

Additional File 14: List of differentially-expressed genes in the *yhr045wΔ* mutant. Genes that were up- or down-regulated in at two independent experiments are listed and categorized according to their cellular functions using the GO biological process from Funspec. The average expression level is shown in logarithmic scale with base of two.

UP-REGULATED GENES

Gene ID	Gene Name	Average expression	Function
<i>Carbohydrate metabolism and energy metabolism (23)</i>			
YAL060W	BDH1	1.17	Butanediol dehydrogenase
YBR126C	TPS1	1.18	Trehalose-6-phosphate synthase
YBR149W	ARA1	1.19	Arabinose dehydrogenase
YCL040W	GLK1	1.57	Glucokinase, specific for aldohexoses
YCR005C	CIT2	1.72	Citrate synthase
YDL021W	GPM2	2.30	Phosphoglycerate mutase
YDL022W	GPD1	0.98	Glycerol-3-phosphate dehydrogenase
YDR074W	TPS2	1.00	Trehalose-6-phosphate phosphatase
YEL071W	DLD3	1.18	D-lactate dehydrogenase
YER178W	PDA1	0.87	Pyruvate dehydrogenase complex alpha subunit
YFR053C	HXK1	1.76	Hexokinase I
YGL156W	AMS1	1.66	Alpha-Mannosidase
YIL070C	MAM33	0.91	Mitochondrial acidic matrix protein
YJL052W	TDH1	0.96	Glyceraldehyde-3-phosphate dehydrogenase 1
YKL085W	MDH1	1.03	Malate dehydrogenase, mitochondrial
YKL150W	MCR1	0.95	NADH-cytochrome b5 reductase
YLR304C	ACO1	1.83	Aconitate hydratase
YMR105C	PGM2	1.88	Phosphoglucomutase
YMR145C	NDE1	1.28	Mitochondrial NADH dehydrogenase
YNR001C	CIT1	1.72	Citrate synthase
YOL136C	PFK27	0.93	6-Phosphofructose-2-kinase
YOR136W	IDH2	2.74	Isocitrate dehydrogenase subunit 2
YOR347C	PYK2	1.30	Pyruvate kinase
<i>Iron metabolism (8)</i>			
YDR270W	CCC2	1.55	Copper-transporting P-type ATPase
YEL065W	SIT1	1.97	Siderophore iron permease
YFL041W	FET5	1.50	Multicopper oxidase involved in ferrous iron transport
YLR136C	TIS11	3.03	Zinc finger containing protein that belongs to iron regulon
YOL158C	ENB1	1.98	Siderophore iron permease
YOR382W	FIT2	4.26	Cell wall mannoprotein of iron transport facilitator
YOR383C	FIT3	4.76	Cell wall mannoprotein of iron transport facilitator
YOR384W	FRE5	1.87	Ferric reductase homologue
<i>Lipid metabolism (7)</i>			
YDR058C	TGL2	0.97	Triglyceride lipase
YGR175C	ERG1	1.12	Squalene monooxygenase
YLR056W	ERG3	1.36	C-5 sterol desaturase
YML008C	ERG6	0.97	S-adenosylmethionine delta-24-sterol-C-methyltransferase
YMR008C	PLB1	1.00	Phospholipase B

Gene ID	Gene Name	Average expression	Function
<i>Lipid metabolism (cont'd)</i>			
YOR049C	RSB1	3.51	Involved in the release of sphingoid long-chain bases
YOR237W	HES1	3.16	Protein implicated in ergosterol biosynthesis
<i>Metal homeostasis (2)</i>			
YGR257C	MTM1	0.95	Putative metal chaperone for Sod2p
YHR053C	CUP1A	1.73	Metallothionein (copper chelatin)
<i>Nucleotide metabolism (14)</i>			
YBL005W	PDR3	1.89	Zinc-finger transcription factor
YBR066C	NRG2	0.89	Suppressor of snf mutations
YCL061C	MRC1	1.02	Component of the replication fork
YEL066W	HPA3	1.31	Histone and other protein acetyltransferase
YER035W	EDC2	1.62	Protein involved in mRNA decapping
YGL037C	PNC1	1.30	Protein with pyrazinamidase and nicotinamidase activity
YHL027W	RIM101	3.08	Transcription factor for sporulation related genes
YHR006W	STP2	1.37	Transcription factor regulating amino acid permease genes
YIR018W	YAP5	1.30	Transcription factor of the basic leucine zipper type
YKL109W	HAP4	1.50	Transcription factor with acidic activation domain
YOR344C	TYE7	1.12	Basic helix-loop-helix transcription factor
YOR360C	PDE2	0.83	3',5'-Cyclic-nucleotide phosphodiesterase
YOR363C	PIP2	1.20	Transcription factor required for induction of peroxisomal proteins
YPL086C	ELP3	1.32	Subunit of the RNA Polymerase II elongator holoenzyme
<i>Others (34)</i>			
YBL034C	STU1	1.34	Suppressor of beta-tubulin mutation
YBL043W	ECM13	2.42	Possibly involved in cell wall structure or biosynthesis
YBL078C	AUT7	1.15	Delivery of autophagic vesicles
YBR105C	VID24	2.23	Vacuolar protein targeting
YBR183W	YPC1	1.39	Alkaline ceramidase
YDL124W	YDL124W	1.61	NAD(P)H-dependent reductase
YDL234C	GYP7	1.24	GTPase-activating protein for Ypt7p
YDR011W	SNQ2	1.25	Drug-efflux pump (ATP-binding cassette superfamily)
YDR072C	IPT1	0.89	Inositolphosphotransferase 1
YER024W	YAT2	1.95	Carnitine acetyltransferase function
YER044C-A	MEI4	1.00	Protein required early in meiosis
YER124C	DSE1	1.27	Protein involved in cell wall metabolism
YER175C	TMT1	2.19	Trans-aconitate methyltransferase
YGL086W	MAD1	0.82	Protein involved in spindle-assembly checkpoint
YGR008C	STF2	1.46	ATPase stabilizing factor
YGR141W	VPS62	0.84	Class F vacuolar protein sorting protein
YGR239C	PEX21	1.16	Peroxisomal biogenesis protein
YHR046C	INM1	1.62	Inositol monophosphatase
YHR179W	OYE2	1.01	NADPH dehydrogenase
YIR038C	GTT1	1.39	Glutathione transferase
YKL008C	LAC1	1.25	Longevity-assurance gene 1 cognate
YKL026C	GPX1	1.09	Glutathione peroxidase
YKR053C	YSR3	1.12	Sphingoid base-phosphate phosphatase
YLR178C	TFS1	2.19	Carboxypeptidase Y inhibitor
YLR286C	CTS1	1.40	Endochitinase
YMR316W	DIA1	1.51	Protein involved in invasive growth
YNL192W	CHS1	0.86	Chitin synthase I
YNL242W	APG2	1.04	Vacuolar protein targeting
YOR036W	PEP12	0.8	Syntaxin homolog involved in Golgi to vacuole transport

Gene ID	Gene Name	Average expression	Function
<i>Others (cont'd)</i>			
<i>YOR153W</i>	<i>PDR5</i>	2.83	Drug-efflux pump (ATP-binding cassette superfamily)
<i>YOR185C</i>	<i>GSP2</i>	1.14	GTP-binding protein member of the ras superfamily
<i>YPL059W</i>	<i>GRX5</i>	1.05	Glutaredoxin
<i>YPL087W</i>	<i>YDC1</i>	1.23	Alkaline ceramidase
<i>YPR149W</i>	<i>NCE102</i>	0.94	Involved in secretion of proteins that lack secretory signal
<i>Protein metabolism (13)</i>			
<i>YDR158W</i>	<i>HOM2</i>	0.90	Aspartate-semialdehyde dehydrogenase
<i>YHR038W</i>	<i>RRF1</i>	0.83	Mitochondrial ribosome recycling factor
<i>YHR047C</i>	<i>AAP1</i>	1.54	Alanine/arginine aminopeptidase
<i>YIL095W</i>	<i>PRK1</i>	1.59	Serine/threonine protein kinase
<i>YJL088W</i>	<i>ARG3</i>	1.18	Ornithine carbamyltransferase
<i>YJR148W</i>	<i>BAT2</i>	1.62	Cytosolic branched-chain amino acid transaminase
<i>YKL103C</i>	<i>LAP4</i>	1.15	Aminopeptidase I of the vacuole
<i>YKL142W</i>	<i>MRP8</i>	1.65	Mitochondrial ribosomal protein
<i>YLR120C</i>	<i>YPS1</i>	0.91	Yapsin 1, GPI-anchored protease
<i>YLR303W</i>	<i>MET17</i>	1.46	O-Acetylhomoserine sulfhydrylase
<i>YNL015W</i>	<i>PBI2</i>	1.28	Protease B
<i>YOR303W</i>	<i>CPA1</i>	1.38	Carbamoylphosphate synthetase
<i>YPL154C</i>	<i>PEP4</i>	1.61	Proteinase A
<i>Stress response (9)</i>			
<i>YDR171W</i>	<i>HSP42</i>	1.28	Heat shock protein
<i>YDR258C</i>	<i>HSP78</i>	1.35	Mitochondrial heat shock protein
<i>YFL014W</i>	<i>HSP12</i>	4.17	Heat shock protein
<i>YGL073W</i>	<i>HSF1</i>	3.71	Heat shock transcription factor
<i>YMR173W</i>	<i>DDR48</i>	1.68	Induced by heat shock, DNA damage, or osmotic stress
<i>YMR251W-A</i>	<i>HOR7</i>	1.26	Protein involved in responsiveness to hyperosmolarity
<i>YNL160W</i>	<i>YGP1</i>	3.86	Secreted glycoprotein in response to nutrient limitation
<i>YOL053C-A</i>	<i>DDR2</i>	1.99	DNA damage responsive protein
<i>YOL151W</i>	<i>GRE2</i>	1.88	Alpha-Acetoxy ketone reductase
<i>Transporters (7)</i>			
<i>YAL067C</i>	<i>SEO1</i>	1.19	Member of the allantate permease family
<i>YHL035C</i>	<i>YHL035C</i>	1.45	Member of the ATP-binding cassette (ABC) superfamily
<i>YJR150C</i>	<i>DAN1</i>	2.19	Cell wall mannoprotein
<i>YKR093W</i>	<i>PTR2</i>	1.19	Peptide permease
<i>YNL055C</i>	<i>POR1</i>	1.07	Outer mitochondrial membrane porin
<i>YOR306C</i>	<i>MCH5</i>	0.94	Monocarboxylate permease homologue
<i>YPR156C</i>	<i>TPO3</i>	0.80	Polyamine transport protein
<i>Functionally unknown genes (90)</i>			
<i>YAL061W</i>	<i>YAL061W</i>	3.31	Member of the zinc-containing alcohol dehydrogenase family
<i>YAL068C</i>	<i>YAL068C</i>	1.40	Possibly required for full induction of IME1 during early meiosis
<i>YAR020C</i>	<i>PAU7</i>	1.64	Member of the seripauperin family
<i>YBL049W</i>	<i>MOH1</i>	1.42	Unknown
<i>YBR005W</i>	<i>YBR005W</i>	1.02	Unknown
<i>YBR046C</i>	<i>ZTA1</i>	1.15	Zeta-crystallin homolog
<i>YBR047W</i>	<i>YBR047W</i>	2.12	Unknown
<i>YBR269C</i>	<i>YBR269C</i>	0.99	Unknown
<i>YCL049C</i>	<i>YCL049C</i>	0.97	Unknown
<i>YDL023C</i>	<i>YDL023C</i>	1.37	Unknown
<i>YDL038C</i>	<i>YDL038C</i>	1.35	Unknown

Gene ID	Gene Name	Average expression	Function
<i>Functionally unknown genes (cont'd)</i>			
YDL048C	STP4	1.59	Similarity to Stp1p
YDL110C	YDL110C	0.81	Unknown
YDL169C	UGX2	1.73	Unknown
YDR032C	PST2	1.09	Similarity to Ycp4p
YDR055W	PST1	1.25	Member of the Sps2p-Ecm33p-Ycl048p family
YDR264C	AKR1	1.09	Protein with palmitoyl transferase activity
YDR271C	YDR271C	1.63	Unknown
YDR516C	EMI2	0.95	Required for full induction of IME1 during early meiosis
YEL049W	PAU2	1.28	Similarity to <i>S. cerevisiae</i> Yal068p
YEL067C	YEL067C	1.09	Unknown
YER038C	KRE29	1.69	Unknown
YER053C	YER053C	2.47	Member of the mitochondrial carrier family of membrane transporters
YER079W	YER079W	1.70	Unknown
YFL020C	PAU5	1.40	Member of the seripauperin (PAU) family
YFL067W	YFL067W	1.10	Unknown
YFR017C	YFR017C	1.73	Unknown
YGL157W	YGL157W	1.69	Unknown
YGL260W	YGL260W	0.97	Unknown
YGR017W	YGR017W	0.97	Unknown
YGR131W	YGR131W	1.19	Unknown
YGR146C	YGR146C	1.01	Unknown
YGR161C	RTS3	1.94	Unknown
YGR213C	RTA1	1.38	Involved in 7-amincholesterol resistance
YHR016C	YSC84	0.97	Protein involved in cortical actin patch polarization with Lsb5p
YHR070W	TRM5	1.29	Unknown
YHR113W	YHR113W	1.62	Unknown
YHR138C	YHR138C	1.21	Unknown
YHR140W	YHR140W	0.92	Unknown
YIL015C-A	YIL014C-A	1.03	Unknown
YJL066C	MPM1	0.96	Unknown
YJL067W	YJL067W	0.98	Unknown
YJL079C	PRY1	1.38	Protein with similarity to plant pathogenesis-related proteins
YJL116C	NCA3	1.58	Protein involved in regulation of synthesis of the Fo-F1 ATP synthase
YJL161W	YJL161W	1.43	Unknown
YKL071W	YKL071W	1.10	Unknown
YKL151C	YKL151C	1.51	Unknown
YKR076W	ECM4	1.39	Unknown
YLL019C	KNS1	1.26	Serine/threonine protein kinase
YLL025W	YLL025W	1.38	Unknown
YLL056C	YLL056C	2.01	Unknown
YLR037C	DAN2	1.66	Member of the seripauperin (PAU) family
YLR089C	YLR089C	0.96	Putative mitochondrial alanine aminotransferase
YLR099C	ICT1	1.39	Required for normal sensitivity to copper
YLR152C	YLR152C	1.16	Unknown
YLR194C	YLR194C	1.46	GPI-anchored protein
YLR270W	DCS1	1.31	Trehalase-associated protein
YLR297W	YLR297W	1.43	Unknown

Gene ID	Gene Name	Average log ₂ expression	Function
<i>Functionally unknown genes (cont'd)</i>			
<i>YLR327C</i>	<i>YLR327C</i>	3.10	Protein with high similarity to <i>S. cerevisiae</i> Stf2p
<i>YLR345W</i>	<i>YLR345W</i>	1.02	Similarity to fructose-2,6-bisphosphatases
<i>YLR346C</i>	<i>YLR346C</i>	3.34	Unknown
<i>YML047C</i>	<i>PRM6</i>	0.96	Pheromone-Regulated Membrane protein
<i>YMR041C</i>	<i>YMR041C</i>	0.85	Protein containing an aldo-keto reductase family domain
<i>YMR095C</i>	<i>SNO1</i>	4.50	Putative pyridoxine biosynthetic enzyme
<i>YMR096W</i>	<i>SNZ1</i>	3.20	Putative pyridoxine biosynthetic enzyme
<i>YMR102C</i>	<i>YMR102C</i>	2.63	Unknown
<i>YMR134W</i>	<i>YMR134W</i>	0.87	Unknown
<i>YMR173W-A</i>	<i>YMR173W-A</i>	1.74	Unknown
<i>YMR195W</i>	<i>ICY1</i>	1.58	Unknown
<i>YMR244C-A</i>	<i>YMR244C-A</i>	1.38	Unknown
<i>YMR245W</i>	<i>YMR245W</i>	1.04	Unknown
<i>YMR291W</i>	<i>YMR291W</i>	1.15	Serine/threonine protein kinase of unknown function
<i>YMR316C-A</i>	<i>YMR316C-A</i>	1.40	Unknown
<i>YNL040W</i>	<i>YNL040W</i>	0.92	Unknown
<i>YNL200C</i>	<i>YNL200C</i>	1.28	Unknown
<i>YNL208W</i>	<i>YNL208W</i>	1.22	Unknown
<i>YNL234W</i>	<i>YNL234W</i>	1.02	Hemoprotein with similarity to mammalian globins
<i>YOL150C</i>	<i>YOL150C</i>	1.78	Unknown
<i>YOL161C</i>	<i>YOL161C</i>	1.22	Member of the seripauperin (PAU) family
<i>YOR135C</i>	<i>YOR135C</i>	3.01	Required for full induction of IME1 during early meiosis
<i>YOR137C</i>	<i>SIA1</i>	0.95	Suppressor of eIF5A
<i>YOR173W</i>	<i>DCS2</i>	1.31	Protein with high similarity to <i>S. cerevisiae</i> Dcs1p
<i>YOR289W</i>	<i>YOR289W</i>	2.31	Unknown
<i>YOR338W</i>	<i>YOR338W</i>	3.73	Possibly required for full induction of IME1 during early meiosis
<i>YOR394W</i>	<i>YOR394W</i>	1.81	Similarity to <i>S. cerevisiae</i> Yir041p
<i>YPL159C</i>	<i>YPL159C</i>	0.93	Unknown
<i>YPL250C</i>	<i>ICY2</i>	1.64	Unknown
<i>YPL272C</i>	<i>YPL272C</i>	2.32	Unknown
<i>YPL282C</i>	<i>YPL282C</i>	1.40	Similarity to <i>S. cerevisiae</i> Yir041p
<i>YPR002W</i>	<i>PDH1</i>	2.30	Involved in propionate utilization

DOWN-REGULATED GENES

Gene ID	Gene Name	Average expression	Function
<i>Nucleotide metabolism (9)</i>			
YBR021W	FUR4	-0.98	Uracil permease
YDR216W	ADR1	-0.89	Zinc-finger transcription factor
YDR399W	HPT1	-1.05	Hypoxanthine-guanine phosphoribosyl transferase
YER060W-A	FCY22	-1.35	Purine/cytosine permease
YGL241W	KAP114	-3.09	Protein of the karyopherin-beta family
YGR109C	CLB6	-1.18	B-type cyclin appearing late in G1
YLR359W	ADE13	-1.04	Adenylosuccinate lyase
YLR449W	FPR4	-0.88	Nucleolar peptidylprolyl cis-trans isomerase
YPR065W	ROX1	-1.56	Heme-dependent transcriptional repressor
<i>Others (8)</i>			
YBR092C	PHO3	-1.28	Acid phosphatase
YBR093C	PHO5	-1.43	Acid phosphatase
YBR244W	GPX2	-1.17	Glutathione peroxidase
YER174C	GRX4	-0.93	Glutaredoxin
YHR051W	COX6	-0.86	Cytochrome c oxidase subunit VI
YHR096C	HXT5	-3.21	Glucose transporter
YKL096W	CWPI	-0.97	Mannoprotein of the cell wall
YPL274W	SAM3	-1.48	High affinity S-adenosylmethionine permease
<i>Protein metabolism (22)</i>			
YDL184C	RPL41A	-1.35	Ribosomal protein L41A
YDR382W	RPP2B	-0.86	Acidic ribosomal protein P2B
YGL009C	LEU1	-1.04	3-Isopropylmalate dehydratase
YGR034W	RPL26B	-1.32	Ribosomal protein L26
YHL001W	RPL14B	-0.91	Ribosomal protein L14
YHR010W	RPL27A	-0.94	Ribosomal protein L27
YHR021C	RPS27B	-1.06	Ribosomal protein S27
YJL136C	RPS21B	-1.02	Ribosomal protein S21
YJL189W	RPL39	-1.02	Ribosomal protein L39
YJR094W-A	RPL43B	-1.04	Ribosomal protein L43B
YKR057W	RPS21A	-1.12	Ribosomal protein S21
YLR167W	RPS31	-1.10	Ribosomal protein S31
YLR264W	RPS28B	-1.07	Ribosomal protein S28
YLR325C	RPL38	-1.31	Ribosomal protein L38
YLR344W	RPL26A	-1.23	Ribosomal protein L26
YML024W	RPS17A	-0.90	Ribosomal protein S17
YML026C	RPS18B	-1.05	Ribosomal protein S18
YMR230W	RPS10B	-1.27	Ribosomal protein S10
YOR096W	RPS7A	-1.29	Ribosomal protein S7
YOR167C	RPS28A	-1.40	Ribosomal protein S28
YPL143W	RPL33A	-1.07	Ribosomal protein L33
YPR167C	MET16	-2.32	3'-Phosphoadenylylsulfate reductase
<i>Functionally unknown genes (27)</i>			
YAR070C	YAR070C	-1.34	Unknown
YBR108W	YBR108W	-1.40	Unknown
YCR102C	YCR102C	-1.22	Similarity to Bacillus subtilis sorbitol dehydrogenase
YDL241W	YDL241W	-1.18	Unknown
YDR111C	YDR111C	-0.93	Similarity to S. cerevisiae Ylr089p

Gene ID	Gene Name	Average expression	Function
<i>Functionally unknown genes (cont'd)</i>			
<i>YEL033W</i>	<i>YEL033W</i>	-1.10	Required for invasive growth and pseudohyphal development
<i>YGL010W</i>	<i>YGL010W</i>	-0.80	Unknown
<i>YGR043C</i>	<i>YGR043C</i>	-2.93	Involved in signal transduction
<i>YGR164W</i>	<i>YGR164W</i>	-1.56	Unknown
<i>YGR270W</i>	<i>YTA7</i>	-1.58	Member of the AAA ATPase protein family
<i>YHL037C</i>	<i>YHL037C</i>	-1.57	Unknown
<i>YIL025C</i>	<i>YIL025C</i>	-2.51	Unknown
<i>YIL146C</i>	<i>ECM37</i>	-1.53	Possibly involved in cell wall structure
<i>YIR014W</i>	<i>YIR014W</i>	-1.15	Unknown
<i>YJL188C</i>	<i>BUD19</i>	-0.94	Involved in bud site selection
<i>YJL200C</i>	<i>YJL200C</i>	-0.96	Protein with similarity to aconitase
<i>YLL014W</i>	<i>YLL014W</i>	-0.83	Unknown
<i>YMR321C</i>	<i>YMR321C</i>	-0.99	Unknown
<i>YNL109W</i>	<i>YNL109W</i>	-1.19	Unknown
<i>YNL303W</i>	<i>YNL303W</i>	-1.39	Unknown
<i>YOL109W</i>	<i>YOL109W</i>	-0.86	Unknown
<i>YOL155C</i>	<i>YOL155C</i>	-1.06	Similarity to <i>S. cerevisiae</i> glucan 1,4-alpha-glucosidase
<i>YOR271C</i>	<i>YOR271C</i>	-0.87	Member of the mitochondrial tricarboxylate carrier family
<i>YOR366W</i>	<i>YOR366W</i>	-1.92	Unknown
<i>YPL263C</i>	<i>KEL3</i>	-0.81	Protein containing three Kelch motifs
<i>YPR044C</i>	<i>YPR044C</i>	-0.94	Unknown
<i>YPR077C</i>	<i>YPR077C</i>	-1.90	Unknown