

Table 1. Genes that are expressed differentially (≥ 2.0 -fold) upon surplus iron for 1 h^a.

Genes expression induced by more than 2-fold upon surplus iron for 1 h (9 ORFs)				
Gene	ORF	Induction fold	GO term^b	Gene description
<i>CUP1-1</i>	YHR053C	5.83	GO:0046872	Copper ion binding (response to copper ion)
<i>CUP1-2</i>	YHR056C	5.83	GO:0008270	Copper ion binding (response to copper ion)
<i>PDR12</i>	YPL058C	4.90	GO:0016887	Xenobiotic-transporting ATPase (response to copper ion)
<i>HSP12</i>	YFL014W	4.61	GO:0008289	Protects membranes from desiccation (response to stress)
<i>CRS5</i>	YOR031W	2.48	GO:0005507	Copper ion binding (response to metal ion)
<i>RGS2</i>	YOR107W	2.41	GO:0005096	GTPase activator activity (G-protein signaling)
<i>MTH1</i>	YDR277C	2.27	GO:0003674	Negative regulator of glucose-sensing signal transduction
<i>CHA1</i>	YCL064C	2.13	GO:0003941	Catabolic L-serine (L-threonine) deaminase
-	YKR075C	2.23	-	Molecular function unknown, expression regulated by glucose
<i>MSN4^c</i>	YKL062W	1.50	GO:0003700	Transcriptional activator (activated in stress conditions)
Genes expression repressed by more than 2-fold upon surplus iron for 1 h (39 ORFs)				
Gene	ORF	Repression fold	GO term^b	Gene description
Iron homeostasis (17 ORFs)				
<i>ARN1</i>	YHL040C	0.43	GO:0015343	Siderophore-iron transport
<i>ARN2</i>	YHL047C	0.23	GO:0015343	Siderophore-iron transport
<i>CCC2</i>	YDR270W	0.50	GO:0019829	Siderophore-iron transport
<i>ENB1</i>	YOL158C	0.09	GO:0015620	Siderophore transport
<i>FET3</i>	YMR058W	0.06	GO:0004322	High affinity iron ion transport
<i>FET4</i>	YMR319C	0.38	GO:0005381	Low-affinity Fe ²⁺ transporter of the plasma membrane
<i>FIT1</i>	YDR534C	0.12	GO:0003674	Mannoprotein for retention of siderophore-iron in cell wall
<i>FIT2</i>	YOR382W	0.08	GO:0003674	Mannoprotein for retention of siderophore-iron in cell wall
<i>FIT3</i>	YOR383C	0.37	GO:0003674	Mannoprotein for retention of siderophore-iron in cell wall
<i>FRE1</i>	YLR214W	0.04	GO:0000293	Ferric-chelate reductase activity
<i>FRE2</i>	YKL220C	0.14	GO:0000293	Ferric-chelate reductase activity
<i>FRE6</i>	YLL051C	0.47	GO:0000293	Ferric-chelate reductase activity
<i>FRE7</i>	YOL152W	0.08	GO:0000293	Ferric-chelate reductase activity
<i>FTR1</i>	YER145C	0.16	GO:0005381	High affinity iron ion transport
<i>SIT1</i>	YEL065W	0.07	GO:0015344	Siderophore transport
<i>SMF3</i>	YLR034C	0.44	GO:0005381	Divalent metal ion transporter involved in iron homeostasis
<i>TIS11</i>	YLR136C	0.08	GO:0003729	mRNA-binding protein expressed during iron starvation
Others (22 ORFs)				

The genes are up-regulated or down-regulated both in 1h and 4h are in bold font.

^aGenes were grouped into these categories according to the *S. cerevisiae* Genome Database and the Munich Information Center for Protein Sequence (<http://www.mips.biochem.mpg.de/proj/yeast>).

^bThe GO term is assigned based on the molecular function.

^cThe genes that are induced between 1.5-fold and 2.0-fold upon surplus iron.

Table 2. Genes that are expressed differentially (≥ 2.0 -fold) upon surplus iron for 4 h^a.

Genes expression induced by more than 2-fold upon surplus iron for 4 h (140 ORFs)				
Gene	ORF	Induction fold	GO term^b	Gene description
<i>TCA cycle, electron transport, and oxidative phosphorylation (43 ORFs)</i>				
<i>CYT1</i>	YOR065W	28.77	GO:0045153	Cytochrome c1, component of mitochondrial respiratory chain
<i>CYC1</i>	YJR048W	17.20	GO:0009055	Cytochrome c, isoform 1
<i>SDH1</i>	YKL148C	12.47	GO:0008177	Flavoprotein subunit of succinate dehydrogenase
<i>QCR2</i>	YPR191W	6.87	GO:0008177	Subunit 2 of the ubiquinol cytochrome-c reductase complex
<i>QCR7</i>	YDR529C	6.34	GO:0008121	Subunit 7 of the ubiquinol cytochrome-c reductase complex
<i>RIP1</i>	YEL024W	5.96	GO:0008121	Ubiquinol-cytochrome-c reductase
<i>INH1</i>	YDL181W	5.92	GO:0004857	Inhibits ATP hydrolysis by the F ₁ F ₀ ATP synthase
<i>COR1</i>	YBL045C	4.71	GO:0008121	Core subunit of the ubiquinol-cytochrome c reductase complex
<i>BNA4</i>	YBL098W	3.82	GO:0004502	Kynurenine 3-mono oxygenase of the TCA cycle
<i>COX7</i>	YMR256C	3.73	GO:0004129	Subunit VII of cytochrome c oxidase
<i>COX17</i>	YLL009C	3.71	GO:0008379	Copper metallochaperone
<i>SDH4</i>	YDR178W	3.46	GO:0008177	Membrane anchor subunit of succinate dehydrogenase
<i>SDH3</i>	YKL141W	3.39	GO:0008177	Cytochrome b subunit of succinate dehydrogenase
<i>COX12</i>	YLR038C	3.28	GO:0004129	Subunit VIb of cytochrome c oxidase
<i>QCR9</i>	YGR183C	3.26	GO:0008121	Subunit 9 of the ubiquinol cytochrome-c reductase complex
<i>QCR8</i>	YJL166W	3.22	GO:0008121	Subunit 8 of the ubiquinol cytochrome-c reductase complex
<i>PHO3</i>	YBR092C	3.12	GO:0003993	Constitutively expressed acid phosphatase, aerobic respiration
<i>TIM11</i>	YDR322C-A	3.04	GO:0005198	Subunit e of mitochondrial F ₁ F ₀ ATPase
<i>COX5B</i>	YIL111W	3.01	GO:0004129	Subunit Vb of cytochrome c oxidase
<i>COX8</i>	YLR395C	3.00	GO:0004129	Subunit VIII of cytochrome c oxidase
<i>FMP10</i>	YER182W	2.92	GO:0003674	Found in mitochondrial proteome
<i>ATP19</i>	YOL077W-A	2.84	GO:0046933	Subunit k of the mitochondrial F ₁ F ₀ ATP synthase
<i>ATP20</i>	YPR020W	2.80	GO:0005198	Subunit g of the mitochondrial F ₁ F ₀ ATP synthase
<i>UGP1</i>	YKL035W	2.59	GO:0003983	UDP-glucose pyrophosphorylase
<i>MDH1</i>	YKL085W	2.57	GO:0030060	Mitochondrial malate dehydrogenase

<i>COX5A</i>	YNL052W	2.46	GO:0004129	Subunit Va of cytochrome c oxidase
<i>COX15</i>	YER141W	2.41	GO:0016653	An prosthetic group for cytochrome c oxidase
<i>ATP4</i>	YPL078C	2.40	GO:0046933	Subunit b of stator stalk of mitochondrial F ₁ F _o ATP synthase
<i>ATP7</i>	YKL016C	2.37	GO:0046933	Subunit d of stator stalk of mitochondrial F ₁ F _o ATP synthase
<i>PPA2</i>	YMR267 W	2.36	GO:0004427	Mitochondrial inorganic pyrophosphatase
<i>COX13</i>	YGL191W	2.21	GO:0004129	Subunit VIa of cytochrome c oxidase
<i>HEM15</i>	YOR176W	2.18	GO:0004325	Ferrochelatase
<i>ATP5</i>	YDR298C	2.12	GO:0046933	Subunit 5 of stator stalk of mitochondrial F ₁ F _o ATP synthase
<i>FMC1</i>	YIL098C	2.08	GO:0003674	Required for assembly of mitochondrial F ₁ F _o ATP synthase
<i>LSC2</i>	YGR244C	2.07	GO:0004775	Beta subunit of succinyl-CoA ligase
<i>KGD1</i>	YIL125W	2.07	GO:0004591	Oxidative decarboxylation of alpha-ketoglutarate
<i>SCO2</i>	YBR024W	2.06	GO:0008379	Delivery of copper to cytochrome c oxidase
<i>MBA1</i>	YBR185C	2.06	GO:0043022	Involved in assembly of mitochondrial respiratory complexes
<i>PET100</i>	YDR079W	2.03	GO:0051082	Chaperone that facilitates assembly of cytochrome c oxidase
<i>ATP11</i>	YNL315C	2.03	GO:0051082	Required for assembly of mitochondrial F ₁ F _o ATP synthase
<i>CIT1</i>	YNR001C	2.00	GO:0004108	Citrate synthase
<i>STF2^b</i>	YGR008C	1.61		Regulation of the mitochondrial F ₁ F _o ATP synthase
<i>Stress response (9 ORFs)</i>				
<i>CCP1</i>	YKR066C	5.53	GO:0004130	Mitochondrial cytochrome c peroxidase
<i>HSP12</i>	YFL014W	4.78	GO:0008289	Protects membranes from desiccation (response to stress)
<i>HOR7</i>	YMR251 W-A	3.50	GO:0003674	Glycine dehydrogenase, induced under hyperosmotic stress
<i>YFH1</i>	YDL120W	2.74	GO:0008198	Regulates mitochondrial iron accumulation
<i>NFU1</i>	YKL040C	2.33	GO:0003674	Protein involved in iron metabolism in mitochondria
<i>LSP1</i>	YPL004C	2.32	GO:0004860	Involved in activation of stress resistance pathways
<i>SOD2</i>	YHR008C	2.18	GO:0008383	Superoxide dismutase, protects cells against oxygen toxicity
<i>GRX4</i>	YER174C	2.15	GO:0030508	Monothiol glutaredoxin, protects cells from oxidative damage
<i>HSP10</i>	YOR020C	2.10	GO:0051082	A mitochondrial chaperonin
<i>CCC1</i>	YLR220W	2.03	GO:0005384	Fe ²⁺ /Mn ²⁺ transporter preventing iron accumulation
<i>MTH1</i>	YDR277C	2.03	GO:0003674	Negative regulator of glucose-sensing signal transduction
<i>GSY1</i>	YFR015C	2.03	GO:0004373	Glycogen synthase, expression induced by stress conditions
<i>MSN4^b</i>	YKL062 W	1.75	GO:0003700	Transcriptional activator (activated in stress conditions)

HSP31^b YDR533C 1.68 GO:0008234 Chaperone and cysteine protease

Amino acid/protein biosynthesis, assembly and modification (10 ORFs)

OPT2 YPR194C 30.57 GO:0015198 Oligopeptide transporter
GLT1 YDL171C 3.80 GO:0016040 NAD⁺-dependent glutamate synthase
LEU1 YGL009C 3.60 GO:0003861 Isopropylmalate isomerase, involved in the leucine biosynthesis
CPR5 YDR304C 3.22 GO:0003755 Peptidyl-prolyl cis-trans isomerase
MRP2 YPR166C 2.72 GO:0003735 Mitochondrial ribosomal protein of the small subunit
HOM6 YJR139C 2.60 GO:0004412 Homoserine dehydrogenase in methionine biosynthesis
MEF2 YJL102W 2.32 GO:0003746 Mitochondrial elongation factor in translational elongation
YPR1 YDR368W 2.29 GO:0004032 2-methylbutyraldehyde reductase in isoleucine catabolism
SHM2 YLR058C 2.17 GO:0004372 Cytosolic serine hydroxymethyltransferase
DPH2 YKL191W 2.16 GO:0003674 Required for synthesis of diphthamide
SER3 YER081W 2.10 GO:0004617 3-phosphoglycerate dehydrogenase in serine biosynthesis

Sugar and lipid synthesis (9 ORFs)

UGP1 YKL035W 2.59 GO:0003983 UDP-glucose pyrophosphorylase (UGPase)
FAA1 YOR317W 2.54 GO:0004467 Long chain fatty acyl-CoA synthetase
LPD1 YFL018C 2.33 GO:0004375 Dihydrolipoamide dehydrogenase
DLD2 YDL178W 2.21 GO:0004458 D-lactate dehydrogenase
MNT3 YIL014W 2.07 GO:0000033 Alpha-1,3-mannosyltransferase in protein O-glycosylation
REG2 YBR050C 2.06 GO:0008599 Regulatory subunit of the Glc7p type-1 protein phosphatase
EEB1 YPL095C 2.06 GO:0004026 Acyl-coenzymeA:ethanol O-acyltransferase
HXK1 YFR053C 2.02 GO:0004396 Hexokinase isoenzyme 1
IMD2 YHR216W 2.01 GO:0003938 Inosine monophosphate dehydrogenase
GPH1^c YPR160W 1.93 GO:0008184 Glycogen phosphorylase
NCE102^c YPR149W 1.50 GO:0003674 Component of the glycolipid-enriched complexes

Cell wall synthesis (4 ORFs)

CWP1 YKL096W 6.39 GO:0005199 Cell wall mannoprotein, involved in cell wall organization
CWP2 YKL096W -A 5.14 GO:0005199 Cell wall mannoprotein, major constituent of the cell wall
KTR6 YPL053C 2.31 GO:0000031 Mannosylphosphate transferase
ZEO1 YOL109W 2.10 GO:0003674 Peripheral membrane protein, regulates cell integrity pathway

Cell fusion, mating and cycle (10 ORFs)

MF(ALPHA) YGL089C 15.41 GO:0000772 Mating pheromone alpha-factor

<i>FUS1</i>	YCL027W	10.81	GO:0003674	Membrane protein, required for cell fusion
<i>MF(ALPHA)</i> <i>1</i>	YPL187W	8.24	GO:0000772	Mating pheromone alpha-factor
<i>STE3</i>	YKL178C	7.33	GO:0004933	Receptor for apha-factor receptor, required for mating
<i>FAR1</i>	YJL157C	3.25	GO:0004861	Cyclin-dependent kinase inhibitor
<i>PBI2</i>	YNL015W	2.26	GO:0004866	Cytosolic inhibitor of vacuolar proteinase B
<i>PNC1</i>	YGL037C	2.25	GO:0008936	Nicotinamidase, required for life span extension
<i>GPA1</i>	YHR005C	2.12	GO:0003924	GTP-binding alpha subunit, negatively regulates mating
<i>HMLALPHA</i> <i>1</i>	YCL066W	2.03	GO:0003713	Transcriptional activator, involved in mating gene expression
<i>MATALPHA1</i>	YCR040W	2.03	GO:0003713	Transcriptional activator, involved in mating gene expression
<i>MSC1</i>	YML128C	2.02	GO:0003674	Mutants are defective in directing meiotic recombination event

Others (55 ORFs)

Genes expression repressed by more than 2-fold upon surplus iron for 4 h (206 ORFs)

Gene	ORF	Repression fold	GO term ^b	Gene description
<i>Iron homeostasis</i> (26 ORFs)				
<i>FIT3</i>	YOR383C	0.02	GO:0003674	Mannoprotein for retention of siderophore-iron in cell wall
<i>FIT2</i>	YOR382 W	0.03	GO:0003674	Mannoprotein for retention of siderophore-iron in cell wall
<i>FIT1</i>	YDR534C	0.03	GO:0003674	Mannoprotein for retention of siderophore-iron in cell wall
<i>TIS11</i>	YLR136C	0.04	GO:0003729	mRNA-binding protein expressed during iron starvation
<i>ARN1</i>	YHL040C	0.04	GO:0015343	Transporter, siderophore-iron transport
<i>ARN2</i>	YHL047C	0.05	GO:0015343	Transporter, siderophore-iron transport
<i>SIT1</i>	YEL065W	0.07	GO:0015344	Siderophore-iron (ferrioxamine) uptake transporter activity
<i>FRE2</i>	YKL220C	0.08	GO:0000293	Ferric-chelate reductase activity
<i>ENB1</i>	YOL158C	0.08	GO:0015620	Ferric-enterobactin transport activity
<i>FET3</i>	YMR058 W	0.12	GO:0004322	High affinity iron ion transport
<i>FRE3</i>	YOR381W	0.15	GO:0000293	Iron ion homeostasis
<i>ISU2</i>	YOR226C	0.18	GO:0003674	Iron ion homeostasis
<i>ECL1</i>	YGR146C	0.18	GO:0003674	Induced by iron homeostasis transcription factor Aft2p
<i>FET4</i>	YMR319C	0.21	GO:0005381	Low-affinity Fe ²⁺ transporter of the plasma membrane
<i>ISU1</i>	YPL135W	0.22	GO:0005515	Iron ion homeostasis
<i>MRS4</i>	YKR052C	0.23	GO:0005381	Mitochondrial iron transporter of the mitochondrial

				carrier family
<i>HMX1</i>	YLR205C	0.24	GO:0004601	Heme-binding, iron ion homeostasis
<i>FTH1</i>	YBR207W	0.24	GO:0005381	High affinity iron transporter
<i>CCC2</i>	YDR270 W	0.24	GO:0019829	Cu²⁺-transporting P-type ATPase, iron ion homeostasis
<i>FTR1</i>	YER145C	0.27	GO:0005381	High affinity iron ion transport
<i>FRE1</i>	YLR214W	0.27	GO:0000293	Ferric-chelate reductase activity
<i>SMF3</i>	YLR034C	0.31	GO:0005381	Divalent metal ion transporter involved in iron homeostasis
<i>VHT1</i>	YGR065C	0.31	GO:0015225	Vitamin H symporter, negatively regulated by iron deprivation
<i>RCS1</i>	YGL071W	0.33	GO:0003700	Transcription factor in iron utilization and homeostasis
<i>FRE6</i>	YLL051C	0.39	GO:0000293	Ferric-chelate reductase activity
<i>FRE7</i>	YOL152 W	0.41	GO:0000293	Ferric-chelate reductase activity

Anaerobic respiration (10 ORFs)

<i>DAN4</i>	YJR151C	0.20	GO:0003674	Cell wall mannoprotein, expressed under anaerobic condition
<i>TIR3</i>	YIL011W	0.21	GO:0003674	Cell wall mannoprotein, expressed under anaerobic condition
<i>TIR1</i>	YER011W	0.24	GO:0005199	Cell wall mannoprotein, expressed under anaerobic condition
<i>TIR4</i>	YOR009W	0.27	GO:0003674	Cell wall mannoprotein, expressed under anaerobic condition
<i>PAU2</i>	YEL049W	0.30	GO:0003674	Part of seripauperin family, negatively regulated by oxygen
<i>DAN2</i>	YLR037C	0.30	GO:0003674	Cell wall mannoprotein, expressed under anaerobic condition
<i>PAU7</i>	YAR020C	0.31	GO:0003674	Part of seripauperin family, negatively regulated by oxygen
<i>PAU5</i>	YFL020C	0.35	GO:0003674	Part of seripauperin family, negatively regulated by oxygen
<i>DAN3</i>	YBR301W	0.36	GO:0003674	Cell wall mannoprotein, expressed under anaerobic condition
<i>NCE103</i>	YNL036W	0.37	GO:0004089	Carbonic anhydrase poorly transcribed under aerobic condition

Others (170 ORFs)

The genes are up-regulated or down-regulated both in 1h and 4h are in bold font, and the target genes of Msn2/4 are also underlined.

^aGenes were grouped into these categories according to the *S. cerevisiae* Genome Database and the Munich Information Center for Protein Sequence (<http://www.mips.biochem.mpg.de/proj/yeast>).

^bThe GO term is assigned based on the molecular function.

^cThe genes that are induced between 1.5-fold and 2.0-fold upon surplus iron.