Name of orthologs	Gene ID	Assigned function
SLN1	LCor00162.1.t1 LCor00877.1.t1 LCor02767.1.t1 LCor03837.1.t1 LCor04582.1.t1 LCor05933.1.t1 LCor07413.1.t1 LCor07770.1.t1 LCor08728.1.t1 LCor1074.1.t1 LCor11074.1.t1 LCor11494.1.t1 LCor112256.1.t1* LCor12257.1.t1* LCor12312.1.t1	Histidine kinase osmosensor that regulates a MAP kinase cascade; transmembrane protein with an intracellular kinase domain that signals to Ypd1p and Ssk1p, thereby forming a phosphorelay system similar to bacterial two component regulators
SLT2	LCor06339.1.t1 LCor07992.1.t2	Serine/threonine MAP kinase; involved in regulating maintenance of cell wall integrity, progression through the cell cycle, and nuclear mRNA retention in heat shock; required for mitophagy and pexophagy; affects recruitment of mitochondria to the phagophore assembly site (PAS); regulated by the PKC1 mediated signaling pathway
VCX1	LCor01072.1.t1 LCor01703.1.t1 LCor02873.1.t1* LCor02874.1.t1* LCor03175.1.t1 LCor04086.1.t1 LCor07712.1.t1 LCor08010.1.t1 LCor10259.1.t1	Vacuolar membrane antiporter with Ca2+/H+ and K+/H+ exchange activity, involved in control of cytosolic Ca2+ and K+ concentrations; has similarity to sodium/calcium exchangers, including the bovine Na+/Ca2+, K+ antiporter
YPS1	LCor00186.1.t1 LCor02028.1.t1 LCor02157.1.t1* LCor02158.1.t1* LCor02462.1.t1* LCor02463.1.t1* LCor03453.1.t1 LCor03813.1.t1 LCor03873.1.t1 LCor05667.1.t1 LCor08530.1.t1 LCor08737.1.t1 LCor09727.1.t1	Aspartic protease, member of the yapsin family of proteases involved in cell wall growth and maintenance; attached to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor

	T Q Q Q Q Q Q I Q I I I	T
BCK1	LCor00818.1.t1	Mitogen activated protein (MAP) kinase
	LCor08890.1.t1	kinase kinase acting in the protein kinase C
		signaling pathway, which controls cell
		integrity; upon activation by Pkc1p
		phosphorylates downstream kinases Mkk1p and
		Mkk2p
BCK2		Protein rich in serine and threonine
		residues involved in protein kinase C
		signaling pathway, which controls cell
		integrity; overproduction suppresses pkc1
		mutations
BEM1	LCor03278.1.t1	Protein containing SH3 domains, involved in
	LCor04465.1.t1	establishing cell polarity and
		morphogenesis; functions as a scaffold
		protein for complexes that include Cdc24p,
		Ste5p, Ste20p, and Rsr1p
BEM2	LCor00141.1.t1	Rho GTPase activating protein (RhoGAP)
	LCor00193.1.t1	involved in the control of cytoskeleton
	LCor01150.1.t1	organization and cellular morphogenesis;
	LCor02720.1.t1	required for bud emergence
	LCor05601.1.t1	
	LCor05860.1.t1	
	LCor07378.1.t1 LCor07454.1.t1	
	LCor07434.1.11 LCor07731.1.t1	
	LCor08677.1.t1	
	LCor09304.1.t1	
	LCor11327.1.t1	
	LCor11602.1.t1	
BNI1	LCor01281.1.t1	Formin, nucleates the formation of linear
	LCor01609.1.t1	actin filaments, involved in cell processes
	LCor03044.1.t1	such as budding and mitotic spindle
	LCor04838.1.t1	orientation which require the formation of
	LCor07542.1.t1	polarized actin cables, functionally
	LCor09714.1.t1	redundant with BNR1
	LCor12294.1.t1	
ССН1	LCor01676.1.t1	Voltage gated high affinity calcium channel
CCHI	LCor07804.1.t1	involved in calcium influx in response to
	LCor08750.1.t1	some environmental stresses as well as
	LCor10564.1.t1	exposure to mating pheromones; interacts and
		colocalizes with Midlp, suggesting Cch1p and
		Midlp function together
CDC24	LCor01389.1.t1	Guanine nucleotide exchange factor (GEF or
	LCor01389.1.11 LCor01904.1.t1	-
	LCor02636.1.t1	GDP release factor) for Cdc42p; required for polarity establishment and maintenance, and
	LCor06659.1.t1	mutants have morphological defects in bud
	LCor08112.1.t1	formation and shmooing
	LCor11357.1.t1	Tormation and Simoorny
CDC42	LCor01683.1.t1	Small rho like GTPase, essential for
	LCor07636.1.t1	establishment and maintenance of cell
	TCOT0/020.1.01	polarity; mutants have defects in the
		organization of actin and septins
		organization of actin and septims

CLA4	LCor01190.1.t1 LCor02719.1.t1 LCor06587.1.t1	Cdc42pactivated signal transducing kinase of the PAK (p21activated kinase) family, along with Ste20p and Skm1p; involved in septin ring assembly, vacuole inheritance, cytokinesis, sterol uptake regulation; phosphorylates Cdc3p and Cdc10p
CMD1	LCor04968.1.t1 LCor06171.1.t1 LCor10629.1.t1	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 Nuflp, Myo2p and calcineurin
CMP2	LCor02879.1.t2 LCor09841.1.t1	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
CNA1	LCor09841.1.t1 LCor02879.1.t2	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
CNB1	LCor05632.1.t1	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
CPR1	LCor00421.1.t1 LCor01642.1.t1 LCor02166.1.t1 LCor03788.1.t1 LCor05112.1.t1 LCor05866.1.t1 LCor07472.1.t1 LCor08282.1.t1 LCor09667.1.t1	Cytoplasmic peptidylprolyl cis-trans isomerase (cyclophilin), catalyzes the cis- trans isomerization of peptide bonds N' terminal to proline residues; binds the drug cyclosporin A
CRZ1	LCor00138.1.t1 LCor00424.1.t1 LCor01236.1.t1 LCor01802.1.t1 LCor01959.1.t1 LCor05575.1.t1 LCor12103.1.t1 LCor12188.1.t1	Transcription factor that activates transcription of genes involved in stress response; nuclear localization is positively regulated by calcineurin mediated dephosphorylation

DIG1		MAP kinas responsive inhibitor of the Stel2p transcription factor, involved in the regulation of mating specific genes and the invasive growth pathway; related regulators Dig1p and Dig2p bind to Stel2p
DIG2		MAP kinas responsive inhibitor of the Stel2p transcription factor, involved in the regulation of mating specific genes and the invasive growth pathway; related regulators Dig1p and Dig2p bind to Stel2p
FAR1		Cyclin dependent kinase inhibitor that mediates cell cycle arrest in response to pheromone; also forms a complex with Cdc24p, Ste4p, and Ste18p that may specify the direction of polarized growth during mating; potential Cdc28p substrate
FIG1		Integral membrane protein required for efficient mating; may participate in or regulate the low affinity Ca2+ influx system, which affects intracellular signaling and cell cell fusion during mating
FPR1	LCor02490.1.t1 LCor02934.1.t1 LCor05180.1.t1 LCor07780.1.t1 LCor08903.1.t1	Peptidylprolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the non histone chromatin binding protein Hmolp and may regulate its assembly or function
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
FUS3	LCor04911.1.t1	Mitogen activated serine/threonine protein kinase involved in mating; phospho-activated by Ste7p; substrates include Ste12p, Far1p, Bni1p, Sst2p; inhibits invasive growth during mating by phosphorylating Tec1p, promoting its degradation
GPA1	LCor00522.1.t1 LCor02271.1.t1 LCor02939.1.t1 LCor02948.1.t1 LCor06277.1.t1 LCor06418.1.t1 LCor07162.1.t1 LCor07353.1.t1 LCor08481.1.t1 LCor10460.1.t1	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

HOG1	LCor01571.1.t1 LCor01831.1.t1	Mitogen activated protein kinase involved in osmoregulation; acts via three independent osmosensors; mitophagy specific regulator; mediates the recruitment and activation of RNA Pol II at Hot1pdependent promoters; localization regulated by Ptp2p and Ptp3p
HOT1	LCor11021.1.t1	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
HRR25	LCor01591.1.t1 LCor09119.1.t3	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)
KSS1	Same as FUS3	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
MCM1	LCor01758.1.t1 LCor06393.1.t1 LCor07433.1.t1 LCor08527.1.t1 LCor08806.1.t1 LCor09108.1.t1 LCor10278.1.t1 LCor12313.1.t1	Transcription factor involved in celltype specific transcription and pheromone response; plays a central role in the formation of both repressor and activator complexes
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
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
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

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
MID1	LCor10558.1.t1	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; interacts with Cch1p
MID2		O glycosylated plasma membrane protein that acts as a sensor for cell wall integrity signaling and activates the pathway; interacts with Rom2p, a guanine nucleotide exchange factor for Rho1p, and with cell integrity pathway protein Zeo1p
MKK1	LCor03536.1.t1 LCor04751.1.t1 LCor08249.1.t1	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
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
MSG5	LCor05433.1.t1	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
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
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

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MSN4	LCor00249.1.t1	Transcriptional activator related to Msn2p;
	LCor01478.1.t1	activated in stress conditions, which
	LCor02196.1.t1	results in translocation from the cytoplasm
	LCor04997.1.t1	to the nucleus; binds DNA at stress response
	LCor07383.1.t1	elements of responsive genes, inducing gene
		expression
MTL1		Putative plasma membrane sensor, involved in
		cell integrity signaling and stress response
		during glucose starvation and oxidative
		stress; has structural and functional
		similarity to Mid2p
PBS2	LCor00564.1.t1	MAP kinase kinase of the HOG signaling
		pathway; activated under severe osmotic
		<pre>stress; mitophagy specific regulator; plays</pre>
		a role in regulating Ty1 transposition
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
DV01	LCor02728.1.t1	
PKC1	LCor02728.1.tl LCor04156.1.tl	Protein serine/threonine kinase essential
	100104130.1.01	for cell wall remodeling during growth;
		localized to sites of polarized growth and
		the mother daughter bud neck; homolog of the
		alpha, beta, and gamma isoforms of mammalian
		protein kinase C (PKC)
PMC1	LCor02317.1.t1	Vacuolar Ca2+ ATPase involved in depleting
	LCor07996.1.t1	cytosol of Ca2+ ions; prevents growth
	LCor06558.1.t1	inhibition by activation of calcineurin in
	LCor10117.1.t1	the presence of elevated concentrations of
	LCor07729.1.t1	calcium; similar to mammalian PMCA1a
	LCor11865.1.t1	
PMR1	LCor11533.1.t1	High affinity Ca2+/Mn2+ Ptype ATPase
		required for Ca2+ and Mn2+ transport into
		Golgi; involved in Ca2+ dependent protein
		sorting and processing; mutations in human
		homolog ATP2C1 cause a cantholytic skin
		condition Hailey Hailey disease
PPZ1/PPZ2	LCor01164.1.t1	Serine/threonine protein phosphatases Z,
	LCor03163.1.t1	isoform of Ppz2p; involved in regulation of
	LCor03495.1.t1	potassium transport, which affects osmotic
		stability, cell cycle progression, and halo tolerance
PRM5		Pheromone regulated protein, predicted to
		have 1 transmembrane segment; induced during
		cell integrity signaling
		construction organization

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PST1	LCor04890.1.t1	Cell wall protein that contains a putative
	LCor12329.1.t1	GPI attachment site; secreted by
	LCor04695.1.t1	regenerating protoplasts; up regulated by
	LCor06520.1.t1	activation of the cell integrity pathway, as
		mediated by Rlm1p; up regulated by cell wall
		damage via disruption of FKS1
RAS2	LCor00430.1.t1	GTP binding protein that regulates the
14102	LCor03725.1.t1	nitrogen starvation response, sporulation,
	LCor04610.1.t1	and filamentous growth; farnesylation and
	LCor06688.1.t1	palmitoylation required for activity and
		localization to plasma membrane; homolog of
		mammalian Ras proto oncogenes
		. ,
	T.O	
RCK1/RCK2	LCor00478.1.t1	Protein kinases involved in the response to
	LCor03419.1.t1 LCor03168.1.t1	oxidative stress; identified as suppressor
	LCOr06432.1.t1	of S. pombe cell cycle checkpoint mutations
	LCor07694.1.t1	
RCN1		Protein involved in calcineurin regulation
		during calcium signaling; has similarity to
		H. sapiens DSCR1 which is found in the Down
		Syndrome candidate region
RHO1	LCor08052.1.t2	GTP binding protein of the rho subfamily of
		Ras like proteins, involved in establishment
		of cell polarity; regulates protein kinase C
		(Pkc1p) and the cell wall synthesizing
		enzyme 1,3 beta-glucan synthase (Fks1p and
		Gsc2p)
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
RLM1	LCor05504.1.t1	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
		·····
DON1	ICom010/1 1 ±1	Opp/Cmp enchange anatoing (Cpp) for phot
ROM1	LCor01841.1.t1	GDP/GTP exchange proteins (GEP) for Rholp;
	LCor02021.1.t1 LCor05488.1.t2	mutations are synthetically lethal with
	LCor05488.1.12 LCor07499.1.t1	mutations in rom2, which also encodes a GEP
	LCOr10007.1.t1	
RTN1		ER membrane protein that interacts with
		Sey1p to maintain ER morphology; interacts
		with exocyst subunit Sec6p, with Yip3p, and
		with Sbh1p; null mutant has an altered ER
		morphology; member of the RTNLA (reticulon
		like A) subfamily

RTN2 SAC7	 LCor02140.1.t1 LCor06413.1.t1 LCor10643.1.t1	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon like A) subfamily GTPase activating protein (GAP) for Rholp, involved in signaling to the actin cytoskeleton, null mutations suppress tor2 mutations and temperature sensitive mutations in actin; potential Cdc28p substrate
SHO1	LCor00503.1.t1 LCor01615.1.t1 LCor04563.1.t1 LCor07332.1.t1 LCor07854.1.t1 LCor08971.1.t1	Transmembrane osmosensor involved in activation of the Cdc42p and MAP kinase dependent filamentous growth pathway and the high osmolarity glycerol response pathway; phosphorylated by Hog1p; interacts with Pbs2p, Msb2p, Hkr1p, and Ste11p
SIT4	LCor02322.1.t1 LCor03480.1.t1 LCor03616.1.t1 LCor07635.1.t1 LCor09474.1.t1 LCor10112.1.t1	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
SKO1		Basic leucine zipper transcription factor of the ATF/CREB family; forms a complex with Tuplp and Cyc8p to both activate and repress transcription; cytosolic and nuclear protein involved in osmotic and oxidative stress responses
SLG1		Sensor transducer of the stress activated PKC1 MPK1 kinase pathway; involved in maintenance of cell wall integrity; required for mitophagy; involved in organization of the actin cytoskeleton; secretory pathway Wsc1p is required for the arrest of secretion response
SMP1	LCor03918.1.t1 LCor08105.1.t1 LCor08386.1.t1	Putative transcription factor involved in regulating the response to osmotic stress; member of the MADS box family of transcription factors
SSK1	LCor05616.1.t1 LCor09508.1.t1	Cytoplasmic response regulator; part of a two component signal transducer that mediates osmo-sensing via a phosphorelay mechanism; required for mitophagy; dephosphorylated form is degraded by the ubiquitin proteasome system; potential Cdc28p substrate

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
SSK22	LCor02371.1.t1 LCor09478.1.t1	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
STE11	LCor09357.1.t1	Signal transducing MEK kinase involved in pheromone response and pseudohyphal / invasive growth pathways where it phosphorylates Ste7p, and the high osmolarity response pathway, via phosphorylation of Pbs2p; regulated by Ste20p and Ste50p
STE12	LCor01878.1.t2 LCor11169.1.t1	Transcription factor that is activated by a MAP kinase signaling cascade, activates genes involved in mating or pseudohyphal / invasive growth pathways; cooperates with Teclp transcription factor to regulate genes specific for invasive growth
STE18	LCor03271.1.t1	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
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
STE20	LCor01168.1.t1 LCor04274.1.t1 LCor05516.1.t1 LCor06936.1.t1 LCor07069.1.t1	Cdc42p activated signal transducing kinase of the PAK (p21activated kinase) family; involved in pheromone response, pseudohyphal/invasive growth, vacuole inheritance, down regulation of sterol uptake; GBB motif binds Ste4p
STE3		Receptor for a factor pheromone, couples to MAP kinase cascade to mediate pheromone response; transcribed in alpha cells and required for mating by alpha cells, ligand bound receptors endocytosed and recycled to the plasma membrane; GPCR

-	LCor01272.1.t1	G protein beta subunit, forms a dimer with
	LCor07294.1.t1	Stel8p to activate the mating signaling
	LCor07816.1.t1	pathway, forms a heterotrimer with Gpalp and
	LCor09889.1.t1	Ste18p to dampen signaling; may recruit
	LCor10582.1.t1	Rholp to the polarized growth site during
		mating; contains WD40 repeats
STE5		Pheromone response scaffold protein that
		controls the mating decision; binds Stellp,
		Ste7p, and Fus3p kinases, forming a MAPK
		cascade complex that interacts with the
		plasma membrane and Ste4p Ste18p; allosteric
		activator of Fus3p
STE50		Protein involved in mating response,
91E30		invasive/filamentous growth, and osmo-
		tolerance, acts as an adaptor that links G
		protein associated Cdc42p Ste20p complex to
		the effector Stellp to modulate signal
		transduction
STE7	LCor05404.1.t1	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 Stellp, degraded by ubiquitin pathway
		abrdarttii baciiway
SWI4	LCor01791.1.t1	DNA binding component of the SBF complex
	LCor07806.1.t1	(Swi4p Swi6p), a transcriptional activator
	LCor09533.1.t1	that in concert with MBF (Mbp1 Swi6p)
		regulates late G1specific transcription of
		targets including cyclins and genes required
		for DNA synthesis and repair
TEC1	LCor03533.1.t1	Transcription factor required for full Ty1
	LCor08455.1.t1	expression, Tyl mediated gene activation,
		and haploid invasive and diploid
		pseudohyphal growth; TEA/ATTS DNA binding
		domain family member
TUS1	LCor01842.1.t1	Guanine nucleotide exchange factor (GEF)
	LCor04938.1.t1	that functions to modulate Rholp activity as
	LCor05487.1.t1	part of the cell integrity signaling
		pathway; multicopy suppressor of tor2
		mutation and ypk1 ypk2 double mutation;
		potential Cdc28p substrate
WSC2		Partially redundant sensor transducer of the
MBCZ		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
		-

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
YPD1	LCor00246.1.t1 LCor01065.1.t1	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
YVC1		Vacuolar cation channel, mediates release of Ca (2+) from the vacuole in response to hyper osmotic shock
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

Genes marked with "*" are probable duplications