Supplementary Table 1

Mutants affected in carbon/nitrogen signalling/amino acid metabolism

Locus	Common name	Glutathione excretion (fold parent)	Capacity for respiratory growth	DTT tolerance[a] 48 h; 72 h	Function
Carbon signaling; RAS/cAMP/PKA pathway					
yol081w	*ira2*	25	yes	1; 1	GTPase-acting protein for Ras1p & Ras2p
yor360c	*pde2*	22	yes	4; 4	High-affinity phosphodiesterase
Nitrogen signaling; amino acid metabolism					
ydr300c	*pro1*	18	yes	1; 3	Proline biosynthesis pathway
yel062w	*npr2*	6	yes	2; 3	Nitrogen permease regulator
ygl227w	*vid30*	3	yes	2; 3	Nitrogen metabolism; gene expression
ynl229c	*ure2*	24	yes	2; 3	Regulator nitrogen catabolite repression
yor375c	*gdh1*	5	yes	4; 4	Glutamate dehydrogenase (NADP$^+$)

Glutathione was measured in stationary phase and is expressed as fold relative to the parent. Respiratory capacity was determined by checking growth on YPG medium. Underlined loci denote mutants showing a reduced capacity/inability to utilise 1 mM GSH as a sole nitrogen source. [a]Tolerance to DTT determined after 48 h and 72 h: 1 = no detectable growth; 2 = very poor growth; 3 = poor growth; 4 = minor or no effect relative to the parental strain.

Supplementary Table 2

Mutants affected in mitochondrial function

Locus	Common name	Glutathione excretion (fold parent)	Capacity for respiratory growth	DTT tolerance[a] 48 h; 72 h	Function
Mitochondrial respiratory complexes: subunits and assembly					
ybr003w	*coq1*	12	no	4; 4	Coenzyme Q biosynthesis
ybr037c	*sco1*	10	no	4; 4	Cu^{2+} insertion into cytochrome c oxidase
ydr079w	*pet100*	11	no	4; 4	Assembly of cytochrome c oxidase
ydr204w	*coq4*	9	no	4; 4	Coenzyme Q biosynthesis
ydr298c	*atp5*	10	no	4; 4	Subunit of F_1F_0-ATPase
ydr529c	*qcr7*	10	no	4; 4	Cytochrome c reductase subunit VII
yer141w	*cox15*	11	no	4; 4	Heme A biosynthesis; Cox assembly
yer154w	*oxa1*	11	no	4; 4	Assembly of F_1F_0-ATPase and Cox
ygr062c	*cox18*	6	no	4; 4	Activity of cytochrome c oxidase
yhr051w	*cox6*	7	no	4; 4	Cytochrome c oxidase subunit VI
yil098c	*fmc1*	14	yes	4; 4	Cytochrome assembly
yjl166w	*qcr8*	8	no	4; 4	Cytochrome c reductase subunit VIII
yll009c	*cox17*	2	no	4; 4	Cu^{2+} insertion into cytochrome c oxidase
yll018c-a	*cox19*	10	no	4; 4	Cytochrome c oxidase activity
ypl132w	*cox11*	8	no	4; 4	Heme A biosynthesis
ypr004c		25	yes	4; 4	Electron transfer flavoprotein
ypr191w	*qcr2*	7	no	4; 4	Cytochrome c reductase subunit II
Mitochondrial genome integrity and expression					
ybr268w	*mrpl37*		no	4; 4	Mitochondrial ribosomal protein
ycr046c	*img1*	8	poor	4; 4	Putative mitochondrial ribosomal protein
ydl069c	*cbs1*	10	no	4; 4	Translational activator of COB mRNA
ydl107w	*mss2*	8	no	4; 4	Mitochondrial expression of *COX2*
ydl202w	*mrpl11*		no	4; 4	Mitochondrial ribosomal protein
ydr175c	*rsm24*	9	no	3; 3	Mitochondrial ribosomal protein
ydr197w	*cbs2*	10	no	4; 4	Mitochondrial translational COB mRNA
ydr322w	*mrpl35*	10	no	4; 4	Mitochondrial ribosomal protein
ydr337w	*mrps28*	2	no	4; 4	Mitochondrial ribosomal protein
ydr462w	*mrpl28*	11	no	4; 4	Mitochondrial ribosomal protein
yer153c	*pet122*	9	no	2; 3	Translational activator *COX3* mRNA
ygr171c	*msm1*	11	no	4; 4	Methionyl t-RNA synthetase
yhl038c	*cbp2*	4	no	1; 3	COB aI5 intron splicing
yhr011w	*dia4*	15	no	4; 4	Amino acyl-tRNA synthetase
yhr116w		8	no	4; 4	Putative mitochondrial translation
yhr120w	*msh1*	11	no	4; 4	Mitochondrial DNA repair
yhr147c	*mrpl6*	11	no	4; 4	Mitochondrial ribosomal protein
yil093c	*rsm25*	7	no	4; 4	Mitochondrial ribosomal protein
yir021w	*mrs1*	9	no	4; 4	COB mRNA splicing
yjl063c	*mrpl8*	6	no	1; 1	Mitochondrial ribosomal protein
yjl102w	*mef2*	8	no	4; 4	Putative mitochondrial translation
yjl209w	*cbp1*	8	no	4; 4	COB mRNA stability & 5' processing
yjr144w	*mgm101*	11	no	4; 4	Mitochondrial genome protein

ykl003c	*mrp17*	29[b]	no	1; 2	Mitochondrial ribosomal protein
ykr006c	*mrpl13*	8	no	4; 4	Mitochondrial ribosomal protein
ylr067c	*pet309*	2	no	2; 3	Stability & translation of *COX1*
ylr439w	*mrpl4*	10	no	4; 4	Mitochondrial ribosomal protein
ymr064w	*aep1*	11	no	4; 4	*ATP9*/*OLI1* transcript accumulation
ymr072w	*abf2*	10	no	4; 4	Transmission & recombination mtDNA
ymr193w	*mrpl24*	12	no	4; 4	Mitochondrial ribosomal protein
ymr228w	*mtf1*	8	no	4; 4	mtRNA polymerase specificity factor
ynl177c		8	no	1; 2	Putative mitochondrial translation
ynr036c		11	no	4; 4	Putative mitochondrial ribosomal protein
ynr037c	*rsm19*	4	no	4; 4	Putative mitochondrial ribosomal protein
ynr045w	*pet494*	10	no	1; 3	Translation of *COX3* mRNA
yol033w	*mse1*	9	no	4; 4	Mitochondrial Glutamyl t-RNA synthetase
yol095c	*hmi1*	10	no	4; 4	Mitochondrial DNA helicase
ypl183w-a		12	no	4; 4	Putative mitochondrial ribosomal protein
ypr166c	*mrp2*	8	no	4; 4	Mitochondrial ribosomal protein
Mitochondrial: other					
ybr163w	*dem1*	10	no	4; 4	Putative mt morphology and respiration
ygl237c	*hap2*	3	no	4; 4	Component Hap2,3,4,5p complex
ygr257c		14	poor	4; 4	Mitochondrial carrier family (MCF)
yil006w		6	yes	4; 4	Mitochondrial carrier family (MCF)
yil065c	*fis1*	10	yes	4; 4	Involved in mitochondrial division
yil070c	*mam33*	11	yes	4; 4	Required for normal respiratory growth
ylr139c	*sls1*	4	yes	4; 4	Mitochondrial metabolism
ylr369w	*ssq1*	4	no	4; 4	Mitochondria heat shock protein 70
ymr150c	*imp1*	8	no	4; 4	Mitochondrial inner membrane protein
yol009c	*mdm12*	2	no	4; 4	Mitochondrial inheritance protein

Glutathione was measured in stationary phase and is expressed as fold relative to the parent. Respiratory capacity was determined by checking growth on YPG medium. Underlined loci denote mutants showing a reduced capacity/inability to utilise 1 mM GSH as a sole nitrogen source. [a]Tolerance to DTT determined after 48 h and 72 h: 1 = no detectable growth; 2 = very poor growth; 3 = poor growth; 4 = minor or no effect relative to the parental strain. [b]Since *MRP17* (*YKL003c*; Crick strand) and *VPS2* (*YKL002w*; Watson strand) are in close proximity on opposite DNA strands, deletion of *MRP17* may have disrupted *VPS2* expression.

Supplementary Table 3

Mutants affected in secretory pathway function/vacuolar protein sorting

Locus	Common name	Glutathione excretion (fold parent)	Capacity for respiratory growth	DTT tolerance[a] 48 h; 72 h	Function
Class E vacuolar protein sorting/late endosome (LE) function					
ynr006w	*vps27*	34	yes	2; 3	Ub & PI3P binding; upstream ESCRT-I ?
ycl008c	*vps23*	27	yes	3; 4	ESCRT-I complex
ylr119w	*vps37/srn2*	25	yes	2; 4	ESCRT-I complex
ypl065w	*vps28*	29	ND	ND	ESCRT-I complex
yjr102c	*vps25*	30	poor	1; 3	ESCRT-II complex
ylr417w	*vps36*	26	poor	3; 3	ESCRT-II complex
ypl002c	*vps22/snf8*	35	yes	1; 1	ESCRT-II complex
ykl002w	*vps2/did4*	37	no	1; 2	ESCRT-III complex
ylr025w	*vps32/snf7*	23	yes	1; 2	ESCRT-III complex
ymr077c	*vps20*	29	no	1; 3	ESCRT-III complex
ykl041w	*vps24*	26	yes	4; 4	ESCRT-III complex
ypl084w	*vps31/bro1*	20	ND	ND	Functions downstream ESCRT-III compl.
ykr035w-a	*did2*	21	yes	2; 3	Endosomal protein sorting
ydr486c	*vps60*	19	yes	4; 4	Endosomal protein sorting
ypr173c	*vps4*	12	yes	1; 3	AAA-ATPase, ESCRT complex release
ydr456w	*vps44/nhx1*	6	ND	ND	Na+/H+ antiporter Endosomal/vacuolar
SNAREs					
yor036w	*vps6/pep12*	21	yes	1; 1	SNARE-Syntaxin of the LE
yhl031c	*gos1*	22	yes	4; 4	SNARE-GOlgi SNARE 1
ygl212w	*vam7*	5	yes	4; 4	SNARE-vacuolar morphogenesis
yor106w	*vam3*	6		4; 4	SNARE-Assoc. with Vam7 & Complex C
PI3P Kinases, FYVE domain-containing					
ydr323c	*pep7/vac1*	28	poor	1; 1	FYVE domain-containing vac. inherit.
yfr019w	*fab1*	11	yes	1; 1	FYVE domain-containing PI3(P)5-kinase
ynr006w	*vps27*	34	yes	2; 3	FYVE domain-containing PI3P binding
GTP-related					
ykr001c	*vps1*	8	no	4; 4	GTPase; Golgi-to-LE; sorts Pep12 to LE
ylr262c	*ypt6*	3	poor	4; 4	GTP-binding LE-to-TGN
yml001w	*ypt7*	13	ND	ND	GTP-binding LE-to-vacuole
yor089c	*vps21*	9	yes	4; 4	Rab GTPase activating/GTP-binding
yor070c	*gyp1*	4	yes	4; 4	GTPase-activating protein ER-to-Golgi
ybr131w	*ccz1*	11	ND	ND	Vesicular transport, interacts with Ypt7p
ygl124c	*mon1*	5	yes	4; 4	Complexes with Ccz1p vacuolar delivery
Vacuolar import and degradation					
ybr105c	*vid24*	2	yes	4; 4	Vacuolar import and degradation
ygl227w	*vid30*	3	poor	4; 4	Vacuolar import and degradation
yil017c	*vid28*	9	yes	4; 4	Vacuolar import and degradation
ylr373c	*vid22*	4		4; 4	Vacuolar import and degradation
Class C Complex/vacuolar biogenesis/Ypt7p associated complex					
ylr148w	*vps18/pep3*	21	no	1; 1	Class C complex; vac. biogenesis
ydl077c	*vps39/vam6*	5	ND	ND	Class C complex; Assoc. with Ypt7p
ylr396c	*vps33*	14	no	1; 1	Class C complex vac. morphogenesis

Endosome-to-Golgi retrieval					
yhr012w	*vps29*	8	yes	4; 4	Endosome-to-Golgi retrieval
yjl053w	*vps26*/*pep8*	7	yes	4; 4	Endosome-to-Golgi retrieval
yjl154c	*vps35*	19	yes	4; 4	Endosome-to-Golgi retrieval
yor069w	*vps5*	8	yes	4; 4	Endosome-to-Golgi retrieval
ypl120w	*vps30*	4	poor	4; 4	Endosome-to-Golgi retrieval
ylr360w	*vps38*	6	yes	4; 4	Endosome-to-Golgi retrieval
ydr027c	*vps54*/*luv1*	15	poor	1; 4	Subunit (Sac2p-Vps53p-Luv1p) complex
ydr484w	*vps52*/*sac2*	10	yes	4; 4	Subunit (Sac2p-Vps53p-Luv1p) complex
yjl029c	*vps53*	13	ND	ND	Subunit (Sac2p-Vps53p-Luv1p) complex
Vacuolar protein sorting: other					
yal002w	*vps8*	7	yes	4; 4	Golgi-to-LE transport
ydr495c	*vps3*	16	yes	1; 1	Vacuolar sorting protein and segregation
yll040c	*vps13*	3	yes	4; 4	Protein involved in vacuolar sorting
yml097c	*vps9*	2	yes	4; 4	Protein involved in vacuolar sorting
ymr004w	*mvp1*	3	yes	4; 4	Protein involved in vacuolar sorting
ynl297c	*mon2*	8	poor	4; 4	Protein involved in vacuolar sorting
yor132w	*vps17*	3	ND	ND	Protein involved in vacuolar sorting
ypl045w	*vps16*	2	no	4; 4	Protein involved in vacuolar sorting
Golgi-to-ER retrograde transport					
yer122c	*glo3*	6	no	3; 3	Retrograde transport between Golgi/ER
Glycosylation					
ygl005c	*cod5*	2	poor	4; 4	Component of Sec34p-Sec35p complex
ygl223c	*cod3*	3	yes	4; 4	Component of Sec34p-Sec35p complex
yml071c	*dor1*	5	yes	4; 4	Component of Sec34p-Sec35p complex
ynl041c	*cod2*	3	no	4; 4	Component of Sec34p-Sec35p complex
ynl051w	*cod4*	2	yes	4; 4	Component of Sec34p-Sec35p complex
yel036c	*anp1*	5	yes	4; 4	Subunit of mannosyltransferase complex
yjl183w	*mnn11*	3	yes	2; 3	Subunit of mannosyltransferase complex
yjr075w	*hoc1*	4		4; 4	Subunit of mannosyltransferase complex
ypr159w	*kre6*	5	no	4; 4	Glucan synthase subunit
ER/Golgi: other					
ydr518w	*eug1*	12	no	4; 4	Protein disulfide isomerase
ygl167c	*pmr1*	8	poor	1; 3	Ca^{2+}, Mn^{2+} -transporting ATPase of Golgi
ylr264w	*sec22*	7	yes	4; 4	ER-to-Golgi transp. vesicles (v-SNARE)
yel031w	*cod1*	3	ND	ND	Ca^{2+}-ATPase of the ER
yfl005w	*sec4*	2		4; 4	Golgi-to-plasma membrane transport
ygr284c	*erv29*	4	no	4; 4	Component of COPII-coated vesicles
ykl212w	*sac1*	3	yes	1; 3	PI phosphatase; ATP transport into ER
Autophagy					
ydl149w	*apg9*	2	poor	4; 4	Involved in autophagy pathway
yhr171w	*apg7*	4		1; 3	Involved in autophagy pathway
yll042c	*apg10*	2	yes	4; 4	Involved in autophagy pathway
ylr423c	*apg17*	3	yes	4; 4	Involved in autophagy pathway
ypl149w	*apg5*	3	no	4; 4	Involved in autophagy pathway

Glutathione was measured in stationary phase and is expressed as fold relative to the parent. Respiratory capacity was determined by checking growth on YPG medium. Underlined loci denote mutants showing a reduced capacity/inability to utilise 1 mM GSH as a sole nitrogen source. [a]Tolerance to DTT determined after 48 h and 72 h: 1 = no detectable growth; 2 = very poor growth; 3 = poor growth; 4 = minor or no effect relative to the parental strain.

Supplementary Table 4

Mutants affected in mRNA translation

Locus	Common name	Glutathione excretion (fold parent)	Capacity for respiratory growth	DTT tolerance[a] 48 h; 72 h	Function
ybl027w	*rpl19b*	4	yes	4; 4	Ribosomal protein L19
ybl072c	*rps8a*	3	yes	4; 4	Ribosomal protein S8
ybr191w	*rpl21a*	4	yes	4; 4	Ribosomal protein L21
ydl160c	*dhh1*	3	poor	4; 4	Putative RNA helicase
ydl191w	*rpl35a*	2	yes	4; 4	Ribosomal protein L35
ydr332w		9	yes	4; 4	RNA helicase
yhr169w	*dbp8*	5	yes	4; 4	RNA helicase
yil018w	*rpl2b*	4	yes	4; 4	Ribosomal protein L2
yjl138c	*tif2*	6	yes	4; 4	Translation initiation factor 4A (eIF4A)
ypl037c	*egd1*	11	no	1; 1	Subunit nascent polypeptide-assoc. compl.

Glutathione was measured in stationary phase and is expressed as fold relative to the parent. Respiratory capacity was determined by checking growth on YPG medium. Underlined loci denote mutants showing a reduced capacity/inability to utilise 1 mM GSH as a sole nitrogen source. [a]Tolerance to DTT determined after 48 h and 72 h: 1 = no detectable growth; 2 = very poor growth; 3 = poor growth; 4 = minor or no effect relative to the parental strain.

Supplementary Table 5

Mutants affected in ubiquitin/proteasome related processes

Locus	Common name	Glutathione excretion (fold parent)	Capacity for respiratory growth	DTT tolerance[a] 48 h; 72 h	Function
ybr173c	*ump1*	10	yes	4; 4	Proteasome maturation and assembly
yel012w	*ubc8*	2	poor	4; 4	Ubiquitin-conjugating enzyme
yer151c	*ubp3*	3	yes	4; 4	Ubiquitin-specific protease
yfr010w	*ubp6*	18	yes	1; 1	Putative ubiquitin-specific protease
yil008w	*urm1*	2	yes	4; 4	Ubiquitin-related protein
ykl213c	*doa1*	25	yes	1; 1	Protein required in ubiquitin proteolysis
ynr051c	*bre5*	9	yes	4; 4	Protein with an RNA recognition motif
yol138c		7	poor	4; 4	Protein contains WD (WD-40) repeats
ypl074w	*yta6*	11	no	4; 4	Probable component 26S proteasome

Glutathione was measured in stationary phase and is expressed as fold relative to the parent. Respiratory capacity was determined by checking growth on YPG medium. Underlined loci denote mutants showing a reduced capacity/inability to utilise 1 mM GSH as a sole nitrogen source. [a]Tolerance to DTT determined after 48 h and 72 h: 1 = no detectable growth; 2 = very poor growth; 3 = poor growth; 4 = minor or no effect relative to the parental strain.

Supplementary Table 6

Mutants affected in cell integrity/cytoskeleton/inositol metabolism

Locus	Common name	Glutathione excretion (fold parent)	Capacity for respiratory growth	DTT tolerance[a] 48 h; 72 h	Function
yal047c	*spc72*	5	no	1; 2	Cytoplasmic plaque of spindle pole body
ybl007c		9	no	4; 4	Assembly of cortical actin cytoskeleton
ycl007c	*cwh36*	7	no	1; 1	Generation of mannoprotein layer
yhr030c	*mpk1*	5	yes	1; 1	Serine/threonine protein kinase
yhr129c	*arp1*	3	yes	4; 4	Actin related protein
yjl042w	*mhp1*	10	no	1; 1	Microtubule-interacting protein
yjl095w	*bck1*	2	yes	1; 1	Serine/threonine protein kinase
yjl188c	*bud19*	7	yes	4; 4	Possibly involved in bud site selection
yjl201w	*ecm25*	21	yes	4; 4	Possibly involved in cell wall structure
ylr006c	*ssk1*	6	yes	4; 4	Component of MAP kinase pathway
ylr330w	*chs5*	5	yes	4; 4	Chitin synthase III activity
ynl225c		2	yes	1; 1	Component of spindle pole body
yor026w	*bub3*	5	poor	4; 4	Cell cycle arrest; microtubule function
yor043w	*whi2*	4	yes	4; 4	DNA repair protein
Inositol metabolism					
yjl153c	*ino1*	14	yes	4; 4	Inositol biosynthesis
yol108c	*ino4*	13	poor	4; 4	Activation phospholipid synthetic genes
ydr017c	*kcs1*	7	yes	2; 4	Inositol hexaphosphate kinase
ydr497c	*itr1*	2	yes	4; 4	Myo-inositol permease
yfr019w	*fab1*	11	yes	1; 1	PI3P-5-kinase

Glutathione was measured in stationary phase and is expressed as fold relative to the parent. Respiratory capacity was determined by checking growth on YPG medium. Underlined loci denote mutants showing a reduced capacity/inability to utilise 1 mM GSH as a sole nitrogen source. [a]Tolerance to DTT determined after 48 h and 72 h: 1 = no detectable growth; 2 = very poor growth; 3 = poor growth; 4 = minor or no effect relative to the parental strain.

Supplementary Table 7

Mutants affected in Ion homeostasis/transport

Locus	Common name	Glutathione excretion (fold parent)	Capacity for respiratory growth	DTT tolerance[a] 48 h; 72 h	Function
Vacuolar ATPase related					
ybr127c	*vma2*	6	no	1; 1	Required for vacuolar H$^+$-ATPase activity
ylr477c	*vma6*	6	no	1; 1	Required for vacuolar H$^+$-ATPase activity
yor332w	*vma4*	6	no	1; 1	Required for vacuolar H$^+$-ATPase activity
ypr036w	*vma13*	2	no	1; 1	Required for vacuolar H$^+$-ATPase activity
Calcium related					
ybr036c	*csg2*	2	yes	4; 4	Ca^{2+} homeostasis protein (CHP) family
yel031w	*cod1*	3	ND	ND	Ca^{2+}-ATPase of the ER
ygl167c	*pmr1*	8	poor	1; 3	Ca^{2+}, Mn^{2+} -transporting ATPase of Golgi
ygr217w	*cch1*	2	yes	4; 4	Voltage-gated Ca^{2+} channel
yor088w	*yvc1*	3	yes	4; 4	Ca^{2+}-activated vacuolar ion channel
Other					
ydr276c	*pmp3*	6	yes	4; 4	Plasma membrane proteolipid
ydr456w	*nhx1*	6	yes	4; 4	Endosomal/vacuolar Na+/H+ antiporter
yhl011c	*prs3*	8	poor	3; 3	Cell cycle regulation; critical cell size
yjl056c	*zap1*	5	yes	4; 4	Zn^{2+} responsive transcription activator
yjr059w	*ptk2*	11	yes	4; 4	Stimulates H$^+$-pumping via Pma1p
yjl212c	*hgt1*	3	yes	4; 4	Glutathione uptake transporter
yll010c	*psr1*	2	yes	4; 4	Na$^+$ stress response; plasma membrane
yol001w	*pho80*	4	yes	4; 4	Cyclin interacting with Pho85p
ypl058c	*pdr12*	7	no	4; 4	Weak organic acid resistance

Glutathione was measured in stationary phase and is expressed as fold relative to the parent. Respiratory capacity was determined by checking growth on YPG medium. Underlined loci denote mutants showing a reduced capacity/inability to utilise 1 mM GSH as a sole nitrogen source. [a]Tolerance to DTT determined after 48 h and 72 h: 1 = no detectable growth; 2 = very poor growth; 3 = poor growth; 4 = minor or no effect relative to the parental strain.

Supplementary Table 8

Mutants affected in transcription; chromatin remodelling

Locus	Common name	Glutathione excretion (fold parent)	Capacity for respiratory growth	DTT tolerance[a] 48 h; 72 h	Function
ybr279w	*paf1*	10	poor	1; 4	Protein associated with RNA polyerase II
ybr289w	*snf5*	11	No	4; 4	Component of SWI-SNF complex
ydl194w	*snf3*	2	Yes	4; 4	High-affinity glucose sensor
ydr448w	*ada2*	2	Yes	1; 3	Component of SAGA & ADA complexes
yel009c	*gcn4*	2	yes	4; 4	Transcription factor
ygl025c	*pgd1*	3	yes	4; 4	Component RNA polymerase II holoenz.
ygl115w		2	yes	4; 4	Derepression of glucose-repressed genes
ygl244w	*rtf1*	3	poor	1; 2	Regulation of transcription elongation
ygr252w	*gcn5*	7	poor	2; 4	Component of SAGA & ADA complexes
yhl025w	*snf6*	3	yes	4; 4	Component of SWI-SNF complex
yjl176c	*swi3*	3	yes	4; 4	Component of SWI-SNF complex
yjr063w	*rpa12*	7	yes	4; 4	RNA polymerase I subunit
ylr226w	*bur2*	6	yes	2; 4	Regulation of transcription
ylr357w	*rsc2*	2	yes	2; 4	Component of the abundant RSC complex
yol004w	*sin3*	7	no	1; 2	Component of histone deacetylase B
ypl254w	*hfi1*	5	no	1; 2	Component of the ADA complex

Glutathione was measured in stationary phase and is expressed as fold relative to the parent. Respiratory capacity was determined by checking growth on YPG medium. Underlined loci denote mutants showing a reduced capacity/inability to utilise 1 mM GSH as a sole nitrogen source. [a] Tolerance to DTT determined after 48 h and 72 h: 1 = no detectable growth; 2 = very poor growth; 3 = poor growth; 4 = minor or no effect relative to the parental strain.

Supplementary Table 9

Miscellaneous/Ungrouped deletants

Locus	Common name	Glutathione excretion (fold parent)	Capacity for respiratory growth	DTT Tolerance[a] 48 h; 72 h	Function
ybr041w	*fat1*	2	yes	4; 4	Very long-chain acyl-CoA synthetase
ybr059c	*akl1*	3	yes	4; 4	Serine/threonine protein kinase
ydr264c	*akr1*	5	no	1; 1	Pheromone signaling pathway
yer056c	*fcy2*	7	no	2; 3	Cytosine/purine permease
yer116c	*slx8*	5	yes	1; 1	Subunit of Hex3p-Slx8p complex
yhr185c	*pfs1*	2	yes	4; 4	Prospore membrane formation
ynl280c	*erg24*	4	poor	4; 4	C-14 sterol reductase
ypl091w	*glr1*	2	yes	4; 4	Glutathione reductase
ydl179w	*pcl9*	2	yes	4; 4	Cyclin that associates with the Pho85p

Glutathione was measured in stationary phase and is expressed as fold relative to the parent. Respiratory capacity was determined by checking growth on YPG medium. Underlined loci denote mutants showing a reduced capacity/inability to utilise 1 mM GSH as a sole nitrogen source. [a]Tolerance to DTT determined after 48 h and 72 h: 1 = no detectable growth; 2 = very poor growth; 3 = poor growth; 4 = minor or no effect relative to the parental strain.

Supplementary Table 10

Mutations in genes of unknown function

Locus	Common name	Glutathione excretion (fold parent)	Capacity for respiratory growth	DTT tolerance[a] 48 h; 72 h	Function
yal024c	*lte1*	2	poor	2; 3	Required for termination of M phase
ybl100c		8	no	1; 4	Protein of unknown function
ybr056w		3	yes	4; 4	Protein of unknown function
ybr162c	*tos1*	2	yes	4; 4	Protein of unknown function
ybr220c		7	yes	4; 4	Similar to human acetyl CoA transporter
ydl023c		5	yes	4; 4	Protein of unknown function
ydl039c	*prm7*	6	yes	1; 3	Protein of unknown function
ydl074c	*bre1*	5	yes	1; 1	Protein of unknown function
ydr200c		3	yes	4; 4	Protein of unknown function
ydr475c		3	yes	4; 4	Protein of unknown function
ydr533c		9	no	4; 4	Protein of unknown function
yel007w	*tos9*	2	yes	2; 4	Protein of unknown function
ygl107c		9	yes	4; 4	Protein of unknown function
ygl127c	*soh1*	3	yes	4; 4	Allows hpr1 null mutant to grow at 37°C
ygr150c		10	poor	4; 4	Protein of unknown function
yhl023c		6	yes	1; 3	Protein of unknown function
yil029c		10	yes	4; 4	Protein of unknown function
yil041w		13	yes	4; 4	Protein of unknown function
yil077c		12	yes	4; 4	Protein of unknown function
yil092w		3	yes	4; 4	Protein of unknown function
yil097w	*fyv10*	2	yes	1; 2	Protein of unknown function
yil110w		5	yes	4; 4	Protein of unknown function
ykr035c		12	yes	2; 3	Protein of unknown function
ylr114c	*efr4*	15	yes	4; 4	Null is synthetically lethal with *pho85*
ylr261c		4	yes	4; 4	Protein of unknown function
ylr322w		12	yes	4; 4	Protein of unknown function
yml048w	*gsf2*	2	yes	4; 4	Protein involved in glucose repression
ymr066w	*sov1*	6	no	4; 4	Protein of unknown function
ymr123w	*pkr1*	4	no	2; 3	Protein of unknown function
ymr151w	*yim2*	7	ND	4; 4	Protein of unknown function
ynl215w		3	yes	1; 3	Protein of unknown function
ynl296w	*kre25*	5	poor	4; 4	Questionable ORF; overlaps *MON2*
yol027c		7	no	4; 4	Protein of unknown function
yor384w	*fre5*	2	yes	4; 4	Protein with similarity to Fre2p
ypl017c		2	yes	2; 2	Protein with similarity to Lpd1p
ybl009w		6	no	4; 4	Protein of unknown function
ypr099c		12	yes	4; 4	Protein of unknown function
yol008w		5	no	4; 4	Protein of unknown function
ylr193c		11	no	4; 4	Protein of unknown function
ypr100w		8	yes	4; 4	Protein of unknown function
ynl183c		3	yes	2; 3	Protein of unknown function
yol050c		4	yes	4; 4	Protein of unknown function
ylr257w		4	yes	4; 4	Protein of unknown function

ydr230w		3	no	4; 4	Protein of unknown function
ydl072c		2	yes	4; 4	Protein of unknown function
ydl048c	*stp4*	2	yes	4; 4	Protein with strong similarity to Stp1p

Glutathione was measured in stationary phase and is expressed as fold relative to the parent. Respiratory capacity was determined by checking growth on YPG medium. Underlined loci denote mutants showing a reduced capacity/inability to utilise 1 mM GSH as a sole nitrogen source. [a]Tolerance to DTT determined after 48 h and 72 h: 1 = no detectable growth; 2 = very poor growth; 3 = poor growth; 4 = minor or no effect relative to the parental strain.

Supplementary Table 11

Extracellular glutathione (GSH and/or GSSG) accumulated by strains of *S. cerevisiae* following growth to stationary phase (72 h) under various conditions

Locus	Gene name	SD medium GSH + GSSG	S.D.	SD medium 2X BCAA	S.D.	SD medium 4X BCAA	S.D.	SD medium pH 6 GSH + GSSG	S.D.	SD medium GSSG	S.D.
BY4743	parent	4.6	0.4	6.6	0.1	2.8	0.7	BD	0.20	0.89	0.05
BY4743	parent	5.2	1.1	4.7	0.1	4.1	1.6	BD	0.02	0.85	0.07
yal024c	*lte1*	8.9	0.4	13.2	1.0	10.7	4.0	8.34	4.16	0.70	0.05
yal047c	*spc72*	14.1	0.7	14.2	2.9	11.7	1.7	7.43	8.94	1.08	0.08
yar002c-a	*erp1*	5.8	0.3	5.5	0.8	4.9	1.9	BD	0.13	0.89	0.02
ybl007c		37.0	5.1	26.8	0.9	28.1	0.8	0.82	0.30	3.05	0.29
ybl009w	*atp1*	23.5	2.1	21.5	0.7	11.2	2.8	BD	0.08	2.28	0.14
ybl027w		2.9	0.7	2.7	0.2	2.2	0.2	BD	0.10	0.66	0.06
ybl047c		3.8	0.7	2.9	0.2	2.6	0.4	BD	0.09	0.80	0.13
ybl072c		4.8	1.2	3.8	0.5	2.6	0.2	BD	0.20	0.77	0.10
ybl091c		4.7	0.6	4.0	0.6	2.2	0.4	BD	0.05	0.67	0.07
ybl100c		21.4	1.0	21.9	1.4	14.9	5.5	BD	0.03	1.95	0.08
ybr003w	*cox1*	33	0	23	3	6	2	BD	0.13	3.41	0.45
ybr036c	*csg2*	5.1	0.3	4.3	0.4	3.0	0.7	BD	0.28	0.81	0.10
ybr037c	*sco1*	37.3	0.2	22.0	0.9	15.6	1.2	BD	0.08	3.76	0.33
ybr041w	*fat1*	8.5	0.0	7.8	0.1	7.2	1.5	BD	0.18	0.74	0.04
ybr056w		14.7	1.5	16.3	0.4	21.4	5.1	BD	0.09	0.87	0.06
ybr059c	*akl1*	16.4	1.1	7.6	10.1	19.3	3.1	0.21	0.30	1.05	0.08
ybr125c	*ptc4*	12.7	2.0	12.0	1.8	4.1	0.5	BD	0.17	1.05	0.03
ybr131w	*ccz1*	1.0	0.0	1.1	0.2	-0.9	0.2	BD	0.06	0.67	0.01
ybr162c	*tos1*	19.3	5.4	21.6	0.3	13.7	7.3	BD	0.18	2.35	0.66
ybr163w	*dem1*	34.2	1.4	22.5	1.5	22.0	1.0	BD	0.12	3.47	0.07

ybr279w	*paf1*	24.9	0.9	19.0	0.8	16.7	2.9	8.79	1.53	1.38	0.06
ybr289w	*snf5*	18.5	0.9	14.0	2.1	8.8	0.4	8.15	0.63	1.05	0.04
ycl007c	*cwh36*	14.0	2.4	12.4	1.9	10.6	0.5	0.95	0.28	1.14	0.02
ycl008c	*vps23*	38	10	14	1	8	2	1.52	0.56	1.99	0.66
ycr046c	*img1*	32.8	1.0	21.0	1.4	18.8	1.9	BD	0.13	3.26	0.03
ycr063w	*bud31*	11.3	0.6	14.0	0.6	7.0	1.2	3.41	0.98	0.86	0.09
ycr077c	*pat1*	5.4	0.1	6.7	1.9	5.3	2.6	0.07	0.40	0.80	0.01
ycr086w	*csm1*	3.1	0.0	8.2	5.4	2.4	0.4	0.11	0.82	0.69	0.19
ydl023c		42.6	0.1	25.5	4.6	24.1	2.9	BD	0.05	2.12	0.00
ydl039c	*prm7*	28.0	5.7	17.8	8.8	10.4	6.7	BD	0.10	2.71	0.63
ydl069c	*cbs1*	36.6	0.5	22.0	0.4	20.5	2.8	BD	0.07	3.25	0.18
ydl074c	*bre1*	22.5	5.8	15.7	1.0	21.1	3.6	4.12	3.44	1.77	0.64
ydl106c	*pho2*	5.7	0.0	4.4	0.0	8.1	4.3	BD	0.24	0.77	0.07
ydl107w	*mss2*	31.7	2.4	20.4	0.6	12.4	3.4	BD	0.05	3.00	0.33
ydl179w	*pcl9*	4.3	0.6	4.4	0.8	2.1	1.0	BD	0.15	0.88	0.01
ydl191w	*rpl35a*	7.4	0.7	6.9	0.8	5.2	1.0	BD	0.19	0.86	0.16
ydl202w	*mrpl11*	28.4	2.2	17.1	4.2	13.4	1.1	BD	0.09	3.07	0.49
ydr017c	*kcs1*	13.4	5.0	12.3	0.8	4.6	1.2	BD	0.17	1.42	0.84
ydr027c	*luv1*	32.1	1.9	31.0	1.4	34.7	2.7	0.89	0.33	1.53	0.14
ydr175c	*rsm24*	30.5	6.9	22.1	1.4	19.7	0.7	BD	0.02	3.24	0.44
ydr197w	*cbs2*	33.5	4.1	23.2	0.7	20.8	1.4	BD	0.05	3.81	1.00
ydr200c		14.2	1.9	9.8	1.1	10.0	3.0	1.16	0.57	1.08	0.13
ydr204w	*coq4*	29.7	2.7	19.5	1.9	18.0	0.9	BD	0.04	3.21	0.54
ydr230w		32.4	2.1	20.2	2.7	20.9	0.8	BD	0.08	3.13	0.90
ydr264c	*akr1*	18.0	0.9	12.1	4.3	19.4	3.8	10.91	10.77	1.90	1.15
ydr276c	*pmp3*	29	6	16	5	7	1	0.17	0.32	1.57	1.26
ydr298c	*atp5*	34.9	1.5	23.1	3.8	19.3	0.6	BD	0.02	3.22	0.44
ydr300c	*pro1*	20.8	6.0	18.1	1.4	13.2	3.1	1.94	0.12	1.52	0.14
ydr322w	*mrpl35*	36.7	3.8	24.8	3.9	20.3	1.5	BD	0.09	1.08	0.51
ydr323c	*pep7*	30.5	1.2	35.1	4.9	25.6	5.1	4.20	1.11	1.37	0.10

ydr332w		32.0	3.9	22.0	5.4	20.4	1.6	BD	0.05	1.73	1.34
ydr337w	*mrps28*	31.5	3.8	18.5	3.1	14.4	0.5	BD	0.11	2.59	1.35
ydr440w	*dot1*	4.5	0.2	6.2	0.7	4.3	1.2	BD	0.34	0.91	0.05
ydr448w	*ada2*	5.2	0.5	4.6	0.0	6.9	4.7	0.13	0.54	0.75	0.05
ydr462w	*mrpl28*	33.9	0.5	25.2	3.9	19.7	4.0	BD	0.12	3.25	0.07
ydr475c		26.5	6.3	25.9	1.5	13.2	4.9	BD	0.26	3.05	0.96
ydr484w	*sac2*	34.8	4.0	31.6	3.5	26.9	0.9	4.77	1.96	1.49	0.18
ydr486c	*vps60*	37	2	28	3	9	7	BD	0.06	3.72	0.15
ydr495c	*vps3*	23.1	0.7	28.1	0.1	18.3	2.2	3.91	0.81	1.27	0.10
ydr497c	*itr1*	5.7	0.8	6.6	0.0	5.3	2.4	BD	0.18	0.84	0.06
ydr518w	*eug1*	36.2	1.3	26.0	4.6	21.7	3.8	BD	0.02	3.08	0.00
ydr529c	*qcr7*	33.3	0.4	27.2	4.4	15.1	0.6	BD	0.03	3.33	0.28
ydr533c		35.9	1.1	25.2	4.7	12.4	2.2	BD	0.06	3.46	0.56
yel007w	*tos9*	13.2	1.1	14.8	3.5	10.4	1.3	BD	0.13	1.05	0.21
yel009c	*gcn4*	6.8	1.2	7.0	1.0	3.9	1.2	1.69	1.37	0.84	0.06
yel051w	*vma8*	4.6	0.5	5.2	1.0	2.7	0.9	BD	0.05	1.75	1.30
yel062w	*npr2*	35	2	22	5	5	2	BD	0.04	1.37	0.91
yer004w		4.6	0.6	6.2	0.4	2.3	0.5	BD	0.06	0.86	0.21
yer005w	*ynd1*	6.7	1.1	9.2	1.2	3.2	0.3	BD	0.06	0.77	0.05
yer017c	*afg3*	12.9	3.7	10.8	2.7	5.8	0.8	BD	0.09	1.41	0.75
yer056c	*fcy2*	36.2	3.2	22.5	3.5	19.2	1.0	BD	0.09	2.19	2.06
yer116c	*slx8*	15.1	3.5	21.0	0.4	23.6	6.5	BD	0.10	1.45	0.01
yer119c-a		5.2	0.5	6.0	0.3	4.6	1.1	2.29	1.92	0.73	0.01
yer122c	*glo3*	21.6	1.1	20.7	0.4	12.5	2.4	BD	0.06	2.17	0.21
yer141w	*cox15*	35.5	1.7	21.8	2.2	19.1	3.6	BD	0.10	3.60	0.42
yer151c	*ubp3*	6.6	0.1	7.4	0.2	3.9	1.4	0.14	0.58	0.82	0.05
yer153c	*pet122*	34.3	1.1	25.4	4.1	22.4	5.0	BD	0.05	3.21	0.06
yer154w	*oxa1*	30.0	1.5	23.1	1.1	10.3	1.1	BD	0.06	3.05	0.10
yfl034w	*mrpl7*	5.7	1.5	4.1	0.4	3.3	0.8	BD	0.04	0.76	0.06
yfr010w	*ubp6*	20	2	11	2	6	1	0.04	0.28	1.25	0.08

yfr019w	*fab1*	7.8	0.1	8.6	0.3	4.6	0.7	BD	0.19	0.94	0.03
yfr019w	*fab1*	28.0	0.2	27.6	0.3	25.7	3.8	BD	0.17	2.91	0.04
ygl025c	*pgd1*	7.1	0.5	8.1	1.1	4.3	0.5	0.05	0.62	0.80	0.04
ygl066w		10.3	1.4	10.5	0.3	7.5	0.8	BD	0.22	0.86	0.03
ygl101w		39.5	1.4	31.6	3.1	21.2	3.0	BD	0.11	3.96	0.06
ygl107c		28.5	0.5	28.0	3.1	17.8	1.8	BD	0.05	3.51	0.43
ygl115w		9.9	0.2	11.4	0.4	6.8	0.5	0.77	0.60	0.81	0.09
ygl124c	*mon1*	5.8	0.3	15.8	5.7	6.1	1.0	0.25	0.13	0.99	0.06
ygl127c	*soh1*	9.5	0.9	10.4	0.9	7.0	0.8	4.35	0.86	1.10	0.04
ygl167c	*pmr1*	29.7	4.0	21.3	0.3	13.7	1.0	15.34	3.51	7.11	0.40
ygl168w		0.7	0.3	0.7	0.1	-0.9	0.2	BD	0.21	0.64	0.15
ygl194c	*hos2*	4.2	0.5	5.1	0.4	3.1	0.6	BD	0.09	0.77	0.06
ygl223c	*tfi1*	8	6	13	4	1	5	BD	0.20	1.11	0.53
ygl227w	*vid30*	8.7	0.2	15.7	0.5	5.2	0.6	BD	0.09	0.86	0.00
ygl237c	*hap2*	10	2	3.3	0.5	1.0	0.6	BD	0.15	0.99	0.04
ygl244w	*rtf1*	11.9	0.8	10.2	0.7	5.6	1.4	BD	0.15	0.93	0.01
ygl252c	*rtg2*	9.8	0.1	11.3	0.3	7.3	0.1	BD	0.24	0.95	0.00
ygr021w		3.9	0.2	6.0	0.5	4.9	1.4	BD	0.11	0.69	0.10
ygr123c	*ppt1*	5.1	0.4	5.5	0.8	3.0	0.1	BD	0.08	0.73	0.05
ygr150c		35.8	3.5	24.0	4.6	18.1	0.8	BD	0.53	3.88	0.82
ygr171c	*msm1*	33.0	1.5	23.2	3.9	20.9	0.6	BD	0.52	2.91	0.17
ygr206w		11	1	8	1	3	1	0.08	0.92	1.13	0.20
ygr217w	*cch1*	8.5	1.7	21.2	6.4	14.7	12.7	BD	0.83	3.28	3.34
ygr252w	*gcn5*	22.7	4.2	11.9	0.6	12.1	0.7	2.93	0.50	1.67	0.33
ygr257c		24.6	1.9	16.1	1.7	9.7	2.6	BD	0.15	1.84	0.10
yhl011c	*prs3*	31.4	3.1	22.4	4.1	11.2	2.0	BD	0.06	3.52	0.90
yhl023c		33	3	20	4	4.2	0.3	BD	0.12	1.74	1.25
yhl025w	*snf6*	12.6	1.0	12.4	1.4	8.3	0.8	4.63	0.15	1.06	0.06
yhl031c	*gos1*	23.1	4.8	15.5	4.7	8.3	8.9	BD	0.12	3.12	0.11
yhl038c	*cbp2*	32.9	3.4	20.7	3.1	20.9	1.2	BD	0.21	2.55	1.76

yhl044w		3.5	0.9	4.4	0.4	4.0	1.1	BD	0.06	0.70	0.29
yhr010w	*rpi27A*	6.9	1.3	6.4	1.8	5.9	0.7	BD	0.27	1.63	1.06
yhr011w	*dia4*	30.8	5.4	24.7	4.0	19.6	0.7	BD	0.10	2.31	0.72
yhr030c	*mpk1*	12.1	2.9	11.9	1.4	15.1	0.2	2.95	0.89	2.16	1.31
yhr034c		5.1	0.6	6.0	0.2	3.5	0.4	BD	0.11	1.82	1.20
yhr051w	*cox6*	28.8	0.2	21.0	0.7	18.3	1.7	BD	0.13	2.95	0.26
yhr116w		25.5	15.3	10.6	3.2	14.9	1.4	BD	0.18	2.57	1.42
yhr120w	*msh1*	35.6	5.6	21.0	2.0	23.8	2.3	BD	0.16	3.57	0.68
yhr129c	*arp1*	8.5	2.1	9.7	0.5	7.3	1.3	BD	0.18	0.81	0.07
yhr147c	*mrpl6*	30.8	3.4	21.3	0.6	20.6	1.7	BD	0.07	3.20	0.11
yhr185c	*pfs1*	8.0	0.0	8.5	1.3	5.1	1.3	BD	0.34	0.79	0.12
yil001w		5.2	0.1	7.7	0.8	6.5	0.4	BD	0.68	0.80	0.11
yil006w		7.4	0.5	9.5	1.7	7.2	1.2	BD	0.17	0.99	0.20
yil008w	*urm1*	8.7	0.7	13.7	3.5	11.5	1.0	0.82	1.52	0.96	0.17
yil017c	*vid28*	40.8	1.4	26.9	2.1	21.8	0.3	0.12	0.22	2.01	0.38
yil018w	*rpl2B*	19.7	4.3	17.8	8.1	10.7	4.6	BD	0.07	2.22	0.67
yil029c		32.9	1.3	26.4	2.6	25.4	1.2	BD	0.69	1.87	0.09
yil041w		35.5	4.7	26.1	2.6	22.0	0.5	BD	0.09	2.17	0.08
yil053w	*rhr2*	20.4	4.7	20.9	1.4	10.1	1.5	BD	0.66	1.40	0.53
yil065c	*fis1*	34.7	7.2	25.3	2.0	19.9	1.5	BD	0.07	2.65	0.24
yil070c	*mam33*	34.0	1.6	25.3	4.0	21.1	1.7	BD	0.21	4.58	0.69
yil077c		39.5	2.3	27.8	6.1	24.4	0.3	BD	0.10	1.87	1.10
yil092w		8.1	0.1	11.3	0.8	10.6	1.7	BD	0.17	1.03	0.02
yil093c	*rsm25*	33.6	1.3	21.5	3.9	14.1	1.8	BD	0.11	3.26	0.21
yil097w	*fyv10*	15.9	1.2	23.4	2.7	9.7	1.8	0.28	1.15	1.30	0.39
yil098c	*fmc1*	54.1	2.9	43.3	3.7	39.3	1.9	0.22	0.69	3.69	0.43
yil110w		30.6	0.0	19.5	0.3	23.1	3.0	BD	0.16	1.88	0.07
yir017c	*met28*	3.9	5.6	2.0	0.4	-0.5	0.5	BD	0.06	0.68	0.16
yir021w	*mrs1*	30.7	4.6	20.8	2.0	17.1	0.3	BD	0.06	2.90	0.39
yjl004c	*sys1*	8.4	0.6	9.5	1.2	6.1	0.5	BD	0.40	0.90	0.04

yjl022w		34.2	0.0	24.6	4.3	23.5	2.8	BD	0.02	3.01	0.04
yjl042w	*mhp1*	29.0	1.0	26.3	0.8	25.0	2.6	BD	0.05	2.99	0.17
yjl056c	*zap1*	25	7	15	7	5	1	0.02	0.23	1.46	0.12
yjl063c	*mrpl8*	31.9	7.1	23.2	0.8	20.6	2.1	BD	0.03	2.70	0.14
yjl095w	*bck1*	13.2	2.4	15.5	0.6	18.0	1.1	12.84	10.39	1.20	0.09
yjl102w	*mef2*	24.4	2.0	22.4	1.0	23.5	3.1	BD	0.07	1.78	2.02
yjl117w	*pho86*	7.2	1.5	6.3	0.4	9.8	1.2	0.41	0.67	0.87	0.03
yjl128c	*pbs2*	4.5	0.2	5.1	0.4	3.0	0.2	BD	0.06	0.77	0.03
yjl138c	*tif2*	31.9	5.1	21.4	5.7	19.1	2.3	BD	0.16	3.89	0.73
yjl152w	*ino1*	39.9	2.9	36.6	1.4	39.4	6.2	27.42	2.52	1.51	0.18
yjl166w	*qcr8*	29.7	3.3	22.2	0.8	19.4	1.5	BD	0.16	3.03	0.42
yjl176c	*swi3*	10.4	1.5	11.3	1.1	13.5	0.7	1.02	0.22	1.04	0.13
yjl183w	*mnn11*	13.6	3.1	12.1	0.5	9.8	2.1	1.95	1.22	0.96	0.04
yjl188c	*bud19*	32	6	18	0	8	1	BD	0.15	2.27	0.55
yjl201w	*ecm25*	35.8	4.1	23.5	3.3	20.5	0.5	BD	0.25	4.36	0.46
yjl204c	*rcy1*	13.0	1.8	9.4	0.7	6.6	0.1	0.15	0.34	0.95	0.03
yjl209w	*cbp1*	30.9	3.6	21.1	0.3	19.0	0.9	BD	0.05	3.09	0.58
yjl212c	*opt1*	6.8	0.7	7.3	1.6	5.4	0.5	BD	0.16	0.92	0.03
yjr059w	*ptk2*	32.3	4.8	23.6	3.0	19.7	1.5	BD	0.22	2.10	0.62
yjr063w	*rpa12*	31.2	3.2	23.9	1.1	20.5	1.3	BD	0.18	2.02	0.45
yjr102c	*vps25*	40	8	16	0	9	1	2.61	1.29	1.70	0.52
yjr144w	*mgm101*	34.8	1.0	22.6	0.0	23.0	0.6	BD	0.18	3.25	0.22
ykl002w	*did4*	52	0	28	3	14	1	0.82	0.45	1.92	0.13
ykl003c	*mrp17*	53	3	30	4	15	1	0.61	0.41	1.85	0.00
ykl007w	*cap1*	12.8	4.1	8.4	1.9	5.4	0.4	BD	0.10	0.92	0.13
ykl032c	*ixr1*	12	3	10	0	1.9	0.2	BD	0.09	1.37	0.31
ykl041w	*vps24*	35.5	1.3	25.3	3.3	16.0	0.7	0.25	0.20	1.40	0.09
ykl055c	*oar1*	11.9	9.5	7.4	3.0	4.3	1.6	BD	0.12	2.23	1.56
ykl212w	*sac1*	15.6	0.5	12.6	2.7	11.8	2.0	1.62	0.48	0.99	0.10
ykl213c	*doa1*	24	5	16	1	7.6	0.1	1.78	0.99	1.48	0.15

ykr001c	*vps13*	22.8	3.2	22.1	1.2	25.1	1.0	1.67	1.10	1.15	0.02
ykr006c	*mrpl13*	29.9	2.5	20.2	2.0	17.7	2.4	BD	0.38	3.11	0.34
ykr035c		24.8	8.3	13.9	1.5	11.8	5.1	2.58	1.34	1.09	0.70
ykr035w-a	*did2*	24	9	14	2	7	2	1.23	0.85	1.35	0.15
ykr054c	*dyn1*	8.4	2.8	6.6	0.8	6.0	4.2	BD	0.19	0.78	0.08
ykr067w	*gpt2*	4.2	1.3	3.5	0.4	2.8	0.6	BD	0.14	0.65	0.11
yll009c	*cox17*	9.2	0.5	10.7	1.8	4.7	3.7	BD	0.40	0.91	0.02
yll010c	*psr1*	8.2	1.1	9.5	0.7	6.1	1.4	BD	0.10	0.81	0.13
yll018c-a	*cox19*	35.6	0.6	26.3	1.1	20.7	7.9	BD	0.08	3.15	0.09
yll040c	*vps13*	9.7	1.6	10.4	3.0	6.4	0.8	BD	0.44	0.87	0.09
ylr006c	*ssk1*	8.6	2.2	11.1	0.6	4.4	1.3	BD	0.21	0.82	0.01
ylr018c	*pom34*	5.1	0.9	5.8	1.3	3.0	0.8	BD	0.37	0.67	0.03
ylr025w	*vps32*	40	7	19	1	12	2	3.52	0.88	1.92	0.20
ylr067c	*pet309*	5.7	1.3	4.8	0.0	4.7	0.8	BD	0.64	0.73	0.04
ylr1148w	*pep3*	50.2	0.6	48.0	2.1	50.5	2.3	13.57	1.47	1.57	0.07
ylr114c	*erf4*	44.1	3.6	35.0	1.9	35.7	1.3	11.92	2.59	1.57	0.08
ylr119w	*srn2*	38	8	10	1	7	1	1.81	0.59	1.65	0.32
ylr139c	*sls1*	5.9	0.9	5.4	0.3	3.7	0.6	BD	0.06	0.66	0.03
ylr193c		32.4	5.2	21.5	2.0	19.0	2.2	BD	0.08	3.08	0.58
ylr226w	*bur2*	14.1	2.7	9.3	3.7	14.4	2.7	12.13	2.07	1.08	0.20
ylr234w	*top3*	8.5	1.5	7.9	0.9	6.9	2.5	15.16	8.54	0.93	0.10
ylr239c	*lip2*	9.0	1.0	10.7	0.8	6.4	1.1	0.74	0.88	0.92	0.08
ylr257w		6.1	1.6	5.4	1.4	4.0	0.8	BD	0.29	0.85	0.02
ylr261c		17.7	3.4	15.1	0.6	12.4	2.1	3.20	0.68	1.14	0.08
ylr262c	*ypt6*	14.5	2.2	13.1	1.7	8.1	0.2	1.31	0.21	1.02	0.08
ylr295c	*hsp60*	6.6	1.1	6.4	0.7	3.2	0.2	BD	0.09	0.94	0.02
ylr322w		20.4	1.9	18.8	2.1	14.9	1.6	6.28	1.45	2.04	0.16
ylr324w		7.6	2.2	6.5	0.6	3.1	1.8	BD	0.13	0.81	0.13
ylr330w	*chs5*	17.9	0.9	16.1	1.3	9.5	0.7	BD	0.17	1.16	0.04
ylr342w	*fks1*	3.3	0.9	7.2	4.4	5.3	5.8	BD	0.10	0.69	0.06

ylr357w	*rsc2*	10.6	3.0	7.8	1.3	11.8	2.5	BD	0.34	1.23	0.24
ylr360w	*vps38*	28.0	10.1	10.4	2.3	14.0	3.8	1.67	0.48	1.42	0.48
ylr369w	*ssq1*	13	4	7.4	2.5	2	2	BD	0.11	1.14	0.15
ylr396c	*vps33*	23.5	5.7	30.2	5.8	41.3	6.2	5.05	0.35	1.58	0.39
ylr417w	*vps36*	36	7	15	1	10	1	3.15	1.30	1.59	0.29
ylr423c	*apg17*	7.5	0.1	8.0	0.2	5.9	2.1	1.14	0.96	0.97	0.03
ylr439w	*mrpl4*	4.8	0.2	6.1	0.4	3.0	0.9	BD	0.16	0.78	0.00
yml048w	*gsf2*	8.3	0.5	4.9	0.4	2.7	0.3	BD	0.12	0.84	
yml071c	*dor1*	20.0	3.6	14.1	1.5	11.8	4.4	3.41	2.30	0.95	0.32
yml078w	*cpr3*	4.2	0.5	6.2	0.3	2.4	0.4	BD	0.04	0.02	1.15
yml097c	*vps9*	6.5	0.9	7.8	1.3	9.1	0.8	0.69	0.18	0.89	0.04
ymr004w	*mvp1*	7.0	1.2	6.2	1.0	4.8	0.5	BD	0.11	0.79	0.04
ymr063w	*rim9*	4.9	1.1	3.3	0.5	2.4	0.8	BD	0.18	0.76	0.10
ymr064w	*aep1*	33.4	6.8	21.5	0.5	24.2	3.5	BD	0.08	3.08	0.93
ymr066w	*sov1*	33.5	2.9	22.0	2.0	20.0	0.6	BD	0.07	3.24	0.37
ymr072w	*abf2*	28.5	2.7	23.0	0.7	16.8	2.7	BD	0.03	2.98	0.46
ymr077c	*vps20*	35.3	4.6	15.7	1.3	12	3	3.28	0.54	1.53	0.28
ymr123w	*pkr1*	8.3	0.4	7.5	1.1	5.3	1.3	0.02	0.21	0.92	0.08
ymr150c	*imp1*	34.3	2.2	20.7	3.1	20.3	1.3	BD	0.36	3.03	0.36
ymr151w	*yim2*	37.1	5.3	20.4	1.4	21.0	2.5	BD	0.17	3.25	0.57
ymr193w	*mrpl24*	36.7	4.3	22.1	1.2	22.0	1.6	BD	0.37	3.41	0.37
ymr228w	*mtf1*	39.5	6.2	22.7	1.2	21.9	2.8	BD	0.21	3.56	0.49
ynl080c		19.3	3.7	11.7	2.6	16.0	2.2	1.58	0.64	1.92	0.18
ynl098c	*ras2*	10.9	0.2	12.5	2.2	4.8	1.2	BD	0.23	0.95	0.06
ynl106c	*inp52*	5.1	0.3	4.9	0.4	2.9	0.3	BD	0.16	0.84	0.02
ynl119w		7.7	0.8	7.0	1.1	7.4	0.6	0.02	0.53	0.82	0.00
ynl148c	*alf1*	6.2	1.0	7.8	0.6	2.9	0.2	BD	0.12	0.84	0.05
ynl154c	*yck2*	5.2	1.0	5.1	0.6	5.5	1.8	BD	0.16	2.50	2.31
ynl159c	*asi2*	4.8	0.7	5.2	0.9	6.6	0.7	BD	0.06	0.97	0.19
ynl177c		27.8	1.0	24.2	2.9	18.9	0.2	BD	0.21	1.66	1.01

ynl183c		7	2	2.7	0.1	1.1	0.3	BD	0.09	2.01	1.66
ynl215w		6.6	1.4	5.5	0.6	4.7	0.6	3.38	0.33	1.73	1.23
ynl225c		10.2	1.5	8.8	1.3	7.6	1.2	1.59	0.44	0.89	0.08
ynl229c	*ure2*	26	7	2.8	0.5	1.9	0.5	2.25	0.43	1.40	0.83
ynl280c	*erg24*	10.4	0.6	12.1	0.1	10.1	0.8	1.79	2.11	0.74	0.03
ynl296w	*kre25*	7.2	0.4	8.6	1.6	8.3	2.1	1.58	0.68	0.71	0.01
ynl297c	*mon2*	23.2	3.9	19.8	5.5	18.2	2.4	3.05	1.49	1.13	0.30
ynr005c		38	11	12	1	8	1	0.66	0.51	1.85	0.64
ynr006w	*vps27*	51.7	10.3	23.1	0.7	18.5	2.5	2.20	0.48	2.29	0.73
ynr036c		23.2	2.0	23.9	2.6	21.3	1.2	BD	0.08	3.22	0.15
ynr037c	*rsm19*	34.6	6.0	22.5	2.5	16.3	1.1	BD	0.10	3.57	0.86
ynr045w	*pet494*	38.5	3.2	23.4	1.8	19.7	0.9	BD	0.14	3.64	0.73
ynr050c	*lys9*	3.6	0.0	5.2	0.6	4.0	0.6	BD	0.22	1.25	0.02
ynr051c	*bre5*	8.4	0.3	8.7	1.2	7.5	3.9	0.43	0.70	0.79	0.06
yol001w	*pho80*	17.7	3.4	8.1	6.0	12.2	1.9	BD	0.21	2.42	1.53
yol004w	*sin3*	37	6	11	1	9	1	BD	0.16	2.25	0.10
yol008w		32.0	7.3	20.0	3.3	13.9	1.1	BD	0.03	1.23	0.53
yol009c	*mdm12*	24.4	2.8	16.7	3.0	13.7	2.3	BD	0.21	1.98	0.16
yol018c	*tlg2*	4.6	0.6	6.5	1.1	3.5	0.7	BD	0.01	2.09	1.87
yol027c		30	1	12	1	5	1	BD	0.17	1.85	0.97
yol033w	*mse1*	35.1	2.6	23.9	2.5	20.9	1.2	BD	0.19	1.80	1.49
yol050c		16	1	12	1	3	0	BD	0.32	2.32	1.57
yol081w	*ira2*	18.3	2.6	18.1	0.7	16.6	2.8	BD	0.57	1.25	0.10
yol095c	*hmi1*	31.7	4.8	22.6	2.1	23.2	0.8	BD	0.11	3.60	0.53
yol108c	*ino4*	14.5	3.4	14.9	1.8	16.5	0.5	21.69	1.63	1.22	0.09
yol138c		34	1	16	1	4.8	0.4	BD	0.24	2.36	0.18
yor008c	*slg1*	24.1	4.5	21.0	3.4	9.0	1.0	BD	0.06	2.77	0.53
yor026w	*bub3*	10.7	0.7	9.6	1.0	11.7	2.1	1.22	0.31	0.90	0.01
yor036w	*pep12*	34.6	1.8	37.5	5.4	28.3	1.1	3.22	0.36	1.61	0.09
yor043w	*whi2*	30.8	1.4	27.6	2.5	21.8	1.2	BD	0.04	1.84	0.05

yor069w	*vps5*	0.9	0.0	0.9	0.2	-0.8	0.1	BD	0.17	0.60	0.01
yor070c	*gyp1*	18.4	2.2	19.1	0.5	17.4	0.3	2.56	0.10	0.94	0.03
yor088w	*yvc1*	4.5	0.5	5.3	0.3	3.9	0.8	BD	0.19	0.79	0.07
yor089c	*vps21*	14.0	1.0	11.6	1.2	7.4	1.1	2.25	0.10	0.84	0.50
yor360c	*pde2*	13.9	4.0	12.5	1.9	7.8	1.0	BD	0.23	1.27	0.61
yor375c	*gdh1*	12	5	4	0	3	1	BD	0.18	1.46	0.43
yor384w	*fre5*	4.6	0.4	6.8	0.9	4.7	0.6	BD	0.17	1.88	1.73
ypl003w	*vps22*	49.7	1.4	41.9	2.0	27.6	1.6	21.47	3.87	1.78	0.03
ypl017c		5.4	0.0	6.9	0.2	4.2	1.3	BD	0.29	0.81	0.06
ypl022w	*rad1*	53.3	5.5	23.1	0.3	19.7	1.8	5.95	1.59	2.16	0.14
ypl026c	*sha3*	10	1	10	0	2	1	BD	0.05	0.99	0.09
ypl037c	*egd1*	19.0	1.2	21.3	0.1	13.1	1.6	1.35	0.70	1.09	0.10
ypl058c	*pdr12*	34.3	5.3	19.7	0.5	15.5	4.3	BD	0.21	3.19	0.75
ypl074w	*yta6*	37.2	9.4	21.2	1.5	22.5	1.8	BD	0.05	3.30	0.85
ypl091w	*glr1*	5.5	1.6	4.8	0.2	3.3	0.7	BD	0.14	0.78	0.07
ypl132w	*cox11*	33.8	3.1	22.0	4.4	18.1	1.6	BD	0.09	3.57	0.24
ypl254w	*hfi1*	19.6	7.2	13.4	0.4	11.9	8.6	BD	0.52	0.95	0.12
ypl272c		5.4	1.1	5.1	1.0	6.0	0.3	BD	0.38	0.74	0.10
ypr004c		34	2	15	1	9	1	2.47	0.42	1.71	0.15
ypr036w	*vma13*	14.9	2.3	14.8	2.7	11.1	1.1	0.54	0.31	0.97	0.17
ypr099c		35.7	5.3	21.3	1.7	20.1	1.3	BD	0.14	3.21	1.27
ypr100w		38.5	4.1	21.9	0.4	21.5	2.4	BD	0.19	3.67	0.59
ypr138c	*mep3*	9	3	2.8	0.5	2.6	0.5	BD	0.08	0.98	0.27
ypr166c	*mrp2*	33.2	4.0	20.2	0.6	17.8	2.0	BD	0.15	3.41	0.54
ypr173c	*vps4*	45.9	2.6	30.7	0.5	19.2	0.6	2.56	1.18	1.85	0.11
ypr191w	*qcr2*	31.4	3.7	21.3	2.5	19.2	1.8	BD	0.01	3.10	0.77

All data shown are means ± S.D. for triplicate values expressed in µM. All values were obtained following growth of strains in 96-well plates at 30°C without shaking. GSH + GSSG (column 3) = Extracellular total glutathione following growth in SD medium to stationary phase (72 h); 2XBCAA (column 5) = As for GSH + GSSG (column 3) but supplemented with 2-times standard BCAA (see methods section for concentrations used); 4X BCAA (column 7) = As for GSH+ GSSG (column 3) but supplemented with 4-times BCAA (see methods section for concentrations used); GSH + GSSG pH 6.0 (column 9) = As for GSH + GSSG (column 3) but SD medium was buffered to pH 6.0 (25 mM PIPPS); GSSG (column

11) = Extracellular GSSG following growth in SD medium to stationary phase (72 h). Abbreviations: BCAA = branched-chain amino acids; BD = below detection limits.