

Additional File 7: Differentially-expressed genes in nutritional iron-deficient yeast model. Yeast wild type was treated with 100 μ M BPS for 1 hour. Genes that were up or down-regulated in at least two out of three independent experiments are listed. The average expression level is shown in logarithmic scale with base of two. Genes were categorized according to their cellular functions using the GO biological process from Funspec (<http://funspec.med.utoronto.ca/>).

Up regulated genes (n = 100)

Gene ID	Gene Name	Average expression level	Localization	Function/ Activity
Carbohydrate metabolism (4)				
<i>YAL038W</i>	<i>CDC19</i>	0.83	Cytoplasm; Nucleus	Pyruvate kinase, catalyzes final step in glycolysis
<i>YBR110W</i>	<i>ALG1</i>	0.33	ER	Beta-mannosyltransferase involved in protein N-glycosylation
<i>YCL040W</i>	<i>GLK1</i>	0.49	Cytoplasm	Glucokinase
<i>YGR254W</i>	<i>ENO1</i>	0.8	Cytoplasm	Enolase in glycolysis
Iron metabolism (17)				
<i>YDR270W</i>	<i>CCC2</i>	0.63	Golgi	Copper-transporting P-type ATPase
<i>YDR534C</i>	<i>FIT1</i>	1.46	Cell wall	Cell wall mannoprotein of iron transport facilitator
<i>YEL065W</i>	<i>SIT1</i>	1.34	Endosome	Siderophore iron (Ferrioxamine B) permease
<i>YFL041W</i>	<i>FET5</i>	0.57	Vacuole	Multicopper oxidase involved in ferrous iron transport
<i>YGL071W</i>	<i>AFT1</i>	0.52	Nucleus; Cytoplasm	Iron responsive transcription activator that regulates genes involved in iron homeostasis
<i>YKL220C</i>	<i>FRE2</i>	0.85	Plasma membrane	Ferric and cupric reductase
<i>YKR052C</i>	<i>MRS4</i>	0.5	Mitochondria	Member of the mitochondrial carrier family of membrane transporters involved in iron transport
<i>YLR136C</i>	<i>TIS11</i>	1.38	ER	Zinc finger containing protein that belongs to iron regulon
<i>YLR205C</i>	<i>HMX1</i>	0.89	Unknown	Homology to heme oxygenases
<i>YLR214W</i>	<i>FRE1</i>	0.93	Plasma membrane	Ferric and cupric reductase

Gene ID	Gene Name	Average expression level	Localization	Function/ Activity
Iron metabolism (cont'd)				
<i>YMR058W</i>	<i>FET3</i>	0.76	Plasma membrane	Cell surface ferroxidase, required for high-affinity ferrous iron uptake
<i>YMR319C</i>	<i>FET4</i>	0.5	Plasma membrane	Low-affinity iron (copper and zinc) transport protein
<i>YOL158C</i>	<i>ARN4</i>	1.23	Endosome	Protein involved in iron uptake via a siderophore enterobactin
<i>YOR381W</i>	<i>FRE3</i>	1.18	Plasma membrane	Ferric reductase involved in siderophore iron transport
<i>YOR382W</i>	<i>FIT2</i>	2.13	Cell wall	Cell wall mannoprotein of iron transport facilitator
<i>YOR383C</i>	<i>FIT3</i>	2.02	Cell wall	Cell wall mannoprotein of iron transport facilitator
<i>YOR384W</i>	<i>FRE5</i>	1.27	Unknown	Protein with similarity to Fre2p
Lipid metabolism (2)				
<i>YGL055W</i>	<i>OLE1</i>	0.54	ER	Delta-9-fatty acid desaturase for synthesis of unsaturated fatty acids
<i>YJR073C</i>	<i>OPI3</i>	0.47	ER	Phospholipid-N-methyltransferase in the phosphatidylcholine biosynthesis pathway
Metal homeostasis (4)				
<i>YGL255W</i>	<i>ZRT1</i>	1.13	Plasma membrane	High-affinity zinc transport protein
<i>YHR175W</i>	<i>CTR2</i>	0.49	Vacuole	Low-affinity copper transport protein
<i>YKL175W</i>	<i>ZRT3</i>	0.52	Vacuole	Vacuolar membrane protein involved in zinc transport and the regulation of zinc storage
<i>YLR034C</i>	<i>SMF3</i>	0.46	Vacuole	Metal transporter
Nucleotide metabolism (15)				
<i>YBL002W</i>	<i>HTB2</i>	0.69	Nucleus	Histone H2B
<i>YBL005W-A</i>	<i>YBL005W-A</i>	0.91	Nucleus	TyA Gag protein
<i>YBL034C</i>	<i>STU1</i>	0.85	Nucleus	Suppressor of beta-tubulin mutation that is required for assembly of the mitotic spindle
<i>YBL101W-A</i>	<i>YBL101W-A</i>	0.50	Nucleus	TyA Gag protein
<i>YBR012W-A</i>	<i>YBR012W-A</i>	1.08	Nucleus	TyA Gag protein
<i>YDR118W</i>	<i>APC4</i>	0.39	Nucleus	Component of the anaphase-promoting complex
<i>YDR263C</i>	<i>DIN7</i>	0.38	Mitochondria	Nuclease with a role in stabilizing the mitochondrial genome, expression is induced by DNA damage

Gene ID	Gene Name	Average expression level	Localization	Function/ Activity
Nucleotide metabolism (cont'd)				
YDR423C	CAD1	0.4	Cytoplasm; Nucleus	Transcriptional activator of the basic leucine zipper (bZIP) family, involved in regulation of multidrug resistance
YEL042W	GDA1	0.52	Golgi	Guanosine diphosphatase
YHL027W	RIM101	0.76	Cytoplasm; Nucleus	Transcription factor involved in induction of IME1, IME2, DIT1, and DIT2 transcription, has three C2H2-type zinc fingers
YIL126W	STH1	0.34	Nucleus	Component of abundant chromatin remodeling complex
YJR105W	ADO1	0.53	Cytoplasm	Adenosine kinase
YKL043W	PHD1	0.45	Cytoplasm; Nucleus	Transcription factor involved in regulation of filamentous growth
YMR287C	MSU1	0.36	Mitochondria	Component of a mitochondrial 3'-5' exonuclease complex
YML039W	YML039W	0.31	nucleus	TyB Gag-Pol protein
Others (9)				
YAL012W	CYS3	0.42	Cytoplasm	Cystathionine gamma-lyase in sulfur assimilation pathway
YDL234C	GYP7	0.45	Unknown	GTPase-activating protein for Ypt7p
YDR264C	AKR1	0.73	Plasma membrane; Cytoplasm	Protein with palmitoyl transferase activity and ankyrin repeats
YER024W	YAT2	1.17	Cytosol; Mitochondrion	Protein with carnitine acetyltransferase function
YLR109W	AHP1	0.72	Cytosol; Mitochondrion; Peroxisome	Alkyl hydroperoxide reductase
YML121W	GTR1	0.99	Cytoplasm	GTP-binding protein involved in the function of the Pho84p phosphate transporter
YNL192W	CHS1	0.46	Membrane	Chitin synthase I
YOL016C	CMK2	0.59	Cytoplasm	Calcium/calmodulin-dependent serine/threonine protein kinase type II
YPL171C	OYE3	0.44	Cytoplasm	NADPH dehydrogenase, isoform 3
Protein metabolism (5)				
YBR118W	TEF2	0.76	Ribosome	Translation elongation factor
YGL123W	RPS2	0.66	Cytoplasm	Ribosomal protein S2

Gene ID	Gene Name	Average expression level	Localization	Function/ Activity
Protein metabolism (cont'd)				
<i>YJL138C</i>	<i>TIF2</i>	0.69	Cytoplasm; Ribosome	Translation initiation factor 4A
<i>YLR121C</i>	<i>YPS3</i>	0.31	Plasma membrane; Cell wall	GPI-anchored aspartic protease
<i>YPL154C</i>	<i>PEP4</i>	0.44	Vacuole	Proteinase A, aspartyl protease required for activation of various degradative enzymes
Stress (2)				
<i>YDR171W</i>	<i>HSP42</i>	0.53	Cytoplasm	Heat shock protein
<i>YGL073W</i>	<i>HSF1</i>	2.18	Nucleus	Heat shock transcription factor
Transporters (6)				
<i>YEL063C</i>	<i>CAN1</i>	0.79	Plasma membrane	Permease for basic amino acids
<i>YGL006W</i>	<i>PMC1</i>	0.33	Vacuole	Ca ²⁺ -transporting P-type ATPase
<i>YGR138C</i>	<i>TPO2</i>	0.43	Vacuole; Plasma membrane	Polyamine transporter
<i>YHL035C</i>	<i>YHL035C</i>	0.83	Membrane	Member of the ATP-binding cassette (ABC) superfamily
<i>YJL094C</i>	<i>KHA1</i>	0.4	Plasma membrane	Putative H ⁺ /K ⁺ antiporter
<i>YNL003C</i>	<i>PET8</i>	0.33	Mitochondria	Protein of the mitochondrial carrier (MCF) family of membrane transporters, has similarity to Mrs4p and Mrs3p
Functionally unknown genes (36)				
<i>YAL061W</i>	<i>YAL061W</i>	0.38	Unknown	Unknown
<i>YAL065C</i>	<i>YAL065C</i>	0.31	Unknown	Unknown
<i>YAR068W</i>	<i>YAR068W</i>	0.41	Unknown	Unknown
<i>YBL111C</i>	<i>YBL111C</i>	0.39	Unknown	Unknown
<i>YBR005W</i>	<i>YBR005W</i>	0.38	Unknown	Unknown
<i>YBR047W</i>	<i>YBR047W</i>	0.56	Unknown	Unknown
<i>YCR007C</i>	<i>YCR007C</i>	0.47	Unknown	Unknown
<i>YDL048C</i>	<i>STP4</i>	0.34	Chromatin	Protein with strong similarity to Stp1p, which is involved in tRNA splicing and branched-chain amino acid uptake
<i>YDL124W</i>	<i>YDL124W</i>	0.56	Unknown	Unknown

Gene ID	Gene Name	Average expression level	Localization	Function/ Activity
Functionally unknown genes (cont'd)				
<i>YDR033W</i>	<i>MRH1</i>	0.73	Plasma membrane; Nucleus	Protein with similarity to Yro2p
<i>YDR271C</i>	<i>YDR271C</i>	0.82	Unknown	Unknown
<i>YEL076C-A</i>	<i>YEL076C-A</i>	0.34	Unknown	Unknown
<i>YEL076W-C</i>	<i>YEL076W-C</i>	0.34	Unknown	Unknown
<i>YER053C</i>	<i>YER053C</i>	0.32	Vacuole	Protein with homology to mitochondrial phosphate transporter, but not itself
<i>YFL010C</i>	<i>WWM1</i>	0.43	Cytoplasm; Nucleus	Protein that may be involved in regulation of metacaspase (Mca1p) function in control of cell proliferation
<i>YFR024C</i>	<i>YFR024C</i>	0.48	Unknown	Unknown
<i>YFR024C-A</i>	<i>LSB3</i>	0.42	Unknown	Protein with high similarity to <i>S. cerevisiae</i> Ysc84p
<i>YGR053C</i>	<i>YGR053C</i>	0.43	Unknown	Unknown
<i>YHR214W-A</i>	<i>YHR214W-A</i>	0.47	Unknown	Unknown
<i>YIL028W</i>	<i>YIL028W</i>	0.48	Unknown	Unknown
<i>YIL146C</i>	<i>ECM37</i>	0.52	Unknown	Protein possibly involved in cell wall structure or biosynthesis
<i>YJL078C</i>	<i>PRY3</i>	0.35	Cell wall; Cytoplasm	Protein with similarity to plant pathogenesis-related proteins
<i>YKL153W</i>	<i>YKL153W</i>	0.62	Unknown	Unknown
<i>YLR126C</i>	<i>YLR126C</i>	0.54	Unknown	Unknown
<i>YLR194C</i>	<i>YLR194C</i>	0.59	Unknown	Unknown
<i>YLR280C</i>	<i>YLR280C</i>	0.46	Unknown	Unknown
<i>YLR297W</i>	<i>YLR297W</i>	0.35	Unknown	Unknown
<i>YLR327C</i>	<i>YLR327C</i>	0.41	Unknown	Unknown
<i>YLR443W</i>	<i>ECM7</i>	0.78	Unknown	Protein possibly involved in cell wall structure or biosynthesis
<i>YMR084W</i>	<i>YMR084W</i>	0.72	Unknown	Unknown
<i>YMR251W</i>	<i>YMR251W</i>	1.4	Unknown	Unknown
<i>YNL143C</i>	<i>YNL143C</i>	0.54	Unknown	Unknown
<i>YOL098C</i>	<i>YOL098C</i>	0.7	Unknown	Unknown
<i>YOR247W</i>	<i>SRL1</i>	0.55	Cell wall	Protein with similarity to Svs1p
<i>YOR291W</i>	<i>YOR291W</i>	0.68	Membrane	Unknown
<i>YPR157W</i>	<i>YPR157W</i>	0.43	Unknown	Unknown

Down-regulated genes (n = 42)

Gene ID	Gene Name	Average expression level	Localization	Function/ Activity
Energy metabolism (5)				
<i>YDR178W</i>	<i>SDH4</i>	-0.42	Mitochondria	Succinate dehydrogenase membrane anchor subunit
<i>YGR174C</i>	<i>CBP4</i>	-0.49	Mitochondria	Ubiquinol-cytochrome c reductase assembly factor
<i>YKL087C</i>	<i>CYT2</i>	-0.32	Mitochondria	Cytochrome c1 heme lyase
<i>YLR304C</i>	<i>ACO1</i>	-0.82	Mitochondria	Aconitase
<i>YPR191W</i>	<i>QCR2</i>	-0.58	Mitochondria	Ubiquinol cytochrome-c reductase core protein 2
Nucleotide metabolism (5)				
<i>YGR092W</i>	<i>DBF2</i>	-0.49	Spindle pole body; Nucleus; Bud neck	Serine/threonine protein kinase related to Dbf20p, required for events in anaphase/telophase
<i>YKL109W</i>	<i>HAP4</i>	-0.45	Nucleus	Transcription factor with acidic activation domain, component of Hap2p-Hap3p-Hap4p-Hap5p complex involved in activation of CCAAT box-containing genes
<i>YLR398C</i>	<i>SKI2</i>	-0.56	Cytoplasm; Nucleolus	Helicase (probable)
<i>YML061C</i>	<i>PIF1</i>	-0.47	Nucleus; Mitochondria	Single-stranded DNA-dependent ATPase and 5'-3' DNA helicase required for maintenance and repair of mitochondrial DNA, also functions in nucleus to regulate telomere length
<i>YPL001W</i>	<i>HAT1</i>	-0.49	Cytoplasm; Nucleus	Histone acetyltransferase
Others (7)				
<i>YBR093C</i>	<i>PHO5</i>	-0.38	Cell wall; Periplasmic space	Acid phosphatase in phosphate metabolism
<i>YGL032C</i>	<i>AGA2</i>	-0.48	Shmoo tip; ER; Bud tip; Cell wall	α -agglutinin adhesion subunit involved in cellular fusion
<i>YHR096C</i>	<i>HXT5</i>	-0.42	Plasma membrane	Hexose transporter
<i>YLL009C</i>	<i>COX17</i>	-0.72	Mitochondrion; Cytoplasm	Protein involved in delivery of copper ions to mitochondrial cytochrome oxidase

Gene ID	Gene Name	Average expression level	Localization	Function/ Activity
Others (cont'd)				
<i>YMR015C</i>	<i>ERG5</i>	-0.36	Cytoplasm; Microsome; Nucleus	Cytochrome P450-involved in C-22 denaturation of the ergosterol side-chain
<i>YNL111C</i>	<i>CYB5</i>	-0.34	ER	Cytochrome b5 in sterol metabolism
<i>YPL170W</i>	<i>DAP1</i>	-0.32	Membrane	Protein involved in ergosterol biosynthesis, response to UV, mitochondrial genome maintenance, and telomere maintenance, member of the membrane-associated progesterone receptor family
Protein metabolism (5)				
<i>YDL184C</i>	<i>RPL41A</i>	-0.5	Cytosol	Ribosomal protein L41A
<i>YGL009C</i>	<i>LEU1</i>	-1.19	Cytosol	3-Isopropylmalate dehydratase in leucine biosynthesis
<i>YGR084C</i>	<i>MRP13</i>	-0.89	Mitochondria	Mitochondrial ribosomal protein
<i>YIL018W</i>	<i>RPL2B</i>	-0.63	Cytosol	Ribosomal protein L2B
<i>YLR325C</i>	<i>RPL38</i>	-0.52	Cytosol	Ribosomal protein L38
Stress (2)				
<i>YER174C</i>	<i>GRX4</i>	-0.64	Unknown	Glutaredoxin
<i>YKR066C</i>	<i>CCP1</i>	-0.93	Mitochondria	Cytochrome c peroxidase
Functionally unknown genes (18)				
<i>YBL044W</i>	<i>YBL044W</i>	-0.53	Unknown	Unknown
<i>YDL162C</i>	<i>YDL162C</i>	-0.9	Unknown	Unknown
<i>YDR154C</i>	<i>YDR154C</i>	-0.46	Unknown	Unknown
<i>YDR494W</i>	<i>RSM28</i>	-0.31	Unknown	Unknown
<i>YER156C</i>	<i>YER156C</i>	-0.42	Unknown	Unknown
<i>YFL012W</i>	<i>YFL012W</i>	-0.76	Unknown	Unknown
<i>YGR226C</i>	<i>YGR226C</i>	-0.67	Unknown	Unknown
<i>YGR270W</i>	<i>YTA7</i>	-1.54	Unknown	ATPase activity
<i>YJL200C</i>	<i>YJL200C</i>	-0.38	Unknown	Protein with homology to aconitase
<i>YKL208W</i>	<i>CBT1</i>	-0.53	Unknown	Unknown
<i>YNL109W</i>	<i>YNL109W</i>	-0.67	Unknown	Unknown
<i>YNL120C</i>	<i>YNL120C</i>	-0.49	Unknown	Unknown
<i>YNL122C</i>	<i>YNL122C</i>	-0.46	Unknown	Unknown
<i>YNL303W</i>	<i>YNL303W</i>	-0.45	Unknown	Unknown
<i>YNR025C</i>	<i>YNR025C</i>	-0.33	Unknown	Unknown
<i>YOL109W</i>	<i>YOL109W</i>	-0.5	Unknown	Unknown
<i>YOR338W</i>	<i>YOR338W</i>	-0.31	Unknown	Unknown
<i>YPL182C</i>	<i>YPL182C</i>	-0.29	Unknown	Unknown