

Additional File 13: List of differentially-expressed genes in the *mrs4Δ* mutant. Genes that were up- or down-regulated in at least two out of three 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 / Activity
<i>Carbohydrate and energy metabolism (25)</i>			
YBR126C	TPS1	2.20	Trehalose-6-phosphate synthase
YCL040W	GLK1	3.52	Glucokinase
YCR005C	CIT2	1.66	Citrate synthase
YDL021W	GPM2	3.15	Phosphoglycerate mutase
YDL022W	GPD1	1.59	Glycerol-3-phosphate dehydrogenase
YDL124W	YDL124W	2.49	NAD(P)H-dependent reductase
YDR074W	TPS2	1.50	Trehalose-6-phosphate phosphatase
YDR342C	HXT7	2.70	High-affinity hexose transporter
YEL011W	GLC3	3.31	Glycogen branching enzyme
YER062C	HOR2	2.51	DL-glycerol phosphate phosphatase
YER175C	TMT1	2.58	Trans-aconitate methyltransferase
YFR015C	GSY1	3.15	Glycogen synthetase isoform 1
YFR053C	HXK1	2.82	Hexokinase I
YHR044C	DOG1	1.66	2-Deoxyglucose-6-phosphate phosphatase
YJL052W	TDH1	1.83	Glyceraldehyde-3-phosphate dehydrogenase 1
YKL150W	MCR1	1.48	NADH-cytochrome b5 reductase
YKR058W	GLG1	2.00	Self-glucosylating initiator of glycogen synthesis
YLR258W	GSY2	2.15	Glycogen synthetase isoform 2
YMR011W	HXT2	1.45	High-affinity hexose transporter
YMR105C	PGM2	3.42	Phosphoglucomutase
YNL037C	IDH1	3.09	Isocitrate dehydrogenase subunit 1
YNR001C	CIT1	2.67	Citrate synthase
YOL059W	GPD2	2.17	Glycerol-3-phosphate dehydrogenase
YOR347C	PYK2	1.50	Pyruvate kinase
YPR160W	GPH1	3.99	Glycogen phosphorylase
<i>Iron metabolism (11)</i>			
YDR270W	CCC2	1.61	Copper-transporting P-type ATPase
YDR534C	FIT1	4.60	Cell wall mannoprotein of iron transport facilitator
YHL040C	ARN1	2.58	Protein involved in iron uptake via a siderophore
YHL047C	ARN2	2.56	Protein involved in iron uptake via a siderophore
YKL220C	FRE2	1.56	Ferric and cupric reductase
YLR136C	TIS11	2.63	Zinc finger containing protein that belongs to iron regulon
YMR058W	FET3	1.73	Cell surface ferroxidase, required for high-affinity ferrous iron uptake

Gene ID	Gene Name	Average expression	Function / Activity
<i>Iron metabolism (cont'd)</i>			
<i>YOL158C</i>	<i>ENB1; ARN4</i>	2.42	Protein involved in iron uptake via a siderophore
<i>YOR381W</i>	<i>FRE3</i>	1.60	Ferric reductase involved in siderophore iron transport
<i>YOR382W</i>	<i>FIT2</i>	4.99	Cell wall mannoprotein of iron transport facilitator
<i>YOR383C</i>	<i>FIT3</i>	5.23	Cell wall mannoprotein of iron transport facilitator
<i>Nucleotide metabolism (6)</i>			
<i>YDL048C</i>	<i>STP4</i>	2.35	Strong similarity to Stp1p
<i>YDR043C</i>	<i>NRG1</i>	1.40	Transcriptional repressor involved in glucose repression
<i>YGL073W</i>	<i>HSF1</i>	3.58	Heat shock transcription factor
<i>YHL027W</i>	<i>RIM101</i>	3.05	Transcription factor for sporulation related genes
<i>YKL062W</i>	<i>MSN4</i>	2.35	Zinc-finger transcriptional activator
<i>YKL109W</i>	<i>HAP4</i>	2.06	Transcription factor with acidic activation domain, component of Hap2p-Hap3p-Hap4p-Hap5p complex involved in activation of CCAAT box-containing genes
<i>Others (15)</i>			
<i>YBL034C</i>	<i>STU1</i>	1.66	Suppressor of beta-tubulin mutation
<i>YBR046C</i>	<i>ZTA1</i>	2.04	Zeta-crystallin homolog
<i>YDL234C</i>	<i>GYP7</i>	1.72	GTPase-activating protein for Ypt7p
<i>YER024W</i>	<i>YAT2</i>	2.10	Protein with carnitine acetyltransferase function
<i>YGR008C</i>	<i>STF2</i>	3.50	ATPase stabilizing factor
<i>YHR053C</i>	<i>CUP1A</i>	3.34	Copper metallothionein
<i>YLR178C</i>	<i>TFS1</i>	2.82	Cell cycle regulator
<i>YLR286C</i>	<i>CTS1</i>	1.64	Endochitinase
<i>YMR008C</i>	<i>PLB1</i>	1.66	Phospholipase B
<i>YNL145W</i>	<i>MFA2</i>	3.36	Mating pheromone a-factor
<i>YOR036W</i>	<i>PEP12</i>	1.43	Syntaxin homolog
<i>YOR360C</i>	<i>PDE2</i>	1.43	3',5'-Cyclic-nucleotide phosphodiesterase
<i>YPL087W</i>	<i>YDC1</i>	1.64	Alkaline ceramidase
<i>YPL154C</i>	<i>PEP4</i>	2.00	Proteinase A
<i>YPL171C</i>	<i>OYE3</i>	1.42	NADPH dehydrogenase isoform 3
<i>Protein metabolism (8)</i>			
<i>YCL064C</i>	<i>CHAI</i>	1.40	L-serine/L-threonine deaminase
<i>YDR059C</i>	<i>UBC5</i>	1.73	Ubiquitin-conjugating enzyme
<i>YDR247W</i>	<i>YDR247W</i>	1.74	Serine/threonine protein kinase
<i>YER098W</i>	<i>UBP9</i>	1.81	Ubiquitin C-terminal hydrolase
<i>YJR148W</i>	<i>BAT2</i>	2.13	Branched-chain amino acid transaminase
<i>YKL103C</i>	<i>LAP4</i>	2.24	Aminopeptidase I
<i>YKL142W</i>	<i>MRP8</i>	2.08	Ribosomal protein of the small subunit
<i>YKR093W</i>	<i>PTR2</i>	1.65	Peptide permease
<i>Stress response (9)</i>			
<i>YBR054W</i>	<i>YRO2</i>	3.35	Protein paralog of Mrh1p
<i>YCR021C</i>	<i>HSP30; YRO1</i>	4.28	Heat shock protein
<i>YDR171W</i>	<i>HSP42</i>	2.47	Heat shock protein
<i>YDR258C</i>	<i>HSP78</i>	1.86	Heat shock protein
<i>YFL014W</i>	<i>HSP12</i>	3.61	Heat shock protein
<i>YGL037C</i>	<i>PNC1</i>	2.14	Pyrazinamidase and nicotinamidase
<i>YIR038C</i>	<i>GTT1</i>	1.72	Glutathione transferase
<i>YKL026C</i>	<i>GPX1</i>	1.60	Glutathione peroxidase
<i>YMR173W</i>	<i>DDR48</i>	2.19	Induced by heat shock, DNA damage, or osmotic stress
<i>Transporters (4)</i>			
<i>YER053C</i>	<i>YER053C</i>	3.82	Member of the mitochondrial carrier family of membrane transporters

Gene ID	Gene Name	Average expression	Function / Activity
<i>Transporters (cont'd)</i>			
<i>YGR138C</i>	<i>TPO2</i>	1.80	Polyamine transport protein
<i>YOR153W</i>	<i>PDR5</i>	2.07	Drug-efflux pump involved in resistance to multiple drugs
<i>YPR036W</i>	<i>VMA13</i>	1.53	Vacuolar H(+)-ATPase
<i>Functionally unknown genes (30)</i>			
<i>YBR047W</i>	<i>YBR047W</i>	2.68	Unknown
<i>YCL042W</i>	<i>YCL042W</i>	2.81	Unknown
<i>YCL049C</i>	<i>YCL049C</i>	1.63	Unknown
<i>YDL023C</i>	<i>YDL023C</i>	2.03	Unknown
<i>YDL169C</i>	<i>UGX2</i>	3.25	Unknown
<i>YDR055W</i>	<i>PST1</i>	2.50	Member of the Sps2p-Ecm33p-Ycl048p family
<i>YDR391C</i>	<i>YDR391C</i>	2.34	Unknown
<i>YER067W</i>	<i>YER067W</i>	4.97	Unknown
<i>YFL020C</i>	<i>PAU5</i>	2.28	Member of the seripauperin (PAU) family
<i>YHR016C</i>	<i>YSC84</i>	2.19	Protein involved in cortical actin patch polarization with Lsb5p
<i>YJL079C</i>	<i>PRY1</i>	2.32	Protein with similarity to plant pathogenesis-related proteins
<i>YKR075C</i>	<i>YKR075C</i>	1.92	Unknown
<i>YLR297W</i>	<i>YLR297W</i>	1.78	Unknown
<i>YLR327C</i>	<i>YLR327C</i>	4.70	Protein with high similarity to <i>S. cerevisiae</i> Stf2p
<i>YLR346C</i>	<i>YLR346C</i>	2.72	Unknown
<i>YMR020W</i>	<i>FMS1</i>	1.39	Protein involved in the biosynthesis of pantothenic acid
<i>YMR173W-A</i>	<i>YMR173W-A</i>	2.09	Unknown
<i>YMR181C</i>	<i>YMR181C</i>	2.31	Unknown
<i>YMR251W-A</i>	<i>HOR7</i>	2.23	Protein involved in responsiveness to hyperosmolarity
<i>YMR315W</i>	<i>YMR315W</i>	1.48	Unknown
<i>YNL160W</i>	<i>YGP1</i>	5.44	Secreted glycoprotein produced in response to nutrient limitation
<i>YNL200C</i>	<i>YNL200C</i>	2.34	Unknown
<i>YNL208W</i>	<i>YNL208W</i>	1.92	Unknown
<i>YOL163W</i>	<i>YOL163W</i>	1.87	Unknown
<i>YOR135C</i>	<i>YOR135C</i>	2.30	Unknown
<i>YOR285W</i>	<i>YOR285W</i>	1.62	Unknown
<i>YOR289W</i>	<i>YOR289W</i>	2.74	Unknown
<i>YOR338W</i>	<i>YOR338W</i>	3.42	Unknown
<i>YPL004C</i>	<i>YPL004C</i>	1.83	Protein with weak similarity to tropomyosin
<i>YPL250C</i>	<i>YPL250C</i>	2.21	Unknown

DOWN-REGULATED GENES

Gene ID	Gene Name	Average expression	Function / Activity
<i>Nucleotide metabolism (3)</i>			
<i>YGR109C</i>	<i>CLB6</i>	-1.89	Involved in initiation of DNA synthesis
<i>YJL033W</i>	<i>HCA4</i>	-1.42	Involved in ribosomal RNA processing
<i>YMR260C</i>	<i>TIF11</i>	-1.64	Translation initiation factor eIF1A
<i>Others (7)</i>			
<i>YAR071W</i>	<i>PHO11</i>	-1.68	Acid phosphatase
<i>YBR093C</i>	<i>PHO5</i>	-2.00	Acid phosphatase
<i>YHR215W</i>	<i>PHO12</i>	-1.81	Acid phosphatase
<i>YIL011W</i>	<i>TIR3</i>	-0.16	Member of the seripauperin family
<i>YKR052C</i>	<i>MRS4</i>	-2.62	Mitochondrial iron transporter
<i>YNL111C</i>	<i>CYB5</i>	-1.62	Cytochrome b5
<i>YPL060W</i>	<i>LPE10;</i> <i>(MRS7)</i>	-0.67	Involved in mitochondrial magnesium homeostasis
<i>Protein metabolism (4)</i>			
<i>YDR234W</i>	<i>LYS4</i>	-1.62	Homoaconitate hydratase
<i>YGL009C</i>	<i>LEU1</i>	-2.78	3-Isopropylmalate dehydratase
<i>YHR208W</i>	<i>BAT1</i>	-1.95	Mitochondrial branched-chain amino acid transaminase
<i>YMR230W</i>	<i>RPS10B</i>	-1.27	Ribosomal protein S10
<i>Functionally unknown genes (6)</i>			
<i>YDR281C</i>	<i>PHM6</i>	-1.44	Predicted to have a role in phosphate metabolism
<i>YEL033W</i>	<i>YEL033W</i>	-1.99	Required for invasive growth and pseudohyphal development
<i>YER156C</i>	<i>YER156C</i>	-1.54	Unknown
<i>YGR164W</i>	<i>YGR164W</i>	-1.55	Unknown
<i>YLR205C</i>	<i>HMX1</i>	-0.02	Unknown
<i>YOR237W</i>	<i>HES1</i>	-0.66	Protein implicated in ergosterol biosynthesis