

S3 Table. UMCC 2581 compared to UMCC 855 as determined by RNA-seq.

Genes with a significant expression change (FDR < 0.05) are shown, excluding those on chromosome 1 because of aneuploidy.

Systematic gene name	Standard gene name	Gene description	Fold change	p-adjusted
YPL265W	<i>DIP5</i>	Dicarboxylic amino acid permease	20.44	7.31E-15
YDR536W	<i>STL1</i>	Glycerol proton symporter of the plasma membrane	18.73	1.40E-06
YMR011W	<i>HXT2</i>	High-affinity glucose transporter of the major facilitator superfamily	16.20	6.06E-14
YHR033W		Putative protein of unknown function	12.00	1.76E-25
YHR096C	<i>HXT5</i>	Hexose transporter with moderate affinity for glucose	10.94	9.69E-06
YLR413W	<i>INA1</i>	Putative protein of unknown function	10.73	7.89E-27
YDR508C	<i>GNP1</i>	High-affinity glutamine permease	10.45	1.93E-12
YFL053W	<i>DAK2</i>	Dihydroxyacetone kinase	9.64	4.13E-02
YKL187C	<i>FAT3</i>	Protein required for fatty acid uptake	8.91	1.68E-02
YGL089C	<i>MF(ALPHA) 2</i>	Mating pheromone alpha-factor, made by alpha cells	8.50	4.51E-02
YBR296C	<i>PHO89</i>	Plasma membrane Na ⁺ /Pi cotransporter	8.17	1.55E-02
YOL013W-A		Putative protein of unknown function	7.59	2.23E-04
YEL065W	<i>SIT1</i>	Ferrioxamine B transporter	6.75	1.76E-25
YNL194C		Integral membrane protein	6.40	2.40E-06
YBR294W	<i>SUL1</i>	High affinity sulfate permease of the SulP anion transporter family	6.31	4.94E-14
YDL222C	<i>FMP45</i>	Integral membrane protein localized to mitochondria	6.12	3.99E-14
YBR117C	<i>TKL2</i>	Transketolase	6.02	1.00E-04
YLR265C	<i>NEJ1</i>	Protein involved in regulation of nonhomologous end joining	5.97	9.33E-04
YDL241W		Putative protein of unknown function	5.34	1.73E-02
YOR028C	<i>CIN5</i>	Basic leucine zipper (bZIP) transcription factor of the yAP-1 family	4.85	4.98E-07
YPL223C	<i>GRE1</i>	Hydrophilin essential in desiccation-rehydration process	4.82	5.07E-15
YKR093W	<i>PTR2</i>	Integral membrane peptide transporter	4.49	3.17E-03
YDR342C	<i>HXT7</i>	High-affinity glucose transporter	4.28	4.89E-02
YFR032C	<i>RRT5</i>	Putative protein of unknown function	4.27	9.73E-03
YOL052C-A	<i>DDR2</i>	Multi-stress response protein	4.21	6.83E-07
YNL195C		Protein of unknown function	4.00	9.78E-09
YNL145W	<i>MFA2</i>	Mating pheromone a-factor	3.49	1.73E-02
YJL089W	<i>SIP4</i>	C6 zinc cluster transcriptional activator	3.29	3.41E-03
YEL039C	<i>CYC7</i>	Cytochrome c isoform 2, expressed under hypoxic conditions	3.12	1.71E-02
YMR085W		Putative protein of unknown function	3.09	2.35E-06
YGR043C	<i>NQM1</i>	Transaldolase of unknown function	3.07	1.48E-03
YHR022C		Putative protein of unknown function	3.05	1.22E-02

YDL039C	<i>PRM7</i>	Pheromone-regulated protein	3.05	1.49E-05
YNR014W		Putative protein of unknown function	3.03	1.34E-06
YPR002W	<i>PDH1</i>	Putative 2-methylcitrate dehydratase	3.03	2.27E-17
YHL026C		Putative protein of unknown function	2.97	2.61E-05
YDR534C	<i>FIT1</i>	Mannoprotein that is incorporated into the cell wall	2.86	3.52E-03
YOR161C	<i>PNS1</i>	Protein of unknown function	2.85	3.99E-07
YML116W	<i>ATR1</i>	Multidrug efflux pump of the major facilitator superfamily	2.72	3.55E-21
YIL121W	<i>QDR2</i>	Plasma membrane transporter of the major facilitator superfamily	2.68	8.79E-13
YLR174W	<i>IDP2</i>	Cytosolic NADP-specific isocitrate dehydrogenase	2.68	3.57E-09
YOL047C	<i>LDS2</i>	Protein Involved in spore wall assembly	2.65	2.44E-02
YNL279W	<i>PRM1</i>	Pheromone-regulated multispinning membrane protein	2.57	5.41E-04
YLL061W	<i>MMP1</i>	High-affinity S-methylmethionine permease	2.54	2.61E-05
YGR248W	<i>SOL4</i>	6-phosphogluconolactonase	2.51	5.32E-03
YDL214C	<i>PRR2</i>	Serine/threonine protein kinase	2.48	1.80E-02
YGR121C	<i>MEP1</i>	Ammonium permease	2.38	1.22E-09
YDL223C	<i>HBT1</i>	Shmoo tip protein, substrate of Hub1p ubiquitin-like protein	2.37	2.23E-04
YOL158C	<i>ENB1</i>	Endosomal ferric enterobactin transporter	2.34	8.98E-08
YOL155C	<i>HPF1</i>	Haze-protective mannoprotein	2.34	2.90E-09
YBR244W	<i>GPX2</i>	Phospholipid hydroperoxide glutathione peroxidase	2.34	6.51E-04
YDL049C	<i>KNH1</i>	Protein with similarity to Kre9p	2.32	1.09E-04
YBR008C	<i>FLR1</i>	Plasma membrane transporter of the major facilitator superfamily	2.29	2.40E-11
YCR021C	<i>HSP30</i>	Negative regulator of the H(+)-ATPase Pma1p	2.22	2.06E-07
YLL057C	<i>JLP1</i>	Fe(II)-dependent sulfonate/alpha-ketoglutarate dioxygenase	2.20	1.19E-02
YJL108C	<i>PRM10</i>	Pheromone-regulated protein	2.19	1.41E-09
YGR197C	<i>SNG1</i>	Protein involved in resistance to nitrosoguanidine and 6-azauracil	2.19	2.09E-02
YOL020W	<i>TAT2</i>	High affinity tryptophan and tyrosine permease	2.19	2.48E-03
YDR011W	<i>SNQ2</i>	Plasma membrane ATP-binding cassette (ABC) transporter	2.16	2.61E-05
YJL191W	<i>RPS14B</i>	Protein component of the small (40S) ribosomal subunit	2.15	1.21E-06
YIR032C	<i>DAL3</i>	Ureidoglycolate lyase	2.13	1.57E-03
YHL016C	<i>DUR3</i>	Plasma membrane transporter for both urea and polyamines	2.12	6.87E-03
YNL058C		Putative protein of unknown function	2.09	2.61E-03
YFL026W	<i>STE2</i>	Receptor for alpha-factor pheromone	2.05	6.33E-03
YCL025C	<i>AGP1</i>	Low-affinity amino acid permease with broad substrate range	2.05	1.24E-04
YDR216W	<i>ADR1</i>	Carbon source-responsive zinc-finger transcription factor	2.02	1.61E-02
YLL055W	<i>YCT1</i>	High-affinity cysteine-specific transporter	2.00	1.65E-04
YML091C	<i>RPM2</i>	Protein subunit of mitochondrial RNase P	1.98	3.73E-07
YJL107C		Putative protein of unknown function	1.98	1.26E-02
YMR169C	<i>ALD3</i>	Cytoplasmic aldehyde dehydrogenase	1.98	7.98E-05

YIR031C	<i>DAL7</i>	Malate synthase	1.97	1.58E-04
YOR374W	<i>ALD4</i>	Mitochondrial aldehyde dehydrogenase	1.96	7.12E-05
YKL161C	<i>KDX1</i>	Protein kinase	1.94	6.85E-08
YDL171C	<i>GLT1</i>	NAD(+)-dependent glutamate synthase (GOGAT)	1.94	6.35E-08
YIL101C	<i>XBPI</i>	Transcriptional repressor	1.93	3.08E-02
YGR243W	<i>MPC3</i>	Highly conserved subunit of mitochondrial pyruvate carrier	1.93	7.25E-03
YOR346W	<i>REV1</i>	Deoxycytidyl transferase	1.92	4.94E-03
YDR259C	<i>YAP6</i>	Basic leucine zipper (bZIP) transcription factor	1.91	6.87E-03
YOR356W	<i>CIR2</i>	Putative ortholog of human ETF-dH	1.91	5.73E-05
YEL040W	<i>UTR2</i>	Chitin transglycosylase	1.91	2.84E-06
YMR058W	<i>FET3</i>	Ferro-O ₂ -oxidoreductase	1.90	1.83E-06
YHR023W	<i>MYO1</i>	Type II myosin heavy chain	1.87	3.11E-03
YIR027C	<i>DAL1</i>	Allantoinase	1.85	2.73E-02
YBR021W	<i>FUR4</i>	Plasma membrane localized uracil permease	1.85	2.31E-02
YGR052W	<i>FMP48</i>	Putative protein of unknown function	1.83	3.36E-06
YMR032W	<i>HOF1</i>	Protein that regulates actin cytoskeleton organization	1.83	3.92E-02
YNR044W	<i>AGA1</i>	Anchorage subunit of a-agglutinin of a-cells	1.82	3.24E-02
YLR297W		Protein of unknown function	1.81	1.19E-02
YOL084W	<i>PHM7</i>	Protein of unknown function	1.80	3.44E-05
YLR304C	<i>ACO1</i>	Aconitase	1.79	6.05E-10
YPR149W	<i>NCE102</i>	Protein of unknown function	1.79	8.67E-05
YIL024C		Putative protein of unknown function	1.79	4.51E-02
YGR088W	<i>CTT1</i>	Cytosolic catalase T	1.77	1.46E-02
YJR124C		Putative protein of unknown function	1.75	5.32E-03
YBR150C	<i>TBS1</i>	Putative protein of unknown function	1.74	1.73E-02
YOL126C	<i>MDH2</i>	Cytoplasmic malate dehydrogenase	1.73	1.07E-03
YNL129W	<i>NRK1</i>	Nicotinamide riboside kinase	1.72	3.59E-03
YMR246W	<i>FAA4</i>	Long chain fatty acyl-CoA synthetase	1.68	1.34E-05
YBR293W	<i>VBA2</i>	Permease of basic amino acids in the vacuolar membrane	1.68	2.44E-02
YML076C	<i>WAR1</i>	Homodimeric Zn ₂ Cys ₆ zinc finger transcription factor	1.65	3.05E-03
YPL017C	<i>IRC15</i>	Microtubule associated protein	1.65	8.88E-03
YER024W	<i>YAT2</i>	Carnitine acetyltransferase	1.63	1.08E-02
YLR108C		Protein of unknown function	1.61	3.88E-04
YJL172W	<i>CPS1</i>	Vacuolar carboxypeptidase S	1.60	1.61E-04
YHR097C		Putative protein of unknown function	1.60	2.01E-02
YBR005W	<i>RCR1</i>	Protein of the ER membrane involved in cell wall chitin deposition	1.60	1.25E-02
YIR029W	<i>DAL2</i>	Allantoicase	1.60	3.82E-02
YLR346C		Putative protein of unknown function found in mitochondria	1.59	4.58E-02
YJL078C	<i>PRY3</i>	Cell wall-associated protein involved in export of acetylated sterols	1.59	4.99E-03
YGR023W	<i>MTL1</i>	Putative plasma membrane sensor	1.59	3.60E-02
YER081W	<i>SER3</i>	3-phosphoglycerate dehydrogenase	1.59	3.31E-05
YDL025C	<i>RTK1</i>	Putative protein kinase, potentially phosphorylated by Cdc28p	1.59	4.45E-04

YGL114W		Putative protein of unknown function	1.58	3.24E-03
YPR160W	<i>GPH1</i>	Glycogen phosphorylase required for the mobilization of glycogen	1.58	6.87E-03
YIL155C	<i>GUT2</i>	Mitochondrial glycerol-3-phosphate dehydrogenase	1.57	4.51E-02
YOR382W	<i>FIT2</i>	Mannoprotein that is incorporated into the cell wall	1.57	1.73E-02
YKR039W	<i>GAP1</i>	General amino acid permease	1.57	4.94E-02
YLR401C	<i>DUS3</i>	Dihydrouridine synthase	1.56	3.79E-02
YJL035C	<i>TAD2</i>	Subunit of tRNA-specific adenosine-34 deaminase	1.56	4.06E-02
YLL027W	<i>ISA1</i>	Protein required for maturation of mitochondrial [4Fe-4S] proteins	1.55	1.70E-02
YNL068C	<i>FKH2</i>	Forkhead family transcription factor	1.55	4.80E-02
YKL051W	<i>SFK1</i>	Plasma membrane protein that may act to generate normal levels of PI4P	1.55	4.80E-02
YGR092W	<i>DBF2</i>	Ser/Thr kinase involved in transcription and stress response	1.55	2.54E-02
YBR183W	<i>YPC1</i>	Alkaline ceramidase	1.55	4.56E-02
YDR334W	<i>SWR1</i>	Swi2/Snf2-related ATPase	1.54	1.69E-02
YGR238C	<i>KEL2</i>	Protein that negatively regulates mitotic exit	1.54	3.12E-02
YLR299W	<i>ECM38</i>	Gamma-glutamyltranspeptidase	1.54	1.71E-03
YPL014W		Putative protein of unknown function	1.53	1.88E-02
YGR239C	<i>PEX21</i>	Peroxin required for peroxisomal matrix protein targeting	1.53	1.36E-02
YLR168C	<i>UPS2</i>	Mitochondrial intermembrane space protein	1.53	3.03E-03
YBR291C	<i>CTP1</i>	Mitochondrial inner membrane citrate transporter	1.53	2.73E-02
YHR146W	<i>CRP1</i>	Protein that binds to cruciform DNA structures	1.52	6.25E-03
YDR034C	<i>LYS14</i>	Transcriptional activator involved in regulating lysine biosynthesis	1.52	1.51E-03
YMR189W	<i>GCV2</i>	P subunit of the mitochondrial glycine decarboxylase complex	1.51	3.24E-03
YNL074C	<i>MLF3</i>	Serine-rich protein of unknown function	1.49	9.65E-03
YNL311C	<i>SKP2</i>	F-box protein of unknown function	1.49	4.51E-02
YLR414C	<i>PUN1</i>	Plasma membrane protein with a role in cell wall integrity	1.48	5.57E-03
YJL088W	<i>ARG3</i>	Ornithine carbamoyltransferase	1.47	6.69E-03
YGR090W	<i>UTP22</i>	Component of the small-subunit processome	1.47	4.33E-02
YMR318C	<i>ADH6</i>	NADPH-dependent medium chain alcohol dehydrogenase	1.46	4.46E-03
YMR300C	<i>ADE4</i>	Phosphoribosylpyrophosphate amidotransferase (PRPPAT)	1.46	2.61E-03
YHL036W	<i>MUP3</i>	Low affinity methionine permease	1.45	4.51E-02
YOR120W	<i>GCY1</i>	Glycerol dehydrogenase	1.45	2.93E-02
YHR216W	<i>IMD2</i>	Inosine monophosphate dehydrogenase	1.43	1.46E-02
YMR016C	<i>SOK2</i>	Nuclear protein that negatively regulates pseudohyphal differentiation	1.43	4.13E-02
YER164W	<i>CHD1</i>	Chromatin remodeler that regulates various aspects of transcription	1.42	4.51E-02
YER056C	<i>FCY2</i>	Purine-cytosine permease	1.41	1.80E-02
YOR136W	<i>IDH2</i>	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase	1.40	1.17E-02

YNL037C	<i>IDH1</i>	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase	1.39	1.48E-02
YJL200C	<i>ACO2</i>	Putative mitochondrial aconitase isozyme	1.38	9.84E-03
YJL141C	<i>YAK1</i>	Serine-threonine protein kinase	1.38	4.86E-02
YMR070W	<i>MOT3</i>	Transcriptional repressor and activator with two C2-H2 zinc fingers	1.37	4.51E-02
YGR061C	<i>ADE6</i>	Formylglycinamide-ribonucleotide (FGAM)-synthetase	1.37	1.46E-02
YNR016C	<i>ACC1</i>	Acetyl-CoA carboxylase, biotin containing enzyme	1.36	5.09E-03
YER069W	<i>ARG5,6</i>	Acetylglutamate kinase and N-acetyl-gamma-glutamyl-phosphate reductase	1.36	1.73E-02
YDL140C	<i>RPO21</i>	RNA polymerase II largest subunit B220	1.36	1.80E-02
YDR135C	<i>YCF1</i>	Vacuolar glutathione S-conjugate transporter	1.36	3.08E-02
YGL009C	<i>LEU1</i>	Isopropylmalate isomerase	1.35	1.33E-02
YGL077C	<i>HNMI</i>	Plasma membrane transporter for choline, ethanolamine, and carnitine	1.35	3.79E-02
YDR074W	<i>TPS2</i>	Phosphatase subunit of the trehalose-6-P synthase/phosphatase complex	1.35	1.66E-02
YJR137C	<i>MET5</i>	Sulfite reductase beta subunit	1.31	4.00E-02
YBR214W	<i>SDS24</i>	Protein involved in cell separation during budding	0.75	4.85E-02
YNL160W	<i>YGP1</i>	Cell wall-related secretory glycoprotein	0.74	4.80E-02
YER152C		Protein with 2-aminoadipate transaminase activity	0.72	3.44E-02
YDL048C	<i>STP4</i>	Protein containing a Kruppel-type zinc-finger domain	0.71	3.16E-02
YJL056C	<i>ZAP1</i>	Zinc-regulated transcription factor	0.71	2.73E-02
YOR188W	<i>MSB1</i>	Protein of unknown function	0.71	4.51E-02
YER088C	<i>DOT6</i>	Protein involved in rRNA and ribosome biogenesis	0.70	4.48E-03
YLR136C	<i>TIS11</i>	mRNA-binding protein expressed during iron starvation	0.70	4.51E-02
YHR188C	<i>GPI16</i>	Subunit of the glycosylphosphatidylinositol transamidase complex	0.70	1.28E-02
YNL200C		NADHX epimerase	0.70	4.80E-02
YCR098C	<i>GIT1</i>	Plasma membrane permease	0.69	4.28E-02
YFL042C	<i>LAM5</i>	Putative sterol transfer protein	0.69	4.50E-02
YGL156W	<i>AMS1</i>	Vacuolar alpha mannosidase	0.68	3.21E-03
YOR344C	<i>TYE7</i>	Serine-rich protein that contains a bHLH DNA binding motif	0.68	1.73E-02
YNR039C	<i>ZRG17</i>	Endoplasmic reticulum zinc transporter	0.68	1.01E-02
YBR169C	<i>SSE2</i>	Member of the heat shock protein 70 (HSP70) family	0.68	1.14E-02
YBR201W	<i>DER1</i>	ER membrane protein that promotes export of misfolded polypeptides	0.68	4.80E-02
YPL026C	<i>SKS1</i>	Putative serine/threonine protein kinase	0.68	4.91E-02
YJL082W	<i>IML2</i>	Protein of unknown function	0.67	5.54E-03
YOR321W	<i>PMT3</i>	Protein O-mannosyltransferase	0.67	5.77E-03
YJL020C	<i>BBC1</i>	Protein possibly involved in assembly of actin patches	0.67	2.50E-03
YLR045C	<i>STU2</i>	Microtubule-associated protein (MAP) of the XMAP215/Dis1 family	0.66	2.40E-02

YKL029C	<i>MAE1</i>	Mitochondrial malic enzyme	0.66	3.24E-03
YOL007C	<i>CSI2</i>	Protein of unknown function	0.66	2.12E-02
YNR026C	<i>SEC12</i>	Guanine nucleotide exchange factor (GEF)	0.66	2.51E-02
YNL289W	<i>PCL1</i>	Cyclin, interacts with cyclin-dependent kinase Pho85p	0.66	6.69E-03
YOL055C	<i>THI20</i>	Trifunctional enzyme of thiamine biosynthesis, degradation and salvage	0.65	7.80E-04
YJR061W		Putative protein of unknown function	0.65	3.05E-03
YPR091C	<i>NVJ2</i>	Lipid-binding ER protein, enriched at nucleus-vacuolar junctions (NVJ)	0.65	4.44E-02
YNL168C	<i>FMP41</i>	Putative protein of unknown function	0.64	2.42E-02
YIR035C		Putative cytoplasmic short-chain dehydrogenase/reductase	0.64	7.93E-03
YNR040W		Putative protein of unknown function	0.64	4.85E-02
YDR320C	<i>SWA2</i>	Auxilin-like protein involved in vesicular transport	0.64	1.76E-03
YOR274W	<i>MOD5</i>	Delta 2-isopentenyl pyrophosphate:tRNA isopentenyl transferase	0.64	4.32E-03
YIL124W	<i>AYR1</i>	Bifunctional triacylglycerol lipase and 1-acyl DHAP reductase	0.63	1.14E-02
YPL134C	<i>ODC1</i>	Mitochondrial inner membrane transporter	0.63	2.55E-02
YER175C	<i>TMT1</i>	Trans-aconitate methyltransferase	0.63	3.34E-02
YGL256W	<i>ADH4</i>	Alcohol dehydrogenase isoenzyme type IV	0.63	1.25E-02
YOL082W	<i>ATG19</i>	Receptor protein for the cytoplasm-to-vacuole targeting (Cvt) pathway	0.63	3.01E-03
YLR126C		Putative glutamine amidotransferase	0.63	4.81E-03
YKR003W	<i>OSH6</i>	Member of an oxysterol-binding protein family	0.62	1.43E-02
YCL028W	<i>RNQ1</i>	[PIN(+)] prion	0.62	1.51E-03
YPL277C		Putative protein of unknown function	0.62	1.44E-03
YOL083W	<i>ATG34</i>	Receptor protein involved in selective autophagy during starvation	0.61	4.86E-02
YMR170C	<i>ALD2</i>	Cytoplasmic aldehyde dehydrogenase	0.61	2.52E-02
YIL119C	<i>RPI1</i>	Transcription factor, allelic differences between S288C and Sigma1278b	0.60	4.45E-02
YOR003W	<i>YSP3</i>	Putative precursor to the subtilisin-like protease III	0.60	4.35E-02
YER158C		Protein of unknown function	0.60	3.05E-03
YLR059C	<i>REX2</i>	3'-5' RNA exonuclease	0.59	1.25E-02
YPR196W		Putative maltose-responsive transcription factor	0.59	4.42E-04
YBR045C	<i>GIP1</i>	Meiosis-specific regulatory subunit of the Glc7p protein phosphatase	0.59	4.32E-03
YDR205W	<i>MSC2</i>	Endoplasmic reticulum zinc transporter	0.59	4.53E-03
YOR125C	<i>CAT5</i>	Protein required for ubiquinone (Coenzyme Q) biosynthesis	0.58	1.70E-02
YMR096W	<i>SNZ1</i>	Protein involved in vitamin B6 biosynthesis	0.58	1.80E-04
YDR400W	<i>URH1</i>	Uridine nucleosidase (uridine-cytidine N-ribohydrolase)	0.58	3.51E-04
YCL049C		Protein of unknown function	0.57	2.01E-04
YJL157C	<i>FAR1</i>	CDK inhibitor and nuclear anchor	0.56	1.77E-04
YGR144W	<i>THI4</i>	Thiazole synthase	0.56	3.01E-03
YOL128C	<i>YGK3</i>	Protein kinase related to mammalian GSK-3 glycogen synthase kinases	0.56	1.97E-03
YDR506C	<i>GMC1</i>	Protein involved in meiotic progression	0.55	3.79E-02

YER015W	<i>FAA2</i>	Medium chain fatty acyl-CoA synthetase	0.55	4.50E-06
YMR020W	<i>FMS1</i>	Polyamine oxidase	0.55	1.04E-02
YML054C	<i>CYB2</i>	Cytochrome b2 (L-lactate cytochrome-c oxidoreductase)	0.55	6.29E-03
YLR231C	<i>BNA5</i>	Kynureninase	0.54	5.13E-06
YKL049C	<i>CSE4</i>	Centromere protein that resembles histone H3	0.54	3.63E-02
YGL185C		Putative protein with sequence similar to hydroxyacid dehydrogenases	0.53	3.47E-03
YNR075W	<i>COS10</i>	Protein of unknown function	0.53	1.61E-04
YBL049W	<i>MOH1</i>	Protein of unknown function, essential for stationary phase survival	0.53	1.13E-02
YOR092W	<i>ECM3</i>	Non-essential protein of unknown function	0.52	7.10E-04
YJR025C	<i>BNA1</i>	3-hydroxyanthranilic acid dioxygenase	0.52	4.14E-04
YOR071C	<i>NRT1</i>	High-affinity nicotinamide riboside transporter	0.52	2.14E-02
YFR055W	<i>IRC7</i>	Beta-lyase involved in the production of thiols	0.51	3.72E-06
YGL121C	<i>GPG1</i>	Proposed gamma subunit of the heterotrimeric G protein	0.50	1.07E-03
YER130C	<i>COM2</i>	Transcription factor that binds IME1 Upstream Activation Signal (UAS) _{ru}	0.50	3.35E-06
YLR237W	<i>THI7</i>	Plasma membrane transporter responsible for the uptake of thiamine	0.50	8.73E-10
YJR149W		Putative protein of unknown function	0.50	1.15E-02
YLR154C	<i>RNH203</i>	Ribonuclease H2 subunit	0.49	1.68E-02
YOR301W	<i>RAX1</i>	Protein involved in bud site selection during bipolar budding	0.48	1.61E-04
YFL050C	<i>ALR2</i>	Probable Mg(2+) transporter	0.48	9.41E-08
YGL257C	<i>MNT2</i>	Mannosyltransferase	0.47	8.65E-07
YDR379C-A	<i>SDH6</i>	Mitochondrial protein involved in assembly of succinate dehydrogenase	0.47	4.03E-02
YGL262W		Putative protein of unknown function	0.47	9.84E-03
YIL072W	<i>HOP1</i>	Meiosis-specific protein required for chromosome synapsis	0.47	3.17E-03
YLR004C	<i>THI73</i>	Putative plasma membrane permease	0.47	1.34E-09
YPL191C		Putative protein of unknown function	0.46	5.64E-03
YIL099W	<i>SGA1</i>	Intracellular sporulation-specific glucoamylase	0.46	8.08E-03
YDR461C-A		Putative protein of unknown function	0.46	2.72E-03
YDR503C	<i>LPP1</i>	Lipid phosphate phosphatase	0.45	1.44E-04
YNL254C	<i>RTC4</i>	Protein of unknown function	0.45	6.80E-07
YHL028W	<i>WSC4</i>	Endoplasmic reticulum (ER) membrane protein	0.45	1.80E-04
YHL048W	<i>COS8</i>	Nuclear membrane protein	0.45	4.92E-05
YPR006C	<i>ICL2</i>	2-methylisocitrate lyase of the mitochondrial matrix	0.44	2.24E-02
YMR095C	<i>SNO1</i>	Protein of unconfirmed function	0.44	9.73E-03
YMR199W	<i>CLN1</i>	G1 cyclin involved in regulation of the cell cycle	0.43	4.05E-10
YOR386W	<i>PHR1</i>	DNA photolyase involved in photoreactivation	0.43	3.96E-02
YDR243C	<i>PRP28</i>	RNA binding protein	0.43	3.03E-04
YPL248C	<i>GAL4</i>	DNA-binding transcription factor required for activating GAL genes	0.43	1.13E-04
YBL029W		Non-essential protein of unknown function	0.42	6.28E-08
YKL043W	<i>PHD1</i>	Transcriptional activator that enhances	0.42	4.98E-12

		pseudohyphal growth		
YGL205W	<i>POX1</i>	Fatty-acyl coenzyme A oxidase	0.41	2.86E-08
YOR049C	<i>RSB1</i>	Suppressor of sphingoid LCB sensitivity of an LCB-lyase mutation	0.41	4.98E-03
YHR140W		Putative integral membrane protein of unknown function	0.40	7.25E-03
YBR033W	<i>EDS1</i>	Putative zinc cluster protein, predicted to be a transcription factor	0.40	2.97E-02
YPL258C	<i>THI21</i>	Hydroxymethylpyrimidine (HMP) and HMP-phosphate kinase	0.39	1.21E-12
YBR072W	<i>HSP26</i>	Small heat shock protein (sHSP) with chaperone activity	0.38	3.06E-09
YDR406W	<i>PDR15</i>	Plasma membrane ATP binding cassette (ABC) transporter	0.38	4.47E-17
YJR079W		Putative protein of unknown function	0.38	5.69E-03
YKL132C	<i>RMA1</i>	Putative dihydrofolate synthetase	0.35	4.19E-05
YLR070C	<i>XYL2</i>	Xylitol dehydrogenase	0.34	4.34E-03
YBR240C	<i>THI2</i>	Transcriptional activator of thiamine biosynthetic genes	0.34	1.42E-14
YBL048W	<i>RRT1</i>	Protein of unknown function	0.34	1.83E-02
YNL065W	<i>AQR1</i>	Plasma membrane transporter of the major facilitator superfamily	0.32	1.80E-15
YMR182C	<i>RGM1</i>	Putative zinc finger DNA binding transcription factor	0.32	4.81E-02
YER060W-A	<i>FCY22</i>	Putative purine-cytosine permease	0.30	1.52E-02
YEL049W	<i>PAU2</i>	Member of the seripauperin multigene family	0.29	3.79E-02
YIL160C	<i>POT1</i>	3-ketoacyl-CoA thiolase with broad chain length specificity	0.29	7.72E-06
YPR121W	<i>THI22</i>	Protein with similarity to hydroxymethylpyrimidine phosphate kinases	0.29	1.99E-10
YJR156C	<i>THI11</i>	Protein involved in synthesis of the thiamine precursor HMP	0.28	3.53E-07
YIR039C	<i>YPS6</i>	Putative GPI-anchored aspartic protease	0.26	3.43E-04
YER060W	<i>FCY21</i>	Putative purine-cytosine permease	0.25	6.94E-11
YGR287C	<i>IMA1</i>	Major isomaltase (alpha-1,6-glucosidase/alpha-methylglucosidase)	0.24	9.68E-10
YFR026C	<i>ULI1</i>	Putative protein of unknown function	0.23	4.82E-07
YGL258W	<i>VEL1</i>	Protein of unknown function	0.18	5.41E-09
YOR161W-B		Protein of unknown function	0.15	3.24E-03
YOL131W		Putative protein of unknown function	0.15	3.17E-05
YNL012W	<i>SPO1</i>	Meiosis-specific prospore protein	0.15	7.30E-03
YDL244W	<i>THI13</i>	Protein involved in synthesis of the thiamine precursor HMP	0.14	2.51E-16
YDR380W	<i>ARO10</i>	Phenylpyruvate decarboxylase	0.12	1.80E-02
YOR387C		Putative protein of unknown function	0.09	6.50E-30
YMR319C	<i>FET4</i>	Low-affinity Fe(II) transporter of the plasma membrane	0.07	3.64E-32
YGR108W	<i>CLB1</i>	B-type cyclin involved in cell cycle progression	0	7.49E-22
YGR109C	<i>CLB6</i>	B-type cyclin involved in DNA replication during S phase	0	5.59E-03
YGR288W	<i>MAL13</i>	MAL-activator protein	0	8.99E-17

YGR289C	<i>MAL11</i>	High-affinity maltose transporter (alpha-glucoside transporter)	0	2.17E-06
YIR042C		Putative protein of unknown function	0	5.17E-14