

Spreadsheet contains the T-profiler analyses output carried out on microarray data and MAVisto gene network motifs.

Table 1. The description and gene ontology for transcripts whose $O > 0.66$.

ORF	GENE	Description	Process	Component	Function	ϕ	O
YGR067C		Hypothetical protein; has similarity to Adr1p DNA-binding domain				96°	1.17
YER045C	ACA1	Basic leucine zipper (bZIP) transcription factor of the ATF/CREB family, may regulate transcription of genes involved in utilization of non-optimal carbon sources	transcription initiation from RNA polymerase II promoter	nucleus	specific RNA polymerase II transcription factor activity	257°	1.09
YAL054C	ACS1	Acetyl-coA synthetase isoform, expressed during growth on nonfermentable carbon sources and under aerobic conditions	acetyl-CoA biosynthesis acetate fermentation	mitochondrion cytosol	acetate-CoA ligase activity	159°	0.89
YMR303C	ADH2	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1	ethanol metabolism fermentation	cytoplasm	alcohol dehydrogenase activity	168°	0.82
YPL202C	AFT2	Iron-regulated transcriptional activator, required for iron homeostasis and resistance to oxidative stress; similar to Aft1p	transcription initiation from RNA polymerase II promoter iron ion homeostasis response to oxidative stress positive regulation of transcription	nucleus nucleus mitochondrion	transcription factor activity specific RNA polymerase II	100°	0.69
YER073W	ALD5	Mitochondrial aldehyde dehydrogenase, involved in regulation or biosynthesis of electron transport chain components and acetate formation; activated by K ⁺ ; utilizes NADP ⁺ as the preferred coenzyme; constitutively expressed	electron transport acetate biosynthesis	mitochondrion	aldehyde dehydrogenase activity	87°	0.97
YPL061W	ALD6	Cytosolic aldehyde dehydrogenase that is activated by Mg ²⁺ and utilizes NADP ⁺ as the preferred coenzyme; required for the conversion of acetaldehyde to acetate; constitutively expressed	acetate biosynthesis	cytoplasm mitochondrion	aldehyde dehydrogenase activity	196°	0.68
YMR042W	ARG80	Transcription factor involved in regulation of arginine-responsive genes; acts with Arg81p and Arg82p	arginine metabolism positive regulation of transcription from RNA polymerase II promoter	nucleus	DNA binding specific RNA polymerase II transcription factor activity	92°	0.87
YML099C	ARG81	Zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type, involved in the regulation of arginine-responsive genes; acts with Arg80p and Arg82p	arginine metabolism negative regulation of calcium ion-dependent exocytosis	nucleus	transcription cofactor activity	88°	
YDR173C	ARG82	Protein involved in regulation of arginine-responsive and Mcm1p-dependent genes; has a dual-specificity inositol polyphosphate kinase activity required for regulation of phosphate- and nitrogen-responsive genes	arginine metabolism phosphorylation	nucleus	inositol or phosphatidylinositol kinase activity	270°	0.72
YKR099W	BAS1	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways	histidine biosynthesis transcription from RNA polymerase II promoter purine base biosynthesis	nucleus	RNA polymerase II transcription factor activity	91°	0.78
YDR423C	CAD1	AP-1-like bZIP transcriptional activator involved in multiple stress responses, iron metabolism, and pleiotropic drug resistance; controls a set of genes involved in stabilizing proteins, binds consensus sequence TACTAA; 5' UTR contains uORFs	positive regulation of transcription from RNA polymerase II promoter response to cadmium ion	nucleus nucleus cytoplasm	RNA polymerase II transcription factor activity	264°	0.75
YMR280C	CAT8	Zinc cluster transcriptional activator necessary for derepression of a variety of genes under non-fermentative growth conditions, active after diauxic shift, binds carbon source responsive elements	positive regulation of gluconeogenesis positive regulation of transcription from RNA polymerase II promoter	nucleus	specific RNA polymerase II transcription factor activity	257°	0.68
YJR060W	CBF1	Helix-loop-helix protein that binds the motif CACRTG, which is present at several sites including MET gene promoters and centromere DNA element I (CDEI); required for nucleosome positioning at this motif; targets lsw1p to DNA	DNA replication and chromosome cycle chromatin assembly or disassembly methionine biosynthesis	kinetochore nucleus mitochondrion	DNA binding centromeric DNA binding	85°	
YOR028C	CIN5	Basic leucine zipper transcriptional factor of the yAP-1 family that mediates pleiotropic drug resistance and salt tolerance; localizes constitutively to the nucleus	regulation of transcription from RNA polymerase II promoter response to salt stress response to drug	nucleus	DNA binding RNA polymerase II transcription factor activity	267°	0.98
YDR256C	CTA1	Catalase A, breaks down hydrogen peroxide in the peroxisomal matrix formed by acyl-CoA oxidase (Pox1p) during fatty acid beta-oxidation	oxygen and reactive oxygen species metabolism	mitochondrion peroxisomal matrix	catalase activity	240°	1.05
YGR088W	CTT1	Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide	response to stress	cytoplasm	catalase activity	261°	0.77

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YAL012W	CYS3	Cystathionine gamma-lyase, catalyzes one of the two reactions involved in the transsulfuration pathway that yields cysteine from homocysteine with the intermediary formation of cystathionine;	sulfur amino acid metabolism cysteine metabolism trans-sulfuration	cytoplasm	cystathionine gamma-lyase activity	63°	1.17
YGR155W	CYS4	Cystathionine beta-synthase, catalyzes the synthesis of cystathionine from serine and homocysteine, the first committed step in cysteine biosynthesis	cysteine biosynthesis	cytoplasm mitochondrion	cystathionine beta-synthase activity	68°	0.83
YKR034W	DAL80	Negative regulator of genes in multiple nitrogen degradation pathways; expression is regulated by nitrogen levels and by Gln3p; member of the GATA-binding family, forms homodimers and heterodimers with Deh1p	transcription transcription regulation of nitrogen utilization	nucleus	transcription factor activity	152°	0.67
YJR137C	ECM17	Sulfite reductase beta subunit, involved in amino acid biosynthesis, transcription repressed by methionine	sulfate assimilation cell wall organization and biogenesis amino acid biosynthesis	cytoplasm cytoplasm sulfite reductase complex (NADPH)	sulfite reductase (NADPH) activity	99°	1.01
YFL021W	GAT1	Transcriptional activator of genes involved in nitrogen catabolite repression, member of the GATA family of DNA binding proteins; activity and localization regulated by nitrogen limitation and Ure2p	transcription initiation from RNA polymerase II promoter regulation of nitrogen utilization positive regulation of transcription	nucleus	specific RNA polymerase II transcription factor activity transcriptional activator activity	308°	0.80
YMR136W	GAT2	Protein containing GATA family zinc finger motifs; similar to Gln3p and Dal80p; expression repressed by leucine	transcription	nucleus	transcription factor activity	245°	0.78
YEL009C	GCN4	Transcriptional activator of amino acid biosynthetic genes in response to amino acid starvation; expression is tightly regulated at both the transcriptional and translational levels	regulation of transcription from RNA polymerase II promoter amino acid biosynthesis	nucleus	DNA binding transcriptional activator activity	277°	0.33
YER040W	GLN3	Transcriptional activator of genes regulated by nitrogen catabolite repression (NCR), localization and activity regulated by quality of nitrogen source	nitrogen compound metabolism regulation of nitrogen utilization positive regulation of transcription positive regulation of transcription from RNA polymerase II promoter	nucleus cytosol	transcription factor activity transcriptional activator activity	164°	
YEL046C	GLY1	Threonine aldolase, catalyzes the cleavage of L-allo-threonine and L-threonine to glycine; involved in glycine biosynthesis	glycine biosynthesis threonine catabolism	cytosol	threonine aldolase activity	194°	0.83
YKL026C	GPX1	Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and nonphospholipid peroxides during oxidative stress			glutathione peroxidase activity	262°	1.04
YBR244W	GPX2	Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and nonphospholipid peroxides during oxidative stress	response to oxidative stress	nucleus cytoplasm	glutathione peroxidase activity	237°	0.68
YCL035C	GRX1	Hydroperoxide and superoxide-radical responsive heat-stable glutathione-dependent disulfide oxidoreductase with active site cysteine pair; protects cells from oxidative damage	response to oxidative stress regulation of cell redox homeostasis	nucleus cytoplasm	glutathione transferase activity glutathione peroxidase activity thiol-disulfide exchange intermediate activity	296°	0.88
YGL073W	HSF1	Trimeric heat shock transcription factor, activates multiple genes in response to hyperthermia; recognizes variable heat shock elements (HSEs) consisting of inverted NGAAN repeats; constitutively DNA-bound; post-translationally regulated	regulation of transcription from RNA polymerase II promoter response to stress response to heat spindle pole body duplication	nucleus mitochondrion	transcription factor activity	259°	
YDR123C	INO2	Component of the heteromeric Ino2p/Ino4p basic helix-loop-helix transcription activator that binds inositol/choline-responsive elements (ICREs), required for derepression of phospholipid biosynthetic genes in response to inositol depletion	phospholipid biosynthesis positive regulation of transcription from RNA polymerase II promoter positive regulation of transcription from RNA polymerase II promoter	nucleus	specific RNA polymerase II transcription factor activity	82°	0.78
YOL108C	INO4	Transcription factor required for derepression of inositol-choline-regulated genes involved in phospholipid synthesis; forms a complex, with Ino2p, that binds the inositol-choline-responsive element through a basic helix-loop-helix domain	phospholipid biosynthesis positive regulation of transcription from RNA polymerase II promoter	nucleus	DNA binding specific RNA polymerase II transcription factor activity	264°	
YNL182C	IP13	Protein required for cell viability; computational analysis of large-scale protein-protein interaction data suggests a possible role in assembly of the ribosomal large subunit	ribosomal large subunit assembly and maintenance ribosomal large subunit assembly and maintenance 35S primary transcript processing	nucleus nucleoplasm		26°	0.94

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YMR043W	MCM1	Transcription factor involved in cell-type-specific transcription and pheromone response; plays a central role in the formation of both repressor and activator complexes	DNA replication initiation regulation of transcription from RNA polymerase II promoter	nuclear chromatin nucleus	DNA binding DNA replication origin binding RNA polymerase II transcription factor activity	274°	
YFR030W	MET10	Subunit alpha of assimilatory sulfite reductase, which is responsible for the conversion of sulfite into sulfide	sulfate assimilation	cytoplasm sulfite reductase complex (NADPH)	sulfite reductase (NADPH) activity	83°	1.11
YKL001C	MET14	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism	sulfate assimilation methionine metabolism	intracellular cytoplasm	adenylyl-sulfate kinase activity	60°	1.30
YPR167C	MET16	3'-phosphoadenylylsulfate reductase, reduces 3'-phosphoadenylyl sulfate to adenosine-3',5'-bisphosphate and free sulfite using reduced thioredoxin as cosubstrate, involved in sulfate assimilation and methionine metabolism	sulfate assimilation methionine metabolism	intracellular cytoplasm	phosphoadenylyl-sulfate reductase (thioredoxin) activity	53°	1.34
YLR303W	MET17	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis	methionine metabolism cysteine biosynthesis	cytoplasm	O-acetylhomoserine aminocarboxypropyltransferase activity cysteine synthase activity	108°	0.82
YLR303W	MET17	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis	methionine metabolism cysteine biosynthesis	cytoplasm	O-acetylhomoserine aminocarboxypropyltransferase activity cysteine synthase activity	108°	0.82
YNL277W	MET2	L-homoserine-O-acetyltransferase, catalyzes the conversion of homoserine to O-acetyl homoserine which is the first step of the methionine biosynthetic pathway	methionine biosynthesis homoserine metabolism	cytoplasm	homoserine O-acetyltransferase activity	43°	1.22
YIR017C	MET28	Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism	sulfur amino acid biosynthesis regulation of transcription from RNA polymerase II promoter regulation of sulfur metabolism	nucleus	DNA binding specific RNA polymerase II transcription factor activity transcriptional activator activity	45°	1.25
YJR010W	MET3	ATP sulfurylase, catalyzes the primary step of intracellular sulfate activation, essential for assimilatory reduction of sulfate to sulfide, involved in methionine metabolism	sulfate assimilation methionine metabolism	cytoplasm mitochondrion	sulfate adenylyltransferase (ATP) activity	77°	1.22
YIL046W	MET30	F-box protein containing five copies of the WD40 motif, controls cell cycle function, sulfur metabolism, and methionine biosynthesis as part of the ubiquitin ligase complex; interacts with and regulates Met4p, localizes within the nucleus	cell cycle protein ubiquitination SCF-dependent proteasomal ubiquitin-dependent protein catabolism response to arsenic response to cadmium ion	SCF ubiquitin ligase complex nuclear SCF ubiquitin ligase complex	protein binding	36°	0.92
YPL038W	MET31	Zinc-finger DNA-binding protein, involved in regulating expression of the methionine biosynthetic genes, similar to Met32p	sulfur amino acid metabolism regulation of transcription	nucleus nucleus cytoplasm	DNA binding specific RNA polymerase II transcription factor activity	331°	
YDR253C	MET32	Zinc-finger DNA-binding protein, involved in regulating expression of the methionine biosynthetic genes, similar to Met31p	sulfur amino acid metabolism	nucleus	DNA binding specific RNA polymerase II transcription factor activity	41°	1.39
YNL103W	MET4	Lecine-zipper transcriptional activator, responsible for the regulation of the sulfur amino acid pathway, requires different combinations of the auxiliary factors Cbf1p, Met28p, Met31p and Met32p	sulfur amino acid metabolism positive regulation of transcription from RNA polymerase II promoter response to arsenic response to cadmium ion	nucleus	transcription co activator activity	39°	1.13
YGR249W	MGA1	Protein similar to heat shock transcription factor; multicopy suppressor of pseudohyphal growth defects of ammonium permease mutants	filamentous growth			212°	0.82
YOL116W	MSN1	Transcriptional activator involved in regulation of invertase and glucoamylase expression, invasive growth and pseudohyphal differentiation, iron uptake, chromium accumulation, and response to osmotic stress; localizes to the nucleus	invasive growth (<i>sensu Saccharomyces</i>) hyperosmotic response	nucleus	transcriptional activator activity	267°	0.68

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YMR037C	MSN2	Transcriptional activator related to Msn4p; activated in stress conditions, which results in translocation from the cytoplasm to the nucleus; binds DNA at stress response elements of responsive genes, inducing gene expression	replicative cell aging age-dependent response to oxidative stress during chronological cell aging regulation of transcription, DNA-dependent response to stress	nucleus cytosol	DNA binding transcription factor activity	274°	0.39
YKL062W	MSN4	Transcriptional activator related to Msn2p; activated in stress conditions, which results in translocation from the cytoplasm to the nucleus; binds DNA at stress response elements of responsive genes, inducing gene expression	replicative cell aging age-dependent response to oxidative stress during chronological cell aging regulation of transcription, DNA-dependent response to stress	nucleus cytoplasm	DNA binding transcription factor activity	245°	0.79
YKL043W	PHD1	Transcriptional activator that enhances pseudohyphal growth; regulates expression of FLO11, an adhesin required for pseudohyphal filament formation; similar to StuA, an A. nidulans developmental regulator; potential Cdc28p substrate	pseudohyphal growth	nucleus	specific RNA polymerase II transcription factor activity	254°	0.86
YBL064C	PRX1	Mitochondrial peroxiredoxin (1-Cys Prx) with thioredoxin peroxidase activity, has a role in reduction of hydroperoxides; induced during respiratory growth and under conditions of oxidative stress	regulation of cell redox homeostasis	mitochondrion	thioredoxin peroxidase activity	299°	0.82
YOR207C	RET1	Second-largest subunit of RNA polymerase III, which is responsible for the transcription of tRNA and 5S RNA genes, and other low molecular weight RNAs	transcription from RNA polymerase III promoter	DNA-directed RNA polymerase III complex	DNA-directed RNA polymerase activity	63°	0.77
YKL038W	RGT1	Glucose-responsive transcription factor that regulates expression of several glucose transporter (HXT) genes in response to glucose; binds to promoters and acts both as a transcriptional activator and repressor	glucose metabolism negative regulation of transcription regulation of glucose import inferred from expression pattern	nucleus	DNA binding RNA polymerase II transcription factor activity transcription co-repressor activity transcriptional activator activity transcriptional repressor activity	252°	0.76
YPR065W	ROX1	Heme-dependent repressor of hypoxic genes; contains an HMG domain that is responsible for DNA bending activity	negative regulation of transcription from RNA polymerase II promoter	nuclear chromosome	DNA bending activity specific transcriptional repressor activity	227°	0.75
YIL119C	RPI1	Putative transcriptional regulator; over-expression suppresses the heat shock sensitivity of wild-type RAS2 over-expression and also suppresses the cell lysis defect of an mpk1 mutation	RAS protein signal transduction thiamine biosynthesis	nucleus	small GTPase regulator activity	244°	0.97
YJL089W	SIP4	C6 zinc cluster transcriptional activator that binds to the carbon source-responsive element (CSRE) of gluconeogenic genes; involved in the positive regulation of gluconeogenesis; regulated by Snf1p protein kinase; localized to the nucleus	regulation of transcription from RNA polymerase II promoter positive regulation of gluconeogenesis	nucleus	specific RNA polymerase II transcription factor activity	130°	0.98
YHR206W	SKN7	Nuclear response regulator and transcription factor, part of a branched two-component signaling system; required for optimal induction of heat-shock genes in response to oxidative stress; involved in osmoregulation	transcription response to osmotic stress response to oxidative stress	nucleus	two-component response regulator activity transcription factor activity	227°	
YHR008C	SOD2	Manganese-containing superoxide dismutase	replicative cell aging age-dependent response to reactive oxygen species during chronological cell aging age-dependent response to oxidative stress during chronological cell aging oxygen and reactive oxygen species metabolism	mitochondrion mitochondrial matrix	manganese superoxide dismutase activity	263°	1.04
YMR016C	SOK2	Nuclear protein that plays a regulatory role in the cyclic AMP (cAMP)-dependent protein kinase (PKA) signal transduction pathway; negatively regulates pseudohyphal differentiation; homologous to several transcription factors	pseudohyphal growth	nucleus	transcription factor activity	252°	0.79

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YDL048C	STP4	Protein involved in pre-tRNA splicing and in uptake of branched-chain amino acids		nucleus cytoplasm mitochondrion		241°	0.95
YBR294W	SUL1	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates	sulfate transport	plasma membrane	sulfate transporter activity	94°	1.05
YLR092W	SUL2	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates	sulfate transport	plasma membrane	sulfate transporter activity	61°	1.24
YGL162W	SUT1	Transcription factor of the Zn[II]2Cys6 family involved in sterol uptake; involved in induction of hypoxic gene expression	regulation of transcription from RNA polymerase II promoter sterol transport regulation of transcription	nucleus	transcription factor activity specific RNA polymerase II	84°	0.85
YGL096W	TOS8	Homeodomain-containing transcription factor; SBF regulated target gene that in turn regulates expression of genes involved in G1/S phase events such as bud site selection, bud emergence and cell cycle progression; similarity to Cup9p	G1/S-specific transcription in mitotic cell cycle	nucleus	transcription factor activity	243°	0.91
YDR513W	TTR1	Cytoplasmic glutaredoxin, thioltransferase, glutathione-dependent disulfide oxidoreductase involved in maintaining redox state of target proteins, also exhibits glutathione peroxidase activity, expression induced in response to stress	response to oxidative stress regulation of cell redox homeostasis	mitochondrion cytosol	glutathione transferase activity thiol-disulfide exchange intermediate activity	260°	0.97
YDL170W	UGA3	Transcriptional activator necessary for gamma-aminobutyrate (GABA)-dependent induction of GABA genes (such as UGA1, UGA2, UGA4); zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type; localized to the nucleus	regulation of transcription from RNA polymerase II promoter nitrogen utilization positive regulation of transcription, DNA-dependent	nucleus	transcription factor activity specific RNA polymerase II transcription factor activity	123°	0.72
YDR207C	UME6	Key transcriptional regulator of early meiotic genes, binds URS1 upstream regulatory sequence, couples metabolic responses to nutritional cues with initiation and progression of meiosis, forms complex with Ime1p, and also with Sin3p-Rpd3p	chromosome organization and biogenesis (sensu Eukaryota) negative regulation of transcription, mitotic meiotic recombination sporulation (sensu Fungi) positive regulation of meiosis	nucleus	DNA binding transcription regulator activity	235°	
YML076C	WAR1	Homodimeric Zn2Cys6 zinc finger transcription factor; binds to a weak acid response element to induce transcription of PDR12 and FUN34, encoding an acid transporter and a putative ammonia transporter, respectively	response to acid	nucleus mitochondrion	transcription factor activity	104°	0.73
YOR230W	WTM1	Transcriptional repressor involved in regulation of meiosis and silencing; contains WD repeats	regulation of meiosis	nucleus	transcription corepressor activity	279°	0.86
YIL101C	XBP1	Transcriptional repressor that binds to promoter sequences of the cyclin genes, CYS3, and SMF2; expression is induced by stress or starvation during mitosis, and late in meiosis; member of the Swi4p/Mbp1p family; potential Cdc28p substrate	response to stress	nucleus	transcription factor activity	247°	0.87
YML007W	YAP1	Basic leucine zipper (bZIP) transcription factor required for oxidative stress tolerance; mediates pleiotropic drug and metal resistance; localized to the nucleus in response to the presence of oxidants	transcription response to oxidative stress response to drug response to arsenic	nucleus cytoplasm	transcription factor activity	271°	0.92
YDR451C	YHP1	One of two homeobox transcriptional repressors (see also Yox1p), that bind to Mcm1p and to early cell cycle box (ECB) elements of cell cycle regulated genes, thereby restricting ECB-mediated transcription to the M/G ₁ interval	G ₁ /S-specific transcription in mitotic cell cycle negative regulation of transcription from RNA polymerase II promoter regulation of mitotic cell cycle regulation of meiosis	nuclear chromosome	DNA binding specific transcriptional repressor activity	235°	0.84
YOR162C	YRR1	Zn2-Cys6 zinc-finger transcription factor that activates genes involved in multidrug resistance; paralog of Yrm1p, acting on an overlapping set of target genes	multidrug transport positive regulation of transcription from RNA polymerase II promoter	nucleus	specific RNA polymerase II transcription factor activity	260°	0.79
YJR127C	ZMS1	Zinc-finger protein that localizes to the nucleus, putative transcriptional regulator of ALD6		nucleus	transcription factor activity	261°	0.69