

S4 Table. Gene Ontology - Process.

Comparison between gene expression levels of the UMCC 2581 and UMCC 855 strains. Gene Ontology (GO) process enriched for up-regulated and down-regulated genes in UMCC 2581 are reported.

Process Ontology							
Gene Ontology Enrichment, <u>up-regulated genes</u>							
Gene Ontology ID	Gene Ontology term	Cluster frequency	Background frequency	p-value	FDR	Expected False Positives	Genes annotated to the term
6820	anion transport	19 out of 140 genes, 13.6%	119 out of 4737 background genes, 2.5%	5.42E-07	0.00	0.00	<i>CTP1/ YBR291C, VBA2/ YBR293W, SUL1/ YBR294W, PHO89/ YBR296C, AGP1/ YCL025C, YCF1/ YDR135C, GNP1/ YDR508C, HNM1/ YGL077C, MPC3/ YGR243W, MUP3/ YHL036W, FAT3/ YKL187C, GAP1/ YKR039W, YCT1/ YLL055W, ATR1/ YML116W, FET3/ YMR058W, FAA4/ YMR246W, TAT2/ YOL020W, ENB1/ YOL158C, DIP5/ YPL265W</i>
46942	carboxylic acid transport	14 out of 140 genes, 10.0%	67 out of 4737 background genes, 1.4%	2.71E-06	0.00	0.00	<i>CTP1/ YBR291C, VBA2/ YBR293W, AGP1/ YCL025C, YCF1/ YDR135C, GNP1/ YDR508C, HNM1/ YGL077C, MPC3/ YGR243W, MUP3/ YHL036W, FAT3/ YKL187C, GAP1/ YKR039W, YCT1/ YLL055W, FAA4/ YMR246W, TAT2/ YOL020W, DIP5/ YPL265W</i>
15849	organic acid transport	14 out of 140 genes, 10.0%	68 out of 4737 background genes, 1.4%	3.33E-06	0.00	0.00	<i>CTP1/ YBR291C, VBA2/ YBR293W, AGP1/ YCL025C, YCF1/ YDR135C, GNP1/ YDR508C, HNM1/ YGL077C, MPC3/ YGR243W, MUP3/ YHL036W, FAT3/ YKL187C, GAP1/ YKR039W, YCT1/ YLL055W, FAA4/ YMR246W, TAT2/ YOL020W, DIP5/ YPL265W</i>
15711	organic anion transport	15 out of 140 genes, 10.7%	100 out of 4737 background genes, 2.1%	8.37E-05	0.00	0.00	<i>CTP1/ YBR291C, VBA2/ YBR293W, AGP1/ YCL025C, YCF1/ YDR135C, GNP1/ YDR508C, HNM1/ YGL077C, MPC3/ YGR243W, MUP3/ YHL036W, FAT3/ YKL187C, GAP1/ YKR039W, YCT1/ YLL055W, FAA4/ YMR246W,</i>

6811	ion transport	22 out of 140 genes, 15.7%	215 out of 4737 background genes, 4.5%	0.00011	0.00	0.00	<i>TAT2/ YOL020W, ENB1/ YOL158C, DIP5/ YPL265W CTP1/ YBR291C, VBA2/ YBR293W, SUL1/ YBR294W, PHO89/ YBR296C, AGP1/ YCL025C, YCF1/ YDR135C, GNP1/ YDR508C, HNM1/ YGL077C, MEP1/ YGR121C, MPC3/ YGR243W, DUR3/ YHL016C, MUP3/ YHL036W, QDR2/ YIL121W, FAT3/ YKL187C, GAP1/ YKR039W, YCT1/ YLL055W, ATR1/ YML116W, FET3/ YMR058W, FAA4/ YMR246W, TAT2/ YOL020W, ENB1/ YOL158C, DIP5/ YPL265W</i>
43605	cellular amide catabolic process	5 out of 140 genes, 3.6%	9 out of 4737 background genes, 0.2%	0.00126	0.00	0.00	<i>DUR3/ YHL016C, DAL1/ YIR027C, DAL2/ YIR029W, DAL7/ YIR031C, DAL3/ YIR032C</i>
71705	nitrogen compound transport	18 out of 140 genes, 12.9%	192 out of 4737 background genes, 4.1%	0.00564	0.00	0.02	<i>FUR4/ YBR021W, VBA2/ YBR293W, AGP1/ YCL025C, YCF1/ YDR135C, GNP1/ YDR508C, FCY2/ YER056C, HNM1/ YGL077C, YGL114W, UTP22/ YGR090W, MEP1/ YGR121C, DUR3/ YHL016C, MUP3/ YHL036W, GAP1/ YKR039W, PTR2/ YKR093W, YCT1/ YLL055W, MMP1/ YLL061W, TAT2/ YOL020W, DIP5/ YPL265W</i>
6865	amino acid transport	8 out of 140 genes, 5.7%	39 out of 4737 background genes, 0.8%	0.00708	0.00	0.02	<i>VBA2/ YBR293W, AGP1/ YCL025C, GNP1/ YDR508C, MUP3/ YHL036W, GAP1/ YKR039W, YCT1/ YLL055W, TAT2/ YOL020W, DIP5/ YPL265W</i>

Gene Ontology Enrichment, down-regulated genes

Gene Ontology ID	Gene Ontology term	Cluster frequency	Background frequency	p-value	FDR	Expected False Positives	Genes annotated to the term
42723	thiamine-containing compound metabolic process	4 out of 109 genes, 3.7%	5 out of 4737 background genes, 0.1%	0.00055	0.02	0.02	<i>THI2/ YBR240C, THI4/ YGR144W, THI20/ YOL055C, THI21/ YPL258C</i>
42724	thiamine-containing compound biosynthetic	4 out of 109 genes, 3.7%	5 out of 4737 background genes, 0.1%	0.00055	0.01	0.02	<i>THI2/ YBR240C, THI4/ YGR144W, THI20/ YOL055C, THI21/ YPL258C</i>

	process						
6772	thiamine metabolic process	4 out of 109 genes, 3.7%	5 out of 4737 background genes, 0.1%	0.00055	0.01	0.02	<i>THI2/ YBR240C, THI4/ YGR144W, THI20/ YOL055C, THI21/ YPL258C</i>
9228	thiamine biosynthetic process	4 out of 109 genes, 3.7%	5 out of 4737 background genes, 0.1%	0.00055	0.01	0.02	<i>THI2/ YBR240C, THI4/ YGR144W, THI20/ YOL055C, THI21/ YPL258C</i>