

**Supplementary data 1.** Microsoft excel file containing the lists of gene deletions determined to be sensitive to each metal. Gene functions listed and taken from [www.yeastgenome.org](http://www.yeastgenome.org).

GENE	RATIO	P-VALUE	FUNCTION
AAT2	0.279409892	0.004466638	Cytosolic aspartate aminotransferase, involved in nitrogen metabolism; localizes to peroxisomes in oleate-grown cells
ABM1	0.439672485	1.63188E-11	Protein of unknown function, required for normal microtubule organization
ADK1	0.342970399	0	Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; lacks cleavable signal sequence
AFT1	0.062296826	0	Transcription factor involved in iron utilization and homeostasis
ALG9	0.383502637	0	Mannosyltransferase, involved in N-linked glycosylation; catalyzes the transfer of mannose from Dol-P-Man to lipid-linked oligosaccharides
APQ12	0.140645221	0	Protein involved in nucleocytoplasmic transport of mRNA
ARE1	0.317873164	0	Acyl-CoA:sterol acyltransferase, isozyme of Are2p; endoplasmic reticulum enzyme that contributes the major sterol esterification activity in the absence of oxygen
ARF1	0.151197323	0	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
ARL1	0.281441505	0	Soluble GTPase with a role in regulation of membrane traffic; regulates potassium influx;
ARO1	0.263396129	1.36807E-10	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids
ARO2	0.469966873	3.08309E-13	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
ARO7	0.182867439	0	Chorismate mutase, catalyzes the conversion of chorismate to prephenate to initiate the tyrosine/phenylalanine-specific branch of aromatic amino acid biosynthesis
ASH1	0.315272509	0	Zinc-finger inhibitor of HO transcription; mRNA is localized and translated in the distal tip of anaphase cells, resulting in accumulation of Ash1p in daughter cell nuclei and inhibition of HO expression;
ATG11	0.159818	0	Adapter protein for pexophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway
ATG22	0.422863037	7.73248E-06	Vacuolar integral membrane protein required for efflux of amino acids during autophagic body breakdown in the vacuole
ATX1	0.308917665	0	Cytosolic copper metallochaperone that transports copper to the secretory vesicle copper transporter Ccc2p for eventual insertion into Fet3p
BRO1	0.387336235	0.001747918	Cytoplasmic class E vacuolar protein sorting (VPS) factor that coordinates deubiquitination in the multivesicular body (MVB) pathway by recruiting Doa4p to endosomes
BUB3	0.225721485	1.1706E-06	Kinetochore checkpoint WD40 repeat protein that localizes to kinetochores during prophase and metaphase, delays anaphase in the presence of unattached kinetochores;
CAC2	0.239059372	0	Component of the chromatin assembly complex (with Rif2p and Msi1p) that assembles newly synthesized histones onto recently replicated DNA, required for building functional kinetochores, conserved from yeast to humans
CCC2	0.05341047	0	Cu(+2)-transporting P-type ATPase, required for export of copper from the cytosol into an extracytosolic compartment
CCR4	0.199875288	7.55951E-13	Component of the CCR4-NOT transcriptional complex, which is involved in regulation of gene expression
CCS1	0.132569633	0	Copper chaperone for superoxide dismutase Sod1p, involved in oxidative stress protection
CDC50	0.051960042	0	Endosomal protein that regulates cell polarity, controls polarized growth; similar to Ynr048wp and Lem3p
CIK1	0.199109159	0	Kinesin-associated protein required for both karyogamy and mitotic spindle organization
CIN5	0.207100244	0	Basic leucine zipper (bZIP) transcriptional factor of the yAP-1 family that mediates pleiotropic drug resistance and salt tolerance
CKB1	0.428123948	6.68698E-12	Beta regulatory subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation
CKB2	0.279212406	0	Beta' regulatory subunit of casein kinase 2, a Ser/Thr protein kinase with roles in cell growth and proliferation;
COG6	0.482671959	0	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
COT1	0.113326701	0	Vacuolar transporter that mediates zinc transport into the vacuole; overexpression confers resistance to cobalt and rhodium
CUE1	0.268208256	5.7664E-08	Endoplasmic reticulum membrane protein that recruits the ubiquitin-conjugating enzyme Ubc7p to the ER where it functions in protein degradation;
CYS3	0.33869265	0	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
CYS4	0.150886314	0	Cystathionine beta-synthase, catalyzes the synthesis of cystathionine from serine and homocysteine, the first committed step in cysteine biosynthesis
DBF2	0.318606726	0	Ser/Thr kinase involved in transcription and stress response; functions as part of a network of genes in exit from mitosis
DCW1	0.387328029	2.22045E-16	Putative mannosidase, GPI-anchored membrane protein required for cell wall biosynthesis in bud formation;homologous to Dfg5p
DEF1	0.085581367	0	RNAPII degradation factor, forms a complex with Rad26p in chromatin
DEG1	0.309417996	3.35393E-06	Non-essential tRNA:pseudouridine synthase, introduces pseudouridines at position 38 or 39 in tRNA, important for maintenance of translation efficiency and normal cell growth
DEM1	0.236241357	0.000304753	Mitochondrial protein of unknown function
DHH1	0.258846878	2.02162E-09	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
DID2	0.417910377	2.20291E-07	Class E protein of the vacuolar protein-sorting (Vps) pathway
DID4	0.219020007	0	Class E Vps protein of the ESCRT-III complex, required for sorting of integral membrane proteins into luminal vesicles of multivesicular bodies, and for delivery of newly synthesized vacuolar enzymes to the vacuole, involved in endocytosis
DOA1	0.336070159	0	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
DOA4	0.224372379	5.66069E-12	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
DRS2	0.061940993	0	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
EAP1	0.203992034	0	eIF4E-associated protein, binds eIF4E and inhibits cap-dependent translation, also functions independently of eIF4E to maintain genetic stability; plays a role in cell growth, implicated in the TOR signaling cascade
ELM1	0.260853899	4.79727E-13	Serine/threonine protein kinase that regulates cellular morphogenesis, septin behavior, and cytokinesis;
ERG3	0.268039707	0	C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into episterol, a precursor in ergosterol biosynthesis
FAB1	0.286476877	0	1-phosphatidylinositol-3-phosphate 5-kinase; vacuolar membrane kinase that generates phosphatidylinositol (3,5)P2, which is involved in vacuolar sorting and homeostasis
FET3	0.056132816	0	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity
FRE1	0.325845098	8.0591E-07	Ferric reductase and cupric reductase, reduces siderophore-bound iron and oxidized copper prior to uptake by transporters
FTR1	0.0530946	0	High affinity iron permease involved in the transport of iron across the plasma membrane;
FYV6	0.246814248	0	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
GEF1	0.124293176	0	Voltage-gated chloride channel localized to the golgi, the endosomal system, and plasma membrane, and involved in cation homeostasis
GLO4	0.430660428	0	Mitochondrial glyoxalase II, catalyzes the hydrolysis of S-D-lactoylglutathione into glutathione and D-lactate
GYP1	0.135924681	0	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
HNM1	0.382853462	0.000523312	Choline/ethanolamine transporter; involved in the uptake of nitrogen mustard and the uptake of glycine betaine during hypersaline stress;
HPF1	0.169717218	0	Haze-protective mannoprotein that reduces the particle size of aggregated proteins in white wines
HSL7	0.478564132	0	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
ICE2	0.292373261	0	Integral ER membrane protein with type-III transmembrane domains; mutations cause defects in cortical ER morphology in both the mother and daughter cells
IRS4	0.147470028	0	EH domain-containing protein involved in regulating phosphatidylinositol 4,5-bisphosphate levels and autophagy
KEM1	0.173143986	0	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
KEX2	0.1342448	0	Subtilisin-like protease (proprotein convertase), a calcium-dependent serine protease involved in the activation of proproteins of the secretory pathway
KRE1	0.267064072	0	Cell wall glycoprotein involved in beta-glucan assembly
KTI12	0.218078962	0	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
MAC1	0.24588381	0	Copper-sensing transcription factor involved in regulation of genes required for high affinity copper transport
MCH5	0.217193108	0	Plasma membrane riboflavin transporter; facilitates the uptake of vitamin B2; required for FAD-dependent processes
MDM10	0.313651742	2.44249E-15	Subunit of both the Mdm10-Mdm12-Mmm1 complex and the mitochondrial sorting and assembly machinery (SAM complex);
MDM12	0.303310567	0	Mitochondrial outer membrane protein, required for transmission of mitochondria to daughter cells;
MGA2	0.13881104	0	ER membrane protein involved in regulation of OLE1 transcription
MGR2	0.28300121	1.73676E-10	Protein required for growth of cells lacking the mitochondrial genome
MIC17	0.154549516	0	Mitochondrial intermembrane space cysteine motif protein;
MID1	0.291880046	1.57763E-13	N-glycosylated integral membrane protein of the ER membrane and plasma membrane, functions as a stretch-activated Ca2+-permeable cation channel required for Ca2+ influx stimulated by pheromone
MNN10	0.349173363	0	Subunit of a Golgi mannosyltransferase complex also containing Anp1p, Mnn9p, Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan backbone
MNN11	0.33671476	0.000101918	Subunit of a Golgi mannosyltransferase complex that also contains Anp1p, Mnn9p, Mnn10p, and Hoc1p, and mediates elongation of the polysaccharide mannan backbone;

MON1	0.044743917	0	Protein required for fusion of cvt-vesicles and autophagosomes with the vacuole
MRE11	0.135650265	0	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
MRP1	0.15769405	0.000229571	Mitochondrial ribosomal protein of the small subunit
MRPL3	0.077505102	0	Mitochondrial ribosomal protein of the large subunit
MRPL36	0.316419181	1.89959E-08	Mitochondrial ribosomal protein of the large subunit
MRPL7	0.373995029	1.96065E-06	Mitochondrial ribosomal protein of the large subunit
MRPS5	0.121448173	0	overlaps the verified gene MRPL38
MRPS8	0.443740131	0	Mitochondrial ribosomal protein of the small subunit
MTD1	0.45481692	1.1969E-07	NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase, plays a catalytic role in oxidation of cytoplasmic one-carbon units
MTG1	0.430890615	2.15294E-05	Peripheral GTPase of the mitochondrial inner membrane, essential for respiratory competence, likely functions in assembly of the large ribosomal subunit, has homologs in plants and animals
NBP2	0.407021937	0	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
NCS2	0.216062217	0	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
NCS6	0.448411954	0	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;
NDE1	0.337616317	1.52995E-05	Mitochondrial external NADH dehydrogenase, a type II NAD(P)H:quinone oxidoreductase that catalyzes the oxidation of cytosolic NADH
NHX1	0.059384051	0	Endosomal Na <sup>+</sup> /H <sup>+</sup> exchanger, required for intracellular sequestration of Na <sup>+</sup> ; required for osmotolerance to acute hypertonic shock
NOP16	0.312386137	4.04099E-12	Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis
NUP188	0.251303205	0	Subunit of the nuclear pore complex (NPC), involved in the structural organization of the complex and of the nuclear envelope
OPI8	0.46342933	1.53814E-10	Dubious open reading frame, partially overlaps verified gene DID2
OPT2	0.086217256	0	Oligopeptide transporter; member of the OPT family
PDR16	0.363685965	1.28114E-10	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p
PEA2	0.347284322	4.8597E-10	Coiled-coil polarisome protein required for polarized morphogenesis, cell fusion, and low affinity Ca <sup>2+</sup> influx; forms polarisome complex with Bni1p, Bud6p, and Spa2p; localizes to sites of polarized growth
PEP12	0.076081989	0	Target membrane receptor (t-SNARE) for vesicular intermediates traveling between the Golgi apparatus and the vacuole
PFS1	0.241482008	0	Sporulation protein required for prospore membrane formation at selected spindle pole
PHO86	0.148733568	0	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
PHO88	0.222274299	9.64446E-09	Probable membrane protein, involved in phosphate transport
PIL1	0.266144844	0	Primary component of eisosomes, which are large immobile cell cortex structures associated with endocytosis
PKR1	0.082922168	0	V-ATPase assembly factor, functions with other V-ATPase assembly factors in the ER to efficiently assemble the V-ATPase membrane sector
PLC1	0.360595592	0.000932711	Phospholipase C, hydrolyzes phosphatidylinositol 4,5-bisphosphate (PIP2) to generate the signaling molecules inositol 1,4,5-triphosphate (IP3) and 1,2-diaclyglycerol (DAG); involved in regulating many cellular processes
POP2	0.143331799	0	RNase of the DEDD superfamily, subunit of the Ccr4-Not complex that mediates 3' to 5' mRNA deadenylation
PTC1	0.267004227	0	Type 2C protein phosphatase (PP2C); inactivates the osmosensing MAPK cascade by dephosphorylating Hog1p
PTC6	0.268692385	0	Mitochondrial protein phosphatase of type 2C with similarity to mammalian PP1Ks
PUB1	0.319797121	1.36511E-10	Poly (A) <sup>+</sup> 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
QRI8	0.268499902	0	Ubiquitin conjugating enzyme, involved in the ER-associated protein degradation pathway; requires Cue1p for recruitment to the ER membrane
RAV1	0.221476835	0	Subunit of the RAVE complex (Rav1p, Rav2p, Skp1p), which promotes assembly of the V-ATPase holoenzyme
RAV2	0.340028993	0	Subunit of RAVE (Rav1p, Rav2p, Skp1p), a complex that associates with the V1 domain of the vacuolar membrane (H <sup>+</sup> )-ATPase (V-ATPase) and promotes assembly and reassembly of the holoenzyme
RCY1	0.079114783	0	F-box protein involved in recycling plasma membrane proteins internalized by endocytosis; localized to sites of polarized growth
RHO4	0.167039182	0	Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins
RIP1	0.138649209	0	Ubiquinol-cytochrome-c reductase, a Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex; transfers electrons from ubiquinol to cytochrome c1 during respiration
RPL14A	0.242770558	0	N-terminally acetylated protein component of the large (60S) ribosomal subunit
RPL42A	0.37139954	0	Protein component of the large (60S) ribosomal subunit,
RPN4	0.058946659	0	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
RPS17A	0.348886799	0.003837145	Ribosomal protein 51 (rp51) of the small (40s) subunit
RPS22A	0.387414585	3.33416E-11	Protein component of the small (40S) ribosomal subunit;
RPS25A	0.238556452	0	Protein component of the small (40S) ribosomal subunit
RPS4A	0.389415896	2.36676E-08	Protein component of the small (40S) ribosomal subunit
SAC1	0.074621214	0	Phosphatidylinositol phosphate (PtdInsP) phosphatase involved in hydrolysis of PtdIns[4]P
SAC7	0.380757907	9.74423E-05	GTPase activating protein (GAP) for Rho1p, involved in signaling to the actin cytoskeleton,
SAM37	0.334452537	7.77156E-16	Component of the mitochondrial outer membrane sorting and assembly machinery (SAM) complex
SEL1	0.123216515	0	Protein involved in ER-associated protein degradation
SHE4	0.075458186	0	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
SLA1	0.419715392	0	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
SNF12	0.180789803	3.88578E-15	73 kDa subunit of the SWI/SNF chromatin remodeling complex involved in transcriptional regulation
SOD1	0.076325748	0	Cytosolic superoxide dismutase; some mutations are analogous to those that cause ALS (amyotrophic lateral sclerosis) in humans
SPO11	0.23175225	0	Meiosis-specific protein that initiates meiotic recombination by catalyzing the formation of double-strand breaks in DNA via a transesterification reaction
SPT10	0.211100813	0	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
SPT2	0.375103179	0.000801271	Protein involved in negative regulation of transcription; required for RNA polyadenylation; exhibits regulated interactions with both histones and SWI-SNF components
SPT2	0.39320317	0.000426315	Protein involved in negative regulation of transcription; required for RNA polyadenylation; exhibits regulated interactions with both histones and SWI-SNF components,
SPT20	0.265974532	6.94825E-06	Subunit of the SAGA transcriptional regulatory complex, involved in maintaining the integrity of the complex
SPT7	0.308176303	4.37098E-05	Subunit of the SAGA transcriptional regulatory complex, involved in proper assembly of the complex
SSN3	0.064071564	0	Cyclin-dependent protein kinase, component of RNA polymerase II holoenzyme;
SSN8	0.052775514	0	Cyclin-like component of the RNA polymerase II holoenzyme
STE24	0.452382264	3.00259E-09	Highly conserved zinc metalloprotease that functions in two steps of a-factor maturation
SWI3	0.159752155	0	Subunit of the SWI/SNF chromatin remodeling complex, which regulates transcription by remodeling chromosomes
SWP82	0.352135037	0	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
TCM62	0.284555762	0	Protein involved in the assembly of the mitochondrial succinate dehydrogenase complex; putative chaperone
TEF4	0.12320827	0	Translation elongation factor EF-1 gamma
TFP1	0.165397668	0	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites;
TFP3	0.190693983	0	Vacuolar ATPase V0 domain subunit c', involved in proton transport activit
TLG2	0.157675252	0	Syntaxin-like t-SNARE that forms a complex with Tlg1p and Vti1p and mediates fusion of endosome-derived vesicles with the late Golgi
TOM5	0.380454189	9.04738E-07	Small mitochondrial outer membrane protein crucial to a binding relay for the import of proteins into mitochondria
TOP1	0.067788256	0	Topoisomerase I, nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone
TPD3	0.182282178	0	Regulatory subunit A of the heterotrimeric protein phosphatase 2A, which also contains regulatory subunit Cdc55p and either catalytic subunit Pph21p or Pph22p; required for cell morphogenesis and for transcription by RNA polymerase III
TRM9	0.357527351	0	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
TRP1	0.164507258	0	Phosphoribosylanthranilate isomerase that catalyzes the third step in tryptophan biosynthesis
TRP2	0.0982352	0	Anthranilate synthase, catalyzes the initial step of tryptophan biosynthesis
TRP3	0.105691851	0	Bifunctional enzyme exhibiting both indole-3-glycerol-phosphate synthase and anthranilate synthase activities
TRP4	0.080306926	0	Anthranilate phosphoribosyl transferase of the tryptophan biosynthetic pathway
UBA4	0.213372873	6.77236E-15	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
UBC13	0.3854464871	0	Ubiquitin-conjugating enzyme involved in the error-free DNA postreplication repair pathway;

UBX4	0.34647126	4.5387E-12	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p
UFD2	0.175300179	0	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
UMP1	0.272116228	7.31637E-12	Short-lived chaperone required for correct maturation of the 20S proteasome;
VAN1	0.415352326	3.75255E-14	Component of the mannan polymerase I
VMA13	0.101306302	0	Subunit H of the eight-subunit V1 peripheral membrane domain of the vacuolar H <sup>+</sup> -ATPase (V-ATPase),
VMA5	0.158692689	0	Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H <sup>+</sup> -ATPase (V-ATPase)
VMA8	0.199478926	0	Subunit D of the eight-subunit V1 peripheral membrane domain of the vacuolar H <sup>+</sup> -ATPase (V-ATPase)
VPH1	0.161090328	0	Subunit a of vacuolar-ATPase V0 domain,
VPS15	0.313341466	2.24631E-10	Myristoylated serine/threonine protein kinase involved in vacuolar protein sorting; functions as a membrane-associated complex with Vps34p
VPS16	0.091857699	0	Subunit of the vacuole fusion and protein sorting HOPS complex and the CORVET tethering complex
VPS24	0.320153004	0	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
VPS27	0.208046933	0	Endosomal protein that forms a complex with Hse1p; required for recycling Golgi proteins, forming luminal membranes and sorting ubiquitinated proteins destined for degradation;
VPS3	0.134580741	0	Component of CORVET tethering complex; cytoplasmic protein required for the sorting and processing of soluble vacuolar proteins, acidification of the vacuolar lumen, and assembly of the vacuolar H <sup>+</sup> -ATPase
VPS34	0.122210165	0	Phosphatidylinositol 3-kinase responsible for the synthesis of phosphatidylinositol 3-phosphate; forms membrane-associated signal transduction complex with Vps15p to regulate protein sorting
VPS4	0.243602504	0	AAA-ATPase involved in multivesicular body (MVB) protein sorting, ATP-bound Vps4p localizes to endosomes and catalyzes ESCRT-III disassembly and membrane release;
VPS51	0.204593138	0	Component of the GARP (Golgi-associated retrograde protein) complex
VPS52	0.114381382	0	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;
VPS53	0.107379217	0	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
VPS66	0.133800607	0	Cytoplasmic protein of unknown function involved in vacuolar protein sorting.
VPS8	0.461767234	0	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
VPS9	0.401637094	5.32907E-15	A guanine nucleotide exchange factor involved in vesicle-mediated vacuolar protein transport
YAR1	0.081309679	0	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
YBR255W	0.177360834	0	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
YCK3	0.291332132	0	Palmitoylated, vacuolar membrane-localized casein kinase I isoform; negatively regulates vacuole fusion during hypertonic stress via phosphorylation of the HOPS complex subunit,
YCL033C	0.33966797	0	Putative protein-methionine-R-oxide reductase; involved in response to oxidative stress;
YCL045C	0.366115739	8.51541E-14	Protein of unknown function, overlaps EMC1 and MGR1
YCR050C	0.176501079	0	Non-essential protein of unknown function; deletion mutant is synthetically sick or lethal with alpha-synuclein, overlaps ARE1
YDL057W	0.370344179	0.024079705	Putative protein of unknown function
YDL183C	0.411322492	0	Putative protein of unknown function
YDL206W	0.237682629	0	Putative protein of unknown function
YDR008C	0.182999018	0	Dubious open reading frame, overlaps TRP1
YDR203W	0.380296141	4.44089E-16	Dubious open reading frame, overlaps RAV2
YDR269C	0.046907107	0	Dubious open reading frame, overlaps ccc2
YDR271C	0.070996629	0	Dubious open reading, partially overlaps the verified ORF CCC2
YDR287W	0.347640507	0	Inositol monophosphatase, involved in biosynthesis of inositol; enzymatic activity requires magnesium ions and is inhibited by lithium and sodium ions
YDR455C	0.131100682	0	Dubious open reading, overlaps the verified gene NHX1
YET1	0.390608398	0	Endoplasmic reticulum transmembrane protein; may interact with ribosomes,
YFL015C	0.246587246	0	Dubious open reading frame adjacent to MDJ1
YFL019C	0.331796706	0	Dubious open reading frame
YGL081W	0.060928748	0	Putative protein of unknown function; non-essential gene; interacts genetically with CHS5, a gene involved in chitin biosynthesis
YGL214W	0.118072363	0	Dubious open reading, overlaps SKI8
YGL218W	0.389249466	0.000272675	Dubious open reading frame, overlaps the verified gene MDM34; deletion in cyr1 mutant results in loss of stress resistance
YGR064W	0.101236771	0	Dubious open reading frame, overlaps SPT4
YHR033W	0.147251079	0	Putative protein of unknown function
YHR151C	0.144570483	0	Protein of unknown function, mtc6 is synthetically sick with cdc13-1
YIL092W	0.459943553	0	Putative protein of unknown function
YJL142C	0.406398751	7.01973E-11	Dubious open reading frame, partially overlaps verified gene YJL141C
YJL175W	0.147948467	0	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
YJR020W	0.307685784	0.001791415	Dubious open reading frame, overlaps TES1
YKL136W	0.421115144	0	Dubious open reading frame, partially overlaps the verified ORF APL2
YKL169C	0.121094586	0	Dubious open reading frame, overlaps the verified gene MRPL38
YLL029W	0.178813288	1.11022E-16	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
YLR065C	0.426802438	6.51948E-07	Putative protein of unknown function
YML012C-A	0.117247625	0	Dubious open reading, overlaps SEL1
YML037C	0.389701756	0	Putative protein of unknown function with some characteristics of a transcriptional activator;
YMR057C	0.229292173	0	Dubious open reading frame, overlaps AAC1
YMR1	0.25359479	1.19885E-07	Phosphatidylinositol 3-phosphate (PI3P) phosphatase; involved in various protein sorting pathways, including CVT targeting and endosome to vacuole transport;
YMR126C	0.173298609	0	Protein of unknown function, mutant sensitive to 6-azauracil (6AU) and mycophenolic acid (MPA)
YNL080C	0.105482692	0	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
YNL105W	0.378976727	0	Dubious open reading frame, overlaps the verified gene INP52
YNL120C	0.044505974	0	Dubious open reading frame, enhances replication of Brome mosaic virus in <i>S. cerevisiae</i> , but likely due to effects on the overlapping gene NCS2
YOL162W	0.442595552	2.33147E-15	Putative protein of unknown function
YOR251C	0.152257849	0	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)
YOR331C	0.16924285	0	Dubious open reading frame, overlaps VMA4
YPR090W	0.290354619	0	Merged with YPR089W, unknown function
YPR123C	0.468127409	0	Hypothetical protein, overlaps CTR1
YPR170C	0.424014092	0	Dubious open reading frame, partially overlaps the dubious ORFs YPR169W-A and YPR170W-B
YPR197C	0.402283224	0	Dubious open reading frame, overlaps SGE1
YPT31	0.292384947	0	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
YPT7	0.146674597	0	GTPase; GTP-binding protein of the rab family; required for homotypic fusion event in vacuole inheritance, for endosome-endosome fusion, similar to mammalian Rab7
YSA1	0.117071919	0	Nudix hydrolase family member with ADP-ribose pyrophosphatase activity
ZAP1	0.280784219	0	Zinc-regulated transcription factor, binds to zinc-responsive promoter elements to induce transcription of certain genes in the presence of zinc; regulates its own transcription; contains seven zinc-finger domains
ZRC1	0.353590889	0	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
ZUO1	0.332167736	3.71028E-07	Cytosolic ribosome-associated chaperone that acts, together with Ssz1p and the Ssb proteins, as a chaperone for nascent polypeptide chains