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No.	BG ID	ORF	Gene	Description	Verification (Check PCR)
<i>S. cerevisiae</i> VN-Fusion Library (5,809 strains) : Order (vn-support@bioneer.com)					
1	VN_0001	YLR106C	MDN1	Huge dynein-related AAA-type ATPase (midasin), forms extended pre-60S particle with the Rix1 complex (Rix1p-Ipi1p-Ipi3p), may mediate ATP-dependent remodeling of 60S subunits and subsequent export from nucleoplasm to cytoplasm	Strain failed to verify via PCR
2	VN_0002	YLR454W	FMP27	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3	VN_0003	YJL130C	URA2	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP	Q
4	VN_0004	YKL182W	FAS1	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities	Q
5	VN_0005	YNL339C	YRF1-6	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p	Q
6	VN_0006	YBR208C	DUR1,2	Urea amidolyase, contains both urea carboxylase and allophanate hydrolase activities, degrades urea to CO ₂ and NH ₃ ; expression sensitive to nitrogen catabolite repression and induced by allophanate, an intermediate in allantoin degradation	Q
7	VN_0007	YNL172W	APC1	Largest subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition	Q
8	VN_0008	YOR341W	RPA190	RNA polymerase I subunit; largest subunit of RNA polymerase I	Q
9	VN_0009	YOR326W	MYO2	One of two type V myosin motors (along with MYO4) involved in actin-based transport of cargos; required for the polarized delivery of secretory vesicles, the vacuole, late Golgi elements, peroxisomes, and the mitotic spindle	Q
10	VN_0010	YGL173C	KEM1	Evolutionarily-conserved 5'-3' exonuclease component of cytoplasmic processing (P) bodies involved in mRNA decay; plays a role in microtubule-mediated processes, filamentous growth, ribosomal RNA maturation, and telomere maintenance	Q
11	VN_0011	YDR180W	SCC2	Subunit of cohesin loading factor (Scc2p-Scc4p), a complex required for loading of cohesin complexes onto chromosomes; involved in establishing sister chromatid cohesion during DSB repair via histone H2AX; evolutionarily-conserved adherin	Q
12	VN_0012	YKR054C	DYN1	Cytoplasmic heavy chain dynein, microtubule motor protein, required for anaphase spindle elongation; involved in spindle assembly, chromosome movement, and spindle orientation during cell division, targeted to microtubule tips by Pac1p	Q
13	VN_0013	YPR117W	YPR117W	Putative protein of unknown function	Q
14	VN_0014	YPL085W	SEC16	COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p	Q
15	VN_0015	YJL207C	LAA1	AP-1 accessory protein; colocalizes with clathrin to the late-Golgi apparatus; involved in TGN-endosome transport; physically interacts	Q

				with AP-1; similar to the mammalian p200; may interact with ribosomes; YJL207C is a non-essential gene	
16	VN_0016	YLR305C	STT4	Phosphatidylinositol-4-kinase that functions in the Pkc1p protein kinase pathway; required for normal vacuole morphology, cell wall integrity, and actin cytoskeleton organization	Strain failed to verify via PCR
17	VN_0017	YDR545W	YRF1-1	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p	Q
18	VN_0018	YDL140C	RPO21	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime	Q
19	VN_0019	YDR283C	GCN2	Protein kinase, phosphorylates the alpha-subunit of translation initiation factor eIF2 (Sui2p) in response to starvation; activated by uncharged tRNAs and the Gcn1p-Gcn20p complex; contributes to DNA damage checkpoint control	Q
20	VN_0020	YOR191W	ULS1	RING finger protein involved in proteolytic control of sumoylated substrates; interacts with SUMO (Smt3p); member of the SWI/SNF family of DNA-dependent ATPases; plays a role in antagonizing silencing during mating-type switching	Q
21	VN_0021	YMR247C	RKR1	Nuclear RING domain protein with functional connections to chromatin modification; may interact with ribosomes, based on co-purification experiments; YMR247C is not an essential gene	Q
22	VN_0022	YHR164C	DNA2	Tripartite DNA replication factor with single-stranded DNA-dependent ATPase, ATP-dependent nuclease, and helicase activities; required for Okazaki fragment processing; involved in DNA repair; cell-cycle dependent localization	Q
23	VN_0023	YGL150C	INO80	ATPase, subunit of a complex containing actin and several actin-related proteins that has chromatin remodeling activity and 3' to 5' DNA helicase activity in vitro; has a role in modulating stress gene transcription	Q
24	VN_0024	YHR099W	TRA1	Subunit of SAGA and NuA4 histone acetyltransferase complexes; interacts with acidic activators (e.g., Gal4p) which leads to transcription activation; similar to human TRRAP, which is a cofactor for c-Myc mediated oncogenic transformation	Strain failed to verify via PCR
25	VN_0025	YHR165C	PRP8	Component of the U4/U6-U5 snRNP complex, involved in the second catalytic step of splicing; mutations of human Prp8 cause retinitis pigmentosa	Q
26	VN_0026	YGR271W	SLH1	Putative RNA helicase related to Ski2p, involved in translation inhibition of non-poly(A) mRNAs; required for repressing propagation of dsRNA viruses	Q
27	VN_0027	YIL177C	YIL177C	Putative protein of unknown function; similarity to DNA helicases that are encoded within subtelomeric Y' elements and induced in telomerase deficient survivors	Q
28	VN_0028	YLR467W	YRF1-5	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p	Q
29	VN_0029	YMR229C	RRP5	RNA binding protein with preference for single stranded tracts of U's involved in synthesis of both 18S and 5.8S rRNAs; component of both the ribosomal small subunit (SSU) processosome and the 90S preribosome	Q
30	VN_0030	YMR219W	ESC1	Protein localized to the nuclear periphery, involved in telomeric silencing; interacts with PAD4-domain of Sir4p	Q
31	VN_0031	YCR089W	FIG2	Cell wall adhesin, expressed specifically during mating; may be involved in maintenance of cell wall integrity during mating	Q
32	VN_0032	YKL101W	HSL1	Nim1p-related protein kinase that regulates the morphogenesis and septin checkpoints; associates with the assembled septin filament; required along with Hsl7p for bud neck recruitment, phosphorylation, and degradation of Swe1p	Q
33	VN_0033	YGL197W	MDS3	Protein with an N-terminal kelch-like domain, putative negative regulator of early meiotic gene expression; required, with Pmd1p, for growth under alkaline conditions	Q
34	VN_0034	YDR457W	TOM1	E3 ubiquitin ligase of the hect-domain class; has a role in mRNA	Q

				export from the nucleus and may regulate transcriptional coactivators; involved in degradation of excess histones	
35	VN_0035	YIL129C	TAO3	Component of the RAM signaling network that is involved in regulation of Ace2p activity and cellular morphogenesis, interacts with protein kinase Cbk1p and also with Kic1p	Q
36	VN_0036	YER155C	BEM2	Rho GTPase activating protein (RhoGAP) involved in the control of cytoskeleton organization and cellular morphogenesis; required for bud emergence	Q
37	VN_0037	YNL271C	BNI1	Formin, nucleates the formation of linear actin filaments, involved in cell processes such as budding and mitotic spindle orientation which require the formation of polarized actin cables, functionally redundant with BNR1	Q
38	VN_0038	YJL225C	YJL225C	Putative protein of unknown function; similarity to DNA helicases that are also encoded within subtelomeric Y' elements and induced in telomerase deficient survivors	Q
39	VN_0039	YMR306W	FKS3	Protein involved in spore wall assembly, has similarity to 1,3-beta-D-glucan synthase catalytic subunits Fks1p and Gsc2p; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
40	VN_0040	YOR290C	SNF2	Catalytic subunit of the SWI/SNF chromatin remodeling complex involved in transcriptional regulation; contains DNA-stimulated ATPase activity; functions interdependently in transcriptional activation with Snf5p and Snf6p	Q
41	VN_0041	YGL206C	CHC1	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function	Q
42	VN_0042	YNL139C	THO2	Subunit of the THO complex, which is required for efficient transcription elongation and involved in transcriptional elongation-associated recombination; required for LacZ RNA expression from certain plasmids	Q
43	VN_0043	YLR247C	IRC20	Putative helicase; localizes to the mitochondrion and the nucleus; YLR247C is not an essential gene; null mutant displays increased levels of spontaneous Rad52p foci	Q
44	VN_0044	YDR334W	SWR1	Swi2/Snf2-related ATPase that is the structural component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A	Q
45	VN_0045	YKL010C	UFD4	Ubiquitin-protein ligase (E3) that interacts with Rpt4p and Rpt6p, two subunits of the 19S particle of the 26S proteasome; cytoplasmic E3 involved in the degradation of ubiquitin fusion proteins	Q
46	VN_0046	YLR087C	CSF1	Protein required for fermentation at low temperature; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
47	VN_0047	YFR019W	FAB1	1-phosphatidylinositol-3-phosphate 5-kinase; vacuolar membrane kinase that generates phosphatidylinositol (3,5)P ₂ , which is involved in vacuolar sorting and homeostasis	Q
48	VN_0048	YER172C	BRR2	RNA-dependent ATPase RNA helicase (DEIH box); required for disruption of U4/U6 base-pairing in native snRNPs to activate the spliceosome for catalysis; homologous to human U5-200kD	Q
49	VN_0049	YPL231W	FAS2	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; phosphorylated	Q
50	VN_0050	YFL033C	RIM15	Glucose-repressible protein kinase involved in signal transduction during cell proliferation in response to nutrients, specifically the establishment of stationary phase; identified as a regulator of IME2; substrate of Pho80p-Pho85p kinase	Q
51	VN_0051	YJR140C	HIR3	Subunit of the HIR complex, a nucleosome assembly complex involved in regulation of histone gene transcription; involved in position-dependent gene silencing and nucleosome reassembly	Q
52	VN_0052	YNL242W	ATG2	Peripheral membrane protein required for vesicle formation during autophagy, pexophagy, and the cytoplasm-to-vacuole targeting (Cvt) pathway; involved in Atg9p cycling between the phagophore assembly site and mitochondria	Q

53	VN_0053	YML072C	TCB3	Lipid-binding protein, localized to the bud via specific mRNA transport; non-tagged protein detected in a phosphorylated state in mitochondria; GFP-fusion protein localizes to the cell periphery; C-termini of Tcb1p, Tcb2p and Tcb3p interact	Q
54	VN_0054	YBL034C	STU1	Component of the mitotic spindle that binds to interpolar microtubules via its association with beta-tubulin (Tub2p); required for interpolar microtubules to provide an outward force on the spindle poles	Q
55	VN_0055	YJL095W	BCK1	Mitogen-activated protein (MAP) kinase kinase kinase acting in the protein kinase C signaling pathway, which controls cell integrity; upon activation by Pkc1p phosphorylates downstream kinases Mkk1p and Mkk2p	Q
56	VN_0056	YBL088C	TEL1	Protein kinase primarily involved in telomere length regulation; contributes to cell cycle checkpoint control in response to DNA damage; functionally redundant with Mec1p; homolog of human ataxia telangiectasia (ATM) gene	Q
57	VN_0057	YNR016C	ACC1	Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids	Q
58	VN_0058	YDL171C	GLT1	NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with Gln1p, forms the secondary pathway for glutamate biosynthesis from ammonia; expression regulated by nitrogen source	Q
59	VN_0059	YLR422W	YLR422W	Protein of unknown function with similarity to human DOCK proteins (guanine nucleotide exchange factors); interacts with Ino4p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, YLR422W is not an essential protein	Q
60	VN_0060	YLR024C	UBR2	Cytoplasmic ubiquitin-protein ligase (E3); required for ubiquitylation of Rpn4p; mediates formation of a Mub1p-Ubr2p-Rad6p complex	Q
61	VN_0061	YJL109C	UTP10	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA	Q
62	VN_0062	YKR031C	SPO14	Phospholipase D, catalyzes the hydrolysis of phosphatidylcholine, producing choline and phosphatidic acid; involved in Sec14p-independent secretion; required for meiosis and spore formation; differently regulated in secretion and meiosis	Q
63	VN_0063	YDR127W	ARO1	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids	Q
64	VN_0064	YAR050W	FLO1	Lectin-like protein involved in flocculation, cell wall protein that binds to mannose chains on the surface of other cells, confers floc-forming ability that is chymotrypsin sensitive and heat resistant; similar to Flo5p	Q
65	VN_0065	YPL167C	REV3	Catalytic subunit of DNA polymerase zeta, which is involved in DNA repair and translesion synthesis; required for mutagenesis induced by DNA damage	Q
66	VN_0066	YAL029C	MYO4	One of two type V myosin motors (along with MYO2) involved in actin-based transport of cargos; required for mRNA transport, including ASH1 mRNA, and facilitating the growth and movement of ER tubules into the growing bud along with She3p	Q
67	VN_0067	YDR150W	NUM1	Protein required for nuclear migration, localizes to the mother cell cortex and the bud tip; may mediate interactions of dynein and cytoplasmic microtubules with the cell cortex	Q
68	VN_0068	YLR430W	SEN1	Presumed helicase required for RNA polymerase II transcription termination and processing of RNAs; homolog of Senataxin which causes Ataxia-Oculomotor Apraxia 2 and a dominant form of amyotrophic lateral sclerosis	Q
69	VN_0069	YMR207C	HFA1	Mitochondrial acetyl-coenzyme A carboxylase, catalyzes the production of malonyl-CoA in mitochondrial fatty acid biosynthesis	Q
70	VN_0070	YHR023W	MYO1	Type II myosin heavy chain, required for wild-type cytokinesis and cell separation; localizes to the actomyosin ring; binds to myosin light chains Mlc1p and Mlc2p through its IQ1 and IQ2 motifs respectively	Q
71	VN_0071	YHL030W	ECM29	Major component of the proteasome; tethers the proteasome core particle to the regulatory particle, and enhances the stability of the proteasome	Q

72	VN_0072	YKL014C	URB1	Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs, associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the biogenesis of the 60S ribosomal subunit	Q
73	VN_0073	YER190W	YRF1-2	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p; induced by treatment with 8-methoxypsoralen and UVA irradiation	Q
74	VN_0074	YCL014W	BUD3	Protein involved in bud-site selection and required for axial budding pattern; localizes with septins to bud neck in mitosis and may constitute an axial landmark for next round of budding	Q
75	VN_0075	YJR138W	IML1	Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the vacuolar membrane	Q
76	VN_0076	YOL004W	SIN3	Component of the Sin3p-Rpd3p histone deacetylase complex, involved in transcriptional repression and activation of diverse processes, including mating-type switching and meiosis; involved in the maintenance of chromosomal integrity	Q
77	VN_0077	YLR256W	HAP1	Zinc finger transcription factor involved in the complex regulation of gene expression in response to levels of heme and oxygen; the S288C sequence differs from other strain backgrounds due to a Ty1 insertion in the carboxy terminus	Strain failed to verify via PCR
78	VN_0078	YER164W	CHD1	Nucleosome remodeling factor that functions in regulation of transcription elongation; contains a chromo domain, a helicase domain and a DNA-binding domain; component of both the SAGA and SLIK complexes	Q
79	VN_0079	YGL195W	GCN1	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA	Q
80	VN_0080	YNL262W	POL2	Catalytic subunit of DNA polymerase (II) epsilon, a chromosomal DNA replication polymerase that exhibits processivity and proofreading exonuclease activity; also involved in DNA synthesis during DNA repair; interacts extensively with Mrc1p	Q
81	VN_0081	YCR093W	CDC39	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor	Q
82	VN_0082	YBR275C	RIF1	Protein that binds to the Rap1p C-terminus and acts synergistically with Rif2p to help control telomere length and establish telomeric silencing; deletion results in telomere elongation	Q
83	VN_0083	YPL082C	MOT1	Essential abundant protein involved in regulation of transcription, removes Spt15p (TBP) from DNA via its C-terminal ATPase activity, forms a complex with TBP that binds TATA DNA with high affinity but with altered specificity	Q
84	VN_0084	YER132C	PMD1	Protein with an N-terminal kelch-like domain, putative negative regulator of early meiotic gene expression; required, with Mds3p, for growth under alkaline conditions	Q
85	VN_0085	YML059C	NTE1	Serine esterase, homolog of human neuropathy target esterase (NTE); Nte1p-mediated phosphatidylcholine turnover influences transcription factor Opi1p localization, affecting transcriptional regulation of phospholipid biosynthesis genes	Q
86	VN_0086	YNL297C	MON2	Peripheral membrane protein with a role in endocytosis and vacuole integrity, interacts with Arl1p and localizes to the endosome; member of the Sec7p family of proteins	Q
87	VN_0087	YNR031C	SSK2	MAP kinase kinase kinase of the HOG1 mitogen-activated signaling pathway; interacts with Ssk1p, leading to autophosphorylation and activation of Ssk2p which phosphorylates Pbs2p; also mediates actin cytoskeleton recovery from osmotic stress	Q
88	VN_0088	YPR184W	GDB1	Glycogen debranching enzyme containing glucanotransferase and alpha-1,6-amyloglucosidase activities, required for glycogen degradation; phosphorylated in mitochondria	Q
89	VN_0089	YPL242C	IQG1	Essential protein required for determination of budding pattern, promotes localization of axial markers Bud4p and Cdc12p and functionally interacts with Sec3p, localizes to the contractile ring during anaphase, member of the IQGAP family	Q
90	VN_0090	YNL102W	POL1	Catalytic subunit of the DNA polymerase I alpha-primase complex, required for the initiation of DNA replication during mitotic DNA	Q

				synthesis and premeiotic DNA synthesis	
91	VN_0091	YLL021W	SPA2	Component of the polarisome, which functions in actin cytoskeletal organization during polarized growth; acts as a scaffold for Mkk1p and Mpk1p cell wall integrity signaling components; potential Cdc28p substrate	Q
92	VN_0092	YDL112W	TRM3	2'-O-ribose methyltransferase, catalyzes the ribose methylation of the guanosine nucleotide at position 18 of tRNAs	Q
93	VN_0093	YCR081W	SRB8	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation; involved in glucose repression	Q
94	VN_0094	YPR164W	MMS1	Subunit of an E3 ubiquitin ligase complex involved in resolving replication intermediates or preventing the damage caused by blocked replication forks; regulates Ty1 transposition; involved with Rtt101p in nonfunctional rRNA decay	Q
95	VN_0095	YIL159W	BNR1	Formin, nucleates the formation of linear actin filaments, involved in cell processes such as budding and mitotic spindle orientation which require the formation of polarized actin cables, functionally redundant with BNI1	Strain failed to verify via PCR
96	VN_0096	YCR073C	SSK22	MAP kinase kinase kinase of the HOG1 mitogen-activated signaling pathway; functionally redundant with, and homologous to, Ssk2p; interacts with and is activated by Ssk1p; phosphorylates Pbs2p	Q
97	VN_0097	YDR159W	SAC3	Nuclear pore-associated protein, forms a complex with Thp1p that is involved in transcription and in mRNA export from the nucleus	Q
98	VN_0098	YJL197W	UBP12	Ubiquitin carboxyl-terminal hydrolase, ubiquitin-specific protease present in the nucleus and cytoplasm that cleaves ubiquitin from ubiquitinated proteins	Q
99	VN_0099	YLL066C	YLL066C	Putative protein of unknown function with similarity to helicases; YLL066C is not an essential gene	Q
100	VN_0100	YNL257C	SIP3	Protein that activates transcription through interaction with DNA-bound Snf1p, C-terminal region has a putative leucine zipper motif; potential Cdc28p substrate	Q
101	VN_0101	YOR116C	RPO31	RNA polymerase III subunit C160, part of core enzyme; similar to bacterial beta-prime subunit	Q
102	VN_0102	YAL024C	LTE1	Protein similar to GDP/GTP exchange factors but without detectable GEF activity; required for asymmetric localization of Bfa1p at daughter-directed spindle pole bodies and for mitotic exit at low temperatures	Q
103	VN_0103	YDR443C	SSN2	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; required for stable association of Srb10p-Srb11p kinase; essential for transcriptional regulation	Q
104	VN_0104	YGL131C	SNT2	DNA binding protein with similarity to the S. pombe Snt2 protein; computational analysis suggests a role in regulation of expression of genes encoding amine transporters	Q
105	VN_0105	YIR019C	MUC1	GPI-anchored cell surface glycoprotein (flocculin) required for pseudohyphal formation, invasive growth, flocculation, and biofilms; transcriptionally regulated by the MAPK pathway (via Ste12p and Tec1p) and the cAMP pathway (via Flo8p)	Strain failed to verify via PCR
106	VN_0106	YDR216W	ADR1	Carbon source-responsive zinc-finger transcription factor, required for transcription of the glucose-repressed gene ADH2, of peroxisomal protein genes, and of genes required for ethanol, glycerol, and fatty acid utilization	Q
107	VN_0107	YOR296W	YOR296W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; expressed during copper starvation; YOR296W is not an essential gene	Q
108	VN_0108	YML081W	YML081W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; YML081w is not an essential gene	Q
109	VN_0109	YLL067C	YLL067C	Putative protein of unknown function with similarity to helicases	Q
110	VN_0110	YHR155W	YSP1	Mitochondrial protein with a potential role in promoting mitochondrial fragmentation during programmed cell death in response to high levels of alpha-factor mating pheromone or the drug amiodarone	Q

111	VN_0111	YMR259C	YMR259C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YMR259C is not an essential gene	Q
112	VN_0112	YOR336W	KRE5	Protein required for beta-1,6 glucan biosynthesis; mutations result in aberrant morphology and severe growth defects	Q
113	VN_0113	YFL036W	RPO41	Mitochondrial RNA polymerase; single subunit enzyme similar to those of T3 and T7 bacteriophages; requires a specificity subunit encoded by MTF1 for promoter recognition	Strain failed to verify via PCR
114	VN_0114	YAL063C	FLO9	Lectin-like protein with similarity to Flo1p, thought to be expressed and involved in flocculation	Q
115	VN_0115	YLR436C	ECM30	Non-essential protein of unknown function	Q
116	VN_0116	YDR293C	SSD1	Protein with a role in maintenance of cellular integrity, interacts with components of the TOR pathway; ssd1 mutant of a clinical S. cerevisiae strain displays elevated virulence	Q
117	VN_0117	YNL273W	TOF1	Subunit of a replication-pausing checkpoint complex (Tof1p-Mrc1p-Csm3p) that acts at the stalled replication fork to promote sister chromatid cohesion after DNA damage, facilitating gap repair of damaged DNA; interacts with the MCM helicase	Q
118	VN_0118	YPL012W	RRP12	Protein required for export of the ribosomal subunits; associates with the RNA components of the pre-ribosomes; contains HEAT-repeats	Q
119	VN_0119	YLR320W	MMS22	Protein that acts with Mms1p in a repair pathway that may be involved in resolving replication intermediates or preventing the damage caused by blocked replication forks; required for accurate meiotic chromosome segregation	Q
120	VN_0120	YLR419W	YLR419W	Putative helicase with limited sequence similarity to human Rb protein; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YLR419W is not an essential gene	Q
121	VN_0121	YLR086W	SMC4	Subunit of the condensin complex; reorganizes chromosomes during cell division; forms a complex with Smc2p that has ATP-hydrolyzing and DNA-binding activity; required for tRNA gene clustering at the nucleolus; potential Cdc28p substrate	Q
122	VN_0122	YBR115C	LYS2	Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine; activation requires posttranslational phosphopantetheinylation by Lys5p	Q
123	VN_0123	YML049C	RSE1	Protein involved in pre-mRNA splicing; component of the pre-spliceosome; associates with U2 snRNA; involved in ER to Golgi transport	Q
124	VN_0124	YLR384C	IKI3	Subunit of Elongator complex, which is required for modification of wobble nucleosides in tRNA; maintains structural integrity of Elongator; homolog of human IKAP, mutations in which cause familial dysautonomia (FD)	Q
125	VN_0125	YJR092W	BUD4	Protein involved in bud-site selection and required for axial budding pattern; localizes with septins to bud neck in mitosis and may constitute an axial landmark for next round of budding; potential Cdc28p substrate	Q
126	VN_0126	YKL215C	YKL215C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
127	VN_0127	YDL195W	SEC31	Essential phosphoprotein component (p150) of the COPII coat of secretory pathway vesicles, in complex with Sec13p; required for ER-derived transport vesicle formation	Q
128	VN_0128	YOR227W	HER1	Protein of unknown function required for proliferation or remodeling of the ER that is caused by overexpression of Hmg2p; may interact with ribosomes, based on co-purification experiments	Q
129	VN_0129	YGL251C	HFM1	Meiosis specific DNA helicase involved in the conversion of double-stranded breaks to later recombination intermediates and in crossover control; catalyzes the unwinding of Holliday junctions; has ssDNA and dsDNA stimulated ATPase activity	Q
130	VN_0130	YCR033W	SNT1	Subunit of the Set3C deacetylase complex that interacts directly with the Set3C subunit, Sif2p; putative DNA-binding protein	Q
131	VN_0131	YMR280C	CAT8	Zinc cluster transcriptional activator necessary for derepression of a	Q

				variety of genes under non-fermentative growth conditions, active after diauxic shift, binds carbon source responsive elements	
132	VN_0132	YMR176W	ECM5	Non-essential protein of unknown function, contains ATP/GTP-binding site motif A; null mutant exhibits cellular volume up to four times greater than wild-type, also large drooping buds with elongated necks	Q
133	VN_0133	YHR080C	YHR080C	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
134	VN_0134	YPL016W	SWI1	Subunit of the SWI/SNF chromatin remodeling complex, which regulates transcription by remodeling chromosomes; required for transcription of many genes, including ADH1, ADH2, GAL1, HO, INO1 and SUC2; can form the prion [SWI+]	Q
135	VN_0135	YDL019C	OSH2	Member of an oxysterol-binding protein family with seven members in <i>S. cerevisiae</i> ; family members have overlapping, redundant functions in sterol metabolism and collectively perform a function essential for viability	Q
136	VN_0136	YOR124C	UBP2	Ubiquitin-specific protease that removes ubiquitin from ubiquitinated proteins; interacts with Rsp5p and is required for MVB sorting of membrane proteins; can cleave polyubiquitin and has isopeptidase activity	Q
137	VN_0137	YDR104C	SPO71	Meiosis-specific protein of unknown function, required for spore wall formation during sporulation; dispensable for both nuclear divisions during meiosis	Q
138	VN_0138	YGR090W	UTP22	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data	Q
139	VN_0139	YMR190C	SGS1	Nucleolar DNA helicase of the RecQ family involved in genome integrity maintenance; regulates chromosome synapsis and meiotic joint molecule/crossover formation; similar to human BLM and WRN proteins implicated in Bloom and Werner syndromes	Q
140	VN_0140	YPR189W	SKI3	Ski complex component and TPR protein, mediates 3'-5' RNA degradation by the cytoplasmic exosome; null mutants have superkiller phenotype of increased viral dsRNAs and are synthetic lethal with mutations in 5'-3' mRNA decay	Q
141	VN_0141	YJR031C	GEA1	Guanine nucleotide exchange factor for ADP ribosylation factors (ARFs), involved in vesicular transport between the Golgi and ER, Golgi organization, and actin cytoskeleton organization; similar to but not functionally redundant with Gea2p	Q
142	VN_0142	YBL047C	EDE1	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins	Q
143	VN_0143	YDR227W	SIR4	Silent information regulator that, together with SIR2 and SIR3, is involved in assembly of silent chromatin domains at telomeres and the silent mating-type loci; potentially phosphorylated by Cdc28p; some alleles of SIR4 prolong lifespan	Q
144	VN_0144	YLR278C	YLR278C	Zinc-cluster protein; GFP-fusion protein localizes to the nucleus; mutant shows moderate growth defect on caffeine; has a prion-domain like fragment that increases frequency of [URE3]; YLR278C is not an essential gene	Q
145	VN_0145	YNL250W	RAD50	Subunit of MRX complex, with Mre11p and Xrs2p, involved in processing double-strand DNA breaks in vegetative cells, initiation of meiotic DSBs, telomere maintenance, and nonhomologous end joining	Q
146	VN_0146	YKL129C	MYO3	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization	Q
147	VN_0147	YBL007C	SLA1	Cytoskeletal protein binding protein required for assembly of the cortical actin cytoskeleton; interacts with proteins regulating actin dynamics and proteins required for endocytosis; found in the nucleus and cell cortex; has 3 SH3 domains	Q
148	VN_0148	YFR016C	YFR016C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and bud; interacts with Spa2p; YFR016C is not an essential gene	Q

149	VN_0149	YJR137C	MET5	Sulfite reductase beta subunit, involved in amino acid biosynthesis, transcription repressed by methionine	Q
150	VN_0150	YCR042C	TAF2	TFIID subunit (150 kDa), involved in RNA polymerase II transcription initiation	Q
151	VN_0151	YJR127C	RSF2	Zinc-finger protein involved in transcriptional control of both nuclear and mitochondrial genes, many of which specify products required for glycerol-based growth, respiration, and other functions	Q
152	VN_0152	YGR061C	ADE6	Formylglycinamide-ribonucleotide (FGAM)-synthetase, catalyzes a step in the 'de novo' purine nucleotide biosynthetic pathway	Q
153	VN_0153	YOL138C	RTC1	Protein of unknown function; may interact with ribosomes, based on co-purification experiments; null mutation suppresses cdc13-1 temperature sensitivity	Q
154	VN_0154	YDR217C	RAD9	DNA damage-dependent checkpoint protein, required for cell-cycle arrest in G1/S, intra-S, and G2/M; transmits checkpoint signal by activating Rad53p and Chk1p; hyperphosphorylated by Mec1p and Tel1p; potential Cdc28p substrate	Strain failed to verify via PCR
155	VN_0155	YDR326C	YSP2	Protein involved in programmed cell death; mutant shows resistance to cell death induced by amiodarone or intracellular acidification	Q
156	VN_0156	YML133C	YML133C	Putative protein of unknown function with similarity to helicases; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YML133C contains an intron	Q
157	VN_0157	YGR270W	YTA7	Protein that localizes to chromatin and has a role in regulation of histone gene expression; has a bromodomain-like region that interacts with the N-terminal tail of histone H3, and an ATPase domain; potentially phosphorylated by Cdc28p	Q
158	VN_0158	YDR301W	CFT1	RNA-binding subunit of the mRNA cleavage and polyadenylation factor; involved in poly(A) site recognition and required for both pre-mRNA cleavage and polyadenylation, 51% sequence similarity with mammalian AAUAA-binding subunit of CPSF	Q
159	VN_0159	YLR425W	TUS1	Guanine nucleotide exchange factor (GEF) that functions to modulate Rho1p activity as part of the cell integrity signaling pathway; multicopy suppressor of tor2 mutation and ypk1 ypk2 double mutation; potential Cdc28p substrate	Q
160	VN_0160	YMR012W	CLU1	eIF3 component of unknown function; deletion causes defects in mitochondrial organization but not in growth or translation initiation, can rescue cytokinesis and mitochondrial organization defects of the Dictyostelium cluA- mutant	Q
161	VN_0161	YNL091W	NST1	Protein of unknown function, mediates sensitivity to salt stress; interacts physically with the splicing factor Msl1p and also displays genetic interaction with MSL1	Q
162	VN_0162	YMR304W	UBP15	Ubiquitin-specific protease that may play a role in ubiquitin precursor processing	Q
163	VN_0163	YOR151C	RPB2	RNA polymerase II second largest subunit B150, part of central core; similar to bacterial beta subunit	Q
164	VN_0164	YOR396W	YRF1-8	One of several telomeric Y' element-encoded DNA helicases, known as Y'-Help1 (Y'-HELicase Protein 1)	Q
165	VN_0165	YML091C	RPM2	Protein subunit of mitochondrial RNase P, has roles in nuclear transcription, cytoplasmic and mitochondrial RNA processing, and mitochondrial translation; distributed to mitochondria, cytoplasmic processing bodies, and the nucleus	Q
166	VN_0166	YOR086C	TCB1	Lipid-binding protein containing three calcium and lipid binding domains; non-tagged protein localizes to mitochondria and GFP-fusion protein localizes to the cell periphery; C-termini of Tcb1p, Tcb2p and Tcb3p interact	Q
167	VN_0167	YOL078W	AVO1	Component of a membrane-bound complex containing the Tor2p kinase and other proteins, which may have a role in regulation of cell growth	Q
168	VN_0168	YJR151C	DAN4	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p; expressed under anaerobic conditions, completely repressed during aerobic growth	Q
169	VN_0169	YGR097W	ASK10	Component of the RNA polymerase II holoenzyme, phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response genes	Q

170	VN_0170	YOR188W	MSB1	Protein involved in positive regulation of both 1,3-beta-glucan synthesis and the Pkc1p-MAPK pathway, potential Cdc28p substrate; multicopy suppressor of temperature-sensitive mutations in CDC24 and CDC42, and of mutations in BEM4	Q
171	VN_0171	YML104C	MDM1	Intermediate filament protein, required for nuclear and mitochondrial transmission to daughter buds; contains a Phox homology (PX) domain and specifically binds phosphatidylinositol 3-phosphate (PtdIns-3-P)	Q
172	VN_0172	YIL151C	YIL151C	Putative protein of unknown function, predicted to contain a PINc domain	Q
173	VN_0173	YER110C	KAP123	Karyopherin beta, mediates nuclear import of ribosomal proteins prior to assembly into ribosomes and import of histones H3 and H4; localizes to the nuclear pore, nucleus, and cytoplasm; exhibits genetic interactions with RAI1	Q
174	VN_0174	YPL216W	YPL216W	Putative protein of unknown function; YPL216W is not an essential gene	Q
175	VN_0175	YBR150C	TBS1	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Strain failed to verify via PCR
176	VN_0176	YPL110C	GDE1	Glycerophosphocholine (GroPCho) phosphodiesterase; hydrolyzes GroPCho to choline and glycerolphosphate, for use as a phosphate source and as a precursor for phosphocholine synthesis; may interact with ribosomes	Q
177	VN_0177	YLR189C	ATG26	UDP-glucose:sterol glucosyltransferase, conserved enzyme involved in synthesis of sterol glucoside membrane lipids; in contrast to ATG26 from <i>P. pastoris</i> , <i>S. cerevisiae</i> ATG26 is not involved in autophagy	Q
178	VN_0178	YNL106C	INP52	Polyphosphatidylinositol phosphatase, dephosphorylates a number of phosphatidylinositols (PIs) to PI; involved in endocytosis; hyperosmotic stress causes translocation to actin patches; synaptojanin-like protein with a Sac1 domain	Q
179	VN_0179	YJL092W	SRS2	DNA helicase and DNA-dependent ATPase involved in DNA repair, needed for proper timing of commitment to meiotic recombination and transition from Meiosis I to II; blocks trinucleotide repeat expansion; affects genome stability	Q
180	VN_0180	YGR070W	ROM1	GDP/GTP exchange protein (GEP) for Rho1p; mutations are synthetically lethal with mutations in rom2, which also encodes a GEP	Q
181	VN_0181	YHL023C	NPR3	Component, with Npr2p, of an evolutionarily conserved complex that mediates downregulation of TOR Complex 1 activity in response to amino acid limitation; null mutant displays delayed meiotic DNA replication and double-strand break repair	Q
182	VN_0182	YML117W	NAB6	Putative RNA-binding protein that associates with mRNAs encoding cell wall proteins in high-throughput studies; deletion mutants display increased sensitivity to some cell wall disrupting agents; expression negatively regulated by cAMP	Q
183	VN_0183	YHR077C	NMD2	Protein involved in the nonsense-mediated mRNA decay (NMD) pathway; interacts with Nam7p and Upf3p; involved in telomere maintenance	Q
184	VN_0184	YJR109C	CPA2	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor	Q
185	VN_0185	YBL063W	KIP1	Kinesin-related motor protein required for mitotic spindle assembly, chromosome segregation, and 2 micron plasmid partitioning; functionally redundant with Cin8p for chromosomal but not plasmid functions	Q
186	VN_0186	YOL045W	PSK2	One of two (see also PSK1) PAS domain containing S/T protein kinases; regulates sugar flux and translation in response to an unknown metabolite by phosphorylating Ugp1p and Gsy2p (sugar flux) and Caf20p, Tif11p and Sro9p (translation)	Q
187	VN_0187	YER111C	SWI4	DNA binding component of the SBF complex (Swi4p-Swi6p), a transcriptional activator that in concert with MBF (Mbp1-Swi6p) regulates late G1-specific transcription of targets including cyclins and genes required for DNA synthesis and repair	Q
188	VN_0188	YLR084C	RAX2	N-glycosylated protein involved in the maintenance of bud site selection during bipolar budding; localization requires Rax1p; RAX2 mRNA stability is regulated by Mpt5p	Q

189	VN_0189	YAR009C	YAR009C	Retrotransposon TYA Gag and TYB Pol genes; in YARCTY1-1 TYB is mutant and probably non-functional	Q
190	VN_0190	YJR041C	URB2	Nucleolar protein required for normal metabolism of the rRNA primary transcript, proposed to be involved in ribosome biogenesis	Q
191	VN_0191	YLR035C-A	YLR035C-A	Retrotransposon TYA Gag and TYB Pol genes; polypeptide is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); YLR035C-A is part of a mutant retrotransposon	Q
192	VN_0192	YLR410W	VIP1	Inositol hexakisphosphate (IP6) and inositol heptakisphosphate (IP7) kinase; generation of IP7 by Vip1p is important for phosphate signaling; likely involved in cortical actin cytoskeleton function, by analogy with <i>S. pombe</i> ortholog asp1	Q
193	VN_0193	YPR022C	YPR022C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus and is induced in response to the DNA-damaging agent MMS	Q
194	VN_0194	YDL231C	BRE4	Zinc finger protein containing five transmembrane domains; null mutant exhibits strongly fragmented vacuoles and sensitivity to brefeldin A, a drug which is known to affect intracellular transport	Q
195	VN_0195	YBL101C	ECM21	Protein involved in regulating the endocytosis of plasma membrane proteins; identified as a substrate for ubiquitination by Rsp5p and deubiquitination by Ubp2p; promoter contains several Gcn4p binding elements	Q
196	VN_0196	YNL163C	RIA1	Cytoplasmic GTPase involved in biogenesis of the 60S ribosome; has similarity to translation elongation factor 2 (Eft1p and Eft2p)	Strain failed to verify via PCR
197	VN_0197	YKL205W	LOS1	Nuclear pore protein involved in nuclear export of pre-tRNA	Strain failed to verify via PCR
198	VN_0198	YOL034W	SMC5	Structural maintenance of chromosomes (SMC) protein; essential subunit of the Mms21-Smc5-Smc6 complex; required for growth and DNA repair; <i>S. pombe</i> homolog forms a heterodimer with <i>S. pombe</i> Rad18p that is involved in DNA repair	Strain failed to verify via PCR
199	VN_0199	YGL140C	YGL140C	Putative protein of unknown function; non-essential gene; contains multiple predicted transmembrane domains	Q
200	VN_0200	YPL226W	NEW1	ATP binding cassette family member; Asn/Gln-rich rich region supports [NU+] prion formation and susceptibility to [PSI+] prion induction; homologous to mRNA export factor from <i>S. pombe</i> and similar protein from <i>C. albicans</i>	Q
201	VN_0201	YBR218C	PYC2	Pyruvate carboxylase isoform, cytoplasmic enzyme that converts pyruvate to oxaloacetate; highly similar to isoform Pyc1p but differentially regulated; mutations in the human homolog are associated with lactic acidosis	Q
202	VN_0202	YFR031C	SMC2	Subunit of the condensin complex; essential SMC chromosomal ATPase family member that forms a complex with Smc4p to form the active ATPase; Smc2p/Smc4p complex binds DNA; required for clustering of tRNA genes at the nucleolus	Strain failed to verify via PCR
203	VN_0203	YER013W	PRP22	DEAH-box RNA-dependent ATPase/ATP-dependent RNA helicase, associates with lariat intermediates before the second catalytic step of splicing; mediates ATP-dependent mRNA release from the spliceosome and unwinds RNA duplexes	Q
204	VN_0204	YGL151W	NUT1	Component of the RNA polymerase II mediator complex, which is required for transcriptional activation and also has a role in basal transcription	Q
205	VN_0205	YGR134W	CAF130	Part of the evolutionarily-conserved CCR4-NOT transcriptional regulatory complex involved in controlling mRNA initiation, elongation, and degradation	Q
206	VN_0206	YNR067C	DSE4	Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother	Q
207	VN_0207	YBR059C	AKL1	Ser-Thr protein kinase, member (with Ark1p and Prk1p) of the Ark kinase family; involved in endocytosis and actin cytoskeleton organization	Q
208	VN_0208	YPL022W	RAD1	Single-stranded DNA endonuclease (with Rad10p), cleaves single-	Q

				stranded DNA during nucleotide excision repair and double-strand break repair; subunit of Nucleotide Excision Repair Factor 1 (NEF1); homolog of human XPF protein	
209	VN_0209	YDL215C	GDH2	NAD(+)-dependent glutamate dehydrogenase, degrades glutamate to ammonia and alpha-ketoglutarate; expression sensitive to nitrogen catabolite repression and intracellular ammonia levels	Q
210	VN_0210	YMR109W	MYO5	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization	Q
211	VN_0211	YKR096W	YKR096W	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the nucleus and cytoplasm; predicted to contain a PINc domain	Q
212	VN_0212	YGL062W	PYC1	Pyruvate carboxylase isoform, cytoplasmic enzyme that converts pyruvate to oxaloacetate; highly similar to isoform Pyc2p but differentially regulated; mutations in the human homolog are associated with lactic acidosis	Q
213	VN_0213	YKL038W	RGT1	Glucose-responsive transcription factor that regulates expression of several glucose transporter (HXT) genes in response to glucose; binds to promoters and acts both as a transcriptional activator and repressor	Q
214	VN_0214	YJR090C	GRR1	F-box protein component of the SCF ubiquitin-ligase complex; involved in carbon catabolite repression, glucose-dependent divalent cation transport, high-affinity glucose transport, morphogenesis, and sulfite detoxification	Q
215	VN_0215	YDR507C	GIN4	Protein kinase involved in bud growth and assembly of the septin ring, proposed to have kinase-dependent and kinase-independent activities; undergoes autophosphorylation; similar to Kcc4p and Hsl1p	Q
216	VN_0216	YKL105C	YKL105C	Putative protein of unknown function	Q
217	VN_0217	YNR065C	YNR065C	Protein of unknown function; protein-protein interactions suggest a possible role in actin patch formation; YNR065C is not an essential gene	Q
218	VN_0218	YOR109W	INP53	Polyphosphatidylinositol phosphatase, dephosphorylates multiple phosphatidylinositols; involved in trans Golgi network-to-early endosome pathway; hyperosmotic stress causes translocation to actin patches; contains Sac1 and 5-ptase domains	Q
219	VN_0219	YKR028W	SAP190	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap185p	Q
220	VN_0220	YJR091C	JSN1	Member of the Puf family of RNA-binding proteins, interacts with mRNAs encoding membrane-associated proteins; involved in localizing the Arp2/3 complex to mitochondria; overexpression causes increased sensitivity to benomyl	Q
221	VN_0221	YPR026W	ATH1	Acid trehalase required for utilization of extracellular trehalose	Q
222	VN_0222	YGR233C	PHO81	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p-Pho85p cyclin-CDK complexes in response to phosphate levels; inhibitory activity for Pho80p-Pho85p requires myo-D-inositol heptakisphosphate (IP7) generated by Vip1p	Q
223	VN_0223	YKR102W	FLO10	Lectin-like protein with similarity to Flo1p, thought to be involved in flocculation	Q
224	VN_0224	YIL026C	IRR1	Subunit of the cohesin complex, which is required for sister chromatid cohesion during mitosis and meiosis and interacts with centromeres and chromosome arms, essential for viability	Q
225	VN_0225	YER129W	SAK1	Upstream serine/threonine kinase for the SNF1 complex; partially redundant with Elm1p and Tos3p; members of this family have functional orthology with LKB1, a mammalian kinase associated with Peutz-Jeghers cancer-susceptibility syndrome	Q
226	VN_0226	YJR039W	YJR039W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
227	VN_0227	YOL087C	YOL087C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; deletion mutant is	Q

				sensitive to various chemicals including phenanthroline, sanguinarine, and nordihydroguaiaretic acid	
228	VN_0228	YGR094W	VAS1	Mitochondrial and cytoplasmic valyl-tRNA synthetase	Q
229	VN_0229	YML100W	TSL1	Large subunit of trehalose 6-phosphate synthase (Tps1p)/phosphatase (Tps2p) complex, which converts uridine-5'-diphosphoglucose and glucose 6-phosphate to trehalose, homologous to Tps3p and may share function	Q
230	VN_0230	YPL160W	CDC60	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA	Q
231	VN_0231	YPR122W	AXL1	Haploid specific endoprotease that performs one of two N-terminal cleavages during maturation of a-factor mating pheromone; required for axial budding pattern of haploid cells	Q
232	VN_0232	YJL076W	NET1	Core subunit of the RENT complex, which is a complex involved in nucleolar silencing and telophase exit; stimulates transcription by RNA polymerase I and regulates nucleolar structure	Q
233	VN_0233	YPR049C	ATG11	Adapter protein for pexophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; directs receptor-bound cargo to the phagophore assembly site (PAS) for packaging into vesicles; required for recruiting other proteins to the (PAS)	Q
234	VN_0234	YLR032W	RAD5	DNA helicase proposed to promote replication fork regression during postreplication repair by template switching; RING finger containing ubiquitin ligase; stimulates the synthesis of free and PCNA-bound polyubiquitin chains by Ubc13p-Mms2p	Q
235	VN_0235	YOR207C	RET1	Second-largest subunit of RNA polymerase III, which is responsible for the transcription of tRNA and 5S RNA genes, and other low molecular weight RNAs	Q
236	VN_0236	YMR317W	YMR317W	Putative protein of unknown function with some similarity to sialidase from Trypanosoma; YMR317W is not an essential gene	Q
237	VN_0237	YBR245C	ISW1	Member of the imitation-switch (ISWI) class of ATP-dependent chromatin remodeling complexes; ATPase that forms a complex with Ioc2p and Ioc4p to regulate transcription elongation, and a complex with Ioc3p to repress transcription initiation	Q
238	VN_0238	YPR030W	CSR2	Nuclear protein proposed to regulate utilization of nonfermentable carbon sources and endocytosis of plasma membrane proteins; overproduction suppresses chs5 spa2 lethality at high temp; ubiquitinated by Rsp5p, deubiquitinated by Ubp2p	Q
239	VN_0239	YGL094C	PAN2	Essential subunit of the Pan2p-Pan3p poly(A)-ribonuclease complex, which acts to control poly(A) tail length and regulate the stoichiometry and activity of postreplication repair complexes	Q
240	VN_0240	YKL092C	BUD2	GTPase activating factor for Rsr1p/Bud1p required for both axial and bipolar budding patterns; mutants exhibit random budding in all cell types	Q
241	VN_0241	YMR308C	PSE1	Karyopherin/importin that interacts with the nuclear pore complex; acts as the nuclear import receptor for specific proteins, including Pdr1p, Yap1p, Ste12p, and Aft1p	Q
242	VN_0242	YPR010C	RPA135	RNA polymerase I subunit A135	Q
243	VN_0243	YEL025C	YEL025C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
244	VN_0244	YLR272C	YCS4	Subunit of the condensin complex; required for establishment and maintenance of chromosome condensation, chromosome segregation, chromatin binding of condensin, tRNA gene clustering at the nucleolus, and silencing at the mating type locus	Q
245	VN_0245	YHR158C	KEL1	Protein required for proper cell fusion and cell morphology; functions in a complex with Kel2p to negatively regulate mitotic exit, interacts with Tem1p and Lte1p; localizes to regions of polarized growth; potential Cdc28p substrate	Q
246	VN_0246	YDR128W	MTC5	Protein of unknown function; mtc5 is synthetically sick with cdc13-1	Q
247	VN_0247	YGR170W	PSD2	Phosphatidylserine decarboxylase of the Golgi and vacuolar membranes, converts phosphatidylserine to phosphatidylethanolamine	Q
248	VN_0248	YPL115C	BEM3	Rho GTPase activating protein (RhoGAP) involved in control of the cytoskeleton organization; targets the essential Rho-GTPase Cdc42p,	Q

				which controls establishment and maintenance of cell polarity, including bud-site assembly	
249	VN_0249	YOR304W	ISW2	ATP-dependent DNA translocase involved in chromatin remodeling; ATPase component that, with Itc1p, forms a complex required for repression of a-specific genes, INO1, and early meiotic genes during mitotic growth	Q
250	VN_0250	YMR218C	TRS130	One of 10 subunits of the transport protein particle (TRAPP) complex of the cis-Golgi which mediates vesicle docking and fusion; involved in ER to Golgi membrane traffic; mutation activates transcription of OCH1	Q
251	VN_0251	YCL061C	MRC1	S-phase checkpoint protein required for DNA replication; interacts with and stabilizes Pol2p at stalled replication forks during stress, where it forms a pausing complex with Tof1p and is phosphorylated by Mec1p; protects uncapped telomeres	Q
252	VN_0252	YMR196W	YMR196W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YMR196W is not an essential gene	Q
253	VN_0253	YJR035W	RAD26	Protein involved in transcription-coupled repair nucleotide excision repair of UV-induced DNA lesions; homolog of human CSB protein	Q
254	VN_0254	YHR102W	KIC1	Protein kinase of the PAK/Ste20 kinase family, required for cell integrity possibly through regulating 1,6-beta-glucan levels in the wall; physically interacts with Cdc31p (centrin), which is a component of the spindle pole body	Q
255	VN_0255	YJL050W	MTR4	ATP-dependent 3'-5' RNA helicase, involved in nuclear RNA processing and degradation both as a component of the TRAMP complex and in TRAMP independent processes; member of the Dead-box family of helicases	Q
256	VN_0256	YGR274C	TAF1	TFIID subunit (145 kDa), involved in RNA polymerase II transcription initiation; possesses in vitro histone acetyltransferase activity but its role in vivo appears to be minor; involved in promoter binding and G1/S progression	Q
257	VN_0257	YBL066C	SEF1	Putative transcription factor, has homolog in Kluyveromyces lactis	Strain failed to verify via PCR
258	VN_0258	YCR092C	MSH3	Mismatch repair protein, forms dimers with Msh2p that mediate repair of insertion or deletion mutations and removal of nonhomologous DNA ends, contains a PCNA (Pol30p) binding motif required for genome stability	Q
259	VN_0259	YEL061C	CIN8	Kinesin motor protein involved in mitotic spindle assembly and chromosome segregation	Q
260	VN_0260	YMR189W	GCV2	P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of 5,10-methylene-THF in the cytoplasm	Q
261	VN_0261	YDR060W	MAK21	Constituent of 66S pre-ribosomal particles, required for large (60S) ribosomal subunit biogenesis; involved in nuclear export of pre-ribosomes; required for maintenance of dsRNA virus; homolog of human CAATT-binding protein	Q
262	VN_0262	YDR028C	REG1	Regulatory subunit of type 1 protein phosphatase Glc7p, involved in negative regulation of glucose-repressible genes	Q
263	VN_0263	YOR048C	RAT1	Nuclear 5' to 3' single-stranded RNA exonuclease, involved in RNA metabolism, including rRNA and snRNA processing as well as poly (A+) dependent and independent mRNA transcription termination	Q
264	VN_0264	YLR223C	IFH1	Essential protein with a highly acidic N-terminal domain; IFH1 exhibits genetic interactions with FHL1, overexpression interferes with silencing at telomeres and HM loci; potential Cdc28p substrate	Q
265	VN_0265	YHR119W	SET1	Histone methyltransferase, subunit of the COMPASS (Set1C) complex which methylates histone H3 on lysine 4; required in transcriptional silencing near telomeres and at the silent mating type loci; contains a SET domain	Q
266	VN_0266	YPR097W	YPR097W	Protein that contains a Phox homology (PX) domain and binds phosphoinositides; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q

267	VN_0267	YNL267W	PIK1	Phosphatidylinositol 4-kinase; catalyzes first step in the biosynthesis of phosphatidylinositol-4,5-bisphosphate; may control cytokinesis through the actin cytoskeleton	Q
268	VN_0268	YLR039C	RIC1	Protein involved in retrograde transport to the cis-Golgi network; forms heterodimer with Rgp1p that acts as a GTP exchange factor for Ypt6p; involved in transcription of rRNA and ribosomal protein genes	Q
269	VN_0269	YDL223C	HBT1	Substrate of the Hub1p ubiquitin-like protein that localizes to the shmoo tip (mating projection); mutants are defective for mating projection formation, thereby implicating Hbt1p in polarized cell morphogenesis	Q
270	VN_0270	YKL033W	TTI1	Putative protein of unknown function; subunit of the ASTRA complex which is part of the chromatin remodeling machinery; similar to S. pombe Tti1p; detected in highly purified mitochondria in high-throughput studies	Q
271	VN_0271	YIL128W	MET18	DNA repair and TFIIH regulator, required for both nucleotide excision repair (NER) and RNA polymerase II (RNAP II) transcription; involved in telomere maintenance	Q
272	VN_0272	YIL125W	KGD1	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA	Q
273	VN_0273	YGL241W	KAP114	Karyopherin, responsible for nuclear import of Spt15p, histones H2A and H2B, and Nap1p; amino terminus shows similarity to those of other importins, particularly Cse1p; localization is primarily nuclear	Q
274	VN_0274	YIL169C	YIL169C	Putative protein of unknown function; serine/threonine rich and highly similar to YOL155C, a putative glucan alpha-1,4-glucosidase; transcript is induced in both high and low pH environments; YIL169C is a non-essential gene	Q
275	VN_0275	YGR218W	CRM1	Major karyopherin, involved in export of proteins, RNAs, and ribosomal subunits from the nucleus; exportin	Q
276	VN_0276	YDR291W	HRQ1	Putative RecQ helicase; belongs to the widely conserved RecQ family of proteins which are involved in maintaining genomic integrity; similar to the human RecQ4p implicated in Rothmund-Thomson syndrome(RTS)	Q
277	VN_0277	YGL178W	MPT5	Member of the Puf family of RNA-binding proteins; binds to mRNAs encoding chromatin modifiers and spindle pole body components; involved in longevity, maintenance of cell wall integrity, and sensitivity to and recovery from pheromone arrest	Q
278	VN_0278	YML010W	SPT5	Protein involved in regulating Pol I and Pol II transcription and pre-mRNA processing; forms a complex with Spt4p; contains a C-terminal repeat domain that is a target for phosphorylation by Sgv1p	Q
279	VN_0279	YNL132W	KRE33	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance	Strain failed to verify via PCR
280	VN_0280	YJL084C	ALY2	Protein proposed to regulate the endocytosis of plasma membrane proteins; interacts with the cyclin Pcl7p and ubiquitin ligase Rsp5p; phosphorylated by the cyclin-CDK complex, Pcl7p-Pho85p; mRNA is cell cycle regulated, peaking in M phase	Q
281	VN_0281	YPL009C	YPL009C	Protein of unknown function; may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YPL009C is not an essential gene	Q
282	VN_0282	YPR204W	YPR204W	Helicase-like protein encoded within the telomeric Y' element	Q
283	VN_0283	YKL210W	UBA1	Ubiquitin activating enzyme (E1), involved in ubiquitin-mediated protein degradation and essential for viability	Q
284	VN_0284	YAL035W	FUN12	GTPase, required for general translation initiation by promoting Met-tRNA ^{iMet} binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2	Q
285	VN_0285	YIL112W	HOS4	Subunit of the Set3 complex, which is a meiotic-specific repressor of sporulation specific genes that contains deacetylase activity; potential Cdc28p substrate	Q
286	VN_0286	YOL145C	CTR9	Component of the Paf1p complex that binds to and modulates the activity of RNA polymerases I and II; required for expression of a subset of genes, including cyclin genes; contains TPR repeats	Q

287	VN_0287	YBL076C	ILS1	Cytoplasmic isoleucine-tRNA synthetase, target of the G1-specific inhibitor reveromycin A	Q
288	VN_0288	YKL157W	APE2	Aminopeptidase yscII; may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W	Q
289	VN_0289	YMR261C	TPS3	Regulatory subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway	Q
290	VN_0290	YLR249W	YEF3	Translational elongation factor 3, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP	Q
291	VN_0291	YCL024W	KCC4	Protein kinase of the bud neck involved in the septin checkpoint, associates with septin proteins, negatively regulates Swe1p by phosphorylation, shows structural homology to bud neck kinases Gin4p and Hsl1p	Q
292	VN_0292	YGR258C	RAD2	Single-stranded DNA endonuclease, cleaves single-stranded DNA during nucleotide excision repair to excise damaged DNA; subunit of Nucleotide Excision Repair Factor 3 (NEF3); homolog of human XPG protein	Q
293	VN_0293	YEL055C	POL5	DNA Polymerase phi; has sequence similarity to the human MybBP1A and weak sequence similarity to B-type DNA polymerases, not required for chromosomal DNA replication; required for the synthesis of rRNA	Q
294	VN_0294	YPL183C	RTT10	Cytoplasmic protein with a role in regulation of Ty1 transposition	Q
295	VN_0295	YPL040C	ISM1	Mitochondrial isoleucyl-tRNA synthetase, null mutant is deficient in respiratory growth	Q
296	VN_0296	YDR430C	CYM1	Lysine-specific metalloprotease of the mitochondrial intermembrane space, member of the pitrilysin family; degrades proteins and presequence peptides cleaved from imported proteins; required for normal mitochondrial morphology	Q
297	VN_0297	YPR115W	RGC1	Pleckstrin homology domain containing protein proposed to function as a glycerol channel activator; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
298	VN_0298	YER033C	ZRG8	Protein of unknown function; authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; GFP-fusion protein is localized to the cytoplasm; transcription induced under conditions of zinc deficiency	Q
299	VN_0299	YAL051W	OAF1	Oleate-activated transcription factor, acts alone and as a heterodimer with Pip2p; activates genes involved in beta-oxidation of fatty acids and peroxisome organization and biogenesis	Q
300	VN_0300	YDR325W	YCG1	Subunit of the condensin complex; required for establishment and maintenance of chromosome condensation, chromosome segregation and chromatin binding of the condensin complex; required for clustering of tRNA genes at the nucleolus	Q
301	VN_0301	YNL014W	HEF3	Translational elongation factor EF-3; paralog of YEF3 and member of the ABC superfamily; stimulates EF-1 alpha-dependent binding of aminoacyl-tRNA by the ribosome; normally expressed in zinc deficient cells	Q
302	VN_0302	YOL098C	YOL098C	Putative metalloprotease	Q
303	VN_0303	YOL089C	HAL9	Putative transcription factor containing a zinc finger; overexpression increases salt tolerance through increased expression of the ENA1 (Na ⁺ /Li ⁺ extrusion pump) gene while gene disruption decreases both salt tolerance and ENA1 expression	Q
304	VN_0304	YGR188C	BUB1	Protein kinase that forms a complex with Mad1p and Bub3p that is crucial in the checkpoint mechanism required to prevent cell cycle progression into anaphase in the presence of spindle damage, associates with centromere DNA via Skp1p	Q
305	VN_0305	YDR495C	VPS3	Component of CORVET tethering complex; cytoplasmic protein required for the sorting and processing of soluble vacuolar proteins,	Q

				acidification of the vacuolar lumen, and assembly of the vacuolar H ⁺ -ATPase	
306	VN_0306	YOL021C	DIS3	Exosome core complex catalytic subunit; possesses both endonuclease and 3'-5' exonuclease activity; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; has similarity to E. coli RNase R and to human DIS3	Q
307	VN_0307	YLR389C	STE23	Metalloprotease involved, with homolog Axl1p, in N-terminal processing of pro-a-factor to the mature form; member of the insulin-degrading enzyme family	Strain failed to verify via PCR
308	VN_0308	YLR071C	RGR1	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; required for glucose repression, HO repression, RME1 repression and sporulation	Q
309	VN_0309	YHR211W	FLO5	Lectin-like cell wall protein (flocculin) involved in flocculation, binds to mannose chains on the surface of other cells, confers floc-forming ability that is chymotrypsin resistant but heat labile; similar to Flo1p	Q
310	VN_0310	YKR086W	PRP16	RNA helicase in the DEAH-box family involved in the second catalytic step of splicing, exhibits ATP-dependent RNA unwinding activity	Q
311	VN_0311	YDR310C	SUM1	Transcriptional repressor required for mitotic repression of middle sporulation-specific genes; also acts as general replication initiation factor; involved in telomere maintenance, chromatin silencing; regulated by pachytene checkpoint	Q
312	VN_0312	YDR017C	KCS1	Inositol hexakisphosphate (IP6) and inositol heptakisphosphate (IP7) kinase; generation of high energy inositol pyrophosphates by Kcs1p is required for many processes such as vacuolar biogenesis, stress response and telomere maintenance	Q
313	VN_0313	YKL197C	PEX1	AAA-peroxin that heterodimerizes with AAA-peroxin Pex6p and participates in the recycling of peroxisomal signal receptor Pex5p from the peroxisomal membrane to the cytosol; induced by oleic acid and upregulated during anaerobiosis	Q
314	VN_0314	YPL075W	GCR1	Transcriptional activator of genes involved in glycolysis; DNA-binding protein that interacts and functions with the transcriptional activator Gcr2p	Q
315	VN_0315	YHR082C	KSP1	Ser/thr protein kinase; nuclear translocation required for haploid filamentous growth; regulates filamentous growth induced nuclear translocation of Bcy1p, Fus3p, and Sks1p; overproduction causes allele-specific suppression of prp20-10	Q
316	VN_0316	YDL240W	LRG1	Putative GTPase-activating protein (GAP) involved in the Pkc1p-mediated signaling pathway that controls cell wall integrity; appears to specifically regulate 1,3-beta-glucan synthesis	Q
317	VN_0317	YDR379W	RGA2	GTPase-activating protein for the polarity-establishment protein Cdc42p; implicated in control of septin organization, pheromone response, and haploid invasive growth; regulated by Pho85p and Cdc28p	Q
318	VN_0318	YGR240C	PFK1	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes	Q
319	VN_0319	YOL051W	GAL11	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; affects transcription by acting as target of activators and repressors	Q
320	VN_0320	YPR042C	PUF2	Member of the PUF protein family, which is defined by the presence of Pumilio homology domains that confer RNA binding activity; preferentially binds mRNAs encoding membrane-associated proteins	Q
321	VN_0321	YNL278W	CAF120	Part of the evolutionarily-conserved CCR4-NOT transcriptional regulatory complex involved in controlling mRNA initiation, elongation, and degradation	Q
322	VN_0322	YJR132W	NMD5	Karyopherin, a carrier protein involved in nuclear import of proteins; importin beta homolog	Q
323	VN_0323	YNL327W	EGT2	Glycosylphosphatidylinositol (GPI)-anchored cell wall endoglucanase required for proper cell separation after cytokinesis, expression is activated by Swi5p and tightly regulated in a cell cycle-dependent manner	Q

324	VN_0324	YGL207W	SPT16	Subunit of the heterodimeric FACT complex (Spt16p-Pob3p), facilitates RNA Polymerase II transcription elongation through nucleosomes by destabilizing and then reassembling nucleosome structure	Q
325	VN_0325	YLR187W	SKG3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; potential Cdc28p substrate; similar to Caf120p and Skg4p	Q
326	VN_0326	YGL201C	MCM6	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex	Q
327	VN_0327	YKL173W	SNU114	GTPase component of U5 snRNP involved in mRNA splicing via spliceosome; binds directly to U5 snRNA; proposed to be involved in conformational changes of the spliceosome; similarity to ribosomal translocation factor EF-2	Q
328	VN_0328	YOL100W	PKH2	Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling cascade required for maintenance of cell wall integrity; redundant with Pkh1p	Q
329	VN_0329	YFL034W	YFL034W	Putative integral membrane protein that interacts with Rpp0p, which is a component of the ribosomal stalk	Q
330	VN_0330	YGL013C	PDR1	Zinc cluster protein that is a master regulator involved in recruiting other zinc cluster proteins to pleiotropic drug response elements (PDREs) to fine tune the regulation of multidrug resistance genes	Q
331	VN_0331	YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p	Q
332	VN_0332	YLL016W	SDC25	Non-essential Ras guanine nucleotide exchange factor (GEF) localized to the membrane; expressed in poor nutrients and on non-fermentable carbon sources; homologous to CDC25; contains a stop codon in S288C; full-length gene includes YLL017W	Q
333	VN_0333	YER114C	BOI2	Protein implicated in polar growth, functionally redundant with Boi1p; interacts with bud-emergence protein Bem1p; contains an SH3 (src homology 3) domain and a PH (pleckstrin homology) domain	Q
334	VN_0334	YIL031W	ULP2	Peptidase that deconjugates Smt3/SUMO-1 peptides from proteins, plays a role in chromosome cohesion at centromeric regions and recovery from checkpoint arrest induced by DNA damage or DNA replication defects; potential Cdc28p substrate	Q
335	VN_0335	YBL037W	APL3	Alpha-adaptin, large subunit of the clathrin associated protein complex (AP-2); involved in vesicle mediated transport	Q
336	VN_0336	YLL031C	GPI13	ER membrane localized phosphoryltransferase that adds phosphoethanolamine onto the third mannose residue of the glycosylphosphatidylinositol (GPI) anchor precursor; similar to human PIG-O protein	Q
337	VN_0337	YOR127W	RGA1	GTPase-activating protein for the polarity-establishment protein Cdc42p; implicated in control of septin organization, pheromone response, and haploid invasive growth	Q
338	VN_0338	YOR363C	PIP2	Autoregulatory oleate-specific transcriptional activator of peroxisome proliferation, contains Zn(2)-Cys(6) cluster domain, forms heterodimer with Oaf1p, binds oleate response elements (OREs), activates beta-oxidation genes	Q
339	VN_0339	YDL073W	YDL073W	Putative protein of unknown function; YDL073W is not an essential gene	Strain failed to verify via PCR
340	VN_0340	YMR185W	YMR185W	Putative protein of unknown function; conflicting evidence on whether null mutant is viable with elongated buds, or inviable	Q
341	VN_0341	YNL236W	SIN4	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; contributes to both positive and negative transcriptional regulation; dispensable for basal transcription	Q
342	VN_0342	YMR125W	STO1	Large subunit of the nuclear mRNA cap-binding protein complex, interacts with Npl3p to carry nuclear poly(A)+ mRNA to cytoplasm; also involved in nuclear mRNA degradation and telomere maintenance; orthologous to mammalian CBP80	Q

343	VN_0343	YMR086W	YMR086W	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; GFP-fusion protein localizes to the cell periphery; possible component of the eisosome; expression is repressed by cAMP	Q
344	VN_0344	YEL043W	YEL043W	Predicted cytoskeleton protein involved in intracellular signalling based on quantitative analysis of protein-protein interaction maps; may interact with ribosomes, based on co-purification studies; contains fibronectin type III domain fold	Q
345	VN_0345	YMR019W	STB4	Protein that binds Sin3p in a two-hybrid assay; contains a Zn(II)2Cys6 zinc finger domain characteristic of DNA-binding proteins; computational analysis suggests a role in regulation of expression of genes encoding transporters	Q
346	VN_0346	YJL154C	VPS35	Endosomal subunit of membrane-associated retromer complex required for retrograde transport; receptor that recognizes retrieval signals on cargo proteins, forms subcomplex with Vps26p and Vps29p that selects cargo proteins for retrieval	Q
347	VN_0347	YDR069C	DOA4	Ubiquitin isopeptidase, required for recycling ubiquitin from proteasome-bound ubiquitinated intermediates, acts at the late endosome/prevacuolar compartment to recover ubiquitin from ubiquitinated membrane proteins en route to the vacuole	Q
348	VN_0348	YKL050C	YKL050C	Protein of unknown function; the YKL050W protein is a target of the SCFCdc4 ubiquitin ligase complex and YKL050W transcription is regulated by Azf1p	Q
349	VN_0349	YML065W	ORC1	Largest subunit of the origin recognition complex, which directs DNA replication by binding to replication origins and is also involved in transcriptional silencing; exhibits ATPase activity	Q
350	VN_0350	YBR289W	SNF5	Subunit of the SWI/SNF chromatin remodeling complex involved in transcriptional regulation; functions interdependently in transcriptional activation with Snf2p and Snf6p	Q
351	VN_0351	YBL085W	BOI1	Protein implicated in polar growth, functionally redundant with Boi2p; interacts with bud-emergence protein Bem1p; contains an SH3 (src homology 3) domain and a PH (pleckstrin homology) domain	Q
352	VN_0352	YOR160W	MTR10	Nuclear import receptor, mediates the nuclear localization of proteins involved in mRNA-nucleus export; promotes dissociation of mRNAs from the nucleus-cytoplasm mRNA shuttling protein Npl3p	Q
353	VN_0353	YOL155C	HPF1	Haze-protective mannoprotein that reduces the particle size of aggregated proteins in white wines	Q
354	VN_0354	YDR359C	EAF1	Component of the NuA4 histone acetyltransferase complex; acts as a platform for assembly of NuA4 subunits into the native complex; required for initiation of pre-meiotic DNA replication, likely due to its requirement for expression of IME1	Q
355	VN_0355	YGR140W	CBF2	Essential kinetochore protein, component of the CBF3 multisubunit complex that binds to the CDEIII region of the centromere; Cbf2p also binds to the CDEII region possibly forming a different multimeric complex, ubiquitinated in vivo	Q
356	VN_0356	YML076C	WAR1	Homodimeric Zn2Cys6 zinc finger transcription factor; binds to a weak acid response element to induce transcription of PDR12 and FUN34, encoding an acid transporter and a putative ammonia transporter, respectively	Q
357	VN_0357	YPR104C	FHL1	Transcriptional activator with similarity to DNA-binding domain of Drosophila forkhead but unable to bind DNA in vitro; required for rRNA processing; isolated as a suppressor of splicing factor prp4	Strain failed to verify via PCR
358	VN_0358	YBL104C	YBL104C	Putative protein of unknown function, promoter contains multiple GCN4 binding sites	Q
359	VN_0359	YIL017C	VID28	Protein involved in proteasome-dependent catabolite degradation of fructose-1,6-bisphosphatase (FBPase); localized to the nucleus and the cytoplasm	Q
360	VN_0360	YOR113W	AZF1	Zinc-finger transcription factor, involved in induction of CLN3 transcription in response to glucose; genetic and physical interactions indicate a possible role in mitochondrial transcription or genome maintenance	Q
361	VN_0361	YFR040W	SAP155	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap185p, and Sap190p	Q

362	VN_0362	YKL015W	PUT3	Transcriptional activator of proline utilization genes, constitutively binds PUT1 and PUT2 promoter sequences and undergoes a conformational change to form the active state; has a Zn(2)-Cys(6) binuclear cluster domain	Q
363	VN_0363	YEL032W	MCM3	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex	Strain failed to verify via PCR
364	VN_0364	YBR112C	CYC8	General transcriptional co-repressor, acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters; can form the prion [OCT+]	Q
365	VN_0365	YHR120W	MSH1	DNA-binding protein of the mitochondria involved in repair of mitochondrial DNA, has ATPase activity and binds to DNA mismatches; has homology to E. coli MutS; transcription is induced during meiosis	Q
366	VN_0366	YHL050C	YHL050C	Putative protein of unknown function, potential Cdc28p substrate	Q
367	VN_0367	YIL002C	INP51	Phosphatidylinositol 4,5-bisphosphate 5-phosphatase, synaptojanin-like protein with an N-terminal Sac1 domain, plays a role in phosphatidylinositol 4,5-bisphosphate homeostasis and in endocytosis; null mutation confers cold-tolerant growth	Q
368	VN_0368	YOR005C	DNL4	DNA ligase required for nonhomologous end-joining (NHEJ), forms stable heterodimer with required cofactor Lif1p, interacts with Nej1p; involved in meiosis, not essential for vegetative growth	Q
369	VN_0369	YJR061W	YJR061W	Putative protein of unknown function; non-essential gene with similarity to Mnn4, a putative membrane protein involved in glycosylation; transcription repressed by Rm101p	Q
370	VN_0370	YDR081C	PDC2	Transcription factor required for the synthesis of the glycolytic enzyme pyruvate decarboxylase, required for high level expression of both the THI and the PDC genes	Q
371	VN_0371	YML111W	BUL2	Component of the Rsp5p E3-ubiquitin ligase complex, involved in intracellular amino acid permease sorting, functions in heat shock element mediated gene expression, essential for growth in stress conditions, functional homolog of BUL1	Q
372	VN_0372	YDR213W	UPC2	Sterol regulatory element binding protein, induces transcription of sterol biosynthetic genes and of DAN/TIR gene products; Ecm22p homolog; relocates from intracellular membranes to perinuclear foci on sterol depletion	Strain failed to verify via PCR
373	VN_0373	YDR409W	SIZ1	SUMO/Smt3 ligase that promotes the attachment of sumo (Smt3p; small ubiquitin-related modifier) to proteins; binds Ubc9p and may bind septins; specifically required for sumoylation of septins in vivo; localized to the septin ring	Q
374	VN_0374	YLR442C	SIR3	Silencing protein that interacts with Sir2p and Sir4p, and histone H3 and H4 tails, to establish a transcriptionally silent chromatin state; required for spreading of silenced chromatin; recruited to chromatin through interaction with Rap1p	Q
375	VN_0375	YMR080C	NAM7	ATP-dependent RNA helicase of the SFI superfamily involved in nonsense mediated mRNA decay; required for efficient translation termination at nonsense codons and targeting of NMD substrates to P-bodies; involved in telomere maintenance	Q
376	VN_0376	YNL023C	FAP1	Protein that binds to Fpr1p, conferring rapamycin resistance by competing with rapamycin for Fpr1p binding; accumulates in the nucleus upon treatment of cells with rapamycin; has similarity to D. melanogaster shuttle craft and human NFX1	Q
377	VN_0377	YMR205C	PFK2	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes	Q
378	VN_0378	YJR089W	BIR1	Subunit of chromosomal passenger complex (CPC; Ipl1p-Sli15p-Bir1p-Nbl1p), which regulates chromosome segregation; required for chromosome bi-orientation and for spindle assembly checkpoint activation upon reduced sister kinetochore tension	Q
379	VN_0379	YIL137C	TMA108	Protein that associates with ribosomes; putative metalloprotease	Q

380	VN_0380	YLR129W	DIP2	Nucleolar protein, specifically associated with the U3 snoRNA, part of the large ribonucleoprotein complex known as the small subunit (SSU) processome, required for 18S rRNA biogenesis, part of the active pre-rRNA processing complex	Strain failed to verify via PCR
381	VN_0381	YPR019W	MCM4	Essential helicase component of heterohexameric MCM2-7 complexes which bind pre-replication complexes on DNA and melt the DNA prior to replication; accumulates in the nucleus in G1; homolog of <i>S. pombe</i> Cdc21p	Q
382	VN_0382	YER032W	FIR1	Protein involved in 3' mRNA processing, interacts with Ref2p; potential Cdc28p substrate	Q
383	VN_0383	YER151C	UBP3	Ubiquitin-specific protease that interacts with Bre5p to co-regulate anterograde and retrograde transport between endoplasmic reticulum and Golgi compartments; inhibitor of gene silencing; cleaves ubiquitin fusions but not polyubiquitin	Q
384	VN_0384	YLR014C	PPR1	Zinc finger transcription factor containing a Zn(2)-Cys(6) binuclear cluster domain, positively regulates transcription of genes involved in uracil biosynthesis; activity may be modulated by interaction with Tup1p	Q
385	VN_0385	YBL005W	PDR3	Transcriptional activator of the pleiotropic drug resistance network, regulates expression of ATP-binding cassette (ABC) transporters through binding to cis-acting sites known as PDREs (PDR responsive elements)	Q
386	VN_0386	YMR288W	HSH155	U2-snRNP associated splicing factor that forms extensive associations with the branch site-3' splice site-3' exon region upon prespliceosome formation; similarity to the mammalian U2 snRNP-associated splicing factor SAP155	Q
387	VN_0387	YBR079C	RPG1	eIF3a subunit of the core complex of translation initiation factor 3 (eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes	Q
388	VN_0388	YBR073W	RDH54	DNA-dependent ATPase, stimulates strand exchange by modifying the topology of double-stranded DNA; involved in recombinational repair of DNA double-strand breaks during mitosis and meiosis; proposed to be involved in crossover interference	Q
389	VN_0389	YNL127W	FAR11	Protein involved in recovery from cell cycle arrest in response to pheromone, in a Far1p-independent pathway; interacts with Far3p, Far7p, Far8p, Far9p, and Far10p; has similarity to the N- and C-termini of <i>N. crassa</i> HAM-2	Q
390	VN_0390	YLL003W	SFI1	Centrin (Cdc31p)-binding protein required for spindle pole body (SPB) duplication, localizes to the half-bridge of the SPB, required for progression through G(2)-M transition, has similarity to <i>Xenopus laevis</i> XCAP-C	Q
391	VN_0391	YMR124W	YMR124W	Protein of unknown function; GFP-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; interacts with Crm1p in two-hybrid assay; YMR124W is not an essential gene; predicted to have a role in organelle organization	Q
392	VN_0392	YER075C	PTP3	Phosphotyrosine-specific protein phosphatase involved in the inactivation of mitogen-activated protein kinase (MAPK) during osmolarity sensing; dephosphorylates Hog1p MAPK and regulates its localization; localized to the cytoplasm	Q
393	VN_0393	YDR103W	STE5	Pheromone-response scaffold protein; binds Ste11p, Ste7p, and Fus3p kinases, forming a MAPK cascade complex that interacts with the plasma membrane and Ste4p-Ste18p; allosteric activator of Fus3p that facilitates Ste7p-mediated activation	Q
394	VN_0394	YGL141W	HUL5	Ubiquitin-conjugating enzyme (E4), elongates polyubiquitin chains on substrate proteins; works in opposition to Ubp6p polyubiquitin-shortening activity; required for retrograde transport of misfolded proteins into cytoplasm during ERAD	Q
395	VN_0395	YNL082W	PMS1	ATP-binding protein required for mismatch repair in mitosis and meiosis; functions as a heterodimer with Mlh1p, binds double- and single-stranded DNA via its N-terminal domain, similar to <i>E. coli</i> MutL	Q
396	VN_0396	YMR275C	BUL1	Ubiquitin-binding component of the Rsp5p E3-ubiquitin ligase complex, functional homolog of Bul2p, disruption causes temperature-	Q

				sensitive growth, overexpression causes missorting of amino acid permeases	
397	VN_0397	YIL130W	ASG1	Zinc cluster protein proposed to function as a transcriptional regulator involved in the stress response; null mutants have a respiratory deficiency, calcofluor white sensitivity and slightly increased cycloheximide resistance	Q
398	VN_0398	YGL227W	VID30	Protein involved in proteasome-dependent catabolite degradation of fructose-1,6-bisphosphatase (FBPase); binds FBPase; shifts the balance of nitrogen metabolism toward glutamate production; localizes to the nucleus and the cytoplasm	Q
399	VN_0399	YGR162W	TIF4631	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p	Q
400	VN_0400	YIL075C	RPN2	Subunit of the 26S proteasome, substrate of the N-acetyltransferase Nat1p	Q
401	VN_0401	YML109W	ZDS2	Protein that interacts with silencing proteins at the telomere, involved in transcriptional silencing; implicated in the mitotic exit network through regulation of Cdc14p localization; paralog of Zds1p	Q
402	VN_0402	YGR056W	RSC1	Component of the RSC chromatin remodeling complex; required for expression of mid-late sporulation-specific genes; contains two essential bromodomains, a bromo-adjacent homology (BAH) domain, and an AT hook	Q
403	VN_0403	YDL220C	CDC13	Single stranded DNA-binding protein found at TG1-3 telomere G-tails; regulates telomere replication through recruitment of specific sub-complexes, but the essential function is telomere capping	Q
404	VN_0404	YGL093W	SPC105	Subunit of a kinetochore-microtubule binding complex with Kre28p that bridges centromeric heterochromatin and kinetochore MAPs and motors; required for sister chromatid bi-orientation and kinetochore binding of SAC components	Q
405	VN_0405	YKR089C	TGL4	Triacylglycerol lipase involved in triacylglycerol mobilization and degradation; found in lipid particles; phosphorylated and activated by Cdc28p; required with Tgl3p for timely bud formation	Q
406	VN_0406	YNL313C	YNL313C	Essential protein of unknown function; fluorescent protein (GFP or YFP)-tagged protein localizes to cytoplasm and nucleus	Q
407	VN_0407	YBR084W	MIS1	Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase	Q
408	VN_0408	YNL118C	DCP2	Catalytic subunit of the Dcp1p-Dcp2p decapping enzyme complex, which removes the 5' cap structure from mRNAs prior to their degradation; member of the Nudix hydrolase family	Q
409	VN_0409	YOL090W	MSH2	Protein that forms heterodimers with Msh3p and Msh6p that bind to DNA mismatches to initiate the mismatch repair process; contains a Walker ATP-binding motif required for repair activity; Msh2p-Msh6p binds to and hydrolyzes ATP	Q
410	VN_0410	YOR335C	ALA1	Cytoplasmic and mitochondrial alanyl-tRNA synthetase, required for protein synthesis; point mutation (cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally complemented by human homolog	Q
411	VN_0411	YDR421W	ARO80	Zinc finger transcriptional activator of the Zn2Cys6 family; activates transcription of aromatic amino acid catabolic genes in the presence of aromatic amino acids	Q
412	VN_0412	YDR356W	SPC110	Inner plaque spindle pole body (SPB) component, ortholog of human kendrin; involved in connecting nuclear microtubules to SPB; interacts with Tub4p-complex and calmodulin; phosphorylated by Mps1p in cell cycle-dependent manner	Q
413	VN_0413	YHL007C	STE20	Cdc42p-activated signal transducing kinase of the PAK (p21-activated kinase) family, involved in pheromone response, pseudohyphal/invasive growth, and vacuole inheritance; GBB motif (found in noncatalytic domains of PAKs) binds Ste4p	Q
414	VN_0414	YKL171W	YKL171W	Putative protein kinase; implicated in proteasome function; epitope-tagged protein localizes to the cytoplasm	Q

415	VN_0415	YCR057C	PWP2	Conserved 90S pre-ribosomal component essential for proper endonucleolytic cleavage of the 35 S rRNA precursor at A0, A1, and A2 sites; contains eight WD-repeats; PWP2 deletion leads to defects in cell cycle and bud morphogenesis	Q
416	VN_0416	YGL036W	YGL036W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YGL036W is not an essential gene	Q
417	VN_0417	YPR160W	GPH1	Non-essential glycogen phosphorylase required for the mobilization of glycogen, activity is regulated by cyclic AMP-mediated phosphorylation, expression is regulated by stress-response elements and by the HOG MAP kinase pathway	Q
418	VN_0418	YAR019C	CDC15	Protein kinase of the Mitotic Exit Network that is localized to the spindle pole bodies at late anaphase; promotes mitotic exit by directly switching on the kinase activity of Dbf2p; required for spindle disassembly after meiosis II	Q
419	VN_0419	YDL190C	UFD2	Ubiquitin chain assembly factor (E4) that cooperates with a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a ubiquitin protein ligase (E3) to conjugate ubiquitin to substrates; also functions as an E3	Q
420	VN_0420	YOL063C	CRT10	Protein involved in transcriptional regulation of RNR2 and RNR3; expression of the gene is induced by DNA damage and null mutations confer increased resistance to hydroxyurea; N-terminal region has a leucine repeat and a WD40 repeat	Q
421	VN_0421	YGR100W	MDR1	Cytoplasmic GTPase-activating protein for Ypt/Rab transport GTPases Ypt6p, Ypt31p and Sec4p; involved in recycling of internalized proteins and regulation of Golgi secretory function	Q
422	VN_0422	YDR395W	SXM1	Nuclear transport factor (karyopherin) involved in protein transport between the cytoplasm and nucleoplasm; similar to Nmd5p, Cse1p, Lph2p, and the human cellular apoptosis susceptibility protein, CAS1	Q
423	VN_0423	YLR409C	UTP21	Subunit of U3-containing 90S preribosome and Small Subunit (SSU) processome complexes involved in production of 18S rRNA and assembly of small ribosomal subunit; synthetic defect with STI1 Hsp90 cochaperone; human homolog linked to glaucoma	Q
424	VN_0424	YPR135W	CTF4	Chromatin-associated protein, required for sister chromatid cohesion; interacts with DNA polymerase alpha (Pol1p) and may link DNA synthesis to sister chromatid cohesion	Q
425	VN_0425	YER024W	YAT2	Carnitine acetyltransferase; has similarity to Yat1p, which is a carnitine acetyltransferase associated with the mitochondrial outer membrane	Q
426	VN_0426	YGL049C	TIF4632	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4631p	Q
427	VN_0427	YLL026W	HSP104	Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved in [PSI ⁺] propagation	Q
428	VN_0428	YDL154W	MSH5	Protein of the MutS family, forms a dimer with Msh4p that facilitates crossovers between homologs during meiosis; msh5-Y823H mutation confers tolerance to DNA alkylating agents; homologs present in C. elegans and humans	Q
429	VN_0429	YDR006C	SOK1	Protein whose overexpression suppresses the growth defect of mutants lacking protein kinase A activity; involved in cAMP-mediated signaling; localized to the nucleus; similar to the mouse testis-specific protein PBS13	Q
430	VN_0430	YGL163C	RAD54	DNA-dependent ATPase, stimulates strand exchange by modifying the topology of double-stranded DNA; involved in the recombinational repair of double-strand breaks in DNA during vegetative growth and meiosis; member of the SWI/SNF family	Q
431	VN_0431	YDR096W	GIS1	JmjC domain-containing histone demethylase; transcription factor involved in the expression of genes during nutrient limitation; also involved in the negative regulation of DPP1 and PHR1	Q
432	VN_0432	YER070W	RNR1	One of two large regulatory subunits of ribonucleotide-diphosphate reductase; the RNR complex catalyzes rate-limiting step in dNTP	Q

				synthesis, regulated by DNA replication and DNA damage checkpoint pathways via localization of small subunits	
433	VN_0433	YPL248C	GAL4	DNA-binding transcription factor required for the activation of the GAL genes in response to galactose; repressed by Gal80p and activated by Gal3p	Q
434	VN_0434	YFL003C	MSH4	Protein involved in meiotic recombination, required for normal levels of crossing over, colocalizes with Zip2p to discrete foci on meiotic chromosomes, has homology to bacterial MutS protein	Q
435	VN_0435	YDR089W	YDR089W	Protein of unknown function; deletion confers resistance to Nickel	Q
436	VN_0436	YER069W	ARG5,6	Protein that is processed in the mitochondrion to yield acetylglutamate kinase and N-acetyl-gamma-glutamyl-phosphate reductase, which catalyze the 2nd and 3rd steps in arginine biosynthesis; enzymes form a complex with Arg2p	Q
437	VN_0437	YPR105C	COG4	Essential component of the conserved oligomeric Golgi complex (Cog1p through Cog8p), a cytosolic tethering complex that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments	Q
438	VN_0438	YJL165C	HAL5	Putative protein kinase; overexpression increases sodium and lithium tolerance, whereas gene disruption increases cation and low pH sensitivity and impairs potassium uptake, suggesting a role in regulation of Trk1p and/or Trk2p transporters	Q
439	VN_0439	YMR053C	STB2	Protein that interacts with Sin3p in a two-hybrid assay and is part of a large protein complex with Sin3p and Stb1p	Q
440	VN_0440	YPL150W	YPL150W	Putative protein kinase of unknown cellular role	Q
441	VN_0441	YMR066W	SOV1	Mitochondrial protein of unknown function	Q
442	VN_0442	YLR382C	NAM2	Mitochondrial leucyl-tRNA synthetase, also has a direct role in splicing of several mitochondrial group I introns; indirectly required for mitochondrial genome maintenance	Q
443	VN_0443	YGL014W	PUF4	Member of the PUF protein family, which is defined by the presence of Pumilio homology domains that confer RNA binding activity; preferentially binds mRNAs encoding nucleolar ribosomal RNA-processing factors	Q
444	VN_0444	YOR058C	ASE1	Mitotic spindle midzone localized microtubule-associated protein (MAP) family member; required for spindle elongation and stabilization; undergoes cell cycle-regulated degradation by anaphase promoting complex; potential Cdc28p substrate	Q
445	VN_0445	YJL056C	ZAP1	Zinc-regulated transcription factor; binds to zinc-responsive promoters to induce transcription of certain genes in presence of zinc, represses other genes in low zinc; regulates its own transcription; contains seven zinc-finger domains	Q
446	VN_0446	YDR186C	YDR186C	Putative protein of unknown function; may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
447	VN_0447	YIL066C	RNR3	One of two large regulatory subunits of ribonucleotide-diphosphate reductase; the RNR complex catalyzes rate-limiting step in dNTP synthesis, regulated by DNA replication and DNA damage checkpoint pathways via localization of small subunits	Q
448	VN_0448	YKR064W	OAF3	Zinc cluster protein; regulates transcription in response to oleate levels; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
449	VN_0449	YGR071C	YGR071C	Putative protein of unknown function; deletion mutant has increased glycogen accumulation and displays elongated buds; green fluorescent protein (GFP)-fusion protein localizes to the nucleus	Q
450	VN_0450	YAL041W	CDC24	Guanine nucleotide exchange factor (GEF or GDP-release factor) for Cdc42p; required for polarity establishment and maintenance, and mutants have morphological defects in bud formation and shmooing	Strain failed to verify via PCR
451	VN_0451	YBR237W	PRP5	RNA helicase in the DEAD-box family, necessary for prespliceosome formation, bridges U1 and U2 snRNPs and enables stable U2 snRNP association with intron RNA	Q
452	VN_0452	YBR225W	YBR225W	Putative protein of unknown function; non-essential gene identified in a screen for mutants affected in mannosylphosphorylation of cell wall	Q

				components	
453	VN_0453	YER047C	SAP1	Putative ATPase of the AAA family, interacts with the Sin1p transcriptional repressor in the two-hybrid system	Q
454	VN_0454	YPL249C	GYP5	GTPase-activating protein (GAP) for yeast Rab family members, involved in ER to Golgi trafficking; exhibits GAP activity toward Ypt1p that is stimulated by Gyl1p, also acts on Sec4p; interacts with Gyl1p, Rvs161p and Rvs167p	Q
455	VN_0455	YJL070C	YJL070C	Putative protein of unknown function with similarity to AMP deaminases; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YJL070C is a non-essential gene	Q
456	VN_0456	YDR206W	EBS1	Protein involved in inhibition of translation and nonsense-mediated decay; interacts with cap binding protein Cdc33p and with Nam7p; localizes to P-bodies upon glucose starvation; mRNA abundance regulated by mRNA decay factors	Q
457	VN_0457	YLR386W	VAC14	Protein involved in regulated synthesis of PtdIns(3,5)P(2), in control of trafficking of some proteins to the vacuole lumen via the MVB, and in maintenance of vacuole size and acidity; interacts with Fig4p; activator of Fab1p	Q
458	VN_0458	YML034W	SRC1	Inner nuclear membrane protein that functions in regulation of subtelomeric genes and is linked to TREX (transcription export) factors; SRC1 produces 2 splice variant proteins with different functions; possible role in chromatid segregation	Q
459	VN_0459	YLR001C	YLR001C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; predicted to be palmitoylated	Q
460	VN_0460	YAR044W	YAR044W , SWH1	#N/A	Q
461	VN_0461	YDL040C	NAT1	Subunit of the N-terminal acetyltransferase NatA (Nat1p, Ard1p, Nat5p); N-terminally acetylates many proteins, which influences multiple processes such as the cell cycle, heat-shock resistance, mating, sporulation, and telomeric silencing	Q
462	VN_0462	YKR009C	FOX2	Multifunctional enzyme of the peroxisomal fatty acid beta-oxidation pathway; has 3-hydroxyacyl-CoA dehydrogenase and enoyl-CoA hydratase activities	Q
463	VN_0463	YGL180W	ATG1	Protein ser/thr kinase required for vesicle formation in autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; structurally required for phagophore assembly site formation; during autophagy forms a complex with Atg13p and Atg17p	Q
464	VN_0464	YNR047W	FPK1	Ser/Thr protein kinase that regulates the putative phospholipid translocases Lem3p-Dnf1p/Dnf2p; phosphorylates and inhibits upstream inhibitory kinase, Ypk1p; localizes to the cytoplasm, early endosome/TGN compartments, and plasma membrane	Q
465	VN_0465	YLR045C	STU2	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family; regulates microtubule dynamics during spindle orientation and metaphase chromosome alignment; interacts with spindle pole body component Spc72p	Q
466	VN_0466	YML099C	ARG81	Zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type, involved in the regulation of arginine-responsive genes; acts with Arg80p and Arg82p	Q
467	VN_0467	YNR011C	PRP2	RNA-dependent ATPase in the DEAH-box family, required for activation of the spliceosome before the first transesterification step in RNA splicing	Q
468	VN_0468	YPL174C	NIP100	Large subunit of the dynactin complex, which is involved in partitioning the mitotic spindle between mother and daughter cells; putative ortholog of mammalian p150(glued)	Q
469	VN_0469	YMR165C	PAH1	Mg ²⁺ -dependent phosphatidate (PA) phosphatase, catalyzes the dephosphorylation of PA to yield diacylglycerol and P _i , responsible for de novo lipid synthesis; homologous to mammalian lipin 1	Q
470	VN_0470	YDR416W	SYF1	Member of the NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 snRNAs; null mutant has splicing defect and arrests in	Q

				G2/M; homologs in human and <i>C. elegans</i>	
471	VN_0471	YDR369C	XRS2	Protein required for DNA repair; component of the Mre11 complex, which is involved in double strand breaks, meiotic recombination, telomere maintenance, and checkpoint signaling	Q
472	VN_0472	YPL105C	SYH1	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
473	VN_0473	YBR055C	PRP6	Splicing factor, component of the U4/U6-U5 snRNP complex	Q
474	VN_0474	YOR371C	GPB1	Multistep regulator of cAMP-PKA signaling; inhibits PKA downstream of Gpa2p and Cyr1p, thereby increasing cAMP dependency; inhibits Ras activity through direct interactions with Ira1p/2p; regulated by G-alpha protein Gpa2p; homolog of Gpb2p	Q
475	VN_0475	YOR129C	AFI1	Arf3p polarization-specific docking factor, required for the polarized distribution of the ADP-ribosylation factor, Arf3p; participates in polarity development and maintenance of a normal haploid budding pattern; interacts with Cnm7p	Q
476	VN_0476	YGR238C	KEL2	Protein that functions in a complex with Kel1p to negatively regulate mitotic exit, interacts with Tem1p and Lte1p; localizes to regions of polarized growth; potential Cdc28p substrate	Q
477	VN_0477	YDR285W	ZIP1	Transverse filament protein of the synaptonemal complex; required for normal levels of meiotic recombination and pairing between homologous chromosome during meiosis; potential Cdc28p substrate	Q
478	VN_0478	YPL141C	YPL141C	Putative protein kinase; similar to Kin4p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YPL141C is not an essential gene	Q
479	VN_0479	YNL068C	FKH2	Forkhead family transcription factor with a major role in the expression of G2/M phase genes; positively regulates transcriptional elongation; negative role in chromatin silencing at HML and HMR; substrate of the Cdc28p/Cln5p kinase	Q
480	VN_0480	YLR115W	CFT2	Subunit of the mRNA cleavage and polyadenylation factor (CPF); required for pre-mRNA cleavage, polyadenylation and poly(A) site recognition, 43% similarity with the mammalian CPSF-100 protein.	Q
481	VN_0481	YBR108W	AIM3	Protein interacting with Rvs167p; null mutant is viable and displays elevated frequency of mitochondrial genome loss	Q
482	VN_0482	YLR336C	SGD1	Essential nuclear protein with a possible role in the osmoregulatory glycerol response; interacts with phospholipase C (Plc1p); putative homolog of human NOM1 which is implicated in acute myeloid leukemia	Q
483	VN_0483	YDR074W	TPS2	Phosphatase subunit of the trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway	Q
484	VN_0484	YJR036C	HUL4	Protein with similarity to hect domain E3 ubiquitin-protein ligases, not essential for viability	Q
485	VN_0485	YIL073C	SPO22	Meiosis-specific protein essential for chromosome synapsis, involved in completion of nuclear divisions during meiosis; induced early in meiosis	Q
486	VN_0486	YJL078C	PRY3	Protein of unknown function	Q
487	VN_0487	YLL013C	PUF3	Protein of the mitochondrial outer surface, links the Arp2/3 complex with the mitochore during anterograde mitochondrial movement; also binds to and promotes degradation of mRNAs for select nuclear-encoded mitochondrial proteins	Q
488	VN_0488	YNL221C	POP1	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends; binds to the RPR1 RNA subunit in RNase P	Q
489	VN_0489	YGR150C	CCM1	Protein required for intron removal of COB and COX1 pre-mRNAs; contains pentatricopeptide repeat (PPR) motifs; mutant is respiratory deficient and has defective plasma membrane electron transport	Q
490	VN_0490	YLR347C	KAP95	Karyopherin beta, forms a complex with Srp1p/Kap60p; interacts with nucleoporins to mediate nuclear import of NLS-containing cargo proteins via the nuclear pore complex; regulates PC biosynthesis;	Q

				GDP-to-GTP exchange factor for Gsp1p	
491	VN_0491	YML061C	PIF1	DNA helicase; exists in two forms; the nuclear form is involved in telomere formation and elongation; acts as a catalytic inhibitor of telomerase; the mitochondrial form is involved in repair and recombination of mitochondrial DNA	Q
492	VN_0492	YKL121W	DGR2	Protein of unknown function; null mutant is resistant to 2-deoxy-D-glucose and displays abnormally elongated buds	Q
493	VN_0493	YAL056W	GPB2	Multistep regulator of cAMP-PKA signaling; inhibits PKA downstream of Gpa2p and Cyr1p, thereby increasing cAMP dependency; inhibits Ras activity through direct interactions with Ira1p/2p; regulated by G-alpha protein Gpa2p; homolog of Gpb1p	Q
494	VN_0494	YML093W	UTP14	Subunit of U3-containing Small Subunit (SSU) processome complex involved in production of 18S rRNA and assembly of small ribosomal subunit	Q
495	VN_0495	YNL233W	BNI4	Targeting subunit for Glc7p protein phosphatase, localized to the bud neck, required for localization of chitin synthase III to the bud neck via interaction with the chitin synthase III regulatory subunit Skt5p	Q
496	VN_0496	YLR451W	LEU3	Zinc-finger transcription factor that regulates genes involved in branched chain amino acid biosynthesis and ammonia assimilation; positively regulated by alpha-isopropylmalate, an intermediate in leucine biosynthesis	Q
497	VN_0497	YKL073W	LHS1	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; nucleotide exchange factor for the ER luminal Hsp70 chaperone Kar2p; regulated by the unfolded protein response pathway	Q
498	VN_0498	YNL325C	FIG4	Phosphatidylinositol 3,5-bisphosphate (PtdIns[3,5]P) phosphatase; required for efficient mating and response to osmotic shock; physically associates with and regulated by Vac14p; contains a SAC1-like domain	Q
499	VN_0499	YOR038C	HIR2	Subunit of the HIR complex, a nucleosome assembly complex involved in regulation of histone gene transcription; recruits Swi-Snf complexes to histone gene promoters; promotes heterochromatic gene silencing with Asf1p	Q
500	VN_0500	YNL256W	FOL1	Multifunctional enzyme of the folic acid biosynthesis pathway, has dihydropteroate synthetase, dihydro-6-hydroxymethylpterin pyrophosphokinase, and dihydroneopterin aldolase activities	Q
501	VN_0501	YOR217W	RFC1	Subunit of heteropentameric Replication factor C (RF-C), which is a DNA binding protein and ATPase that acts as a clamp loader of the proliferating cell nuclear antigen (PCNA) processivity factor for DNA polymerases delta and epsilon	Q
502	VN_0502	YNL201C	PSY2	Putative subunit of an evolutionarily conserved protein phosphatase complex containing the catalytic subunit Pph3p and the regulatory subunit Psy4p; required for cisplatin and oxaliplatin resistance; putative homolog of mammalian R3	Q
503	VN_0503	YER167W	BCK2	Protein rich in serine and threonine residues involved in protein kinase C signaling pathway, which controls cell integrity; overproduction suppresses pkc1 mutations	Q
504	VN_0504	YDR466W	PKH3	Protein kinase with similarity to mammalian phosphoinositide-dependent kinase 1 (PDK1) and yeast Pkh1p and Pkh2p, two redundant upstream activators of Pkc1p; identified as a multicopy suppressor of a pkh1 pkh2 double mutant	Q
505	VN_0505	YBL014C	RRN6	Component of the core factor (CF) rDNA transcription factor complex; CF is required for transcription of 35S rRNA genes by RNA polymerase I and is composed of Rrn6p, Rrn7p, and Rrn11p	Q
506	VN_0506	YLR357W	RSC2	Component of the RSC chromatin remodeling complex; required for expression of mid-late sporulation-specific genes; involved in telomere maintenance	Q
507	VN_0507	YDL117W	CYK3	SH3-domain protein located in the mother-bud neck and the cytokinetic actin ring; mutant phenotype and genetic interactions suggest a role in cytokinesis	Q
508	VN_0508	YOR141C	ARP8	Nuclear actin-related protein involved in chromatin remodeling, component of chromatin-remodeling enzyme complexes	Q

509	VN_0509	YBR281C	DUG2	Probable di- and tri-peptidase; forms a complex with Dug1p and Dug3p to degrade glutathione (GSH) and other peptides containing a gamma-glu-X bond in an alternative pathway to GSH degradation by gamma-glutamyl transpeptidase (Ecm38p)	Q
510	VN_0510	YCR030C	SYP1	Protein of unknown function that may regulate assembly and disassembly of the septin ring; colocalizes and interacts with septin subunits; potential role in actin cytoskeletal organization	Q
511	VN_0511	YDR422C	SIP1	Alternate beta-subunit of the Snf1p kinase complex, may confer substrate specificity; vacuolar protein containing KIS (Kinase-Interacting Sequence) and ASC (Association with Snf1 kinase Complex) domains involved in protein interactions	Q
512	VN_0512	YPL008W	CHL1	Conserved nuclear protein required to establish sister-chromatid pairing during S-phase, probable DNA helicase with similarity to human BACH1, which associates with tumor suppressor BRCA1; associates with acetyltransferase Ctf7p	Q
513	VN_0513	YHR047C	AAP1	Arginine/alanine aminopeptidase, overproduction stimulates glycogen accumulation	Q
514	VN_0514	YOR373W	NUD1	Component of the spindle pole body outer plaque, required for exit from mitosis	Q
515	VN_0515	YBR202W	MCM7	Component of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent helicase that promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase	Q
516	VN_0516	YPL084W	BRO1	Cytoplasmic class E vacuolar protein sorting (VPS) factor that coordinates deubiquitination in the multivesicular body (MVB) pathway by recruiting Doa4p to endosomes	Q
517	VN_0517	YDR505C	PSP1	Asn and gln rich protein of unknown function; high-copy suppressor of POL1 (DNA polymerase alpha) and partial suppressor of CDC2 (polymerase delta) and CDC6 (pre-RC loading factor) mutations; overexpression results in growth inhibition	Q
518	VN_0518	YAL021C	CCR4	Component of the CCR4-NOT transcriptional complex, which is involved in regulation of gene expression; component of the major cytoplasmic deadenylase, which is involved in mRNA poly(A) tail shortening	Q
519	VN_0519	YGL073W	HSF1	Trimeric heat shock transcription factor, activates multiple genes in response to stresses that include hyperthermia; recognizes variable heat shock elements (HSEs) consisting of inverted NGAAN repeats; posttranslationally regulated	Q
520	VN_0520	YNL085W	MKT1	Protein that forms a complex with Pbp1p that may mediate posttranscriptional regulation of HO endonuclease; involved in propagation of M2 dsRNA satellite of L-A virus; allelic variation affects mitochondrial genome stability	Q
521	VN_0521	YLL032C	YLL032C	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLL032C is not an essential gene	Q
522	VN_0522	YJL187C	SWE1	Protein kinase that regulates the G2/M transition by inhibition of Cdc28p kinase activity; localizes to the nucleus and to the daughter side of the mother-bud neck; homolog of S. pombe Wee1p; potential Cdc28p substrate	Q
523	VN_0523	YGR130C	YGR130C	Putative protein of unknown function; GFP-fusion protein localizes to the cytoplasm; possible component of the eisosome; specifically phosphorylated in vitro by mammalian diphosphoinositol pentakisphosphate (IP7)	Q
524	VN_0524	YKR099W	BAS1	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways; also involved in regulation of meiotic recombination at specific genes	Q
525	VN_0525	YPL207W	TYW1	Protein required for the synthesis of wybutosine, a modified guanosine found at the 3'-position adjacent to the anticodon of phenylalanine tRNA which supports reading frame maintenance by stabilizing codon-anticodon interactions	Q
526	VN_0526	YMR049C	ERB1	Constituent of 66S pre-ribosomal particles, forms a complex with Nop7p and Ytm1p that is required for maturation of the large ribosomal subunit; required for maturation of the 25S and 5.8S	Strain failed to verify via PCR

				ribosomal RNAs; homologous to mammalian Bop1	
527	VN_0527	YIL143C	SSL2	Component of the holoenzyme form of RNA polymerase transcription factor TFIIF, has DNA-dependent ATPase/helicase activity and is required, with Rad3p, for unwinding promoter DNA; involved in DNA repair; homolog of human ERCC3	Q
528	VN_0528	YBL008W	HIR1	Subunit of the HIR complex, a nucleosome assembly complex involved in regulation of histone gene transcription; contributes to nucleosome formation, heterochromatic gene silencing, and formation of functional kinetochores	Q
529	VN_0529	YLL034C	RIX7	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions	Q
530	VN_0530	YCR106W	RDS1	Zinc cluster transcription factor involved in conferring resistance to cycloheximide	Q
531	VN_0531	YJL089W	SIP4	C6 zinc cluster transcriptional activator that binds to the carbon source-responsive element (CSRE) of gluconeogenic genes; involved in the positive regulation of gluconeogenesis; regulated by Snf1p protein kinase; localized to the nucleus	Q
532	VN_0532	YPL032C	SVL3	Protein of unknown function, mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck	Strain failed to verify via PCR
533	VN_0533	YGL229C	SAP4	Protein required for function of the Sit4p protein phosphatase, member of a family of similar proteins that form complexes with Sit4p, including Sap15p, Sap185p, and Sap190p	Q
534	VN_0534	YLR176C	RFX1	Major transcriptional repressor of DNA-damage-regulated genes, recruits repressors Tup1p and Cyc8p to their promoters; involved in DNA damage and replication checkpoint pathway; similar to a family of mammalian DNA binding RFX1-4 proteins	Q
535	VN_0535	YDL122W	UBP1	Ubiquitin-specific protease that removes ubiquitin from ubiquitinated proteins; cleaves at the C terminus of ubiquitin fusions irrespective of their size; capable of cleaving polyubiquitin chains	Q
536	VN_0536	YER144C	UBP5	Putative ubiquitin-specific protease, closest paralog of Doa4p but has no functional overlap; concentrates at the bud neck	Q
537	VN_0537	YOR233W	KIN4	Serine/threonine protein kinase that inhibits the mitotic exit network (MEN) when the spindle position checkpoint is activated; localized asymmetrically to mother cell cortex, spindle pole body and bud neck	Q
538	VN_0538	YMR031C	YMR031C	Protein of unknown function with similarity to Ykl050cp and Uso1p; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies; possible component of the eisosome	Q
539	VN_0539	YHR131C	YHR131C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; overexpression causes a cell cycle delay or arrest	Q
540	VN_0540	YOR018W	ROD1	Membrane protein that binds the ubiquitin ligase Rsp5p via its 2 PY motifs; overexpression confers resistance to the GST substrate o-dinitrobenzene, zinc, and calcium; proposed to regulate the endocytosis of plasma membrane proteins	Q
541	VN_0541	YFL024C	EPL1	Component of NuA4, which is an essential histone H4/H2A acetyltransferase complex; homologous to Drosophila Enhancer of Polycomb	Q
542	VN_0542	YBR133C	HSL7	Protein arginine N-methyltransferase that exhibits septin and Hsl1p-dependent bud neck localization and periodic Hsl1p-dependent phosphorylation; required along with Hsl1p for bud neck recruitment, phosphorylation, and degradation of Swe1p	Q
543	VN_0543	YJR059W	PTK2	Putative serine/threonine protein kinase involved in regulation of ion transport across plasma membrane; enhances spermine uptake	Q
544	VN_0544	YGL216W	KIP3	Kinesin-related motor protein involved in mitotic spindle positioning	Q
545	VN_0545	YCL030C	HIS4	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; catalyzes the second, third, ninth and tenth steps in histidine biosynthesis	Q

546	VN_0546	YDR207C	UME6	Key transcriptional regulator of early meiotic genes, binds URS1 upstream regulatory sequence, couples metabolic responses to nutritional cues with initiation and progression of meiosis, forms complex with Ime1p, and also with Sin3p-Rpd3p	Q
547	VN_0547	YHR056C	RSC30	Component of the RSC chromatin remodeling complex; non-essential gene required for regulation of ribosomal protein genes and the cell wall/stress response; highly similar to Rsc3p; null mutants are osmosensitive	Q
548	VN_0548	YIL107C	PFK26	6-phosphofructo-2-kinase, inhibited by phosphoenolpyruvate and sn-glycerol 3-phosphate; has negligible fructose-2,6-bisphosphatase activity; transcriptional regulation involves protein kinase A	Q
549	VN_0549	YHR172W	SPC97	Component of the microtubule-nucleating Tub4p (gamma-tubulin) complex; interacts with Spc110p at the spindle pole body (SPB) inner plaque and with Spc72p at the SPB outer plaque	Q
550	VN_0550	YOR322C	LDB19	Protein involved in regulating the endocytosis of plasma membrane proteins by recruiting the ubiquitin ligase Rsp5p to its target; localization changes in response to nutrient levels; null mutant has reduced affinity for alcian blue dye	Q
551	VN_0551	YLR228C	ECM22	Sterol regulatory element binding protein, regulates transcription of sterol biosynthetic genes; contains Zn[2]-Cys[6] binuclear cluster; homologous to Upc2p; relocates from intracellular membranes to perinuclear foci on sterol depletion	Q
552	VN_0552	YDL148C	NOP14	Nucleolar protein, forms a complex with Noc4p that mediates maturation and nuclear export of 40S ribosomal subunits; also present in the small subunit processome complex, which is required for processing of pre-18S rRNA	Q
553	VN_0553	YOR168W	GLN4	Glutamine tRNA synthetase, monomeric class I tRNA synthetase that catalyzes the specific glutaminylation of tRNA(Glu); N-terminal domain proposed to be involved in enzyme-tRNA interactions	Q
554	VN_0554	YGL083W	SCY1	Putative kinase, suppressor of GTPase mutant, similar to bovine rhodopsin kinase	Q
555	VN_0555	YER109C	FLO8	Transcription factor required for flocculation, diploid filamentous growth, and haploid invasive growth; genome reference strain S288C and most laboratory strains have a mutation in this gene	Q
556	VN_0556	YJL047C	RTT101	Cullin subunit of a Roc1p-dependent E3 ubiquitin ligase complex with a role in anaphase progression; implicated in Mms22-dependent DNA repair; involved with Mms1p in nonfunctional rRNA decay; modified by the ubiquitin-like protein, Rub1p	Q
557	VN_0557	YKL022C	CDC16	Subunit of the anaphase-promoting complex/cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition; required for sporulation	Q
558	VN_0558	YIL038C	NOT3	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation	Q
559	VN_0559	YPR029C	APL4	Gamma-adaptin, large subunit of the clathrin-associated protein (AP-1) complex; binds clathrin; involved in vesicle mediated transport	Q
560	VN_0560	YJL087C	TRL1	tRNA ligase, required for tRNA splicing; composed of three essential domains containing the phosphodiesterase, polynucleotide kinase, and ligase activities required for ligation; localized at the inner membrane of the nuclear envelope	Q
561	VN_0561	YJL051W	IRC8	Bud tip localized protein of unknown function; mRNA is targeted to the bud by a She2p dependent transport system; mRNA is cell cycle regulated via Fkh2p, peaking in G2/M phase; null mutant displays increased levels of spontaneous Rad52p foci	Q
562	VN_0562	YGR196C	FYV8	Protein of unknown function, required for survival upon exposure to K1 killer toxin	Q
563	VN_0563	YLR095C	IOC2	Member of a complex (Isw1b) with Isw1p and Ioc4p that exhibits nucleosome-stimulated ATPase activity and acts within coding regions to coordinate transcription elongation with termination and processing, contains a PHD finger motif	Strain failed to verify via PCR
564	VN_0564	YDR485C	VPS72	Htz1p-binding component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A; required for vacuolar protein sorting	Q

565	VN_0565	YOR256C	TRE2	Protein that functions with Tre1p to regulate ubiquitylation and vacuolar degradation of the metal transporter Smf1p; has similarity to transferrin receptors; inviability of null mutant in systematic studies is due to proximity to CDC31	Q
566	VN_0566	YPL180W	TCO89	Subunit of TORC1 (Tor1p or Tor2p-Kog1p-Lst8p-Tco89p), a complex that regulates growth in response to nutrient availability; cooperates with Ssd1p in the maintenance of cellular integrity; deletion strains are hypersensitive to rapamycin	Q
567	VN_0567	YNL298W	CLA4	Cdc42p-activated signal transducing kinase of the PAK (p21-activated kinase) family, which also includes Ste20p and Skm1p; involved in septin ring assembly, vacuole inheritance, and cytokinesis; phosphorylates septins Cdc3p and Cdc10p	Q
568	VN_0568	YNL041C	COG6	Component of the conserved oligomeric Golgi complex (Cog1p through Cog8p), a cytosolic tethering complex that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments	Q
569	VN_0569	YDL126C	CDC48	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome	Q
570	VN_0570	YBL052C	SAS3	Histone acetyltransferase catalytic subunit of NuA3 complex that acetylates histone H3, involved in transcriptional silencing; homolog of the mammalian MOZ proto-oncogene; sas3 gcn5 double mutation confers lethality	Q
571	VN_0571	YLR263W	RED1	Protein component of the axial elements of the synaptonemal complex, involved in chromosome segregation during the first meiotic division; interacts with Hop1p; required for wild-type levels of Mek1p kinase activity	Q
572	VN_0572	YOR195W	SLK19	Kinetochore-associated protein required for normal segregation of chromosomes in meiosis and mitosis; component of the FEAR regulatory network, which promotes Cdc14p release from the nucleolus during anaphase; potential Cdc28p substrate	Q
573	VN_0573	YGR198W	YPP1	Cargo-transport protein involved in endocytosis; interacts with phosphatidylinositol-4-kinase Stt4; GFP-fusion protein localizes to the cytoplasm; YGR198W is an essential gene	Q
574	VN_0574	YMR309C	NIP1	eIF3c subunit of the eukaryotic translation initiation factor 3 (eIF3), involved in the assembly of preinitiation complex and start codon selection	Q
575	VN_0575	YIL095W	PRK1	Protein serine/threonine kinase; regulates the organization and function of the actin cytoskeleton through the phosphorylation of the Pan1p-Sla1p-End3p protein complex	Q
576	VN_0576	YBR276C	PPS1	Protein phosphatase with specificity for serine, threonine, and tyrosine residues; has a role in the DNA synthesis phase of the cell cycle	Q
577	VN_0577	YLR182W	SWI6	Transcription cofactor, forms complexes with DNA-binding proteins Swi4p and Mbp1p to regulate transcription at the G1/S transition; involved in meiotic gene expression; localization regulated by phosphorylation; potential Cdc28p substrate	Q
578	VN_0578	YOR133W	EFT1	Elongation factor 2 (EF-2), also encoded by EFT2; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin	Q
579	VN_0579	YKR079C	TRZ1	tRNA 3'-end processing endonuclease tRNase Z; also localized to mitochondria and interacts genetically with Rex2 exonuclease; homolog of the human candidate prostate cancer susceptibility gene ELAC2	Q
580	VN_0580	YMR102C	YMR102C	Protein of unknown function; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance; mutant shows increased resistance to azoles; YMR102C is not an essential gene	Q
581	VN_0581	YDR251W	PAM1	Essential protein of unknown function; exhibits variable expression during colony morphogenesis; overexpression permits survival without protein phosphatase 2A, inhibits growth, and induces a filamentous phenotype	Q

582	VN_0582	YNL216W	RAP1	DNA-binding protein involved in either activation or repression of transcription, depending on binding site context; also binds telomere sequences and plays a role in telomeric position effect (silencing) and telomere structure	Q
583	VN_0583	YPL153C	RAD53	Protein kinase, required for cell-cycle arrest in response to DNA damage; activated by trans autophosphorylation when interacting with hyperphosphorylated Rad9p; also interacts with ARS1 and plays a role in initiation of DNA replication	Q
584	VN_0584	YLR222C	UTP13	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA	Q
585	VN_0585	YDR258C	HSP78	Oligomeric mitochondrial matrix chaperone that cooperates with Ssc1p in mitochondrial thermotolerance after heat shock; able to prevent the aggregation of misfolded proteins as well as resolubilize protein aggregates	Q
586	VN_0586	YML035C	AMD1	AMP deaminase, tetrameric enzyme that catalyzes the deamination of AMP to form IMP and ammonia; may be involved in regulation of intracellular adenine nucleotide pools	Q
587	VN_0587	YJL141C	YAK1	Serine-threonine protein kinase that is part of a glucose-sensing system involved in growth control in response to glucose availability; translocates from the cytoplasm to the nucleus and phosphorylates Pop2p in response to a glucose signal	Q
588	VN_0588	YGL139W	FLC3	Putative FAD transporter, similar to Flc1p and Flc2p; localized to the ER	Q
589	VN_0589	YPL045W	VPS16	Subunit of the vacuole fusion and protein sorting HOPS complex and the CORVET tethering complex; part of the Class C Vps complex essential for membrane docking and fusion at Golgi-to-endosome and endosome-to-vacuole protein transport stages	Q
590	VN_0590	YCL054W	SPB1	AdoMet-dependent methyltransferase involved in rRNA processing and 60S ribosomal subunit maturation; methylates G2922 in the tRNA docking site of the large subunit rRNA and in the absence of snR52, U2921; suppressor of PAB1 mutants	Q
591	VN_0591	YML029W	USA1	Protein involved in ER-associated protein degradation (ERAD); component of the Hrd1p complex; interacts with the U1 snRNP-specific protein, Snp1p	Q
592	VN_0592	YDL056W	MBP1	Transcription factor involved in regulation of cell cycle progression from G1 to S phase, forms a complex with Swi6p that binds to MluI cell cycle box regulatory element in promoters of DNA synthesis genes	Strain failed to verify via PCR
593	VN_0593	YJL102W	MEF2	Mitochondrial elongation factor involved in translational elongation	Q
594	VN_0594	YLR337C	VRP1	Proline-rich actin-associated protein involved in cytoskeletal organization and cytokinesis; related to mammalian Wiskott-Aldrich syndrome protein (WASP)-interacting protein (WIP)	Q
595	VN_0595	YJR126C	VPS70	Protein of unknown function involved in vacuolar protein sorting	Q
596	VN_0596	YOR162C	YRR1	Zn2-Cys6 zinc-finger transcription factor that activates genes involved in multidrug resistance; paralog of Yrm1p, acting on an overlapping set of target genes	Q
597	VN_0597	YLR352W	YLR352W	Putative protein of unknown function with similarity to F-box proteins; interacts with Skp1p and Cdc53p; YLR352W is not an essential gene	Q
598	VN_0598	YGL234W	ADE5,7	Bifunctional enzyme of the 'de novo' purine nucleotide biosynthetic pathway, contains aminoimidazole ribotide synthetase and glycinamide ribotide synthetase activities	Q
599	VN_0599	YBR284W	YBR284W	Putative protein of unknown function; YBR284W is not an essential gene; null mutant exhibits decreased resistance to rapamycin and wortmannin and synthetic phenotype with alpha-synuclein	Q
600	VN_0600	YCR077C	PAT1	Topoisomerase II-associated deadenylation-dependent mRNA-decapping factor; also required for faithful chromosome transmission, maintenance of rDNA locus stability, and protection of mRNA 3'-UTRs from trimming; functionally linked to Pab1p	Q
601	VN_0601	YBL113C	YBL113C	Helicase-like protein encoded within the telomeric Y' element	Q

602	VN_0602	YNL183C	NPR1	Protein kinase that stabilizes several plasma membrane amino acid transporters by antagonizing their ubiquitin-mediated degradation	Q
603	VN_0603	YNR033W	ABZ1	Para-aminobenzoate (PABA) synthase, has similarity to Escherichia coli PABA synthase components PabA and PabB	Q
604	VN_0604	YBR001C	NTH2	Putative neutral trehalase, required for thermotolerance and may mediate resistance to other cellular stresses	Q
605	VN_0605	YFR038W	IRC5	Putative ATPase containing the DEAD/H helicase-related sequence motif; null mutant displays increased levels of spontaneous Rad52p foci	Q
606	VN_0606	YJL020C	BBC1	Protein possibly involved in assembly of actin patches; interacts with an actin assembly factor Las17p and with the SH3 domains of Type I myosins Myo3p and Myo5p; localized predominantly to cortical actin patches	Q
607	VN_0607	YOL006C	TOP1	Topoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone; relaxes both positively and negatively supercoiled DNA; functions in replication, transcription, and recombination	Q
608	VN_0608	YOR140W	SFL1	Transcriptional repressor and activator; involved in repression of flocculation-related genes, and activation of stress responsive genes; negatively regulated by cAMP-dependent protein kinase A subunit Tpk2p	Q
609	VN_0609	YOR361C	PRT1	eIF3b subunit of the core complex of translation initiation factor 3 (eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes	Q
610	VN_0610	YDL164C	CDC9	DNA ligase found in the nucleus and mitochondria, an essential enzyme that joins Okazaki fragments during DNA replication; also acts in nucleotide excision repair, base excision repair, and recombination	Q
611	VN_0611	YER169W	RPH1	JmjC domain-containing histone demethylase which can specifically demethylate H3K36 tri- and dimethyl modification states; transcriptional repressor of PHR1; Rph1p phosphorylation during DNA damage is under control of the MEC1-RAD53 pathway	Q
612	VN_0612	YNL186W	UBP10	Ubiquitin-specific protease that deubiquitinates ubiquitin-protein moieties; may regulate silencing by acting on Sir4p; involved in posttranscriptionally regulating Gap1p and possibly other transporters; primarily located in the nucleus	Q
613	VN_0613	YJL200C	ACO2	Putative mitochondrial aconitase isozyme; similarity to Aco1p, an aconitase required for the TCA cycle; expression induced during growth on glucose, by amino acid starvation via Gcn4p, and repressed on ethanol	Q
614	VN_0614	YOR172W	YRM1	Zn2-Cys6 zinc-finger transcription factor that activates genes involved in multidrug resistance; paralog of Yrr1p, acting on an overlapping set of target genes	Q
615	VN_0615	YLR304C	ACO1	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; phosphorylated; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy	Q
616	VN_0616	YKR010C	TOF2	Protein required for rDNA silencing and mitotic rDNA condensation; stimulates Cdc14p phosphatase activity and biphasic release to promote rDNA repeat segregation; required for condensin recruitment to the replication fork barrier site	Q
617	VN_0617	YER091C	MET6	Cobalamin-independent methionine synthase, involved in methionine biosynthesis and regeneration; requires a minimum of two glutamates on the methyltetrahydrofolate substrate, similar to bacterial metE homologs	Q
618	VN_0618	YKR027W	BCH2	Member of the ChAPs family of proteins (Chs5p-Arf1p-binding proteins: Bch1p, Bch2p, Bud7p, Chs6p), that forms the exomer complex with Chs5p to mediate export of specific cargo proteins, including Chs3p, from the Golgi to the plasma membrane	Q
619	VN_0619	YLR069C	MEF1	Mitochondrial elongation factor involved in translational elongation	Q
620	VN_0620	YJL206C	YJL206C	Putative protein of unknown function; similar to transcriptional regulators from the Zn[2]-Cys[6] binuclear cluster protein family;	Q

				mRNA is weakly cell cycle regulated, peaking in S phase; induced rapidly upon MMS treatment	
621	VN_0621	YFL023W	BUD27	Protein involved in bud-site selection, nutrient signaling, and gene expression controlled by TOR kinase; diploid mutants show a random budding pattern rather than the wild-type bipolar pattern; plays a role in regulating Ty1 transposition	Q
622	VN_0622	YOR144C	ELG1	Protein required for S phase progression and telomere homeostasis, forms an alternative replication factor C complex important for DNA replication and genome integrity; involved in homologous recombination-mediated DNA repair	Q
623	VN_0623	YOR035C	SHE4	Protein containing a UCS (UNC-45/CRO1/SHE4) domain, binds to myosin motor domains to regulate myosin function; involved in endocytosis, polarization of the actin cytoskeleton, and asymmetric mRNA localization	Q
624	VN_0624	YDR208W	MSS4	Phosphatidylinositol-4-phosphate 5-kinase, involved in actin cytoskeleton organization and cell morphogenesis; multicopy suppressor of stt4 mutation	Q
625	VN_0625	YDR324C	UTP4	Subunit of U3-containing 90S preribosome and Small Subunit (SSU) processome complexes involved in production of 18S rRNA and assembly of small ribosomal subunit; member of t-Utp subcomplex involved with transcription of 35S rRNA transcript	Q
626	VN_0626	YJL033W	HCA4	Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 18S rRNA synthesis	Strain failed to verify via PCR
627	VN_0627	YGL120C	PRP43	RNA helicase in the DEAH-box family, functions in both RNA polymerase I and polymerase II transcript metabolism, involved in release of the lariat-intron from the spliceosome	Strain failed to verify via PCR
628	VN_0628	YOL036W	YOL036W	Protein of unknown function; potential Cdc28p substrate	Q
629	VN_0629	YKL034W	TUL1	Golgi-localized RING-finger ubiquitin ligase (E3), involved in ubiquitinating and sorting membrane proteins that contain polar transmembrane domains to multivesicular bodies for delivery to the vacuole for quality control purposes	Q
630	VN_0630	YER098W	UBP9	Ubiquitin carboxyl-terminal hydrolase, ubiquitin-specific protease that cleaves ubiquitin-protein fusions	Q
631	VN_0631	YHR204W	MNL1	Alpha mannosidase-like protein of the endoplasmic reticulum required for degradation of glycoproteins but not for processing of N-linked oligosaccharides	Q
632	VN_0632	YOR353C	SOG2	Key component of the RAM signaling network, required for proper cell morphogenesis and cell separation after mitosis	Q
633	VN_0633	YDL060W	TSR1	Protein required for processing of 20S pre-rRNA in the cytoplasm, associates with pre-40S ribosomal particles	Q
634	VN_0634	YGR237C	YGR237C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
635	VN_0635	YFL009W	CDC4	F-box protein required for G1/S and G2/M transition, associates with Skp1p and Cdc53p to form a complex, SCFCdc4, which acts as ubiquitin-protein ligase directing ubiquitination of the phosphorylated CDK inhibitor Sic1p	Q
636	VN_0636	YOR165W	SEY1	GTPase with a role in ER morphology; interacts physically and genetically with Yop1p and Rtn1p; possible functional ortholog of mammalian atlastins, defects in which cause a form of hereditary spastic paraplegia; homolog of Arabidopsis RHD3	Q
637	VN_0637	YKL134C	40452	Mitochondrial intermediate peptidase, cleaves N-terminal residues of a subset of proteins upon import, after their cleavage by mitochondrial processing peptidase (Mas1p-Mas2p); may contribute to mitochondrial iron homeostasis	Q
638	VN_0638	YGR245C	SDA1	Highly conserved nuclear protein required for actin cytoskeleton organization and passage through Start, plays a critical role in G1 events, binds Nap1p, also involved in 60S ribosome biogenesis	Strain failed to verify via PCR
639	VN_0639	YIR007W	YIR007W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YIR007W is a non-essential gene	Q
640	VN_0640	YOR112W	CEX1	Cytoplasmic component of the nuclear aminoacylation-dependent	Q

				tRNA export pathway; interacts with nuclear pore component Nup116p; copurifies with tRNA export receptors Los1p and Msn5p, as well as eIF-1a and the RAN GTPase Gsp1p	
641	VN_0641	YMR164C	MSS11	Transcription factor involved in regulation of invasive growth and starch degradation; controls the activation of MUC1 and STA2 in response to nutritional signals	Q
642	VN_0642	YER162C	RAD4	Protein that recognizes and binds damaged DNA (with Rad23p) during nucleotide excision repair; subunit of Nuclear Excision Repair Factor 2 (NEF2); homolog of human XPC protein	Q
643	VN_0643	YOL076W	MDM20	Non-catalytic subunit of the NatB N-terminal acetyltransferase, which catalyzes N-acetylation of proteins with specific N-terminal sequences; involved in mitochondrial inheritance and actin assembly	Q
644	VN_0644	YBR114W	RAD16	Protein that recognizes and binds damaged DNA in an ATP-dependent manner (with Rad7p) during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 4 (NEF4) and the Elongin-Cullin-Socs (ECS) ligase complex	Q
645	VN_0645	YGR200C	ELP2	Subunit of Elongator complex, which is required for modification of wobble nucleosides in tRNA; target of Kluyveromyces lactis zymocin	Q
646	VN_0646	YHR182W	YHR182W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery and cytoplasm	Q
647	VN_0647	YGL009C	LEU1	Isopropylmalate isomerase, catalyzes the second step in the leucine biosynthesis pathway	Q
648	VN_0648	YLR274W	MCM5	Component of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent helicase that promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase	Q
649	VN_0649	YLR131C	ACE2	Transcription factor that activates expression of early G1-specific genes, localizes to daughter cell nuclei after cytokinesis and delays G1 progression in daughters, localization is regulated by phosphorylation; potential Cdc28p substrate	Q
650	VN_0650	YNL224C	SQS1	Stimulates the ATPase and helicase activities of Prp43p; acts with Prp43p to stimulate 18s rRNA maturation by Nob1p; overexpression antagonizes the suppression of splicing defects by spp382 mutants; component of pre-ribosomal particles	Q
651	VN_0651	YJL090C	DPB11	Replication initiation protein that loads DNA pol epsilon onto pre-replication complexes at origins; checkpoint sensor recruited to stalled replication forks by the checkpoint clamp complex where it activates Mec1p; ortholog of human TopBP1	Q
652	VN_0652	YAL031C	GIP4	Cytoplasmic Glc7-interacting protein whose overexpression relocates Glc7p from the nucleus and prevents chromosome segregation; potential Cdc28p substrate	Q
653	VN_0653	YMR179W	SPT21	Protein required for normal transcription at several loci including HTA2-HTB2 and HHF2-HHT2, but not required at the other histone loci; functionally related to Spt10p; involved in telomere maintenance	Q
654	VN_0654	YNL258C	DSL1	Peripheral membrane protein needed for Golgi-to-ER retrograde traffic; forms a complex with Sec39p and Tip20p that interacts with ER SNAREs Sec20p and Use1p; component of the ER target site that interacts with coatomer; interacts with Cin5p	Q
655	VN_0655	YER184C	YER184C	Putative zinc cluster protein; deletion confers sensitivity to Calcufluor white, and prevents growth on glycerol or lactate as sole carbon source	Q
656	VN_0656	YBR172C	SMY2	Protein of unknown function involved in COPII vesicle formation; interacts with the Sec23p/Sec24p subcomplex; overexpression suppresses the temperature sensitivity of a myo2 mutant; has similarity to S. pombe Mpd2	Q
657	VN_0657	YLR319C	BUD6	Actin- and formin-interacting protein, involved in actin cable nucleation and polarized cell growth; isolated as bipolar budding mutant; potential Cdc28p substrate	Q
658	VN_0658	YMR016C	SOK2	Nuclear protein that plays a regulatory role in the cyclic AMP (cAMP)-dependent protein kinase (PKA) signal transduction pathway; negatively regulates pseudohyphal differentiation; homologous to several transcription factors	Q
659	VN_0659	YLR144C	ACF2	Intracellular beta-1,3-endoglucanase, expression is induced during sporulation; may have a role in cortical actin cytoskeleton assembly	Q

660	VN_0660	YML006C	GIS4	CAAX box containing protein of unknown function, proposed to be involved in the RAS/cAMP signaling pathway	Q
661	VN_0661	YPR091C	YPR091C	Putative protein of unknown function; may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YPR091C is not an essential gene	Q
662	VN_0662	YLR114C	AVL9	Conserved protein involved in exocytic transport from the Golgi; mutation is synthetically lethal with <i>apl2 vps1</i> double mutation; member of a protein superfamily with orthologs in diverse organisms	Q
663	VN_0663	YER041W	YEN1	Holliday junction resolvase; localization is cell-cycle dependent and regulated by Cdc28p phosphorylation; homolog of human GEN1 and has similarity to <i>S. cerevisiae</i> endonuclease Rth1p	Q
664	VN_0664	YPL158C	AIM44	Protein of unknown function; GFP-fusion protein localizes to the bud neck; transcription is regulated by Swi5p; null mutant displays elevated frequency of mitochondrial genome loss	Q
665	VN_0665	YPL074W	YTA6	Putative ATPase of the CDC48/PAS1/SEC18 (AAA) family, localized to the cortex of mother cells but not to daughter cells	Q
666	VN_0666	YGR067C	YGR067C	Putative protein of unknown function; contains a zinc finger motif similar to that of Adr1p	Q
667	VN_0667	YDL239C	ADY3	Protein required for spore wall formation, thought to mediate assembly of a Don1p-containing structure at the leading edge of the prospore membrane via interaction with spindle pole body components; potentially phosphorylated by Cdc28p	Strain failed to verify via PCR
668	VN_0668	YDR239C	YDR239C	Protein of unknown function that may interact with ribosomes, based on co-purification experiments	Q
669	VN_0669	YPL176C	TRE1	Plasma membrane protein that binds to Bsd2p and regulates ubiquitylation and vacuolar degradation of the metal transporter Smf1p; function is redundant with that of Tre2p; has similarity to transferrin receptors	Q
670	VN_0670	YBR142W	MAK5	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits	Q
671	VN_0671	YLL054C	YLL054C	Putative protein of unknown function with similarity to Pip2p, an oleate-specific transcriptional activator of peroxisome proliferation; YLL054C is not an essential gene	Q
672	VN_0672	YDR490C	PKH1	Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway that controls endocytosis; activates Ypk1p and Ykr2p, components of signaling cascade required for maintenance of cell wall integrity; redundant with Pkh2p	Q
673	VN_0673	YHR197W	RIX1	Essential component of the Rix1 complex (Rix1p, Ipi1p, Ipi3p) that is required for processing of ITS2 sequences from 35S pre-rRNA; Rix1 complex associates with Mdn1p in pre-60S ribosomal particles	Q
674	VN_0674	YOR267C	HRK1	Protein kinase implicated in activation of the plasma membrane H(+)-ATPase Pma1p in response to glucose metabolism; plays a role in ion homeostasis	Q
675	VN_0675	YOR014W	RTS1	B-type regulatory subunit of protein phosphatase 2A (PP2A); homolog of the mammalian B' subunit of PP2A	Q
676	VN_0676	YBR094W	PBY1	Putative tubulin tyrosine ligase associated with P-bodies	Q
677	VN_0677	YOR178C	GAC1	Regulatory subunit for Glc7p type-1 protein phosphatase (PP1), tethers Glc7p to Gsy2p glycogen synthase, binds Hsf1p heat shock transcription factor, required for induction of some HSF-regulated genes under heat shock	Q
678	VN_0678	YDR034C	LYS14	Transcriptional activator involved in regulation of genes of the lysine biosynthesis pathway; requires 2-aminoadipate semialdehyde as co-inducer	Q
679	VN_0679	YFR013W	IOC3	Member of a complex (Isw1a) with Isw1p that has nucleosome-stimulated ATPase activity and represses transcription initiation by specific positioning of a promoter proximal dinucleosome; has homology to Esc8p, which is involved in silencing	Q
680	VN_0680	YGR250C	YGR250C	Putative RNA binding protein; localizes to stress granules induced by glucose deprivation; interacts with Rbg1p in a two-hybrid	Q

681	VN_0681	YDR520C	URC2	Putative Zn(II)2Cys6 motif containing transcription factor; non-essential gene identified in a screen for mutants with increased levels of rDNA transcription; similar to <i>S. kluyveri</i> Urc2p involved in uracil catabolism	Q
682	VN_0682	YMR167W	MLH1	Protein required for mismatch repair in mitosis and meiosis as well as crossing over during meiosis; forms a complex with Pms1p and Msh2p-Msh3p during mismatch repair; human homolog is associated with hereditary non-polyposis colon cancer	Q
683	VN_0683	YKL072W	STB6	Protein that binds Sin3p in a two-hybrid assay	Q
684	VN_0684	YNL311C	YNL311C	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; putative F-box protein; analysis of integrated high-throughput datasets predicts involvement in ubiquitin-dependent protein catabolism	Q
685	VN_0685	YNL161W	CBK1	Serine/threonine protein kinase that regulates cell morphogenesis pathways; involved in cell wall biosynthesis, apical growth, proper mating projection morphology, bipolar bud site selection in diploid cells, and cell separation	Q
686	VN_0686	YBR102C	EXO84	Essential protein with dual roles in spliceosome assembly and exocytosis; the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, and Exo84p) mediates polarized targeting of secretory vesicles to active sites of exocytosis	Q
687	VN_0687	YDR138W	HPR1	Subunit of THO/TREX complexes that couple transcription elongation with mitotic recombination and with mRNA metabolism and export, subunit of an RNA Pol II complex; regulates lifespan; involved in telomere maintenance; similar to Top1p	Q
688	VN_0688	YOR208W	PTP2	Phosphotyrosine-specific protein phosphatase involved in the inactivation of mitogen-activated protein kinase (MAPK) during osmolarity sensing; dephosphorylates Hog1p MAPK and regulates its localization; localized to the nucleus	Q
689	VN_0689	YDR499W	LCD1	Essential protein required for the DNA integrity checkpoint pathways; interacts physically with Mec1p; putative homolog of <i>S. pombe</i> Rad26 and human ATRIP	Q
690	VN_0690	YGR003W	CUL3	Ubiquitin-protein ligase, member of the cullin family with similarity to Cdc53p and human CUL3; required for ubiquitin-dependent degradation of the RNA Polymerase II subunit RPO21	Q
691	VN_0691	YLL019C	KNS1	Nonessential putative protein kinase of unknown cellular role; member of the LAMMER family of protein kinases, which are serine/threonine kinases also capable of phosphorylating tyrosine residues	Q
692	VN_0692	YKL168C	KKQ8	Putative serine/threonine protein kinase with unknown cellular role	Q
693	VN_0693	YJL082W	IML2	Protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
694	VN_0694	YLR219W	MSC3	Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; msc3 mutants are defective in directing meiotic recombination events to homologous chromatids; potential Cdc28p substrate	Q
695	VN_0695	YMR237W	BCH1	Member of the ChAPs family (Chs5p-Arf1p-binding proteins: Bch1p, Bch2p, Bud7p, Chs6p), that forms the exomer complex with Chs5p to mediate export of specific cargo proteins from the Golgi to the plasma membrane; may interact with ribosomes	Q
696	VN_0696	YDL167C	NRP1	Putative RNA binding protein of unknown function; localizes to stress granules induced by glucose deprivation; predicted to be involved in ribosome biogenesis	Q
697	VN_0697	YPL164C	MLH3	Protein involved in DNA mismatch repair and crossing-over during meiotic recombination; forms a complex with Mlh1p; mammalian homolog is implicated mammalian microsatellite instability	Q
698	VN_0698	YCL057W	PRD1	Zinc metalloendopeptidase, found in the cytoplasm and intermembrane space of mitochondria; with Cym1p, involved in degradation of mitochondrial proteins and of presequence peptides cleaved from imported proteins	Q
699	VN_0699	YFR009W	GCN20	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA	Q

700	VN_0700	YGL086W	MAD1	Coiled-coil protein involved in the spindle-assembly checkpoint; phosphorylated by Mps1p upon checkpoint activation which leads to inhibition of the activity of the anaphase promoting complex; forms a complex with Mad2p	Q
701	VN_0701	YOR076C	SKI7	Coupling protein that mediates interactions between the Ski complex and the cytoplasmic exosome during 3'-5' RNA degradation; eRF3-like domain targets nonstop mRNA for degradation; null mutants have superkiller phenotype	Q
702	VN_0702	YHR178W	STB5	Transcription factor, involved in regulating multidrug resistance and oxidative stress response; forms a heterodimer with Pdr1p; contains a Zn(II)2Cys6 zinc finger domain that interacts with a pleiotropic drug resistance element in vitro	Q
703	VN_0703	YPL029W	SUV3	ATP-dependent RNA helicase, component of the mitochondrial degradosome along with the RNase Dss1p; the degradosome associates with the ribosome and mediates turnover of aberrant or unprocessed RNAs	Q
704	VN_0704	YEL053C	MAK10	Non-catalytic subunit of N-terminal acetyltransferase of the NatC type, required for replication of dsRNA virus; expression is glucose-repressible	Q
705	VN_0705	YKL112W	ABF1	DNA binding protein with possible chromatin-reorganizing activity involved in transcriptional activation, gene silencing, and DNA replication and repair	Q
706	VN_0706	YMR154C	RIM13	Calpain-like cysteine protease involved in proteolytic activation of Rim101p in response to alkaline pH; has similarity to <i>A. nidulans</i> palB	Q
707	VN_0707	YDR333C	YDR333C	Putative protein of unknown function	Q
708	VN_0708	YMR172W	HOT1	Transcription factor required for the transient induction of glycerol biosynthetic genes GPD1 and GPP2 in response to high osmolarity; targets Hog1p to osmostress responsive promoters; has similarity to Msn1p and Gcr1p	Q
709	VN_0709	YFL047W	RGD2	GTPase-activating protein (RhoGAP) for Cdc42p and Rho5p	Q
710	VN_0710	YDR211W	GCD6	Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression	Q
711	VN_0711	YLL008W	DRS1	Nucleolar DEAD-box protein required for ribosome assembly and function, including synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles	Strain failed to verify via PCR
712	VN_0712	YLL029W	FRA1	Protein involved in negative regulation of transcription of iron regulon; forms an iron independent complex with Fra2p, Grx3p, and Grx4p; cytosolic; mutant fails to repress transcription of iron regulon and is defective in spore formation	Q
713	VN_0713	YKR024C	DBP7	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; essential for growth under anaerobic conditions	Q
714	VN_0714	YBR007C	DSF2	Deletion suppressor of mpt5 mutation	Q
715	VN_0715	YFR022W	ROG3	Protein that binds the ubiquitin ligase Rsp5p via its 2 PY motifs; has similarity to Rod1p; mutation suppresses the temperature sensitivity of an mck1 rim11 double mutant; proposed to regulate the endocytosis of plasma membrane proteins	Q
716	VN_0716	YER040W	GLN3	Transcriptional activator of genes regulated by nitrogen catabolite repression (NCR), localization and activity regulated by quality of nitrogen source	Q
717	VN_0717	YKL135C	APL2	Beta-adaptin, large subunit of the clathrin-associated protein (AP-1) complex; binds clathrin; involved in clathrin-dependent Golgi protein sorting	Q
718	VN_0718	YHR031C	RRM3	DNA helicase involved in rDNA replication and Ty1 transposition; relieves replication fork pauses at telomeric regions; structurally and functionally related to Pif1p	Strain failed to verify via PCR
719	VN_0719	YKL104C	GFA1	Glutamine-fructose-6-phosphate amidotransferase, catalyzes the formation of glucosamine-6-P and glutamate from fructose-6-P and glutamine in the first step of chitin biosynthesis	Q

720	VN_0720	YHR074W	QNS1	Glutamine-dependent NAD(+) synthetase, essential for the formation of NAD(+) from nicotinic acid adenine dinucleotide	Q
721	VN_0721	YLR006C	SSK1	Cytoplasmic response regulator, part of a two-component signal transducer that mediates osmosensing via a phosphorelay mechanism; dephosphorylated form is degraded by the ubiquitin-proteasome system; potential Cdc28p substrate	Q
722	VN_0722	YDR001C	NTH1	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; may be phosphorylated by Cdc28p	Q
723	VN_0723	YOR034C	AKR2	Ankyrin repeat-containing protein similar to Akrlp; member of a family of putative palmitoyltransferases containing an Asp-His-His-Cys-cysteine rich (DHHC-CRD) domain; possibly involved in constitutive endocytosis of Ste3p	Q
724	VN_0724	YJL099W	CHS6	Member of the ChAPs family of proteins (Chs5p-Arf1p-binding proteins: Bch1p, Bch2p, Bud7p, Chs6p), that forms the exomer complex with Chs5p to mediate export of specific cargo proteins, including Chs3p, from the Golgi to the plasma membrane	Q
725	VN_0725	YMR216C	SKY1	SR protein kinase (SRPK) involved in regulating proteins involved in mRNA metabolism and cation homeostasis; similar to human SRPK1	Q
726	VN_0726	YPR090W	YPR090W	#N/A	Q
727	VN_0727	YJL168C	SET2	Histone methyltransferase with a role in transcriptional elongation, methylates a lysine residue of histone H3; associates with the C-terminal domain of Rpo21p; histone methylation activity is regulated by phosphorylation status of Rpo21p	Q
728	VN_0728	YLR149C	YLR149C	Putative protein of unknown function; overexpression causes a cell cycle delay or arrest; null mutation results in a decrease in plasma membrane electron transport; YLR149C is not an essential gene	Q
729	VN_0729	YOR156C	NFI1	SUMO ligase, catalyzes the covalent attachment of SUMO (Smt3p) to proteins; involved in maintenance of proper telomere length	Q
730	VN_0730	YGR178C	PBP1	Component of glucose deprivation induced stress granules, involved in P-body-dependent granule assembly; similar to human ataxin-2; interacts with Pab1p to regulate mRNA polyadenylation; interacts with Mkt1p to regulate HO translation	Q
731	VN_0731	YKR098C	UBP11	Ubiquitin-specific protease that cleaves ubiquitin from ubiquitinated proteins	Q
732	VN_0732	YOL017W	ESC8	Protein involved in telomeric and mating-type locus silencing, interacts with Sir2p and also interacts with the Gal11p, which is a component of the RNA pol II mediator complex	Q
733	VN_0733	YOL057W	YOL057W	Dipeptidyl-peptidase III; cleaves dipeptides from the amino terminus of target proteins; highly active on synthetic substrate Arg-Arg-2-naphthylamide; mammalian ortholog may be a biomarker for some cancers	Q
734	VN_0734	YGR264C	MES1	Methionyl-tRNA synthetase, forms a complex with glutamyl-tRNA synthetase (Gus1p) and Arc1p, which increases the catalytic efficiency of both tRNA synthetases; also has a role in nuclear export of tRNAs	Q
735	VN_0735	YOR081C	TGL5	Triacylglycerol lipase involved in TAG mobilization; localizes to lipid particles; potential Cdc28p substrate	Q
736	VN_0736	YMR078C	CTF18	Subunit of a complex with Ctf8p that shares some subunits with Replication Factor C and is required for sister chromatid cohesion; may have overlapping functions with Rad24p in the DNA damage replication checkpoint	Q
737	VN_0737	YLR381W	CTF3	Outer kinetochore protein that forms a complex with Mcm16p and Mcm22p; may bind the kinetochore to spindle microtubules	Q
738	VN_0738	YOR019W	YOR019W	Protein of unknown function that may interact with ribosomes, based on co-purification experiments	Q
739	VN_0739	YKR018C	YKR018C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	Q
740	VN_0740	YIL091C	YIL091C	Nucleolar protein of unknown function; proposed to function as an RNA helicase based on structure prediction and remote homology searches; essential for viability	Q
741	VN_0741	YLR362W	STE11	Signal transducing MEK kinase involved in pheromone response and pseudohyphal/invasive growth pathways where it phosphorylates	Q

				Ste7p, and the high osmolarity response pathway, via phosphorylation of Pbs2p; regulated by Ste20p and Ste50p	
742	VN_0742	YAL054C	ACS1	Acetyl-coA synthetase isoform which, along with Acs2p, is the nuclear source of acetyl-coA for histone acetylation; expressed during growth on nonfermentable carbon sources and under aerobic conditions	Q
743	VN_0743	YDR436W	PPZ2	Serine/threonine protein phosphatase Z, isoform of Ppz1p; involved in regulation of potassium transport, which affects osmotic stability, cell cycle progression, and halotolerance	Q
744	VN_0744	YKR029C	SET3	Defining member of the SET3 histone deacetylase complex which is a meiosis-specific repressor of sporulation genes; necessary for efficient transcription by RNAPII; one of two yeast proteins that contains both SET and PHD domains	Q
745	VN_0745	YGL205W	POX1	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta-oxidation pathway; localized to the peroxisomal matrix	Q
746	VN_0746	YOR299W	BUD7	Member of the ChAPs family of proteins (Chs5p-Arf1p-binding proteins: Bch1p, Bch2p, Bud7p, Chs6p), that forms the exomer complex with Chs5p to mediate export of specific cargo proteins, including Chs3p, from the Golgi to the plasma membrane	Q
747	VN_0747	YNL144C	YNL144C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YNL144C is not an essential gene	Q
748	VN_0748	YKL078W	DHR2	Predominantly nucleolar DEAH-box ATP-dependent RNA helicase, required for 18S rRNA synthesis	Q
749	VN_0749	YOR001W	RRP6	Nuclear exosome exonuclease component; has 3'-5' exonuclease activity; involved in RNA processing, maturation, surveillance, degradation, tethering, and export; has similarity to E. coli RNase D and to human PM-Sc1 100 (EXOSC10)	Q
750	VN_0750	YPR141C	KAR3	Minus-end-directed microtubule motor that functions in mitosis and meiosis, localizes to the spindle pole body and localization is dependent on functional Cik1p, required for nuclear fusion during mating; potential Cdc28p substrate	Q
751	VN_0751	YNR044W	AGA1	Anchorage subunit of a-agglutinin of a-cells, highly O-glycosylated protein with N-terminal secretion signal and C-terminal signal for addition of GPI anchor to cell wall, linked to adhesion subunit Aga2p via two disulfide bonds	Q
752	VN_0752	YCR091W	KIN82	Putative serine/threonine protein kinase implicated in the regulation of phospholipid asymmetry through the activation of phospholipid translocases (flippases) Lem3p-Dnf1p/Dnf2p; similar to Fpk1p	Q
753	VN_0753	YDR109C	YDR109C	Putative kinase	Q
754	VN_0754	YCR084C	TUP1	General repressor of transcription, forms complex with Cyc8p, involved in the establishment of repressive chromatin structure through interactions with histones H3 and H4, appears to enhance expression of some genes	Q
755	VN_0755	YOR206W	NOC2	Protein that forms a nucleolar complex with Mak21p that binds to 90S and 66S pre-ribosomes, as well as a nuclear complex with Noc3p that binds to 66S pre-ribosomes; both complexes mediate intranuclear transport of ribosomal precursors	Q
756	VN_0756	YJL132W	YJL132W	Putative protein of unknown function; localizes to the membrane fraction; possible Zap1p-regulated target gene induced by zinc deficiency; YJL132W is a non-essential gene	Q
757	VN_0757	YLR135W	SLX4	Endonuclease involved in processing DNA during recombination and repair; cleaves branched structures in a complex with Slx1p; involved in Rad1p/Rad10p-dependent removal of 3'-nonhomologous tails during DSB repair via single-strand annealing	Q
758	VN_0758	YCL039W	GID7	Protein of unknown function, involved in proteasome-dependent catabolite inactivation of fructose-1,6-bisphosphatase; contains six WD40 repeats; computational analysis suggests that Gid7p and Moh1p have similar functions	Q
759	VN_0759	YKL054C	DEF1	RNAPII degradation factor, forms a complex with Rad26p in chromatin, enables ubiquitination and proteolysis of RNAPII present in an elongation complex; mutant is deficient in Zip1p loading onto chromosomes during meiosis	Q

760	VN_0760	YHR149C	SKG6	Integral membrane protein that localizes primarily to growing sites such as the bud tip or the cell periphery; potential Cdc28p substrate; Skg6p interacts with Zds1p and Zds2p	Q
761	VN_0761	YMR277W	FCP1	Carboxy-terminal domain (CTD) phosphatase, essential for dephosphorylation of the repeated C-terminal domain of the RNA polymerase II large subunit (Rpo21p)	Q
762	VN_0762	YBL097W	BRN1	Subunit of the condensin complex; required for chromosome condensation and for clustering of tRNA genes at the nucleolus; may influence multiple aspects of chromosome transmission	Q
763	VN_0763	YDR164C	SEC1	Sm-like protein involved in docking and fusion of exocytic vesicles through binding to assembled SNARE complexes at the membrane; localization to sites of secretion (bud neck and bud tip) is dependent on SNARE function	Q
764	VN_0764	YLR335W	NUP2	Nucleoporin involved in nucleocytoplasmic transport, binds to either the nucleoplasmic or cytoplasmic faces of the nuclear pore complex depending on Ran-GTP levels; also has a role in chromatin organization	Q
765	VN_0765	YKL213C	DOA1	WD repeat protein required for ubiquitin-mediated protein degradation, forms complex with Cdc48p, plays a role in controlling cellular ubiquitin concentration; also promotes efficient NHEJ in postdiauxic/stationary phase	Q
766	VN_0766	YGR128C	UTP8	Nucleolar protein required for export of tRNAs from the nucleus; also copurifies with the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA	Q
767	VN_0767	YDR146C	SWI5	Transcription factor that activates transcription of genes expressed at the M/G1 phase boundary and in G1 phase; localization to the nucleus occurs during G1 and appears to be regulated by phosphorylation by Cdc28p kinase	Q
768	VN_0768	YKL187C	YKL187C	Putative protein of unknown function; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies	Q
769	VN_0769	YPR031W	NTO1	Subunit of the NuA3 histone acetyltransferase complex that acetylates histone H3; contains PHD finger domain that interacts with methylated histone H3	Q
770	VN_0770	YJR030C	YJR030C	Putative protein of unknown function; expression repressed in carbon limited vs carbon replete chemostat cultures; YJR030C is a non-essential gene	Q
771	VN_0771	YPR185W	ATG13	Regulatory subunit of the Atg1p signaling complex; stimulates Atg1p kinase activity; required for vesicle formation during autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; involved in Atg9p, Atg23p, and Atg27p cycling	Q
772	VN_0772	YIL078W	THS1	Threonyl-tRNA synthetase, essential cytoplasmic protein	Q
773	VN_0773	YBR238C	YBR238C	Mitochondrial membrane protein with similarity to Rmd9p; not required for respiratory growth but causes a synthetic respiratory defect in combination with rmd9 mutations; transcriptionally up-regulated by TOR; deletion increases life span	Q
774	VN_0774	YJR119C	JHD2	JmjC domain family histone demethylase specific for H3-K4 (histone H3 Lys4); removes methyl groups specifically added by Set1p methyltransferase; protein levels regulated by Not4p (E3 ubiquitin ligase) polyubiquitin-mediated degradation	Q
775	VN_0775	YGL245W	GUS1	Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Met1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm	Q
776	VN_0776	YMR192W	GYL1	Putative GTPase activating protein (GAP) that may have a role in polarized exocytosis; stimulates Gyp5p GAP activity on Ypt1p, colocalizes with Gyp5p at sites of polarized growth; interacts with Gyp5p, Rvs161p, and Rvs167p	Q
777	VN_0777	YOR022C	YOR022C	Protein with similarity to bovine phospholipase A1; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
778	VN_0778	YHL024W	RIM4	Putative RNA-binding protein required for the expression of early and middle sporulation genes	Q

779	VN_0779	YHL032C	GUT1	Glycerol kinase, converts glycerol to glycerol-3-phosphate; glucose repression of expression is mediated by Adr1p and Ino2p-Ino4p; derepression of expression on non-fermentable carbon sources is mediated by Opi1p and Rsf1p	Q
780	VN_0780	YLR440C	SEC39	Component of the Dsl1p tethering complex that interacts with ER SNAREs Sec20p and Use1p; proposed to be involved in protein secretion; localizes to the ER and nuclear envelope	Q
781	VN_0781	YKR090W	PXL1	LIM domain-containing protein that localizes to sites of polarized growth, required for selection and/or maintenance of polarized growth sites, may modulate signaling by the GTPases Cdc42p and Rho1p; has similarity to metazoan paxillin	Q
782	VN_0782	YMR163C	INP2	Peroxisome-specific receptor important for peroxisome inheritance; co-fractionates with peroxisome membranes and co-localizes with peroxisomes in vivo; physically interacts with the myosin V motor Myo2p; INP2 is not an essential gene	Q
783	VN_0783	YAR014C	BUD14	Protein involved in bud-site selection, Bud14p-Glc7p complex is a cortical regulator of dynein; inhibitor of the actin assembly factor Bnr1p (formin); diploid mutants display a random budding pattern instead of the wild-type bipolar pattern	Q
784	VN_0784	YOR317W	FAA1	Long chain fatty acyl-CoA synthetase with a preference for C12:0-C16:0 fatty acids; involved in the activation of imported fatty acids; localized to both lipid particles and mitochondrial outer membrane; essential for stationary phase	Q
785	VN_0785	YIL108W	YIL108W	Putative metalloprotease	Q
786	VN_0786	YDR234W	LYS4	Homoaconitase, catalyzes the conversion of homocitrate to homoisocitrate, which is a step in the lysine biosynthesis pathway	Q
787	VN_0787	YPR175W	DPB2	Second largest subunit of DNA polymerase II (DNA polymerase epsilon), required for normal yeast chromosomal replication; expression peaks at the G1/S phase boundary; potential Cdc28p substrate	Q
788	VN_0788	YGR099W	TEL2	Essential DNA-binding protein specific to single-stranded yeast telomeric DNA repeats, required for telomere length regulation and telomere position effect	Q
789	VN_0789	YLR117C	CLF1	Member of the NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 snRNAs; homolog of Drosophila crooked neck protein; interacts with U1 snRNP proteins	Q
790	VN_0790	YLR143W	YLR143W	Putative protein of unknown function; green fluorescent protein (GFP)-tagged protein localizes to the cytoplasm; YLR143W is not an essential gene	Q
791	VN_0791	YEL023C	YEL023C	Putative protein of unknown function; expression is increased greatly during sporulation; YEL023C is not an essential gene	Q
792	VN_0792	YPL240C	HSP82	Hsp90 chaperone required for pheromone signaling and negative regulation of Hsf1p; docks with Tom70p for mitochondrial preprotein delivery; promotes telomerase DNA binding and nucleotide addition; interacts with Cns1p, Cpr6p, Cpr7p, Sti1p	Q
793	VN_0793	YMR006C	PLB2	Phospholipase B (lysophospholipase) involved in phospholipid metabolism; displays transacylase activity in vitro; overproduction confers resistance to lysophosphatidylcholine	Q
794	VN_0794	YMR186W	HSC82	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10-fold higher basal levels than HSP82 and induced 2-3 fold by heat shock	Q
795	VN_0795	YDR176W	NGG1	Transcriptional regulator involved in glucose repression of Gal4p-regulated genes; component of transcriptional adaptor and histone acetyltransferase complexes, the ADA complex, the SAGA complex, and the SLIK complex	Q
796	VN_0796	YBR019C	GAL10	UDP-glucose-4-epimerase, catalyzes the interconversion of UDP-galactose and UDP-D-glucose in galactose metabolism; also catalyzes the conversion of alpha-D-glucose or alpha-D-galactose to their beta-anomers	Q
797	VN_0797	YLR035C	MLH2	Protein involved in the mismatch repair of certain frameshift intermediates and involved in meiotic recombination; forms a complex	Q

				with Mlh1p	
798	VN_0798	YLR072W	YLR072W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; YLR072W is not an essential gene	Q
799	VN_0799	YIL144W	TID3	Component of the evolutionarily conserved kinetochore-associated Ndc80 complex (Ndc80p-Nuf2p-Spc24p-Spc25p); conserved coiled-coil protein involved in chromosome segregation, spindle checkpoint activity, kinetochore assembly and clustering	Q
800	VN_0800	YLR260W	LCB5	Minor sphingoid long-chain base kinase, paralog of Lcb4p responsible for few percent of the total activity, possibly involved in synthesis of long-chain base phosphates, which function as signaling molecules	Q
801	VN_0801	YOR249C	APC5	Subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition	Q
802	VN_0802	YDL176W	YDL176W	Protein of unknown function, predicted by computational methods to be involved in fructose-1,6-bisphosphatase (Fbp1p) degradation; interacts with components of the GID complex; YDL176W is not an essential gene	Q
803	VN_0803	YNL021W	HDA1	Putative catalytic subunit of a class II histone deacetylase complex that also contains Hda2p and Hda3p; Hda1p interacts with the Hda2p-Hda3p subcomplex to form an active tetramer; deletion increases histone H2B, H3 and H4 acetylation	Q
804	VN_0804	YBR131W	CCZ1	Protein involved in vacuolar assembly, essential for autophagy and the cytoplasm-to-vacuole pathway	Q
805	VN_0805	YDL214C	PRR2	Serine/threonine protein kinase that inhibits pheromone induced signalling downstream of MAPK, possibly at the level of the Ste12p transcription factor	Q
806	VN_0806	YOL141W	PPM2	AdoMet-dependent tRNA methyltransferase also involved in methoxycarbonylation; required for the synthesis of wybutosine (yW), a modified guanosine found at the 3'-position adjacent to the anticodon of phe-tRNA; similarity to Ppm1p	Q
807	VN_0807	YDL141W	BPL1	Biotin:apoprotein ligase, covalently modifies proteins with the addition of biotin, required for acetyl-CoA carboxylase (Acc1p) holoenzyme formation	Q
808	VN_0808	YHR084W	STE12	Transcription factor that is activated by a MAP kinase signaling cascade, activates genes involved in mating or pseudohyphal/invasive growth pathways; cooperates with Tec1p transcription factor to regulate genes specific for invasive growth	Q
809	VN_0809	YMR108W	ILV2	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control	Q
810	VN_0810	YBR117C	TKL2	Transketolase, similar to Tkl1p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids	Q
811	VN_0811	YFR015C	GSY1	Glycogen synthase with similarity to Gsy2p, the more highly expressed yeast homolog; expression induced by glucose limitation, nitrogen starvation, environmental stress, and entry into stationary phase	Q
812	VN_0812	YPL155C	KIP2	Kinesin-related motor protein involved in mitotic spindle positioning, stabilizes microtubules by targeting Bik1p to the plus end; Kip2p levels are controlled during the cell cycle	Q
813	VN_0813	YDR052C	DBF4	Regulatory subunit of Cdc7p-Dbf4p kinase complex, required for Cdc7p kinase activity and initiation of DNA replication; phosphorylates the Mcm2-7 family of proteins; cell cycle regulated	Q
814	VN_0814	YOR033C	EXO1	5'-3' exonuclease and flap-endonuclease involved in recombination, double-strand break repair and DNA mismatch repair; member of the Rad2p nuclease family, with conserved N and I nuclease domains	Q
815	VN_0815	YLR233C	EST1	TLC1 RNA-associated factor involved in telomere length regulation as the recruitment subunit of the telomerase holoenzyme, has a possible role in activating Est2p-TLC1-RNA bound to the telomere	Q

816	VN_0816	YBR255W	MTC4	Protein of unknown function, required for normal growth rate at 15 degrees C; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; mtc4 is synthetically sick with cdc13-1	Q
817	VN_0817	YDR314C	RAD34	Protein involved in nucleotide excision repair (NER); homologous to RAD4	Q
818	VN_0818	YGL071W	AFT1	Transcription factor involved in iron utilization and homeostasis; binds the consensus site PyPuCACCCPu and activates the expression of target genes in response to changes in iron availability	Q
819	VN_0819	YJR110W	YMR1	Phosphatidylinositol 3-phosphate (PI3P) phosphatase; involved in various protein sorting pathways, including CVT targeting and endosome to vacuole transport; has similarity to the conserved myotubularin dual specificity phosphatase family	Q
820	VN_0820	YIL105C	SLM1	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm2p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; phosphorylated by the TORC2 complex	Q
821	VN_0821	YBL024W	NCL1	S-adenosyl-L-methionine-dependent tRNA: m5C-methyltransferase, methylates cytosine to m5C at several positions in tRNAs and intron-containing pre-tRNAs; similar to Nop2p and human proliferation associated nucleolar protein p120	Q
822	VN_0822	YLR424W	SPP382	Essential protein that forms a dimer with Ntr2p; also forms a trimer, with Ntr2p and Prp43p, that is involved in spliceosome disassembly; found also in a multisubunit complex with the splicing factor Clf1p; suppressor of prp38-1 mutation	Q
823	VN_0823	YBL035C	POL12	B subunit of DNA polymerase alpha-primase complex, required for initiation of DNA replication during mitotic and premeiotic DNA synthesis; also functions in telomere capping and length regulation	Q
824	VN_0824	YEL011W	GLC3	Glycogen branching enzyme, involved in glycogen accumulation; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Strain failed to verify via PCR
825	VN_0825	YGR266W	YGR266W	Protein of unknown function, predicted to contain a single transmembrane domain; localized to both the mitochondrial outer membrane and the plasma membrane	Q
826	VN_0826	YBR156C	SLI15	Subunit of the conserved chromosomal passenger complex (CPC; Ipl1p-Sli15p-Bir1p-Nbl1p), which regulates kinetochore-microtubule attachments, activation of the spindle tension checkpoint, and mitotic spindle disassembly	Q
827	VN_0827	YIL009W	FAA3	Long chain fatty acyl-CoA synthetase, has a preference for C16 and C18 fatty acids; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery	Q
828	VN_0828	YFL013C	IES1	Subunit of the INO80 chromatin remodeling complex	Q
829	VN_0829	YDR332W	IRC3	Putative RNA helicase of the DEAH/D-box family; null mutant displays increased levels of spontaneous Rad52p foci; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion	Q
830	VN_0830	YPL222W	FMP40	Putative protein of unknown function; proposed to be involved in responding to environmental stresses; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
831	VN_0831	YLR047C	FRE8	Protein with sequence similarity to iron/copper reductases, involved in iron homeostasis; deletion mutant has iron deficiency/accumulation growth defects; expression increased in the absence of copper-responsive transcription factor Mac1p	Q
832	VN_0832	YMR075W	RCO1	Essential subunit of the histone deacetylase Rpd3S complex; interacts with Eaf3p	Q
833	VN_0833	YPR007C	REC8	Meiosis-specific component of sister chromatid cohesion complex; maintains cohesion between sister chromatids during meiosis I; maintains cohesion between centromeres of sister chromatids until meiosis II; homolog of S. pombe Rec8p	Strain failed to verify via PCR
834	VN_0834	YGL026C	TRP5	Tryptophan synthase, catalyzes the last step of tryptophan biosynthesis; regulated by the general control system of amino acid biosynthesis	Q

835	VN_0835	YKL222C	YKL222C	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; similar to transcriptional regulators from the zinc cluster (binuclear cluster) family; null mutant is sensitive to caffeine	Q
836	VN_0836	YGL249W	ZIP2	Meiosis-specific protein involved in normal synaptonemal complex formation and pairing between homologous chromosomes during meiosis	Q
837	VN_0837	YLR266C	PDR8	Transcription factor; targets include ATP-binding cassette (ABC) transporters, major facilitator superfamily transporters, and other genes involved in the pleiotropic drug resistance (PDR) phenomenon	Q
838	VN_0838	YDR108W	GSG1	Subunit of TRAPP (transport protein particle), a multi-subunit complex involved in targeting and/or fusion of ER-to-Golgi transport vesicles with their acceptor compartment; protein has late meiotic role, following DNA replication	Q
839	VN_0839	YMR246W	FAA4	Long chain fatty acyl-CoA synthetase, regulates protein modification during growth in the presence of ethanol, functions to incorporate palmitic acid into phospholipids and neutral lipids	Q
840	VN_0840	YML016C	PPZ1	Serine/threonine protein phosphatase Z, isoform of Ppz2p; involved in regulation of potassium transport, which affects osmotic stability, cell cycle progression, and halotolerance	Q
841	VN_0841	YBL067C	UBP13	Putative ubiquitin carboxyl-terminal hydrolase, ubiquitin-specific protease that cleaves ubiquitin-protein fusions	Q
842	VN_0842	YBL060W	YEL1	Guanine nucleotide exchange factor specific for Arf3p; localized to the bud neck and tip; required for localization of Arf3p to the bud neck and tip	Q
843	VN_0843	YLR399C	BDF1	Protein involved in transcription initiation at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p	Q
844	VN_0844	YKL017C	HCS1	Hexameric DNA polymerase alpha-associated DNA helicase A involved in lagging strand DNA synthesis; contains single-stranded DNA stimulated ATPase and dATPase activities; replication protein A stimulates helicase and ATPase activities	Q
845	VN_0845	YPR074C	TKL1	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids	Q
846	VN_0846	YLR258W	GSY2	Glycogen synthase, similar to Gsy1p; expression induced by glucose limitation, nitrogen starvation, heat shock, and stationary phase; activity regulated by cAMP-dependent, Snf1p and Pho85p kinases as well as by the Gac1p-Glc7p phosphatase	Q
847	VN_0847	YMR037C	MSN2	Transcriptional activator related to Msn4p; activated in stress conditions, which results in translocation from the cytoplasm to the nucleus; binds DNA at stress response elements of responsive genes, inducing gene expression	Q
848	VN_0848	YBL111C	YBL111C	Helicase-like protein encoded within the telomeric Y' element	Q
849	VN_0849	YLR452C	SST2	GTPase-activating protein for Gpa1p, regulates desensitization to alpha factor pheromone; also required to prevent receptor-independent signaling of the mating pathway; member of the RGS (regulator of G-protein signaling) family	Q
850	VN_0850	YPR008W	HAA1	Transcriptional activator involved in the transcription of TPO2, YRO2, and other genes putatively encoding membrane stress proteins; involved in adaptation to weak acid stress	Q
851	VN_0851	YMR224C	MRE11	Subunit of a complex with Rad50p and Xrs2p (MRX complex) that functions in repair of DNA double-strand breaks and in telomere stability, exhibits nuclease activity that appears to be required for MRX function; widely conserved	Q
852	VN_0852	YBR259W	YBR259W	Putative protein of unknown function; YBR259W is not an essential gene	Q
853	VN_0853	YDR444W	YDR444W	Putative protein of unknown function	Q
854	VN_0854	YDR172W	SUP35	Translation termination factor eRF3; altered protein conformation creates the [PSI(+)] prion, a dominant cytoplasmically inherited	Q

				protein aggregate that alters translational fidelity and creates a nonsense suppressor phenotype	
855	VN_0855	YLR153C	ACS2	Acetyl-coA synthetase isoform which, along with Acs1p, is the nuclear source of acetyl-coA for histone acetylation; mutants affect global transcription; required for growth on glucose; expressed under anaerobic conditions	Q
856	VN_0856	YDR129C	SAC6	Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the organization and maintenance of the actin cytoskeleton	Q
857	VN_0857	YJR134C	SGM1	Protein of unknown function, required for wild-type growth rate on galactose and mannose; localizes to COPI coated vesicles and the Golgi apparatus	Q
858	VN_0858	YMR001C	CDC5	Polo-like kinase with similarity to Xenopus Plx1 and S. pombe Plo1p; found at bud neck, nucleus and SPBs; has multiple functions in mitosis and cytokinesis through phosphorylation of substrates; may be a Cdc28p substrate	Q
859	VN_0859	YOR365C	YOR365C	Putative protein of unknown function; YOR365C is not an essential protein	Q
860	VN_0860	YDL074C	BRE1	E3 ubiquitin ligase, forms heterodimer with Rad6p to monoubiquitinate histone H2B-K123, which is required for the subsequent methylation of histone H3-K4 and H3-K79; required for DSBR, transcription, silencing, and checkpoint control	Q
861	VN_0861	YPL116W	HOS3	Trichostatin A-insensitive homodimeric histone deacetylase (HDAC) with specificity in vitro for histones H3, H4, H2A, and H2B; similar to Hda1p, Rpd3p, Hos1p, and Hos2p; deletion results in increased histone acetylation at rDNA repeats	Q
862	VN_0862	YBR169C	SSE2	Member of the heat shock protein 70 (HSP70) family; may be involved in protein folding; localized to the cytoplasm; highly homologous to the heat shock protein Sse1p	Q
863	VN_0863	YOR354C	MSC6	Protein of unknown function; mutant is defective in directing meiotic recombination events to homologous chromatids; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
864	VN_0864	YER077C	YER077C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion; null mutation results in a decrease in plasma membrane electron transport	Q
865	VN_0865	YER022W	SRB4	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation	Q
866	VN_0866	YGL144C	ROG1	Protein with putative serine active lipase domain	Q
867	VN_0867	YLR403W	SFP1	Transcription factor that controls expression of ribosome biogenesis genes in response to nutrients and stress, regulates G2/M transitions during mitotic cell cycle and DNA-damage response, modulates cell size; regulated by TORC1 and Mrs6p	Q
868	VN_0868	YGL236C	MTO1	Mitochondrial protein, forms a heterodimer complex with Mss1p that performs the 5-carboxymethylaminomethyl modification of the wobble uridine base in mitochondrial tRNAs; required for respiration in paromomycin-resistant 15S rRNA mutants	Q
869	VN_0869	YHL029C	OCA5	Cytoplasmic protein required for replication of Brome mosaic virus in S. cerevisiae, which is a model system for studying replication of positive-strand RNA viruses in their natural hosts	Q
870	VN_0870	YMR104C	YPK2	Protein kinase with similarity to serine/threonine protein kinase Ypk1p; functionally redundant with YPK1 at the genetic level; participates in a signaling pathway required for optimal cell wall integrity; homolog of mammalian kinase SGK	Q
871	VN_0871	YDR452W	PPN1	Vacuolar endopolyphosphatase with a role in phosphate metabolism; functions as a homodimer	Q
872	VN_0872	YER088C	DOT6	Protein involved in rRNA and ribosome biogenesis; binds polymerase A and C motif; subunit of the RPD3L histone deacetylase complex; similar to Tod6p; has chromatin specific SANT domain; involved in telomeric gene silencing and filamentation	Q
873	VN_0873	YGL113W	SLD3	Protein involved in the initiation of DNA replication, required for proper assembly of replication proteins at the origins of replication;	Q

				interacts with Cdc45p	
874	VN_0874	YLL007C	YLL007C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLL007C is not an essential gene	Q
875	VN_0875	YNR053C	NOG2	Putative GTPase that associates with pre-60S ribosomal subunits in the nucleolus and is required for their nuclear export and maturation	Q
876	VN_0876	YOR275C	RIM20	Protein involved in proteolytic activation of Rim101p in response to alkaline pH; PalA/AIP1/Alix family member; interaction with the ESCRT-III subunit Snf7p suggests a relationship between pH response and multivesicular body formation	Q
877	VN_0877	YPL104W	MSD1	Mitochondrial aspartyl-tRNA synthetase, required for acylation of aspartyl-tRNA; yeast and bacterial aspartyl-, asparaginyl-, and lysyl-tRNA synthetases contain regions with high sequence similarity, suggesting a common ancestral gene	Q
878	VN_0878	YNL047C	SLM2	Phosphoinositide PI4,5P(2) binding protein, forms a complex with Slm1p; acts downstream of Mss4p in a pathway regulating actin cytoskeleton organization in response to stress; phosphorylated by the TORC2 complex	Q
879	VN_0879	YOR147W	MDM32	Mitochondrial inner membrane protein with similarity to Mdm31p, required for normal mitochondrial morphology and inheritance; interacts genetically with MMM1, MDM10, MDM12, and MDM34	Q
880	VN_0880	YBR123C	TFC1	One of six subunits of the RNA polymerase III transcription initiation factor complex (TFIIIC); part of the TauA globular domain of TFIIIC that binds DNA at the BoxA promoter sites of tRNA and similar genes; human homolog is TFIIIC-63	Strain failed to verify via PCR
881	VN_0881	YIR003W	AIM21	Protein of unknown function involved in mitochondrial migration along actin filament; may interact with ribosomes; GFP-fusion protein colocalizes with Sac1p to the actin cytoskeleton	Q
882	VN_0882	YMR232W	FUS2	Cytoplasmic protein localized to the shmoo tip; required for the alignment of parental nuclei before nuclear fusion during mating	Q
883	VN_0883	YOR054C	VHS3	Negative regulatory subunit of protein phosphatase 1 Ppz1p and also a subunit of the phosphopantothienylcysteine decarboxylase (PPCDC; Cab3p, Sis2p, Vhs3p) complex, which catalyzes the third step of coenzyme A biosynthesis	Q
884	VN_0884	YLR427W	MAG2	Cytoplasmic protein of unknown function; induced in response to mycotoxin patulin; ubiquitinated protein similar to the human ring finger motif protein RNF10; predicted to be involved in repair of alkylated DNA due to interaction with MAG1	Q
885	VN_0885	YJL128C	PBS2	MAP kinase kinase that plays a pivotal role in the osmosensing signal-transduction pathway, activated under severe osmotic stress; plays a role in regulating Ty1 transposition	Q
886	VN_0886	YDR194C	MSS116	DEAD-box protein required for efficient splicing of mitochondrial Group I and II introns; non-polar RNA helicase that also facilitates strand annealing	Q
887	VN_0887	YOR350C	MNE1	Mitochondrial protein similar to <i>Lucilia illustris</i> mitochondrial cytochrome oxidase	Q
888	VN_0888	YLR299W	ECM38	Gamma-glutamyltranspeptidase, major glutathione-degrading enzyme; involved in detoxification of electrophilic xenobiotics; expression induced mainly by nitrogen starvation	Q
889	VN_0889	YGL066W	SGF73	Subunit of SAGA histone acetyltransferase complex; involved in formation of the preinitiation complex assembly at promoters; null mutant displays defects in premeiotic DNA synthesis	Q
890	VN_0890	YJR098C	YJR098C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
891	VN_0891	YDR118W	APC4	Subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition	Q
892	VN_0892	YDL224C	WHI4	Putative RNA binding protein and partially redundant Whi3p homolog that regulates the cell size requirement for passage through Start and commitment to cell division	Q

893	VN_0893	YKL025C	PAN3	Essential subunit of the Pan2p-Pan3p poly(A)-ribonuclease complex, which acts to control poly(A) tail length and regulate the stoichiometry and activity of postreplication repair complexes	Q
894	VN_0894	YBL009W	ALK2	Protein kinase; accumulation and phosphorylation are periodic during the cell cycle; phosphorylated in response to DNA damage; contains characteristic motifs for degradation via the APC pathway; similar to Alk1p and to mammalian haspkins	Q
895	VN_0895	YBR212W	NGR1	RNA binding protein that negatively regulates growth rate; interacts with the 3' UTR of the mitochondrial porin (POR1) mRNA and enhances its degradation; overexpression impairs mitochondrial function; expressed in stationary phase	Q
896	VN_0896	YML042W	CAT2	Carnitine acetyl-CoA transferase present in both mitochondria and peroxisomes, transfers activated acetyl groups to carnitine to form acetylcarnitine which can be shuttled across membranes	Q
897	VN_0897	YML088W	UFO1	F-box receptor protein, subunit of the Skp1-Cdc53-F-box receptor (SCF) E3 ubiquitin ligase complex; binds to phosphorylated Ho endonuclease, allowing its ubiquitylation by SCF and subsequent degradation	Q
898	VN_0898	YML020W	YML020W	Putative protein of unknown function	Q
899	VN_0899	YAL048C	GEM1	Evolutionarily-conserved tail-anchored outer mitochondrial membrane GTPase which regulates mitochondrial morphology; cells lacking Gem1p contain collapsed, globular, or grape-like mitochondria; not required for pheromone-induced cell death	Q
900	VN_0900	YML056C	IMD4	Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis, member of a four-gene family in <i>S. cerevisiae</i> , constitutively expressed	Q
901	VN_0901	YLR369W	SSQ1	Mitochondrial hsp70-type molecular chaperone, required for assembly of iron/sulfur clusters into proteins at a step after cluster synthesis, and for maturation of Yfh1p, which is a homolog of human frataxin implicated in Friedreich's ataxia	Q
902	VN_0902	YGR083C	GCD2	Delta subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression	Q
903	VN_0903	YIL155C	GUT2	Mitochondrial glycerol-3-phosphate dehydrogenase; expression is repressed by both glucose and cAMP and derepressed by non-fermentable carbon sources in a Snf1p, Rsf1p, Hap2/3/4/5 complex dependent manner	Q
904	VN_0904	YKL179C	COY1	Golgi membrane protein with similarity to mammalian CASP; genetic interactions with GOS1 (encoding a Golgi snare protein) suggest a role in Golgi function	Q
905	VN_0905	YOL023W	IFM1	Mitochondrial translation initiation factor 2	Q
906	VN_0906	YDR362C	TFC6	One of six subunits of RNA polymerase III transcription initiation factor complex (TFIIIC); part of TFIIIC TauB domain that binds BoxB promoter sites of tRNA and other genes; cooperates with Tfc3p in DNA binding; human homolog is TFIIIC-110	Q
907	VN_0907	YKL029C	MAE1	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids	Q
908	VN_0908	YBR121C	GRS1	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation	Q
909	VN_0909	YDR307W	YDR307W	Putative protein of unknown function	Q
910	VN_0910	YOL025W	LAG2	Protein involved in the determination of longevity and also in the negative regulation of SCF E3-ubiquitin ligase function; LAG2 is preferentially expressed in young cells; overexpression extends the mean and maximum life span of cells	Q
911	VN_0911	YPR179C	HDA3	Subunit of a possibly tetrameric trichostatin A-sensitive class II histone deacetylase complex that contains an Hda1p homodimer and an Hda2p-Hda3p heterodimer; required for the activity of the complex; has similarity to Hda2p	Q

912	VN_0912	YLR429W	CRN1	Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; plays a role in regulation of actin patch assembly	Q
913	VN_0913	YML082W	YML082W	Putative protein predicted to have carbon-sulfur lyase activity; green fluorescent protein (GFP)-fusion protein localizes to the nucleus and the cytoplasm; YNML082W is not an essential gene	Q
914	VN_0914	YJL101C	GSH1	Gamma glutamylcysteine synthetase catalyzes the first step in glutathione (GSH) biosynthesis; expression induced by oxidants, cadmium, and mercury	Q
915	VN_0915	YOR243C	PUS7	Pseudouridine synthase, catalyzes pseudouridylation at position 35 in U2 snRNA, position 50 in 5S rRNA, position 13 in cytoplasmic tRNAs, and position 35 in pre-tRNA(Tyr); conserved in archaea, vertebrates, and some bacteria	Q
916	VN_0916	YNL103W	MET4	Leucine-zipper transcriptional activator, responsible for the regulation of the sulfur amino acid pathway, requires different combinations of the auxiliary factors Cbf1p, Met28p, Met31p and Met32p	Q
917	VN_0917	YMR032W	HOF1	Bud neck-localized, SH3 domain-containing protein required for cytokinesis; regulates actomyosin ring dynamics and septin localization; interacts with the formins, Bni1p and Bnr1p, and with Cyk3p, Vrp1p, and Bni5p	Q
918	VN_0918	YJL057C	IKS1	Putative serine/threonine kinase; expression is induced during mild heat stress; deletion mutants are hypersensitive to copper sulphate and resistant to sorbate; interacts with an N-terminal fragment of Sst2p	Q
919	VN_0919	YDR137W	RGP1	Subunit of a Golgi membrane exchange factor (Ric1p-Rgp1p) that catalyzes nucleotide exchange on Ypt6p	Q
920	VN_0920	YFR048W	RMD8	Cytosolic protein required for sporulation	Q
921	VN_0921	YER173W	RAD24	Checkpoint protein, involved in the activation of the DNA damage and meiotic pachytene checkpoints; subunit of a clamp loader that loads Rad17p-Mec3p-Ddc1p onto DNA; homolog of human and S. pombe Rad17 protein	Strain failed to verify via PCR
922	VN_0922	YDR389W	SAC7	GTPase activating protein (GAP) for Rho1p, involved in signaling to the actin cytoskeleton, null mutations suppress tor2 mutations and temperature sensitive mutations in actin; potential Cdc28p substrate	Q
923	VN_0923	YPL263C	KEL3	Cytoplasmic protein of unknown function	Q
924	VN_0924	YKR101W	SIR1	Protein involved in repression of transcription at the silent mating-type loci HML and HMR; recruitment to silent chromatin requires interactions with Orc1p and with Sir4p, through a common Sir1p domain; binds to centromeric chromatin	Q
925	VN_0925	YPL089C	RLM1	MADS-box transcription factor, component of the protein kinase C-mediated MAP kinase pathway involved in the maintenance of cell integrity; phosphorylated and activated by the MAP-kinase Slt2p	Q
926	VN_0926	YLR330W	CHS5	Component of the exomer complex, which also contains Csh6p, Bch1p, Bch2p, and Bud7p and is involved in export of selected proteins, such as chitin synthase Chs3p, from the Golgi to the plasma membrane	Q
927	VN_0927	YNL008C	ASI3	Putative integral membrane E3 ubiquitin ligase; acts with Asi1p and Asi2p to ensure the fidelity of SPS-sensor signalling by maintaining the dormant repressed state of gene expression in the absence of inducing signals	Q
928	VN_0928	YBR260C	RGD1	GTPase-activating protein (RhoGAP) for Rho3p and Rho4p, possibly involved in control of actin cytoskeleton organization	Q
929	VN_0929	YDR458C	HEH2	Inner nuclear membrane (INM) protein; contains helix-extension-helix (HEH) motif, nuclear localization signal sequence; targeting to the INM requires the Srp1p-Kap95p karyopherins and the Ran cycle	Strain failed to verify via PCR
930	VN_0930	YMR137C	PSO2	Required for a post-incision step in the repair of DNA single and double-strand breaks that result from interstrand crosslinks produced by a variety of mono- and bi-functional psoralen derivatives; induced by UV-irradiation	Q
931	VN_0931	YHR015W	MIP6	Putative RNA-binding protein, interacts with Mex67p, which is a component of the nuclear pore involved in nuclear mRNA export	Q
932	VN_0932	YDR496C	PUF6	Pumilio-homology domain protein that binds ASH1 mRNA at PUF consensus sequences in the 3' UTR and represses its translation,	Q

				resulting in proper asymmetric localization of ASH1 mRNA	
933	VN_0933	YJL209W	CBP1	Mitochondrial protein that interacts with the 5'-untranslated region of the COB mRNA and has a role in its stability and translation; found in a complex at the inner membrane along with Pet309p	Q
934	VN_0934	YLR103C	CDC45	DNA replication initiation factor; recruited to MCM pre-RC complexes at replication origins; promotes release of MCM from Mcm10p, recruits elongation machinery; mutants in human homolog may cause velocardiofacial and DiGeorge syndromes	Q
935	VN_0935	YLR273C	PIG1	Putative targeting subunit for the type-1 protein phosphatase Glc7p that tethers it to the Gsy2p glycogen synthase	Q
936	VN_0936	YNL027W	CRZ1	Transcription factor that activates transcription of genes involved in stress response; nuclear localization is positively regulated by calcineurin-mediated dephosphorylation	Q
937	VN_0937	YBR216C	YBP1	Protein required for oxidation of specific cysteine residues of the transcription factor Yap1p, resulting in the nuclear localization of Yap1p in response to stress	Q
938	VN_0938	YNL045W	LAP2	Leucyl aminopeptidase yscIV (leukotriene A4 hydrolase) with epoxide hydrolase activity, metalloenzyme containing one zinc atom; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	Q
939	VN_0939	YBL051C	PIN4	Protein involved in G2/M phase progression and response to DNA damage, interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage	Q
940	VN_0940	YEL007W	YEL007W	Putative protein with sequence similarity to S. pombe gti1+ (gluconate transport inducer 1)	Q
941	VN_0941	YJL149W	DAS1	Putative SCF ubiquitin ligase F-box protein; interacts physically with both Cdc53p and Skp1 and genetically with CDC34; similar to putative F-box protein YDR131C	Q
942	VN_0942	YNL197C	WHI3	RNA binding protein that sequesters CLN3 mRNA in cytoplasmic foci; cytoplasmic retention factor for Cdc28p and associated cyclins; regulates cell fate and dose-dependently regulates the critical cell size required for passage through Start	Q
943	VN_0943	YKR036C	CAF4	WD40 repeat-containing protein associated with the CCR4-NOT complex, interacts in a Ccr4p-dependent manner with Ssn2p; also interacts with Fis1p, Mdv1p and Dnm1p and plays a role in mitochondrial fission	Q
944	VN_0944	YKL079W	SMY1	Protein that interacts with Myo2p, proposed to be involved in exocytosis; N-terminal domain is related to the motor domain of kinesins	Q
945	VN_0945	YML007W	YAP1	Basic leucine zipper (bZIP) transcription factor required for oxidative stress tolerance; activated by H2O2 through the multistep formation of disulfide bonds and transit from the cytoplasm to the nucleus; mediates resistance to cadmium	Q
946	VN_0946	YDL109C	YDL109C	Putative lipase; involved in lipid metabolism; YDL109C is not an essential gene	Q
947	VN_0947	YMR061W	RNA14	Cleavage and polyadenylation factor I (CF I) component involved in cleavage and polyadenylation of mRNA 3' ends; bridges interaction between Rna15p and Hrp1p in the CF I complex	Q
948	VN_0948	YDR295C	HDA2	Subunit of a possibly tetrameric trichostatin A-sensitive class II histone deacetylase complex containing an Hda1p homodimer and an Hda2p-Hda3p heterodimer; involved in telomere maintenance	Q
949	VN_0949	YOR138C	RUP1	Protein involved in regulation of Rsp5p, which is an essential HECT ubiquitin ligase; has a WW domain consensus motif of PPPSY (residues 131-135) that mediates binding of Rsp5p to Ubp2p; contains an UBA domain	Q
950	VN_0950	YDR320C	SWA2	Auxilin-like protein involved in vesicular transport; clathrin-binding protein required for uncoating of clathrin-coated vesicles	Q
951	VN_0951	YJL010C	NOP9	Essential subunit of U3-containing 90S preribosome involved in production of 18S rRNA and assembly of small ribosomal subunit; also part of pre-40S ribosome and required for its export into cytoplasm; binds RNA and contains pumilio domain	Q

952	VN_0952	YLR002C	NOC3	Protein that forms a nuclear complex with Noc2p that binds to 66S ribosomal precursors to mediate their intranuclear transport; also binds to chromatin to promote the association of DNA replication factors and replication initiation	Q
953	VN_0953	YNR008W	LRO1	Acyltransferase that catalyzes diacylglycerol esterification; one of several acyltransferases that contribute to triglyceride synthesis; putative homolog of human lecithin cholesterol acyltransferase	Q
954	VN_0954	YNL012W	SPO1	Meiosis-specific prospore protein; required for meiotic spindle pole body duplication and separation; required to produce bending force necessary for proper prospore membrane assembly during sporulation; has similarity to phospholipase B	Q
955	VN_0955	YLR234W	TOP3	DNA Topoisomerase III, conserved protein that functions in a complex with Sgs1p and Rmi1p to relax single-stranded negatively-supercoiled DNA preferentially, involved in telomere stability and regulation of mitotic recombination	Q
956	VN_0956	YPR190C	RPC82	RNA polymerase III subunit C82	Strain failed to verify via PCR
957	VN_0957	YBL075C	SSA3	ATPase involved in protein folding and the response to stress; plays a role in SRP-dependent cotranslational protein-membrane targeting and translocation; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm	Q
958	VN_0958	YDR014W	RAD61	Subunit of a complex (Scc3p, Pds5p, Rad61p) that inhibits sister chromatid cohesion; inhibited by Eco1p-acetylated cohesin subunits Smc3p and Mcd1p; related to the human Wapl protein that controls the association of cohesin with chromatin	Q
959	VN_0959	YIL101C	XPB1	Transcriptional repressor that binds to promoter sequences of the cyclin genes, CYS3, and SMF2; expression is induced by stress or starvation during mitosis, and late in meiosis; member of the Swi4p/Mbp1p family; potential Cdc28p substrate	Q
960	VN_0960	YLR289W	GUF1	Mitochondrial matrix GTPase that associates with mitochondrial ribosomes; important for translation under temperature and nutrient stress; may have a role in translational fidelity; similar to bacterial LepA elongation factor	Q
961	VN_0961	YAL005C	SSA1	ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall	Q
962	VN_0962	YDL113C	ATG20	Sorting nexin family member required for the cytoplasm-to-vacuole targeting (Cvt) pathway and for endosomal sorting; has a Phox homology domain that binds phosphatidylinositol-3-phosphate; interacts with Snx4p; potential Cdc28p substrate	Q
963	VN_0963	YLL024C	SSA2	ATP binding protein involved in protein folding and vacuolar import of proteins; member of heat shock protein 70 (HSP70) family; associated with the chaperonin-containing T-complex; present in the cytoplasm, vacuolar membrane and cell wall	Q
964	VN_0964	YNL176C	YNL176C	Cell cycle-regulated gene of unknown function, promoter bound by Fkh2p	Q
965	VN_0965	YNL293W	MSB3	GTPase-activating protein for Sec4p and several other Rab GTPases, regulates exocytosis via its action on Sec4p, also required for proper actin organization; similar to Msb4p; both Msb3p and Msb4p localize to sites of polarized growth	Q
966	VN_0966	YCR061W	YCR061W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; induced by treatment with 8-methoxypsoralen and UVA irradiation	Q
967	VN_0967	YNR038W	DBP6	Essential protein involved in ribosome biogenesis; putative ATP-dependent RNA helicase of the DEAD-box protein family	Q
968	VN_0968	YHR124W	NDT80	Meiosis-specific transcription factor required for exit from pachytene and for full meiotic recombination; activates middle sporulation genes; competes with Sum1p for binding to promoters containing middle sporulation elements (MSE)	Q
969	VN_0969	YNL299W	TRF5	Non-canonical poly(A) polymerase, involved in nuclear RNA degradation as a component of the TRAMP complex; catalyzes polyadenylation of hypomodified tRNAs, and snoRNA and rRNA	Q

				precursors; overlapping but non-redundant functions with Pap2p	
970	VN_0970	YBR215W	HPC2	Subunit of the HIR complex, a nucleosome assembly complex involved in regulation of histone gene transcription; mutants display synthetic defects with subunits of FACT, a complex that allows passage of RNA Pol II through nucleosomes	Q
971	VN_0971	YNL167C	SKO1	Basic leucine zipper (bZIP) transcription factor of the ATF/CREB family, forms a complex with Tup1p and Ssn6p to both activate and repress transcription; cytosolic and nuclear protein involved in osmotic and oxidative stress responses	Q
972	VN_0972	YOL117W	RRI2	Subunit of the COP9 signalosome (CSN) complex that cleaves the ubiquitin-like protein Nedd8 from SCF ubiquitin ligases; plays a role in the mating pheromone response	Q
973	VN_0973	YBR280C	SAF1	F-Box protein involved in proteasome-dependent degradation of Aah1p during entry of cells into quiescence; interacts with Skp1	Q
974	VN_0974	YGL099W	LSG1	Putative GTPase involved in 60S ribosomal subunit biogenesis; required for the release of Nmd3p from 60S subunits in the cytoplasm	Q
975	VN_0975	YAL011W	SWC3	Protein of unknown function, component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A; required for formation of nuclear-associated array of smooth endoplasmic reticulum known as karmellae	Q
976	VN_0976	YAL016W	TPD3	Regulatory subunit A of the heterotrimeric protein phosphatase 2A (PP2A), which also contains regulatory subunit Cdc55p and either catalytic subunit Pph21p or Pph22p; required for cell morphogenesis and transcription by RNA polymerase III	Q
977	VN_0977	YOR181W	LAS17	Actin assembly factor, activates the Arp2/3 protein complex that nucleates branched actin filaments; localizes with the Arp2/3 complex to actin patches; homolog of the human Wiskott-Aldrich syndrome protein (WASP)	Q
978	VN_0978	YOR356W	YOR356W	Mitochondrial protein with similarity to flavoprotein-type oxidoreductases; found in a large supramolecular complex with other mitochondrial dehydrogenases	Q
979	VN_0979	YOL152W	FRE7	Putative ferric reductase with similarity to Fre2p; expression induced by low copper levels	Q
980	VN_0980	YIL055C	YIL055C	Putative protein of unknown function	Q
981	VN_0981	YEL062W	NPR2	Component, with Npr3p, of an evolutionarily conserved complex that mediates downregulation of TOR Complex 1 activity in response to amino acid limitation; transcription is induced in response to proline and urea	Q
982	VN_0982	YDL203C	ACK1	Protein that functions upstream of Pkc1p in the cell wall integrity pathway; GFP-fusion protein expression is induced in response to the DNA-damaging agent MMS; non-tagged Ack1p is detected in purified mitochondria	Q
983	VN_0983	YPL093W	NOG1	Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus and is required for 60S ribosomal subunit biogenesis; constituent of 66S pre-ribosomal particles; member of the ODN family of nucleolar G-proteins	Q
984	VN_0984	YEL030W	ECM10	Heat shock protein of the Hsp70 family, localized in mitochondrial nucleoids, plays a role in protein translocation, interacts with Mge1p in an ATP-dependent manner; overexpression induces extensive mitochondrial DNA aggregations	Q
985	VN_0985	YCR038C	BUD5	GTP/GDP exchange factor for Rsr1p (Bud1p) required for both axial and bipolar budding patterns; mutants exhibit random budding in all cell types	Q
986	VN_0986	YIL046W	MET30	F-box protein containing five copies of the WD40 motif, controls cell cycle function, sulfur metabolism, and methionine biosynthesis as part of the ubiquitin ligase complex; interacts with and regulates Met4p, localizes within the nucleus	Q
987	VN_0987	YDL070W	BDF2	Protein involved in transcription initiation at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf1p	Q

988	VN_0988	YDR380W	ARO10	Phenylpyruvate decarboxylase, catalyzes decarboxylation of phenylpyruvate to phenylacetaldehyde, which is the first specific step in the Ehrlich pathway	Q
989	VN_0989	YPL161C	BEM4	Protein involved in establishment of cell polarity and bud emergence; interacts with the Rho1p small GTP-binding protein and with the Rho-type GTPase Cdc42p; involved in maintenance of proper telomere length	Q
990	VN_0990	YHL038C	CBP2	Mitochondrial protein required for splicing of the group I intron aI5 of the COB pre-mRNA, binds to the RNA to promote splicing; also involved in but not essential for splicing of the COB bI2 intron and the intron in the 21S rRNA gene	Q
991	VN_0991	YOR066W	MSA1	Activator of G1-specific transcription factors, MBF and SBF; involved in regulation of the timing of G1-specific gene transcription and cell cycle initiation; localization is cell-cycle dependent and regulated by Cdc28p phosphorylation	Q
992	VN_0992	YKL125W	RRN3	Protein required for transcription of rDNA by RNA polymerase I; transcription factor independent of DNA template; involved in recruitment of RNA polymerase I to rDNA	Strain failed to verify via PCR
993	VN_0993	YER147C	SCC4	Subunit of cohesin loading factor (Scc2p-Scc4p), a complex required for the loading of cohesin complexes onto chromosomes; involved in establishing sister chromatid cohesion during double-strand break repair via phosphorylated histone H2AX	Q
994	VN_0994	YFL049W	SWP82	Member of the SWI/SNF chromatin remodeling complex in which it plays an as yet unidentified role; has identifiable counterparts in closely related yeast species; abundantly expressed in many growth conditions; paralog of Npl6p	Q
995	VN_0995	YPL253C	VIK1	Protein that forms a complex with Kar3p at the spindle pole body, possible regulator of Kar3p function in microtubule-mediated processes; required for sister chromatid cohesion; has similarity to Cik1p	Strain failed to verify via PCR
996	VN_0996	YER049W	TPA1	Poly(rA)-binding protein involved in translation termination efficiency, mRNA poly(A) tail length and mRNA stability; interacts with Sup45p (eRF1), Sup35p (eRF3) and Pab1p; similar to prolyl 4-hydroxylases; binds Fe(III) and 2-oxoglutarate	Q
997	VN_0997	YDR311W	TFB1	Subunit of TFIIH and nucleotide excision repair factor 3 complexes, required for nucleotide excision repair, target for transcriptional activators	Q
998	VN_0998	YIL056W	VHR1	Transcriptional activator, required for the vitamin H-responsive element (VHRE) mediated induction of VHT1 (Vitamin H transporter) and BIO5 (biotin biosynthesis intermediate transporter) in response to low biotin concentrations	Q
999	VN_0999	YNL020C	ARK1	Serine/threonine protein kinase involved in regulation of the cortical actin cytoskeleton; involved in control of endocytosis	Q
1000	VN_1000	YEL060C	PRB1	Vacuolar proteinase B (yscB), a serine protease of the subtilisin family; involved in protein degradation in the vacuole and required for full protein degradation during sporulation	Q
1001	VN_1001	YDR049W	YDR049W	Zinc finger protein; putative transcription factor that may interact with proteins involved in histone acetylation or deacetylation; may be involved in altering acetylation on histone lysines	Q
1002	VN_1002	YHR035W	YHR035W	Putative protein of unknown function; not an essential gene	Q
1003	VN_1003	YOR239W	ABP140	Nonessential protein that binds actin filaments and localizes to actin patches and cables, has similarity to S-adenosylmethionine (AdoMet)-dependent methyltransferases	Q
1004	VN_1004	YDR228C	PCF11	mRNA 3' end processing factor, essential component of cleavage and polyadenylation factor IA (CF IA), involved in pre-mRNA 3' end processing and in transcription termination; binds C-terminal domain of largest subunit of RNA pol II (Rpo21p)	Q
1005	VN_1005	YGL110C	CUE3	Protein of unknown function; has a CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination	Q
1006	VN_1006	YAL047C	SPC72	Component of the cytoplasmic Tub4p (gamma-tubulin) complex, binds spindle pole bodies and links them to microtubules; has roles in astral microtubule formation and stabilization	Q

1007	VN_1007	YGL107C	RMD9	Mitochondrial protein required for respiratory growth; mutant phenotype and genetic interactions suggest a role in delivering mt mRNAs to ribosomes; located on matrix face of the inner membrane and loosely associated with mitoribosomes	Q
1008	VN_1008	YGL124C	MON1	Protein required for fusion of cvt-vesicles and autophagosomes with the vacuole; associates, as a complex with Ccz1p, with a perivacuolar compartment; potential Cdc28p substrate	Q
1009	VN_1009	YER103W	SSA4	Heat shock protein that is highly induced upon stress; plays a role in SRP-dependent cotranslational protein-membrane targeting and translocation; member of the HSP70 family; cytoplasmic protein that concentrates in nuclei upon starvation	Q
1010	VN_1010	YJL127C	SPT10	Putative histone acetylase, sequence-specific activator of histone genes, binds specifically and highly cooperatively to pairs of UAS elements in core histone promoters, functions at or near the TATA box	Q
1011	VN_1011	YHR161C	YAP1801	Protein involved in clathrin cage assembly; binds Pan1p and clathrin; homologous to Yap1802p, member of the AP180 protein family	Q
1012	VN_1012	YGL023C	PIB2	Protein binding phosphatidylinositol 3-phosphate, involved in telomere-proximal repression of gene expression; similar to Fab1 and Vps27	Q
1013	VN_1013	YDR386W	MUS81	Subunit of the structure-specific Mms4p-Mus81p endonuclease that cleaves branched DNA; involved in DNA repair, replication fork stability, and joint molecule formation/resolution during meiotic recombination; helix-hairpin-helix protein	Q
1014	VN_1014	YIL014W	MNT3	Alpha-1,3-mannosyltransferase, adds the fourth and fifth alpha-1,3-linked mannose residues to O-linked glycans during protein O-glycosylation	Q
1015	VN_1015	YHR219W	YHR219W	Putative protein of unknown function with similarity to helicases; located in the telomere region on the right arm of chromosome VIII	Q
1016	VN_1016	YGR221C	TOS2	Protein involved in localization of Cdc24p to the site of bud growth; may act as a membrane anchor; localizes to the bud neck and bud tip; potentially phosphorylated by Cdc28p	Q
1017	VN_1017	YOL164W	BDS1	Bacterially-derived sulfatase required for use of alkyl- and aryl-sulfates as sulfur sources	Strain failed to verify via PCR
1018	VN_1018	YPL269W	KAR9	Karyogamy protein required for correct positioning of the mitotic spindle and for orienting cytoplasmic microtubules, localizes at the shmoo tip in mating cells and at the tip of the growing bud in small-budded cells through anaphase	Q
1019	VN_1019	YGR054W	YGR054W	Eukaryotic initiation factor (eIF) 2A; associates specifically with both 40S subunits and 80 S ribosomes, and interacts genetically with both eIF5b and eIF4E; homologous to mammalian eIF2A	Q
1020	VN_1020	YKL048C	ELM1	Serine/threonine protein kinase that regulates cellular morphogenesis, septin behavior, and cytokinesis; required for the regulation of other kinases; forms part of the bud neck ring	Q
1021	VN_1021	YOR070C	GYP1	Cis-golgi GTPase-activating protein (GAP) for the Rab family members Ypt1p (in vivo) and for Ypt1p, Sec4p, Ypt7p, and Ypt51p (in vitro); involved in vesicle docking and fusion	Q
1022	VN_1022	YDR477W	SNF1	AMP-activated serine/threonine protein kinase found in a complex containing Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis	Q
1023	VN_1023	YDR419W	RAD30	DNA polymerase eta, involved in the predominantly error-free bypass replication of DNA lesions, catalyzes the efficient and accurate synthesis of DNA opposite cyclobutane pyrimidine dimers; homolog of human POLH and bacterial DinB proteins	Q
1024	VN_1024	YKL062W	MSN4	Transcriptional activator related to Msn2p; activated in stress conditions, which results in translocation from the cytoplasm to the nucleus; binds DNA at stress response elements of responsive genes, inducing gene expression	Q
1025	VN_1025	YKL155C	RSM22	Mitochondrial ribosomal protein of the small subunit; also predicted to be an S-adenosylmethionine-dependent methyltransferase	Q
1026	VN_1026	YDR425W	SNX41	Sorting nexin, involved in the retrieval of late-Golgi SNAREs from the post-Golgi endosome to the trans-Golgi network; interacts with Snx4p	Q

1027	VN_1027	YMR119W	ASI1	Putative integral membrane E3 ubiquitin ligase; acts with Asi2p and Asi3p to ensure the fidelity of SPS-sensor signalling by maintaining the dormant repressed state of gene expression in the absence of inducing signals	Q
1028	VN_1028	YPL210C	SRP72	Core component of the signal recognition particle (SRP) ribonucleoprotein (RNP) complex that functions in targeting nascent secretory proteins to the endoplasmic reticulum (ER) membrane	Q
1029	VN_1029	YDR398W	UTP5	Subunit of U3-containing Small Subunit (SSU) processome complex involved in production of 18S rRNA and assembly of small ribosomal subunit	Q
1030	VN_1030	YMR313C	TGL3	Triacylglycerol lipase of the lipid particle, responsible for all the TAG lipase activity of the lipid particle; contains the consensus sequence motif GX SXG, which is found in lipolytic enzymes; required with Tgl4p for timely bud formation	Q
1031	VN_1031	YDR266C	YDR266C	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; contains a RING finger domain	Q
1032	VN_1032	YDR390C	UBA2	Nuclear protein that acts as a heterodimer with Aos1p to activate Smt3p (SUMO) before its conjugation to proteins (sumoylation), which may play a role in protein targeting; essential for viability	Q
1033	VN_1033	YHR114W	BZZ1	SH3 domain protein implicated in the regulation of actin polymerization, able to recruit actin polymerization machinery through its SH3 domains, colocalizes with cortical actin patches and Las17p, interacts with type I myosins	Q
1034	VN_1034	YKL204W	EAP1	eIF4E-associated protein, competes with eIF4G for binding to eIF4E; inhibits cap-dependent translation; functions independently of eIF4E to maintain genetic stability; plays a role in cell growth, implicated in the TOR signaling cascade	Q
1035	VN_1035	YML046W	PRP39	U1 snRNP protein involved in splicing, contains multiple tetrapeptide repeats	Q
1036	VN_1036	YLR177W	YLR177W	Putative protein of unknown function; phosphorylated by Dbf2p-Mob1p in vitro; some strains contain microsatellite polymorphisms at this locus; YLR177W is not an essential gene	Q
1037	VN_1037	YHL027W	RIM101	Transcriptional repressor involved in response to pH and in cell wall construction; required for alkaline pH-stimulated haploid invasive growth and sporulation; activated by proteolytic processing; similar to A. nidulans PacC	Q
1038	VN_1038	YOR171C	LCB4	Sphingoid long-chain base kinase, responsible for synthesis of long-chain base phosphates, which function as signaling molecules, regulates synthesis of ceramide from exogenous long-chain bases, localizes to the Golgi and late endosomes	Q
1039	VN_1039	YMR278W	PGM3	Phosphoglucosyltransferase, catalyzes interconversion of glucose-1-phosphate and glucose-6-phosphate; transcription induced in response to stress; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; non-essential	Q
1040	VN_1040	YJL106W	IME2	Serine/threonine protein kinase involved in activation of meiosis, associates with Ime1p and mediates its stability, activates Ndt80p; IME2 expression is positively regulated by Ime1p	Q
1041	VN_1041	YHR091C	MSR1	Mitochondrial arginyl-tRNA synthetase	Strain failed to verify via PCR
1042	VN_1042	YGL060W	YBP2	Central kinetochore associated protein that mediates mitotic progression; interacts with several central kinetochore proteins and the centromeric histone Cse4p; role in resistance to oxidative stress; similarity to Ybp1p and Slk19p	Q
1043	VN_1043	YJR130C	STR2	Cystathionine gamma-synthase, converts cysteine into cystathionine	Q
1044	VN_1044	YHR218W	YHR218W	Helicase-like protein encoded within the telomeric Y' element	Q
1045	VN_1045	YIL092W	YIL092W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to the nucleus	Q
1046	VN_1046	YMR106C	YKU80	Subunit of the telomeric Ku complex (Yku70p-Yku80p), involved in telomere length maintenance, structure and telomere position effect; relocates to sites of double-strand cleavage to promote nonhomologous	Q

				end joining during DSB repair	
1047	VN_1047	YKR008W	RSC4	Component of the RSC chromatin remodeling complex; found in close proximity to nucleosomal DNA; displaced from the surface of nucleosomal DNA after chromatin remodeling	Q
1048	VN_1048	YOR389W	YOR389W	Putative protein of unknown function; expression regulated by copper levels	Q
1049	VN_1049	YNR006W	VPS27	Endosomal protein that forms a complex with Hse1p; required for recycling Golgi proteins, forming luminal membranes and sorting ubiquitinated proteins destined for degradation; has Ubiquitin Interaction Motifs which bind ubiquitin (Ubi4p)	Q
1050	VN_1050	YOR137C	SIA1	Protein of unassigned function involved in activation of the Pma1p plasma membrane H ⁺ -ATPase by glucose	Q
1051	VN_1051	YKR056W	TRM2	tRNA methyltransferase, 5-methylates the uridine residue at position 54 of tRNAs and may also have a role in tRNA stabilization or maturation; endo-exonuclease with a role in DNA repair	Q
1052	VN_1052	YLR206W	ENT2	Epsin-like protein required for endocytosis and actin patch assembly and functionally redundant with Ent1p; contains clathrin-binding motif at C-terminus	Q
1053	VN_1053	YDR350C	ATP22	Mitochondrial inner membrane protein required for assembly of the F0 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis	Strain failed to verify via PCR
1054	VN_1054	YHR188C	GPI16	Transmembrane protein subunit of the glycosylphosphatidylinositol transamidase complex that adds GPIs to newly synthesized proteins; human PIG-Tp homolog	Strain failed to verify via PCR
1055	VN_1055	YMR168C	CEP3	Essential kinetochore protein, component of the CBF3 complex that binds the CDEIII region of the centromere; contains an N-terminal Zn2Cys6 type zinc finger domain, a C-terminal acidic domain, and a putative coiled coil dimerization domain	Q
1056	VN_1056	YGR103W	NOP7	Component of several different pre-ribosomal particles; forms a complex with Ytm1p and Erb1p that is required for maturation of the large ribosomal subunit; required for exit from G ₀ and the initiation of cell proliferation	Q
1057	VN_1057	YGL192W	IME4	Probable mRNA N6-adenosine methyltransferase required for entry into meiosis; transcribed in diploid cells; haploids repress IME4 transcription via production of antisense IME4 transcripts; antisense transcription is repressed in diploids	Q
1058	VN_1058	YKL032C	IXR1	Protein that binds DNA containing intrastrand cross-links formed by cisplatin, contains two HMG (high mobility group box) domains, which confer the ability to bend cisplatin-modified DNA; mediates aerobic transcriptional repression of COX5b	Q
1059	VN_1059	YMR198W	CIK1	Kinesin-associated protein required for both karyogamy and mitotic spindle organization, interacts stably and specifically with Kar3p and may function to target this kinesin to a specific cellular role; has similarity to Vik1p	Q
1060	VN_1060	YMR100W	MUB1	Protein that interacts with E2 and E3 enzymes Ubr2p and Rad6p and is required for ubiquitylation and degradation of Rpn4p; contains a MYND domain (residues 512 to 555); has a short half-life; has similarity to Aspergillus nidulans samB gene	Q
1061	VN_1061	YPL119C	DBP1	Putative ATP-dependent RNA helicase of the DEAD-box protein family; mutants show reduced stability of the 40S ribosomal subunit scanning through 5' untranslated regions of mRNAs	Q
1062	VN_1062	YNL209W	SSB2	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in the folding of newly-synthesized polypeptide chains; member of the HSP70 family; homolog of SSB1	Q
1063	VN_1063	YFR023W	PES4	Poly(A) binding protein, suppressor of DNA polymerase epsilon mutation, similar to Mip6p	Q
1064	VN_1064	YLR248W	RCK2	Protein kinase involved in the response to oxidative and osmotic stress; identified as suppressor of S. pombe cell cycle checkpoint mutations	Q
1065	VN_1065	YDR341C	YDR341C	Arginyl-tRNA synthetase, proposed to be cytoplasmic but the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q

1066	VN_1066	YIL072W	HOP1	Meiosis-specific DNA binding protein that displays Red1p dependent localization to the unsynapsed axial-lateral elements of the synaptonemal complex; required for homologous chromosome synapsis and chiasma formation	Q
1067	VN_1067	YCR008W	SAT4	Ser/Thr protein kinase involved in salt tolerance; functions in regulation of Trk1p-Trk2p potassium transporter; partially redundant with Hal5p; has similarity to Npr1p	Q
1068	VN_1068	YGR194C	XKS1	Xylulokinase, converts D-xylulose and ATP to xylulose 5-phosphate and ADP; rate limiting step in fermentation of xylulose; required for xylose fermentation by recombinant <i>S. cerevisiae</i> strains	Q
1069	VN_1069	YDR144C	MKC7	GPI-anchored aspartyl protease (yapsin) involved in protein processing; shares functions with Yap3p and Kex2p	Q
1070	VN_1070	YNL039W	BDP1	Essential subunit of RNA polymerase III transcription factor (TFIIIB), which is involved in transcription of genes encoding tRNAs, 5S rRNA, U6 snRNA, and other small RNAs	Q
1071	VN_1071	YPL020C	ULP1	Ubl (ubiquitin-like protein)-specific protease that cleaves Smt3p protein conjugates; specifically required for cell cycle progression; associates with nucleoporins and may interact with septin rings during telophase	Q
1072	VN_1072	YDL013W	SLX5	Subunit of the Slx5-Slx8 SUMO-targeted ubiquitin ligase (STUbL) complex, stimulated by SUMO-modified substrates; contains a RING domain and two SIMs (SUMO-interacting motifs); forms SUMO-dependent nuclear foci, including DNA repair centers	Q
1073	VN_1073	YGL142C	GPI10	Integral membrane protein involved in glycosylphosphatidylinositol (GPI) anchor synthesis; putative alpha 1,2 mannosyltransferase required for addition of the third mannose onto the GPI core structure; human PIG-Bp is a functional homolog	Q
1074	VN_1074	YMR098C	ATP25	Mitochondrial protein required for the stability of Oli1p (Atp9p) mRNA and for the Oli1p ring formation; YMR098C is not an essential gene	Q
1075	VN_1075	YJL181W	YJL181W	Putative protein of unknown function; expression is cell-cycle regulated as shown by microarray analysis	Q
1076	VN_1076	YBR148W	YSW1	Protein required for normal prospore membrane formation; interacts with Gip1p, which is the meiosis-specific regulatory subunit of the Glc7p protein phosphatase; expressed specifically in spores and localizes to the prospore membrane	Q
1077	VN_1077	YJL100W	LSB6	Type II phosphatidylinositol 4-kinase that binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization	Q
1078	VN_1078	YDR200C	VPS64	Protein required for cytoplasm to vacuole targeting of proteins; forms a complex with Far3p and Far7p to Far11p involved in recovery from pheromone-induced cell cycle arrest; localizes to the cytoplasm and endoplasmic reticulum membrane	Q
1079	VN_1079	YLR353W	BUD8	Protein involved in bud-site selection; diploid mutants display a unipolar budding pattern instead of the wild-type bipolar pattern, and bud at the proximal pole	Q
1080	VN_1080	YGL125W	MET13	Major isozyme of methylenetetrahydrofolate reductase, catalyzes the reduction of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate in the methionine biosynthesis pathway	Q
1081	VN_1081	YDR349C	YPS7	Putative GPI-anchored aspartic protease, located in the cytoplasm and endoplasmic reticulum	Q
1082	VN_1082	YDR101C	ARX1	Shuttling pre-60S factor; involved in the biogenesis of ribosomal large subunit biogenesis; interacts directly with Alb1; responsible for Tif6 recycling defects in absence of Rei1; associated with the ribosomal export complex	Q
1083	VN_1083	YBR060C	ORC2	Subunit of the origin recognition complex, which directs DNA replication by binding to replication origins and is also involved in transcriptional silencing; interacts with Spp1p and with trimethylated histone H3; phosphorylated by Cdc28p	Q
1084	VN_1084	YNL104C	LEU4	Alpha-isopropylmalate synthase (2-isopropylmalate synthase); the main isozyme responsible for the first step in the leucine biosynthesis pathway	Q
1085	VN_1085	YNL018C	YNL018C	Putative protein of unknown function	Q

1086	VN_1086	YKR084C	HBS1	GTP binding protein with sequence similarity to the elongation factor class of G proteins, EF-1alpha and Sup35p; associates with Dom34p, and shares a similar genetic relationship with genes that encode ribosomal protein components	Q
1087	VN_1087	YDL080C	THI3	Probable alpha-ketoisocaproate decarboxylase, may have a role in catabolism of amino acids to long-chain and complex alcohols; required for expression of enzymes involved in thiamine biosynthesis	Q
1088	VN_1088	YML071C	COG8	Component of the conserved oligomeric Golgi complex (Cog1p through Cog8p), a cytosolic tethering complex that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments	Q
1089	VN_1089	YJL083W	TAX4	EH domain-containing protein involved in regulating phosphatidylinositol 4,5-bisphosphate levels and autophagy; Irs4p and Tax4p bind and activate the PtdIns phosphatase Inp51p; Irs4p and Tax4p are involved in localizing Atg17p to the PAS	Q
1090	VN_1090	YJL201W	ECM25	Non-essential protein of unknown function; promoter contains a consensus binding sequence for factor Abf1p	Q
1091	VN_1091	YGR246C	BRF1	TFIIB B-related factor, one of three subunits of RNA polymerase III transcription initiation factor TFIIB, binds TFIIC and TBP and recruits RNA pol III to promoters, amino-terminal half is homologous to TFIIB	Q
1092	VN_1092	YGR225W	AMA1	Activator of meiotic anaphase promoting complex (APC/C); Cdc20p family member; required for initiation of spore wall assembly; required for Clb1p degradation during meiosis	Q
1093	VN_1093	YDL025C	YDL025C	Putative protein kinase, potentially phosphorylated by Cdc28p; YDL025C is not an essential gene	Q
1094	VN_1094	YOR030W	DFG16	Probable multiple transmembrane protein, involved in diploid invasive and pseudohyphal growth upon nitrogen starvation; required for accumulation of processed Rim101p	Q
1095	VN_1095	YPR155C	NCA2	Protein involved in regulation of mitochondrial expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase; functions with Nca3p	Q
1096	VN_1096	YNL034W	YNL034W	Putative protein of unknown function; YNL034W is not an essential gene	Q
1097	VN_1097	YDL153C	SAS10	Essential subunit of U3-containing Small Subunit (SSU) processome complex involved in production of 18S rRNA and assembly of small ribosomal subunit; disrupts silencing when overproduced	Q
1098	VN_1098	YLR401C	DUS3	Dihydrouridine synthase, member of a widespread family of conserved proteins including Smm1p, Dus1p, and Dus4p; contains a consensus oleate response element (ORE) in its promoter region	Q
1099	VN_1099	YNR063W	YNR063W	Putative zinc-cluster protein of unknown function	Q
1100	VN_1100	YJR046W	TAH11	DNA replication licensing factor, required for pre-replication complex assembly	Q
1101	VN_1101	YLR055C	SPT8	Subunit of the SAGA transcriptional regulatory complex but not present in SAGA-like complex SLIK/SALSA, required for SAGA-mediated inhibition at some promoters	Q
1102	VN_1102	YJR002W	MPP10	Component of the SSU processome and 90S preribosome, required for pre-18S rRNA processing, interacts with and controls the stability of Imp3p and Imp4p, essential for viability; similar to human Mpp10p	Strain failed to verify via PCR
1103	VN_1103	YDL063C	YDL063C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; predicted to be involved in ribosome biogenesis	Q
1104	VN_1104	YJL103C	GSM1	Putative zinc cluster protein of unknown function; proposed to be involved in the regulation of energy metabolism, based on patterns of expression and sequence analysis	Q
1105	VN_1105	YKR019C	IRS4	EH domain-containing protein involved in regulating phosphatidylinositol 4,5-bisphosphate levels and autophagy; Irs4p and Tax4p bind and activate the PtdIns phosphatase Inp51p; Irs4p and Tax4p are involved in localizing Atg17p to the PAS	Q
1106	VN_1106	YPL070W	MUK1	Cytoplasmic protein of unknown function containing a Vps9 domain; computational analysis of large-scale protein-protein interaction data suggests a possible role in transcriptional regulation	Q

1107	VN_1107	YDR143C	SAN1	Ubiquitin-protein ligase, involved in the proteasome-dependent degradation of aberrant nuclear proteins	Q
1108	VN_1108	YOL091W	SPO21	Component of the meiotic outer plaque of the spindle pole body, involved in modifying the meiotic outer plaque that is required prior to prospore membrane formation	Q
1109	VN_1109	YFL002C	SPB4	Putative ATP-dependent RNA helicase, nucleolar protein required for synthesis of 60S ribosomal subunits at a late step in the pathway; sediments with 66S pre-ribosomes in sucrose gradients	Q
1110	VN_1110	YML057W	CMP2	Calcineurin A; one isoform (the other is CNA1) of the catalytic subunit of calcineurin, a Ca^{++} /calmodulin-regulated protein phosphatase which regulates Crz1p (a stress-response transcription factor), the other calcineurin subunit is CNB1	Q
1111	VN_1111	YMR284W	YKU70	Subunit of the telomeric Ku complex (Yku70p-Yku80p), involved in telomere length maintenance, structure and telomere position effect; relocates to sites of double-strand cleavage to promote nonhomologous end joining during DSB repair	Q
1112	VN_1112	YPL243W	SRP68	Core component of the signal recognition particle (SRP) ribonucleoprotein (RNP) complex that functions in targeting nascent secretory proteins to the endoplasmic reticulum (ER) membrane	Q
1113	VN_1113	YJL069C	UTP18	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data	Q
1114	VN_1114	YKR069W	MET1	S-adenosyl-L-methionine uroporphyrinogen III transmethylese, involved in the biosynthesis of siroheme, a prosthetic group used by sulfite reductase; required for sulfate assimilation and methionine biosynthesis	Q
1115	VN_1115	YDR085C	AFR1	Protein required for pheromone-induced projection (shmoo) formation; regulates septin architecture during mating; has an RVXF motif that mediates targeting of Glc7p to mating projections; interacts with Cdc12p	Q
1116	VN_1116	YNL061W	NOP2	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus; constituent of 66S pre-ribosomal particles	Q
1117	VN_1117	YMR092C	AIP1	Actin cortical patch component, interacts with the actin depolymerizing factor cofilin; required to restrict cofilin localization to cortical patches; contains WD repeats	Q
1118	VN_1118	YPL184C	MRN1	RNA-binding protein proposed to be involved in translational regulation; binds specific categories of mRNAs, including those that contain upstream open reading frames (uORFs) and internal ribosome entry sites (IRES)	Q
1119	VN_1119	YER036C	ARB1	ATPase of the ATP-binding cassette (ABC) family involved in 40S and 60S ribosome biogenesis, has similarity to Gcn20p; shuttles from nucleus to cytoplasm, physically interacts with Tif6p, Lsg1p	Q
1120	VN_1120	YPL005W	AEP3	Peripheral mitochondrial inner membrane protein, located on the matrix face of the membrane; stabilizes the bicistronic AAP1-ATP6 mRNA encoding subunits 6 and 8 of the ATP synthase complex	Q
1121	VN_1121	YOL148C	SPT20	Subunit of the SAGA transcriptional regulatory complex, involved in maintaining the integrity of the complex	Q
1122	VN_1122	YOR324C	FRT1	Tail-anchored, endoplasmic reticulum membrane protein that is a substrate of the phosphatase calcineurin, interacts with homolog Frt2p, promotes cell growth in conditions of high Na^{+} , alkaline pH, and cell wall stress	Q
1123	VN_1123	YDL079C	MRK1	Glycogen synthase kinase 3 (GSK-3) homolog; one of four GSK-3 homologs in <i>S. cerevisiae</i> that function to activate Msn2p-dependent transcription of stress responsive genes and that function in protein degradation	Q
1124	VN_1124	YKL005C	BYE1	Negative regulator of transcription elongation, contains a TFIIS-like domain and a PHD finger, multicopy suppressor of temperature-sensitive <i>ess1</i> mutations, probably binds RNA polymerase II large subunit	Q
1125	VN_1125	YCR088W	ABP1	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization	Q

1126	VN_1126	YGR013W	SNU71	Component of U1 snRNP required for mRNA splicing via spliceosome; yeast specific, no metazoan counterpart	Q
1127	VN_1127	YPR081C	GRS2	Protein with sequence similarity to Grs1p, which is a glycyl-tRNA synthetase; cannot substitute for Grs1p; possible pseudogene that is expressed at very low levels	Q
1128	VN_1128	YDL229W	SSB1	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p	Q
1129	VN_1129	YPL194W	DDC1	DNA damage checkpoint protein, part of a PCNA-like complex required for DNA damage response, required for pachytene checkpoint to inhibit cell cycle in response to unrepaired recombination intermediates; potential Cdc28p substrate	Q
1130	VN_1130	YGL116W	CDC20	Cell-cycle regulated activator of anaphase-promoting complex/cyclosome (APC/C), which is required for metaphase/anaphase transition; directs ubiquitination of mitotic cyclins, Pds1p, and other anaphase inhibitors; potential Cdc28p substrate	Strain failed to verify via PCR
1131	VN_1131	YLR173W	YLR173W	Putative protein of unknown function	Q
1132	VN_1132	YPR018W	RLF2	Largest subunit (p90) of the Chromatin Assembly Complex (CAF-1) with Cac2p and Msi1p that assembles newly synthesized histones onto recently replicated DNA; involved in the maintenance of transcriptionally silent chromatin	Q
1133	VN_1133	YOR108W	LEU9	Alpha-isopropylmalate synthase II (2-isopropylmalate synthase), catalyzes the first step in the leucine biosynthesis pathway; the minor isozyme, responsible for the residual alpha-IPMS activity detected in a leu4 null mutant	Q
1134	VN_1134	YBR186W	PCH2	Nucleolar component of the pachytene checkpoint, which prevents chromosome segregation when recombination and chromosome synapsis are defective; also represses meiotic interhomolog recombination in the rDNA	Q
1135	VN_1135	YLR368W	MDM30	F-box protein; associates with mitochondria and has a role in mitochondrial fusion; stimulates nuclear export of specific mRNAs; promotes ubiquitin-mediated degradation of Gal4p in some strains	Q
1136	VN_1136	YLR276C	DBP9	ATP-dependent RNA helicase of the DEAD-box family involved in biogenesis of the 60S ribosomal subunit	Q
1137	VN_1137	YLR089C	ALT1	Alanine transaminase (glutamic pyruvic transaminase); involved in alanine biosynthetic and catabolic processes; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
1138	VN_1138	YMR120C	ADE17	Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4-carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities, isozyme of Ade16p; ade16 ade17 mutants require adenine and histidine	Q
1139	VN_1139	YMR227C	TAF7	TFIID subunit (67 kDa), involved in RNA polymerase II transcription initiation	Q
1140	VN_1140	YOR027W	STI1	Hsp90 cochaperone, interacts with the Ssa group of the cytosolic Hsp70 chaperones; activates the ATPase activity of Ssa1p; homolog of mammalian Hop protein	Q
1141	VN_1141	YIL036W	CST6	Basic leucine zipper (bZIP) transcription factor of the ATF/CREB family, activates transcription of genes involved in utilization of non-optimal carbon sources; involved in telomere maintenance	Q
1142	VN_1142	YMR291W	YMR291W	Putative kinase of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YMR291W is not an essential gene	Q
1143	VN_1143	YKR078W	YKR078W	Cytoplasmic protein of unknown function, has similarity to Vps5p; potential Cdc28p substrate; contains a Phox homology (PX) domain and specifically binds phosphatidylinositol 3-phosphate (PtdIns-3-P)	Q
1144	VN_1144	YCL051W	LRE1	Protein involved in control of cell wall structure and stress response; inhibits Cbk1p protein kinase activity; overproduction confers resistance to cell-wall degrading enzymes	Q
1145	VN_1145	YJL216C	YJL216C	Protein of unknown function, similar to alpha-D-glucosidases; transcriptionally activated by both Pdr8p and Yrm1p, along with	Q

				transporters and other genes involved in the pleiotropic drug resistance (PDR) phenomenon	
1146	VN_1146	YBL039C	URA7	Major CTP synthase isozyme (see also URA8), catalyzes the ATP-dependent transfer of the amide nitrogen from glutamine to UTP, forming CTP, the final step in de novo biosynthesis of pyrimidines; involved in phospholipid biosynthesis	Q
1147	VN_1147	YOR260W	GCD1	Gamma subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression	Q
1148	VN_1148	YJL172W	CPS1	Vacuolar carboxypeptidase yscS; expression is induced under low-nitrogen conditions	Q
1149	VN_1149	YNL227C	JJJ1	Co-chaperone that stimulates the ATPase activity of Ssa1p, required for a late step of ribosome biogenesis; associated with the cytosolic large ribosomal subunit; contains a J-domain; mutation causes defects in fluid-phase endocytosis	Q
1150	VN_1150	YDR243C	PRP28	RNA helicase in the DEAD-box family, involved in RNA isomerization at the 5' splice site	Q
1151	VN_1151	YNL094W	APP1	Protein of unknown function, interacts with Rvs161p and Rvs167p; computational analysis of protein-protein interactions in large-scale studies suggests a possible role in actin filament organization	Q
1152	VN_1152	YOL015W	IRC10	Putative protein of unknown function; null mutant displays increased levels of spontaneous Rad52p foci	Q
1153	VN_1153	YMR250W	GAD1	Glutamate decarboxylase, converts glutamate into gamma-aminobutyric acid (GABA) during glutamate catabolism; involved in response to oxidative stress	Q
1154	VN_1154	YDL038C	YDL039C, PRM7	#N/A	Q
1155	VN_1155	YML127W	RSC9	Component of the RSC chromatin remodeling complex; DNA-binding protein involved in the synthesis of rRNA and in transcriptional repression and activation of genes regulated by the Target of Rapamycin (TOR) pathway	Q
1156	VN_1156	YHR150W	PEX28	Peroxisomal integral membrane peroxin, involved in the regulation of peroxisomal size, number and distribution; genetic interactions suggest that Pex28p and Pex29p act at steps upstream of those mediated by Pex30p, Pex31p, and Pex32p	Q
1157	VN_1157	YDR463W	STP1	Transcription factor, undergoes proteolytic processing by SPS (Ssy1p-Ptr3p-Ssy5p)-sensor component Ssy5p in response to extracellular amino acids; activates transcription of amino acid permease genes and may have a role in tRNA processing	Q
1158	VN_1158	YLR196W	PWP1	Protein with WD-40 repeats involved in rRNA processing; associates with trans-acting ribosome biogenesis factors; similar to beta-transducin superfamily	Q
1159	VN_1159	YPR006C	ICL2	2-methylisocitrate lyase of the mitochondrial matrix, functions in the methylcitrate cycle to catalyze the conversion of 2-methylisocitrate to succinate and pyruvate; ICL2 transcription is repressed by glucose and induced by ethanol	Q
1160	VN_1160	YFL053W	DAK2	Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress adaptation	Q
1161	VN_1161	YOR073W	SGO1	Component of the spindle checkpoint, involved in sensing lack of tension on mitotic chromosomes; protects centromeric Rec8p at meiosis I; required for accurate chromosomal segregation at meiosis II and for mitotic chromosome stability	Q
1162	VN_1162	YGL252C	RTG2	Sensor of mitochondrial dysfunction; regulates the subcellular location of Rtg1p and Rtg3p, transcriptional activators of the retrograde (RTG) and TOR pathways; Rtg2p is inhibited by the phosphorylated form of Mks1p	Q
1163	VN_1163	YNL218W	MGS1	Protein with DNA-dependent ATPase and ssDNA annealing activities involved in maintenance of genome; interacts functionally with DNA polymerase delta; homolog of human Werner helicase interacting protein (WHIP)	Q
1164	VN_1164	YBR163W	DEM1	Mitochondrial protein of unknown function; null mutant has defects in cell morphology and in response to air drying; may be regulated by the	Q

				transcription factor Ace2	
1165	VN_1165	YBR299W	MAL32	Maltase (alpha-D-glucosidase), inducible protein involved in maltose catabolism; encoded in the MAL3 complex locus; functional in genomic reference strain S288C	Q
1166	VN_1166	YKL012W	PRP40	U1 snRNP protein involved in splicing, interacts with the branchpoint-binding protein during the formation of the second commitment complex	Q
1167	VN_1167	YNL225C	CNM67	Component of the spindle pole body outer plaque; required for spindle orientation and mitotic nuclear migration	Q
1168	VN_1168	YHR194W	MDM31	Mitochondrial inner membrane protein with similarity to Mdm32p, required for normal mitochondrial morphology and inheritance; interacts genetically with MMM1, MDM10, MDM12, and MDM34	Q
1169	VN_1169	YER165W	PAB1	Poly(A) binding protein, part of the 3'-end RNA-processing complex, mediates interactions between the 5' cap structure and the 3' mRNA poly(A) tail, involved in control of poly(A) tail length, interacts with translation factor eIF-4G	Q
1170	VN_1170	YNL073W	MSK1	Mitochondrial lysine-tRNA synthetase, required for import of both aminoacylated and deacylated forms of tRNA(Lys) into mitochondria and for aminoacylation of mitochondrially encoded tRNA(Lys)	Q
1171	VN_1171	YJL071W	ARG2	Acetylglutamate synthase (glutamate N-acetyltransferase), mitochondrial enzyme that catalyzes the first step in the biosynthesis of the arginine precursor ornithine; forms a complex with Arg5,6p	Q
1172	VN_1172	YLR028C	ADE16	Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4-carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities, isozyme of Ade17p; ade16 ade17 mutants require adenine and histidine	Q
1173	VN_1173	YDR294C	DPL1	Dihydrosphingosine phosphate lyase, regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases, prefers C16 dihydrosphingosine-1-phosphate as a substrate	Q
1174	VN_1174	YOR154W	SLP1	Integral membrane protein of unknown function; member of the SUN-like family of proteins; genetic interactions suggest a role in folding of ER membrane proteins	Q
1175	VN_1175	YHL010C	ETP1	Putative protein of unknown function that is required for growth on ethanol; contains a zinc finger region and has homology to human BRAP2, which is a cytoplasmic protein that binds nuclear localization sequences	Q
1176	VN_1176	YLR077W	FMP25	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
1177	VN_1177	YOL153C	YOL153C	Hypothetical protein	Q
1178	VN_1178	YKL124W	SSH4	Specificity factor required for Rsp5p-dependent ubiquitination and sorting of cargo proteins at the multivesicular body; identified as a high-copy suppressor of a SHR3 deletion, increasing steady-state levels of amino acid permeases	Q
1179	VN_1179	YGL228W	SHE10	Putative glycosylphosphatidylinositol (GPI)-anchored protein of unknown function; overexpression causes growth arrest	Q
1180	VN_1180	YPR171W	BSP1	Adapter that links synaptojanins Inp52p and Inp53p to the cortical actin cytoskeleton	Q
1181	VN_1181	YJR053W	BFA1	Component of the GTPase-activating Bfa1p-Bub2p complex involved in multiple cell cycle checkpoint pathways that control exit from mitosis	Q
1182	VN_1182	YML054C	CYB2	Cytochrome b2 (L-lactate cytochrome-c oxidoreductase), component of the mitochondrial intermembrane space, required for lactate utilization; expression is repressed by glucose and anaerobic conditions	Q
1183	VN_1183	YGR287C	YGR287C	Isomaltase (alpha-D-glucosidase); may interact with ribosomes, based on co-purification experiments; authentic, non-tagged protein detected in purified mitochondria in high-throughput studies	Q
1184	VN_1184	YPL007C	TFC8	One of six subunits of RNA polymerase III transcription initiation factor complex (TFIIIC); part of TFIIIC TauB domain that binds BoxB promoter sites of tRNA and other genes; linker between TauB and	Q

				TauA domains; human homolog is TFIIC-90	
1185	VN_1185	YOR308C	SNU66	Component of the U4/U6.U5 snRNP complex involved in pre-mRNA splicing via spliceosome; has homology to human SART-1 and to an <i>S. pombe</i> protein; <i>snu66</i> null mutation confers cold-sensitivity but is not lethal at normal growth temperatures	Q
1186	VN_1186	YHL039W	YHL039W	Putative protein of unknown function; contains a SET-domain; predicted to be involved in ribosome biogenesis; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
1187	VN_1187	YML013W	UBX2	Protein involved in ER-associated protein degradation; proposed to coordinate the assembly of proteins involved in ERAD; contains a UBX (ubiquitin regulatory X) domain and a ubiquitin-associated (UBA) domain	Q
1188	VN_1188	YPL208W	RKM1	SET-domain lysine-N-methyltransferase, catalyzes the formation of dimethyllysine residues on the large ribosomal subunit protein L23a (RPL23A and RPL23B)	Q
1189	VN_1189	YAL040C	CLN3	G1 cyclin involved in cell cycle progression; activates Cdc28p kinase to promote the G1 to S phase transition; plays a role in regulating transcription of the other G1 cyclins, CLN1 and CLN2; regulated by phosphorylation and proteolysis	Q
1190	VN_1190	YPR083W	MDM36	Protein required for normal mitochondrial morphology and inheritance	Q
1191	VN_1191	YGR278W	CWC22	Essential protein, component of a complex containing Cef1p, has similarity to <i>S. pombe</i> Cwf22p; putative spliceosomal component, based on computational analysis of large-scale protein-protein interaction data	Q
1192	VN_1192	YGR171C	MSM1	Mitochondrial methionyl-tRNA synthetase (MetRS), functions as a monomer in mitochondrial protein synthesis; functions similarly to cytoplasmic MetRS although the cytoplasmic form contains a zinc-binding domain not found in Msm1p	Q
1193	VN_1193	YBR045C	GIP1	Meiosis-specific regulatory subunit of the Glc7p protein phosphatase, regulates spore wall formation and septin organization, required for expression of some late meiotic genes and for normal localization of Glc7p	Q
1194	VN_1194	YNL308C	KRI1	Essential nucleolar protein required for 40S ribosome biogenesis; physically and functionally interacts with Krr1p	Q
1195	VN_1195	YIL172C	YIL172C	Putative protein of unknown function with similarity to glucosidases; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
1196	VN_1196	YDL174C	DLD1	D-lactate dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane	Q
1197	VN_1197	YDL227C	HO	Site-specific endonuclease required for gene conversion at the MAT locus (homothallic switching) through the generation of a ds DNA break; expression restricted to mother cells in late G1 as controlled by Swi4p-Swi6p, Swi5p and Ash1p	Q
1198	VN_1198	YHR108W	GGA2	Golgi-localized protein with homology to gamma-adaptin, interacts with and regulates Arf1p and Arf2p in a GTP-dependent manner in order to facilitate traffic through the late Golgi	Q
1199	VN_1199	YML070W	DAK1	Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress adaptation	Q
1200	VN_1200	YCR014C	POL4	DNA polymerase IV, undergoes pair-wise interactions with Dnl4p-Lif1p and Rad27p to mediate repair of DNA double-strand breaks by non-homologous end joining (NHEJ); homologous to mammalian DNA polymerase beta	Q
1201	VN_1201	YBR170C	NPL4	Endoplasmic reticulum and nuclear membrane protein, forms a complex with Cdc48p and Ufd1p that recognizes ubiquitinated proteins in the endoplasmic reticulum and delivers them to the proteasome for degradation	Q
1202	VN_1202	YBR078W	ECM33	GPI-anchored protein of unknown function, has a possible role in apical bud growth; GPI-anchoring on the plasma membrane crucial to function; phosphorylated in mitochondria; similar to Sps2p and Pst1p	Q
1203	VN_1203	YER086W	ILV1	Threonine deaminase, catalyzes the first step in isoleucine biosynthesis; expression is under general amino acid control; ILV1	Q

				locus exhibits highly positioned nucleosomes whose organization is independent of known ILV1 regulation	
1204	VN_1204	YHR037W	PUT2	Delta-1-pyrroline-5-carboxylate dehydrogenase, nuclear-encoded mitochondrial protein involved in utilization of proline as sole nitrogen source; deficiency of the human homolog causes HPIL, an autosomal recessive inborn error of metabolism	Q
1205	VN_1205	YER124C	DSE1	Daughter cell-specific protein, may regulate cross-talk between the mating and filamentation pathways; deletion affects cell separation after division and sensitivity to alpha-factor and drugs affecting the cell wall	Q
1206	VN_1206	YOL066C	RIB2	Bifunctional enzyme with DRAP deaminase and tRNA:pseudouridine synthase activity; the deaminase catalyzes the third step in riboflavin biosynthesis and the synthase catalyzes formation of pseudouridine at position 32 in cytoplasmic tRNAs	Q
1207	VN_1207	YJL221C	FSP2	Protein of unknown function, expression is induced during nitrogen limitation	Q
1208	VN_1208	YER068W	MOT2	Subunit of the CCR4-NOT complex, which has roles in transcription regulation, mRNA degradation, and post-transcriptional modifications; with Ubc4p, ubiquitinates nascent polypeptide-associated complex subunits and histone demethylase Jhd2p	Q
1209	VN_1209	YGR068C	ART5	Protein proposed to regulate the endocytosis of plasma membrane proteins by recruiting the ubiquitin ligase Rsp5p to its target in the plasma membrane	Q
1210	VN_1210	YHR109W	CTM1	Cytochrome c lysine methyltransferase, trimethylates residue 72 of apo-cytochrome c (Cyc1p) in the cytosol; not required for normal respiratory growth	Q
1211	VN_1211	YNL076W	MKS1	Pleiotropic negative transcriptional regulator involved in Ras-CAMP and lysine biosynthetic pathways and nitrogen regulation; involved in retrograde (RTG) mitochondria-to-nucleus signaling	Q
1212	VN_1212	YDR440W	DOT1	Nucleosomal histone H3-Lys79 methylase; methylation is required for telomeric silencing, meiotic checkpoint control, and DNA damage response	Q
1213	VN_1213	YMR282C	AEP2	Mitochondrial protein, likely involved in translation of the mitochondrial OLI1 mRNA; exhibits genetic interaction with the OLI1 mRNA 5'-untranslated leader	Q
1214	VN_1214	YLR361C	DCR2	Phosphoesterase involved in downregulation of the unfolded protein response, at least in part via dephosphorylation of Ire1p; dosage-dependent positive regulator of the G1/S phase transition through control of the timing of START	Q
1215	VN_1215	YER087W	AIM10	Protein with similarity to tRNA synthetases; non-tagged protein is detected in purified mitochondria; null mutant is viable and displays elevated frequency of mitochondrial genome loss	Q
1216	VN_1216	YHR196W	UTP9	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA	Q
1217	VN_1217	YER158C	YER158C	Protein of unknown function, has similarity to Afr1p; potentially phosphorylated by Cdc28p	Q
1218	VN_1218	YMR213W	CEF1	Essential splicing factor; associated with Prp19p and the spliceosome, contains an N-terminal c-Myb DNA binding motif necessary for cell viability but not for Prp19p association, evolutionarily conserved and homologous to S. pombe Cdc5p	Q
1219	VN_1219	YOL157C	YOL157C	Putative protein of unknown function	Q
1220	VN_1220	YIL015W	BAR1	Aspartyl protease secreted into the periplasmic space of mating type a cells, helps cells find mating partners, cleaves and inactivates alpha factor allowing cells to recover from alpha-factor-induced cell cycle arrest	Q
1221	VN_1221	YJL186W	MNN5	Alpha-1,2-mannosyltransferase, responsible for addition of the second alpha-1,2-linked mannose of the branches on the mannan backbone of oligosaccharides, localizes to an early Golgi compartment	Q
1222	VN_1222	YJR016C	ILV3	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids	Q
1223	VN_1223	YOL115W	PAP2	Non-canonical poly(A) polymerase, involved in nuclear RNA	Q

				degradation as a component of the TRAMP complex; catalyzes polyadenylation of hypomodified tRNAs, and snoRNA and rRNA precursors; overlapping but non-redundant functions with Trf5p	
1224	VN_1224	YLR133W	CKI1	Choline kinase, catalyzing the first step in phosphatidylcholine synthesis via the CDP-choline (Kennedy pathway); exhibits some ethanolamine kinase activity contributing to phosphatidylethanolamine synthesis via the CDP-ethanolamine pathway	Q
1225	VN_1225	YNR059W	MNT4	Putative alpha-1,3-mannosyltransferase, not required for protein O-glycosylation	Strain failed to verify via PCR
1226	VN_1226	YML017W	PSP2	Asn rich cytoplasmic protein that contains RGG motifs; high-copy suppressor of group II intron-splicing defects of a mutation in MRS2 and of a conditional mutation in POL1 (DNA polymerase alpha); possible role in mitochondrial mRNA splicing	Q
1227	VN_1227	YIR010W	DSN1	Essential component of the MIND kinetochore complex (Mtw1p Including Nnf1p-Nsl1p-Dsn1p) which joins kinetochore subunits contacting DNA to those contacting microtubules; important for chromosome segregation	Q
1228	VN_1228	YLL058W	YLL058W	Putative protein of unknown function with similarity to Str2p, which is a cystathionine gamma-synthase important in sulfur metabolism; YLL058W is not an essential gene	Q
1229	VN_1229	YGR088W	CTT1	Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide	Q
1230	VN_1230	YLL012W	YEH1	Steryl ester hydrolase, one of three gene products (Yeh1p, Yeh2p, Tgl1p) responsible for steryl ester hydrolase activity and involved in sterol homeostasis; localized to lipid particle membranes	Q
1231	VN_1231	YGL160W	AIM14	Putative protein of with similarity to iron/copper reductases (FRE1-8), possibly involved in iron homeostasis; may interact with ribosomes; null mutant displays elevated frequency of mitochondrial genome loss	Q
1232	VN_1232	YKR002W	PAP1	Poly(A) polymerase, one of three factors required for mRNA 3'-end polyadenylation, forms multiprotein complex with polyadenylation factor I (PF I), also required for mRNA nuclear export; may also polyadenylate rRNAs	Q
1233	VN_1233	YLR417W	VPS36	Component of the ESCRT-II complex; contains the GLUE (GRAM Like Ubiquitin binding in EAP45) domain which is involved in interactions with ESCRT-I and ubiquitin-dependent sorting of proteins into the endosome	Q
1234	VN_1234	YCR065W	HCM1	Forkhead transcription factor that drives S-phase specific expression of genes involved in chromosome segregation, spindle dynamics, and budding; suppressor of calmodulin mutants with specific SPB assembly defects; telomere maintenance role	Q
1235	VN_1235	YLR134W	PDC5	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and ethanol-dependent, repressed by thiamine, involved in amino acid catabolism	Q
1236	VN_1236	YEL020C	YEL020C	Hypothetical protein with low sequence identity to Pdc1p	Q
1237	VN_1237	YDR212W	TCP1	Alpha subunit of chaperonin-containing T-complex, which mediates protein folding in the cytosol; involved in actin cytoskeleton maintenance; overexpression in neurons suppresses formation of pathogenic conformations of huntingtin protein	Q
1238	VN_1238	YLL018C	DPS1	Aspartyl-tRNA synthetase, primarily cytoplasmic; homodimeric enzyme that catalyzes the specific aspartylation of tRNA(Asp); class II aminoacyl tRNA synthetase; binding to its own mRNA may confer autoregulation	Q
1239	VN_1239	YJL153C	INO1	Inositol 1-phosphate synthase, involved in synthesis of inositol phosphates and inositol-containing phospholipids; transcription is coregulated with other phospholipid biosynthetic genes by Ino2p and Ino4p, which bind the UASINO DNA element	Q
1240	VN_1240	YOL027C	MDM38	Mitochondrial inner membrane protein, involved in membrane integration of a subset of mitochondrial proteins; required for K ⁺ /H ⁺ exchange; associates with mitochondrial ribosomes; human ortholog Letm1 implicated in Wolf-Hirschhorn syndrome	Q

1241	VN_1241	YPR145W	ASN1	Asparagine synthetase, isozyme of Asn2p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway	Strain failed to verify via PCR
1242	VN_1242	YKL127W	PGM1	Phosphoglucosyltransferase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism	Q
1243	VN_1243	YKR015C	YKR015C	Putative protein of unknown function	Q
1244	VN_1244	YNR023W	SNF12	73 kDa subunit of the SWI/SNF chromatin remodeling complex involved in transcriptional regulation; homolog of Rsc6p subunit of the RSC chromatin remodeling complex; deletion mutants are temperature-sensitive	Strain failed to verify via PCR
1245	VN_1245	YGL171W	ROK1	ATP-dependent RNA helicase of the DEAD box family; required for 18S rRNA synthesis	Q
1246	VN_1246	YDL042C	SIR2	Conserved NAD ⁺ dependent histone deacetylase of the Sirtuin family involved in regulation of lifespan; plays roles in silencing at HML, HMR, telomeres, and the rDNA locus; negatively regulates initiation of DNA replication	Q
1247	VN_1247	YGL179C	TOS3	Protein kinase, related to and functionally redundant with Elm1p and Sak1p for the phosphorylation and activation of Snf1p; functionally orthologous to LKB1, a mammalian kinase associated with Peutz-Jeghers cancer-susceptibility syndrome	Q
1248	VN_1248	YGL244W	RTF1	Subunit of the RNA polymerase II-associated Paf1 complex; directly or indirectly regulates DNA-binding properties of Spt15p and relative activities of different TATA elements; involved in telomere maintenance	Q
1249	VN_1249	YPL086C	ELP3	Subunit of Elongator complex, which is required for modification of wobble nucleosides in tRNA; exhibits histone acetyltransferase activity that is directed to histones H3 and H4; disruption confers resistance to K. lactis zymotoxin	Q
1250	VN_1250	YLR343W	GAS2	1,3-beta-glucanosyltransferase, involved with Gas4p in spore wall assembly; has similarity to Gas1p	Q
1251	VN_1251	YIR031C	DAL7	Malate synthase, role in allantoin degradation unknown; expression sensitive to nitrogen catabolite repression and induced by allophanate, an intermediate in allantoin degradation	Q
1252	VN_1252	YPR137W	RRP9	Protein involved in pre-rRNA processing, associated with U3 snRNP; component of small ribosomal subunit (SSU) processosome; ortholog of the human U3-55k protein	Q
1253	VN_1253	YHR184W	SSP1	Protein involved in the control of meiotic nuclear division and coordination of meiosis with spore formation; transcription is induced midway through meiosis	Q
1254	VN_1254	YLR267W	BOP2	Protein of unknown function	Q
1255	VN_1255	YOR118W	RTC5	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; null mutation suppresses cdc13-1 temperature sensitivity	Q
1256	VN_1256	YOR023C	AHC1	Subunit of the Ada histone acetyltransferase complex, required for structural integrity of the complex	Q
1257	VN_1257	YJR103W	URA8	Minor CTP synthase isozyme (see also URA7), catalyzes the ATP-dependent transfer of the amide nitrogen from glutamine to UTP, forming CTP, the final step in de novo biosynthesis of pyrimidines; involved in phospholipid biosynthesis	Q
1258	VN_1258	YDR261C	EXG2	Exo-1,3-beta-glucanase, involved in cell wall beta-glucan assembly; may be anchored to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor	Q
1259	VN_1259	YGR166W	KRE11	Protein involved in biosynthesis of cell wall beta-glucans; subunit of the TRAPP (transport protein particle) complex, which is involved in the late steps of endoplasmic reticulum to Golgi transport	Q
1260	VN_1260	YGL257C	MNT2	Mannosyltransferase involved in adding the 4th and 5th mannose residues of O-linked glycans	Q
1261	VN_1261	YDR131C	YDR131C	F-box protein, substrate-specific adaptor subunit that recruits substrates to a core ubiquitination complex	Q
1262	VN_1262	YNL182C	IPI3	Essential component of the Rix1 complex (Rix1p, Ipi1p, Ipi3p) that is	Strain failed

				required for processing of ITS2 sequences from 35S pre-rRNA; highly conserved and contains WD40 motifs; Rix1 complex associates with Mdn1p in pre-60S ribosomal particles	to verify via PCR
1263	VN_1263	YKL109W	HAP4	Subunit of the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression; provides the principal activation function of the complex	Strain failed to verify via PCR
1264	VN_1264	YGR092W	DBF2	Ser/Thr kinase involved in transcription and stress response; functions as part of a network of genes in exit from mitosis; localization is cell cycle regulated; activated by Cdc15p during the exit from mitosis	Q
1265	VN_1265	YIL150C	MCM10	Essential chromatin-associated protein involved in the initiation of DNA replication; required for the association of the MCM2-7 complex with replication origins	Q
1266	VN_1266	YLR120C	YPS1	Aspartic protease, attached to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor	Q
1267	VN_1267	YPL030W	TRM44	tRNA(Ser) Um(44) 2'-O-methyltransferase; involved in maintaining levels of the tRNA-Ser species tS(CGA) and tS(UGA); conserved among metazoans and fungi but there does not appear to be a homolog in plants; TRM44 is a non-essential gene	Q
1268	VN_1268	YPR070W	MED1	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation	Q
1269	VN_1269	YPR111W	DBF20	Ser/Thr kinase involved in late nuclear division, one of the mitotic exit network (MEN) proteins; necessary for the execution of cytokinesis	Q
1270	VN_1270	YJR064W	CCT5	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	Strain failed to verify via PCR
1271	VN_1271	YJL105W	SET4	Protein of unknown function, contains a SET domain	Q
1272	VN_1272	YNL193W	YNL193W	Putative protein of unknown function; exhibits a two-hybrid interaction with Yhr151cp in a large-scale analysis	Q
1273	VN_1273	YER140W	YER140W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; genetic interactions suggest a role in folding of ER membrane proteins	Q
1274	VN_1274	YMR036C	MIH1	Protein tyrosine phosphatase involved in cell cycle control; regulates the phosphorylation state of Cdc28p; homolog of <i>S. pombe</i> cdc25	Strain failed to verify via PCR
1275	VN_1275	YGR124W	ASN2	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway	Q
1276	VN_1276	YKL088W	CAB3	Subunit of a phosphopantothienoylcysteine decarboxylase (PPCDC; Cab3p, Sis2p, Vhs3p) complex, which catalyzes the third step of coenzyme A biosynthesis; null mutant lethality is complemented by <i>E. coli</i> coaBC	Q
1277	VN_1277	YLR253W	YLR253W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; transcription is periodic during the metabolic cycle; YLR253W is not an essential gene	Q
1278	VN_1278	YCL036W	GFD2	Protein of unknown function, identified as a high-copy suppressor of a dbp5 mutation	Q
1279	VN_1279	YBR263W	SHM1	Mitochondrial serine hydroxymethyltransferase, converts serine to glycine plus 5,10 methylenetetrahydrofolate; involved in generating precursors for purine, pyrimidine, amino acid, and lipid biosynthesis; reverse reaction generates serine	Q
1280	VN_1280	YBR286W	APE3	Vacuolar aminopeptidase Y, processed to mature form by Prb1p	Q
1281	VN_1281	YKR072C	SIS2	Negative regulatory subunit of protein phosphatase 1 Ppz1p and also a subunit of the phosphopantothienoylcysteine decarboxylase (PPCDC; Cab3p, Sis2p, Vhs3p) complex, which catalyzes the third step of coenzyme A biosynthesis	Q
1282	VN_1282	YMR136W	GAT2	Protein containing GATA family zinc finger motifs; similar to Gln3p and Dal80p; expression repressed by leucine	Q
1283	VN_1283	YDR358W	GGA1	Golgi-localized protein with homology to gamma-adaptin, interacts	Q

				with and regulates Arf1p and Arf2p in a GTP-dependent manner in order to facilitate traffic through the late Golgi	
1284	VN_1284	YML023C	NSE5	Essential subunit of the Mms21-Smc5-Smc6 complex; required for cell viability and DNA repair	Strain failed to verify via PCR
1285	VN_1285	YBR196C	PGI1	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression and completion of the gluconeogenic events of sporulation	Strain failed to verify via PCR
1286	VN_1286	YNL117W	MLS1	Malate synthase, enzyme of the glyoxylate cycle, involved in utilization of non-fermentable carbon sources; expression is subject to carbon catabolite repression; localizes in peroxisomes during growth in oleic acid medium	Strain failed to verify via PCR
1287	VN_1287	YHR064C	SSZ1	Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome-associated complex that binds the ribosome via the Zuo1p subunit; also involved in pleiotropic drug resistance via sequential activation of PDR1 and PDR5; binds ATP	Strain failed to verify via PCR
1288	VN_1288	YOR128C	ADE2	Phosphoribosylaminoimidazole carboxylase, catalyzes a step in the 'de novo' purine nucleotide biosynthetic pathway; red pigment accumulates in mutant cells deprived of adenine	Q
1289	VN_1289	YMR105C	PGM2	Phosphoglucomutase, catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; functions as the acceptor for a Glc-phosphotransferase	Q
1290	VN_1290	YDL003W	MCD1	Essential subunit of the cohesin complex required for sister chromatid cohesion in mitosis and meiosis; apoptosis induces cleavage and translocation of a C-terminal fragment to mitochondria; expression peaks in S phase	Q
1291	VN_1291	YDR117C	TMA64	Protein of unknown function that associates with ribosomes; has a putative RNA binding domain	Q
1292	VN_1292	YCR054C	CTR86	Essential protein of unknown function; upstream region contains a Gcn4p responsive site suggesting a possible role in amino acid biosynthesis	Q
1293	VN_1293	YLR286C	CTS1	Endochitinase, required for cell separation after mitosis; transcriptional activation during the G1 phase of the cell cycle is mediated by transcription factor Ace2p	Q
1294	VN_1294	YMR145C	NDE1	Mitochondrial external NADH dehydrogenase, a type II NAD(P)H:quinone oxidoreductase that catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p provide cytosolic NADH to the mitochondrial respiratory chain	Q
1295	VN_1295	YEL058W	PCM1	Essential N-acetylglucosamine-phosphate mutase; converts GlcNAc-6-P to GlcNAc-1-P, which is a precursor for the biosynthesis of chitin and for the formation of N-glycosylated mannoproteins and glycosylphosphatidylinositol anchors	Q
1296	VN_1296	YOR205C	GEP3	Protein of unknown function; null mutant is defective in respiration and interacts synthetically with prohibitin (phb1); the authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies	Q
1297	VN_1297	YDR479C	PEX29	Peroxisomal integral membrane peroxin, involved in the regulation of peroxisomal size, number and distribution; genetic interactions suggest that Pex28p and Pex29p act at steps upstream of those mediated by Pex30p, Pex31p, and Pex32p	Q
1298	VN_1298	YOR372C	NDD1	Transcriptional activator essential for nuclear division; localized to the nucleus; essential component of the mechanism that activates the expression of a set of late-S-phase-specific genes	Q
1299	VN_1299	YLR259C	HSP60	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; phosphorylated	Q
1300	VN_1300	YDR026C	YDR026C	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; Myb-like DNA-binding protein that may bind to the Ter region of rDNA; interacts physically with Fob1p	Q
1301	VN_1301	YGR241C	YAP1802	Protein involved in clathrin cage assembly; binds Pan1p and clathrin; homologous to Yap1801p, member of the AP180 protein family	Q

1302	VN_1302	YDR110W	FOB1	Nucleolar protein that binds the rDNA replication fork barrier (RFB) site; required for replication fork blocking, recombinational hotspot activity, condensin recruitment to RFB and rDNA repeat segregation; related to retroviral integrases	Q
1303	VN_1303	YJR052W	RAD7	Protein that recognizes and binds damaged DNA in an ATP-dependent manner (with Rad16p) during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 4 (NEF4) and the Elongin-Cullin-Socs (ECS) ligase complex	Q
1304	VN_1304	YGR087C	PDC6	Minor isoform of pyruvate decarboxylase, decarboxylates pyruvate to acetaldehyde, involved in amino acid catabolism; transcription is glucose- and ethanol-dependent, and is strongly induced during sulfur limitation	Strain failed to verify via PCR
1305	VN_1305	YPL128C	TBF1	Telobox-containing general regulatory factor; binds to TTAGGG repeats within subtelomeric anti-silencing regions (STARs) and possibly throughout the genome and mediates their insulating capacity by blocking silent chromatin propagation	Q
1306	VN_1306	YPR072W	NOT5	Subunit of the CCR4-NOT complex, which is a global transcriptional regulator with roles in transcription initiation and elongation and in mRNA degradation	Q
1307	VN_1307	YER065C	ICL1	Isocitrate lyase, catalyzes the formation of succinate and glyoxylate from isocitrate, a key reaction of the glyoxylate cycle; expression of ICL1 is induced by growth on ethanol and repressed by growth on glucose	Q
1308	VN_1308	YDR474C	d8035.17	#N/A	Q
1309	VN_1309	YER082C	UTP7	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA	Q
1310	VN_1310	YGL076C	RPL7A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2)	Q
1311	VN_1311	YOR090C	PTC5	Mitochondrial type 2C protein phosphatase involved in regulation of pyruvate dehydrogenase activity by dephosphorylating the ser-133 residue of the Pda1p subunit; acts in concert with kinases Pkp1p and Pkp2p and phosphatase Ptc6p	Q
1312	VN_1312	YDR120C	TRM1	tRNA methyltransferase; two forms of the protein are made by alternative translation starts; localizes to both the nucleus and mitochondrion to produce the modified base N2,N2-dimethylguanosine in tRNAs in both compartments	Q
1313	VN_1313	YJL008C	CCT8	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	Strain failed to verify via PCR
1314	VN_1314	YGL003C	CDH1	Cell-cycle regulated activator of the anaphase-promoting complex/cyclosome (APC/C), which directs ubiquitination of cyclins resulting in mitotic exit; targets the APC/C to specific substrates including Cdc20p, Ase1p, Cin8p and Fin1p	Q
1315	VN_1315	YOR386W	PHR1	DNA photolyase involved in photoreactivation, repairs pyrimidine dimers in the presence of visible light; induced by DNA damage; regulated by transcriptional repressor Rph1p	Q
1316	VN_1316	YLR044C	PDC1	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism	Q
1317	VN_1317	YGL064C	MRH4	Mitochondrial ATP-dependent RNA helicase of the DEAD-box family, plays an essential role in mitochondrial function	Q
1318	VN_1318	YDL106C	PHO2	Homeobox transcription factor; regulatory targets include genes involved in phosphate metabolism; binds cooperatively with Pho4p to the PHO5 promoter; phosphorylation of Pho2p facilitates interaction with Pho4p	Q
1319	VN_1319	YFR037C	RSC8	Component of the RSC chromatin remodeling complex; essential for viability and mitotic growth; homolog of SWI/SNF subunit Swi3p, but unlike Swi3p, does not activate transcription of reporters	Q

1320	VN_1320	YFL042C	YFL042C	Putative protein of unknown function; YFL042C is not an essential gene	Strain failed to verify via PCR
1321	VN_1321	YGL176C	YGL176C	Putative protein of unknown function; deletion mutant is viable and has no detectable phenotype	Q
1322	VN_1322	YLR433C	CNA1	Calcineurin A; one isoform (the other is CMP2) of the catalytic subunit of calcineurin, a Ca ⁺⁺ /calmodulin-regulated protein phosphatase which regulates Crz1p (a stress-response transcription factor), the other calcineurin subunit is CNB1	Q
1323	VN_1323	YEL015W	EDC3	Non-essential conserved protein of unknown function, plays a role in mRNA decapping by specifically affecting the function of the decapping enzyme Dcp1p; localizes to cytoplasmic mRNA processing bodies	Q
1324	VN_1324	YJL111W	CCT7	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	Q
1325	VN_1325	YPL228W	CET1	Beta (RNA 5'-triphosphatase) subunit of the mRNA capping enzyme, a heterodimer (the other subunit is CEG1, a guanylyltransferase) involved in adding the 5' cap to mRNA; the mammalian enzyme is a single bifunctional polypeptide	Q
1326	VN_1326	YMR199W	CLN1	G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends on transcription factor complexes, MBF (Swi6p-Mbp1p) and SBF (Swi6p-Swi4p)	Q
1327	VN_1327	YDR235W	PRP42	U1 snRNP protein involved in splicing, required for U1 snRNP biogenesis; contains multiple tetra-tricopeptide repeats	Q
1328	VN_1328	YGL028C	SCW11	Cell wall protein with similarity to glucanases; may play a role in conjugation during mating based on its regulation by Ste12p	Q
1329	VN_1329	YDR061W	YDR061W	Protein with similarity to ATP-binding cassette (ABC) transporter family members; lacks predicted membrane-spanning regions; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance	Q
1330	VN_1330	YOL033W	MSE1	Mitochondrial glutamyl-tRNA synthetase, predicted to be palmitoylated	Q
1331	VN_1331	YJL014W	CCT3	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	Q
1332	VN_1332	YMR110C	HFD1	Putative fatty aldehyde dehydrogenase, located in the mitochondrial outer membrane and also in lipid particles; has similarity to human fatty aldehyde dehydrogenase (FALDH) which is implicated in Sjogren-Larsson syndrome	Q
1333	VN_1333	YBR239C	YBR239C	Putative protein of unknown function; GFP-fusion protein localizes to the cytoplasm and nucleus; null mutation affects periodicity of transcriptional and metabolic oscillation; plays a role in restricting Ty1 transposition	Q
1334	VN_1334	YMR258C	YMR258C	Protein of unknown function with similarity to F-box proteins; physically interacts with Skp1p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YMR258C is not an essential gene	Q
1335	VN_1335	YFR028C	CDC14	Protein phosphatase required for mitotic exit; located in the nucleolus until liberated by the FEAR and Mitotic Exit Network in anaphase, enabling it to act on key substrates to effect a decrease in CDK/B-cyclin activity and mitotic exit	Q
1336	VN_1336	YMR171C	EAR1	Specificity factor required for Rsp5p-dependent ubiquitination and sorting of specific cargo proteins at the multivesicular body; mRNA is targeted to the bud via the mRNA transport system involving She2p	Q
1337	VN_1337	YDR232W	HEM1	5-aminolevulinate synthase, catalyzes the first step in the heme biosynthetic pathway; an N-terminal signal sequence is required for localization to the mitochondrial matrix; expression is regulated by Hap2p-Hap3p	Q
1338	VN_1338	YOR380W	RDR1	Transcriptional repressor involved in the control of multidrug resistance; negatively regulates expression of the PDR5 gene; member of the Gal4p family of zinc cluster proteins	Q
1339	VN_1339	YOR002W	ALG6	Alpha 1,3 glucosyltransferase, involved in transfer of oligosaccharides from dolichyl pyrophosphate to asparagine residues of proteins during	Q

				N-linked protein glycosylation; mutations in human ortholog are associated with disease	
1340	VN_1340	YNL189W	SRP1	Karyopherin alpha homolog, forms a dimer with karyopherin beta Kap95p to mediate import of nuclear proteins, binds the nuclear localization signal of the substrate during import; may also play a role in regulation of protein degradation	Q
1341	VN_1341	YDR145W	TAF12	Subunit (61/68 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, similar to histone H2A	Q
1342	VN_1342	YBR103W	SIF2	WD40 repeat-containing subunit of the Set3C histone deacetylase complex, which represses early/middle sporulation genes; antagonizes telomeric silencing; binds specifically to the Sir4p N-terminus	Q
1343	VN_1343	YKL191W	DPH2	Protein required, along with Dph1p, Kti11p, Jjj3p, and Dph5p, for synthesis of diphthamide, which is a modified histidine residue of translation elongation factor 2 (Eft1p or Eft2p); may act in a complex with Dph1p and Kti11p	Q
1344	VN_1344	YMR297W	PRC1	Vacuolar carboxypeptidase Y (proteinase C; CPY), broad-specificity C-terminal exopeptidase involved in non-specific protein degradation in the vacuole; member of the serine carboxypeptidase family	Q
1345	VN_1345	YIL146C	ATG32	Mitochondrial-anchored transmembrane receptor that interacts with the autophagy adaptor protein, Atg11p, and is essential for mitophagy, the selective vacuolar degradation of mitochondria in response to starvation	Q
1346	VN_1346	YBR030W	RKM3	Ribosomal lysine methyltransferase specific for monomethylation of Rpl42ap and Rpl42bp (lysine 40); nuclear SET domain containing protein	Q
1347	VN_1347	YGR023W	MTL1	Protein with both structural and functional similarity to Mid2p, which is a plasma membrane sensor required for cell integrity signaling during pheromone-induced morphogenesis; suppresses rgd1 null mutations	Q
1348	VN_1348	YBR158W	AMN1	Protein required for daughter cell separation, multiple mitotic checkpoints, and chromosome stability; contains 12 degenerate leucine-rich repeat motifs; expression is induced by the Mitotic Exit Network (MEN)	Q
1349	VN_1349	YER054C	GIP2	Putative regulatory subunit of the protein phosphatase Glc7p, involved in glycogen metabolism; contains a conserved motif (GVNK motif) that is also found in Gac1p, Pig1p, and Pig2p	Q
1350	VN_1350	YPR033C	HTS1	Cytoplasmic and mitochondrial histidine tRNA synthetase; encoded by a single nuclear gene that specifies two messages; efficient mitochondrial localization requires both a presequence and an amino-terminal sequence	Q
1351	VN_1351	YPL212C	PUS1	tRNA:pseudouridine synthase, introduces pseudouridines at positions 26-28, 34-36, 65, and 67 of tRNA; nuclear protein that appears to be involved in tRNA export; also acts on U2 snRNA	Q
1352	VN_1352	YNL249C	MPA43	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
1353	VN_1353	YJR003C	YJR003C	Putative protein of unknown function; detected in highly purified mitochondria in high-throughput studies; predicted to be involved in ribosome biogenesis	Q
1354	VN_1354	YNL199C	GCR2	Transcriptional activator of genes involved in glycolysis; interacts and functions with the DNA-binding protein Gcr1p	Q
1355	VN_1355	YDL020C	RPN4	Transcription factor that stimulates expression of proteasome genes; Rpn4p levels are in turn regulated by the 26S proteasome in a negative feedback control mechanism; RPN4 is transcriptionally regulated by various stress responses	Strain failed to verify via PCR
1356	VN_1356	YBR248C	HIS7	Imidazole glycerol phosphate synthase (glutamine amidotransferase:cyclase), catalyzes the fifth and sixth steps of histidine biosynthesis and also produces 5-aminoimidazole-4-carboxamide ribotide (AICAR), a purine precursor	Q
1357	VN_1357	YJL110C	GZF3	GATA zinc finger protein and Dal80p homolog that negatively regulates nitrogen catabolic gene expression by competing with Gat1p for GATA site binding; function requires a repressive carbon source; dimerizes with Dal80p and binds to Tor1p	Q

1358	VN_1358	YDR242W	AMD2	Putative amidase	Q
1359	VN_1359	YKL140W	TGL1	Steryl ester hydrolase, one of three gene products (Yeh1p, Yeh2p, Tgl1p) responsible for steryl ester hydrolase activity and involved in sterol homeostasis; localized to lipid particle membranes	Q
1360	VN_1360	YBR270C	BIT2	Subunit of TORC2, a membrane-associated complex that regulates actin cytoskeletal dynamics during polarized growth and cell wall integrity; interacts with Slm1p and Slm2p, homologous PH domain-containing TORC2 substrates; similar to Bit61p	Q
1361	VN_1361	YBL080C	PET112	Subunit of the trimeric GatFAB AmidoTransferase(AdT) complex; involved in the formation of Q-tRNAQ; mutation is functionally complemented by the bacterial GatB ortholog	Q
1362	VN_1362	YIL045W	PIG2	Putative type-1 protein phosphatase targeting subunit that tethers Glc7p type-1 protein phosphatase to Gsy2p glycogen synthase	Q
1363	VN_1363	YGR177C	ATF2	Alcohol acetyltransferase, may play a role in steroid detoxification; forms volatile esters during fermentation, which is important in brewing	Q
1364	VN_1364	YOL123W	HRP1	Subunit of cleavage factor I, a five-subunit complex required for the cleavage and polyadenylation of pre-mRNA 3' ends; RRM-containing heteronuclear RNA binding protein and hnRNPA/B family member that binds to poly (A) signal sequences	Q
1365	VN_1365	YDL030W	PRP9	Subunit of the SF3a splicing factor complex, required for spliceosome assembly; acts after the formation of the U1 snRNP-pre-mRNA complex	Q
1366	VN_1366	YAL028W	FRT2	Tail-anchored endoplasmic reticulum membrane protein, interacts with homolog Frt1p but is not a substrate of calcineurin (unlike Frt1p), promotes growth in conditions of high Na ⁺ , alkaline pH, or cell wall stress; potential Cdc28p substrate	Q
1367	VN_1367	YKR017C	YKR017C	Putative protein of unknown function; contains a RING finger motif	Q
1368	VN_1368	YIL099W	SGA1	Intracellular sporulation-specific glucoamylase involved in glycogen degradation; induced during starvation of a/a diploids late in sporulation, but dispensable for sporulation	Q
1369	VN_1369	YOR241W	MET7	Folylpolyglutamate synthetase, catalyzes extension of the glutamate chains of the folate coenzymes, required for methionine synthesis and for maintenance of mitochondrial DNA	Q
1370	VN_1370	YDL085W	NDE2	Mitochondrial external NADH dehydrogenase, catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p are involved in providing the cytosolic NADH to the mitochondrial respiratory chain	Q
1371	VN_1371	YJL058C	BIT61	Subunit of TORC2 (Tor2p-Lst8p-Avo1-Avo2-Tsc11p-Bit61p-Slm1p-Slm2p), a membrane-associated complex that regulates cell cycle-dependent actin cytoskeletal dynamics during polarized growth and cell wall integrity	Q
1372	VN_1372	YHR006W	STP2	Transcription factor, activated by proteolytic processing in response to signals from the SPS sensor system for external amino acids; activates transcription of amino acid permease genes	Q
1373	VN_1373	YLR020C	YEH2	Steryl ester hydrolase, catalyzes steryl ester hydrolysis at the plasma membrane; involved in sterol metabolism	Q
1374	VN_1374	YML115C	VAN1	Component of the mannan polymerase I, which contains Van1p and Mnn9p and is involved in the first steps of mannan synthesis; mutants are vanadate-resistant	Q
1375	VN_1375	YDR195W	REF2	RNA-binding protein involved in the cleavage step of mRNA 3'-end formation prior to polyadenylation, and in snoRNA maturation; part of holo-CPF subcomplex APT, which associates with 3'-ends of snoRNA- and mRNA-encoding genes	Q
1376	VN_1376	YDL178W	DLD2	D-lactate dehydrogenase, located in the mitochondrial matrix	Q
1377	VN_1377	YBR020W	GAL1	Galactokinase, phosphorylates alpha-D-galactose to alpha-D-galactose-1-phosphate in the first step of galactose catabolism; expression regulated by Gal4p	Q
1378	VN_1378	YPR144C	NOC4	Nucleolar protein, forms a complex with Nop14p that mediates maturation and nuclear export of 40S ribosomal subunits	Q
1379	VN_1379	YOL055C	THI20	Multifunctional protein with hydroxymethylpyrimidine phosphate (HMP-P) kinase and thiaminase activities; involved in thiamine	Q

				biosynthesis and degradation; in a gene family with THI21 and THI22; HMP-P kinase activity redundant with Thi21p	
1380	VN_1380	YKL089W	MIF2	Kinetochore protein with homology to human CENP-C, required for structural integrity of the spindle during anaphase spindle elongation, interacts with histones H2A, H2B, and H4, phosphorylated by Ipl1p	Q
1381	VN_1381	YGR041W	BUD9	Protein involved in bud-site selection; diploid mutants display a unipolar budding pattern instead of the wild-type bipolar pattern, and bud at the distal pole	Q
1382	VN_1382	YPL256C	CLN2	G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends on transcription factor complexes, MBF (Swi6p-Mbp1p) and SBF (Swi6p-Swi4p)	Q
1383	VN_1383	YLR023C	IZH3	Membrane protein involved in zinc ion homeostasis, member of the four-protein IZH family, expression induced by zinc deficiency; deletion reduces sensitivity to elevated zinc and shortens lag phase, overexpression reduces Zap1p activity	Q
1384	VN_1384	YPR088C	SRP54	Signal recognition particle (SRP) subunit (homolog of mammalian SRP54); contains the signal sequence-binding activity of SRP, interacts with the SRP RNA, and mediates binding of SRP to signal receptor; contains GTPase domain	Strain failed to verify via PCR
1385	VN_1385	YMR015C	ERG5	C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a target of azole antifungal drugs	Q
1386	VN_1386	YDR147W	EK11	Ethanolamine kinase, primarily responsible for phosphatidylethanolamine synthesis via the CDP-ethanolamine pathway; exhibits some choline kinase activity, thus contributing to phosphatidylcholine synthesis via the CDP-choline pathway	Q
1387	VN_1387	YDR488C	PAC11	Dynein intermediate chain, acts in the cytoplasmic dynein pathway, forms cortical cytoplasmic microtubule capture site with Num1p; null mutant is defective in nuclear migration, essential in the absence of CIN8	Q
1388	VN_1388	YJR049C	UTR1	ATP-NADH kinase; phosphorylates both NAD and NADH; active as a hexamer; enhances the activity of ferric reductase (Fre1p)	Q
1389	VN_1389	YDL143W	CCT4	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	Q
1390	VN_1390	YBR200W	BEM1	Protein containing SH3-domains, involved in establishing cell polarity and morphogenesis; functions as a scaffold protein for complexes that include Cdc24p, Ste5p, Ste20p, and Rsr1p	Q
1391	VN_1391	YPL258C	THI21	Hydroxymethylpyrimidine phosphate kinase, involved in the last steps in thiamine biosynthesis; member of a gene family with THI20 and THI22; Thi20p also has this activity	Q
1392	VN_1392	YKR097W	PCK1	Phosphoenolpyruvate carboxykinase, key enzyme in gluconeogenesis, catalyzes early reaction in carbohydrate biosynthesis, glucose represses transcription and accelerates mRNA degradation, regulated by Mcm1p and Cat8p, located in the cytosol	Q
1393	VN_1393	YDR188W	CCT6	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, essential protein that is required for the assembly of actin and tubulins in vivo; contains an ATP-binding motif	Q
1394	VN_1394	YML124C	TUB3	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; expressed at lower level than Tub1p	Q
1395	VN_1395	YPL109C	YPL109C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
1396	VN_1396	YKR016W	FCJ1	Mitochondrial inner membrane protein involved in formation and molecular structure of crista junctions; impairs oligomerization of F1F0-ATP synthase; null shows altered mitochondrial morphology and abnormal mitochondrial genome maintenance	Q
1397	VN_1397	YIR039C	YPS6	Putative GPI-anchored aspartic protease	Q
1398	VN_1398	YDR299W	BFR2	Essential protein that is a component of 90S preribosomes; may be involved in rRNA processing; multicopy suppressor of sensitivity to Brefeldin A; expression is induced during lag phase and also by cold shock	Q

1399	VN_1399	YNL294C	RIM21	Component of the RIM101 pathway, has a role in cell wall construction and alkaline pH response; has similarity to A. nidulans PalH	Q
1400	VN_1400	YKR023W	YKR023W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
1401	VN_1401	YDL170W	UGA3	Transcriptional activator necessary for gamma-aminobutyrate (GABA)-dependent induction of GABA genes (such as UGA1, UGA2, UGA4); zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type; localized to the nucleus	Q
1402	VN_1402	YDL225W	SHS1	One of five related septins (Cdc3p, Cdc10p, Cdc11p, Cdc12p, Shs1p) that form a cortical filamentous collar at the mother-bud neck which is necessary for normal morphogenesis and cytokinesis	Q
1403	VN_1403	YPL260W	YPL260W	Putative substrate of cAMP-dependent protein kinase (PKA); green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YPL260W is not an essential gene	Q
1404	VN_1404	YPL179W	PPQ1	Putative protein serine/threonine phosphatase; null mutation enhances efficiency of translational suppressors	Q
1405	VN_1405	YBR223C	TDP1	Tyrosyl-DNA Phosphodiesterase I, hydrolyzes 3' and 5'-phosphotyrosyl bonds, involved in the repair of DNA lesions created by topoisomerase I and topoisomerase II; mutations in human homolog result in the neurodegenerative disease SCAN1	Q
1406	VN_1406	YDR057W	YOS9	ER quality-control lectin; integral subunit of the HRD ligase; binds to glycans with terminal alpha-1,6 linked mannose on misfolded N-glycosylated proteins and participates in targeting proteins to ERAD; member of the OS-9 protein family	Q
1407	VN_1407	YPL214C	THI6	Bifunctional enzyme with thiamine-phosphate pyrophosphorylase and 4-methyl-5-beta-hydroxyethylthiazole kinase activities, required for thiamine biosynthesis; GFP-fusion protein localizes to the cytoplasm in a punctate pattern	Q
1408	VN_1408	YDR403W	DIT1	Sporulation-specific enzyme required for spore wall maturation, involved in the production of a soluble LL-dityrosine-containing precursor of the spore wall; transcripts accumulate at the time of prospore enclosure	Q
1409	VN_1409	YDR434W	GPI17	Transmembrane protein subunit of the glycosylphosphatidylinositol transamidase complex that adds GPIs to newly synthesized proteins; human PIG-Sp homolog	Q
1410	VN_1410	YIL162W	SUC2	Invertase, sucrose hydrolyzing enzyme; a secreted, glycosylated form is regulated by glucose repression, and an intracellular, nonglycosylated enzyme is produced constitutively	Q
1411	VN_1411	YLR313C	SPH1	Protein involved in shmoo formation and bipolar bud site selection; homologous to Spa2p, localizes to sites of polarized growth in a cell cycle dependent- and Spa2p-dependent manner, interacts with MAPKKs Mkk1p, Mkk2p, and Ste7p	Q
1412	VN_1412	YDR534C	FIT1	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall	Q
1413	VN_1413	YKL045W	PRI2	Subunit of DNA primase, which is required for DNA synthesis and double-strand break repair	Q
1414	VN_1414	YIL142W	CCT2	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	Q
1415	VN_1415	YNL138W	SRV2	CAP (cyclase-associated protein) subunit of adenylyl cyclase complex; N-terminus binds adenylyl cyclase and facilitates activation by RAS; C-terminus binds ADP-actin monomers, facilitating regulation of actin dynamics and cell morphogenesis	Q
1416	VN_1416	YOR359W	VTS1	Post-transcriptional gene regulator, flap-structured DNA-binding and RNA-binding protein; shows genetic interactions with Vti1p, a v-SNARE involved in cis-Golgi membrane traffic; stimulates Dna2p endonuclease activity; contains a SAM domain	Q
1417	VN_1417	YBL019W	APN2	Class II basic (AP) endonuclease involved in repair of DNA damage; homolog of human HAP1 and E. coli exoIII	Q
1418	VN_1418	YER007W	PAC2	Microtubule effector required for tubulin heterodimer formation, binds alpha-tubulin, required for normal microtubule function, null mutant	Q

				exhibits cold-sensitive microtubules and sensitivity to benomyl	
1419	VN_1419	YIL097W	FYV10	Protein of unknown function, required for survival upon exposure to K1 killer toxin; involved in proteasome-dependent catabolite inactivation of FBPAse; contains CTLH domain; plays role in anti-apoptosis	Q
1420	VN_1420	YJL013C	MAD3	Subunit of the spindle-assembly checkpoint complex, which delays anaphase onset in cells with defects in mitotic spindle assembly; pseudosubstrate inhibitor of APC(Cdc20), the anaphase promoting complex involved in securin (Pds1p) turnover	Q
1421	VN_1421	YDL101C	DUN1	Cell-cycle checkpoint serine-threonine kinase required for DNA damage-induced transcription of certain target genes, phosphorylation of Rad55p and Sml1p, and transient G2/M arrest after DNA damage; also regulates postreplicative DNA repair	Q
1422	VN_1422	YMR093W	UTP15	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA	Q
1423	VN_1423	YKL139W	CTK1	Catalytic (alpha) subunit of C-terminal domain kinase I (CTDK-I), which phosphorylates both RNA pol II subunit Rpo21p to affect transcription and pre-mRNA 3' end processing, and ribosomal protein Rps2p to increase translational fidelity	Q
1424	VN_1424	YKL074C	MUD2	Protein involved in early pre-mRNA splicing; component of the pre-mRNA-U1 snRNP complex, the commitment complex; interacts with Msl5p/BBP splicing factor and Sub2p; similar to metazoan splicing factor U2AF65	Q
1425	VN_1425	YOR360C	PDE2	High-affinity cyclic AMP phosphodiesterase, component of the cAMP-dependent protein kinase signaling system, protects the cell from extracellular cAMP, contains readthrough motif surrounding termination codon	Q
1426	VN_1426	YOR377W	ATF1	Alcohol acetyltransferase with potential roles in lipid and sterol metabolism; responsible for the major part of volatile acetate ester production during fermentation	Q
1427	VN_1427	YGL078C	DBP3	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis	Q
1428	VN_1428	YPL247C	YPL247C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; similar to the petunia WD repeat protein an11; overexpression causes a cell cycle delay or arrest	Q
1429	VN_1429	YBR227C	MCX1	Mitochondrial matrix protein; putative ATP-binding chaperone with non-proteolytic function; similar to bacterial ClpX proteins	Q
1430	VN_1430	YHR170W	NMD3	Protein involved in nuclear export of the large ribosomal subunit; acts as a Crm1p-dependent adapter protein for export of nascent ribosomal subunits through the nuclear pore complex	Q
1431	VN_1431	YKL047W	YKL047W	Putative protein of unknown function, predicted to be palmitoylated; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
1432	VN_1432	YMR285C	NGL2	Protein involved in 5.8S rRNA processing; Ccr4p-like RNase required for correct 3'-end formation of 5.8S rRNA at site E; similar to Ngl1p and Ngl3p	Q
1433	VN_1433	YDR169C	STB3	Ribosomal RNA processing element (RRPE)-binding protein involved in the induction of non-ribosomal protein growth genes by glucose; binds Sin3p in a two-hybrid assay	Q
1434	VN_1434	YMR283C	RIT1	2'-O-ribosyl phosphate transferase, modifies the initiator methionine tRNA at position 64 to distinguish it from elongator methionine tRNA	Q
1435	VN_1435	YNL077W	APJ1	Putative chaperone of the HSP40 (DNAJ) family; overexpression interferes with propagation of the [Psi ⁺] prion; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
1436	VN_1436	YBL015W	ACH1	Protein with CoA transferase activity, particularly for CoASH transfer from succinyl-CoA to acetate; has minor acetyl-CoA-hydrolase activity; phosphorylated; required for acetate utilization and for diploid pseudohyphal growth	Q
1437	VN_1437	YBL054W	TOD6	PAC motif binding protein involved in rRNA and ribosome biogenesis; subunit of the RPD3L histone deacetylase complex; Myb-	Q

				like HTH transcription factor, similar to Dot6p; hypophosphorylated by rapamycin treatment in a Sch9p-dependent manner	
1438	VN_1438	YBR138C	YBR138C	Cytoplasmic protein of unknown function, potentially phosphorylated by Cdc28p; YBR138C is not an essential gene	Q
1439	VN_1439	YHR009C	YHR009C	Putative protein of unknown function; not an essential gene	Strain failed to verify via PCR
1440	VN_1440	YDR009W	GAL3	Transcriptional regulator involved in activation of the GAL genes in response to galactose; forms a complex with Gal80p to relieve Gal80p inhibition of Gal4p; binds galactose and ATP but does not have galactokinase activity	Q
1441	VN_1441	YKL116C	PRR1	Serine/threonine protein kinase that inhibits pheromone induced signalling downstream of MAPK, possibly at the level of the Ste12p transcription factor	Q
1442	VN_1442	YOR149C	SMP3	Alpha 1,2-mannosyltransferase involved in glycosyl phosphatidyl inositol (GPI) biosynthesis; required for addition of the fourth, side branching mannose to the GPI core structure	Q
1443	VN_1443	YNR051C	BRE5	Ubiquitin protease cofactor, forms deubiquitination complex with Ubp3p that coregulates anterograde and retrograde transport between the endoplasmic reticulum and Golgi compartments; null is sensitive to brefeldin A	Q
1444	VN_1444	YGR123C	PPT1	Protein serine/threonine phosphatase with similarity to human phosphatase PP5; present in both the nucleus and cytoplasm; expressed during logarithmic growth; computational analyses suggest roles in phosphate metabolism and rRNA processing	Q
1445	VN_1445	YPL122C	TFB2	Subunit of TFIIH and nucleotide excision repair factor 3 complexes, involved in transcription initiation, required for nucleotide excision repair, similar to 52 kDa subunit of human TFIIH	Q
1446	VN_1446	YBR214W	SDS24	One of two <i>S. cerevisiae</i> homologs (Sds23p and Sds24p) of the <i>S. pombe</i> Sds23 protein, which is implicated in APC/cytosome regulation; involved in cell separation during budding; may play an indirect role in fluid-phase endocytosis	Q
1447	VN_1447	YBR028C	YBR028C	Putative protein kinase, possible substrate of cAMP-dependent protein kinase (PKA)	Q
1448	VN_1448	YHR016C	YSC84	Actin-binding protein involved in bundling of actin filaments and endocytosis of actin cortical patches; activity stimulated by Las17p; contains SH3 domain similar to Rvs167p	Q
1449	VN_1449	YHR086W	NAM8	RNA binding protein, component of the U1 snRNP protein; mutants are defective in meiotic recombination and in formation of viable spores, involved in the formation of DSBs through meiosis-specific splicing of MER2 pre-mRNA	Q
1450	VN_1450	YDL156W	YDL156W	Putative protein of unknown function; protein sequence contains three WD domains (WD-40 repeat); green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	Q
1451	VN_1451	YLR392C	ART10	Protein of unknown function that contains 2 PY motifs and is ubiquitinated by Rsp5p; green fluorescent protein (GFP)-fusion protein localizes it to the cytoplasm; non-essential gene	Q
1452	VN_1452	YPL198W	RPL7B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Ap and has similarity to <i>E. coli</i> L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2)	Q
1453	VN_1453	YCR053W	THR4	Threonine synthase, conserved protein that catalyzes formation of threonine from O-phosphohomoserine; expression is regulated by the GCN4-mediated general amino acid control pathway	Q
1454	VN_1454	YHR137W	ARO9	Aromatic aminotransferase II, catalyzes the first step of tryptophan, phenylalanine, and tyrosine catabolism	Q
1455	VN_1455	YER096W	SHC1	Sporulation-specific activator of Chs3p (chitin synthase III), required for the synthesis of the chitosan layer of ascospores; has similarity to Skt5p, which activates Chs3p during vegetative growth; transcriptionally induced at alkaline pH	Q
1456	VN_1456	YBR274W	CHK1	Serine/threonine kinase and DNA damage checkpoint effector, mediates cell cycle arrest via phosphorylation of Pds1p; phosphorylated by checkpoint signal transducer Mec1p; homolog of <i>S.</i>	Strain failed to verify via PCR

				pombe and mammalian Chk1 checkpoint kinase	
1457	VN_1457	YHR151C	MTC6	Protein of unknown function; mtc6 is synthetically sick with cdc13-1	Q
1458	VN_1458	YDL197C	ASF2	Anti-silencing protein that causes derepression of silent loci when overexpressed	Q
1459	VN_1459	YHR216W	IMD2	Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis, expression is induced by mycophenolic acid resulting in resistance to the drug, expression is repressed by nutrient limitation	Q
1460	VN_1460	YNL116W	DMA2	Protein involved in ubiquitination; plays a role in regulating spindle position and orientation; functionally redundant with Dma1p; orthologous to human RNF8 protein, also has sequence similarity to human Chfr	Q
1461	VN_1461	YER073W	ALD5	Mitochondrial aldehyde dehydrogenase, involved in regulation or biosynthesis of electron transport chain components and acetate formation; activated by K ⁺ ; utilizes NADP ⁺ as the preferred coenzyme; constitutively expressed	Q
1462	VN_1462	YMR064W	AEP1	Protein required for expression of the mitochondrial OLI1 gene encoding subunit 9 of F1-F0 ATP synthase	Q
1463	VN_1463	YPR002W	PDH1	Mitochondrial protein that participates in respiration, induced by diauxic shift; homologous to E. coli PrpD, may take part in the conversion of 2-methylcitrate to 2-methylisocitrate	Q
1464	VN_1464	YJL025W	RRN7	Component of the core factor (CF) rDNA transcription factor complex; CF is required for transcription of 35S rRNA genes by RNA polymerase I and is composed of Rrn6p, Rrn7p, and Rrn11p	Q
1465	VN_1465	YIL001W	YIL001W	Putative protein of unknown function; contains a BTB/POZ domain which generally function in protein interactions; deletion slightly improved competitive fitness in rich media; GFP-tagged protein is localized to the cytoplasm	Q
1466	VN_1466	YGL158W	RCK1	Protein kinase involved in the response to oxidative stress; identified as suppressor of S. pombe cell cycle checkpoint mutations	Q
1467	VN_1467	YER025W	GCD11	Gamma subunit of the translation initiation factor eIF2, involved in the identification of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-Met	Q
1468	VN_1468	YHR207C	SET5	Zinc-finger protein of unknown function, contains one canonical and two unusual fingers in unusual arrangements; deletion enhances replication of positive-strand RNA virus	Q
1469	VN_1469	YGL122C	NAB2	Nuclear polyadenylated RNA-binding protein required for nuclear mRNA export and poly(A) tail length control; binds nuclear pore protein Mlp1p; autoregulates mRNA levels; related to human hnRNPs; nuclear localization sequence binds Kap104p	Q
1470	VN_1470	YNL295W	YNL295W	Putative protein of unknown function	Q
1471	VN_1471	YLR324W	PEX30	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome number; partially functionally redundant with Pex31p; genetic interactions suggest action at a step downstream of steps mediated by Pex28p and Pex29p	Q
1472	VN_1472	YOR355W	GDS1	Protein of unknown function, required for growth on glycerol as a carbon source; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
1473	VN_1473	YLR314C	CDC3	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM	Q
1474	VN_1474	YDR518W	EUG1	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER	Q
1475	VN_1475	YKL103C	LAP4	Vacuolar aminopeptidase yscI; zinc metalloproteinase that belongs to the peptidase family M18; often used as a marker protein in studies of autophagy and cytosol to vacuole targeting (CVT) pathway	Q
1476	VN_1476	YJL194W	CDC6	Essential ATP-binding protein required for DNA replication, component of the pre-replicative complex (pre-RC) which requires ORC to associate with chromatin and is in turn required for Mcm2-7p	Q

				DNA association; homologous to <i>S. pombe</i> Cdc18p	
1477	VN_1477	YGR059W	SPR3	Sporulation-specific homolog of the yeast CDC3/10/11/12 family of bud neck microfilament genes; septin protein involved in sporulation; regulated by ABFI	Q
1478	VN_1478	YER052C	HOM3	Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis	Q
1479	VN_1479	YML086C	ALO1	D-Arabinono-1,4-lactone oxidase, catalyzes the final step in biosynthesis of dehydro-D-arabinono-1,4-lactone, which is protective against oxidative stress	Q
1480	VN_1480	YGR227W	DIE2	Dolichyl-phosphoglucose-dependent alpha-1,2 glucosyltransferase of the ER, functions in the pathway that synthesizes the dolichol-linked oligosaccharide precursor for N-linked protein glycosylation, has a role in regulation of ITR1 and INO1	Q
1481	VN_1481	YBR184W	YBR184W	Putative protein of unknown function; YBR184W is not an essential gene	Q
1482	VN_1482	YLR432W	IMD3	Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis, member of a four-gene family in <i>S. cerevisiae</i> , constitutively expressed	Q
1483	VN_1483	YDR501W	PLM2	Forkhead Associated domain containing protein and putative transcription factor found associated with chromatin; target of SBF transcription factor; induced in response to DNA damaging agents and deletion of telomerase; similar to TOS4	Q
1484	VN_1484	YMR014W	BUD22	Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern	Q
1485	VN_1485	YPL272C	YPL272C	Putative protein of unknown function; gene expression induced in response to ketoconazole; YPL272C is not an essential gene	Q
1486	VN_1486	YDL159W	STE7	Signal transducing MAP kinase kinase involved in pheromone response, where it phosphorylates Fus3p, and in the pseudohyphal/invasive growth pathway, through phosphorylation of Kss1p; phosphorylated by Ste11p, degraded by ubiquitin pathway	Q
1487	VN_1487	YMR018W	YMR018W	Putative protein of unknown function with similarity to human PEX5Rp (peroxin protein 5 related protein); transcription increases during colony development similar to genes involved in peroxisome biogenesis; YMR018W is not an essential gene	Q
1488	VN_1488	YML120C	NDI1	NADH:ubiquinone oxidoreductase, transfers electrons from NADH to ubiquinone in the respiratory chain but does not pump protons, in contrast to the higher eukaryotic multisubunit respiratory complex I; phosphorylated; homolog of human AMID	Q
1489	VN_1489	YLR054C	OSW2	Protein of unknown function proposed to be involved in the assembly of the spore wall	Q
1490	VN_1490	YGL056C	SDS23	One of two <i>S. cerevisiae</i> homologs (Sds23p and Sds24p) of the <i>S. pombe</i> Sds23 protein, which is implicated in APC/cyclosome regulation; involved in cell separation during budding	Q
1491	VN_1491	YMR023C	MSS1	Mitochondrial protein, forms a heterodimer complex with Mto1p that performs the 5-carboxymethylaminomethyl modification of the wobble uridine base in mitochondrial tRNAs; similar to human GTPBP3	Q
1492	VN_1492	YML096W	YML096W	Putative protein of unknown function with similarity to asparagine synthetases; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YML096W is not an essential gene and partially overlaps the verified gene RAD10	Q
1493	VN_1493	YBR250W	SPO23	Protein of unknown function; associates with meiosis-specific protein Spo1p	Q
1494	VN_1494	YMR029C	FAR8	Protein involved in recovery from cell cycle arrest in response to pheromone, in a Far1p-independent pathway; interacts with Far3p, Far7p, Far9p, Far10p, and Far11p	Q
1495	VN_1495	YKL081W	TEF4	Translation elongation factor EF-1 gamma	Q
1496	VN_1496	YOR374W	ALD4	Mitochondrial aldehyde dehydrogenase, required for growth on ethanol and conversion of acetaldehyde to acetate; phosphorylated; activity is K ⁺ dependent; utilizes NADP ⁺ or NAD ⁺ equally as	Q

				coenzymes; expression is glucose repressed	
1497	VN_1497	YDR256C	CTA1	Catalase A, breaks down hydrogen peroxide in the peroxisomal matrix formed by acyl-CoA oxidase (Pox1p) during fatty acid beta-oxidation	Q
1498	VN_1498	YPR169W	JIP5	Essential protein of unknown function; interacts with proteins involved in RNA processing, ribosome biogenesis, ubiquitination and demethylation; tagged protein localizes to nucleus and nucleolus; similar to WDR55, a human WD repeat protein	Q
1499	VN_1499	YML128C	MSC1	Protein of unknown function; mutant is defective in directing meiotic recombination events to homologous chromatids; the authentic, non-tagged protein is detected in highly purified mitochondria and is phosphorylated	Q
1500	VN_1500	YDR371W	CTS2	Protein similar to <i>Ashbya gossypii</i> sporulation-specific chitinase	Q
1501	VN_1501	YER078C	ICP55	Mitochondrial aminopeptidase; cleaves the N termini of at least 38 imported proteins after cleavage by the mitochondrial processing peptidase (MPP), thereby increasing their stability; member of the aminopeptidase P family	Q
1502	VN_1502	YMR300C	ADE4	Phosphoribosylpyrophosphate amidotransferase (PRPPAT; amidophosphoribosyltransferase), catalyzes first step of the 'de novo' purine nucleotide biosynthetic pathway	Q
1503	VN_1503	YDR111C	ALT2	Putative alanine transaminase (glutamic pyruvic transaminase)	Q
1504	VN_1504	YDR030C	RAD28	Protein involved in DNA repair, related to the human CSA protein that is involved in transcription-coupled repair nucleotide excision repair	Q
1505	VN_1505	YGR229C	SMI1	Protein involved in the regulation of cell wall synthesis; proposed to be involved in coordinating cell cycle progression with cell wall integrity	Q
1506	VN_1506	YML032C	RAD52	Protein that stimulates strand exchange by facilitating Rad51p binding to single-stranded DNA; anneals complementary single-stranded DNA; involved in the repair of double-strand breaks in DNA during vegetative growth and meiosis	Q
1507	VN_1507	YEL070W	DSF1	Deletion suppressor of mpt5 mutation	Q
1508	VN_1508	YJR051W	OSM1	Fumarate reductase, catalyzes the reduction of fumarate to succinate, required for the reoxidation of intracellular NADH under anaerobic conditions; mutations cause osmotic sensitivity	Q
1509	VN_1509	YDR516C	EMI2	Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1; required for sporulation; expression is regulated by glucose-repression transcription factors Mig1/2p	Q
1510	VN_1510	YOR351C	MEK1	Meiosis-specific serine/threonine protein kinase, functions in meiotic checkpoint, promotes recombination between homologous chromosomes by suppressing double strand break repair between sister chromatids	Q
1511	VN_1511	YJR010W	MET3	ATP sulfurylase, catalyzes the primary step of intracellular sulfate activation, essential for assimilatory reduction of sulfate to sulfide, involved in methionine metabolism	Q
1512	VN_1512	YEL052W	AFG1	Conserved protein that may act as a chaperone in the degradation of misfolded or unassembled cytochrome c oxidase subunits; localized to matrix face of the mitochondrial inner membrane; member of the AAA family but lacks a protease domain	Q
1513	VN_1513	YER090W	TRP2	Anthranilate synthase, catalyzes the initial step of tryptophan biosynthesis, forms multifunctional hetero-oligomeric anthranilate synthase:indole-3-glycerol phosphate synthase enzyme complex with Trp3p	Q
1514	VN_1514	YDR168W	CDC37	Essential Hsp90p co-chaperone; necessary for passage through the START phase of the cell cycle; stabilizes protein kinase nascent chains and participates along with Hsp90p in their folding	Q
1515	VN_1515	YLR015W	BRE2	Subunit of COMPASS (Set1C) complex, which methylates Lys4 of histone H3 and functions in silencing at telomeres; has a C-terminal Sdc1 Dpy-30 Interaction (SDI) domain that mediates binding to Sdc1p; similar to trithorax-group protein ASH2L	Q
1516	VN_1516	YDR539W	YDR539W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YDR539W is not an	Q

				essential gene; homolog of E. coli UbiD	
1517	VN_1517	YKR063C	LAS1	Essential nuclear protein possibly involved in bud formation and morphogenesis; mutants require the SSD1-v allele for viability	Q
1518	VN_1518	YMR115W	MGR3	Subunit of the mitochondrial (mt) i-AAA protease supercomplex, which degrades misfolded mitochondrial proteins; forms a subcomplex with Mgr1p that binds to substrates to facilitate proteolysis; required for growth of cells lacking mtDNA	Q
1519	VN_1519	YFR021W	ATG18	Phosphoinositide binding protein required for vesicle formation in autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; binds both phosphatidylinositol (3,5)-bisphosphate and phosphatidylinositol 3-phosphate; WD-40 repeat protein	Q
1520	VN_1520	YKL035W	UGP1	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p	Q
1521	VN_1521	YEL071W	DLD3	D-lactate dehydrogenase, part of the retrograde regulon which consists of genes whose expression is stimulated by damage to mitochondria and reduced in cells grown with glutamate as the sole nitrogen source, located in the cytoplasm	Q
1522	VN_1522	YDR257C	RKM4	Ribosomal lysine methyltransferase specific for monomethylation of Rpl42ap and Rpl42bp (lysine 55); nuclear SET-domain containing protein	Q
1523	VN_1523	YLR345W	YLR345W	Similar to 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase enzymes responsible for the metabolism of fructoso-2,6-bisphosphate; mRNA expression is repressed by the Rfx1p-Tup1p-Ssn6p repressor complex; YLR345W is not an essential gene	Q
1524	VN_1524	YGR093W	YGR093W	Putative protein of unconfirmed function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus	Q
1525	VN_1525	YMR169C	ALD3	Cytoplasmic aldehyde dehydrogenase, involved in beta-alanine synthesis; uses NAD ⁺ as the preferred coenzyme; very similar to Ald2p; expression is induced by stress and repressed by glucose	Q
1526	VN_1526	YML118W	NGL3	Putative endonuclease, has a domain similar to a magnesium-dependent endonuclease motif in mRNA deadenylase Ccr4p; similar to Ngl1p and Ngl2p	Q
1527	VN_1527	YFL022C	FRS2	Alpha subunit of cytoplasmic phenylalanyl-tRNA synthetase, forms a tetramer with Frs1p to form active enzyme; evolutionarily distant from mitochondrial phenylalanyl-tRNA synthetase based on protein sequence, but substrate binding is similar	Strain failed to verify via PCR
1528	VN_1528	YLR033W	RSC58	Component of the RSC chromatin remodeling complex; RSC functions in transcriptional regulation and elongation, chromosome stability, and establishing sister chromatid cohesion; involved in telomere maintenance	Q
1529	VN_1529	YNR012W	URK1	Uridine/cytidine kinase, component of the pyrimidine ribonucleotide salvage pathway that converts uridine into UMP and cytidine into CMP; involved in the pyrimidine deoxyribonucleotide salvage pathway, converting deoxycytidine into dCMP	Q
1530	VN_1530	YGL202W	ARO8	Aromatic aminotransferase I, expression is regulated by general control of amino acid biosynthesis	Q
1531	VN_1531	YPL017C	IRC15	Microtubule associated protein; regulates microtubule dynamics; required for accurate meiotic chromosome segregation; null mutant displays large budded cells due to delayed mitotic progression, increased levels of spontaneous Rad52 foci	Q
1532	VN_1532	YOL061W	PRS5	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, synthesizes PRPP, which is required for nucleotide, histidine, and tryptophan biosynthesis; one of five related enzymes, which are active as heteromultimeric complexes	Q
1533	VN_1533	YGR091W	PRP31	Splicing factor, component of the U4/U6-U5 snRNP complex	Q
1534	VN_1534	YOR310C	NOP58	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA	Q
1535	VN_1535	YBR139W	YBR139W	Putative serine type carboxypeptidase with a role in phytochelatin synthesis; green fluorescent protein (GFP)-fusion protein localizes to	Q

				the vacuole; expression induced by nitrogen limitation in a GLN3, GAT1-independent manner	
1536	VN_1536	YGR155W	CYS4	Cystathionine beta-synthase, catalyzes synthesis of cystathionine from serine and homocysteine, the first committed step in cysteine biosynthesis; responsible for hydrogen sulfide generation; mutations in human ortholog cause homocystinuria	Q
1537	VN_1537	YMR170C	ALD2	Cytoplasmic aldehyde dehydrogenase, involved in ethanol oxidation and beta-alanine biosynthesis; uses NAD ⁺ as the preferred coenzyme; expression is stress induced and glucose repressed; very similar to Ald3p	Q
1538	VN_1538	YMR290C	HAS1	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles	Q
1539	VN_1539	YGL017W	ATE1	Arginyl-tRNA-protein transferase, catalyzes post-translational conjugation of arginine to the amino termini of acceptor proteins which are then subject to degradation via the N-end rule pathway	Q
1540	VN_1540	YLR094C	GIS3	Protein of unknown function	Q
1541	VN_1541	YOL070C	NBA1	Protein of unknown function, localizes to the bud neck and cytoplasm; interacts with Nap1p; may interact with ribosomes, based on co-purification experiments; potential Cdc28p substrate	Q
1542	VN_1542	YPL061W	ALD6	Cytosolic aldehyde dehydrogenase, activated by Mg ²⁺ and utilizes NADP ⁺ as the preferred coenzyme; required for conversion of acetaldehyde to acetate; constitutively expressed; locates to the mitochondrial outer surface upon oxidative stress	Q
1543	VN_1543	YPL072W	UBP16	Deubiquitinating enzyme anchored to the outer mitochondrial membrane, probably not important for general mitochondrial functioning, but may perform a more specialized function at mitochondria	Q
1544	VN_1544	YPL100W	ATG21	Phosphoinositide binding protein required for vesicle formation in the cytoplasm-to-vacuole targeting (Cvt) pathway; binds both phosphatidylinositol (3,5)-bisphosphate and phosphatidylinositol 3-phosphate; WD-40 repeat protein	Q
1545	VN_1545	YOR269W	PAC1	Protein involved in nuclear migration, part of the dynein/dynactin pathway; targets dynein to microtubule tips, which is necessary for sliding of microtubules along bud cortex; synthetic lethal with bni1; homolog of human LIS1	Q
1546	VN_1546	YFL021W	GAT1	Transcriptional activator of genes involved in nitrogen catabolite repression; contains a GATA-1-type zinc finger DNA-binding motif; activity and localization regulated by nitrogen limitation and Ure2p	Q
1547	VN_1547	YLR121C	YPS3	Aspartic protease, attached to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor	Q
1548	VN_1548	YGR189C	CRH1	Chitin transglycosylase that functions in the transfer of chitin to beta(1-6) and beta(1-3) glucans in the cell wall; similar and functionally redundant to Utr2; localizes to sites of polarized growth; expression induced by cell wall stress	Q
1549	VN_1549	YNL223W	ATG4	Conserved cysteine protease required for autophagy; cleaves Atg8p to a form required for autophagosome and Cvt vesicle generation	Q
1550	VN_1550	YNL241C	ZWF1	Glucose-6-phosphate dehydrogenase (G6PD), catalyzes the first step of the pentose phosphate pathway; involved in adapting to oxidative stress; homolog of the human G6PD which is deficient in patients with hemolytic anemia	Q
1551	VN_1551	YGL065C	ALG2	Mannosyltransferase that catalyzes two consecutive steps in the N-linked glycosylation pathway; alg2 mutants exhibit temperature-sensitive growth and abnormal accumulation of the lipid-linked oligosaccharide Man2GlcNAc2-PP-Dol	Q
1552	VN_1552	YNR073C	YNR073C	Putative mannitol dehydrogenase	Q
1553	VN_1553	YAL038W	CDC19	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration	Q
1554	VN_1554	YBR006W	UGA2	Succinate semialdehyde dehydrogenase involved in the utilization of gamma-aminobutyrate (GABA) as a nitrogen source; part of the 4-aminobutyrate and glutamate degradation pathways; localized to the	Q

				cytoplasm	
1555	VN_1555	YMR033W	ARP9	Component of both the SWI/SNF and RSC chromatin remodeling complexes; actin-related protein involved in transcriptional regulation	Q
1556	VN_1556	YPL204W	HRR25	Protein kinase involved in regulating diverse events including vesicular trafficking, DNA repair, and chromosome segregation; binds the CTD of RNA pol II; homolog of mammalian casein kinase 1delta (CK1delta)	Q
1557	VN_1557	YFR039C	YFR039C	Putative protein of unknown function; may be involved in response to high salt and changes in carbon source; deletion mutant has decreased spore survival in <i>Drosophila</i> feces	Q
1558	VN_1558	YMR020W	FMS1	Polyamine oxidase, converts spermine to spermidine, which is required for the essential hypusination modification of translation factor eIF-5A; also involved in pantothenic acid biosynthesis	Q
1559	VN_1559	YIL104C	SHQ1	Chaperone protein required for the assembly of box H/ACA snoRNPs and thus for pre-rRNA processing, forms a complex with Naf1p and interacts with H/ACA snoRNP components Nhp2p and Cbf5p; homology with known Hsp90p cochaperones	Q
1560	VN_1560	YOR347C	PYK2	Pyruvate kinase that appears to be modulated by phosphorylation; PYK2 transcription is repressed by glucose, and Pyk2p may be active under low glycolytic flux	Q
1561	VN_1561	YGL035C	MIG1	Transcription factor involved in glucose repression; sequence specific DNA binding protein containing two Cys2His2 zinc finger motifs; regulated by the SNF1 kinase and the GLC7 phosphatase	Q
1562	VN_1562	YLL036C	PRP19	Splicing factor associated with the spliceosome; contains a U-box, a motif found in a class of ubiquitin ligases	Q
1563	VN_1563	YPL026C	SKS1	Putative serine/threonine protein kinase; involved in the adaptation to low concentrations of glucose independent of the SNF3 regulated pathway	Q
1564	VN_1564	YCL040W	GLK1	Glucokinase, catalyzes the phosphorylation of glucose at C6 in the first irreversible step of glucose metabolism; one of three glucose phosphorylating enzymes; expression regulated by non-fermentable carbon sources	Q
1565	VN_1565	YFL018C	LPD1	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes	Q
1566	VN_1566	YCL017C	NFS1	Cysteine desulfurase involved in iron-sulfur cluster (Fe/S) biogenesis; required for the post-transcriptional thio-modification of mitochondrial and cytoplasmic tRNAs; essential protein located predominantly in mitochondria	Q
1567	VN_1567	YBR126C	TPS1	Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway	Q
1568	VN_1568	YEL016C	NPP2	Nucleotide pyrophosphatase/phosphodiesterase family member; mediates extracellular nucleotide phosphate hydrolysis along with Npp1p and Pho5p; activity and expression enhanced during conditions of phosphate starvation	Q
1569	VN_1569	YJR015W	YJR015W	Putative protein of unknown function; localizes to the endoplasmic reticulum and cytoplasm; predicted to encode a membrane transporter based on phylogenetic analysis; YJR015W is a non-essential gene	Q
1570	VN_1570	YOR231W	MKK1	Mitogen-activated kinase kinase involved in protein kinase C signaling pathway that controls cell integrity; upon activation by Bck1p phosphorylates downstream target, Slt2p; functionally redundant with Mkk2p	Q
1571	VN_1571	YML043C	RRN11	Component of the core factor (CF) rDNA transcription factor complex; CF is required for transcription of 35S rRNA genes by RNA polymerase I and is composed of Rrn6p, Rrn7p, and Rrn11p	Q
1572	VN_1572	YPL140C	MKK2	Mitogen-activated kinase kinase involved in protein kinase C signaling pathway that controls cell integrity; upon activation by Bck1p phosphorylates downstream target, Slt2p; functionally redundant with Mkk1p	Q
1573	VN_1573	YHR159W	YHR159W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; potential Cdc28p	Q

				substrate	
1574	VN_1574	YOL068C	HST1	NAD(+)-dependent histone deacetylase; essential subunit of the Sum1p/Rfm1p/Hst1p complex required for ORC-dependent silencing and mitotic repression; non-essential subunit of the Set3C deacetylase complex; involved in telomere maintenance	Q
1575	VN_1575	YBR056W	YBR056W	Putative cytoplasmic protein of unknown function	Q
1576	VN_1576	YDR036C	EHD3	3-hydroxyisobutyryl-CoA hydrolase, member of a family of enoyl-CoA hydratase/isomerases; non-tagged protein is detected in highly purified mitochondria in high-throughput studies; phosphorylated; mutation affects fluid-phase endocytosis	Q
1577	VN_1577	YFR010W	UBP6	Ubiquitin-specific protease situated in the base subcomplex of the 26S proteasome, releases free ubiquitin from branched polyubiquitin chains; works in opposition to polyubiquitin elongation activity of Hul5p	Q
1578	VN_1578	YFL027C	GYP8	GTPase-activating protein for yeast Rab family members; Ypt1p is the preferred in vitro substrate but also acts on Sec4p, Ypt31p and Ypt32p; involved in the regulation of ER to Golgi vesicle transport	Q
1579	VN_1579	YDR132C	YDR132C	Putative protein of unknown function	Q
1580	VN_1580	YER122C	GLO3	ADP-ribosylation factor GTPase activating protein (ARF GAP), involved in ER-Golgi transport; shares functional similarity with Gcs1p	Q
1581	VN_1581	YDL017W	CDC7	DDK (Dbf4-dependent kinase) catalytic subunit required for firing origins and replication fork progression in mitosis through phosphorylation of Mcm2-7p complexes and Cdc45p; kinase activity correlates with cyclical DBF4 expression	Q
1582	VN_1582	YDL160C	DHH1	Cytoplasmic DEXD/H-box helicase, stimulates mRNA decapping, coordinates distinct steps in mRNA function and decay, interacts with both the decapping and deadenylase complexes, may have a role in mRNA export and translation	Q
1583	VN_1583	YPL181W	CTI6	Protein that relieves transcriptional repression by binding to the Cyc8p-Tup1p corepressor and recruiting the SAGA complex to the repressed promoter; contains a PHD finger domain	Q
1584	VN_1584	YLR197W	NOP56	Essential evolutionarily-conserved nucleolar protein component of the box C/D snoRNP complexes that direct 2'-O-methylation of pre-rRNA during its maturation; overexpression causes spindle orientation defects	Q
1585	VN_1585	YDR522C	SPS2	Protein expressed during sporulation, redundant with Sps22p for organization of the beta-glucan layer of the spore wall; S. pombe ortholog is a spore wall component	Q
1586	VN_1586	YGL119W	ABC1	Protein required for ubiquinone (coenzyme Q) biosynthesis and for respiratory growth; exhibits genetic interaction with COQ9, suggesting a common function; similar to prokaryotic proteins involved in early steps of ubiquinone biosynthesis	Q
1587	VN_1587	YDR330W	UBX5	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p	Q
1588	VN_1588	YHR070W	TRM5	tRNA(m(1)G37)methyltransferase, methylates a tRNA base adjacent to the anticodon that has a role in prevention of frameshifting; highly conserved across Archaea, Bacteria, and Eukarya	Q
1589	VN_1589	YJR122W	IBA57	Mitochondrial matrix protein involved in the incorporation of iron-sulfur clusters into mitochondrial aconitase-type proteins; activates the radical-SAM family members Bio2p and Lip5p; interacts with Ccr4p in the two-hybrid system	Q
1590	VN_1590	YEL041W	YEF1	ATP-NADH kinase; phosphorylates both NAD and NADH; homooctameric structure consisting of 60-kDa subunits; sequence similarity to Utr1p and Pos5p; overexpression complements certain pos5 phenotypes	Q
1591	VN_1591	YHL012W	YHL012W	Putative protein of unknown function, has some homology to Ugp1p, which encodes UDP-glucose pyrophosphorylase	Q
1592	VN_1592	YLR227C	ADY4	Structural component of the meiotic outer plaque, which is a membrane-organizing center that assembles on the cytoplasmic face of the spindle pole body during meiosis II and triggers the formation of	Q

				the prospore membrane	
1593	VN_1593	YPL097W	MSY1	Mitochondrial tyrosyl-tRNA synthetase	Q
1594	VN_1594	YOL049W	GSH2	Glutathione synthetase, catalyzes the ATP-dependent synthesis of glutathione (GSH) from gamma-glutamylcysteine and glycine; induced by oxidative stress and heat shock	Q
1595	VN_1595	YDL238C	GUD1	Guanine deaminase, a catabolic enzyme of the guanine salvage pathway producing xanthine and ammonia from guanine; activity is low in exponentially-growing cultures but expression is increased in post-diauxic and stationary-phase cultures	Q
1596	VN_1596	YNL053W	MSG5	Dual-specificity protein phosphatase; exists in 2 isoforms; required for maintenance of a low level of signaling through the cell integrity pathway, adaptive response to pheromone; regulates and is regulated by Slt2p; dephosphorylates Fus3p	Q
1597	VN_1597	YPL277C	YPL277C	Putative protein of unknown function; localized to the membranes; gene expression regulated by copper levels	Q
1598	VN_1598	YOR043W	WHI2	Protein required, with binding partner Psr1p, for full activation of the general stress response, possibly through Msn2p dephosphorylation; regulates growth during the diauxic shift; negative regulator of G1 cyclin expression	Q
1599	VN_1599	YKL211C	TRP3	Bifunctional enzyme exhibiting both indole-3-glycerol-phosphate synthase and anthranilate synthase activities, forms multifunctional hetero-oligomeric anthranilate synthase:indole-3-glycerol phosphate synthase enzyme complex with Trp2p	Q
1600	VN_1600	YCR052W	RSC6	Component of the RSC chromatin remodeling complex; essential for mitotic growth; homolog of SWI/SNF subunit Swp73p	Q
1601	VN_1601	YHR024C	MAS2	Larger subunit of the mitochondrial processing protease (MPP), essential processing enzyme that cleaves the N-terminal targeting sequences from mitochondrially imported proteins	Q
1602	VN_1602	YGR255C	COQ6	Putative flavin-dependent monooxygenase, involved in ubiquinone (Coenzyme Q) biosynthesis; localizes to the matrix face of the mitochondrial inner membrane in a large complex with other ubiquinone biosynthetic enzymes	Q
1603	VN_1603	YNL119W	NCS2	Protein required for thiolation of the uridine at the wobble position of Lys(UUU) and Glu(UUC) tRNAs; has a role in urmylation and in invasive and pseudohyphal growth; inhibits replication of Brome mosaic virus in <i>S. cerevisiae</i>	Q
1604	VN_1604	YPL219W	PCL8	Cyclin, interacts with Pho85p cyclin-dependent kinase (Cdk) to phosphorylate and regulate glycogen synthase, also activates Pho85p for Glc8p phosphorylation	Q
1605	VN_1605	YPR119W	CLB2	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the transition from G2 to M phase; accumulates during G2 and M, then targeted via a destruction box motif for ubiquitin-mediated degradation by the proteasome	Q
1606	VN_1606	YDR402C	DIT2	N-formyltyrosine oxidase, sporulation-specific microsomal enzyme involved in the production of N,N-bisformyl dityrosine required for spore wall maturation, homologous to cytochrome P-450s	Q
1607	VN_1607	YNR069C	BSC5	Protein of unknown function, ORF exhibits genomic organization compatible with a translational readthrough-dependent mode of expression	Q
1608	VN_1608	YBL103C	RTG3	Basic helix-loop-helix-leucine zipper (bHLH/Zip) transcription factor that forms a complex with another bHLH/Zip protein, Rtg1p, to activate the retrograde (RTG) and TOR pathways	Q
1609	VN_1609	YPR001W	CIT3	Dual specificity mitochondrial citrate and methylcitrate synthase; catalyzes the condensation of acetyl-CoA and oxaloacetate to form citrate and that of propionyl-CoA and oxaloacetate to form 2-methylcitrate	Q
1610	VN_1610	YNL026W	SAM50	Essential component of the Sorting and Assembly Machinery (SAM or TOB complex) of the mitochondrial outer membrane, which binds precursors of beta-barrel proteins and facilitates their outer membrane insertion; homologous to bacterial Omp85	Q
1611	VN_1611	YDR514C	YDR514C	Putative protein of unknown function	Q

1612	VN_1612	YJL162C	JJJ2	Protein of unknown function, contains a J-domain, which is a region with homology to the E. coli DnaJ protein	Q
1613	VN_1613	YDR181C	SAS4	Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones and nucleosomes and regulates transcriptional silencing; required for the HAT activity of Sas2p	Q
1614	VN_1614	YCR024C	SLM5	Mitochondrial asparaginyl-tRNA synthetase	Q
1615	VN_1615	YCR045C	RRT12	Probable subtilisin-family protease with a role in formation of the dityrosine layer of spore walls; localizes to the spore wall and also the nuclear envelope and ER region in mature spores	Q
1616	VN_1616	YFR024C-A	LSB3	Protein containing a C-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization	Q
1617	VN_1617	YER045C	ACA1	Basic leucine zipper (bZIP) transcription factor of the ATF/CREB family, may regulate transcription of genes involved in utilization of non-optimal carbon sources	Q
1618	VN_1618	YPL254W	HFI1	Adaptor protein required for structural integrity of the SAGA complex, a histone acetyltransferase-coactivator complex that is involved in global regulation of gene expression through acetylation and transcription functions	Q
1619	VN_1619	YBR083W	TEC1	Transcription factor required for full Ty1 expression, Ty1-mediated gene activation, and haploid invasive and diploid pseudohyphal growth; TEA/ATTS DNA-binding domain family member	Q
1620	VN_1620	YML085C	TUB1	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules	Q
1621	VN_1621	YOL030W	GAS5	1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the cell wall	Q
1622	VN_1622	YLR175W	CBF5	Pseudouridine synthase catalytic subunit of box H/ACA small nucleolar ribonucleoprotein particles (snoRNPs), acts on both large and small rRNAs and on snRNA U2; mutations in human ortholog dyskerin cause the disorder dyskeratosis congenita	Q
1623	VN_1623	YDR346C	SVF1	Protein with a potential role in cell survival pathways, required for the diauxic growth shift; expression in mammalian cells increases survival under conditions inducing apoptosis	Q
1624	VN_1624	YNR001C	CIT1	Citrate synthase, catalyzes the condensation of acetyl coenzyme A and oxaloacetate to form citrate; the rate-limiting enzyme of the TCA cycle; nuclear encoded mitochondrial protein	Q
1625	VN_1625	YDR240C	SNU56	Component of U1 snRNP required for mRNA splicing via spliceosome; yeast specific, no metazoan counterpart; interacts with mRNA in commitment complex	Q
1626	VN_1626	YDL146W	LDB17	Protein involved in the regulation of endocytosis; transiently recruited to actin cortical patches in a SLA1-dependent manner after late coat component assembly; GFP-fusion protein localizes to the periphery, cytoplasm, bud, and bud neck	Q
1627	VN_1627	YDL048C	STP4	Protein containing a Kruppel-type zinc-finger domain; has similarity to Stp1p, Stp2p, and Stp3p	Q
1628	VN_1628	YHR183W	GND1	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress	Q
1629	VN_1629	YPL262W	FUM1	Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and mitochondrial distribution determined by the N-terminal targeting sequence, protein conformation, and status of glyoxylate shunt; phosphorylated in mitochondria	Q
1630	VN_1630	YER141W	COX15	Protein required for the hydroxylation of heme O to form heme A, which is an essential prosthetic group for cytochrome c oxidase	Q
1631	VN_1631	YFR053C	HXK1	Hexokinase isoenzyme 1, a cytosolic protein that catalyzes phosphorylation of glucose during glucose metabolism; expression is highest during growth on non-glucose carbon sources; glucose-induced repression involves the hexokinase Hxk2p	Q
1632	VN_1632	YOL144W	NOP8	Nucleolar protein required for 60S ribosomal subunit biogenesis	Q
1633	VN_1633	YNL239W	LAP3	Cysteine aminopeptidase with homocysteine-thiolactonase activity;	Q

				protects cells against homocysteine toxicity; has bleomycin hydrolase activity in vitro; transcription is regulated by galactose via Gal4p; orthologous to human BLMH	
1634	VN_1634	YFR044C	DUG1	Cys-Gly metallo-di-peptidase; forms a complex with Dug2p and Dug3p to degrade glutathione (GSH) and other peptides containing a gamma-glu-X bond in an alternative pathway to GSH degradation by gamma-glutamyl transpeptidase (Ecm38p)	Q
1635	VN_1635	YOR298W	MUM3	Protein of unknown function involved in the organization of the outer spore wall layers; has similarity to the tafazzins superfamily of acyltransferases	Q
1636	VN_1636	YER051W	JHD1	JmjC domain family histone demethylase specific for H3-K36, similar to proteins found in human, mouse, drosophila, X. laevis, C. elegans, and S. pombe	Q
1637	VN_1637	YDR182W	CDC1	Putative lipid phosphatase of the endoplasmic reticulum; shows Mn2+ dependence and may affect Ca2+ signaling; mutants display actin and general growth defects and pleiotropic defects in cell cycle progression and organelle distribution	Q
1638	VN_1638	YDR523C	SPS1	Putative protein serine/threonine kinase expressed at the end of meiosis and localized to the prospore membrane, required for correct localization of enzymes involved in spore wall synthesis	Q
1639	VN_1639	YCR066W	RAD18	E3 ubiquitin ligase, forms heterodimer with Rad6p to monoubiquitinate PCNA-K164; heterodimer binds single-stranded DNA and has single-stranded DNA dependent ATPase activity; required for postreplication repair	Q
1640	VN_1640	YGL253W	HXK2	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; predominant hexokinase during growth on glucose; functions in the nucleus to repress expression of HXK1 and GLK1 and to induce expression of its own gene	Q
1641	VN_1641	YLR108C	YLR108C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; YLR108C is not an essential gene	Q
1642	VN_1642	YOR119C	RIO1	Essential serine kinase involved in cell cycle progression and processing of the 20S pre-rRNA into mature 18S rRNA	Q
1643	VN_1643	YPL091W	GLR1	Cytosolic and mitochondrial glutathione oxidoreductase, converts oxidized glutathione to reduced glutathione; mitochondrial but not cytosolic form has a role in resistance to hyperoxia	Q
1644	VN_1644	YLR394W	CST9	SUMO E3 ligase; required for synaptonemal complex formation; localizes to synapsis initiation sites on meiotic chromosomes; potential Cdc28p substrate	Q
1645	VN_1645	YBR272C	HSM3	Proteasome-interacting protein involved in the assembly of the base subcomplex of the 19S proteasomal regulatory particle (RP); involved in DNA mismatch repair during slow growth; weak similarity to Msh1p; related to human 19S subunit S5b	Q
1646	VN_1646	YPL066W	YPL066W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the bud neck and cytoplasm; null mutant is viable and exhibits growth defect on a non-fermentable (respiratory) carbon source	Q
1647	VN_1647	YGR256W	GND2	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone	Q
1648	VN_1648	YLR190W	MMR1	Phosphorylated protein of the mitochondrial outer membrane, localizes only to mitochondria of the bud; interacts with Myo2p to mediate mitochondrial distribution to buds; mRNA is targeted to the bud via the transport system involving She2p	Q
1649	VN_1649	YHR113W	YHR113W	Cytoplasmic aspartyl aminopeptidase; cleaves unblocked N-terminal acidic amino acid residues from peptide substrates; forms a 12 subunit homo-oligomeric complex; M18 metalloprotease family member; may interact with ribosomes	Q
1650	VN_1650	YLL011W	SOF1	Essential protein required for biogenesis of 40S (small) ribosomal subunit; has similarity to the beta subunit of trimeric G-proteins and the splicing factor Prp4p	Q
1651	VN_1651	YER133W	GLC7	Type 1 serine/threonine protein phosphatase catalytic subunit, involved in many processes (eg: glycogen metabolism, sporulation, mitosis); accumulates at mating projections by interaction with Afr1p; interacts with many regulatory subunits	Q

1652	VN_1652	YGR211W	ZPR1	Essential protein with two zinc fingers, present in the nucleus of growing cells but relocates to the cytoplasm in starved cells via a process mediated by Cpr1p; binds to translation elongation factor eEF-1 (Tef1p)	Q
1653	VN_1653	YDL089W	NUR1	Protein of unknown function; interacts with Csm1p, Lrs4p; required for rDNA repeat stability; null mutant causes increase in unequal sister-chromatid exchange; GFP-fusion protein localizes to the nuclear periphery, possible Cdc28p substrate	Q
1654	VN_1654	YOR216C	RUD3	Golgi matrix protein involved in the structural organization of the cis-Golgi; interacts genetically with COG3 and USO1	Q
1655	VN_1655	YDR388W	RVS167	Actin-associated protein, interacts with Rvs161p to regulate actin cytoskeleton, endocytosis, and viability following starvation or osmotic stress; homolog of mammalian amphiphysin	Q
1656	VN_1656	YKR058W	GLG1	Self-glucosylating initiator of glycogen synthesis, also glucosylates n-dodecyl-beta-D-maltoside; similar to mammalian glycogenin	Q
1657	VN_1657	YDR306C	YDR306C	F-box protein of unknown function; interacts with Sgt1p via a Leucine-Rich Repeat (LRR) domain	Q
1658	VN_1658	YNL124W	NAF1	RNA-binding protein required for the assembly of box H/ACA snoRNPs and thus for pre-rRNA processing, forms a complex with Shq1p and interacts with H/ACA snoRNP components Nhp2p and Cbf5p; similar to Gar1p	Q
1659	VN_1659	YML126C	ERG13	3-hydroxy-3-methylglutaryl-CoA (HMG-CoA) synthase, catalyzes the formation of HMG-CoA from acetyl-CoA and acetoacetyl-CoA; involved in the second step in mevalonate biosynthesis	Q
1660	VN_1660	YMR070W	MOT3	Nuclear transcription factor with two Cys2-His2 zinc fingers; involved in repression of a subset of hypoxic genes by Rox1p, repression of several DAN/TIR genes during aerobic growth, and repression of ergosterol biosynthetic genes	Q
1661	VN_1661	YLR183C	TOS4	Forkhead Associated domain containing protein and putative transcription factor found associated with chromatin; target of SBF transcription factor; expression is periodic and peaks in G1; similar to PLM2	Q
1662	VN_1662	YJR006W	POL31	DNA polymerase III (delta) subunit, essential for cell viability; involved in DNA replication and DNA repair	Q
1663	VN_1663	YNL137C	NAM9	Mitochondrial ribosomal component of the small subunit	Q
1664	VN_1664	YHR030C	SLT2	Serine/threonine MAP kinase involved in regulating the maintenance of cell wall integrity and progression through the cell cycle; regulated by the PKC1-mediated signaling pathway	Q
1665	VN_1665	YBR247C	ENP1	Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and 40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the nucleolus	Q
1666	VN_1666	YDR524C	AGE1	ADP-ribosylation factor (ARF) GTPase activating protein (GAP) effector, involved in the secretory and endocytic pathways; contains C2C2H2 cysteine/histidine motif	Q
1667	VN_1667	YOR046C	DBP5	Cytoplasmic ATP-dependent RNA helicase of the DEAD-box family involved in mRNA export from the nucleus; involved in translation termination	Q
1668	VN_1668	YNR058W	BIO3	7,8-diamino-pelargonic acid aminotransferase (DAPA), catalyzes the second step in the biotin biosynthesis pathway; BIO3 is in a cluster of 3 genes (BIO3, BIO4, and BIO5) that mediate biotin synthesis	Strain failed to verify via PCR
1669	VN_1669	YJL123C	MTC1	Protein of unknown function that may interact with ribosomes; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to COPI-coated vesicles (early Golgi); mtc1 is synthetically lethal with cdc13-1	Q
1670	VN_1670	YOL112W	MSB4	GTPase-activating protein of the Ras superfamily that acts primarily on Sec4p, localizes to the bud site and bud tip, has similarity to Msb3p; msb3 msb4 double mutation causes defects in secretion and actin organization	Q
1671	VN_1671	YNL240C	NAR1	Component of the cytosolic iron-sulfur (FeS) protein assembly machinery, required for maturation of cytosolic and nuclear FeS proteins and for normal resistance to oxidative stress; homologous to human Narf	Q

1672	VN_1672	YNL022C	YNL022C	Putative cytosine 5-methyltransferase, contains seven beta-strand methyltransferase motif similar to NOP2/YNL061W; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; predicted to be involved in ribosome biogenesis	Q
1673	VN_1673	YMR140W	SIP5	Protein of unknown function; interacts with both the Reg1p/Glc7p phosphatase and the Snf1p kinase	Q
1674	VN_1674	YOR009W	TIR4	Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins; expressed under anaerobic conditions and required for anaerobic growth; transcription is also induced by cold shock	Q
1675	VN_1675	YNL277W	MET2	L-homoserine-O-acetyltransferase, catalyzes the conversion of homoserine to O-acetyl homoserine which is the first step of the methionine biosynthetic pathway	Q
1676	VN_1676	YIL131C	FKH1	Forkhead family transcription factor with a minor role in the expression of G2/M phase genes; negatively regulates transcriptional elongation; positive role in chromatin silencing at HML and HMR; regulates donor preference during switching	Q
1677	VN_1677	YBR288C	APM3	Mu3-like subunit of the clathrin associated protein complex (AP-3); functions in transport of alkaline phosphatase to the vacuole via the alternate pathway	Q
1678	VN_1678	YGL097W	SRM1	Nucleotide exchange factor for Gsp1p, localizes to the nucleus, required for nucleocytoplasmic trafficking of macromolecules; suppressor of the pheromone response pathway; potentially phosphorylated by Cdc28p	Q
1679	VN_1679	YOR088W	YOR087W, YVC1	#N/A	Q
1680	VN_1680	YDR198C	RKM2	Ribosomal protein lysine methyltransferase, responsible for trimethylation of the lysine residue at position 3 of Rpl12Ap and Rpl12Bp	Q
1681	VN_1681	YLR238W	FAR10	Protein involved in recovery from cell cycle arrest in response to pheromone, in a Far1p-independent pathway; interacts with Far3p, Far7p, Far8p, Far9p, and Far11p; potential Cdc28p substrate	Q
1682	VN_1682	YGR002C	SWC4	Component of the Swr1p complex that incorporates Htz1p into chromatin; component of the NuA4 histone acetyltransferase complex	Q
1683	VN_1683	YMR211W	DML1	Essential protein involved in mtDNA inheritance, may also function in the partitioning of the mitochondrial organelle or in the segregation of chromosomes, exhibits regions similar to members of a GTPase family	Q
1684	VN_1684	YLR212C	TUB4	Gamma-tubulin, involved in nucleating microtubules from both the cytoplasmic and nuclear faces of the spindle pole body	Q
1685	VN_1685	YOL132W	GAS4	1,3-beta-glucanosyltransferase, involved with Gas2p in spore wall assembly; has similarity to Gas1p; localizes to the cell wall	Q
1686	VN_1686	YDR473C	PRP3	Splicing factor, component of the U4/U6-U5 snRNP complex	Q
1687	VN_1687	YGR212W	SLI1	N-acetyltransferase, confers resistance to the sphingolipid biosynthesis inhibitor myriocin (ISP-1) by converting it into N-acetyl-myriocin, co-operates with Ypk1p in mediating resistance to myriocin	Q
1688	VN_1688	YGR141W	VPS62	Vacuolar protein sorting (VPS) protein required for cytoplasm to vacuole targeting of proteins	Q
1689	VN_1689	YCL037C	SRO9	Cytoplasmic RNA-binding protein that associates with translating ribosomes; involved in heme regulation of Hap1p as a component of the HMC complex, also involved in the organization of actin filaments; contains a La motif	Q
1690	VN_1690	YNL317W	PFS2	Integral subunit of the pre-mRNA cleavage and polyadenylation factor (CPF) complex; plays an essential role in mRNA 3'-end formation by bridging different processing factors and thereby promoting the assembly of the processing complex	Q
1691	VN_1691	YOR177C	MPC54	Component of the meiotic outer plaque, a membrane-organizing center which is assembled on the cytoplasmic face of the spindle pole body during meiosis II and triggers the formation of the prospore membrane; potential Cdc28p substrate	Q
1692	VN_1692	YDL036C	PUS9	Mitochondrial tRNA:pseudouridine synthase, catalyzes the formation of pseudouridine at position 32 in mitochondrial tRNAs; contains an N-terminal mitochondrial targeting sequence	Q

1693	VN_1693	YNL062C	GCD10	Subunit of tRNA (1-methyladenosine) methyltransferase with Gcd14p, required for the modification of the adenine at position 58 in tRNAs, especially tRNA ⁱ -Met; first identified as a negative regulator of GCN4 expression	Q
1694	VN_1694	YGR117C	YGR117C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
1695	VN_1695	YLL063C	AYT1	Acetyltransferase; catalyzes trichothecene 3-O-acetylation, suggesting a possible role in trichothecene biosynthesis	Q
1696	VN_1696	YBR098W	MMS4	Subunit of the structure-specific Mms4p-Mus81p endonuclease that cleaves branched DNA; involved in recombination, DNA repair, and joint molecule formation/resolution during meiotic recombination	Q
1697	VN_1697	YPL235W	RVB2	Essential protein involved in transcription regulation; component of chromatin remodeling complexes; required for assembly and function of the INO80 complex; also referred to as reptin; member of the RUVB-like protein family	Q
1698	VN_1698	YER081W	SER3	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser33p	Q
1699	VN_1699	YML102W	CAC2	Component of the chromatin assembly complex (with Rlf2p and Msi1p) that assembles newly synthesized histones onto recently replicated DNA, required for building functional kinetochores, conserved from yeast to humans	Q
1700	VN_1700	YHR215W	PHO12	One of three repressible acid phosphatases, a glycoprotein that is transported to the cell surface by the secretory pathway; nearly identical to Pho11p; upregulated by phosphate starvation	Q
1701	VN_1701	YKL184W	SPE1	Ornithine decarboxylase, catalyzes the first step in polyamine biosynthesis; degraded in a proteasome-dependent manner in the presence of excess polyamines; deletion decreases lifespan, and increases necrotic cell death and ROS generation	Q
1702	VN_1702	YPR152C	URN1	Putative protein of unknown function containing WW and FF domains; overexpression causes accumulation of cells in G1 phase	Q
1703	VN_1703	YAL034C	FUN19	Non-essential protein of unknown function; expression induced in response to heat stress	Q
1704	VN_1704	YDR023W	SES1	Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate, interacts with peroxin Pex21p	Strain failed to verify via PCR
1705	VN_1705	YOR003W	YSP3	Putative precursor to the subtilisin-like protease III	Q
1706	VN_1706	YLR116W	MSL5	Component of the commitment complex, which defines the first step in the splicing pathway; essential protein that interacts with Mud2p and Prp40p, forming a bridge between the intron ends; also involved in nuclear retention of pre-mRNA	Q
1707	VN_1707	YLR288C	MEC3	DNA damage and meiotic pachytene checkpoint protein; subunit of a heterotrimeric complex (Rad17p-Mec3p-Ddc1p) that forms a sliding clamp, loaded onto partial duplex DNA by a clamp loader complex; homolog of human and <i>S. pombe</i> Hus1	Q
1708	VN_1708	YDR316W	OMS1	Protein integral to the mitochondrial membrane; has a conserved methyltransferase motif; multicopy suppressor of respiratory defects caused by OXA1 mutations	Q
1709	VN_1709	YEL047C	YEL047C	Soluble fumarate reductase, required with isoenzyme Osm1p for anaerobic growth; may interact with ribosomes, based on co-purification experiments; authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies	Q
1710	VN_1710	YIL074C	SER33	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p	Q
1711	VN_1711	YPL103C	FMP30	Protein of unknown function proposed to be involved in N-acylethanolamine metabolism; related to human NAPE-selective phospholipase D enzyme; native protein is detected in highly purified mitochondria in high-throughput studies	Q
1712	VN_1712	YKL145W	RPT1	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for optimal CDC20 transcription; interacts with Rpn12p and the E3 ubiquitin-protein ligase Ubr1p	Strain failed to verify via PCR

1713	VN_1713	YDR219C	MFB1	Mitochondria-associated F-box protein involved in maintenance of normal mitochondrial morphology; interacts with Skp1p through the F-box motif; preferentially localizes to the mother cell during budding	Q
1714	VN_1714	YPR178W	PRP4	Splicing factor, component of the U4/U6-U5 snRNP complex	Q
1715	VN_1715	YDR148C	KGD2	Dihydrolipoyl transsuccinylase, component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes the oxidative decarboxylation of alpha-ketoglutarate to succinyl-CoA in the TCA cycle; phosphorylated	Q
1716	VN_1716	YGR004W	PEX31	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome size; partially functionally redundant with Pex30p and Pex32p; probably acts at a step downstream of steps mediated by Pex28p and Pex29p	Q
1717	VN_1717	YLR142W	PUT1	Proline oxidase, nuclear-encoded mitochondrial protein involved in utilization of proline as sole nitrogen source; PUT1 transcription is induced by Put3p in the presence of proline and the absence of a preferred nitrogen source	Q
1718	VN_1718	YPR047W	MSF1	Mitochondrial phenylalanyl-tRNA synthetase, active as a monomer, unlike the cytoplasmic subunit which is active as a dimer complexed to a beta subunit dimer; similar to the alpha subunit of E. coli phenylalanyl-tRNA synthetase	Q
1719	VN_1719	YGR019W	UGA1	Gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase) involved in the 4-aminobutyrate and glutamate degradation pathways; required for normal oxidative stress tolerance and nitrogen utilization	Q
1720	VN_1720	YMR027W	YMR027W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus and cytoplasm; YMR027W is not an essential gene	Q
1721	VN_1721	YJL146W	IDS2	Protein involved in modulation of Ime2p activity during meiosis, appears to act indirectly to promote Ime2p-mediated late meiotic functions; found in growing cells and degraded during sporulation	Q
1722	VN_1722	YAR071W	PHO11	One of three repressible acid phosphatases, a glycoprotein that is transported to the cell surface by the secretory pathway; induced by phosphate starvation and coordinately regulated by PHO4 and PHO2	Q
1723	VN_1723	YOR229W	WTM2	Transcriptional modulator involved in regulation of meiosis, silencing, and expression of RNR genes; involved in response to replication stress; contains WD repeats	Q
1724	VN_1724	YFL052W	YFL052W	Putative zinc cluster protein that contains a DNA binding domain; null mutant sensitive to calcofluor white, low osmolarity and heat, suggesting a role for YFL052Wp in cell wall integrity	Q
1725	VN_1725	YER038C	KRE29	Essential subunit of the Mms21-Smc5-Smc6 complex, required for growth and DNA repair; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance	Q
1726	VN_1726	YDR190C	RVB1	Essential protein involved in transcription regulation; component of chromatin remodeling complexes; required for assembly and function of the INO80 complex; also referred to as pontin; member of the RUVB-like protein family	Q
1727	VN_1727	YKL194C	MST1	Mitochondrial threonyl-tRNA synthetase	Q
1728	VN_1728	YDL103C	QRI1	UDP-N-acetylglucosamine pyrophosphorylase, catalyzes the formation of UDP-N-acetylglucosamine (UDP-GlcNAc), which is important in cell wall biosynthesis, protein N-glycosylation, and GPI anchor biosynthesis	Q
1729	VN_1729	YOL125W	TRM13	2'-O-methyltransferase responsible for modification of tRNA at position 4; C-terminal domain has similarity to Rossmann-fold (RFM) superfamily of RNA methyltransferases	Q
1730	VN_1730	YDR105C	TMS1	Vacuolar membrane protein of unknown function that is conserved in mammals; predicted to contain eleven transmembrane helices; interacts with Pdr5p, a protein involved in multidrug resistance	Q
1731	VN_1731	YGR108W	CLB1	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the transition from G2 to M phase; accumulates during G2 and M, then targeted via a destruction box motif for ubiquitin-mediated degradation by the proteasome	Q

1732	VN_1732	YOR198C	BFR1	Component of mRNP complexes associated with polyribosomes; implicated in secretion and nuclear segregation; multicopy suppressor of BFA (Brefeldin A) sensitivity	Q
1733	VN_1733	YLR058C	SHM2	Cytosolic serine hydroxymethyltransferase, converts serine to glycine plus 5,10 methylenetetrahydrofolate; major isoform involved in generating precursors for purine, pyrimidine, amino acid, and lipid biosynthesis	Q
1734	VN_1734	YBR092C	PHO3	Constitutively expressed acid phosphatase similar to Pho5p; brought to the cell surface by transport vesicles; hydrolyzes thiamin phosphates in the periplasmic space, increasing cellular thiamin uptake; expression is repressed by thiamin	Q
1735	VN_1735	YPL083C	SEN54	Subunit of the tRNA splicing endonuclease, which is composed of Sen2p, Sen15p, Sen34p, and Sen54p	Q
1736	VN_1736	YGL184C	STR3	Cystathionine beta-lyase, converts cystathionine into homocysteine	Q
1737	VN_1737	YER089C	PTC2	Type 2C protein phosphatase; dephosphorylates Hog1p to limit maximal osmotic stress induced kinase activity; dephosphorylates Ire1p to downregulate the unfolded protein response; dephosphorylates Cdc28p; role in DNA checkpoint inactivation	Q
1738	VN_1738	YGL111W	NSA1	Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis	Q
1739	VN_1739	YLR163C	MAS1	Smaller subunit of the mitochondrial processing protease (MPP), essential processing enzyme that cleaves the N-terminal targeting sequences from mitochondrially imported proteins	Q
1740	VN_1740	YER019W	ISC1	Mitochondrial membrane localized inositol phosphosphingolipid phospholipase C, hydrolyzes complex sphingolipids to produce ceramide; activated by phosphatidylserine, cardiolipin, and phosphatidylglycerol; mediates Na ⁺ and Li ⁺ halotolerance	Q
1741	VN_1741	YPL063W	TIM50	Essential component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); acts as receptor for the TIM23 complex guiding incoming precursors from the TOM complex; may control the gating of the Tim23p-Tim17p channel	Q
1742	VN_1742	YGR288W	MAL13	MAL-activator protein, part of complex locus MAL1; nonfunctional in genomic reference strain S288C	Q
1743	VN_1743	YHR036W	BRL1	Essential nuclear envelope integral membrane protein identified as a suppressor of a conditional mutation in the major karyopherin, CRM1; homologous to and interacts with Brr6p, a nuclear envelope protein involved in nuclear export	Q
1744	VN_1744	YPR045C	YPR045C	Protein of unknown function; involvement in splicing based on pre-mRNA accumulation defect for many intron-containing genes; contains a SAC3 domain; physically interacts with Csn12p; YPR045C is not an essential gene	Q
1745	VN_1745	YBL056W	PTC3	Type 2C protein phosphatase; dephosphorylates Hog1p (see also Ptc2p) to limit maximal kinase activity induced by osmotic stress; dephosphorylates T169 phosphorylated Cdc28p (see also Ptc2p); role in DNA checkpoint inactivation	Q
1746	VN_1746	YBR093C	PHO5	Repressible acid phosphatase (1 of 3) that also mediates extracellular nucleotide-derived phosphate hydrolysis; secretory pathway derived cell surface glycoprotein; induced by phosphate starvation and coordinately regulated by PHO4 and PHO2	Q
1747	VN_1747	YPR157W	YPR157W	Putative protein of unknown function; induced by treatment with 8-methoxypsoralen and UVA irradiation	Q
1748	VN_1748	YGL256W	ADH4	Alcohol dehydrogenase isoenzyme type IV, dimeric enzyme demonstrated to be zinc-dependent despite sequence similarity to iron-activated alcohol dehydrogenases; transcription is induced in response to zinc deficiency	Q
1749	VN_1749	YML068W	ITT1	Protein that modulates the efficiency of translation termination, interacts with translation release factors eRF1 (Sup45p) and eRF3 (Sup35p) in vitro, contains a zinc finger domain characteristic of the TRIAD class of proteins	Q
1750	VN_1750	YHR018C	ARG4	Argininosuccinate lyase, catalyzes the final step in the arginine biosynthesis pathway	Q
1751	VN_1751	YML005W	TRM12	S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; required for wybutosine formation in phenylalanine-	Q

				accepting tRNA	
1752	VN_1752	YLR341W	SPO77	Meiosis-specific protein of unknown function, required for spore wall formation during sporulation; dispensable for both nuclear divisions during meiosis	Q
1753	VN_1753	YIL123W	SIM1	Protein of the SUN family (Sim1p, Uth1p, Nca3p, Sun4p) that may participate in DNA replication, promoter contains SCB regulation box at -300 bp indicating that expression may be cell cycle-regulated	Q
1754	VN_1754	YIL039W	TED1	Conserved phosphoesterase domain-containing protein that acts together with Emp24p/Erv25p in cargo exit from the ER; deletion confers sensitivity to 4-(N-(S-glutathionylacetyl)amino) phenylarsenoxide (GSAO)	Q
1755	VN_1755	YMR223W	UBP8	Ubiquitin-specific protease that is a component of the SAGA (Spt-Ada-Gcn5-Acetyltransferase) acetylation complex; required for SAGA-mediated deubiquitination of histone H2B	Q
1756	VN_1756	YPR068C	HOS1	Putative class I histone deacetylase (HDAC) with sequence similarity to Hda1p, Rpd3p, Hos2p, and Hos3p; deletion results in increased histone acetylation at rDNA repeats; interacts with the Tup1p-Ssn6p corepressor complex	Q
1757	VN_1757	YBR297W	MAL33	MAL-activator protein, part of complex locus MAL3; nonfunctional in genomic reference strain S288C	Q
1758	VN_1758	YDR223W	CRF1	Transcriptional corepressor involved in repression of ribosomal protein (RP) gene transcription via the TOR signaling pathway which promotes accumulation of Crf1p in the nucleus; role in repression of RP genes varies by strain	Q
1759	VN_1759	YMR133W	REC114	Protein involved in early stages of meiotic recombination; possibly involved in the coordination of recombination and meiotic division; mutations lead to premature initiation of the first meiotic division	Q
1760	VN_1760	YHL021C	AIM17	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; null mutant displays reduced frequency of mitochondrial genome loss	Q
1761	VN_1761	YMR293C	HER2	Subunit of the trimeric GatFAB AmidoTransferase(AdT) complex; involved in the formation of Q-tRNA ^Q ; required for remodeling of ER caused by Hmg2p overexpression; similar to bacterial GatA glutamyl-tRNA amidotransferase	Q
1762	VN_1762	YKL133C	YKL133C	Putative protein of unknown function; has similarity to Mgr3p, but unlike MGR3, is not required for growth of cells lacking the mitochondrial genome (null mutation does not confer a petite-negative phenotype)	Q
1763	VN_1763	YMR111C	YMR111C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; YMR111C is not an essential gene	Q
1764	VN_1764	YPR034W	ARP7	Component of both the SWI/SNF and RSC chromatin remodeling complexes; actin-related protein involved in transcriptional regulation	Strain failed to verify via PCR
1765	VN_1765	YMR044W	IOC4	Member of a complex (Isw1b) with Isw1p and Ioc2p that exhibits nucleosome-stimulated ATPase activity and acts within coding regions to coordinate transcription elongation with termination and processing, contains a PWWP motif	Q
1766	VN_1766	YLR034C	SMF3	Putative divalent metal ion transporter involved in iron homeostasis; transcriptionally regulated by metal ions; member of the Nramp family of metal transport proteins	Q
1767	VN_1767	YMR239C	RNT1	RNAase III; involved in rDNA transcription and rRNA processing; also cleaves a stem-loop structure at the 3' end of U2 snRNA to ensure formation of the correct U2 3' end; involved in polyadenylation-independent transcription termination	Q
1768	VN_1768	YPR196W	YPR196W	Putative maltose activator	Q
1769	VN_1769	YDL024C	DIA3	Protein of unknown function, involved in invasive and pseudohyphal growth	Q
1770	VN_1770	YEL040W	UTR2	Chitin transglycosylase that functions in the transfer of chitin to beta(1-6) and beta(1-3) glucans in the cell wall; similar to and functionally redundant with Crh1; glycosylphosphatidylinositol (GPI)-anchored protein localized to bud neck	Q

1771	VN_1771	YBL086C	YBL086C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery	Q
1772	VN_1772	YHR146W	CRP1	Protein that binds to cruciform DNA structures	Q
1773	VN_1773	YKL143W	LTV1	Component of the GSE complex, which is required for proper sorting of amino acid permease Gap1p; required for ribosomal small subunit export from nucleus; required for growth at low temperature	Q
1774	VN_1774	YDR247W	VHS1	Cytoplasmic serine/threonine protein kinase; identified as a high-copy suppressor of the synthetic lethality of a <i>sis2 sit4</i> double mutant, suggesting a role in G1/S phase progression; homolog of Sks1p	Q
1775	VN_1775	YIR027C	DAL1	Allantoinase, converts allantoin to allantate in the first step of allantoin degradation; expression sensitive to nitrogen catabolite repression	Q
1776	VN_1776	YOL041C	NOP12	Nucleolar protein involved in pre-25S rRNA processing and biogenesis of large 60S ribosomal subunit; contains an RNA recognition motif (RRM); binds to Ebp2; similar to Nop13p and Nsr1p	Strain failed to verify via PCR
1777	VN_1777	YOR166C	SWT1	RNA endoribonuclease involved in perinuclear mRNP quality control via the turnover of aberrant, unprocessed pre-mRNAs; interacts with subunits of THO/TREX, TREX-2, and RNA polymerase II; contains a PIN (PiIT N terminus) domain	Q
1778	VN_1778	YDR393W	SHE9	Mitochondrial inner membrane protein required for normal mitochondrial morphology, may be involved in fission of the inner membrane; forms a homo-oligomeric complex	Q
1779	VN_1779	YDL091C	UBX3	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p, green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Q
1780	VN_1780	YDL161W	ENT1	Epsin-like protein involved in endocytosis and actin patch assembly and functionally redundant with Ent2p; binds clathrin via a clathrin-binding domain motif at C-terminus	Q
1781	VN_1781	YHR066W	SSF1	Constituent of 66S pre-ribosomal particles, required for ribosomal large subunit maturation; functionally redundant with Ssf2p; member of the Brix family	Q
1782	VN_1782	YBR177C	EHT1	Acyl-coenzymeA:ethanol O-acyltransferase that plays a minor role in medium-chain fatty acid ethyl ester biosynthesis; possesses short-chain esterase activity; localizes to lipid particles and the mitochondrial outer membrane	Q
1783	VN_1783	YBR240C	THI2	Zinc finger protein of the Zn(II) ₂ Cys ₆ type, probable transcriptional activator of thiamine biosynthetic genes	Q
1784	VN_1784	YKL046C	DCW1	Putative mannosidase, GPI-anchored membrane protein required for cell wall biosynthesis in bud formation; homologous to Dfg5p	Q
1785	VN_1785	YLR005W	SSL1	Component of the core form of RNA polymerase transcription factor TFIIH, which has both protein kinase and DNA-dependent ATPase/helicase activities and is essential for transcription and nucleotide excision repair; interacts with Tfb4p	Q
1786	VN_1786	YLR210W	CLB4	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the G2/M transition; may be involved in DNA replication and spindle assembly; accumulates during S phase and G2, then targeted for ubiquitin-mediated degradation	Q
1787	VN_1787	YOR056C	NOB1	Essential nuclear protein involved in proteasome maturation and synthesis of 40S ribosomal subunits; required for cleavage of the 20S pre-rRNA to generate the mature 18S rRNA	Q
1788	VN_1788	YPR080W	TEF1	Translational elongation factor EF-1 alpha; also encoded by TEF2; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes	Q
1789	VN_1789	YGR249W	MGA1	Protein similar to heat shock transcription factor; multicopy suppressor of pseudohyphal growth defects of ammonium permease mutants	Q
1790	VN_1790	YDL216C	RRI1	Catalytic subunit of the COP9 signalosome (CSN) complex that acts as an isopeptidase in cleaving the ubiquitin-like protein Nedd8 from SCF ubiquitin ligases; metalloendopeptidase involved in the adaptation to pheromone signaling	Q
1791	VN_1791	YOR375C	GDH1	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh3p; expression regulated by nitrogen and	Q

				carbon sources	
1792	VN_1792	YHR177W	YHR177W	Putative protein of unknown function; overexpression causes a cell cycle delay or arrest	Q
1793	VN_1793	YBR182C	SMP1	Putative transcription factor involved in regulating the response to osmotic stress; member of the MADS-box family of transcription factors	Q
1794	VN_1794	YJL046W	AIM22	Putative lipote-protein ligase, required along with Lip2 and Lip5 for lipoylation of Lat1p and Kgd2p; similar to E. coli LplA; null mutant displays reduced frequency of mitochondrial genome loss	Q
1795	VN_1795	YJL049W	YJL049W	Putative protein of unknown function; YJL049W is a non-essential gene	Q
1796	VN_1796	YMR210W	YMR210W	Putative acyltransferase with similarity to Eeb1p and Eht1p, has a minor role in medium-chain fatty acid ethyl ester biosynthesis; may be involved in lipid metabolism and detoxification	Q
1797	VN_1797	YMR265C	YMR265C	Putative protein of unknown function	Q
1798	VN_1798	YOR272W	YTM1	Constituent of 66S pre-ribosomal particles, forms a complex with Nop7p and Erb1p that is required for maturation of the large ribosomal subunit; has seven C-terminal WD repeats	Strain failed to verify via PCR
1799	VN_1799	YBL082C	ALG3	Dolichol-P-Man dependent alpha(1-3) mannosyltransferase, involved in the synthesis of dolichol-linked oligosaccharide donor for N-linked glycosylation of proteins	Q
1800	VN_1800	YAL062W	GDH3	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh1p; expression regulated by nitrogen and carbon sources	Strain failed to verify via PCR
1801	VN_1801	YDR364C	CDC40	Pre-mRNA splicing factor, important for catalytic step II of pre-mRNA splicing and plays a role in cell cycle progression; required for DNA synthesis during mitosis and meiosis; has WD repeats	Q
1802	VN_1802	YPL245W	YPL245W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the nucleus and the cytoplasm	Q
1803	VN_1803	YJR078W	BNA2	Putative tryptophan 2,3-dioxygenase or indoleamine 2,3-dioxygenase, required for the de novo biosynthesis of NAD from tryptophan via kynurenine; expression is upregulated upon telomere uncapping; regulated by Hst1p and Aft2p	Q
1804	VN_1804	YGL194C	HOS2	Histone deacetylase required for gene activation via specific deacetylation of lysines in H3 and H4 histone tails; subunit of the Set3 complex, a meiotic-specific repressor of sporulation specific genes that contains deacetylase activity	Q
1805	VN_1805	YKL106W	AAT1	Mitochondrial aspartate aminotransferase, catalyzes the conversion of oxaloacetate to aspartate in aspartate and asparagine biosynthesis	Q
1806	VN_1806	YKL075C	YKL075C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; proposed to be involved in resistance to streptozotocin and camptothecin	Q
1807	VN_1807	YFR005C	SAD1	Conserved zinc-finger domain protein involved in pre-mRNA splicing, required for assembly of U4 snRNA into the U4/U6 particle	Q
1808	VN_1808	YPL201C	YIG1	Protein that interacts with glycerol 3-phosphatase and plays a role in anaerobic glycerol production; localizes to the nucleus and cytosol	Q
1809	VN_1809	YPL139C	UME1	Negative regulator of meiosis, required for repression of a subset of meiotic genes during vegetative growth, binding of histone deacetylase Rpd3p required for activity, contains a NEE box and a WD repeat motif; homologous with Wtm1p, Wtm2p	Q
1810	VN_1810	YBR118W	TEF2	Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes	Q
1811	VN_1811	YDL189W	RBS1	Protein of unknown function, identified as a high copy suppressor of psk1 psk2 mutations that confer temperature-sensitivity for galactose utilization; proposed to bind single-stranded nucleic acids via its R3H domain	Q
1812	VN_1812	YOR323C	PRO2	Gamma-glutamyl phosphate reductase, catalyzes the second step in proline biosynthesis	Q

1813	VN_1813	YLR195C	NMT1	N-myristoyl transferase, catalyzes the cotranslational, covalent attachment of myristic acid to the N-terminal glycine residue of several proteins involved in cellular growth and signal transduction	Q
1814	VN_1814	YPR125W	YLH47	Mitochondrial inner membrane protein exposed to the mitochondrial matrix, associates with mitochondrial ribosomes, NOT required for respiratory growth; homolog of human Letm1, a protein implicated in Wolf-Hirschhorn syndrome	Q
1815	VN_1815	YKL108W	SLD2	Protein required for DNA replication, phosphorylated in S phase by S-phase cyclin-dependent kinases (Cdks), phosphorylation is essential for DNA replication and for complex formation with Dpb11p; potential Cdc28p substrate	Q
1816	VN_1816	YGL215W	CLG1	Cyclin-like protein that interacts with Pho85p; has sequence similarity to G1 cyclins PCL1 and PCL2	Q
1817	VN_1817	YML097C	VPS9	A guanine nucleotide exchange factor involved in vesicle-mediated vacuolar protein transport; specifically stimulates the intrinsic guanine nucleotide exchange activity of Vps21p/Rab5: similar to mammalian ras inhibitors; binds ubiquitin	Q
1818	VN_1818	YKR042W	UTH1	Mitochondrial outer membrane and cell wall localized SUN family member required for mitochondrial autophagy; involved in the oxidative stress response, life span during starvation, mitochondrial biogenesis, and cell death	Q
1819	VN_1819	YGR223C	HSV2	Phosphatidylinositol 3,5-bisphosphate-binding protein, plays a role in micronucleophagy; predicted to fold as a seven-bladed beta-propeller; displays punctate cytoplasmic localization	Q
1820	VN_1820	YBL098W	BNA4	Kynurenine 3-mono oxygenase, required for the de novo biosynthesis of NAD from tryptophan via kynurenine; expression regulated by Hst1p; putative therapeutic target for Huntington disease	Strain failed to verify via PCR
1821	VN_1821	YGL130W	CEG1	Alpha (guanylyltransferase) subunit of the mRNA capping enzyme, a heterodimer (the other subunit is CET1, an RNA 5'-triphosphatase) involved in adding the 5' cap to mRNA; the mammalian enzyme is a single bifunctional polypeptide	Strain failed to verify via PCR
1822	VN_1822	YDL233W	YDL233W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YDL233W is not an essential gene	Q
1823	VN_1823	YPL095C	EEB1	Acyl-coenzymeA:ethanol O-acyltransferase responsible for the major part of medium-chain fatty acid ethyl ester biosynthesis during fermentation; possesses short-chain esterase activity; may be involved in lipid metabolism and detoxification	Q
1824	VN_1824	YMR135C	GID8	Protein of unknown function, involved in proteasome-dependent catabolite inactivation of fructose-1,6-bisphosphatase; contains LisH and CTLH domains, like Vid30p; dosage-dependent regulator of START	Q
1825	VN_1825	YBR095C	RXT2	Subunit of the histone deacetylase Rpd3L complex; possibly involved in cell fusion and invasive growth	Q
1826	VN_1826	YLR231C	BNA5	Kynureninase, required for the de novo biosynthesis of NAD from tryptophan via kynurenine; expression regulated by Hst1p	Q
1827	VN_1827	YHL002W	HSE1	Subunit of the endosomal Vps27p-Hse1p complex required for sorting of ubiquitinated membrane proteins into intraluminal vesicles prior to vacuolar degradation, as well as for recycling of Golgi proteins and formation of luminal membranes	Q
1828	VN_1828	YMR220W	ERG8	Phosphomevalonate kinase, an essential cytosolic enzyme that acts in the biosynthesis of isoprenoids and sterols, including ergosterol, from mevalonate	Q
1829	VN_1829	YOR059C	YOR059C	Hypothetical protein	Strain failed to verify via PCR
1830	VN_1830	YKR003W	OSH6	Member of an oxysterol-binding protein family with overlapping, redundant functions in sterol metabolism and which collectively perform a function essential for viability; GFP-fusion protein localizes to the cell periphery	Q
1831	VN_1831	YGL219C	MDM34	Mitochondrial component of the ERMES complex that links the ER to mitochondria and may promote inter-organellar calcium and phospholipid exchange as well as coordinating mitochondrial DNA replication and growth	Q

1832	VN_1832	YDR254W	CHL4	Outer kinetochore protein required for chromosome stability, interacts with kinetochore proteins Ctf19p, Ctf3p, and Iml3p; exhibits a two-hybrid interaction with Mif2p; association with CEN DNA requires Ctf19p	Q
1833	VN_1833	YJR062C	NTA1	Amidase, removes the amide group from N-terminal asparagine and glutamine residues to generate proteins with N-terminal aspartate and glutamate residues that are targets of ubiquitin-mediated degradation	Q
1834	VN_1834	YPL101W	ELP4	Subunit of Elongator complex, which is required for modification of wobble nucleosides in tRNA; required for Elongator structural integrity	Q
1835	VN_1835	YNL206C	RTT106	Histone chaperone, involved in regulation of chromatin structure in both transcribed and silenced chromosomal regions; affects transcriptional elongation; has a role in regulation of Ty1 transposition	Q
1836	VN_1836	YDR125C	ECM18	Protein of unknown function, similar to Rlp24p	Q
1837	VN_1837	YLR431C	ATG23	Peripheral membrane protein required for the cytoplasm-to-vacuole targeting (Cvt) pathway and efficient macroautophagy; cycles between the phagophore assembly site (PAS) and non-PAS locations; forms a complex with Atg9p and Atg27p	Q
1838	VN_1838	YJL155C	FBP26	Fructose-2,6-bisphosphatase, required for glucose metabolism	Q
1839	VN_1839	YOL069W	NUF2	Component of the evolutionarily conserved kinetochore-associated Ndc80 complex (Ndc80p-Nuf2p-Spc24p-Spc25p); involved in chromosome segregation, spindle checkpoint activity and kinetochore clustering	Q
1840	VN_1840	YOR155C	ISN1	Inosine 5'-monophosphate (IMP)-specific 5'-nucleotidase, catalyzes the breakdown of IMP to inosine, does not show similarity to known 5'-nucleotidases from other organisms	Q
1841	VN_1841	YLR300W	EXG1	Major exo-1,3-beta-glucanase of the cell wall, involved in cell wall beta-glucan assembly; exists as three differentially glycosylated isoenzymes	Q
1842	VN_1842	YDR004W	RAD57	Protein that stimulates strand exchange by stabilizing the binding of Rad51p to single-stranded DNA; involved in the recombinational repair of double-strand breaks in DNA during vegetative growth and meiosis; forms heterodimer with Rad55p	Q
1843	VN_1843	YLR090W	XDJ1	Putative chaperone, homolog of E. coli DnaJ, closely related to Ydj1p; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
1844	VN_1844	YJL044C	GYP6	GTPase-activating protein (GAP) for the yeast Rab family member, Ypt6p; involved in vesicle mediated protein transport	Q
1845	VN_1845	YMR209C	YMR209C	Putative S-adenosylmethionine-dependent methyltransferase; YMR209C is not an essential gene	Q
1846	VN_1846	YPR084W	YPR084W	Putative protein of unknown function	Q
1847	VN_1847	YOL072W	THP1	Nuclear pore-associated protein, forms a complex with Sac3p that is involved in transcription and in mRNA export from the nucleus; contains a PAM domain implicated in protein-protein binding	Q
1848	VN_1848	YDR229W	IVY1	Phospholipid-binding protein that interacts with both Ypt7p and Vps33p, may partially counteract the action of Vps33p and vice versa, localizes to the rim of the vacuole as cells approach stationary phase	Q
1849	VN_1849	YNL016W	PUB1	Poly (A)+ RNA-binding protein, abundant mRNP-component protein that binds mRNA and is required for stability of many mRNAs; component of glucose deprivation induced stress granules, involved in P-body-dependent granule assembly	Q
1850	VN_1850	YNL074C	MLF3	Serine-rich protein of unknown function, predicted to be palmitoylated; overproduction suppresses the growth inhibition caused by exposure to the immunosuppressant leflunomide	Q
1851	VN_1851	YOR221C	MCT1	Predicted malonyl-CoA:ACP transferase, putative component of a type-II mitochondrial fatty acid synthase that produces intermediates for phospholipid remodeling	Q
1852	VN_1852	YER043C	SAH1	S-adenosyl-L-homocysteine hydrolase, catabolizes S-adenosyl-L-homocysteine which is formed after donation of the activated methyl group of S-adenosyl-L-methionine (AdoMet) to an acceptor	Strain failed to verify via PCR

1853	VN_1853	YNL166C	BNI5	Protein involved in organization of septins at the mother-bud neck, may interact directly with the Cdc11p septin, localizes to bud neck in a septin-dependent manner	Q
1854	VN_1854	YER003C	PMI40	Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P; required for early steps in protein mannosylation	Q
1855	VN_1855	YNL309W	STB1	Protein with a role in regulation of MBF-specific transcription at Start, phosphorylated by Cln-Cdc28p kinases in vitro; unphosphorylated form binds Swi6p and binding is required for Stb1p function; expression is cell-cycle regulated	Q
1856	VN_1856	YMR191W	SPG5	Protein required for survival at high temperature during stationary phase; not required for growth on nonfermentable carbon sources	Q
1857	VN_1857	YDR363W	ESC2	Protein involved in silencing; may recruit or stabilize Sir proteins; role in Rad51-dependent homologous recombination repair and intra S-phase DNA damage checkpoint; member of the RENi (Rad60-Esc2-Nip45) family of SUMO-like domain proteins	Q
1858	VN_1858	YBR162C	TOS1	Covalently-bound cell wall protein of unknown function; identified as a cell cycle regulated SBF target gene; deletion mutants are highly resistant to treatment with beta-1,3-glucanase; has sequence similarity to YJL171C	Q
1859	VN_1859	YPL146C	NOP53	Nucleolar protein; involved in biogenesis of the 60S subunit of the ribosome; interacts with rRNA processing factors Cbf5p and Nop2p; null mutant is viable but growth is severely impaired	Q
1860	VN_1860	YDR312W	SSF2	Protein required for ribosomal large subunit maturation, functionally redundant with Ssf1p; member of the Brix family	Q
1861	VN_1861	YOR197W	MCA1	Putative cysteine protease similar to mammalian caspases; involved in regulation of apoptosis upon hydrogen peroxide treatment; proposed to be involved in cell cycle progression	Q
1862	VN_1862	YPL049C	DIG1	Regulatory protein of unknown function, constitutively-expressed, involved in the regulation of mating-specific genes and the invasive growth pathway, required for MAP-kinase imposed repression, inhibits pheromone-responsive transcription	Q
1863	VN_1863	YPL151C	PRP46	Member of the NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 snRNAs	Q
1864	VN_1864	YPR085C	ASA1	Putative protein of unknown function; subunit of the ASTRA complex (Rvb1p, Rvb2p, Tra1p, Tti1p, Tti2, Asa1p and Tra1p) which is part of the chromatin remodeling machinery	Q
1865	VN_1865	YDR515W	SLF1	RNA binding protein that associates with polysomes; proposed to be involved in regulating mRNA translation; involved in the copper-dependent mineralization of copper sulfide complexes on cell surface in cells cultured in copper salts	Q
1866	VN_1866	YHR011W	DIA4	Probable mitochondrial seryl-tRNA synthetase, mutant displays increased invasive and pseudohyphal growth	Q
1867	VN_1867	YOR244W	ESA1	Catalytic subunit of the histone acetyltransferase complex (NuA4) that acetylates four conserved internal lysines of histone H4 N-terminal tail; required for cell cycle progression and transcriptional silencing at the rDNA locus	Q
1868	VN_1868	YMR268C	PRP24	Splicing factor that reanneals U4 and U6 snRNPs during spliceosome recycling	Q
1869	VN_1869	YMR208W	ERG12	Mevalonate kinase, acts in the biosynthesis of isoprenoids and sterols, including ergosterol, from mevalonate	Q
1870	VN_1870	YMR062C	ARG7	Mitochondrial ornithine acetyltransferase, catalyzes the fifth step in arginine biosynthesis; also possesses acetylglutamate synthase activity, regenerates acetylglutamate while forming ornithine	Q
1871	VN_1871	YOL059W	GPD2	NAD-dependent glycerol 3-phosphate dehydrogenase, homolog of Gpd1p, expression is controlled by an oxygen-independent signaling pathway required to regulate metabolism under anoxic conditions; located in cytosol and mitochondria	Q
1872	VN_1872	YGR254W	ENO1	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose	Q

1873	VN_1873	YPL281C	ERR2	Protein of unknown function, has similarity to enolases	Q
1874	VN_1874	YPR163C	TIF3	Translation initiation factor eIF-4B, has RNA annealing activity; contains an RNA recognition motif and binds to single-stranded RNA	Q
1875	VN_1875	YPR120C	CLB5	B-type cyclin involved in DNA replication during S phase; activates Cdc28p to promote initiation of DNA synthesis; functions in formation of mitotic spindles along with Clb3p and Clb4p; most abundant during late G1 phase	Q
1876	VN_1876	YKL027W	YKL027W	Protein of unknown function, localized to the mitochondrial outer membrane	Q
1877	VN_1877	YNR050C	LYS9	Saccharopine dehydrogenase (NADP+, L-glutamate-forming); catalyzes the formation of saccharopine from alpha-aminoadipate 6-semialdehyde, the seventh step in lysine biosynthesis pathway; exhibits genetic and physical interactions with TRM112	Q
1878	VN_1878	YOR250C	CLP1	Subunit of cleavage factor I (CFI), involved in both the endonucleolytic cleavage and polyadenylation steps of mRNA 3'-end maturation	Strain failed to verify via PCR
1879	VN_1879	YNL011C	YNL011C	Putative protein of unknown function; YNL011C is not an essential gene	Q
1880	VN_1880	YPR106W	ISR1	Predicted protein kinase, overexpression causes sensitivity to staurosporine, which is a potent inhibitor of protein kinase C	Q
1881	VN_1881	YCL029C	BIK1	Microtubule-associated protein, component of the interface between microtubules and kinetochore, involved in sister chromatid separation; essential in polyploid cells but not in haploid or diploid cells; ortholog of mammalian CLIP-170	Q
1882	VN_1882	YDR527W	RBA50	Protein involved in transcription; interacts with RNA polymerase II subunits Rpb2p, Rpb3, and Rpb11p; has similarity to human RPAP1	Q
1883	VN_1883	YHR001W	OSH7	Member of an oxysterol-binding protein family with seven members in <i>S. cerevisiae</i> ; family members have overlapping, redundant functions in sterol metabolism and collectively perform a function essential for viability	Q
1884	VN_1884	YBR236C	ABD1	Methyltransferase, catalyzes the transfer of a methyl group from S-adenosylmethionine to the GpppN terminus of capped mRNA	Q
1885	VN_1885	YAR018C	KIN3	Nonessential protein kinase with unknown cellular role	Strain failed to verify via PCR
1886	VN_1886	YPR148C	YPR148C	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Q
1887	VN_1887	YOR237W	HES1	Protein implicated in the regulation of ergosterol biosynthesis; one of a seven member gene family with a common essential function and non-essential unique functions; similar to human oxysterol binding protein (OSBP)	Q
1888	VN_1888	YKR005C	YKR005C	Putative protein of unknown function	Q
1889	VN_1889	YPL133C	RDS2	Zinc cluster transcriptional activator involved in conferring resistance to ketoconazole	Q
1890	VN_1890	YDR055W	PST1	Cell wall protein that contains a putative GPI-attachment site; secreted by regenerating protoplasts; up-regulated by activation of the cell integrity pathway, as mediated by Rlm1p; upregulated by cell wall damage via disruption of FKS1	Q
1891	VN_1891	YOR047C	STD1	Protein involved in control of glucose-regulated gene expression; interacts with protein kinase Snf1p, glucose sensors Snf3p and Rgt2p, and TATA-binding protein Spt15p; acts as a regulator of the transcription factor Rgt1p	Q
1892	VN_1892	YCR079W	PTC6	Mitochondrial protein phosphatase of type 2C with similarity to mammalian PP1Ks; involved in mitophagy; null mutant is sensitive to rapamycin and has decreased phosphorylation of the Pda1 subunit of pyruvate dehydrogenase	Q
1893	VN_1893	YDL044C	MTF2	Mitochondrial matrix protein that interacts with an N-terminal region of mitochondrial RNA polymerase (Rpo41p) and couples RNA processing and translation to transcription	Q
1894	VN_1894	YGR252W	GCN5	Histone acetyltransferase, acetylates N-terminal lysines on histones	Q

				H2B and H3; catalytic subunit of the ADA and SAGA histone acetyltransferase complexes; founding member of the Gcn5p-related N-acetyltransferase superfamily	
1895	VN_1895	YHR174W	ENO2	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose	Q
1896	VN_1896	YBR273C	UBX7	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p	Q
1897	VN_1897	YHR118C	ORC6	Subunit of the origin recognition complex, which directs DNA replication by binding to replication origins and is also involved in transcriptional silencing; phosphorylated by Cdc28p	Q
1898	VN_1898	YDL097C	RPN6	Essential, non-ATPase regulatory subunit of the 26S proteasome lid required for the assembly and activity of the 26S proteasome; the human homolog (S9 protein) partially rescues Rpn6p depletion	Q
1899	VN_1899	YPL123C	RNY1	Vacuolar RNase of the T(2) family, relocalizes to the cytosol where it cleaves tRNAs upon oxidative or stationary phase stress; promotes apoptosis under stress conditions and this function is independent of its catalytic activity	Q
1900	VN_1900	YOL016C	CMK2	Calmodulin-dependent protein kinase; may play a role in stress response, many CA ⁺⁺ /calmodulin dependent phosphorylation substrates demonstrated in vitro, amino acid sequence similar to Cmk1p and mammalian Cam Kinase II	Q
1901	VN_1901	YBR279W	PAF1	Component of the Paf1p complex that binds to and modulates the activity of RNA polymerases I and II; required for expression of a subset of genes, including cell cycle-regulated genes; homolog of human PD2/hPAF1	Q
1902	VN_1902	YDR165W	TRM82	Subunit of a tRNA methyltransferase complex composed of Trm8p and Trm82p that catalyzes 7-methylguanosine modification of tRNA	Q
1903	VN_1903	YER130C	YER130C	Protein of unknown function	Q
1904	VN_1904	YDR370C	YDR370C	Putative protein of unknown function	Q
1905	VN_1905	YDL131W	LYS21	Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p	Q
1906	VN_1906	YLR085C	ARP6	Actin-related protein that binds nucleosomes; a component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A	Q
1907	VN_1907	YMR323W	ERR3	Protein of unknown function, has similarity to enolases	Q
1908	VN_1908	YIL135C	VHS2	Cytoplasmic protein of unknown function; identified as a high-copy suppressor of the synthetic lethality of a sis2 sit4 double mutant, suggesting a role in G1/S phase progression; similar to Mlf3p	Q
1909	VN_1909	YLR113W	HOG1	Mitogen-activated protein kinase involved in osmoregulation via three independent osmosensors; mediates the recruitment and activation of RNA Pol II at Hot1p-dependent promoters; localization regulated by Ptp2p and Ptp3p	Q
1910	VN_1910	YDR448W	ADA2	Transcription coactivator, component of the ADA and SAGA transcriptional adaptor/HAT (histone acetyltransferase) complexes	Strain failed to verify via PCR
1911	VN_1911	YPL145C	KES1	Member of the oxysterol binding protein family, which includes seven yeast homologs; involved in negative regulation of Sec14p-dependent Golgi complex secretory functions, peripheral membrane protein that localizes to the Golgi complex	Q
1912	VN_1912	YOR025W	HST3	Member of the Sir2 family of NAD(+)-dependent protein deacetylases; involved along with Hst4p in telomeric silencing, cell cycle progression, radiation resistance, genomic stability and short-chain fatty acid metabolism	Q
1913	VN_1913	YDL147W	RPN5	Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to mammalian p55 subunit and to another <i>S. cerevisiae</i> regulatory subunit, Rpn7p	Q

1914	VN_1914	YIL071C	PCI8	Possible shared subunit of Cop9 signalosome (CSN) and eIF3, binds eIF3b subunit Prt1p, has possible dual functions in transcriptional and translational control, contains a PCI (Proteasome-COP9 signalosome (CSN)-eIF3) domain	Q
1915	VN_1915	YER152C	YER152C	Protein with 2-aminoadipate transaminase activity; shares amino acid similarity with the aminotransferases Aro8p and Aro9p; YER152C is not an essential gene	Q
1916	VN_1916	YER061C	CEM1	Mitochondrial beta-keto-acyl synthase with possible role in fatty acid synthesis; required for mitochondrial respiration	Q
1917	VN_1917	YDR170W-A	YDR170W-A	Retrotransposon TYA Gag gene; Gag is a nucleocapsid protein that is the structural constituent of virus-like particles (VLPs); similar to retroviral Gag; YDR170W-A is part of a mutant retrotransposon	Q
1918	VN_1918	YER044C-A	MEI4	Meiosis-specific protein involved in double-strand break formation during meiotic recombination; required for chromosome synapsis and production of viable spores	Q
1919	VN_1919	YOR187W	TUF1	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in <i>S. pombe</i> and humans	Q
1920	VN_1920	YLL002W	RTT109	Histone acetyltransferase critical for cell survival in the presence of DNA damage during S phase; acetylates H3-K56 and H3-K9; involved in non-homologous end joining and in regulation of Ty1 transposition; interacts physically with Vps75p	Q
1921	VN_1921	YML051W	GAL80	Transcriptional regulator involved in the repression of GAL genes in the absence of galactose; inhibits transcriptional activation by Gal4p; inhibition relieved by Gal3p or Gal1p binding	Q
1922	VN_1922	YKL082C	RRP14	Essential protein, constituent of 66S pre-ribosomal particles; interacts with proteins involved in ribosomal biogenesis and cell polarity; member of the SURF-6 family	Q
1923	VN_1923	YDL084W	SUB2	Component of the TREX complex required for nuclear mRNA export; member of the DEAD-box RNA helicase superfamily and is involved in early and late steps of spliceosome assembly; homolog of the human splicing factor hUAP56	Strain failed to verify via PCR
1924	VN_1924	YGL059W	PKP2	Mitochondrial protein kinase that negatively regulates activity of the pyruvate dehydrogenase complex by phosphorylating the ser-133 residue of the Pda1p subunit; acts in concert with kinase Pkp1p and phosphatases Ptc5p and Ptc6p	Q
1925	VN_1925	YJL060W	BNA3	Kynurenine aminotransferase, catalyzes formation of kynurenic acid from kynurenine; potential Cdc28p substrate	Q
1926	VN_1926	YER178W	PDA1	E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA; phosphorylated; regulated by glucose	Q
1927	VN_1927	YFL001W	DEG1	tRNA:pseudouridine synthase, introduces pseudouridines at position 38 or 39 in tRNA, important for maintenance of translation efficiency and normal cell growth, localizes to both the nucleus and cytoplasm; non-essential for viability	Q
1928	VN_1928	YDR449C	UTP6	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA	Q
1929	VN_1929	YBR143C	SUP45	Polypeptide release factor (eRF1) in translation termination; mutant form acts as a recessive omnipotent suppressor; methylated by Mtr2p-Trm112p in ternary complex eRF1-eRF3-GTP; mutation of methylation site confers resistance to zymocin	Q
1930	VN_1930	YOR230W	WTM1	Transcriptional modulator involved in regulation of meiosis, silencing, and expression of RNR genes; required for nuclear localization of the ribonucleotide reductase small subunit Rnr2p and Rnr4p; contains WD repeats	Q
1931	VN_1931	YLR203C	MSS51	Specific translational activator for the mitochondrial COX1 mRNA; loosely associated with the matrix face of the mitochondrial inner membrane; influences both COX1 mRNA translation and Cox1p assembly into cytochrome c oxidase	Q
1932	VN_1932	YMR091C	NPL6	Component of the RSC chromatin remodeling complex; interacts with Rsc3p, Rsc30p, Ldb7p, and Htl1p to form a module important for a broad range of RSC functions; involved in nuclear protein import and maintenance of proper telomere length	Q

1933	VN_1933	YMR034C	YMR034C	Putative transporter, member of the SLC10 carrier family; identified in a transposon mutagenesis screen as a gene involved in azole resistance; YMR034C is not an essential gene	Strain failed to verify via PCR
1934	VN_1934	YDR277C	MTH1	Negative regulator of the glucose-sensing signal transduction pathway, required for repression of transcription by Rgt1p; interacts with Rgt1p and the Snf3p and Rgt2p glucose sensors; phosphorylated by Yck1p, triggering Mth1p degradation	Q
1935	VN_1935	YFR014C	CMK1	Calmodulin-dependent protein kinase; may play a role in stress response, many CA ⁺⁺ /calmodulin dependent phosphorylation substrates demonstrated in vitro, amino acid sequence similar to Cmk2p and mammalian Cam Kinase II	Q
1936	VN_1936	YGR110W	CLD1	Mitochondrial cardiolipin-specific phospholipase; functions upstream of Taz1p to generate monolyso-cardiolipin; transcription increases upon genotoxic stress; involved in restricting Ty1 transposition; has homology to mammalian CGI-58	Q
1937	VN_1937	YLR080W	EMP46	Integral membrane component of endoplasmic reticulum-derived COPII-coated vesicles, which function in ER to Golgi transport	Q
1938	VN_1938	YKL090W	CUE2	Protein of unknown function; has two CUE domains that bind ubiquitin, which may facilitate intramolecular monoubiquitination	Q
1939	VN_1939	YBL046W	PSY4	Putative regulatory subunit of an evolutionarily conserved protein phosphatase; localization is cell-cycle dependent and regulated by Cdc28p phosphorylation; required for cisplatin resistance; homolog of mammalian R2	Q
1940	VN_1940	YGL164C	YRB30	RanGTP-binding protein, inhibits RanGAP1 (Rna1p)-mediated GTP hydrolysis of RanGTP (Gsp1p); shares similarity to proteins in other fungi but not in higher eukaryotes	Q
1941	VN_1941	YDL007W	RPT2	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for normal peptide hydrolysis by the core 20S particle	Q
1942	VN_1942	YOR259C	RPT4	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle	Q
1943	VN_1943	YMR240C	CUS1	Protein required for assembly of U2 snRNP into the spliceosome, forms a complex with Hsh49p and Hsh155p	Q
1944	VN_1944	YOR110W	TFC7	One of six subunits of the RNA polymerase III transcription initiation factor complex (TFIIIC); part of the TauA globular domain of TFIIIC that binds DNA at the BoxA promoter sites of tRNA and similar genes	Q
1945	VN_1945	YNL128W	TEP1	Homolog of human tumor suppressor gene PTEN/MMAC1/TEP1 that has lipid phosphatase activity and is linked to the phosphatidylinositol signaling pathway; plays a role in normal sporulation	Q
1946	VN_1946	YGL134W	PCL10	Pho85p cyclin; recruits, activates, and targets Pho85p cyclin-dependent protein kinase to its substrate	Q
1947	VN_1947	YHR004C	NEM1	Probable catalytic subunit of Nem1p-Spo7p phosphatase holoenzyme; regulates nuclear growth by controlling phospholipid biosynthesis, required for normal nuclear envelope morphology and sporulation; homolog of the human protein Dullard	Strain failed to verify via PCR
1948	VN_1948	YOR190W	SPR1	Sporulation-specific exo-1,3-beta-glucanase; contributes to ascospore thermoresistance	Q
1949	VN_1949	YKR044W	UIP5	Protein of unknown function that interacts with Ulp1p, a Ubl (ubiquitin-like protein)-specific protease for Smt3p protein conjugates	Q
1950	VN_1950	YKL059C	MPE1	Essential conserved subunit of CPF (cleavage and polyadenylation factor), plays a role in 3' end formation of mRNA via the specific cleavage and polyadenylation of pre-mRNA, contains a putative RNA-binding zinc knuckle motif	Q
1951	VN_1951	YHR111W	UBA4	Protein that activates Urm1p before its conjugation to proteins (urmylation); one target is the thioredoxin peroxidase Ahp1p, suggesting a role of urmylation in the oxidative stress response	Q
1952	VN_1952	YDL133W	YDL133W	Putative protein of unknown function	Strain failed to verify via PCR
1953	VN_1953	YOR393W	ERR1	Protein of unknown function, has similarity to enolases	Q

1954	VN_1954	YNR066C	YNR066C	Putative membrane-localized protein of unknown function	Strain failed to verify via PCR
1955	VN_1955	YOR301W	RAX1	Protein involved in bud site selection during bipolar budding; localization requires Rax2p; has similarity to members of the insulin-related peptide superfamily	Q
1956	VN_1956	YOR032C	HMS1	Basic helix-loop-helix (bHLH) protein with similarity to myc-family transcription factors; overexpression confers hyperfilamentous growth and suppresses the pseudohyphal filamentation defect of a diploid mep1 mep2 homozygous null mutant	Strain failed to verify via PCR
1957	VN_1957	YGR285C	ZUO1	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb proteins, as a chaperone for nascent polypeptide chains; contains a DnaJ domain and functions as a J-protein partner for Ssb1p and Ssb2p	Q
1958	VN_1958	YKL161C	YKL161C	Protein kinase implicated in the Slt2p mitogen-activated (MAP) kinase signaling pathway; associates with Rlm1p	Q
1959	VN_1959	YGR149W	YGR149W	Putative protein of unknown function; predicted to be an integral membrane protein	Q
1960	VN_1960	YHR169W	DBP8	ATPase, putative RNA helicase of the DEAD-box family; component of 90S preribosome complex involved in production of 18S rRNA and assembly of 40S small ribosomal subunit; ATPase activity stimulated by association with Esp2p	Q
1961	VN_1961	YMR173W	DDR48	DNA damage-responsive protein, expression is increased in response to heat-shock stress or treatments that produce DNA lesions; contains multiple repeats of the amino acid sequence NNDSYGS	Strain failed to verify via PCR
1962	VN_1962	YPR186C	PZF1	Transcription factor IIIA (TFIIIA), essential protein with nine C2H2 Zn-fingers, binds the 5S rRNA gene through the zinc finger domain and directs assembly of a multiprotein initiation complex for RNA polymerase III; also binds DNA	Q
1963	VN_1963	YDL155W	CLB3	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the G2/M transition; may be involved in DNA replication and spindle assembly; accumulates during S phase and G2, then targeted for ubiquitin-mediated degradation	Q
1964	VN_1964	YLR321C	SFH1	Component of the RSC chromatin remodeling complex; essential gene required for cell cycle progression and maintenance of proper ploidy; phosphorylated in the G1 phase of the cell cycle; Snf5p paralog	Q
1965	VN_1965	YGR202C	PCT1	Cholinephosphate cytidyltransferase, also known as CTP:phosphocholine cytidyltransferase, rate-determining enzyme of the CDP-choline pathway for phosphatidylcholine synthesis, inhibited by Sec14p, activated upon lipid-binding	Q
1966	VN_1966	YJR084W	CSN12	Subunit of the Cop9 signalosome, which is required for deneddylation, or removal of the ubiquitin-like protein Rub1p from Cdc53p (cullin); involved in mRNA splicing and adaptation to pheromone signaling	Q
1967	VN_1967	YDR005C	MAF1	Negative regulator of RNA polymerase III; component of several signaling pathways that repress polymerase III transcription in response to changes in cellular environment; targets the initiation factor TFIIB	Q
1968	VN_1968	YER059W	PCL6	Pho85p cyclin of the Pho80p subfamily; forms the major Glc8p kinase together with Pcl7p and Pho85p; involved in the control of glycogen storage by Pho85p; stabilized by Elongin C binding	Q
1969	VN_1969	YML083C	YML083C	Putative protein of unknown function; strong increase in transcript abundance during anaerobic growth compared to aerobic growth; cells deleted for YML083C do not exhibit growth defects in anaerobic or anaerobic conditions	Q
1970	VN_1970	YLR446W	YLR446W	Putative protein of unknown function with similarity to hexokinases; transcript is upregulated during sporulation and the unfolded protein response; YLR446W is not an essential gene	Q
1971	VN_1971	YLR027C	AAT2	Cytosolic aspartate aminotransferase, involved in nitrogen metabolism; localizes to peroxisomes in oleate-grown cells	Q
1972	VN_1972	YIR012W	SQT1	Essential protein involved in a late step of 60S ribosomal subunit assembly or modification; contains multiple WD repeats; interacts with Qsr1p in a two-hybrid assay	Q
1973	VN_1973	YOR264W	DSE3	Daughter cell-specific protein, may help establish daughter fate	Q

1974	VN_1974	YDL066W	IDP1	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes	Q
1975	VN_1975	YGR244C	LSC2	Beta subunit of succinyl-CoA ligase, which is a mitochondrial enzyme of the TCA cycle that catalyzes the nucleotide-dependent conversion of succinyl-CoA to succinate	Strain failed to verify via PCR
1976	VN_1976	YMR068W	AVO2	Component of a complex containing the Tor2p kinase and other proteins, which may have a role in regulation of cell growth	Q
1977	VN_1977	YGR263C	SAY1	Sterol deacetylase; component of the sterol acetylation/deacetylation cycle along with Atf2p; integral membrane protein with active site in the ER lumen; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum	Q
1978	VN_1978	YML080W	DUS1	Dihydrouridine synthase, member of a widespread family of conserved proteins including Smm1p, Dus3p, and Dus4p; modifies pre-tRNA(Phe) at U17	Q
1979	VN_1979	YBL091C	MAP2	Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map1p	Q
1980	VN_1980	YER149C	PEA2	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca ²⁺ influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth	Q
1981	VN_1981	YOR245C	DGA1	Diacylglycerol acyltransferase, catalyzes the terminal step of triacylglycerol (TAG) formation, acylates diacylglycerol using acyl-CoA as an acyl donor, localized to lipid particles	Q
1982	VN_1982	YLR387C	REH1	Cytoplasmic 60S subunit biogenesis factor, associates with pre-60S particles; similar to Rei1p and shares partially redundant function in cytoplasmic 60S subunit maturation; contains dispersed C2H2 zinc finger domains	Q
1983	VN_1983	YMR187C	YMR187C	Putative protein of unknown function; YMR187C is not an essential gene	Q
1984	VN_1984	YPL168W	YPL168W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion; expression may be cell cycle-regulated	Q
1985	VN_1985	YDL182W	LYS20	Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p	Q
1986	VN_1986	YKL172W	EBP2	Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit assembly, localizes to the nucleolus; constituent of 66S pre-ribosomal particles	Q
1987	VN_1987	YNL234W	YNL234W	Protein of unknown function with similarity to globins; has a functional heme-binding domain; transcription is induced by hypoxia and other stress conditions; proposed to be involved in glucose signaling or metabolism; regulated by Rgt1p	Q
1988	VN_1988	YLR438W	CAR2	L-ornithine transaminase (OTase), catalyzes the second step of arginine degradation, expression is dually-regulated by allophanate induction and a specific arginine induction process; not nitrogen catabolite repression sensitive	Q
1989	VN_1989	YOL126C	MDH2	Cytoplasmic malate dehydrogenase, one of three isozymes that catalyze interconversion of malate and oxaloacetate; involved in the glyoxylate cycle and gluconeogenesis during growth on two-carbon compounds; interacts with Pck1p and Fbp1	Q
1990	VN_1990	YDR255C	RMD5	Conserved protein that has an E3-like ubiquitin ligase activity necessary for polyubiquitination and degradation of the gluconeogenic enzyme fructose-1,6-bisphosphatase; also required for sporulation; has a degenerate RING finger domain	Q
1991	VN_1991	YMR204C	INP1	Peripheral membrane protein of peroxisomes involved in peroxisomal inheritance; recruitment to peroxisomes is mediated by interaction with Pex3p at the peroxisomal membrane	Q
1992	VN_1992	YAL061W	BDH2	Putative medium-chain alcohol dehydrogenase with similarity to BDH1; transcription induced by constitutively active PDR1 and PDR3	Q
1993	VN_1993	YNL220W	ADE12	Adenylosuccinate synthase, catalyzes the first step in synthesis of	Q

				adenosine monophosphate from inosine 5'monophosphate during purine nucleotide biosynthesis; exhibits binding to single-stranded autonomously replicating (ARS) core sequence	
1994	VN_1994	YMR085W	YMR085W	Putative protein of unknown function; YMR085W and adjacent ORF YMR084W are merged in related strains	Q
1995	VN_1995	YDL001W	RMD1	Cytoplasmic protein required for sporulation	Q
1996	VN_1996	YHR003C	YHR003C	Protein of unknown function, localized to the mitochondrial outer membrane	Q
1997	VN_1997	YDR300C	PRO1	Gamma-glutamyl kinase, catalyzes the first step in proline biosynthesis	Q
1998	VN_1998	YKL181W	PRS1	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, synthesizes PRPP, which is required for nucleotide, histidine, and tryptophan biosynthesis; one of five related enzymes, which are active as heteromultimeric complexes	Q
1999	VN_1999	YBR130C	SHE3	Protein that acts as an adaptor between Myo4p and the She2p-mRNA complex; part of the mRNA localization machinery that restricts accumulation of certain proteins to the bud; also required for cortical ER inheritance	Q
2000	VN_2000	YBL058W	SHP1	UBX (ubiquitin regulatory X) domain-containing protein that regulates Glc7p phosphatase activity and interacts with Cdc48p; interacts with ubiquitylated proteins in vivo and is required for degradation of a ubiquitylated model substrate	Q
2001	VN_2001	YOL140W	ARG8	Acetylornithine aminotransferase, catalyzes the fourth step in the biosynthesis of the arginine precursor ornithine	Q
2002	VN_2002	YGL090W	LIF1	Component of the DNA ligase IV complex that mediates nonhomologous end joining in DNA double-strand break repair; physically interacts with Dnl4p and Nej1p; homologous to mammalian XRCC4 protein	Q
2003	VN_2003	YNL009W	IDP3	Peroxisomal NADP-dependent isocitrate dehydrogenase, catalyzes oxidation of isocitrate to alpha-ketoglutarate with the formation of NADP(H+), required for growth on unsaturated fatty acids	Q
2004	VN_2004	YCL044C	MGR1	Subunit of the mitochondrial (mt) i-AAA protease supercomplex, which degrades misfolded mitochondrial proteins; forms a subcomplex with Mgr3p that binds to substrates to facilitate proteolysis; required for growth of cells lacking mtDNA	Q
2005	VN_2005	YNL330C	RPD3	Histone deacetylase; regulates transcription and silencing; plays a role in regulating Ty1 transposition	Q
2006	VN_2006	YOL097C	WRS1	Cytoplasmic tryptophanyl-tRNA synthetase, aminoacylates tryptophanyl-tRNA	Q
2007	VN_2007	YDR263C	DIN7	Mitochondrial nuclease functioning in DNA repair and replication, modulates the stability of the mitochondrial genome, induced by exposure to mutagens, also induced during meiosis at a time nearly coincident with commitment to recombination	Q
2008	VN_2008	YNL004W	HRB1	Poly(A+) RNA-binding protein, involved in the export of mRNAs from the nucleus to the cytoplasm; similar to Gbp2p and Npl3p	Q
2009	VN_2009	YDR394W	RPT3	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; substrate of N-acetyltransferase B	Q
2010	VN_2010	YKL195W	MIA40	Essential protein of the mitochondrial intermembrane space (IMS); promotes retention of newly imported proteins; may do so by stabilizing client protein folding as part of a disulfide relay system or transferring metal to client proteins	Strain failed to verify via PCR
2011	VN_2011	YCL063W	VAC17	Phosphoprotein involved in vacuole inheritance; degraded in late M phase of the cell cycle; acts as a vacuole-specific receptor for myosin Myo2p	Q
2012	VN_2012	YBR195C	MSI1	Subunit of chromatin assembly factor I (CAF-1), negative regulator of the RAS/cAMP pathway via sequestration of Npr1p kinase; localizes to the nucleus and cytoplasm; homologous to human retinoblastoma binding proteins RbAp48 and RbAp46	Q
2013	VN_2013	YJR136C	TTI2	Putative protein of unknown function; subunit of the ASTRA complex which is part of the chromatin remodeling machinery; similar to S. pombe Tti2p; may interact with Rsm23p; GFP-fusion protein localizes to the cytoplasm	Q

2014	VN_2014	YNL066W	SUN4	Cell wall protein related to glucanases, possibly involved in cell wall septation; member of the SUN family	Q
2015	VN_2015	YDL033C	SLM3	tRNA-specific 2-thiouridylase, responsible for 2-thiolation of the wobble base of mitochondrial tRNAs; human ortholog is implicated in myoclonus epilepsy associated with ragged red fibers (MERRF)	Q
2016	VN_2016	YNR052C	POP2	RNase of the DEDD superfamily, subunit of the Ccr4-Not complex that mediates 3' to 5' mRNA deadenylation	Q
2017	VN_2017	YDL005C	MED2	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation	Q
2018	VN_2018	YER101C	AST2	Protein that may have a role in targeting of plasma membrane [H ⁺]ATPase (Pma1p) to the plasma membrane, as suggested by analysis of genetic interactions	Q
2019	VN_2019	YNR029C	YNR029C	Putative protein of unknown function, deletion confers reduced fitness in saline	Q
2020	VN_2020	YLR049C	YLR049C	Putative protein of unknown function	Q
2021	VN_2021	YMR113W	FOL3	Dihydrofolate synthetase, involved in folic acid biosynthesis; catalyzes the conversion of dihydropteroate to dihydrofolate in folate coenzyme biosynthesis	Q
2022	VN_2022	YIL103W	DPH1	Protein required, along with Dph2p, Kti11p, Jjj3p, and Dph5p, for synthesis of diphthamide, which is a modified histidine residue of translation elongation factor 2 (Eft1p or Eft2p); may act in a complex with Dph2p and Kti11p	Q
2023	VN_2023	YDR218C	SPR28	Sporulation-specific homolog of the yeast CDC3/10/11/12 family of bud neck microfilament genes; meiotic septin expressed at high levels during meiotic divisions and ascospore formation	Q
2024	VN_2024	YDL150W	RPC53	RNA polymerase III subunit C53	Q
2025	VN_2025	YKR038C	KAE1	Highly conserved putative glycoprotease proposed to be involved in transcription as a component of the EKC protein complex with Bud32p, Cgi121p, Pcc1p, and Gon7p; also identified as a component of the KEOPS protein complex	Q
2026	VN_2026	YOL058W	ARG1	Arginosuccinate synthetase, catalyzes the formation of L-argininosuccinate from citrulline and L-aspartate in the arginine biosynthesis pathway; potential Cdc28p substrate	Q
2027	VN_2027	YER027C	GAL83	One of three possible beta-subunits of the Snf1 kinase complex, allows nuclear localization of the Snf1 kinase complex in the presence of a nonfermentable carbon source; contains glycogen-binding domain	Q
2028	VN_2028	YOL124C	TRM11	Catalytic subunit of an adoMet-dependent tRNA methyltransferase complex (Trm11p-Trm112p), required for the methylation of the guanosine nucleotide at position 10 (m2G10) in tRNAs; contains a THUMP domain and a methyltransferase domain	Q
2029	VN_2029	YDL090C	RAM1	Beta subunit of the CAAX farnesyltransferase (FTase) that prenylates the a-factor mating pheromone and Ras proteins; required for the membrane localization of Ras proteins and a-factor; homolog of the mammalian FTase beta subunit	Q
2030	VN_2030	YHR132C	ECM14	Putative metalloprotease with similarity to the zinc carboxypeptidase family, required for normal cell wall assembly	Q
2031	VN_2031	YOR209C	NPT1	Nicotinate phosphoribosyltransferase, acts in the salvage pathway of NAD ⁺ biosynthesis; required for silencing at rDNA and telomeres and has a role in silencing at mating-type loci; localized to the nucleus	Q
2032	VN_2032	YOR274W	MOD5	Delta 2-isopentenyl pyrophosphate:tRNA isopentenyl transferase, required for biosynthesis of the modified base isopentenyladenosine in mitochondrial and cytoplasmic tRNAs; gene is nuclear and encodes two isozymic forms	Q
2033	VN_2033	YAR003W	SWD1	Subunit of the COMPASS (Set1C) complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres; WD40 beta propeller superfamily member with similarity to mammalian Rbbp7	Q
2034	VN_2034	YNL136W	EAF7	Subunit of the NuA4 histone acetyltransferase complex, which acetylates the N-terminal tails of histones H4 and H2A	Q
2035	VN_2035	YDR528W	HLR1	Protein involved in regulation of cell wall composition and integrity	Q

				and response to osmotic stress; overproduction suppresses a lysis sensitive PKC mutation; similar to Lre1p, which functions antagonistically to protein kinase A	
2036	VN_2036	YLR213C	CRR1	Putative glycoside hydrolase of the spore wall envelope; required for normal spore wall assembly, possibly for cross-linking between the glucan and chitosan layers; expressed during sporulation	Q
2037	VN_2037	YOL031C	SIL1	Nucleotide exchange factor for the endoplasmic reticulum (ER) luminal Hsp70 chaperone Kar2p, required for protein translocation into the ER; homolog of <i>Yarrowia lipolytica</i> SLS1; GrpE-like protein	Q
2038	VN_2038	YBR271W	YBR271W	Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; predicted to be involved in ribosome biogenesis	Q
2039	VN_2039	YGL004C	RPN14	Proteasome-interacting protein involved in the assembly of the base subcomplex of the 19S proteasome regulatory particle (RP); null mutants accumulate ubiquitinated Gcn4p and display decreased 26S proteasome stability; interacts with Rpt5p	Q
2040	VN_2040	YGL025C	PGD1	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for basal and activated transcription; direct target of Cyc8p-Tup1p transcriptional corepressor	Q
2041	VN_2041	YKL132C	RMA1	Putative dihydrofolate synthetase; has similarity to Fol3p and to <i>E. coli</i> folylpolyglutamate synthetase/dihydrofolate synthetase; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2042	VN_2042	YPR108W	RPN7	Essential, non-ATPase regulatory subunit of the 26S proteasome, similar to another <i>S. cerevisiae</i> regulatory subunit, Rpn5p, as well as to mammalian proteasome subunits	Q
2043	VN_2043	YCL011C	GBP2	Poly(A+) RNA-binding protein, involved in the export of mRNAs from the nucleus to the cytoplasm; similar to Hrb1p and Npl3p; also binds single-stranded telomeric repeat sequence in vitro	Q
2044	VN_2044	YGL169W	SUA5	Single-stranded telomeric DNA-binding protein, required for normal telomere length; null mutant lacks N6-threonylcarbamoyl adenosine (t6A) modification in the anticodon loop of ANN-decoding tRNA; member of conserved YrdC/Sua5 family	Q
2045	VN_2045	YNL207W	RIO2	Essential serine kinase involved in the processing of the 20S pre-rRNA into mature 18S rRNA; has similarity to Rio1p	Q
2046	VN_2046	YJL036W	SNX4	Sorting nexin, involved in retrieval of late-Golgi SNAREs from post-Golgi endosomes to the trans-Golgi network and in cytoplasm to vacuole transport; contains a PX phosphoinositide-binding domain; forms complexes with Snx41p and with Atg20p	Q
2047	VN_2047	YNL253W	TEX1	Protein involved in mRNA export, component of the transcription export (TREX) complex	Q
2048	VN_2048	YDL027C	YDL027C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YDL027C is not an essential gene	Q
2049	VN_2049	YBL055C	YBL055C	3'→5' exonuclease and endonuclease with a possible role in apoptosis; has similarity to mammalian and <i>C. elegans</i> apoptotic nucleases	Q
2050	VN_2050	YGL223C	COG1	Essential component of the conserved oligomeric Golgi complex (Cog1p through Cog8p), a cytosolic tethering complex that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments	Q
2051	VN_2051	YIL160C	POT1	3-ketoacyl-CoA thiolase with broad chain length specificity, cleaves 3-ketoacyl-CoA into acyl-CoA and acetyl-CoA during beta-oxidation of fatty acids	Q
2052	VN_2052	YPL202C	AFT2	Iron-regulated transcriptional activator; activates genes involved in intracellular iron use and required for iron homeostasis and resistance to oxidative stress; similar to Aft1p	Q
2053	VN_2053	YDR317W	HIM1	Protein of unknown function involved in DNA repair	Q
2054	VN_2054	YBR233W	PBP2	RNA binding protein with similarity to mammalian heterogeneous nuclear RNP K protein, involved in the regulation of telomere position effect and telomere length	Q

2055	VN_2055	YOR051C	YOR051C	Nuclear protein that inhibits replication of Brome mosaic virus in <i>S. cerevisiae</i> , which is a model system for studying replication of positive-strand RNA viruses in their natural hosts	Q
2056	VN_2056	YGR142W	BTN2	v-SNARE binding protein that facilitates specific protein retrieval from a late endosome to the Golgi; modulates arginine uptake, possible role in mediating pH homeostasis between the vacuole and plasma membrane H(+)-ATPase	Q
2057	VN_2057	YOR134W	BAG7	Rho GTPase activating protein (RhoGAP), stimulates the intrinsic GTPase activity of Rho1p, which plays a role in actin cytoskeleton organization and control of cell wall synthesis; structurally and functionally related to Sac7p	Q
2058	VN_2058	YLR225C	YLR225C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLR225C is not an essential gene	Q
2059	VN_2059	YOL054W	PSH1	Nuclear protein, putative RNA polymerase II elongation factor; isolated as Pob3p/Spt16p-binding protein	Q
2060	VN_2060	YBR063C	YBR063C	Putative protein of unknown function; YBR063C is not an essential gene	Q
2061	VN_2061	YGR214W	RPS0A	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Bp; required for maturation of 18S rRNA along with Rps0Bp; deletion of either RPS0 gene reduces growth rate, deletion of both genes is lethal	Q
2062	VN_2062	YKL162C	YKL162C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion	Q
2063	VN_2063	YKR048C	NAP1	Protein that interacts with mitotic cyclin Clb2p; required for the regulation of microtubule dynamics during mitosis; controls bud morphogenesis; involved in the transport of H2A and H2B histones to the nucleus; phosphorylated by CK2	Q
2064	VN_2064	YDR222W	YDR222W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Q
2065	VN_2065	YDR432W	NPL3	RNA-binding protein that promotes elongation, regulates termination, and carries poly(A) mRNA from nucleus to cytoplasm; required for pre-mRNA splicing; dissociation from mRNAs promoted by Mtr10p; phosphorylated by Sky1p in the cytoplasm	Q
2066	VN_2066	YGL143C	MRF1	Mitochondrial translation release factor, involved in stop codon recognition and hydrolysis of the peptidyl-tRNA bond during mitochondrial translation; lack of MRF1 causes mitochondrial genome instability	Q
2067	VN_2067	YOR201C	MRM1	Ribose methyltransferase that modifies a functionally critical, conserved nucleotide in mitochondrial 21S rRNA	Q
2068	VN_2068	YGR193C	PDX1	Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core	Strain failed to verify via PCR
2069	VN_2069	YMR235C	RNA1	GTPase activating protein (GAP) for Gsp1p, involved in nuclear transport	Q
2070	VN_2070	YCL028W	RNQ1	[PIN(+)] prion, an infectious protein conformation that is generally an ordered protein aggregate	Q
2071	VN_2071	YGR169C	PUS6	tRNA:pseudouridine synthase, catalyzes the conversion of uridine to pseudouridine at position 31 in cytoplasmic and mitochondrial tRNAs; mutation of Asp168 to Ala abolishes enzyme activity; not essential for viability	Q
2072	VN_2072	YEL056W	HAT2	Subunit of the Hat1p-Hat2p histone acetyltransferase complex; required for high affinity binding of the complex to free histone H4, thereby enhancing Hat1p activity; similar to human RbAp46 and 48; has a role in telomeric silencing	Q
2073	VN_2073	YLR423C	ATG17	Scaffold protein responsible for phagophore assembly site organization; regulatory subunit of an autophagy-specific complex that includes Atg1p and Atg13p; stimulates Atg1p kinase activity	Q
2074	VN_2074	YGL208W	SIP2	One of three beta subunits of the Snf1 serine/threonine protein kinase complex involved in the response to glucose starvation; null mutants exhibit accelerated aging; N-myristoylprotein localized to the cytoplasm and the plasma membrane	Q

2075	VN_2075	YGR159C	NSR1	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis	Q
2076	VN_2076	YGL170C	SPO74	Component of the meiotic outer plaque of the spindle pole body, involved in modifying the meiotic outer plaque that is required prior to prospore membrane formation	Q
2077	VN_2077	YDR153C	ENT5	Protein containing an N-terminal epsin-like domain involved in clathrin recruitment and traffic between the Golgi and endosomes; associates with the clathrin adaptor Gga2p, clathrin adaptor complex AP-1, and clathrin	Q
2078	VN_2078	YOL022C	TSR4	Cytoplasmic protein of unknown function; essential gene in S288C background, while tsr4 null mutations in a CEN.PK2 background confer a reduced growth rate	Strain failed to verify via PCR
2079	VN_2079	YNL078W	NIS1	Protein localized in the bud neck at G2/M phase; physically interacts with septins; possibly involved in a mitotic signaling network	Q
2080	VN_2080	YGL048C	RPT6	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; bound by ubiquitin-protein ligases Ubr1p and Ufd4p; localized mainly to the nucleus throughout the cell cycle	Strain failed to verify via PCR
2081	VN_2081	YHL020C	OPI1	Transcriptional regulator of a variety of genes; phosphorylation by protein kinase A stimulates Opi1p function in negative regulation of phospholipid biosynthetic genes; involved in telomere maintenance	Q
2082	VN_2082	YNL051W	COG5	Component of the conserved oligomeric Golgi complex (Cog1p through Cog8p), a cytosolic tethering complex that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments	Q
2083	VN_2083	YLR328W	NMA1	Nicotinic acid mononucleotide adenylyltransferase, involved in pathways of NAD biosynthesis, including the de novo, NAD(+) salvage, and nicotinamide riboside salvage pathways	Q
2084	VN_2084	YMR021C	MAC1	Copper-sensing transcription factor involved in regulation of genes required for high affinity copper transport	Q
2085	VN_2085	YJR076C	CDC11	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM	Q
2086	VN_2086	YMR253C	YMR253C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; YMR253C is not an essential gene	Q
2087	VN_2087	YPL060W	LPE10	Mitochondrial inner membrane magnesium transporter, involved in maintenance of magnesium concentrations inside mitochondria; indirectly affects splicing of group II introns; functionally and structurally related to Mrs2p	Q
2088	VN_2088	YGR210C	YGR210C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2089	VN_2089	YPR133C	SPN1	Protein that interacts with Spt6p and copurifies with Spt5p and RNA polymerase II, probable transcriptional elongation factor; metazoan homologs contain an acidic N terminus; mutations in the gene confer an Spt- phenotype	Q
2090	VN_2090	YHR097C	YHR097C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus	Q
2091	VN_2091	YNL181W	YNL181W	Putative oxidoreductase; required for cell viability	Q
2092	VN_2092	YHL014C	YLF2	Protein of unknown function, has weak similarity to E. coli GTP-binding protein gtp1; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2093	VN_2093	YJR149W	YJR149W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2094	VN_2094	YNL175C	NOP13	Nucleolar protein found in preribosomal complexes; contains an RNA recognition motif (RRM)	Q
2095	VN_2095	YNL254C	RTC4	Protein of unknown function; null mutation suppresses cdc13-1 temperature sensitivity; (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
2096	VN_2096	YCR012W	PGK1	3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate	Q

				to ADP to produce ATP; key enzyme in glycolysis and gluconeogenesis	
2097	VN_2097	YNL248C	RPA49	RNA polymerase I subunit A49	Q
2098	VN_2098	YOR196C	LIP5	Protein involved in biosynthesis of the coenzyme lipoic acid, has similarity to E. coli lipoic acid synthase	Q
2099	VN_2099	YDR465C	RMT2	Arginine methyltransferase; ribosomal protein L12 is a substrate	Q
2100	VN_2100	YML074C	FPR3	Nucleolar peptidyl-prolyl cis-trans isomerase (PPIase); FK506 binding protein; phosphorylated by casein kinase II (Cka1p-Cka2p-Ckb1p-Ckb2p) and dephosphorylated by Ptp1p	Q
2101	VN_2101	YDR289C	RTT103	Protein that interacts with exonuclease Rat1p and Rai1p and plays a role in transcription termination by RNA polymerase II, has an RPR domain (carboxy-terminal domain interacting domain); also involved in regulation of Ty1 transposition	Q
2102	VN_2102	YDL104C	QRI7	Highly conserved mitochondrial protein, essential for stability of the mitochondrial genome; functional homolog of the essential E. coli <i>ygjD</i> gene; member of a family of proteins putatively involved in genome maintenance	Q
2103	VN_2103	YDR076W	RAD55	Protein that stimulates strand exchange by stabilizing the binding of Rad51p to single-stranded DNA; involved in the recombinational repair of double-strand breaks in DNA during vegetative growth and meiosis; forms heterodimer with Rad57p	Q
2104	VN_2104	YKL149C	DBR1	RNA lariat debranching enzyme, involved in intron turnover; required for efficient Ty1 transposition	Q
2105	VN_2105	YKR053C	YSR3	Dihydrosphingosine 1-phosphate phosphatase, membrane protein involved in sphingolipid metabolism; has similarity to Lcb3p	Q
2106	VN_2106	YNL292W	PUS4	Pseudouridine synthase, catalyzes only the formation of pseudouridine-55 (Psi55), a highly conserved tRNA modification, in mitochondrial and cytoplasmic tRNAs; PUS4 overexpression leads to translational derepression of GCN4 (Gcd- phenotype)	Q
2107	VN_2107	YOR091W	TMA46	Protein of unknown function that associates with ribosomes; interacts with GTPase Rbg1p	Q
2108	VN_2108	YHR115C	DMA1	Protein involved in ubiquitin ligation; plays a role in regulating spindle position and orientation; functionally redundant with Dma2p; orthologous to human RNF8 protein, also has sequence similarity to human Chfr.	Q
2109	VN_2109	YOL082W	ATG19	Receptor protein specific for the cytoplasm-to-vacuole targeting (Cvt) pathway; delivers cargo proteins aminopeptidase I (Lap4p) and alpha-mannosidase (Ams1p) to the phagophore assembly site for packaging into Cvt vesicles	Q
2110	VN_2110	YPL188W	POS5	Mitochondrial NADH kinase, phosphorylates NADH; also phosphorylates NAD(+) with lower specificity; required for the response to oxidative stress	Q
2111	VN_2111	YLL057C	JLP1	Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase, involved in sulfonate catabolism for use as a sulfur source; contains sequence that resembles a J domain (typified by the E. coli DnaJ protein); induced by sulphur starvation	Q
2112	VN_2112	YOR042W	CUE5	Protein containing a CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Q
2113	VN_2113	YDR423C	CAD1	AP-1-like basic leucine zipper (bZIP) transcriptional activator involved in stress responses, iron metabolism, and pleiotropic drug resistance; controls a set of genes involved in stabilizing proteins; binds consensus sequence TTAATA	Q
2114	VN_2114	YGR179C	OKP1	Outer kinetochore protein, required for accurate mitotic chromosome segregation; component of the kinetochore sub-complex COMA (Ctf19p, Okp1p, Mcm21p, Ame1p) that functions as a platform for kinetochore assembly	Q
2115	VN_2115	YMR010W	YMR010W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YMR010W is not an essential gene; YMR010W mRNA is transcribed with ADI1	Q
2116	VN_2116	YLR107W	REX3	RNA exonuclease; required for maturation of the RNA component of RNase MRP; functions redundantly with Rnh70p and Rex2p in	Q

				processing of U5 snRNA and RNase P RNA; member of RNase D family of exonucleases	
2117	VN_2117	YDL105W	NSE4	Nuclear protein that plays a role in the function of the Smc5p-Rhc18p complex	Q
2118	VN_2118	YOR368W	RAD17	Checkpoint protein, involved in the activation of the DNA damage and meiotic pachytene checkpoints; with Mec3p and Ddc1p, forms a clamp that is loaded onto partial duplex DNA; homolog of human and S. pombe Rad1 and U. maydis Rec1 proteins	Q
2119	VN_2119	YIL033C	BCY1	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation	Q
2120	VN_2120	YPL048W	CAM1	Nuclear protein required for transcription of MXR1; binds the MXR1 promoter in the presence of other nuclear factors; binds calcium and phospholipids; has similarity to translational cofactor EF-1 gamma	Q
2121	VN_2121	YBR074W	YBR074W	Putative metalloprotease	Q
2122	VN_2122	YLR174W	IDP2	Cytosolic NADP-specific isocitrate dehydrogenase, catalyzes oxidation of isocitrate to alpha-ketoglutarate; levels are elevated during growth on non-fermentable carbon sources and reduced during growth on glucose	Q
2123	VN_2123	YOR303W	CPA1	Small subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor; translationally regulated by an attenuator peptide encoded by YOR302W within the CPA1 mRNA 5'-leader	Q
2124	VN_2124	YIR008C	PRI1	Subunit of DNA primase, which is required for DNA synthesis and double-strand break repair	Q
2125	VN_2125	YIL119C	RPI1	Putative transcriptional regulator; overexpression suppresses the heat shock sensitivity of wild-type RAS2 overexpression and also suppresses the cell lysis defect of an mpk1 mutation	Q
2126	VN_2126	YKR092C	SRP40	Nucleolar, serine-rich protein with a role in preribosome assembly or transport; may function as a chaperone of small nucleolar ribonucleoprotein particles (snoRNPs); immunologically and structurally to rat Nopp140	Q
2127	VN_2127	YMR214W	SCJ1	One of several homologs of bacterial chaperone DnaJ, located in the ER lumen where it cooperates with Kar2p to mediate maturation of proteins	Strain failed to verify via PCR
2128	VN_2128	YDR083W	RRP8	Nucleolar protein involved in rRNA processing, pre-rRNA cleavage at site A2; also involved in telomere maintenance; mutation is synthetically lethal with a gar1 mutation	Q
2129	VN_2129	YPR023C	EAF3	Esa1p-associated factor, nonessential component of the NuA4 acetyltransferase complex, homologous to Drosophila dosage compensation protein MSL3; plays a role in regulating Ty1 transposition	Q
2130	VN_2130	YMR067C	UBX4	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p	Q
2131	VN_2131	YDR282C	YDR282C	Putative protein of unknown function	Q
2132	VN_2132	YBR168W	PEX32	Peroxisomal integral membrane protein, involved in negative regulation of peroxisome size; partially functionally redundant with Pex31p; genetic interactions suggest action at a step downstream of steps mediated by Pex28p and Pex29p	Q
2133	VN_2133	YOL083W	YOL083W	Putative protein of unknown function	Strain failed to verify via PCR
2134	VN_2134	YPR118W	MRI1	5'-methylthioribose-1-phosphate isomerase; catalyzes the isomerization of 5-methylthioribose-1-phosphate to 5-methylthioribulose-1-phosphate in the methionine salvage pathway	Q
2135	VN_2135	YNL152W	INN1	Essential protein that associates with the contractile actomyosin ring, required for ingress of the plasma membrane into the bud neck during cytokinesis; C2 domain, a membrane targeting module, is required for function	Q
2136	VN_2136	YKL219W	COS9	Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	Q

2137	VN_2137	YNL165W	YNL165W	Putative protein of unknown function; YNL165W is not an essential gene	Q
2138	VN_2138	YPR041W	TIF5	Translation initiation factor eIF-5; N-terminal domain functions as a GTPase-activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation	Q
2139	VN_2139	YNR021W	YNR021W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YNR021W is not an essential gene	Q
2140	VN_2140	YGR122W	YGR122W	Probable ortholog of <i>A. nidulans</i> PalC, which is involved in pH regulation and binds to the ESCRT-III complex; null mutant does not properly process Rim101p and has decreased resistance to rapamycin; GFP-fusion protein is cytoplasmic	Q
2141	VN_2141	YDR019C	GCV1	T subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm	Q
2142	VN_2142	YER095W	RAD51	Strand exchange protein, forms a helical filament with DNA that searches for homology; involved in the recombinational repair of double-strand breaks in DNA during vegetative growth and meiosis; homolog of Dmc1p and bacterial RecA protein	Q
2143	VN_2143	YAL015C	NTG1	DNA N-glycosylase and apurinic/apyrimidinic (AP) lyase involved in base excision repair; distribution between nucleus and mitochondrion varies according to which compartment is under oxidative stress and is also sumoylation-dependent	Q
2144	VN_2144	YHL022C	SPO11	Meiosis-specific protein that initiates meiotic recombination by catalyzing the formation of double-strand breaks in DNA via a transesterification reaction; required for homologous chromosome pairing and synaptonemal complex formation	Q
2145	VN_2145	YOR173W	DCS2	Non-essential, stress induced regulatory protein containing a HIT (histidine triad) motif; modulates m7G-oligoribonucleotide metabolism; inhibits Dcs1p; regulated by Msn2p, Msn4p, and the Ras-cAMP-CAPK signaling pathway, similar to Dcs1p.	Q
2146	VN_2146	YIL042C	PKP1	Mitochondrial protein kinase involved in negative regulation of pyruvate dehydrogenase complex activity by phosphorylating the ser-133 residue of the Pda1p subunit; acts in concert with kinase Pkp2p and phosphatases Ptc5p and Ptc6p	Q
2147	VN_2147	YDL204W	RTN2	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily	Q
2148	VN_2148	YNR048W	YNR048W	Protein that interacts specifically in vivo with phospholipid translocase (flippase) Dnf3p; similar to Cdc50p, which is an essential interaction partner of the flippase Drs2p	Q
2149	VN_2149	YDL022W	GPD1	NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high-osmolarity glycerol response pathway; homolog of Gpd2p	Q
2150	VN_2150	YNL035C	YNL035C	Putative protein of unknown function with similarity to proteins containing WD-40 domains; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; YNL035C is not an essential gene	Q
2151	VN_2151	YGR072W	UPF3	Component of the nonsense-mediated mRNA decay (NMD) pathway, along with Nam7p and Nmd2p; involved in decay of mRNA containing nonsense codons; involved in telomere maintenance	Q
2152	VN_2152	YGL243W	TAD1	tRNA-specific adenosine deaminase, deaminates adenosine-37 to inosine in tRNA-Ala	Q
2153	VN_2153	YDR021W	FAL1	Nucleolar protein required for maturation of 18S rRNA, member of the eIF4A subfamily of DEAD-box ATP-dependent RNA helicases	Q
2154	VN_2154	YLR312C	YLR312C	Putative protein of unknown function	Q
2155	VN_2155	YDR018C	YDR018C	Probable membrane protein with three predicted transmembrane domains; homologous to Ybr042cp, similar to <i>C. elegans</i> F55A11.5 and maize 1-acyl-glycerol-3-phosphate acyltransferase	Strain failed to verify via PCR
2156	VN_2156	YJL138C	TIF2	Translation initiation factor eIF4A, identical to Tif1p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains	Q

				connected by a linker; interacts with eIF4G	
2157	VN_2157	YAL012W	CYS3	Cystathionine gamma-lyase, catalyzes one of the two reactions involved in the transsulfuration pathway that yields cysteine from homocysteine with the intermediary formation of cystathionine	Q
2158	VN_2158	YJR080C	AIM24	Protein of unknown function; the authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies; null mutant displays reduced respiratory growth and elevated frequency of mitochondrial genome loss	Q
2159	VN_2159	YDR427W	RPN9	Non-ATPase regulatory subunit of the 26S proteasome, has similarity to putative proteasomal subunits in other species; null mutant is temperature sensitive and exhibits cell cycle and proteasome assembly defects	Q
2160	VN_2160	YPR025C	CCL1	Cyclin associated with protein kinase Kin28p, which is the TFIIF-associated carboxy-terminal domain (CTD) kinase involved in transcription initiation at RNA polymerase II promoters	Q
2161	VN_2161	YMR005W	TAF4	TFIID subunit (48 kDa), involved in RNA polymerase II transcription initiation; potential Cdc28p substrate	Strain failed to verify via PCR
2162	VN_2162	YHR068W	DYS1	Deoxyhypusine synthase, catalyzes formation of deoxyhypusine, the first step in hypusine biosynthesis; triggers posttranslational hypusination of translation elongation factor eIF-5A and regulates its intracellular levels; tetrameric	Q
2163	VN_2163	YGR005C	TFG2	TFIIF (Transcription Factor II) middle subunit; involved in both transcription initiation and elongation of RNA polymerase II; homologous to human RAP30	Q
2164	VN_2164	YGR234W	YHB1	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses	Q
2165	VN_2165	YPL028W	ERG10	Acetyl-CoA C-acetyltransferase (acetoacetyl-CoA thiolase), cytosolic enzyme that transfers an acetyl group from one acetyl-CoA molecule to another, forming acetoacetyl-CoA; involved in the first step in mevalonate biosynthesis	Q
2166	VN_2166	YGL181W	GTS1	Protein that localizes to the nucleus and is involved in transcription regulation; also localizes to actin patches and plays a role in endocytosis; N-terminus contains an ARF-GAP domain and C-terminus contains a Gln-rich domain	Q
2167	VN_2167	YKR059W	TIF1	Translation initiation factor eIF4A, identical to Tif2p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G	Q
2168	VN_2168	YBR025C	OLA1	P-loop ATPase with similarity to human OLA1 and bacterial YchF; identified as specifically interacting with the proteasome; protein levels are induced by hydrogen peroxide	Q
2169	VN_2169	YLR099C	ICT1	Lysophosphatidic acid acyltransferase, responsible for enhanced phospholipid synthesis during organic solvent stress; null displays increased sensitivity to Calcofluor white; highly expressed during organic solvent stress	Q
2170	VN_2170	YEL050C	RML2	Mitochondrial ribosomal protein of the large subunit, has similarity to E. coli L2 ribosomal protein; fat21 mutant allele causes inability to utilize oleate and may interfere with activity of the Adr1p transcription factor	Q
2171	VN_2171	YFL066C	YFL066C	Helicase-like protein encoded within the telomeric Y' element; induced by treatment with 8-methoxypsoralen and UVA irradiation	Q
2172	VN_2172	YPL230W	USV1	Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes involved in growth on non-fermentable carbon sources, response to salt stress and cell wall biosynthesis	Q
2173	VN_2173	YPR054W	SMK1	Middle sporulation-specific mitogen-activated protein kinase (MAPK) required for production of the outer spore wall layers; negatively regulates activity of the glucan synthase subunit Gsc2p	Q
2174	VN_2174	YJL107C	YJL107C	Putative protein of unknown function; expression is induced by activation of the HOG1 mitogen-activated signaling pathway and this induction is Hog1p/Pbs2p dependent; YJL107C and adjacent ORF,	Strain failed to verify via PCR

				YJL108C are merged in related fungi	
2175	VN_2175	YGR111W	YGR111W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
2176	VN_2176	YJL026W	RNR2	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits	Strain failed to verify via PCR
2177	VN_2177	YGL213C	SKI8	Ski complex component and WD-repeat protein, mediates 3'-5' RNA degradation by the cytoplasmic exosome; also required for meiotic double-strand break recombination; null mutants have superkiller phenotype	Strain failed to verify via PCR
2178	VN_2178	YLR226W	BUR2	Cyclin for the Sgv1p (Bur1p) protein kinase; Sgv1p and Bur2p comprise a CDK-cyclin complex involved in transcriptional regulation through its phosphorylation of the carboxy-terminal domain of the largest subunit of RNA polymerase II	Q
2179	VN_2179	YCR035C	RRP43	Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; has similarity to E. coli RNase PH and to human hRrp43p (OIP2, EXOSC8)	Q
2180	VN_2180	YMR173W-A	YMR173W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the verified gene DDR48/YML173W	Q
2181	VN_2181	YGR012W	YGR012W	Putative cysteine synthase, localized to the mitochondrial outer membrane	Q
2182	VN_2182	YKL077W	YKL077W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole	Q
2183	VN_2183	YDL237W	AIM6	Putative protein of unknown function, required for respiratory growth; YDL237W is not an essential gene	Q
2184	VN_2184	YIL018W	RPL2B	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Ap and has similarity to E. coli L2 and rat L8 ribosomal proteins; expression is upregulated at low temperatures	Strain failed to verify via PCR
2185	VN_2185	YLR244C	MAP1	Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map2p	Q
2186	VN_2186	YHR075C	PPE1	Protein with carboxyl methyl esterase activity that may have a role in demethylation of the phosphoprotein phosphatase catalytic subunit; also identified as a small subunit mitochondrial ribosomal protein	Strain failed to verify via PCR
2187	VN_2187	YKL189W	HYM1	Component of the RAM signaling network that is involved in regulation of Ace2p activity and cellular morphogenesis, interacts with Kic1p and Sog2p, localizes to sites of polarized growth during budding and during the mating response	Q
2188	VN_2188	YHR201C	PPX1	Exopolyphosphatase, hydrolyzes inorganic polyphosphate (poly P) into Pi residues; located in the cytosol, plasma membrane, and mitochondrial matrix	Q
2189	VN_2189	YNL042W	BOP3	Protein of unknown function, potential Cdc28p substrate; overproduction confers resistance to methylmercury	Q
2190	VN_2190	YER028C	MIG3	Probable transcriptional repressor involved in response to toxic agents such as hydroxyurea that inhibit ribonucleotide reductase; phosphorylation by Snf1p or the Mec1p pathway inactivates Mig3p, allowing induction of damage response genes	Q
2191	VN_2191	YPL112C	PEX25	Peripheral peroxisomal membrane peroxin required for the regulation of peroxisome size and maintenance, recruits GTPase Rho1p to peroxisomes, induced by oleate, interacts with homologous protein Pex27p	Q
2192	VN_2192	YHR208W	BAT1	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase	Q
2193	VN_2193	YLR082C	SRL2	Protein of unknown function; overexpression suppresses the lethality caused by a rad53 null mutation	Q
2194	VN_2194	YMR024W	MRPL3	Mitochondrial ribosomal protein of the large subunit	Strain failed to verify via PCR

2195	VN_2195	YBR246W	RRT2	Putative protein of unknown function; non-essential gene identified in a screen for mutants with increased levels of rDNA transcription; null mutants display a weak carboxypeptidase Y missorting/secretion phenotype	Q
2196	VN_2196	YOR063W	RPL3	Protein component of the large (60S) ribosomal subunit, has similarity to E. coli L3 and rat L3 ribosomal proteins; involved in the replication and maintenance of killer double stranded RNA virus	Strain failed to verify via PCR
2197	VN_2197	YHR179W	OYE2	Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to Oye3p with slight differences in ligand binding and catalytic properties; may be involved in sterol metabolism	Q
2198	VN_2198	YKL198C	PTK1	Putative serine/threonine protein kinase that regulates spermine uptake; involved in polyamine transport; possible mitochondrial protein	Q
2199	VN_2199	YJL164C	TPK1	cAMP-dependent protein kinase catalytic subunit; promotes vegetative growth in response to nutrients via the Ras-cAMP signaling pathway; inhibited by regulatory subunit Bcy1p in the absence of cAMP; partially redundant with Tpk2p and Tpk3p	Q
2200	VN_2200	YNR043W	MVD1	Mevalonate pyrophosphate decarboxylase, essential enzyme involved in the biosynthesis of isoprenoids and sterols, including ergosterol; acts as a homodimer	Q
2201	VN_2201	YLR453C	RIF2	Protein that binds to the Rap1p C-terminus and acts synergistically with Rif1p to help control telomere length and establish telomeric silencing; deletion results in telomere elongation	Q
2202	VN_2202	YGR185C	TYS1	Cytoplasmic tyrosyl-tRNA synthetase, required for cytoplasmic protein synthesis; interacts with positions 34 and 35 of the tRNA ^{Tyr} anticodon; mutations in human ortholog YARS are associated with Charcot-Marie-Tooth (CMT) neuropathies	Q
2203	VN_2203	YBL013W	FMT1	Methionyl-tRNA formyltransferase, catalyzes the formylation of initiator Met-tRNA in mitochondria; potential Cdc28p substrate	Q
2204	VN_2204	YIL153W	RRD1	Peptidyl-prolyl cis/trans-isomerase, activator of the phosphotyrosyl phosphatase activity of PP2A; involved in G1 phase progression, microtubule dynamics, bud morphogenesis and DNA repair; subunit of the Tap42p-Sit4p-Rrd1p complex	Q
2205	VN_2205	YLR449W	FPR4	Peptidyl-prolyl cis-trans isomerase (PPIase) (proline isomerase) localized to the nucleus; catalyzes isomerization of proline residues in histones H3 and H4, which affects lysine methylation of those histones	Q
2206	VN_2206	YDR197W	CBS2	Mitochondrial translational activator of the COB mRNA; interacts with translating ribosomes, acts on the COB mRNA 5'-untranslated leader	Q
2207	VN_2207	YDR161W	YDR161W	Putative protein of unknown function; non-essential gene; proposed function in rRNA and ribosome biosynthesis based on transcriptional co-regulation; genetic interactions suggest a role in ER-associated protein degradation (ERAD)	Q
2208	VN_2208	YOR084W	LPX1	Oleic acid-inducible, peroxisomal matrix localized lipase; transcriptionally activated by Yrm1p along with genes involved in multidrug resistance; peroxisomal import is dependent on the PTS1 receptor, Pex5p and on self-interaction	Strain failed to verify via PCR
2209	VN_2209	YNL092W	YNL092W	Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; YNL092W is not an essential gene	Q
2210	VN_2210	YMR201C	RAD14	Protein that recognizes and binds damaged DNA during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 1 (NEF1); contains zinc finger motif; homolog of human XPA protein	Q
2211	VN_2211	YMR017W	SPO20	Meiosis-specific subunit of the t-SNARE complex, required for prospore membrane formation during sporulation; similar to but not functionally redundant with Sec9p; SNAP-25 homolog	Q
2212	VN_2212	YOL052C	SPE2	S-adenosylmethionine decarboxylase, required for the biosynthesis of spermidine and spermine; cells lacking Spe2p require spermine or spermidine for growth in the presence of oxygen but not when grown anaerobically	Q
2213	VN_2213	YOL053W	AIM39	Putative protein of unknown function; null mutant displays elevated frequency of mitochondrial genome loss	Q
2214	VN_2214	YGR187C	HGH1	Nonessential protein of unknown function; predicted to be involved in	Q

				ribosome biogenesis; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; similar to mammalian BRP16 (Brain protein 16)	
2215	VN_2215	YBR125C	PTC4	Cytoplasmic type 2C protein phosphatase; identified as a high-copy number suppressor of the synthetic lethality of a <i>cnb1 mpk1</i> double deletion; overexpression decreases high-osmolarity induced Hog1p phosphorylation and kinase activity	Q
2216	VN_2216	YJR032W	CPR7	Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; binds to Hsp82p and contributes to chaperone activity	Q
2217	VN_2217	YML062C	MFT1	Subunit of the THO complex, which is a nuclear complex comprised of Hpr1p, Mft1p, Rlr1p, and Thp2p, that is involved in transcription elongation and mitotic recombination; involved in telomere maintenance	Q
2218	VN_2218	YGR112W	SHY1	Mitochondrial inner membrane protein required for assembly of cytochrome c oxidase (complex IV); associates with complex IV assembly intermediates and complex III/complex IV supercomplexes; similar to human SURF1 involved in Leigh Syndrome	Q
2219	VN_2219	YEL046C	GLY1	Threonine aldolase, catalyzes the cleavage of L-allo-threonine and L-threonine to glycine; involved in glycine biosynthesis	Q
2220	VN_2220	YDL168W	SFA1	Bifunctional enzyme containing both alcohol dehydrogenase and glutathione-dependent formaldehyde dehydrogenase activities, functions in formaldehyde detoxification and formation of long chain and complex alcohols, regulated by Hog1p-Sko1p	Q
2221	VN_2221	YPL171C	OYE3	Conserved NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to Oye2p with slight differences in ligand binding and catalytic properties; expression induced in cells treated with the mycotoxin patulin	Strain failed to verify via PCR
2222	VN_2222	YEL037C	RAD23	Protein with ubiquitin-like N terminus, recognizes and binds damaged DNA (with Rad4p) during nucleotide excision repair; regulates Rad4p levels, subunit of Nuclear Excision Repair Factor 2 (NEF2); homolog of human HR23A and HR23B proteins	Q
2223	VN_2223	YOL136C	PFK27	6-phosphofructo-2-kinase, catalyzes synthesis of fructose-2,6-bisphosphate; inhibited by phosphoenolpyruvate and sn-glycerol 3-phosphate, expression induced by glucose and sucrose, transcriptional regulation involves protein kinase A	Q
2224	VN_2224	YPL113C	YPL113C	Glyoxylate reductase; acts on glyoxylate and hydroxypyruvate substrates; YPL113C is not an essential gene	Q
2225	VN_2225	YOR057W	SGT1	Cochaperone protein; regulates activity of adenyl cyclase Cyr1p; involved in kinetochore complex assembly; associates with the SCF (Skp1p/Cdc53p/F box protein) ubiquitin ligase complex; acts as a linker between Skp1p and HSP90 complexes	Strain failed to verify via PCR
2226	VN_2226	YHL004W	MRP4	Mitochondrial ribosomal protein of the small subunit	Q
2227	VN_2227	YBR267W	REI1	Cytoplasmic pre-60S factor; required for the correct recycling of shuttling factors Alb1, Arx1 and Tif6 at the end of the ribosomal large subunit biogenesis; involved in bud growth in the mitotic signaling network	Q
2228	VN_2228	YLR418C	CDC73	Component of the Paf1p complex that binds to and modulates the activity of RNA polymerases I and II; required for expression of certain genes, modification of some histones, and telomere maintenance	Q
2229	VN_2229	YCR094W	CDC50	Endosomal protein that interacts with phospholipid flippase Drs2p; interaction with Cdc50p is essential for Drs2p catalytic activity; mutations affect cell polarity and polarized growth; similar to Ynr048wp and Lem3p	Q
2230	VN_2230	YMR305C	SCW10	Cell wall protein with similarity to glucanases; may play a role in conjugation during mating based on mutant phenotype and its regulation by Ste12p	Q
2231	VN_2231	YGL246C	RAI1	Nuclear protein that binds to and stabilizes the exoribonuclease Rat1p, required for pre-rRNA processing	Q
2232	VN_2232	YGR279C	SCW4	Cell wall protein with similarity to glucanases; <i>scw4 scw10</i> double mutants exhibit defects in mating	Q

2233	VN_2233	YML107C	PML39	Protein required for nuclear retention of unspliced pre-mRNAs along with Mlp1p and Pml1p; anchored to nuclear pore complex via Mlp1p and Mlp2p; found with the subset of nuclear pores farthest from the nucleolus; may interact with ribosomes	Q
2234	VN_2234	YJR072C	NPA3	Essential, conserved, cytoplasmic ATPase; phosphorylated by the Pcl1p-Pho85p kinase complex	Q
2235	VN_2235	YNR015W	SMM1	Dihydrouridine synthase, member of a family of dihydrouridine synthases including Dus1p, Smm1p, Dus3p, and Dus4p; modifies uridine residues at position 20 of cytoplasmic tRNAs	Q
2236	VN_2236	YJL147C	YJL147C	Mitochondrial protein of unknown function; homozygous diploid deletion strain has a sporulation defect characterized by elevated dityrosine in the soluble fraction; expression induced by calcium shortage; YJL147W is a non-essential gene	Q
2237	VN_2237	YHL048W	COS8	Nuclear membrane protein, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins; regulation suggests a potential role in the unfolded protein response	Q
2238	VN_2238	YDR354W	TRP4	Anthranilate phosphoribosyl transferase of the tryptophan biosynthetic pathway, catalyzes the phosphoribosylation of anthranilate, subject to the general control system of amino acid biosynthesis	Q
2239	VN_2239	YGL185C	YGL185C	Putative protein with sequence similarity to hydroxyacid dehydrogenases; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2240	VN_2240	YLR105C	SEN2	Subunit of the tRNA splicing endonuclease, which is composed of Sen2p, Sen15p, Sen34p, and Sen54p; Sen2p contains the active site for tRNA 5' splice site cleavage and has similarity to Sen34p and to Archaeal tRNA splicing endonuclease	Q
2241	VN_2241	YHR052W	CIC1	Essential protein that interacts with proteasome components and has a potential role in proteasome substrate specificity; also copurifies with 66S pre-ribosomal particles	Q
2242	VN_2242	YOR388C	FDH1	NAD(+)-dependent formate dehydrogenase, may protect cells from exogenous formate	Strain failed to verify via PCR
2243	VN_2243	YOL128C	YGK3	Protein kinase related to mammalian glycogen synthase kinases of the GSK-3 family; GSK-3 homologs (Mck1p, Rim11p, Mrk1p, Ygk3p) are involved in control of Msn2p-dependent transcription of stress responsive genes and in protein degradation	Q
2244	VN_2244	YDR249C	YDR249C	Putative protein of unknown function	Q
2245	VN_2245	YNL001W	DOM34	Endoribonuclease; functions in no-go mRNA decay, protein translation to promote G1 progression and differentiation, required for meiotic cell division; similar to the eukaryotic Pelota	Q
2246	VN_2246	YLL022C	HIF1	Non-essential component of the HAT-B histone acetyltransferase complex (Hat1p-Hat2p-Hif1p), localized to the nucleus; has a role in telomeric silencing	Q
2247	VN_2247	YOL065C	INP54	Phosphatidylinositol 4,5-bisphosphate 5-phosphatase with a role in secretion, localizes to the endoplasmic reticulum via the C-terminal tail; lacks the Sac1 domain and proline-rich region found in the other 3 INP proteins	Q
2248	VN_2248	YKL113C	RAD27	5' to 3' exonuclease, 5' flap endonuclease, required for Okazaki fragment processing and maturation as well as for long-patch base-excision repair; member of the S. pombe RAD2/FEN1 family	Q
2249	VN_2249	YLL039C	UBI4	Ubiquitin, becomes conjugated to proteins, marking them for selective degradation via the ubiquitin-26S proteasome system; essential for the cellular stress response; encoded as a polyubiquitin precursor comprised of 5 head-to-tail repeats	Q
2250	VN_2250	YGL126W	SCS3	Protein required for inositol prototrophy, identified as an ortholog of the FIT family of proteins involved in triglyceride droplet biosynthesis; disputed role in the synthesis of inositol phospholipids from inositol	Q
2251	VN_2251	YHR063C	PAN5	2-dehydropantoate 2-reductase, part of the pantothenic acid pathway, structurally homologous to E. coli panE	Q
2252	VN_2252	YOL047C	YOL047C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Strain failed to verify via PCR

2253	VN_2253	YJR148W	BAT2	Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during stationary phase and repressed during logarithmic phase	Q
2254	VN_2254	YBR204C	YBR204C	Serine hydrolase; YBR204C is not an essential gene	Q
2255	VN_2255	YOR390W	YOR390W	Putative protein of unknown function	Q
2256	VN_2256	YFR024C	YFR024C-A	#N/A	Q
2257	VN_2257	YBR155W	CNS1	TPR-containing co-chaperone; binds both Hsp82p (Hsp90) and Ssa1p (Hsp70) and stimulates the ATPase activity of SSA1, ts mutants reduce Hsp82p function while over expression suppresses the phenotypes of an HSP82 ts allele and a cpr7 deletion	Q
2258	VN_2258	YML027W	YOX1	Homeodomain-containing transcriptional repressor, binds to Mcm1p and to early cell cycle boxes (ECBs) in the promoters of cell cycle-regulated genes expressed in M/G1 phase; expression is cell cycle-regulated; potential Cdc28p substrate	Q
2259	VN_2259	YDR259C	YAP6	Putative basic leucine zipper (bZIP) transcription factor; overexpression increases sodium and lithium tolerance; computational analysis suggests a role in regulation of expression of genes involved in carbohydrate metabolism	Strain failed to verify via PCR
2260	VN_2260	YLR180W	SAM1	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p)	Q
2261	VN_2261	YLR291C	GCD7	Beta subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression	Q
2262	VN_2262	YNL230C	ELA1	Elongin A, F-box protein that forms a heterodimer with Elc1p and is required for ubiquitin-dependent degradation of the RNA Polymerase II subunit RPO21; subunit of the Elongin-Cullin-Socs (ECS) ligase complex	Q
2263	VN_2263	YLR460C	YLR460C	Member of the quinone oxidoreductase family, up-regulated in response to the fungicide mancozeb; possibly up-regulated by iodine	Q
2264	VN_2264	YDL193W	NUS1	Putative prenyltransferase, required for cell viability; proposed to be involved in protein trafficking because tet-repressible mutant shows accumulation of hypoglycosylated forms of CPY	Strain failed to verify via PCR
2265	VN_2265	YDR415C	YDR415C	Putative protein of unknown function	Q
2266	VN_2266	YIR034C	LYS1	Saccharopine dehydrogenase (NAD ⁺ , L-lysine-forming), catalyzes the conversion of saccharopine to L-lysine, which is the final step in the lysine biosynthesis pathway	Q
2267	VN_2267	YDR532C	YDR532C	Subunit of a kinetochore-microtubule binding complex with Spc105p that bridges centromeric heterochromatin and kinetochore MAPs and motors, and is also required for sister chromatid bi-orientation and kinetochore binding of SAC components	Q
2268	VN_2268	YBR234C	ARC40	Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches	Q
2269	VN_2269	YDR309C	GIC2	Redundant rho-like GTPase Cdc42p effector; homolog of Gic1p; involved in initiation of budding and cellular polarization; interacts with Cdc42p via the Cdc42/Rac-interactive binding (CRIB) domain and with PI(4,5)P2 via a polybasic region	Q
2270	VN_2270	YOL116W	MSN1	Transcriptional activator involved in regulation of invertase and glucoamylase expression, invasive growth and pseudohyphal differentiation, iron uptake, chromium accumulation, and response to osmotic stress; localizes to the nucleus	Q
2271	VN_2271	YPL014W	YPL014W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to the nucleus	Q
2272	VN_2272	YGR109C	CLB6	B-type cyclin involved in DNA replication during S phase; activates Cdc28p to promote initiation of DNA synthesis; functions in formation of mitotic spindles along with Clb3p and Clb4p; most abundant during late G1	Q
2273	VN_2273	YDR400W	URH1	Uridine nucleosidase (uridine-cytidine N-ribohydrolase), cleaves N-glycosidic bonds in nucleosides; involved in the pyrimidine salvage	Q

				and nicotinamide riboside salvage pathways	
2274	VN_2274	YBR161W	CSH1	Probable catalytic subunit of a mannosylinositol phosphorylceramide (MIPC) synthase, forms a complex with probable regulatory subunit Csg2p; function in sphingolipid biosynthesis is overlapping with that of Sur1p	Q
2275	VN_2275	YML060W	OGG1	Mitochondrial glycosylase/lyase that specifically excises 7,8-dihydro-8-oxoguanine residues located opposite cytosine or thymine residues in DNA, repairs oxidative damage to mitochondrial DNA, contributes to UVA resistance	Q
2276	VN_2276	YDR142C	PEX7	Peroxisomal signal receptor for the N-terminal nonapeptide signal (PTS2) of peroxisomal matrix proteins; WD repeat protein; defects in human homolog cause lethal rhizomelic chondrodysplasia punctata (RCDP)	Q
2277	VN_2277	YMR276W	DSK2	Nuclear-enriched ubiquitin-like polyubiquitin-binding protein, required for spindle pole body (SPB) duplication and for transit through the G2/M phase of the cell cycle, involved in proteolysis, interacts with the proteasome	Q
2278	VN_2278	YFL030W	AGX1	Alanine:glyoxylate aminotransferase (AGT), catalyzes the synthesis of glycine from glyoxylate, which is one of three pathways for glycine biosynthesis in yeast; has similarity to mammalian and plant alanine:glyoxylate aminotransferases	Q
2279	VN_2279	YDR502C	SAM2	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p)	Q
2280	VN_2280	YJL125C	GCD14	Subunit of tRNA (1-methyladenosine) methyltransferase, with Gcd10p, required for the modification of the adenine at position 58 in tRNAs, especially tRNAi-Met; first identified as a negative regulator of GCN4 expression	Q
2281	VN_2281	YBL032W	HEK2	RNA binding protein involved in the asymmetric localization of ASH1 mRNA; represses translation of ASH1 mRNA, an effect reversed by Yck1p-dependent phosphorylation; regulates telomere position effect and length; similarity to hnRNP-K	Q
2282	VN_2282	YPL193W	RSA1	Protein involved in the assembly of 60S ribosomal subunits; functionally interacts with Dbp6p; functions in a late nucleoplasmic step of the assembly	Q
2283	VN_2283	YJL137C	GLG2	Self-glucosylating initiator of glycogen synthesis, also glucosylates n-dodecyl-beta-D-maltoside; similar to mammalian glycogenin	Q
2284	VN_2284	YHR112C	YHR112C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2285	VN_2285	YGL105W	ARC1	Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p), delivering tRNA to them, stimulating catalysis, and ensuring their localization to the cytoplasm; also binds quadruplex nucleic acids	Q
2286	VN_2286	YMR030W	RSF1	Protein required for respiratory growth; localized to both the nucleus and mitochondrion; may interact with transcription factors to mediate the transition to respiratory growth and activate transcription of nuclear and mitochondrial genes	Q
2287	VN_2287	YDR171W	HSP42	Small heat shock protein (sHSP) with chaperone activity; forms barrel-shaped oligomers that suppress unfolded protein aggregation; involved in cytoskeleton reorganization after heat shock	Strain failed to verify via PCR
2288	VN_2288	YMR289W	ABZ2	Aminodeoxychorismate lyase (4-amino-4-deoxychorismate lyase), catalyzes the third step in para-aminobenzoic acid biosynthesis; involved in folic acid biosynthesis	Q
2289	VN_2289	YMR294W	JNM1	Component of the yeast dynactin complex, consisting of Nip100p, Jnm1p, and Arp1p; required for proper nuclear migration and spindle partitioning during mitotic anaphase B	Strain failed to verify via PCR
2290	VN_2290	YGR046W	TAM41	Mitochondrial protein involved in protein import into the mitochondrial matrix; maintains the functional integrity of the TIM23 protein translocator complex; viability of null mutant is strain-dependent; mRNA is targeted to the bud	Strain failed to verify via PCR
2291	VN_2291	YGL067W	NPY1	NADH diphosphatase (pyrophosphatase), hydrolyzes the pyrophosphate linkage in NADH and related nucleotides; localizes to peroxisomes	Strain failed to verify via PCR

2292	VN_2292	YAL060W	BDH1	NAD-dependent (R,R)-butanediol dehydrogenase, catalyzes oxidation of (R,R)-2,3-butanediol to (3R)-acetoin, oxidation of meso-butanediol to (3S)-acetoin, and reduction of acetoin; enhances use of 2,3-butanediol as an aerobic carbon source	Q
2293	VN_2293	YDR321W	ASP1	Cytosolic L-asparaginase, involved in asparagine catabolism	Q
2294	VN_2294	YPR140W	TAZ1	Lyso-phosphatidylcholine acyltransferase, required for normal phospholipid content of mitochondrial membranes; may remodel acyl groups of cardiolipin in the inner membrane; human ortholog tafazzin is implicated in Barth syndrome	Q
2295	VN_2295	YOL043C	NTG2	DNA N-glycosylase and apurinic/apyrimidinic (AP) lyase involved in base excision repair, localizes to the nucleus; sumoylated	Q
2296	VN_2296	YNR074C	AIF1	Mitochondrial cell death effector that translocates to the nucleus in response to apoptotic stimuli, homolog of mammalian Apoptosis-Inducing Factor, putative reductase	Q
2297	VN_2297	YGL148W	ARO2	Bifunctional chorismate synthase and flavin reductase, catalyzes the conversion of 5-enolpyruvylshikimate 3-phosphate (EPSP) to form chorismate, which is a precursor to aromatic amino acids	Q
2298	VN_2298	YNL134C	YNL134C	Putative protein of unknown function with similarity to dehydrogenases from other model organisms; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and nucleus and is induced by the DNA-damaging agent MMS	Q
2299	VN_2299	YGR286C	BIO2	Biotin synthase, catalyzes the conversion of dethiobiotin to biotin, which is the last step of the biotin biosynthesis pathway; complements E. coli bioB mutant	Q
2300	VN_2300	YNR075W	COS10	Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	Q
2301	VN_2301	YNL288W	CAF40	Evolutionarily conserved subunit of the CCR4-NOT complex involved in controlling mRNA initiation, elongation and degradation; binds Cdc39p	Q
2302	VN_2302	YHR129C	ARP1	Actin-related protein of the dynactin complex; required for spindle orientation and nuclear migration; putative ortholog of mammalian centractin	Q
2303	VN_2303	YDR088C	SLU7	RNA splicing factor, required for ATP-independent portion of 2nd catalytic step of spliceosomal RNA splicing; interacts with Prp18p; contains zinc knuckle domain	Q
2304	VN_2304	YGL082W	YGL082W	Putative protein of unknown function; predicted prenylation/proteolysis target of Afc1p and Rce1p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YGL082W is not an essential gene	Q
2305	VN_2305	YBR026C	ETR1	2-enoyl thioester reductase, member of the medium chain dehydrogenase/reductase family; localized to in mitochondria, where it has a probable role in fatty acid synthesis	Q
2306	VN_2306	YAL032C	PRP45	Protein required for pre-mRNA splicing; associates with the spliceosome and interacts with splicing factors Prp22p and Prp46p; orthologous to human transcriptional coactivator SKIP and can activate transcription of a reporter gene	Q
2307	VN_2307	YDL188C	PPH22	Catalytic subunit of protein phosphatase 2A (PP2A), functionally redundant with Pph21p; methylated at C terminus; forms alternate complexes with several regulatory subunits; involved in signal transduction and regulation of mitosis	Q
2308	VN_2308	YGL155W	CDC43	Beta subunit of geranylgeranyltransferase type I, catalyzes geranylgeranylation to the cysteine residue in proteins containing a C-terminal CaaX sequence ending in Leu or Phe; has substrates important for morphogenesis	Q
2309	VN_2309	YNL331C	AAD14	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role	Q
2310	VN_2310	YMR083W	ADH3	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production	Q
2311	VN_2311	YPL001W	HAT1	Catalytic subunit of the Hat1p-Hat2p histone acetyltransferase complex that uses the cofactor acetyl coenzyme A, to acetylate free nuclear and cytoplasmic histone H4; involved in telomeric silencing	Q

				and DNA double-strand break repair	
2312	VN_2312	YPL165C	SET6	SET domain protein of unknown function; deletion heterozygote is sensitive to compounds that target ergosterol biosynthesis, may be involved in compound availability	Q
2313	VN_2313	YIL116W	HIS5	Histidinol-phosphate aminotransferase, catalyzes the seventh step in histidine biosynthesis; responsive to general control of amino acid biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts	Q
2314	VN_2314	YMR272C	SCS7	Sphingolipid alpha-hydroxylase, functions in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids, has both cytochrome b5-like and hydroxylase/desaturase domains, not essential for growth	Q
2315	VN_2315	YGL209W	MIG2	Protein containing zinc fingers, involved in repression, along with Mig1p, of SUC2 (invertase) expression by high levels of glucose; binds to Mig1p-binding sites in SUC2 promoter	Q
2316	VN_2316	YGR295C	COS6	Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	Q
2317	VN_2317	YCL016C	DCC1	Subunit of a complex with Ctf8p and Ctf18p that shares some components with Replication Factor C, required for sister chromatid cohesion and telomere length maintenance	Q
2318	VN_2318	YDR268W	MSW1	Mitochondrial tryptophanyl-tRNA synthetase	Q
2319	VN_2319	YIL110W	MNI1	Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; deletion mutant exhibits a weak vacuolar protein sorting defect, enhanced resistance to caspofungin, and is synthetically lethal with MEN mutants	Q
2320	VN_2320	YOR193W	PEX27	Peripheral peroxisomal membrane protein involved in controlling peroxisome size and number, interacts with homologous protein Pex25p	Q
2321	VN_2321	YNL307C	MCK1	Protein serine/threonine/tyrosine (dual-specificity) kinase involved in control of chromosome segregation and in regulating entry into meiosis; related to mammalian glycogen synthase kinases of the GSK-3 family	Q
2322	VN_2322	YDR113C	PDS1	Securin, inhibits anaphase by binding separin Esp1p; blocks cyclin destruction and mitotic exit, essential for meiotic progression and mitotic cell cycle arrest; localization is cell-cycle dependent and regulated by Cdc28p phosphorylation	Q
2323	VN_2323	YDL211C	YDL211C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole	Strain failed to verify via PCR
2324	VN_2324	YDR517W	GRH1	Acetylated, cis-golgi localized protein involved in ER to Golgi transport; homolog of human GRASP65; forms a complex with the coiled-coil protein Bug1p; mutants are compromised for the fusion of ER-derived vesicles with Golgi membranes	Q
2325	VN_2325	YBR249C	ARO4	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase, catalyzes the first step in aromatic amino acid biosynthesis and is feedback-inhibited by tyrosine or high concentrations of phenylalanine or tryptophan	Q
2326	VN_2326	YMR139W	RIM11	Protein kinase required for signal transduction during entry into meiosis; promotes the formation of the Ime1p-Ume6p complex by phosphorylating Ime1p and Ume6p; shares similarity with mammalian glycogen synthase kinase 3-beta	Q
2327	VN_2327	YOR136W	IDH2	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; phosphorylated	Q
2328	VN_2328	YMR114C	YMR114C	Protein of unknown function; may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the nucleus and cytoplasm; YMR114C is not an essential gene	Q
2329	VN_2329	YLR137W	YLR137W	Putative S-adenosylmethionine-dependent methyltransferase	Q
2330	VN_2330	YHR040W	BCD1	Essential protein required for the accumulation of box C/D snoRNA	Q

2331	VN_2331	YIR026C	YVH1	Protein phosphatase involved in vegetative growth at low temperatures, sporulation, and glycogen accumulation; mutants are defective in 60S ribosome assembly; member of the dual-specificity family of protein phosphatases	Strain failed to verify via PCR
2332	VN_2332	YBR031W	RPL4A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins	Q
2333	VN_2333	YCR105W	ADH7	NADPH-dependent medium chain alcohol dehydrogenase with broad substrate specificity; member of the cinnamyl family of alcohol dehydrogenases; may be involved in fusel alcohol synthesis or in aldehyde tolerance	Q
2334	VN_2334	YIL035C	CKA1	Alpha catalytic subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation; the holoenzyme also contains CKA2, CKB1 and CKB2, the many substrates include transcription factors and all RNA polymerases	Q
2335	VN_2335	YDR035W	ARO3	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase, catalyzes the first step in aromatic amino acid biosynthesis and is feedback-inhibited by phenylalanine or high concentration of tyrosine or tryptophan	Q
2336	VN_2336	YPR035W	GLN1	Glutamine synthetase (GS), synthesizes glutamine from glutamate and ammonia; with Glt1p, forms the secondary pathway for glutamate biosynthesis from ammonia; expression regulated by nitrogen source and by amino acid limitation	Q
2337	VN_2337	YPL018W	CTF19	Outer kinetochore protein, required for accurate mitotic chromosome segregation; component of the kinetochore sub-complex COMA (Ctf19p, Okp1p, Mcm21p, Ame1p) that functions as a platform for kinetochore assembly	Q
2338	VN_2338	YNL316C	PHA2	Prephenate dehydratase, catalyzes the conversion of prephenate to phenylpyruvate, which is a step in the phenylalanine biosynthesis pathway	Q
2339	VN_2339	YLR405W	DUS4	Dihydrouridine synthase, member of a widespread family of conserved proteins including Smm1p, Dus1p, and Dus3p	Q
2340	VN_2340	YKL043W	PHD1	Transcriptional activator that enhances pseudohyphal growth; regulates expression of FLO11, an adhesin required for pseudohyphal filament formation; similar to StuA, an A. nidulans developmental regulator; potential Cdc28p substrate	Q
2341	VN_2341	YJL021C	MTI1	#N/A	Q
2342	VN_2342	YLR420W	URA4	Dihydroorotase, catalyzes the third enzymatic step in the de novo biosynthesis of pyrimidines, converting carbamoyl-L-aspartate into dihydroorotate	Q
2343	VN_2343	YCR095C	OCA4	Cytoplasmic protein required for replication of Brome mosaic virus in S. cerevisiae, which is a model system for studying replication of positive-strand RNA viruses in their natural hosts	Strain failed to verify via PCR
2344	VN_2344	YDL055C	PSA1	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanylttransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure	Strain failed to verify via PCR
2345	VN_2345	YPR078C	YPR078C	Putative protein of unknown function; possible role in DNA metabolism and/or in genome stability; expression is heat-inducible	Q
2346	VN_2346	YDR191W	HST4	Member of the Sir2 family of NAD(+)-dependent protein deacetylases; involved along with Hst3p in silencing at telomeres, cell cycle progression, radiation resistance, genomic stability and short-chain fatty acid metabolism	Q
2347	VN_2347	YAL036C	RBG1	Member of the DRG family of GTP-binding proteins; associates with translating ribosomes; interacts with Tma46p, Ygr250cp, Gir2p and Yap1p via two-hybrid	Q
2348	VN_2348	YBL081W	YBL081W	Non-essential protein of unknown function; null mutation results in a decrease in plasma membrane electron transport	Q
2349	VN_2349	YNR032W	PPG1	Putative serine/threonine protein phosphatase, required for glycogen accumulation; interacts with Tap42p, which binds to and regulates other protein phosphatases	Q
2350	VN_2350	YMR097C	MTG1	Putative GTPase peripheral to the mitochondrial inner membrane, essential for respiratory competence, likely functions in assembly of	Q

				the large ribosomal subunit, has homologs in plants and animals	
2351	VN_2351	YMR028W	TAP42	Essential protein involved in the TOR signaling pathway; physically associates with the protein phosphatase 2A and the SIT4 protein phosphatase catalytic subunits	Q
2352	VN_2352	YLR063W	YLR063W	Putative S-adenosylmethionine-dependent methyltransferase; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLR063W is not an essential gene	Q
2353	VN_2353	YPL081W	RPS9A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins	Q
2354	VN_2354	YKR077W	MSA2	Putative transcriptional activator, that interacts with G1-specific transcription factor, MBF and G1-specific promoters; ortholog of Msa2p, an MBF and SBF activator that regulates G1-specific transcription and cell cycle initiation	Q
2355	VN_2355	YDR012W	RPL4B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Ap and has similarity to E. coli L4 and rat L4 ribosomal proteins	Strain failed to verify via PCR
2356	VN_2356	YFR046C	CNN1	Kinetochore protein of unknown function; associated with the essential kinetochore proteins Nnf1p and Spc24p; phosphorylated by both Clb5-Cdk1 and, to a lesser extent, Clb2-Cdk1.	Q
2357	VN_2357	YLR048W	RPS0B	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap; required for maturation of 18S rRNA along with Rps0Ap; deletion of either RPS0 gene reduces growth rate, deletion of both genes is lethal	Q
2358	VN_2358	YDR438W	THI74	Mitochondrial transporter repressible by thiamine	Q
2359	VN_2359	YDL134C	PPH21	Catalytic subunit of protein phosphatase 2A (PP2A), functionally redundant with Pph22p; methylated at C terminus; forms alternate complexes with several regulatory subunits; involved in signal transduction and regulation of mitosis	Q
2360	VN_2360	YCR102C	YCR102C	Putative protein of unknown function; involved in copper metabolism; similar to C.carbonum toxD gene; YCR102C is not an essential gene	Q
2361	VN_2361	YPR065W	ROX1	Heme-dependent repressor of hypoxic genes; contains an HMG domain that is responsible for DNA bending activity	Q
2362	VN_2362	YOL010W	RCL1	Subunit of U3-containing 90S preribosome processome complex involved in 18S rRNA biogenesis and small ribosomal subunit assembly; stimulates Bms1p GTPase and U3 binding activity; similar to RNA cyclase-like proteins but no activity detected	Q
2363	VN_2363	YMR251W	GTO3	Omega class glutathione transferase; putative cytosolic localization	Q
2364	VN_2364	YML131W	YML131W	Putative protein of unknown function with similarity to medium chain dehydrogenase/reductases; expression induced by stresses including osmotic shock, DNA damaging agents, and other chemicals; GFP-fusion protein localizes to the cytoplasm	Q
2365	VN_2365	YDR047W	HEM12	Uroporphyrinogen decarboxylase, catalyzes the fifth step in the heme biosynthetic pathway; localizes to both the cytoplasm and nucleus; a hem12 mutant has phenotypes similar to patients with porphyria cutanea tarda	Q
2366	VN_2366	YIL094C	LYS12	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate	Q
2367	VN_2367	YGL063W	PUS2	Mitochondrial tRNA:pseudouridine synthase; acts at positions 27 and 28, but not at position 72; efficiently and rapidly targeted to mitochondria, specifically dedicated to mitochondrial tRNA modification	Q
2368	VN_2368	YGL248W	PDE1	Low-affinity cyclic AMP phosphodiesterase, controls glucose and intracellular acidification-induced cAMP signaling, target of the cAMP-protein kinase A (PKA) pathway; glucose induces transcription and inhibits translation	Q
2369	VN_2369	YFL029C	CAK1	Cyclin-dependent kinase-activating kinase required for passage through the cell cycle, phosphorylates and activates Cdc28p; nucleotide-binding pocket differs significantly from those of most	Q

				other protein kinases	
2370	VN_2370	YPL090C	RPS6A	Protein component of the small (40S) ribosomal subunit; identical to Rps6Bp and has similarity to rat S6 ribosomal protein	Q
2371	VN_2371	YNL080C	EOS1	Protein involved in N-glycosylation; deletion mutation confers sensitivity to oxidative stress and shows synthetic lethality with mutations in the spindle checkpoint genes BUB3 and MAD1; YNL080C is not an essential gene	Strain failed to verify via PCR
2372	VN_2372	YMR270C	RRN9	Protein involved in promoting high level transcription of rDNA, subunit of UAF (upstream activation factor) for RNA polymerase I	Q
2373	VN_2373	YLR316C	TAD3	Subunit of tRNA-specific adenosine-34 deaminase, forms a heterodimer with Tad2p that converts adenosine to inosine at the wobble position of several tRNAs	Q
2374	VN_2374	YOL042W	NGL1	Putative endonuclease, has a domain similar to a magnesium-dependent endonuclease motif in mRNA deadenylase Ccr4p; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2375	VN_2375	YLR155C	ASP3-1	Cell-wall L-asparaginase II, involved in asparagine catabolism; expression is induced during nitrogen starvation; four copies of ASP3 are present in the genome reference strain S288C	Q
2376	VN_2376	YJR153W	PGU1	Endo-polygalacturonase, pectolytic enzyme that hydrolyzes the alpha-1,4-glycosidic bonds in the rhamnogalacturonan chains in pectins	Q
2377	VN_2377	YLR216C	CPR6	Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; binds to Hsp82p and contributes to chaperone activity	Q
2378	VN_2378	YGL159W	YGL159W	Putative protein of unknown function; deletion mutant has no detectable phenotype	Q
2379	VN_2379	YGR052W	FMP48	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; induced by treatment with 8-methoxypsoralen and UVA irradiation	Q
2380	VN_2380	YGR040W	KSS1	Mitogen-activated protein kinase (MAPK) involved in signal transduction pathways that control filamentous growth and pheromone response; the KSS1 gene is nonfunctional in S288C strains and functional in W303 strains	Q
2381	VN_2381	YDR322W	MRPL35	Mitochondrial ribosomal protein of the large subunit	Q
2382	VN_2382	YBR018C	GAL7	Galactose-1-phosphate uridyl transferase, synthesizes glucose-1-phosphate and UDP-galactose from UDP-D-glucose and alpha-D-galactose-1-phosphate in the second step of galactose catabolism	Q
2383	VN_2383	YDR065W	RRG1	Protein of unknown function, required for vacuolar acidification and mitochondrial genome maintenance; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2384	VN_2384	YER179W	DMC1	Meiosis-specific protein required for repair of double-strand breaks and pairing between homologous chromosomes; homolog of Rad51p and the bacterial RecA protein	Q
2385	VN_2385	YCR019W	MAK32	Protein necessary for structural stability of L-A double-stranded RNA-containing particles	Q
2386	VN_2386	YOR338W	YOR338W	Putative protein of unknown function; YOR338W transcription is regulated by Azf1p and its transcript is a specific target of the G protein effector Scp160p; identified as being required for sporulation in a high-throughput mutant screen	Q
2387	VN_2387	YLR157C	ASP3-2	Cell-wall L-asparaginase II, involved in asparagine catabolism; expression is induced during nitrogen starvation; four copies of ASP3 are present in the genome reference strain S288C	Q
2388	VN_2388	YKR066C	CCP1	Mitochondrial cytochrome-c peroxidase; degrades reactive oxygen species in mitochondria, involved in the response to oxidative stress	Q
2389	VN_2389	YNL005C	MRP7	Mitochondrial ribosomal protein of the large subunit	Q
2390	VN_2390	YGR079W	YGR079W	Putative protein of unknown function; YGR079W is not an essential gene	Q
2391	VN_2391	YLR224W	YLR224W	F-box protein and component of SCF ubiquitin ligase complexes involved in ubiquitin-dependent protein catabolism; readily	Q

				monoubiquitinated in vitro by SCF-Ubc4 complexes; YLR224W is not an essential gene	
2392	VN_2392	YGR173W	RBG2	Protein with similarity to mammalian developmentally regulated GTP-binding protein	Q
2393	VN_2393	YDR531W	CAB1	Pantothenate kinase (ATP:D-pantothenate 4'-phosphotransferase, EC 2.7.1.33); catalyzes the first committed step in the universal biosynthetic pathway for synthesis of coenzyme A (CoA)	Q
2394	VN_2394	YBR057C	MUM2	Cytoplasmic protein essential for meiotic DNA replication and sporulation; interacts with Orc2p, which is a component of the origin recognition complex	Q
2395	VN_2395	YDR158W	HOM2	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis	Q
2396	VN_2396	YBR065C	ECM2	Pre-mRNA splicing factor, facilitates the cooperative formation of U2/U6 helix II in association with stem II in the spliceosome, function may be regulated by Slu7p	Q
2397	VN_2397	YCR107W	AAD3	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role	Q
2398	VN_2398	YPL096W	PNG1	Conserved peptide N-glycanase required for deglycosylation of misfolded glycoproteins during proteasome-dependent degradation, localizes to the cytoplasm and nucleus, interacts with the DNA repair protein Rad23p	Q
2399	VN_2399	YLR158C	ASP3-3	Cell-wall L-asparaginase II, involved in asparagine catabolism; expression is induced during nitrogen starvation; four copies of ASP3 are present in the genome reference strain S288C	Q
2400	VN_2400	YCL064C	CHA1	Catabolic L-serine (L-threonine) deaminase, catalyzes the degradation of both L-serine and L-threonine; required to use serine or threonine as the sole nitrogen source, transcriptionally induced by serine and threonine	Q
2401	VN_2401	YOR242C	SSP2	Sporulation specific protein that localizes to the spore wall; required for sporulation at a point after meiosis II and during spore wall formation; SSP2 expression is induced midway in meiosis	Strain failed to verify via PCR
2402	VN_2402	YKR076W	ECM4	Omega class glutathione transferase; not essential; similar to Ygr154cp; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2403	VN_2403	YML066C	SMA2	Meiosis-specific prospore membrane protein; required to produce bending force necessary for proper assembly of the prospore membrane during sporulation	Q
2404	VN_2404	YIR025W	MND2	Subunit of the anaphase-promoting complex (APC); necessary for maintaining sister chromatid cohesion in prophase I of meiosis by inhibiting premature ubiquitination and subsequent degradation of substrates by the APC(Ama1) ubiquitin ligase	Q
2405	VN_2405	YKL114C	APN1	Major apurinic/apyrimidinic endonuclease, 3'-repair diesterase involved in repair of DNA damage by oxidation and alkylating agents; also functions as a 3'-5' exonuclease to repair 7,8-dihydro-8-oxodeoxyguanosine	Q
2406	VN_2406	YBR221C	PDB1	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria	Q
2407	VN_2407	YDR273W	DON1	Meiosis-specific component of the spindle pole body, part of the leading edge protein (LEP) coat, forms a ring-like structure at the leading edge of the prospore membrane during meiosis II	Q
2408	VN_2408	YCL018W	LEU2	Beta-isopropylmalate dehydrogenase (IMDH), catalyzes the third step in the leucine biosynthesis pathway	Strain failed to verify via PCR
2409	VN_2409	YFR018C	YFR018C	Putative protein of unknown function	Q
2410	VN_2410	YAL013W	DEP1	Transcriptional modulator involved in regulation of structural phospholipid biosynthesis genes and metabolically unrelated genes, as well as maintenance of telomeres, mating efficiency, and sporulation	Q
2411	VN_2411	YLR160C	ASP3-4	Cell-wall L-asparaginase II, involved in asparagine catabolism;	Q

				expression is induced during nitrogen starvation; four copies of ASP3 are present in the genome reference strain S288C	
2412	VN_2412	YIL079C	AIR1	Zinc knuckle protein, involved in nuclear RNA processing and degradation as a component of the TRAMP complex; stimulates the poly(A) polymerase activity of Pap2p in vitro; functionally redundant with Air2p	Q
2413	VN_2413	YJR094C	IME1	Master regulator of meiosis that is active only during meiotic events, activates transcription of early meiotic genes through interaction with Ume6p, degraded by the 26S proteasome following phosphorylation by Ime2p	Q
2414	VN_2414	YJR139C	HOM6	Homoserine dehydrogenase (L-homoserine:NADP oxidoreductase), dimeric enzyme that catalyzes the third step in the common pathway for methionine and threonine biosynthesis; enzyme has nucleotide-binding, dimerization and catalytic regions	Q
2415	VN_2415	YER127W	LCP5	Essential protein involved in maturation of 18S rRNA; depletion leads to inhibited pre-rRNA processing and reduced polysome levels; localizes primarily to the nucleolus	Q
2416	VN_2416	YPL015C	HST2	Cytoplasmic member of the silencing information regulator 2 (Sir2) family of NAD(+)-dependent protein deacetylases; modulates nucleolar (rDNA) and telomeric silencing; possesses NAD(+)-dependent histone deacetylase activity in vitro	Q
2417	VN_2417	YLR287C	YLR287C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLR287C is not an essential gene	Q
2418	VN_2418	YNL229C	URE2	Nitrogen catabolite repression transcriptional regulator that acts by inhibition of GLN3 transcription in good nitrogen source; has glutathione peroxidase activity and can mutate to acquire GST activity; altered form creates [URE3] prion	Q
2419	VN_2419	YKR011C	YKR011C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus	Q
2420	VN_2420	YBR145W	ADH5	Alcohol dehydrogenase isoenzyme V; involved in ethanol production	Q
2421	VN_2421	YDR214W	AHA1	Co-chaperone that binds to Hsp82p and activates its ATPase activity; similar to Hch1p; expression is regulated by stresses such as heat shock	Q
2422	VN_2422	YJR019C	TES1	Peroxisomal acyl-CoA thioesterase likely to be involved in fatty acid oxidation rather than fatty acid synthesis; conserved protein also found in human peroxisomes; TES1 mRNA levels increase during growth on fatty acids	Q
2423	VN_2423	YMR234W	RNH1	Ribonuclease H1; able to bind double-stranded RNAs and RNA-DNA hybrids; associates with RNase polymerase I; the homolog of mammalian RNase HII (the S. cerevisiae homolog of mammalian RNase HI is RNH201)	Q
2424	VN_2424	YJR141W	YJR141W	Essential protein of unknown function	Q
2425	VN_2425	YLR215C	CDC123	Protein involved in nutritional control of the cell cycle; regulates abundance of the translation initiation factor eIF2; ortholog of human D123 protein	Q
2426	VN_2426	YKL060C	FBA1	Fructose 1,6-bisphosphate aldolase, required for glycolysis and gluconeogenesis; catalyzes conversion of fructose 1,6 bisphosphate to glyceraldehyde-3-P and dihydroxyacetone-P; locates to mitochondrial outer surface upon oxidative stress	Q
2427	VN_2427	YHR025W	THR1	Homoserine kinase, conserved protein required for threonine biosynthesis; expression is regulated by the GCN4-mediated general amino acid control pathway	Q
2428	VN_2428	YGR154C	GTO1	Omega-class glutathione transferase; induced under oxidative stress; putative peroxisomal localization	Q
2429	VN_2429	YMR244W	YMR244W	Putative protein of unknown function	Q
2430	VN_2430	YOR049C	RSB1	Suppressor of sphingoid long chain base (LCB) sensitivity of an LCB-lyase mutation; putative integral membrane transporter or flippase that may transport LCBs from the cytoplasmic side toward the extracytoplasmic side of the membrane	Q

2431	VN_2431	YPL011C	TAF3	TFIID subunit (47 kDa), involved in promoter binding and RNA polymerase II transcription initiation	Q
2432	VN_2432	YDL107W	MSS2	Peripherally bound inner membrane protein of the mitochondrial matrix involved in membrane insertion of C-terminus of Cox2p, interacts genetically and physically with Cox18p	Q
2433	VN_2433	YDR279W	RNH202	Ribonuclease H2 subunit, required for RNase H2 activity; related to human AGS2 that causes Aicardi-Goutieres syndrome	Q
2434	VN_2434	YMR315W	YMR315W	Protein with NADP(H) oxidoreductase activity; transcription is regulated by Stb5p in response to NADPH depletion induced by diamide; promoter contains a putative Stb5p binding site	Q
2435	VN_2435	YMR303C	ADH2	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1	Q
2436	VN_2436	YLR100W	ERG27	3-keto sterol reductase, catalyzes the last of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; mutants are sterol auxotrophs	Strain failed to verify via PCR
2437	VN_2437	YMR318C	ADH6	NADPH-dependent medium chain alcohol dehydrogenase with broad substrate specificity; member of the cinnamyl family of alcohol dehydrogenases; may be involved in fusel alcohol synthesis or in aldehyde tolerance	Q
2438	VN_2438	YML021C	UNG1	Uracil-DNA glycosylase, required for repair of uracil in DNA formed by spontaneous cytosine deamination, not required for strand-specific mismatch repair, cell-cycle regulated, expressed in late G1, localizes to mitochondria and nucleus	Q
2439	VN_2439	YJR159W	SOR1	Sorbitol dehydrogenase; expression is induced in the presence of sorbitol or xylose	Q
2440	VN_2440	YJL131C	AIM23	Putative protein of unknown function; the authentic non-tagged protein is detected in highly purified mitochondria; null mutant is viable, displays severe respiratory growth defect and elevated frequency of mitochondrial genome loss	Q
2441	VN_2441	YNL304W	YPT11	Rab-type small GTPase that interacts with the C-terminal tail domain of Myo2p; mediates distribution of mitochondria and endoplasmic reticuli to daughter cells	Q
2442	VN_2442	YBR181C	RPS6B	Protein component of the small (40S) ribosomal subunit; identical to Rps6Ap and has similarity to rat S6 ribosomal protein	Q
2443	VN_2443	YPL138C	SPP1	Subunit of COMPASS (Set1C), a complex which methylates histone H3 on lysine 4 and is required in telomeric transcriptional silencing; interacts with Orc2p; PHD finger domain protein similar to human CGBP, an unmethylated CpG binding protein	Q
2444	VN_2444	YIL122W	POG1	Putative transcriptional activator that promotes recovery from pheromone induced arrest; inhibits both alpha-factor induced G1 arrest and repression of CLN1 and CLN2 via SCB/MCB promoter elements; potential Cdc28p substrate; SBF regulated	Q
2445	VN_2445	YJR043C	POL32	Third subunit of DNA polymerase delta, involved in chromosomal DNA replication; required for error-prone DNA synthesis in the presence of DNA damage and processivity; interacts with Hys2p, PCNA (Pol30p), and Pol1p	Q
2446	VN_2446	YNL084C	END3	EH domain-containing protein involved in endocytosis, actin cytoskeletal organization and cell wall morphogenesis; forms a complex with Sla1p and Pan1p	Q
2447	VN_2447	YMR146C	TIF34	eIF3i subunit of the core complex of translation initiation factor 3 (eIF3), which is essential for translation	Q
2448	VN_2448	YNL037C	IDH1	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle	Q
2449	VN_2449	YBR053C	YBR053C	Putative protein of unknown function; induced by cell wall perturbation	Q
2450	VN_2450	YKL098W	MTC2	Protein of unknown function; mtc2 is synthetically sick with cdc13-1	Q
2451	VN_2451	YLR070C	XYL2	Xylitol dehydrogenase, converts xylitol to D-xylulose; expression induced by xylose, even though this pentose sugar is not well utilized by <i>S. cerevisiae</i> ; null mutant has cell wall defect	Q

2452	VN_2452	YBR087W	RFC5	Subunit of heteropentameric Replication factor C (RF-C), which is a DNA binding protein and ATPase that acts as a clamp loader of the proliferating cell nuclear antigen (PCNA) processivity factor for DNA polymerases delta and epsilon	Q
2453	VN_2453	YBL016W	FUS3	Mitogen-activated serine/threonine protein kinase involved in mating; phosphoactivated by Ste7p; substrates include Ste12p, Far1p, Bni1p, Sst2p; inhibits invasive growth during mating by phosphorylating Tec1p, promoting its degradation	Q
2454	VN_2454	YDL226C	GCS1	ADP-ribosylation factor GTPase activating protein (ARF GAP), involved in ER-Golgi transport; shares functional similarity with Glo3p	Q
2455	VN_2455	YJR060W	CBF1	Helix-loop-helix protein that binds the motif CACRTG, which is present at several sites including MET gene promoters and centromere DNA element I (CDEI); required for nucleosome positioning at this motif; targets Isw1p to DNA	Q
2456	VN_2456	YLR270W	DCS1	Non-essential hydrolase involved in mRNA decapping, may function in a feedback mechanism to regulate deadenylation, contains pyrophosphatase activity and a HIT (histidine triad) motif; interacts with neutral trehalase Nth1p	Q
2457	VN_2457	YPR129W	SCD6	Protein containing an Lsm domain, may bind RNA and have a role in RNA processing; overproduction suppresses a null mutation in CHC1, which encodes the heavy chain of clathrin	Q
2458	VN_2458	YNL141W	AAH1	Adenine deaminase (adenine aminohydrolase), converts adenine to hypoxanthine; involved in purine salvage; transcriptionally regulated by nutrient levels and growth phase; Aah1p degraded upon entry into quiescence via SCF and the proteasome	Q
2459	VN_2459	YPL191C	YPL191C	Putative protein of unknown function; diploid deletion strain exhibits high budding index; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2460	VN_2460	YJR147W	HMS2	Protein with similarity to heat shock transcription factors; overexpression suppresses the pseudohyphal filamentation defect of a diploid mep1 mep2 homozygous null mutant	Q
2461	VN_2461	YML119W	YML119W	Putative protein of unknown function; YML119W is not an essential gene; potential Cdc28p substrate	Q
2462	VN_2462	YPR040W	TIP41	Protein that interacts physically and genetically with Tap42p, which regulates protein phosphatase 2A; component of the TOR (target of rapamycin) signaling pathway	Q
2463	VN_2463	YCL034W	LSB5	Protein of unknown function; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization; may mediate disassembly of the Pan1 complex from the endocytic coat	Q
2464	VN_2464	YDR451C	YHP1	One of two homeobox transcriptional repressors (see also Yox1p), that bind to Mcm1p and to early cell cycle box (ECB) elements of cell cycle regulated genes, thereby restricting ECB-mediated transcription to the M/G1 interval	Q
2465	VN_2465	YJL167W	ERG20	Farnesyl pyrophosphate synthetase, has both dimethylallyltransferase and geranyltransferase activities; catalyzes the formation of C15 farnesyl pyrophosphate units for isoprenoid and sterol biosynthesis	Strain failed to verify via PCR
2466	VN_2466	YNL164C	IBD2	Component of the BUB2-dependent spindle checkpoint pathway, interacts with Bfa1p and functions upstream of Bub2p and Bfa1p	Q
2467	VN_2467	YNL264C	PDR17	Phosphatidylinositol transfer protein (PITP), downregulates Plb1p-mediated turnover of phosphatidylcholine, found in the cytosol and microsomes, homologous to Pdr16p, deletion affects phospholipid composition	Q
2468	VN_2468	YBR034C	HMT1	Nuclear SAM-dependent mono- and asymmetric arginine dimethylating methyltransferase that modifies hnRNPs, including Npl3p and Hrp1p, thus facilitating nuclear export of these proteins; also methylates ribosomal protein Rps2p	Q
2469	VN_2469	YDR439W	LRS4	Nucleolar protein that forms a complex with Csm1p, and then Mam1p at kinetochores during meiosis I to mediate accurate homolog segregation; required for condensin recruitment to the replication fork barrier site and rDNA repeat segregation	Q

2470	VN_2470	YOR262W	YOR262W	Protein of unknown function required for establishment of sister chromatid cohesion; contains an ATP/GTP binding site motif; similar to YLR243W and is highly conserved across species and homologous to human gene GPN2/ATPBD1B	Q
2471	VN_2471	YPR075C	OPY2	Integral membrane protein that functions in the signaling branch of the high-osmolarity glycerol (HOG) pathway; interacts with Ste50p; overproduction blocks cell cycle arrest in the presence of mating pheromone	Q
2472	VN_2472	YPL152W	RRD2	Activator of the phosphotyrosyl phosphatase activity of PP2A, peptidyl-prolyl cis/trans-isomerase; regulates G1 phase progression, the osmoresponse, microtubule dynamics; subunit of the Tap42p-Pph21p-Rrd2p complex	Q
2473	VN_2473	YNL187W	SWT21	Protein involved in mRNA splicing; contains a consensus nuclear export signal (NES) sequence similar to the consensus sequence recognized by Crm1p; interacts genetically with Prp40p and Tgs1p; contains WD40 repeats	Q
2474	VN_2474	YBL068W	PRS4	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, synthesizes PRPP, which is required for nucleotide, histidine, and tryptophan biosynthesis; one of five related enzymes, which are active as heteromultimeric complexes	Q
2475	VN_2475	YDL100C	GET3	Guanine nucleotide exchange factor for Gpa1p; amplifies G protein signaling; subunit of the GET complex, which is involved in Golgi to ER trafficking and insertion of proteins into the ER membrane; has low-level ATPase activity	Q
2476	VN_2476	YFR007W	YFH7	Putative kinase with similarity to the phosphoribulokinase/uridine kinase/bacterial pantothenate kinase (PRK/URK/PANK) subfamily of P-loop kinases	Q
2477	VN_2477	YKR070W	YKR070W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2478	VN_2478	YNL231C	PDR16	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p	Q
2479	VN_2479	YNL274C	GOR1	Glyoxylate reductase; null mutation results in increased biomass after diauxic shift; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2480	VN_2480	YGL039W	YGL039W	Oxidoreductase shown to reduce carbonyl compounds to chiral alcohols	Q
2481	VN_2481	YPR180W	AOS1	Nuclear protein that acts as a heterodimer with Uba2p to activate Smt3p (SUMO) before its conjugation to proteins (sumoylation), which may play a role in protein targeting; essential for viability	Q
2482	VN_2482	YDL144C	YDL144C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YDL144C is not an essential gene.	Q
2483	VN_2483	YBR084C-A	RPL19A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl19Bp and has similarity to rat L19 ribosomal protein; rpl19a and rpl19b single null mutations result in slow growth, while the double null mutation is lethal	Q
2484	VN_2484	YNL191W	DUG3	Probable glutamine amidotransferase, forms a complex with Dug1p and Dug2p to degrade glutathione (GSH) and other peptides containing a gamma-glu-X bond in an alternative pathway to GSH degradation by gamma-glutamyl transpeptidase (Ecm38p)	Q
2485	VN_2485	YBL074C	AAR2	Component of the U5 snRNP, required for splicing of U3 precursors; originally described as a splicing factor specifically required for splicing pre-mRNA of the MATa1 cistron	Q
2486	VN_2486	YHR054C	YHR054C	Putative protein of unknown function	Q
2487	VN_2487	YJR068W	RFC2	Subunit of heteropentameric Replication factor C (RF-C), which is a DNA binding protein and ATPase that acts as a clamp loader of the proliferating cell nuclear antigen (PCNA) processivity factor for DNA polymerases delta and epsilon	Q
2488	VN_2488	YNL007C	SIS1	Type II HSP40 co-chaperone that interacts with the HSP70 protein Ssa1p; not functionally redundant with Ydj1p due to substrate	Q

				specificity; shares similarity with bacterial DnaJ proteins	
2489	VN_2489	YHR203C	RPS4B	Protein component of the small (40S) ribosomal subunit; identical to Rps4Ap and has similarity to rat S4 ribosomal protein	Q
2490	VN_2490	YLR426W	YLR426W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; proposed to be involved in resistance to mechlorethamine and streptozotocin	Q
2491	VN_2491	YKR071C	DRE2	Protein that may prevent apoptosis by forming a complex with Tah18p in the absence of stress; required for iron-sulfur cluster assembly and sister chromatid cohesion; homolog of human anti-apoptotic protein Ciapin1	Q
2492	VN_2492	YGL157W	YGL157W	NADPH-dependent aldehyde reductase, utilizes aromatic and alicyclic aldehyde substrates; member of the short-chain dehydrogenase/reductase superfamily	Q
2493	VN_2493	YJR145C	RPS4A	Protein component of the small (40S) ribosomal subunit; mutation affects 20S pre-rRNA processing; identical to Rps4Bp and has similarity to rat S4 ribosomal protein	Strain failed to verify via PCR
2494	VN_2494	YHR069C	RRP4	Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; predicted to contain RNA binding domains; has similarity to human hRrp4p (EXOSC2)	Q
2495	VN_2495	YDL246C	SOR2	Protein of unknown function; protein sequence is 99% identical to the Sor1p sorbitol dehydrogenase; computational analysis of large-scale protein-protein interaction data also suggests a role in fructose or mannose metabolism	Q
2496	VN_2496	YOL064C	MET22	Bisphosphate-3'-nucleotidase, involved in salt tolerance and methionine biogenesis; dephosphorylates 3'-phosphoadenosine-5'-phosphate and 3'-phosphoadenosine-5'-phosphosulfate, intermediates of the sulfate assimilation pathway	Q
2497	VN_2497	YDR173C	ARG82	Inositol polyphosphate multikinase (IPMK), sequentially phosphorylates Ins(1,4,5)P3 to form Ins(1,3,4,5,6)P5; also has diphosphoinositol polyphosphate synthase activity; regulates arginine-, phosphate-, and nitrogen-responsive genes	Q
2498	VN_2498	YNL160W	YGP1	Cell wall-related secretory glycoprotein; induced by nutrient deprivation-associated growth arrest and upon entry into stationary phase; may be involved in adaptation prior to stationary phase entry; has similarity to Sps100p	Q
2499	VN_2499	YKL011C	CCE1	Mitochondrial cruciform cutting endonuclease, cleaves Holliday junctions formed during recombination of mitochondrial DNA	Q
2500	VN_2500	YOL104C	NDJ1	Meiosis-specific telomere protein, required for bouquet formation, effective homolog pairing, ordered cross-over distribution, sister chromatid cohesion at meiotic telomeres, chromosomal segregation and telomere-led rapid prophase movement	Q
2501	VN_2501	YDL065C	PEX19	Chaperone and import receptor for newly-synthesized class I peroxisomal membrane proteins (PMPs), binds PMPs in the cytoplasm and delivers them to the peroxisome for subsequent insertion into the peroxisomal membrane	Q
2502	VN_2502	YLR377C	FBP1	Fructose-1,6-bisphosphatase, key regulatory enzyme in the gluconeogenesis pathway, required for glucose metabolism; undergoes either proteasome-mediated or autophagy-mediated degradation depending on growth conditions; interacts with Vid30p	Q
2503	VN_2503	YJL023C	PET130	Protein required for respiratory growth; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2504	VN_2504	YCL032W	STE50	Protein involved in mating response, invasive/filamentous growth, and osmotolerance, acts as an adaptor that links G protein-associated Cdc42p-Ste20p complex to the effector Ste11p to modulate signal transduction	Q
2505	VN_2505	YGR101W	PCP1	Mitochondrial serine protease required for the processing of various mitochondrial proteins and maintenance of mitochondrial DNA and morphology; belongs to the rhomboid-GlpG superfamily of intramembrane peptidases	Q

2506	VN_2506	YDR372C	VPS74	Protein required for Golgi localization of glycosyltransferases; binds the cytosolic domains of Golgi glycosyltransferases; functions as a heterotetramer	Q
2507	VN_2507	YBR149W	ARA1	NADP ⁺ dependent arabinose dehydrogenase, involved in carbohydrate metabolism; purified as homodimer; naturally occurs with a N-terminus degradation product	Q
2508	VN_2508	YPL118W	MRP51	Mitochondrial ribosomal protein of the small subunit; MRP51 exhibits genetic interactions with mutations in the COX2 and COX3 mRNA 5'-untranslated leader sequences	Q
2509	VN_2509	YEL004W	YEA4	Uridine diphosphate-N-acetylglucosamine (UDP-GlcNAc) transporter required for cell wall chitin synthesis; localized to the ER	Q
2510	VN_2510	YNR035C	ARC35	Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches; required for cortical localization of calmodulin	Q
2511	VN_2511	YHR210C	YHR210C	Putative protein of unknown function; non-essential gene; highly expressed under anaerobic conditions; sequence similarity to aldose 1-epimerases such as GAL10	Strain failed to verify via PCR
2512	VN_2512	YDL244W	THI13	Protein involved in synthesis of the thiamine precursor hydroxymethylpyrimidine (HMP); member of a subtelomeric gene family including THI5, THI11, THI12, and THI13	Q
2513	VN_2513	YNL290W	RFC3	Subunit of heteropentameric Replication factor C (RF-C), which is a DNA binding protein and ATPase that acts as a clamp loader of the proliferating cell nuclear antigen (PCNA) processivity factor for DNA polymerases delta and epsilon	Q
2514	VN_2514	YOR061W	CKA2	Alpha' catalytic subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation; the holoenzyme also contains CKA1, CKB1 and CKB2, the many substrates include transcription factors and all RNA polymerases	Q
2515	VN_2515	YKL193C	SDS22	Conserved nuclear regulatory subunit of Glc7p type 1 protein serine-threonine phosphatase (PP1), functions positively with Glc7p to promote dephosphorylation of nuclear substrates required for chromosome transmission during mitosis	Q
2516	VN_2516	YEL017W	GTT3	Protein of unknown function with a possible role in glutathione metabolism, as suggested by computational analysis of large-scale protein-protein interaction data; GFP-fusion protein localizes to the nuclear periphery	Q
2517	VN_2517	YIL019W	FAF1	Protein required for pre-rRNA processing and 40S ribosomal subunit assembly	Q
2518	VN_2518	YGL138C	YGL138C	Putative protein of unknown function; has no significant sequence similarity to any known protein	Q
2519	VN_2519	YDL175C	AIR2	Zinc knuckle protein, involved in nuclear RNA processing and degradation as a component of the TRAMP complex; stimulates the poly(A) polymerase activity of Pap2p in vitro; functionally redundant with Air1p	Q
2520	VN_2520	YPR004C	AIM45	Protein with similarity to mammalian electron transfer flavoprotein complex subunit ETF-alpha; interacts with frataxin, Yfh1p; null mutant displays elevated frequency of mitochondrial genome loss	Q
2521	VN_2521	YGL040C	HEM2	Aminolevulinatase dehydratase, a homo-octameric enzyme, catalyzes the conversion of 5-aminolevulinatase to porphobilinogen, the second step in heme biosynthesis; enzymatic activity is zinc-dependent; localizes to the cytoplasm and nucleus	Q
2522	VN_2522	YNR071C	YNR071C	Putative protein of unknown function	Q
2523	VN_2523	YKL164C	PIR1	O-glycosylated protein required for cell wall stability; attached to the cell wall via beta-1,3-glucan; mediates mitochondrial translocation of Apn1p; expression regulated by the cell integrity pathway and by Swi5p during the cell cycle	Q
2524	VN_2524	YFL058W	THI5	Protein involved in synthesis of the thiamine precursor hydroxymethylpyrimidine (HMP); member of a subtelomeric gene family including THI5, THI11, THI12, and THI13	Q
2525	VN_2525	YNL332W	THI12	Protein involved in synthesis of the thiamine precursor hydroxymethylpyrimidine (HMP); member of a subtelomeric gene family including THI5, THI11, THI12, and THI13	Q

2526	VN_2526	YPL031C	PHO85	Cyclin-dependent kinase, with ten cyclin partners; involved in regulating the cellular response to nutrient levels and environmental conditions and progression through the cell cycle	Q
2527	VN_2527	YMR081C	ISF1	Serine-rich, hydrophilic protein with similarity to Mbr1p; overexpression suppresses growth defects of hap2, hap3, and hap4 mutants; expression is under glucose control; cotranscribed with NAM7 in a cyp1 mutant	Q
2528	VN_2528	YJL116C	NCA3	Protein that functions with Nca2p to regulate mitochondrial expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase; member of the SUN family; expression induced in cells treated with the mycotoxin patulin	Q
2529	VN_2529	YIL154C	IMP2'	Transcriptional activator involved in maintenance of ion homeostasis and protection against DNA damage caused by bleomycin and other oxidants, contains a C-terminal leucine-rich repeat	Q
2530	VN_2530	YGL175C	SAE2	Endonuclease that processes hairpin DNA structures with the MRX complex; involved in meiotic and mitotic double-strand break repair; phosphorylated in response to DNA damage and required for normal resistance to DNA-damaging agents	Q
2531	VN_2531	YDR541C	YDR541C	Putative dihydrokaempferol 4-reductase	Q
2532	VN_2532	YDL078C	MDH3	Peroxisomal malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the glyoxylate cycle	Q
2533	VN_2533	YGR031W	YGR031W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Strain failed to verify via PCR
2534	VN_2534	YOL151W	GRE2	3-methylbutanal reductase and NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway	Q
2535	VN_2535	YMR228W	MTF1	Mitochondrial RNA polymerase specificity factor with structural similarity to S-adenosylmethionine-dependent methyltransferases and functional similarity to bacterial sigma-factors, interacts with mitochondrial core polymerase Rpo41p	Strain failed to verify via PCR
2536	VN_2536	YFR055W	IRC7	Putative cystathionine beta-lyase; involved in copper ion homeostasis and sulfur metabolism; null mutant displays increased levels of spontaneous Rad52p foci; expression induced by nitrogen limitation in a GLN3, GAT1-dependent manner	Q
2537	VN_2537	YBR076W	ECM8	Non-essential protein of unknown function	Q
2538	VN_2538	YBL031W	SHE1	Mitotic spindle protein that interacts with components of the Dam1 (DASH) complex, its effector Sli15p, and microtubule-associated protein Bim1p; also localizes to nuclear microtubules and to the bud neck in a ring-shaped structure	Strain failed to verify via PCR
2539	VN_2539	YMR127C	SAS2	Histone acetyltransferase (HAT) catalytic subunit of the SAS complex (Sas2p-Sas4p-Sas5p), which acetylates free histones and nucleosomes and regulates transcriptional silencing; member of the MYSTacetyltransferase family	Q
2540	VN_2540	YKL151C	YKL151C	Putative protein of unknown function; YKL151C promoter contains STREs (stress response elements) and expression is induced by heat shock or methyl methanesulfonate; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2541	VN_2541	YJR154W	YJR154W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2542	VN_2542	YGR165W	MRPS35	Mitochondrial ribosomal protein of the small subunit	Q
2543	VN_2543	YER016W	BIM1	Microtubule-binding protein that together with Kar9p makes up the cortical microtubule capture site and delays the exit from mitosis when the spindle is oriented abnormally	Q
2544	VN_2544	YIR029W	DAL2	Allantoicase, converts allantoate to urea and ureidoglycolate in the second step of allantoin degradation; expression sensitive to nitrogen catabolite repression and induced by allophanate, an intermediate in allantoin degradation	Q
2545	VN_2545	YHR106W	TRR2	Mitochondrial thioredoxin reductase involved in protection against oxidative stress, required with Glr1p to maintain the redox state of	Q

				Trx3p; contains active-site motif (CAVC) present in prokaryotic orthologs; binds NADPH and FAD	
2546	VN_2546	YPL088W	YPL088W	Putative aryl alcohol dehydrogenase; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance	Q
2547	VN_2547	YOL007C	CSI2	Protein of unknown function; green fluorescent protein (GFP)- fusion protein localizes to the mother side of the bud neck and the vacuole; YOL007C is not an essential gene	Q
2548	VN_2548	YHR156C	LIN1	Non-essential component of U5 snRNP; nuclear protein; physically interacts with Irr1p of cohesin complex; may link together proteins involved in chromosome segregation, mRNA splicing and DNA replication	Q
2549	VN_2549	YDL209C	CWC2	Member of the NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 snRNAs; binds directly to U6 snRNA; similar to <i>S. pombe</i> Cwf2	Q
2550	VN_2550	YBR050C	REG2	Regulatory subunit of the Glc7p type-1 protein phosphatase; involved with Reg1p, Glc7p, and Snf1p in regulation of glucose-repressible genes, also involved in glucose-induced proteolysis of maltose permease	Q
2551	VN_2551	YOR261C	RPN8	Essential, non-ATPase regulatory subunit of the 26S proteasome; has similarity to the human p40 proteasomal subunit and to another <i>S. cerevisiae</i> regulatory subunit, Rpn11p	Q
2552	VN_2552	YLR017W	MEU1	Methylthioadenosine phosphorylase (MTAP), catalyzes the initial step in the methionine salvage pathway; affects polyamine biosynthesis through regulation of ornithine decarboxylase (Spe1p) activity; regulates ADH2 gene expression	Q
2553	VN_2553	YML015C	TAF11	TFIID subunit (40 kDa), involved in RNA polymerase II transcription initiation, similar to histone H3 with atypical histone fold motif of Spt3-like transcription factors	Q
2554	VN_2554	YGR180C	RNR4	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits	Q
2555	VN_2555	YHR034C	PIH1	Protein of unresolved function; may function in protein folding and/or rRNA processing, interacts with a chaperone (Hsp82p), two chromatin remodeling factors (Rvb1p, Rvb2p) and two rRNA processing factors (Rrp43p, Nop58p)	Q
2556	VN_2556	YLR375W	STP3	Zinc-finger protein of unknown function, possibly involved in pre-tRNA splicing and in uptake of branched-chain amino acids	Q
2557	VN_2557	YJR142W	YJR142W	Putative protein of unknown function; GST fusion protein is a Dbf2-Mob1 phosphorylation target in a proteome chip analysis; synthetic lethal with PH085 deletion; plays a role in restricting Ty1 transposition	Q
2558	VN_2558	YDL099W	BUG1	Cis-golgi localized protein involved in ER to Golgi transport; forms a complex with the mammalian GRASP65 homolog, Grh1p; mutants are compromised for the fusion of ER-derived vesicles with Golgi membranes	Q
2559	VN_2559	YOR026W	BUB3	Kinetochore checkpoint WD40 repeat protein that localizes to kinetochores during prophase and metaphase, delays anaphase in the presence of unattached kinetochores; forms complexes with Mad1p-Bub1p and with Cdc20p, binds Mad2p and Mad3p	Q
2560	VN_2560	YJR105W	ADO1	Adenosine kinase, required for the utilization of S-adenosylmethionine (AdoMet); may be involved in recycling adenosine produced through the methyl cycle	Q
2561	VN_2561	YGR084C	MRP13	Mitochondrial ribosomal protein of the small subunit	Q
2562	VN_2562	YDR077W	SED1	Major stress-induced structural GPI-cell wall glycoprotein in stationary-phase cells, associates with translating ribosomes, possible role in mitochondrial genome maintenance; ORF contains two distinct variable minisatellites	Q
2563	VN_2563	YOR313C	SPS4	Protein whose expression is induced during sporulation; not required for sporulation; heterologous expression in <i>E. coli</i> induces the SOS response that senses DNA damage	Q

2564	VN_2564	YIL096C	YIL096C	Putative protein of unknown function; associates with precursors of the 60S ribosomal subunit; predicted to be involved in ribosome biogenesis	Q
2565	VN_2565	YOR007C	SGT2	Glutamine-rich cytoplasmic protein of unknown function; contains tetratricopeptide (TPR) repeats, which often mediate protein-protein interactions; has similarity to human SGT, which is a cochaperone that negatively regulates Hsp70	Q
2566	VN_2566	YIL145C	PAN6	Pantothenate synthase, also known as pantoate-beta-alanine ligase, required for pantothenic acid biosynthesis, deletion causes pantothenic acid auxotrophy, homologous to E. coli panC	Q
2567	VN_2567	YJR079W	YJR079W	Putative protein of unknown function; mutation results in impaired mitochondrial respiration	Q
2568	VN_2568	YMR101C	SRT1	Cis-prenyltransferase involved in synthesis of long-chain dolichols (19-22 isoprene units; as opposed to Rer2p which synthesizes shorter-chain dolichols); localizes to lipid bodies; transcription is induced during stationary phase	Q
2569	VN_2569	YLR265C	NEJ1	Protein involved in regulation of nonhomologous end joining; interacts with DNA ligase IV components Dnl4p and Lif1p; repressed by MAT heterozygosity; regulates cellular distribution of Lif1p	Q
2570	VN_2570	YDR411C	DFM1	ER localized derlin-like family member involved in ER stress and homeostasis; not involved in ERAD or substrate retrotranslocation; interacts with CDC48; contains four transmembrane domains and two SHP boxes	Q
2571	VN_2571	YPL004C	LSP1	Primary component of eisosomes, which are large immobile patch structures at the cell cortex associated with endocytosis, along with Pil1p and Sur7p; null mutants show activation of Pkc1p/Ypk1p stress resistance pathways	Q
2572	VN_2572	YJR156C	THI11	Protein involved in synthesis of the thiamine precursor hydroxymethylpyrimidine (HMP); member of a subtelomeric gene family including THI5, THI11, THI12, and THI13	Q
2573	VN_2573	YGR086C	PIL1	Primary component of eisosomes, which are large immobile cell cortex structures associated with endocytosis; null mutants show activation of Pkc1p/Ypk1p stress resistance pathways; detected in phosphorylated state in mitochondria	Strain failed to verify via PCR
2574	VN_2574	YER156C	YER156C	Putative protein of unknown function; interacts with Hsp82p and copurifies with Ipl1p; expression is copper responsive and downregulated in strains deleted for MAC1, a copper-responsive transcription factor; similarity to mammalian MYG1	Q
2575	VN_2575	YPR056W	TFB4	Subunit of TFIIF complex, involved in transcription initiation, similar to 34 kDa subunit of human TFIIF; interacts with Ssl1p	Q
2576	VN_2576	YLR007W	NSE1	Essential subunit of the Mms21-Smc5-Smc6 complex; nuclear protein required for DNA repair and growth; has a nonstructural role in the maintenance of chromosomes	Q
2577	VN_2577	YOR315W	SFG1	Nuclear protein, putative transcription factor required for growth of superficial pseudohyphae (which do not invade the agar substrate) but not for invasive pseudohyphal growth; may act together with Phd1p; potential Cdc28p substrate	Q
2578	VN_2578	YPR086W	SUA7	Transcription factor TFIIB, a general transcription factor required for transcription initiation and start site selection by RNA polymerase II	Q
2579	VN_2579	YKR081C	RPF2	Essential protein involved in the processing of pre-rRNA and the assembly of the 60S ribosomal subunit; interacts with ribosomal protein L11; localizes predominantly to the nucleolus; constituent of 66S pre-ribosomal particles	Q
2580	VN_2580	YOR352W	YOR352W	Putative protein of unknown function; expression levels regulated by Arg5,6p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	Q
2581	VN_2581	YMR126C	DLT1	Protein of unknown function, mutant sensitive to 6-azauracil (6AU) and mycophenolic acid (MPA)	Q
2582	VN_2582	YGR163W	GTR2	Putative GTP binding protein that negatively regulates Ran/Tc4 GTPase cycle; activates transcription; subunit of EGO and GSE complexes; required for sorting of Gap1p; localizes to cytoplasm and to chromatin; homolog of human RagC and RagD	Q
2583	VN_2583	YPR057W	BRR1	snRNP protein component of spliceosomal snRNPs, required for pre-	Q

				mRNA splicing and snRNP biogenesis; in null mutant newly-synthesized snRNAs are destabilized and 3'-end processing is slowed	
2584	VN_2584	YLR151C	PCD1	Peroxisomal nudix pyrophosphatase with specificity for coenzyme A and CoA derivatives, may function to remove potentially toxic oxidized CoA disulfide from peroxisomes to maintain the capacity for beta-oxidation of fatty acids	Q
2585	VN_2585	YJR129C	YJR129C	Putative protein of unknown function; predicted S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2586	VN_2586	YJL088W	ARG3	Ornithine carbamoyltransferase (carbamoylphosphate:L-ornithine carbamoyltransferase), catalyzes the sixth step in the biosynthesis of the arginine precursor ornithine	Q
2587	VN_2587	YBR141C	YBR141C	Putative S-adenosylmethionine-dependent methyltransferase; green fluorescent protein (GFP)-fusion protein localizes to the nucleolus; YBR141C is not an essential gene	Q
2588	VN_2588	YMR316W	DIA1	Protein of unknown function, involved in invasive and pseudohyphal growth; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Q
2589	VN_2589	YBL033C	RIB1	GTP cyclohydrolase II; catalyzes the first step of the riboflavin biosynthesis pathway	Q
2590	VN_2590	YPR127W	YPR127W	Protein of unknown function, differentially expressed during alcoholic fermentation; expression activated by transcription factor YRM1/YOR172W; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
2591	VN_2591	YLR097C	HRT3	Putative SCF-ubiquitin ligase F-box protein, based on both genetic and physical interactions and sequence similarity; identified in association with Cdc53p, Skp1p and Ubi4 in large and small-scale studies	Q
2592	VN_2592	YIL106W	MOB1	Component of the mitotic exit network; associates with and is required for the activation and Cdc15p-dependent phosphorylation of the Dbf2p kinase; required for cytokinesis and cell separation; component of the CCR4 transcriptional complex	Strain failed to verify via PCR
2593	VN_2593	YMR144W	YMR144W	Putative protein of unknown function; localized to the nucleus; YMR144W is not an essential gene	Q
2594	VN_2594	YGR283C	YGR283C	Protein of unknown function; may interact with ribosomes, based on co-purification experiments; predicted to be involved in ribosome biogenesis; null mutant is resistant to fluconazole; GFP-fusion protein localizes to the nucleolus	Q
2595	VN_2595	YJR021C	REC107	Protein involved in early stages of meiotic recombination; involved in coordination between the initiation of recombination and the first division of meiosis; part of a complex (Rec107p-Mei4p-Rec114p) required for ds break formation	Q
2596	VN_2596	YML037C	YML037C	Putative protein of unknown function with some characteristics of a transcriptional activator; may be a target of Dbf2p-Mob1p kinase; GFP-fusion protein co-localizes with clathrin-coated vesicles; YML037C is not an essential gene	Q
2597	VN_2597	YKL093W	MBR1	Protein involved in mitochondrial functions and stress response; overexpression suppresses growth defects of hap2, hap3, and hap4 mutants	Q
2598	VN_2598	YJR008W	YJR008W	Putative protein of unknown function; expression repressed by inosine and choline in an Opi1p-dependent manner; expression induced by mild heat-stress on a non-fermentable carbon source.	Q
2599	VN_2599	YDR392W	SPT3	Subunit of the SAGA and SAGA-like transcriptional regulatory complexes, interacts with Spt15p to activate transcription of some RNA polymerase II-dependent genes, also functions to inhibit transcription at some promoters	Q
2600	VN_2600	YCL055W	KAR4	Transcription factor required for gene regulation in response to pheromones; also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone	Q
2601	VN_2601	YDL230W	PTP1	Phosphotyrosine-specific protein phosphatase that dephosphorylates a broad range of substrates in vivo, including Fpr3p; localized to the cytoplasm and the mitochondria	Q

2602	VN_2602	YPL069C	BTS1	Geranylgeranyl diphosphate synthase, increases the intracellular pool of geranylgeranyl diphosphate, suppressor of bet2 mutation that causes defective geranylgeranylation of small GTP-binding proteins that mediate vesicular traffic	Q
2603	VN_2603	YDL108W	KIN28	Serine/threonine protein kinase, subunit of the transcription factor TFIIH; involved in transcription initiation at RNA polymerase II promoters	Strain failed to verify via PCR
2604	VN_2604	YGR192C	TDH3	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell wall	Q
2605	VN_2605	YHL009C	YAP3	Basic leucine zipper (bZIP) transcription factor	Q
2606	VN_2606	YDR435C	PPM1	Carboxyl methyltransferase, methylates the C terminus of the protein phosphatase 2A catalytic subunit (Pph21p or Pph22p), which is important for complex formation with regulatory subunits	Strain failed to verify via PCR
2607	VN_2607	YBR048W	RPS11B	Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and has similarity to E. coli S17 and rat S11 ribosomal proteins	Q
2608	VN_2608	YOR340C	RPA43	RNA polymerase I subunit A43	Q
2609	VN_2609	YKL163W	PIR3	O-glycosylated covalently-bound cell wall protein required for cell wall stability; expression is cell cycle regulated, peaking in M/G1 and also subject to regulation by the cell integrity pathway	Q
2610	VN_2610	YDR480W	DIG2	Regulatory protein of unknown function, pheromone-inducible, involved in the regulation of mating-specific genes and the invasive growth pathway, required for MAP-kinase imposed repression, inhibits pheromone-responsive transcription	Q
2611	VN_2611	YDR204W	COQ4	Protein with a role in ubiquinone (Coenzyme Q) biosynthesis, possibly functioning in stabilization of Coq7p; located on the matrix face of the mitochondrial inner membrane; component of a mitochondrial ubiquinone-synthesizing complex	Strain failed to verify via PCR
2612	VN_2612	YPR110C	RPC40	RNA polymerase subunit, common to RNA polymerase I and III	Q
2613	VN_2613	YER161C	SPT2	Protein involved in negative regulation of transcription; required for RNA polyadenylation; exhibits regulated interactions with both histones and SWI-SNF components, has similarity to mammalian HMG1 proteins	Q
2614	VN_2614	YHL025W	SNF6	Subunit of the SWI/SNF chromatin remodeling complex involved in transcriptional regulation; functions interdependently in transcriptional activation with Snf2p and Snf5p	Q
2615	VN_2615	YLR181C	VT A1	Multivesicular body (MVB) protein involved in endosomal protein sorting; regulates Vps4p activity by promoting its oligomerization; has an N-terminal Vps60- and Did2- binding domain, a linker region, and a C-terminal Vps4p binding domain	Q
2616	VN_2616	YKR013W	PRY2	Protein of unknown function	Q
2617	VN_2617	YGL091C	NBP35	Essential iron-sulfur cluster binding protein localized in the cytoplasm; forms a complex with Cfd1p that is involved in iron-sulfur protein assembly in the cytosol; similar to P-loop NTPases	Q
2618	VN_2618	YDL205C	HEM3	Porphobilinogen deaminase, catalyzes the conversion of 4-porphobilinogen to hydroxymethylbilane, the third step in heme biosynthesis; localizes to the cytoplasm and nucleus; expression is regulated by Hap2p-Hap3p, but not by levels of heme	Strain failed to verify via PCR
2619	VN_2619	YDR058C	TGL2	Protein with lipolytic activity towards triacylglycerols and diacylglycerols when expressed in E. coli; role in yeast lipid degradation is unclear	Q
2620	VN_2620	YDR151C	CTH1	Member of the CCCH zinc finger family; has similarity to mammalian Tis11 protein, which activates transcription and also has a role in mRNA degradation; may function with Tis11p in iron homeostasis	Q
2621	VN_2621	YPL273W	SAM4	S-adenosylmethionine-homocysteine methyltransferase, functions along with Mht1p in the conversion of S-adenosylmethionine (AdoMet) to methionine to control the methionine/AdoMet ratio	Q
2622	VN_2622	YGR007W	MUQ1	Choline phosphate cytidyltransferase, catalyzes the second step of	Q

				phosphatidylethanolamine biosynthesis; involved in the maintenance of plasma membrane; similar to mammalian CTP: phosphocholine cytidyl-yl-transferases	
2623	VN_2623	YFR025C	HIS2	Histidinolphosphatase, catalyzes the eighth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; transcription is regulated by general amino acid control	Q
2624	VN_2624	YBR046C	ZTA1	NADPH-dependent quinone reductase, GFP-tagged protein localizes to the cytoplasm and nucleus; has similarity to E. coli quinone oxidoreductase and to human zeta-crystallin	Q
2625	VN_2625	YGR043C	NQM1	Transaldolase of unknown function; transcription is repressed by Mot1p and induced by alpha-factor and during diauxic shift	Q
2626	VN_2626	YJL052W	TDH1	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell wall	Q
2627	VN_2627	YNL097C	PHO23	Probable component of the Rpd3 histone deacetylase complex, involved in transcriptional regulation of PHO5; C-terminus has similarity to human candidate tumor suppressor p33(ING1) and its isoform ING3	Q
2628	VN_2628	YOR142W	LSC1	Alpha subunit of succinyl-CoA ligase, which is a mitochondrial enzyme of the TCA cycle that catalyzes the nucleotide-dependent conversion of succinyl-CoA to succinate; phosphorylated	Q
2629	VN_2629	YGR015C	YGR015C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion	Q
2630	VN_2630	YHR104W	GRE3	Aldose reductase involved in methylglyoxal, d-xylose, arabinose, and galactose metabolism; stress induced (osmotic, ionic, oxidative, heat shock, starvation and heavy metals); regulated by the HOG pathway	Q
2631	VN_2631	YGR144W	THI4	Thiazole synthase, catalyzes formation of a thiazole intermediate during thiamine biosynthesis; required for mitochondrial genome stability in response to DNA damaging agents	Q
2632	VN_2632	YDR530C	APA2	Diadenosine 5',5'-P1,P4-tetraphosphate phosphorylase II (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa1p	Q
2633	VN_2633	YPR176C	BET2	Beta subunit of Type II geranylgeranyltransferase required for vesicular transport between the endoplasmic reticulum and the Golgi; provides a membrane attachment moiety to Rab-like proteins Ypt1p and Sec4p	Q
2634	VN_2634	YHR010W	RPL27A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Bp and has similarity to rat L27 ribosomal protein	Q
2635	VN_2635	YGR058W	PEF1	Penta-EF-hand protein required for polar bud growth and cell wall abscission; binds calcium and zinc with different affinity; localizes to bud site in G1, bud neck in G2	Q
2636	VN_2636	YDR051C	DET1	Acid phosphatase involved in the non-vesicular transport of sterols in both directions between the endoplasmic reticulum and plasma membrane; deletion confers sensitivity to nickel	Q
2637	VN_2637	YMR142C	RPL13B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl13Ap; not essential for viability; has similarity to rat L13 ribosomal protein	Q
2638	VN_2638	YJR009C	TDH2	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell wall	Strain failed to verify via PCR
2639	VN_2639	YNL301C	RPL18B	Protein component of the large (60S) ribosomal subunit, identical to Rpl18Ap and has similarity to rat L18 ribosomal protein	Q
2640	VN_2640	YJR107W	YJR107W	Putative protein of unknown function; has sequence or structural similarity to lipases	Q
2641	VN_2641	YIL063C	YRB2	Protein of unknown function involved in nuclear processes of the Ran-GTPase cycle; involved in nuclear protein export; contains Ran Binding Domain and FxFG repeats; interacts with Srm1p, GTP-Gsp1p, Rna1p and Crm1p; is not essential	Q
2642	VN_2642	YHR139C	SPS100	Protein required for spore wall maturation; expressed during sporulation; may be a component of the spore wall; expression also	Q

				induced in cells treated with the mycotoxin patulin	
2643	VN_2643	YFL034C-B	MOB2	Component of the RAM signaling network, that activates the Cbk1p kinase, thereby facilitating the Ace2p-dependent daughter cell-specific transcription of genes involved in cell separation; similar to Mob1p	Q
2644	VN_2644	YMR143W	RPS16A	Protein component of the small (40S) ribosomal subunit; identical to Rps16Bp and has similarity to E. coli S9 and rat S16 ribosomal proteins	Q
2645	VN_2645	YJL006C	CTK2	Beta subunit of C-terminal domain kinase I (CTDK-I), which phosphorylates both RNA pol II subunit Rpo21p to affect transcription and pre-mRNA 3' end processing, and ribosomal protein Rps2p to increase translational fidelity	Q
2646	VN_2646	YHR085W	IPI1	Essential component of the Rix1 complex (with Rix1p and Ipi3p) that is required for processing of ITS2 sequences from 35S pre-rRNA; Rix1 complex associates with Mdn1p in pre-60S ribosomal particles	Q
2647	VN_2647	YNL265C	IST1	Protein with a positive role in the multivesicular body sorting pathway; functions and forms a complex with Did2p; recruitment to endosomes is mediated by the Vps2p-Vps24p subcomplex of ESCRT-III; also interacts with Vps4p	Q
2648	VN_2648	YPL055C	LGE1	Protein of unknown function; null mutant forms abnormally large cells, and homozygous diploid null mutant displays delayed premeiotic DNA synthesis and reduced efficiency of meiotic nuclear division	Strain failed to verify via PCR
2649	VN_2649	YOR246C	YOR246C	Protein with similarity to oxidoreductases, found in lipid particles; required for replication of Brome mosaic virus in S. cerevisiae, which is a model system for studying replication of positive-strand RNA viruses in their natural hosts	Q
2650	VN_2650	YBR129C	OPY1	Protein of unknown function, overproduction blocks cell cycle arrest in the presence of mating pheromone; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2651	VN_2651	YKR062W	TFA2	TFIIE small subunit, involved in RNA polymerase II transcription initiation	Q
2652	VN_2652	YIL084C	SDS3	Component of the Rpd3p/Sin3p deacetylase complex required for its structural integrity and catalytic activity, involved in transcriptional silencing and required for sporulation; cells defective in SDS3 display pleiotropic phenotypes	Q
2653	VN_2653	YIL041W	GVP36	BAR domain-containing protein that localizes to both early and late Golgi vesicles; required for adaptation to varying nutrient concentrations, fluid-phase endocytosis, polarization of the actin cytoskeleton, and vacuole biogenesis	Q
2654	VN_2654	YHR143W	DSE2	Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother; expression is repressed by cAMP	Q
2655	VN_2655	YBR211C	AME1	Essential kinetochore protein associated with microtubules and spindle pole bodies; component of the kinetochore sub-complex COMA (Ctf19p, Okp1p, Mcm21p, Ame1p); involved in spindle checkpoint maintenance	Q
2656	VN_2656	YNL025C	SSN8	Cyclin-like component of the RNA polymerase II holoenzyme, involved in phosphorylation of the RNA polymerase II C-terminal domain; involved in glucose repression and telomere maintenance	Q
2657	VN_2657	YLR354C	TAL1	Transaldolase, enzyme in the non-oxidative pentose phosphate pathway; converts sedoheptulose 7-phosphate and glyceraldehyde 3-phosphate to erythrose 4-phosphate and fructose 6-phosphate	Q
2658	VN_2658	YKL085W	MDH1	Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; phosphorylated	Q
2659	VN_2659	YPL111W	CAR1	Arginase, responsible for arginine degradation, expression responds to both induction by arginine and nitrogen catabolite repression; disruption enhances freeze tolerance	Q
2660	VN_2660	YJL213W	YJL213W	Protein of unknown function that may interact with ribosomes; periodically expressed during the yeast metabolic cycle; phosphorylated in vitro by the mitotic exit network (MEN) kinase complex, Dbf2p/Mob1p	Q

2661	VN_2661	YDL243C	AAD4	Putative aryl-alcohol dehydrogenase with similarity to <i>P. chrysosporium</i> aryl-alcohol dehydrogenase, involved in the oxidative stress response; expression induced in cells treated with the mycotoxin patulin	Q
2662	VN_2662	YDL037C	BSC1	Protein of unconfirmed function, similar to cell surface flocculin Muc1p; ORF exhibits genomic organization compatible with a translational readthrough-dependent mode of expression	Q
2663	VN_2663	YJR093C	FIP1	Subunit of cleavage polyadenylation factor (CPF), interacts directly with poly(A) polymerase (Pap1p) to regulate its activity	Q
2664	VN_2664	YKL218C	SRY1	3-hydroxyaspartate dehydratase, deaminates L-threo-3-hydroxyaspartate to form oxaloacetate and ammonia; required in the presence of hydroxyaspartate; highly similar to mouse serine racemase (Srr) but has no serine racemase activity	Q
2665	VN_2665	YJL017W	YJL017W, YJL016W	#N/A	Q
2666	VN_2666	YDR124W	YDR124W	Putative protein of unknown function; non-essential gene; expression is strongly induced by alpha factor	Strain failed to verify via PCR
2667	VN_2667	YOL094C	RFC4	Subunit of heteropentameric Replication factor C (RF-C), which is a DNA binding protein and ATPase that acts as a clamp loader of the proliferating cell nuclear antigen (PCNA) processivity factor for DNA polymerases delta and epsilon	Strain failed to verify via PCR
2668	VN_2668	YMR041C	ARA2	NAD-dependent arabinose dehydrogenase, involved in biosynthesis of dehydro-D-arabinono-1,4-lactone; similar to plant L-galactose dehydrogenase	Q
2669	VN_2669	YAL020C	ATS1	Protein required, with Elongator complex, Kti11p, and Kti12p, for modification of wobble nucleosides in tRNA; has a potential role in regulatory interactions between microtubules and the cell cycle	Q
2670	VN_2670	YBR189W	RPS9B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Ap and has similarity to <i>E. coli</i> S4 and rat S9 ribosomal proteins	Q
2671	VN_2671	YHR083W	SAM35	Essential component of the sorting and assembly machinery (SAM complex or TOB complex) of the mitochondrial outer membrane, which binds precursors of beta-barrel proteins and facilitates their insertion into the outer membrane	Q
2672	VN_2672	YDL057W	YDL057W	Putative protein of unknown function; YDL057W is not an essential gene	Q
2673	VN_2673	YBR119W	MUD1	U1 snRNP A protein, homolog of human U1-A; involved in nuclear mRNA splicing	Q
2674	VN_2674	YJR100C	AIM25	Putative protein of unknown function; non-tagged protein is detected in purified mitochondria in high-throughput studies; similar to murine NOR1; null mutant is viable and displays elevated frequency of mitochondrial genome loss	Q
2675	VN_2675	YML004C	GLO1	Monomeric glyoxalase I, catalyzes the detoxification of methylglyoxal (a by-product of glycolysis) via condensation with glutathione to produce S-D-lactoylglutathione; expression regulated by methylglyoxal levels and osmotic stress	Q
2676	VN_2676	YJL180C	ATP12	Conserved protein required for assembly of alpha and beta subunits into the F1 sector of mitochondrial F1F0 ATP synthase; mutation of human ATP12 reduces active ATP synthase levels and is associated with the disorder ATPAF2 deficiency	Q
2677	VN_2677	YLL062C	MHT1	S-methylmethionine-homocysteine methyltransferase, functions along with Sam4p in the conversion of S-adenosylmethionine (AdoMet) to methionine to control the methionine/AdoMet ratio	Q
2678	VN_2678	YER014C-A	BUD25	Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern	Strain failed to verify via PCR
2679	VN_2679	YCR036W	RBK1	Putative ribokinase	Q
2680	VN_2680	YGR080W	TWF1	Twinfilin, highly conserved actin monomer-sequestering protein involved in regulation of the cortical actin cytoskeleton, composed of two cofilin-like regions, localizes actin monomers to sites of rapid filament assembly	Q

2681	VN_2681	YDR267C	CIA1	WD40 repeat protein involved in assembly of cytosolic and nuclear iron-sulfur proteins; similar to the human Ciao1 protein; YDR267C is an essential gene	Q
2682	VN_2682	YJL208C	NUC1	Major mitochondrial nuclease, has RNase and DNA endo- and exonucleolytic activities; has roles in mitochondrial recombination, apoptosis and maintenance of polyploidy	Q
2683	VN_2683	YDR044W	HEM13	Coproporphyrinogen III oxidase, an oxygen requiring enzyme that catalyzes the sixth step in the heme biosynthetic pathway; transcription is repressed by oxygen and heme (via Rox1p and Hap1p)	Q
2684	VN_2684	YNL302C	RPS19B	Protein component of the small (40S) ribosomal subunit, required for assembly and maturation of pre-40 S particles; mutations in human RPS19 are associated with Diamond Blackfan anemia; nearly identical to Rps19Ap	Strain failed to verify via PCR
2685	VN_2685	YNR062C	YNR062C	Putative membrane protein of unknown function	Q
2686	VN_2686	YNL217W	YNL217W	Hypothetical protein	Q
2687	VN_2687	YJR070C	LIA1	Deoxyhypusine hydroxylase, a HEAT-repeat containing metalloenzyme that catalyzes hypusine formation; binds to and is required for the modification of Hyp2p (eIF5A); complements <i>S. pombe</i> mmd1 mutants defective in mitochondrial positioning	Q
2688	VN_2688	YOR096W	RPS7A	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps7Bp; interacts with Kti11p; deletion causes hypersensitivity to zymocin; has similarity to rat S7 and <i>Xenopus</i> S8 ribosomal proteins	Strain failed to verify via PCR
2689	VN_2689	YCR002C	CDC10	Component of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM	Q
2690	VN_2690	YGL115W	SNF4	Activating gamma subunit of the AMP-activated Snf1p kinase complex (contains Snf1p and a Sip1p/Sip2p/Gal83p family member); activates glucose-repressed genes, represses glucose-induced genes; role in sporulation, and peroxisome biogenesis	Q
2691	VN_2691	YER037W	PHM8	Protein of unknown function, expression is induced by low phosphate levels and by inactivation of Pho85p	Q
2692	VN_2692	YGL136C	MRM2	Mitochondrial 2' O-ribose methyltransferase, required for methylation of U(2791) in 21S rRNA; MRM2 deletion confers thermosensitive respiration and loss of mitochondrial DNA; has similarity to Spb1p and Trm7p, and to <i>E. coli</i> FtsJ/RmJ	Strain failed to verify via PCR
2693	VN_2693	YDR353W	TRR1	Cytoplasmic thioredoxin reductase, key regulatory enzyme that determines the redox state of the thioredoxin system, which acts as a disulfide reductase system and protects cells against both oxidative and reductive stress	Q
2694	VN_2694	YIL021W	RPB3	RNA polymerase II third largest subunit B44, part of central core; similar to prokaryotic alpha subunit	Q
2695	VN_2695	YDR352W	YDR352W	Putative protein of unknown function	Q
2696	VN_2696	YCL059C	KRR1	Essential nucleolar protein required for the synthesis of 18S rRNA and for the assembly of 40S ribosomal subunit	Strain failed to verify via PCR
2697	VN_2697	YGR231C	PHB2	Subunit of the prohibitin complex (Phb1p-Phb2p), a 1.2 MDa ring-shaped inner mitochondrial membrane chaperone that stabilizes newly synthesized proteins; determinant of replicative life span; involved in mitochondrial segregation	Q
2698	VN_2698	YNL063W	MTQ1	S-adenosylmethionine-dependent methyltransferase; methylates translational release factor Mrf1p; similar to <i>E.coli</i> PrmC; is not an essential gene	Strain failed to verify via PCR
2699	VN_2699	YOR006C	TSR3	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
2700	VN_2700	YGR127W	YGR127W	Putative protein of unknown function; expression is regulated by Msn2p/Msn4p, indicating a possible role in stress response	Q
2701	VN_2701	YDL021W	GPM2	Homolog of Gpm1p phosphoglycerate mutase, which converts 3-phosphoglycerate to 2-phosphoglycerate in glycolysis; may be non-functional derivative of a gene duplication event	Strain failed to verify via PCR

2702	VN_2702	YIL043C	CBR1	Microsomal cytochrome b reductase, not essential for viability; also detected in mitochondria; mutation in conserved NADH binding domain of the human ortholog results in type I methemoglobinemia	Q
2703	VN_2703	YHR198C	AIM18	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; null mutant displays elevated frequency of mitochondrial genome loss	Strain failed to verify via PCR
2704	VN_2704	YHL011C	PRS3	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, synthesizes PRPP, which is required for nucleotide, histidine, and tryptophan biosynthesis; one of five related enzymes, which are active as heteromultimeric complexes	Q
2705	VN_2705	YIR011C	STS1	Protein that interacts with the karyopherin Srp1p; may have a role with Srp1p in ubiquitin-mediated protein degradation	Strain failed to verify via PCR
2706	VN_2706	YNL315C	ATP11	Molecular chaperone, required for the assembly of alpha and beta subunits into the F1 sector of mitochondrial F1F0 ATP synthase	Q
2707	VN_2707	YGR213C	RTA1	Protein involved in 7-aminosterol resistance; has seven potential membrane-spanning regions; expression is induced under both low-heme and low-oxygen conditions; member of the fungal lipid-translocating exporter (LTE) family of protein	Q
2708	VN_2708	YCR100C	YCR100C	Putative protein of unknown function	Q
2709	VN_2709	YPL157W	TGS1	Trimethyl guanosine synthase, conserved nucleolar methyl transferase that converts the m(7)G cap structure of snRNAs, snoRNAs, and telomerase TLC1 RNA to m(2,2,7)G; also required for ribosome synthesis and nucleolar morphology	Q
2710	VN_2710	YNL263C	YIF1	Integral membrane protein required for the fusion of ER-derived COPII transport vesicles with the Golgi; interacts with Yip1p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles	Q
2711	VN_2711	YBR176W	ECM31	Ketopantoate hydroxymethyltransferase, required for pantothenic acid biosynthesis, converts 2-oxoisovalerate into 2-dehydropantoate	Q
2712	VN_2712	YHR144C	DCD1	Deoxycytidine monophosphate (dCMP) deaminase required for dCTP and dTTP synthesis; expression is NOT cell cycle regulated	Strain failed to verify via PCR
2713	VN_2713	YDL047W	SIT4	Type 2A-related serine-threonine phosphatase that functions in the G1/S transition of the mitotic cycle; cytoplasmic and nuclear protein that modulates functions mediated by Pkc1p including cell wall and actin cytoskeleton organization	Strain failed to verify via PCR
2714	VN_2714	YKR022C	NTR2	Essential protein that forms a dimer with Ntr1p; also forms a trimer, with Ntr2p and the DExD/H-box RNA helicase Prp43p, that is involved in spliceosome disassembly	Q
2715	VN_2715	YLR257W	YLR257W	Putative protein of unknown function	Q
2716	VN_2716	YIL077C	YIL077C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; deletion confers sensitivity to 4-(N-(S-glutathionylacetyl)amino) phenylarsenoxide (GSAO)	Q
2717	VN_2717	YLR439W	MRPL4	Mitochondrial ribosomal protein of the large subunit	Q
2718	VN_2718	YOR158W	PET123	Mitochondrial ribosomal protein of the small subunit; PET123 exhibits genetic interactions with PET122, which encodes a COX3 mRNA-specific translational activator	Q
2719	VN_2719	YMR048W	CSM3	Protein required for accurate chromosome segregation during meiosis	Q
2720	VN_2720	YKL019W	RAM2	Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase that catalyze prenylation of proteins containing a CAAX consensus motif; essential protein required for membrane localization of Ras proteins and a-factor	Q
2721	VN_2721	YGR282C	BGL2	Endo-beta-1,3-glucanase, major protein of the cell wall, involved in cell wall maintenance	Q
2722	VN_2722	YCL049C	YCL049C	Protein of unknown function; localizes to membrane fraction; YCL049C is not an essential gene;	Q
2723	VN_2723	YLR308W	CDA2	Chitin deacetylase, together with Cda1p involved in the biosynthesis ascospore wall component, chitosan; required for proper rigidity of the	Q

				ascospore wall	
2724	VN_2724	YGL146C	RRT6	Putative protein of unknown function; non-essential gene identified in a screen for mutants with increased levels of rDNA transcription; contains two putative transmembrane spans, but no significant homology to other known proteins	Q
2725	VN_2725	YNL002C	RLP7	Nucleolar protein with similarity to large ribosomal subunit L7 proteins; constituent of 66S pre-ribosomal particles; plays an essential role in processing of precursors to the large ribosomal subunit RNAs	Strain failed to verify via PCR
2726	VN_2726	YNR034W	SOL1	Protein with a possible role in tRNA export; shows similarity to 6-phosphogluconolactonase non-catalytic domains but does not exhibit this enzymatic activity; homologous to Sol2p, Sol3p, and Sol4p	Strain failed to verify via PCR
2727	VN_2727	YKR080W	MTD1	NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase, plays a catalytic role in oxidation of cytoplasmic one-carbon units; expression is regulated by Bas1p and Bas2p, repressed by adenine, and may be induced by inositol and choline	Q
2728	VN_2728	YLR457C	NBP1	Spindle pole body (SPB) component, required for the insertion of the duplication plaque into the nuclear membrane during SPB duplication; essential for bipolar spindle formation; component of the Mps2p-Bbp1p complex	Q
2729	VN_2729	YOR288C	MPD1	Member of the protein disulfide isomerase (PDI) family; interacts with and inhibits the chaperone activity of Cne1p; MPD1 overexpression in a pdi1 null mutant suppresses defects in Pdi1p functions such as carboxypeptidase Y maturation	Q
2730	VN_2730	YMR310C	YMR310C	Putative protein of unknown function; predicted to be involved in ribosome biogenesis; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; YMR310C is not an essential gene	Strain failed to verify via PCR
2731	VN_2731	YNL058C	YNL058C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; YNL058C is not an essential gene	Q
2732	VN_2732	YDR336W	YDR336W	Putative protein of unknown function; sumoylated under stress conditions in a genome wide study; YDR336W is not an essential gene	Q
2733	VN_2733	YKL094W	YJU3	Serine hydrolase with sequence similarity to monoglyceride lipase (MGL), localizes to lipid particles	Q
2734	VN_2734	YDL124W	YDL124W	NADPH-dependent alpha-keto amide reductase; reduces aromatic alpha-keto amides, aliphatic alpha-keto esters, and aromatic alpha-keto esters; member of the aldo-keto reductase (AKR) family	Q
2735	VN_2735	YLR209C	PNP1	Purine nucleoside phosphorylase, specifically metabolizes inosine and guanosine nucleosides; involved in the nicotinamide riboside salvage pathway	Q
2736	VN_2736	YNL284C	MRPL10	Mitochondrial ribosomal protein of the large subunit; appears as two protein spots (YmL10 and YmL18) on two-dimensional SDS gels	Q
2737	VN_2737	YPL206C	PGC1	Phosphatidyl Glycerol phospholipase C; regulates the phosphatidylglycerol (PG) content via a phospholipase C-type degradation mechanism; contains glycerophosphodiester phosphodiesterase motifs	Q
2738	VN_2738	YMR180C	CTL1	RNA 5'-triphosphatase, localizes to both the nucleus and cytoplasm	Q
2739	VN_2739	YML025C	YML6	Mitochondrial ribosomal protein of the large subunit, has similarity to E. coli L4 ribosomal protein and human mitoribosomal MRP-L4 protein; essential for viability, unlike most other mitoribosomal proteins	Q
2740	VN_2740	YNR003C	RPC34	RNA polymerase III subunit C34; interacts with TFIIB70 and is a key determinant in pol III recruitment by the preinitiation complex	Q
2741	VN_2741	YNR054C	ESF2	Essential nucleolar protein involved in pre-18S rRNA processing; binds to RNA and stimulates ATPase activity of Dbp8; involved in assembly of the small subunit (SSU) processome	Q
2742	VN_2742	YHR061C	GIC1	Protein of unknown function involved in initiation of budding and cellular polarization, interacts with Cdc42p via the Cdc42/Rac-interactive binding (CRIB) domain	Q
2743	VN_2743	YKL110C	KTI12	Protein that plays a role, with Elongator complex, in modification of wobble nucleosides in tRNA; involved in sensitivity to G1 arrest induced by zymocin; interacts with chromatin throughout the genome; also interacts with Cdc19p	Q

2744	VN_2744	YDL236W	PHO13	Alkaline phosphatase specific for p-nitrophenyl phosphate; also has protein phosphatase activity	Strain failed to verify via PCR
2745	VN_2745	YML087C	AIM33	Putative protein of unknown function, highly conserved across species and orthologous to human CYB5R4; null mutant displays reduced frequency of mitochondrial genome loss	Q
2746	VN_2746	YML050W	AIM32	Putative protein of unknown function; null mutant is viable and displays elevated frequency of mitochondrial genome loss	Q
2747	VN_2747	YCL050C	APA1	Diadenosine 5',5''-P ₁ ,P ₄ -tetrphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetrphosphates; has similarity to Apa2p	Q
2748	VN_2748	YDL082W	RPL13A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl13Bp; not essential for viability; has similarity to rat L13 ribosomal protein	Q
2749	VN_2749	YNL215W	IES2	Protein that associates with the INO80 chromatin remodeling complex under low-salt conditions; essential for growth under anaerobic conditions	Strain failed to verify via PCR
2750	VN_2750	YOR143C	THI80	Thiamine pyrophosphokinase, phosphorylates thiamine to produce the coenzyme thiamine pyrophosphate (thiamine diphosphate)	Q
2751	VN_2751	YNR027W	BUD17	Putative pyridoxal kinase, a key enzyme in vitamin B6 metabolism; involved in bud-site selection; diploid mutants display a random rather than a bipolar budding pattern; similarity to yeast BUD16 and human pyridoxal kinase (PDXK)	Q
2752	VN_2752	YKL216W	URA1	Dihydroorotate dehydrogenase, catalyzes the fourth enzymatic step in the de novo biosynthesis of pyrimidines, converting dihydroorotic acid into orotic acid	Q
2753	VN_2753	YMR206W	YMR206W	Putative protein of unknown function; YMR206W is not an essential gene	Q
2754	VN_2754	YDR368W	YPR1	NADPH-dependent aldo-keto reductase, reduces multiple substrates including 2-methylbutyraldehyde and D,L-glyceraldehyde, expression is induced by osmotic and oxidative stress; functionally redundant with other aldo-keto reductases	Q
2755	VN_2755	YMR299C	DYN3	Dynein light intermediate chain (LIC); localizes with dynein, null mutant is defective in nuclear migration	Q
2756	VN_2756	YBR061C	TRM7	2'-O-ribose methyltransferase, methylates the 2'-O-ribose of nucleotides at positions 32 and 34 of the tRNA anticodon loop	Q
2757	VN_2757	YDR347W	MRP1	Mitochondrial ribosomal protein of the small subunit; MRP1 exhibits genetic interactions with PET122, encoding a COX3-specific translational activator, and with PET123, encoding a small subunit mitochondrial ribosomal protein	Q
2758	VN_2758	YDL183C	YDL183C	Putative protein of unknown function; YDL183C is not an essential gene	Q
2759	VN_2759	YGL103W	RPL28	Ribosomal protein of the large (60S) ribosomal subunit, has similarity to E. coli L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can mutate to cycloheximide resistance	Strain failed to verify via PCR
2760	VN_2760	YOR342C	YOR342C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus	Q
2761	VN_2761	YPR013C	YPR013C	Putative zinc finger protein; YPR013C is not an essential gene	Q
2762	VN_2762	YBR175W	SWD3	Essential subunit of the COMPASS (Set1C) complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres; WD40 beta propeller superfamily member and ortholog of mammalian WDR5	Q
2763	VN_2763	YKR087C	OMA1	Metalloendopeptidase of the mitochondrial inner membrane, involved in turnover of membrane-embedded proteins; member of a family of predicted membrane-bound metallopeptidases in prokaryotes and higher eukaryotes	Q
2764	VN_2764	YMR262W	YMR262W	Protein of unknown function; interacts weakly with Knr4p; YMR262W is not an essential gene	Q
2765	VN_2765	YEL029C	BUD16	Putative pyridoxal kinase, a key enzyme involved in pyridoxal 5'-phosphate synthesis, the active form of vitamin B6; required for genome integrity; involved in bud-site selection; similarity to yeast BUD17 and human pyridoxal kinase (PDXK)	Q

2766	VN_2766	YOR120W	GCY1	Putative NADP(+) coupled glycerol dehydrogenase, proposed to be involved in an alternative pathway for glycerol catabolism; member of the aldo-keto reductase (AKR) family	Q
2767	VN_2767	YDR068W	DOS2	Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2768	VN_2768	YDR460W	TFB3	Subunit of TFIIF and nucleotide excision repair factor 3 complexes, involved in transcription initiation, required for nucleotide excision repair; ring finger protein similar to mammalian CAK and TFIIF subunit	Q
2769	VN_2769	YGL081W	YGL081W	Putative protein of unknown function; non-essential gene; interacts genetically with CHS5, a gene involved in chitin biosynthesis	Q
2770	VN_2770	YDR175C	RSM24	Mitochondrial ribosomal protein of the small subunit	Q
2771	VN_2771	YER099C	PRS2	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, synthesizes PRPP, which is required for nucleotide, histidine, and tryptophan biosynthesis; one of five related enzymes, which are active as heteromultimeric complexes	Q
2772	VN_2772	YDL218W	YDL218W	Putative protein of unknown function; YDL218W transcription is regulated by Azf1p and induced by starvation and aerobic conditions; expression also induced in cells treated with the mycotoxin patulin	Q
2773	VN_2773	YBR151W	APD1	Protein of unknown function, required for normal localization of actin patches and for normal tolerance of sodium ions and hydrogen peroxide; localizes to both cytoplasm and nucleus	Strain failed to verify via PCR
2774	VN_2774	YCR073W-A	SOL2	Protein with a possible role in tRNA export; shows similarity to 6-phosphogluconolactonase non-catalytic domains but does not exhibit this enzymatic activity; homologous to Sol1p, Sol3p, and Sol4p	Strain failed to verify via PCR
2775	VN_2775	YLR283W	YLR283W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria; YLR283W is not an essential gene	Q
2776	VN_2776	YNL322C	KRE1	Cell wall glycoprotein involved in beta-glucan assembly; serves as a K1 killer toxin membrane receptor	Q
2777	VN_2777	YOR164C	GET4	Protein of unknown function, highly conserved across species and homologous to human gene C7orf20; interacts with Mdy2p; genetic interactions predict a role in insertion of tail-anchored proteins into the ER membrane	Q
2778	VN_2778	YDR090C	YDR090C	Putative protein of unknown function	Q
2779	VN_2779	YGL161C	YIP5	Protein that interacts with Rab GTPases, localized to late Golgi vesicles; computational analysis of large-scale protein-protein interaction data suggests a possible role in vesicle-mediated transport	Q
2780	VN_2780	YPR093C	ASR1	Ubiquitin ligase that modifies and regulates RNA Pol II; involved in a putative alcohol-responsive signaling pathway; accumulates in the nucleus under alcohol stress; contains a Ring/PHD finger domain similar to the mammalian rA9 protein	Q
2781	VN_2781	YJR083C	ACF4	Protein of unknown function, computational analysis of large-scale protein-protein interaction data suggests a possible role in actin cytoskeleton organization; potential Cdc28p substrate	Q
2782	VN_2782	YDL114W	YDL114W	Putative protein of unknown function with similarity to acyl-carrier-protein reductases; YDL114W is not an essential gene	Strain failed to verify via PCR
2783	VN_2783	YML110C	COQ5	2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase, involved in ubiquinone (Coenzyme Q) biosynthesis; localizes to the matrix face of the mitochondrial inner membrane in a large complex with other ubiquinone biosynthetic enzymes	Strain failed to verify via PCR
2784	VN_2784	YKL183W	LOT5	Protein of unknown function; gene expression increases in cultures shifted to a lower temperature	Q
2785	VN_2785	YNL096C	RPS7B	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps7Ap; interacts with Kti11p; deletion causes hypersensitivity to zymocin; has similarity to rat S7 and Xenopus S8 ribosomal proteins	Q
2786	VN_2786	YOR251C	TUM1	Mitochondrial protein, required for formation of the 2-thio group of the 5-methoxycarbonylmethyl-2-thiouridine modified base in some tRNAs; has similarity to mammalian thiosulfate sulfurtransferase (rhodanese)	Q

2787	VN_2787	YOL056W	GPM3	Homolog of Gpm1p phosphoglycerate mutase, which converts 3-phosphoglycerate to 2-phosphoglycerate in glycolysis; may be non-functional derivative of a gene duplication event	Q
2788	VN_2788	YLR307W	CDA1	Chitin deacetylase, together with Cda2p involved in the biosynthesis ascospore wall component, chitosan; required for proper rigidity of the ascospore wall	Q
2789	VN_2789	YIL061C	SNP1	Component of U1 snRNP required for mRNA splicing via spliceosome; may interact with poly(A) polymerase to regulate polyadenylation; homolog of human U1 70K protein	Q
2790	VN_2790	YGL162W	SUT1	Transcription factor of the Zn[II]2Cys6 family involved in sterol uptake; involved in induction of hypoxic gene expression	Q
2791	VN_2791	YHR199C	AIM46	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; null mutant displays elevated frequency of mitochondrial genome loss	Q
2792	VN_2792	YOR312C	RPL20B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Ap and has similarity to rat L18a ribosomal protein	Strain failed to verify via PCR
2793	VN_2793	YKL107W	YKL107W	Putative protein of unknown function; proposed to be a palmitoylated membrane protein	Q
2794	VN_2794	YDR075W	PPH3	Catalytic subunit of an evolutionarily conserved protein phosphatase complex containing Psy2p and the regulatory subunit Psy4p; required for cisplatin resistance; involved in activation of Gln3p	Q
2795	VN_2795	YNL072W	RNH201	Ribonuclease H2 catalytic subunit, removes RNA primers during Okazaki fragment synthesis; homolog of RNase HI (the <i>S. cerevisiae</i> homolog of mammalian RNase HII is RNH1); related to human AGS4 that causes Aicardi-Goutieres syndrome	Q
2796	VN_2796	YMR055C	BUB2	Mitotic exit network regulator, forms GTPase-activating Bfa1p-Bub2p complex that binds Tem1p and spindle pole bodies, blocks cell cycle progression before anaphase in response to spindle and kinetochore damage	Strain failed to verify via PCR
2797	VN_2797	YBR228W	SLX1	Subunit of a complex, with Slx4p, that hydrolyzes 5' branches from duplex DNA in response to stalled or converging replication forks; function overlaps with that of Sgs1p-Top3p	Q
2798	VN_2798	YPL186C	UIP4	Protein that interacts with Ulp1p, a Ubl (ubiquitin-like protein)-specific protease for Smt3p protein conjugates; detected in a phosphorylated state in the mitochondrial outer membrane; also detected in ER and nuclear envelope	Q
2799	VN_2799	YDR446W	ECM11	Non-essential protein apparently involved in meiosis, GFP fusion protein is present in discrete clusters in the nucleus throughout mitosis; may be involved in maintaining chromatin structure	Q
2800	VN_2800	YPL054W	LEE1	Zinc-finger protein of unknown function	Q
2801	VN_2801	YLR093C	NYV1	v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion; inhibits ATP-dependent Ca(2+) transport activity of Pmc1p in the vacuolar membrane	Q
2802	VN_2802	YGL254W	FZF1	Transcription factor involved in sulfite metabolism, sole identified regulatory target is SSU1, overexpression suppresses sulfite-sensitivity of many unrelated mutants due to hyperactivation of SSU1, contains five zinc fingers	Q
2803	VN_2803	YJL159W	HSP150	O-mannosylated heat shock protein that is secreted and covalently attached to the cell wall via beta-1,3-glucan and disulfide bridges; required for cell wall stability; induced by heat shock, oxidative stress, and nitrogen limitation	Q
2804	VN_2804	YCL009C	ILV6	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria	Q
2805	VN_2805	YLR464W	YLR464W	Putative protein of unknown function; intron is predicted but not detected experimentally; YLR464W overlaps the verified gene YRF1-4/YLR466W and two dubious ORFs YLR463C and YLR465C	Q
2806	VN_2806	YBR251W	MRPS5	Mitochondrial ribosomal protein of the small subunit	Q
2807	VN_2807	YAL025C	MAK16	Essential nuclear protein, constituent of 66S pre-ribosomal particles; required for maturation of 25S and 5.8S rRNAs; required for	Strain failed to verify via

				maintenance of M1 satellite double-stranded RNA of the L-A virus	PCR
2808	VN_2808	YOR238W	YOR238W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
2809	VN_2809	YDL179W	PCL9	Cyclin, forms a functional kinase complex with Pho85p cyclin-dependent kinase (Cdk), expressed in late M/early G1 phase, activated by Swi5p	Q
2810	VN_2810	YPR147C	YPR147C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and is induced in response to the DNA-damaging agent MMS	Q
2811	VN_2811	YER076C	YER076C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; analysis of HA-tagged protein suggests a membrane localization	Q
2812	VN_2812	YPL064C	CWC27	Component of a complex containing Cef1p, putatively involved in pre-mRNA splicing; has similarity to <i>S. pombe</i> Cwf27p	Q
2813	VN_2813	YLR146C	SPE4	Spermine synthase, required for the biosynthesis of spermine and also involved in biosynthesis of pantothenic acid	Q
2814	VN_2814	YJL068C	YJL068C	Non-essential intracellular esterase that can function as an S-formylglutathione hydrolase; may be involved in the detoxification of formaldehyde, which can be metabolized to S-formylglutathione; similar to human esterase D	Q
2815	VN_2815	YKL091C	YKL091C	Putative homolog of Sec14p, which is a phosphatidylinositol/phosphatidylcholine transfer protein involved in lipid metabolism; localizes to the nucleus	Q
2816	VN_2816	YDL222C	FMP45	Integral membrane protein localized to mitochondria (untagged protein); required for sporulation and maintaining sphingolipid content; has sequence similarity to SUR7 and YNL194C	Q
2817	VN_2817	YNL177C	MRPL22	Mitochondrial ribosomal protein of the large subunit	Strain failed to verify via PCR
2818	VN_2818	YER083C	GET2	Subunit of the GET complex; involved in insertion of proteins into the ER membrane; required for the retrieval of HDEL proteins from the Golgi to the ER in an ERD2 dependent fashion and for meiotic nuclear division	Q
2819	VN_2819	YAR015W	ADE1	N-succinyl-5-aminoimidazole-4-carboxamide ribotide (SAICAR) synthetase, required for 'de novo' purine nucleotide biosynthesis; red pigment accumulates in mutant cells deprived of adenine	Q
2820	VN_2820	YPL177C	CUP9	Homeodomain-containing transcriptional repressor of PTR2, which encodes a major peptide transporter; imported peptides activate ubiquitin-dependent proteolysis, resulting in degradation of Cup9p and de-repression of PTR2 transcription	Q
2821	VN_2821	YDR123C	INO2	Component of the heteromeric Ino2p/Ino4p basic helix-loop-helix transcription activator that binds inositol/choline-responsive elements (ICREs), required for derepression of phospholipid biosynthetic genes in response to inositol depletion	Q
2822	VN_2822	YBR231C	SWC5	Protein of unknown function, component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A	Strain failed to verify via PCR
2823	VN_2823	YER106W	MAM1	Monopolin, kinetochore associated protein involved in chromosome attachment to meiotic spindle	Q
2824	VN_2824	YPR061C	JID1	Probable Hsp40p co-chaperone, has a DnaJ-like domain and appears to be involved in ER-associated degradation of misfolded proteins containing a tightly folded cytoplasmic domain; inhibits replication of Brome mosaic virus in <i>S. cerevisiae</i>	Q
2825	VN_2825	YLR172C	DPH5	Methyltransferase required for synthesis of diphthamide, which is a modified histidine residue of translation elongation factor 2 (Eft1p or Eft2p); not essential for viability; GFP-Dph5p fusion protein localizes to the cytoplasm	Q
2826	VN_2826	YJL079C	PRY1	Protein of unknown function	Q
2827	VN_2827	YML121W	GTR1	Cytoplasmic GTP binding protein and negative regulator of the Ran/Tc4 GTPase cycle; component of GSE complex, which is required for sorting of Gap1p; involved in phosphate transport and	Q

				telomeric silencing; similar to human RagA and RagB	
2828	VN_2828	YEL076C-A	YEL076C-A	Putative protein of unknown function	Q
2829	VN_2829	YNL312W	RFA2	Subunit of heterotrimeric Replication Protein A (RPA), which is a highly conserved single-stranded DNA binding protein involved in DNA replication, repair, and recombination	Q
2830	VN_2830	YGR104C	SRB5	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation; involved in telomere maintenance	Q
2831	VN_2831	YDL045C	FAD1	Flavin adenine dinucleotide (FAD) synthetase, performs the second step in synthesis of FAD from riboflavin	Q
2832	VN_2832	YBL087C	RPL23A	Protein component of the large (60S) ribosomal subunit, identical to Rpl23Bp and has similarity to E. coli L14 and rat L23 ribosomal proteins	Strain failed to verify via PCR
2833	VN_2833	YJR007W	SUI2	Alpha subunit of the translation initiation factor eIF2, involved in the identification of the start codon; phosphorylation of Ser51 is required for regulation of translation by inhibiting the exchange of GDP for GTP	Strain failed to verify via PCR
2834	VN_2834	YDR288W	NSE3	Essential subunit of the Mms21-Smc5-Smc6 complex; protein of unknown function; required for DNA repair and growth	Q
2835	VN_2835	YKL150W	MCR1	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis	Q
2836	VN_2836	YLR128W	DCN1	Putative Nedd8 ligase; binds Nedd8; involved in cullin neddylation; not essential; similar to C.elegans DCN-1; contains UBA-like ubiquitin-binding domain and a DUF298 domain	Q
2837	VN_2837	YNL204C	SPS18	Protein of unknown function, contains a putative zinc-binding domain; expressed during sporulation	Strain failed to verify via PCR
2838	VN_2838	YNL156C	NSG2	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins	Q
2839	VN_2839	YGL043W	DST1	General transcription elongation factor TFIIS, enables RNA polymerase II to read through blocks to elongation by stimulating cleavage of nascent transcripts stalled at transcription arrest sites	Q
2840	VN_2840	YOR107W	RGS2	Negative regulator of glucose-induced cAMP signaling; directly activates the GTPase activity of the heterotrimeric G protein alpha subunit Gpa2p	Q
2841	VN_2841	YHL013C	OTU2	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; member of the ovarian tumor-like (OTU) superfamily of predicted cysteine proteases; shows cytoplasmic localization	Q
2842	VN_2842	YDR374C	YDR374C	Putative protein of unknown function	Q
2843	VN_2843	YDR280W	RRP45	Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; has similarity to E. coli RNase PH and to human hRrp45p (PM/SCL-75, EXOSC9)	Strain failed to verify via PCR
2844	VN_2844	YLR448W	RPL6B	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Ap and to rat L6 ribosomal protein; binds to 5.8S rRNA	Q
2845	VN_2845	YER185W	PUG1	Plasma membrane protein with roles in the uptake of protoporphyrin IX and the efflux of heme; expression is induced under both low-heme and low-oxygen conditions; member of the fungal lipid-translocating exporter (LTE) family of proteins	Q
2846	VN_2846	YOR287C	YOR287C	Putative protein of unknown function; may play a role in the ribosome and rRNA biosynthesis based on expression profiles and mutant phenotype	Q
2847	VN_2847	YPR066W	UBA3	Protein that acts together with Ula1p to activate Rub1p before its conjugation to proteins (neddylation), which may play a role in protein degradation; GFP-fusion protein localizes to the cytoplasm in a punctate pattern	Q

2848	VN_2848	YNR007C	ATG3	E2-like enzyme involved in autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; plays a role in formation of Atg8p-phosphatidylethanolamine conjugates, which are involved in membrane dynamics during autophagy and Cvt	Q
2849	VN_2849	YGR208W	SER2	Phosphoserine phosphatase of the phosphoglycerate pathway, involved in serine and glycine biosynthesis, expression is regulated by the available nitrogen source	Q
2850	VN_2850	YOR292C	YOR292C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; YOR292C is not an essential gene	Strain failed to verify via PCR
2851	VN_2851	YJL126W	NIT2	Nit protein, one of two proteins in <i>S. cerevisiae</i> with similarity to the Nit domain of NitFhit from fly and worm and to the mouse and human Nit protein which interacts with the Fhit tumor suppressor; nitrilase superfamily member	Q
2852	VN_2852	YER186C	YER186C	Putative protein of unknown function	Q
2853	VN_2853	YGR277C	CAB4	Probable pantetheine-phosphate adenylyltransferase (PPAT), which catalyzes the fourth step in the biosynthesis of coenzyme A from pantothenate; null mutant lethality is complemented by <i>E. coli</i> coaD (encoding PPAT); widely conserved	Q
2854	VN_2854	YLR455W	YLR455W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus; deletion confers sensitivity to 4-(N-(S-glutathionylacetyl)amino) phenylarsenoxide (GSAO)	Q
2855	VN_2855	YFR031C-A	RPL2A	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to <i>E. coli</i> L2 and rat L8 ribosomal proteins	Q
2856	VN_2856	YOR228C	YOR228C	Protein of unknown function, localized to the mitochondrial outer membrane	Q
2857	VN_2857	YPL079W	RPL21B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl21Ap and has similarity to rat L21 ribosomal protein	Q
2858	VN_2858	YGR001C	YGR001C	Putative protein of unknown function with similarity to methyltransferase family members; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; required for replication of Brome mosaic virus in <i>S. cerevisiae</i>	Q
2859	VN_2859	YBR160W	CDC28	Catalytic subunit of the main cell cycle cyclin-dependent kinase (CDK); alternately associates with G1 cyclins (CLNs) and G2/M cyclins (CLBs) which direct the CDK to specific substrates	Q
2860	VN_2860	YOR279C	RFM1	DNA-binding protein required for vegetative repression of middle sporulation genes; specificity factor that directs the Hst1p histone deacetylase to some of the promoters regulated by Sum1p; involved in telomere maintenance	Q
2861	VN_2861	YHR187W	IKI1	Subunit of Elongator complex, which is required for modification of wobble nucleosides in tRNA; <i>iki1</i> mutations confer resistance to the <i>K. lactis</i> toxin zymocin	Q
2862	VN_2862	YGL232W	TAN1	Putative tRNA acetyltransferase, RNA-binding protein required for the formation of the modified nucleoside N(4)-acetylcytidine in serine and leucine tRNAs but not required for the same modification in 18S rRNA	Q
2863	VN_2863	YKR075C	YKR075C	Protein of unknown function; similar to YOR062Cp and Reg1p; expression regulated by glucose and Rgt1p; GFP-fusion protein is induced in response to the DNA-damaging agent MMS	Q
2864	VN_2864	YFR004W	RPN11	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; couples the deubiquitination and degradation of proteasome substrates; involved, independent of catalytic activity, in fission of mitochondria and peroxisomes	Q
2865	VN_2865	YJR013W	GPI14	Glycosylphosphatidylinositol- α 1,4 mannosyltransferase I, involved in GPI anchor biosynthesis, requires Pbn1p for function; homolog of mammalian PIG-M	Strain failed to verify via PCR
2866	VN_2866	YMR281W	GPI12	ER membrane protein involved in the second step of glycosylphosphatidylinositol (GPI) anchor assembly, the de-N-acetylation of the N-acetylglucosaminylphosphatidylinositol intermediate; functional homolog of human PIG-Lp	Q
2867	VN_2867	YFL044C	OTU1	Deubiquitylation enzyme that binds to the chaperone-ATPase Cdc48p; may contribute to regulation of protein degradation by	Strain failed to verify via

				deubiquitylating substrates that have been ubiquitylated by Ufd2p; member of the Ovarian Tumor (OTU) family	PCR
2868	VN_2868	YGR044C	RME1	Zinc finger protein involved in control of meiosis; prevents meiosis by repressing IME1 expression and promotes mitosis by activating CLN2 expression; directly repressed by a1-alpha2 regulator; mediates cell type control of sporulation	Q
2869	VN_2869	YER175C	TMT1	Trans-aconitate methyltransferase, cytosolic enzyme that catalyzes the methyl esterification of 3-isopropylmalate, an intermediate of the leucine biosynthetic pathway, and trans-aconitate, which inhibits the citric acid cycle	Q
2870	VN_2870	YFL059W	SNZ3	Member of a stationary phase-induced gene family; transcription of SNZ2 is induced prior to diauxic shift, and also in the absence of thiamin in a Thi2p-dependent manner; forms a coregulated gene pair with SNO3	Q
2871	VN_2871	YIL044C	AGE2	ADP-ribosylation factor (ARF) GTPase activating protein (GAP) effector, involved in Trans-Golgi-Network (TGN) transport; contains C2C2H2 cysteine/histidine motif	Q
2872	VN_2872	YMR096W	SNZ1	Protein involved in vitamin B6 biosynthesis; member of a stationary phase-induced gene family; coregulated with SNO1; interacts with Sno1p and with Yhr198p, perhaps as a multiprotein complex containing other Snz and Sno proteins	Strain failed to verify via PCR
2873	VN_2873	YML112W	CTK3	Gamma subunit of C-terminal domain kinase I (CTDK-I), which phosphorylates both RNA pol II subunit Rpo21p to affect transcription and pre-mRNA 3' end processing, and ribosomal protein Rps2p to increase translational fidelity	Q
2874	VN_2874	YHR046C	INM1	Inositol monophosphatase, involved in biosynthesis of inositol and in phosphoinositide second messenger signaling; INM1 expression increases in the presence of inositol and decreases upon exposure to antibipolar drugs lithium and valproate	Q
2875	VN_2875	YOR083W	WHI5	Repressor of G1 transcription that binds to SCB binding factor (SBF) at SCB target promoters in early G1; phosphorylation of Whi5p by the CDK, Cln3p/Cdc28p relieves repression and promoter binding by Whi5; periodically expressed in G1	Q
2876	VN_2876	YJL145W	SFH5	Non-classical phosphatidylinositol transfer protein (PITP); exhibits PI-but not PC-transfer activity; localizes to the peripheral endoplasmic reticulum, cytosol and microsomes; similar to Sec14p	Q
2877	VN_2877	YIL003W	CFD1	Highly conserved, iron-sulfur cluster binding protein localized in the cytoplasm; forms a complex with Nbp35p that is involved in iron-sulfur protein assembly in the cytosol	Q
2878	VN_2878	YDR287W	INM2	Inositol monophosphatase, involved in biosynthesis of inositol; enzymatic activity requires magnesium ions and is inhibited by lithium and sodium ions; inm1 inm2 double mutant lacks inositol auxotrophy	Q
2879	VN_2879	YBR152W	SPP381	mRNA splicing factor, component of U4/U6.U5 tri-snRNP; interacts genetically and physically with Prp38p	Q
2880	VN_2880	YLR367W	RPS22B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Ap and has similarity to E. coli S8 and rat S15a ribosomal proteins	Q
2881	VN_2881	YJL031C	BET4	Alpha subunit of Type II geranylgeranyltransferase required for vesicular transport between the endoplasmic reticulum and the Golgi; provides a membrane attachment moiety to Rab-like proteins Ypt1p and Sec4p	Strain failed to verify via PCR
2882	VN_2882	YAL034W-A	MTW1	Essential component of the MIND kinetochore complex (Mtw1p Including Nnf1p-Nsl1p-Dsn1p) which joins kinetochore subunits contacting DNA to those contacting microtubules; critical to kinetochore assembly	Q
2883	VN_2883	YJR150C	DAN1	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p; expressed under anaerobic conditions, completely repressed during aerobic growth	Strain failed to verify via PCR
2884	VN_2884	YMR099C	YMR099C	Glucose-6-phosphate 1-epimerase (hexose-6-phosphate mutarotase), likely involved in carbohydrate metabolism; GFP-fusion protein localizes to both the nucleus and cytoplasm and is induced in response to the DNA-damaging agent MMS	Q
2885	VN_2885	YIL133C	RPL16A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rpl16Bp, E.	Q

				coli L13 and rat L13a ribosomal proteins; transcriptionally regulated by Rap1p	
2886	VN_2886	YHR058C	MED6	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation	Q
2887	VN_2887	YPL241C	CIN2	GTPase-activating protein (GAP) for Cin4p; tubulin folding factor C involved in beta-tubulin (Tub2p) folding; mutants display increased chromosome loss and benomyl sensitivity; deletion complemented by human GAP, retinitis pigmentosa 2	Q
2888	VN_2888	YOR114W	YOR114W	Putative protein of unknown function; null mutant is viable	Strain failed to verify via PCR
2889	VN_2889	YJL185C	YJL185C	Putative protein of unknown function; mRNA is weakly cell cycle regulated, peaking in G2 phase; YJL185C is a non-essential gene	Q
2890	VN_2890	YGR066C	YGR066C	Putative protein of unknown function	Q
2891	VN_2891	YDL129W	YDL129W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus; YDL129W is not an essential gene	Q
2892	VN_2892	YOL077C	BRX1	Nucleolar protein, constituent of 66S pre-ribosomal particles; depletion leads to defects in rRNA processing and a block in the assembly of large ribosomal subunits; possesses a sigma(70)-like RNA-binding motif	Q
2893	VN_2893	YLR132C	YLR132C	Essential protein of unknown function; fluorescent protein (GFP or YFP)-tagged protein localizes to mitochondria, cytoplasm and nucleus	Q
2894	VN_2894	YFL028C	CAF16	Part of evolutionarily-conserved CCR4-NOT regulatory complex; contains single ABC-type ATPase domain but no transmembrane domain; interacts with several subunits of Mediator	Q
2895	VN_2895	YNL196C	SLZ1	Sporulation-specific protein with a leucine zipper motif	Q
2896	VN_2896	YPL131W	RPL5	Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rat L5 ribosomal proteins; binds 5S rRNA and is required for 60S subunit assembly	Q
2897	VN_2897	YNL246W	VPS75	NAP family histone chaperone; binds to histones and Rtt109p, stimulating histone acetyltransferase activity; possesses nucleosome assembly activity in vitro; proposed role in vacuolar protein sorting and in double-strand break repair	Q
2898	VN_2898	YHR088W	RPF1	Nucleolar protein involved in the assembly and export of the large ribosomal subunit; constituent of 66S pre-ribosomal particles; contains a sigma(70)-like motif, which is thought to bind RNA	Strain failed to verify via PCR
2899	VN_2899	YDL076C	RXT3	Subunit of the RPD3L complex; involved in histone deacetylation	Q
2900	VN_2900	YPL149W	ATG5	Conserved protein involved in autophagy and the Cvt pathway; undergoes conjugation with Atg12p to form a complex involved in Atg8p lipidation; conjugated Atg12p also forms a complex with Atg16p that is essential for autophagosome formation	Q
2901	VN_2901	YLR091W	GEP5	Protein of unknown function, required for mitochondrial genome maintenance; detected in highly purified mitochondria in high-throughput studies; null mutant has decreased levels of cardiolipin and phosphatidylethanolamine	Q
2902	VN_2902	YJR088C	EMC2	Member of a transmembrane complex required for efficient folding of proteins in the ER; null mutant displays induction of the unfolded protein response	Q
2903	VN_2903	YDR130C	FIN1	Spindle pole body-related intermediate filament protein, forms cell cycle-specific filaments between spindle pole bodies in mother and daughter cells, able to self-assemble, expression induced during S/G2, localization cell-cycle dependent	Q
2904	VN_2904	YOR344C	TYE7	Serine-rich protein that contains a basic-helix-loop-helix (bHLH) DNA binding motif; binds E-boxes of glycolytic genes and contributes to their activation; may function as a transcriptional activator in Ty1-mediated gene expression	Q
2905	VN_2905	YML003W	YML003W	Putative protein of unknown function	Strain failed to verify via PCR

2906	VN_2906	YFR032C	RRT5	Putative protein of unknown function; non-essential gene identified in a screen for mutants with increased levels of rDNA transcription; expressed at high levels during sporulation	Q
2907	VN_2907	YNL333W	SNZ2	Member of a stationary phase-induced gene family; transcription of SNZ2 is induced prior to diauxic shift, and also in the absence of thiamin in a Thi2p-dependent manner; forms a coregulated gene pair with SNO2; interacts with Thi11p	Q
2908	VN_2908	YPL173W	MRPL40	Mitochondrial ribosomal protein of the large subunit	Q
2909	VN_2909	YDL173W	PAR32	Putative protein of unknown function; hyperphosphorylated upon rapamycin treatment in a Tap42p-dependent manner; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; PAR32 is not an essential gene	Q
2910	VN_2910	YKL128C	PMU1	Putative phosphomutase, contains a region homologous to the active site of phosphomutases; overexpression suppresses the histidine auxotrophy of an ade3 ade16 ade17 triple mutant and the temperature sensitivity of a tps2 mutant	Q
2911	VN_2911	YDR184C	ATC1	Nuclear protein, possibly involved in regulation of cation stress responses and/or in the establishment of bipolar budding pattern	Q
2912	VN_2912	YPR005C	HAL1	Cytoplasmic protein involved in halotolerance; decreases intracellular Na ⁺ (via Ena1p) and increases intracellular K ⁺ by decreasing efflux; expression repressed by Ssn6p-Tup1p and Sko1p and induced by NaCl, KCl, and sorbitol through Gcn4p	Q
2913	VN_2913	YOL001W	PHO80	Cyclin, interacts with cyclin-dependent kinase Pho85p; regulates the response to nutrient levels and environmental conditions, including the response to phosphate limitation and stress-dependent calcium signaling	Q
2914	VN_2914	YKL052C	ASK1	Essential subunit of the Dam1 complex (aka DASH complex), couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; phosphorylated during the cell cycle by cyclin-dependent kinases	Q
2915	VN_2915	YDR450W	RPS18A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps18Bp and has similarity to E. coli S13 and rat S18 ribosomal proteins	Strain failed to verify via PCR
2916	VN_2916	YER074W	RPS24A	Protein component of the small (40S) ribosomal subunit; identical to Rps24Bp and has similarity to rat S24 ribosomal protein	Strain failed to verify via PCR
2917	VN_2917	YOL080C	REX4	Putative RNA exonuclease possibly involved in pre-rRNA processing and ribosome assembly	Q
2918	VN_2918	YCL031C	RRP7	Essential protein involved in rRNA processing and ribosome biogenesis	Q
2919	VN_2919	YBR147W	RTC2	Protein of unknown function; identified in a screen for mutants with decreased levels of rDNA transcription; detected in highly purified mitochondria; null mutant suppresses cdc13-1; similar to a G-protein coupled receptor from S. pombe	Q
2920	VN_2920	YDR054C	CDC34	Ubiquitin-conjugating enzyme (E2) and catalytic subunit of SCF ubiquitin-protein ligase complex (together with Skp1p, Rbx1p, Cdc53p, and an F-box protein) that regulates cell cycle progression by targeting key substrates for degradation	Q
2921	VN_2921	YKR037C	SPC34	Essential subunit of the Dam1 complex (aka DASH complex), couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; also localized to nuclear side of spindle pole body	Q
2922	VN_2922	YDR489W	SLD5	Subunit of the GINS complex (Sld5p, Psf1p, Psf2p, Psf3p), which is localized to DNA replication origins and implicated in assembly of the DNA replication machinery	Q
2923	VN_2923	YPR109W	YPR109W	Predicted membrane protein; diploid deletion strain has high budding index	Q
2924	VN_2924	YOL093W	TRM10	tRNA methyltransferase, methylates the N-1 position of guanosine in tRNAs	Q
2925	VN_2925	YKR004C	ECM9	Non-essential protein of unknown function	Q
2926	VN_2926	YHR014W	SPO13	Meiosis-specific protein, involved in maintaining sister chromatid cohesion during meiosis I as well as promoting proper attachment of	Q

				kinetochores to the spindle during meiosis I and meiosis II	
2927	VN_2927	YBR101C	FES1	Hsp70 (Ssa1p) nucleotide exchange factor, cytosolic homolog of Sil1p, which is the nucleotide exchange factor for BiP (Kar2p) in the endoplasmic reticulum	Q
2928	VN_2928	YNR064C	YNR064C	Epoxide hydrolase, member of the alpha/beta hydrolase fold family; may have a role in detoxification of epoxides	Q
2929	VN_2929	YDR494W	RSM28	Mitochondrial ribosomal protein of the small subunit; genetic interactions suggest a possible role in promoting translation initiation	Q
2930	VN_2930	YCL008C	STP22	Component of the ESCRT-I complex, which is involved in ubiquitin-dependent sorting of proteins into the endosome; homologous to the mouse and human Tsg101 tumor susceptibility gene; mutants exhibit a Class E Vps phenotype	Strain failed to verify via PCR
2931	VN_2931	YDR233C	RTN1	ER membrane protein that interacts with Sey1p to maintain ER morphology; interacts with exocyst subunit Sec6p, with Yip3p, and with Shh1p; null mutant has an altered ER morphology; member of the RTNLA (reticulon-like A) subfamily	Q
2932	VN_2932	YMR025W	CSI1	Subunit of the Cop9 signalosome, which is required for deneddylation, or removal of the ubiquitin-like protein Rub1p from Cdc53p (cullin); involved in adaptation to pheromone signaling	Q
2933	VN_2933	YER117W	RPL23B	Protein component of the large (60S) ribosomal subunit, identical to Rpl23Ap and has similarity to E. coli L14 and rat L23 ribosomal proteins	Strain failed to verify via PCR
2934	VN_2934	YPR199C	ARR1	Transcriptional activator of the basic leucine zipper (bZIP) family, required for transcription of genes involved in resistance to arsenic compounds	Q
2935	VN_2935	YPL068C	YPL068C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus and is induced in response to the DNA-damaging agent MMS	Strain failed to verify via PCR
2936	VN_2936	YMR039C	SUB1	Transcriptional coactivator, facilitates elongation through factors that modify RNAP II; role in peroxide resistance involving Rad2p; role in the hyperosmotic stress response through polymerase recruitment at RNAP II and RNAP III genes	Q
2937	VN_2937	YHR209W	CRG1	Putative S-adenosylmethionine-dependent methyltransferase; mediates cantharidin resistance	Strain failed to verify via PCR
2938	VN_2938	YCR016W	YCR016W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleolus and nucleus; predicted to be involved in ribosome biogenesis	Q
2939	VN_2939	YOR385W	YOR385W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YOR385W is not an essential gene	Q
2940	VN_2940	YGL221C	NIF3	Protein of unknown function, similar to Listeria monocytogenes major sigma factor (rpoD gene product); the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2941	VN_2941	YGR017W	YGR017W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the nucleus and the cytoplasm	Q
2942	VN_2942	YFR041C	ERJ5	Type I membrane protein with a J domain is required to preserve the folding capacity of the endoplasmic reticulum; loss of the non-essential ERJ5 gene leads to a constitutively induced unfolded protein response	Q
2943	VN_2943	YNL202W	SPS19	Peroxisomal 2,4-dienoyl-CoA reductase, auxiliary enzyme of fatty acid beta-oxidation; homodimeric enzyme required for growth and sporulation on petroselinic acid medium; expression induced during late sporulation and in the presence of oleate	Q
2944	VN_2944	YHL034C	SBP1	Putative RNA binding protein; involved in translational repression and found in cytoplasmic P bodies; found associated with small nucleolar RNAs snR10 and snR11	Q
2945	VN_2945	YGR222W	PET54	Mitochondrial inner membrane protein that binds to the 5' UTR of the COX3 mRNA to activate its translation together with Pet122p and Pet494p; also binds to the COX1 Group I intron A15 beta to facilitate exon ligation during splicing	Q
2946	VN_2946	YPR069C	SPE3	Spermidine synthase, involved in biosynthesis of spermidine and also	Q

				in biosynthesis of pantothenic acid; spermidine is required for growth of wild-type cells	
2947	VN_2947	YNL232W	CSL4	Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; predicted to contain an S1 RNA binding domain; has similarity to human hCsl4p (EXOSC1)	Q
2948	VN_2948	YLR003C	CMS1	Subunit of U3-containing 90S preribosome processome complex involved in production of 18S rRNA and assembly of small ribosomal subunit; overexpression rescues suppressor mutant of mcm10; null mutant is viable	Q
2949	VN_2949	YGR021W	YGR021W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2950	VN_2950	YJL177W	RPL17B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl17Ap and has similarity to E. coli L22 and rat L17 ribosomal proteins	Q
2951	VN_2951	YGR147C	NAT2	Protein with an apparent role in acetylation of N-terminal methionine residues	Q
2952	VN_2952	YIL124W	AYR1	NADPH-dependent 1-acyl dihydroxyacetone phosphate reductase found in lipid particles, ER, and mitochondrial outer membrane; involved in phosphatidic acid biosynthesis; required for spore germination; capable of metabolizing steroid hormones	Q
2953	VN_2953	YGL044C	RNA15	Cleavage and polyadenylation factor I (CF I) component involved in cleavage and polyadenylation of mRNA 3' ends; interacts with the A-rich polyadenylation signal in complex with Rna14p and Hrp1p	Q
2954	VN_2954	YFR047C	BNA6	Quinolinate phosphoribosyl transferase, required for the de novo biosynthesis of NAD from tryptophan via kynurenine; expression regulated by Hst1p	Q
2955	VN_2955	YOR028C	CIN5	Basic leucine zipper (bZIP) transcription factor of the yAP-1 family, mediates pleiotropic drug resistance and salt tolerance; nuclearly localized under oxidative stress and sequestered in the cytoplasm by Lot6p under reducing conditions	Q
2956	VN_2956	YHR029C	YHI9	Protein of unknown function; null mutant is defective in unfolded protein response; possibly involved in a membrane regulation metabolic pathway; member of the PhzF superfamily, though most likely not involved in phenazine production	Q
2957	VN_2957	YHR062C	RPP1	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends	Q
2958	VN_2958	YDR237W	MRPL7	Mitochondrial ribosomal protein of the large subunit	Strain failed to verify via PCR
2959	VN_2959	YOR223W	YOR223W	Putative protein of unknown function	Q
2960	VN_2960	YLR351C	NIT3	Nit protein, one of two proteins in S. cerevisiae with similarity to the Nit domain of NitFhit from fly and worm and to the mouse and human Nit protein which interacts with the Fhit tumor suppressor; nitrilase superfamily member	Q
2961	VN_2961	YGR205W	YGR205W	ATP-binding protein of unknown function; crystal structure resembles that of E.coli pantothenate kinase and other small kinases	Q
2962	VN_2962	YBR191W	RPL21A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl21Bp and has similarity to rat L21 ribosomal protein	Strain failed to verify via PCR
2963	VN_2963	YGR239C	PEX21	Peroxin required for targeting of peroxisomal matrix proteins containing PTS2; interacts with Pex7p; partially redundant with Pex18p	Q
2964	VN_2964	YJR155W	AAD10	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role	Q
2965	VN_2965	YIL034C	CAP2	Beta subunit of the capping protein (CP) heterodimer (Cap1p and Cap2p) which binds to the barbed ends of actin filaments preventing further polymerization; localized predominantly to cortical actin patches	Q
2966	VN_2966	YMR069W	NAT4	N alpha-acetyl-transferase, involved in acetylation of the N-terminal	Q

				residues of histones H4 and H2A	
2967	VN_2967	YNL033W	YNL033W	Putative protein of unknown function	Q
2968	VN_2968	YJR111C	YJR111C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondria	Q
2969	VN_2969	YGL224C	SDT1	Pyrimidine nucleotidase; overexpression suppresses the 6-AU sensitivity of transcription elongation factor S-II, as well as resistance to other pyrimidine derivatives	Q
2970	VN_2970	YBR257W	POP4	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends; binds to the RPR1 RNA subunit in RNase P	Q
2971	VN_2971	YNL289W	PCL1	Cyclin, interacts with cyclin-dependent kinase Pho85p; member of the Pcl1,2-like subfamily, involved in the regulation of polarized growth and morphogenesis and progression through the cell cycle; localizes to sites of polarized cell growth	Q
2972	VN_2972	YKL095W	YJU2	) and acts after Prp2p to promote the first catalytic reaction of splicing	Strain failed to verify via PCR
2973	VN_2973	YPR116W	RRG8	Putative protein of unknown function, required for mitochondrial genome maintenance; null mutation results in a decrease in plasma membrane electron transport	Strain failed to verify via PCR
2974	VN_2974	YOR362C	PRE10	Alpha 7 subunit of the 20S proteasome	Strain failed to verify via PCR
2975	VN_2975	YPR103W	PRE2	Beta 5 subunit of the 20S proteasome, responsible for the chymotryptic activity of the proteasome	Q
2976	VN_2976	YDR098C	GRX3	Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; monothiol glutaredoxin subfamily member along with Grx4p and Grx5p; protects cells from oxidative damage	Q
2977	VN_2977	YNL286W	CUS2	Protein that binds to U2 snRNA and Prp11p, may be involved in U2 snRNA folding; contains two RNA recognition motifs (RRMs)	Q
2978	VN_2978	YNL320W	YNL320W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
2979	VN_2979	YKR046C	PET10	Protein of unknown function that co-purifies with lipid particles; expression pattern suggests a role in respiratory growth; computational analysis of large-scale protein-protein interaction data suggests a role in ATP/ADP exchange	Q
2980	VN_2980	YDL006W	PTC1	Type 2C protein phosphatase (PP2C); inactivates the osmosensing MAPK cascade by dephosphorylating Hog1p; mutation delays mitochondrial inheritance; deletion reveals defects in precursor tRNA splicing, sporulation and cell separation	Q
2981	VN_2981	YHR067W	HTD2	Mitochondrial 3-hydroxyacyl-thioester dehydratase involved in fatty acid biosynthesis, required for respiratory growth and for normal mitochondrial morphology	Q
2982	VN_2982	YDL127W	PCL2	Cyclin, interacts with cyclin-dependent kinase Pho85p; member of the Pcl1,2-like subfamily, involved in the regulation of polarized growth and morphogenesis and progression through the cell cycle; localizes to sites of polarized cell growth	Q
2983	VN_2983	YPL129W	TAF14	Subunit of TFIID, TFIIF, INO80, SWI/SNF, and NuA3 complexes, involved in RNA polymerase II transcription initiation and in chromatin modification; contains a YEATS domain	Q
2984	VN_2984	YOR255W	OSW1	Protein involved in sporulation; required for the construction of the outer spore wall layers; required for proper localization of Spo14p	Q
2985	VN_2985	YNL162W	RPL42A	Protein component of the large (60S) ribosomal subunit, identical to Rpl42Bp and has similarity to rat L44 ribosomal protein	Q
2986	VN_2986	YPL117C	IDI1	Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP isomerase), catalyzes an essential activation step in the isoprenoid biosynthetic pathway; required for viability	Q
2987	VN_2987	YDL201W	TRM8	Subunit of a tRNA methyltransferase complex composed of Trm8p and Trm82p that catalyzes 7-methylguanosine modification of tRNA	Q

2988	VN_2988	YDR116C	MRPL1	Mitochondrial ribosomal protein of the large subunit	Q
2989	VN_2989	YOR040W	GLO4	Mitochondrial glyoxalase II, catalyzes the hydrolysis of S-D-lactoylglutathione into glutathione and D-lactate	Q
2990	VN_2990	YOR174W	MED4	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation	Q
2991	VN_2991	YOR234C	RPL33B	Ribosomal protein L37 of the large (60S) ribosomal subunit, nearly identical to Rpl33Ap and has similarity to rat L35a; rpl33b null mutant exhibits normal growth while rpl33a rpl33b double null mutant is inviable	Q
2992	VN_2992	YEL009C	GCN4	Basic leucine zipper (bZIP) transcriptional activator of amino acid biosynthetic genes in response to amino acid starvation; expression is tightly regulated at both the transcriptional and translational levels	Q
2993	VN_2993	YHR163W	SOL3	6-phosphogluconolactonase, catalyzes the second step of the pentose phosphate pathway; weak multicopy suppressor of los1-1 mutation; homologous to Sol2p and Sol1p	Q
2994	VN_2994	YEL018W	EA5	Esa1p-associated factor, non-essential subunit of the NuA4 acetyltransferase complex	Q
2995	VN_2995	YIL052C	RPL34B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl34Ap and has similarity to rat L34 ribosomal protein	Q
2996	VN_2996	YBR165W	UBS1	Ubiquitin-conjugating enzyme suppressor that functions as a general positive regulator of Cdc34p activity; nuclear protein that may represent a link between nucleocytoplasmic transport and ubiquitin ligase activity	Q
2997	VN_2997	YGL096W	TOS8	Homeodomain-containing protein and putative transcription factor found associated with chromatin; target of SBF transcription factor; induced during meiosis and under cell-damaging conditions; similar to Cup9p transcription factor	Q
2998	VN_2998	YPR202W	YPR202W	Putative protein of unknown function with similarity to telomere-encoded helicases; YPR202W is not an essential gene; transcript is predicted to be spliced but there is no evidence that it is spliced in vivo	Q
2999	VN_2999	YDR337W	MRPS28	Mitochondrial ribosomal protein of the small subunit	Q
3000	VN_3000	YIL050W	PCL7	Pho85p cyclin of the Pho80p subfamily, forms a functional kinase complex with Pho85p which phosphorylates Mmr1p and is regulated by Pho81p; involved in glycogen metabolism, expression is cell-cycle regulated	Q
3001	VN_3001	YPL237W	SUI3	Beta subunit of the translation initiation factor eIF2, involved in the identification of the start codon; proposed to be involved in mRNA binding	Q
3002	VN_3002	YEL005C	VAB2	Protein with a potential role in vacuolar function, as suggested by its ability to bind Vac8p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Q
3003	VN_3003	YFR027W	ECO1	Acetyltransferase required for sister chromatid cohesion; modifies Smc3p at DNA replication forks during S-phase; modifies Mcd1p in response to double-strand DNA breaks during G2/M; acetylation of cohesin subunits antagonizes Rad61p	Q
3004	VN_3004	YJL203W	PRP21	Subunit of the SF3a splicing factor complex, required for spliceosome assembly	Q
3005	VN_3005	YGL005C	COG7	Component of the conserved oligomeric Golgi complex (Cog1p through Cog8p), a cytosolic tethering complex that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments	Q
3006	VN_3006	YBR146W	MRPS9	Mitochondrial ribosomal protein of the small subunit	Q
3007	VN_3007	YDL186W	YDL186W	Putative protein of unknown function; YDL186W is not an essential gene	Strain failed to verify via PCR
3008	VN_3008	YJL174W	KRE9	Glycoprotein involved in cell wall beta-glucan assembly; null mutation leads to severe growth defects, aberrant multibudded morphology, and mating defects	Q
3009	VN_3009	YBR011C	IPP1	Cytoplasmic inorganic pyrophosphatase (PPase), homodimer that catalyzes the rapid exchange of oxygens from Pi with water, highly	Q

				expressed and essential for viability, active-site residues show identity to those from <i>E. coli</i> PPase	
3010	VN_3010	YER023W	PRO3	Delta 1-pyrroline-5-carboxylate reductase, catalyzes the last step in proline biosynthesis	Q
3011	VN_3011	YLR136C	TIS11	mRNA-binding protein expressed during iron starvation; binds to a sequence element in the 3'-untranslated regions of specific mRNAs to mediate their degradation; involved in iron homeostasis	Q
3012	VN_3012	YDR106W	ARP10	Component of the dynactin complex, localized to the pointed end of the Arp1p filament; may regulate membrane association of the complex	Q
3013	VN_3013	YDR361C	BCP1	Essential protein involved in nuclear export of Mss4p, which is a lipid kinase that generates phosphatidylinositol 4,5-bisphosphate and plays a role in actin cytoskeleton organization and vesicular transport	Q
3014	VN_3014	YHR090C	YNG2	Subunit of the NuA4 histone acetyltransferase complex that acetylates histone H4 and H2A; has similarity to the human tumor suppressor ING1 and its isoforms ING4 and ING5	Q
3015	VN_3015	YNL032W	SIW14	Tyrosine phosphatase that plays a role in actin filament organization and endocytosis; localized to the cytoplasm	Q
3016	VN_3016	YLR284C	ECI1	Peroxisomal delta3,delta2-enoyl-CoA isomerase, hexameric protein that converts 3-hexenoyl-CoA to trans-2-hexenoyl-CoA, essential for the beta-oxidation of unsaturated fatty acids, oleate-induced	Q
3017	VN_3017	YJL115W	ASF1	Nucleosome assembly factor, involved in chromatin assembly and disassembly, anti-silencing protein that causes derepression of silent loci when overexpressed; plays a role in regulating Ty1 transposition	Q
3018	VN_3018	YDR087C	RRP1	Essential evolutionarily conserved nucleolar protein necessary for biogenesis of 60S ribosomal subunits and processing of pre-rRNAs to mature rRNAs, associated with several distinct 66S pre-ribosomal particles	Q
3019	VN_3019	YKL023W	YKL023W	Putative protein of unknown function, predicted by computational methods to be involved in mRNA degradation; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
3020	VN_3020	YLR344W	RPL26A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Bp and has similarity to <i>E. coli</i> L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA	Q
3021	VN_3021	YDL083C	RPS16B	Protein component of the small (40S) ribosomal subunit; identical to Rps16Ap and has similarity to <i>E. coli</i> S9 and rat S16 ribosomal proteins	Q
3022	VN_3022	YLR312W-A	MRPL15	Mitochondrial ribosomal protein of the large subunit	Q
3023	VN_3023	YLR079W	SIC1	Inhibitor of Cdc28-Clb kinase complexes that controls G1/S phase transition, preventing premature S phase and ensuring genomic integrity; phosphorylation targets Sic1p for SCF(CDC4)-dependent turnover; functional homolog of mammalian Kip1	Q
3024	VN_3024	YGL240W	DOC1	Processivity factor required for the ubiquitination activity of the anaphase promoting complex (APC), mediates the activity of the APC by contributing to substrate recognition; involved in cyclin proteolysis	Q
3025	VN_3025	YJR096W	YJR096W	Putative xylose and arabinose reductase; member of the aldo-keto reductase (AKR) family; GFP-fusion protein is induced in response to the DNA-damaging agent MMS	Q
3026	VN_3026	YNL252C	MRPL17	Mitochondrial ribosomal protein of the large subunit	Q
3027	VN_3027	YML041C	VPS71	Nucleosome-binding component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A; required for vacuolar protein sorting	Q
3028	VN_3028	YJR116W	YJR116W	Putative protein of unknown function	Q
3029	VN_3029	YGL019W	CKB1	Beta regulatory subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation; the holoenzyme also contains CKA1, CKA2 and CKB2, the many substrates include transcription factors and all RNA polymerases	Q
3030	VN_3030	YLR290C	YLR290C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YLR290C is not an essential gene	Q

3031	VN_3031	YGL057C	GEP7	Protein of unknown function; null mutant exhibits a respiratory growth defect and synthetic interactions with prohibitin (phb1) and gem1; authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3032	VN_3032	YMR043W	MCM1	Transcription factor involved in cell-type-specific transcription and pheromone response; plays a central role in the formation of both repressor and activator complexes	Q
3033	VN_3033	YLR338W	OPI9	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF VRP1/YLR337C	Q
3034	VN_3034	YMR087W	YMR087W	Putative ADP-ribose-1"-monophosphatase that converts ADP-ribose-1"-monophosphate to ADP-ribose; may have a role in tRNA splicing; contains an A1pp domain	Q
3035	VN_3035	YGR053C	YGR053C	Putative protein of unknown function	Q
3036	VN_3036	YKR025W	RPC37	RNA polymerase III subunit C37	Q
3037	VN_3037	YPL033C	SRL4	Protein of unknown function; involved in regulation of dNTP production; null mutant suppresses the lethality of lcd1 and rad53 mutations; expression is induced by Kar4p	Q
3038	VN_3038	YKL199C	PTK1	#N/A	Q
3039	VN_3039	YHR192W	YHR192W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and is induced in response to the DNA-damaging agent MMS	Q
3040	VN_3040	YOL088C	MPD2	Member of the protein disulfide isomerase (PDI) family, exhibits chaperone activity; overexpression suppresses the lethality of a pdi1 deletion but does not complement all Pdi1p functions; undergoes oxidation by Ero1p	Q
3041	VN_3041	YCR047C	BUD23	Methyltransferase, methylates residue G1575 of 18S rRNA; required for rRNA processing and nuclear export of 40S ribosomal subunits independently of methylation activity; diploid mutant displays random budding pattern	Q
3042	VN_3042	YGR132C	PHB1	Subunit of the prohibitin complex (Phb1p-Phb2p), a 1.2 MDa ring-shaped inner mitochondrial membrane chaperone that stabilizes newly synthesized proteins; determinant of replicative life span; involved in mitochondrial segregation	Q
3043	VN_3043	YOR194C	TOA1	TFIIA large subunit; involved in transcriptional activation, acts as antirepressor or as coactivator; homologous to largest and second largest subunits of human and Drosophila TFIIA	Q
3044	VN_3044	YLR404W	FLD1	Seipin protein involved in lipid droplet morphology, number, and size; proposed to be involved in lipid metabolism; related to the human BSCL2 which is associated with lipodystrophy	Q
3045	VN_3045	YNL019C	YNL019C	Putative protein of unknown function	Strain failed to verify via PCR
3046	VN_3046	YHR160C	PEX18	Peroxin required for targeting of peroxisomal matrix proteins containing PTS2; interacts with Pex7p; partially redundant with Pex21p	Q
3047	VN_3047	YOR104W	PIN2	Protein that induces appearance of [PIN+] prion when overproduced; predicted to be palmitoylated	Q
3048	VN_3048	YBL010C	YBL010C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein colocalizes with clathrin-coated vesicles	Q
3049	VN_3049	YML026C	RPS18B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps18Ap and has similarity to E. coli S13 and rat S18 ribosomal proteins	Q
3050	VN_3050	YML014W	TRM9	tRNA methyltransferase, catalyzes esterification of modified uridine nucleotides in tRNA(Arg3) and tRNA(Glu), likely as part of a complex with Trm112p; deletion confers resistance to zymocin	Q
3051	VN_3051	YKL055C	OAR1	Mitochondrial 3-oxoacyl-[acyl-carrier-protein] reductase, may comprise a type II mitochondrial fatty acid synthase along with Mct1p	Q
3052	VN_3052	YPR027C	YPR027C	Putative protein of unknown function	Q

3053	VN_3053	YDL051W	LHP1	RNA binding protein required for maturation of tRNA and U6 snRNA precursors; acts as a molecular chaperone for RNAs transcribed by polymerase III; homologous to human La (SS-B) autoantigen	Q
3054	VN_3054	YDR384C	ATO3	Plasma membrane protein, regulation pattern suggests a possible role in export of ammonia from the cell; phosphorylated in mitochondria; member of the TC 9.B.33 YaaH family of putative transporters	Q
3055	VN_3055	YFR052W	RPN12	Subunit of the 19S regulatory particle of the 26S proteasome lid; synthetically lethal with RPT1, which is an ATPase component of the 19S regulatory particle; physically interacts with Nob1p and Rpn3p	Q
3056	VN_3056	YNL155W	YNL155W	Putative protein of unknown function, contains DHHC domain, also predicted to have thiol-disulfide oxidoreductase active site	Strain failed to verify via PCR
3057	VN_3057	YLR205C	HMX1	ER localized, heme-binding peroxidase involved in the degradation of heme; does not exhibit heme oxygenase activity despite similarity to heme oxygenases; expression regulated by AFT1	Q
3058	VN_3058	YNR068C	YNR068C	Putative protein of unknown function	Q
3059	VN_3059	YOR180C	DCI1	Peroxisomal protein; identification as a delta(3,5)-delta(2,4)-dienoyl-CoA isomerase involved in fatty acid metabolism is disputed	Q
3060	VN_3060	YDR025W	RPS11A	Protein component of the small (40S) ribosomal subunit; identical to Rps11Bp and has similarity to E. coli S17 and rat S11 ribosomal proteins	Q
3061	VN_3061	YDL049C	KNH1	Protein with similarity to Kre9p, which is involved in cell wall beta 1,6-glucan synthesis; overproduction suppresses growth defects of a kre9 null mutant; required for propionic acid resistance	Q
3062	VN_3062	YAL037W	YAL037W	Putative protein of unknown function	Q
3063	VN_3063	YDL043C	PRP11	Subunit of the SF3a splicing factor complex, required for spliceosome assembly	Q
3064	VN_3064	YDL111C	RRP42	Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; has similarity to E. coli RNase PH and to human hRrp42p (EXOSC7)	Q
3065	VN_3065	YDR471W	RPL27B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein	Strain failed to verify via PCR
3066	VN_3066	YKR006C	MRPL13	Mitochondrial ribosomal protein of the large subunit, not essential for mitochondrial translation	Strain failed to verify via PCR
3067	VN_3067	YGL085W	YGL085W	Putative protein of unknown function, has homology to Staphylococcus aureus nuclease; green fluorescent protein (GFP)-fusion protein localizes to mitochondria and is induced in response to the DNA-damaging agent MMS	Q
3068	VN_3068	YOL121C	RPS19A	Protein component of the small (40S) ribosomal subunit, required for assembly and maturation of pre-40 S particles; mutations in human RPS19 are associated with Diamond Blackfan anemia; nearly identical to Rps19Bp	Strain failed to verify via PCR
3069	VN_3069	YML105C	SEC65	Subunit of the signal recognition particle (SRP), involved in protein targeting to the ER; interacts with Srp54p; homolog of mammalian SRP19	Strain failed to verify via PCR
3070	VN_3070	YIL069C	RPS24B	Protein component of the small (40S) ribosomal subunit; identical to Rps24Ap and has similarity to rat S24 ribosomal protein	Q
3071	VN_3071	YHL001W	RPL14B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl14Ap and has similarity to rat L14 ribosomal protein	Q
3072	VN_3072	YGR220C	MRPL9	Mitochondrial ribosomal protein of the large subunit	Q
3073	VN_3073	YDR179W-A	YDR179W-A	Putative protein of unknown function	Q
3074	VN_3074	YEL019C	MMS21	SUMO ligase involved in chromosomal organization and DNA repair; essential subunit of the Mms21-Smc5-Smc6 complex; mutants are sensitive to methyl methanesulfonate and show increased spontaneous mutation and mitotic recombination	Q
3075	VN_3075	YFR050C	PRE4	Beta 7 subunit of the 20S proteasome	Strain failed to verify via

					PCR
3076	VN_3076	YDR152W	GIR2	Highly-acidic cytoplasmic RWD domain-containing protein of unknown function; interacts with Rbg1p and Gcn1p; associates with translating ribosomes; putative intrinsically unstructured protein	Strain failed to verify via PCR
3077	VN_3077	YIL093C	RSM25	Mitochondrial ribosomal protein of the small subunit	Strain failed to verify via PCR
3078	VN_3078	YOR278W	HEM4	Uroporphyrinogen III synthase, catalyzes the conversion of hydroxymethylbilane to uroporphyrinogen III, the fourth step in heme biosynthesis; deficiency in the human homolog can result in the disease congenital erythropoietic porphyria	Q
3079	VN_3079	YGR201C	YGR201C	Putative protein of unknown function	Q
3080	VN_3080	YOR145C	PNO1	Essential nucleolar protein required for pre-18S rRNA processing, interacts with Dim1p, an 18S rRNA dimethyltransferase, and also with Nob1p, which is involved in proteasome biogenesis; contains a KH domain	Strain failed to verify via PCR
3081	VN_3081	YMR312W	ELP6	Subunit of Elongator complex, which is required for modification of wobble nucleosides in tRNA; required for Elongator structural integrity	Q
3082	VN_3082	YGR042W	YGR042W	Putative protein of unknown function; involved in maintenance of proper telomere length; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
3083	VN_3083	YKL006W	RPL14A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl14Bp and has similarity to rat L14 ribosomal protein; rpl14a csh5 double null mutant exhibits synthetic slow growth	Strain failed to verify via PCR
3084	VN_3084	YHR134W	WSS1	Sumoylated protein of unknown function, identified based on genetic interactions with SMT3; UV-sensitive mutant phenotype and genetic interactions suggest a role in the DNA damage response, processing stalled or collapsed replication forks	Strain failed to verify via PCR
3085	VN_3085	YHR200W	RPN10	Non-ATPase base subunit of the 19S regulatory particle (RP) of the 26S proteasome; N-terminus plays a role in maintaining the structural integrity of the RP; binds selectively to polyubiquitin chains; homolog of the mammalian S5a protein	Q
3086	VN_3086	YEL021W	URA3	Orotidine-5'-phosphate (OMP) decarboxylase, catalyzes the sixth enzymatic step in the de novo biosynthesis of pyrimidines, converting OMP into uridine monophosphate (UMP); converts 5-FOA into 5-fluorouracil, a toxic compound	Strain failed to verify via PCR
3087	VN_3087	YGL174W	BUD13	Subunit of the RES complex, which is required for nuclear pre-mRNA retention and splicing; involved in bud-site selection; diploid mutants display a unipolar budding pattern instead of the wild-type bipolar pattern	Strain failed to verify via PCR
3088	VN_3088	YGL117W	YGL117W	Putative protein of unknown function	Q
3089	VN_3089	YDR405W	MRP20	Mitochondrial ribosomal protein of the large subunit	Q
3090	VN_3090	YBR213W	MET8	Bifunctional dehydrogenase and ferroxidase, involved in the biosynthesis of siroheme, a prosthetic group used by sulfite reductase; required for sulfate assimilation and methionine biosynthesis	Q
3091	VN_3091	YJL191W	RPS14B	Ribosomal protein 59 of the small subunit, required for ribosome assembly and 20S pre-rRNA processing; mutations confer cryptopleurine resistance; nearly identical to Rps14Ap and similar to E. coli S11 and rat S14 ribosomal proteins	Q
3092	VN_3092	YDL086W	YDL086W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YDL086W is not an essential gene	Q
3093	VN_3093	YPL196W	OXR1	Protein of unknown function required for normal levels of resistance to oxidative damage, null mutants are sensitive to hydrogen peroxide; member of a conserved family of proteins found in eukaryotes but not in prokaryotes	Q
3094	VN_3094	YGR280C	PXR1	Essential protein involved in rRNA and snoRNA maturation; competes with TLC1 RNA for binding to Est2p, suggesting a role in negative regulation of telomerase; human homolog inhibits telomerase; contains	Q

				a G-patch RNA interacting domain	
3095	VN_3095	YBL095W	YBL095W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3096	VN_3096	YIL011W	TIR3	Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins; expressed under anaerobic conditions and required for anaerobic growth	Q
3097	VN_3097	YKL007W	CAP1	Alpha subunit of the capping protein (CP) heterodimer (Cap1p and Cap2p) which binds to the barbed ends of actin filaments preventing further polymerization; localized predominantly to cortical actin patches	Q
3098	VN_3098	YER177W	BMH1	14-3-3 protein, major isoform; controls proteome at post-transcriptional level, binds proteins and DNA, involved in regulation of many processes including exocytosis, vesicle transport, Ras/MAPK signaling, and rapamycin-sensitive signaling	Q
3099	VN_3099	YIL070C	MAM33	Acidic protein of the mitochondrial matrix involved in oxidative phosphorylation; related to the human complement receptor gC1q-R	Strain failed to verify via PCR
3100	VN_3100	YGL237C	HAP2	Subunit of the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression; contains sequences sufficient for both complex assembly and DNA binding	Q
3101	VN_3101	YGR161C	RTS3	Putative component of the protein phosphatase type 2A complex	Q
3102	VN_3102	YDR272W	GLO2	Cytoplasmic glyoxalase II, catalyzes the hydrolysis of S-D-lactoylglutathione into glutathione and D-lactate	Strain failed to verify via PCR
3103	VN_3103	YKR060W	UTP30	Subunit of U3-containing 90S preribosome complex involved in production of 18S rRNA and assembly of small ribosomal subunit	Q
3104	VN_3104	YDR099W	BMH2	14-3-3 protein, minor isoform; controls proteome at post-transcriptional level, binds proteins and DNA, involved in regulation of many processes including exocytosis, vesicle transport, Ras/MAPK signaling, and rapamycin-sensitive signaling	Q
3105	VN_3105	YIL148W	RPL40A	Fusion protein, identical to Rpl40Bp, that is cleaved to yield ubiquitin and a ribosomal protein of the large (60S) ribosomal subunit with similarity to rat L40; ubiquitin may facilitate assembly of the ribosomal protein into ribosomes	Strain failed to verify via PCR
3106	VN_3106	YHL049C	YHL049C	Putative protein of unknown function	Q
3107	VN_3107	YLR046C	YLR046C	Putative membrane protein; member of the fungal lipid-translocating exporter (LTE) family of proteins; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance	Q
3108	VN_3108	YJR144W	MGM101	Protein involved in mitochondrial genome maintenance; component of the mitochondrial nucleoid, required for the repair of oxidative mtDNA damage	Q
3109	VN_3109	YOR062C	YOR062C	Protein of unknown function; similar to YKR075Cp and Reg1p; expression regulated by glucose and Rgt1p; GFP-fusion protein is induced in response to the DNA-damaging agent MMS	Q
3110	VN_3110	YER180C	ISC10	Protein required for sporulation, transcript is induced 7.5 hours after induction of meiosis, expected to play significant role in the formation of reproductive cells	Q
3111	VN_3111	YJR101W	RSM26	Mitochondrial ribosomal protein of the small subunit	Strain failed to verify via PCR
3112	VN_3112	YIR016W	YIR016W	Putative protein of unknown function; expression directly regulated by the metabolic and meiotic transcriptional regulator Ume6p; overexpression causes a cell cycle delay or arrest; YIR016W is a non-essential gene	Q
3113	VN_3113	YIR036C	IRC24	Putative benzil reductase;(GFP)-fusion protein localizes to the cytoplasm and is induced by the DNA-damaging agent MMS; sequence similarity with short-chain dehydrogenase/reductases; null mutant has increased spontaneous Rad52p foci	Q

3114	VN_3114	YDR319C	YDR319C	Putative protein of unknown function, identified as an ortholog of the highly conserved FIT family of proteins involved in triglyceride droplet biosynthesis; interacts with Sst2p and Hsp82p in high-throughput two-hybrid screens	Q
3115	VN_3115	YLR271W	YLR271W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus and is induced in response to the DNA-damaging agent MMS	Q
3116	VN_3116	YGL050W	TYW3	tRNA methyltransferase required for synthesis of wybutosine, a modified guanosine found at the 3'-position adjacent to the anticodon of phenylalanine tRNA which supports reading frame maintenance by stabilizing codon-anticodon interactions	Q
3117	VN_3117	YDR262W	YDR262W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole and is induced in response to the DNA-damaging agent MMS; gene expression increases in response to Zymolase treatment	Q
3118	VN_3118	YIL053W	RHR2	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress	Q
3119	VN_3119	YNL108C	YNL108C	Putative protein of unknown function with similarity to Tfc7p and prokaryotic phosphotransfer enzymes; null mutant shows alterations in glucose metabolism; GFP-fusion protein localizes to the cytoplasm and nucleus	Q
3120	VN_3120	YKR034W	DAL80	Negative regulator of genes in multiple nitrogen degradation pathways; expression is regulated by nitrogen levels and by Gln3p; member of the GATA-binding family, forms homodimers and heterodimers with Deh1p	Strain failed to verify via PCR
3121	VN_3121	YPR009W	SUT2	Putative transcription factor; multicopy suppressor of mutations that cause low activity of the cAMP/protein kinase A pathway; highly similar to Sut1p	Q
3122	VN_3122	YKL206C	ADD66	Protein involved in 20S proteasome assembly; forms a heterodimer with Pba1p that binds to proteasome precursors; similar to human PAC2 constituent of the PAC1-PAC2 complex involved in proteasome assembly	Q
3123	VN_3123	YLR102C	APC9	Subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition	Q
3124	VN_3124	YLR030W	YLR030W	Putative protein of unknown function	Q
3125	VN_3125	YDR429C	TIF35	eIF3g subunit of the core complex of translation initiation factor 3 (eIF3), which is essential for translation	Strain failed to verify via PCR
3126	VN_3126	YLR412W	BER1	Protein involved in microtubule-related processes, N-acetylation; GFP-fusion protein localizes to the cytoplasm and is induced in response to the DNA-damaging agent MMS; YLR412W is not an essential gene; similar to Arabidopsis SRR1 gene	Q
3127	VN_3127	YLR064W	YLR064W	Putative protein of unknown function; highly conserved across species and orthologous to human TMEM33; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YLR064W is not an essential gene	Q
3128	VN_3128	YGL154C	LYS5	Phosphopantetheinyl transferase involved in lysine biosynthesis; converts inactive apo-form of Lys2p (alpha-aminoadipate reductase) into catalytically active holo-form by posttranslational addition of phosphopantetheine	Q
3129	VN_3129	YKL208W	CBT1	Protein involved in 5' end processing of mitochondrial COB, 15S_rRNA, and RPM1 transcripts; may also have a role in 3' end processing of the COB pre-mRNA; displays genetic interaction with cell cycle-regulated kinase Dbf2p	Q
3130	VN_3130	YNL210W	MER1	Protein with RNA-binding motifs required for meiosis-specific mRNA splicing; required for chromosome pairing and meiotic recombination	Q
3131	VN_3131	YLR059C	REX2	3'-5' RNA exonuclease; involved in 3'-end processing of U4 and U5 snRNAs, 5S and 5.8S rRNAs, and RNase P and RNase MRP RNA; localized to mitochondria and null suppresses escape of mtDNA to nucleus in yme1 yme2 mutants; RNase D exonuclease	Q

3132	VN_3132	YPR134W	MSS18	Nuclear encoded protein needed for efficient splicing of mitochondrial COX1 aI5beta intron; mss18 mutations block cleavage of 5' exon - intron junction; phenotype of intronless strain suggests additional functions	Q
3133	VN_3133	YMR226C	YMR226C	NADP(+)-dependent dehydrogenase; acts on serine, L-allo-threonine, and other 3-hydroxy acids; green fluorescent protein fusion protein localizes to the cytoplasm and nucleus; may interact with ribosomes, based on co-purification experiments	Q
3134	VN_3134	YHR021C	RPS27B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps27Ap and has similarity to rat S27 ribosomal protein	Strain failed to verify via PCR
3135	VN_3135	YLR192C	HCR1	Dual function protein involved in translation initiation as a substoichiometric component (eIF3j) of translation initiation factor 3 (eIF3) and required for processing of 20S pre-rRNA; binds to eIF3 subunits Rpg1p and Prt1p and 18S rRNA	Q
3136	VN_3136	YLR414C	YLR414C	Putative protein of unknown function; localizes to bud and cytoplasm; co-localizes with Sur7p in punctate patches in the plasma membrane; null mutant displays decreased thermotolerance; transcription induced on cell wall damage	Q
3137	VN_3137	YER116C	SLX8	Subunit of the Slx5-Slx8 SUMO-targeted ubiquitin ligase (STUbL) complex; stimulated by prior attachment of SUMO to the substrate; contains a C-terminal RING domain	Q
3138	VN_3138	YMR178W	YMR178W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and nucleus and is induced in response to the DNA-damaging agent MMS; YMR178W is not an essential gene	Q
3139	VN_3139	YLR150W	STM1	Protein required for optimal translation under nutrient stress; perturbs association of Yef3p with ribosomes; involved in TOR signaling; binds G4 quadruplex and purine motif triplex nucleic acid; helps maintain telomere structure	Q
3140	VN_3140	YLR243W	YLR243W	Putative protein of unknown function; YLR243W is an essential gene	Strain failed to verify via PCR
3141	VN_3141	YKR043C	YKR043C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	Q
3142	VN_3142	YNR020C	ATP23	Putative metalloprotease of the mitochondrial inner membrane, required for processing of Atp6p; has an additional role in assembly of the F0 sector of the F1F0 ATP synthase complex	Q
3143	VN_3143	YML024W	RPS17A	Ribosomal protein 51 (rp51) of the small (40s) subunit; nearly identical to Rps17Bp and has similarity to rat S17 ribosomal protein	Q
3144	VN_3144	YBR219C	YBR219C	Putative protein of unknown function; YBR219C is not an essential gene	Q
3145	VN_3145	YPR132W	RPS23B	Ribosomal protein 28 (rp28) of the small (40S) ribosomal subunit, required for translational accuracy; nearly identical to Rps23Ap and similar to E. coli S12 and rat S23 ribosomal proteins; deletion of both RPS23A and RPS23B is lethal	Strain failed to verify via PCR
3146	VN_3146	YCR009C	RVS161	Amphiphysin-like lipid raft protein; interacts with Rvs167p and regulates polarization of the actin cytoskeleton, endocytosis, cell polarity, cell fusion and viability following starvation or osmotic stress	Q
3147	VN_3147	YOR220W	RCN2	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and is induced in response to the DNA-damaging agent MMS; phosphorylated in response to alpha factor	Q
3148	VN_3148	YDR486C	VPS60	Cytoplasmic and vacuolar membrane protein involved in late endosome to vacuole transport; required for normal filament maturation during pseudohyphal growth; may function in targeting cargo proteins for degradation; interacts with Vta1p	Q
3149	VN_3149	YGL046W	PAL3	#N/A	Q
3150	VN_3150	YGR262C	BUD32	Protein kinase proposed to be involved in bud-site selection, telomere uncapping and elongation, and transcription; component of the EKC/KEOPS protein complex with Kae1p, Cgi121p, Pcc1p, and Gon7p	Q

3151	VN_3151	YGR253C	PUP2	Alpha 5 subunit of the 20S proteasome involved in ubiquitin-dependent catabolism; human homolog is subunit zeta	Q
3152	VN_3152	YLR323C	CWC24	Essential protein, component of a complex containing Cef1p; has similarity to <i>S. pombe</i> Cwf24p	Q
3153	VN_3153	YOR039W	CKB2	Beta' regulatory subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation; the holoenzyme also contains CKA1, CKA2 and CKB1, the many substrates include transcription factors and all RNA polymerases	Q
3154	VN_3154	YAR042W	SWH1	Protein similar to mammalian oxysterol-binding protein; contains ankyrin repeats; localizes to the Golgi and the nucleus-vacuole junction	Q
3155	VN_3155	YLL045C	RPL8B	Ribosomal protein L4 of the large (60S) ribosomal subunit, nearly identical to Rpl8Ap and has similarity to rat L7a ribosomal protein; mutation results in decreased amounts of free 60S subunits	Q
3156	VN_3156	YMR157C	AIM36	Protein of unknown function; null mutant displays reduced respiratory growth and elevated frequency of mitochondrial genome loss; the authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies	Q
3157	VN_3157	YDL075W	RPL31A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; loss of both Rpl31p and Rpl39p confers lethality	Strain failed to verify via PCR
3158	VN_3158	YJL066C	MPM1	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches	Q
3159	VN_3159	YNL151C	RPC31	RNA polymerase III subunit C31; contains HMG-like C-terminal domain	Strain failed to verify via PCR
3160	VN_3160	YMR084W	YMR084W	Putative protein of unknown function; YMR084W and adjacent ORF YMR085W are merged in related strains	Q
3161	VN_3161	YHR167W	THP2	Subunit of the THO complex, which connects transcription elongation and mitotic recombination, and of the TREX complex, which is recruited to activated genes and couples transcription to mRNA export; involved in telomere maintenance	Q
3162	VN_3162	YKL207W	AIM27	Member of a transmembrane complex required for efficient folding of proteins in the ER; required for respiratory growth; null mutant displays induction of the unfolded protein response	Q
3163	VN_3163	YNL168C	FMP41	Putative protein of unknown function; GFP-fusion protein is induced in response to the DNA-damaging agent MMS; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3164	VN_3164	YOR095C	RK11	Ribose-5-phosphate ketol-isomerase, catalyzes the interconversion of ribose 5-phosphate and ribulose 5-phosphate in the pentose phosphate pathway; participates in pyridoxine biosynthesis	Q
3165	VN_3165	YCL005W	LDB16	Protein of unknown function; null mutants have decreased net negative cell surface charge; GFP-fusion protein expression is induced in response to the DNA-damaging agent MMS; native protein is detected in purified mitochondria	Q
3166	VN_3166	YNR040W	YNR040W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3167	VN_3167	YNL314W	DAL82	Positive regulator of allophanate inducible genes; binds a dodecanucleotide sequence upstream of all genes that are induced by allophanate; contains an UISALL DNA-binding, a transcriptional activation, and a coiled-coil domain	Q
3168	VN_3168	YIR035C	YIR035C	Putative cytoplasmic protein of unknown function	Q
3169	VN_3169	YER056C-A	RPL34A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl34Bp and has similarity to rat L34 ribosomal protein	Q
3170	VN_3170	YLR186W	EMG1	Member of the alpha/beta knot fold methyltransferase superfamily; required for maturation of 18S rRNA and for 40S ribosome production; interacts with RNA and with S-adenosylmethionine; associates with spindle/microtubules; forms homodimers	Strain failed to verify via PCR
3171	VN_3171	YOR010C	TIR2	Putative cell wall mannoprotein of the Srp1p/Tip1p family of serine-	Q

				alanine-rich proteins; transcription is induced by cold shock and anaerobiosis	
3172	VN_3172	YAL027W	SAW1	Protein involved in Rad1p/Rad10p-dependent removal of 3'-nonhomologous tails during double-strand break repair via single-strand annealing; green fluorescent protein (GFP)-fusion protein localizes to the nucleus	Q
3173	VN_3173	YIL020C	HIS6	Phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase, catalyzes the fourth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts	Q
3174	VN_3174	YLR201C	COQ9	Protein required for ubiquinone (coenzyme Q) biosynthesis and respiratory growth; localizes to the matrix face of the mitochondrial inner membrane in a large complex with ubiquinone biosynthetic enzymes	Q
3175	VN_3175	YBR088C	POL30	Proliferating cell nuclear antigen (PCNA), functions as the sliding clamp for DNA polymerase delta; may function as a docking site for other proteins required for mitotic and meiotic chromosomal DNA replication and for DNA repair	Strain failed to verify via PCR
3176	VN_3176	YPL127C	HHO1	Histone H1, a linker histone required for nucleosome packaging at restricted sites; suppresses DNA repair involving homologous recombination; not required for telomeric silencing, basal transcriptional repression, or efficient sporulation	Q
3177	VN_3177	YGR095C	RRP46	Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; has similarity to E. coli RNase PH and to human hRrp46p (EXOSC5)	Q
3178	VN_3178	YOR152C	YOR152C	Putative protein of unknown function; has no similarity to any known protein; YOR152C is not an essential gene	Q
3179	VN_3179	YDR367W	KEI1	Component of inositol phosphorylceramide (IPC) synthase; forms a complex with Aur1p and regulates its activity; required for IPC synthase complex localization to the Golgi; post-translationally processed by Kex2p; KEI1 is an essential gene	Q
3180	VN_3180	YLR165C	PUS5	Pseudouridine synthase, catalyzes only the formation of pseudouridine (Psi)-2819 in mitochondrial 21S rRNA; not essential for viability	Q
3181	VN_3181	YHR141C	RPL42B	Protein component of the large (60S) ribosomal subunit, identical to Rpl42Ap and has similarity to rat L44; required for propagation of the killer toxin-encoding M1 double-stranded RNA satellite of the L-A double-stranded RNA virus	Strain failed to verify via PCR
3182	VN_3182	YPR158W	CUR1	Protein of unknown function involved in destabilization of [URE3] prions; similar in sequence to Btn2p	Q
3183	VN_3183	YOR289W	YOR289W	Putative protein of unknown function; transcription induced by the unfolded protein response; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
3184	VN_3184	YBL064C	PRX1	Mitochondrial peroxiredoxin (1-Cys Prx) with thioredoxin peroxidase activity, has a role in reduction of hydroperoxides; reactivation requires Trp2p and glutathione; induced during respiratory growth and oxidative stress; phosphorylated	Q
3185	VN_3185	YJR011C	YJR011C	Putative protein of unknown function; GFP-fusion protein expression is induced in response to the DNA-damaging agent MMS	Q
3186	VN_3186	YPL163C	SVS1	Cell wall and vacuolar protein, required for wild-type resistance to vanadate	Q
3187	VN_3187	YCL047C	YCL047C	Putative protein of unknown function	Q
3188	VN_3188	YBL036C	YBL036C	Putative non-specific single-domain racemase based on structural similarity; binds pyridoxal 5'-phosphate; expression of GFP-fusion protein induced in response to the DNA-damaging agent MMS	Q
3189	VN_3189	YHL033C	RPL8A	Ribosomal protein L4 of the large (60S) ribosomal subunit, nearly identical to Rpl8Bp and has similarity to rat L7a ribosomal protein; mutation results in decreased amounts of free 60S subunits	Q
3190	VN_3190	YPR060C	ARO7	Chorismate mutase, catalyzes the conversion of chorismate to prephenate to initiate the tyrosine/phenylalanine-specific branch of aromatic amino acid biosynthesis	Strain failed to verify via PCR
3191	VN_3191	YKL002W	DID4	Class E Vps protein of the ESCRT-III complex, required for sorting of integral membrane proteins into luminal vesicles of multivesicular	Q

				bodies, and for delivery of newly synthesized vacuolar enzymes to the vacuole, involved in endocytosis	
3192	VN_3192	YLR194C	YLR194C	Structural constituent of the cell wall attached to the plasma membrane by a GPI-anchor; expression is upregulated in response to cell wall stress	Q
3193	VN_3193	YGR118W	RPS23A	Ribosomal protein 28 (rp28) of the small (40S) ribosomal subunit, required for translational accuracy; nearly identical to Rps23Bp and similar to E. coli S12 and rat S23 ribosomal proteins; deletion of both RPS23A and RPS23B is lethal	Strain failed to verify via PCR
3194	VN_3194	YPR131C	NAT3	Catalytic subunit of the NatB N-terminal acetyltransferase, which catalyzes acetylation of the amino-terminal methionine residues of all proteins beginning with Met-Asp or Met-Glu and of some proteins beginning with Met-Asn or Met-Met	Q
3195	VN_3195	YDL087C	LUC7	Essential protein associated with the U1 snRNP complex; splicing factor involved in recognition of 5' splice site; contains two zinc finger motifs; N-terminal zinc finger binds pre-mRNA	Q
3196	VN_3196	YLR285W	NNT1	Putative nicotinamide N-methyltransferase, has a role in rDNA silencing and in lifespan determination	Q
3197	VN_3197	YAL009W	SPO7	Putative regulatory subunit of Nem1p-Spo7p phosphatase holoenzyme, regulates nuclear growth by controlling phospholipid biosynthesis, required for normal nuclear envelope morphology, premeiotic replication, and sporulation	Q
3198	VN_3198	YCR059C	YIH1	Protein that inhibits activation of Gcn2p, an eIF2 alpha subunit protein kinase, by competing for Gcn1p binding, thus impacting gene expression in response to starvation; has sequence and functional similarity to the mouse IMPACT gene	Q
3199	VN_3199	YBL043W	ECM13	Non-essential protein of unknown function; induced by treatment with 8-methoxypsoralen and UVA irradiation	Q
3200	VN_3200	YDL136W	RPL35B	Protein component of the large (60S) ribosomal subunit, identical to Rpl35Ap and has similarity to rat L35 ribosomal protein	Q
3201	VN_3201	YMR194W	RPL36A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl36Bp and has similarity to rat L36 ribosomal protein; binds to 5.8 S rRNA	Q
3202	VN_3202	YNL148C	ALF1	Alpha-tubulin folding protein, similar to mammalian cofactor B; Alf1p-GFP localizes to cytoplasmic microtubules; required for the folding of alpha-tubulin and may play an additional role in microtubule maintenance	Q
3203	VN_3203	YPL124W	SPC29	Inner plaque spindle pole body (SPB) component, links the central plaque component Spc42p to the inner plaque component Spc110p; required for SPB duplication	Q
3204	VN_3204	YDR535C	YDR535C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YDR535C is not an essential gene.	Q
3205	VN_3205	YKR094C	RPL40B	Fusion protein, identical to Rpl40Ap, that is cleaved to yield ubiquitin and a ribosomal protein of the large (60S) ribosomal subunit with similarity to rat L40; ubiquitin may facilitate assembly of the ribosomal protein into ribosomes	Q
3206	VN_3206	YOR157C	PUP1	Beta 2 subunit of the 20S proteasome; endopeptidase with trypsin-like activity that cleaves after basic residues; synthesized as a proprotein before being proteolytically processed for assembly into 20S particle; human homolog is subunit Z	Q
3207	VN_3207	YCL010C	SGF29	Probable subunit of SAGA histone acetyltransferase complex	Q
3208	VN_3208	YIL064W	SEE1	Protein with a role in intracellular transport; has sequence similarity to S-adenosylmethionine-dependent methyltransferases of the seven beta-strand family	Q
3209	VN_3209	YKL040C	NFU1	Protein involved in iron metabolism in mitochondria; similar to NifU, which is a protein required for the maturation of the Fe/S clusters of nitrogenase in nitrogen-fixing bacteria	Q
3210	VN_3210	YGR248W	SOL4	6-phosphogluconolactonase with similarity to Sol3p	Q
3211	VN_3211	YER011W	TIR1	Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins; expression is downregulated at acidic pH and induced by cold shock and anaerobiosis; abundance is increased in cells cultured	Q

				without shaking	
3212	VN_3212	YOL038W	PRE6	Alpha 4 subunit of the 20S proteasome; may replace alpha 3 subunit (Pre9p) under stress conditions to create a more active proteasomal isoform; GFP-fusion protein relocates from cytosol to the mitochondrial surface upon oxidative stress	Q
3213	VN_3213	YPL159C	PET20	Mitochondrial protein, required for respiratory growth under some conditions and for stability of the mitochondrial genome	Strain failed to verify via PCR
3214	VN_3214	YDR318W	MCM21	Protein involved in minichromosome maintenance; component of the COMA complex (Ctf19p, Okp1p, Mcm21p, Ame1p) that bridges kinetochore subunits that are in contact with centromeric DNA and the subunits bound to microtubules	Q
3215	VN_3215	YLR061W	RPL22A	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl22Bp and to rat L22 ribosomal protein	Q
3216	VN_3216	YER126C	NSA2	Protein constituent of 66S pre-ribosomal particles, contributes to processing of the 27S pre-rRNA	Q
3217	VN_3217	YPR167C	MET16	3'-phosphoadenylsulfate reductase, reduces 3'-phosphoadenyl sulfate to adenosine-3',5'-bisphosphate and free sulfite using reduced thioredoxin as cosubstrate, involved in sulfate assimilation and methionine metabolism	Q
3218	VN_3218	YEL012W	UBC8	Ubiquitin-conjugating enzyme that negatively regulates gluconeogenesis by mediating the glucose-induced ubiquitination of fructose-1,6-bisphosphatase (FBPase); cytoplasmic enzyme that catalyzes the ubiquitination of histones in vitro	Q
3219	VN_3219	YMR193W	MRPL24	Mitochondrial ribosomal protein of the large subunit	Q
3220	VN_3220	YJL043W	YJL043W	Putative protein of unknown function; YJL043W is a non-essential gene	Q
3221	VN_3221	YKL071W	YKL071W	Putative protein of unknown function; expression induced in cells treated with the mycotoxin patulin, and also the quinone methide triterpene celastrol; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
3222	VN_3222	YLR441C	RPS1A	Ribosomal protein 10 (rp10) of the small (40S) subunit; nearly identical to Rps1Bp and has similarity to rat S3a ribosomal protein	Q
3223	VN_3223	YER153C	PET122	Mitochondrial translational activator specific for the COX3 mRNA, acts together with Pet54p and Pet494p; located in the mitochondrial inner membrane	Q
3224	VN_3224	YOR004W	UTP23	Essential nucleolar protein that is a component of the SSU (small subunit) processome involved in 40S ribosomal subunit biogenesis; has homology to PINc domain protein Fcf1p, although the PINc domain of Utp23p is not required for function	Q
3225	VN_3225	YOR293W	RPS10A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps10Bp and has similarity to rat ribosomal protein S10	Q
3226	VN_3226	YGR207C	YGR207C	Protein that interacts with frataxin (Yfh1p); putative homolog of mammalian electron transfer flavoprotein complex subunit ETF-beta; authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3227	VN_3227	YCL068C	YCL068C	Putative protein of unknown function	Q
3228	VN_3228	YGR115C	YGR115C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified and essential ORF SPT6/YGR115C	Strain failed to verify via PCR
3229	VN_3229	YNL228W	YNL228W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data; almost completely overlaps ORF YNL227C/JJJ1	Strain failed to verify via PCR
3230	VN_3230	YOR060C	YOR060C	Protein of unknown function required for cell viability; deletion mutant harbors aberrant mitochondria	Q
3231	VN_3231	YKL099C	UTP11	Subunit of U3-containing Small Subunit (SSU) processome complex involved in production of 18S rRNA and assembly of small ribosomal subunit	Q
3232	VN_3232	YML063W	RPS1B	Ribosomal protein 10 (rp10) of the small (40S) subunit; nearly identical to Rps1Ap and has similarity to rat S3a ribosomal protein	Q

3233	VN_3233	YFL006W		#N/A	Q
3234	VN_3234	YJL001W	PRE3	Beta 1 subunit of the 20S proteasome, responsible for cleavage after acidic residues in peptides	Strain failed to verify via PCR
3235	VN_3235	YGL011C	SCL1	Alpha 1 subunit of the 20S proteasome involved in the degradation of ubiquitinated substrates; 20S proteasome is the core complex of the 26S proteasome; essential for growth; detected in the mitochondria	Strain failed to verify via PCR
3236	VN_3236	YLR126C	YLR126C	Putative protein of unknown function with similarity to glutamine amidotransferase proteins; has Aft1p-binding motif in the promoter; may be involved in copper and iron homeostasis; YLR126C is not an essential protein	Q
3237	VN_3237	YCR076C	YCR076C	Putative protein of unknown function; YCR076C is not an essential gene	Q
3238	VN_3238	YER062C	HOR2	One of two redundant DL-glycerol-3-phosphatases (RHR2/GPP1 encodes the other) involved in glycerol biosynthesis; induced in response to hyperosmotic stress and oxidative stress, and during the diauxic transition	Q
3239	VN_3239	YML092C	PRE8	Alpha 2 subunit of the 20S proteasome	Q
3240	VN_3240	YDR050C	TPI1	Triose phosphate isomerase, abundant glycolytic enzyme; mRNA half-life is regulated by iron availability; transcription is controlled by activators Reb1p, Gcr1p, and Rap1p through binding sites in the 5' non-coding region	Q
3241	VN_3241	YGR034W	RPL26B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA	Q
3242	VN_3242	YDR174W	HMO1	Chromatin associated high mobility group (HMG) family member involved in genome maintenance; rDNA-binding component of the Pol I transcription system; associates with a 5'-3' DNA helicase and Fpr1p, a prolyl isomerase	Q
3243	VN_3243	YLR211C	YLR211C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLR211C is not an essential gene; ORF contains an intron	Strain failed to verify via PCR
3244	VN_3244	YPL027W	SMA1	Protein of unknown function involved in the assembly of the prospore membrane during sporulation; interacts with Spo14p	Q
3245	VN_3245	YHR041C	SRB2	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; general transcription factor involved in telomere maintenance	Q
3246	VN_3246	YGR075C	PRP38	Unique component of the U4/U6.U5 tri-snRNP particle, required for conformational changes which result in the catalytic activation of the spliceosome; dispensable for spliceosome assembly	Q
3247	VN_3247	YBR090C	YBR090C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	Q
3248	VN_3248	YJL136C	RPS21B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps21Ap and has similarity to rat S21 ribosomal protein	Strain failed to verify via PCR
3249	VN_3249	YPL199C	YPL199C	Putative protein of unknown function, predicted to be palmitoylated	Strain failed to verify via PCR
3250	VN_3250	YGR158C	MTR3	Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; has similarity to E. coli RNase PH and to human hMtr3p (EXOSC6)	Strain failed to verify via PCR
3251	VN_3251	YPR143W	RRP15	Nucleolar protein, constituent of pre-60S ribosomal particles; required for proper processing of the 27S pre-rRNA at the A3 and B1 sites to yield mature 5.8S and 25S rRNAs	Q
3252	VN_3252	YML113W	DAT1	DNA binding protein that recognizes oligo(dA).oligo(dT) tracts; Arg side chain in its N-terminal pentad Gly-Arg-Lys-Pro-Gly repeat is required for DNA-binding; not essential for viability	Q
3253	VN_3253	YJR113C	RSM7	Mitochondrial ribosomal protein of the small subunit, has similarity to E. coli S7 ribosomal protein	Q
3254	VN_3254	YGR195W	SKI6	Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; has	Q

				similarity to E. coli RNase PH and to human hRrp41p (EXOSC4)	
3255	VN_3255	YBR107C	IML3	Protein with a role in kinetochore function, localizes to the outer kinetochore in a Ctf19p-dependent manner, interacts with Chl4p and Ctf19p	Q
3256	VN_3256	YPR016C	TIF6	Constituent of 66S pre-ribosomal particles, has similarity to human translation initiation factor 6 (eIF6); may be involved in the biogenesis and or stability of 60S ribosomal subunits	Strain failed to verify via PCR
3257	VN_3257	YLR376C	PSY3	Protein involved in a Rad51p-, Rad54p-dependent pathway for homologous recombination repair; deletion results in a mutator phenotype; deletion increases sensitivity to anticancer drugs oxaliplatin and cisplatin but not mitomycin C	Q
3258	VN_3258	YDR196C	CAB5	Probable dephospho-CoA kinase (DPCK) that catalyzes the last step in coenzyme A biosynthesis; null mutant lethality is complemented by E. coli coaE (encoding DPCK); detected in purified mitochondria in high-throughput studies	Q
3259	VN_3259	YDL115C	IWR1	Protein involved in transcription from polymerase II promoters; interacts with with most of the polymerase II subunits; nucleocytoplasmic shuttling protein; deletion causes hypersensitivity to the K1 killer toxin	Q
3260	VN_3260	YIR001C	SGN1	Cytoplasmic RNA-binding protein, contains an RNA recognition motif (RRM); may have a role in mRNA translation, as suggested by genetic interactions with genes encoding proteins involved in translational initiation	Q
3261	VN_3261	YDL202W	MRPL11	Mitochondrial ribosomal protein of the large subunit	Q
3262	VN_3262	YOR213C	SAS5	Subunit of the SAS complex (Sas2p, Sas4p, Sas5p), which acetylates free histones and nucleosomes and regulates transcriptional silencing; stimulates Sas2p HAT activity	Q
3263	VN_3263	YKL152C	GPM1	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis	Q
3264	VN_3264	YHR043C	DOG2	2-deoxyglucose-6-phosphate phosphatase, member of a family of low molecular weight phosphatases, similar to Dog1p, induced by oxidative and osmotic stress, confers 2-deoxyglucose resistance when overexpressed	Q
3265	VN_3265	YGL250W	RMR1	Protein required for meiotic recombination and gene conversion; null mutant displays reduced PIS1 expression and growth defects on non-fermentable carbon sources and minimal media; GFP-fusion protein localizes to both cytoplasm and nucleus	Q
3266	VN_3266	YBR153W	RIB7	Diaminohydroxyphosphoribosylaminopyrimidine deaminase; catalyzes the second step of the riboflavin biosynthesis pathway	Q
3267	VN_3267	YHR049W	FSH1	Putative serine hydrolase that localizes to both the nucleus and cytoplasm; sequence is similar to S. cerevisiae Fsh2p and Fsh3p and the human candidate tumor suppressor OVCA2	Q
3268	VN_3268	YOR305W	RRG7	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion; deletion confers sensitivity to 4-(N-(S-glutathionylacetyl)amino) phenylarsenoxide (GSAO); YOR305W is not an essential gene	Q
3269	VN_3269	YEL038W	UTR4	Protein with sequence similarity to 2,3-diketo-5-methylthiopentyl-1-phosphate enolase-phosphatases, involved in methionine salvage; found in both the cytoplasm and nucleus	Q
3270	VN_3270	YCR007C	YCR007C	Putative integral membrane protein, member of DUP240 gene family; YCR007C is not an essential gene	Q
3271	VN_3271	YJL035C	TAD2	Subunit of tRNA-specific adenosine-34 deaminase, forms a heterodimer with Tad3p that converts adenosine to inosine at the wobble position of several tRNAs	Q
3272	VN_3272	YLL046C	RNP1	Ribonucleoprotein that contains two RNA recognition motifs (RRM)	Q
3273	VN_3273	YPL107W	YPL107W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria; YPL107W is not an essential gene	Q
3274	VN_3274	YLL038C	ENT4	Protein of unknown function, contains an N-terminal epsin-like domain; proposed to be involved in the trafficking of Arn1p in the	Q

				absence of ferrichrome	
3275	VN_3275	YHR044C	DOG1	2-deoxyglucose-6-phosphate phosphatase, similar to Dog2p, member of a family of low molecular weight phosphatases; confers 2-deoxyglucose resistance when overexpressed, in vivo substrate has not yet been identified	Q
3276	VN_3276	YGR057C	LST7	Protein possibly involved in a post-Golgi secretory pathway; required for the transport of nitrogen-regulated amino acid permease Gap1p from the Golgi to the cell surface	Q
3277	VN_3277	YER174C	GRX4	Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; monothiol glutaredoxin subfamily member along with Grx3p and Grx5p; protects cells from oxidative damage	Q
3278	VN_3278	YHR127W	YHR127W	Protein of unknown function; localizes to the nucleus; required for asymmetric localization of Kar9p during mitosis	Q
3279	VN_3279	YOR358W	HAP5	Subunit of the heme-activated, glucose-repressed Hap2/3/4/5 CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression; required for assembly and DNA binding activity of the complex	Q
3280	VN_3280	YGR136W	LSB1	Protein containing an N-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization	Q
3281	VN_3281	YLR326W	YLR326W	Putative protein of unknown function, predicted to be palmitoylated	Q
3282	VN_3282	YER188W	YER188W	Hypothetical protein	Q
3283	VN_3283	YKR041W	YKR041W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	Q
3284	VN_3284	YLR435W	TSR2	Protein with a potential role in pre-rRNA processing	Q
3285	VN_3285	YCL076W	YCL076W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
3286	VN_3286	YOR087W	YVC1	Vacuolar cation channel, mediates release of Ca(2+) from the vacuole in response to hyperosmotic shock	Q
3287	VN_3287	YKL130C	SHE2	RNA-binding protein that binds specific mRNAs and interacts with She3p; part of the mRNA localization machinery that restricts accumulation of certain proteins to the bud	Q
3288	VN_3288	YIL139C	REV7	Processivity subunit of DNA polymerase zeta, which is involved in DNA repair and translesion synthesis; required for mutagenesis induced by DNA damage	Q
3289	VN_3289	YER182W	FMP10	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3290	VN_3290	YNL195C	YNL195C	Putative protein of unknown function; shares a promoter with YNL194C; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3291	VN_3291	YPL065W	VPS28	Component of the ESCRT-I complex (Stp22p, Sm2p, Vps28p, and Mvb12p), which is involved in ubiquitin-dependent sorting of proteins into the endosome; conserved C-terminal domain interacts with ESCRT-III subunit Vps20p	Q
3292	VN_3292	YKR100C	SKG1	Transmembrane protein with a role in cell wall polymer composition; localizes on the inner surface of the plasma membrane at the bud and in the daughter cell	Q
3293	VN_3293	YNL129W	NRK1	Nicotinamide riboside kinase, catalyzes the phosphorylation of nicotinamide riboside and nicotinic acid riboside in salvage pathways for NAD+ biosynthesis	Q
3294	VN_3294	YGR033C	TIM21	Nonessential subunit of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); interacts with the Translocase of the Outer Mitochondrial membrane (TOM complex) and with respiratory enzymes; may regulate TIM23 complex activity	Q
3295	VN_3295	YLL027W	ISA1	Mitochondrial matrix protein involved in biogenesis of the iron-sulfur (Fe/S) cluster of Fe/S proteins, isa1 deletion causes loss of mitochondrial DNA and respiratory deficiency; depletion reduces growth on nonfermentable carbon sources	Q

3296	VN_3296	YMR038C	CCS1	Copper chaperone for superoxide dismutase Sod1p, involved in oxidative stress protection; Met-X-Cys-X2-Cys motif within the N-terminal portion is involved in insertion of copper into Sod1p under conditions of copper deprivation	Q
3297	VN_3297	YCR004C	YCP4	Protein of unknown function, has sequence and structural similarity to flavodoxins; predicted to be palmitoylated; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3298	VN_3298	YPR015C	YPR015C	Putative protein of unknown function; overexpression causes a cell cycle delay or arrest	Q
3299	VN_3299	YNL024C	YNL024C	Putative protein of unknown function with seven beta-strand methyltransferase motif; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YNL024C is not an essential gene	Q
3300	VN_3300	YIR018W	YAP5	Basic leucine zipper (bZIP) transcription factor	Q
3301	VN_3301	YIR030C	DCG1	Protein of unknown function, expression is sensitive to nitrogen catabolite repression and regulated by Dal80p; contains transmembrane domain	Q
3302	VN_3302	YOR284W	HUA2	Cytoplasmic protein of unknown function; computational analysis of large-scale protein-protein interaction data suggests a possible role in actin patch assembly	Q
3303	VN_3303	YMR230W	RPS10B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps10Ap and has similarity to rat ribosomal protein S10	Q
3304	VN_3304	YNL010W	YNL010W	Putative protein of unknown function with similarity to phosphoserine phosphatases; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; homozygous diploid mutant shows an increase in glycogen accumulation	Q
3305	VN_3305	YNL178W	RPS3	Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic (AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat S3 ribosomal proteins	Q
3306	VN_3306	YGR036C	CAX4	Dolichyl pyrophosphate (Dol-P-P) phosphatase with a lumenally oriented active site in the ER, cleaves the anhydride linkage in Dol-P-P, required for Dol-P-P-linked oligosaccharide intermediate synthesis and protein N-glycosylation	Q
3307	VN_3307	YLR022C	SDO1	Essential protein involved in 60S ribosome maturation; ortholog of the human protein (SBDS) responsible for autosomal recessive Shwachman-Bodian-Diamond Syndrome; highly conserved across archae and eukaryotes	Q
3308	VN_3308	YNR009W	NRM1	Transcriptional co-repressor of MBF (MCB binding factor)-regulated gene expression; Nrm1p associates stably with promoters via MBF to repress transcription upon exit from G1 phase	Q
3309	VN_3309	YDL139C	SCM3	Nonhistone component of centromeric chromatin that binds stoichiometrically to CenH3-H4 histones, required for kinetochore assembly; contains nuclear export signal (NES); required for G2/M progression and localization of Cse4p	Q
3310	VN_3310	YDR305C	HNT2	Dinucleoside triphosphate hydrolase; has similarity to the tumor suppressor FHIT and belongs to the histidine triad (HIT) superfamily of nucleotide-binding proteins	Q
3311	VN_3311	YNL200C	YNL200C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3312	VN_3312	YJL055W	YJL055W	Putative protein of unknown function, proposed to be involved in the metabolism of purine and pyrimidine base analogues; deletion mutants are sensitive to HAP and AHA; overexpression confers resistance to 5-FOA and 5-FU	Q
3313	VN_3313	YJR024C	MDE1	5'-methylthioribulose-1-phosphate dehydratase; acts in the methionine salvage pathway; potential Smt3p sumoylation substrate; expression downregulated by caspofungin and deletion mutant is caspofungin resistant	Q
3314	VN_3314	YDR092W	UBC13	Ubiquitin-conjugating enzyme involved in the error-free DNA postreplication repair pathway; interacts with Mms2p to assemble ubiquitin chains at the Ub Lys-63 residue; DNA damage triggers redistribution from the cytoplasm to the nucleus	Q

3315	VN_3315	YGL033W	HOP2	Meiosis-specific protein that localizes to chromosomes, preventing synapsis between nonhomologous chromosomes and ensuring synapsis between homologs; complexes with Mnd1p to promote homolog pairing and meiotic double-strand break repair	Q
3316	VN_3316	YPL024W	RMI1	Subunit of the RecQ (Sgs1p) - Topo III (Top3p) complex; stimulates superhelical relaxing and ssDNA binding activities of Top3p; involved in response to DNA damage; null mutants display increased rates of recombination and delayed S phase	Q
3317	VN_3317	YOL142W	RRP40	Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; predicted to contain both S1 and KH RNA binding domains; has similarity to human hRrp40p (EXOSC3)	Q
3318	VN_3318	YGR247W	CPD1	Cyclic nucleotide phosphodiesterase, hydrolyzes ADP-ribose 1", 2"-cyclic phosphate to ADP-ribose 1"-phosphate; may have a role in tRNA splicing; no detectable phenotype is conferred by null mutation or by overexpression	Q
3319	VN_3319	YLR052W	IES3	Subunit of the INO80 chromatin remodeling complex	Q
3320	VN_3320	YOL154W	ZPS1	Putative GPI-anchored protein; transcription is induced under low-zinc conditions, as mediated by the Zap1p transcription factor, and at alkaline pH	Q
3321	VN_3321	YGL061C	DUO1	Essential subunit of the Dam1 complex (aka DASH complex), couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; is transferred to the kinetochore prior to mitosis	Q
3322	VN_3322	YAL049C	AIM2	Cytoplasmic protein involved in mitochondrial function or organization; null mutant displays reduced frequency of mitochondrial genome loss; potential Hsp82p interactor	Q
3323	VN_3323	YOL032W	OPI10	Protein with a possible role in phospholipid biosynthesis, based on inositol-excreting phenotype of the null mutant and its suppression by exogenous choline	Q
3324	VN_3324	YOL028C	YAP7	Putative basic leucine zipper (bZIP) transcription factor	Q
3325	VN_3325	YLR301W	YLR301W	Protein of unknown function that interacts with Sec72p	Q
3326	VN_3326	YDR538W	PAD1	Phenylacrylic acid decarboxylase, confers resistance to cinnamic acid, decarboxylates aromatic carboxylic acids to the corresponding vinyl derivatives; homolog of E. coli UbiX	Q
3327	VN_3327	YDR447C	RPS17B	Ribosomal protein 51 (rp51) of the small (40s) subunit; nearly identical to Rps17Ap and has similarity to rat S17 ribosomal protein	Q
3328	VN_3328	YPL077C	YPL077C	Putative protein of unknown function; regulates PIS1 expression; mutant displays spore wall assembly defect in ether sensitivity screen; YPL077C is not an essential gene	Q
3329	VN_3329	YJR135C	MCM22	Protein involved in minichromosome maintenance; component of the kinetochore; binds to centromeric DNA in a Ctf19p-dependent manner	Q
3330	VN_3330	YKL096W	CWP1	Cell wall mannoprotein, linked to a beta-1,3- and beta-1,6-glucan heteropolymer through a phosphodiester bond; involved in cell wall organization; required for propionic acid resistance	Q
3331	VN_3331	YLR390W-A	CCW14	Covalently linked cell wall glycoprotein, present in the inner layer of the cell wall	Q
3332	VN_3332	YHR185C	PFS1	Sporulation protein required for prospore membrane formation at selected spindle poles, ensures functionality of all four spindle pole bodies during meiosis II; not required for meiotic recombination or meiotic chromosome segregation	Q
3333	VN_3333	YDR162C	NBP2	Protein involved in the HOG (high osmolarity glycerol) pathway, negatively regulates Hog1p by recruitment of phosphatase Ptc1p the Pbs2p-Hog1p complex, found in the nucleus and cytoplasm, contains an SH3 domain that binds Pbs2p	Q
3334	VN_3334	YDR149C	YDR149C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data; overlaps the verified gene NUM1; null mutation blocks anaerobic growth	Q
3335	VN_3335	YGL051W	MST27	Putative integral membrane protein, involved in vesicle formation; forms complex with Mst28p; member of DUP240 gene family; binds	Q

				COPI and COPII vesicles	
3336	VN_3336	YHR008C	SOD2	Mitochondrial superoxide dismutase, protects cells against oxygen toxicity; phosphorylated	Q
3337	VN_3337	YDR391C	YDR391C	Putative protein of unknown function, possibly involved in zinc homeostasis; Bdf1p-dependent transcription induced by salt stress; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
3338	VN_3338	YEL072W	RMD6	Protein required for sporulation	Q
3339	VN_3339	YGR126W	YGR126W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus and is induced in response to the DNA-damaging agent MMS	Q
3340	VN_3340	YFL034C-A	RPL22B	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl22Ap and to rat L22 ribosomal protein	Q
3341	VN_3341	YOR295W	UAF30	Subunit of UAF (upstream activation factor), which is an RNA polymerase I specific transcription stimulatory factor composed of Uaf30p, Rrn5p, Rrn9p, Rrn10p, histones H3 and H4; deletion decreases cellular growth rate	Q
3342	VN_3342	YMR063W	RIM9	Protein of unknown function, involved in the proteolytic activation of Rim101p in response to alkaline pH; has similarity to A. nidulans PalI; putative membrane protein	Q
3343	VN_3343	YMR156C	TPP1	DNA 3'-phosphatase that functions in repair of endogenous damage of double-stranded DNA, activity is specific for removal of 3' phosphates at strand breaks; has similarity to the 1-2-haloacid dehalogenase superfamily	Q
3344	VN_3344	YMR134W	YMR134W	Protein of unknown function that may be involved in iron metabolism; mutant bm-8 has a growth defect on iron-limited medium that is complemented by overexpression of Yfh1p; shows localization to the ER; highly conserved in ascomycetes	Q
3345	VN_3345	YIR042C	YIR042C	Putative protein of unknown function; YIR042C is a non-essential gene	Q
3346	VN_3346	YDR275W	BSC2	Protein of unknown function, ORF exhibits genomic organization compatible with a translational readthrough-dependent mode of expression	Q
3347	VN_3347	YIR038C	GTT1	ER associated glutathione S-transferase capable of homodimerization; expression induced during the diauxic shift and throughout stationary phase; functional overlap with Gtt2p, Grx1p, and Grx2p	Q
3348	VN_3348	YJL148W	RPA34	RNA polymerase I subunit A34.5	Q
3349	VN_3349	YER163C	YER163C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; periodically expressed during the metabolic cycle; weak similarity to bacterial cation transport protein	Q
3350	VN_3350	YER002W	NOP16	Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis	Q
3351	VN_3351	YHR038W	RRF1	Mitochondrial ribosome recycling factor, essential for mitochondrial protein synthesis and for the maintenance of the respiratory function of mitochondria	Strain failed to verify via PCR
3352	VN_3352	YGL045W	RIM8	Protein involved in proteolytic activation of Rim101p in response to alkaline pH; similar to A. nidulans PalF; essential for anaerobic growth; member of the arrestin-related trafficking adaptor family	Q
3353	VN_3353	YLR118C	YLR118C	Acyl-protein thioesterase responsible for depalmitoylation of Gpa1p; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and nucleus and is induced in response to the DNA-damaging agent MMS	Q
3354	VN_3354	YBR242W	YBR242W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YBR242W is not an essential gene	Q
3355	VN_3355	YNL099C	OCA1	Putative protein tyrosine phosphatase, required for cell cycle arrest in response to oxidative damage of DNA	Q
3356	VN_3356	YMR188C	MRPS17	Mitochondrial ribosomal protein of the small subunit	Q

3357	VN_3357	YJR056C	YJR056C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
3358	VN_3358	YDR412W	RRP17	Component of the pre-60S pre-ribosomal particle; required for cell viability under standard (aerobic) conditions but not under anaerobic conditions	Q
3359	VN_3359	YLR250W	SSP120	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Q
3360	VN_3360	YJL195C	YJL195C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YJL194W/CDC6	Q
3361	VN_3361	YFR020W	YFR020W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3362	VN_3362	YER004W	FMP52	Protein of unknown function, localized to the mitochondrial outer membrane; induced by treatment with 8-methoxypsoralen and UVA irradiation	Q
3363	VN_3363	YIR043C	YIR043C	Possible pseudogene in strain S288C; YIR043C and the adjacent ORF, YIR044C, together may encode a non-functional member of the conserved, often subtelomerically-encoded Cos protein family	Q
3364	VN_3364	YHR071W	PCL5	Cyclin, interacts with and phosphorylated by Pho85p cyclin-dependent kinase (Cdk), induced by Gcn4p at level of transcription, specifically required for Gcn4p degradation, may be sensor of cellular protein biosynthetic capacity	Q
3365	VN_3365	YMR090W	YMR090W	Putative protein of unknown function with similarity to DTDP-glucose 4,6-dehydratases; GFP-fusion protein localizes to the cytoplasm; up-regulated in response to the fungicide mancozeb; not essential for viability	Q
3366	VN_3366	YBR256C	RIB5	Riboflavin synthase; catalyzes the last step of the riboflavin biosynthesis pathway	Q
3367	VN_3367	YOR126C	IAH1	Isoamyl acetate-hydrolyzing esterase, required in balance with alcohol acetyltransferase to maintain optimal amounts of isoamyl acetate, which is particularly important in sake brewing	Q
3368	VN_3368	YMR322C	SNO4	Possible chaperone and cysteine protease, similar to bacterial Hsp31 and yeast Hsp31p, Hsp32p, and Hsp33p; DJ-1/ThiJ/PfpI superfamily member; predicted involvement in pyridoxine metabolism; induced by mild heat stress and copper deprivation	Q
3369	VN_3369	YJR099W	YUH1	Ubiquitin C-terminal hydrolase that cleaves ubiquitin-protein fusions to generate monomeric ubiquitin; hydrolyzes the peptide bond at the C-terminus of ubiquitin; also the major processing enzyme for the ubiquitin-like protein Rub1p	Q
3370	VN_3370	YHL044W	YHL044W	Putative integral membrane protein, member of DUP240 gene family; green fluorescent protein (GFP)-fusion protein localizes to the plasma membrane in a punctate pattern	Q
3371	VN_3371	YMR314W	PRE5	Alpha 6 subunit of the 20S proteasome	Q
3372	VN_3372	YPL002C	SNF8	Component of the ESCRT-II complex, which is involved in ubiquitin-dependent sorting of proteins into the endosome; appears to be functionally related to SNF7; involved in glucose derepression	Q
3373	VN_3373	YOR077W	RTS2	Basic zinc-finger protein, similar to human and mouse Kin17 proteins which are chromatin-associated proteins involved in UV response and DNA replication	Q
3374	VN_3374	YHR122W	YHR122W	Protein of unknown function required for establishment of sister chromatid cohesion; synthetically lethal with RFC5, an RF-C subunit that links replication to cohesion establishment; YHR122W is an essential gene	Q
3375	VN_3375	YLL033W	IRC19	Putative protein of unknown function; YLL033W is not an essential gene but mutant is defective in spore formation; null mutant displays increased levels of spontaneous Rad52p foci	Q
3376	VN_3376	YLR407W	YLR407W	Putative protein of unknown function; null mutant displays elongated buds and a large fraction of budded cells have only one nucleus	Q
3377	VN_3377	YMR271C	URA10	Minor orotate phosphoribosyltransferase (OPRTase) isozyme that catalyzes the fifth enzymatic step in the de novo biosynthesis of pyrimidines, converting orotate into orotidine-5'-phosphate; major OPRTase encoded by URA5	Q

3378	VN_3378	YDL059C	RAD59	Protein involved in the repair of double-strand breaks in DNA during vegetative growth via recombination and single-strand annealing; anneals complementary single-stranded DNA; homologous to Rad52p	Q
3379	VN_3379	YPL213W	LEA1	Component of U2 snRNP; disruption causes reduced U2 snRNP levels; physically interacts with Msl1p; involved in telomere maintenance; putative homolog of human U2A' snRNP protein	Q
3380	VN_3380	YNR057C	BIO4	Dethiobiotin synthetase, catalyzes the third step in the biotin biosynthesis pathway; BIO4 is in a cluster of 3 genes (BIO3, BIO4, and BIO5) that mediate biotin synthesis; expression appears to be repressed at low iron levels	Q
3381	VN_3381	YKL009W	MRT4	Protein involved in mRNA turnover and ribosome assembly, localizes to the nucleolus	Q
3382	VN_3382	YIL152W	YIL152W	Putative protein of unknown function	Q
3383	VN_3383	YNL100W	AIM37	Putative protein of unknown function; non-tagged protein is detected in purified mitochondria; null mutant is viable and displays reduced respiratory growth and reduced frequency of mitochondrial genome loss	Q
3384	VN_3384	YLR306W	UBC12	Enzyme that mediates the conjugation of Rub1p, a ubiquitin-like protein, to other proteins; related to E2 ubiquitin-conjugating enzymes	Q
3385	VN_3385	YOR111W	YOR111W	Putative protein of unknown function	Q
3386	VN_3386	YLR298C	YHC1	Component of the U1 snRNP complex required for pre-mRNA splicing; putative ortholog of human U1C protein, which is involved in formation of a complex between U1 snRNP and the pre-mRNA 5' splice site	Q
3387	VN_3387	YLR168C	UPS2	Mitochondrial intermembrane space protein involved in regulation of mitochondrial cardiolipin and phosphatidylethanolamine levels; null has defects in mitochondrial morphology; similar to Ups1p, Ups3p and to human PRELI	Q
3388	VN_3388	YMR311C	GLC8	Regulatory subunit of protein phosphatase 1 (Glc7p), involved in glycogen metabolism and chromosome segregation; proposed to regulate Glc7p activity via conformational alteration; ortholog of the mammalian protein phosphatase inhibitor 2	Q
3389	VN_3389	YPR043W	RPL43A	Protein component of the large (60S) ribosomal subunit, identical to Rpl43Bp and has similarity to rat L37a ribosomal protein; null mutation confers a dominant lethal phenotype	Q
3390	VN_3390	YHR013C	ARD1	Subunit of N-terminal acetyltransferase NatA (Nat1p, Ard1p, Nat5p); acetylates many proteins and thus affects telomeric silencing, cell cycle, heat-shock resistance, mating, and sporulation; human Ard1p levels are elevated in cancer cells	Q
3391	VN_3391	YDR533C	HSP31	Possible chaperone and cysteine protease with similarity to E. coli Hsp31; member of the DJ-1/ThiJ/PfpI superfamily, which includes human DJ-1 involved in Parkinson's disease; exists as a dimer and contains a putative metal-binding site	Q
3392	VN_3392	YOL110W	SHR5	Subunit of a palmitoyltransferase, composed of Shr5p and Erf2p, that adds a palmitoyl lipid moiety to heterolipidated substrates such as Ras1p and Ras2p through a thioester linkage; palmitoylation is required for Ras2p membrane localization	Q
3393	VN_3393	YOL146W	PSF3	Subunit of the GINS complex (Sld5p, Psf1p, Psf2p, Psf3p), which is localized to DNA replication origins and implicated in assembly of the DNA replication machinery	Q
3394	VN_3394	YIL161W	YIL161W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; mRNA is enriched in Scp160p-associated mRNPs; YIL161W is a non-essential gene	Q
3395	VN_3395	YDL069C	CBS1	Mitochondrial translational activator of the COB mRNA; membrane protein that interacts with translating ribosomes, acts on the COB mRNA 5'-untranslated leader	Q
3396	VN_3396	YBL038W	MRPL16	Mitochondrial ribosomal protein of the large subunit	Q
3397	VN_3397	YBR111C	YSA1	Nudix hydrolase family member with ADP-ribose pyrophosphatase activity; shown to metabolize O-acetyl-ADP-ribose to AMP and acetylated ribose 5'-phosphate	Q

3398	VN_3398	YOL149W	DCP1	Subunit of the Dcp1p-Dcp2p decapping enzyme complex, which removes the 5' cap structure from mRNAs prior to their degradation; enhances the activity of catalytic subunit Dcp2p; regulated by DEAD box protein Dhh1p	Q
3399	VN_3399	YOL102C	TPT1	tRNA 2'-phosphotransferase, catalyzes the final step in yeast tRNA splicing: the transfer of the 2'-PO(4) from the splice junction to NAD(+) to form ADP-ribose 1"-2" cyclic phosphate and nicotinamide	Q
3400	VN_3400	YDR296W	MHR1	Protein involved in homologous recombination in mitochondria and in transcription regulation in nucleus; binds to activation domains of acidic activators; required for recombination-dependent mtDNA partitioning	Q
3401	VN_3401	YJL063C	MRPL8	Mitochondrial ribosomal protein of the large subunit	Q
3402	VN_3402	YFR043C	IRC6	Putative protein of unknown function; null mutant displays increased levels of spontaneous Rad52p foci	Q
3403	VN_3403	YOR391C	HSP33	Possible chaperone and cysteine protease with similarity to E. coli Hsp31 and S. cerevisiae Hsp31p, Hsp32p, and Sno4p; member of the DJ-1/ThiJ/PfpI superfamily, which includes human DJ-1 involved in Parkinson's disease	Q
3404	VN_3404	YOR214C	YOR214C	Putative protein of unknown function; YOR214C is not an essential gene	Q
3405	VN_3405	YJR050W	ISY1	Member of NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of spliceosome containing U2, U5, and U6 snRNAs, interacts with Prp16p to modulate splicing fidelity; isy1 syf2 cells have defective spindles	Q
3406	VN_3406	YEL057C	YEL057C	Protein of unknown function involved in telomere maintenance; target of UME6 regulation	Q
3407	VN_3407	YBR261C	TAE1	Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; has a role in protein synthesis; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YBR261C is not an essential gene	Q
3408	VN_3408	YDL010W	GRX6	Cis-golgi localized monothiol glutaredoxin that binds an iron-sulfur cluster; more similar in activity to dithiol than other monothiol glutaredoxins; involved in the oxidative stress response; functional overlap with GRX7	Q
3409	VN_3409	YBR096W	YBR096W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the ER	Q
3410	VN_3410	YOR283W	YOR283W	Phosphatase with some similarity to GPM1/YKL152C, a phosphoglycerate mutase; YOR283W is not an essential gene	Q
3411	VN_3411	YGR232W	NAS6	Proteasome-interacting protein involved in the assembly of the base subcomplex of the 19S proteasomal regulatory particle (RP); ortholog of human oncoprotein gankyrin, which interacts with the Rb tumor suppressor and CDK4/6	Q
3412	VN_3412	YER139C	RTR1	CTD phosphatase; dephosphorylates S5-P in the C-terminal domain of Rpo21p; has a cysteine-rich motif required for function and conserved in eukaryotes; shuttles between the nucleus and cytoplasm	Q
3413	VN_3413	YJL121C	RPE1	D-ribulose-5-phosphate 3-epimerase, catalyzes a reaction in the non-oxidative part of the pentose-phosphate pathway; mutants are sensitive to oxidative stress	Q
3414	VN_3414	YGR024C	THG1	tRNAHis guanylyltransferase, adds a guanosine residue to the 5' end of tRNAHis after transcription and RNase P cleavage; couples nuclear division and migration to cell budding and cytokinesis; essential enzyme conserved among eukaryotes	Q
3415	VN_3415	YPL280W	HSP32	Possible chaperone and cysteine protease with similarity to E. coli Hsp31 and S. cerevisiae Hsp31p, Hsp33p, and Sno4p; member of the DJ-1/ThiJ/PfpI superfamily, which includes human DJ-1 involved in Parkinson's disease	Q
3416	VN_3416	YPL275W	FDH2	NAD(+)-dependent formate dehydrogenase, may protect cells from exogenous formate; YPL275W and YPL276W comprise a continuous open reading frame in some S. cerevisiae strains but not in the genomic reference strain S288C	Q
3417	VN_3417	YER010C	YER010C	Protein of unknown function, forms a ring-shaped homotrimer; has similarity to members of the prokaryotic rraA family; possibly involved in a phosphotransfer reaction	Q

3418	VN_3418	YGR235C	YGR235C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3419	VN_3419	YDR020C	DAS2	Putative protein of unknown function; non-essential gene identified in a screen for mutants with increased levels of rDNA transcription; weak similarity with uridine kinases and with phosphoribokinases	Q
3420	VN_3420	YDR043C	NRG1	Transcriptional repressor that recruits the Cyc8p-Tup1p complex to promoters; mediates glucose repression and negatively regulates a variety of processes including filamentous growth and alkaline pH response	Q
3421	VN_3421	YDR183W	PLP1	Protein that interacts with CCT (chaperonin containing TCP-1) complex and has a role in actin and tubulin folding; has weak similarity to phosducins, which are G-protein regulators	Q
3422	VN_3422	YLR406C	RPL31B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Ap and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; loss of both Rpl31p and Rpl39p confers lethality	Q
3423	VN_3423	YOR232W	MGE1	Mitochondrial matrix cochaperone, acts as a nucleotide release factor for Ssc1p in protein translocation and folding; also acts as cochaperone for Ssq1p in folding of Fe-S cluster proteins; homolog of E. coli GrpE	Strain failed to verify via PCR
3424	VN_3424	YML106W	URA5	Major orotate phosphoribosyltransferase (OPRTase) isozyme that catalyzes the fifth enzymatic step in de novo biosynthesis of pyrimidines, converting orotate into orotidine-5'-phosphate; minor OPRTase encoded by URA10	Q
3425	VN_3425	YMR233W	TRI1	Non-essential sumoylated protein of unknown function with similarity to components of human SWI/SNF complex including SMRD3; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm, nucleus and nucleolus	Q
3426	VN_3426	YNL335W	DDI3	Protein of unknown function; expression is induced over 100-fold by DNA damage; induction decreased in rad6 and rad18 mutants	Q
3427	VN_3427	YMR161W	HLJ1	Co-chaperone for Hsp40p, anchored in the ER membrane; with its homolog Ydj1p promotes ER-associated protein degradation (ERAD) of integral membrane substrates; similar to E. coli DnaJ	Q
3428	VN_3428	YPL130W	SPO19	Meiosis-specific prospore protein; required to produce bending force necessary for proper assembly of the prospore membrane during sporulation; identified as a weak high-copy suppressor of the spo1-1 ts mutation	Q
3429	VN_3429	YCR018C	SRD1	Protein involved in the processing of pre-rRNA to mature rRNA; contains a C2/C2 zinc finger motif; srd1 mutation suppresses defects caused by the rrp1-1 mutation	Strain failed to verify via PCR
3430	VN_3430	YNL036W	NCE103	Carbonic anhydrase; poorly transcribed under aerobic conditions and at an undetectable level under anaerobic conditions; involved in non-classical protein export pathway	Q
3431	VN_3431	YOR202W	HIS3	Imidazoleglycerol-phosphate dehydratase, catalyzes the sixth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; transcription is regulated by general amino acid control via Gcn4p	Q
3432	VN_3432	YDR236C	FMN1	Riboflavin kinase, phosphorylates riboflavin to form riboflavin monophosphate (FMN), which is a necessary cofactor for many enzymes; localizes to microsomes and to the mitochondrial inner membrane	Q
3433	VN_3433	YGL135W	RPL1B	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Ap and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal	Q
3434	VN_3434	YBL059W	YBL059W	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3435	VN_3435	YER007C-A	TMA20	Protein of unknown function that associates with ribosomes and has a putative RNA binding domain; interacts with Tma22p; null mutant exhibits translation defects; has homology to human oncogene MCT-1	Q
3436	VN_3436	YIL010W	DOT5	Nuclear thiol peroxidase which functions as an alkyl-hydroperoxide reductase during post-diauxic growth	Q

3437	VN_3437	YNL107W	YAF9	Subunit of both the NuA4 histone H4 acetyltransferase complex and the SWR1 complex, may function to antagonize silencing near telomeres; interacts directly with Swc4p, has homology to human leukemogenic protein AF9, contains a YEATS domain	Strain failed to verify via PCR
3438	VN_3438	YDR007W	TRP1	Phosphoribosylanthranilate isomerase that catalyzes the third step in tryptophan biosynthesis; in 2004, the sequence of TRP1 from strain S228C was updated by changing the previously annotated internal STOP (TAA) to serine (TCA)	Q
3439	VN_3439	YNR018W	AIM38	Putative protein of unknown function; non-tagged protein is detected in purified mitochondria; may interact with respiratory chain complex IV; null mutant is viable and displays reduced frequency of mitochondrial genome loss	Q
3440	VN_3440	YCR051W	YCR051W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; contains ankyrin (Ank) repeats; YCR051W is not an essential gene	Q
3441	VN_3441	YDR140W	MTQ2	S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family; subunit of complex with Trm112p that methylates translation release factor Sup45p (eRF1) in the ternary complex eRF1-eRF3-GTP; similar to E.coli PrmC	Q
3442	VN_3442	YPR174C	YPR174C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nuclear periphery; potential Cdc28p substrate	Q
3443	VN_3443	YDR302W	GPI11	ER membrane protein involved in a late step of glycosylphosphatidylinositol (GPI) anchor assembly; involved in the addition of phosphoethanolamine to the multiply mannosylated GPI intermediate; human PIG-Fp is a functional homolog	Q
3444	VN_3444	YER063W	THO1	Conserved nuclear RNA-binding protein; specifically binds to transcribed chromatin in a THO- and RNA-dependent manner, genetically interacts with shuttling hnRNP NAB2; overproduction suppresses transcriptional defect caused by hpr1 mutation	Q
3445	VN_3445	YGR153W	YGR153W	Putative protein of unknown function	Q
3446	VN_3446	YEL076C	YEL076C	Putative protein of unknown function	Q
3447	VN_3447	YAL004W	YAL004W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps verified gene SSA1/YAL005C	Q
3448	VN_3448	YOL162W	YOL162W	Putative protein of unknown function; member of the Dal5p subfamily of the major facilitator family	Q
3449	VN_3449	YDL213C	NOP6	Putative RNA-binding protein implicated in ribosome biogenesis; contains an RNA recognition motif (RRM) and has similarity to hydrophilins; NOP6 may be a fungal-specific gene as no homologs have been yet identified in higher eukaryotes	Q
3450	VN_3450	YDR067C	OCA6	Cytoplasmic protein required for replication of Brome mosaic virus in <i>S. cerevisiae</i> , which is a model system for studying positive-strand RNA virus replication; null mutation confers sensitivity to tunicamycin and DTT	Q
3451	VN_3451	YOL046C	YOL046C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; almost completely overlaps the verified gene PSK2/YOL045W	Q
3452	VN_3452	YDR226W	ADK1	Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; lacks cleavable signal sequence	Q
3453	VN_3453	YDR399W	HPT1	Dimeric hypoxanthine-guanine phosphoribosyltransferase, catalyzes the formation of both inosine monophosphate and guanosine monophosphate; mutations in the human homolog HPRT1 can cause Lesch-Nyhan syndrome and Kelley-Seegmiller syndrome	Q
3454	VN_3454	YBL093C	ROX3	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme	Q
3455	VN_3455	YGL079W	YGL079W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endosome; identified as a transcriptional activator in a high-throughput yeast one-hybrid assay	Q
3456	VN_3456	YLR051C	FCF2	Essential nucleolar protein involved in the early steps of 35S rRNA processing; interacts with Faf1p; member of a transcriptionally co-regulated set of genes called the RRB regulon	Q

3457	VN_3457	YGL037C	PNC1	Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span	Q
3458	VN_3458	YBR154C	RPB5	RNA polymerase subunit ABC27, common to RNA polymerases I, II, and III; contacts DNA and affects transactivation	Strain failed to verify via PCR
3459	VN_3459	YPR154W	PIN3	Protein that induces appearance of [PIN+] prion when overproduced	Strain failed to verify via PCR
3460	VN_3460	YDR476C	YDR476C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YDR476C is not an essential gene	Q
3461	VN_3461	YBR193C	MED8	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation	Q
3462	VN_3462	YFL060C	SNO3	Protein of unknown function, nearly identical to Sno2p; expression is induced before the diauxic shift and also in the absence of thiamin	Q
3463	VN_3463	YER018C	SPC25	Component of the evolutionarily conserved kinetochore-associated Ndc80 complex (Ndc80p-Nuf2p-Spc24p-Spc25p); involved in chromosome segregation, spindle checkpoint activity and kinetochore clustering	Q
3464	VN_3464	YBR066C	NRG2	Transcriptional repressor that mediates glucose repression and negatively regulates filamentous growth; has similarity to Nrg1p	Q
3465	VN_3465	YJL038C	LOH1	Protein of unknown function with proposed roles in maintenance of genome integrity and also in spore wall assembly; induced during sporulation; repressed during vegetative growth by Sum1p and Hst1p; sequence similar to IRC1	Q
3466	VN_3466	YJR074W	MOG1	Conserved nuclear protein that interacts with GTP-Gsp1p, which is a Ran homolog of the Ras GTPase family, and stimulates nucleotide release, involved in nuclear protein import, nucleotide release is inhibited by Yrb1p	Q
3467	VN_3467	YNL306W	MRPS18	Mitochondrial ribosomal protein of the small subunit; essential for viability, unlike most other mitoribosomal proteins	Q
3468	VN_3468	YGL218W	YGL218W	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 93% of ORF overlaps the verified gene MDM34; deletion in <i>cyr1</i> mutant results in loss of stress resistance	Q
3469	VN_3469	YBL057C	PTH2	One of two (see also PTH1) mitochondrially-localized peptidyl-tRNA hydrolases; negatively regulates the ubiquitin-proteasome pathway via interactions with ubiquitin-like ubiquitin-associated proteins; dispensable for cell growth	Strain failed to verify via PCR
3470	VN_3470	YFL061W	DDI2	Protein of unknown function; expression is induced over 100-fold by DNA damage; induction decreased in <i>rad6</i> and <i>rad18</i> mutants	Q
3471	VN_3471	YJL037W	IRC18	Putative protein of unknown function; expression induced in respiratory-deficient cells and in carbon-limited chemostat cultures; similar to adjacent ORF, YJL038C; null mutant displays increased levels of spontaneous Rad52p foci	Q
3472	VN_3472	YDL169C	UGX2	Protein of unknown function, transcript accumulates in response to any combination of stress conditions	Q
3473	VN_3473	YGR038W	ORM1	Evolutionarily conserved protein with similarity to Orm2p, required for resistance to agents that induce the unfolded protein response; human ortholog is located in the endoplasmic reticulum	Q
3474	VN_3474	YFR008W	FAR7	Protein involved in recovery from cell cycle arrest in response to pheromone, in a Far1p-independent pathway; interacts with Far3p, Far8p, Far9p, Far10p, and Far11p	Q
3475	VN_3475	YIL007C	NAS2	Proteasome-interacting protein involved in the assembly of the base subcomplex of the 19S proteasomal regulatory particle (RP); similar to mammalian proteasomal modulator subunit; non-essential gene; interacts with Rpn4p	Q
3476	VN_3476	YJL118W	YJL118W	Putative protein of unknown function; may interact with ribosomes, based on co-purification experiments; YJL118W is a non-essential gene; deletion enhances the toxicity of heterologously expressed	Q

				human alpha-synuclein	
3477	VN_3477	YLR363C	NMD4	Protein interacting with Nam7p, may be involved in the nonsense-mediated mRNA decay pathway	Q
3478	VN_3478	YOR258W	HNT3	Member of the third branch of the histidine triad (HIT) superfamily of nucleotide-binding proteins; similar to Aprataxin, a Hint related protein that is mutated in individuals with ataxia with oculomotor apraxia	Q
3479	VN_3479	YIR024C	YIR024C	Protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; interacts with Arh1p, a mitochondrial oxidoreductase; deletion mutant has a respiratory growth defect	Q
3480	VN_3480	YCR020C	PET18	Protein of unknown function, has weak similarity to proteins involved in thiamin metabolism; expression is induced in the absence of thiamin	Q
3481	VN_3481	YBR072W	HSP26	Small heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation; oligomer activation requires a heat-induced conformational change; not expressed in unstressed cells	Q
3482	VN_3482	YGL152C	YGL152C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF PEX14/YGL153W	Q
3483	VN_3483	YJL096W	MRPL49	Mitochondrial ribosomal protein of the large subunit	Q
3484	VN_3484	YDR078C	SHU2	Protein involved in a Rad51p-, Rad54p-dependent pathway for homologous recombination repair, important for error-free repair of spontaneous and induced DNA lesions to protect the genome from mutation; associates with Shu1p, Psy3p, and Csm2p	Q
3485	VN_3485	YNL334C	SNO2	Protein of unknown function, nearly identical to Sno3p; expression is induced before the diauxic shift and also in the absence of thiamin	Strain failed to verify via PCR
3486	VN_3486	YJL140W	RPB4	RNA polymerase II subunit B32; forms two subunit dissociable complex with Rpb7p; involved recruitment of 3'-end processing factors to transcribing RNA polymerase II complex and in export of mRNA to cytoplasm under stress conditions	Strain failed to verify via PCR
3487	VN_3487	YLR199C	PBA1	Protein involved in 20S proteasome assembly; forms a heterodimer with Add66p that binds to proteasome precursors; similar to human PAC1 constituent of the PAC1-PAC2 complex involved in proteasome assembly	Strain failed to verify via PCR
3488	VN_3488	YKL142W	MRP8	Protein of unknown function; undergoes sumoylation; transcription induced under cell wall stress; protein levels are reduced under anaerobic conditions; originally thought to be a mitochondrial ribosomal protein based on sequence analysis	Q
3489	VN_3489	YOR131C	YOR131C	Putative protein of unknown function; non-essential gene; overexpression causes a cell cycle delay or arrest	Q
3490	VN_3490	YPL220W	RPL1A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal	Q
3491	VN_3491	YJR057W	CDC8	Thymidylate and uridylate kinase, functions in de novo biosynthesis of pyrimidine deoxyribonucleotides; converts dTMP to dTDP and dUMP to dUTP; essential for mitotic and meiotic DNA replication; homologous to S. pombe Tmp1p	Q
3492	VN_3492	YDR177W	UBC1	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response	Q
3493	VN_3493	YDR408C	ADE8	Phosphoribosyl-glycinamide transformylase, catalyzes a step in the 'de novo' purine nucleotide biosynthetic pathway	Q
3494	VN_3494	YGL166W	CUP2	Copper-binding transcription factor; activates transcription of the metallothionein genes CUP1-1 and CUP1-2 in response to elevated copper concentrations	Q
3495	VN_3495	YLR040C	YLR040C	Putative protein of unknown function; localizes to the cell wall; predicted to be a GPI-attached protein; upregulated by Mcm1p-Alpha1p transcription factor; partially overlaps the dubious ORF	Q

				YLR041W; YLR040C is not essential	
3496	VN_3496	YMR147W	YMR147W	Putative protein of unknown function	Q
3497	VN_3497	YOL135C	MED7	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation	Q
3498	VN_3498	YLR221C	RSA3	Protein with a likely role in ribosomal maturation, required for accumulation of wild-type levels of large (60S) ribosomal subunits; binds to the helicase Dbp6p in pre-60S ribosomal particles in the nucleolus	Q
3499	VN_3499	YLR178C	TFS1	Protein that interacts with and inhibits carboxypeptidase Y and Ira2p; phosphatidylethanolamine-binding protein (PEBP) family member; targets to vacuolar membranes during stationary phase; acetylated by NatB N-terminal acetyltransferase	Q
3500	VN_3500	YDR500C	RPL37B	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl37Ap and to rat L37 ribosomal protein	Q
3501	VN_3501	YKL117W	SBA1	Co-chaperone that binds to and regulates Hsp90 family chaperones; important for pp60v-src activity in yeast; homologous to the mammalian p23 proteins and like p23 can regulate telomerase activity	Q
3502	VN_3502	YGL101W	YGL101W	Putative protein of unknown function; non-essential gene with similarity to YBR242W; interacts with the DNA helicase Hpr5p	Q
3503	VN_3503	YHR105W	YPT35	Endosomal protein of unknown function that contains a phox (PX) homology domain and binds to both phosphatidylinositol-3-phosphate (PtdIns(3)P) and proteins involved in ER-Golgi or vesicular transport	Q
3504	VN_3504	YMR095C	SNO1	Protein of unconfirmed function, involved in pyridoxine metabolism; expression is induced during stationary phase; forms a putative glutamine amidotransferase complex with Snz1p, with Sno1p serving as the glutaminase	Q
3505	VN_3505	YMR222C	FSH2	Putative serine hydrolase that localizes to the cytoplasm; sequence is similar to <i>S. cerevisiae</i> Fsh1p and Fsh3p and the human candidate tumor suppressor OVCA2	Q
3506	VN_3506	YPL121C	MEI5	Meiosis specific protein involved in DMC1-dependent meiotic recombination, forms heterodimer with Sae3p; proposed to be an assembly factor for Dmc1p	Q
3507	VN_3507	YMR077C	VPS20	Myristoylated subunit of ESCRTIII, the endosomal sorting complex required for transport of transmembrane proteins into the multivesicular body pathway to the lysosomal/vacuolar lumen; cytoplasmic protein recruited to endosomal membranes	Q
3508	VN_3508	YNL110C	NOP15	Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis; localizes to both nucleolus and cytoplasm	Q
3509	VN_3509	YOR064C	YNG1	Subunit of the NuA3 histone acetyltransferase complex that acetylates histone H3; contains PHD finger domain that interacts with methylated histone H3, has similarity to the human tumor suppressor ING1	Q
3510	VN_3510	YBR197C	YBR197C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YBR197C is not an essential gene	Q
3511	VN_3511	YOR318C	YOR318C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; transcript is predicted to be spliced but there is no evidence that it is spliced in vivo	Q
3512	VN_3512	YPL233W	NSL1	Essential component of the MIND kinetochore complex (Mtw1p Including Nnf1p-Nsl1p-Dsn1p) which joins kinetochore subunits contacting DNA to those contacting microtubules; required for accurate chromosome segregation	Q
3513	VN_3513	YGR129W	SYF2	Member of the NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 snRNAs; <i>isy1 syf2</i> cells have defective spindles activating cell cycle arrest	Q
3514	VN_3514	YHR147C	MRPL6	Mitochondrial ribosomal protein of the large subunit	Q
3515	VN_3515	YNL213C	RRG9	Protein of unknown function; null mutant lacks mitochondrial DNA and cannot grow on glycerol; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q

3516	VN_3516	YMR117C	SPC24	Component of the evolutionarily conserved kinetochore-associated Ndc80 complex (Ndc80p-Nuf2p-Spc24p-Spc25p); involved in chromosome segregation, spindle checkpoint activity and kinetochore clustering	Q
3517	VN_3517	YNL038W	GPI15	Protein involved in the synthesis of N-acetylglucosaminyl phosphatidylinositol (GlcNAc-PI), the first intermediate in the synthesis of glycosylphosphatidylinositol (GPI) anchors; homologous to the human PIG-H protein	Strain failed to verify via PCR
3518	VN_3518	YKL159C	RCN1	Protein involved in calcineurin regulation during calcium signaling; has similarity to H. sapiens DSCR1 which is found in the Down Syndrome candidate region	Q
3519	VN_3519	YDR003W	RCR2	Vacuolar protein that presumably functions within the endosomal-vacuolar trafficking pathway, affecting events that determine whether plasma membrane proteins are degraded or routed to the plasma membrane; similar to Rcr1p	Q
3520	VN_3520	YPL267W	ACM1	Pseudosubstrate inhibitor of the anaphase-promoting complex/cyclosome (APC/C), that suppresses APC/C [Cdh1]-mediated proteolysis of mitotic cyclins; associates with Cdh1p, Bmh1p and Bmh2p; cell cycle regulated protein	Q
3521	VN_3521	YFL046W	FMP32	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3522	VN_3522	YGL258W	VEL1	Protein of unknown function; highly induced in zinc-depleted conditions and has increased expression in NAP1 deletion mutants	Q
3523	VN_3523	YDR056C	YDR056C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YDR056C is not an essential protein	Q
3524	VN_3524	YFR001W	LOC1	Nuclear protein involved in asymmetric localization of ASH1 mRNA; binds double-stranded RNA in vitro; constituent of 66S pre-ribosomal particles	Q
3525	VN_3525	YMR052W	FAR3	Protein involved in recovery from cell cycle arrest in response to pheromone, in a Far1p-independent pathway; interacts with Far7p, Far8p, Far9p, Far10p, and Far11p; localizes to the endoplasmic reticulum	Q
3526	VN_3526	YDR041W	RSM10	Mitochondrial ribosomal protein of the small subunit, has similarity to E. coli S10 ribosomal protein; essential for viability, unlike most other mitoribosomal proteins	Q
3527	VN_3527	YOR078W	BUD21	Component of small ribosomal subunit (SSU) processosome that contains U3 snoRNA; originally isolated as bud-site selection mutant that displays a random budding pattern	Q
3528	VN_3528	YOL139C	CDC33	Cytoplasmic mRNA cap binding protein and translation initiation factor eIF4E; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with translation initiation factor eIF4G (Tif4631p or Tif4632p)	Q
3529	VN_3529	YNR014W	YNR014W	Putative protein of unknown function; expression is cell-cycle regulated, Azf1p-dependent, and heat-inducible	Q
3530	VN_3530	YMR182C	RGM1	Putative transcriptional repressor with proline-rich zinc fingers; overproduction impairs cell growth	Q
3531	VN_3531	YER079W	YER079W	Putative protein of unknown function	Q
3532	VN_3532	YJR012C	YJR012C	Essential protein of unknown function; proposed involvement in transport based on mass spectrometry analysis of copurifying proteins; partially overlaps neighboring ORF, GPI14/YJR013W	Q
3533	VN_3533	YIL127C	RRT14	Putative protein of unknown function; identified in a screen for mutants with decreased levels of rDNA transcription; green fluorescent protein (GFP)-fusion protein localizes to the nucleolus; predicted to be involved in ribosome biogenesis	Q
3534	VN_3534	YDR231C	COX20	Mitochondrial inner membrane protein, required for proteolytic processing of Cox2p and its assembly into cytochrome c oxidase	Q
3535	VN_3535	YIL158W	AIM20	Putative protein of unknown function; overexpression causes a cell cycle delay or arrest; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; null mutant displays elevated frequency of mitochondrial genome loss	Q

3536	VN_3536	YMR121C	RPL15B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl15Ap and has similarity to rat L15 ribosomal protein; binds to 5.8 S rRNA	Q
3537	VN_3537	YEL076W-C		#N/A	Q
3538	VN_3538	YBR005W	RCR1	Protein of the ER membrane involved in cell wall chitin deposition; may function in the endosomal-vacuolar trafficking pathway, helping determine whether plasma membrane proteins are degraded or routed to the plasma membrane	Q
3539	VN_3539	YOR021C	YOR021C	Putative protein of unknown function; YOR021C is not an essential gene; predicted to be involved in rRNA processing and ribosome biogenesis and in biopolymer catabolism	Q
3540	VN_3540	YOL111C	MDY2	Protein required for efficient mating; involved in shmoo formation and nuclear migration in the pre-zygote; associates with ribosomes and interacts with Get4p; has a possible role in insertion of tail-anchored proteins into the ER membrane	Q
3541	VN_3541	YOR236W	DFR1	Dihydrofolate reductase, part of the dTTP biosynthetic pathway, involved in folate metabolism, possibly required for mitochondrial function	Q
3542	VN_3542	YGR081C	SLX9	Protein required for pre-rRNA processing; associated with the 90S pre-ribosome and 43S small ribosomal subunit precursor; interacts with U3 snoRNA; deletion mutant has synthetic fitness defect with an sgs1 deletion mutant	Q
3543	VN_3543	YDR487C	RIB3	3,4-dihydroxy-2-butanone-4-phosphate synthase (DHBP synthase), required for riboflavin biosynthesis from ribulose-5-phosphate, also has an unrelated function in mitochondrial respiration	Q
3544	VN_3544	YOL008W	COQ10	Coenzyme Q (ubiquinone) binding protein, functions in the delivery of Q ₆ to its proper location for electron transport during respiration; START domain protein with homologs in bacteria and eukaryotes	Q
3545	VN_3545	YMR245W	YMR245W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3546	VN_3546	YKL024C	URA6	Uridylate kinase, catalyzes the seventh enzymatic step in the de novo biosynthesis of pyrimidines, converting uridine monophosphate (UMP) into uridine-5'-diphosphate (UDP)	Q
3547	VN_3547	YNL190W	YNL190W	Cell wall protein of unknown function; proposed role as a hydrophilin induced by osmotic stress; contains a putative GPI-attachment site	Q
3548	VN_3548	YER128W	YER128W	Putative protein of unknown function	Q
3549	VN_3549	YDL228C	YDL228C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; almost completely overlaps the verified gene SSB1	Q
3550	VN_3550	YOR319W	HSH49	U2-snRNP associated splicing factor with similarity to the mammalian splicing factor SAP49; proposed to function as a U2-snRNP assembly factor along with Hsh155p and binding partner Cus1p; contains two RNA recognition motifs (RRM)	Q
3551	VN_3551	YBR071W	YBR071W	Putative protein of unknown function; (GFP)-fusion and epitope-tagged proteins localize to the cytoplasm; mRNA expression may be regulated by the cell cycle and/or cell wall stress	Q
3552	VN_3552	YPR071W	YPR071W	Putative membrane protein; YPR071W is not an essential gene	Q
3553	VN_3553	YIL167W	SDL1	Open reading frame, unlikely to produce a functional protein in S288C; in closely related species and other <i>S. cerevisiae</i> strain backgrounds YIL167W and adjacent ORF, YIL168W, constitute a single ORF encoding L-serine dehydratase	Q
3554	VN_3554	YER104W	RTT105	Protein with a role in regulation of Ty1 transposition	Q
3555	VN_3555	YPL041C	YPL041C	Protein of unknown function involved in maintenance of proper telomere length	Q
3556	VN_3556	YNL222W	SSU72	Transcription/RNA-processing factor that associates with TFIIB and cleavage/polyadenylation factor Pta1p; exhibits phosphatase activity on serine-5 of the RNA polymerase II C-terminal domain; affects start site selection in vivo	Q

3557	VN_3557	YHR057C	CPR2	Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; has a potential role in the secretory pathway	Q
3558	VN_3558	YNL208W	YNL208W	Protein of unknown function; may interact with ribosomes, based on co-purification experiments; authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies; potential orthologs found in other fungi	Q
3559	VN_3559	YGR160W	YGR160W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
3560	VN_3560	YIL132C	CSM2	Protein involved in a Rad51p-, Rad54p-dependent pathway for homologous recombination repair, required for accurate chromosome segregation during meiosis	Q
3561	VN_3561	YPL166W	ATG29	Autophagy-specific protein that is required for recruitment of other ATG proteins to the pre-autophagosomal structure (PAS); interacts with Atg17p and localizes to the PAS in a manner interdependent with Atg17p and Cts1p; not conserved	Q
3562	VN_3562	YBR201W	DER1	Endoplasmic reticulum membrane protein, required for ER-associated protein degradation of misfolded or unassembled proteins; N- and C-termini protrude into the cytoplasm, has similarity to Dfm1p	Q
3563	VN_3563	YBR052C	RFS1	Protein of unknown function; member of a flavodoxin-like fold protein family that includes Pst2p and Ycp4p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Q
3564	VN_3564	YML095C	RAD10	Single-stranded DNA endonuclease (with Rad1p), cleaves single-stranded DNA during nucleotide excision repair and double-strand break repair; subunit of Nucleotide Excision Repair Factor 1 (NEF1); homolog of human ERCC1 protein	Q
3565	VN_3565	YMR132C	JLP2	Protein of unknown function, contains sequence that closely resembles a J domain (typified by the E. coli DnaJ protein)	Q
3566	VN_3566	YDL130W	RPP1B	Ribosomal protein P1 beta, component of the ribosomal stalk, which is involved in interaction of translational elongation factors with ribosome; accumulation is regulated by phosphorylation and interaction with the P2 stalk component	Q
3567	VN_3567	YOR387C	YOR387C	Putative protein of unknown function; regulated by the metal-responsive Aft1p transcription factor; highly inducible in zinc-depleted conditions; localizes to the soluble fraction	Q
3568	VN_3568	YHR089C	GAR1	Protein component of the H/ACA snoRNP pseudouridylation complex, involved in the modification and cleavage of the 18S pre-rRNA	Q
3569	VN_3569	YKR035W-A	DID2	Class E protein of the vacuolar protein-sorting (Vps) pathway; binds Vps4p and directs it to dissociate ESCRT-III complexes; forms a functional and physical complex with Ist1p; human ortholog may be altered in breast tumors	Q
3570	VN_3570	YOR383C	FIT3	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall	Strain failed to verify via PCR
3571	VN_3571	YHR214W	YHR214W	Putative protein of unknown function; predicted to be a glycosylphosphatidylinositol-modified (GPI) protein	Q
3572	VN_3572	YJL072C	PSF2	Subunit of the GINS complex (Sld5p, Psf1p, Psf2p, Psf3p), which is localized to DNA replication origins and implicated in assembly of the DNA replication machinery	Q
3573	VN_3573	YFL056C	AAD6	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase, involved in the oxidative stress response; expression induced in cells treated with the mycotoxin patulin	Q
3574	VN_3574	YER183C	FAU1	5,10-methenyltetrahydrofolate synthetase, involved in folic acid biosynthesis	Q
3575	VN_3575	YBR067C	TIP1	Major cell wall mannoprotein with possible lipase activity; transcription is induced by heat- and cold-shock; member of the Srp1p/Tip1p family of serine-alanine-rich proteins	Q
3576	VN_3576	YOR247W	SRL1	Mannoprotein that exhibits a tight association with the cell wall, required for cell wall stability in the absence of GPI-anchored mannoproteins; has a high serine-threonine content; expression is induced in cell wall mutants	Q

3577	VN_3577	YPL178W	CBC2	Small subunit of the heterodimeric cap binding complex that also contains Sto1p, component of the spliceosomal commitment complex; interacts with Npl3p, possibly to package mRNA for export from the nucleus; contains an RNA-binding motif	Q
3578	VN_3578	YLR287C-A	RPS30A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps30Bp and has similarity to rat S30 ribosomal protein	Q
3579	VN_3579	YPL229W	YPL229W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YPL229W is not an essential gene	Q
3580	VN_3580	YIL089W	YIL089W	Putative protein of unknown function	Q
3581	VN_3581	YLR016C	PML1	Subunit of the RES complex, which is required for nuclear retention of unspliced pre-mRNAs; acts in the same pathway as Pml39p and Mlp1p	Q
3582	VN_3582	YAR066W	YAR066W	Putative GPI protein	Q
3583	VN_3583	YKL214C	YRA2	Member of the REF (RNA and export factor binding proteins) family; when overexpressed, can substitute for the function of Yra1p in export of poly(A)+ mRNA from the nucleus	Q
3584	VN_3584	YKR035C	OPI8	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene DID2/YKR035W-A	Q
3585	VN_3585	YKL144C	RPC25	RNA polymerase III subunit C25, required for transcription initiation; forms a heterodimer with Rpc17p; paralog of Rpb7p	Q
3586	VN_3586	YFL010C	WWM1	WW domain containing protein of unknown function; binds to Mca1p, a caspase-related protease that regulates H2O2-induced apoptosis; overexpression causes G1 phase growth arrest and clonal death that is suppressed by overexpression of MCA1	Q
3587	VN_3587	YCL067C	HMLALPHA2	Silenced copy of ALPHA2 at HML; homeobox-domain protein that associates with Mcm1p in haploid cells to repress a-specific gene expression and interacts with a1p in diploid cells to repress haploid-specific gene expression	Q
3588	VN_3588	YIL113W	SDP1	Stress-inducible dual-specificity MAP kinase phosphatase, negatively regulates Sit2p MAP kinase by direct dephosphorylation, diffuse localization under normal conditions shifts to punctate localization after heat shock	Q
3589	VN_3589	YPR107C	YTH1	Essential RNA-binding component of cleavage and polyadenylation factor, contains five zinc fingers; required for pre-mRNA 3'-end processing and polyadenylation	Q
3590	VN_3590	YDL200C	MGT1	DNA repair methyltransferase (6-O-methylguanine-DNA methylase) involved in protection against DNA alkylation damage	Q
3591	VN_3591	YPR151C	SUE1	Mitochondrial protein required for degradation of unstable forms of cytochrome c	Q
3592	VN_3592	YKL147C	YKL147C	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; partially overlaps the verified gene AVT3	Q
3593	VN_3593	YLR029C	RPL15A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl15Bp and has similarity to rat L15 ribosomal protein; binds to 5.8 S rRNA	Strain failed to verify via PCR
3594	VN_3594	YBR014C	GRX7	Cis-golgi localized monothiol glutaredoxin; more similar in activity to dithiol than other monothiol glutaredoxins; involved in the oxidative stress response; does not bind metal ions; functional overlap with GRX6	Q
3595	VN_3595	YLR036C	YLR036C	Putative protein of unknown function predicted to have transmembrane domains; interacts with HSP90 by yeast two-hybrid analysis; YLR036C is not an essential protein	Q
3596	VN_3596	YLR119W	SRN2	Component of the ESCRT-I complex, which is involved in ubiquitin-dependent sorting of proteins into the endosome; suppressor of rna1-1 mutation; may be involved in RNA export from nucleus	Q
3597	VN_3597	YML053C	YML053C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and the nucleus; overexpression causes a cell cycle delay or arrest; YML053C is not an essential gene	Q

3598	VN_3598	YGR146C	ECL1	Protein of unknown function, affects chronological lifespan; induced by iron homeostasis transcription factor Aft2p; multicopy suppressor of temperature sensitive hsf1 mutant; induced by treatment with 8-methoxypsoralen and UVA irradiation	Q
3599	VN_3599	YJR133W	XPT1	Xanthine-guanine phosphoribosyl transferase, required for xanthine utilization and for optimal utilization of guanine	Q
3600	VN_3600	YLR185W	RPL37A	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl37Bp and to rat L37 ribosomal protein	Q
3601	VN_3601	YDR167W	TAF10	Subunit (145 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification	Q
3602	VN_3602	YAL014C	SYN8	Endosomal SNARE related to mammalian syntaxin 8	Q
3603	VN_3603	YNL310C	ZIM17	Heat shock protein with a zinc finger motif; essential for protein import into mitochondria; may act with Pam18p to facilitate recognition and folding of imported proteins by Ssc1p (mtHSP70) in the mitochondrial matrix	Q
3604	VN_3604	YLR456W	YLR456W	Putative protein of unknown function; null mutant displays increased resistance to antifungal agents gliotoxin, cycloheximide and H2O2	Q
3605	VN_3605	YDL002C	NHP10	Protein related to mammalian high mobility group proteins; binds preferentially to DNA ends and is able to protect them from exonuclease cleavage; likely component of the INO80 complex, which is an ATP-dependent chromatin-remodeling complex	Q
3606	VN_3606	YNL203C	YNL203C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3607	VN_3607	YLR462W	YLR462W	Putative protein of unknown function with similarity to helicases; YLR462W is within the telomere on the right arm of chromosome XII	Q
3608	VN_3608	YLR179C	YLR179C	Protein of unknown function with similarity to Tfs1p; transcription is activated by paralogous proteins Yrm1p and Yrr1p along with proteins involved in multidrug resistance; GFP-tagged protein localizes to the cytoplasm and nucleus	Q
3609	VN_3609	YDR042C	YDR042C	Putative protein of unknown function; expression is increased in ssu72-ts69 mutant	Q
3610	VN_3610	YPL239W	YAR1	Cytoplasmic ankyrin-repeat containing protein of unknown function, proposed to link the processes of 40S ribosomal subunit biogenesis and adaptation to osmotic and oxidative stress; expression repressed by heat shock	Q
3611	VN_3611	YKL156W	RPS27A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps27Bp and has similarity to rat S27 ribosomal protein	Q
3612	VN_3612	YHR213W	YHR213W	Possible pseudogene; has similarity to Flo1p, which is a lectin-like protein involved in flocculation	Q
3613	VN_3613	YPL067C	YPL067C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YPL067C is not an essential gene	Q
3614	VN_3614	YMR295C	YMR295C	Protein of unknown function that associates with ribosomes; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery and bud; YMR295C is not an essential gene	Strain failed to verify via PCR
3615	VN_3615	YER029C	SMB1	Core Sm protein Sm B; part of heteroheptameric complex (with Smd1p, Smd2p, Smd3p, Sme1p, Smx3p, and Smx2p) that is part of the spliceosomal U1, U2, U4, and U5 snRNPs; homolog of human Sm B and Sm B'	Q
3616	VN_3616	YOR122C	PFY1	Profilin, actin- and phosphatidylinositol 4,5-bisphosphate-binding protein, involved in cytoskeleton organization, required for normal timing of actin polymerization in response to thermal stress; localizes to plasma membrane and cytosol	Strain failed to verify via PCR
3617	VN_3617	YDR328C	SKP1	Evolutionarily conserved kinetochore protein that is part of multiple protein complexes, including the SCF ubiquitin ligase complex, the CBF3 complex that binds centromeric DNA, and the RAVE complex that regulates assembly of the V-ATPase	Strain failed to verify via PCR
3618	VN_3618	YLL050C	COF1	Cofilin, promotes actin filament depolarization in a pH-dependent manner; binds both actin monomers and filaments and severs filaments; thought to be regulated by phosphorylation at SER4; ubiquitous and essential in eukaryotes	Q

3619	VN_3619	YOL114C	YOL114C	Putative protein of unknown function with similarity to human ICT1 and prokaryotic factors that may function in translation termination; YOL114C is not an essential gene	Q
3620	VN_3620	YML079W	YML079W	Non-essential protein of unknown function with structural resemblance to plant storage and ligand binding proteins (canavalin, glycinin, auxin binding protein) and to some enzymes (epimerase, germin); localizes to the nucleus and cytoplasm	Q
3621	VN_3621	YER102W	RPS8B	Protein component of the small (40S) ribosomal subunit; identical to Rps8Ap and has similarity to rat S8 ribosomal protein	Strain failed to verify via PCR
3622	VN_3622	YPR172W	YPR172W	Protein of unknown function, transcriptionally activated by Yrm1p along with genes involved in multidrug resistance	Q
3623	VN_3623	YAL008W	FUN14	Mitochondrial protein of unknown function	Q
3624	VN_3624	YJL217W	REE1	Cytoplasmic protein involved in the regulation of enolase (ENO1); mRNA expression is induced by calcium shortage, copper deficiency (via Mac1p) and the presence of galactose (via Gal4p); mRNA expression is also regulated by the cell cycle	Strain failed to verify via PCR
3625	VN_3625	YDL166C	FAP7	Essential NTPase required for small ribosome subunit synthesis, mediates processing of the 20S pre-rRNA at site D in the cytoplasm but associates only transiently with 43S preribosomes via Rps14p, may be the endonuclease for site D	Q
3626	VN_3626	YNL056W	OCA2	Putative protein with similarity to predicted tyrosine phosphatases Oca1p and Siw14p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YNL056W is not an essential gene	Q
3627	VN_3627	YGR251W	YGR251W	Essential protein required for maturation of 18S rRNA; green fluorescent protein (GFP)-fusion protein localizes to both the nucleus and the nucleolus	Q
3628	VN_3628	YDL125C	HNT1	Adenosine 5'-monophosphoramidase; interacts physically and genetically with Kin28p, a CDK and TFIIF subunit, and genetically with CAK1; member of the histidine triad (HIT) superfamily of nucleotide-binding proteins and similar to Hint	Q
3629	VN_3629	YGL068W	MNP1	Protein associated with the mitochondrial nucleoid; putative mitochondrial ribosomal protein with similarity to E. coli L7/L12 ribosomal protein; required for normal respiratory growth	Q
3630	VN_3630	YDL135C	RDI1	Rho GDP dissociation inhibitor involved in the localization and regulation of Cdc42p	Q
3631	VN_3631	YBR278W	DPB3	Third-largest subunit of DNA polymerase II (DNA polymerase epsilon), required to maintain fidelity of chromosomal replication and also for inheritance of telomeric silencing; mRNA abundance peaks at the G1/S boundary of the cell cycle	Q
3632	VN_3632	YMR073C	IRC21	Putative protein of unknown function; proposed to be involved in resistance to carboplatin and cisplatin; shares similarity to a human cytochrome oxidoreductase; null mutant displays increased levels of spontaneous Rad52p foci	Q
3633	VN_3633	YFL031W	HAC1	Basic leucine zipper (bZIP) transcription factor (ATF/CREB1 homolog) that regulates the unfolded protein response, via UPR binding, and membrane biogenesis; ER stress-induced splicing pathway facilitates efficient Hac1p synthesis	Q
3634	VN_3634	YAR062W	YAR062W	Pseudogene with similarity to Flo1p, which is a lectin-like protein involved in flocculation	Q
3635	VN_3635	YJR014W	TMA22	Protein of unknown function; associates with ribosomes and has a putative RNA binding domain; interacts with Tma20p; similar to human GRAP and human DRP1, which interacts with human Tma20p homolog MCT-1	Q
3636	VN_3636	YBL107C	YBL107C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YBL107C is not an essential gene	Q
3637	VN_3637	YJL030W	MAD2	Component of the spindle-assembly checkpoint complex, which delays the onset of anaphase in cells with defects in mitotic spindle assembly; forms a complex with Mad1p	Q
3638	VN_3638	YEL067C	YEL067C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q

3639	VN_3639	YDL064W	UBC9	SUMO-conjugating enzyme involved in the Smt3p conjugation pathway; nuclear protein required for S- and M-phase cyclin degradation and mitotic control; involved in proteolysis mediated by the anaphase-promoting complex cyclosome (APCC)	Strain failed to verify via PCR
3640	VN_3640	YER050C	RSM18	Mitochondrial ribosomal protein of the small subunit, has similarity to E. coli S18 ribosomal protein	Q
3641	VN_3641	YMR263W	SAP30	Subunit of a histone deacetylase complex, along with Rpd3p and Sin3p, that is involved in silencing at telomeres, rDNA, and silent mating-type loci; involved in telomere maintenance	Q
3642	VN_3642	YDR032C	PST2	Protein with similarity to members of a family of flavodoxin-like proteins; induced by oxidative stress in a Yap1p dependent manner; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3643	VN_3643	YMR003W	AIM34	Protein of unknown function; GFP-fusion protein localizes to the mitochondria; null mutant is viable and displays reduced frequency of mitochondrial genome loss	Q
3644	VN_3644	YGL247W	BRR6	Essential nuclear envelope integral membrane protein required for nuclear transport; depletion alters nucleoporin distribution and nuclear envelope morphology, suggesting a role in the spatial organization of nuclear pores	Q
3645	VN_3645	YBR122C	MRPL36	Mitochondrial ribosomal protein of the large subunit; overproduction suppresses mutations in the COX2 leader peptide-encoding region	Strain failed to verify via PCR
3646	VN_3646	YJL178C	ATG27	Type I membrane protein involved in autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; may be involved in membrane delivery to the phagophore assembly site	Q
3647	VN_3647	YFR017C	YFR017C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and is induced in response to the DNA-damaging agent MMS; YFR017C is not an essential gene	Q
3648	VN_3648	YCL026C-A	FRM2	Protein of unknown function, involved in the integration of lipid signaling pathways with cellular homeostasis; expression induced in cells treated with the mycotoxin patulin; has similarity to bacterial nitroreductases	Q
3649	VN_3649	YFR012W	YFR012W	Putative protein of unknown function	Q
3650	VN_3650	YDR537C	YDR537C	Dubious open reading frame unlikely to encode a protein, almost completely overlaps verified ORF PAD1/YDR538W	Q
3651	VN_3651	YOL029C	YOL029C	Putative protein of unknown function; identified as interacting with Hsc82p and Hsp82p in high-throughput two-hybrid screens	Q
3652	VN_3652	YLR073C	RFU1	Protein that inhibits Doa4p deubiquitinating activity; contributes to ubiquitin homeostasis by regulating the conversion of free ubiquitin chains to ubiquitin monomers by Doa4p; GFP-fusion protein localizes to endosomes	Q
3653	VN_3653	YGR226C	YGR226C	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; overlaps significantly with a verified ORF, AMA1/YGR225W	Q
3654	VN_3654	YDR478W	SNM1	Subunit of RNase MRP, which cleaves pre-rRNA and has a role in cell cycle-regulated degradation of daughter cell-specific mRNAs; binds to the NME1 RNA subunit of RNase MRP	Strain failed to verify via PCR
3655	VN_3655	YIL157C	COA1	Mitochondrial inner membrane protein required for assembly of the cytochrome c oxidase complex (complex IV); interacts with complex IV assembly factor Shy1p during the early stages of assembly	Q
3656	VN_3656	YDR022C	CIS1	Autophagy-specific protein required for autophagosome formation; may form a complex with Atg17p and Atg29p that localizes other proteins to the pre-autophagosomal structure; high-copy suppressor of CIK1 deletion	Q
3657	VN_3657	YJL218W	YJL218W	Putative protein of unknown function, similar to bacterial galactoside O-acetyltransferases; induced by oleate in an OAF1/PIP2-dependent manner; promoter contains an oleate response element consensus sequence; non-essential gene	Q
3658	VN_3658	YKR085C	MRPL20	Mitochondrial ribosomal protein of the large subunit	Q

3659	VN_3659	YCL027C-A		#N/A	Strain failed to verify via PCR
3660	VN_3660	YGL047W	ALG13	Catalytic component of UDP-GlcNAc transferase, required for the second step of dolichyl-linked oligosaccharide synthesis; anchored to the ER membrane via interaction with Alg14p; similar to bacterial and human glycosyltransferases	Q
3661	VN_3661	YJR112W	NNF1	Essential component of the MIND kinetochore complex (Mtw1p Including Nnf1p-Nsl1p-Dsn1p) which joins kinetochore subunits contacting DNA to those contacting microtubules; required for accurate chromosome segregation	Q
3662	VN_3662	YPL052W	OAZ1	Regulator of ornithine decarboxylase (Spe1p), antizyme that binds to Spe1p to regulate ubiquitin-independent degradation; ribosomal frameshifting during synthesis of Oaz1p and its ubiquitin-mediated degradation are both polyamine-regulated	Q
3663	VN_3663	YLR329W	REC102	Protein involved in early stages of meiotic recombination; required for chromosome synapsis; forms a complex with Rec104p and Spo11p necessary during the initiation of recombination	Q
3664	VN_3664	YIL164C	NIT1	Nitrilase, member of the nitrilase branch of the nitrilase superfamily; in closely related species and other <i>S. cerevisiae</i> strain backgrounds YIL164C and adjacent ORF, YIL165C, likely constitute a single ORF encoding a nitrilase gene	Q
3665	VN_3665	YER012W	PRE1	Beta 4 subunit of the 20S proteasome; localizes to the nucleus throughout the cell cycle	Strain failed to verify via PCR
3666	VN_3666	YNL158W	PGA1	Essential component of GPI-mannosyltransferase II, responsible for second mannose addition to GPI precursors as a partner of Gpi18p; required for maturation of Gas1p and Pho8p; has synthetic genetic interactions with secretory pathway genes	Q
3667	VN_3667	YJR069C	HAM1	Conserved protein with deoxyribonucleoside triphosphate pyrophosphohydrolase activity, mediates exclusion of noncanonical purines from deoxyribonucleoside triphosphate pools; mutant is sensitive to the base analog 6-N-hydroxylaminopurine	Q
3668	VN_3668	YDR066C	RTR2	Protein of unknown function with high similarity to Rtr1p; exhibits genetic interactions with Rtr1p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YDR066C is not an essential gene	Q
3669	VN_3669	YML028W	TSA1	Thioredoxin peroxidase, acts as both a ribosome-associated and free cytoplasmic antioxidant; self-associates to form a high-molecular weight chaperone complex under oxidative stress; deletion results in mutator phenotype	Q
3670	VN_3670	YNL282W	POP3	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends	Q
3671	VN_3671	YJR102C	VPS25	Component of the ESCRT-II complex, which is involved in ubiquitin-dependent sorting of proteins into the endosome	Strain failed to verify via PCR
3672	VN_3672	YKL030W	YKL030W	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; partially overlaps the verified gene MAE1	Q
3673	VN_3673	YKL190W	CNB1	Calcineurin B; the regulatory subunit of calcineurin, a Ca ⁺⁺ /calmodulin-regulated type 2B protein phosphatase which regulates Crz1p (a stress-response transcription factor), the other calcineurin subunit is encoded by CNA1 and/or CMP1	Q
3674	VN_3674	YOR182C	RPS30B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps30Ap and has similarity to rat S30 ribosomal protein	Q
3675	VN_3675	YLR009W	RLP24	Essential protein with similarity to Rpl24Ap and Rpl24Bp, associated with pre-60S ribosomal subunits and required for ribosomal large subunit biogenesis	Strain failed to verify via PCR
3676	VN_3676	YGR268C	HUA1	Cytoplasmic protein containing a zinc finger domain with sequence similarity to that of Type I J-proteins; computational analysis of large-scale protein-protein interaction data suggests a possible role in actin patch assembly	Q
3677	VN_3677	YNL260C	YNL260C	Putative protein of unknown function with similarity to a human protein overexpressed in oral cancers; essential gene with defects in anaerobic and filamentous growth; localizes to the nucleus and	Q

				cytoplasm	
3678	VN_3678	YKR065C	PAM17	Constituent of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); proposed alternatively to be a component of the import motor (PAM complex) or to interact with and modulate the core TIM23 complex	Q
3679	VN_3679	YDR121W	DPB4	Shared subunit of DNA polymerase (II) epsilon and of ISW2/yCHRAC chromatin accessibility complex; involved in both chromosomal DNA replication and in inheritance of telomeric silencing	Q
3680	VN_3680	YMR118C	YMR118C	Protein of unknown function with similarity to succinate dehydrogenase cytochrome b subunit; YMR118C is not an essential gene	Q
3681	VN_3681	YKR057W	RPS21A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps21Bp and has similarity to rat S21 ribosomal protein	Q
3682	VN_3682	YDR248C	YDR248C	Putative protein of unknown function; sequence similarity to bacterial and human gluconokinase; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; upregulated by deletion of the RNAP-II associated factor, PAF1	Q
3683	VN_3683	YKL001C	MET14	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism	Q
3684	VN_3684	YLR145W	RMP1	Subunit of RNase MRP, which processes pre-rRNA and has a role in cell cycle-regulated degradation of daughter cell-specific mRNAs; unlike most subunits, not shared between RNase MRP and nuclear RNase P	Q
3685	VN_3685	YBL072C	RPS8A	Protein component of the small (40S) ribosomal subunit; identical to Rps8Bp and has similarity to rat S8 ribosomal protein	Strain failed to verify via PCR
3686	VN_3686	YOR367W	SCP1	Component of yeast cortical actin cytoskeleton, binds and cross links actin filaments; originally identified by its homology to calponin (contains a calponin-like repeat) but the Scp1p domain structure is more similar to transgelin	Q
3687	VN_3687	YNL079C	TPM1	Major isoform of tropomyosin; binds to and stabilizes actin cables and filaments, which direct polarized cell growth and the distribution of several organelles; acetylated by the NatB complex and acetylated form binds actin most efficiently	Strain failed to verify via PCR
3688	VN_3688	YHR153C	SPO16	Meiosis-specific protein involved in synaptonemal complex assembly; implicated in regulation of crossover formation; required for sporulation	Q
3689	VN_3689	YPL051W	ARL3	GTPase of the Ras superfamily required to recruit Arl1p to the Golgi; similar to ADP-ribosylation factor	Q
3690	VN_3690	YLR251W	SYM1	Protein required for ethanol metabolism; induced by heat shock and localized to the inner mitochondrial membrane; homologous to mammalian peroxisomal membrane protein Mpv17	Q
3691	VN_3691	YDR453C	TSA2	Stress inducible cytoplasmic thioredoxin peroxidase; cooperates with Tsa1p in the removal of reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; deletion enhances the mutator phenotype of tsa1 mutants	Q
3692	VN_3692	YPR037C	ERV2	Flavin-linked sulfhydryl oxidase localized to the endoplasmic reticulum lumen, involved in disulfide bond formation within the ER	Q
3693	VN_3693	YDL098C	SNU23	Component of U4/U6.U5 snRNP involved in mRNA splicing via spliceosome	Q
3694	VN_3694	YGL211W	NCS6	Protein required for thiolation of the uridine at the wobble position of Gln, Lys, and Glu tRNAs; has a role in urmylation and in invasive and pseudohyphal growth; inhibits replication of Brome mosaic virus in <i>S. cerevisiae</i>	Strain failed to verify via PCR
3695	VN_3695	YKL202W	YKL202W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3696	VN_3696	YDR413C	YDR413C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the essential uncharacterized ORF YDR412W that is implicated in rRNA processing	Q
3697	VN_3697	YCR086W	CSM1	Nucleolar protein that forms a complex with Lrs4p and then Mam1p at	Q

				kinetochores during meiosis I to mediate accurate homolog segregation; required for condensin recruitment to the replication fork barrier site and rDNA repeat segregation	
3698	VN_3698	YHR175W	CTR2	Putative low-affinity copper transporter of the vacuolar membrane; mutation confers resistance to toxic copper concentrations, while overexpression confers resistance to copper starvation	Q
3699	VN_3699	YOR179C	SYC1	Subunit of the APT subcomplex of cleavage and polyadenylation factor, may have a role in 3' end formation of both polyadenylated and non-polyadenylated RNAs	Q
3700	VN_3700	YLR358C	YLR358C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF RSC2/YLR357W	Strain failed to verify via PCR
3701	VN_3701	YNR024W	MPP6	Nuclear exosome-associated RNA binding protein; involved in surveillance of pre-rRNAs and pre-mRNAs, and the degradation of cryptic non-coding RNAs (ncRNA); copurifies with ribosomes	Q
3702	VN_3702	YPL025C	YPL025C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
3703	VN_3703	YJR094W-A	RPL43B	Protein component of the large (60S) ribosomal subunit, identical to Rpl43Ap and has similarity to rat L37a ribosomal protein	Q
3704	VN_3704	YMR072W	ABF2	Mitochondrial DNA-binding protein involved in mitochondrial DNA replication and recombination, member of HMG1 DNA-binding protein family; activity may be regulated by protein kinase A phosphorylation	Strain failed to verify via PCR
3705	VN_3705	YGL030W	RPL30	Protein component of the large (60S) ribosomal subunit, has similarity to rat L30 ribosomal protein; involved in pre-rRNA processing in the nucleolus; autoregulates splicing of its transcript	Strain failed to verify via PCR
3706	VN_3706	YPR187W	RPO26	RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III; part of central core; similar to bacterial omega subunit	Strain failed to verify via PCR
3707	VN_3707	YKR068C	BET3	Hydrophilic protein that acts in conjunction with SNARE proteins in targeting and fusion of ER to Golgi transport vesicles; component of the TRAPP (transport protein particle) complex	Q
3708	VN_3708	YER115C	SPR6	Protein of unknown function, expressed during sporulation; not required for sporulation, but gene exhibits genetic interactions with other genes required for sporulation	Q
3709	VN_3709	YDR136C	VPS61	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 4% of ORF overlaps the verified gene RGP1; deletion causes a vacuolar protein sorting defect	Q
3710	VN_3710	YIL024C	YIL024C	Putative protein of unknown function; non-essential gene; expression directly regulated by the metabolic and meiotic transcriptional regulator Ume6p	Q
3711	VN_3711	YDR401W	YDR401W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3712	VN_3712	YML022W	APT1	Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis	Q
3713	VN_3713	YDL053C	PBP4	Pbp1p binding protein, interacts strongly with Pab1p-binding protein 1 (Pbp1p) in the yeast two-hybrid system; also interacts with Lsm12p in a copurification assay	Q
3714	VN_3714	YPR067W	ISA2	Protein required for maturation of mitochondrial and cytosolic Fe/S proteins, localizes to the mitochondrial intermembrane space, overexpression of ISA2 suppresses grx5 mutations	Q
3715	VN_3715	YCR003W	MRPL32	Mitochondrial ribosomal protein of the large subunit	Q
3716	VN_3716	YCR090C	YCR090C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YCR090C is not an essential gene	Q
3717	VN_3717	YIL009C-A	EST3	Component of the telomerase holoenzyme, involved in telomere replication	Q
3718	VN_3718	YAL055W	PEX22	Putative peroxisomal membrane protein required for import of peroxisomal proteins, functionally complements a Pichia pastoris pex22 mutation	Q

3719	VN_3719	YPL257W	YPL257W	Putative protein of unknown function; homozygous diploid deletion strain exhibits low budding index; physically interacts with Hsp82p; YPL257W is not an essential gene	Q
3720	VN_3720	YGL147C	RPL9A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl9Bp and has similarity to E. coli L6 and rat L9 ribosomal proteins	Q
3721	VN_3721	YGL231C	EMC4	Member of a transmembrane complex required for efficient folding of proteins in the ER; null mutant displays induction of the unfolded protein response; human ortholog TMEM85 may function in apoptosis	Q
3722	VN_3722	YLR254C	NDL1	Homolog of nuclear distribution factor NudE, NUDEL; interacts with Pac1p and regulates dynein targeting to microtubule plus ends	Q
3723	VN_3723	YDR454C	GUK1	Guanylate kinase, converts GMP to GDP; required for growth and mannose outer chain elongation of cell wall N-linked glycoproteins	Q
3724	VN_3724	YPL021W	ECM23	Non-essential protein of unconfirmed function; affects pre-rRNA processing, may act as a negative regulator of the transcription of genes involved in pseudohyphal growth; homologous to Srd1p	Q
3725	VN_3725	YER034W	YER034W	Putative protein of unknown function; non-essential gene; expression induced upon calcium shortage	Q
3726	VN_3726	YER042W	MXR1	Methionine-S-sulfoxide reductase, involved in the response to oxidative stress; protects iron-sulfur clusters from oxidative inactivation along with MXR2; involved in the regulation of lifespan	Q
3727	VN_3727	YCR101C	YCR101C	Putative protein of unknown function; localizes to the membrane fraction; YCR101C is not an essential gene	Q
3728	VN_3728	YDR441C	APT2	Apparent pseudogene, not transcribed or translated under normal conditions; encodes a protein with similarity to adenine phosphoribosyltransferase, but artificially expressed protein exhibits no enzymatic activity	Q
3729	VN_3729	YJL160C	YJL160C	Putative protein of unknown function; member of the PIR (proteins with internal repeats) family of cell wall proteins; non-essential gene that is required for sporulation; mRNA is weakly cell cycle regulated, peaking in mitosis	Q
3730	VN_3730	YFR054C	YFR054C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3731	VN_3731	YKR045C	YKR045C	Putative protein of unknown function; epitope-tagged protein localizes to the cytoplasm	Q
3732	VN_3732	YGR016W	YGR016W	Putative protein of unknown function	Q
3733	VN_3733	YML036W	CGI121	Protein involved in telomere uncapping and elongation as component of the KEOPS protein complex with Bud32p, Kae1p, Pcc1p, and Gon7p; also shown to be a component of the EKC protein complex; homolog of human CGI-121	Q
3734	VN_3734	YDR512C	EMI1	Non-essential protein required for transcriptional induction of the early meiotic-specific transcription factor IME1, also required for sporulation; contains twin cysteine-x9-cysteine motifs	Q
3735	VN_3735	YPR142C	YPR142C	Hypothetical protein; open reading frame overlaps 5' end of essential RRP15 gene required for ribosomal RNA processing	Q
3736	VN_3736	YER066W	RRT13	Putative protein of unknown function; non-essential gene identified in a screen for mutants with decreased levels of rDNA transcription	Q
3737	VN_3737	YGL018C	JAC1	Specialized J-protein that functions with Hsp70 in Fe-S cluster biogenesis in mitochondria, involved in iron metabolism; contains a J domain typical to J-type chaperones; localizes to the mitochondrial matrix	Q
3738	VN_3738	YGR102C	YGR102C	Subunit of the trimeric GatFAB AmidoTransferase(AdT) complex; involved in the formation of Q-tRNA ^{Glu} ; transposon insertion mutant is salt sensitive and null mutant has growth defects; non-tagged protein is detected in purified mitochondria	Q
3739	VN_3739	YHR093W	AHT1	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; multicopy suppressor of glucose transport defects, likely due to the presence of an HXT4 regulatory element in the region	Q
3740	VN_3740	YGL242C	YGL242C	Putative protein of unknown function; deletion mutant is viable	Q

3741	VN_3741	YJL161W	FMP33	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3742	VN_3742	YGL165C	YGL165C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF CUP2/YGL166W	Q
3743	VN_3743	YLR011W	LOT6	FMN-dependent NAD(P)H:quinone reductase, may be involved in quinone detoxification; expression elevated at low temperature; sequesters the Cin5p transcription factor in the cytoplasm in complex with the proteasome under reducing conditions	Q
3744	VN_3744	YHR189W	PTH1	One of two (see also PTH2) mitochondrially-localized peptidyl-tRNA hydrolases; dispensable for respiratory growth on rich medium, but required for respiratory growth on minimal medium	Q
3745	VN_3745	YNL140C	YNL140C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene THO2/YNL139C	Q
3746	VN_3746	YER112W	LSM4	Lsm (Like Sm) protein; part of heteroheptameric complexes (Lsm2p-7p and either Lsm1p or 8p); cytoplasmic Lsm1p complex involved in mRNA decay; nuclear Lsm8p complex part of U6 snRNP and possibly involved in processing tRNA, snoRNA, and rRNA	Q
3747	VN_3747	YPR197C	YPR197C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3748	VN_3748	YHR100C	GEP4	Protein of unknown function required for respiratory growth; detected in highly purified mitochondria in high-throughput studies; null mutation confers sensitivity to tunicamycin and DTT and decreased levels of phosphatidylethanol	Q
3749	VN_3749	YHR081W	LRP1	Nuclear exosome-associated nucleic acid binding protein; involved in RNA processing, surveillance, degradation, tethering, and export; homolog of mammalian nuclear matrix protein C1D involved in regulation of DNA repair and recombination	Q
3750	VN_3750	YHR157W	REC104	Protein involved in early stages of meiotic recombination; required for meiotic crossing over; forms a complex with Rec102p and Spo11p necessary during the initiation of recombination	Strain failed to verify via PCR
3751	VN_3751	YLR065C	YLR065C	Putative protein of unknown function; YLR065C is not an essential gene	Strain failed to verify via PCR
3752	VN_3752	YKL069W	YKL069W	Methionine-R-sulfoxide reductase, reduces the R enantiomer of free Met-SO, in contrast to Ycl033Cp which reduces Met-R-SO in a peptide linkage; has a role in protection against oxidative stress	Q
3753	VN_3753	YDL165W	CDC36	Component of the CCR4-NOT complex, which has multiple roles in regulating mRNA levels including regulation of transcription and destabilizing mRNAs by deadenylation; basal transcription factor	Q
3754	VN_3754	YMR138W	CIN4	GTP-binding protein involved in beta-tubulin (Tub2p) folding; isolated as mutant with increased chromosome loss and sensitivity to benomyl; regulated by the GTPase-activating protein, Cin2p, the human retinitis pigmentosa 2 (RP2) homolog	Q
3755	VN_3755	YJR017C	ESS1	Peptidylprolyl-cis/trans-isomerase (PPIase) specific for phosphorylated serine and threonine residues N-terminal to proline; regulates phosphorylation of the RNA polymerase II large subunit (Rpo21p) C-terminal domain	Q
3756	VN_3756	YBR106W	PHO88	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations	Q
3757	VN_3757	YGR049W	SCM4	Potential regulatory effector of CDC4 function, suppresses a temperature-sensitive allele of CDC4, tripartite protein structure in which a charged region separates two uncharged domains, not essential for mitosis or meiosis	Q
3758	VN_3758	YBR217W	ATG12	Conserved ubiquitin-like modifier involved in autophagy and the Cvt pathway; conjugated to Atg5p to form a complex involved in Atg8p lipidation; Atg12p-Atg5p also forms a complex with Atg16p that is required for autophagosome formation	Q
3759	VN_3759	YOR148C	SPP2	Essential protein that promotes the first step of splicing and is required for the final stages of spliceosome maturation; interacts with Prp2p, which may release Spp2p from the spliceosome following the first	Q

				cleavage reaction	
3760	VN_3760	YKL186C	MTR2	mRNA transport regulator, essential nuclear protein; Mex67p and Mtr2p form a mRNA export complex which binds to RNA	Strain failed to verify via PCR
3761	VN_3761	YJL170C	ASG7	Protein that regulates signaling from a G protein beta subunit Ste4p and its relocalization within the cell; specific to a-cells and induced by alpha-factor	Q
3762	VN_3762	YML078W	CPR3	Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; involved in protein refolding after import into mitochondria	Q
3763	VN_3763	YNL109W	YNL109W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YNL108C	Q
3764	VN_3764	YMR242C	RPL20A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Bp and has similarity to rat L18a ribosomal protein	Q
3765	VN_3765	YDR071C	PAA1	Polyamine acetyltransferase; acetylates polyamines (e.g. putrescine, spermidine, spermine) and also aralkylamines (e.g. tryptamine, phenylethylamine); may be involved in transcription and/or DNA replication	Q
3766	VN_3766	YNL067W	RPL9B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl9Ap and has similarity to E. coli L6 and rat L9 ribosomal proteins	Q
3767	VN_3767	YNL174W	YNL174W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the verified gene NOP13/YNL175C	Q
3768	VN_3768	YMR255W	GFD1	Coiled-coiled protein of unknown function, identified as a high-copy suppressor of a dbp5 mutation	Q
3769	VN_3769	YHR121W	LSM12	Protein of unknown function that may function in RNA processing; interacts with Pbp1p and Pbp4p and associates with ribosomes; contains an RNA-binding LSM domain and an AD domain; GFP-fusion protein is induced by the DNA-damaging agent MMS	Q
3770	VN_3770	YGR275W	RTT102	Component of both the SWI/SNF and RSC chromatin remodeling complexes, suggested role in chromosome maintenance; possible weak regulator of Ty1 transposition	Q
3771	VN_3771	YOR215C	AIM41	Putative protein of unknown function; the authentic protein is detected in highly purified mitochondria in high-throughput studies; null mutant displays reduced frequency of mitochondrial genome loss	Q
3772	VN_3772	YKR007W	MEH1	Component of the EGO complex, which is involved in the regulation of microautophagy, and of the GSE complex, which is required for proper sorting of amino acid permease Gap1p; loss results in a defect in vacuolar acidification	Q
3773	VN_3773	YLR339C	YLR339C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the essential gene RPP0	Strain failed to verify via PCR
3774	VN_3774	YPL044C	YPL044C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene NOP4/YPL043W	Strain failed to verify via PCR
3775	VN_3775	YPL211W	NIP7	Nucleolar protein required for 60S ribosome subunit biogenesis, constituent of 66S pre-ribosomal particles; physically interacts with Nop8p and the exosome subunit Rrp43p	Q
3776	VN_3776	YBR082C	UBC4	Ubiquitin-conjugating enzyme (E2), mediates degradation of abnormal or excess proteins, including calmodulin and histone H3; interacts with many SCF ubiquitin protein ligases; component of the cellular stress response	Q
3777	VN_3777	YDR253C	MET32	Zinc-finger DNA-binding protein, involved in transcriptional regulation of the methionine biosynthetic genes, similar to Met31p	Q
3778	VN_3778	YML094W	GIM5	Subunit of the heterohexameric cochaperone prefoldin complex which binds specifically to cytosolic chaperonin and transfers target proteins to it	Q
3779	VN_3779	YOR163W	DDP1	Polyphosphate phosphatase; hydrolyzes diphosphorylated inositol polyphosphates and diadenosine polyphosphates; has high specificity	Q

				for diadenosine hexa- and pentaphosphates; member of the MutT family of nucleotide hydrolases	
3780	VN_3780	YIR017C	MET28	Basic leucine zipper (bZIP) transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism	Q
3781	VN_3781	YLR031W	YLR031W	Putative protein of unknown function	Q
3782	VN_3782	YOR331C	YOR331C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; open reading frame overlaps the verified gene VMA4/YOR332W	Q
3783	VN_3783	YOL129W	VPS68	Vacuolar membrane protein of unknown function involved in vacuolar protein sorting; also detected in the mitochondria	Q
3784	VN_3784	YLR463C	YLR463C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the uncharacterized ORFs YLR462W and YLR464W	Q
3785	VN_3785	YPL099C	AIM43	Protein of unknown function; the authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies; null mutant displays elevated frequency of mitochondrial genome loss	Q
3786	VN_3786	YPR046W	MCM16	Protein involved in kinetochore-microtubule mediated chromosome segregation; binds to centromere DNA	Q
3787	VN_3787	YJL189W	RPL39	Protein component of the large (60S) ribosomal subunit, has similarity to rat L39 ribosomal protein; required for ribosome biogenesis; loss of both Rpl31p and Rpl39p confers lethality; also exhibits genetic interactions with SIS1 and PAB1	Strain failed to verify via PCR
3788	VN_3788	YPL249C-A	RPL36B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl36Ap and has similarity to rat L36 ribosomal protein; binds to 5.8 S rRNA	Q
3789	VN_3789	YNL245C	CWC25	Heat-stable protein required for the first step of pre-mRNA splicing; component of a complex containing Cef1p; has similarity to S. pombe Cwf25p	Q
3790	VN_3790	YBR022W	POA1	Phosphatase that is highly specific for ADP-ribose 1"-phosphate, a tRNA splicing metabolite; may have a role in regulation of tRNA splicing	Q
3791	VN_3791	YDR397C	NCB2	Subunit of a heterodimeric NC2 transcription regulator complex with Bur6p; complex binds to TBP and can repress transcription by preventing preinitiation complex assembly or stimulate activated transcription; homologous to human NC2beta	Q
3792	VN_3792	YDR163W	CWC15	Non-essential protein involved in pre-mRNA splicing, component of a complex containing Cef1p; has similarity to S. pombe Cwf15p	Q
3793	VN_3793	YDL120W	YFH1	Mitochondrial matrix iron chaperone; oxidizes and stores iron; interacts with Isu1p to promote Fe-S cluster assembly; mutation results in multiple Fe/S-dependent enzyme deficiencies; human frataxin homolog is mutated in Friedrich's ataxia	Q
3794	VN_3794	YDL219W	DTD1	D-Tyr-tRNA(Tyr) deacylase, functions in protein translation, may affect nonsense suppression via alteration of the protein synthesis machinery; ubiquitous among eukaryotes	Q
3795	VN_3795	YPR150W	YPR150W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene SUE1/YPR151C	Q
3796	VN_3796	YBR224W	YBR224W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene TDP1	Q
3797	VN_3797	YDL177C	YDL177C	Putative protein of unknown function; similar to the mouse IMPACT gene; YDL177C is not an essential gene	Q
3798	VN_3798	YDR073W	SNF11	Subunit of the SWI/SNF chromatin remodeling complex involved in transcriptional regulation; interacts with a highly conserved 40-residue sequence of Snf2p	Q
3799	VN_3799	YCL033C	MXR2	Methionine-R-sulfoxide reductase, involved in the response to oxidative stress; protects iron-sulfur clusters from oxidative inactivation along with MXR1; involved in the regulation of lifespan	Q
3800	VN_3800	YBR137W	YBR137W	Protein of unknown function; localized to the cytoplasm; binds to Replication Protein A (RPA); YBR137W is not an essential gene	Q

3801	VN_3801	YDR059C	UBC5	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived, abnormal, or excess proteins, including histone H3; central component of the cellular stress response; expression is heat inducible	Q
3802	VN_3802	YJR025C	BNA1	3-hydroxyanthranilic acid dioxygenase, required for the de novo biosynthesis of NAD from tryptophan via kynurenine; expression regulated by Hst1p	Q
3803	VN_3803	YLR109W	AHP1	Thiol-specific peroxiredoxin, reduces hydroperoxides to protect against oxidative damage; function in vivo requires covalent conjugation to Urm1p	Q
3804	VN_3804	YDR469W	SDC1	Subunit of the COMPASS (Set1C) complex, which methylates lysine 4 of histone H3 and is required in chromatin silencing at telomeres; contains a Dpy-30 domain that mediates interaction with Bre2p; similar to <i>C. elegans</i> and human DPY-30	Q
3805	VN_3805	YFL064C	YFL064C	Putative protein of unknown function	Q
3806	VN_3806	YAL033W	POP5	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends	Q
3807	VN_3807	YDR187C	YDR187C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified, essential ORF CCT6/YDR188W	Q
3808	VN_3808	YCL022C	YCL022C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps verified gene KCC4/YCL024W	Q
3809	VN_3809	YDR260C	SWM1	Subunit of the anaphase-promoting complex, which is an E3 ubiquitin ligase that regulates the metaphase-anaphase transition and exit from mitosis; required for activation of the daughter-specific gene expression and spore wall maturation	Q
3810	VN_3810	YLL059C	YLL059C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
3811	VN_3811	YDR185C	UPS3	Mitochondrial protein of unknown function; similar to Ups1p and Ups2p which are involved in regulation of mitochondrial cardiolipin and phosphatidylethanolamine levels; null is viable but interacts synthetically with ups1 and ups2 mutations	Q
3812	VN_3812	YER134C	YER134C	Putative protein of unknown function; non-essential gene	Q
3813	VN_3813	YML011C	RAD33	Protein involved in nucleotide excision repair; green fluorescent protein (GFP)-fusion protein localizes to the nucleus	Q
3814	VN_3814	YOR253W	NAT5	Subunit of the N-terminal acetyltransferase NatA (Nat1p, Ard1p, Nat5p); N-terminally acetylates many proteins, which influences multiple processes such as the cell cycle, heat-shock resistance, mating, sporulation, and telomeric silencing	Q
3815	VN_3815	YGL222C	EDC1	RNA-binding protein, activates mRNA decapping directly by binding to the mRNA substrate and enhancing the activity of the decapping proteins Dcp1p and Dcp2p; has a role in translation during heat stress	Q
3816	VN_3816	YGL183C	MND1	Protein required for recombination and meiotic nuclear division; forms a complex with Hop2p, which is involved in chromosome pairing and repair of meiotic double-strand breaks	Strain failed to verify via PCR
3817	VN_3817	YDL046W	NPC2	Functional homolog of human NPC2/He1, which is a cholesterol-binding protein whose deficiency causes Niemann-Pick type C2 disease involving retention of cholesterol in lysosomes	Q
3818	VN_3818	YGL058W	RAD6	Ubiquitin-conjugating enzyme (E2), involved in postreplication repair (as a heterodimer with Rad18p), DSB and checkpoint control (as a heterodimer with Bre1p), ubiquitin-mediated N-end rule protein degradation (as a heterodimer with Ubr1p)	Q
3819	VN_3819	YCR087W	YCR087W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps uncharacterized gene YCR087C-A; YCR087W is not an essential gene	Q
3820	VN_3820	YFR011C	AIM13	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria; null mutant displays reduced respiratory growth and reduced frequency of mitochondrial genome loss	Q
3821	VN_3821	YJR115W	YJR115W	Putative protein of unknown function	Q

3822	VN_3822	YLR008C	PAM18	Constituent of the import motor (PAM complex) component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); essential J-protein cochaperone that stimulates Ssc1p ATPase activity to drive import; inhibited by Pam16p	Q
3823	VN_3823	YDR540C	IRC4	Putative protein of unknown function; null mutant displays increased levels of spontaneous Rad52p foci; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	Q
3824	VN_3824	YGL235W	YGL235W	Putative protein of unknown function; potential Cdc28p substrate; null mutant displays increased resistance to antifungal agents gliotoxin, cycloheximide and H2O2	Q
3825	VN_3825	YMR042W	ARG80	Transcription factor involved in regulation of arginine-responsive genes; acts with Arg81p and Arg82p	Q
3826	VN_3826	YPR051W	MAK3	Catalytic subunit of N-terminal acetyltransferase of the NatC type; required for replication of dsRNA virus	Q
3827	VN_3827	YGL262W	YGL262W	Putative protein of unknown function; null mutant displays elevated sensitivity to expression of a mutant huntingtin fragment or of alpha-synuclein; YGL262W is not an essential gene	Q
3828	VN_3828	YGR085C	RPL11B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11	Strain failed to verify via PCR
3829	VN_3829	YDL208W	NHP2	Nuclear protein related to mammalian high mobility group (HMG) proteins, essential for function of H/ACA-type snoRNPs, which are involved in 18S rRNA processing	Q
3830	VN_3830	YJL124C	LSM1	Lsm (Like Sm) protein; forms heteroheptameric complex (with Lsm2p, Lsm3p, Lsm4p, Lsm5p, Lsm6p, and Lsm7p) involved in degradation of cytoplasmic mRNAs	Q
3831	VN_3831	YDR404C	RPB7	RNA polymerase II subunit B16; forms two subunit dissociable complex with Rpb4p	Q
3832	VN_3832	YHL043W	ECM34	Putative protein of unknown function; member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	Q
3833	VN_3833	YKL070W	YKL070W	Putative protein of unknown function; expression induced in cells treated with mycotoxins patulin or citrinin; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
3834	VN_3834	YLR164W	YLR164W	Mitochondrial inner membrane of unknown function; similar to Tim18p and Sdh4p; expression induced by nitrogen limitation in a GLN3, GAT1-dependent manner	Q
3835	VN_3835	YEL066W	HPA3	D-Amino acid N-acetyltransferase, catalyzes N-acetylation of D-amino acids through ordered bi-bi mechanism in which acetyl-CoA is first substrate bound and CoA is last product liberated; similar to Hpa2p, acetylates histones weakly in vitro	Q
3836	VN_3836	YLR370C	ARC18	Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches	Q
3837	VN_3837	YMR135W-A	YMR135W-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3838	VN_3838	YBR047W	FMP23	Putative protein of unknown function; proposed to be involved in iron or copper homeostasis; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Strain failed to verify via PCR
3839	VN_3839	YJL122W	ALB1	Shuttling pre-60S factor; involved in the biogenesis of ribosomal large subunit; interacts directly with Arx1p; responsible for Tif6p recycling defects in absence of Rei1p	Q
3840	VN_3840	YGR131W	YGR131W	Protein of unknown function; expression induced in response to ketoconazole; promoter region contains a sterol regulatory element motif, which has been identified as a Upc2p-binding site	Q
3841	VN_3841	YER085C	YER085C	Putative protein of unknown function	Q
3842	VN_3842	YJR097W	JJJ3	Protein of unknown function, contains a J-domain, which is a region with homology to the E. coli DnaJ protein	Strain failed to verify via PCR
3843	VN_3843	YJL016W	YJL016W	Putative protein of unknown function; GFP-fusion protein localizes to the cytoplasm; conserved in closely related Saccharomyces species	Q

3844	VN_3844	YJL175W	YJL175W	Dubious open reading frame unlikely to encode a functional protein; deletion confers resistance to cisplatin, hypersensitivity to 5-fluorouracil, and growth defect at high pH with high calcium; overlaps gene for SWI3 transcription factor	Q
3845	VN_3845	YLR349W	YLR349W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the verified ORF DIC1/YLR348C	Q
3846	VN_3846	YLL049W	LDB18	Protein of unknown function; required for nuclear migration; null mutant shows a reduced affinity for the alcian blue dye suggesting a decreased net negative charge of the cell surface	Q
3847	VN_3847	YML055W	SPC2	Subunit of signal peptidase complex (Spc1p, Spc2p, Spc3p, Sec11p), which catalyzes cleavage of N-terminal signal sequences of proteins targeted to the secretory pathway; homologous to mammalian SPC25	Q
3848	VN_3848	YOL067C	RTG1	Transcription factor (bHLH) involved in interorganelle communication between mitochondria, peroxisomes, and nucleus	Q
3849	VN_3849	YBR116C	YBR116C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene TKL2	Q
3850	VN_3850	YLR193C	UPS1	Mitochondrial intermembrane space protein that regulates mitochondrial cardiolipin levels, null has defects in Mgm1p processing, integrity of mitochondrial inner membrane complexes, and mitochondrial morphology; ortholog of human PRELI	Q
3851	VN_3851	YGR273C	YGR273C	Putative protein of unknown function; expression downregulated by treatment with 8-methoxypsoralen plus UVA irradiation; YGR273C is not an essential gene	Q
3852	VN_3852	YHR152W	SPO12	Nucleolar protein of unknown function, positive regulator of mitotic exit; involved in regulating release of Cdc14p from the nucleolus in early anaphase, may play similar role in meiosis	Q
3853	VN_3853	YNL046W	YNL046W	Putative protein of unknown function; expression depends on Swi5p; GFP-fusion protein localizes to the endoplasmic reticulum; deletion confers sensitivity to 4-(N-(S-glutathionylacetyl)amino) phenylarsenoxide (GSAO)	Q
3854	VN_3854	YOL143C	RIB4	Lumazine synthase (6,7-dimethyl-8-ribityllumazine synthase, also known as DMRL synthase); catalyzes synthesis of immediate precursor to riboflavin	Q
3855	VN_3855	YNL157W	YNL157W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	Strain failed to verify via PCR
3856	VN_3856	YLR021W	IRC25	Component of a heterodimeric Poc4p-Irc25p chaperone involved in assembly of alpha subunits into the 20S proteasome; may regulate formation of proteasome isoforms with alternative subunits under different conditions	Q
3857	VN_3857	YAL044C	GCV3	H subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; also required for all protein lipoylation; expression is regulated by levels of 5,10-methylene-THF	Q
3858	VN_3858	YPL038W	MET31	Zinc-finger DNA-binding protein, involved in transcriptional regulation of the methionine biosynthetic genes, similar to Met32p	Q
3859	VN_3859	YCL066W	HMLALPHA1	Silenced copy of ALPHA1 at HML, encoding a transcriptional coactivator involved in the regulation of mating-type alpha-specific gene expression	Strain failed to verify via PCR
3860	VN_3860	YOR097C	YOR097C	Putative protein of unknown function; identified as interacting with Hsp82p in a high-throughput two-hybrid screen; YOR097C is not an essential gene	Q
3861	VN_3861	YHR193C	EGD2	Alpha subunit of the heteromeric nascent polypeptide-associated complex (NAC) involved in protein sorting and translocation, associated with cytoplasmic ribosomes	Q
3862	VN_3862	YKL131W	YKL131W	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3863	VN_3863	YOL024W	YOL024W	Putative protein of unknown function; predicted to have thiol-disulfide oxidoreductase active site	Q
3864	VN_3864	YCR046C	IMG1	Mitochondrial ribosomal protein of the large subunit, required for respiration and for maintenance of the mitochondrial genome	Q

3865	VN_3865	YOL163W	YOL163W	Putative protein of unknown function; member of the Dal5p subfamily of the major facilitator family	Q
3866	VN_3866	YPL108W	YPL108W	Cytoplasmic protein of unknown function; non-essential gene that is induced in a GDH1 deleted strain with altered redox metabolism; GFP-fusion protein is induced in response to the DNA-damaging agent MMS	Q
3867	VN_3867	YMR009W	ADI1	Acireductone dioxygenase involved in the methionine salvage pathway; ortholog of human MTCBP-1; transcribed with YMR010W and regulated post-transcriptionally by RNase III (Rnt1p) cleavage; ADI1 mRNA is induced in heat shock conditions	Q
3868	VN_3868	YBL090W	MRP21	Mitochondrial ribosomal protein of the small subunit; MRP21 exhibits genetic interactions with mutations in the COX2 and COX3 mRNA 5'-untranslated leader sequences	Q
3869	VN_3869	YPL148C	PPT2	Phosphopantetheine:protein transferase (PPTase), activates mitochondrial acyl carrier protein (Acp1p) by phosphopantetheinylation	Q
3870	VN_3870	YPR101W	SNT309	Member of the NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 snRNAs; interacts physically and genetically with Prp19p	Q
3871	VN_3871	YPR102C	RPL11A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Bp; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11	Q
3872	VN_3872	YNL133C	FYV6	Protein of unknown function, required for survival upon exposure to K1 killer toxin; proposed to regulate double-strand break repair via non-homologous end-joining	Q
3873	VN_3873	YPL252C	YAH1	Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur proteins; involved in heme A biosynthesis; homologous to human adrenodoxin	Q
3874	VN_3874	YOL159C	YOL159C	Soluble protein of unknown function; deletion mutants are viable and have elevated levels of Ty1 retrotransposition and Ty1 cDNA	Q
3875	VN_3875	YDL094C	YDL094C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene PMT5/YDL093W; YDL094C is not essential	Q
3876	VN_3876	YPR063C	YPR063C	ER-localized protein of unknown function	Q
3877	VN_3877	YPL223C	GRE1	Hydrophilin of unknown function; stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway	Q
3878	VN_3878	YDL235C	YPD1	Phosphorelay intermediate protein, phosphorylated by the plasma membrane sensor Sln1p in response to osmotic stress and then in turn phosphorylates the response regulators Ssk1p in the cytosol and Skn7p in the nucleus	Q
3879	VN_3879	YML098W	TAF13	TFIID subunit (19 kDa), involved in RNA polymerase II transcription initiation, similar to histone H4 with atypical histone fold motif of Spt3-like transcription factors	Q
3880	VN_3880	YBR300C	YBR300C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YBR301W; YBR300C is not an essential gene	Q
3881	VN_3881	YPL135W	ISU1	Conserved protein of the mitochondrial matrix, performs a scaffolding function during assembly of iron-sulfur clusters, interacts physically and functionally with yeast frataxin (Yfh1p); isu1 isu2 double mutant is inviable	Q
3882	VN_3882	YPL282C	PAU22	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions; identical to Pau21p; encodes 2 proteins that are translated from 2 different start codons	Q
3883	VN_3883	YBR120C	CBP6	Mitochondrial translational activator of the COB mRNA; phosphorylated	Q
3884	VN_3884	YCR097W	HMRA1	Silenced copy of a1 at HMR; homeobox corepressor that interacts with Alpha2p to repress haploid-specific gene transcription in diploid cells	Q
3885	VN_3885	YNL120C	YNL120C	Dubious open reading frame unlikely to encode a protein, based on	Q

				available experimental and comparative sequence data; deletion enhances replication of Brome mosaic virus in <i>S. cerevisiae</i> , but likely due to effects on the overlapping gene	
3886	VN_3886	YGR030C	POP6	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends	Q
3887	VN_3887	YEL034W	HYP2	Translation elongation factor eIF-5A, previously thought to function in translation initiation; similar to and functionally redundant with Anb1p; structural homolog of bacterial EF-P; undergoes an essential hypusination modification	Strain failed to verify via PCR
3888	VN_3888	YPL037C	EGD1	Subunit beta1 of the nascent polypeptide-associated complex (NAC) involved in protein targeting, associated with cytoplasmic ribosomes; enhances DNA binding of the Gal4p activator; homolog of human BTF3b	Q
3889	VN_3889	YJL065C	DLS1	Subunit of ISW2/yCHRAC chromatin accessibility complex along with Itc1p, Isw2p, and Dpb4p; involved in inheritance of telomeric silencing	Q
3890	VN_3890	YBR230C	OM14	Integral mitochondrial outer membrane protein; abundance is decreased in cells grown in glucose relative to other carbon sources; appears to contain 3 alpha-helical transmembrane segments; ORF encodes a 97-basepair intron	Q
3891	VN_3891	YDL008W	APC11	Catalytic core subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition	Q
3892	VN_3892	YPL187W	MF(ALPHA)1	Mating pheromone alpha-factor, made by alpha cells; interacts with mating type a cells to induce cell cycle arrest and other responses leading to mating; also encoded by MF(ALPHA)2, although MF(ALPHA)1 produces most alpha-factor	Q
3893	VN_3893	YHR180W	YHR180W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
3894	VN_3894	YBR244W	GPX2	Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and nonphospholipid peroxides during oxidative stress	Q
3895	VN_3895	YDR024W	FYV1	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; mutation decreases survival upon exposure to K1 killer toxin	Q
3896	VN_3896	YOR276W	CAF20	Phosphoprotein of the mRNA cap-binding complex involved in translational control, repressor of cap-dependent translation initiation, competes with eIF4G for binding to eIF4E	Q
3897	VN_3897	YDL172C	YDL172C	Dubious ORF unlikely to encode a protein, based on available experimental and comparative sequence data	Q
3898	VN_3898	YML010W-A		#N/A	Q
3899	VN_3899	YGR076C	MRPL25	Mitochondrial ribosomal protein of the large subunit	Q
3900	VN_3900	YPR168W	NUT2	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; required for transcriptional activation and has a role in basal transcription	Q
3901	VN_3901	YKL026C	GPX1	Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and nonphospholipid peroxides during oxidative stress	Q
3902	VN_3902	YDR201W	SPC19	Essential subunit of the Dam1 complex (aka DASH complex), couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; also localized to nuclear side of spindle pole body	Q
3903	VN_3903	YIR037W	HYR1	Thiol peroxidase that functions as a hydroperoxide receptor to sense intracellular hydroperoxide levels and transduce a redox signal to the Yap1p transcription factor	Q
3904	VN_3904	YDR155C	CPR1	Cytoplasmic peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; binds the drug cyclosporin A	Q
3905	VN_3905	YER067W	YER067W	Putative protein of unknown function; green fluorescent protein	Q

				(GFP)-fusion protein localizes to the cytoplasm and nucleus; YER067W is not an essential gene; protein abundance is increased upon intracellular iron depletion	
3906	VN_3906	YPL073C	YPL073C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps with verified gene UBP16/YPL072W; may interact with ribosome based on co-purification experiments	Q
3907	VN_3907	YFL017C	GNA1	Evolutionarily conserved glucosamine-6-phosphate acetyltransferase required for multiple cell cycle events including passage through START, DNA synthesis, and mitosis; involved in UDP-N-acetylglucosamine synthesis, forms GlcNAc6P from AcCoA	Q
3908	VN_3908	YNL089C	YNL089C	Dubious open reading frame unlikely to encode a functional protein; almost completely overlaps YNL090W/RHO2 which encodes a small GTPase of the Rho/Rac subfamily of Ras-like proteins	Q
3909	VN_3909	YIL087C	AIM19	Putative protein of unknown function; the authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies; null mutant displays reduced respiratory growth	Q
3910	VN_3910	YKL056C	TMA19	Protein that associates with ribosomes; homolog of translationally controlled tumor protein; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and relocates to the mitochondrial outer surface upon oxidative stress	Q
3911	VN_3911	YEL035C	UTR5	Protein of unknown function; transcription may be regulated by Gcr1p; essential for growth under standard (aerobic) conditions but not under anaerobic conditions	Q
3912	VN_3912	YDR418W	RPL12B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins	Q
3913	VN_3913	YFL015C	YFL015C	Dubious open reading frame unlikely to encode a protein; partially overlaps dubious ORF YFL015W-A; YFL015C is not an essential gene	Q
3914	VN_3914	YOL099C	YOL099C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene PKH2/YOL100W; may interact with ribosomes	Q
3915	VN_3915	YDR179C	CSN9	Subunit of the Cop9 signalosome, which is required for deneddylation, or removal of the ubiquitin-like protein Rub1p from Cdc53p (cullin); involved in adaptation to pheromone signaling	Q
3916	VN_3916	YHR214W-A	YHR214W-A	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; similar to the fungal specific protein encoded by YAR068W; induced by zinc deficiency	Q
3917	VN_3917	YPR073C	LTP1	Protein phosphotyrosine phosphatase of unknown cellular role; activated by adenine	Q
3918	VN_3918	YHL006C	SHU1	Protein involved in a Rad51p-, Rad54p-dependent pathway for homologous recombination repair, important for error-free repair of spontaneous and induced DNA lesions to protect the genome from mutation; associates with Shu2p, Psy3p, and Csm2p	Q
3919	VN_3919	YNL185C	MRPL19	Mitochondrial ribosomal protein of the large subunit	Q
3920	VN_3920	YJR047C	ANB1	Translation elongation factor eIF-5A, previously thought to function in translation initiation; similar to and functionally redundant with Hyp2p; undergoes an essential hypusination modification; expressed under anaerobic conditions	Q
3921	VN_3921	YGL199C	YGL199C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF YIP4/YGL198W	Q
3922	VN_3922	YKL063C	YKL063C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the Golgi	Q
3923	VN_3923	YEL044W	IES6	Protein that associates with the INO80 chromatin remodeling complex under low-salt conditions; human ortholog INO80C is a member of the human INO80 complex; implicated in DNA repair based on genetic interactions with RAD52 epistasis genes	Q
3924	VN_3924	YEL054C	RPL12A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Bp; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12	Q

				ribosomal proteins	
3925	VN_3925	YIL057C	YIL057C	Putative protein of unknown function; expression induced under carbon limitation and repressed under high glucose	Q
3926	VN_3926	YOR150W	MRPL23	Mitochondrial ribosomal protein of the large subunit	Q
3927	VN_3927	YER093C-A	AIM11	Protein of unknown function; null mutant is viable but shows increased loss of mitochondrial genome and synthetic interaction with prohibitin (phb1); contains an intron	Q
3928	VN_3928	YIL138C	TPM2	Minor isoform of tropomyosin, binds to and stabilizes actin cables and filaments, which direct polarized cell growth and the distribution of several organelles; appears to have distinct and also overlapping functions with Tpm1p	Q
3929	VN_3929	YBR113W	YBR113W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene CYC8	Q
3930	VN_3930	YHL037C	YHL037C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3931	VN_3931	YPR062W	FCY1	Cytosine deaminase, zinc metalloenzyme that catalyzes the hydrolytic deamination of cytosine to uracil; of biomedical interest because it also catalyzes the deamination of 5-fluorocytosine (5FC) to form anticancer drug 5-fluorouracil (5FU)	Q
3932	VN_3932	YLR400W	YLR400W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3933	VN_3933	YLR421C	RPN13	Subunit of the 19S regulatory particle of the 26S proteasome lid; acts as a ubiquitin receptor for the proteasome; null mutants accumulate ubiquitinated Gcn4p and display decreased 26S proteasome stability	Q
3934	VN_3934	YKL122C	SRP21	Subunit of the signal recognition particle (SRP), which functions in protein targeting to the endoplasmic reticulum membrane; not found in mammalian SRP; forms a pre-SRP structure in the nucleolus that is translocated to the cytoplasm	Q
3935	VN_3935	YER066C-A	YER066C-A	Dubious open reading frame unlikely to encode a protein, partially overlaps uncharacterized ORF YER067W	Q
3936	VN_3936	YGL196W	DSD1	D-serine dehydratase (aka D-serine ammonia-lyase); converts D-serine to pyruvate and ammonia by a reaction dependent on pyridoxal 5'-phosphate and zinc; may play a role in D-serine detoxification; L-serine is not a substrate	Q
3937	VN_3937	YJR055W	HIT1	Protein of unknown function, required for growth at high temperature	Q
3938	VN_3938	YPR188C	MLC2	Regulatory light chain for the type II myosin, Myo1p; binds to an IQ motif of Myo1p, localization to the bud neck depends on Myo1p; involved in the disassembly of the Myo1p ring	Q
3939	VN_3939	YGL214W	YGL214W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; deletion mutation phenotype is likely due to the overlapping verified ORF SKI8/YGL213C	Q
3940	VN_3940	YER030W	CHZ1	Histone chaperone for Htz1p/H2A-H2B dimer; required for the stabilization of the Chz1p-Htz1-H2B complex; has overlapping function with Nap1p; null mutant displays weak sensitivity to MMS and benomyl; contains a highly conserved CHZ motif	Q
3941	VN_3941	YHR126C	ANS1	Putative protein of unknown function; transcription dependent upon Azf1p	Q
3942	VN_3942	YMR236W	TAF9	Subunit (17 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation and in chromatin modification, similar to histone H3	Q
3943	VN_3943	YMR002W	MIC17	Mitochondrial intermembrane space protein; contains twin cysteine-x9-cysteine motifs; MIC17 is not an essential gene	Q
3944	VN_3944	YLR074C	BUD20	Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern	Q
3945	VN_3945	YMR022W	UBC7	Ubiquitin conjugating enzyme, involved in the ER-associated protein degradation pathway; requires Cue1p for recruitment to the ER membrane; proposed to be involved in chromatin assembly	Q
3946	VN_3946	YKR020W	VPS51	Component of the GARP (Golgi-associated retrograde protein)	Q

				complex, Vps51p-Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; links the (VFT/GARP) complex to the SNARE Tlg1p	
3947	VN_3947	YCR028C-A	RIM1	Single-stranded DNA-binding protein essential for mitochondrial genome maintenance; involved in mitochondrial DNA replication	Q
3948	VN_3948	YOL071W	EMI5	Subunit of succinate dehydrogenase, which couples succinate oxidation to ubiquinone reduction; required for FAD cofactor attachment to Sdh1p; mutations in human ortholog PGL2 are associated with neuroendocrine tumors (paraganglioma)	Q
3949	VN_3949	YLR042C	YLR042C	Protein of unknown function; localizes to the cytoplasm; YLL042C is not an essential gene	Q
3950	VN_3950	YFL051C	YFL051C	Putative protein of unknown function; YFL051C is not an essential gene	Q
3951	VN_3951	YML030W	AIM31	Putative protein of unknown function; GFP-fusion protein localizes to mitochondria; may interact with respiratory chain complexes III or IV; null mutant is viable and displays reduced frequency of mitochondrial genome loss	Q
3952	VN_3952	YCR006C	YCR006C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
3953	VN_3953	YOR044W	IRC23	Putative protein of unknown function; green fluorescent protein (GFP)-fusion localizes to the ER; null mutant displays increased levels of spontaneous Rad52p foci	Q
3954	VN_3954	YOR013W	IRC11	Dubious opening reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized gene YOR012C; null mutant displays increased levels of spontaneous Rad52 foci	Q
3955	VN_3955	YLL042C	ATG10	Conserved E2-like conjugating enzyme that mediates formation of the Atg12p-Atg5p conjugate, which is a critical step in autophagy	Q
3956	VN_3956	YPL034W	YPL034W	Putative protein of unknown function; YPL034W is not essential gene	Q
3957	VN_3957	YOR394W	PAU21	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions; identical to Pau22p; encodes 2 proteins that are translated from 2 different start codons	Q
3958	VN_3958	YBR077C	SLM4	Component of the EGO complex, which is involved in the regulation of microautophagy, and of the GSE complex, which is required for proper sorting of amino acid permease Gap1p; gene exhibits synthetic genetic interaction with MSS4	Q
3959	VN_3959	YOR357C	SNX3	Sorting nexin required to maintain late-Golgi resident enzymes in their proper location by recycling molecules from the prevacuolar compartment; contains a PX domain and sequence similarity to human Snx3p	Q
3960	VN_3960	YLR050C	YLR050C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YLR050C is not an essential gene	Q
3961	VN_3961	YBL018C	POP8	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends	Q
3962	VN_3962	YCR063W	BUD31	Component of the SF3b subcomplex of the U2 snRNP; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern	Q
3963	VN_3963	YOR325W	YOR325W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the verified ORF FRT1	Q
3964	VN_3964	YOR226C	ISU2	Conserved protein of the mitochondrial matrix, required for synthesis of mitochondrial and cytosolic iron-sulfur proteins, performs a scaffolding function in mitochondria during Fe/S cluster assembly; isu1 isu2 double mutant is inviable	Q
3965	VN_3965	YOR339C	UBC11	Ubiquitin-conjugating enzyme most similar in sequence to Xenopus ubiquitin-conjugating enzyme E2-C, but not a true functional homolog of this E2; unlike E2-C, not required for the degradation of mitotic cyclin Clb2	Q
3966	VN_3966	YGR148C	RPL24B	Ribosomal protein L30 of the large (60S) ribosomal subunit, nearly identical to Rpl24Ap and has similarity to rat L24 ribosomal protein; not essential for translation but may be required for normal translation	Q

				rate	
3967	VN_3967	YJR104C	SOD1	Cytosolic copper-zinc superoxide dismutase; some mutations are analogous to those that cause ALS (amyotrophic lateral sclerosis) in humans	Q
3968	VN_3968	YKL067W	YNK1	Nucleoside diphosphate kinase, catalyzes the transfer of gamma phosphates from nucleoside triphosphates, usually ATP, to nucleoside diphosphates by a mechanism that involves formation of an autophosphorylated enzyme intermediate	Q
3969	VN_3969	YCL058C	FYV5	Protein of unknown function, required for survival upon exposure to K1 killer toxin; involved in ion homeostasis	Q
3970	VN_3970	YFR057W	YFR057W	Putative protein of unknown function	Q
3971	VN_3971	YDL110C	TMA17	Protein of unknown function that associates with ribosomes; heterozygous deletion demonstrated increases in chromosome instability in a rad9 deletion background; protein abundance is decreased upon intracellular iron depletion	Q
3972	VN_3972	YDL121C	YDL121C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YDL121C is not an essential protein	Q
3973	VN_3973	YOR286W	RDL2	Protein with rhodanese activity; contains a rhodanese-like domain similar to Rdl1p, Uba4p, Tum1p, and Ych1p; overexpression causes a cell cycle delay; null mutant displays elevated frequency of mitochondrial genome loss	Q
3974	VN_3974	YHR136C	SPL2	Protein with similarity to cyclin-dependent kinase inhibitors; downregulates low-affinity phosphate transport during phosphate limitation; overproduction suppresses a plc1 null mutation; GFP-fusion protein localizes to the cytoplasm	Q
3975	VN_3975	YDR344C	YDR344C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
3976	VN_3976	YOR392W	YOR392W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; gene expression induced by heat	Q
3977	VN_3977	YPL071C	YPL071C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
3978	VN_3978	YIL098C	FMC1	Mitochondrial matrix protein, required for assembly or stability at high temperature of the F1 sector of mitochondrial F1F0 ATP synthase; null mutant temperature sensitive growth on glycerol is suppressed by multicopy expression of Odc1p	Strain failed to verify via PCR
3979	VN_3979	YMR181C	YMR181C	Protein of unknown function; mRNA transcribed as part of a bicistronic transcript with a predicted transcriptional repressor RGM1/YMR182C; mRNA is destroyed by nonsense-mediated decay (NMD); YMR181C is not an essential gene	Q
3980	VN_3980	YLR315W	NKP2	Non-essential kinetochore protein, subunit of the Ctf19 central kinetochore complex (Ctf19p-Mcm21p-Okp1p-Mcm22p-Mcm16p-Ctf3p-Chl4p-Mcm19p-Nkp1p-Nkp2p-Ame1p-Mtw1p)	Q
3981	VN_3981	YEL048C	TCA17	Protein that interacts with subunits of the TRAPP complex and may play a role its assembly or stability; mutation is synthetically lethal with gcs1 deletion; Sedlin_N family member; human Sedlin mutations cause the skeletal disorder SEDT	Q
3982	VN_3982	YHR021W-A	ECM12	Non-essential protein of unknown function	Q
3983	VN_3983	YHL042W	YHL042W	Putative protein of unknown function; member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	Q
3984	VN_3984	YDR063W	AIM7	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; null mutant is viable and displays elevated frequency of mitochondrial genome loss	Q
3985	VN_3985	YBR173C	UMP1	Short-lived chaperone required for correct maturation of the 20S proteasome; may inhibit premature dimerization of proteasome half-mers; degraded by proteasome upon completion of its assembly	Q
3986	VN_3986	YIR005W	IST3	Component of the U2 snRNP, required for the first catalytic step of splicing and for spliceosomal assembly; interacts with Rds3p and is required for Mer1p-activated splicing	Q

3987	VN_3987	YDR462W	MRPL28	Mitochondrial ribosomal protein of the large subunit	Q
3988	VN_3988	YLR202C	YLR202C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF YLR201C; ORF contains a putative intron	Strain failed to verify via PCR
3989	VN_3989	YPL200W	CSM4	Protein required for accurate chromosome segregation during meiosis; involved in meiotic telomere clustering (bouquet formation) and telomere-led rapid prophase movements	Q
3990	VN_3990	YKR074W	AIM29	Putative protein of unknown function; epitope-tagged protein localizes to the cytoplasm; YKR074W is not an essential gene; null mutant displays elevated frequency of mitochondrial genome loss	Q
3991	VN_3991	YMR260C	TIF11	Translation initiation factor eIF1A, essential protein that forms a complex with Sui1p (eIF1) and the 40S ribosomal subunit and scans for the start codon; C-terminus associates with Fun12p (eIF5B); N terminus interacts with eIF2 and eIF3	Q
3992	VN_3992	YFL057C	AAD16	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role	Q
3993	VN_3993	YHR116W	COX23	Mitochondrial intermembrane space protein that functions in mitochondrial copper homeostasis, essential for functional cytochrome oxidase expression; homologous to Cox17p; contains twin cysteine-x9-cysteine motifs	Q
3994	VN_3994	YJL220W	YJL220W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YJL221C/FSP2	Q
3995	VN_3995	YDR252W	BTT1	Beta3 subunit of the heterotrimeric nascent polypeptide-associated complex which binds ribosomes via its beta-subunits in close proximity to nascent polypeptides; interacts with Caf130p of the CCR4-NOT complex; similar to human BTF3	Q
3996	VN_3996	YCR049C	YCR049C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
3997	VN_3997	YLL044W	YLL044W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; transcription of both YLL044W and the overlapping gene RPL8B is reduced in the gcr1 null mutant	Q
3998	VN_3998	YGL230C	YGL230C	Putative protein of unknown function; non-essential gene	Q
3999	VN_3999	YBR282W	MRPL27	Mitochondrial ribosomal protein of the large subunit	Q
4000	VN_4000	YPR193C	HPA2	Tetrameric histone acetyltransferase with similarity to Gcn5p, Hat1p, Elp3p, and Hpa3p; acetylates histones H3 and H4 in vitro and exhibits autoacetylation activity	Q
4001	VN_4001	YLR281C	YLR281C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria; YLR281C is not an essential gene	Q
4002	VN_4002	YCL001W-A	YCL001W-A	Putative protein of unknown function; YCL001W-A is not an essential gene	Q
4003	VN_4003	YNL255C	GIS2	Protein with seven cysteine-rich CCHC zinc-finger motifs, similar to human CNBP, proposed to be involved in the RAS/cAMP signaling pathway	Q
4004	VN_4004	YLR068W	FYV7	Essential protein required for maturation of 18S rRNA; required for survival upon exposure to K1 killer toxin	Q
4005	VN_4005	YLR218C	YLR218C	Protein that localizes to the mitochondrial intermembrane space via the Mia40p-Erv1p system; mutants exhibit glycogen storage defects and growth defects on a non-fermentable carbon source; contains twin cysteine-x9-cysteine motifs	Q
4006	VN_4006	YER044C	ERG28	Endoplasmic reticulum membrane protein, may facilitate protein-protein interactions between the Erg26p dehydrogenase and the Erg27p 3-ketoreductase and/or tether these enzymes to the ER, also interacts with Erg6p	Q
4007	VN_4007	YMR059W	SEN15	Subunit of the tRNA splicing endonuclease, which is composed of Sen2p, Sen15p, Sen34p, and Sen54p	Q
4008	VN_4008	YGR290W	YGR290W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; putative HLH	Q

				protein; partially overlaps the verified ORF MAL11/YGR289C (a high-affinity maltose transporter)	
4009	VN_4009	YCL075W	YCL075W	Pseudogene: encodes fragment of Ty Pol protein	Strain failed to verify via PCR
4010	VN_4010	YCR099C	YCR099C	Putative protein of unknown function	Q
4011	VN_4011	YMR158W	MRPS8	Mitochondrial ribosomal protein of the small subunit	Q
4012	VN_4012	YCR087C-A	YCR087C-A	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleolus; YCR087C-A is not an essential gene	Q
4013	VN_4013	YNL281W	HCH1	Heat shock protein regulator that binds to Hsp90p and may stimulate ATPase activity; originally identified as a high-copy number suppressor of a HSP90 loss-of-function mutation; GFP-fusion protein localizes to the cytoplasm and nucleus	Q
4014	VN_4014	YKR091W	SRL3	Cytoplasmic protein that, when overexpressed, suppresses the lethality of a rad53 null mutation; potential Cdc28p substrate	Q
4015	VN_4015	YOL108C	INO4	Transcription factor required for derepression of inositol-choline-regulated genes involved in phospholipid synthesis; forms a complex, with Ino2p, that binds the inositol-choline-responsive element through a basic helix-loop-helix domain	Q
4016	VN_4016	YMR159C	ATG16	Conserved protein that interacts with Atg12p-Atg5p conjugates to form Atg12p-Atg5p-Atg16p multimers, which localize to the pre-autophagosomal structure and are required for autophagy	Q
4017	VN_4017	YGR107W	YGR107W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4018	VN_4018	YMR148W	OSW5	Protein of unknown function that may play a role in spore wall assembly; predicted to contain an N-terminal transmembrane domain; osw5 null mutant spores exhibit increased spore wall permeability and sensitivity to beta-glucanase digestion	Q
4019	VN_4019	YJL211C	YJL211C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YJL210W/PEX2	Q
4020	VN_4020	YCR071C	IMG2	Mitochondrial ribosomal protein of the small subunit	Q
4021	VN_4021	YDR475C	JIP4	Protein of unknown function; previously annotated as two separate ORFs, YDR474C and YDR475C, which were merged as a result of corrections to the systematic reference sequence	Q
4022	VN_4022	YPR089W	YPR089W	Protein of unknown function; exhibits genetic interaction with ERG11 and protein-protein interaction with Hsp82p	Q
4023	VN_4023	YEL028W	YEL028W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4024	VN_4024	YNR036C	MRPS12	Mitochondrial protein; may interact with ribosomes based on co-purification experiments; similar to E. coli and human mitochondrial S12 ribosomal proteins	Q
4025	VN_4025	YLL053C	YLL053C	Putative protein; in the Sigma 1278B strain background YLL053C is contiguous with AQY2 which encodes an aquaporin	Q
4026	VN_4026	YPR053C	YPR053C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene NHP6A/YPR052C	Q
4027	VN_4027	YHL041W	YHL041W	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data	Q
4028	VN_4028	YER150W	SPI1	GPI-anchored cell wall protein involved in weak acid resistance; basal expression requires Msn2p/Msn4p; expression is induced under conditions of stress and during the diauxic shift; similar to Sed1p	Q
4029	VN_4029	YPL144W	POC4	Component of a heterodimeric Poc4p-Irc25p chaperone involved in assembly of alpha subunits into the 20S proteasome; may regulate formation of proteasome isoforms with alternative subunits under different conditions	Q
4030	VN_4030	YKL066W	YKL066W	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; partially overlaps the verified gene YNK1	Q

4031	VN_4031	YDL092W	SRP14	Signal recognition particle (SRP) subunit, interacts with the RNA component of SRP to form the Alu domain, which is the region of SRP responsible for arrest of nascent chain elongation during membrane targeting; homolog of mammalian SRP14	Q
4032	VN_4032	YFR003C	YPI1	Inhibitor of the type I protein phosphatase Glc7p, which is involved in regulation of a variety of metabolic processes; overproduction causes decreased cellular content of glycogen	Q
4033	VN_4033	YGL069C	YGL069C	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 92% of ORF overlaps the uncharacterized ORF YGL068W; deletion in <i>cyr1</i> mutant results in loss of stress resistance	Q
4034	VN_4034	YGR293C	YGR293C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YGR294W	Q
4035	VN_4035	YOR382W	FIT2	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall	Q
4036	VN_4036	YDR424C	DYN2	Cytoplasmic light chain dynein, microtubule motor protein; proposed to be involved in the assembly of the nuclear pore complex	Q
4037	VN_4037	YOR052C	YOR052C	Nuclear protein of unknown function; expression induced by nitrogen limitation in a <i>GLN3</i> , <i>GAT1</i> -independent manner and by weak acid	Q
4038	VN_4038	YJL104W	PAM16	Constituent of the import motor (PAM complex) component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); forms a 1:1 subcomplex with Pam18p and inhibits its cochaperone activity; contains a J-like domain	Q
4039	VN_4039	YFL012W	YFL012W	Putative protein of unknown function; transcribed during sporulation; null mutant exhibits increased resistance to rapamycin	Q
4040	VN_4040	YBR109C	CMD1	Calmodulin; Ca ⁺⁺ binding protein that regulates Ca ⁺⁺ independent processes (mitosis, bud growth, actin organization, endocytosis, etc.) and Ca ⁺⁺ dependent processes (stress-activated pathways), targets include Nuf1p, Myo2p and calcineurin	Strain failed to verify via PCR
4041	VN_4041	YMR225C	MRPL44	Mitochondrial ribosomal protein of the large subunit	Q
4042	VN_4042	YDR433W	YDR433W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4043	VN_4043	YGL031C	RPL24A	Ribosomal protein L30 of the large (60S) ribosomal subunit, nearly identical to Rpl24Bp and has similarity to rat L24 ribosomal protein; not essential for translation but may be required for normal translation rate	Q
4044	VN_4044	YIL062C	ARC15	Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches	Q
4045	VN_4045	YHR217C	YHR217C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; located in the telomeric region TEL08R.	Strain failed to verify via PCR
4046	VN_4046	YCL002C	YCL002C	Putative protein of unknown function; YCL002C is not an essential gene	Q
4047	VN_4047	YBR135W	CKS1	Cyclin-dependent protein kinase regulatory subunit and adaptor; modulates proteolysis of M-phase targets through interactions with the proteasome; role in transcriptional regulation, recruiting proteasomal subunits to target gene promoters	Q
4048	VN_4048	YPL059W	GRX5	Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; mitochondrial matrix protein involved in the synthesis/assembly of iron-sulfur centers; monothiol glutaredoxin subfamily member along with Grx3p and Grx4p	Q
4049	VN_4049	YNR010W	CSE2	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; component of the Med9/10 module; required for regulation of RNA polymerase II activity	Q
4050	VN_4050	YGR203W	YCH1	Phosphatase with sequence similarity to Cdc25p, Arr2p and Mih1p; member of the single-domain rhodanese homology superfamily; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	Q
4051	VN_4051	YBR252W	DUT1	dUTPase, catalyzes hydrolysis of dUTP to dUMP and PPi, thereby	Q

				preventing incorporation of uracil into DNA during replication; critical for the maintenance of genetic stability	
4052	VN_4052	YNL147W	LSM7	Lsm (Like Sm) protein; part of heteroheptameric complexes (Lsm2p-7p and either Lsm1p or 8p); cytoplasmic Lsm1p complex involved in mRNA decay; nuclear Lsm8p complex part of U6 snRNP and possibly involved in processing tRNA, snoRNA, and rRNA	Q
4053	VN_4053	YGR074W	SMD1	Core Sm protein Sm D1; part of heteroheptameric complex (with Smb1p, Smd2p, Smd3p, Sme1p, Smx3p, and Smx2p) that is part of the spliceosomal U1, U2, U4, and U5 snRNPs; homolog of human Sm D1	Q
4054	VN_4054	YGR243W	FMP43	Putative protein of unknown function; expression regulated by osmotic and alkaline stresses; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
4055	VN_4055	YER035W	EDC2	RNA-binding protein, activates mRNA decapping directly by binding to the mRNA substrate and enhancing the activity of the decapping proteins Dcp1p and Dcp2p; has a role in translation during heat stress	Q
4056	VN_4056	YPL276W	YPL276W	NAD(+)-dependent formate dehydrogenase, may protect cells from exogenous formate; YPL275W and YPL276W comprise a continuous open reading frame in some <i>S. cerevisiae</i> strains but not in the genomic reference strain S288C	Q
4057	VN_4057	YOR055W	YOR055W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4058	VN_4058	YNL081C	SWS2	Putative mitochondrial ribosomal protein of the small subunit, has similarity to <i>E. coli</i> S13 ribosomal protein; participates in controlling sporulation efficiency	Q
4059	VN_4059	YBR258C	SHG1	Subunit of the COMPASS (Set1C) complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres	Q
4060	VN_4060	YNL113W	RPC19	RNA polymerase subunit, common to RNA polymerases I and III	Q
4061	VN_4061	YJR067C	YAE1	Protein of unknown function, essential for growth under standard (aerobic) conditions but not under anaerobic conditions	Q
4062	VN_4062	YDR437W	GPI19	Subunit of GPI-GlcNAc transferase involved in synthesis of N-acetylglucosaminyl phosphatidylinositol (GlcNAc-PI), which is the first intermediate in glycosylphosphatidylinositol (GPI) anchor synthesis, shares similarity with mammalian PIG-P	Q
4063	VN_4063	YEL033W	MTC7	Predicted metabolic role based on network analysis derived from ChIP experiments, a large-scale deletion study and localization of transcription factor binding sites; null mutant is sensitive to temperature oscillation in a <i>cdc13-1</i> mutant	Q
4064	VN_4064	YBL049W	MOH1	Protein of unknown function, has homology to kinase Snf7p; not required for growth on nonfermentable carbon sources; essential for viability in stationary phase	Q
4065	VN_4065	YDR156W	RPA14	RNA polymerase I subunit A14	Q
4066	VN_4066	YGR259C	YGR259C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps almost completely with the verified ORF TNA1/YGR260W	Strain failed to verify via PCR
4067	VN_4067	YFL043C		#N/A	Q
4068	VN_4068	YBL021C	HAP3	Subunit of the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression; contains sequences contributing to both complex assembly and DNA binding	Q
4069	VN_4069	YOR186W	YOR186W	Putative protein of unknown function; proper regulation of expression during heat stress is sphingolipid-dependent	Q
4070	VN_4070	YNL235C	YNL235C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF SIN4/YNL236W, a subunit of the mediator complex	Q
4071	VN_4071	YDR544C	YDR544C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4072	VN_4072	YNR042W	YNR042W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely	Q

				overlaps verified gene COQ2	
4073	VN_4073	YKR033C	YKR033C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene DAL80	Q
4074	VN_4074	YGL108C	YGL108C	Protein of unknown function, predicted to be palmitoylated; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery	Q
4075	VN_4075	YLR112W	YLR112W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4076	VN_4076	YIL040W	APQ12	Protein involved in nucleocytoplasmic transport of mRNA	Strain failed to verify via PCR
4077	VN_4077	YDR209C	YDR209C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps uncharacterized gene YDR210W.	Q
4078	VN_4078	YNL319W	YNL319W	Dubious open reading frame unlikely to encode a protein; partially overlaps the verified gene HXT14	Q
4079	VN_4079	YGL118C	YGL118C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4080	VN_4080	YBR285W	YBR285W	Putative protein of unknown function; YBR285W is not an essential gene and deletion of YBR285W leads to poor growth on glucose-minimal medium at 15C	Q
4081	VN_4081	YPR123C	YPR123C	Hypothetical protein	Q
4082	VN_4082	YOL165C	AAD15	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role	Q
4083	VN_4083	YER159C	BUR6	Subunit of a heterodimeric NC2 transcription regulator complex with Ncb2p; complex binds to TBP and can repress transcription by preventing preinitiation complex assembly or stimulate activated transcription; homologous to human NC2alpha	Q
4084	VN_4084	YLR013W	GAT3	Protein containing GATA family zinc finger motifs	Q
4085	VN_4085	YJR044C	VPS55	Late endosomal protein involved in late endosome to vacuole trafficking; functional homolog of human obesity receptor gene-related protein (OB-RGRP)	Q
4086	VN_4086	YNL266W	YNL266W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF IST1/YNL265C	Q
4087	VN_4087	YJL027C	YJL027C	Putative protein of unknown function	Q
4088	VN_4088	YGR230W	BNS1	Protein with some similarity to Spo12p; overexpression bypasses need for Spo12p, but not required for meiosis	Q
4089	VN_4089	YNR004W	YNR004W	Putative protein of unknown function; haploid disruptant exhibits cold-sensitive growth and elongated buds	Q
4090	VN_4090	YIL051C	MMF1	Mitochondrial protein involved in maintenance of the mitochondrial genome	Q
4091	VN_4091	YCL056C	YCL056C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; null mutant displays decreased thermotolerance	Q
4092	VN_4092	YPR153W	YPR153W	Putative protein of unknown function	Q
4093	VN_4093	YOR041C	YOR041C	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 85% of ORF overlaps the uncharacterized gene CUE5; deletion in cyr1 mutant results in loss of stress resistance	Q
4094	VN_4094	YBL083C	YBL083C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps verified ORF ALG3	Q
4095	VN_4095	YOR252W	TMA16	Protein of unknown function that associates with ribosomes	Q
4096	VN_4096	YNR022C	MRPL50	Mitochondrial ribosomal protein of the large subunit, not essential for mitochondrial translation	Q

4097	VN_4097	YJL075C	APQ13	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 85% of ORF overlaps the verified gene NET1; null mutant is sensitive to sorbate	Strain failed to verify via PCR
4098	VN_4098	YKL031W	YKL031W	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species	Q
4099	VN_4099	YOR224C	RPB8	RNA polymerase subunit ABC14.5, common to RNA polymerases I, II, and III	Strain failed to verify via PCR
4100	VN_4100	YKL160W	ELF1	Transcription elongation factor that contains a conserved zinc finger domain; implicated in the maintenance of proper chromatin structure in actively transcribed regions; deletion inhibits Brome mosaic virus (BMV) gene expression	Q
4101	VN_4101	YHR095W	YHR095W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4102	VN_4102	YIL029C	YIL029C	Putative protein of unknown function; deletion confers sensitivity to 4-(N-(S-glutathionylacetyl)amino) phenylarsenoxide (GSAO)	Q
4103	VN_4103	YDL062W	YDL062W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps uncharacterized ORF YDL063C; YDL062W is not essential	Q
4104	VN_4104	YBR167C	POP7	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends	Q
4105	VN_4105	YLR275W	SMD2	Core Sm protein Sm D2; part of heteroheptameric complex (with Smb1p, Smd1p, Smd3p, Sme1p, Smx3p, and Smx2p) that is part of the spliceosomal U1, U2, U4, and U5 snRNPs; homolog of human Sm D2	Q
4106	VN_4106	YOR218C	YOR218C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; open reading frame overlaps the verified gene RFC1/YOR217W	Strain failed to verify via PCR
4107	VN_4107	YKL170W	MRPL38	Mitochondrial ribosomal protein of the large subunit; appears as two protein spots (YmL34 and YmL38) on two-dimensional SDS gels	Q
4108	VN_4108	YKL049C	CSE4	Centromere protein that resembles histone H3, required for proper kinetochore function; homolog of human CENP-A	Q
4109	VN_4109	YPL225W	YPL225W	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
4110	VN_4110	YMR074C	YMR074C	Protein with homology to human PDCD5, which is involved in programmed cell death; N-terminal region forms a conserved triple-helix bundle structure; overexpression promotes H2O2-induced apoptosis; YMR074C is not an essential gene	Q
4111	VN_4111	YIL060W	YIL060W	Putative protein of unknown function; mutant accumulates less glycogen than does wild type; null mutation results in a decrease in plasma membrane electron transport; YIL060W is not an essential gene	Q
4112	VN_4112	YDR100W	TVP15	Integral membrane protein localized to late Golgi vesicles along with the v-SNARE Tlg2p	Q
4113	VN_4113	YPR082C	DIB1	17-kDa component of the U4/U6aU5 tri-snRNP, plays an essential role in pre-mRNA splicing, orthologue of hDIM1, the human U5-specific 15-kDa protein	Q
4114	VN_4114	YLR245C	CDD1	Cytidine deaminase; catalyzes the modification of cytidine to uridine in vitro but native RNA substrates have not been identified, localizes to both the nucleus and cytoplasm	Q
4115	VN_4115	YBR188C	NTC20	Member of the NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 snRNAs	Q
4116	VN_4116	YNL205C	YNL205C	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4117	VN_4117	YOR285W	RDL1	Protein of unknown function containing a rhodanese-like domain; localized to the mitochondrial outer membrane	Q
4118	VN_4118	YKL167C	MRP49	Mitochondrial ribosomal protein of the large subunit, not essential for mitochondrial translation	Strain failed to verify via PCR
4119	VN_4119	YBL006C	LDB7	Component of the RSC chromatin remodeling complex; interacts with Rsc3p, Rsc30p, Npl6p, and Htl1p to form a module important for a	Q

				broad range of RSC functions	
4120	VN_4120	YMR151W	YIM2	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 5% of ORF overlaps the verified gene IMP1	Q
4121	VN_4121	YIR015W	RPR2	Subunit of nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends; not shared between RNase MRP and RNase P, in contrast to all other RNase P protein subunits	Q
4122	VN_4122	YDR513W	GRX2	Cytoplasmic glutaredoxin, thioltransferase, glutathione-dependent disulfide oxidoreductase involved in maintaining redox state of target proteins, also exhibits glutathione peroxidase activity, expression induced in response to stress	Q
4123	VN_4123	YBR064W	YBR064W	Dubious open reading frame unlikely to encode a protein; partially overlaps the uncharacterized ORF YBR063C	Q
4124	VN_4124	YMR269W	TMA23	Nucleolar protein of unknown function implicated in ribosome biogenesis; TMA23 may be a fungal-specific gene as no homologs have been yet identified in higher eukaryotes	Q
4125	VN_4125	YER187W	YER187W	Putative protein of unknown function; induced in respiratory-deficient cells	Strain failed to verify via PCR
4126	VN_4126	YDL123W	SNA4	Protein of unknown function, localized to the vacuolar outer membrane; predicted to be palmitoylated	Q
4127	VN_4127	YPR100W	MRPL51	Mitochondrial ribosomal protein of the large subunit	Q
4128	VN_4128	YPL114W	YPL114W	Dubious open reading frame, unlikely to encode a functional protein; largely overlaps ORF YPL113C; diploid deletion in BY4743 strain background exhibits high budding index	Q
4129	VN_4129	YOR012W	YOR012W	Putative protein of unknown function	Q
4130	VN_4130	YBL025W	RRN10	Protein involved in promoting high level transcription of rDNA, subunit of UAF (upstream activation factor) for RNA polymerase I	Q
4131	VN_4131	YNL179C	YNL179C	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; deletion in <i>cyr1</i> mutant results in loss of stress resistance	Q
4132	VN_4132	YER046W	SPO73	Meiosis-specific protein of unknown function, required for spore wall formation during sporulation; dispensable for both nuclear divisions during meiosis	Q
4133	VN_4133	YBR210W	ERV15	Protein involved in export of proteins from the endoplasmic reticulum, has similarity to Erv14p	Q
4134	VN_4134	YNL105W	RRT16	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene INP52; identified in a screen for mutants with decreased levels of rDNA transcription	Q
4135	VN_4135	YIL027C	KRE27	Member of a transmembrane complex required for efficient folding of proteins in the ER; null mutant displays induction of the unfolded protein response, and also shows K1 killer toxin resistance	Q
4136	VN_4136	YDR308C	SRB7	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation; target of the global repressor Tup1p	Strain failed to verify via PCR
4137	VN_4137	YBR012C	YBR012C	Dubious open reading frame, unlikely to encode a functional protein; expression induced by iron-regulated transcriptional activator Aft2p	Q
4138	VN_4138	YPR064W	YPR064W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4139	VN_4139	YBL059C-A	CMC2	Protein of the mitochondrial intermembrane space with a role in respiratory chain complex assembly or maintenance; contains twin Cx9C motifs that can form coiled coil-helix-coiled-coil helix fold	Q
4140	VN_4140	YPL197C	YPL197C	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; partially overlaps the ribosomal gene RPB7B	Q
4141	VN_4141	YPR050C	YPR050C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene MAK3/YPR051W	Q

4142	VN_4142	YKL097C	YKL097C	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species	Q
4143	VN_4143	YPL062W	YPL062W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YPL062W is not an essential gene; homozygous diploid mutant shows a decrease in glycogen accumulation	Q
4144	VN_4144	YDR366C	YDR366C	Putative protein of unknown function	Strain failed to verify via PCR
4145	VN_4145	YOR200W	YOR200W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF MRM1/YOR201c	Strain failed to verify via PCR
4146	VN_4146	YKL003C	MRP17	Mitochondrial ribosomal protein of the small subunit; MRP17 exhibits genetic interactions with PET122, encoding a COX3-specific translational activator	Q
4147	VN_4147	YNL324W	YNL324W	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4148	VN_4148	YGL080W	FMP37	Putative protein of unknown function; highly conserved across species and orthologous to human gene BRP44L; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Strain failed to verify via PCR
4149	VN_4149	YGR114C	YGR114C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; open reading frame overlaps 5' end of the essential gene SPT6	Strain failed to verify via PCR
4150	VN_4150	YBR010W	HHT1	Histone H3, core histone protein required for chromatin assembly, part of heterochromatin-mediated telomeric and HM silencing; one of two identical histone H3 proteins (see HHT2); regulated by acetylation, methylation, and phosphorylation	Q
4151	VN_4151	YLR125W	YLR125W	Putative protein of unknown function; mutant has decreased Ty3 transposition; YLR125W is not an essential gene	Q
4152	VN_4152	YNR046W	TRM112	Subunit of tRNA methyltransferase (MTase) complexes in combination with Trm9p and Trm11p; subunit of complex with Mtt2p that methylates Sup45p (eRF1) in the ternary complex eRF1-eRF3-GTP; deletion confers resistance to zymocin	Q
4153	VN_4153	YBL012C	YBL012C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4154	VN_4154	YKR049C	FMP46	Putative redox protein containing a thioredoxin fold; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
4155	VN_4155	YIL028W	YIL028W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4156	VN_4156	YOR268C	YOR268C	Putative protein of unknown function; sporulation is abnormal in homozygous diploid; YOR268C is not an essential gene	Q
4157	VN_4157	YKL138C	MRPL31	Mitochondrial ribosomal protein of the large subunit	Q
4158	VN_4158	YPL185W	YPL185W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene UIP4/YPL186C	Q
4159	VN_4159	YHL005C	YHL005C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF YHL004W	Q
4160	VN_4160	YNL143C	YNL143C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4161	VN_4161	YGR236C	SPG1	Protein required for survival at high temperature during stationary phase; not required for growth on nonfermentable carbon sources; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
4162	VN_4162	YBR226C	YBR226C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YBR225W	Q
4163	VN_4163	YNL031C	HHT2	Histone H3, core histone protein required for chromatin assembly, part of heterochromatin-mediated telomeric and HM silencing; one of two identical histone H3 proteins (see HHT1); regulated by acetylation,	Strain failed to verify via PCR

				methylation, and phosphorylation	
4164	VN_4164	YOR263C	YOR263C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF DES3/YOR264W	Q
4165	VN_4165	YBR134W	YBR134W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4166	VN_4166	YKR083C	DAD2	Essential subunit of the Dam1 complex (aka DASH complex), couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; is transferred to the kinetochore prior to mitosis	Strain failed to verify via PCR
4167	VN_4167	YKL136W	YKL136W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF APL2/YKL135C	Q
4168	VN_4168	YBL092W	RPL32	Protein component of the large (60S) ribosomal subunit, has similarity to rat L32 ribosomal protein; overexpression disrupts telomeric silencing	Strain failed to verify via PCR
4169	VN_4169	YHR059W	FYV4	Protein of unknown function, required for survival upon exposure to K1 killer toxin	Q
4170	VN_4170	YOR139C	YOR139C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF SFL1/YOR140W	Q
4171	VN_4171	YHR162W	YHR162W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion	Q
4172	VN_4172	YCR025C	YCR025C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YCR025C is not an essential gene	Q
4173	VN_4173	YNL226W	YNL226W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the verified gene JJJ1/YNL227C	Q
4174	VN_4174	YPR130C	YPR130C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4175	VN_4175	YBR277C	YBR277C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YBR278W	Q
4176	VN_4176	YLR437C	DIF1	Protein that regulates the nuclear localization of ribonucleotide reductase Rnr2p and Rnr4p subunits; phosphorylated by Dun1p in response to DNA damage and degraded; N-terminal half has similarity to S. pombe Spd1 protein	Q
4177	VN_4177	YDR053W	YDR053W	Putative protein of unknown function; open reading frame overlaps 5' end of essential DBF4 gene encoding the regulatory subunit of the Cdc7p-Dbf4p kinase complex	Q
4178	VN_4178	YLR104W	YLR104W	Putative protein of unknown function; mutant is deficient in amounts of cell wall mannosylphosphate; genetic interactions suggest a role in ER-associated protein degradation (ERAD)	Q
4179	VN_4179	YBR269C	FMP21	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
4180	VN_4180	YIL012W	YIL012W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4181	VN_4181	YIL141W	YIL141W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4182	VN_4182	YCR064C	YCR064C	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; partially overlaps the verified gene BUD31	Q
4183	VN_4183	YPL250C	ICY2	Protein of unknown function; mobilized into polysomes upon a shift from a fermentable to nonfermentable carbon source; potential Cdc28p substrate	Q
4184	VN_4184	YLR445W	YLR445W	Putative protein of unknown function; transcription is regulated by Ume6p and induced in response to alpha factor	Q
4185	VN_4185	YDR157W	YDR157W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q

4186	VN_4186	YML095C-A		#N/A	Q
4187	VN_4187	YLR385C	SWC7	Protein of unknown function, component of the Swr1p complex that incorporates Htz1p into chromatin	Q
4188	VN_4188	YCL007C	YCL007C	Dubious ORF unlikely to encode a protein; overlaps verified ORF YCL005W-A; mutations in YCL007C were thought to confer sensitivity to calcofluor white, but this phenotype was later shown to be due to the defect in YCL005W-A	Q
4189	VN_4189	YJL142C	IRC9	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene YJL141C; null mutant displays increased levels of spontaneous Rad52p foci	Q
4190	VN_4190	YBR013C	YBR013C	Putative protein of unknown function, haploid deletion mutant exhibits synthetic phenotype with alpha-synuclein	Q
4191	VN_4191	YLR171W	YLR171W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4192	VN_4192	YDR095C	YDR095C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4193	VN_4193	YDL012C	YDL012C	Plasma membrane protein of unknown function; may contribute to Non-homologous end-joining (NHEJ) based on double deletion with htz1; YDL012C is not an essential gene	Q
4194	VN_4194	YMR252C	YMR252C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria; YMR252C is not an essential gene	Q
4195	VN_4195	YDR511W	ACN9	Protein of the mitochondrial intermembrane space, required for acetate utilization and gluconeogenesis; has orthologs in higher eukaryotes	Q
4196	VN_4196	YLR416C	YLR416C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4197	VN_4197	YHR132W-A	YHR132W-A	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; protein abundance is decreased upon intracellular iron depletion	Q
4198	VN_4198	YNL170W	YNL170W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4199	VN_4199	YJL190C	RPS22A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Bp and has similarity to E. coli S8 and rat S15a ribosomal proteins	Q
4200	VN_4200	YDR015C	YDR015C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the verified gene HED1/YDR014W-A	Q
4201	VN_4201	YLR279W	YLR279W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4202	VN_4202	YDR134C	YDR134C	Hypothetical protein	Q
4203	VN_4203	YDR445C	YDR445C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4204	VN_4204	YNR005C	YNR005C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4205	VN_4205	YHR191C	CTF8	Subunit of a complex with Ctf18p that shares some subunits with Replication Factor C and is required for sister chromatid cohesion	Q
4206	VN_4206	YDR193W	YDR193W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4207	VN_4207	YML035C-A		#N/A	Q
4208	VN_4208	YJL064W	YJL064W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the verified gene YJL065C/DLS1	Q
4209	VN_4209	YNL269W	BSC4	Protein of unknown function, ORF exhibits genomic organization compatible with a translational readthrough-dependent mode of expression; readthrough is increased upon depletion of Sup35p	Q
4210	VN_4210	YER135C	YER135C	Dubious open reading frame unlikely to encode a protein; YER135C is not an essential gene	Q

4211	VN_4211	YJR114W	YJR114W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF RSM7/YJR113C	Q
4212	VN_4212	YER057C	HMF1	Member of the p14.5 protein family with similarity to Mmf1p, functionally complements Mmf1p function when targeted to mitochondria; heat shock inducible; high-dosage growth inhibitor; forms a homotrimer in vitro	Q
4213	VN_4213	YLR297W	YLR297W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; YLR297W is not an essential gene; induced by treatment with 8-methoxypsoralen and UVA irradiation	Q
4214	VN_4214	YGR265W	YGR265W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF MES1/YGR264C, which encodes methionyl-tRNA synthetase	Q
4215	VN_4215	YDR482C	CWC21	Component of a complex containing Cef1p, putatively involved in pre-mRNA splicing; may bind RNA; has similarity to <i>S. pombe</i> Cwf21p	Q
4216	VN_4216	YOL012C	HTZ1	Histone variant H2AZ, exchanged for histone H2A in nucleosomes by the SWR1 complex; involved in transcriptional regulation through prevention of the spread of silent heterochromatin	Q
4217	VN_4217	YJL151C	SNA3	Integral membrane protein localized to vacuolar intraluminal vesicles, computational analysis of large-scale protein-protein interaction data suggests a possible role in either cell wall synthesis or protein-vacuolar targeting	Q
4218	VN_4218	YDR225W	HTA1	Histone H2A, core histone protein required for chromatin assembly and chromosome function; one of two nearly identical subtypes (see also HTA2); DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p	Strain failed to verify via PCR
4219	VN_4219	YOL079W	YOL079W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4220	VN_4220	YJL077C	ICS3	Protein of unknown function	Q
4221	VN_4221	YNL276C	YNL276C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the verified gene MET2/YNL277W	Q
4222	VN_4222	YGL015C	YGL015C	Hypothetical protein	Q
4223	VN_4223	YKL036C	YKL036C	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; partially overlaps the essential gene UGP1 gene and uncharacterized ORF YKL037W	Q
4224	VN_4224	YGL191W	COX13	Subunit VIa of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; not essential for cytochrome c oxidase activity but may modulate activity in response to ATP	Q
4225	VN_4225	YLR374C	YLR374C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF STP3/YLR375W	Q
4226	VN_4226	YML058C-A		#N/A	Q
4227	VN_4227	YBR016W	YBR016W	Plasma membrane protein of unknown function, predicted to be palmitoylated; has similarity to hydrophilins, which are hydrophilic, glycine-rich proteins involved in the adaptive response to hyperosmotic conditions	Q
4228	VN_4228	YBR099C	YBR099C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the verified gene MMS4	Q
4229	VN_4229	YKL076C	PSY1	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 69% of ORF overlaps the uncharacterized ORF YKL075C	Q
4230	VN_4230	YAL064C-A	YAL064C-A	Putative protein of unknown function; YAL064C-A is not an essential gene	Q
4231	VN_4231	YKL123W	YKL123W	Dubious open reading frame, unlikely to encode a protein; partially overlaps the verified gene SSH4	Q

4232	VN_4232	YCL021W-A	YCL021W-A	Putative protein of unknown function	Q
4233	VN_4233	YDL071C	YDL071C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF BDF2/YDL070W	Q
4234	VN_4234	YLL025W	PAU17	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions; YLL025W is not an essential gene	Q
4235	VN_4235	YPR076W	YPR076W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4236	VN_4236	YDR417C	YDR417C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF RPL12B/YDR418W	Q
4237	VN_4237	YMR306C-A	YMR306C-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4238	VN_4238	YCR082W	AHC2	Protein of unknown function, putative transcriptional regulator; proposed to be a Ada Histone acetyltransferase complex component; GFP tagged protein is localized to the cytoplasm and nucleus	Q
4239	VN_4239	YCR043C	YCR043C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the Golgi apparatus; YCR043C is not an essential gene	Q
4240	VN_4240	YKL086W	SRX1	Sulfiredoxin, contributes to oxidative stress resistance by reducing cysteine-sulfinic acid groups in the peroxiredoxins Tsa1p and Ahp1p that are formed upon exposure to oxidants; conserved in higher eukaryotes	Q
4241	VN_4241	YAL064W-B	YAL064W-B	Fungal-specific protein of unknown function	Q
4242	VN_4242	YDR426C	YDR426C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF SNX41	Q
4243	VN_4243	YLR122C	YLR122C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the dubious ORF YLR123C	Q
4244	VN_4244	YFL013W-A	YFL013W-A	Dubious ORF unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps IES1/YFL013C; identified by gene-trapping, microarray expression analysis, and genome-wide homology searching	Q
4245	VN_4245	YLR037C	PAU23	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p; member of the seripauperin multigene family encoded mainly in subtelomeric regions; expressed under anaerobic conditions, completely repressed during aerobic growth	Q
4246	VN_4246	YBR194W	AIM4	Protein proposed to be associated with the nuclear pore complex; null mutant is viable, displays elevated frequency of mitochondrial genome loss and is sensitive to freeze-thaw stress	Q
4247	VN_4247	YDR493W	AIM8	Protein of unknown function; overexpression causes a cell cycle delay or arrest; null mutant displays severe respiratory growth defect and elevated frequency of mitochondrial genome loss; detected in mitochondria in high-throughput studies	Q
4248	VN_4248	YNL149C	PGA2	Essential protein required for maturation of Gas1p and Pho8p; involved in protein trafficking; GFP-fusion protein localizes to the ER and YFP-fusion protein to the nuclear envelope-ER network; null mutants have a cell separation defect	Q
4249	VN_4249	YDR360W	OPI7	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene VID21/YDR359C.	Q
4250	VN_4250	YCR083W	TRX3	Mitochondrial thioredoxin, highly conserved oxidoreductase required to maintain the redox homeostasis of the cell, forms the mitochondrial thioredoxin system with Trx2p, redox state is maintained by both Trx2p and Glr1p	Q
4251	VN_4251	YBL062W	YBL062W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4252	VN_4252	YLR334C	YLR334C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps a	Q

				stand-alone long terminal repeat sequence whose presence indicates a retrotransposition event occurred here	
4253	VN_4253	YER009W	NTF2	Nuclear envelope protein, interacts with GDP-bound Gsp1p and with proteins of the nuclear pore to transport Gsp1p into the nucleus where it is an essential player in nucleocytoplasmic transport	Strain failed to verify via PCR
4254	VN_4254	YLR331C	JIP3	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 98% of ORF overlaps the verified gene MID2	Q
4255	VN_4255	YFR036W	CDC26	Subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition	Q
4256	VN_4256	YLR295C	ATP14	Subunit h of the F0 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis	Q
4257	VN_4257	YBR292C	YBR292C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YBR292C is not an essential gene	Q
4258	VN_4258	YEL003W	GIM4	Subunit of the heterohexameric cochaperone prefoldin complex which binds specifically to cytosolic chaperonin and transfers target proteins to it	Q
4259	VN_4259	YNL153C	GIM3	Subunit of the heterohexameric cochaperone prefoldin complex which binds specifically to cytosolic chaperonin and transfers target proteins to it	Q
4260	VN_4260	YER084W	YER084W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4261	VN_4261	YDR215C	YDR215C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; null mutant displays elevated sensitivity to expression of a mutant huntingtin fragment or of alpha-synuclein	Q
4262	VN_4262	YLL047W	YLL047W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene RNP1	Q
4263	VN_4263	YDL118W	YDL118W	Non-essential protein of unconfirmed function; mutants are defective in telomere maintenance, and are synthetically sick or lethal with alpha-synuclein	Q
4264	VN_4264	YLR458W	YLR458W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data; overlaps 5' end of essential NBP1 gene required for mitosis	Q
4265	VN_4265	YER092W	IES5	Protein that associates with the INO80 chromatin remodeling complex under low-salt conditions	Q
4266	VN_4266	YML013C-A		#N/A	Strain failed to verify via PCR
4267	VN_4267	YGR137W	YGR137W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4268	VN_4268	YLR379W	YLR379W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the essential ORF SEC61/YLR378C	Q
4269	VN_4269	YDL050C	YDL050C	Dubious ORF unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4270	VN_4270	YER119C-A	YER119C-A	Dubious open reading frame, not conserved in closely related <i>Saccharomyces</i> species; deletion mutation blocks replication of Brome mosaic virus in <i>S. cerevisiae</i> , but this is likely due to effects on the overlapping gene SCS2	Q
4271	VN_4271	YOL134C	YOL134C	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; partially overlaps HRT1, a verified gene that encodes an SCF ubiquitin ligase subunit	Strain failed to verify via PCR
4272	VN_4272	YJR022W	LSM8	Lsm (Like Sm) protein; forms heteroheptameric complex (with Lsm2p, Lsm3p, Lsm4p, Lsm5p, Lsm6p, and Lsm7p) that is part of spliceosomal U6 snRNP and is also implicated in processing of pre-tRNA, pre-snoRNA, and pre-rRNA	Q

4273	VN_4273	YDR504C	SPG3	Protein required for survival at high temperature during stationary phase; not required for growth on nonfermentable carbon sources	Q
4274	VN_4274	YLR434C	YLR434C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF TSR2/YLR435W	Q
4275	VN_4275	YEL008W	YEL008W	Hypothetical protein predicted to be involved in metabolism	Q
4276	VN_4276	YML122C	YML122C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4277	VN_4277	YGL007W	BRP1	Dubious ORF located in the upstream region of PMA1, deletion leads to polyamine resistance due to downregulation of PMA1	Q
4278	VN_4278	YNL013C	YNL013C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF HEF3/YNL014W	Strain failed to verify via PCR
4279	VN_4279	YIL025C	YIL025C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4280	VN_4280	YMR119W-A	YMR119W-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4281	VN_4281	YDL241W	YDL241W	Putative protein of unknown function; YDL241W is not an essential gene	Q
4282	VN_4282	YFR049W	YMR31	Mitochondrial ribosomal protein of the small subunit, has similarity to human mitochondrial ribosomal protein MRP-S36	Q
4283	VN_4283	YOR183W	FYV12	Protein of unknown function, required for survival upon exposure to K1 killer toxin	Q
4284	VN_4284	YML090W	YML090W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the dubious ORF YML089C; exhibits growth defect on a non-fermentable (respiratory) carbon source	Q
4285	VN_4285	YGL127C	SOH1	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; involved in telomere maintenance; conserved with other metazoan MED31 subunits	Q
4286	VN_4286	YMR172C-A	YMR172C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4287	VN_4287	YEL026W	SNU13	RNA binding protein, part of U3 snoRNP involved in rRNA processing, part of U4/U6-U5 tri-snoRNP involved in mRNA splicing, similar to human 15.5K protein	Q
4288	VN_4288	YMR007W	YMR007W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4289	VN_4289	YJR063W	RPA12	RNA polymerase I subunit A12.2; contains two zinc binding domains, and the N terminal domain is responsible for anchoring to the RNA pol I complex	Q
4290	VN_4290	YBL053W	YBL053W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4291	VN_4291	YIR041W	PAU15	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions	Q
4292	VN_4292	YMR122C	YMR122C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4293	VN_4293	YDR271C	YDR271C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF CCC2/YDR270W	Q
4294	VN_4294	YGL226W	MTC3	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the mitochondrion; mtc3 is synthetically sick with cdc13-1	Q
4295	VN_4295	YPL238C	YPL238C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data; partially overlaps 5' end of the verified essential gene SUI3/YPL237W	Strain failed to verify via PCR
4296	VN_4296	YIL168W	YIL168W	Open reading frame, unlikely to produce a functional protein in S288C; in closely related species and other <i>S. cerevisiae</i> strain backgrounds YIL168W and adjacent ORF, YIL167W, constitute a single ORF encoding L-serine dehydratase	Q

4297	VN_4297	YMR195W	ICY1	Protein of unknown function, required for viability in rich media of cells lacking mitochondrial DNA; mutants have an invasive growth defect with elongated morphology; induced by amino acid starvation	Q
4298	VN_4298	YER071C	YER071C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Q
4299	VN_4299	YOR309C	YOR309C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene NOP58	Q
4300	VN_4300	YKL192C	ACP1	Mitochondrial matrix acyl carrier protein, involved in biosynthesis of octanoate, which is a precursor to lipoic acid; activated by phosphopantetheinylation catalyzed by Ppt2p	Strain failed to verify via PCR
4301	VN_4301	YBR178W	YBR178W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YBR177C	Q
4302	VN_4302	YJL015C	YJL015C	Dubious open reading frame unlikely to encode a functional protein; expression if heat-inducible; located in promoter region of essential CCT3 gene encoding a subunit of the cytosolic chaperonin Cct ring complex, overlaps ORF YJL016W	Q
4303	VN_4303	YMR325W	PAU19	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions	Q
4304	VN_4304	YDR274C	YDR274C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4305	VN_4305	YGR073C	YGR073C	Dubious open reading frame unlikely to encode a functional protein, extensively overlaps essential SMD1 gene encoding a U6 snRNP protein	Q
4306	VN_4306	YAL065C	YAL065C	Putative protein of unknown function; has homology to FLO1; possible pseudogene	Q
4307	VN_4307	YPR059C	YPR059C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YMC1/YPR058W	Q
4308	VN_4308	YJR037W	YJR037W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene HUL4/YJR036C; deletion mutant has decreased spore survival in Drosophila feces	Q
4309	VN_4309	YPL182C	YPL182C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene CTI6/YPL181W	Q
4310	VN_4310	YGL121C	GPG1	Proposed gamma subunit of the heterotrimeric G protein that interacts with the receptor Gpr1p; involved in regulation of pseudohyphal growth; requires Gpb1p or Gpb2p to interact with Gpa2p; overproduction causes prion curing	Q
4311	VN_4311	YKR012C	YKR012C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene PRY2	Q
4312	VN_4312	YCR104W	PAU3	Member of the seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme	Q
4313	VN_4313	YKL053W	YKL053W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified ORF ASK1	Q
4314	VN_4314	YOL014W	YOL014W	Putative protein of unknown function	Q
4315	VN_4315	YDR378C	LSM6	Lsm (Like Sm) protein; part of heteroheptameric complexes (Lsm2p-7p and either Lsm1p or 8p); cytoplasmic Lsm1p complex involved in mRNA decay; nuclear Lsm8p complex part of U6 snRNP and possibly involved in processing tRNA, snoRNA, and rRNA	Q
4316	VN_4316	YJL184W	GON7	Protein proposed to be involved in the modification of N-linked oligosaccharides, osmotic stress response, telomere uncapping and elongation, transcription; component of the EKC/KEOPS protein complex with Kae1p, Cgi121p, Pcc1p, and Bud32p	Q
4317	VN_4317	YJR108W	ABM1	Protein of unknown function, required for normal microtubule organization	Strain failed to verify via PCR

4318	VN_4318	YCL065W	YCL065W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps HMLALPHA1	Strain failed to verify via PCR
4319	VN_4319	YJL086C	YJL086C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified genes YJL085W/EXO70 and YJL087C/TRL1	Q
4320	VN_4320	YMR123W	PKR1	V-ATPase assembly factor, functions with other V-ATPase assembly factors in the ER to efficiently assemble the V-ATPase membrane sector (V0)	Q
4321	VN_4321	YGL034C	YGL034C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4322	VN_4322	YMR075C-A	YMR075C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the verified ORF RCO1/YMR075W	Strain failed to verify via PCR
4323	VN_4323	YGL089C	MF(ALPHA)2	Mating pheromone alpha-factor, made by alpha cells; interacts with mating type a cells to induce cell cycle arrest and other responses leading to mating; also encoded by MF(ALPHA)1, which is more highly expressed than MF(ALPHA)2	Strain failed to verify via PCR
4324	VN_4324	YJL223C	PAU1	Member of the seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme; identical to Pau14p	Strain failed to verify via PCR
4325	VN_4325	YNL111C	CYB5	Cytochrome b5, involved in the sterol and lipid biosynthesis pathways; acts as an electron donor to support sterol C5-6 desaturation	Strain failed to verify via PCR
4326	VN_4326	YER131W	RPS26B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps26Ap and has similarity to rat S26 ribosomal protein	Strain failed to verify via PCR
4327	VN_4327	YMR294W-A	YMR294W-A	Dubious open reading frame unlikely to encode a functional protein, substantially overlaps YMR295C; deletion causes sensitivity to unfolded protein response-inducing agents	Q
4328	VN_4328	YHR145C	YHR145C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4329	VN_4329	YKL224C	PAU16	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions	Strain failed to verify via PCR
4330	VN_4330	YDR357C	YDR357C	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Strain failed to verify via PCR
4331	VN_4331	YJL169W	YJL169W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YJL168C/SET2	Strain failed to verify via PCR
4332	VN_4332	YNL171C	YNL171C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4333	VN_4333	YGL088W	YGL088W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps snR10, a snoRNA required for preRNA processing	Strain failed to verify via PCR
4334	VN_4334	YOL133W	HRT1	RING finger containing subunit of Skp1-Cullin-F-box ubiquitin protein ligases (SCF); required for Gic2p, Far1p, Sic1p and Cln2p degradation; may tether Cdc34p (a ubiquitin conjugating enzyme or E2) and Cdc53p (a cullin) subunits of SCF	Strain failed to verify via PCR
4335	VN_4335	YGL220W	FRA2	Protein involved in negative regulation of transcription of iron regulon; forms an iron independent complex with Fra2p, Grx3p, and Grx4p; null mutant fails to repress iron regulon and is sensitive to nickel	Q
4336	VN_4336	YJR018W	YJR018W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4337	VN_4337	YNR076W	PAU6	Member of the seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme; identical to Pau18p	Q

4338	VN_4338	YGL072C	YGL072C	Dubious open reading frame unlikely to encode a protein; partially overlaps the verified gene HSF1; null mutant displays increased resistance to antifungal agents gliotoxin, cycloheximide and H2O2	Strain failed to verify via PCR
4339	VN_4339	YNR025C	YNR025C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data; deletion reduces expression of PIS1 gene encoding phosphatidylinositol synthase	Strain failed to verify via PCR
4340	VN_4340	YIL032C	YIL032C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4341	VN_4341	YMR057C	YMR057C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified ORF AAC1	Strain failed to verify via PCR
4342	VN_4342	YEL075C	YEL075C	Putative protein of unknown function	Strain failed to verify via PCR
4343	VN_4343	YJL173C	RFA3	Subunit of heterotrimeric Replication Protein A (RPA), which is a highly conserved single-stranded DNA binding protein involved in DNA replication, repair, and recombination	Strain failed to verify via PCR
4344	VN_4344	YOR364W	YOR364W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YOR365C	Q
4345	VN_4345	YGR190C	YGR190C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the verified gene HIP1/YGR191W	Strain failed to verify via PCR
4346	VN_4346	YPL013C	MRPS16	Mitochondrial ribosomal protein of the small subunit	Strain failed to verify via PCR
4347	VN_4347	YGL261C	PAU11	Putative protein of unknown function and member of the seripauperin multigene family encoded mainly in subtelomeric regions; mRNA expression appears to be regulated by SUT1 and UPC2	Strain failed to verify via PCR
4348	VN_4348	YJR038C	YJR038C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4349	VN_4349	YOL005C	RPB11	RNA polymerase II subunit B12.5; part of central core; similar to Rpc19p and bacterial alpha subunit	Q
4350	VN_4350	YGL189C	RPS26A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps26Bp and has similarity to rat S26 ribosomal protein	Strain failed to verify via PCR
4351	VN_4351	YOR015W	YOR015W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4352	VN_4352	YJL003W	COX16	Mitochondrial inner membrane protein, required for assembly of cytochrome c oxidase	Strain failed to verify via PCR
4353	VN_4353	YNL114C	YNL114C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the verified ORF RPC19/YNL113W, an RNA polymerase subunit	Strain failed to verify via PCR
4354	VN_4354	YER189W	YER189W	Putative protein of unknown function	Strain failed to verify via PCR
4355	VN_4355	YJR071W	YJR071W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4356	VN_4356	YOR376W	YOR376W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YOR376W is not an essential gene.	Strain failed to verify via PCR
4357	VN_4357	YAL068C	PAU8	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions	Strain failed to verify via PCR
4358	VN_4358	YGR045C	YGR045C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR

4359	VN_4359	YJR157W	YJR157W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4360	VN_4360	YOL161C	PAU20	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions; expression induced by low temperature and also by anaerobic conditions; induced during alcoholic fermentation	Q
4361	VN_4361	YIL165C	YIL165C	Putative protein of unknown function; in closely related species and other <i>S. cerevisiae</i> strain backgrounds YIL165C and adjacent ORF, YIL164C, likely constitute a single ORF encoding a nitrilase gene	Q
4362	VN_4362	YPR038W	IRC16	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene YPR037C; null mutant displays increased levels of spontaneous Rad52p foci	Strain failed to verify via PCR
4363	VN_4363	YKL037W	AIM26	Putative protein of unknown function; null mutant is viable and displays elevated frequency of mitochondrial genome loss; null mutation confers sensitivity to tunicamycin and DTT	Strain failed to verify via PCR
4364	VN_4364	YNL285W	YNL285W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4365	VN_4365	YFL020C	PAU5	Member of the seripauperin multigene family encoded mainly in subtelomeric regions; induced during alcoholic fermentation; induced by low temperature and also by anaerobic conditions; negatively regulated by oxygen and repressed by heme	Q
4366	VN_4366	YPL136W	YPL136W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the verified gene GIP3/YPL137C	Q
4367	VN_4367	YIL059C	YIL059C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YIL060W	Strain failed to verify via PCR
4368	VN_4368	YBR301W	PAU24	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p; member of the seripauperin multigene family encoded mainly in subtelomeric regions; expressed under anaerobic conditions, completely repressed during aerobic growth	Q
4369	VN_4369	YGR294W	PAU12	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions	Q
4370	VN_4370	YLL064C	PAU18	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions; identical to Pau6p	Q
4371	VN_4371	YBR124W	YBR124W	Putative protein of unknown function	Strain failed to verify via PCR
4372	VN_4372	YJL152W	YJL152W	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4373	VN_4373	YAL046C	AIM1	Protein involved in mitochondrial function or organization; null mutant displays elevated frequency of mitochondrial genome loss	Strain failed to verify via PCR
4374	VN_4374	YLR162W	YLR162W	Putative protein of unknown function; overexpression confers resistance to the antimicrobial peptide MiAMP1	Strain failed to verify via PCR
4375	VN_4375	YPR077C	YPR077C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data; expression increased by deletion of NAP1	Strain failed to verify via PCR
4376	VN_4376	YFR056C	YFR056C	Dubious open reading frame unlikely to encode a protein based on available experimental and comparative sequence data; partially overlaps the uncharacterized gene YFR055W	Q
4377	VN_4377	YLR012C	YLR012C	Putative protein of unknown function; YLR012C is not an essential gene	Q
4378	VN_4378	YBR253W	SRB6	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation	Strain failed to verify via PCR
4379	VN_4379	YIR013C	GAT4	Protein containing GATA family zinc finger motifs	Strain failed to verify via PCR

4380	VN_4380	YDR542W	PAU10	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions	Q
4381	VN_4381	YHL018W	YHL018W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria and is induced in response to the DNA-damaging agent MMS	Strain failed to verify via PCR
4382	VN_4382	YLR302C	YLR302C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4383	VN_4383	YBR232C	YBR232C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4384	VN_4384	YJL215C	YJL215C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4385	VN_4385	YDL157C	YDL157C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Strain failed to verify via PCR
4386	VN_4386	YMR082C	YMR082C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4387	VN_4387	YPR177C	YPR177C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the 5' end of the essential PRP4 gene encoding a component of the U4/U6-U5 snRNP complex	Q
4388	VN_4388	YGL070C	RPB9	RNA polymerase II subunit B12.6; contacts DNA; mutations affect transcription start site; involved in telomere maintenance	Strain failed to verify via PCR
4389	VN_4389	YLR408C	YLR408C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endosome; YLR408C is not an essential gene	Strain failed to verify via PCR
4390	VN_4390	YDL152W	YDL152W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF SAS10/YDL153C, a component of the small ribosomal subunit processosome	Q
4391	VN_4391	YML048W-A		#N/A	Strain failed to verify via PCR
4392	VN_4392	YEL049W	PAU2	Member of the seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme	Strain failed to verify via PCR
4393	VN_4393	YHL046C	PAU13	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions; expression is induced after ethanol shock	Q
4394	VN_4394	YLR461W	PAU4	Member of the seripauperin multigene family encoded mainly in subtelomeric regions; active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme	Q
4395	VN_4395	YCL042W	YCL042W	Putative protein of unknown function; epitope-tagged protein localizes to the cytoplasm	Strain failed to verify via PCR
4396	VN_4396	YJR128W	YJR128W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF RSF2	Strain failed to verify via PCR
4397	VN_4397	YDL162C	YDL162C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps ENT1/YDL161W, a verified gene involved in endocytosis and actin cortical patch assembly	Strain failed to verify via PCR
4398	VN_4398	YPR099C	YPR099C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene MRPL51/YPR100W	Strain failed to verify via PCR
4399	VN_4399	YBL044W	YBL044W	Putative protein of unknown function; YBL044W is not an essential protein	Strain failed to verify via PCR
4400	VN_4400	YGR064W	YGR064W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially	Q

				overlaps the verified ORF SPT4/YGR063C	
4401	VN_4401	YML089C	YML089C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data; expression induced by calcium shortage	Strain failed to verify via PCR
4402	VN_4402	YDR199W	YDR199W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene VPS64; computationally predicted to have thiol-disulfide oxidoreductase activity	Strain failed to verify via PCR
4403	VN_4403	YMR052C-A	YMR052C-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4404	VN_4404	YGL029W	CGR1	Protein involved in nucleolar integrity and processing of the pre-rRNA for the 60S ribosome subunit; transcript is induced in response to cytotoxic stress but not genotoxic stress	Strain failed to verify via PCR
4405	VN_4405	YIL176C	PAU14	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions; identical to Pau1p	Strain failed to verify via PCR
4406	VN_4406	YMR103C	YMR103C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4407	VN_4407	YCR096C	HMRA2	Silenced copy of a2 at HMR; similarity to Alpha2p; required along with a1p for inhibiting expression of the HO endonuclease in a/alpha HO/HO diploid cells with an active mating-type interconversion system	Strain failed to verify via PCR
4408	VN_4408	YGR050C	YGR050C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4409	VN_4409	YAL035C-A		#N/A	Strain failed to verify via PCR
4410	VN_4410	YCR085W	YCR085W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4411	VN_4411	YJR146W	YJR146W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene HMS2	Q
4412	VN_4412	YJR087W	YJR087W	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; partially overlaps the verified gene STE18 and uncharacterized ORF YJR088C	Q
4413	VN_4413	YGR176W	YGR176W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4414	VN_4414	YMR290W-A	YMR290W-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data; overlaps 5' end of essential HAS1 gene which encodes an ATP-dependent RNA helicase	Strain failed to verify via PCR
4415	VN_4415	YDL034W	YDL034W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps with verified gene GPR1/YDL035C; YDL034W is not an essential gene	Q
4416	VN_4416	YLR161W	YLR161W	Putative protein of unknown function; YLR156W, YLR159W, and YLR161W are three identical open reading frames encoded near the ribosomal DNA region of chromosome 12	Q
4417	VN_4417	YGR219W	YGR219W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF MRPL9/YGR220C	Q
4418	VN_4418	YOL160W	YOL160W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4419	VN_4419	YHR173C	YHR173C	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4420	VN_4420	YDL041W	YDL041W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the verified gene SIR2/YDL042C	Q

4421	VN_4421	YLR169W	YLR169W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4422	VN_4422	YAL058C-A		#N/A	Q
4423	VN_4423	YJR120W	YJR120W	Protein of unknown function; essential for growth under anaerobic conditions; mutation causes decreased expression of ATP2, impaired respiration, defective sterol uptake, and altered levels/localization of ABC transporters Aus1p and Pdr11p	Q
4424	VN_4424	YOR189W	IES4	Component of the INO80 chromatin remodeling complex and target of the Mec1p/Tel1p DNA damage signaling pathway; proposed to link chromatin remodeling to replication checkpoint responses	Q
4425	VN_4425	YHL045W	YHL045W	Putative protein of unknown function; not an essential gene	Q
4426	VN_4426	YNL122C	YNL122C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria; YNL122C is not an essential gene	Q
4427	VN_4427	YDR286C	YDR286C	Putative protein of unknown function; predicted to have thiol-disulfide oxidoreductase active site	Q
4428	VN_4428	YLR200W	YKE2	Subunit of the heterohexameric Gim/prefoldin protein complex involved in the folding of alpha-tubulin, beta-tubulin, and actin	Q
4429	VN_4429	YJR082C	EAF6	Subunit of the NuA4 acetyltransferase complex that acetylates histone H4 and NuA3 acetyltransferase complex that acetylates histone H3	Q
4430	VN_4430	YOR053W	YOR053W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene VHS3/YOR054C	Q
4431	VN_4431	YKL177W	YKL177W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene STE3	Q
4432	VN_4432	YDL242W	YDL242W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4433	VN_4433	YLR255C	YLR255C	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4434	VN_4434	YBR051W	YBR051W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the REG2/YBR050C regulatory subunit of the Glc7p type-1 protein phosphatase	Q
4435	VN_4435	YJR162C	YJR162C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4436	VN_4436	YOR345C	YOR345C	Dubious ORF unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the verified gene REV1; null mutant displays increased resistance to antifungal agents gliotoxin, cycloheximide and H2O2	Q
4437	VN_4437	YNL303W	YNL303W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4438	VN_4438	YER121W	YER121W	Putative protein of unknown function; may be involved in phosphatase regulation and/or generation of precursor metabolites and energy	Q
4439	VN_4439	YLR428C	YLR428C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF CRN1	Q
4440	VN_4440	YKL061W	YKL061W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endosome	Q
4441	VN_4441	YOR082C	YOR082C	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; partially overlaps the verified gene YOR083W	Q
4442	VN_4442	YLR390W	ECM19	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
4443	VN_4443	YDR031W	MIC14	Mitochondrial intermembrane space protein; contains twin cysteine-x9-cysteine motifs	Q
4444	VN_4444	YML101C	CUE4	Protein of unknown function; has a CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination	Q

4445	VN_4445	YDR008C	YDR008C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4446	VN_4446	YKL084W	HOT13	Mitochondrial intermembrane space protein, first component of a pathway mediating assembly of small TIM (Translocase of the Inner Membrane) complexes which escort hydrophobic inner membrane proteins en route to the TIM22 complex	Q
4447	VN_4447	YBR062C	YBR062C	Hypothetical protein	Q
4448	VN_4448	YKL225W	YKL225W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4449	VN_4449	YOR050C	YOR050C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; null mutation is viable	Q
4450	VN_4450	YFR035C	YFR035C	Putative protein of unknown function, deletion mutant exhibits synthetic phenotype with alpha-synuclein	Strain failed to verify via PCR
4451	VN_4451	YNL135C	FPR1	Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function	Q
4452	VN_4452	YLL030C	RRT7	Identified in a screen for mutants with increased levels of rDNA transcription; dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4453	VN_4453	YOR135C	IRC14	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YOR136W; null mutant displays increased levels of spontaneous Rad52 foci	Q
4454	VN_4454	YLR415C	YLR415C	Putative protein of unknown function; YLR415C is not an essential gene	Q
4455	VN_4455	YFL019C	YFL019C	Dubious open reading frame unlikely to encode a protein; YFL019C is not an essential gene	Q
4456	VN_4456	YOL037C	YOL037C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YOL036W	Strain failed to verify via PCR
4457	VN_4457	YDR154C	YDR154C	Dubious open reading frame, null mutant exhibits synthetic phenotype with alpha-synuclein	Q
4458	VN_4458	YLL065W	YLL065W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps chromosome XII telomeric element core sequences	Strain failed to verify via PCR
4459	VN_4459	YCL023C	YCL023C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified ORF KCC4	Q
4460	VN_4460	YLR184W	YLR184W	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4461	VN_4461	YPL035C	YPL035C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized gene YPL034W; YPL035C is not an essential gene	Q
4462	VN_4462	YHR138C	YHR138C	Putative protein of unknown function; has similarity to Pbi2p; double null mutant lacking Pbi2p and Yhr138p exhibits highly fragmented vacuoles	Q
4463	VN_4463	YOR068C	VAM10	Protein involved in vacuole morphogenesis; acts at an early step of homotypic vacuole fusion that is required for vacuole tethering	Q
4464	VN_4464	YLR282C	YLR282C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data; deletion mutation confers an increase in Ty1 transposition	Strain failed to verify via PCR
4465	VN_4465	YPL098C	MGR2	Protein required for growth of cells lacking the mitochondrial genome	Strain failed to verify via PCR
4466	VN_4466	YMR086C-A	YMR086C-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4467	VN_4467	YGR182C	YGR182C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially	Q

				overlaps the verified ORF TIM13/YGR181W	
4468	VN_4468	YEL010W	YEL010W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4469	VN_4469	YLR269C	YLR269C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4470	VN_4470	YDR230W	YDR230W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene COX20	Q
4471	VN_4471	YLR232W	YLR232W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene BNA5	Q
4472	VN_4472	YLR124W	YLR124W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4473	VN_4473	YPL205C	YPL205C	Hypothetical protein; deletion of locus affects telomere length	Strain failed to verify via PCR
4474	VN_4474	YOL026C	MIM1	Mitochondrial outer membrane protein, required for assembly of the translocase of the outer membrane (TOM) complex and thereby for mitochondrial protein import; N terminus is exposed to the cytosol: transmembrane segment is highly conserved	Q
4475	VN_4475	YBR100W		#N/A	Q
4476	VN_4476	YNL017C	YNL017C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the tRNA ORF tI(AAU)N2	Strain failed to verify via PCR
4477	VN_4477	YIL100W	YIL100W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the dubious ORF YIL100C-A	Strain failed to verify via PCR
4478	VN_4478	YGR035C	YGR035C	Putative protein of unknown function, potential Cdc28p substrate; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p along with genes involved in multidrug resistance	Q
4479	VN_4479	YLR280C	YLR280C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4480	VN_4480	YLR311C	YLR311C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4481	VN_4481	YBL065W	YBL065W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified ORF SEF1/YBL066C; YBL065W is a non-essential gene	Q
4482	VN_4482	YLR156W	YLR156W	Putative protein of unknown function; exhibits a two-hybrid interaction with Jsn1p in a large-scale analysis	Q
4483	VN_4483	YAR030C	YAR030C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YAR029W and the verified gene PRM9	Strain failed to verify via PCR
4484	VN_4484	YOL085C	YOL085C	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; partially overlaps the dubious gene YOL085W-A	Q
4485	VN_4485	YEL074W	YEL074W	Hypothetical protein	Q
4486	VN_4486	YIL163C	YIL163C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4487	VN_4487	YOR366W	YOR366W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YOR365C	Q
4488	VN_4488	YJL067W	YJL067W	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4489	VN_4489	YMR304C-A	YMR304C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene SCW10	Q
4490	VN_4490	YGL177W	YGL177W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q

4491	VN_4491	YMR107W	SPG4	Protein required for survival at high temperature during stationary phase; not required for growth on nonfermentable carbon sources	Q
4492	VN_4492	YCR022C	YCR022C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YCR022C is not an essential gene	Q
4493	VN_4493	YLR159W	YLR159W	Putative protein of unknown function; YLR156W, YLR159W, and YLR161W are three identical open reading frames encoded near the ribosomal DNA region of chromosome 12	Q
4494	VN_4494	YGL217C	YGL217C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF KIP3/YGL216W	Q
4495	VN_4495	YOL109W	ZEO1	Peripheral membrane protein of the plasma membrane that interacts with Mid2p; regulates the cell integrity pathway mediated by Pkc1p and Slt2p; the authentic protein is detected in a phosphorylated state in highly purified mitochondria	Q
4496	VN_4496	YGR139W	YGR139W	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4497	VN_4497	YOR379C	YOR379C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YOR378W	Q
4498	VN_4498	YAR060C	YAR060C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4499	VN_4499	YGR069W	YGR069W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4500	VN_4500	YKL111C	YKL111C	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; partially overlaps the verified essential gene ABF1	Q
4501	VN_4501	YBR027C	YBR027C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4502	VN_4502	YGL168W	HUR1	Protein of unknown function; reported null mutant phenotype of hydroxyurea sensitivity may be due to effects on overlapping PMR1 gene	Q
4503	VN_4503	YNL057W	YNL057W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4504	VN_4504	YGR018C	YGR018C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YGR017W	Q
4505	VN_4505	YML100W-A	YML100W-A	Putative protein of unknown function; identified by gene-trapping, microarray-based expression analysis, and genome-wide homology searching	Q
4506	VN_4506	YDL096C	OPI6	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene PMT1/YDL095W; YDL096C is not essential	Q
4507	VN_4507	YJL199C	MBB1	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; protein detected in large-scale protein-protein interaction studies	Q
4508	VN_4508	YML010C-B		#N/A	Q
4509	VN_4509	YPR098C	YPR098C	Protein of unknown function, localized to the mitochondrial outer membrane	Q
4510	VN_4510	YBL109W	YBL109W	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data	Q
4511	VN_4511	YGR151C	YGR151C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps almost completely with the verified ORF RSR1/BUD1/YGR152C	Q
4512	VN_4512	YLR204W	QRI5	Mitochondrial inner membrane protein, required for accumulation of spliced COX1 mRNA; may have an additional role in translation of COX1 mRNA	Q
4513	VN_4513	YCL035C	GRX1	Hydroperoxide and superoxide-radical responsive heat-stable glutathione-dependent disulfide oxidoreductase with active site cysteine pair; protects cells from oxidative damage	Q

4514	VN_4514	YGR215W	RSM27	Mitochondrial ribosomal protein of the small subunit	Q
4515	VN_4515	YDL068W	YDL068W	Dubious ORF unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4516	VN_4516	YGR022C	YGR022C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps almost completely with the verified ORF MTL1/YGR023W	Strain failed to verify via PCR
4517	VN_4517	YOR199W	YOR199W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4518	VN_4518	YJR034W	PET191	Protein required for assembly of cytochrome c oxidase; exists as an oligomer that is integral to the mitochondrial inner membrane and faces the intermembrane space; contains a twin Cx9C motif	Strain failed to verify via PCR
4519	VN_4519	YMR031W-A	YMR031W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; null mutant displays shortened telomeres; partially overlaps the uncharacterized ORF YMR031C	Strain failed to verify via PCR
4520	VN_4520	YBR206W	YBR206W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene KTR3	Q
4521	VN_4521	YCR060W	TAH1	HSP90 cofactor; interacts with Hsp82p, Pih1p, Rvb1 and Rvb2, contains a single TPR domain with at least two TPR motifs	Q
4522	VN_4522	YGR164W	YGR164W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4523	VN_4523	YMR153C-A	YMR153C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene NUP53	Q
4524	VN_4524	YCR041W	YCR041W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4525	VN_4525	YIR040C	YIR040C	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data	Strain failed to verify via PCR
4526	VN_4526	YDL187C	YDL187C	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4527	VN_4527	YIL171W	YIL171W	Possible pseudogene in strain S288C; YIL171W and the adjacent ORF, YIL170W/HXT12, together encode a non-functional member of the hexose transporter family	Q
4528	VN_4528	YOR225W	YOR225W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4529	VN_4529	YDR467C	YDR467C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4530	VN_4530	YLL014W	EMC6	Member of a transmembrane complex required for efficient folding of proteins in the ER; null mutant displays induction of the unfolded protein response	Q
4531	VN_4531	YNL184C	YNL184C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4532	VN_4532	YCL046W	YCL046W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YCL045C	Q
4533	VN_4533	YDR079W	PET100	Chaperone that specifically facilitates the assembly of cytochrome c oxidase, integral to the mitochondrial inner membrane; interacts with a subcomplex of subunits VII, VIIa, and VIII (Cox7p, Cox9p, and Cox8p) but not with the holoenzyme	Q
4534	VN_4534	YHR087W	RTC3	Protein of unknown function involved in RNA metabolism; has structural similarity to SBDS, the human protein mutated in Shwachman-Diamond Syndrome (the yeast SBDS ortholog = SDO1); null mutation suppresses cdc13-1 temperature sensitivity	Q
4535	VN_4535	YOR029W	YOR029W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4536	VN_4536	YDR010C	YDR010C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q

4537	VN_4537	YJR020W	YJR020W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4538	VN_4538	YDL196W	YDL196W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; open reading frame is located in promoter region of essential gene SEC31	Q
4539	VN_4539	YJL179W	PFD1	Subunit of heterohexameric prefoldin, which binds cytosolic chaperonin and transfers target proteins to it; involved in the biogenesis of actin and of alpha- and gamma-tubulin	Q
4540	VN_4540	YGL074C	YGL074C	Dubious open reading frame unlikely to encode a functional protein; overlaps 5' end of essential HSF1 gene encoding heat shock transcription factor	Q
4541	VN_4541	YLR053C	YLR053C	Putative protein of unknown function	Q
4542	VN_4542	YDL009C	YDL009C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YDL010W; YDL009C is not an essential gene	Q
4543	VN_4543	YDR094W	YDR094W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified ORF DNF2	Q
4544	VN_4544	YHR130C	YHR130C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4545	VN_4545	YPR039W	YPR039W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified non essential genes ERV2/YPR037C and TIP41/YPR040W	Q
4546	VN_4546	YDR045C	RPC11	RNA polymerase III subunit C11; mediates pol III RNA cleavage activity and is important for termination of transcription; homologous to TFIIIS	Q
4547	VN_4547	YKL223W	YKL223W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4548	VN_4548	YDR290W	YDR290W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF RTT103	Q
4549	VN_4549	YJR048W	CYC1	Cytochrome c, isoform 1; electron carrier of the mitochondrial intermembrane space that transfers electrons from ubiquinone-cytochrome c oxidoreductase to cytochrome c oxidase during cellular respiration	Q
4550	VN_4550	YPR014C	YPR014C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YPR014C is not an essential gene	Q
4551	VN_4551	YGR011W	YGR011W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4552	VN_4552	YLR140W	YLR140W	Dubious open reading frame unlikely to encode a functional protein; overlaps essential RRN5 gene which encodes a member of the UAF transcription factor involved in transcription of rDNA by RNA polymerase I	Strain failed to verify via PCR
4553	VN_4553	YOL131W	YOL131W	Putative protein of unknown function	Q
4554	VN_4554	YDL011C	YDL011C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the uncharacterized ORF YDL010W	Q
4555	VN_4555	YDR133C	YDR133C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps YDR134C	Strain failed to verify via PCR
4556	VN_4556	YHR212C	YHR212C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4557	VN_4557	YPR170C	YPR170C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the dubious ORFs YPR169W-A and YPR170W-B	Q
4558	VN_4558	YDR102C	YDR102C	Dubious open reading frame; homozygous diploid deletion strain exhibits high budding index	Q

4559	VN_4559	YDR525W	API2	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 26% of ORF overlaps the dubious ORF YDR524C-A; insertion mutation in a <i>cdc34-2</i> mutant background causes altered bud morphology	Q
4560	VN_4560	YLR123C	YLR123C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the dubious ORF YLR122C; contains characteristic aminoacyl-tRNA motif	Q
4561	VN_4561	YPR146C	YPR146C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4562	VN_4562	YGR027C	RPS25A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein	Strain failed to verify via PCR
4563	VN_4563	YLR261C	VPS63	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 98% of ORF overlaps the verified gene YPT6; deletion causes a vacuolar protein sorting defect	Q
4564	VN_4564	YOR105W	YOR105W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4565	VN_4565	YDR269C	YDR269C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4566	VN_4566	YDR521W	YDR521W	Dubious ORF that overlaps YDR520C; mutant increases expression of PIS1 and RPL3 in glycerol	Q
4567	VN_4567	YIR009W	MSL1	U2B component of U2 snRNP, involved in splicing, binds the U2 snRNA stem-loop IV in vitro but requires association of Lea1p for in vivo binding; does not contain the conserved C-terminal RNA binding domain found in other family members	Q
4568	VN_4568	YAL044W-A	YAL044W-A	Putative protein of unknown function; similar to <i>S. pombe</i> uvi31 which is a putative DNA repair protein	Q
4569	VN_4569	YDR382W	RPP2B	Ribosomal protein P2 beta, a component of the ribosomal stalk, which is involved in the interaction between translational elongation factors and the ribosome; regulates the accumulation of P1 (Rpp1Ap and Rpp1Bp) in the cytoplasm	Q
4570	VN_4570	YER097W	YER097W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4571	VN_4571	YLR294C	YLR294C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene ATP14	Q
4572	VN_4572	YPR195C	YPR195C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4573	VN_4573	YGR269W	YGR269W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF HUA1/YGR268C	Q
4574	VN_4574	YLR296W	YLR296W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4575	VN_4575	YOR343C	YOR343C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4576	VN_4576	YEL073C	YEL073C	Putative protein of unknown function; located adjacent to ARS503 and the telomere on the left arm of chromosome V; regulated by inositol/choline	Q
4577	VN_4577	YGL132W	YGL132W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the verified gene SNT2/YGL131C	Q
4578	VN_4578	YJL028W	YJL028W	Protein of unknown function; may interact with ribosomes, based on co-purification experiments	Q
4579	VN_4579	YBL094C	YBL094C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps uncharacterized ORF YBL095W	Q
4580	VN_4580	YEL068C	YEL068C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4581	VN_4581	YLR365W	YLR365W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially	Q

				overlaps dubious gene YLR364C-A; YLR365W is not an essential gene	
4582	VN_4582	YFL014W	HSP12	Plasma membrane localized protein that protects membranes from desiccation; induced by heat shock, oxidative stress, osmostress, stationary phase entry, glucose depletion, oleate and alcohol; regulated by the HOG and Ras-Pka pathways	Q
4583	VN_4583	YLR364W	GRX8	Glutaredoxin that employs a dithiol mechanism of catalysis; monomeric; activity is low and null mutation does not affect sensitivity to oxidative stress; GFP-fusion protein localizes to the cytoplasm; expression strongly induced by arsenic	Q
4584	VN_4584	YAL064W	YAL064W	Protein of unknown function; may interact with ribosomes, based on co-purification experiments	Q
4585	VN_4585	YJL009W	YJL009W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps CCT8/YJL008C, a verified gene encoding a subunit of the cytosolic chaperonin Cct ring complex	Strain failed to verify via PCR
4586	VN_4586	YLR333C	RPS25B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Ap and has similarity to rat S25 ribosomal protein	Strain failed to verify via PCR
4587	VN_4587	YPL080C	YPL080C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4588	VN_4588	YER058W	PET117	Protein required for assembly of cytochrome c oxidase	Q
4589	VN_4589	YER181C	YER181C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative data; extensively overlaps a Ty1 LTR; protein product is detected in highly purified mitochondria in high-throughput studies	Q
4590	VN_4590	YOR024W	YOR024W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4591	VN_4591	YDL081C	RPP1A	Ribosomal stalk protein P1 alpha, involved in the interaction between translational elongation factors and the ribosome; accumulation of P1 in the cytoplasm is regulated by phosphorylation and interaction with the P2 stalk component	Strain failed to verify via PCR
4592	VN_4592	YOL048C	RRT8	Putative protein of unknown function; identified in a screen for mutants with increased levels of rDNA transcription; green fluorescent protein (GFP)-fusion protein localizes to lipid particles	Q
4593	VN_4593	YBR268W	MRPL37	Mitochondrial ribosomal protein of the large subunit	Q
4594	VN_4594	YJL182C	YJL182C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps uncharacterized ORF YJL181W	Q
4595	VN_4595	YBL001C	ECM15	Non-essential protein of unknown function, likely exists as tetramer, may be regulated by the binding of small-molecule ligands (possibly sulfate ions), may have a role in yeast cell-wall biogenesis	Q
4596	VN_4596	YGL041C	YGL041C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4597	VN_4597	YLR322W	VPS65	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 75% of ORF overlaps the verified gene SFH1; deletion causes a vacuolar protein sorting defect and blocks anaerobic growth	Q
4598	VN_4598	YBR009C	HHF1	Histone H4, core histone protein required for chromatin assembly and chromosome function; one of two identical histone proteins (see also HHF2); contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity	Q
4599	VN_4599	YHR139C-A	YHR139C-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4600	VN_4600	YAL066W	YAL066W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4601	VN_4601	YGL109W	YGL109W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the uncharacterized gene YGL108C	Q
4602	VN_4602	YPR094W	RDS3	Component of the SF3b subcomplex of the U2 snRNP, zinc cluster protein involved in pre-mRNA splicing and cycloheximide resistance	Strain failed to verify via

					PCR
4603	VN_4603	YFL032W	YFL032W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene HAC1/YFL031W; YFL032W is not an essential gene	Q
4604	VN_4604	YOL050C	YOL050C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps verified gene GAL11; deletion confers sensitivity to 4-(N-(S-glutathionylacetyl)amino) phenylarsenoxide (GSAO)	Q
4605	VN_4605	YDR115W	YDR115W	Putative mitochondrial ribosomal protein of the large subunit, has similarity to E. coli L34 ribosomal protein; required for respiratory growth, as are most mitochondrial ribosomal proteins	Q
4606	VN_4606	YJR085C	YJR085C	Putative protein of unknown function; GFP-fusion protein is induced in response to the DNA-damaging agent MMS; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
4607	VN_4607	YBL100C	YBL100C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; almost completely overlaps the 5' end of ATP1	Q
4608	VN_4608	YGL239C	YGL239C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene CSE1	Q
4609	VN_4609	YML058W	SML1	Ribonucleotide reductase inhibitor involved in regulating dNTP production; regulated by Mec1p and Rad53p during DNA damage and S phase	Q
4610	VN_4610	YBR190W	YBR190W	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; partially overlaps the verified ribosomal protein gene RPL21A/YBR191W	Strain failed to verify via PCR
4611	VN_4611	YKL118W	YKL118W	Dubious open reading frame, unlikely to encode a protein; partially overlaps the verified gene VPH2	Q
4612	VN_4612	YBL071C	YBL071C	Dubious open reading frame, predicted protein contains a peroxisomal targeting signal	Q
4613	VN_4613	YGL182C	YGL182C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF MND1/YGL183C	Q
4614	VN_4614	YAR047C	YAR047C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4615	VN_4615	YKL044W	YKL044W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4616	VN_4616	YOR020C	HSP10	Mitochondrial matrix co-chaperonin that inhibits the ATPase activity of Hsp60p, a mitochondrial chaperonin; involved in protein folding and sorting in the mitochondria; 10 kD heat shock protein with similarity to E. coli groES	Strain failed to verify via PCR
4617	VN_4617	YDR203W	YDR203W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4618	VN_4618	YML102C-A		#N/A	Q
4619	VN_4619	YBR144C	YBR144C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YBR144C is not an essential gene	Q
4620	VN_4620	YIL015C-A		#N/A	Q
4621	VN_4621	YMR244C-A	YMR244C-A	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and nucleus and is induced in response to the DNA-damaging agent MMS; YMR244C-A is not an essential gene	Q
4622	VN_4622	YDL026W	YDL026W	Dubious ORF unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4623	VN_4623	YKL137W	CMC1	Evolutionarily conserved copper-binding protein of the mitochondrial intermembrane space, may be involved in delivering copper from the matrix to the cytochrome c oxidase complex; contains a twin CX9C motif	Q

4624	VN_4624	YBL096C	YBL096C	Non-essential protein of unknown function	Q
4625	VN_4625	YGR051C	YGR051C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YGR051C is not an essential gene	Q
4626	VN_4626	YBL028C	YBL028C	Protein of unknown function that may interact with ribosomes; green fluorescent protein (GFP)-fusion protein localizes to the nucleolus; predicted to be involved in ribosome biogenesis	Q
4627	VN_4627	YKR073C	YKR073C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4628	VN_4628	YOR265W	RBL2	Protein involved in microtubule morphogenesis, required for protection from excess free beta-tubulin; proposed to be involved the folding of beta-tubulin; similar to mouse beta-tubulin cofactor A	Q
4629	VN_4629	YDR278C	YDR278C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4630	VN_4630	YML108W	YML108W	Putative protein of unknown function whose structure defines a new subfamily of the split beta-alpha-beta sandwiches; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YML108W is not an essential gene	Q
4631	VN_4631	YBR174C	YBR174C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF YBR175W; null mutant is viable and sporulation defective	Q
4632	VN_4632	YJL007C	YJL007C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4633	VN_4633	YNL296W	YNL296W	Dubious open reading frame unlikely to encode a functional protein; deletion adversely affects sporulation; deletion mutant exhibits synthetic phenotype under expression of mutant huntingtin fragment, but gene does not have human ortholog	Q
4634	VN_4634	YDL032W	YDL032W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps verified gene SLM3/YDL033C; YDL032W is not an essential gene	Q
4635	VN_4635	YLL017W	YLL017W	Non-essential Ras guanine nucleotide exchange factor (GEF) localized to the membrane; expressed in poor nutrients and on non-fermentable carbon sources; homologous to CDC25; contains a stop codon in S288C; full-length gene includes YLL016W	Q
4636	VN_4636	YJL119C	YJL119C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4637	VN_4637	YBL070C	YBL070C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4638	VN_4638	YLR041W	YLR041W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the uncharacterized ORF YLR040C	Q
4639	VN_4639	YOR282W	YOR282W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps essential, verified gene PLP2/YOR281C	Q
4640	VN_4640	YGR181W	TIM13	Mitochondrial intermembrane space protein, forms a complex with Tim8p that delivers a subset of hydrophobic proteins to the TIM22 complex for insertion into the inner membrane	Q
4641	VN_4641	YMR321C	YMR321C	Putative protein of unknown function; proposed to be a palmitoylated membrane protein	Strain failed to verify via PCR
4642	VN_4642	YCR001W	YCR001W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YCR001W is not an essential gene	Q
4643	VN_4643	YJL018W		#N/A	Q
4644	VN_4644	YOR072W	YOR072W	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; partially overlaps the dubious gene YOR072W-A; diploid deletion strains are methotrexate, paraquat and wortmannin sensitive	Q

4645	VN_4645	YDR431W	YDR431W	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4646	VN_4646	YMR316C-A	YMR316C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the verified gene DIA1/YMR316W	Q
4647	VN_4647	YDL158C	YDL158C	Dubious ORF unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4648	VN_4648	YJL120W	YJL120W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YJL121C/RPE1; deletion confers sensitivity to GSAO	Q
4649	VN_4649	YBR157C	ICS2	Protein of unknown function; null mutation does not confer any obvious defects in growth, spore germination, viability, or carbohydrate utilization	Q
4650	VN_4650	YMR158W-A		#N/A	Q
4651	VN_4651	YPR087W	VPS69	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 85% of ORF overlaps the verified gene SRP54; deletion causes a vacuolar protein sorting defect	Q
4652	VN_4652	YIL054W	YIL054W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4653	VN_4653	YNL028W	YNL028W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4654	VN_4654	YDR029W	YDR029W	Dubious ORF unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4655	VN_4655	YJL032W	YJL032W	Dubious open reading frame unlikely to encode a functional protein; overlaps 3' end of essential BET4 gene encoding the alpha subunit of Type II geranylgeranyltransferase	Strain failed to verify via PCR
4656	VN_4656	YOR235W	IRC13	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; null mutant displays increased levels of spontaneous Rad52 foci	Q
4657	VN_4657	YGL193C	YGL193C	Haploid-specific gene repressed by a1-alpha2, turned off in sir3 null strains, absence enhances the sensitivity of rad52-327 cells to camptothecin almost 100-fold	Q
4658	VN_4658	YNL030W	HHF2	Histone H4, core histone protein required for chromatin assembly and chromosome function; one of two identical histone proteins (see also HHF1); contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity	Strain failed to verify via PCR
4659	VN_4659	YDR112W	IRC2	Dubious open reading frame, unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps YDR111C; null mutant displays increased levels of spontaneous Rad52p foci	Q
4660	VN_4660	YLR217W	YLR217W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene CPR6	Q
4661	VN_4661	YBR262C	AIM5	Protein of unknown function; the authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies; null mutant displays elevated frequency of mitochondrial genome loss	Q
4662	VN_4662	YNL043C	YNL043C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YIP3/YNL044W	Q
4663	VN_4663	YBL112C	YBL112C	Putative protein of unknown function; YBL112C is contained within TEL02L	Q
4664	VN_4664	YIL175W	YIL175W	Hypothetical protein	Q
4665	VN_4665	YDR048C	YDR048C	Dubious ORF unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4666	VN_4666	YJL144W	YJL144W	Cytoplasmic hydrophilin of unknown function, possibly involved in the desiccation response; expression induced by osmotic stress, starvation and during stationary phase; GFP-fusion protein is induced by the DNA-damaging agent MMS	Q

4667	VN_4667	YBL048W	RRT1	Identified in a screen for mutants with increased levels of rDNA transcription; dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data	Q
4668	VN_4668	YGR039W	YGR039W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the Autonomously Replicating Sequence ARS722	Q
4669	VN_4669	YOL150C	YOL150C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4670	VN_4670	YDR455C	YDR455C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YDR456W	Q
4671	VN_4671	YLR236C	YLR236C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4672	VN_4672	YDL023C	YDL023C	Dubious open reading frame, unlikely to encode a protein; not conserved in other <i>Saccharomyces</i> species; overlaps the verified gene GPD1; deletion confers sensitivity to GSAO; deletion in <i>cyr1</i> mutant results in loss of stress resistance	Q
4673	VN_4673	YOL039W	RPP2A	Ribosomal protein P2 alpha, a component of the ribosomal stalk, which is involved in the interaction between translational elongation factors and the ribosome; regulates the accumulation of P1 (Rpp1Ap and Rpp1Bp) in the cytoplasm	Q
4674	VN_4674	YBR209W	YBR209W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YBR209W is not an essential gene	Q
4675	VN_4675	YJL135W	YJL135W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified genes YJL134W/LCB3	Q
4676	VN_4676	YAL069W	YAL069W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4677	VN_4677	YDR281C	PHM6	Protein of unknown function, expression is regulated by phosphate levels	Q
4678	VN_4678	YKR032W	YKR032W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4679	VN_4679	YBL073W	YBL073W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the essential gene AAR2/YBL074C	Strain failed to verify via PCR
4680	VN_4680	YHR049C-A	YHR049C-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4681	VN_4681	YAL045C	YAL045C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; almost completely overlaps YAL044W-A	Q
4682	VN_4682	YFL065C	YFL065C	Putative protein of unknown function; induced by treatment with 8-methoxypsoralen and UVA irradiation	Q
4683	VN_4683	YMR141C	YMR141C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4684	VN_4684	YOR300W	YOR300W	Dubious open reading frame, unlikely to encode a protein; overlaps with verified gene BUD7/YOR299W; mutation affects bipolar budding and bud site selection, though phenotype could be due to the mutation's effects on BUD7	Q
4685	VN_4685	YEL014C	YEL014C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4686	VN_4686	YKR047W	YKR047W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene NAP1	Q
4687	VN_4687	YOR121C	YOR121C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; open reading frame overlaps the verified gene GCY1/YOR120W	Q
4688	VN_4688	YDL163W	YDL163W	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; partially overlaps the verified gene CDC9/YDL164C encoding DNA ligase	Q

4689	VN_4689	YNL146W	YNL146W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YNL146W is not an essential gene	Q
4690	VN_4690	YAR070C	YAR070C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4691	VN_4691	YHR001W-A	QCR10	Subunit of the ubiquinol-cytochrome c oxidoreductase complex which includes Cobp, Rip1p, Cyt1p, Cor1p, Qcr2p, Qcr6p, Qcr7p, Qcr8p, Qcr9p, and Qcr10p and comprises part of the mitochondrial respiratory chain	Q
4692	VN_4692	YBL029C-A	YBL029C-A	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; has potential orthologs in <i>Saccharomyces</i> species and in <i>Yarrowia lipolytica</i>	Q
4693	VN_4693	YDR070C	FMP16	Putative protein of unknown function; proposed to be involved in responding to conditions of stress; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
4694	VN_4694	YGR063C	SPT4	Protein involved in the regulating Pol I and Pol II transcription, pre-mRNA processing, kinetochore function, and gene silencing; forms a complex with Spt5p	Q
4695	VN_4695	YMR254C	YMR254C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4696	VN_4696	YPL261C	YPL261C	Dubious open reading frame unlikely to encode a protein; partially overlaps the uncharacterized ORF YPL260W	Q
4697	VN_4697	YGL052W	YGL052W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF MST27	Q
4698	VN_4698	YLL020C	YLL020C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene KNS1	Q
4699	VN_4699	YDR114C	YDR114C	Putative protein of unknown function; deletion mutant exhibits poor growth at elevated pH and calcium	Q
4700	VN_4700	YNL198C	YNL198C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4701	VN_4701	YBL091C-A	SCS22	Protein involved in regulation of phospholipid metabolism; homolog of Scs2p; similar to <i>D. melanogaster</i> intuned protein	Q
4702	VN_4702	YLL018C-A	COX19	Protein required for cytochrome c oxidase assembly, located in the cytosol and mitochondrial intermembrane space; putative copper metallochaperone that delivers copper to cytochrome c oxidase; contains twin cysteine-x9-cysteine motifs	Q
4703	VN_4703	YBR233W-A	DAD3	Essential subunit of the Dam1 complex (aka DASH complex), couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; is transferred to the kinetochore prior to mitosis	Strain failed to verify via PCR
4704	VN_4704	YER146W	LSM5	Lsm (Like Sm) protein; part of heteroheptameric complexes (Lsm2p-7p and either Lsm1p or 8p); cytoplasmic Lsm1p complex involved in mRNA decay; nuclear Lsm8p complex part of U6 snRNP and possibly involved in processing tRNA, snoRNA, and rRNA	Q
4705	VN_4705	YGR242W	YGR242W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF YAP1802/YGR241C	Q
4706	VN_4706	YMR316C-B	YMR316C-B	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4707	VN_4707	YPR126C	YPR126C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4708	VN_4708	YGL149W	YGL149W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF INO80/YGL150C.	Q
4709	VN_4709	YLR147C	SMD3	Core Sm protein Sm D3; part of heteroheptameric complex (with Smb1p, Smd1p, Smd2p, Sme1p, Smx3p, and Smx2p) that is part of the spliceosomal U1, U2, U4, and U5 snRNPs; homolog of human Sm D3	Strain failed to verify via PCR
4710	VN_4710	YOR170W	YOR170W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially	Q

				overlaps the verified gene LCB4	
4711	VN_4711	YDR340W	YDR340W	Putative protein of unknown function	Strain failed to verify via PCR
4712	VN_4712	YOL035C	YOL035C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4713	VN_4713	YBR089C-A	NHP6B	High-mobility group non-histone chromatin protein, functionally redundant with Nhp6Ap; homologous to mammalian high mobility group proteins 1 and 2; acts to recruit transcription factor Rcs1p to certain promoters	Q
4714	VN_4714	YNR034W-A	YNR034W-A	Putative protein of unknown function; expression is regulated by Msn2p/Msn4p	Q
4715	VN_4715	YHR005C-A	TIM10	Essential protein of the mitochondrial intermembrane space, forms a complex with Tim9p (TIM10 complex) that delivers hydrophobic proteins to the TIM22 complex for insertion into the inner membrane	Q
4716	VN_4716	YIL086C	YIL086C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4717	VN_4717	YMR326C	YMR326C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; overlaps the telomere on the right arm of chromosome 13	Strain failed to verify via PCR
4718	VN_4718	YPR203W	YPR203W	Putative protein of unknown function	Q
4719	VN_4719	YGL204C	YGL204C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4720	VN_4720	YLR230W	YLR230W	Dubious open reading frame unlikely to encode a functional protein; overlaps 5' end of essential CDC42 gene which encodes a small Rho-like GTPase essential for establishment and maintenance of cell polarity	Strain failed to verify via PCR
4721	VN_4721	YPL056C	YPL056C	Putative protein of unknown function; deletion mutant is fluconazole resistant	Q
4722	VN_4722	YDR355C	YDR355C	Dubious: Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified essential ORF SPC110/YDR356W	Q
4723	VN_4723	YOR248W	YOR248W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4724	VN_4724	YDR543C	YDR543C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4725	VN_4725	YDR220C	YDR220C	Dubious open reading frame, null mutant exhibits synthetic phenotype with alpha-synuclein	Q
4726	VN_4726	YER048W-A	ISD11	Protein required for mitochondrial iron-sulfur cluster biosynthesis	Q
4727	VN_4727	YPL183W-A	RTC6	Homolog of the prokaryotic ribosomal protein L36, likely to be a mitochondrial ribosomal protein coded in the nuclear genome; null mutation suppresses cdc13-1 temperature sensitivity	Q
4728	VN_4728	YJL022W	YJL022W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene PET130	Q
4729	VN_4729	YNL086W	YNL086W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to endosomes	Q
4730	VN_4730	YDR139C	RUB1	Ubiquitin-like protein with similarity to mammalian NEDD8; conjugation (neddylation) substrates include the cullins Cdc53p, Rtt101p, and Cul3p; activated by Ula1p and Uba3p (E1 enzyme pair); conjugation mediated by Ubc12p (E2 enzyme)	Q
4731	VN_4731	YGR206W	MVB12	ESCRT-I subunit required to stabilize oligomers of the ESCRT-I core complex (Stp22p, Vps28p, Srm2p), which is involved in ubiquitin-dependent sorting of proteins into the endosome; deletion mutant is sensitive to rapamycin and nystatin	Q
4732	VN_4732	YLR252W	YLR252W	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; partially overlaps the verified gene SYM1, a mitochondrial protein involved in ethanol metabolism	Q

4733	VN_4733	YPR092W	YPR092W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4734	VN_4734	YGR025W	YGR025W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4735	VN_4735	YPL102C	YPL102C	Dubious open reading frame, not conserved in closely related <i>Saccharomyces</i> species; deletion mutation enhances replication of Brome mosaic virus in <i>S. cerevisiae</i> , but this is likely due to effects on the overlapping gene ELP4	Q
4736	VN_4736	YIL008W	URM1	Ubiquitin-like protein with weak sequence similarity to ubiquitin; depends on the E1-like activating enzyme Uba4p; molecular function of the Urm1p pathway is unknown, but it is required for normal growth, particularly at high temperature	Q
4737	VN_4737	YDR322C-A	TIM11	Subunit e of mitochondrial F1F0-ATPase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis; essential for the dimeric and oligomeric state of ATP synthase	Q
4738	VN_4738	YFL010W-A	AUA1	Protein required for the negative regulation by ammonia of Gap1p, which is a general amino acid permease	Q
4739	VN_4739	YPR052C	NHP6A	High-mobility group non-histone chromatin protein, functionally redundant with Nhp6Bp; homologous to mammalian high mobility group proteins 1 and 2; acts to recruit transcription factor Rcs1p to certain promoters	Q
4740	VN_4740	YNL300W	TOS6	Glycosylphosphatidylinositol-dependent cell wall protein, expression is periodic and decreases in response to ergosterol perturbation or upon entry into stationary phase; depletion increases resistance to lactic acid	Q
4741	VN_4741	YBL108W	YBL108W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4742	VN_4742	YHR125W	YHR125W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4743	VN_4743	YLR346C	YLR346C	Putative protein of unknown function found in mitochondria; expression is regulated by transcription factors involved in pleiotropic drug resistance, Pdr1p and Yrr1p; YLR346C is not an essential gene	Q
4744	VN_4744	YJL205C-A		#N/A	Q
4745	VN_4745	YIR020C	YIR020C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4746	VN_4746	YPL251W	YPL251W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data; partially overlaps 5' end of the verified, essential gene YAH1/YPL252C	Q
4747	VN_4747	YKL018C-A	YKL018C-A	Putative protein of unknown function; identified by homology; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	Q
4748	VN_4748	YOL013W-A	YOL013W-A	Putative protein of unknown function; identified by SAGE	Q
4749	VN_4749	YIL058W	YIL058W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4750	VN_4750	YKL096W-A	CWP2	Covalently linked cell wall mannoprotein, major constituent of the cell wall; plays a role in stabilizing the cell wall; involved in low pH resistance; precursor is GPI-anchored	Q
4751	VN_4751	YLR465C	BSC3	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 100% of YLR465C overlaps the uncharacterized ORF YLR464W and 86% of YLR465C overlaps the verified gene YRF1-4	Q
4752	VN_4752	YOL118C	YOL118C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4753	VN_4753	YDR377W	ATP17	Subunit f of the F0 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis	Q
4754	VN_4754	YIL102C	YIL102C	Putative protein of unknown function	Q
4755	VN_4755	YLR366W	YLR366W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the dubious ORF YLR364C-A	Q

4756	VN_4756	YBR032W	YBR032W	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data	Q
4757	VN_4757	YJL150W	YJL150W	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4758	VN_4758	YPL278C	YPL278C	Putative protein of unknown function; gene expression regulated by copper levels	Q
4759	VN_4759	YPL046C	ELC1	Elongin C, involved in transcription elongation as a heterodimer with Ela1p; required for ubiquitin-dependent degradation of Rpo21p; plays a role in global genomic nucleotide excision repair; expression highly upregulated during sporulation	Q
4760	VN_4760	YDL045W-A	MRP10	Mitochondrial ribosomal protein of the small subunit; contains twin cysteine-x9-cysteine motifs	Q
4761	VN_4761	YJL166W	QCR8	Subunit 8 of ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; oriented facing the intermembrane space; expression is regulated by Abf1p and Cpf1p	Q
4762	VN_4762	YDR250C	YDR250C	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data	Q
4763	VN_4763	YML084W	YML084W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4764	VN_4764	YOR277C	YOR277C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; almost completely overlaps the verified gene CAF20	Q
4765	VN_4765	YDR510W	SMT3	Ubiquitin-like protein of the SUMO family, conjugated to lysine residues of target proteins; regulates chromatid cohesion, chromosome segregation, APC-mediated proteolysis, DNA replication and septin ring dynamics; phosphorylated at Ser2	Q
4766	VN_4766	YKL102C	YKL102C	Dubious open reading frame unlikely to encode a functional protein; deletion confers sensitivity to citric acid; predicted protein would include a thiol-disulfide oxidoreductase active site	Q
4767	VN_4767	YMR320W	YMR320W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4768	VN_4768	YML117W-A		#N/A	Strain failed to verify via PCR
4769	VN_4769	YPR096C	YPR096C	Protein of unknown function that may interact with ribosomes, based on co-purification experiments	Q
4770	VN_4770	YPL047W	SGF11	Integral subunit of SAGA histone acetyltransferase complex, regulates transcription of a subset of SAGA-regulated genes, required for the Ubp8p association with SAGA and for H2B deubiquitylation	Q
4771	VN_4771	YDR241W	BUD26	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related <i>Saccharomyces</i> species; 1% of ORF overlaps the verified gene SNU56; diploid mutant displays a weak budding pattern phenotype in a systematic assay	Q
4772	VN_4772	YOR159C	SME1	Core Sm protein Sm E; part of heteroheptameric complex (with Smb1p, Smd1p, Smd2p, Smd3p, Smx3p, and Smx2p) that is part of the spliceosomal U1, U2, U4, and U5 snRNPs; homolog of human Sm E	Q
4773	VN_4773	YGR037C	ACB1	Acyl-CoA-binding protein, transports newly synthesized acyl-CoA esters from fatty acid synthetase (Fas1p-Fas2p) to acyl-CoA-consuming processes	Q
4774	VN_4774	YPR016W-A	YPR016W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4775	VN_4775	YGR008C	STF2	Protein involved in regulation of the mitochondrial F1F0-ATP synthase; Stf1p and Stf2p may act as stabilizing factors that enhance inhibitory action of the Inh1p protein	Q
4776	VN_4776	YMR324C	YMR324C	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; transcription is AZF1 dependent in glycerol-lactate medium and SLT2 dependent in response to the lipid hydroperoxides	Strain failed to verify via PCR
4777	VN_4777	YGL258W-A	YGL258W-A	Putative protein of unknown function	Q

4778	VN_4778	YEL059C-A	SOM1	Subunit of the mitochondrial inner membrane peptidase, which is required for maturation of mitochondrial proteins of the intermembrane space; Som1p facilitates cleavage of a subset of substrates; contains twin cysteine-x9-cysteine motifs	Q
4779	VN_4779	YDR079C-A	TFB5	Component of the RNA polymerase II general transcription and DNA repair factor TFIIF; involved in transcription initiation and in nucleotide-excision repair; homolog of Chlamydomonas reinhardtii REX1-S protein involved in DNA repair	Q
4780	VN_4780	YLL009C	COX17	Copper metallochaperone that transfers copper to Sco1p and Cox11p for eventual delivery to cytochrome c oxidase; contains twin cysteine-x9-cysteine motifs	Q
4781	VN_4781	YBR162W-A	YSY6	Protein whose expression suppresses a secretory pathway mutation in E. coli; has similarity to the mammalian RAMP4 protein involved in secretion	Q
4782	VN_4782	YIR044C	YIR044C	Possible pseudogene in strain S288C; YIR044C and the adjacent ORF, YIR043C, together may encode a non-functional member of the conserved, often subtelomerically-encoded Cos protein family	Strain failed to verify via PCR
4783	VN_4783	YOR298C-A	MBF1	Transcriptional coactivator that bridges the DNA-binding region of Gcn4p and TATA-binding protein Spt15p; suppressor of frameshift mutations	Q
4784	VN_4784	YOL159C-A	YOL159C-A	Putative protein of unknown function; identified by sequence comparison with hemiascomycetous yeast species	Q
4785	VN_4785	YJR135W-A	TIM8	Mitochondrial intermembrane space protein, forms a complex with Tim13p that delivers a subset of hydrophobic proteins to the TIM22 complex for inner membrane insertion; homolog of human TIMM8A, implicated in Mohr-Tranebjaerg syndrome	Q
4786	VN_4786	YPR182W	SMX3	Core Sm protein Sm F; part of heteroheptameric complex (with Smb1p, Smd1p, Smd2p, Smd3p, Sme1p, and Smx2p) that is part of the spliceosomal U1, U2, U4, and U5 snRNPs; homolog of human Sm F	Q
4787	VN_4787	YMR122W-A	YMR122W-A	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and endoplasmic reticulum	Q
4788	VN_4788	YDR379C-A	YDR379C-A	Putative protein of unknown function; identified by homology with other fungi; GFP-fusion protein localized to the mitochondrion	Q
4789	VN_4789	YKL165C-A	YKL165C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4790	VN_4790	YMR194C-A	YMR194C-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4791	VN_4791	YDR320C-A	DAD4	Essential subunit of the Dam1 complex (aka DASH complex), couples kinetochores to the force produced by MT depolymerization thereby aiding in chromosome segregation; is transferred to the kinetochore prior to mitosis	Q
4792	VN_4792	YOR031W	CRS5	Copper-binding metallothionein, required for wild-type copper resistance	Q
4793	VN_4793	YCR102W-A	YCR102W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4794	VN_4794	YOL052C-A	DDR2	Multistress response protein, expression is activated by a variety of xenobiotic agents and environmental or physiological stresses	Q
4795	VN_4795	YGL188C	YGL188C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
4796	VN_4796	YDR363W-A	SEM1	Component of the lid subcomplex of the regulatory subunit of the 26S proteasome; involved in mRNA export mediated by the TREX-2 complex (Sac3p-Thp1p); ortholog of human DSS1	Q
4797	VN_4797	YLR099W-A	YLR099W-A	Putative protein of unknown function	Strain failed to verify via PCR
4798	VN_4798	YBR085C-A	YBR085C-A	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to the nucleus	Q
4799	VN_4799	YNL337W	YNL337W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4800	VN_4800	YDR525W-A	SNA2	Protein of unknown function, has similarity to Pmp3p, which is involved in cation transport; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Strain failed to verify via PCR

4801	VN_4801	YGL260W	YGL260W	Putative protein of unknown function; transcription is significantly increased in a NAP1 deletion background; deletion mutant has increased accumulation of nickel and selenium	Q
4802	VN_4802	YOR008C-A	YOR008C-A	Putative protein of unknown function, includes a potential transmembrane domain; deletion results in slightly lengthened telomeres	Q
4803	VN_4803	YER039C-A	YER039C-A	Putative protein of unknown function; YER039C-A is not an essential gene	Q
4804	VN_4804	YDL085C-A	YDL085C-A	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus	Q
4805	VN_4805	YJL012C-A		#N/A	Q
4806	VN_4806	YKL033W-A	YKL033W-A	Putative protein of unknown function; similar to uncharacterized proteins from other fungi	Q
4807	VN_4807	YDL061C	RPS29B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps29Ap and has similarity to rat S29 and E. coli S14 ribosomal proteins	Q
4808	VN_4808	YLR438C-A	LSM3	Lsm (Like Sm) protein; part of heteroheptameric complexes (Lsm2p-7p and either Lsm1p or 8p); cytoplasmic Lsm1p complex involved in mRNA decay; nuclear Lsm8p complex part of U6 snRNP and possibly involved in processing tRNA, snoRNA, and rRNA	Q
4809	VN_4809	YDL130W-A	STF1	Protein involved in regulation of the mitochondrial F1F0-ATP synthase; Stf1p and Stf2p may act as stabilizing factors that enhance inhibitory action of the Inh1p protein	Q
4810	VN_4810	YDL181W	INH1	Protein that inhibits ATP hydrolysis by the F1F0-ATP synthase; inhibitory function is enhanced by stabilizing proteins Stf1p and Stf2p; has similarity to Stf1p; has a calmodulin-binding motif and binds calmodulin in vitro	Q
4811	VN_4811	YNR077C	YNR077C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4812	VN_4812	YMR175W	SIP18	Phospholipid-binding protein; expression is induced by osmotic stress	Q
4813	VN_4813	YOR304C-A	YOR304C-A	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck	Q
4814	VN_4814	YER091C-A	YER091C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4815	VN_4815	YNL162W-A	YNL162W-A	Putative protein of unknown function; identified by homology	Q
4816	VN_4816	YML058W-A	HUG1	Protein involved in the Mec1p-mediated checkpoint pathway that responds to DNA damage or replication arrest, transcription is induced by DNA damage	Q
4817	VN_4817	YPR002C-A	YPR002C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the Ty1 long terminal repeat, YPRWdelta12	Strain failed to verify via PCR
4818	VN_4818	YDL067C	COX9	Subunit VIIa of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain	Q
4819	VN_4819	YLR388W	RPS29A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps29Bp and has similarity to rat S29 and E. coli S14 ribosomal proteins	Q
4820	VN_4820	YCR020C-A	MAK31	Non-catalytic subunit of N-terminal acetyltransferase of the NatC type; required for replication of dsRNA virus; member of the Sm protein family	Q
4821	VN_4821	YKL053C-A	MDM35	Mitochondrial intermembrane space protein; mutation affects mitochondrial distribution and morphology; contains twin cysteine-x9-cysteine motifs	Q
4822	VN_4822	YJL062W-A	RRG10	Putative protein of unknown function, proposed to be involved in the expression of mitochondrial proteins; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
4823	VN_4823	YPR012W	YPR012W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; YPR012W is not an essential gene	Q
4824	VN_4824	YCR020W-B	HTL1	Component of the RSC chromatin remodeling complex; RSC functions in transcriptional regulation and elongation, chromosome	Q

				stability, and establishing sister chromatid cohesion; involved in telomere maintenance	
4825	VN_4825	YDL185C-A	YDL185C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified gene YDL185W; identified by homology with hemiascomycetous yeast species	Q
4826	VN_4826	YGR291C	YGR291C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4827	VN_4827	YNR001W-A	YNR001W-A	Dubious open reading frame unlikely to encode a functional protein; identified by homology	Q
4828	VN_4828	YMR174C	PAI3	Cytoplasmic proteinase A (Pep4p) inhibitor, dependent on Pbs2p and Hog1p protein kinases for osmotic induction; intrinsically unstructured, N-terminal half becomes ordered in the active site of proteinase A upon contact	Q
4829	VN_4829	YLR262C-A	TMA7	Protein of unknown that associates with ribosomes; null mutant exhibits translation defects, altered polyribosome profiles, and resistance to the translation inhibitor anisomycin	Q
4830	VN_4830	YFR032C-A	RPL29	Protein component of the large (60S) ribosomal subunit, has similarity to rat L29 ribosomal protein; not essential for translation, but required for proper joining of the large and small ribosomal subunits and for normal translation rate	Strain failed to verify via PCR
4831	VN_4831	YPR074W-A	YPR074W-A	Hypothetical protein identified by homology	Q
4832	VN_4832	YLR327C	TMA10	Protein of unknown function that associates with ribosomes	Q
4833	VN_4833	YLR363W-A	YLR363W-A	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus	Q
4834	VN_4834	YLR038C	COX12	Subunit VIb of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; required for assembly of cytochrome c oxidase but not required for activity after assembly; phosphorylated	Q
4835	VN_4835	YLR325C	RPL38	Protein component of the large (60S) ribosomal subunit, has similarity to rat L38 ribosomal protein	Strain failed to verify via PCR
4836	VN_4836	YDR210W	YDR210W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery	Q
4837	VN_4837	YJL156W-A	YJL156W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4838	VN_4838	YHR143W-A	RPC10	RNA polymerase subunit, found in RNA polymerase complexes I, II, and III	Strain failed to verify via PCR
4839	VN_4839	YAR061W	YAR061W	Pseudogene with similarity to Flo1p, which is a lectin-like protein involved in flocculation	Q
4840	VN_4840	YGR271C-A	EFG1	Essential protein required for maturation of 18S rRNA; null mutant is sensitive to hydroxyurea and is delayed in recovering from alpha-factor arrest; green fluorescent protein (GFP)-fusion protein localizes to the nucleolus	Q
4841	VN_4841	YMR251W-A	HOR7	Protein of unknown function; overexpression suppresses Ca ²⁺ sensitivity of mutants lacking inositol phosphorylceramide mannosyltransferases Csg1p and Csh1p; transcription is induced under hyperosmotic stress and repressed by alpha factor	Q
4842	VN_4842	YAR020C	PAU7	Member of the seripauperin multigene family, active during alcoholic fermentation, regulated by anaerobiosis, inhibited by oxygen, repressed by heme	Q
4843	VN_4843	YER019C-A	SBH2	Ssh1p-Sss1p-Sbh2p complex component, involved in protein translocation into the endoplasmic reticulum; homologous to Sbh1p	Q
4844	VN_4844	YMR286W	MRPL33	Mitochondrial ribosomal protein of the large subunit	Q
4845	VN_4845	YCL001W-B	YCL001W-B	Putative protein of unknown function; identified by homology	Q
4846	VN_4846	YBL071W-A	KTI11	Zn-ribbon protein that co-purifies with Dph1 and Dph2 in a complex required for synthesis of diphthamide on translation factor eEF2 and with Elongator subunits Iki3p, Elp2p, and Elp3p involved in	Q

				modification of wobble nucleosides in tRNAs	
4847	VN_4847	YLR395C	COX8	Subunit VIII of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain	Q
4848	VN_4848	YIL174W	YIL174W	Hypothetical protein	Q
4849	VN_4849	YNL259C	ATX1	Cytosolic copper metallochaperone that transports copper to the secretory vesicle copper transporter Ccc2p for eventual insertion into Fet3p, which is a multicopper oxidase required for high-affinity iron uptake	Q
4850	VN_4850	YML009C	MRPL39	Mitochondrial ribosomal protein of the large subunit	Strain failed to verify via PCR
4851	VN_4851	YLR264W	RPS28B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Ap and has similarity to rat S28 ribosomal protein	Q
4852	VN_4852	YHR053C	CUP1-1	Metallothionein, binds copper and mediates resistance to high concentrations of copper and cadmium; locus is variably amplified in different strains, with two copies, CUP1-1 and CUP1-2, in the genomic sequence reference strain S288C	Q
4853	VN_4853	YDR034C-A	YDR034C-A	Putative protein of unknown function; contained within the solo Ty1 LTR element YDRWdelta7	Q
4854	VN_4854	YNL338W	YNL338W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps TEL14L-XC, which is Telomeric X element Core sequence on the left arm of Chromosome XIV	Strain failed to verify via PCR
4855	VN_4855	YGL032C	AGA2	Adhesion subunit of a-agglutinin of a-cells, C-terminal sequence acts as a ligand for alpha-agglutinin (Sag1p) during agglutination, modified with O-linked oligomannosyl chains, linked to anchorage subunit Aga1p via two disulfide bonds	Q
4856	VN_4856	YNL211C	YNL211C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria; YNL211C is not an essential gene	Q
4857	VN_4857	YIR020W-B		#N/A	Q
4858	VN_4858	YFL017W-A	SMX2	Core Sm protein Sm G; part of heteroheptameric complex (with Smb1p, Smd1p, Smd2p, Smd3p, Sme1p, and Smx3p) that is part of the spliceosomal U1, U2, U4, and U5 snRNPs; homolog of human Sm G	Q
4859	VN_4859	YNL015W	PBI2	Cytosolic inhibitor of vacuolar proteinase B, required for efficient vacuole inheritance; with thioredoxin forms protein complex LMA1, which assists in priming SNARE molecules and promotes vacuole fusion	Q
4860	VN_4860	YNR032C-A	HUB1	Ubiquitin-like protein modifier, may function in modification of Sph1p and Hbt1p, functionally complemented by the human or S. pombe ortholog; mechanism of Hub1p adduct formation not yet clear	Q
4861	VN_4861	YOR210W	RPB10	RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III	Strain failed to verify via PCR
4862	VN_4862	YOR167C	RPS28A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp and has similarity to rat S28 ribosomal protein	Q
4863	VN_4863	YHR055C	CUP1-2	Metallothionein, binds copper and mediates resistance to high concentrations of copper and cadmium; locus is variably amplified in different strains, with two copies, CUP1-1 and CUP1-2, in the genomic sequence reference strain S288C	Q
4864	VN_4864	YDR034W-B	YDR034W-B	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery	Q
4865	VN_4865	YHR079C-A	SAE3	Meiosis specific protein involved in DMC1-dependent meiotic recombination, forms heterodimer with Mei5p; proposed to be an assembly factor for Dmc1p	Q
4866	VN_4866	YGR122C-A	YGR122C-A	Dubious open reading frame unlikely to encode a functional protein, similar to YLR334C and YOL106W	Strain failed to verify via PCR
4867	VN_4867	YDL114W-A	YDL114W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; identified based on homology to hemiascomycetous yeasts	Strain failed to verify via PCR

4868	VN_4868	YMR013W-A	YMR013W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the characterized snoRNA gene snR73	Q
4869	VN_4869	YKL162C-A	YKL162C-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4870	VN_4870	YMR046W-A	YMR046W-A	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4871	VN_4871	YER053C-A	YER053C-A	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum	Strain failed to verify via PCR
4872	VN_4872	YDL133C-A	RPL41B	Ribosomal protein L47 of the large (60S) ribosomal subunit, identical to Rpl41Ap and has similarity to rat L41 ribosomal protein; comprised of only 25 amino acids; rpl41a rpl41b double null mutant is viable	Strain failed to verify via PCR
4873	VN_4873	YNL067W-A	YNL067W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
4874	VN_4874	YCR038W-A	YCR038W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; completely overlaps the verified gene BUD5/YCR038C; identified by homology with hemiascomycetous yeast species	Strain failed to verify via PCR
4875	VN_4875	YDR461W	MFA1	Mating pheromone a-factor, made by a cells; interacts with alpha cells to induce cell cycle arrest and other responses leading to mating; biogenesis involves C-terminal modification, N-terminal proteolysis, and export; also encoded by MFA2	Strain failed to verify via PCR
4876	VN_4876	YDL184C	RPL41A	Ribosomal protein L47 of the large (60S) ribosomal subunit, identical to Rpl41Bp and has similarity to rat L41 ribosomal protein; comprised of only 25 amino acids; rpl41a rpl41b double null mutant is viable	Strain failed to verify via PCR
4877	VN_4877	YBR103C-A	YBR103C-A	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; identified by homology to related yeast	Strain failed to verify via PCR
4878	VN_4878	YJL052C-A	YJL052C-A	Putative protein of unknown function, identified based on comparison to related yeast species	Strain failed to verify via PCR
4879	VN_4879	YML007C-A	YML007C-A	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria	Strain failed to verify via PCR
4880	VN_4880	YOR302W	YOR302W	CPA1 uORF , Arginine attenuator peptide, regulates translation of the CPA1 mRNA	Strain failed to verify via PCR
4881	VN_4881	YDL240C-A	YDL240C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; identified by sequence comparison with hemiascomycetous yeast species	Strain failed to verify via PCR
4882	VN_4882	YKL003W-A		#N/A	Strain failed to verify via PCR
4883	VN_4883	YOR314W-A	YOR314W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4884	VN_4884	YBR191W-A	YBR191W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4885	VN_4885	YMR158C-B		#N/A	Strain failed to verify via PCR
4886	VN_4886	YKL106C-A	YKL106C-A	Putative protein of unknown function; identified by homology to uncharacterized proteins in other fungi	Strain failed to verify via PCR
4887	VN_4887	YOR008W-B	YOR008W-B	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4888	VN_4888	YDL247W-A	YDL247W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; identified by	Strain failed to verify via

				sequence comparison with hemiascomycetous yeast species	PCR
4889	VN_4889	YDL159W-A	YDL159W-A	Putative protein of unknown function; identified by sequence comparison with hemiascomycetous yeast species	Strain failed to verify via PCR
4890	VN_4890	YJL127W-A	YJL127W-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4891	VN_4891	YFR012W-A	YFR012W-A	Putative protein of unknown function; identified by homology	Strain failed to verify via PCR
4892	VN_4892	YBL108C-A	PAU9	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions	Strain failed to verify via PCR
4893	VN_4893	YNL145W	MFA2	Mating pheromone a-factor, made by a cells; interacts with alpha cells to induce cell cycle arrest and other responses leading to mating; biogenesis involves C-terminal modification, N-terminal proteolysis, and export; also encoded by MFA1	Strain failed to verify via PCR
4894	VN_4894	YLR149C-A	YLR149C-A	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
4895	VN_4895	YLL040C	VPS13	Protein of unknown function; heterooligomeric or homooligomeric complex; peripherally associated with membranes; homologous to human COH1; involved in sporulation, vacuolar protein sorting and protein-Golgi retention	Strain failed to verify via PCR
4896	VN_4896	YJL005W	CYR1	Adenylate cyclase, required for cAMP production and cAMP-dependent protein kinase signaling; the cAMP pathway controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation	Q
4897	VN_4897	YDR420W	HKR1	Mucin family member that functions as an osmosensor in the Sho1p-mediated HOG pathway with Msb2p; proposed to be a negative regulator of filamentous growth; mutant displays defects in beta-1,3 glucan synthesis and bud site selection	Q
4898	VN_4898	YHL035C	VMR1	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; member of the ATP-binding cassette (ABC) family; potential Cdc28p substrate; detected in purified mitochondria in high-throughput studies	Q
4899	VN_4899	YDR406W	PDR15	Plasma membrane ATP binding cassette (ABC) transporter, multidrug transporter and general stress response factor implicated in cellular detoxification; regulated by Pdr1p, Pdr3p and Pdr8p; promoter contains a PDR responsive element	Q
4900	VN_4900	YOR291W	YPK9	Vacuolar protein with a possible role in sequestering heavy metals; has similarity to the type V P-type ATPase Spf1p; homolog of human ATP13A2 (PARK9), mutations in which are associated with Parkinson disease and Kufo?Rakeb syndrome	Strain failed to verify via PCR
4901	VN_4901	YMR129W	POM152	Nuclear pore membrane glycoprotein; may be involved in duplication of nuclear pores and nuclear pore complexes during S-phase;	Strain failed to verify via PCR
4902	VN_4902	YDR407C	TRS120	One of 10 subunits of the transport protein particle (TRAPP) complex of the cis-Golgi which mediates vesicle docking and fusion; involved in endoplasmic reticulum (ER) to Golgi membrane traffic	Q
4903	VN_4903	YKL201C	MNN4	Putative positive regulator of mannosylphosphate transferase (Mnn6p), involved in mannosylphosphorylation of N-linked oligosaccharides; expression increases in late-logarithmic and stationary growth phases	Q
4904	VN_4904	YIL048W	NEO1	Putative aminophospholipid translocase (flippase) involved in endocytosis and vacuolar biogenesis; localizes to endosomes and the Golgi apparatus	Q
4905	VN_4905	YDR038C	ENA5	Protein with similarity to P-type ATPase sodium pumps, member of the Na ⁺ efflux ATPase family	Q
4906	VN_4906	YCR067C	SED4	Integral endoplasmic reticulum membrane protein, functions as a positive regulator of Sar1p probably through inhibition of GTPase activation by Sec23p; binds Sec16p, participates in vesicle formation, similar to Sec12p	Q

4907	VN_4907	YBR140C	IRA1	GTPase-activating protein that negatively regulates RAS by converting it from the GTP- to the GDP-bound inactive form, required for reducing cAMP levels under nutrient limiting conditions, mediates membrane association of adenylate cyclase	Strain failed to verify via PCR
4908	VN_4908	YDR170C	SEC7	Guanine nucleotide exchange factor (GEF) for ADP ribosylation factors involved in proliferation of the Golgi, intra-Golgi transport and ER-to-Golgi transport; found in the cytoplasm and on Golgi-associated coated vesicles	Q
4909	VN_4909	YDL058W	USO1	Essential protein involved in intracellular protein transport, coiled-coil protein necessary for transport from ER to Golgi; required for assembly of the ER-to-Golgi SNARE complex	Q
4910	VN_4910	YLR310C	CDC25	Membrane bound guanine nucleotide exchange factor (GEF or GDP-release factor); indirectly regulates adenylate cyclase through activation of Ras1p and Ras2p by stimulating the exchange of GDP for GTP; required for progression through G1	Q
4911	VN_4911	YDR135C	YCF1	Vacuolar glutathione S-conjugate transporter of the ATP-binding cassette family, has a role in detoxifying metals such as cadmium, mercury, and arsenite; also transports unconjugated bilirubin; similar to human cystic fibrosis protein CFTR	Q
4912	VN_4912	YIL115C	NUP159	Nucleoporin, subunit of the nuclear pore complex that is found exclusively on the cytoplasmic side, member of the Nup82 subcomplex, required for mRNA export	Q
4913	VN_4913	YER008C	SEC3	Subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p) which mediates targeting of post-Golgi vesicles to sites of active exocytosis; Sec3p specifically is a spatial landmark for secretion	Q
4914	VN_4914	YJL129C	TRK1	Component of the Trk1p-Trk2p potassium transport system; 180 kDa high affinity potassium transporter; phosphorylated in vivo and interacts physically with the phosphatase Ppz1p, suggesting Trk1p activity is regulated by phosphorylation	Q
4915	VN_4915	YNL087W	TCB2	Bud-specific protein with a potential role in membrane trafficking; GFP-fusion protein migrates from the cell surface to intracellular vesicles near vacuole; contains 3 calcium and lipid binding domains; mRNA is targeted to the bud	Q
4916	VN_4916	YLR096W	KIN2	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; closely related to Kin1p	Q
4917	VN_4917	YDR039C	ENA2	P-type ATPase sodium pump, involved in Na ⁺ efflux to allow salt tolerance; likely not involved in Li ⁺ efflux	Q
4918	VN_4918	YPR055W	SEC8	Essential 121kDa subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, and Exo84p), which has the essential function of mediating polarized targeting of secretory vesicles to active sites of exocytosis	Strain failed to verify via PCR
4919	VN_4919	YOL081W	IRA2	GTPase-activating protein that negatively regulates RAS by converting it from the GTP- to the GDP-bound inactive form, required for reducing cAMP levels under nutrient limiting conditions, has similarity to Ira1p and human neurofibromin	Q
4920	VN_4920	YGR296W	YRF1-3	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p	Q
4921	VN_4921	YJL039C	NUP192	Essential structural subunit of the nuclear pore complex (NPC), localizes to the nuclear periphery of nuclear pores, homologous to human p205	Q
4922	VN_4922	YBL017C	PEP1	Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles between the late-Golgi and prevacuolar endosome-like compartments	Q
4923	VN_4923	YOR153W	PDR5	Plasma membrane ATP-binding cassette (ABC) transporter, multidrug transporter actively regulated by Pdr1p; also involved in steroid transport, cation resistance, and cellular detoxification during exponential growth	Q
4924	VN_4924	YBR097W	VPS15	Myristoylated serine/threonine protein kinase involved in vacuolar protein sorting; functions as a membrane-associated complex with Vps34p; active form recruits Vps34p to the Golgi membrane; interacts with the GDP-bound form of Gpa1p	Q

4925	VN_4925	YNR070W	PDR18	Putative transporter of the ATP-binding cassette (ABC) family, implicated in pleiotropic drug resistance; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
4926	VN_4926	YJL080C	SCP160	Essential RNA-binding G protein effector of mating response pathway, mainly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with translating ribosomes via multiple KH domains, similar to vertebrate vigilins	Strain failed to verify via PCR
4927	VN_4927	YAL002W	VPS8	Membrane-associated protein that interacts with Vps21p to facilitate soluble vacuolar protein localization; component of the CORVET complex; required for localization and trafficking of the CPY sorting receptor; contains RING finger motif	Q
4928	VN_4928	YBL022C	PIM1	ATP-dependent Lon protease, involved in degradation of misfolded proteins in mitochondria; required for biogenesis and maintenance of mitochondria	Q
4929	VN_4929	YDR040C	ENA1	P-type ATPase sodium pump, involved in Na ⁺ and Li ⁺ efflux to allow salt tolerance	Strain failed to verify via PCR
4930	VN_4930	YDR122W	KIN1	Serine/threonine protein kinase involved in regulation of exocytosis; localizes to the cytoplasmic face of the plasma membrane; closely related to Kin2p	Q
4931	VN_4931	YBL004W	UTP20	Component of the small-subunit (SSU) processome, which is involved in the biogenesis of the 18S rRNA	Q
4932	VN_4932	YIL149C	MLP2	Myosin-like protein associated with the nuclear envelope, connects the nuclear pore complex with the nuclear interior; involved in the Tel1p pathway that controls telomere length	Q
4933	VN_4933	YER166W	DNF1	Aminophospholipid translocase (flippase) that localizes primarily to the plasma membrane; contributes to endocytosis, protein transport and cell polarity; type 4 P-type ATPase	Q
4934	VN_4934	YPL058C	PDR12	Plasma membrane ATP-binding cassette (ABC) transporter, weak-acid-inducible multidrug transporter required for weak organic acid resistance; induced by sorbate and benzoate and regulated by War1p; mutants exhibit sorbate hypersensitivity	Q
4935	VN_4935	YIL013C	PDR11	ATP-binding cassette (ABC) transporter, multidrug transporter involved in multiple drug resistance; mediates sterol uptake when sterol biosynthesis is compromisedregulated by Pdr1p; required for anaerobic growth	Q
4936	VN_4936	YIL030C	SSM4	Ubiquitin-protein ligase involved in ER-associated protein degradation; located in the ER/nuclear envelope; ssm4 mutation suppresses mRNA instability caused by an rna14 mutation	Q
4937	VN_4937	YGL006W	PMC1	Vacuolar Ca ²⁺ ATPase involved in depleting cytosol of Ca ²⁺ ions; prevents growth inhibition by activation of calcineurin in the presence of elevated concentrations of calcium; similar to mammalian PMCA1a	Q
4938	VN_4938	YNL192W	CHS1	Chitin synthase I, requires activation from zymogenic form in order to catalyze the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for repairing the chitin septum during cytokinesis; transcription activated by mating factor	Q
4939	VN_4939	YGL156W	AMS1	Vacuolar alpha mannosidase, involved in free oligosaccharide (fOS) degradation; delivered to the vacuole in a novel pathway separate from the secretory pathway	Q
4940	VN_4940	YML075C	HMG1	One of two isozymes of HMG-CoA reductase that catalyzes the conversion of HMG-CoA to mevalonate, which is a rate-limiting step in sterol biosynthesis; localizes to the nuclear envelope; overproduction induces the formation of karmellae	Q
4941	VN_4941	YKL203C	TOR2	PIK-related protein kinase and rapamycin target; subunit of TORC1, a complex that regulates growth in response to nutrients and TORC2, a complex that regulates cell-cycle dependent polarization of the actin cytoskeleton; involved in meiosis	Strain failed to verify via PCR
4942	VN_4942	YGR032W	GSC2	Catalytic subunit of 1,3-beta-glucan synthase, involved in formation of the inner layer of the spore wall; activity positively regulated by Rho1p and negatively by Smk1p; has similarity to an alternate catalytic subunit, Fks1p (Gsc1p)	Q
4943	VN_4943	YLL048C	YBT1	Transporter of the ATP-binding cassette (ABC) family involved in bile acid transport; similar to mammalian bile transporters	Strain failed to verify via

					PCR
4944	VN_4944	YOR328W	PDR10	ATP-binding cassette (ABC) transporter, multidrug transporter involved in the pleiotropic drug resistance network; regulated by Pdr1p and Pdr3p	Q
4945	VN_4945	YBL079W	NUP170	Subunit of the nuclear pore complex (NPC), required for NPC localization of specific nucleoporins; involved in nuclear envelope permeability and chromosome segregation; has similar to Nup157p; essential role, with Nup157p, in NPC assembly	Q
4946	VN_4946	YGL092W	NUP145	Essential nucleoporin, catalyzes its own cleavage in vivo to generate a C-terminal fragment that assembles into the Nup84p subcomplex of the nuclear pore complex, and an N-terminal fragment of unknown function that is homologous to Nup100p	Q
4947	VN_4947	YKR103W	NFT1	Putative transporter of the multidrug resistance-associated protein (MRP) subfamily; adjacent ORFs YKR103W and YKR104W are merged in different strain backgrounds.	Q
4948	VN_4948	YPL006W	NCR1	Vacuolar membrane protein that transits through the biosynthetic vacuolar protein sorting pathway, involved in sphingolipid metabolism; glycoprotein and functional orthologue of human Niemann Pick C1 (NPC1) protein	Q
4949	VN_4949	YBR235W	YBR235W	Putative ion transporter, similar to mammalian electroneutral Na ⁽⁺⁾ -(K ⁺)-C1- cotransporter family; YBR235W is not an essential gene	Q
4950	VN_4950	YKL020C	SPT23	ER membrane protein involved in regulation of OLE1 transcription, acts with homolog Mga2p; inactive ER form dimerizes and one subunit is then activated by ubiquitin/proteasome-dependent processing followed by nuclear targeting	Q
4951	VN_4951	YCR011C	ADP1	Putative ATP-dependent permease of the ABC transporter family of proteins	Q
4952	VN_4952	YJR066W	TOR1	PIK-related protein kinase and rapamycin target; subunit of TORC1, a complex that controls growth in response to nutrients by regulating translation, transcription, ribosome biogenesis, nutrient transport and autophagy; involved in meiosis	Q
4953	VN_4953	YMR162C	DNF3	Aminophospholipid translocase (flippase) that maintains membrane lipid asymmetry in post-Golgi secretory vesicles; localizes to the trans-Golgi network; likely involved in protein transport; type 4 P-type ATPase	Q
4954	VN_4954	YLL015W	BPT1	ABC type transmembrane transporter of MRP/CFTR family, found in vacuolar membrane, involved in the transport of unconjugated bilirubin and in heavy metal detoxification via glutathione conjugates, along with Ycf1p	Q
4955	VN_4955	YDR011W	SNQ2	Plasma membrane ATP-binding cassette (ABC) transporter, multidrug transporter involved in multidrug resistance and resistance to singlet oxygen species	Q
4956	VN_4956	YER105C	NUP157	Abundant subunit of the nuclear pore complex (NPC), present on both sides of the NPC; has similarity to Nup170p; essential role, with Nup170p, in NPC assembly	Q
4957	VN_4957	YGR014W	MSB2	Mucin family member involved in the Cdc42p- and MAP kinase-dependent filamentous growth signaling pathway; also functions as an osmosensor in parallel to the Sho1p-mediated pathway; potential Cdc28p substrate	Q
4958	VN_4958	YBR295W	PCA1	Cadmium transporting P-type ATPase; may also have a role in copper and iron homeostasis; stabilized by Cd binding, which prevents ubiquitination; S288C and other lab strains contain a G970R mutation which eliminates Cd transport function	Q
4959	VN_4959	YBR023C	CHS3	Chitin synthase III, catalyzes the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for synthesis of the majority of cell wall chitin, the chitin ring during bud emergence, and spore wall chitosan	Q
4960	VN_4960	YHR079C	IRE1	Serine-threonine kinase and endoribonuclease; transmembrane protein that mediates the unfolded protein response (UPR) by regulating Hac1p synthesis through HAC1 mRNA splicing; Kar2p binds inactive Ire1p and releases from it upon ER stress	Q
4961	VN_4961	YGL016W	KAP122	Karyopherin beta, responsible for import of the Toa1p-Toa2p complex into the nucleus; binds to nucleoporins Nup1p and Nup2p; may play a role in regulation of pleiotropic drug resistance	Q

4962	VN_4962	YKR095W	MLP1	Myosin-like protein associated with the nuclear envelope, connects the nuclear pore complex with the nuclear interior; involved with Tel1p in telomere length control; involved with Pml1p and Pml39p in nuclear retention of unspliced mRNAs	Strain failed to verify via PCR
4963	VN_4963	YML103C	NUP188	Subunit of the nuclear pore complex (NPC), involved in the structural organization of the complex and of the nuclear envelope, also involved in nuclear envelope permeability, interacts with Pom152p and Nic96p	Q
4964	VN_4964	YIL173W	VTH1	Putative membrane glycoprotein with strong similarity to Vth2p and Pep1p/Vps10p, may be involved in vacuolar protein sorting	Q
4965	VN_4965	YIR006C	PAN1	Part of actin cytoskeleton-regulatory complex Pan1p-Sla1p-End3p, associates with actin patches on the cell cortex; promotes protein-protein interactions essential for endocytosis; previously thought to be a subunit of poly(A) ribonuclease	Q
4966	VN_4966	YJR033C	RAV1	Subunit of the RAVE complex (Rav1p, Rav2p, Skp1p), which promotes assembly of the V-ATPase holoenzyme; required for transport between the early and late endosome/PVC and for localization of TGN membrane proteins; potential Cdc28p substrate	Q
4967	VN_4967	YOL075C	YOL075C	Putative ABC transporter	Strain failed to verify via PCR
4968	VN_4968	YEL031W	SPF1	P-type ATPase, ion transporter of the ER membrane involved in ER function and Ca ²⁺ homeostasis; required for regulating Hmg2p degradation; confers sensitivity to a killer toxin (SMKT) produced by <i>Pichia farinosa</i> KK1	Q
4969	VN_4969	YNL054W	VAC7	Integral vacuolar membrane protein involved in vacuole inheritance and morphology; activates Fab1p kinase activity under basal conditions and also after hyperosmotic shock	Strain failed to verify via PCR
4970	VN_4970	YIR033W	MGA2	ER membrane protein involved in regulation of OLE1 transcription, acts with homolog Spt23p; inactive ER form dimerizes and one subunit is then activated by ubiquitin/proteasome-dependent processing followed by nuclear targeting	Strain failed to verify via PCR
4971	VN_4971	YOR098C	NUP1	Nuclear pore complex (NPC) subunit, involved in protein import/export and in export of RNAs, possible karyopherin release factor that accelerates release of karyopherin-cargo complexes after transport across NPC; potential Cdc28p substrate	Q
4972	VN_4972	YLR450W	HMG2	One of two isozymes of HMG-CoA reductase that convert HMG-CoA to mevalonate, a rate-limiting step in sterol biosynthesis; overproduction induces assembly of peripheral ER membrane arrays and short nuclear-associated membrane stacks	Q
4973	VN_4973	YGR217W	CCH1	Voltage-gated high-affinity calcium channel involved in calcium influx in response to some environmental stresses as well as exposure to mating pheromones; interacts and co-localizes with Mid1p, suggesting Cch1p and Mid1p function together	Q
4974	VN_4974	YFL007W	BLM10	Proteasome activator subunit; found in association with core particles, with and without the 19S regulatory particle; required for resistance to bleomycin, may be involved in protecting against oxidative damage; similar to mammalian PA200	Strain failed to verify via PCR
4975	VN_4975	YDR093W	DNF2	Aminophospholipid translocase (flippase) that localizes primarily to the plasma membrane; contributes to endocytosis, protein transport and cell polarity; type 4 P-type ATPase	Q
4976	VN_4976	YJL222W	VTH2	Putative membrane glycoprotein with strong similarity to Vth1p and Pep1p/Vps10p, may be involved in vacuolar protein sorting	Q
4977	VN_4977	YGR281W	YOR1	Plasma membrane ATP-binding cassette (ABC) transporter, multidrug transporter mediates export of many different organic anions including oligomycin; similar to human cystic fibrosis transmembrane receptor (CFTR)	Q
4978	VN_4978	YAL026C	DRS2	Aminophospholipid translocase (flippase) that maintains membrane lipid asymmetry in post-Golgi secretory vesicles; contributes to clathrin-coated vesicle formation and endocytosis; mutations in human homolog ATP8B1 result in liver disease	Q
4979	VN_4979	YKL209C	STE6	Plasma membrane ATP-binding cassette (ABC) transporter required for the export of a-factor, catalyzes ATP hydrolysis coupled to a-factor transport; contains 12 transmembrane domains and two ATP binding domains; expressed only in MATa cells	Q

4980	VN_4980	YDL145C	COP1	Alpha subunit of COPI vesicle coatamer complex, which surrounds transport vesicles in the early secretory pathway	Strain failed to verify via PCR
4981	VN_4981	YKR082W	NUP133	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), localizes to both sides of the NPC, required to establish a normal nucleocytoplasmic concentration gradient of the GTPase Gsp1p	Q
4982	VN_4982	YMR047C	NUP116	Subunit of the Nup82 subcomplex of the nuclear pore complex; localized to both sides of the pore; contains a repetitive GLFG motif that interacts with mRNA export factor Mex67p and with karyopherin Kap95p; homologous to Nup100p	Strain failed to verify via PCR
4983	VN_4983	YDL185W	TFP1	Subunit A of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-SceI), which is a site-specific endonuclease	Strain failed to verify via PCR
4984	VN_4984	YDR270W	CCC2	Cu(+2)-transporting P-type ATPase, required for export of copper from the cytosol into an extracytosolic compartment; has similarity to human proteins involved in Menkes and Wilsons diseases	Strain failed to verify via PCR
4985	VN_4985	YKL064W	MNR2	Vacuolar membrane protein required for magnesium homeostasis; putative magnesium transporter; has similarity to Alr1p and Alr2p, which mediate influx of Mg ²⁺ and other divalent cations	Q
4986	VN_4986	YBR229C	ROT2	Glucosidase II catalytic subunit required for normal cell wall synthesis; mutations in rot2 suppress tor2 mutations, and are synthetically lethal with rot1 mutations	Q
4987	VN_4987	YOR219C	STE13	Dipeptidyl aminopeptidase, Golgi integral membrane protein that cleaves on the carboxyl side of repeating -X-Ala- sequences, required for maturation of alpha factor, transcription is induced by a-factor	Q
4988	VN_4988	YMR273C	ZDS1	Protein that interacts with silencing proteins at the telomere, involved in transcriptional silencing; has a role in localization of PKA subunit Bcy1p; implicated in mRNA nuclear export; involved in mitotic exit through regulation of Cdc14p	Q
4989	VN_4989	YNR013C	PHO91	Low-affinity phosphate transporter of the vacuolar membrane; deletion of pho84, pho87, pho89, pho90, and pho91 causes synthetic lethality; transcription independent of Pi and Pho4p activity; overexpression results in vigorous growth	Q
4990	VN_4990	YNL049C	SFB2	Probable component of COPII coated vesicles that binds to Sec23p; similar to and functionally redundant with Sec24p, but expressed at low levels; involved in ER to Golgi transport and in autophagy	Q
4991	VN_4991	YDR160W	SSY1	Component of the SPS plasma membrane amino acid sensor system (Ssy1p-Ptr3p-Ssy5p), which senses external amino acid concentration and transmits intracellular signals that result in regulation of expression of amino acid permease genes	Q
4992	VN_4992	YJL062W	LAS21	Integral plasma membrane protein involved in the synthesis of the glycosylphosphatidylinositol (GPI) core structure; mutations affect cell wall integrity	Q
4993	VN_4993	YDL095W	PMT1	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; one of seven related proteins involved in O-glycosylation which is essential for cell wall rigidity	Q
4994	VN_4994	YFR030W	MET10	Subunit alpha of assimilatory sulfite reductase, which converts sulfite into sulfide	Q
4995	VN_4995	YDL149W	ATG9	Transmembrane protein involved in forming Cvt and autophagic vesicles; cycles between the phagophore assembly site (PAS) and other cytosolic punctate structures, not found in autophagosomes; may be involved in membrane delivery to the PAS	Q
4996	VN_4996	YNL243W	SLA2	Transmembrane actin-binding protein involved in membrane cytoskeleton assembly and cell polarization; adaptor protein that links actin to clathrin and endocytosis; present in the actin cortical patch of the emerging bud tip; dimer in vivo	Q
4997	VN_4997	YHR098C	SFB3	Member of the Sec24p family; forms a complex, with Sec23p, that is involved in sorting of Pma1p into COPII vesicles; peripheral ER membrane protein; potential Cdc28p substrate	Q
4998	VN_4998	YLR309C	IMH1	Protein involved in vesicular transport, mediates transport between an endosomal compartment and the Golgi, contains a Golgi-localization	Q

				(GRIP) domain that interacts with activated Arl1p-GTP to localize Imh1p to the Golgi	
4999	VN_4999	YLR092W	SUL2	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates	Q
5000	VN_5000	YLR240W	VPS34	Phosphatidylinositol 3-kinase responsible for the synthesis of phosphatidylinositol 3-phosphate; forms membrane-associated signal transduction complex with Vps15p to regulate protein sorting; activated by the GTP-bound form of Gpa1p	Q
5001	VN_5001	YDR351W	SBE2	Protein involved in the transport of cell wall components from the Golgi to the cell surface; required for bud growth	Q
5002	VN_5002	YHR103W	SBE22	Protein involved in the transport of cell wall components from the Golgi to the cell surface; similar in structure and functionally redundant with Sbe2p; involved in bud growth	Q
5003	VN_5003	YFL004W	VTC2	Subunit of the vacuolar transporter chaperone (VTC) complex involved in membrane trafficking, vacuolar polyphosphate accumulation, microautophagy and non-autophagic vacuolar fusion	Q
5004	VN_5004	YNL238W	KEX2	Subtilisin-like protease (proprotein convertase), a calcium-dependent serine protease involved in the activation of proproteins of the secretory pathway	Q
5005	VN_5005	YPR032W	SRO7	Effector of Rab GTPase Sec4p, forms a complex with Sec4p and t-SNARE Sec9p; involved in exocytosis and docking and fusion of post-Golgi vesicles with plasma membrane; homolog of Sro77p and Drosophila lgl tumor suppressor	Q
5006	VN_5006	YHR027C	RPN1	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine-rich repeat (LRR) domain, a site for protein-protein interactions	Q
5007	VN_5007	YLR067C	PET309	Specific translational activator for the COX1 mRNA, also influences stability of intron-containing COX1 primary transcripts; localizes to the mitochondrial inner membrane; contains seven pentatricopeptide repeats (PPRs)	Q
5008	VN_5008	YMR266W	RSN1	Membrane protein of unknown function; overexpression suppresses NaCl sensitivity of sro7 mutant cells by restoring sodium pump (Ena1p) localization to the plasma membrane	Q
5009	VN_5009	YIL109C	SEC24	Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the binding of the Sec13 complex to ER membranes; homologous to Lst1p and Lss1p	Strain failed to verify via PCR
5010	VN_5010	YGL233W	SEC15	Essential 113kDa subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, and Exo84p), which mediates polarized targeting of vesicles to active sites of exocytosis; Sec15p associates with Sec4p and vesicles	Q
5011	VN_5011	YMR054W	STV1	Subunit a of the vacuolar-ATPase V0 domain, one of two isoforms (Stv1p and Vph1p); Stv1p is located in V-ATPase complexes of the Golgi and endosomes while Vph1p is located in V-ATPase complexes of the vacuole	Q
5012	VN_5012	YJL094C	KHA1	Putative K ⁺ /H ⁺ antiporter with a probable role in intracellular cation homeostasis, localized to Golgi vesicles and detected in highly purified mitochondria in high-throughput studies	Q
5013	VN_5013	YJL041W	NSP1	Essential component of the nuclear pore complex, which mediates nuclear import and export, found in both the Nup82 and Nic96 complexes	Q
5014	VN_5014	YMR302C	YME2	Integral inner mitochondrial membrane protein with a role in maintaining mitochondrial nucleoid structure and number; mutants exhibit an increased rate of mitochondrial DNA escape; shows some sequence similarity to exonucleases	Q
5015	VN_5015	YKL176C	LST4	Protein possibly involved in a post-Golgi secretory pathway; required for the transport of nitrogen-regulated amino acid permease Gap1p from the Golgi to the cell surface	Strain failed to verify via PCR
5016	VN_5016	YGR261C	APL6	Beta3-like subunit of the yeast AP-3 complex; functions in transport of alkaline phosphatase to the vacuole via the alternate pathway; exists in both cytosolic and peripherally associated membrane-bound pools	Q

5017	VN_5017	YPL125W	KAP120	Karyopherin responsible for the nuclear import of ribosome maturation factor Rfp1p	Strain failed to verify via PCR
5018	VN_5018	YDR080W	VPS41	Vacuolar membrane protein that is a subunit of the homotypic vacuole fusion and vacuole protein sorting (HOPS) complex; essential for membrane docking and fusion at the Golgi-to-endosome and endosome-to-vacuole stages of protein transport	Q
5019	VN_5019	YBR038W	CHS2	Chitin synthase II; catalyzes transfer of N-acetylglucosamine (GlcNAc) to chitin upon activation of zymogenic form; required for chitin synthesis in the primary septum during cytokinesis; localization regulated by Cdk1p during mitosis	Q
5020	VN_5020	YGL167C	PMR1	High affinity Ca ²⁺ /Mn ²⁺ P-type ATPase required for Ca ²⁺ and Mn ²⁺ transport into Golgi; involved in Ca ²⁺ dependent protein sorting and processing; mutations in human homolog ATP2C1 cause acantholytic skin condition Hailey-Hailey disease	Q
5021	VN_5021	YCR037C	PHO87	Low-affinity inorganic phosphate (Pi) transporter, involved in activation of PHO pathway; expression is independent of Pi concentration and Pho4p activity; contains 12 membrane-spanning segments	Q
5022	VN_5022	YNL321W	VNX1	Low affinity vacuolar membrane localized monovalent cation/H ⁺ antiporter; member of the calcium exchanger (CAX) family; potential Cdc28p substrate	Q
5023	VN_5023	YDR027C	VPS54	Component of the GARP (Golgi-associated retrograde protein) complex, Vps51p-Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; potentially phosphorylated by Cdc28p	Q
5024	VN_5024	YOR329C	SCD5	Protein required for normal actin organization and endocytosis; targeting subunit for protein phosphatase type 1; undergoes Crm1p-dependent nuclear-cytoplasmic shuttling; multicopy suppressor of clathrin deficiency	Q
5025	VN_5025	YBR294W	SUL1	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates	Q
5026	VN_5026	YOR270C	VPB1	Subunit a of vacuolar-ATPase V0 domain, one of two isoforms (Vph1p and Stv1p); Vph1p is located in V-ATPase complexes of the vacuole while Stv1p is located in V-ATPase complexes of the Golgi and endosomes	Q
5027	VN_5027	YMR089C	YTA12	Component, with Afg3p, of the mitochondrial inner membrane m-AAA protease that mediates degradation of misfolded or unassembled proteins and is also required for correct assembly of mitochondrial enzyme complexes	Q
5028	VN_5028	YIL068C	SEC6	Essential 88kDa subunit of the exocyst complex, which mediates polarized targeting of secretory vesicles to active sites of exocytosis; dimeric form of Sec6p interacts with Sec9p in vitro and inhibits t-SNARE assembly	Q
5029	VN_5029	YNL329C	PEX6	AAA-peroxin that heterodimerizes with AAA-peroxin Pex1p and participates in the recycling of peroxisomal signal receptor Pex5p from the peroxisomal membrane to the cytosol	Q
5030	VN_5030	YOL084W	PHM7	Protein of unknown function, expression is regulated by phosphate levels; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery and vacuole	Strain failed to verify via PCR
5031	VN_5031	YDL035C	GPR1	Plasma membrane G protein coupled receptor (GPCR) that interacts with the heterotrimeric G protein alpha subunit, Gpa2p, and with Plc1p; sensor that integrates nutritional signals with the modulation of cell fate via PKA and cAMP synthesis	Q
5032	VN_5032	YPL036W	PMA2	Plasma membrane H ⁺ -ATPase, isoform of Pma1p, involved in pumping protons out of the cell; regulator of cytoplasmic pH and plasma membrane potential	Q
5033	VN_5033	YBR033W	EDS1	Putative zinc cluster protein; YBR033W is not an essential gene	Q
5034	VN_5034	YIL047C	SYG1	Plasma membrane protein of unknown function; truncation and overexpression suppresses lethality of G-alpha protein deficiency	Q
5035	VN_5035	YKR050W	TRK2	Component of the Trk1p-Trk2p potassium transport system	Q

5036	VN_5036	YLR166C	SEC10	Essential 100kDa subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, and Exo84p), which has the essential function of mediating polarized targeting of secretory vesicles to active sites of exocytosis	Q
5037	VN_5037	YOL130W	ALR1	Plasma membrane Mg(2+) transporter, expression and turnover are regulated by Mg(2+) concentration; overexpression confers increased tolerance to Al(3+) and Ga(3+) ions	Q
5038	VN_5038	YFR002W	NIC96	Component of the nuclear pore complex, required for nuclear pore formation; forms a subcomplex with Nsp1p, Nup57p, and Nup49p	Q
5039	VN_5039	YIL140W	AXL2	Integral plasma membrane protein required for axial budding in haploid cells, localizes to the incipient bud site and bud neck; glycosylated by Pmt4p; potential Cdc28p substrate	Q
5040	VN_5040	YER157W	COG3	Essential component of the conserved oligomeric Golgi complex (Cog1p through Cog8p), a cytosolic tethering complex that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments	Q
5041	VN_5041	YFL025C	BST1	GPI inositol deacylase of the ER that negatively regulates COPII vesicle formation, prevents production of vesicles with defective subunits, required for proper discrimination between resident ER proteins and Golgi-bound cargo molecules	Q
5042	VN_5042	YLR138W	NHA1	Na ⁺ /H ⁺ antiporter involved in sodium and potassium efflux through the plasma membrane; required for alkali cation tolerance at acidic pH	Q
5043	VN_5043	YGL238W	CSE1	Nuclear envelope protein that mediates the nuclear export of importin alpha (Srp1p), homolog of metazoan CAS protein, required for accurate chromosome segregation	Q
5044	VN_5044	YBR086C	IST2	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process	Q
5045	VN_5045	YKL165C	MCD4	Protein involved in glycosylphosphatidylinositol (GPI) anchor synthesis; multimembrane-spanning protein that localizes to the endoplasmic reticulum; highly conserved among eukaryotes	Q
5046	VN_5046	YOR211C	MGM1	Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p and Fzo1p; required for normal morphology of cristae and for stability of Tim11p; homolog of human OPA1 involved in autosomal dominant optic atrophy	Q
5047	VN_5047	YDL194W	SNF3	Plasma membrane low glucose sensor that regulates glucose transport; contains 12 predicted transmembrane segments and a long C-terminal tail required for induction of hexose transporters; also senses fructose and mannose; similar to Rgt2p	Q
5048	VN_5048	YPL147W	PXA1	Subunit of a heterodimeric peroxisomal ATP-binding cassette transporter complex (Pxa1p-Pxa2p), required for import of long-chain fatty acids into peroxisomes; similarity to human adrenoleukodystrophy transporter and ALD-related proteins	Q
5049	VN_5049	YFL050C	ALR2	Probable Mg(2+) transporter; overexpression confers increased tolerance to Al(3+) and Ga(3+) ions; plays a role in regulating Ty1 transposition	Strain failed to verify via PCR
5050	VN_5050	YPL019C	VTC3	Subunit of the vacuolar transporter chaperone (VTC) complex involved in membrane trafficking, vacuolar polyphosphate accumulation, microautophagy and non-autophagic vacuolar fusion	Q
5051	VN_5051	YMR257C	PET111	Mitochondrial translational activator specific for the COX2 mRNA; located in the mitochondrial inner membrane	Q
5052	VN_5052	YMR231W	PEP5	Component of CORVET tethering complex; peripheral vacuolar membrane protein required for protein trafficking and vacuole biogenesis; interacts with Pep7p	Q
5053	VN_5053	YDR238C	SEC26	Essential beta-coat protein of the COPI coatomer, involved in ER-to-Golgi protein trafficking and maintenance of normal ER morphology; shares 43% sequence identity with mammalian beta-coat protein (beta-COP)	Q
5054	VN_5054	YKL068W	NUP100	Subunit of the nuclear pore complex (NPC) that is localized to both sides of the pore; contains a repetitive GLFG motif that interacts with mRNA export factor Mex67p and with karyopherin Kap95p; homologous to Nup116p	Q

5055	VN_5055	YNL287W	SEC21	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo	Q
5056	VN_5056	YGL008C	PMA1	Plasma membrane H ⁺ -ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases	Q
5057	VN_5057	YJL198W	PHO90	Low-affinity phosphate transporter; deletion of pho84, pho87, pho89, pho90, and pho91 causes synthetic lethality; transcription independent of Pi and Pho4p activity; overexpression results in vigorous growth	Q
5058	VN_5058	YGR157W	CHO2	Phosphatidylethanolamine methyltransferase (PEMT), catalyzes the first step in the conversion of phosphatidylethanolamine to phosphatidylcholine during the methylation pathway of phosphatidylcholine biosynthesis	Q
5059	VN_5059	YBR179C	FZO1	Mitofusin, mitochondrial integral membrane protein involved in mitochondrial fusion and mitochondrial genome maintenance; contains N-terminal GTPase domain; targeted for destruction by cytosolic components of the ubiquitin-proteasome system	Q
5060	VN_5060	YPL270W	MDL2	Mitochondrial inner membrane half-type ATP-binding cassette (ABC) transporter	Q
5061	VN_5061	YOR017W	PET127	Protein with a role in 5'-end processing of mitochondrial RNAs, located in the mitochondrial membrane	Q
5062	VN_5062	YBL106C	SRO77	Protein with roles in exocytosis and cation homeostasis; functions in docking and fusion of post-Golgi vesicles with plasma membrane; homolog of Sro7p and Drosophila lethal giant larvae tumor suppressor; interacts with SNARE protein Sec9p	Q
5063	VN_5063	YDR166C	SEC5	Essential 107kDa subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, and Exo84p), which has the essential function of mediating polarized targeting of secretory vesicles to active sites of exocytosis	Q
5064	VN_5064	YGL137W	SEC27	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP	Q
5065	VN_5065	YPL195W	APL5	Delta adaptin-like subunit of the clathrin associated protein complex (AP-3); functions in transport of alkaline phosphatase to the vacuole via the alternate pathway, suppressor of loss of casein kinase 1 function	Q
5066	VN_5066	YLR148W	PEP3	Component of CORVET tethering complex; vacuolar peripheral membrane protein that promotes vesicular docking/fusion reactions in conjunction with SNARE proteins, required for vacuolar biogenesis	Q
5067	VN_5067	YLR373C	VID22	Glycosylated integral membrane protein localized to the plasma membrane; plays a role in fructose-1,6-bisphosphatase (FBPase) degradation; involved in FBPase transport from the cytosol to Vid (vacuole import and degradation) vesicles	Q
5068	VN_5068	YPR194C	OPT2	Oligopeptide transporter; member of the OPT family, with potential orthologs in <i>S. pombe</i> and <i>C. albicans</i> ; also plays a role in formation of mature vacuoles	Q
5069	VN_5069	YKL188C	PXA2	Subunit of a heterodimeric peroxisomal ATP-binding cassette transporter complex (Pxa1p-Pxa2p), required for import of long-chain fatty acids into peroxisomes; similarity to human adrenoleukodystrophy transporter and ALD-related proteins	Q
5070	VN_5070	YLR207W	HRD3	Resident protein of the ER membrane that plays a central role in ER-associated protein degradation (ERAD), forms HRD complex with Hrd1p and ERAD determinants that engages in lumen to cytosol communication and coordination of ERAD events	Q
5071	VN_5071	YJL212C	OPT1	Proton-coupled oligopeptide transporter of the plasma membrane; also transports glutathione and phytochelatins; member of the OPT family	Q
5072	VN_5072	YPL221W	FLC1	Putative FAD transporter; required for uptake of FAD into endoplasmic reticulum; involved in cell wall maintenance	Strain failed to verify via PCR
5073	VN_5073	YPR181C	SEC23	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p	Strain failed to verify via PCR

5074	VN_5074	YGL021W	ALK1	Protein kinase; accumulation and phosphorylation are periodic during the cell cycle; phosphorylated in response to DNA damage; contains characteristic motifs for degradation via the APC pathway; similar to Alk2p and to mammalian haspkins	Q
5075	VN_5075	YOR321W	PMT3	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex with Pmt5p, can instead interact with Pmt1p in some conditions; target for new antifungals	Q
5076	VN_5076	YNR060W	FRE4	Ferric reductase, reduces a specific subset of siderophore-bound iron prior to uptake by transporters; expression induced by low iron levels	Strain failed to verify via PCR
5077	VN_5077	YER113C	TMN3	Protein with a role in cellular adhesion and filamentous growth; similar to Emp70p and Tmn2p; member of Transmembrane Nine family with 9 transmembrane segments; localizes to Golgi; induced by 8-methoxypsoralen plus UVA irradiation	Q
5078	VN_5078	YDR338C	YDR338C	Putative protein of unknown function	Q
5079	VN_5079	YBR043C	QDR3	Multidrug transporter of the major facilitator superfamily, required for resistance to quinidine, barban, cisplatin, and bleomycin	Strain failed to verify via PCR
5080	VN_5080	YLR413W	YLR413W	Putative protein of unknown function; YLR413W is not an essential gene	Strain failed to verify via PCR
5081	VN_5081	YNL279W	PRM1	Pheromone-regulated multispinning membrane protein involved in membrane fusion during mating; predicted to have 5 transmembrane segments and a coiled coil domain; localizes to the shmoo tip; regulated by Ste12p	Q
5082	VN_5082	YJL073W	JEM1	DnaJ-like chaperone required for nuclear membrane fusion during mating, localizes to the ER membrane; exhibits genetic interactions with KAR2	Strain failed to verify via PCR
5083	VN_5083	YAL053W	FLC2	Putative FAD transporter; required for uptake of FAD into endoplasmic reticulum; involved in cell wall maintenance	Q
5084	VN_5084	YDR264C	AKR1	Palmitoyl transferase involved in protein palmitoylation; acts as a negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; contains ankyrin repeats	Q
5085	VN_5085	YBL011W	SCT1	Glycerol 3-phosphate/dihydroxyacetone phosphate dual substrate-specific sn-1 acyltransferase of the glycerolipid biosynthesis pathway, prefers 16-carbon fatty acids, similar to Gpt2p, gene is constitutively transcribed	Strain failed to verify via PCR
5086	VN_5086	YPR024W	YME1	Catalytic subunit of the mitochondrial inner membrane i-AAA protease complex, which is responsible for degradation of unfolded or misfolded mitochondrial gene products; mutation causes an elevated rate of mitochondrial turnover	Strain failed to verify via PCR
5087	VN_5087	YGL022W	STT3	Subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; forms a subcomplex with Ost3p and Ost4p and is directly involved in catalysis	Q
5088	VN_5088	YOL060C	MAM3	Protein required for normal mitochondrial morphology, has similarity to hemolysins	Q
5089	VN_5089	YLR188W	MDL1	Mitochondrial inner membrane half-type ATP-binding cassette (ABC) transporter, mediates export of peptides generated upon proteolysis of mitochondrial proteins, plays a role in the regulation of cellular resistance to oxidative stress	Strain failed to verify via PCR
5090	VN_5090	YAR035W	YAT1	Outer mitochondrial carnitine acetyltransferase, minor ethanol-inducible enzyme involved in transport of activated acyl groups from the cytoplasm into the mitochondrial matrix; phosphorylated	Strain failed to verify via PCR
5091	VN_5091	YNL125C	ESBP6	Protein with similarity to monocarboxylate permeases, appears not to be involved in transport of monocarboxylates such as lactate, pyruvate or acetate across the plasma membrane	Q
5092	VN_5092	YOR273C	TPO4	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major facilitator superfamily	Q

5093	VN_5093	YLR241W	YLR241W	Putative protein of unknown function, may be involved in detoxification	Q
5094	VN_5094	YDL138W	RGT2	Plasma membrane high glucose sensor that regulates glucose transport; contains 12 predicted transmembrane segments and a long C-terminal tail required for induction of hexose transporters; highly similar to Snf3p	Q
5095	VN_5095	YGR199W	PMT6	Protein O-mannosyltransferase, transfers mannose from dolichyl phosphate-D-mannose to protein serine/threonine residues of secretory proteins; reaction is essential for cell wall rigidity; member of a family of mannosyltransferases	Q
5096	VN_5096	YER015W	FAA2	Long chain fatty acyl-CoA synthetase; accepts a wider range of acyl chain lengths than Faa1p, preferring C9:0-C13:0; involved in the activation of endogenous pools of fatty acids	Q
5097	VN_5097	YHR072W	ERG7	Lanosterol synthase, an essential enzyme that catalyzes the cyclization of squalene 2,3-epoxide, a step in ergosterol biosynthesis	Q
5098	VN_5098	YJL112W	MDV1	Peripheral protein of the cytosolic face of the mitochondrial outer membrane, required for mitochondrial fission; interacts with Fis1p and with the dynamin-related GTPase Dnm1p; contains WD repeats	Q
5099	VN_5099	YOL095C	HMI1	Mitochondrial inner membrane localized ATP-dependent DNA helicase, required for the maintenance of the mitochondrial genome; not required for mitochondrial transcription; has homology to E. coli helicase uvrD	Q
5100	VN_5100	YOR384W	FRE5	Putative ferric reductase with similarity to Fre2p; expression induced by low iron levels; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Strain failed to verify via PCR
5101	VN_5101	YDL199C	YDL199C	Putative transporter, member of the sugar porter family	Q
5102	VN_5102	YDR107C	TMN2	Protein with a role in cellular adhesion and filamentous growth; similar to Emp70p and Tmn3p; member of the evolutionarily conserved Transmembrane Nine family of proteins with nine membrane-spanning segments	Q
5103	VN_5103	YIL037C	PRM2	Pheromone-regulated protein, predicted to have 4 transmembrane segments and a coiled coil domain; regulated by Ste12p; required for efficient nuclear fusion	Q
5104	VN_5104	YNL115C	YNL115C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria; YNL115C is not an essential gene	Q
5105	VN_5105	YMR212C	EFR3	Non-essential protein of unknown function; exhibits synthetic lethal genetic interactions with PHO85; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies and is phosphorylated	Q
5106	VN_5106	YDL206W	YDL206W	Putative protein of unknown function; YDL206W is not an essential protein	Q
5107	VN_5107	YNL272C	SEC2	Guanylnucleotide exchange factor for the small G-protein Sec4p; essential for post-Golgi vesicle transport; associates with the exocyst, via exocyst subunit Sec15p, on secretory vesicles	Q
5108	VN_5108	YJR042W	NUP85	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC), required for assembly of the subcomplex and also for formation of the nucleocytoplasmic Gsp1p concentration gradient that plays a role in nuclear trafficking	Q
5109	VN_5109	YGL203C	KEX1	Protease involved in the processing of killer toxin and alpha factor precursor; cleaves Lys and Arg residues from the C-terminus of peptides and proteins	Strain failed to verify via PCR
5110	VN_5110	YJL061W	NUP82	Nucleoporin, subunit of the nuclear pore complex (NPC); forms a subcomplex with Gle2p, Nup159p, Nsp1p, and Nup116p and is required for proper localization of Nup116p in the NPC	Q
5111	VN_5111	YKR001C	VPS1	Dynamin-like GTPase required for vacuolar sorting; also involved in actin cytoskeleton organization, late Golgi-retention of some proteins, regulating peroxisome biogenesis	Strain failed to verify via PCR
5112	VN_5112	YKL146W	AVT3	Vacuolar transporter, exports large neutral amino acids from the vacuole; member of a family of seven S. cerevisiae genes (AVT1-7) related to vesicular GABA-glycine transporters	Strain failed to verify via PCR
5113	VN_5113	YJL156C	SSY5	Serine protease of SPS plasma membrane amino acid sensor system	Q

				(Ssy1p-Ptr3p-Ssy5p); contains an inhibitory domain that dissociates in response to extracellular amino acids, freeing a catalytic domain to activate transcription factor Stp1p	
5114	VN_5114	YLL043W	FPS1	Plasma membrane channel, member of major intrinsic protein (MIP) family; involved in efflux of glycerol and in uptake of acetic acid and the trivalent metalloids arsenite and antimonite; phosphorylated by Hog1p MAPK under acetate stress	Q
5115	VN_5115	YML031W	NDC1	Nuclear envelope protein with multiple putative transmembrane domains, required for nuclear pore complex assembly and spindle pole body duplication; required for meiosis II	Q
5116	VN_5116	YLR139C	SLS1	Mitochondrial membrane protein that coordinates expression of mitochondrially-encoded genes; may facilitate delivery of mRNA to membrane-bound translation machinery	Q
5117	VN_5117	YNL212W	VID27	Cytoplasmic protein of unknown function; possibly involved in vacuolar protein degradation; not essential for proteasome-dependent degradation of fructose-1,6-bisphosphatase (FBPase); null mutants exhibit normal growth	Q
5118	VN_5118	YER001W	MNN1	Alpha-1,3-mannosyltransferase, integral membrane glycoprotein of the Golgi complex, required for addition of alpha1,3-mannose linkages to N-linked and O-linked oligosaccharides, one of five <i>S. cerevisiae</i> proteins of the MNN1 family	Q
5119	VN_5119	YAL023C	PMT2	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex with Pmt1p, can instead interact with Pmt5p in some conditions; target for new antifungals	Q
5120	VN_5120	YDL093W	PMT5	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex with Pmt3p, can instead interact with Pmt2p in some conditions; target for new antifungals	Q
5121	VN_5121	YDL116W	NUP84	Subunit of the nuclear pore complex (NPC), forms a subcomplex with Nup85p, Nup120p, Nup145p-C, Sec13p, and Seh1p that plays a role in nuclear mRNA export and NPC biogenesis	Q
5122	VN_5122	YNL101W	AVT4	Vacuolar transporter, exports large neutral amino acids from the vacuole; member of a family of seven <i>S. cerevisiae</i> genes (AVT1-7) related to vesicular GABA-glycine transporters	Q
5123	VN_5123	YGL145W	TIP20	Peripheral membrane protein required for fusion of COPI vesicles with the ER; prohibits back-fusion of COPII vesicles with the ER; forms a tethering complex with Sec39p and Dsl1p that interacts with ER SNAREs Sec20p and Use1p	Q
5124	VN_5124	YHR042W	NCP1	NADP-cytochrome P450 reductase; involved in ergosterol biosynthesis; associated and coordinately regulated with Erg11p	Q
5125	VN_5125	YLR214W	FRE1	Ferric reductase and cupric reductase, reduces siderophore-bound iron and oxidized copper prior to uptake by transporters; expression induced by low copper and iron levels	Q
5126	VN_5126	YLR083C	EMP70	Protein with a role in cellular adhesion and filamentous growth; similar to Tmn2p and Tmn3p; member of Transmembrane Nine family of proteins with 9 transmembrane segments; 24kDa cleavage product found in endosome-enriched membrane fractions	Q
5127	VN_5127	YNL095C	YNL095C	Putative protein of unknown function predicted to contain a transmembrane domain; YNL095C is not an essential gene	Strain failed to verify via PCR
5128	VN_5128	YJR040W	GEF1	Voltage-gated chloride channel localized to the golgi, the endosomal system, and plasma membrane, and involved in cation homeostasis; highly homologous to vertebrate voltage-gated chloride channels	Q
5129	VN_5129	YJR143C	PMT4	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; appears to form homodimers in vivo and does not complex with other Pmt proteins; target for new antifungals	Q
5130	VN_5130	YKR067W	GPT2	Glycerol-3-phosphate/dihydroxyacetone phosphate dual substrate-specific sn-1 acyltransferase located in lipid particles and the ER; involved in the stepwise acylation of glycerol-3-phosphate and dihydroxyacetone in lipid biosynthesis	Strain failed to verify via PCR
5131	VN_5131	YLL051C	FRE6	Putative ferric reductase with similarity to Fre2p; expression induced by low iron levels	Q

5132	VN_5132	YIL005W	EPS1	ER protein with chaperone and co-chaperone activity, involved in retention of resident ER proteins; has a role in recognizing proteins targeted for ER-associated degradation (ERAD), member of the protein disulfide isomerase family	Strain failed to verify via PCR
5133	VN_5133	YOL011W	PLB3	Phospholipase B (lysophospholipase) involved in phospholipid metabolism; hydrolyzes phosphatidylinositol and phosphatidylserine and displays transacylase activity in vitro	Strain failed to verify via PCR
5134	VN_5134	YDR189W	SLY1	Hydrophilic protein involved in vesicle trafficking between the ER and Golgi; SM (Sec1/Munc-18) family protein that binds the tSNARE Sed5p and stimulates its assembly into a trans-SNARE membrane-protein complex	Q
5135	VN_5135	YJR004C	SAG1	Alpha-agglutinin of alpha-cells, binds to Aga1p during agglutination, N-terminal half is homologous to the immunoglobulin superfamily and contains binding site for a-agglutinin, C-terminal half is highly glycosylated and contains GPI anchor	Q
5136	VN_5136	YNR019W	ARE2	Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the major sterol esterification activity in the presence of oxygen	Q
5137	VN_5137	YGR143W	SKN1	Protein involved in sphingolipid biosynthesis; type II membrane protein with similarity to Kre6p	Strain failed to verify via PCR
5138	VN_5138	YER017C	AFG3	Component, with Yta12p, of the mitochondrial inner membrane m-AAA protease that mediates degradation of misfolded or unassembled proteins and is also required for correct assembly of mitochondrial enzyme complexes	Strain failed to verify via PCR
5139	VN_5139	YCR026C	NPP1	Nucleotide pyrophosphatase/phosphodiesterase family member; mediates extracellular nucleotide phosphate hydrolysis along with Npp2p and Pho5p; activity and expression enhanced during conditions of phosphate starvation	Q
5140	VN_5140	YJR106W	ECM27	Non-essential protein of unknown function	Q
5141	VN_5141	YJR005W	APL1	Beta-adaptin, large subunit of the clathrin associated protein complex (AP-2); involved in vesicle mediated transport; similar to mammalian beta-chain of the clathrin associated protein complex	Strain failed to verify via PCR
5142	VN_5142	YFR029W	PTR3	Component of the SPS plasma membrane amino acid sensor system (Ssy1p-Ptr3p-Ssy5p), which senses external amino acid concentration and transmits intracellular signals that result in regulation of expression of amino acid permease genes	Strain failed to verify via PCR
5143	VN_5143	YDR508C	GNP1	High-affinity glutamine permease, also transports Leu, Ser, Thr, Cys, Met and Asn; expression is fully dependent on Grr1p and modulated by the Ssy1p-Ptr3p-Ssy5p (SPS) sensor of extracellular amino acids	Q
5144	VN_5144	YJL012C	VTC4	Vacuolar membrane polyphosphate polymerase; subunit of the vacuolar transporter chaperone (VTC) complex involved in synthesis and transfer of polyP to the vacuole; regulates membrane trafficking; role in non-autophagic vacuolar fusion	Q
5145	VN_5145	YDR484W	VPS52	Component of the GARP (Golgi-associated retrograde protein) complex, Vps51p-Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; involved in localization of actin and chitin	Q
5146	VN_5146	YDR119W	VBA4	Protein of unknown function with proposed role as a basic amino acid permease based on phylogeny; GFP-fusion protein localizes to vacuolar membrane; physical interaction with Atg27p suggests a possible role in autophagy; non-essential gene	Strain failed to verify via PCR
5147	VN_5147	YCL045C	EMC1	Member of a transmembrane complex required for efficient folding of proteins in the ER; null mutant displays induction of the unfolded protein response; interacts with Gal80p	Strain failed to verify via PCR
5148	VN_5148	YPR003C	YPR003C	Putative sulfate permease; physically interacts with Hsp82p; green fluorescent protein (GFP)-fusion protein localizes to the ER; YPR003C is not an essential gene	Strain failed to verify via PCR
5149	VN_5149	YDR205W	MSC2	Member of the cation diffusion facilitator family, localizes to the endoplasmic reticulum and nucleus; mutations affect the cellular distribution of zinc and also confer defects in meiotic recombination between homologous chromatids	Q

5150	VN_5150	YPR159W	KRE6	Protein required for beta-1,6 glucan biosynthesis; putative beta-glucan synthase; appears functionally redundant with Skn1p	Strain failed to verify via PCR
5151	VN_5151	YOR381W	FRE3	Ferric reductase, reduces siderophore-bound iron prior to uptake by transporters; expression induced by low iron levels	Q
5152	VN_5152	YBL061C	SKT5	Activator of Chs3p (chitin synthase III), recruits Chs3p to the bud neck via interaction with Bni4p; has similarity to Shc1p, which activates Chs3p during sporulation	Q
5153	VN_5153	YMR301C	ATM1	Mitochondrial inner membrane ATP-binding cassette (ABC) transporter, exports mitochondrially synthesized precursors of iron-sulfur (Fe/S) clusters to the cytosol	Q
5154	VN_5154	YIL067C	YIL067C	Uncharacterized protein of unknown function	Q
5155	VN_5155	YOR254C	SEC63	Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-dependent and post-translational SRP-independent protein targeting and import into the ER	Q
5156	VN_5156	YFL054C	YFL054C	Putative channel-like protein; similar to Fps1p; mediates passive diffusion of glycerol in the presence of ethanol	Q
5157	VN_5157	YBL042C	FUI1	High affinity uridine permease, localizes to the plasma membrane; also mediates low but significant transport of the cytotoxic nucleoside analog 5-fluorouridine; not involved in uracil transport	Q
5158	VN_5158	YKL212W	SAC1	Phosphatidylinositol phosphate (PtdInsP) phosphatase involved in hydrolysis of PtdIns[4]P; transmembrane protein localizes to ER and Golgi; involved in protein trafficking and processing, secretion, and cell wall maintenance	Q
5159	VN_5159	YNL121C	TOM70	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins	Q
5160	VN_5160	YGR224W	AZR1	Plasma membrane transporter of the major facilitator superfamily, involved in resistance to azole drugs such as ketoconazole and fluconazole	Strain failed to verify via PCR
5161	VN_5161	YDL247W	MPH2	Alpha-glucoside permease, transports maltose, maltotriose, alpha-methylglucoside, and turanose; identical to Mph3p; encoded in a subtelomeric position in a region likely to have undergone duplication	Strain failed to verify via PCR
5162	VN_5162	YNR039C	ZRG17	Endoplasmic reticulum protein of unknown function, transcription is induced under conditions of zinc deficiency; mutant phenotype suggests a role in uptake of zinc	Q
5163	VN_5163	YOR192C	THI72	Transporter of thiamine or related compound; shares sequence similarity with Thi7p	Q
5164	VN_5164	YHR096C	HXT5	Hexose transporter with moderate affinity for glucose, induced in the presence of non-fermentable carbon sources, induced by a decrease in growth rate, contains an extended N-terminal domain relative to other HXTs	Q
5165	VN_5165	YNL065W	AQR1	Plasma membrane multidrug transporter of the major facilitator superfamily, confers resistance to short-chain monocarboxylic acids and quinidine; involved in the excretion of excess amino acids	Q
5166	VN_5166	YGL095C	VPS45	Protein of the Sec1p/Munc-18 family, essential for vacuolar protein sorting; required for the function of Pep12p and the early endosome/late Golgi SNARE Tlg2p; essential for fusion of Golgi-derived vesicles with the prevacuolar compartment	Q
5167	VN_5167	YLR081W	GAL2	Galactose permease, required for utilization of galactose; also able to transport glucose	Q
5168	VN_5168	YHR117W	TOM71	Mitochondrial outer membrane protein with similarity to Tom70p; probable minor component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochondrially directed proteins	Q
5169	VN_5169	YHR171W	ATG7	Autophagy-related protein and dual specificity member of the E1 family of ubiquitin-activating enzymes; mediates the conjugation of Atg12p with Atg5p and Atg8p with phosphatidylethanolamine, required steps in autophagosome formation	Q
5170	VN_5170	YPR048W	TAH18	Protein of unknown function that plays a pro-death role in response to	Strain failed

				oxidative stress; highly conserved across species and similar to human protein NDOR1; allele is synthetically lethal with the pol3-13 allele of DNA polymerase delta	to verify via PCR
5171	VN_5171	YOR092W	ECM3	Non-essential protein of unknown function; involved in signal transduction and the genotoxic response; induced rapidly in response to treatment with 8-methoxypsoralen and UVA irradiation	Q
5172	VN_5172	YGR216C	GPI1	Membrane protein involved in the synthesis of N-acetylglucosaminyl phosphatidylinositol (GlcNAc-PI), the first intermediate in the synthesis of glycosylphosphatidylinositol (GPI) anchors; human and mouse GPI1p are functional homologs	Q
5173	VN_5173	YDR046C	BAP3	Amino acid permease involved in the uptake of cysteine, leucine, isoleucine and valine	Q
5174	VN_5174	YOR067C	ALG8	Glucosyl transferase, involved in N-linked glycosylation; adds glucose to the dolichol-linked oligosaccharide precursor prior to transfer to protein during lipid-linked oligosaccharide biosynthesis; similar to Alg6p	Q
5175	VN_5175	YBR044C	TCM62	Protein involved in the assembly of the mitochondrial succinate dehydrogenase complex; putative chaperone	Strain failed to verify via PCR
5176	VN_5176	YHL047C	ARN2	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to the siderophore triacetylfusarinine C	Q
5177	VN_5177	YEL065W	SIT1	Ferrioxamine B transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; transcription is induced during iron deprivation and diauxic shift; potentially phosphorylated by Cdc28p	Q
5178	VN_5178	YFL041W	FET5	Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport	Q
5179	VN_5179	YDR244W	PEX5	Peroxisomal membrane signal receptor for the C-terminal tripeptide signal sequence (PTS1) of peroxisomal matrix proteins, required for peroxisomal matrix protein import; also proposed to have PTS1-receptor independent functions	Q
5180	VN_5180	YPL189W	GUP2	Probable membrane protein with a possible role in proton symport of glycerol; member of the MBOAT family of putative membrane-bound O-acyltransferases; Gup1p homolog	Q
5181	VN_5181	YGR191W	HIP1	High-affinity histidine permease, also involved in the transport of manganese ions	Strain failed to verify via PCR
5182	VN_5182	YOR071C	NRT1	High-affinity nicotinamide riboside transporter; also transports thiamine with low affinity; shares sequence similarity with Thi7p and Thi72p; proposed to be involved in 5-fluorocytosine sensitivity	Strain failed to verify via PCR
5183	VN_5183	YDR497C	ITR1	Myo-inositol transporter with strong similarity to the minor myo-inositol transporter Itr2p, member of the sugar transporter superfamily; expression is repressed by inositol and choline via Opi1p and derepressed via Ino2p and Ino4p	Q
5184	VN_5184	YLR152C	YLR152C	Putative protein of unknown function; YLR152C is not an essential gene	Q
5185	VN_5185	YNL270C	ALP1	Arginine transporter; expression is normally very low and it is unclear what conditions would induce significant expression	Q
5186	VN_5186	YMR058W	FET3	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases	Q
5187	VN_5187	YPR156C	TPO3	Polyamine transport protein specific for spermine; localizes to the plasma membrane; member of the major facilitator superfamily	Q
5188	VN_5188	YDR091C	RLI1	Essential iron-sulfur protein required for ribosome biogenesis and translation initiation; facilitates binding of a multifactor complex (MFC) of translation initiation factors to the small ribosomal subunit; predicted ABC family ATPase	Q
5189	VN_5189	YOR370C	MRS6	Rab escort protein, forms a complex with the Ras-like small GTPase Ypt1p that is required for the prenylation of Ypt1p by protein geranylgeranyltransferase type II (Bet2p-Bet4p); sequence similarity to mammalian choroideraemia gene	Q

5190	VN_5190	YBR015C	MNN2	Alpha-1,2-mannosyltransferase, responsible for addition of the first alpha-1,2-linked mannose to form the branches on the mannan backbone of oligosaccharides, localizes to an early Golgi compartment	Strain failed to verify via PCR
5191	VN_5191	YGR077C	PEX8	Intraperoxisomal organizer of the peroxisomal import machinery, tightly associated with the luminal face of the peroxisomal membrane, essential for peroxisome biogenesis, binds PTS1-signal receptor Pex5p	Strain failed to verify via PCR
5192	VN_5192	YLL061W	MMP1	High-affinity S-methylmethionine permease, required for utilization of S-methylmethionine as a sulfur source; has similarity to S-adenosylmethionine permease Sam3p	Strain failed to verify via PCR
5193	VN_5193	YNL275W	BOR1	Boron efflux transporter of the plasma membrane; binds HCO ₃ ⁻ , I ⁻ , Br ⁻ , NO ₃ ⁻ and Cl ⁻ ; has similarity to the characterized boron efflux transporter <i>A. thaliana</i> BOR1	Q
5194	VN_5194	YBR180W	DTR1	Putative dityrosine transporter, required for spore wall synthesis; expressed during sporulation; member of the major facilitator superfamily (DHA1 family) of multidrug resistance transporters	Q
5195	VN_5195	YIR028W	DAL4	Allantoin permease; expression sensitive to nitrogen catabolite repression and induced by allophanate, an intermediate in allantoin degradation	Q
5196	VN_5196	YHL040C	ARN1	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores	Q
5197	VN_5197	YKR106W	YKR106W	Protein of unconfirmed function; displays a topology characteristic of the Major Facilitators Superfamily of membrane proteins; coding sequence 98% identical to that of YCL073C	Q
5198	VN_5198	YCR023C	YCR023C	Vacuolar membrane protein of unknown function; member of the multidrug resistance family; YCR023C is not an essential gene	Q
5199	VN_5199	YPL265W	DIP5	Dicarboxylic amino acid permease, mediates high-affinity and high-capacity transport of L-glutamate and L-aspartate; also a transporter for Gln, Asn, Ser, Ala, and Gly	Q
5200	VN_5200	YJR001W	AVT1	Vacuolar transporter, imports large neutral amino acids into the vacuole; member of a family of seven <i>S. cerevisiae</i> genes (AVT1-7) related to vesicular GABA-glycine transporters	Q
5201	VN_5201	YBR132C	AGP2	High affinity polyamine permease, preferentially uses spermidine over putrescine; expression is down-regulated by osmotic stress; plasma membrane carnitine transporter, also functions as a low-affinity amino acid permease	Strain failed to verify via PCR
5202	VN_5202	YKR105C	VBA5	Putative transporter of the Major Facilitator Superfamily (MFS); proposed role as a basic amino acid permease based on phylogeny	Q
5203	VN_5203	YDL210W	UGA4	Permease that serves as a gamma-aminobutyrate (GABA) transport protein involved in the utilization of GABA as a nitrogen source; catalyzes the transport of putrescine and delta-aminolevulinic acid (ALA); localized to the vacuolar membrane	Q
5204	VN_5204	YJL045W	YJL045W	Minor succinate dehydrogenase isozyme; homologous to Sdh1p, the major isozyme responsible for the oxidation of succinate and transfer of electrons to ubiquinone; induced during the diauxic shift in a Cat8p-dependent manner	Q
5205	VN_5205	YOR348C	PUT4	Proline permease, required for high-affinity transport of proline; also transports the toxic proline analog azetidine-2-carboxylate (AzC); PUT4 transcription is repressed in ammonia-grown cells	Strain failed to verify via PCR
5206	VN_5206	YBR298C	MAL31	Maltose permease, high-affinity maltose transporter (alpha-glucoside transporter); encoded in the MAL3 complex locus; member of the 12 transmembrane domain superfamily of sugar transporters; functional in genomic reference strain S288C	Strain failed to verify via PCR
5207	VN_5207	YNL268W	LYP1	Lysine permease; one of three amino acid permeases (Alp1p, Can1p, Lyp1p) responsible for uptake of cationic amino acids	Strain failed to verify via PCR
5208	VN_5208	YOL158C	ENB1	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment	Q
5209	VN_5209	YJR160C	MPH3	Alpha-glucoside permease, transports maltose, maltotriose, alpha-methylglucoside, and turanose; identical to Mph2p; encoded in a	Q

				subtelomeric position in a region likely to have undergone duplication	
5210	VN_5210	YCL025C	AGP1	Low-affinity amino acid permease with broad substrate range, involved in uptake of asparagine, glutamine, and other amino acids; expression is regulated by the SPS plasma membrane amino acid sensor system (Ssy1p-Ptr3p-Ssy5p)	Q
5211	VN_5211	YML123C	PHO84	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; exit from the ER during maturation requires Pho86p	Strain failed to verify via PCR
5212	VN_5212	YHR032W	YHR032W	Putative protein of unknown function; putative substrate of the cAMP-dependent protein kinase (PKA)	Q
5213	VN_5213	YBL020W	RFT1	Essential integral membrane protein that is required for translocation of Man5GlcNac2-PP-Dol from the cytoplasmic side to the lumenal side of the ER membrane but is not the flippase; mutation is suppressed by expression of human p53 protein	Q
5214	VN_5214	YDR342C	HXT7	High-affinity glucose transporter of the major facilitator superfamily, nearly identical to Hxt6p, expressed at high basal levels relative to other HXTs, expression repressed by high glucose levels	Q
5215	VN_5215	YBR021W	FUR4	Uracil permease, localized to the plasma membrane; expression is tightly regulated by uracil levels and environmental cues	Q
5216	VN_5216	YBR041W	FAT1	Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a complex with Faa1p or Faa4p that imports and activates exogenous fatty acids	Strain failed to verify via PCR
5217	VN_5217	YOR175C	ALE1	Broad-specificity lysophospholipid acyltransferase, part of MBOAT family of membrane-bound O-acyltransferases; key component of Lands cycle; may have role in fatty acid exchange at sn-2 position of mature glycerophospholipids	Strain failed to verify via PCR
5218	VN_5218	YGR138C	TPO2	Polyamine transport protein specific for spermine; localizes to the plasma membrane; transcription of TPO2 is regulated by Haa1p; member of the major facilitator superfamily	Q
5219	VN_5219	YCR048W	ARE1	Acyl-CoA:sterol acyltransferase, isozyme of Are2p; endoplasmic reticulum enzyme that contributes the major sterol esterification activity in the absence of oxygen	Q
5220	VN_5220	YHL019C	APM2	Protein of unknown function, homologous to the medium chain of mammalian clathrin-associated protein complex; involved in vesicular transport	Q
5221	VN_5221	YKR039W	GAP1	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source	Q
5222	VN_5222	YAL067C	SEO1	Putative permease, member of the allantoin transporter subfamily of the major facilitator superfamily; mutation confers resistance to ethionine sulfoxide	Strain failed to verify via PCR
5223	VN_5223	YPL274W	SAM3	High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a sulfur source; has similarity to S-methylmethionine permease Mmp1p	Strain failed to verify via PCR
5224	VN_5224	YGL186C	TPN1	Plasma membrane pyridoxine (vitamin B6) transporter; member of the purine-cytosine permease subfamily within the major facilitator superfamily; proton symporter with similarity to Fcy21p, Fcy2p, and Fcy22p	Strain failed to verify via PCR
5225	VN_5225	YBR296C	PHO89	Na ⁺ /Pi cotransporter, active in early growth phase; similar to phosphate transporters of <i>Neurospora crassa</i> ; transcription regulated by inorganic phosphate concentrations and Pho4p	Q
5226	VN_5226	YDR343C	HXT6	High-affinity glucose transporter of the major facilitator superfamily, nearly identical to Hxt7p, expressed at high basal levels relative to other HXTs, repression of expression by high glucose requires SNF3	Q
5227	VN_5227	YDR456W	NHX1	Endosomal Na ⁺ /H ⁺ exchanger, required for intracellular sequestration of Na ⁺ ; required for osmotolerance to acute hypertonic shock	Q
5228	VN_5228	YJL085W	EXO70	Subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, and Exo84p), which directs secretory vesicles to active sites of exocytosis; acts with Sec3p in membrane targeting of the exocyst via PI(4,5)P2 binding	Q
5229	VN_5229	YKL174C	TPO5	Protein involved in excretion of putrescine and spermidine; putative polyamine transporter in the Golgi or post-Golgi vesicles	Q

5230	VN_5230	YLR088W	GAA1	Subunit of the GPI (glycosylphosphatidylinositol):protein transamidase complex, removes the GPI-anchoring signal and attaches GPI to proteins in the ER	Q
5231	VN_5231	YBR068C	BAP2	High-affinity leucine permease, functions as a branched-chain amino acid permease involved in the uptake of leucine, isoleucine and valine; contains 12 predicted transmembrane domains	Q
5232	VN_5232	YHL028W	WSC4	ER membrane protein involved in the translocation of soluble secretory proteins and insertion of membrane proteins into the ER membrane; may also have a role in the stress response but has only partial functional overlap with WSC1-3	Q
5233	VN_5233	YKR093W	PTR2	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains; PTR2 expression is regulated by the N-end rule pathway via repression by Cup9p	Q
5234	VN_5234	YGR065C	VHT1	High-affinity plasma membrane H ⁺ -biotin (vitamin H) symporter; mutation results in fatty acid auxotrophy; 12 transmembrane domain containing major facilitator subfamily member; mRNA levels negatively regulated by iron deprivation and biotin	Q
5235	VN_5235	YLL028W	TPO1	Polyamine transporter that recognizes spermine, putrescine, and spermidine; catalyzes uptake of polyamines at alkaline pH and excretion at acidic pH; phosphorylation enhances activity and sorting to the plasma membrane	Q
5236	VN_5236	YEL013W	VAC8	Phosphorylated and palmitoylated vacuolar membrane protein that interacts with Atg13p, required for the cytoplasm-to-vacuole targeting (Cvt) pathway; interacts with Nvj1p to form nucleus-vacuole junctions	Q
5237	VN_5237	YGR055W	MUP1	High affinity methionine permease, integral membrane protein with 13 putative membrane-spanning regions; also involved in cysteine uptake	Q
5238	VN_5238	YHR094C	HXT1	Low-affinity glucose transporter of the major facilitator superfamily, expression is induced by Hxk2p in the presence of glucose and repressed by Rgt1p when glucose is limiting	Q
5239	VN_5239	YDR536W	STL1	Glycerol proton symporter of the plasma membrane, subject to glucose-induced inactivation, strongly but transiently induced when cells are subjected to osmotic shock	Q
5240	VN_5240	YEL069C	HXT13	Hexose transporter, induced in the presence of non-fermentable carbon sources, induced by low levels of glucose, repressed by high levels of glucose	Q
5241	VN_5241	YBR220C	YBR220C	Putative protein of unknown function; YBR220C is not an essential gene	Q
5242	VN_5242	YOL105C	WSC3	Partially redundant sensor-transducer of the stress-activated PKC1-MPK1 signaling pathway involved in maintenance of cell wall integrity; involved in the response to heat shock and other stressors; regulates 1,3-beta-glucan synthesis	Q
5243	VN_5243	YOL019W	YOL019W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery and vacuole	Q
5244	VN_5244	YGR197C	SNG1	Protein involved in nitrosoguanidine (MNNG) resistance; expression is regulated by transcription factors involved in multidrug resistance	Q
5245	VN_5245	YJR152W	DAL5	Allantoate permease; ureidosuccinate permease; also transports dipeptides, though with lower affinity than for allantoate and ureidosuccinate; expression is constitutive but sensitive to nitrogen catabolite repression	Q
5246	VN_5246	YMR279C	YMR279C	Putative protein of unknown function; identified as a heat-induced gene in a high-throughout screen; YMR279C is not an essential gene	Q
5247	VN_5247	YER056C	FCY2	Purine-cytosine permease, mediates purine (adenine, guanine, and hypoxanthine) and cytosine accumulation	Strain failed to verify via PCR
5248	VN_5248	YDL088C	ASM4	Nuclear pore complex subunit, part of a subcomplex also containing Nup53p, Nup170p, and Pse1p	Q
5249	VN_5249	YCR068W	ATG15	Lipase required for intravacuolar lysis of autophagic bodies and Cvt bodies; targeted to intravacuolar vesicles during autophagy via the multivesicular body (MVB) pathway	Q
5250	VN_5250	YOR378W	YOR378W	Putative protein of unknown function; belongs to the DHA2 family of drug:H ⁺ antiporters; YOR378W is not an essential gene	Q

5251	VN_5251	YJL214W	HXT8	Protein of unknown function with similarity to hexose transporter family members, expression is induced by low levels of glucose and repressed by high levels of glucose	Q
5252	VN_5252	YNR072W	HXT17	Hexose transporter, up-regulated in media containing raffinose and galactose at pH 7.7 versus pH 4.7, repressed by high levels of glucose	Q
5253	VN_5253	YGL084C	GUP1	Plasma membrane protein involved in remodeling GPI anchors; member of the MBOAT family of putative membrane-bound O-acyltransferases; proposed to be involved in glycerol transport	Q
5254	VN_5254	YDR387C	YDR387C	Putative transporter, member of the sugar porter family; YDR387C is not an essential gene	Q
5255	VN_5255	YOR132W	VPS17	Subunit of the membrane-associated retromer complex essential for endosome-to-Golgi retrograde protein transport; peripheral membrane protein that assembles onto the membrane with Vps5p to promote vesicle formation	Q
5256	VN_5256	YMR155W	YMR155W	Putative protein of unknown function; identified as interacting with Hsp82p in a high-throughput two-hybrid screen	Q
5257	VN_5257	YPR198W	SGE1	Plasma membrane multidrug transporter of the major facilitator superfamily, acts as an extrusion permease; partial multicopy suppressor of gal11 mutations	Q
5258	VN_5258	YNL130C	CPT1	Cholinephosphotransferase, required for phosphatidylcholine biosynthesis and for inositol-dependent regulation of EPT1 transcription	Q
5259	VN_5259	YER060W	FCY21	Putative purine-cytosine permease, very similar to Fcy2p but cannot substitute for its function	Q
5260	VN_5260	YMR013C	SEC59	Dolichol kinase, catalyzes the terminal step in dolichyl monophosphate (Dol-P) biosynthesis; required for viability and for normal rates of lipid intermediate synthesis and protein N-glycosylation	Q
5261	VN_5261	YHR048W	YHK8	Presumed antiporter of the DHA1 family of multidrug resistance transporters; contains 12 predicted transmembrane spans; expression of gene is up-regulated in cells exhibiting reduced susceptibility to azoles	Q
5262	VN_5262	YDL245C	HXT15	Protein of unknown function with similarity to hexose transporter family members, expression is induced by low levels of glucose and repressed by high levels of glucose	Strain failed to verify via PCR
5263	VN_5263	YGL077C	HNH1	Choline/ethanolamine transporter; involved in the uptake of nitrogen mustard and the uptake of glycine betaine during hypersaline stress; co-regulated with phospholipid biosynthetic genes and negatively regulated by choline and myo-inositol	Q
5264	VN_5264	YHR045W	YHR045W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum	Q
5265	VN_5265	YJL163C	YJL163C	Putative protein of unknown function	Q
5266	VN_5266	YHR050W	SMF2	Divalent metal ion transporter involved in manganese homeostasis; has broad specificity for di-valent and tri-valent metals; post-translationally regulated by levels of metal ions; member of the Nramp family of metal transport proteins	Q
5267	VN_5267	YIL121W	QDR2	Multidrug transporter of the major facilitator superfamily, required for resistance to quinidine, barban, cisplatin, and bleomycin; may have a role in potassium uptake	Q
5268	VN_5268	YAR002W	NUP60	Subunit of the nuclear pore complex (NPC), functions to anchor Nup2p to the NPC in a process controlled by the nucleoplasmic concentration of Gsp1p-GTP; potential Cdc28p substrate; involved in telomere maintenance	Q
5269	VN_5269	YHL017W	YHL017W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein co-localizes with clathrin-coated vesicles	Q
5270	VN_5270	YDR072C	IPT1	Inositolphosphotransferase, involved in synthesis of mannose-(inositol-P) ₂ -ceramide (M(IP) ₂ C), the most abundant sphingolipid; can mutate to resistance to the antifungals syringomycin E and DmAMP1 and to K. lactis zymocin	Q
5271	VN_5271	YCR098C	GIT1	Plasma membrane permease, mediates uptake of glycerophosphoinositol and glycerophosphocholine as sources of the nutrients inositol and phosphate; expression and transport rate are regulated by phosphate and inositol availability	Q

5272	VN_5272	YCL027W	FUS1	Membrane protein localized to the shmoo tip, required for cell fusion; expression regulated by mating pheromone; proposed to coordinate signaling, fusion, and polarization events required for fusion; potential Cdc28p substrate	Q
5273	VN_5273	YDR345C	HXT3	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions	Q
5274	VN_5274	YIL120W	QDR1	Multidrug transporter of the major facilitator superfamily, required for resistance to quinidine, ketoconazole, fluconazole, and barban	Q
5275	VN_5275	YNL219C	ALG9	Mannosyltransferase, involved in N-linked glycosylation; catalyzes the transfer of mannose from Dol-P-Man to lipid-linked oligosaccharides; mutation of the human ortholog causes type 1 congenital disorders of glycosylation	Strain failed to verify via PCR
5276	VN_5276	YJR131W	MNS1	Alpha-1,2-mannosidase involved in ER quality control; catalyzes the removal of one mannose residue from Man9GlcNAc to produce a single isomer of Man8GlcNAc in N-linked oligosaccharide biosynthesis; integral to ER membrane	Q
5277	VN_5277	YFR051C	RET2	Delta subunit of the coatamer complex (COPI), which coats Golgi-derived transport vesicles; involved in retrograde transport between Golgi and ER	Q
5278	VN_5278	YIL166C	YIL166C	Putative protein with similarity to the allantate permease (Dal5p) subfamily of the major facilitator superfamily; mRNA expression is elevated by sulfur limitation; YIL166C is a non-essential gene	Q
5279	VN_5279	YER014W	HEM14	Protoporphyrinogen oxidase, a mitochondrial enzyme that catalyzes the seventh step in the heme biosynthetic pathway, converting protoporphyrinogen IX to protoporphyrin IX; inhibited by diphenyl ether-type herbicides	Q
5280	VN_5280	YKL039W	PTM1	Protein of unknown function, copurifies with late Golgi vesicles containing the v-SNARE Tlg2p	Q
5281	VN_5281	YER123W	YCK3	Palmitoylated, vacuolar membrane-localized casein kinase I isoform; negatively regulates vacuole fusion during hypertonic stress via phosphorylation of Vps41p; shares essential functions with Hrr25p; regulates vesicle fusion in AP-3 pathway	Q
5282	VN_5282	YEL042W	GDA1	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate	Q
5283	VN_5283	YCR028C	FEN2	Plasma membrane H ⁺ -pantothenate symporter; confers sensitivity to the antifungal agent fenpropimorph	Q
5284	VN_5284	YJL219W	HXT9	Putative hexose transporter that is nearly identical to Hxt11p, has similarity to major facilitator superfamily (MFS) transporters, expression of HXT9 is regulated by transcription factors Pdr1p and Pdr3p	Q
5285	VN_5285	YML130C	ERO1	Thiol oxidase required for oxidative protein folding in the endoplasmic reticulum	Q
5286	VN_5286	YMR307W	GAS1	Beta-1,3-glucanosyltransferase, required for cell wall assembly and also has a role in transcriptional silencing; localizes to the cell surface via a glycosylphosphatidylinositol (GPI) anchor; also found at the nuclear periphery	Q
5287	VN_5287	YHR078W	YHR078W	High osmolarity-regulated gene of unknown function	Q
5288	VN_5288	YBR008C	FLR1	Plasma membrane multidrug transporter of the major facilitator superfamily, involved in efflux of fluconazole, diazaborine, benomyl, methotrexate, and other drugs; expression induced in cells treated with the mycotoxin patulin	Q
5289	VN_5289	YHL036W	MUP3	Low affinity methionine permease, similar to Mup1p	Q
5290	VN_5290	YML116W	ATR1	Multidrug efflux pump of the major facilitator superfamily, required for resistance to aminotriazole and 4-nitroquinoline-N-oxide	Q
5291	VN_5291	YOR161C	PNS1	Protein of unknown function; has similarity to Torpedo californica tCTL1p, which is postulated to be a choline transporter, neither null mutation nor overexpression affects choline transport	Q
5292	VN_5292	YLL055W	YCT1	High-affinity cysteine-specific transporter with similarity to the Dal5p family of transporters; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YCT1 is not an essential gene	Strain failed to verify via PCR

5293	VN_5293	YLR004C	THI73	Putative plasma membrane permease proposed to be involved in carboxylic acid uptake and repressed by thiamine; substrate of Dbf2p/Mob1p kinase; transcription is altered if mitochondrial dysfunction occurs	Q
5294	VN_5294	YAL022C	FUN26	Nucleoside transporter with broad nucleoside selectivity; localized to intracellular membranes	Q
5295	VN_5295	YFL016C	MDJ1	Co-chaperone that stimulates the ATPase activity of the HSP70 protein Ssc1p; involved in protein folding/refolding in the mitochondrial matrix; required for proteolysis of misfolded proteins; member of the HSP40 (DnaJ) family of chaperones	Q
5296	VN_5296	YMR088C	VBA1	Permease of basic amino acids in the vacuolar membrane	Q
5297	VN_5297	YFL055W	AGP3	Low-affinity amino acid permease, may act to supply the cell with amino acids as nitrogen source in nitrogen-poor conditions; transcription is induced under conditions of sulfur limitation; plays a role in regulating Ty1 transposition	Q
5298	VN_5298	YMR319C	FET4	Low-affinity Fe(II) transporter of the plasma membrane	Q
5299	VN_5299	YNL048W	ALG11	Alpha-1,2-mannosyltransferase, catalyzes sequential addition of the two terminal alpha 1,2-mannose residues to the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER	Q
5300	VN_5300	YNL154C	YCK2	Palmitoylated plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck1p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck1p	Q
5301	VN_5301	YDL207W	GLE1	Cytoplasmic nucleoporin required for polyadenylated RNA export but not for protein import; component of Nup82p nuclear pore subcomplex; contains a nuclear export signal	Q
5302	VN_5302	YNL029C	KTR5	Putative mannosyltransferase involved in protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family	Q
5303	VN_5303	YBR127C	VMA2	Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the cytoplasm	Strain failed to verify via PCR
5304	VN_5304	YOL156W	HXT11	Putative hexose transporter that is nearly identical to Hxt9p, has similarity to major facilitator superfamily (MFS) transporters and is involved in pleiotropic drug resistance	Q
5305	VN_5305	YDR062W	LCB2	Component of serine palmitoyltransferase, responsible along with Lcb1p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine	Q
5306	VN_5306	YMR296C	LCB1	Component of serine palmitoyltransferase, responsible along with Lcb2p for the first committed step in sphingolipid synthesis, which is the condensation of serine with palmitoyl-CoA to form 3-ketosphinganine	Q
5307	VN_5307	YNR030W	ALG12	Alpha-1,6-mannosyltransferase localized to the ER; responsible for the addition of the alpha-1,6 mannose to dolichol-linked Man7GlcNAc2, acts in the dolichol pathway for N-glycosylation	Q
5308	VN_5308	YNL291C	MID1	N-glycosylated integral membrane protein of the ER membrane and plasma membrane, functions as a stretch-activated Ca ²⁺ -permeable cation channel required for Ca ²⁺ influx stimulated by pheromone; interacts with Cch1p; forms an oligomer	Q
5309	VN_5309	YBL099W	ATP1	Alpha subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis; phosphorylated	Q
5310	VN_5310	YHR135C	YCK1	Palmitoylated plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p	Q
5311	VN_5311	YHR007C	ERG11	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4'-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family	Q

5312	VN_5312	YIL085C	KTR7	Putative mannosyltransferase involved in protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family	Q
5313	VN_5313	YMR004W	MVP1	Protein required for sorting proteins to the vacuole; overproduction of Mvp1p suppresses several dominant VPS1 mutations; Mvp1p and Vps1p act in concert to promote membrane traffic to the vacuole	Q
5314	VN_5314	YDR481C	PHO8	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides	Q
5315	VN_5315	YNR056C	BIO5	Putative transmembrane protein involved in the biotin biosynthesis pathway; responsible for uptake of 7-keto 8-aminopelargonic acid; BIO5 is in a cluster of 3 genes (BIO3, BIO4, and BIO5) that mediate biotin synthesis	Q
5316	VN_5316	YPL120W	VPS30	Subunit of phosphatidylinositol (PtdIns) 3-kinase complexes I and II; Complex I is essential in autophagy and Complex II is required for vacuolar protein sorting; ortholog of the higher eukaryotic gene Beclin 1	Q
5317	VN_5317	YOL013C	HRD1	Ubiquitin-protein ligase required for endoplasmic reticulum-associated degradation (ERAD) of misfolded proteins; genetically linked to the unfolded protein response (UPR); regulated through association with Hrd3p; contains an H2 ring finger	Q
5318	VN_5318	YDL180W	YDL180W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole	Strain failed to verify via PCR
5319	VN_5319	YBR222C	PCS60	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase	Q
5320	VN_5320	YFL040W	YFL040W	Putative transporter, member of the sugar porter family; YFL040W is not an essential gene	Q
5321	VN_5321	YGR260W	TNA1	High affinity nicotinic acid plasma membrane permease, responsible for uptake of low levels of nicotinic acid; expression of the gene increases in the absence of extracellular nicotinic acid or para-aminobenzoate (PABA)	Q
5322	VN_5322	YCL038C	ATG22	Vacuolar integral membrane protein required for efflux of amino acids during autophagic body breakdown in the vacuole; null mutation causes a gradual loss of viability during starvation	Q
5323	VN_5323	YOR306C	MCH5	Plasma membrane riboflavin transporter; facilitates the uptake of vitamin B2; required for FAD-dependent processes; sequence similarity to mammalian monocarboxylate permeases, however mutants are not deficient in monocarboxylate transport	Q
5324	VN_5324	YDR323C	PEP7	Multivalent adaptor protein that facilitates vesicle-mediated vacuolar protein sorting by ensuring high-fidelity vesicle docking and fusion, which are essential for targeting of vesicles to the endosome; required for vacuole inheritance	Q
5325	VN_5325	YGL055W	OLE1	Delta(9) fatty acid desaturase, required for monounsaturated fatty acid synthesis and for normal distribution of mitochondria	Q
5326	VN_5326	YMR177W	MMT1	Putative metal transporter involved in mitochondrial iron accumulation; closely related to Mmt2p	Q
5327	VN_5327	YGR175C	ERG1	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine	Q
5328	VN_5328	YBR283C	SSH1	Subunit of the Ssh1 translocon complex; Sec61p homolog involved in co-translational pathway of protein translocation; not essential	Strain failed to verify via PCR
5329	VN_5329	YPL175W	SPT14	UDP-GlcNAc-binding and catalytic subunit of the enzyme that mediates the first step in glycosylphosphatidylinositol (GPI) biosynthesis, mutations cause defects in transcription and in biogenesis of cell wall proteins	Q
5330	VN_5330	YPL259C	APM1	Mu1-like medium subunit of the clathrin-associated protein complex (AP-1); binds clathrin; involved in clathrin-dependent Golgi protein sorting	Q
5331	VN_5331	YKL178C	STE3	Receptor for a factor pheromone, transcribed in alpha cells and required for mating by alpha cells, couples to MAP kinase cascade to	Q

				mediate pheromone response; ligand bound receptors are endocytosed and recycled to the plasma membrane; GPC	
5332	VN_5332	YNL237W	YTP1	Probable type-III integral membrane protein of unknown function, has regions of similarity to mitochondrial electron transport proteins	Strain failed to verify via PCR
5333	VN_5333	YJR117W	STE24	Highly conserved zinc metalloprotease that functions in two steps of a-factor maturation, C-terminal CAAX proteolysis and the first step of N-terminal proteolytic processing; contains multiple transmembrane spans	Q
5334	VN_5334	YJR124C	YJR124C	Putative protein of unknown function; expression induced under calcium shortage	Q
5335	VN_5335	YDR329C	PEX3	Peroxisomal membrane protein (PMP) required for proper localization and stability of PMPs; anchors peroxisome retention factor Inp1p at the peroxisomal membrane; interacts with Pex19p	Q
5336	VN_5336	YDR192C	NUP42	Subunit of the nuclear pore complex (NPC) that localizes exclusively to the cytoplasmic side; involved in RNA export, most likely at a terminal step; interacts with Gle1p	Q
5337	VN_5337	YBL089W	AVT5	Putative transporter, member of a family of seven <i>S. cerevisiae</i> genes (AVT1-7) related to vesicular GABA-glycine transporters	Q
5338	VN_5338	YOL119C	MCH4	Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma membrane; mutant is not deficient in monocarboxylate transport	Q
5339	VN_5339	YNL083W	SAL1	ADP/ATP transporter; member of the Ca ²⁺ -binding subfamily of the mitochondrial carrier family, with two EF-hand motifs; Pet9p and Sal1p have an overlapping function critical for viability; polymorphic in different <i>S. cerevisiae</i> strains	Q
5340	VN_5340	YIL088C	AVT7	Putative transporter, member of a family of seven <i>S. cerevisiae</i> genes (AVT1-7) related to vesicular GABA-glycine transporters	Q
5341	VN_5341	YEL064C	AVT2	Putative transporter, member of a family of seven <i>S. cerevisiae</i> genes (AVT1-7) related to vesicular GABA-glycine transporters	Q
5342	VN_5342	YBR293W	VBA2	Permease of basic amino acids in the vacuolar membrane	Q
5343	VN_5343	YOR334W	MRS2	Mitochondrial inner membrane Mg(2+) channel, required for maintenance of intramitochondrial Mg(2+) concentrations at the correct level to support splicing of group II introns	Q
5344	VN_5344	YCL069W	VBA3	Permease of basic amino acids in the vacuolar membrane	Strain failed to verify via PCR
5345	VN_5345	YOR307C	SLY41	Protein involved in ER-to-Golgi transport	Q
5346	VN_5346	YLR443W	ECM7	Non-essential putative integral membrane protein; mutant has cell wall defects; transcription is induced under conditions of zinc deficiency	Strain failed to verify via PCR
5347	VN_5347	YLR360W	VPS38	Part of a Vps34p phosphatidylinositol 3-kinase complex that functions in carboxypeptidase Y (CPY) sorting; binds Vps30p and Vps34p to promote production of phosphatidylinositol 3-phosphate (PtdIns3P) which stimulates kinase activity	Q
5348	VN_5348	YEL002C	WBP1	Beta subunit of the oligosaccharyl transferase (OST) glycoprotein complex; required for N-linked glycosylation of proteins in the endoplasmic reticulum	Q
5349	VN_5349	YER064C	YER064C	Non-essential nuclear protein; null mutation has global effects on transcription	Q
5350	VN_5350	YEL036C	ANP1	Subunit of the alpha-1,6 mannosyltransferase complex; type II membrane protein; has a role in retention of glycosyltransferases in the Golgi; involved in osmotic sensitivity and resistance to aminonitrophenyl propanediol	Q
5351	VN_5351	YAL010C	MDM10	Subunit of both the ERMES complex that links the ER to mitochondria, and of the mitochondrial sorting and assembly machinery (SAM complex) that functions in import and assembly of outer membrane beta-barrel proteins	Q
5352	VN_5352	YNR045W	PET494	Mitochondrial translational activator specific for the COX3 mRNA, acts together with Pet54p and Pet122p; located in the mitochondrial	Strain failed to verify via

				inner membrane	PCR
5353	VN_5353	YGL038C	OCH1	Mannosyltransferase of the cis-Golgi apparatus, initiates the polymannose outer chain elongation of N-linked oligosaccharides of glycoproteins	Q
5354	VN_5354	YBR003W	COQ1	Hexaprenyl pyrophosphate synthetase, catalyzes the first step in ubiquinone (coenzyme Q) biosynthesis	Q
5355	VN_5355	YKL021C	MAK11	Protein involved in an early, nucleolar step of 60S ribosomal subunit biogenesis; essential for cell growth and replication of killer M1 dsRNA virus; contains four beta-transducin repeats	Q
5356	VN_5356	YMR238W	DFG5	Putative mannosidase, essential glycosylphosphatidylinositol (GPI)-anchored membrane protein required for cell wall biogenesis in bud formation, involved in filamentous growth, homologous to Dcw1p	Q
5357	VN_5357	YER136W	GDI1	GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins	Q
5358	VN_5358	YPL053C	KTR6	Probable mannosylphosphate transferase involved in the synthesis of core oligosaccharides in protein glycosylation pathway; member of the KRE2/MNT1 mannosyltransferase family	Q
5359	VN_5359	YOR316C	COT1	Vacuolar transporter that mediates zinc transport into the vacuole; overexpression confers resistance to cobalt and rhodium	Q
5360	VN_5360	YER143W	DDI1	DNA damage-inducible v-SNARE binding protein, contains a ubiquitin-associated (UBA) domain, may act as a negative regulator of constitutive exocytosis, may play a role in S-phase checkpoint control	Q
5361	VN_5361	YMR065W	KAR5	Protein required for nuclear membrane fusion during karyogamy, localizes to the membrane with a soluble portion in the endoplasmic reticulum lumen, may form a complex with Jem1p and Kar2p; expression of the gene is regulated by pheromone	Strain failed to verify via PCR
5362	VN_5362	YNL169C	PSD1	Phosphatidylserine decarboxylase of the mitochondrial inner membrane, converts phosphatidylserine to phosphatidylethanolamine	Q
5363	VN_5363	YDR376W	ARH1	Oxidoreductase of the mitochondrial inner membrane, involved in cytoplasmic and mitochondrial iron homeostasis and required for activity of Fe-S cluster-containing enzymes; one of the few mitochondrial proteins essential for viability	Q
5364	VN_5364	YLR378C	SEC61	Essential subunit of Sec61 complex (Sec61p, Sbh1p, and Sss1p); forms a channel for SRP-dependent protein import and retrograde transport of misfolded proteins out of the ER; with Sec63 complex allows SRP-independent protein import into ER	Q
5365	VN_5365	YGL012W	ERG4	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants are viable, but lack ergosterol	Q
5366	VN_5366	YBR207W	FTH1	Putative high affinity iron transporter involved in transport of intravacuolar stores of iron; forms complex with Fet5p; expression is regulated by iron; proposed to play indirect role in endocytosis	Q
5367	VN_5367	YPL092W	SSU1	Plasma membrane sulfite pump involved in sulfite metabolism and required for efficient sulfite efflux; major facilitator superfamily protein	Strain failed to verify via PCR
5368	VN_5368	YBR110W	ALG1	Mannosyltransferase, involved in asparagine-linked glycosylation in the endoplasmic reticulum (ER); essential for viability, mutation is functionally complemented by human ortholog	Q
5369	VN_5369	YFL048C	EMP47	Integral membrane component of endoplasmic reticulum-derived COPII-coated vesicles, which function in ER to Golgi transport	Q
5370	VN_5370	YJL139C	YUR1	Mannosyltransferase of the KTR1 family, involved in protein N-glycosylation; located in the Golgi apparatus	Q
5371	VN_5371	YMR221C	YMR221C	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; physical interaction with Atg27p suggests a possible role in autophagy	Q
5372	VN_5372	YNL142W	MEP2	Ammonium permease involved in regulation of pseudohyphal growth; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium (NH ₄ ⁺); expression is under the nitrogen catabolite repression regulation	Q
5373	VN_5373	YGR121C	MEP1	Ammonium permease; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium (NH ₄ ⁺); expression	Q

				is under the nitrogen catabolite repression regulation	
5374	VN_5374	YBR241C	YBR241C	Putative transporter, member of the sugar porter family; green fluorescent protein (GFP)-fusion protein localizes to the vacuolar membrane; YBR241C is not an essential gene	Q
5375	VN_5375	YJL054W	TIM54	Component of the mitochondrial TIM22 complex involved in insertion of polytopic proteins into the inner membrane	Q
5376	VN_5376	YKL221W	MCH2	Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma membrane; mutant is not deficient in monocarboxylate transport	Q
5377	VN_5377	YBR199W	KTR4	Putative mannosyltransferase involved in protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family	Q
5378	VN_5378	YBL045C	COR1	Core subunit of the ubiquinol-cytochrome c reductase complex (bc1 complex), which is a component of the mitochondrial inner membrane electron transport chain	Q
5379	VN_5379	YER020W	GPA2	Nucleotide binding alpha subunit of the heterotrimeric G protein that interacts with the receptor Gpr1p, has signaling role in response to nutrients; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery	Q
5380	VN_5380	YHR190W	ERG9	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway	Q
5381	VN_5381	YPR173C	VPS4	AAA-ATPase involved in multivesicular body (MVB) protein sorting, ATP-bound Vps4p localizes to endosomes and catalyzes ESCRT-III disassembly and membrane release; ATPase activity is activated by Vta1p; regulates cellular sterol metabolism	Q
5382	VN_5382	YBR287W	YBR287W	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the ER; YBR287W is not an essential gene	Q
5383	VN_5383	YKL175W	ZRT3	Vacuolar membrane zinc transporter, transports zinc from storage in the vacuole to the cytoplasm when needed; transcription is induced under conditions of zinc deficiency	Q
5384	VN_5384	YJL091C	GWT1	Protein involved in the inositol acylation of glucosaminyl phosphatidylinositol (GlcN-PI) to form glucosaminyl(acyl)phosphatidylinositol (GlcN(acyl)PI), an intermediate in the biosynthesis of glycosylphosphatidylinositol (GPI) anchors	Q
5385	VN_5385	YIL090W	ICE2	Integral ER membrane protein with type-III transmembrane domains; mutations cause defects in cortical ER morphology in both the mother and daughter cells	Q
5386	VN_5386	YGL129C	RSM23	Mitochondrial ribosomal protein of the small subunit, has similarity to mammalian apoptosis mediator proteins; null mutation prevents induction of apoptosis by overproduction of metacaspase Mca1p	Q
5387	VN_5387	YPR036W	VMA13	Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; serves as an activator or a structural stabilizer of the V-ATPase	Q
5388	VN_5388	YGL172W	NUP49	Subunit of the Nsp1p-Nup57p-Nup49p-Nic96p subcomplex of the nuclear pore complex (NPC), required for nuclear export of ribosomes	Strain failed to verify via PCR
5389	VN_5389	YCL048W	SPS22	Protein of unknown function, redundant with Sps2p for the organization of the beta-glucan layer of the spore wall	Q
5390	VN_5390	YBR029C	CDS1	Phosphatidate cytidyltransferase (CDP-diglyceride synthetase); an enzyme that catalyzes that conversion of CTP + phosphate into diphosphate + CDP-diacylglycerol, a critical step in the synthesis of all major yeast phospholipids	Strain failed to verify via PCR
5391	VN_5391	YPL224C	MMT2	Putative metal transporter involved in mitochondrial iron accumulation; closely related to Mmt1p	Q
5392	VN_5392	YDR483W	KRE2	Alpha1,2-mannosyltransferase of the Golgi involved in protein mannosylation	Q
5393	VN_5393	YIR004W	DJP1	Cytosolic J-domain-containing protein, required for peroxisomal protein import and involved in peroxisome assembly, homologous to E. coli DnaJ	Q

5394	VN_5394	YLL010C	PSR1	Plasma membrane associated protein phosphatase involved in the general stress response; required along with binding partner Whi2p for full activation of STRE-mediated gene expression, possibly through dephosphorylation of Msn2p	Q
5395	VN_5395	YNL283C	WSC2	Partially redundant sensor-transducer of the stress-activated PKC1-MPK1 signaling pathway involved in maintenance of cell wall integrity and recovery from heat shock; secretory pathway Wsc2p is required for the arrest of secretion response	Q
5396	VN_5396	YJR054W	YJR054W	Vacuolar protein of unknown function; potential Cdc28p substrate	Q
5397	VN_5397	YOL062C	APM4	Mu2-like subunit of the clathrin associated protein complex (AP-2); involved in vesicle transport	Q
5398	VN_5398	YDL054C	MCH1	Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma membrane; mutant is not deficient in monocarboxylate transport	Q
5399	VN_5399	YJL002C	OST1	Alpha subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins	Q
5400	VN_5400	YHR005C	GPA1	GTP-binding alpha subunit of the heterotrimeric G protein that couples to pheromone receptors; negatively regulates the mating pathway by sequestering G(beta)gamma and by triggering an adaptive response; activates Vps34p at the endosome	Q
5401	VN_5401	YPL172C	COX10	Heme A:farnesyltransferase, catalyzes the first step in the conversion of protoheme to the heme A prosthetic group required for cytochrome c oxidase activity; human ortholog is associated with mitochondrial disorders	Q
5402	VN_5402	YIL170W	HXT12	Possible pseudogene in strain S288C; YIL170W/HXT12 and the adjacent ORF, YIL171W, together encode a non-functional member of the hexose transporter family	Strain failed to verify via PCR
5403	VN_5403	YBR243C	ALG7	UDP-N-acetyl-glucosamine-1-P transferase, transfers Glc-Nac-P from UDP-GlcNac to Dol-P in the ER in the first step of the dolichol pathway of protein asparagine-linked glycosylation; inhibited by tunicamycin	Strain failed to verify via PCR
5404	VN_5404	YML038C	YMD8	Putative nucleotide sugar transporter, has similarity to Vrg4p	Q
5405	VN_5405	YFL026W	STE2	Receptor for alpha-factor pheromone; seven transmembrane-domain GPCR that interacts with both pheromone and a heterotrimeric G protein to initiate the signaling response that leads to mating between haploid a and alpha cells	Q
5406	VN_5406	YLL006W	MMM1	ER integral membrane protein, component of the ERMES complex that links the ER to mitochondria and may promote inter-organellar calcium and phospholipid exchange as well as coordinating mitochondrial DNA replication and growth	Q
5407	VN_5407	YAL058W	CNE1	Calnexin; integral membrane ER chaperone involved in folding and quality control of glycoproteins; chaperone activity is inhibited by Mpd1p, with which Cne1p interacts; 24% identical to mammalian calnexin; Ca ²⁺ binding not yet shown in yeast	Q
5408	VN_5408	YOL137W	BSC6	Protein of unknown function containing 8 putative transmembrane segments; ORF exhibits genomic organization compatible with a translational readthrough-dependent mode of expression	Q
5409	VN_5409	YOR320C	GNT1	N-acetylglucosaminyltransferase capable of modification of N-linked glycans in the Golgi apparatus	Q
5410	VN_5410	YGL104C	VPS73	Mitochondrial protein; mutation affects vacuolar protein sorting; putative transporter; member of the sugar porter family	Strain failed to verify via PCR
5411	VN_5411	YMR153W	NUP53	Subunit of the nuclear pore complex (NPC), interacts with karyopherin Kap121p or with Nup170p via overlapping regions of Nup53p, involved in activation of the spindle checkpoint mediated by the Mad1p-Mad2p complex	Q
5412	VN_5412	YNR026C	SEC12	Guanine nucleotide exchange factor (GEF); glycosylated integral membrane protein of the endoplasmic reticulum, important for the initiation of transport vesicle budding from the endoplasmic reticulum through activation of the GTPase Sar1p	Q

5413	VN_5413	YBR075W		#N/A	Q
5414	VN_5414	YDR375C	BCS1	Protein of the mitochondrial inner membrane that functions as an ATP-dependent chaperone, required for the incorporation of the Rip1p and Qcr10p subunits into the cytochrome bc(1) complex; member of the CDC48/PAS1/SEC18 ATPase family	Strain failed to verify via PCR
5415	VN_5415	YER119C	AVT6	Vacuolar amino acid transporter, exports aspartate and glutamate from the vacuole; member of a family of seven <i>S. cerevisiae</i> genes (AVT1-7) related to vesicular GABA-glycine transporters	Q
5416	VN_5416	YMR243C	ZRC1	Vacuolar membrane zinc transporter, transports zinc from the cytosol into the vacuole for storage; also has a role in resistance to zinc shock resulting from a sudden influx of zinc into the cytoplasm	Q
5417	VN_5417	YIL022W	TIM44	Essential component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); tethers the import motor and regulatory factors (PAM complex) to the translocation channel (Tim23p-Tim17p core complex)	Strain failed to verify via PCR
5418	VN_5418	YKR061W	KTR2	Mannosyltransferase involved in N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family	Q
5419	VN_5419	YHR033W	YHR033W	Putative protein of unknown function; epitope-tagged protein localizes to the cytoplasm	Q
5420	VN_5420	YCL052C	PBN1	Essential component of glycosylphosphatidylinositol-mannosyltransferase I, required for the autocatalytic post-translational processing of the protease B precursor Prb1p, localizes to ER in luminal orientation; homolog of mammalian PIG-X	Q
5421	VN_5421	YNL064C	YDJ1	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family	Q
5422	VN_5422	YML048W	GSF2	ER localized integral membrane protein that may promote secretion of certain hexose transporters, including Gal2p; involved in glucose-dependent repression	Q
5423	VN_5423	YOL018C	TLG2	Syntaxin-like t-SNARE that forms a complex with Tlg1p and Vti1p and mediates fusion of endosome-derived vesicles with the late Golgi; binds Vps45p, which prevents Tlg2p degradation and also facilitates t-SNARE complex formation	Q
5424	VN_5424	YOR099W	KTR1	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; type II membrane protein; member of the KRE2/MNT1 mannosyltransferase family	Q
5425	VN_5425	YDR498C	SEC20	Membrane glycoprotein v-SNARE involved in retrograde transport from the Golgi to the ER; required for N- and O-glycosylation in the Golgi but not in the ER; interacts with the Dsl1p complex through Tip20p	Q
5426	VN_5426	YPR079W	MRL1	Membrane protein with similarity to mammalian mannose-6-phosphate receptors, possibly functions as a sorting receptor in the delivery of vacuolar hydrolases	Q
5427	VN_5427	YBR192W	RIM2	Mitochondrial pyrimidine nucleotide transporter; imports pyrimidine nucleoside triphosphates and exports pyrimidine nucleoside monophosphates; member of the mitochondrial carrier family	Q
5428	VN_5428	YMR166C	YMR166C	Predicted transporter of the mitochondrial inner membrane; has similarity to human mitochondrial ATP-Mg/Pi carriers; YMR166C is not an essential gene	Q
5429	VN_5429	YHR101C	BIG1	Integral membrane protein of the endoplasmic reticulum, required for normal content of cell wall beta-1,6-glucan	Q
5430	VN_5430	YMR079W	SEC14	Phosphatidylinositol/phosphatidylcholine transfer protein; involved in regulating PtdIns, PtdCho, and ceramide metabolism, products of which regulate intracellular transport and UPR; functionally homologous to mammalian PITPs	Q
5431	VN_5431	YOR212W	STE4	G protein beta subunit, forms a dimer with Ste18p to activate the mating signaling pathway, forms a heterotrimer with Gpa1p and Ste18p to dampen signaling; may recruit Rho1p to the polarized growth site during mating; contains WD40 repeats	Q
5432	VN_5432	YAL042W	ERV46	Protein localized to COPII-coated vesicles, forms a complex with Erv41p; involved in the membrane fusion stage of transport	Q
5433	VN_5433	YJL059W	YHC3	Vacuolar membrane protein involved in the ATP-dependent transport	Q

				of arginine into the vacuole and possibly in balancing ion homeostasis; homolog of human CLN3 involved in Batten disease (juvenile onset neuronal ceroid lipofuscinosis)	
5434	VN_5434	YER154W	OXA1	Mitochondrial inner membrane insertase, mediates the insertion of both mitochondrial- and nuclear-encoded proteins from the matrix into the inner membrane, interacts with mitochondrial ribosomes; conserved from bacteria to animals	Q
5435	VN_5435	YJL171C	YJL171C	GPI-anchored cell wall protein of unknown function; induced in response to cell wall damaging agents and by mutations in genes involved in cell wall biogenesis; sequence similarity to YBR162C/TOS1, a covalently bound cell wall protein	Q
5436	VN_5436	YOR176W	HEM15	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic pathway	Q
5437	VN_5437	YPL203W	TPK2	cAMP-dependent protein kinase catalytic subunit; promotes vegetative growth in response to nutrients via the Ras-cAMP signaling pathway; partially redundant with Tpk1p and Tpk3p; localizes to P-bodies during stationary phase	Q
5438	VN_5438	YGL255W	ZRT1	High-affinity zinc transporter of the plasma membrane, responsible for the majority of zinc uptake; transcription is induced under low-zinc conditions by the Zap1p transcription factor	Q
5439	VN_5439	YPR191W	QCR2	Subunit 2 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; phosphorylated; transcription is regulated by Hap1p, Hap2p/Hap3p, and heme	Q
5440	VN_5440	YBR105C	VID24	Peripheral membrane protein located at Vid (vacuole import and degradation) vesicles; regulates fructose-1,6-bisphosphatase (FBPase) targeting to the vacuole; promotes proteasome-dependent catabolite degradation of FBPase	Q
5441	VN_5441	YKL051W	SFK1	Plasma membrane protein that may act together with or upstream of Stt4p to generate normal levels of the essential phospholipid PI4P, at least partially mediates proper localization of Stt4p to the plasma membrane	Q
5442	VN_5442	YOR266W	PNT1	Mitochondrial integral inner membrane protein involved in membrane insertion of C-terminus of Cox2p, interacts genetically and physically with Cox18p; deletion mutant sensitive to the anti-Pneumocystis carinii drug pentamidine	Strain failed to verify via PCR
5443	VN_5443	YNL323W	LEM3	Membrane protein of the plasma membrane and ER, interacts specifically in vivo with the phospholipid translocase (flippase) Dnf1p; involved in translocation of phospholipids and alkylphosphocholine drugs across the plasma membrane	Q
5444	VN_5444	YLR380W	CSR1	Phosphatidylinositol transfer protein with a potential role in regulating lipid and fatty acid metabolism under heme-depleted conditions; interacts specifically with thioredoxin peroxidase; may have a role in oxidative stress resistance	Q
5445	VN_5445	YJL193W	YJL193W	Putative protein of unknown function, predicted to encode a triose phosphate transporter subfamily member based on phylogenetic analysis; similar to YOR307C/SLY41; deletion mutant has a respiratory growth defect	Q
5446	VN_5446	YJR075W	HOC1	Alpha-1,6-mannosyltransferase involved in cell wall mannan biosynthesis; subunit of a Golgi-localized complex that also contains Anp1p, Mnn9p, Mnn11p, and Mnn10p; identified as a suppressor of a cell lysis sensitive pkc1-371 allele	Q
5447	VN_5447	YKL080W	VMA5	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H ⁺ -ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane	Q
5448	VN_5448	YJR161C	COS5	Protein of unknown function, member the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	Strain failed to verify via PCR
5449	VN_5449	YBR302C	COS2	Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	Q
5450	VN_5450	YLR332W	MID2	O-glycosylated plasma membrane protein that acts as a sensor for cell wall integrity signaling and activates the pathway; interacts with	Q

				Rom2p, a guanine nucleotide exchange factor for Rho1p, and with cell integrity pathway protein Zeo1p	
5451	VN_5451	YER118C	SHO1	Transmembrane osmosensor, participates in activation of both the Cdc42p- and MAP kinase-dependent filamentous growth pathway and the high-osmolarity glycerol response pathway	Q
5452	VN_5452	YDR414C	ERD1	Predicted membrane protein required for the retention of luminal endoplasmic reticulum proteins; mutants secrete the endogenous ER protein, BiP (Kar2p)	Q
5453	VN_5453	YPL264C	YPL264C	Putative membrane protein of unknown function; physically interacts with Hsp82p; YPL264C is not an essential gene	Q
5454	VN_5454	YJL183W	MNN11	Subunit of a Golgi mannosyltransferase complex that also contains Anp1p, Mnn9p, Mnn10p, and Hoc1p, and mediates elongation of the polysaccharide mannan backbone; has homology to Mnn10p	Q
5455	VN_5455	YDL128W	VCX1	Vacuolar H ⁺ /Ca ²⁺ exchanger involved in control of cytosolic Ca ²⁺ concentration; has similarity to sodium/calcium exchangers, including the bovine Na ⁺ /Ca ²⁺ ,K ⁺ antiporter	Q
5456	VN_5456	YPR124W	CTR1	High-affinity copper transporter of the plasma membrane, mediates nearly all copper uptake under low copper conditions; transcriptionally induced at low copper levels and degraded at high copper levels	Q
5457	VN_5457	YKL004W	AUR1	Phosphatidylinositol:ceramide phosphoinositol transferase (IPC synthase), required for sphingolipid synthesis; can mutate to confer aureobasidin A resistance	Q
5458	VN_5458	YPL050C	MNN9	Subunit of Golgi mannosyltransferase complex also containing Anp1p, Mnn10p, Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan backbone; forms a separate complex with Van1p that is also involved in backbone elongation	Q
5459	VN_5459	YGL075C	MPS2	Essential membrane protein localized at the nuclear envelope and spindle pole body (SPB), required for insertion of the newly duplicated SPB into the nuclear envelope; potentially phosphorylated by Cdc28p	Q
5460	VN_5460	YML008C	ERG6	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; localized to both lipid particles and mitochondrial outer membrane	Q
5461	VN_5461	YFL062W	COS4	Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	Q
5462	VN_5462	YPL279C	YPL279C	Putative protein of unknown function	Strain failed to verify via PCR
5463	VN_5463	YGR257C	MTM1	Mitochondrial protein of the mitochondrial carrier family, involved in activating mitochondrial Sod2p probably by facilitating insertion of an essential manganese cofactor	Q
5464	VN_5464	YGR028W	MSP1	Mitochondrial protein involved in sorting of proteins in the mitochondria; putative membrane-spanning ATPase	Q
5465	VN_5465	YML047C	PRM6	Pheromone-regulated protein, predicted to have 2 transmembrane segments; regulated by Ste12p during mating	Q
5466	VN_5466	YLR130C	ZRT2	Low-affinity zinc transporter of the plasma membrane; transcription is induced under low-zinc conditions by the Zap1p transcription factor	Q
5467	VN_5467	YDR331W	GPI8	ER membrane glycoprotein subunit of the glycosylphosphatidylinositol transamidase complex that adds glycosylphosphatidylinositol (GPI) anchors to newly synthesized proteins; human PIG-K protein is a functional homolog	Q
5468	VN_5468	YBR205W	KTR3	Putative alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family	Q
5469	VN_5469	YMR026C	PEX12	C3HC4-type RING-finger peroxisomal membrane peroxin required for peroxisome biogenesis and peroxisomal matrix protein import; forms translocation subcomplex with Pex2p and Pex10p; mutations in human homolog cause peroxisomal disorders	Q
5470	VN_5470	YLR459W	GAB1	GPI transamidase subunit, involved in attachment of glycosylphosphatidylinositol (GPI) anchors to proteins; may have a role in recognition of the attachment signal or of the lipid portion of GPI	Q

5471	VN_5471	YMR203W	TOM40	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; constitutes the core element of the protein conducting pore	Q
5472	VN_5472	YML067C	ERV41	Protein localized to COPII-coated vesicles, forms a complex with Erv46p; involved in the membrane fusion stage of transport; has homology to human ERGIC2 (PTX1) protein	Q
5473	VN_5473	YJL053W	PEP8	Vacuolar protein sorting protein that forms part of the multimeric membrane-associated retromer complex along with Vps35p, Vps29p, Vps17p, and Vps5p; essential for endosome-to-Golgi retrograde protein transport	Strain failed to verify via PCR
5474	VN_5474	YDR459C	PFA5	Palmitoyltransferase with autoacylation activity; likely functions in pathway(s) outside Ras; member of a family of putative palmitoyltransferases containing an Asp-His-His-Cys-cysteine rich (DHHC-CRD) domain	Q
5475	VN_5475	YNL173C	MDG1	Plasma membrane protein involved in G-protein mediated pheromone signaling pathway; overproduction suppresses bem1 mutations	Q
5476	VN_5476	YIL076W	SEC28	Epsilon-COP subunit of the coatomer; regulates retrograde Golgi-to-ER protein traffic; stabilizes Cop1p, the alpha-COP and the coatomer complex; non-essential for cell growth	Q
5477	VN_5477	YDR202C	RAV2	Subunit of RAVE (Rav1p, Rav2p, Skp1p), a complex that associates with the V1 domain of the vacuolar membrane (H ⁺)-ATPase (V-ATPase) and promotes assembly and reassembly of the holoenzyme	Q
5478	VN_5478	YHR123W	EPT1	sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase; not essential for viability	Q
5479	VN_5479	YHL003C	LAG1	Ceramide synthase component, involved in synthesis of ceramide from C26(acyl)-coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to Lac1p	Q
5480	VN_5480	YER145C	FTR1	High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex with Fet3p; expression is regulated by iron	Q
5481	VN_5481	YKL166C	TPK3	cAMP-dependent protein kinase catalytic subunit; promotes vegetative growth in response to nutrients via the Ras-cAMP signaling pathway; partially redundant with Tpk1p and Tpk2p; localizes to P-bodies during stationary phase	Q
5482	VN_5482	YDR245W	MNN10	Subunit of a Golgi mannosyltransferase complex also containing Anp1p, Mnn9p, Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan backbone; membrane protein of the mannosyltransferase family	Strain failed to verify via PCR
5483	VN_5483	YLR191W	PEX13	Integral peroxisomal membrane required for the translocation of peroxisomal matrix proteins, interacts with the PTS1 signal recognition factor Pex5p and the PTS2 signal recognition factor Pex7p, forms a complex with Pex14p and Pex17p	Q
5484	VN_5484	YOL044W	PEX15	Phosphorylated tail-anchored type II integral peroxisomal membrane protein required for peroxisome biogenesis, cells lacking Pex15p mislocalize peroxisomal matrix proteins to cytosol, overexpression results in impaired peroxisome assembly	Q
5485	VN_5485	YML132W	COS3	Protein involved in salt resistance; interacts with sodium:hydrogen antiporter Nha1p; member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	Q
5486	VN_5486	YHR176W	FMO1	Flavin-containing monooxygenase, localized to the cytoplasmic face of the ER membrane; catalyzes oxidation of biological thiols to maintain the ER redox buffer ratio for correct folding of disulfide-bonded proteins	Q
5487	VN_5487	YER107C	GLE2	Component of the Nup82 subcomplex of the nuclear pore complex; required for polyadenylated RNA export but not for protein import; homologous to S. pombe Rae1p	Q
5488	VN_5488	YLR246W	ERF2	Subunit of a palmitoyltransferase, composed of Erf2p and Shr5p, that adds a palmitoyl lipid moiety to heterolipidated substrates such as Ras1p and Ras2p through a thioester linkage; mutants partially mislocalize Ras2p to the vacuole	Q
5489	VN_5489	YOR085W	OST3	Gamma subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; Ost3p is important for N-glycosylation of a	Q

				subset of proteins	
5490	VN_5490	YKL008C	LAC1	Ceramide synthase component, involved in synthesis of ceramide from C26(acyl)-coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to Lag1p	Q
5491	VN_5491	YBR036C	CSG2	Endoplasmic reticulum membrane protein, required for mannosylation of inositolphosphorylceramide and for growth at high calcium concentrations	Q
5492	VN_5492	YOR037W	CYC2	Mitochondrial peripheral inner membrane protein, contains a FAD cofactor in a domain exposed in the intermembrane space; exhibits redox activity in vitro; likely participates in ligation of heme to acytochromes c and c1 (Cyc1p and Cyt1p)	Q
5493	VN_5493	YBR042C	CST26	Protein required for incorporation of stearic acid into phosphatidylinositol; affects chromosome stability when overexpressed	Q
5494	VN_5494	YIL136W	OM45	Protein of unknown function, major constituent of the mitochondrial outer membrane; located on the outer (cytosolic) face of the outer membrane	Q
5495	VN_5495	YPL255W	BBP1	Protein required for the spindle pole body (SPB) duplication, localized at the central plaque periphery; forms a complex with a nuclear envelope protein Mps2p and SPB components Spc29p and Kar1p; required for mitotic functions of Cdc5p	Q
5496	VN_5496	YPL057C	SUR1	Probable catalytic subunit of a mannosylinositol phosphorylceramide (MIPC) synthase, forms a complex with probable regulatory subunit Csg2p; function in sphingolipid biosynthesis is overlapping with that of Csh1p	Q
5497	VN_5497	YOL003C	PFA4	Palmitoyltransferase with autoacylation activity, required for palmitoylation of amino acid permeases containing a C-terminal Phe-Trp-Cys site; required for modification of Chs3p; member of the DHHC family of putative palmitoyltransferases	Q
5498	VN_5498	YIL006W	YIA6	Mitochondrial NAD ⁺ transporter, involved in the transport of NAD ⁺ into the mitochondria (see also YEA6); member of the mitochondrial carrier subfamily; disputed role as a pyruvate transporter; has putative mouse and human orthologs	Q
5499	VN_5499	YLR056W	ERG3	C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow on non-fermentable carbon sources	Q
5500	VN_5500	YCR044C	PER1	Protein of the endoplasmic reticulum, required for GPI-phospholipase A2 activity that remodels the GPI anchor as a prerequisite for association of GPI-anchored proteins with lipid rafts; functionally complemented by human ortholog PERLD1	Q
5501	VN_5501	YDR297W	SUR2	Sphinganine C4-hydroxylase, catalyses the conversion of sphinganine to phytosphingosine in sphingolipid biosynthesis	Q
5502	VN_5502	YKR051W	YKR051W	Putative protein of unknown function	Q
5503	VN_5503	YJL134W	LCB3	Long-chain base-1-phosphate phosphatase with specificity for dihydrosphingosine-1-phosphate, regulates ceramide and long-chain base phosphates levels, involved in incorporation of exogenous long chain bases in sphingolipids	Q
5504	VN_5504	YPR201W	ARR3	Arsenite transporter of the plasma membrane, required for resistance to arsenic compounds; transcription is activated by Arr1p in the presence of arsenite	Q
5505	VN_5505	YLR019W	PSR2	Functionally redundant Psr1p homolog, a plasma membrane phosphatase involved in the general stress response; required with Psr1p and Whi2p for full activation of STRE-mediated gene expression, possibly through dephosphorylation of Msn2p	Q
5506	VN_5506	YML018C	YML018C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the membrane of the vacuole; physical interaction with Atg27p suggests a possible role in autophagy; YML018C is not an essential gene	Q
5507	VN_5507	YDL248W	COS7	Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Strain failed to verify via PCR

5508	VN_5508	YNL336W	COS1	Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	Strain failed to verify via PCR
5509	VN_5509	YOR008C	SLG1	Sensor-transducer of the stress-activated PKC1-MPK1 kinase pathway involved in maintenance of cell wall integrity; involved in organization of the actin cytoskeleton; secretory pathway Wsc1p is required for the arrest of secretion response	Q
5510	VN_5510	YNR041C	COQ2	Para hydroxybenzoate: polyprenyl transferase, catalyzes the second step in ubiquinone (coenzyme Q) biosynthesis	Strain failed to verify via PCR
5511	VN_5511	YMR152W	YIM1	Protein of unknown function; null mutant displays sensitivity to DNA damaging agents; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Strain failed to verify via PCR
5512	VN_5512	YHR002W	LEU5	Mitochondrial carrier protein involved in the accumulation of CoA in the mitochondrial matrix; homolog of human Graves disease protein; does not encode an isozyme of Leu4p, as first hypothesized	Q
5513	VN_5513	YGL100W	SEH1	Nuclear pore protein that is part of the evolutionarily conserved Nup84p complex (Nup84p, Nup85p, Nup120p, Nup145p, and Seh1p); homologous to Sec13p	Q
5514	VN_5514	YBR159W	IFA38	Microsomal beta-keto-reductase; contains oleate response element (ORE) sequence in the promoter region; mutants exhibit reduced VLCFA synthesis, accumulate high levels of dihydrosphingosine, phytosphingosine and medium-chain ceramides	Q
5515	VN_5515	YOL107W	YOL107W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and colocalizes in a punctate pattern with the early golgi/COPI vesicles; YOL107W is not an essential protein	Q
5516	VN_5516	YNL326C	PFA3	Palmitoyltransferase for Vac8p, required for vacuolar membrane fusion; contains an Asp-His-His-Cys-cysteine rich (DHHC-CRD) domain; autoacylates; required for vacuolar integrity under stress conditions	Q
5517	VN_5517	YBR104W	YMC2	Mitochondrial protein, putative inner membrane transporter with a role in oleate metabolism and glutamate biosynthesis; member of the mitochondrial carrier (MCF) family; has similarity with Ymc1p	Q
5518	VN_5518	YAL018C	YAL018C	Putative protein of unknown function	Q
5519	VN_5519	YHR195W	NVJ1	Nuclear envelope protein, anchored to the nuclear inner membrane, that interacts with the vacuolar membrane protein Vac8p to promote formation of nucleus-vacuole junctions during piecemeal microautophagy of the nucleus (PMN)	Q
5520	VN_5520	YBR183W	YPC1	Alkaline ceramidase that also has reverse (CoA-independent) ceramide synthase activity, catalyzes both breakdown and synthesis of phytoceramide; overexpression confers fumonisin B1 resistance	Q
5521	VN_5521	YGR096W	TPC1	Mitochondrial membrane transporter that mediates uptake of the essential cofactor thiamine pyrophosphate (ThPP) into mitochondria; expression appears to be regulated by carbon source; member of the mitochondrial carrier family	Q
5522	VN_5522	YIL134W	FLX1	Protein required for transport of flavin adenine dinucleotide (FAD), a synthesis product of riboflavin, across the mitochondrial membrane	Strain failed to verify via PCR
5523	VN_5523	YMR056C	AAC1	Mitochondrial inner membrane ADP/ATP translocator, exchanges cytosolic ADP for mitochondrially synthesized ATP; phosphorylated; Aac1p is a minor isoform while Pet9p is the major ADP/ATP translocator	Q
5524	VN_5524	YPR058W	YMC1	Mitochondrial protein, putative inner membrane transporter with a role in oleate metabolism and glutamate biosynthesis; member of the mitochondrial carrier (MCF) family; has similarity with Ymc2p	Q
5525	VN_5525	YBR024W	SCO2	Protein anchored to the mitochondrial inner membrane, similar to Sco1p and may have a redundant function with Sco1p in delivery of copper to cytochrome c oxidase; interacts with Cox2p	Strain failed to verify via PCR
5526	VN_5526	YCR034W	FEN1	Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway	Q

5527	VN_5527	YGL153W	PEX14	Peroxisomal membrane peroxin that is a central component of the peroxisomal protein import machinery; interacts with both PTS1 (Pex5p) and PTS2 (Pex7p), peroxisomal matrix protein signal recognition factors and membrane receptor Pex13p	Strain failed to verify via PCR
5528	VN_5528	YEL006W	YEA6	Putative mitochondrial NAD ⁺ transporter, member of the mitochondrial carrier subfamily (see also YIA6); has putative human ortholog	Q
5529	VN_5529	YBL069W	AST1	Peripheral membrane protein that interacts with the plasma membrane ATPase Pma1p and has a role in its targeting to the plasma membrane, possibly by influencing its incorporation into lipid rafts	Q
5530	VN_5530	YKL120W	OAC1	Mitochondrial inner membrane transporter, transports oxaloacetate, sulfate, thiosulfate, and isopropylmalate; member of the mitochondrial carrier family	Q
5531	VN_5531	YLR242C	ARV1	Protein functioning in transport of glycosylphosphatidylinositol intermediates into the ER lumen; required for normal intracellular sterol distribution and for sphingolipid metabolism; similar to Nup120p and C. elegans R05H5.5 protein	Q
5532	VN_5532	YDR492W	IZH1	Membrane protein involved in zinc ion homeostasis, member of the four-protein IZH family; transcription is regulated directly by Zap1p, expression induced by zinc deficiency and fatty acids; deletion increases sensitivity to elevated zinc	Strain failed to verify via PCR
5533	VN_5533	YJL133W	MRS3	Iron transporter that mediates Fe ²⁺ transport across the inner mitochondrial membrane; mitochondrial carrier family member, similar to and functionally redundant with Mrs4p; active under low-iron conditions; may transport other cations	Q
5534	VN_5534	YJL117W	PHO86	Endoplasmic reticulum (ER) resident protein required for ER exit of the high-affinity phosphate transporter Pho84p, specifically required for packaging of Pho84p into COPII vesicles	Q
5535	VN_5535	YOR065W	CYT1	Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex	Q
5536	VN_5536	YKR104W	YKR104W	Putative transporter of the multidrug resistance-associated protein (MRP) subfamily; contains a stop codon in S288C; adjacent ORFs YKR103W and YKR104W are merged in different strain backgrounds	Q
5537	VN_5537	YNL194C	YNL194C	Integral membrane protein required for sporulation and plasma membrane sphingolipid content; has sequence similarity to SUR7 and FMP45; GFP-fusion protein is induced in response to the DNA-damaging agent MMS	Q
5538	VN_5538	YIL023C	YKE4	Zinc transporter; localizes to the ER; null mutant is sensitive to calcofluor white, leads to zinc accumulation in cytosol; ortholog of the mouse KE4 and member of the ZIP (ZRT, IRT-like Protein) family	Q
5539	VN_5539	YLR026C	SED5	cis-Golgi t-SNARE syntaxin required for vesicular transport between the ER and the Golgi complex, binds at least 9 SNARE proteins	Strain failed to verify via PCR
5540	VN_5540	YPL215W	CBP3	Mitochondrial protein required for assembly of ubiquinol cytochrome-c reductase complex (cytochrome bc1 complex); interacts with Cbp4p and function is partially redundant with that of Cbp4p	Q
5541	VN_5541	YPR128C	ANT1	Peroxisomal adenine nucleotide transporter; involved in beta-oxidation of medium-chain fatty acid; required for peroxisome proliferation	Q
5542	VN_5542	YJR095W	SFC1	Mitochondrial succinate-fumarate transporter, transports succinate into and fumarate out of the mitochondrion; required for ethanol and acetate utilization	Q
5543	VN_5543	YBR265W	TSC10	3-ketosphinganine reductase, catalyzes the second step in phytosphingosine synthesis, essential for growth in the absence of exogenous dihydrosphingosine or phytosphingosine, member of short chain dehydrogenase/reductase protein family	Q
5544	VN_5544	YMR241W	YHM2	Mitochondrial DNA-binding protein, component of the mitochondrial nucleoid structure, involved in mtDNA replication and segregation of mitochondrial genomes; member of the mitochondrial carrier protein family	Q
5545	VN_5545	YJR077C	MIR1	Mitochondrial phosphate carrier, imports inorganic phosphate into mitochondria; functionally redundant with Pic2p but more abundant than Pic2p under normal conditions; phosphorylated	Q

5546	VN_5546	YOR101W	RAS1	GTPase involved in G-protein signaling in the adenylate cyclase activating pathway, plays a role in cell proliferation; localized to the plasma membrane; homolog of mammalian RAS proto-oncogenes	Q
5547	VN_5547	YKR026C	GCN3	Alpha subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a positive regulator of GCN4 expression	Q
5548	VN_5548	YDL198C	GGC1	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family	Strain failed to verify via PCR
5549	VN_5549	YPL227C	ALG5	UDP-glucose:dolichyl-phosphate glucosyltransferase, involved in asparagine-linked glycosylation in the endoplasmic reticulum	Q
5550	VN_5550	YMR060C	SAM37	Component of the Sorting and Assembly Machinery (SAM or TOB complex) of the mitochondrial outer membrane, which binds precursors of beta-barrel proteins and facilitates their outer membrane insertion; contributes to SAM complex stability	Q
5551	VN_5551	YLR220W	CCC1	Putative vacuolar Fe ²⁺ /Mn ²⁺ transporter; suppresses respiratory deficit of yfh1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation	Q
5552	VN_5552	YGR062C	COX18	Mitochondrial integral inner membrane protein required for membrane insertion of C-terminus of Cox2p; interacts genetically and physically with Mss2p and Pnt1p; similar to <i>S. cerevisiae</i> Oxa1, <i>N. crassa</i> Oxa2p, and <i>E. coli</i> YidC	Q
5553	VN_5553	YOR079C	ATX2	Golgi membrane protein involved in manganese homeostasis; overproduction suppresses the sod1 (copper, zinc superoxide dismutase) null mutation	Q
5554	VN_5554	YDL015C	TSC13	Enoyl reductase that catalyzes the last step in each cycle of very long chain fatty acid elongation, localizes to the ER, highly enriched in a structure marking nuclear-vacuolar junctions, coimmunoprecipitates with elongases Fen1p and Sur4p	Q
5555	VN_5555	YNR028W	CPR8	Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; similarity to Cpr4p suggests a potential role in the secretory pathway	Q
5556	VN_5556	YPR192W	AQY1	Spore-specific water channel that mediates the transport of water across cell membranes, developmentally controlled; may play a role in spore maturation, probably by allowing water outflow, may be involved in freeze tolerance	Q
5557	VN_5557	YER053C	PIC2	Mitochondrial phosphate carrier, imports inorganic phosphate into mitochondria; functionally redundant with Mir1p but less abundant than Mir1p under normal conditions; expression is induced at high temperature	Q
5558	VN_5558	YLR372W	SUR4	Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis	Q
5559	VN_5559	YDR265W	PEX10	Peroxisomal membrane E3 ubiquitin ligase required for for Ubc4p-dependent Pex5p ubiquitination and peroxisomal matrix protein import; contains zinc-binding RING domain; mutations in human homolog cause various peroxisomal disorders	Q
5560	VN_5560	YCR021C	HSP30	Hydrophobic plasma membrane localized, stress-responsive protein that negatively regulates the H(+)-ATPase Pma1p; induced by heat shock, ethanol treatment, weak organic acid, glucose limitation, and entry into stationary phase	Q
5561	VN_5561	YOL002C	IZH2	Plasma membrane protein involved in zinc homeostasis and osmotin-induced apoptosis; transcription regulated by Zap1p, zinc and fatty acid levels; similar to mammalian adiponectins; deletion increases sensitivity to elevated zinc	Q
5562	VN_5562	YNL098C	RAS2	GTP-binding protein that regulates the nitrogen starvation response, sporulation, and filamentous growth; farnesylation and palmitoylation required for activity and localization to plasma membrane; homolog of mammalian Ras proto-oncogenes	Q
5563	VN_5563	YBL030C	PET9	Major ADP/ATP carrier of the mitochondrial inner membrane, exchanges cytosolic ADP for mitochondrially synthesized ATP; phosphorylated; required for viability in many common lab strains carrying a mutation in the polymorphic SAL1 gene	Strain failed to verify via PCR

5564	VN_5564	YHR142W	CHS7	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p export from the ER	Q
5565	VN_5565	YGR284C	ERV29	Protein localized to COPII-coated vesicles, involved in vesicle formation and incorporation of specific secretory cargo	Strain failed to verify via PCR
5566	VN_5566	YOL092W	YOL092W	Putative protein of unknown function; predicted to contain six transmembrane domains and is 58% similar to the uncharacterized ORF YBR147W	Q
5567	VN_5567	YKR052C	MRS4	Iron transporter that mediates Fe ²⁺ transport across the inner mitochondrial membrane; mitochondrial carrier family member, similar to and functionally redundant with Mrs3p; active under low-iron conditions; may transport other cations	Q
5568	VN_5568	YPL132W	COX11	Mitochondrial inner membrane protein required for delivery of copper to the Cox1p subunit of cytochrome c oxidase; association with mitochondrial ribosomes suggests that copper delivery may occur during translation of Cox1p	Strain failed to verify via PCR
5569	VN_5569	YLR447C	VMA6	Subunit d of the five-subunit V0 integral membrane domain of vacuolar H ⁺ -ATPase (V-ATPase), an electrogenic proton pump found in the endomembrane system; stabilizes VO subunits; required for V1 domain assembly on the vacuolar membrane	Strain failed to verify via PCR
5570	VN_5570	YGL225W	VRG4	Golgi GDP-mannose transporter; regulates Golgi function and glycosylation in Golgi	Strain failed to verify via PCR
5571	VN_5571	YML019W	OST6	Subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins; similar to and partially functionally redundant with Ost3p	Q
5572	VN_5572	YOR100C	CRC1	Mitochondrial inner membrane carnitine transporter, required for carnitine-dependent transport of acetyl-CoA from peroxisomes to mitochondria during fatty acid beta-oxidation	Q
5573	VN_5573	YOL073C	YOL073C	Putative protein of unknown function	Strain failed to verify via PCR
5574	VN_5574	YCR069W	CPR4	Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; has a potential role in the secretory pathway	Q
5575	VN_5575	YOL096C	COQ3	O-methyltransferase, catalyzes two different O-methylation steps in ubiquinone (Coenzyme Q) biosynthesis; component of a mitochondrial ubiquinone-synthesizing complex; phosphoprotein	Q
5576	VN_5576	YOL101C	IZH4	Membrane protein involved in zinc ion homeostasis, member of the four-protein IZH family, expression induced by fatty acids and altered zinc levels; deletion reduces sensitivity to excess zinc; possible role in sterol metabolism	Q
5577	VN_5577	YJL196C	ELO1	Elongase I, medium-chain acyl elongase, catalyzes carboxy-terminal elongation of unsaturated C12-C16 fatty acyl-CoAs to C16-C18 fatty acids	Q
5578	VN_5578	YOR074C	CDC21	Thymidylate synthase, required for de novo biosynthesis of pyrimidine deoxyribonucleotides; expression is induced at G1/S	Strain failed to verify via PCR
5579	VN_5579	YPR139C	VPS66	Cytoplasmic protein of unknown function involved in vacuolar protein sorting.	Q
5580	VN_5580	YBR054W	YRO2	Putative protein of unknown function; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-throughput studies; transcriptionally regulated by Haa1p	Q
5581	VN_5581	YKR088C	TVP38	Integral membrane protein localized to late Golgi vesicles along with the v-SNARE Tlg2p; required for asymmetric localization of Kar9p during mitosis; GFP-fusion protein localizes to the cytoplasm in a punctate pattern	Q
5582	VN_5582	YNL180C	RHO5	Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, likely involved in protein kinase C (Pkc1p)-dependent signal transduction pathway that controls cell integrity	Q
5583	VN_5583	YOR271C	FSF1	Putative protein, predicted to be an alpha-isopropylmalate carrier; belongs to the sideroblastic-associated protein family; non-tagged	Q

				protein is detected in purified mitochondria; likely to play a role in iron homeostasis	
5584	VN_5584	YHR012W	VPS29	Endosomal protein that is a subunit of the membrane-associated retromer complex essential for endosome-to-Golgi retrograde transport; forms a subcomplex with Vps35p and Vps26p that selects cargo proteins for endosome-to-Golgi retrieval	Q
5585	VN_5585	YIL117C	PRM5	Pheromone-regulated protein, predicted to have 1 transmembrane segment; induced during cell integrity signaling	Q
5586	VN_5586	YMR274C	RCE1	Type II CAAX prenyl protease involved in the proteolysis and maturation of Ras and the a-factor mating pheromone	Strain failed to verify via PCR
5587	VN_5587	YOR069W	VPS5	Nexin-1 homolog required for localizing membrane proteins from a prevacuolar/late endosomal compartment back to the late Golgi apparatus; structural component of the retromer membrane coat complex; forms a retromer subcomplex with Vps17p	Q
5588	VN_5588	YPL134C	ODC1	Mitochondrial inner membrane transporter, exports 2-oxoadipate and 2-oxoglutarate from the mitochondrial matrix to the cytosol for lysine and glutamate biosynthesis and lysine catabolism; suppresses, in multicopy, an <i>fmc1</i> null mutation	Q
5589	VN_5589	YDL119C	YDL119C	Putative mitochondrial transport protein; GFP-fusion protein is induced in response to the DNA-damaging agent MMS; the authentic, non-tagged protein is detected in purified mitochondria	Strain failed to verify via PCR
5590	VN_5590	YDL052C	SLC1	1-acyl-sn-glycerol-3-phosphate acyltransferase, catalyzes the acylation of lysophosphatidic acid to form phosphatidic acid, a key intermediate in lipid metabolism; enzymatic activity detected in lipid particles and microsomes	Q
5591	VN_5591	YBR291C	CTP1	Mitochondrial inner membrane citrate transporter, member of the mitochondrial carrier family	Q
5592	VN_5592	YBR128C	ATG14	Autophagy-specific subunit of phosphatidylinositol 3-kinase complex I (with Vps34/15/30p); Atg14p targets complex I to the phagophore assembly site (PAS); required for localizing additional ATG proteins to the PAS; homolog of human Barkor	Q
5593	VN_5593	YDR126W	SWF1	Palmitoyltransferase that acts on the SNAREs Snc1p, Syn8p, Tlg1p and likely on all SNAREs; member of a family of putative palmitoyltransferases containing an Asp-His-His-Cys-cysteine rich (DHHC-CRD) domain; may have a role in vacuole fusion	Q
5594	VN_5594	YPR011C	YPR011C	Putative transporter, member of the mitochondrial carrier family; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
5595	VN_5595	YBR290W	BSD2	Heavy metal ion homeostasis protein, facilitates trafficking of Smf1p and Smf2p metal transporters to the vacuole where they are degraded, controls metal ion transport, prevents metal hyperaccumulation, functions in copper detoxification	Q
5596	VN_5596	YPL087W	YDC1	Alkaline dihydroceramidase, involved in sphingolipid metabolism; preferentially hydrolyzes dihydroceramide to a free fatty acid and dihydrosphingosine; has a minor reverse activity	Q
5597	VN_5597	YPR114W	YPR114W	Putative protein of unknown function	Q
5598	VN_5598	YBR039W	ATP3	Gamma subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis	Q
5599	VN_5599	YGR060W	ERG25	C-4 methyl sterol oxidase, catalyzes the first of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; mutants accumulate the sterol intermediate 4,4-dimethylzymosterol	Q
5600	VN_5600	YML052W	SUR7	Plasma membrane protein that localizes to furrow-like invaginations (MCC patches); component of eisosomes; associated with endocytosis, along with Pil1p and Lsp1p; sporulation and plasma membrane sphingolipid content are altered in mutants	Q
5601	VN_5601	YLR018C	POM34	Integral membrane protein of the nuclear pore; has an important role in maintaining the architecture of the pore complex	Q
5602	VN_5602	YAR031W	PRM9	Pheromone-regulated protein with 3 predicted transmembrane segments and an FF sequence, a motif involved in COPII binding; member of DUP240 gene family	Q

5603	VN_5603	YOR130C	ORT1	Ornithine transporter of the mitochondrial inner membrane, exports ornithine from mitochondria as part of arginine biosynthesis; human ortholog is associated with hyperammonaemia-hyperornithinaemia-homocitrullinuria (HHH) syndrome	Q
5604	VN_5604	YBR002C	RER2	Cis-prenyltransferase involved in dolichol synthesis; participates in endoplasmic reticulum (ER) protein sorting	Q
5605	VN_5605	YNL055C	POR1	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; phosphorylated	Strain failed to verify via PCR
5606	VN_5606	YLL023C	YLL023C	Protein of unknown function; highly conserved across species and orthologous to human TMEM33; may interact with ribosomes, based on co-purification experiments; GFP-fusion protein localizes to the endoplasmic reticulum	Q
5607	VN_5607	YHL026C	YHL026C	Putative protein of unknown function; YHL026C is not an essential gene; in 2005 the start site was moved 141 nt upstream (see Locus History)	Q
5608	VN_5608	YEL051W	VMA8	Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; plays a role in the coupling of proton transport and ATP hydrolysis	Q
5609	VN_5609	YBR070C	ALG14	Component of UDP-GlcNAc transferase required for the second step of dolichyl-linked oligosaccharide synthesis; anchors the catalytic subunit Alg13p to the ER membrane; similar to bacterial and human glycosyltransferases	Q
5610	VN_5610	YJL192C	SOP4	ER-membrane protein; suppressor of pma1-7, deletion of SOP4 slows down the export of wild-type Pma1p and Pma1-7 from the ER	Q
5611	VN_5611	YDL018C	ERP3	Protein with similarity to Emp24p and Erv25p, member of the p24 family involved in ER to Golgi transport	Q
5612	VN_5612	YBR040W	FIG1	Integral membrane protein required for efficient mating; may participate in or regulate the low affinity Ca ²⁺ influx system, which affects intracellular signaling and cell-cell fusion during mating	Q
5613	VN_5613	YHR133C	NSG1	Protein involved in regulation of sterol biosynthesis; specifically stabilizes Hmg2p, one of two HMG-CoA isoenzymes that catalyze the rate-limiting step in sterol biosynthesis; homolog of mammalian INSIG proteins	Q
5614	VN_5614	YOR106W	VAM3	Syntaxin-related protein required for vacuolar assembly; functions with Vam7p in vacuolar protein trafficking; member of the syntaxin family of proteins	Q
5615	VN_5615	YLR393W	ATP10	Mitochondrial inner membrane protein required for assembly of the F ₀ sector of mitochondrial F ₁ F ₀ ATP synthase, interacts genetically with ATP6	Q
5616	VN_5616	YKR030W	GMH1	Golgi membrane protein of unknown function, interacts with Gea1p and Gea2p; required for localization of Gea2p; computational analysis suggests a possible role in either cell wall synthesis or protein-vacuolar targeting	Q
5617	VN_5617	YOR115C	TRS33	One of 10 subunits of the transport protein particle (TRAPP) complex of the cis-Golgi which mediates vesicle docking and fusion; involved in endoplasmic reticulum (ER) to Golgi membrane traffic	Q
5618	VN_5618	YMR200W	ROT1	Molecular chaperone involved in protein folding in the ER; mutation causes defects in cell wall synthesis and in lysis of autophagic bodies, suppresses tor2 mutations, and is synthetically lethal with kar2-1 and with rot2 mutations	Q
5619	VN_5619	YER120W	SCS2	Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog	Q
5620	VN_5620	YGL053W	PRM8	Pheromone-regulated protein with 2 predicted transmembrane segments and an FF sequence, a motif involved in COPII binding; forms a complex with Prp9p in the ER; member of DUP240 gene family	Q
5621	VN_5621	YKR014C	YPT52	GTPase, similar to Ypt51p and Ypt53p and to mammalian rab5; required for vacuolar protein sorting and endocytosis	Q

5622	VN_5622	YEL001C	IRC22	Putative protein of unknown function; green fluorescent protein (GFP)-fusion localizes to the ER; YEL001C is non-essential; null mutant displays increased levels of spontaneous Rad52p foci	Q
5623	VN_5623	YLL056C	YLL056C	Putative protein of unknown function, transcription is activated by paralogous transcription factors Yrm1p and Yrr1p and genes involved in pleiotropic drug resistance (PDR); expression is induced in cells treated with the mycotoxin patulin	Q
5624	VN_5624	YKR055W	RHO4	Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, likely to be involved in the establishment of cell polarity	Q
5625	VN_5625	YMR149W	SWP1	Delta subunit of the oligosaccharyl transferase glycoprotein complex, which is required for N-linked glycosylation of proteins in the endoplasmic reticulum	Q
5626	VN_5626	YPL094C	SEC62	Essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-dependent and post-translational SRP-independent protein targeting and import into the ER	Q
5627	VN_5627	YBR185C	MBA1	Protein involved in assembly of mitochondrial respiratory complexes; may act as a receptor for proteins destined for export from the mitochondrial matrix to the inner membrane	Q
5628	VN_5628	YPL162C	YPL162C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the membrane of vacuole with cell cycle-correlated morphology	Q
5629	VN_5629	YKL154W	SRP102	Signal recognition particle (SRP) receptor beta subunit; involved in SRP-dependent protein targeting; anchors Srp101p to the ER membrane	Q
5630	VN_5630	YGR167W	CLC1	Clathrin light chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; thought to regulate clathrin function; two Clathrin heavy chains (CHC1) form the clathrin triskelion structural component	Q
5631	VN_5631	YER170W	ADK2	Mitochondrial adenylate kinase, catalyzes the reversible synthesis of GTP and AMP from GDP and ADP; may serve as a back-up for synthesizing GTP or ADP depending on metabolic conditions; 3' sequence of ADK2 varies with strain background	Q
5632	VN_5632	YLR348C	DIC1	Mitochondrial dicarboxylate carrier, integral membrane protein, catalyzes a dicarboxylate-phosphate exchange across the inner mitochondrial membrane, transports cytoplasmic dicarboxylates into the mitochondrial matrix	Strain failed to verify via PCR
5633	VN_5633	YOR311C	DGK1	Diacylglycerol kinase, localized to the endoplasmic reticulum (ER); overproduction induces enlargement of ER-like membrane structures and suppresses a temperature-sensitive sly1 mutation; contains a CTP transferase domain	Q
5634	VN_5634	YNL003C	PET8	S-adenosylmethionine transporter of the mitochondrial inner membrane, member of the mitochondrial carrier family; required for biotin biosynthesis and respiratory growth	Q
5635	VN_5635	YNR002C	ATO2	Putative transmembrane protein involved in export of ammonia, a starvation signal that promotes cell death in aging colonies; phosphorylated in mitochondria; member of the TC 9.B.33 YaaH family; homolog of Ady2p and Y. lipolytica Gpr1p	Q
5636	VN_5636	YGR026W	YGR026W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery	Q
5637	VN_5637	YLL041C	SDH2	Iron-sulfur protein subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer of electrons to ubiquinone	Q
5638	VN_5638	YBL040C	ERD2	HDEL receptor, an integral membrane protein that binds to the HDEL motif in proteins destined for retention in the endoplasmic reticulum; has a role in maintenance of normal levels of ER-resident proteins	Q
5639	VN_5639	YPL078C	ATP4	Subunit b of the stator stalk of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis; phosphorylated	Q
5640	VN_5640	YOL147C	PEX11	Peroxisomal membrane protein required for peroxisome proliferation and medium-chain fatty acid oxidation, most abundant protein in the peroxisomal membrane, regulated by Adr1p and Pip2p-Oaf1p, promoter contains ORE and UAS1-like elements	Q

5641	VN_5641	YLL060C	GTT2	Glutathione S-transferase capable of homodimerization; functional overlap with Gtt2p, Grx1p, and Grx2p	Q
5642	VN_5642	YPR028W	YOP1	Membrane protein that interacts with Yip1p to mediate membrane traffic; interacts with Sey1p to maintain ER morphology; overexpression leads to cell death and accumulation of internal cell membranes	Q
5643	VN_5643	YPL232W	SSO1	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane and in vesicle fusion during sporulation; forms a complex with Sec9p that binds v-SNARE Snc2p; syntaxin homolog; functionally redundant with Sso2p	Q
5644	VN_5644	YPL156C	PRM4	Pheromone-regulated protein proposed to be involved in mating; predicted to have 1 transmembrane segment; transcriptionally regulated by Ste12p during mating and by Cat8p during the diauxic shift	Q
5645	VN_5645	YDR315C	IPK1	Inositol 1,3,4,5,6-pentakisphosphate 2-kinase, nuclear protein required for synthesis of 1,2,3,4,5,6-hexakisphosphate (phytate), which is integral to cell function; has 2 motifs conserved in other fungi; ipk1 gle1 double mutant is inviable	Q
5646	VN_5646	YER026C	CHO1	Phosphatidylserine synthase, functions in phospholipid biosynthesis; catalyzes the reaction CDP-diacylglycerol + L-serine = CMP + L-1-phosphatidylserine, transcriptionally repressed by myo-inositol and choline	Strain failed to verify via PCR
5647	VN_5647	YOR125C	CAT5	Protein required for ubiquinone (Coenzyme Q) biosynthesis; localizes to the matrix face of the mitochondrial inner membrane in a large complex with ubiquinone biosynthetic enzymes; required for gluconeogenic gene activation	Q
5648	VN_5648	YER100W	UBC6	Ubiquitin-conjugating enzyme involved in ER-associated protein degradation; located at the cytosolic side of the ER membrane; tail region contains a transmembrane segment at the C-terminus; substrate of the ubiquitin-proteasome pathway	Q
5649	VN_5649	YLR411W	CTR3	High-affinity copper transporter of the plasma membrane, acts as a trimer; gene is disrupted by a Ty2 transposon insertion in many laboratory strains of <i>S. cerevisiae</i>	Q
5650	VN_5650	YOR332W	VMA4	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane	Q
5651	VN_5651	YDR468C	TLG1	Essential t-SNARE that forms a complex with Tlg2p and Vti1p and mediates fusion of endosome-derived vesicles with the late Golgi; binds the docking complex VFT (Vps fifty-three) through interaction with Vps51p	Q
5652	VN_5652	YNL305C	YNL305C	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; YNL305C is not an essential gene	Q
5653	VN_5653	YDR284C	DPP1	Diacylglycerol pyrophosphate (DGPP) phosphatase, zinc-regulated vacuolar membrane-associated lipid phosphatase, dephosphorylates DGPP to phosphatidate (PA) and Pi, then PA to diacylglycerol; involved in lipid signaling and cell metabolism	Q
5654	VN_5654	YCR010C	ADY2	Acetate transporter required for normal sporulation; phosphorylated in mitochondria	Q
5655	VN_5655	YIL114C	POR2	Putative mitochondrial porin (voltage-dependent anion channel), related to Por1p but not required for mitochondrial membrane permeability or mitochondrial osmotic stability	Strain failed to verify via PCR
5656	VN_5656	YIR014W	YIR014W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; expression directly regulated by the metabolic and meiotic transcriptional regulator Ume6p; YIR014W is a non-essential gene	Q
5657	VN_5657	YJL210W	PEX2	RING-finger peroxin, peroxisomal membrane protein with a C-terminal zinc-binding RING domain, forms translocation subcomplex with Pex10p and Pex12p which functions in peroxisomal matrix protein import	Q
5658	VN_5658	YPL246C	RBD2	Possible rhomboid protease, has similarity to eukaryotic rhomboid proteases including Pcp1p	Q

5659	VN_5659	YER039C	HVG1	Protein of unknown function, has homology to Vrg4p	Q
5660	VN_5660	YLR025W	SNF7	One of four subunits of the endosomal sorting complex required for transport III (ESCRT-III); involved in the sorting of transmembrane proteins into the multivesicular body (MVB) pathway; recruited from the cytoplasm to endosomal membranes	Q
5661	VN_5661	YGL020C	GET1	Subunit of the GET complex; involved in insertion of proteins into the ER membrane; required for the retrieval of HDEL proteins from the Golgi to the ER in an ERD2 dependent fashion and for normal mitochondrial morphology and inheritance	Q
5662	VN_5662	YKL041W	VPS24	One of four subunits of the endosomal sorting complex required for transport III (ESCRT-III); forms an ESCRT-III subcomplex with Did4p; involved in the sorting of transmembrane proteins into the multivesicular body (MVB) pathway	Q
5663	VN_5663	YBR037C	SCO1	Copper-binding protein of the mitochondrial inner membrane, required for cytochrome c oxidase activity and respiration; may function to deliver copper to cytochrome c oxidase; has similarity to thioredoxins	Q
5664	VN_5664	YNL159C	ASI2	Integral inner nuclear membrane protein that acts with Asi1p and Asi3p to ensure the fidelity of SPS-sensor signalling by maintaining the dormant repressed state of gene expression in the absence of inducing signals	Q
5665	VN_5665	YDL142C	CRD1	Cardiolipin synthase; produces cardiolipin, which is a phospholipid of the mitochondrial inner membrane that is required for normal mitochondrial membrane potential and function; also required for normal vacuolar ion homeostasis	Q
5666	VN_5666	YBR187W	GDT1	Putative protein of unknown function; expression is reduced in a gcr1 null mutant; GFP-fusion protein localizes to the vacuole; expression pattern and physical interactions suggest a possible role in ribosome biogenesis	Q
5667	VN_5667	YGR120C	COG2	Essential component of the conserved oligomeric Golgi complex (Cog1p through Cog8p), a cytosolic tethering complex that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments	Q
5668	VN_5668	YOL009C	MDM12	Mitochondrial outer membrane protein, required for transmission of mitochondria to daughter cells; component of the ERMES complex that links the ER to mitochondria; may influence import and assembly of outer membrane beta-barrel proteins	Q
5669	VN_5669	YGL198W	YIP4	Protein that interacts with Rab GTPases, localized to late Golgi vesicles; computational analysis of large-scale protein-protein interaction data suggests a possible role in vesicle-mediated transport	Q
5670	VN_5670	YDR410C	STE14	Farnesyl cysteine-carboxyl methyltransferase, mediates the carboxyl methylation step during C-terminal CAAX motif processing of a-factor and RAS proteins in the endoplasmic reticulum, localizes to the ER membrane	Q
5671	VN_5671	YAR028W	YAR028W	Putative integral membrane protein, member of DUP240 gene family; GFP-fusion protein is induced in response to the DNA-damaging agent MMS	Q
5672	VN_5672	YHR181W	SVP26	Integral membrane protein of the early Golgi apparatus and endoplasmic reticulum, involved in COP II vesicle transport; may also function to promote retention of proteins in the early Golgi compartment	Q
5673	VN_5673	YKL087C	CYT2	Cytochrome c1 heme lyase, involved in maturation of cytochrome c1, which is a subunit of the mitochondrial ubiquinol-cytochrome-c reductase; links heme covalently to apocytochrome c1	Q
5674	VN_5674	YMR183C	SSO2	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p	Q
5675	VN_5675	YOR036W	PEP12	Target membrane receptor (t-SNARE) for vesicular intermediates traveling between the Golgi apparatus and the vacuole; controls entry of biosynthetic, endocytic, and retrograde traffic into the prevacuolar compartment; syntaxin	Q
5676	VN_5676	YDR472W	TRS31	One of 10 subunits of the transport protein particle (TRAPP) complex of the cis-Golgi which mediates vesicle docking and fusion; involved in endoplasmic reticulum (ER) to Golgi membrane traffic	Q

5677	VN_5677	YPL076W	GPI2	Protein involved in the synthesis of N-acetylglucosaminyl phosphatidylinositol (GlcNAc-PI), the first intermediate in the synthesis of glycosylphosphatidylinositol (GPI) anchors; homologous to the human PIG-C protein	Q
5678	VN_5678	YDR503C	LPP1	Lipid phosphate phosphatase, catalyzes Mg(2+)-independent dephosphorylation of phosphatidic acid (PA), lysophosphatidic acid, and diacylglycerol pyrophosphate; involved in control of the cellular levels of phosphatidylinositol and PA	Q
5679	VN_5679	YCR075C	ERS1	Protein with similarity to human cystinosin, which is a H(+)-driven transporter involved in L-cystine export from lysosomes and implicated in the disease cystinosis; contains seven transmembrane domains	Q
5680	VN_5680	YGL098W	USE1	Essential SNARE protein localized to the ER, involved in retrograde traffic from the Golgi to the ER; forms a complex with the SNAREs Sec22p, Sec20p and Ufe1p	Q
5681	VN_5681	YAR033W	MST28	Putative integral membrane protein, involved in vesicle formation; forms complex with Mst27p; member of DUP240 gene family; binds COPI and COPII vesicles	Q
5682	VN_5682	YJL158C	CIS3	Mannose-containing glycoprotein constituent of the cell wall; member of the PIR (proteins with internal repeats) family	Q
5683	VN_5683	YER031C	YPT31	GTPase of the Ypt/Rab family, very similar to Ypt32p; involved in the exocytic pathway; mediates intra-Golgi traffic or the budding of post-Golgi vesicles from the trans-Golgi	Q
5684	VN_5684	YAR002C-A	ERP1	Protein that forms a heterotrimeric complex with Erp2p, Emp24p, and Erv25p; member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi transport and localized to COPII-coated vesicles	Q
5685	VN_5685	YLR350W	ORM2	Evolutionarily conserved protein with similarity to Orm1p, required for resistance to agents that induce the unfolded protein response; human ortholog is located in the endoplasmic reticulum	Q
5686	VN_5686	YHR026W	PPA1	Subunit c" of the vacuolar ATPase, which functions in acidification of the vacuole; one of three proteolipid subunits of the V0 domain	Strain failed to verify via PCR
5687	VN_5687	YCR027C	RHB1	Putative Rheb-related GTPase involved in regulating canavanine resistance and arginine uptake; member of the Ras superfamily of G-proteins	Q
5688	VN_5688	YKL065C	YET1	Endoplasmic reticulum transmembrane protein; may interact with ribosomes, based on co-purification experiments; homolog of human BAP31 protein	Q
5689	VN_5689	YDR084C	TVP23	Integral membrane protein localized to late Golgi vesicles along with the v-SNARE Tlg2p; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Q
5690	VN_5690	YLR229C	CDC42	Small rho-like GTPase, essential for establishment and maintenance of cell polarity; mutants have defects in the organization of actin and septins	Strain failed to verify via PCR
5691	VN_5691	YGR082W	TOM20	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins	Q
5692	VN_5692	YAR023C	YAR023C	Putative integral membrane protein, member of DUP240 gene family	Q
5693	VN_5693	YGR174C	CBP4	Mitochondrial protein required for assembly of ubiquinol cytochrome-c reductase complex (cytochrome bc1 complex); interacts with Cbp3p and function is partially redundant with that of Cbp3p	Q
5694	VN_5694	YGL210W	YPT32	GTPase of the Ypt/Rab family, very similar to Ypt31p; involved in the exocytic pathway; mediates intra-Golgi traffic or the budding of post-Golgi vesicles from the trans-Golgi	Q
5695	VN_5695	YDR246W	TRS23	One of 10 subunits of the transport protein particle (TRAPP) complex of the cis-Golgi which mediates vesicle docking and fusion; involved in endoplasmic reticulum (ER) to Golgi membrane traffic; human homolog is TRAPPC4	Q
5696	VN_5696	YAL007C	ERP2	Protein that forms a heterotrimeric complex with Erp1p, Emp24p, and Erv25p; member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi transport and localized to COPII-coated	Q

				vesicles	
5697	VN_5697	YAL059W	ECM1	Protein of unknown function, localized in the nucleoplasm and the nucleolus, genetically interacts with MTR2 in 60S ribosomal protein subunit export	Q
5698	VN_5698	YNL214W	PEX17	Peroxisomal membrane peroxin and subunit of the docking complex that facilitates the import of peroxisomal matrix proteins; required for peroxisome biogenesis	Q
5699	VN_5699	YDR373W	FRQ1	N-myristoylated calcium-binding protein that may have a role in intracellular signaling through its regulation of the phosphatidylinositol 4-kinase Pik1p; member of the recoverin/frequenin branch of the EF-hand superfamily	Q
5700	VN_5700	YGR133W	PEX4	Peroxisomal ubiquitin conjugating enzyme required for peroxisomal matrix protein import and peroxisome biogenesis	Q
5701	VN_5701	YFR045W	YFR045W	Putative mitochondrial transport protein; null mutant is viable, exhibits decreased levels of chitin and normal resistance to calcofluor white	Q
5702	VN_5702	YHR039C-A	VMA10	Subunit G of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; involved in vacuolar acidification	Q
5703	VN_5703	YMR202W	ERG2	C-8 sterol isomerase, catalyzes the isomerization of the delta-8 double bond to the delta-7 position at an intermediate step in ergosterol biosynthesis	Strain failed to verify via PCR
5704	VN_5704	YBL102W	SFT2	Non-essential tetra-spanning membrane protein found mostly in the late Golgi, can suppress some sed5 alleles; may be part of the transport machinery, but precise function is unknown; similar to mammalian syntaxin 5	Q
5705	VN_5705	YDR298C	ATP5	Subunit 5 of the stator stalk of mitochondrial F1F0 ATP synthase, which is an evolutionarily conserved enzyme complex required for ATP synthesis; homologous to bovine subunit OSCP (oligomycin sensitivity-conferring protein); phosphorylated	Q
5706	VN_5706	YML001W	YPT7	GTPase; GTP-binding protein of the rab family; required for homotypic fusion event in vacuole inheritance, for endosome-endosome fusion, similar to mammalian Rab7	Q
5707	VN_5707	YGL200C	EMP24	Integral membrane component of endoplasmic reticulum-derived COPII-coated vesicles, which function in ER to Golgi transport	Q
5708	VN_5708	YKL141W	SDH3	Cytochrome b subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer of electrons to ubiquinone	Q
5709	VN_5709	YMR150C	IMP1	Catalytic subunit of the mitochondrial inner membrane peptidase complex, required for maturation of mitochondrial proteins of the intermembrane space; complex contains Imp1p and Imp2p (both catalytic subunits), and Som1p	Q
5710	VN_5710	YOR094W	ARF3	Glucose-repressible ADP-ribosylation factor, GTPase of the Ras superfamily involved in development of polarity	Q
5711	VN_5711	YMR035W	IMP2	Catalytic subunit of the mitochondrial inner membrane peptidase complex, required for maturation of mitochondrial proteins of the intermembrane space; complex contains Imp1p and Imp2p (both catalytic subunits), and Som1p	Q
5712	VN_5712	YIR022W	SEC11	18kDa catalytic subunit of the Signal Peptidase Complex (SPC; Spc1p, Spc2p, Spc3p, and Sec11p) which cleaves the signal sequence of proteins targeted to the endoplasmic reticulum	Q
5713	VN_5713	YNR017W	TIM23	Essential component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); involved in protein import into mitochondrial matrix and inner membrane; with Tim17p, contributes to architecture and function of the import channel	Q
5714	VN_5714	YNR061C	YNR061C	Putative protein of unknown function	Q
5715	VN_5715	YHR110W	ERP5	Protein with similarity to Emp24p and Erv25p, member of the p24 family involved in ER to Golgi transport	Strain failed to verify via PCR
5716	VN_5716	YDL217C	TIM22	Essential core component of the mitochondrial TIM22 complex involved in insertion of polytopic proteins into the inner membrane; forms the channel through which proteins are imported	Strain failed to verify via PCR

5717	VN_5717	YJL004C	SYS1	Integral membrane protein of the Golgi required for targeting of the Arf-like GTPase Arl3p to the Golgi; multicopy suppressor of ypt6 null mutation	Strain failed to verify via PCR
5718	VN_5718	YPL010W	RET3	Zeta subunit of the coatamer complex (COPI), which coats Golgi-derived transport vesicles; involved in retrograde transport between Golgi and ER	Q
5719	VN_5719	YDL137W	ARF2	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf1p	Q
5720	VN_5720	YBR254C	TRS20	One of 10 subunits of the transport protein particle (TRAPP) complex of the cis-Golgi which mediates vesicle docking and fusion; mutations in the human homolog cause the spondyloepiphyseal dysplasia tarda (SEDL) disorder	Q
5721	VN_5721	YMR071C	TVP18	Integral membrane protein localized to late Golgi vesicles along with the v-SNARE Tlg2p; may interact with ribosomes, based on co-purification experiments	Strain failed to verify via PCR
5722	VN_5722	YNL093W	YPT53	GTPase, similar to Ypt51p and Ypt52p and to mammalian rab5; required for vacuolar protein sorting and endocytosis	Q
5723	VN_5723	YML012W	ERV25	Protein that forms a heterotrimeric complex with Erp1, Erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport	Q
5724	VN_5724	YOR016C	ERP4	Protein with similarity to Emp24p and Erv25p, member of the p24 family involved in ER to Golgi transport	Q
5725	VN_5725	YJR118C	ILM1	Protein of unknown function; may be involved in mitochondrial DNA maintenance; required for slowed DNA synthesis-induced filamentous growth	Q
5726	VN_5726	YIR032C	DAL3	Ureidoglycolate hydrolase, converts ureidoglycolate to glyoxylate and urea in the third step of allantoin degradation; expression sensitive to nitrogen catabolite repression	Q
5727	VN_5727	YCL001W	RER1	Protein involved in retention of membrane proteins, including Sec12p, in the ER; localized to Golgi; functions as a retrieval receptor in returning membrane proteins to the ER	Q
5728	VN_5728	YDL192W	ARF1	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated vesicle formation in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p	Q
5729	VN_5729	YFL067W	YFL067W	Protein of unknown function, down-regulated at low calcium levels	Strain failed to verify via PCR
5730	VN_5730	YMR292W	GOT1	Evolutionarily conserved non-essential protein present in early Golgi cisternae that may be involved in ER-Golgi transport at a step after vesicle tethering to Golgi membranes, exhibits membrane topology similar to that of Sft2p	Q
5731	VN_5731	YFL068W	YFL068W	Putative protein of unknown function	Strain failed to verify via PCR
5732	VN_5732	YOR185C	GSP2	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; interacts with Kap121p, Kap123p and Pdr6p (karyophilin betas); Gsp1p homolog that is not required for viability	Q
5733	VN_5733	YJL097W	PHS1	Essential 3-hydroxyacyl-CoA dehydratase of the ER membrane, involved in elongation of very long-chain fatty acids; evolutionarily conserved, similar to mammalian PTPLA and PTPLB; involved in sphingolipid biosynthesis and protein trafficking	Q
5734	VN_5734	YKL119C	VPH2	Integral membrane protein required for vacuolar H ⁺ -ATPase (V-ATPase) function, although not an actual component of the V-ATPase complex; functions in the assembly of the V-ATPase; localized to the endoplasmic reticulum (ER)	Q
5735	VN_5735	YDL212W	SHR3	Endoplasmic reticulum packaging chaperone, required for incorporation of amino acid permeases into COPII coated vesicles for transport to the cell surface	Q
5736	VN_5736	YBR171W	SEC66	Non-essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-dependent and post-translational SRP-independent	Q

				protein targeting and import into the ER	
5737	VN_5737	YMR264W	CUE1	Endoplasmic reticulum membrane protein that recruits the ubiquitin-conjugating enzyme Ubc7p to the ER where it functions in protein degradation; contains a CUE domain that binds ubiquitin to facilitate intramolecular monoubiquitination	Q
5738	VN_5738	YLR292C	SEC72	Non-essential subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-dependent and post-translational SRP-independent protein targeting and import into the ER	Q
5739	VN_5739	YDR178W	SDH4	Membrane anchor subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer of electrons to ubiquinone	Q
5740	VN_5740	YGL010W	YGL010W	Putative protein of unknown function; YGL010W is not an essential gene	Q
5741	VN_5741	YGL259W	YPS5	Protein with similarity to GPI-anchored aspartic proteases such as Yap1p and Yap3p	Q
5742	VN_5742	YIL016W	SNL1	Protein of unknown function proposed to be involved in nuclear pore complex biogenesis and maintenance as well as protein folding; has similarity to the mammalian BAG-1 protein	Q
5743	VN_5743	YPR113W	PIS1	Phosphatidylinositol synthase, required for biosynthesis of phosphatidylinositol, which is a precursor for polyphosphoinositides, sphingolipids, and glycolipid anchors for some of the plasma membrane proteins	Q
5744	VN_5744	YMR197C	VTI1	Protein involved in cis-Golgi membrane traffic; v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p; required for multiple vacuolar sorting pathways	Q
5745	VN_5745	YLR262C	YPT6	GTPase, Ras-like GTP binding protein involved in the secretory pathway, required for fusion of endosome-derived vesicles with the late Golgi, maturation of the vacuolar carboxypeptidase Y; has similarity to the human GTPase, Rab6	Q
5746	VN_5746	YNR049C	MSO1	Probable component of the secretory vesicle docking complex, acts at a late step in secretion; shows genetic and physical interactions with Sec1p; required for prospore membrane formation during sporulation	Q
5747	VN_5747	YNL044W	YIP3	Protein localized to COPII vesicles, proposed to be involved in ER to Golgi transport; interacts with members of the Rab GTPase family and Yip1p; also interacts with Rtn1p	Q
5748	VN_5748	YLR066W	SPC3	Subunit of signal peptidase complex (Spc1p, Spc2p, Spc3p, Sec11p), which catalyzes cleavage of N-terminal signal sequences of proteins targeted to the secretory pathway; homologous to mammalian SPC22/23	Q
5749	VN_5749	YHR060W	VMA22	Peripheral membrane protein that is required for vacuolar H ⁺ -ATPase (V-ATPase) function, although not an actual component of the V-ATPase complex; functions in the assembly of the V-ATPase; localized to the yeast endoplasmic reticulum (ER)	Q
5750	VN_5750	YKL016C	ATP7	Subunit d of the stator stalk of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis	Q
5751	VN_5751	YJL024C	APS3	Small subunit of the clathrin-associated adaptor complex AP-3, which is involved in vacuolar protein sorting; related to the sigma subunit of the mammalian clathrin AP-3 complex; suppressor of loss of casein kinase 1 function	Q
5752	VN_5752	YGL002W	ERP6	Protein with similarity to Emp24p and Erv25p, member of the p24 family involved in ER to Golgi transport; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	Q
5753	VN_5753	YLR268W	SEC22	R-SNARE protein; assembles into SNARE complex with Bet1p, Bos1p and Sed5p; cycles between the ER and Golgi complex; involved in anterograde and retrograde transport between the ER and Golgi; synaptobrevin homolog	Q
5754	VN_5754	YOR089C	VPS21	GTPase required for transport during endocytosis and for correct sorting of vacuolar hydrolases; localized in endocytic intermediates; detected in mitochondria; geranylgeranylation required for membrane association; mammalian Rab5 homolog	Q

5755	VN_5755	YJR073C	OPI3	Phospholipid methyltransferase (methylene-fatty-acyl-phospholipid synthase), catalyzes the last two steps in phosphatidylcholine biosynthesis	Q
5756	VN_5756	YOR297C	TIM18	Component of the mitochondrial TIM22 complex involved in insertion of polytopic proteins into the inner membrane; may mediate assembly or stability of the complex	Q
5757	VN_5757	YBR164C	ARL1	Soluble GTPase with a role in regulation of membrane traffic; regulates potassium influx; G protein of the Ras superfamily, similar to ADP-ribosylation factor	Q
5758	VN_5758	YPR149W	NCE102	Protein of unknown function; contains transmembrane domains; involved in secretion of proteins that lack classical secretory signal sequences; component of the detergent-insoluble glycolipid-enriched complexes (DIGs)	Q
5759	VN_5759	YDR491C	YDR491C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Q
5760	VN_5760	YJL143W	TIM17	Essential subunit of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); with Tim23p, contributes to the architecture and function of the import channel; may link the import motor to the core TIM23 complex	Strain failed to verify via PCR
5761	VN_5761	YLR170C	APS1	Small subunit of the clathrin-associated adaptor complex AP-1, which is involved in protein sorting at the trans-Golgi network; homolog of the sigma subunit of the mammalian clathrin AP-1 complex	Q
5762	VN_5762	YLL052C	AQY2	Water channel that mediates the transport of water across cell membranes, only expressed in proliferating cells, controlled by osmotic signals, may be involved in freeze tolerance; disrupted by a stop codon in many <i>S. cerevisiae</i> strains	Q
5763	VN_5763	YGR183C	QCR9	Subunit 9 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; required for electron transfer at the ubiquinol oxidase site of the complex	Q
5764	VN_5764	YJR086W	STE18	G protein gamma subunit, forms a dimer with Ste4p to activate the mating signaling pathway, forms a heterotrimer with Gpa1p and Ste4p to dampen signaling; C-terminus is palmitoylated and farnesylated, which are required for normal signaling	Q
5765	VN_5765	YAR069C	YAR069C	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Q
5766	VN_5766	YGL187C	COX4	Subunit IV of cytochrome c oxidase, the terminal member of the mitochondrial inner membrane electron transport chain; precursor N-terminal 25 residues are cleaved during mitochondrial import; phosphorylated; spermidine enhances translation	Strain failed to verify via PCR
5767	VN_5767	YHR051W	COX6	Subunit VI of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; expression is regulated by oxygen levels	Q
5768	VN_5768	YGL226C-A	OST5	Zeta subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes asparagine-linked glycosylation of newly synthesized proteins	Q
5769	VN_5769	YBL078C	ATG8	Component of autophagosomes and Cvt vesicles; undergoes conjugation to phosphatidylethanolamine (PE); Atg8p-PE is anchored to membranes, is involved in phagophore expansion, and may mediate membrane fusion during autophagosome formation	Q
5770	VN_5770	YJR010C-A	SPC1	Subunit of the signal peptidase complex (SPC), which cleaves the signal sequence from proteins targeted to the endoplasmic reticulum (ER), homolog of the SPC12 subunit of mammalian signal peptidase complex	Strain failed to verify via PCR
5771	VN_5771	YOL077W-A	ATP19	Subunit k of the mitochondrial F1F0 ATP synthase, which is a large enzyme complex required for ATP synthesis; associated only with the dimeric form of ATP synthase	Strain failed to verify via PCR
5772	VN_5772	YEL017C-A	PMP2	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p); regulates plasma membrane H(+)-ATPase activity; nearly identical to PMP1	Strain failed to verify via PCR
5773	VN_5773	YIL065C	FIS1	Protein involved in mitochondrial membrane fission and peroxisome abundance; required for localization of Dnm1p and Mdv1p during mitochondrial division; mediates ethanol-induced apoptosis and ethanol-induced mitochondrial fragmentation	Strain failed to verify via PCR

5774	VN_5774	YFR033C	QCR6	Subunit 6 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; highly acidic protein; required for maturation of cytochrome c1	Q
5775	VN_5775	YDR519W	FPR2	Membrane-bound peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; expression pattern suggests possible involvement in ER protein trafficking	Strain failed to verify via PCR
5776	VN_5776	YDL039C	PRM7	Pheromone-regulated protein, predicted to have one transmembrane segment; promoter contains Gcn4p binding elements	Strain failed to verify via PCR
5777	VN_5777	YGR209C	TRX2	Cytoplasmic thioredoxin isoenzyme of the thioredoxin system which protects cells against oxidative and reductive stress, forms LMA1 complex with Pbi2p, acts as a cofactor for Tsa1p, required for ER-Golgi transport and vacuole inheritance	Strain failed to verify via PCR
5778	VN_5778	YPL271W	ATP15	Epsilon subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis; phosphorylated	Strain failed to verify via PCR
5779	VN_5779	YCR024C-A	PMP1	Small single-membrane span proteolipid that functions as a regulatory subunit of the plasma membrane H(+)-ATPase Pma1p, forms unique helix and positively charged cytoplasmic domain that is able to specifically segregate phosphatidylserines	Strain failed to verify via PCR
5780	VN_5780	YAL030W	SNC1	Vesicle membrane receptor protein (v-SNARE) involved in the fusion between Golgi-derived secretory vesicles with the plasma membrane; proposed to be involved in endocytosis; member of the synaptobrevin/VAMP family of R-type v-SNARE proteins	Q
5781	VN_5781	YJR058C	APS2	Small subunit of the clathrin-associated adaptor complex AP-2, which is involved in protein sorting at the plasma membrane; related to the sigma subunit of the mammalian plasma membrane clathrin-associated protein (AP-2) complex	Strain failed to verify via PCR
5782	VN_5782	YLR110C	CCW12	Cell wall mannoprotein, mutants are defective in mating and agglutination, expression is downregulated by alpha-factor	Q
5783	VN_5783	YOR327C	SNC2	Vesicle membrane receptor protein (v-SNARE) involved in the fusion between Golgi-derived secretory vesicles with the plasma membrane; member of the synaptobrevin/VAMP family of R-type v-SNARE proteins	Strain failed to verify via PCR
5784	VN_5784	YLR043C	TRX1	Cytoplasmic thioredoxin isoenzyme of the thioredoxin system which protects cells against oxidative and reductive stress, forms LMA1 complex with Pbi2p, acts as a cofactor for Tsa1p, required for ER-Golgi transport and vacuole inheritance	Strain failed to verify via PCR
5785	VN_5785	YER087C-A	YER087C-A	Dubious open reading frame unlikely to encode a protein, based on experimental and comparative sequence data; overlaps the uncharacterized gene YER087W, a putative tRNA synthetase	Strain failed to verify via PCR
5786	VN_5786	YNL052W	COX5A	Subunit Va of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; predominantly expressed during aerobic growth while its isoform Vb (Cox5Bp) is expressed during anaerobic growth	Strain failed to verify via PCR
5787	VN_5787	YNL328C	MDJ2	Constituent of the mitochondrial import motor associated with the presequence translocase; function overlaps with that of Pam18p; stimulates the ATPase activity of Ssc1p to drive mitochondrial import; contains a J domain	Strain failed to verify via PCR
5788	VN_5788	YGL042C	YGL042C	Dubious open reading frame, not conserved in closely related Saccharomyces species; deletion mutation blocks replication of Brome mosaic virus in S. cerevisiae, but this is likely due to effects on the overlapping gene DST1	Strain failed to verify via PCR
5789	VN_5789	YMR256C	COX7	Subunit VII of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain	Strain failed to verify via PCR
5790	VN_5790	YNL131W	TOM22	Component of the TOM (translocase of outer mitochondrial membrane) complex responsible for initial import of mitochondrially directed proteins; acts as a receptor for precursor proteins and mediates interaction between TOM and TIM complexes	Strain failed to verify via PCR
5791	VN_5791	YKL006C-A	SFT1	Intra-Golgi v-SNARE, required for transport of proteins between an early and a later Golgi compartment	Strain failed to verify via PCR

5792	VN_5792	YPL192C	PRM3	Pheromone-regulated protein required for nuclear envelope fusion during karyogamy; localizes to the outer face of the nuclear membrane; interacts with Kar5p at the spindle pole body	Strain failed to verify via PCR
5793	VN_5793	YGR228W	YGR228W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially overlaps the verified ORF SMI1/YGR229C	Strain failed to verify via PCR
5794	VN_5794	YLR444C	YLR444C	Dubious open reading frame unlikely to encode a functional protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
5795	VN_5795	YDR086C	SSS1	Subunit of the Sec61p translocation complex (Sec61p-Sss1p-Sbh1p) that forms a channel for passage of secretory proteins through the endoplasmic reticulum membrane, and of the Ssh1p complex (Ssh1p-Sbh2p-Sss1p); interacts with Ost4p and Wbp1p	Strain failed to verify via PCR
5796	VN_5796	YPL170W	DAP1	Heme-binding protein involved in regulation of cytochrome P450 protein Erg11p; damage response protein, related to mammalian membrane progesterone receptors; mutations lead to defects in telomeres, mitochondria, and sterol synthesis	Strain failed to verify via PCR
5797	VN_5797	YPR017C	DSS4	Guanine nucleotide dissociation stimulator for Sec4p, functions in the post-Golgi secretory pathway; binds zinc, found both on membranes and in the cytosol	Strain failed to verify via PCR
5798	VN_5798	YER072W	VTC1	Subunit of the vacuolar transporter chaperone (VTC) complex involved in membrane trafficking, vacuolar polyphosphate accumulation, microautophagy and non-autophagic vacuolar fusion	Strain failed to verify via PCR
5799	VN_5799	YEL039C	CYC7	Cytochrome c isoform 2, expressed under hypoxic conditions; electron carrier of the mitochondrial intermembrane space that transfers electrons from ubiquinone-cytochrome c oxidoreductase to cytochrome c oxidase during cellular respiration	Strain failed to verify via PCR
5800	VN_5800	YAR064W	YAR064W	Putative protein of unknown function	Strain failed to verify via PCR
5801	VN_5801	YGR105W	VMA21	Integral membrane protein that is required for vacuolar H ⁺ -ATPase (V-ATPase) function, although not an actual component of the V-ATPase complex; functions in the assembly of the V-ATPase; localized to the yeast endoplasmic reticulum (ER)	Strain failed to verify via PCR
5802	VN_5802	YML081C-A	ATP18	Subunit of the mitochondrial F1F0 ATP synthase, which is a large enzyme complex required for ATP synthesis; termed subunit I or subunit j; does not correspond to known ATP synthase subunits in other organisms	Strain failed to verify via PCR
5803	VN_5803	YBR266C	SLM6	Protein with a potential role in actin cytoskeleton organization; gene exhibits synthetic genetic interaction with MSS4 encoding phosphatidylinositol 4-phosphate kinase	Strain failed to verify via PCR
5804	VN_5804	YGL054C	ERV14	Protein localized to COPII-coated vesicles, involved in vesicle formation and incorporation of specific secretory cargo; required for the delivery of bud-site selection protein Axl2p to cell surface; related to Drosophila cornichon	Strain failed to verify via PCR
5805	VN_5805	YDR529C	QCR7	Subunit 7 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; oriented facing the mitochondrial matrix; N-terminus appears to play a role in complex assembly	Strain failed to verify via PCR
5806	VN_5806	YGL024W	YGL024W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data; partially/completely overlaps the verified ORF PGD1/YGL025C	Strain failed to verify via PCR
5807	VN_5807	YAR053W	YAR053W	Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data	Strain failed to verify via PCR
5808	VN_5808	YAR029W	YAR029W	Member of DUP240 gene family but contains no transmembrane domains; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern	Strain failed to verify via PCR
5809	VN_5809	YDR276C	PMP3	Small plasma membrane protein related to a family of plant polypeptides that are overexpressed under high salt concentration or low temperature, not essential for viability, deletion causes hyperpolarization of the plasma membrane potential	Strain failed to verify via PCR