Dataset S2. Analysis by iTRAQ of SNO-proteins in *Δadh6* versus WT yeast.

iTRAQ ratios of SNO-proteins obtained from *Δadh6* versus WT yeast cells treated with EtCysNO. Represented are averages from 2 or 3 biological replicates. RSD (Relative Standard Deviation) less than 35%.

ORF	Fold Change	Protein name and Function
YOR136W	2.55	IDH2 SGDID:S000005662, Chr XV from 580250-581359, Verified ORF, Subunit of mitochondrial NAD()-dependent isocitrate dehydrogenase
YNL071W	2.10	LAT1 SGDID:S000005015, Chr XIV from 491523-492971, Verified ORF, Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex
YCL040W	1.91	GLK1 SGDID:S000000545, Chr III from 50838-52340, Verified ORF, Glucokinase
YOR374W	1.86	ALD4 SGDID:S000005901, Chr XV from 1039840-1041399, Verified ORF, Mitochondrial aldehyde dehydrogenase
YML008C	1.69	ERG6 SGDID:S000004467, Chr XIII from 252990-251839, reverse complement, Verified ORF, Delta(24)-sterol C-methyltransferase
YLR355C	1.66	ILV5 SGDID:S000004347, Chr XII from 839253-838066, reverse complement, Verified ORF, Acetohydroxyacid reductoisomerase
YPL028W	1.58	ERG10 SGDID:S000005949, Chr XVI from 498096-499292, Verified ORF, Acetyl-CoA C-acetyltransferase (acetoacetyl-CoA thiolase)
YBR221C	1.53	PDB1 SGDID:S000000425, Chr II from 666253-665153, reverse complement, Verified ORF, E1 beta subunit of the pyruvate dehydrogenase (PDH) complex
YKL029C	1.52	MAE1 SGDID:S000001512, Chr XI from 384725-382716, reverse complement, Verified ORF, Mitochondrial malic enzyme
YER003C	1.49	PMI40 SGDID:S000000805, Chr V from 158994-157736,159118-159088, reverse complement, Verified ORF, Mannose-6-phosphate isomerase
YDR385W	1.48	EFT2 SGDID:S000002793, Chr IV from 1243230-1245758, Verified ORF, Elongation factor 2 (EF-2)
YFL018C	1.44	LPD1 SGDID:S000001876, Chr VI from 103127-101628, reverse complement, Verified ORF, Dihydrolipoamide dehydrogenase
YOR335C	1.42	ALA1 SGDID:S000005862, Chr XV from 949109-946233, reverse complement, Verified ORF, Cytoplasmic and mitochondrial alanyl-tRNA synthetase
YJL111W	1.38	CCT7 SGDID:S000003647, Chr X from 207872-209524, Verified ORF, "Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo"
YGL105W	1.35	ARC1 SGDID:S000003073, Chr VII from 307437-308567, Verified ORF, Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Gus1p)
YLR259C	1.34	HSP60 SGDID:S000004249, Chr XII from 665002-663284, reverse complement, Verified ORF, 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""
YGL148W	1.32	ARO2 SGDID:S000003116, Chr VII from 226399-227529, Verified ORF, Bifunctional chorismate synthase and flavin reductase
YDR212W	1.28	TCP1 SGDID:S000002620, Chr IV from 887230-888909, Verified ORF, "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"

YDL126C	1.27	CDC48 SGDID:S000002284, Chr IV from 238664-236157, reverse complement, Verified ORF, "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"
YNL239W	1.26	LAP3 SGDID:S000005183, Chr XIV from 200569-201933, Verified ORF, Cysteine aminopeptidase with homocysteine-thiolactonase activity; protects cells against homocysteine toxicity; has bleomycin hydrolase activity in vitro; transcription is regulated by galactose via Gal4p; orthologous to human BLMH""
YMR108W	1.23	ILV2 SGDID:S000004714, Chr XIII from 484084-486147, Verified ORF, Acetolactate synthase
YNL209W	1.20	SSB2 SGDID:S000005153, Chr XIV from 252059-253900, Verified ORF, Cytoplasmic ATPase that is a ribosome-associated molecular chaperone
YKL157W	1.19	YKL157W APE2 SGDID:S000001640, Chr XI from 154991-155271,155655-158232, Verified ORF, 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""
YGR204W	1.18	ADE3 SGDID:S000003436, Chr VII from 905934-908774, Verified ORF, Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase
YIL125W	1.17	KGD1 SGDID:S000001387, Chr IX from 122689-125733, Verified ORF, Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex
YGR061C	1.16	ADE6 SGDID:S000003293, Chr VII from 615965-611889, reverse complement, Verified ORF, Formylglycinamidine-ribonucleotide (FGAM)-synthetase
YPL111W	1.15	CAR1 SGDID:S000006032, Chr XVI from 339944-340945, Verified ORF, Arginase
YKR059W	1.15	TIF1 SGDID:S000001767, Chr XI from 554629-555816, Verified ORF, "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"
YMR217W	1.13	GUA1 SGDID:S000004830, Chr XIII from 701790-703367, Verified ORF, GMP synthase
YHR208W	1.12	BAT1 SGDID:S000001251, Chr VIII from 517532-518713, Verified ORF, Mitochondrial branched-chain amino acid aminotransferase
YPR033C	1.12	HTS1 SGDID:S000006237, Chr XVI from 639019-637379, reverse complement, Verified ORF, 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""
YNL112W	1.11	DBP2 SGDID:S000005056, Chr XIV from 413639-414911,415914-416281, Verified ORF, Essential ATP-dependent RNA helicase of the DEAD-box protein family
YAL003W	1.10	EFB1 SGDID:S000000003, Chr I from 142174-142253,142620-143160, Verified ORF, Translation elongation factor 1 beta; stimulates nucleotide exchange to regenerate EF-1 alpha-GTP for the next elongation cycle; part of the EF-1 complex
YMR205C	1.10	PFK2 SGDID:S000004818, Chr XIII from 674766-671887, reverse complement, Verified ORF, Beta subunit of heterooctameric phosphofructokinase involved in glycolysis
YDR023W	1.10	SES1 SGDID:S000002430, Chr IV from 489508-490896, Verified ORF, Cytosolic seryl-tRNA synthetase

YGR285C	1.09	ZUO1 SGDID:S000003517, Chr VII from 1063160-1061859, reverse complement, Verified ORF, "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"
YER043C	1.09	SAH1 SGDID:S000000845, Chr V from 237119-235770, reverse complement, Verified ORF, S-adenosyl-L-homocysteine hydrolase
YDR012W	1.08	RPL4B SGDID:S000002419, Chr IV from 471853-472941, Verified ORF, Protein component of the large (60S) ribosomal subunit
YDL182W	1.08	LYS20 SGDID:S000002341, Chr IV from 133437-134723, Verified ORF, Homocitrate synthase isozyme
YGL202W	1.08	ARO8 SGDID:S000003170, Chr VII from 116059-117561, Verified ORF, Aromatic aminotransferase I
YOR209C	1.07	NPT1 SGDID:S000005735, Chr XV from 737726-736437, reverse complement, Verified ORF, Nicotinate phosphoribosyltransferase
YGR180C	1.07	RNR4 SGDID:S000003412, Chr VII from 856301-855264, reverse complement, Verified ORF, Ribonucleotide-diphosphate reductase (RNR)
YGR240C	1.07	PFK1 SGDID:S000003472, Chr VII from 973734-970771, reverse complement, Verified ORF, Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis
YNL014W	1.06	HEF3 SGDID:S000004959, Chr XIV from 606319-609453, Verified ORF, 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""
YOR063W	1.06	RPL3 SGDID:S000005589, Chr XV from 444686-445849, Verified ORF, Protein component of the large (60S) ribosomal subunit
YOR133W	1.05	EFT1 SGDID:S000005659, Chr XV from 575099-577627, Verified ORF, "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"
YGR185C	1.04	TYS1 SGDID:S000003417, Chr VII from 867520-866336, reverse complement, Verified ORF, Cytoplasmic tyrosyl-tRNA synthetase
YEL046C	1.03	GLY1 SGDID:S000000772, Chr V from 68792-67629, reverse complement, Verified ORF, Threonine aldolase
YGL253W	1.03	HXK2 SGDID:S000003222, Chr VII from 23935-25395, Verified ORF, 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""
YLR048W	1.03	RPS0B SGDID:S000004038, Chr XII from 242232-242321,242681-243349, Verified ORF, Protein component of the small (40S) ribosomal subunit
YCR012W	1.02	PGK1 SGDID:S000000605, Chr III from 137746-138996, Verified ORF, 3-phosphoglycerate kinase
YEL071W	1.02	DLD3 SGDID:S000000797, Chr V from 16355-17845, Verified ORF, D-lactate dehydrogenase
YGR087C	1.02	PDC6 SGDID:S000003319, Chr VII from 652981-651290, reverse complement, Verified ORF, Minor isoform of pyruvate decarboxylase
YKL060C	1.02	FBA1 SGDID:S000001543, Chr XI from 327487-326408, reverse complement, Verified ORF, Fructose 1
YGR192C	1.01	TDH3 SGDID:S000003424, Chr VII from 883810-882812, reverse complement, Verified ORF, Glyceraldehyde-3-phosphate dehydrogenase

YHR068W	1.01	DYS1 SGDID:S000001110, Chr VIII from 232133-233296, Verified ORF, Deoxyhypusine synthase
YBR196C	1.01	PGI1 SGDID:S000000400, Chr II from 613900-612236, reverse complement, Verified ORF, Glycolytic enzyme phosphoglucose isomerase
YPR035W	1.00	GLN1 SGDID:S000006239, Chr XVI from 642208-643320, Verified ORF, Glutamine synthetase (GS)
YDL143W	1.00	CCT4 SGDID:S000002302, Chr IV from 199997-201583, Verified ORF, "Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo"
YER052C	0.99	HOM3 SGDID:S000000854, Chr V from 257957-256374, reverse complement, Verified ORF, "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"
YOR347C	0.99	PYK2 SGDID:S000005874, Chr XV from 986459-984939, reverse complement, Verified ORF, "Pyruvate kinase that appears to be modulated by phosphorylation; PYK2 transcription is repressed by glucose, and Pyk2p may be active under low glycolytic flux"
YOL086C	0.98	ADH1 SGDID:S000005446, Chr XV from 160594-159548, reverse complement, Verified ORF, Alcohol dehydrogenase
YDR037W	0.98	KRS1 SGDID:S000002444, Chr IV from 525440-527215, Verified ORF, Lysyl-tRNA synthetase""
YJL167W	0.97	ERG20 SGDID:S000003703, Chr X from 105014-106072, Verified ORF, Farnesyl pyrophosphate synthetase
YBL076C	0.97	ILS1 SGDID:S000000172, Chr II from 84261-81043, reverse complement, Verified ORF, Cytoplasmic isoleucine-tRNA synthetase
YBR121C	0.97	GRS1 SGDID:S000000325, Chr II from 483367-481364, reverse complement, Verified ORF, 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""
YCR053W	0.96	THR4 SGDID:S000000649, Chr III from 216697-218241, Verified ORF, Threonine synthase
YHR183W	0.95	GND1 SGDID:S000001226, Chr VIII from 470960-472429, Verified ORF, 6-phosphogluconate dehydrogenase (decarboxylating)
YER090W	0.95	TRP2 SGDID:S000000892, Chr V from 337949-339472, Verified ORF, Anthranilate synthase
YML126C	0.95	ERG13 SGDID:S000004595, Chr XIII from 20535-19060, reverse complement, Verified ORF, 3-hydroxy-3-methylglutaryl-CoA (HMG-CoA) synthase
YJR016C	0.95	ILV3 SGDID:S000003777, Chr X from 466208-464451, reverse complement, Verified ORF, Dihydroxyacid dehydratase
YGR234W	0.95	YHB1 SGDID:S000003466, Chr VII from 959904-961103, Verified ORF, Nitric oxide oxidoreductase
YDL185W	0.93	VMA1 SGDID:S000002344, Chr IV from 126787-130002, Verified ORF, 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)
YPL061W	0.93	ALD6 SGDID:S000005982, Chr XVI from 432588-434090, Verified ORF, Cytosolic aldehyde dehydrogenase
YOR362C	0.92	PRE10 SGDID:S000005889, Chr XV from 1018746-1017880, reverse complement, Verified ORF, Alpha 7 subunit of the 20S proteasome""
YHR047C	0.92	AAP1 SGDID:S000001089, Chr VIII from 201310-198740, reverse complement, Verified ORF, Arginine/alanine aminopeptidase

YPR080W	0.92	TEF1 SGDID:S000006284, Chr XVI from 700592-701968, Verified ORF, "Translational elongation factor EF-1 alpha; also encoded by TEF2; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes"
YNL134C	0.91	YNL134C SGDID:S000005078, Chr XIV from 373581-372451, reverse complement, Uncharacterized ORF, 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""
YBR249C	0.91	ARO4 SGDID:S000000453, Chr II from 717994-716882, reverse complement, Verified ORF, 3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase
YML070W	0.91	DAK1 SGDID:S000004535, Chr XIII from 133475-135229, Verified ORF, Dihydroxyacetone kinase
YNL178W	0.88	RPS3 SGDID:S000005122, Chr XIV from 302680-303402, Verified ORF, Protein component of the small (40S) ribosomal subunit
YDR158W	0.88	HOM2 SGDID:S000002565, Chr IV from 770357-771454, Verified ORF, Aspartic beta semi-aldehyde dehydrogenase
YHR019C	0.88	DED81 SGDID:S000001061, Chr VIII from 143558-141894, reverse complement, Verified ORF, Cytosolic asparaginyl-tRNA synthetase
YDR035W	0.87	ARO3 SGDID:S000002442, Chr IV from 521816-522928, Verified ORF, 3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase
YML085C	0.86	TUB1 SGDID:S000004550, Chr XIII from 99400-99376,99259-97941, reverse complement, Verified ORF, "Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules"
YLL018C	0.85	DPS1 SGDID:S000003941, Chr XII from 111575-109902, reverse complement, Verified ORF, Aspartyl-tRNA synthetase
YHR137W	0.85	ARO9 SGDID:S000001179, Chr VIII from 375709-377250, Verified ORF, Aromatic aminotransferase II
YBR248C	0.84	HIS7 SGDID:S000000452, Chr II from 716465-714807, reverse complement, Verified ORF, Imidazole glycerol phosphate synthase (glutamine amidotransferase:cyclase)
YPR074C	0.82	TKL1 SGDID:S000006278, Chr XVI from 694838-692796, reverse complement, Verified ORF, Transketolase
YAL038W	0.82	CDC19 SGDID:S000000036, Chr I from 71786-73288, Verified ORF, Pyruvate kinase
YDL055C	0.81	PSA1 SGDID:S000002213, Chr IV from 356759-355674, reverse complement, Verified ORF, GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase)
YLR216C	0.80	CPR6 SGDID:S000004206, Chr XII from 573211-572096, reverse complement, Verified ORF, Peptidyl-prolyl cis-trans isomerase (cyclophilin)
YLR060W	0.78	FRS1 SGDID:S000004050, Chr XII from 260979-262766, Verified ORF, Beta subunit of cytoplasmic phenylalanyl-tRNA synthetase
YER165W	0.77	PAB1 SGDID:S000000967, Chr V from 510373-512106, Verified ORF, Poly(A) binding protein
YLR420W	0.77	URA4 SGDID:S000004412, Chr XII from 963785-964879, Verified ORF, Dihydroorotase
YPL131W	0.77	RPL5 SGDID:S000006052, Chr XVI from 303121-304014, Verified ORF, 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""
YHR074W	0.76	QNS1 SGDID:S000001116, Chr VIII from 246193-248337, Verified ORF, Glutamine-dependent NAD() synthetase
YPR145W	0.74	ASN1 SGDID:S000006349, Chr XVI from 822620-824338, Verified ORF, Asparagine synthetase

YJR148W	0.70	BAT2 SGDID:S000003909, Chr X from 705744-706874, Verified ORF, Cytosolic branched-chain amino acid aminotransferase
YLR028C	0.70	ADE16 SGDID:S000004018, Chr XII from 201315-199540, reverse complement, Verified ORF, Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4-carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities
YML056C	0.69	IMD4 SGDID:S000004520, Chr XIII from 163308-162194,164176-163717, reverse complement, Verified ORF, Inosine monophosphate dehydrogenase
YER091C	0.60	MET6 SGDID:S000000893, Chr V from 342167-339864, reverse complement, Verified ORF, Cobalamin-independent methionine synthase
YPL231W	0.57	FAS2 SGDID:S000006152, Chr XVI from 108652-114315, Verified ORF, Alpha subunit of fatty acid synthetase

iTRAQ ratios of endogenous SNO-proteins obtained from *Δadh6* versus WT yeast cells under basal growth conditions. Represented are averages from 2 or 3 biological replicates. RSD (Relative Standard Deviation) less than 35%. Shared targets of SNO-CoA are indicated bold.

YCL028W	9.72	RNQ1 SGDID:S000000533, Chr III from 70150-71367, Verified ORF;[PIN(+)] prion, an infectious protein conformation that is generally an ordered protein aggregate;
YFL039C	1.51	ACT1 SGDID:S000001855, Chr VI from 54695-54686,54377-53260, reverse complement, Verified ORF;Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions;
YLR259C	1.44	HSP60 SGDID:S000004249, Chr XII from 665004-663286, reverse complement, Verified ORF;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;
YPL090C	1.36	RPS6A SGDID:S000006011, Chr XVI from 378392-378387,377992-377288, reverse complement, Verified ORF;Protein component of the small (40S) ribosomal subunit; identical to Rps6Bp and has similarity to rat S6 ribosomal protein;
YPL028W	1.35	ERG10 SGDID:S000005949, Chr XVI from 498094-499290, Verified ORF;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;
YKL060C	1.28	FBA1 SGDID:S000001543, Chr XI from 327131-326052, reverse complement, Verified ORF;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;
YEL046C	1.26	GLY1 SGDID:S000000772, Chr V from 68792-67629, reverse complement, Verified ORF;Threonine aldolase, catalyzes the cleavage of L-allo-threonine and L-threonine to glycine; involved in glycine biosynthesis;
YDL229W	1.24	SSB1 SGDID:S000002388, Chr IV from 44066-45907, Verified ORF;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;
YDL143W	1.21	CCT4 SGDID:S000002302, Chr IV from 199997-201583, Verified ORF;Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo;

YER043C	1.19	SAH1 SGDID:S000000845, Chr V from 237118-235769, reverse complement, Verified ORF;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;
YER021W	1.16	RPN3 SGDID:S000000823, Chr V from 196947-198518, Verified ORF;Essential, non-ATPase regulatory subunit of the 26S proteasome lid, similar to the p58 subunit of the human 26S proteasome; temperature-sensitive alleles cause metaphase arrest, suggesting a role for the proteasome in cell cycle control;
YGR192C	1.14	TDH3 SGDID:S000003424, Chr VII from 883815-882817, reverse complement, Verified ORF;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;
YDR226W	1.14	ADK1 SGDID:S000002634, Chr IV from 916483-917151, Verified ORF;Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; lacks cleavable signal sequence;
YOR063W	1.12	RPL3 SGDID:S000005589, Chr XV from 444688-445851, Verified ORF;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;
YCR012W	1.11	PGK1 SGDID:S000000605, Chr III from 137744-138994, Verified ORF;3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme in glycolysis and gluconeogenesis;
YIL018W	1.10	RPL2B SGDID:S000001280, Chr IX from 316766-316769,317170-317930, Verified ORF;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;
YPL131W	1.10	RPL5 SGDID:S000006052, Chr XVI from 303120-304013, Verified ORF;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;
YDL055C	1.09	PSA1 SGDID:S000002213, Chr IV from 356759-355674, reverse complement, Verified ORF;GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure;
YGR285C	1.09	ZUO1 SGDID:S000003517, Chr VII from 1063160-1061859, reverse complement, Verified ORF;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;
YOR133W	1.07	EFT1 SGDID:S000005659, Chr XV from 575099-577627, Verified ORF;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;
YKR059W	1.07	TIF1 SGDID:S000001767, Chr XI from 554629-555816, Verified ORF;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;
YER025W	1.06	GCD11 SGDID:S000000827, Chr V from 205250-206833, Verified ORF;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;
YPL240C	1.05	HSP82 SGDID:S000006161, Chr XVI from 98625-96496, reverse complement, Verified ORF;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;

YPL220W	1.05	RPL1A SGDID:S000006141, Chr XVI from 135789-136442, Verified ORF;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;
YLR075W	1.02	RPL10 SGDID:S000004065, Chr XII from 282928-283593, Verified ORF;Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family;
YER178W	1.02	PDA1 SGDID:S000000980, Chr V from 546812-548074, Verified ORF;E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA; phosphorylated; regulated by glucose;
YLR249W	1.01	YEF3 SGDID:S000004239, Chr XII from 636782-639916, Verified ORF;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;
YLR134W	1.01	PDC5 SGDID:S000004124, Chr XII from 410724-412415, Verified ORF;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;
YMR217W	1.00	GUA1 SGDID:S000004830, Chr XIII from 701789-703366, Verified ORF;GMP synthase, an enzyme that catalyzes the second step in the biosynthesis of GMP from inosine 5'-phosphate (IMP); transcription is not subject to regulation by guanine but is negatively regulated by nutrient starvation;
YDR037W	0.99	KRS1 SGDID:S000002444, Chr IV from 525438-527213, Verified ORF;Lysyl-tRNA synthetase;
YPL106C	0.98	SSE1 SGDID:S000006027, Chr XVI from 352272-350191, reverse complement, Verified ORF;ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm;
YMR205C	0.96	PFK2 SGDID:S000004818, Chr XIII from 674765-671886, reverse complement, Verified ORF;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;
YLR109W	0.95	AHP1 SGDID:S000004099, Chr XII from 368782-369312, Verified ORF;Thiol-specific peroxiredoxin, reduces hydroperoxides to protect against oxidative damage; function in vivo requires covalent conjugation to Urm1p;
YGL202W	0.95	ARO8 SGDID:S000003170, Chr VII from 116063-117565, Verified ORF;Aromatic aminotransferase I, expression is regulated by general control of amino acid biosynthesis;
YGL253W	0.95	HXK2 SGDID:S000003222, Chr VII from 23935-25395, Verified ORF;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;
YJR145C	0.94	RPS4A SGDID:S000003906, Chr X from 703058-703045,702788-702017, reverse complement, Verified ORF;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;
YAL038W	0.93	CDC19 SGDID:S000000036, Chr I from 71787-73289, Verified ORF;Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration;

YDR050C	0.92	TPI1 SGDID:S000002457, Chr IV from 556471-555725, reverse complement, Verified ORF;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;
YGR204W	0.92	ADE3 SGDID:S000003436, Chr VII from 905939-908779, Verified ORF;Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; null mutation causes auxotrophy for adenine and histidine;
YER102W	0.88	RPS8B SGDID:S000000904, Chr V from 363096-363698, Verified ORF;Protein component of the small (40S) ribosomal subunit; identical to Rps8Ap and has similarity to rat S8 ribosomal protein;
YBL076C	0.87	ILS1 SGDID:S000000172, Chr II from 84259-81041, reverse complement, Verified ORF;Cytoplasmic isoleucine-tRNA synthetase, target of the G1-specific inhibitor reveromycin A;
YHR208W	0.86	BAT1 SGDID:S000001251, Chr VIII from 517532-518713, Verified ORF;Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase;
YIL078W	0.84	THS1 SGDID:S000001340, Chr IX from 212496-214700, Verified ORF;Threonyl-tRNA synthetase, essential cytoplasmic protein;
YML056C	0.83	IMD4 SGDID:S000004520, Chr XIII from 164176-163717,163308-162194, reverse complement, Verified ORF;Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis, member of a four-gene family in S. cerevisiae, constitutively expressed;
YGL245W	0.83	GUS1 SGDID:S000003214, Chr VII from 39023-41149, Verified ORF;Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and Arc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct localization to the cytoplasm;
YGR240C	0.82	PFK1 SGDID:S000003472, Chr VII from 973739-970776, reverse complement, Verified ORF;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;
YGR094W	0.81	VAS1 SGDID:S000003326, Chr VII from 672190-675504, Verified ORF;Mitochondrial and cytoplasmic valyl-tRNA synthetase;
YLR432W	0.80	IMD3 SGDID:S000004424, Chr XII from 1002554-1004125, Verified ORF;Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis, member of a four-gene family in S. cerevisiae, constitutively expressed;
YBR196C	0.79	PGI1 SGDID:S000000400, Chr II from 613895-612231, reverse complement, Verified ORF;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;
YOR335C	0.77	ALA1 SGDID:S000005862, Chr XV from 949106-946230, reverse complement, Verified ORF;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;
YLR044C	0.60	PDC1 SGDID:S000004034, Chr XII from 234082-232391, reverse complement, Verified ORF;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;