

Sypplementary Table 1

ORF	Gene name	CaFK/Ca	Position of CDRE-like	Position of STRE	Localization	Function/Description
YMR175W	<i>SIP18</i>	2.53		-388 -369 -158	unknown	Phospholipid-binding protein; expression is induced by osmotic stress
YKL035W	<i>UGP1</i>	2.41	GGGGCGCA (-533)	-483 -445 -272 -260	cytoplasm; plasa membrane enriched fraction	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
YBR117C	<i>TKL2</i>	2.39		-77	cytoplasm; nucleus	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
YGR088W	<i>CTT1</i>	2.31		-378 -363 -133	cytoplasm	Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide
YPL186C	<i>UIP4</i>	2.31		-301 -219 -95	ER; nuclear envelope; mitochondrion	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
YFL014W	<i>HSP12</i>	2.06	GGGGCTG (-234)	-435 -414 -377 -232 -190	plasma membrane; cytoplasm; nucleus	Plasma membrane localized protein that protects membranes from desiccation; induced by heat shock, oxidative stress, osmstress, stationary phase entry, glucose depletion, oleate and alcohol; regulated by the HOG and Ras-Pka pathways
YOR173W	<i>DCS2</i>	2.03	GGGGCTG (-190)	-160 -148	cytoplasm	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.
YGR256W	<i>GND2</i>	2.00		-299 -163	cytoplasm	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone
YDR516C	<i>EMI2</i>	2.00		-355 -173	cytoplasm	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
YMR297W	<i>PRC1</i>	1.99		-194 -163	cytoplasm; ER; vacule	Vacuolar carboxypeptidase Y (proteinase C), broad-specificity C-terminal exopeptidase involved in non-specific protein degradation in the vacuole; member of the serine carboxypeptidase family
YNL160W	<i>YGP1</i>	1.97		-434	extracellular region	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 Sps100
YOR382W	<i>FIT2</i>	1.93	GGGGCTT (-420)	-242	cell wall	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall
YCL042W		1.92	GAGGCTG (-441)	-449	cytoplasm	Putative protein of unknown function; epitope-tagged protein localizes to the cytoplasm
YBR183W	<i>YPC1</i>	1.89		-361 -270 -83	ER	Alkaline ceramidase that also has reverse (CoA-independent) ceramide synthase activity, catalyzes both breakdown and synthesis of phytoceramide; overexpression confers fumonisin B1 resistance
YPL004C	<i>LSP1</i>	1.83		-215 -193 -182	cytoplasm; mitochondrion	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
YGR052W	<i>FMP48</i>	1.82		-338	mitochondrion	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

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YNR001C	<i>CIT1</i>	1.81		-159 -134	mitochondrion	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
YOL052C-A	<i>DDR2</i>	1.77		-472 -248 -203 -175	cytoplasm; vacuole	Multistress response protein, expression is activated by a variety of xenobiotic agents and environmental or physiological stresses
YBR105C	<i>VID24</i>	1.76		-356	cytoplasmic membrane-bounded vesicle; extrinsic to	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
YKL150W	<i>MCR1</i>	1.71		-308 -268	mitochondrion	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis
YDR070C	<i>FMP16</i>	1.68		-201	mitochondrion	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
YML004C	<i>GLO1</i>	1.67	GGGGCTT (-228)	-432 -229	cytoplasm; nucleus	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