

Table S6:

Gene Ontology analysis of deregulation of gene expression in *mcd1-1* with respect to cellular component affected. Results of the Gene Ontology Slim Term Mapper searching for all terms from GO Set: Yeast GO slim: component.

GO Terms from the cellular component Ontology GO Term (GO ID)	Percentage of total affected genes	Total no. of genes in component	No. of genes affected within component	Affected genes within component (percentage)
Cytoplasm (GO:0005737)	38.92	2549	369	14.47
Membrane (GO:0016020)	27.53	1972	261	13.24
Nucleus (GO:0005634)	23.20	2350	220	9.36
Mitochondrion (GO:0005739)	13.71	1222	130	10.64
Ribosome (GO:0005840)	12.02	241	114	47.30
Vacuole (GO:0005773)	10.13	516	96	18.60
Plasma membrane (GO:0005886)	8.86	549	84	15.30
Endoplasmic Reticulum (GO:0005783)	6.54	683	62	9.08
Cell Wall (GO:0005618)	6.22	140	59	42.14
Mitochondrial envelope (GO:0005740)	4.11	448	39	8.71
Extracellular region (GO:0005576)	3.38	115	32	27.83
Chromosome (GO:0005694)	2.95	212	28	13.21
Nucleolus (GO:0005730)	2.95	347	28	8.07
Site of polarized growth (GO:0030427)	2.11	279	20	7.17
Cytoskeleton (GO:0005856)	2.00	220	19	8.64
Cellular bud (GO:0005933)	1.90	257	18	7.00
Cell cortex (GO:0005938)	1.69	170	16	9.41
Golgi apparatus (GO:0005794)	1.37	297	13	4.38
Peroxisome (GO:0005777)	1.27	91	12	13.19
Cytoplasmic vesicle (GO:0031410)	0.74	136	7	5.15
Endomembrane system (GO:0012505)	0.21	92	2	2.17
Microtubule organizing center (GO:0005815)	0.11	6	1	16.67
All terms	-	6430	948	14.74