Sequence	Sequence Name(s)	Sequence Description	Ratio	Fold Chang	P-value	Sequence	Sequence I	Accession	Primary Sequence Name
YML123C	PHO84	inorganic phosphate trans	5.61	5.61	3.54E-07	SGD	634086		PHO84
YGR051C	YGR051C		2.23	2.23	5.20E-05	SGD	634299		YGR051C
YBR244W	GPX2,AMI1	Glutathione peroxidase pa	0.47	-2.13	1.07E-18	SGD	634399		GPX2
YML007W	YAP1,PAR1,SNQ3	jun-like transcription factor	0.05	-22.12	3.21E-16	SGD	634566		YAP1
YDR536W	STL1	sugar transporter-like prot	0.4	-2.47	2.12E-11	SGD	634742		STL1
YLR110C	CCW12	cell wall mannoprotein; Nu	2.73	2.73	3.17E-04	SGD	634826		CCW12
YDR134C	YDR134C		2.55	2.55	4.84E-08	SGD	634919		YDR134C
YJR115W	YJR115W		2.43	2.43	9.21E-06	SGD	635706		YJR115W
YML131W	YML131W		0.45	-2.2	5.17E-17	SGD	636011		YML131W
YMR011W	HXT2	hexose transporter; high a	2.5	2.5	7.36E-06	SGD	636206		HXT2
YNL134C	YNL134C		0.43	-2.31	4.15E-05	SGD	636954		YNL134C
YPL171C	OYE3,ZRG6	Old yellow enzyme; NADP	0.3	-3.38	1.30E-23	SGD	636980		OYE3
YNL234W	YNL234W		2.07	2.07	7.84E-05	SGD	637019		YNL234W
YGL158W	RCK1	Serine/threonine protein ki	4.27	4.27	0	SGD	637165		RCK1
YDR380W	ARO10		0.43	-2.33	4.08E-06	SGD	637201		ARO10
YCL026C-A	FRM2	Protein involved in the inte	0.32	-3.14	2.61E-25	SGD	637621		FRM2
YGR052W	YGR052W		3.17	3.17	8.13E-39	SGD	637831		YGR052W
YBR238C	YBR238C		2.1	2.1	2.90E-07	SGD	638088		YBR238C
YGL162W	SUT1	Involved in sterol uptake; M	2.5	2.5	2.55E-04	SGD	638454		SUT1
YGR142W	BTN2	Gene/protein whose expre	0.48	-2.06	9.82E-20	SGD	638550		BTN2
YPL061W	ALD6	Utilizes NADP+ as the pre	3.04	3.04	3.29E-09	SGD	638588		ALD6
YDR055W	PST1	Protoplasts-secreted; the g	2.18	2.18	6.51E-07	SGD	639359		PST1
Q0297	ORF:Q0297	BioProcess=biological_pro	2.25	2.25	6.78E-04	SGD	970694		ORF:Q0297
YML007C-A	ORF:YML007C-A	BioProcess=biological_pro	3.03	3.03	4.77E-19	SGD	970815		ORF:YML007C-A