

Table S1. ORFs whose transcripts are repressed at least 2 fold in an *mtl1* strain compared to the wild-type. Functional annotation is based on the information provided by SGD.

ORF	Gene	Ratio <i>mtl1</i> Δ/wt	Gene description; Function
YBL098W	BNA4	0.500	Kynurenine 3-mono oxygenase, required for biosynthesis of nicotinic acid
YIR035C		0.500	Unknown Function
YKL141W	SDH3	0.500	Cytochrome b subunit of succinate dehydrogenase; respiratory chain complex II
YLR395C	COX8	0.500	Subunit VIII of cytochrome c oxidase; mitochondrial inner membrane electron transport chain
YNL333W	SNZ3	0.500	Member of a stationary phase-induced gene family
YOR065W	CYT1	0.500	Cytochrome c1, component of the mitochondrial respiratory chain; respiratory chain complex III
YAL063C	FLO9	0.491	Lectin-like protein with similarity to Flo1p, involved in flocculation
YDR377W	ATP17	0.491	Subunit f of the F0 sector of mitochondrial F1F0 ATP synthase; proton-transporting ATP synthase complex
YPL078C	ATP4	0.491	Subunit b of the stator stalk of mitochondrial F1F0 ATP synthase; proton-transporting ATP synthase complex
YBR039W	ATP3	0.483	Gamma subunit of the F1 sector of mitochondrial F1F0 ATP synthase; proton-transporting ATP synthase complex
YHR138C		0.483	Unknown function; Homologous to PBI2
YJR019C	TES1	0.483	Peroxisomal acyl-CoA thioesterase; likely to be involved in fatty acid oxidation
YJR077C	MIR1	0.483	Mitochondrial phosphate carrier, imports inorganic phosphate into mitochondria
YDL124W		0.475	NADPH-dependent alpha-keto amide reductase
YLR231C	BNA5	0.475	Kynureninase, required for biosynthesis of nicotinic acid from tryptophan
YOL083W		0.475	Unknown Function
YDL004W	ATP16	0.467	Delta subunit of the central stalk of mitochondrial F1F0 ATP synthase; proton-transporting ATP synthase
YDR148C	KGD2	0.467	Dihydrolipoyl transsuccinylase, a component of the mitochondrial alpha-ketoglutarate dehydrogenase complex
YDR298C	ATP5	0.467	Subunit 5 of the stator stalk of mitochondrial F1F0 ATP synthase; proton-transporting ATP synthase
YIL042C	PKP1	0.467	Mitochondrial protein kinase involved in negative regulation of pyruvate dehydrogenase complex activity
YLR294C		0.467	Unknown Function
YML087C	AIM33	0.467	Unknown Function
YPL271W	ATP15	0.467	Epsilon subunit of the F1 sector of mitochondrial F1F0 ATP synthase; proton-transporting ATP synthase
YGL187C	COX4	0.459	Subunit IV of cytochrome c oxidase; member of the mitochondrial inner membrane electron transport chain
YKL148C	SDH1	0.459	Flavoprotein subunit of succinate dehydrogenase
YER158C		0.451	Unknown function
YGR035C		0.451	Unknown function
YLR295C	ATP14	0.451	Subunit h of the F0 sector of mitochondrial F1F0 ATP synthase; proton-transporting ATP synthase complex
YPR191W	QCR2	0.451	Subunit 2 of the ubiquinol cytochrome-c reductase complex; mitochondrial inner membrane electron transport chain
YBL045C	COR1	0.443	Core subunit of the ubiquinol-cytochrome c reductase complex ; mitochondrial inner membrane electron transport chain
YIL099W	SGA1	0.443	Intracellular sporulation-specific glucoamylase involved in glycogen degradation
YCR083W	TRX3	0.435	Mitochondrial thioredoxin, required to maintain the redox homeostasis of the cell

YGL104C	VPS73	0.435	Mitochondrial protein of unknown function involved in vacuolar protein sorting
YKL150W	MCR1	0.435	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis
YHR001W-A	QCR10	0.428	Subunit of the ubiquinol-cytochrome c oxidoreductase complex, involved in aerobic respiration
YLL053C		0.428	Unknown function
YML070W	DAK1	0.420	Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress adaptation
YNL202W	SPS19	0.420	Peroxisomal 2,4-dienoyl-CoA reductase, auxiliary enzyme of fatty acid beta-oxidation
YJR079W		0.413	Unknown function; mutation results in impaired mitochondrial respiration
YKL016C	ATP7	0.413	Subunit d of the stator stalk of mitochondrial F1F0 ATP synthase; proton-transporting ATP synthase,
YPR020W	ATP20	0.413	Subunit g of the mitochondrial F1F0 ATP synthase; proton-transporting ATP synthase complex
YDL130W-A	STF1	0.406	Protein involved in regulation of the mitochondrial F1F0-ATP synthase; proton-transporting ATP synthase complex
YBR230C	OM14	0.392	Integral mitochondrial outer membrane protein
YIR038C	GTT1	0.392	ER associated glutathione S-transferase capable of homodimerization
YLL052C	AQY2	0.386	Water channel that mediates the transport of water across cell membranes
YPL095C	EEB1	0.386	ethanol O-acyltransferase responsible for short-chain fatty acid ethyl ester production during fermentation
YKR049C	FMP46	0.372	Mitochondrial protein of unknown function
YOR107W	RGS2	0.372	Negative regulator of glucose-induced cAMP signaling
YDR059C	UBC5	0.366	Ubiquitin-conjugating enzyme that mediates selective degradation of abnormal proteins; stress response
YHR033W		0.366	Unknown function
YJL163C		0.366	Unknown function
YKR076W	ECM4	0.366	Unknown function
YLL041C	SDH2	0.366	Iron-sulfur protein subunit of succinate dehydrogenase
YKL093W	MBR1	0.347	Protein involved in mitochondrial functions and stress response
YLR178C	TFS1	0.342	Carboxypeptidase Y inhibitor
YPR127W		0.342	Unknown function
YGR052W	FMP48	0.336	Unknown function; localized in the mitochondria
YJR096W		0.336	Putative xylose and arabinose reductase
YLR356W	ATG33	0.330	Mitochondrial mitophagy-specific protein
YNL015W	PBI2	0.330	Cytosolic inhibitor of vacuolar proteinase B, required for efficient vacuole inheritance
YBR169C	SSE2	0.324	Member of the heat shock protein 70 (HSP70) family
YMR196W		0.319	Unknown function
YJR078W	BNA2	0.313	Tryptophan 2,3-dioxygenase
YKL151C		0.313	Unknown function
YBL043W	ECM13	0.292	Unknown function
YMR090W		0.292	Unknown function
YOR185C	GSP2	0.292	GTP binding protein involved in the maintenance of nuclear organization, RNA processing and transport
YBL015W	ACH1	0.282	Acetyl-coA hydrolase, primarily localized to mitochondria
YDR453C	TSA2	0.277	Stress inducible cytoplasmic thioredoxin peroxidase

YGR248W	SOL4	0.263	6-phosphogluconolactonase with similarity to Sol3p
YOR338W		0.263	Unknown function
YGL156W	AMS1	0.254	Vacuolar alpha mannosidase, involved in free oligosaccharide (fOS) degradation
YBR054W	YRO2	0.250	Putative plasma membrane protein of unknown function
YER103W	SSA4	0.237	Heat shock protein that is highly induced upon stress
YDL085W	NDE2	0.233	Mitochondrial external NADH dehydrogenase, catalyzes the oxidation of cytosolic NADH
YMR250W	GAD1	0.225	Glutamate decarboxylase; involved in response to oxidative stress
YOL155C	HPF1	0.221	Haze-protective mannoprotein
YML123C	PHO84	0.218	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter
YDL222C	FMP45	0.203	Unknown function
YDR034W-B		0.186	Unknown function
YGR088W	CTT1	0.183	Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide
YKL163W	PIR3	0.183	O-glycosylated covalently-bound cell wall protein required for cell wall stability
YOL084W	PHM7	0.183	Unknown function
YDL181W	INH1	0.180	Protein that inhibits ATP hydrolysis by the F1F0-ATP synthase; proton-transporting ATP synthase complex
YML128C	MSC1	0.174	Unknown function
YDL204W	RTN2	0.151	Unknown function
YFL014W	HSP12	0.151	Plasma membrane localized protein that protects membranes from desiccation
YOL053C-A	DDR2	0.151	Multistress response protein
YFL030W	AGX1	0.144	Glyoxylate aminotransferase, catalyzes the synthesis of glycine from glyoxylate
YIL160C	POT1	0.134	3-ketoacyl-CoA thiolase; beta-oxidation of fatty acids
YGR043C	NQM1	0.125	Transaldolase of unknown function
YMR107W	SPG4	0.119	Unknown function
YBR072W	HSP26	0.102	Small heat shock protein with chaperone activity
YMR169C	ALD3	0.098	Cytoplasmic aldehyde dehydrogenase, involved in beta-alanine synthesis
YHR139C	SPS100	0.093	Protein required for spore wall maturation
YGR256W	GND2	0.090	6-phosphogluconate dehydrogenase
YBR116C		0.084	Unknown function
YDL223C	HBT1	0.084	Substrate of the Hub1p ubiquitin-like protein that localizes to the shmoo tip
YDR070C	FMP16	0.076	Unknown function; mitochondrion
YPL223C	GRE1	0.061	Hydrophilin of unknown function; stress induced
YMR175W	SIP18	0.041	Protein of unknown function whose expression is induced by osmotic stress
YBR117C	TKL2	0.016	Transketolase, similar to Tk1p; required for synthesis of aromatic amino acids

Table S2. ORFs whose transcripts are induced at least 2 fold in an *mtl1* strain compared to the wild-type. Functional annotation is based on the information provided by SGD.

ORF	Gene	Ratio <i>mtl1</i> Δ/wt	Gene description; Function
YMR095C	SNO1	3.249	Protein involved in pyridoxine metabolism
YNR060W	FRE4	3.249	Ferric reductase;iron-siderophore transport
YPL250C	ICY2	3.138	Protein involved in chromatin organization and nuclear transport,
YMR011W	HXT2	2.878	High-affinity glucose transporter of the major facilitator superfamily
YIL121W	QDR2	2.828	Multidrug transporter
YBR145W	ADH5	2.685	Alcohol dehydrogenase isoenzyme V
YGL117W		2.685	Unknown Function
YBR244W	GPX2	2.594	Phospholipid hydroperoxide glutathione peroxidase; oxidative stress
YER081W	SER3	2.219	3-phosphoglycerate dehydrogenase
YBR115C	LYS2	2.107	Alpha amino adipate reductase; biosynthesis of lysine
YPL111W	CAR1	2.107	Arginase, responsible for arginine degradation
YMR096W	SNZ1	2.000	Protein involved in vitamin B6 biosynthesis
YOL158C	ENB1	2.000	Endosomal ferric enterobactin transporter

Table S3. Classification of the collection of genes whose expression was lower in *mtl1* than in wild type cells. We present two different classifications. The first according to GO Biological Process and the second according to MIPS functional classification.

GO Biological Process

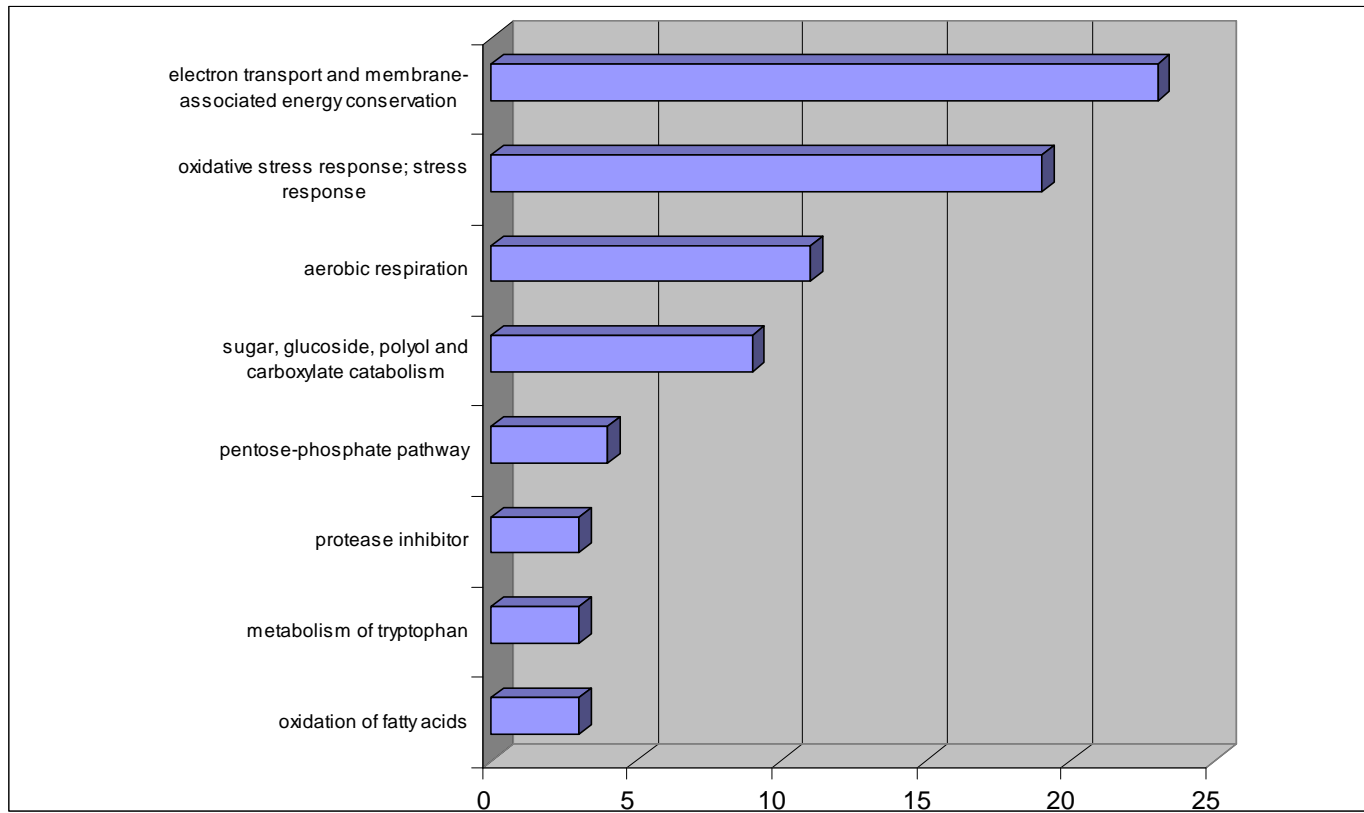
Category	p-value	In Category from Cluster	k
oxidation reduction	5,78E-13	BNA4 LYS2 ADH5 GPX2 NDE2 YDL124W TSA2 SER3 COX4 CTT1 GND2 YIR035C MIR1 BNA2 YJR096W SDH1 MCR1 FMP46 SDH2 COX8 AIM33 ALD3 SPS19 FRE4 ATP20 YPR127W	26
metabolic process	3,96E-05	BNA4 LYS2 TKL2 ADH5 INH1 KGD2 SER3 AGX1 AMS1 NQM1 GND2 SGA1 POT1 YIR035C YMR090W SNZ1 ALD3 SPS19 SNZ2	19
response to oxidative stress; response to stress		GPX2 TRX3 YDL124W TSA2 HSP12 CTT1 YJR096W MCR1 GAD1; HSP26 SSE2 UBC5 SSA4 DAK1 ALD3 DDR2 YOR338W GRE1	18
ATP synthesis coupled proton transport	4,81E-07	ATP3 ATP16 ATP5 ATP17 ATP7 ATP14 ATP4 ATP15 ATP20	9
mitochondrial electron transport		SDH3 SDH1 SDH2; QCR10 CYT1 QCR2	6
aromatic compound metabolic process	0,00298911	ADH5 YDL124W SER3 SNO1 ENB1	5
ascospore formation	0,00962488	FMP45 UBC5 SGA1 SPS19 YOR338W	5
pentose-phosphate shunt	0,00041566	TKL2 NQM1 SOL4 GND2	4
de novo NAD biosynthetic process from tryptophan	5,02E-05	BNA4 BNA2 BNA5	3
pyridoxine biosynthetic process	0,00076692	SNO1 SNZ1 SNZ2	3
cell death	0,00895324	COX4 CYT1 QCR2	3

proton transport [GO:0015992]	2,51E-07	ATP3 ATP16 ATP5 ATP17 ATP7 ATP14 ATP4 ATP15 ATP20	9
negative regulation of nucleotide metabolic process [GO:0045980]	0,00030074	STF1 INH1	2
ATP biosynthetic process [GO:0006754]	7,01E-10	ATP3 ATP16 ATP5 ATP17 ATP7 ATP14 ATP15 ATP20	8

pyridoxine metabolic process [GO:0008614]
ion transport [GO:0006811]
amino acid and derivative metabolic process [GO:0006519]

0,00544529 SNO1 SNZ1 SNZ2
7,21E-07 ATP3 YRO2 ATP16 ATP5 ATP17 ATP7 ATP14 FRE4 ENB1 ATP4 ATP15 ATP20
0,00596414 BNA4 SER3

3
12
2



MIPS Functional Classification		
Category	p-value	In Category from Cluster
electron transport and membrane-associated energy conservation		COR1 ATP3 ATP16 NDE2 STF1 INH1 ATP5 ATP17 COX4 QCR10 ATP7 SDH3 SDH1 M SDH2 ATP14 COX8 ATP4 ATP15 ATP20 QCR2; TRX3 CYT1
oxidative stress response; stress response		GPX2 TRX3 TSA2 HSP12 CTT1 GTT1 MCR1 FMP46 GAD1 GRE1; YRO2 SSE2 PIR3 DA SNO1 SNZ1 ALD3 SNZ2 DDR2
aerobic respiration	7,03E-08	COR1 NDE2 COX4 QCR10 MBR1 SDH3 SDH1 SDH2 COX8 CYT1 QCR2
sugar, glucoside, polyol and carboxylate catabolism	9,83E-06	TKL2 KGD2 AMS1 NQM1 YJR096W SDH3 SDH1 SDH2 HPF1
pentose-phosphate pathway	0,000833	TKL2 NQM1 SOL4 GND2
protease inhibitor	5,02E-05	YHR138C TFS1 PBI2
metabolism of tryptophan	0,00027	BNA4 BNA2 BNA5
oxidation of fatty acids	0,000401	POT1 TES1 SPS19

Fe/S binding [16.21.08]

homeostasis of phosphate [34.01.03.03]

tricarboxylic-acid pathway (citrate cycle, Krebs cycle, TCA cycle)
[02.10]

cation transport (H⁺, Na⁺, K⁺, Ca²⁺, NH₄⁺, etc.) [20.01.01.01]

homeostasis of protons [34.01.01.03]

5,02E-05 SDH3 SDH1 SDH2

0,009994 MIR1 PHO84

0,001911 KGD2 SDH3 SDH1 SDH2

2,05E-05 ATP3 ATP16 ATP5 ATP17 ATP7 ATP14 ATP4 ATP15

1,18E-06 ATP3 ATP16 ATP5 ATP7 ATP14 PHO84 ATP4 ATP15

