Sequence	Sequence Name(s)	Sequence Description	Ratio	Fold Chang	P-value	Sequence	Sequence	Accession	Primary Sequence Name
YDL229W	SSB1,YG101	Stress-Seventy Subfamily	3.09	3.09	9.00E-05	SGD	633280		SSB1
YDL038C	YDL038C		2.06	2.06	1.89E-10	SGD	633290		YDL038C
YGL141W	HUL5	ubiquitin-protein ligase (E3	0.45	-2.22	9.11E-13	SGD	633291		HUL5
YBR067C	TIP1	cold- and heat-shock induc	0.3	-3.36	8.80E-11	SGD	633292		TIP1
YOL121C	RPS19A	Homology to rat S19; ribos	3.7	3.7	1.88E-10	SGD	633300		RPS19A
YPR052C	NHP6A	Homologous to mammalian	2.26	2.26	2.54E-40	SGD	633303		NHP6A
YKL086W	YKL086W		0.34	-2.98	2.18E-06	SGD	633310		YKL086W
YKR066C	CCP1	Cytochrome-c peroxidase;	0.23	-4.27	2.75E-25	SGD	633336		CCP1
YER007C-	YER007C-A		2.27	2.27	2.12E-07	SGD	633337		YER007C-A
YMR307W	GAS1,CWH52,GGP1	Glycophospholipid-anchore	4.8	4.8	4.88E-34	SGD	633348		GAS1
YBL092W	RPL32	Homology to rat L32 and m	3.29	3.29	2.57E-09	SGD	633370		RPL32
YCL001W	RER1	Protein involved in retentio	2.7	2.7	3.27E-05	SGD	633373		RER1
YLR106C	YLR106C		3.01	3.01	1.59E-04	SGD	633377		YLR106C
YER060w-	FCY22	identical to FCY2; purine-c	0.32	-3.12	1.49E-30	SGD	633383		FCY22
YER056C-	RPL34A	Homology to rat L34; ribos	3.09	3.09	3.63E-20	SGD	633385		RPL34A
YBL054W	YBL054W	Homolog to myb transform	0.41	-2.43	4.43E-15	SGD	633391		YBL054W
YDR238C	SEC26	Involved in endoplasmic-to	2.35	2.35	2.50E-08	SGD	633398		SEC26
YMR085W	YMR085W		0.5	-2.01	2.11E-15	SGD	633400		YMR085W
YDR242W	AMD2	putative amidase; amidase	0.3	-3.38	5.25E-11	SGD	633407		AMD2
YJR094W-	RPL43B	Homology to human L37a;	4.77	4.77	1.75E-13	SGD	633410		RPL43B
YLR272C	YCS4,LOC7	loss of cohesion; Null muta	2.28	2.28	2.48E-07	SGD	633428		YCS4
YDR247W	YDR247W		0.49	-2.02	5.06E-09	SGD	633440		YDR247W
YLR287C-/	RPS30A	Homology to mammalian S	2.21	2.21	2.76E-04	SGD	633442		RPS30A
YMR120C	ADE17	AICAR transformylase/IMP	0.1	-10.42	1.39E-17	SGD	633447		ADE17
YMR062C	ECM40,ARG7	ExtraCellular Mutant; acety	0.09	-11.43	1.97E-16	SGD	633448		ECM40
YFR031C-/	RPL2A,RPL5B	Homology to rat L8 and E.	5.71	5.71	5.79E-09	SGD	633449		RPL2A
YML009C	MRPL39,YML39	Mitochondrial ribosomal pr	2.58	2.58	1.32E-11	SGD	633461		MRPL39
YGR014W	MSB2	putative integral membrane	2.08	2.08	1.61E-06	SGD	633462		MSB2
YJR092W	BUD4	co-assembles with Bud3p a	2.85	2.85	1.08E-06	SGD	633469		BUD4
YJR109C	CPA2	carbamyl phosphate synth	0.08	-12.67	0	SGD	633480		CPA2
YPL242C	IQG1,CYK1	Homolog of the mammalian	2.27	2.27	1.46E-16	SGD	633508		IQG1
YJL207C	YJL207C		2.11	2.11	7.47E-04	SGD	633516		YJL207C
YLR311C	YLR311C		0.3	-3.33	6.72E-04	SGD	633541		YLR311C
YNL135C	FPR1,FKB1,RBP1	FK506 binding protein, pro	2.6	2.6	3.37E-04	SGD	633543		FPR1
YGL189C	RPS26A	Homology to rat S26; ribos	3.62	3.62	2.63E-11	SGD	633551		RPS26A
YAR050W	FLO1,FLO2,FLO4	cell wall protein involved in	0.41	-2.45	2.07E-04	SGD	633582		FLO1

YAL024C	LTE1,MSI2	Gdp/GTP exchange factor	4.7	4.7	1.72E-09	SGD	633585	LTE1
YLR086W	SMC4	Stable Maintenance of Chr	2.37	2.37	9.90E-07	SGD	633587	SMC4
YIL159W	BNR1	Bni1p-related protein, help	2.08	2.08	6.81E-04	SGD	633588	BNR1
YLR339C	YLR339C		2.64	2.64	2.76E-16	SGD	633594	YLR339C
YDR185C	YDR185C		0.38	-2.66	3.36E-05	SGD	633597	YDR185C
YGR085C	RPL11B	Homology to rat L11 and E	2.89	2.89	6.01E-15	SGD	633601	RPL11B
YJL142C	YJL142C		0.44	-2.26	4.56E-05	SGD	633608	YJL142C
YJL190C	RPS22A,RPS24	Homology to rat S15a; ribo	3.91	3.91	2.59E-20	SGD	633624	RPS22A
YLR279W	YLR279W		2.3	2.3	5.31E-08	SGD	633642	YLR279W
YNL079C	TPM1	tropomyosin I; Null mutant	2.45	2.45	2.76E-13	SGD	633667	TPM1
YER066W	YER066W		0.27	-3.75	0	SGD	633678	YER066W
YGL242C	YGL242C		2.72	2.72	1.19E-05	SGD	633681	YGL242C
YJR025C	BNA1,HAD1	biosynthesis of nicotinic ac	0.37	-2.73	5.65E-08	SGD	633684	BNA1
YLR193C	YLR193C		0.48	-2.11	1.13E-07	SGD	633686	YLR193C
YBR106W	PHO88	May be a membrane protei	3.46	3.46	0	SGD	633708	PHO88
YNL010W	YNL010W		2.11	2.11	7.25E-07	SGD	633722	YNL010W
YNL178W	RPS3,SUF14	Homology to mammalian S	5.78	5.78	0	SGD	633723	RPS3
YLR356W	YLR356W		0.44	-2.26	4.39E-12	SGD	633735	YLR356W
YML028W	TSA1,TPX1,ZRG14	antioxidant enzyme that pr	2.73	2.73	8.47E-32	SGD	633736	TSA1
YGL147C	RPL9A	Homology to rat L9; riboso	3.31	3.31	1.91E-36	SGD	633740	RPL9A
YBR014C	YBR014C	Glutaredoxin homolog	2.15	2.15	5.40E-09	SGD	633745	YBR014C
YER102W	RPS8B	Homology to mammalian S	2.91	2.91	6.24E-08	SGD	633748	RPS8B
YMR118C	YMR118C		0.43	-2.31	2.01E-17	SGD	633753	YMR118C
YGR026W	YGR026W		2.15	2.15	9.87E-24	SGD	633764	YGR026W
YOL088C	MPD2	protein disulfide isomerase	2.08	2.08	1.63E-11	SGD	633765	MPD2
YGR201C	YGR201C		0.33	-3.06	7.53E-09	SGD	633767	YGR201C
YML105C	SEC65	signal recognition particle s	2.28	2.28	2.72E-16	SGD	633769	SEC65
YIL053W	RHR2,GPP1	DL-glycerol-3-phosphatase	2.64	2.64	4.32E-08	SGD	633770	RHR2
YER039C	HVG1,YEM9	Homologous to VRG4; nuc	0.44	-2.3	1.06E-04	SGD	633777	HVG1
YHR043C	DOG2	2-deoxyglucose-6-phospha	2.69	2.69	4.71E-05	SGD	633779	DOG2
YLR301W	YLR301W		2.93	2.93	5.60E-28	SGD	633781	YLR301W
YMR230W	RPS10B	Homology to rat S10; ribos	3.26	3.26	4.70E-17	SGD	633782	RPS10B
YGR152C	RSR1,BUD1	Gtp-binding protein of the r	2.18	2.18	2.70E-17	SGD	633785	RSR1
YJL210W	PEX2,CRT1,PAS5	Required for peroxisome b	0.44	-2.25	5.69E-05	SGD	633786	PEX2
YJL035C	TAD2	tRNA-specific adenosine-3	4.29	4.29	1.98E-33	SGD	633792	TAD2
YKL152C	GPM1	converts 3-phosphoglycera	2.03	2.03	1.23E-06	SGD	633794	GPM1
YGR058W	YGR058W		0.41	-2.42	3.75E-14	SGD	633805	YGR058W

YCR010C	ADY2	Accumulation of DYads; Nu	2.09	2.09	3.13E-05	SGD	633816	ADY2
YNL289W	PCL1,HCS26	G(sub)1 cyclin that associa	2.56	2.56	9.73E-07	SGD	633820	PCL1
YIL003W	DRE3	Protein required for cell via	0.3	-3.32	4.92E-27	SGD	633824	DRE3
YDL142C	CRD1,CLS1	Cardiolipin synthase; cardi	0.47	-2.13	8.72E-06	SGD	633832	CRD1
YOR239W	ABP140	actin filament binding prote	2.9	2.9	1.92E-26	SGD	633836	ABP140
YLR290C	YLR290C		0.41	-2.43	1.85E-05	SGD	633837	YLR290C
YLR344W	RPL26A	Homology to rat L26; ribos	2.15	2.15	9.92E-04	SGD	633838	RPL26A
YDL175C	YDL175C		0.27	-3.68	1.28E-12	SGD	633844	YDL175C
YOL151W	GRE2	induced by osmotic stress,	2.16	2.16	4.02E-07	SGD	633862	GRE2
YFR025C	HIS2	Histidinolphosphatase; hist	0.45	-2.23	4.51E-35	SGD	633867	HIS2
YBR046C	ZTA1	Zeta-crystallin homolog, ha	0.36	-2.8	5.37E-27	SGD	633868	ZTA1
YCR021C	HSP30,YRO1	Protein induced by heat sh	0.14	-7.27	3.65E-23	SGD	633869	HSP30
YLR372W	SUR4,ELO3,SRE1,VBM1	Required for conversion of	7.92	7.92	0	SGD	633875	SUR4
YBR181C	RPS6B,LPG18,RPS101,F	Homology to rat, human, a	4.78	4.78	0	SGD	633886	RPS6B
YGR286C	BIO2	Biotin synthase; biotin synt	3.71	3.71	2.70E-08	SGD	633887	BIO2
YKR076W	ECM4	ExtraCellular Mutant; A Tn	0.43	-2.33	4.80E-06	SGD	633890	ECM4
YLR056W	ERG3,SYR1	C-5 sterol desaturase; Null	0.4	-2.49	7.13E-07	SGD	633894	ERG3
YKR011C	TOS5	Hypothetical ORF	2.38	2.38	7.05E-05	SGD	633902	TOS5
YER118C	SHO1,SSU81	Transmembrane osmosens	2.2	2.2	5.08E-33	SGD	633908	SHO1
YIR021W	MRS1,PET157	RNA splicing protein of the	2.15	2.15	6.03E-05	SGD	633911	MRS1
YBR105C	VID24	also involved in vacuolar p	0.38	-2.66	4.41E-14	SGD	633912	VID24
YOR049C	YOR049C		0.21	-4.82	4.90E-06	SGD	633917	YOR049C
YNL007C	SIS1	sit4 suppressor, dnaJ hom	0.4	-2.51	6.35E-05	SGD	633919	SIS1
YHR203C	RPS4B	Homology to rat S4 and hu	3.84	3.84	2.64E-09	SGD	633920	RPS4B
YKL027W	YKL027W		2.26	2.26	6.24E-05	SGD	633927	YKL027W
YGR110W	YGR110W		0.35	-2.89	3.09E-05	SGD	633928	YGR110W
YOR393W	ERR1	enolase homolog	0.3	-3.37	6.30E-12	SGD	633949	ERR1
YLR387C	YLR387C		0.45	-2.22	1.20E-09	SGD	633953	YLR387C
YLR049C	YLR049C		2.1	2.1	8.80E-07	SGD	633956	YLR049C
YBR249C	ARO4	3-deoxy-D-arabino-heptulo	0.37	-2.74	1.45E-14	SGD	633960	ARO4
YBR018C	GAL7	galactose-1-phosphate uric	0.31	-3.22	2.83E-12	SGD	633963	GAL7
YBR297W	MAL33,MAL3R	Part of complex locus MAL	0.19	-5.28	4.92E-09	SGD	633966	MAL33
YGL256W	ADH4,NRC465,ZRG5	Alcohol dehydrogenase typ	7.67	7.67	2.71E-27	SGD	633968	ADH4
YBR029C	CDS1,CDG1	CDP-diacylglycerol synthas	2.81	2.81	4.06E-07	SGD	633973	CDS1
YOR375C	GDH1,URE1	NADP-specific glutamate d	2.88	2.88	1.43E-28	SGD	633975	GDH1
YFL037W	TUB2,ARM10,SHE8	beta subunit of tubulin mor	4.82	4.82	4.51E-10	SGD	633989	TUB2
YOR221C	MCT1	malonyl-CoA:ACP transfer	0.26	-3.87	1.37E-29	SGD	633994	MCT1

YER043C	SAH1	putative S-adenosyl-L-hom	5.35	5.35	5.03E-23	SGD	633995	SAH1
YKL090W	YKL090W		0.4	-2.53	2.07E-05	SGD	633999	YKL090W
YPL281C	ERR2	enolase-related subtelome	0.27	-3.67	2.08E-26	SGD	634003	ERR2
YNL220W	ADE12,BRA9	adenylosuccinate syntheta	0.29	-3.43	2.30E-28	SGD	634006	ADE12
YHR006W	STP2	Involved in pre-tRNA splici	0.36	-2.78	4.10E-19	SGD	634025	STP2
YBR093C	PHO5	Acid phosphatase, repress	0.47	-2.14	1.69E-08	SGD	634033	PHO5
YGR004W	YGR004W		2.1	2.1	1.51E-11	SGD	634036	YGR004W
YPL201C	YPL201C		2.22	2.22	4.71E-04	SGD	634037	YPL201C
YGR249W	MGA1	Mga1p shows similarity to	3.94	3.94	8.51E-11	SGD	634040	MGA1
YHR005C	GPA1,CDC70,DAC1,SCG	Involved in the mating phe	0.38	-2.65	9.16E-23	SGD	634046	GPA1
YDR481C	PHO8	repressible alkaline phosph	0.44	-2.28	9.12E-04	SGD	634052	PHO8
YNL117W	MLS1	carbon-catabolite sensitive	0.2	-4.98	1.39E-11	SGD	634059	MLS1
YPL212C	PUS1	Involved in tRNA biogenes	0.49	-2.06	5.10E-14	SGD	634064	PUS1
YGL028C	SCW11	Soluble Cell Wall protein; s	0.41	-2.43	2.81E-28	SGD	634065	SCW11
YJR064W	CCT5,TCP5	Required for assembly of n	2.01	2.01	1.48E-05	SGD	634070	CCT5
YBR248C	HIS7	glutamine amidotransferas	0.2	-5.02	6.38E-10	SGD	634075	HIS7
YGR023W	MTL1	Mid-Two Like 1; acts in cor	0.48	-2.08	9.91E-04	SGD	634076	MTL1
YOR027W	STI1	Heat shock protein also inc	0.35	-2.89	2.91E-07	SGD	634085	STI1
YDR497C	ITR1	member of sugar transport	2.61	2.61	9.99E-23	SGD	634088	ITR1
YDR343C	HXT6	Repression of HXT6 expre	0.23	-4.31	1.68E-04	SGD	634095	HXT6
YNL227C	YNL227C		0.44	-2.27	2.28E-40	SGD	634100	YNL227C
YER124C	DSE1	Hypothetical ORF	0.19	-5.24	0	SGD	634109	DSE1
YBR299W	MAL32,MAL3S	Part of the complex locus M	0.33	-3	5.64E-22	SGD	634119	MAL32
YFR015C	GSY1	Highly similar to GSY2. GS	0.37	-2.7	5.27E-09	SGD	634141	GSY1
YAR014C	BUD14	Null mutant is viable, rando	0.43	-2.3	1.13E-14	SGD	634143	BUD14
YKL187C	YKL187C		3.36	3.36	1.57E-06	SGD	634147	YKL187C
YMR078C	CTF18,CHL12	Chromosome transmission	2.07	2.07	3.54E-24	SGD	634149	CTF18
YDR234W	LYS4,LYS3	homoaconitase; Lysine req	0.34	-2.94	7.49E-27	SGD	634161	LYS4
YLR069C	MEF1	mitochondrial elongation fa	2.71	2.71	4.11E-17	SGD	634170	MEF1
YHR172W	SPC97	Spindle Pole Body compor	2.56	2.56	1.43E-07	SGD	634173	SPC97
YDR034C	LYS14	Transcriptional activator of	0.31	-3.25	4.77E-29	SGD	634180	LYS14
YOR321W	PMT3	Transfers mannose residue	2.19	2.19	9.06E-25	SGD	634189	PMT3
YGL114W	YGL114W		0.41	-2.43	1.20E-17	SGD	634195	YGL114W
YDR086C	SSS1	involved in transfer of secre	2.25	2.25	3.68E-07	SGD	634199	SSS1
YLR325C	RPL38	Homology to rat L38; ribose	2.98	2.98	2.35E-10	SGD	634209	RPL38
YLR264W	RPS28B,RPS33B	Homology to mammalian S	3.4	3.4	3.97E-21	SGD	634210	RPS28B
YOR302W	YOR302W		0.5	-2.01	1.07E-17	SGD	634212	YOR302W

YJL150W	YJL150W		3.13	3.13	2.45E-09	SGD	634215	YJL150W
YPL251W	YPL251W		0.33	-3.06	1.90E-05	SGD	634216	YPL251W
YDR070C	YDR070C		0.33	-3.03	8.76E-29	SGD	634217	YDR070C
YAR029W	YAR029W	membrane protein	0.22	-4.59	0	SGD	634219	YAR029W
YOR167C	RPS28A,RPS33A	Homology to mammalian S	3.52	3.52	0	SGD	634220	RPS28A
YIL140W	AXL2,BUD10,SRO4	involved in polarity establis	2.31	2.31	1.91E-18	SGD	634224	AXL2
YMR309C	NIP1	Protein required for nuclea	2.9	2.9	7.58E-11	SGD	634226	NIP1
YER146W	LSM5	Like Sm-E protein; snRNP	2.07	2.07	1.02E-07	SGD	634233	LSM5
YLR263W	RED1	Required for full chr. pairin	0.48	-2.1	5.51E-04	SGD	634240	RED1
YNR022C	YNR022C		2.25	2.25	9.92E-40	SGD	634254	YNR022C
YOL039W	RPP2A,RPL44,RPLA2	Homology to rat P2, humar	4.83	4.83	1.03E-25	SGD	634285	RPP2A
YDL081C	RPP1A,RPLA1	Homology to rat P1, humar	2.32	2.32	2.54E-04	SGD	634300	RPP1A
YOL048C	YOL048C		0.35	-2.85	3.22E-07	SGD	634301	YOL048C
YIL008W	URM1	ubiquitin-like protein; Null r	2.66	2.66	4.99E-09	SGD	634314	URM1
YLL053C	YLL053C		0.45	-2.2	1.39E-12	SGD	634334	YLL053C
YNL105W	YNL105W		0.3	-3.36	3.71E-13	SGD	634345	YNL105W
YBL003C	HTA2,H2A2	Histone H2A (HTA1 and H	0.49	-2.04	5.52E-10	SGD	634354	HTA2
YNL226W	YNL226W		0.31	-3.25	7.39E-08	SGD	634367	YNL226W
YOL012C	HTZ1,HTA3	Histone-related protein tha	2.01	2.01	1.41E-13	SGD	634368	HTZ1
YBR035C	PDX3	pyridoxine (pyridoxiamine)	0.23	-4.31	3.87E-11	SGD	634379	PDX3
YPR043W	RPL43A	Homology to human L37a;	3.31	3.31	2.70E-22	SGD	634380	RPL43A
YJL097W	YJL097W		2.5	2.5	2.77E-14	SGD	634387	YJL097W
YOR247W	SRL1	Suppressor of Rad53 null l	4.6	4.6	0	SGD	634394	SRL1
YEL054C	RPL12A	Homology to rat L12(a) anc	3.83	3.83	2.40E-39	SGD	634397	RPL12A
YIL057C	YIL057C		2.03	2.03	3.62E-08	SGD	634398	YIL057C
YER067W	YER067W		0.31	-3.2	1.09E-11	SGD	634400	YER067W
YIL087C	YIL087C		0.37	-2.72	0	SGD	634403	YIL087C
YGR148C	RPL24B,RPL30B	Homology to rat L24; ribos	3.84	3.84	1.78E-07	SGD	634405	RPL24B
YLR167W	RPS31,RPS37,UBI3	Homology to rat S27a; ribo	3.35	3.35	9.90E-32	SGD	634409	RPS31
YHL042W	YHL042W		0.4	-2.51	2.01E-05	SGD	634410	YHL042W
YGL196W	YGL196W		0.4	-2.47	1.98E-10	SGD	634414	YGL196W
YHR180W	YHR180W		0.5	-2.01	8.87E-07	SGD	634415	YHR180W
YNL044W	YIP3	Interacts with YPT proteins	3.85	3.85	9.63E-18	SGD	634419	YIP3
YOL038W	PRE6	alpha-type of subunit of 20	2.36	2.36	1.71E-08	SGD	634435	PRE6
YMR271C	URA10	Fifth step in pyrimidine bio	0.31	-3.2	1.49E-07	SGD	634464	URA10
YDL169C	UGX2	Product of gene unknown	0.4	-2.49	5.59E-11	SGD	634467	UGX2
YNL006W	LST8	Required for amino acid pe	0.45	-2.2	1.26E-04	SGD	634472	LST8

YLR128W	YLR128W		0.39	-2.6	1.04E-08	SGD	634473	YLR128W
YER055C	HIS1	involved in the first step of	0.24	-4.22	2.51E-29	SGD	634476	HIS1
YHR029C	YHR029C	Thymidylate synthase (puta	0.1	-10.14	5.88E-16	SGD	634479	YHR029C
YHR199C	YHR199C		0.35	-2.84	5.41E-22	SGD	634481	YHR199C
YOR074C	CDC21,CRT9,TMP1	cell division cycle blocked a	4.81	4.81	0	SGD	634487	CDC21
YOR228C	YOR228C		0.31	-3.2	3.14E-12	SGD	634488	YOR228C
YPL131W	RPL5,LPI14,RPL1	Homology to rat ribosomal	4.95	4.95	7.29E-25	SGD	634492	RPL5
YPR167C	MET16	3'phosphoadenylylsulfate r	0.25	-3.95	0	SGD	634497	MET16
YAR015W	ADE1	phosphoribosyl amino imid	0.17	-5.96	0	SGD	634502	ADE1
YER188W	YER188W		0.46	-2.17	1.92E-29	SGD	634505	YER188W
YBR256C	RIB5	Riboflavin biosynthesis; Nu	0.18	-5.53	2.93E-12	SGD	634506	RIB5
YIL152W	YIL152W		0.36	-2.79	2.39E-05	SGD	634509	YIL152W
YLR441C	RPS1A,RP10A	Homologous to rat S3A; rib	3.18	3.18	2.29E-06	SGD	634517	RPS1A
YDL014W	NOP1	nucleolar protein, homolog	2.63	2.63	1.89E-19	SGD	634527	NOP1
YOR100C	CRC1	carnitine carrier; carnitine t	0.37	-2.7	1.84E-08	SGD	634528	CRC1
YHR143W	DSE2	Hypothetical ORF	0.44	-2.3	1.48E-31	SGD	634529	DSE2
YKR080W	MTD1	NAD-dependent 5,10-meth	0.12	-8.16	5.56E-23	SGD	634533	MTD1
YDL218W	YDL218W		0.27	-3.73	3.00E-07	SGD	634535	YDL218W
YBL103C	RTG3	bHLH/Zip transcription fact	0.35	-2.89	7.51E-08	SGD	634536	RTG3
YOR120W	GCY1	Galactose-induced transcri	0.34	-2.97	2.35E-10	SGD	634541	GCY1
YPL173W	MRPL40	Mitochondrial ribosomal pr	2.12	2.12	1.89E-09	SGD	634554	MRPL40
YFL054C	YFL054C		0.44	-2.25	4.65E-08	SGD	634567	YFL054C
YBR043C	YBR043C		0.31	-3.24	0	SGD	634585	YBR043C
YLR403W	SFP1	Inhibits nuclear protein loca	0.36	-2.77	7.07E-09	SGD	634588	SFP1
YDR508C	GNP1	high-affinity glutamine perm	2.6	2.6	4.07E-08	SGD	634593	GNP1
YLR045C	STU2	May play a role in attachme	2.07	2.07	5.74E-04	SGD	634598	STU2
YKR089C	YKR089C		0.47	-2.12	6.85E-18	SGD	634610	YKR089C
YJR036C	HUL4	ubiquitin-protein ligase (E3	0.49	-2.04	3.52E-09	SGD	634613	HUL4
YOR133W	EFT1	translation elongation facto	2.59	2.59	1.51E-05	SGD	634622	EFT1
YML042W	CAT2	Carnitine O-acetyltransfera	0.26	-3.82	8.85E-11	SGD	634632	CAT2
YOL090W	MSH2,PMS5	Functions with Pms1p and	2.14	2.14	1.32E-12	SGD	634643	MSH2
YMR125W	STO1,CBC1,CBP80,GCR	Large subunit of the nuclea	2.5	2.5	2.29E-12	SGD	634657	STO1
YMR189W	GCV2,GSD2	Glycine CleaVage system;	0.11	-8.8	0	SGD	634671	GCV2
YAL035W	FUN12,yIF2	Function unknown now; 97	2.2	2.2	5.66E-10	SGD	634674	FUN12
YEL055C	POL5	DNA polymerase V that ha	2.06	2.06	2.40E-05	SGD	634688	POL5
YMR019W	STB4	binds Sin3p in two-hybrid a	0.35	-2.88	3.23E-08	SGD	634694	STB4
YJL084C	YJL084C		0.45	-2.2	8.38E-05	SGD	634701	YJL084C

YDR001C	NTH1	hydrolyzes trehalose, may	0.41	-2.47	1.26E-06	SGD	634711	NTH1
YLL051C	FRE6	similar to FRE2	0.44	-2.28	7.23E-06	SGD	634720	FRE6
YMR246W	FAA4	acyl-CoA synthetase (long-	2.67	2.67	5.09E-07	SGD	634725	FAA4
YJL073W	JEM1	DnaJ-like protein of the en	5.97	5.97	7.10E-11	SGD	634726	JEM1
YHR096C	HXT5	Member of superfamily of r	0.14	-7.28	8.32E-31	SGD	634730	HXT5
YJR016C	ILV3	catalyzes third step in com	0.22	-4.6	9.71E-15	SGD	634734	ILV3
YLR152C	YLR152C		0.15	-6.58	1.37E-14	SGD	634738	YLR152C
YJL071W	ARG2,HRB574	First step in ornithine biosy	0.42	-2.36	1.39E-05	SGD	634739	ARG2
YOR128C	ADE2	phosphoribosylamino-imida	0.11	-8.78	2.23E-24	SGD	634741	ADE2
YDR536W	STL1	sugar transporter-like prote	0.46	-2.17	1.13E-06	SGD	634742	STL1
YGL234W	ADE5,7	glycinamide ribotide synthe	0.38	-2.62	1.02E-11	SGD	634747	ADE5,7
YBR001C	NTH2	hydrolyzes trehalose, may	0.3	-3.34	5.88E-12	SGD	634751	NTH2
YER001W	MNN1	Alpha-1,3-mannosyltransfe	2.45	2.45	4.48E-06	SGD	634755	MNN1
YAL023C	PMT2,FUN25	Transfers mannosyl residu	6.8	6.8	2.02E-33	SGD	634756	PMT2
YPL074W	YTA6	Member of CDC48/PAS1/S	0.41	-2.45	1.42E-07	SGD	634758	YTA6
YHL016C	DUR3	Urea active transport prote	0.46	-2.18	8.36E-04	SGD	634762	DUR3
YCR091W	KIN82	Putative serine/threonine p	0.46	-2.18	2.45E-06	SGD	634764	KIN82
YKR098C	UBP11	Ubiquitin-specific protease	0.36	-2.79	3.57E-05	SGD	634766	UBP11
YEL011W	GLC3,GHA1	Glycogen branching enzym	0.35	-2.88	8.89E-38	SGD	634770	GLC3
YLR149C	YLR149C		0.36	-2.81	5.52E-08	SGD	634779	YLR149C
YPL153C	RAD53,LSD1,MEC2,SPK	Required for DNA damage	2.76	2.76	8.48E-24	SGD	634782	RAD53
YMR089C	YTA12,RCA1	Mitochondrial ATPase (sim	2.6	2.6	2.11E-17	SGD	634793	YTA12
YMR049C	ERB1	Eukaryotic Ribosome Biog	2.13	2.13	2.21E-04	SGD	634797	ERB1
YOR195W	SLK19	synthetic lethal KAR3; leuc	2.11	2.11	4.93E-04	SGD	634809	SLK19
YDL095W	PMT1	Transfers mannose residue	3.92	3.92	3.65E-06	SGD	634810	PMT1
YKR099W	BAS1	Transcription factor regulat	0.26	-3.78	0	SGD	634811	BAS1
YDR225W	HTA1,H2A1,SPT11	Histone H2A (HTA1 and H	0.36	-2.81	2.96E-04	SGD	634827	HTA1
YGR039W	YGR039W		2.62	2.62	1.28E-20	SGD	634841	YGR039W
YLR333C	RPS25B	Homology to rat S25, belor	2.97	2.97	1.03E-15	SGD	634848	RPS25B
YBR190W	YBR190W		3.03	3.03	1.80E-09	SGD	634856	YBR190W
YNL300W	TOS6	Hypothetical ORF	2.77	2.77	4.18E-06	SGD	634860	TOS6
YGL193C	YGL193C		0.4	-2.47	3.39E-09	SGD	634873	YGL193C
YGR008C	STF2	ATPase stabilizing factor	2.11	2.11	8.16E-15	SGD	634883	STF2
YOR044W	YOR044W		0.31	-3.18	7.65E-12	SGD	634899	YOR044W
YMR225C	MRPL44,YMR44	Mitochondrial ribosomal pr	2.15	2.15	4.64E-05	SGD	634909	MRPL44
YOR041C	YOR041C		0.33	-3.05	3.11E-08	SGD	634913	YOR041C
YOR369C	RPS12	Homology to rat S12; ribos	2.45	2.45	1.01E-05	SGD	634929	RPS12

YOL040C	RPS15,RPS21	Homology to rat S15 and E	3.62	3.62	1.27E-36	SGD	634930	RPS15
YHR136C	SPL2	Suppressor of plc1-delta. I	0.35	-2.83	9.32E-06	SGD	634940	SPL2
YJL158C	CIS3,CCW11	cik1 suppressor; similar to	3.42	3.42	4.81E-28	SGD	634958	CIS3
YDR500C	RPL37B	Homology to rat L37; ribos	2.21	2.21	7.66E-07	SGD	634965	RPL37B
YPL220W	RPL1A,SSM1	Homology to rat L10a, eub	2.54	2.54	7.00E-18	SGD	634966	RPL1A
YLR349W	YLR349W		4.32	4.32	0	SGD	634973	YLR349W
YER030W	YER030W		2.19	2.19	7.00E-20	SGD	634979	YER030W
YMR158W	YMR158W		2.06	2.06	5.92E-04	SGD	634984	YMR158W
YFL057C	YFL057C		0.47	-2.11	1.73E-26	SGD	634986	YFL057C
YDR418W	RPL12B	Homology to rat L12(a) an	4.12	4.12	2.87E-06	SGD	634991	RPL12B
YPL282C	YPL282C		0.44	-2.27	4.46E-15	SGD	634992	YPL282C
YPL127C	HHO1	Histone H1; histone H1; Nu	2.7	2.7	2.46E-14	SGD	635019	HHO1
YNL314W	DAL82	Positive regulator of alloph	0.47	-2.12	6.99E-15	SGD	635021	DAL82
YLR186W	EMG1	Essential for Mitotic Growt	2.01	2.01	1.57E-06	SGD	635023	EMG1
YHR140W	YHR140W		0.39	-2.57	1.04E-07	SGD	635025	YHR140W
YHR071W	PCL5	PHO85 cyclin; Null mutant	0.2	-4.97	1.60E-33	SGD	635034	PCL5
YML106W	URA5,PYR5	Fifth step in pyrimidine bio	2.07	2.07	7.49E-22	SGD	635035	URA5
YMR095C	SNO1	SNZ1 proximal ORF, static	0.03	-37.68	0	SGD	635037	SNO1
YNL194C	YNL194C		0.42	-2.37	5.41E-31	SGD	635062	YNL194C
YGR044C	RME1,CSP1	mediates cell type control	0.46	-2.16	3.79E-20	SGD	635063	RME1
YLR348C	DIC1	mitochondrial dicarboxylate	0.34	-2.98	7.17E-06	SGD	635065	DIC1
YCL009C	ILV6	acetolactate synthase regu	0.29	-3.41	1.38E-06	SGD	635071	ILV6
YOR222W	ODC2	mitochondrial 2-oxodicarb	0.25	-3.95	2.64E-20	SGD	635074	ODC2
YBR088C	POL30	Accessory factor for DNA	4.12	4.12	7.47E-14	SGD	635087	POL30
YDL075W	RPL31A,RPL34	Homology to rat L31; ribos	3.95	3.95	1.68E-14	SGD	635091	RPL31A
YLL060C	GTT2	Glutathione Transferase; g	0.41	-2.43	1.28E-04	SGD	635099	GTT2
YGL123W	RPS2,RPS4,SUP138,SU	Homology to rat S2 and E.	2.87	2.87	3.33E-07	SGD	635106	RPS2
YHR141C	RPL42B	Homology to rat L36a and	2.82	2.82	1.41E-25	SGD	635107	RPL42B
YLR126C	YLR126C		2.8	2.8	2.94E-18	SGD	635108	YLR126C
YML073C	RPL6A,YL16A	Homology to rat L6 and hu	4.62	4.62	1.77E-13	SGD	635135	RPL6A
YOR292C	YOR292C		0.47	-2.13	3.62E-08	SGD	635142	YOR292C
YER053C	YER053C		0.4	-2.47	2.11E-10	SGD	635148	YER053C
YBR291C	CTP1	citrate transport protein; cit	0.46	-2.17	2.65E-06	SGD	635149	CTP1
YLL056C	YLL056C		0.34	-2.94	4.15E-13	SGD	635150	YLL056C
YMR096W	SNZ1	Snooze: stationary phase-i	0.05	-20.75	5.49E-33	SGD	635151	SNZ1
YEL046C	GLY1	Threonine Aldolase; threor	0.28	-3.58	5.78E-08	SGD	635168	GLY1
YML008C	ERG6,ISE1,LIS1,SED6	ergosterol synthesis; The r	2.23	2.23	2.65E-16	SGD	635171	ERG6

YDR354W	TRP4	anthranilate phosphoribosy	0.28	-3.61	4.69E-09	SGD	635173	TRP4
YLR181C	YLR181C		2.24	2.24	1.78E-35	SGD	635178	YLR181C
YBL030C	PET9,AAC2,ANC2,OP1	the major mitochondrial AD	2.1	2.1	3.07E-05	SGD	635187	PET9
YBL027W	RPL19B	Homology to rat L19; ribos	2.66	2.66	5.64E-06	SGD	635188	RPL19B
YLR380W	CSR1	chs5 spa2 rescue, isolated	2.63	2.63	3.17E-14	SGD	635201	CSR1
YGR234W	YHB1,YHB4	may play a role in the oxida	2.44	2.44	4.27E-26	SGD	635207	YHB1
YLR312C	YLR312C		0.26	-3.78	5.05E-10	SGD	635208	YLR312C
YLR099C	ICT1	Increased Copper Toleranc	2.37	2.37	2.17E-04	SGD	635211	ICT1
YGL126W	SCS3	Required for inositol protot	3.55	3.55	0	SGD	635220	SCS3
YJL026W	RNR2,CRT6	small subunit of ribonucleo	2.3	2.3	1.64E-12	SGD	635223	RNR2
YOR063W	RPL3,MAK8,TCM1	Homology to rat L3; riboso	3.34	3.34	8.58E-23	SGD	635231	RPL3
YML027W	YOX1	Homeodomain protein that	2.68	2.68	1.62E-09	SGD	635232	YOX1
YNR074C	YNR074C		0.35	-2.85	2.22E-37	SGD	635237	YNR074C
YJR148W	BAT2,TWT2	Branched-Chain Amino Ac	0.37	-2.72	3.39E-07	SGD	635238	BAT2
YDR218C	SPR28	Septin-related protein expr	2.14	2.14	1.67E-06	SGD	635247	SPR28
YDL054C	MCH1	Monocarboxylate Permeas	0.09	-11.38	4.00E-19	SGD	635274	MCH1
YMR214W	SCJ1	dnaJ homolog; DnaJ homo	5.36	5.36	4.37E-12	SGD	635275	SCJ1
YHR123W	EPT1	sn-1,2-diacylglycerol ethan	2.69	2.69	2.52E-20	SGD	635281	EPT1
YOL119C	MCH4	monocarboxylate permeas	0.13	-7.58	4.58E-22	SGD	635284	MCH4
YNL022C	YNL022C		0.49	-2.03	3.50E-07	SGD	635290	YNL022C
YLR175W	CBF5	major low affinity 55 kDa C	2.35	2.35	3.10E-07	SGD	635294	CBF5
YNR073C	YNR073C		0.35	-2.83	3.05E-09	SGD	635299	YNR073C
YLR183C	TOS4	Hypothetical ORF	2.54	2.54	8.47E-08	SGD	635306	TOS4
YGL202W	ARO8	aromatic amino acid amino	0.29	-3.43	1.85E-08	SGD	635316	ARO8
YJR054W	YJR054W		2.45	2.45	6.82E-13	SGD	635317	YJR054W
YHR048W	YHR048W		0.41	-2.45	1.20E-04	SGD	635327	YHR048W
YBR103W	SIF2,EMB1	Sir4p-Interacting Factor; N	0.49	-2.03	9.48E-22	SGD	635332	SIF2
YLL055W	YLL055W		0.18	-5.43	0	SGD	635334	YLL055W
YDL170W	UGA3	Transcriptional activator ne	0.17	-5.91	0	SGD	635335	UGA3
YBR250W	YBR250W		0.35	-2.82	7.67E-20	SGD	635338	YBR250W
YER073W	ALD5	Utilizes NADP+ as the pref	0.26	-3.8	2.94E-16	SGD	635340	ALD5
YCL027W	FUS1	cell-surface protein require	0.41	-2.46	1.61E-07	SGD	635344	FUS1
YPL272C	YPL272C		0.39	-2.59	1.67E-10	SGD	635357	YPL272C
YHR137W	ARO9	aromatic amino acid amino	0.1	-10.12	1.21E-16	SGD	635359	ARO9
YGL055W	OLE1,MDM2	delta-9-fatty acid desaturas	3.88	3.88	7.49E-23	SGD	635361	OLE1
YLR432W	IMD3	IMP dehydrogenase homol	3.12	3.12	9.90E-24	SGD	635365	IMD3
YIL056W	YIL056W		0.35	-2.82	3.09E-05	SGD	635372	YIL056W

YDL025C	YDL025C		0.27	-3.65	0	SGD	635373	YDL025C
YKR056W	RNC1,NUC2,NUD1,TRM	tRNA methyltransferase	0.39	-2.56	2.31E-31	SGD	635374	RNC1
YKR019C	IRS4	Increased rDNA silencing;	0.41	-2.42	2.80E-09	SGD	635375	IRS4
YKL212W	SAC1,RSD1	integral membrane protein	2.89	2.89	3.34E-08	SGD	635381	SAC1
YCR023C	YCR023C	Membrane transporter	0.34	-2.92	0	SGD	635392	YCR023C
YGR191W	HIP1	histidine permease; require	0.42	-2.4	1.48E-32	SGD	635396	HIP1
YJL014W	CCT3,BIN2,TCP3	Homolog of mammalian C(	2.14	2.14	8.07E-18	SGD	635398	CCT3
YIL146C	ECM37	ExtraCellular Mutant; A Tn	0.46	-2.16	2.49E-06	SGD	635400	ECM37
YJL034W	KAR2,BIP,GRP78	Involved in translocation of	2.64	2.64	1.37E-07	SGD	635412	KAR2
YKL029C	MAE1	Mitochondrial malic enzym	0.23	-4.32	1.68E-09	SGD	635415	MAE1
YBR121C	GRS1	Glycyl-tRNA synthase; glyc	2.19	2.19	1.76E-13	SGD	635416	GRS1
YBL075C	SSA3,HSP70	heat-inducible cytosolic me	0.16	-6.38	7.09E-14	SGD	635421	SSA3
YER103W	SSA4	member of 70 kDa heat sh	0.27	-3.68	1.13E-27	SGD	635424	SSA4
YJR130C	STR2	Sulfur TRansfer; cystathior	0.27	-3.75	1.07E-13	SGD	635432	STR2
YNL104C	LEU4	leucine biosynthesis; alpha	0.22	-4.58	2.86E-26	SGD	635434	LEU4
YNL209W	SSB2	stress-seventy subfamily B	3.57	3.57	1.16E-04	SGD	635436	SSB2
YOL158C	ENB1,ARN4	Siderophore transporter fo	0.26	-3.82	6.92E-14	SGD	635439	ENB1
YPL141C	YPL141C		2.13	2.13	4.02E-08	SGD	635446	YPL141C
YPL019C	VTC3,PHM2	Phosphate metabolism, tra	2.3	2.3	3.07E-09	SGD	635452	VTC3
YMR108W	ILV2,SMR1	acetolactate synthase; Isol	0.2	-4.96	1.56E-31	SGD	635456	ILV2
YHL029C	YHL029C		0.48	-2.09	4.17E-10	SGD	635458	YHL029C
YNL115C	YNL115C		0.43	-2.34	6.03E-43	SGD	635469	YNL115C
YAR035W	YAT1	Outer carnitine acetyltrans	0.19	-5.19	1.79E-16	SGD	635471	YAT1
YNL103W	MET4	member of the leucine zipp	0.46	-2.17	6.03E-08	SGD	635476	MET4
YKR036C	CAF4	CCR4 associated factor; C	0.49	-2.04	8.56E-06	SGD	635481	CAF4
YLR382C	NAM2	mitochondrial leucyl tRNA	2.24	2.24	1.17E-09	SGD	635484	NAM2
YJL078C	PRY3	Pathogen Related in Sc, c	0.24	-4.11	2.81E-10	SGD	635486	PRY3
YHR047C	AAP1'	arginine/alanine aminopep	0.31	-3.2	4.49E-11	SGD	635491	AAP1'
YBR294W	SUL1	Putative sulfate permease;	0.18	-5.65	0	SGD	635506	SUL1
YER047C	SAP1	interacts with Sin1p; AAA	0.46	-2.19	3.35E-08	SGD	635515	SAP1
YCL014W	BUD3	cell cycle regulated protein	2.02	2.02	3.11E-18	SGD	635522	BUD3
YLR249W	YEF3,TEF3	contains two ABC cassette	2.46	2.46	5.27E-09	SGD	635533	YEF3
YDR421W	ARO80		0.35	-2.87	9.50E-17	SGD	635542	ARO80
YKL165C	MCD4,ZRG16	Required for GPI anchor s	10.01	10.01	0	SGD	635547	MCD4
YPL110C	YPL110C		2.01	2.01	5.72E-06	SGD	635554	YPL110C
YBR218C	PYC2	converts pyruvate to oxalo	0.25	-3.93	5.00E-24	SGD	635556	PYC2
YIL026C	IRR1,SCC3	Irregular, involved in sister	2.89	2.89	5.99E-13	SGD	635558	IRR1

YER024W	YAT2	The Yat2p protein shows s	0.12	-8.11	3.42E-26	SGD	635574	YAT2
YPR135W	CTF4,CHL15,POB1	May function in DNA synth	2.38	2.38	3.34E-06	SGD	635575	CTF4
YGL137W	SEC27	Involved in endoplasmic-to	2.23	2.23	7.97E-06	SGD	635578	SEC27
YAR019C	CDC15,LYT1	Required for mitosis and sp	0.46	-2.16	2.48E-09	SGD	635581	CDC15
YGR098C	ESP1	Esp1 promotes sister chron	3.08	3.08	8.78E-05	SGD	635584	ESP1
YMR012W	CLU1,TIF31	CLU1 is similar to the Dicty	2.51	2.51	1.27E-06	SGD	635587	CLU1
YJL080C	SCP160	May be required during cel	6.63	6.63	0	SGD	635590	SCP160
YMR076C	PDS5	Precocious Dissociation of	4.79	4.79	1.20E-36	SGD	635603	PDS5
YEL031W	SPF1,COD1	Sensitivity to a killer toxin (	2.67	2.67	1.08E-04	SGD	635606	SPF1
YJL092W	HPR5,RADH,RADH1,SRS	Required for proper timing	3.14	3.14	3.54E-10	SGD	635608	HPR5
YDR507C	GIN4,ERC47	Growth inhibitory gene; ser	2.44	2.44	1.37E-29	SGD	635610	GIN4
YNR067C	DSE4	Hypothetical ORF	0.37	-2.74	6.69E-09	SGD	635612	DSE4
YBL063W	KIP1,CIN9	Mitotic spindle assembly; k	2.58	2.58	5.99E-06	SGD	635613	KIP1
YDR127W	ARO1	pentafunctional arom polyp	0.28	-3.54	3.01E-13	SGD	635618	ARO1
YOR153W	PDR5,LEM1,YDR1	multidrug resistance transp	2.08	2.08	1.34E-14	SGD	635620	PDR5
YDL171C	GLT1	Glutamate synthase (NADH	0.48	-2.08	9.74E-07	SGD	635628	GLT1
YGL195W	GCN1	translational activator of G(	3.88	3.88	7.38E-09	SGD	635642	GCN1
YNR016C	ACC1,ABP2,FAS3	acetyl-CoA carboxylase; ac	5.17	5.17	1.32E-15	SGD	635643	ACC1
YBL065W	YBL065W		0.43	-2.33	2.81E-04	SGD	635667	YBL065W
YMR103C	YMR103C		0.32	-3.1	5.91E-07	SGD	635675	YMR103C
YIL165C	YIL165C		0.13	-7.55	6.10E-23	SGD	635676	YIL165C
YBR115C	LYS2	alpha aminoadipate reduct	0.21	-4.81	0	SGD	635696	LYS2
YHL030W	ECM29	ExtraCellular Mutant; A Tn	3.3	3.3	0	SGD	635702	ECM29
YJR115W	YJR115W		0.48	-2.1	8.28E-06	SGD	635706	YJR115W
YLR297W	YLR297W		0.43	-2.34	6.27E-15	SGD	635711	YLR297W
YMR195W	ICY1	Interacting with the cytoske	0.3	-3.3	4.74E-35	SGD	635714	ICY1
YGL015C	YGL015C		0.48	-2.06	1.19E-08	SGD	635725	YGL015C
YMR193C-	YMR193C-A		2.17	2.17	2.35E-37	SGD	635728	YMR193C-A
YOR309C	YOR309C		2.13	2.13	2.64E-04	SGD	635731	YOR309C
YDL208W	NHP2	HMG-like nuclear protein; I	2.02	2.02	6.79E-05	SGD	635753	NHP2
YJL152W	YJL152W		3.04	3.04	8.87E-17	SGD	635759	YJL152W
YIR017C	MET28	Transcriptional activator of	0.33	-3.02	8.98E-11	SGD	635778	MET28
YGL030W	RPL30	Homology to rat and mous	3.53	3.53	0	SGD	635782	RPL30
YJL136C	RPS21B	Homology to rat S21; ribos	3.68	3.68	0	SGD	635808	RPS21B
YPL229W	YPL229W		0.41	-2.46	5.26E-05	SGD	635812	YPL229W
YLR029C	RPL15A,RPL10A	Homology to rat L15; ribos	3.22	3.22	2.98E-41	SGD	635813	RPL15A
YJL217W	YJL217W		0.34	-2.97	9.77E-34	SGD	635819	YJL217W

YDR453C	YDR453C		0.35	-2.87	1.24E-08	SGD	635821	YDR453C
YIL113W	YIL113W		0.28	-3.63	0	SGD	635825	YIL113W
YGL258W	YGL258W		5.58	5.58	1.89E-20	SGD	635827	YGL258W
YHR089C	GAR1	small nucleolar RNP protei	2.31	2.31	5.60E-04	SGD	635828	GAR1
YJR118C	ILM1	Product of gene unknown	2.77	2.77	1.07E-06	SGD	635830	ILM1
YJR014W	YJR014W		2.47	2.47	3.19E-16	SGD	635835	YJR014W
YOR387C	YOR387C		5.34	5.34	4.22E-25	SGD	635843	YOR387C
YKR057W	RPS21A,RPS25	Homology to rat S21; ribos	3.03	3.03	2.24E-18	SGD	635855	RPS21A
YJL191W	RPS14B,CRY2	Homology to human S14 a	2.79	2.79	3.23E-13	SGD	635860	RPS14B
YNR068C	YNR068C		0.06	-17	7.81E-15	SGD	635862	YNR068C
YJR144W	MGM101,MGM9	Involved in mitochondrial g	2.53	2.53	7.98E-09	SGD	635864	MGM101
YGL117W	YGL117W		0.03	-33.28	4.29E-38	SGD	635867	YGL117W
YLR061W	RPL22A	Homology to rat L22; ribos	4.15	4.15	9.04E-13	SGD	635868	RPL22A
YLL027W	ISA1	Iron Sulfur Assembly -- Isc	0.23	-4.44	7.17E-29	SGD	635869	ISA1
YOR213C	SAS5	Involved in silencing at telo	0.44	-2.27	4.44E-08	SGD	635870	SAS5
YIL070C	MAM33	33-kDa mitochondrial acidi	3.05	3.05	1.02E-06	SGD	635882	MAM33
YDR471W	RPL27B	Homology to mammalian L	3.09	3.09	5.11E-14	SGD	635883	RPL27B
YOR293W	RPS10A	Homology to rat S10; ribos	3.23	3.23	0	SGD	635884	RPS10A
YDR447C	RPS17B,RP51B,RPL51B	Homology to rat ribosomal	3.61	3.61	1.66E-12	SGD	635891	RPS17B
YLR091W	YLR091W		0.48	-2.08	7.04E-09	SGD	635910	YLR091W
YDL129W	YDL129W		0.46	-2.2	3.63E-21	SGD	635911	YDL129W
YLR367W	RPS22B	Homology to rat S15a; ribo	4.15	4.15	0	SGD	635912	RPS22B
YIL052C	RPL34B	Homology to rat L34; ribos	3.29	3.29	1.98E-23	SGD	635922	RPL34B
YJL177W	RPL17B	Homology to rat L17, huma	4.1	4.1	3.75E-08	SGD	635929	RPL17B
YPL143W	RPL33A	Homology to rat L35a; ribo	3.54	3.54	8.64E-11	SGD	635935	RPL33A
YPR116W	YPR116W		2.15	2.15	2.09E-11	SGD	635940	YPR116W
YIL082W	YIL082W		2.22	2.22	2.91E-12	SGD	635945	YIL082W
YLR100W	ERG27	3-keto sterol reductase	2.66	2.66	7.61E-13	SGD	635966	ERG27
YFR055W	YFR055W		0.45	-2.22	2.18E-06	SGD	635972	YFR055W
YBR076W	ECM8	ExtraCellular Mutant; A Tn	0.34	-2.94	1.88E-06	SGD	635973	ECM8
YMR081C	ISF1,MBR3	May regulate NAM7 functio	0.46	-2.19	1.91E-08	SGD	635974	ISF1
YPL264C	YPL264C		0.28	-3.64	0	SGD	635978	YPL264C
YBL091C	MAP2	methionine aminopeptidas	2.06	2.06	2.13E-22	SGD	635980	MAP2
YNL069C	RPL16B,RP23	Homology to rat ribosomal	2.62	2.62	4.38E-14	SGD	635981	RPL16B
YBR145W	ADH5	alcohol dehydrogenase iso	0.13	-7.81	1.85E-14	SGD	635994	ADH5
YDR214W	YDR214W		0.29	-3.43	7.24E-07	SGD	635995	YDR214W
YOL007C	CSI2	chitin synthase involved; cl	2.07	2.07	2.54E-27	SGD	636004	CSI2

YIR034C	LYS1	saccharopine dehydrogena	0.14	-7.13	2.55E-14	SGD	636005	LYS1
YPL081W	RPS9A	Homology to rat S9 and E.	5.25	5.25	9.73E-11	SGD	636012	RPS9A
YBR084C-	RPL19A	Homology to rat L19; ribos	2.58	2.58	1.36E-05	SGD	636016	RPL19A
YDR035W	ARO3	DAHP synthase, a.k.a. pho	0.28	-3.57	1.37E-09	SGD	636022	ARO3
YDR012W	RPL4B	Highly similar to ribosomal	2.22	2.22	4.32E-09	SGD	636029	RPL4B
YMR079W	SEC14,PIT1	Required for vesicle buddir	2.56	2.56	3.72E-07	SGD	636033	SEC14
YNR032W	PPG1	Serine/threonine protein ph	0.49	-2.06	1.99E-06	SGD	636040	PPG1
YDR158W	HOM2	threonine and methionine p	0.37	-2.71	1.08E-43	SGD	636042	HOM2
YDR277C	MTH1,BPC1,DGT1,HTR1	Negative regulator of HXT	0.41	-2.44	7.10E-04	SGD	636046	MTH1
YOR264W	DSE3	Hypothetical ORF	0.42	-2.39	1.19E-21	SGD	636080	DSE3
YDL066W	IDP1	Mitochondrial form of NAD	0.36	-2.8	4.50E-10	SGD	636081	IDP1
YPR163C	TIF3,RBL3,STM1	Suppressor of translation n	2.32	2.32	4.19E-05	SGD	636083	TIF3
YPR196W	MAL63	zinc-finger transcription fac	0.49	-2.05	9.02E-10	SGD	636085	MAL63
YDR223W	YDR223W		0.44	-2.26	3.52E-25	SGD	636086	YDR223W
YCL037C	SRO9	Associates with translating	2.88	2.88	7.90E-06	SGD	636087	SRO9
YHR018C	ARG4	argininosuccinate lyase; Ar	0.09	-11.75	2.71E-32	SGD	636089	ARG4
YJL002C	OST1,NLT1	Oligosaccharyltransferase	2.03	2.03	2.14E-05	SGD	636097	OST1
YDL024C	DIA3	involved in invasive and ps	0.26	-3.78	8.90E-11	SGD	636101	DIA3
YEL040W	UTR2,CRH2	Product of gene unknown	2.67	2.67	1.80E-09	SGD	636102	UTR2
YHL021C	YHL021C		0.39	-2.55	4.59E-07	SGD	636103	YHL021C
YGR288W	MAL13	Part of complex locus MAL	0.33	-3.06	2.23E-06	SGD	636116	MAL13
YDL085W	YDL085W		0.43	-2.33	1.27E-12	SGD	636128	YDL085W
YGL076C	RPL7A	Homology to rat L7 and E.	3.53	3.53	1.18E-08	SGD	636139	RPL7A
YPL095C	YPL095C		0.28	-3.61	5.69E-12	SGD	636162	YPL095C
YPR125W	YPR125W		2.26	2.26	8.63E-12	SGD	636163	YPR125W
YGL186C	YGL186C		0.21	-4.8	0	SGD	636168	YGL186C
YDR463W	STP1,BAP1,SSY2	Involved in pre-tRNA splici	0.35	-2.82	2.33E-09	SGD	636169	STP1
YGR055W	MUP1	high affinity methionine per	9.21	9.21	1.06E-25	SGD	636171	MUP1
YML127W	RSC9	Remodels the Structure of	2.09	2.09	2.18E-10	SGD	636183	RSC9
YHR150W	YHR150W		0.48	-2.09	6.38E-07	SGD	636184	YHR150W
YHR037W	PUT2	delta-1-pyrroline-5-carboxy	0.38	-2.62	0	SGD	636186	PUT2
YHR064C	SSZ1,PDR13	DnaK homolog, interacts w	2.36	2.36	8.74E-07	SGD	636188	SSZ1
YHR094C	HXT1,HOR4	High-affinity hexose (gluco	0.3	-3.32	8.98E-08	SGD	636189	HXT1
YLR286C	CTS1	Endochitinase; endochitina	0.43	-2.32	7.21E-06	SGD	636194	CTS1
YJL153C	INO1,APR1	involved in the rate limiting	20.15	20.15	0	SGD	636197	INO1
YKR017C	YKR017C		0.48	-2.09	3.34E-04	SGD	636200	YKR017C
YKR097W	PCK1,JPM2,PPC1	phosphoenolpyruvate carb	0.46	-2.15	5.58E-04	SGD	636201	PCK1

YBR270C	YBR270C	Probable ATP/GTP-binding	0.44	-2.29	7.29E-32	SGD	636203	YBR270C
YGR292W	MAL12	Part of the complex locus M	0.36	-2.8	1.34E-14	SGD	636205	MAL12
YJL163C	YJL163C		0.45	-2.23	9.49E-05	SGD	636214	YJL163C
YGR003W	YGR003W		0.42	-2.4	1.72E-08	SGD	636220	YGR003W
YKL054C	VID31	Vacuole import and degrac	2.1	2.1	1.76E-04	SGD	636221	VID31
YER040W	GLN3	Regulates glutamine-repre	0.33	-3.04	1.20E-29	SGD	636223	GLN3
YCL057W	PRD1	Saccharolysin (oligopeptida	2.44	2.44	5.16E-16	SGD	636227	PRD1
YLR424W	YLR424W		2.2	2.2	6.01E-17	SGD	636228	YLR424W
YBR255W	YBR255W		0.3	-3.35	2.94E-11	SGD	636232	YBR255W
YOR192C	YOR192C		0.43	-2.31	5.66E-05	SGD	636235	YOR192C
YKR069W	MET1,MET20	Methionine metabolism; Nu	0.49	-2.02	2.22E-09	SGD	636237	MET1
YKR039W	GAP1	general amino acid permea	2.33	2.33	1.74E-19	SGD	636250	GAP1
YLL028W	TPO1	Polyamine transport protein	0.34	-2.96	1.85E-05	SGD	636257	TPO1
YOR361C	PRT1,CDC63,DNA26	translation initiation factor e	3	3	2.05E-08	SGD	636264	PRT1
YLR219W	MSC3	Meiotic Sister-Chromatid re	0.47	-2.12	6.45E-05	SGD	636273	MSC3
YNR044W	AGA1	anchorage subunit of a-agg	0.45	-2.23	2.86E-04	SGD	636274	AGA1
YGL026C	TRP5	tryptophan synthetase; Nul	0.43	-2.32	1.39E-41	SGD	636278	TRP5
YER169W	RPH1	Regulator of PHR1; binds t	0.4	-2.49	0	SGD	636280	RPH1
YLR452C	SST2	Protein involved in desensi	0.35	-2.82	5.77E-23	SGD	636282	SST2
YKL104C	GFA1	catalyzes first step in hexos	2.14	2.14	4.04E-07	SGD	636292	GFA1
YOR337W	TEA1	Mutants are defective in Ty	0.32	-3.16	2.68E-06	SGD	636301	TEA1
YDR258C	HSP78	Similar to E. coli ClpB prote	0.36	-2.81	1.22E-23	SGD	636305	HSP78
YCL030C	HIS4	histidinol dehydrogenase; I	0.06	-16.33	3.15E-43	SGD	636308	HIS4
YJL200C	YJL200C		0.45	-2.25	3.14E-07	SGD	636310	YJL200C
YKL134C	1-Oct	mitochondrial protein impor	2	2	8.29E-23	SGD	636313	1-Oct
YGL120C	PRP43,JA1	Pre-mRNA processing fact	3.09	3.09	5.21E-16	SGD	636314	PRP43
YNL311C	YNL311C		0.3	-3.36	8.24E-28	SGD	636315	YNL311C
YLL020C	YLL020C		0.47	-2.12	2.10E-07	SGD	636347	YLL020C
YNL319W	YNL319W		2.49	2.49	4.32E-05	SGD	636378	YNL319W
YOR186W	YOR186W		0.11	-9.07	9.87E-23	SGD	636380	YOR186W
YPL250C	ICY2	Interacting with the cytoske	0.2	-5.04	1.06E-04	SGD	636403	ICY2
YKR049C	YKR049C		0.42	-2.4	8.86E-14	SGD	636405	YKR049C
YBL048W	YBL048W		0.49	-2.04	1.90E-04	SGD	636420	YBL048W
YGR027C	RPS25A,RPS31A	Homology to rat S25; ribos	3.51	3.51	2.97E-22	SGD	636443	RPS25A
YJR104C	SOD1,CRS4	Cu, Zn superoxide dismuta	0.05	-21.6	5.75E-39	SGD	636455	SOD1
YMR260C	TIF11	Translation initiation factor	2.91	2.91	2.11E-06	SGD	636456	TIF11
YGL259W	YPS5	Gpi-anchored aspartic prot	0.45	-2.22	1.05E-07	SGD	636462	YPS5

YMR040W	YMR040W		3.62	3.62	0	SGD	636466	YMR040W
YMR181C	YMR181C		0.48	-2.1	3.54E-30	SGD	636471	YMR181C
YBR173C	UMP1	Involved in ubiquitin-media	2.4	2.4	7.21E-27	SGD	636476	UMP1
YER187W	YER187W	similar to killer toxin	0.43	-2.31	3.10E-21	SGD	636485	YER187W
YDL123W	SNA4	Homology to PMP3/SNA1	0.35	-2.85	5.96E-19	SGD	636486	SNA4
YLR293C	GSP1,CNR1,CST17	maintenance of nuclear org	2.22	2.22	4.97E-08	SGD	636505	GSP1
YDR408C	ADE8	glycinamide ribotide transfo	0.49	-2.04	6.26E-04	SGD	636509	ADE8
YNR014W	YNR014W		0.41	-2.41	9.86E-08	SGD	636511	YNR014W
YOR232W	MGE1,YGE1	involved in protein import in	2.23	2.23	7.42E-21	SGD	636514	MGE1
YDR067C	YDR067C		0.43	-2.34	1.29E-18	SGD	636516	YDR067C
YBL102W	SFT2	similar to mammalian synta	0.49	-2.04	1.28E-25	SGD	636522	SFT2
YAL007C	ERP2	Emp24p/Erv25p related pro	5.29	5.29	8.15E-14	SGD	636524	ERP2
YML012W	ERV25	COPII coat component of c	2.46	2.46	1.03E-04	SGD	636528	ERV25
YDR533C	YDR533C		0.38	-2.66	8.72E-06	SGD	636557	YDR533C
YDR043C	NRG1	involved in regulation of glu	0.17	-5.82	1.82E-16	SGD	636562	NRG1
YML063W	RPS1B,PLC2,RP10B	Homologous to rat ribosom	4.15	4.15	1.29E-10	SGD	636567	RPS1B
YFL045C	SEC53,ALG4	involved in synthesis of GD	4.96	4.96	7.80E-19	SGD	636568	SEC53
YGR036C	CAX4,CWH8	CAX4p contains 3 short str	2.03	2.03	9.16E-04	SGD	636571	CAX4
YHR013C	ARD1	subunit of the major N alph	2.2	2.2	1.17E-04	SGD	636572	ARD1
YMR322C	YMR322C		0.36	-2.76	2.40E-09	SGD	636573	YMR322C
YLR406C	RPL31B	Homology to rat L31; ribos	5.03	5.03	9.21E-33	SGD	636580	RPL31B
YDR399W	HPT1,BRA6	enzyme involved in de nov	0.31	-3.27	4.91E-08	SGD	636585	HPT1
YBR066C	NRG2	homologue of NRG1; NRG	2.03	2.03	1.00E-04	SGD	636586	NRG2
YKR075C	YKR075C		0.34	-2.98	1.48E-15	SGD	636593	YKR075C
YPL186C	YPL186C		0.41	-2.43	3.95E-17	SGD	636596	YPL186C
YDL198C	YHM1	high copy suppressor of ab	0.15	-6.6	1.33E-14	SGD	636598	YHM1
YBL087C	RPL23A	Homology to E. coli L14 an	2.66	2.66	2.91E-05	SGD	636610	RPL23A
YBR147W	YBR147W		0.08	-11.92	6.52E-18	SGD	636617	YBR147W
YLL045C	RPL8B,KRB1,SCL41	Homology to human L7a, r	2.53	2.53	8.94E-06	SGD	636624	RPL8B
YGR247W	YGR247W		0.35	-2.84	8.10E-19	SGD	636629	YGR247W
YAR028W	YAR028W	membrane protein	0.32	-3.16	1.34E-07	SGD	636633	YAR028W
YJL148W	RPA34	RNA polymerase I subunit,	2.1	2.1	2.46E-06	SGD	636634	RPA34
YBR183W	YPC1	Yeast Phyto-ceramidase; a	0.33	-3.04	6.62E-22	SGD	636637	YPC1
YDR064W	RPS13,RPS13B,RPS13C	Homology to rat S13; ribos	3.27	3.27	1.49E-17	SGD	636641	RPS13
YDL243C	AAD4	high degree of similarity wi	0.46	-2.17	8.07E-21	SGD	636642	AAD4
YJR070C	YJR070C		2.48	2.48	0	SGD	636646	YJR070C
YLR340W	RPP0,RPL10E	Homology to rat P0, humar	3.82	3.82	0	SGD	636657	RPP0

YOR312C	RPL20B,RPL18A1	Homology to rat L18a; ribo	3.48	3.48	6.35E-05	SGD	636660	RPL20B
YPL079W	RPL21B	Homology to rat L21; ribos	3.59	3.59	2.02E-13	SGD	636667	RPL21B
YKL113C	RAD27,ERC11,RTH1	DNA repair protein that bel	2.86	2.86	4.24E-08	SGD	636686	RAD27
YOR271C	YOR271C		3.08	3.08	9.96E-08	SGD	636695	YOR271C
YHR195W	NVJ1,VAB36	Vac8p binding protein, nuc	0.45	-2.21	1.61E-10	SGD	636699	NVJ1
YKL216W	URA1	dihydroorotate dehydrogen	2.33	2.33	8.77E-13	SGD	636705	URA1
YCL061C	MRC1	Mediator of the Replication	2.17	2.17	1.78E-05	SGD	636708	MRC1
YHR104W	GRE3	Induced by osmotic stress,	0.44	-2.26	5.64E-08	SGD	636710	GRE3
YBR048W	RPS11B	Homology to rat S11, huma	2.71	2.71	4.12E-04	SGD	636711	RPS11B
YJL180C	ATP12	essential for assembly of a	2.11	2.11	5.43E-04	SGD	636712	ATP12
YOR096W	RPS7A,RPS30	Homology to human S7 an	4.67	4.67	9.49E-37	SGD	636713	RPS7A
YMR272C	SCS7,FAH1	Required for the hydroxylat	0.42	-2.39	4.14E-37	SGD	636733	SCS7
YIL018W	RPL2B,RPL5A	Homology to rat L8 and E.	4.31	4.31	8.64E-12	SGD	636746	RPL2B
YNR015W	SMM1	Suppressor of Mitochondri	2.55	2.55	0	SGD	636749	SMM1
YLR438W	CAR2	ornithine aminotransferase	2.47	2.47	3.35E-04	SGD	636756	CAR2
YOL140W	ARG8	Acetylornithine aminotrans	0.19	-5.32	0	SGD	636757	ARG8
YOL031C	YOL031C		8.16	8.16	2.54E-23	SGD	636758	YOL031C
YBR233W	PBP2	Overexpression confers re	2.45	2.45	2.07E-07	SGD	636762	PBP2
YOR201C	PET56	Ribose methyltransferase f	0.49	-2.05	4.83E-05	SGD	636763	PET56
YOR303W	CPA1	Carbamoyl phosphate synt	0.09	-11.66	0	SGD	636795	CPA1
YML126C	ERG13,HMGS	involved in mevalonate syr	2.17	2.17	6.15E-04	SGD	636798	ERG13
YHR070W	TRM5	tRNA modification enzyme	0.5	-2.01	2.22E-04	SGD	636810	TRM5
YNL240C	NAR1	Nuclear architecture relate	0.29	-3.42	1.98E-04	SGD	636814	NAR1
YNL277W	MET2	homoserine O-trans-acetyl	0.42	-2.4	2.19E-06	SGD	636817	MET2
YKL211C	TRP3	anthranilate synthase Com	0.28	-3.51	0	SGD	636818	TRP3
YLR197W	SIK1,NOP56	homology to microtubule bi	3.83	3.83	0	SGD	636822	SIK1
YHL012W	YHL012W	UDP Glucose pyrophospho	0.41	-2.43	1.65E-25	SGD	636828	YHL012W
YOR043W	WHI2	Protein involved in growth	0.35	-2.85	8.96E-12	SGD	636833	WHI2
YLR378C	SEC61	membrane component of E	3.06	3.06	1.17E-08	SGD	636836	SEC61
YDL156W	YDL156W		2.25	2.25	7.12E-21	SGD	636842	YDL156W
YBR127C	VMA2,ATPVS,VAT2	vacuolar H-ATPase regulat	2.09	2.09	1.90E-29	SGD	636844	VMA2
YDL101C	DUN1	DNA damage response; pr	2.04	2.04	6.96E-06	SGD	636846	DUN1
YOR310C	NOP58	57 kDa nucleolar protein in	3.17	3.17	9.77E-09	SGD	636848	NOP58
YER056C	FCY2,BRA7	purine-cytosine permease;	0.35	-2.83	9.90E-08	SGD	636852	FCY2
YDL143W	CCT4,TCP4	cytoplasmic chaperonin su	2.71	2.71	1.59E-09	SGD	636854	CCT4
YDR518W	EUG1	ER protein functionally like	3.02	3.02	3.61E-12	SGD	636860	EUG1
YBR068C	BAP2	contains 12 predicted trans	0.35	-2.86	7.72E-21	SGD	636883	BAP2

YMR215W	YMR215W		3.5	3.5	1.75E-04	SGD	636893	YMR215W
YEL042W	GDA1	converts nucleoside diphos	3.23	3.23	1.12E-23	SGD	636896	GDA1
YPL198W	RPL7B	Homolog of mammalian rib	3.04	3.04	1.71E-04	SGD	636897	RPL7B
YER090W	TRP2	anthranilate synthase Com	0.25	-3.96	3.75E-11	SGD	636902	TRP2
YDL020C	RPN4,SON1,UFD5	involved in ubiquitin degrac	0.47	-2.12	1.86E-04	SGD	636905	RPN4
YAR007C	RFA1,BUF2,FUN3,RPA1	Required for DNA-damage	3.39	3.39	3.39E-10	SGD	636910	RFA1
YPL161C	BEM4,ROM7	Involved in polarity establis	2.07	2.07	1.39E-05	SGD	636915	BEM4
YBR069C	TAT1,VAP1	Amino acid transport protei	3.25	3.25	9.10E-20	SGD	636919	TAT1
YHL027W	RIM101	Rim101p is similar to the A	0.42	-2.35	2.75E-06	SGD	636928	RIM101
YCL025C	AGP1,YCC5	broad substrate range perr	2.2	2.2	2.60E-09	SGD	636931	AGP1
YOR108W	YOR108W		0.37	-2.72	3.72E-05	SGD	636941	YOR108W
YHR017W	YSC83	similar to S. douglasii YSD	0.4	-2.52	1.53E-09	SGD	636947	YSC83
YNL134C	YNL134C		0.35	-2.87	8.75E-06	SGD	636954	YNL134C
YJL213W	YJL213W		0.14	-7.17	1.40E-44	SGD	636955	YJL213W
YBR104W	YMC2	Mitochondrial carrier protei	0.25	-4.06	2.73E-10	SGD	636956	YMC2
YKL218C	SRY1	Serine Racemase homolog	0.2	-4.94	7.56E-10	SGD	636959	SRY1
YNL025C	SSN8,GIG3,NUT9,SRB11	Component of RNA polyme	0.45	-2.22	3.21E-40	SGD	636961	SSN8
YDL082W	RPL13A	Homology to rat L13; ribos	3.95	3.95	1.19E-13	SGD	636963	RPL13A
YIL117C	PRM5	pheromone-regulated mem	0.37	-2.7	3.91E-07	SGD	636965	PRM5
YOL094C	RFC4	RFC is a DNA binding prot	2.16	2.16	6.07E-35	SGD	636977	RFC4
YOR184W	SER1,ADE9	phosphoserine transamina	0.25	-3.97	3.77E-13	SGD	636984	SER1
YBL013W	FMT1	Formyl-Methionyl-tRNA Tra	2	2	1.14E-05	SGD	636985	FMT1
YIL116W	HIS5	responsive to control of ge	0.09	-11.36	0	SGD	636990	HIS5
YEL037C	RAD23	ubiquitin-like protein; radiat	2.25	2.25	3.29E-31	SGD	636997	RAD23
YPL230W	USV1	Up in StarVation	0.18	-5.69	1.07E-07	SGD	637003	USV1
YDR321W	ASP1	Asparaginase I, intracellula	2.4	2.4	9.69E-15	SGD	637008	ASP1
YGL181W	GTS1,FHT1	Putative zinc-finger transcr	0.39	-2.54	3.63E-15	SGD	637014	GTS1
YLR130C	ZRT2	Low-affinity zinc transport p	0.45	-2.22	4.73E-06	SGD	637021	ZRT2
YNL066W	SUN4	Protein involved in the agir	0.37	-2.74	0	SGD	637022	SUN4
YML074C	FPR3,NPI46	binds the immunosuppress	2.43	2.43	6.62E-04	SGD	637027	FPR3
YDR019C	GCV1,GSD1	Required for metabolizing g	0.08	-11.87	3.23E-17	SGD	637033	GCV1
YOL058W	ARG1,ARG10	arginosuccinate synthetase	0.03	-39.33	0	SGD	637038	ARG1
YLR423C	APG17	required for activation of Ap	9.69	9.69	3.73E-11	SGD	637039	APG17
YDR222W	YDR222W		0.36	-2.76	3.51E-09	SGD	637040	YDR222W
YMR116C	ASC1,CPC2	WD repeat protein (G-beta	8.49	8.49	0	SGD	637043	ASC1
YGR214W	RPS0A,NAB1,NAB1A,YS	Homology to rat Sa; riboso	4.39	4.39	1.04E-40	SGD	637047	RPS0A
YAL061W	YAL061W		0.47	-2.15	2.27E-07	SGD	637054	YAL061W

YMR021C	MAC1,CUA1	metal-binding transcriptiona	0.47	-2.15	1.70E-04	SGD	637055	MAC1
YNL124W	YNL124W		0.29	-3.41	8.83E-05	SGD	637065	YNL124W
YHR183W	GND1	6-phosphogluconate dehyc	2.31	2.31	2.58E-17	SGD	637067	GND1
YJL091C	YJL091C		3.1	3.1	2.78E-29	SGD	637078	YJL091C
YNR069C	YNR069C		0.09	-10.73	1.12E-19	SGD	637083	YNR069C
YKR058W	GLG1	self-glucosylating initiator c	0.21	-4.72	1.01E-15	SGD	637088	GLG1
YEL071W	DLD3	D-lactate dehydrogenase	0.25	-4.01	2.64E-06	SGD	637094	DLD3
YER045C	ACA1	contains an ATF/CREB-like	0.47	-2.11	4.25E-15	SGD	637099	ACA1
YOR046C	DBP5,RAT8	Dead-Box protein 5; RNA h	2.6	2.6	3.34E-11	SGD	637104	DBP5
YOR298W	YOR298W		0.36	-2.79	4.34E-10	SGD	637105	YOR298W
YKL081W	TEF4,EFC1	Translation elongation fact	6.21	6.21	0	SGD	637107	TEF4
YKL047W	YKL047W		0.48	-2.09	4.37E-04	SGD	637109	YKL047W
YOR360C	PDE2,SRA5	low-Km (high-affinity) cAMI	0.48	-2.06	1.85E-04	SGD	637120	PDE2
YMR300C	ADE4	phosphoribosylpyrophosph	0.23	-4.36	6.64E-18	SGD	637129	ADE4
YGL035C	MIG1,CAT4,SSN1,TDS22	Transcription factor involve	0.33	-3.06	0	SGD	637132	MIG1
YOL091W	SPO21,MPC70	sporulation defective; meio	0.19	-5.14	1.21E-08	SGD	637149	SPO21
YCL043C	PDI1,MFP1,TRG1	protein disulfide isomerase	4.71	4.71	8.16E-13	SGD	637160	PDI1
YGL158W	RCK1	Serine/threonine protein ki	0.19	-5.29	0	SGD	637165	RCK1
YNR019W	ARE2,SAT1	Acyl-CoA cholesterol acyltr	2.18	2.18	1.53E-06	SGD	637179	ARE2
YHL047C	TAF1,ARN2	Siderophore transporter for	0.41	-2.45	1.38E-25	SGD	637186	TAF1
YKL148C	SDH1	flavoprotein subunit of succ	0.48	-2.07	2.19E-10	SGD	637187	SDH1
YBR298C	MAL31,MAL3T	Part of the complex locus M	0.27	-3.72	2.75E-07	SGD	637190	MAL31
YEL062W	NPR2	Putative post-transcriptiona	0.5	-2.01	2.65E-05	SGD	637197	NPR2
YDR380W	ARO10		0.03	-38.72	0	SGD	637201	ARO10
YGR289C	MAL11,AGT1	Part of MAL1 complex locu	0.31	-3.28	1.58E-38	SGD	637205	MAL11
YJL100W	LSB6	LAs17 Binding protein	0.39	-2.58	3.99E-09	SGD	637209	LSB6
YHL028W	WSC4,YHC8	cell wall integrity and stress	2.01	2.01	4.86E-19	SGD	637210	WSC4
YFR029W	PTR3,SSY3	Regulator of expression of	0.39	-2.56	3.63E-06	SGD	637215	PTR3
YGL066W	SGF73	SaGa associated Factor 73	0.39	-2.57	4.65E-25	SGD	637237	SGF73
YNL125C	ESBP6	Protein with similarity to ma	0.2	-5.05	1.60E-09	SGD	637248	ESBP6
YAL048C	YAL048C		0.4	-2.48	2.01E-08	SGD	637251	YAL048C
YML056C	IMD4	similar to IMP dehydrogena	2.6	2.6	2.55E-09	SGD	637252	IMD4
YER070W	RNR1,CRT7,RIR1,SDS12	ribonucleotide reductase; r	2.1	2.1	7.65E-09	SGD	637262	RNR1
YDL194W	SNF3	glucose sensor; Null mutar	0.49	-2.04	7.50E-08	SGD	637263	SNF3
YDR385W	EFT2	translation elongation facto	2.64	2.64	6.56E-14	SGD	637270	EFT2
YGL073W	HSF1,EXA3,MAS3	heat shock transcription fac	0.49	-2.05	1.15E-16	SGD	637272	HSF1
YPR160W	GPH1	Releases glucose-1-phosp	0.43	-2.31	3.26E-10	SGD	637278	GPH1

YER069W	ARG5,6	N-acetyl-gamma-glutamyl-p	0.1	-9.6	0	SGD	637285	ARG5,6
YML061C	PIF1,TST1	involved in repair and reco	2.68	2.68	6.83E-11	SGD	637286	PIF1
YOL130W	ALR1	aluminium resistance; ion t	0.45	-2.21	3.99E-06	SGD	637302	ALR1
YOL089C	HAL9	involved in salt tolerance; c	0.45	-2.23	1.26E-13	SGD	637308	HAL9
YDL019C	OSH2	Oxysterol Binding Protein;	0.45	-2.22	7.10E-23	SGD	637343	OSH2
YJL074C	SMC3	involved in sister chromatic	4.2	4.2	2.13E-16	SGD	637345	SMC3
YDL145C	COP1,RET1,SEC33	alpha subunit of the coatar	3.04	3.04	3.40E-06	SGD	637347	COP1
YKR102W	FLO10	Protein with similarity to flo	0.47	-2.14	1.48E-04	SGD	637349	FLO10
YHR154W	ESC4	Establishes Silent Chromat	6.65	6.65	1.48E-33	SGD	637358	ESC4
YDR310C	SUM1	Suppresor of mar1-1 (sir2)	2.71	2.71	3.02E-10	SGD	637359	SUM1
YDL223C	YDL223C		0.28	-3.51	4.69E-18	SGD	637360	YDL223C
YHR098C	SFB3	binds to Sed5p and Sec23	3.25	3.25	8.63E-30	SGD	637367	SFB3
YBR245C	ISW1,SGN2	has strong homology to Dr	2.05	2.05	2.02E-17	SGD	637389	ISW1
YFL008W	SMC1,CHL10	coiled-coil protein involved	2.32	2.32	1.98E-04	SGD	637399	SMC1
YML091C	RPM2	involved in processing of m	0.45	-2.21	4.66E-07	SGD	637400	RPM2
YLR342W	FKS1,CND1,CWH53,ETG	Required for viability of cal	2.62	2.62	6.47E-06	SGD	637405	FKS1
YOR326W	MYO2,CDC66	class V myosin; Null mutar	2.97	2.97	4.97E-28	SGD	637407	MYO2
YPL231W	FAS2	Trifunctional enzyme; fatty	2.96	2.96	3.66E-28	SGD	637418	FAS2
YKL101W	HSL1,NIK1	Negative regulator of swe1	3.78	3.78	5.83E-37	SGD	637424	HSL1
YGR061C	ADE6	5'-phosphoribosylformyl gly	0.35	-2.82	2.89E-06	SGD	637429	ADE6
YJL039C	NUP192	large yeast nucleoporin; Nu	2.33	2.33	9.96E-21	SGD	637434	NUP192
YER131W	RPS26B	Homology to rat S26; ribos	4.53	4.53	6.97E-10	SGD	637435	RPS26B
YDL039C	PRM7	pheromone-regulated mem	2.11	2.11	5.98E-04	SGD	637440	PRM7
YGL024W	YGL024W		0.35	-2.84	1.20E-19	SGD	637446	YGL024W
YOR203W	YOR203W		0.07	-14.34	2.02E-35	SGD	637454	YOR203W
YFR035C	YFR035C		2.85	2.85	4.99E-08	SGD	637458	YFR035C
YDR382W	RPP2B,RPL45,YPA1	Homology to rat P2, humar	2.12	2.12	3.06E-04	SGD	637464	RPP2B
YKL182W	FAS1	pentafunctional enzyme co	2.8	2.8	2.11E-10	SGD	637475	FAS1
YLR104W	YLR104W		3.01	3.01	9.51E-14	SGD	637483	YLR104W
YHL015W	RPS20,URP2	Homology to rat S20, huma	2.92	2.92	4.65E-42	SGD	637497	RPS20
YHR162W	YHR162W		0.2	-5.11	3.34E-29	SGD	637501	YHR162W
YPL252C	YAH1	Yeast Adrenodoxin Homolo	0.38	-2.6	6.57E-08	SGD	637516	YAH1
YCR083W	TRX3	mitochondrial thioredoxin; t	0.48	-2.09	8.99E-04	SGD	637520	TRX3
YLR184W	YLR184W		2.02	2.02	3.44E-15	SGD	637539	YLR184W
YJL170C	ASG7	an a-specific gene that is ir	0.3	-3.3	1.95E-11	SGD	637550	ASG7
YDR178W	SDH4,ACN18	succinate dehydrogenase r	0.46	-2.17	4.38E-04	SGD	637551	SDH4
YMR009W	YMR009W		0.39	-2.54	1.94E-10	SGD	637553	YMR009W

YBR047W	YBR047W		0.08	-12.02	7.06E-16	SGD	637555	YBR047W
YPR102C	RPL11A	Homology to rat L11 and E	3.07	3.07	5.36E-07	SGD	637557	RPL11A
YPR149W	NCE102	involved in secretion of pro	0.18	-5.58	3.69E-07	SGD	637558	NCE102
YJL189W	RPL39,PUB2,RPL46,SPE	Homology to rat L39; ribos	4.13	4.13	6.09E-04	SGD	637568	RPL39
YBR116C	YBR116C		0.13	-7.77	1.09E-12	SGD	637571	YBR116C
YAR023C	YAR023C	membrane protein	0.38	-2.67	1.79E-09	SGD	637585	YAR023C
YAL044C	GCV3	H-protein subunit of the gly	0.16	-6.16	7.46E-18	SGD	637586	GCV3
YNL190W	YNL190W		0.47	-2.15	1.19E-09	SGD	637595	YNL190W
YKL001C	MET14	adenylylsulfate kinase; Nul	2.08	2.08	1.20E-09	SGD	637597	MET14
YOR182C	RPS30B	Homology to mammalian S	2.11	2.11	1.02E-06	SGD	637599	RPS30B
YMR184W	YMR184W		3.01	3.01	3.31E-05	SGD	637601	YMR184W
YFR017C	YFR017C		0.31	-3.26	0	SGD	637604	YFR017C
YBR171W	SEC66,HSS1,SEC71	glycoprotein complexed wi	2.35	2.35	1.38E-13	SGD	637608	SEC66
YMR143W	RPS16A	Homology to rat S16; ribos	3.32	3.32	2.29E-18	SGD	637609	RPS16A
YBL072C	RPS8A	Homology to mammalian S	3.04	3.04	1.24E-07	SGD	637614	RPS8A
YCL026C-A	FRM2	Protein involved in the inte	0.16	-6.31	0	SGD	637621	FRM2
YNL067W	RPL9B	Homology to rat L9; riboso	3.2	3.2	5.70E-09	SGD	637622	RPL9B
YLR185W	RPL37A	Homology to rat L37; ribos	3.06	3.06	4.70E-15	SGD	637623	RPL37A
YGL200C	EMP24,BST2	type I transmembrane prot	2.85	2.85	1.45E-15	SGD	637627	EMP24
YIL164C	NIT1	nitrilase	0.12	-8.38	9.57E-07	SGD	637631	NIT1
YJR069C	HAM1	Product of gene unknown;	2.46	2.46	1.54E-06	SGD	637634	HAM1
YOR280C	YOR280C		2.26	2.26	1.09E-23	SGD	637643	YOR280C
YDR174W	HMO1	High mobility group (HMG)	2.31	2.31	9.41E-08	SGD	637648	HMO1
YDR025W	RPS11A	Homology to rat S11, huma	2.36	2.36	6.13E-04	SGD	637656	RPS11A
YPR183W	DPM1,SED3	dolichol phosphate manno	4.9	4.9	2.28E-14	SGD	637658	DPM1
YHR021C	RPS27B	Homology to mammalian S	3.92	3.92	2.17E-04	SGD	637659	RPS27B
YOL154W	YOL154W		6.38	6.38	2.46E-24	SGD	637662	YOL154W
YGR034W	RPL26B	Homology to rat L26; ribos	2.48	2.48	9.77E-17	SGD	637663	RPL26B
YLR064W	YLR064W		0.49	-2.03	3.30E-09	SGD	637669	YLR064W
YGL154C	LYS5	aminoadipate-semialdehyd	0.35	-2.89	1.05E-31	SGD	637670	LYS5
YHL001W	RPL14B	Homology to mammalian L	2.59	2.59	1.10E-04	SGD	637671	RPL14B
YPR132W	RPS23B	Homology to rat S23 and E	2.96	2.96	2.83E-06	SGD	637674	RPS23B
YNL195C	YNL195C		0.23	-4.36	6.78E-09	SGD	637683	YNL195C
YGL096W	TOS8	Hypothetical ORF	0.37	-2.74	9.56E-06	SGD	637687	TOS8
YFL028C	CAF16	CCR4 associated factor; A	0.25	-3.96	1.21E-11	SGD	637693	CAF16
YKL180W	RPL17A	Homology to rat L17, huma	4.13	4.13	5.85E-11	SGD	637695	RPL17A
YDL191W	RPL35A,SOS1	Homology to rat L35; ribos	2.33	2.33	5.66E-16	SGD	637697	RPL35A

YML026C	RPS18B	Homology to rat S18 and E	3.44	3.44	1.32E-11	SGD	637700	RPS18B
YIR014W	YIR014W		0.48	-2.08	1.50E-11	SGD	637703	YIR014W
YER074W	RPS24A,RPS24EA	Homology to rat S24; ribos	3.93	3.93	7.43E-08	SGD	637707	RPS24A
YGR239C	PEX21	Peroxin, Pex18p and Pex2	0.28	-3.63	1.13E-16	SGD	637709	PEX21
YGL224C	SDT1,SSM1	suppressor of deletion of T	0.4	-2.49	9.62E-09	SGD	637715	SDT1
YBR257W	POP4	Required for normal 5.8S r	0.4	-2.52	7.08E-09	SGD	637716	POP4
YLR150W	STM1,MPT4	Multicopy suppressor of tor	5.2	5.2	3.16E-13	SGD	637723	STM1
YKL006W	RPL14A	Homology to mammalian L	3.46	3.46	5.09E-20	SGD	637725	RPL14A
YJR145C	RPS4A	Homology to rat S4 and hu	3.54	3.54	5.53E-05	SGD	637727	RPS4A
YNR071C	YNR071C		0.38	-2.62	4.19E-16	SGD	637731	YNR071C
YPL111W	CAR1,LPH15	arginase; Null mutant is via	2.88	2.88	5.28E-23	SGD	637738	CAR1
YNL264C	PDR17,ISS1	involved in pleiotropic drug	0.34	-2.94	6.03E-14	SGD	637740	PDR17
YGL157W	YGL157W		2.39	2.39	9.53E-44	SGD	637742	YGL157W
YBR189W	RPS9B,RPS13A,SUP46	Homology to rat S9 and E.	3.34	3.34	1.27E-15	SGD	637754	RPS9B
YJR155W	AAD10	high degree of similarity wi	0.32	-3.08	2.27E-08	SGD	637760	AAD10
YLR136C	TIS11,CTH2	Zinc finger containing hom	3.98	3.98	0	SGD	637762	TIS11
YPL156C	PRM4	pheromone-regulated mem	0.41	-2.46	6.33E-06	SGD	637763	PRM4
YJR111C	YJR111C		0.19	-5.13	9.26E-17	SGD	637764	YJR111C
YOL064C	MET22,HAL2	Putative phosphatase gene	0.47	-2.12	1.38E-19	SGD	637770	MET22
YLR216C	CPR6	a cyclophilin related to the	0.21	-4.76	4.76E-08	SGD	637775	CPR6
YNL160W	YGP1	may be involved in cellular	0.48	-2.07	3.19E-05	SGD	637787	YGP1
YKL051W	YKL051W		0.31	-3.26	1.96E-10	SGD	637788	YKL051W
YNL164C	YNL164C		0.43	-2.31	1.14E-05	SGD	637790	YNL164C
YOR007C	SGT2	small glutamine-rich tetratr	0.46	-2.19	2.40E-05	SGD	637794	SGT2
YBR128C	APG14	Required for autophagy; N	0.5	-2.02	2.25E-20	SGD	637795	APG14
YGL059W	YGL059W		0.13	-7.64	0	SGD	637814	YGL059W
YER061C	CEM1	homology with beta-keto-a	0.31	-3.23	2.56E-05	SGD	637816	CEM1
YHR111W	YHR111W	moeB, thiF, UBA1	0.48	-2.1	1.40E-05	SGD	637817	YHR111W
YNL004W	HRB1,TOM34	an ORF of unknown functio	0.4	-2.5	1.75E-06	SGD	637825	HRB1
YGR028W	MSP1,YTA4	40 kDa putative membrane	2.08	2.08	4.09E-08	SGD	637837	MSP1
YHR002W	LEU5	mitochondrial carrier protei	0.48	-2.08	1.33E-05	SGD	637840	LEU5
YDR249C	YDR249C		0.5	-2.02	2.36E-05	SGD	637844	YDR249C
YPL090C	RPS6A	Homology to rat, mouse, a	4.86	4.86	1.06E-40	SGD	637848	RPS6A
YNL016W	PUB1	poly(A)+ RNA-binding prot	2.06	2.06	8.29E-07	SGD	637856	PUB1
YMR220W	ERG8	Involved in isoprene and e	0.45	-2.24	1.57E-23	SGD	637858	ERG8
YNL166C	BNI5	bud neck involved, localize	2.54	2.54	1.46E-19	SGD	637860	BNI5
YJL088W	ARG3	Sixth step in arginine biosy	0.04	-26.41	0	SGD	637865	ARG3

YBR243C	ALG7,TUR1	ER protein that transfers G	3.99	3.99	2.29E-32	SGD	637875	ALG7
YLR058C	SHM2,SHMT2	serine hydroxymethyltransf	0.27	-3.66	1.93E-16	SGD	637895	SHM2
YFL052W	YFL052W		0.29	-3.41	1.80E-27	SGD	637897	YFL052W
YAL034C	FUN19	Function unknown now; Nu	0.4	-2.49	5.40E-40	SGD	637898	FUN19
YDR023W	SES1	seryl-tRNA synthetase; ser	4.47	4.47	0	SGD	637899	SES1
YER003C	PMI40	catalyzes the interconversi	10.36	10.36	4.13E-12	SGD	637900	PMI40
YAL062W	GDH3,FUN51	Involved in glutamate biosy	0.43	-2.31	7.31E-15	SGD	637902	GDH3
YOR198C	BFR1	Multicopy suppressor of BF	6.3	6.3	0	SGD	637910	BFR1
YHR092C	HXT4,LGT1,RAG1	hexose transporter; high af	0.37	-2.67	4.67E-18	SGD	637930	HXT4
YKL109W	HAP4	Regulates respiratory funct	0.44	-2.29	1.34E-11	SGD	637933	HAP4
YOL019W	TOS7	Hypothetical ORF	2.79	2.79	7.28E-07	SGD	637935	TOS7
YGR197C	SNG1	Involved in nitrosoguanidin	0.44	-2.26	1.31E-16	SGD	637937	SNG1
YIL123W	SIM1	(putative) invovled in contr	3.55	3.55	0	SGD	637944	SIM1
YNL237W	YTP1	Yeast putative Transmemb	0.47	-2.11	3.16E-06	SGD	637953	YTP1
YCR061W	YCR061W		0.36	-2.76	1.67E-14	SGD	637956	YCR061W
YBR078W	ECM33	ExtraCellular Mutant; A Tn	3.25	3.25	1.22E-11	SGD	637958	ECM33
YDR345C	HXT3	Low-affinity glucose transp	0.34	-2.94	2.59E-10	SGD	637964	HXT3
YDL003W	MCD1,PDS3,RHC21,SCC	Mitotic Chromosome Deter	2.61	2.61	8.05E-05	SGD	637965	MCD1
YPR111W	DBF20	kinase required for late nuc	0.31	-3.21	2.34E-15	SGD	637982	DBF20
YFL055W	AGP3	General amino acid perme	0.42	-2.38	1.16E-05	SGD	637985	AGP3
YIL036W	CST6,ACA2	Chromosome STability, co	0.42	-2.38	1.86E-07	SGD	637990	CST6
YMR250W	GAD1	glutamate decarboxylase	0.42	-2.36	3.11E-32	SGD	637992	GAD1
YDL079C	MRK1	putative protein kinase with	0.24	-4.22	1.12E-20	SGD	638017	MRK1
YLR089C	YLR089C		0.24	-4.17	6.56E-13	SGD	638019	YLR089C
YBR169C	SSE2	HSP70 family member, hig	0.45	-2.24	5.88E-11	SGD	638025	SSE2
YLL019C	KNS1,L124	protein kinase homolog; via	0.49	-2.03	8.71E-27	SGD	638029	KNS1
YLR258W	GSY2	Highly similar to GSY1. GS	0.31	-3.21	2.72E-07	SGD	638037	GSY2
YKL220C	FRE2	Ferric reductase, similar to	0.44	-2.25	1.91E-06	SGD	638051	FRE2
YJR143C	PMT4	Transfers mannose residue	3.64	3.64	1.57E-27	SGD	638064	PMT4
YPL032C	SVL3	Styryl dye vacuolar localiza	2.09	2.09	2.03E-11	SGD	638067	SVL3
YMR016C	SOK2	Protein that can when over	2.14	2.14	1.68E-07	SGD	638075	SOK2
YDL164C	CDC9,MMS8	essential for mitosis and m	3.06	3.06	4.47E-18	SGD	638082	CDC9
YOR248W	TOS11	Hypothetical ORF	3.28	3.28	1.48E-05	SGD	638100	TOS11
YGR037C	ACB1	Involved in transport of new	4.24	4.24	7.53E-12	SGD	638102	ACB1
YAL053W	YAL053W		2.13	2.13	1.92E-05	SGD	638116	YAL053W
YJL206C	YJL206C		0.31	-3.26	1.77E-05	SGD	638122	YJL206C
YOR199W	YOR199W		2.85	2.85	5.17E-25	SGD	638134	YOR199W

YNL015W	PBI2	Proteinase inhibitor that inh	2.85	2.85	3.07E-07	SGD	638188	PBI2
YAR020C	PAU7	similar to Pau3, member of	0.44	-2.28	1.29E-22	SGD	638190	PAU7
YDR510W	SMT3	may be involved in functior	2.02	2.02	2.26E-05	SGD	638191	SMT3
YGL032C	AGA2	adhesion subunit of a-aggl	0.31	-3.2	4.41E-05	SGD	638196	AGA2
YOR392W	YOR392W		0.5	-2	9.61E-04	SGD	638206	YOR392W
YBL049W	YBL049W		0.43	-2.35	3.12E-05	SGD	638214	YBL049W
YDR519W	FPR2,FKB2	binds the immunosuppress	3.1	3.1	4.86E-10	SGD	638217	FPR2
YOR103C	OST2	Oligosaccharyltransferase	2.01	2.01	1.10E-16	SGD	638219	OST2
YBR201W	DER1	Degradation in the Endopla	2.85	2.85	2.90E-12	SGD	638227	DER1
YLR112W	YLR112W		0.41	-2.47	2.90E-18	SGD	638246	YLR112W
YPL135W	ISU1,NUA1	Iron-sulfur cluster nifU-like	0.32	-3.09	4.12E-19	SGD	638256	ISU1
YGL031C	RPL24A,RPL30A	Homology to rat L24; ribos	3.32	3.32	3.29E-29	SGD	638263	RPL24A
YBR135W	CKS1	subunit of the Cdc28 prote	2.18	2.18	1.73E-08	SGD	638267	CKS1
YLR164W	YLR164W		0.34	-2.94	1.57E-22	SGD	638269	YLR164W
YOR394W	YOR394W		0.44	-2.28	1.06E-07	SGD	638272	YOR394W
YOR339C	UBC11	homolog of ubiquitin carrie	0.38	-2.63	4.43E-05	SGD	638295	UBC11
YGL135W	RPL1B,SSM2	Homology to rat L10a, eub	2.53	2.53	5.61E-14	SGD	638330	RPL1B
YCR020C	PET18,HIT2	Transcription regulator; pet	0.41	-2.42	1.93E-04	SGD	638332	PET18
YHR022C	YHR022C	RAS-related protein	0.44	-2.26	3.28E-06	SGD	638345	YHR022C
YDL136W	RPL35B,SOS2	Homology to rat L35; ribos	2.33	2.33	1.15E-05	SGD	638346	RPL35B
YHR185C	PFS1,ADY1	Prospore Formation at Sel	2.26	2.26	9.05E-05	SGD	638352	PFS1
YHL044W	YHL044W		0.3	-3.34	5.01E-22	SGD	638354	YHL044W
YHR122W	YHR122W		0.16	-6.25	1.11E-26	SGD	638357	YHR122W
YPL218W	SAR1	Secretion-Associated, Ras	2.51	2.51	1.45E-07	SGD	638359	SAR1
YBL043W	ECM13	ExtraCellular Mutant; A Tn	0.26	-3.81	0	SGD	638361	ECM13
YKL040C	NFU1,NUB1	Nifu-like protein; Null muta	0.46	-2.17	1.41E-18	SGD	638362	NFU1
YMR194W	RPL36A,RPL39B	Homology to rat L36; ribos	2.7	2.7	1.78E-08	SGD	638363	RPL36A
YGR118W	RPS23A	Homology to rat S23 and E	3.21	3.21	2.13E-20	SGD	638365	RPS23A
YKL096W	CWP1,YJU1	cell wall protein, involved ir	5.03	5.03	0	SGD	638367	CWP1
YPL280W	YPL280W		0.34	-2.94	2.85E-07	SGD	638369	YPL280W
YJR123W	RPS5	ribosomal small subunit pr	4.83	4.83	2.13E-13	SGD	638378	RPS5
YMR056C	AAC1	minor species of mitochon	0.47	-2.13	3.56E-21	SGD	638383	AAC1
YPR058W	YMC1	putative mitochondrial carri	0.25	-4.01	2.68E-32	SGD	638385	YMC1
YLR448W	RPL6B	Homology to rat and huma	4.03	4.03	5.67E-11	SGD	638387	RPL6B
YER117W	RPL23B	Homology to rat L23 and E	2.93	2.93	1.51E-05	SGD	638395	RPL23B
YKL150W	MCR1	NADH-cytochrome b5 redu	0.33	-3.01	6.18E-08	SGD	638404	MCR1
YPR061C	YPR061C		0.29	-3.41	4.20E-45	SGD	638405	YPR061C

YER175C	TMT1,TAM1	Trans-aconitate Methyltran	0.15	-6.78	5.49E-07	SGD	638406	TMT1
YIL133C	RPL16A,RPL13	Homology to rat L13a; ribo	2.63	2.63	4.57E-17	SGD	638410	RPL16A
YCR007C	YCR007C		0.45	-2.22	4.07E-06	SGD	638421	YCR007C
YBR211C	AME1,ARP100	associated with microtubul	0.45	-2.24	2.22E-08	SGD	638432	AME1
YGR127W	YGR127W		0.31	-3.25	1.77E-08	SGD	638442	YGR127W
YNL096C	RPS7B	Homology to human S7 an	3.63	3.63	0	SGD	638450	RPS7B
YGL162W	SUT1	Involved in sterol uptake; N	0.26	-3.88	1.97E-07	SGD	638454	SUT1
YNL196C	SLZ1	sporulation-specific protein	3.75	3.75	1.49E-27	SGD	638456	SLZ1
YFR041C	YFR041C		4.46	4.46	1.17E-08	SGD	638458	YFR041C
YMR305C	SCW10	Soluble Cell Wall protein; s	2.14	2.14	3.82E-16	SGD	638462	SCW10
YFL030W	YFL030W		0.49	-2.03	2.38E-14	SGD	638464	YFL030W
YDR502C	SAM2,ETH2	methionine biosynthesis re	6.91	6.91	0	SGD	638465	SAM2
YML060W	OGG1	Excises 7,8-dihydro-8-oxog	2.53	2.53	6.52E-33	SGD	638471	OGG1
YNL301C	RPL18B,RP28B	Homology to rat ribosomal	3.34	3.34	1.36E-08	SGD	638473	RPL18B
YNL302C	RPS19B,RP55B	Homology to rat S19; ribos	3.26	3.26	2.24E-07	SGD	638475	RPS19B
YHR139C	SPS100	involved in spore developm	0.16	-6.39	4.35E-11	SGD	638476	SPS100
YHR010W	RPL27A	Homology to mammalian L	5.86	5.86	5.76E-28	SGD	638478	RPL27A
YNL063W	YNL063W		0.49	-2.05	3.84E-06	SGD	638486	YNL063W
YAL060W	BDH1	(2R,3R)-2,3-butanediol deh	0.4	-2.47	1.92E-23	SGD	638512	BDH1
YHR179W	OYE2	NAPDH dehydrogenase (o	3.52	3.52	1.35E-12	SGD	638531	OYE2
YPL028W	ERG10,LPB3,TSM0115	acetoacetyl CoA thiolase; M	2.67	2.67	2.84E-04	SGD	638534	ERG10
YOR173W	YOR173W		0.42	-2.36	8.08E-05	SGD	638535	YOR173W
YER154W	OXA1,PET-TS1402	Mediates the export of prot	2.05	2.05	6.56E-08	SGD	638539	OXA1
YIL160C	POT1,FOX3,POX3	peroxisomal 3-oxoacyl CoA	2.37	2.37	3.50E-22	SGD	638546	POT1
YLL057C	YLL057C		0.24	-4.09	5.69E-07	SGD	638549	YLL057C
YNL064C	YDJ1,MAS5	yeast dnaJ homolog (nucle	0.35	-2.83	4.12E-12	SGD	638551	YDJ1
YPL188W	POS5	involved in oxidative stress	0.25	-4.06	0	SGD	638565	POS5
YER145C	FTR1	Plasma membrane iron per	2.11	2.11	7.27E-06	SGD	638570	FTR1
YPL017C	YPL017C		0.34	-2.93	3.08E-06	SGD	638573	YPL017C
YPR119W	CLB2	Involved in mitotic induction	2.42	2.42	4.93E-08	SGD	638577	CLB2
YLR359W	ADE13,BRA1,BRA8	Adenylosuccinate Lyase; a	0.22	-4.51	1.12E-27	SGD	638582	ADE13
YPL061W	ALD6	Utilizes NADP+ as the pref	2.03	2.03	1.30E-07	SGD	638588	ALD6
YER051W	YER051W		0.37	-2.72	4.69E-08	SGD	638591	YER051W
YGR189C	CRH1	congo red hypersensitive; c	3.59	3.59	0	SGD	638623	CRH1
YFL022C	FRS2	Phenylalanyl-tRNA synthet	2.79	2.79	3.36E-39	SGD	638626	FRS2
YGL253W	HXK2,HEX1,HKB,SCI2	Glucose phosphorylation; h	4.92	4.92	2.67E-13	SGD	638636	HXK2
YNR001C	CIT1,CS1,LYS6	citrate synthase. Nuclear e	0.47	-2.12	3.00E-14	SGD	638640	CIT1

YAL028W	YAL028W		0.47	-2.15	4.29E-13	SGD	638653	YAL028W
YER052C	HOM3,BOR1,SIL4	First step in common pathv	0.16	-6.18	1.64E-11	SGD	638654	HOM3
YLR314C	CDC3	involved in proper bud grov	2.85	2.85	0	SGD	638658	CDC3
YKL103C	LAP4,APE1,API,YSC1	vacuolar aminopeptidase y	0.28	-3.56	2.83E-04	SGD	638661	LAP4
YLR121C	YPS3,YPS4	Gpi-anchored aspartic prot	2.81	2.81	1.18E-39	SGD	638664	YPS3
YER060W	FCY21	identical to FCY2; purine-c	2.18	2.18	1.88E-04	SGD	638669	FCY21
YDR501W	PLM2	Plasmid Maintenance; Null	2.61	2.61	3.65E-09	SGD	638673	PLM2
YER096W	SHC1	sporulation-specific homolo	0.25	-4.04	0	SGD	638678	SHC1
YJR046W	TAH11	Product of gene unknown;	0.35	-2.85	6.45E-37	SGD	638699	TAH11
YHR161C	YAP1801	Yeast Assembly Polypeptic	0.37	-2.72	3.75E-11	SGD	638706	YAP1801
YGL116W	CDC20,PAC5	Required for onset of anap	0.42	-2.39	6.29E-07	SGD	638712	CDC20
YPL265W	DIP5	dicarboxylic amino acid pe	0.5	-2.02	3.98E-07	SGD	638713	DIP5
YIL092W	YIL092W		0.48	-2.07	1.23E-05	SGD	638720	YIL092W
YHR117W	TOM71,TOM72	Translocase of the Outer M	2.03	2.03	1.76E-12	SGD	638722	TOM71
YGL142C	GPI10	Involved in glycosyl phospl	0.4	-2.5	4.81E-04	SGD	638725	GPI10
YBR117C	TKL2	transketolase, homologous	0.24	-4.1	9.85E-18	SGD	638733	TKL2
YGR054W	YGR054W		2.07	2.07	2.60E-05	SGD	638745	YGR054W
YOR254C	SEC63,PTL1	Protein involved in protein	3.93	3.93	1.02E-09	SGD	638754	SEC63
YIL037C	PRM2	pheromone-regulated mem	0.37	-2.72	3.59E-07	SGD	638756	PRM2
YNL167C	SKO1,ACR1	Suppressor of PKA overex	0.48	-2.07	1.24E-09	SGD	638759	SKO1
YPL269W	KAR9	cortical protein required for	0.46	-2.17	2.60E-26	SGD	638760	KAR9
YMR313C	YMR313C		0.44	-2.28	1.12E-10	SGD	638761	YMR313C
YLR240W	VPS34,END12,PEP15,VF	phosphatidylinositol 3-kina	0.49	-2.06	4.52E-31	SGD	638764	VPS34
YLL034C	YLL034C		2.3	2.3	3.04E-07	SGD	638771	YLL034C
YNL221C	POP1	Required for processing of	0.47	-2.14	2.43E-05	SGD	638780	POP1
YBL024W	NCL1,TRM4	Nuclear protein 1, similar to	2.12	2.12	4.70E-05	SGD	638792	NCL1
YBR084W	MIS1	mitochondrial C1-tetrahydr	2.61	2.61	4.38E-18	SGD	638810	MIS1
YKL073W	LHS1,CER1,SSI1	Required for efficient transl	5.65	5.65	2.42E-13	SGD	638818	LHS1
YBR281C	YBR281C	Probable G-protein, -transc	2.46	2.46	4.42E-28	SGD	638819	YBR281C
YGL180W	APG1,AUT3	Required for autophagy; pr	0.29	-3.45	7.54E-14	SGD	638831	APG1
YGR204W	ADE3	Required for the biosynthes	0.48	-2.09	4.02E-06	SGD	638840	ADE3
YBR203W	YBR203W		0.39	-2.59	1.39E-09	SGD	638853	YBR203W
YJR039W	YJR039W		0.32	-3.17	3.46E-06	SGD	638888	YJR039W
YGL094C	PAN2	Required for Pab1p-stimula	3.42	3.42	0	SGD	638889	PAN2
YER033C	ZRG8	Zinc regulated gene	0.5	-2.01	6.04E-07	SGD	638893	ZRG8
YNL262W	POL2,DUN2	DNA polymerase II	2.34	2.34	1.53E-07	SGD	638909	POL2
YNL087W	YNL087W		2.55	2.55	2.45E-11	SGD	638923	YNL087W

YPR030W	CSR2,MRG19	chs5 spa2 rescue, overexp	0.48	-2.08	2.16E-05	SGD	638927	CSR2
YGR090W	YGR090W		3.62	3.62	1.83E-10	SGD	638936	YGR090W
YEL039C	CYC7	iso-2-cytochrome c; Null m	0.24	-4.18	0	SGD	638940	CYC7
YPL058C	PDR12	similar to Pdr5p; multidrug	0.31	-3.26	8.25E-07	SGD	638948	PDR12
YKL010C	UFD4	Ubiquitin Fusion Degradati	0.48	-2.09	1.31E-22	SGD	638949	UFD4
YBR208C	DUR1,2,DUR80	Urea amidolyase (contains	3.25	3.25	7.34E-27	SGD	638958	DUR1,2
YDR406W	PDR15	similar to Pdr5p and Pdr10	0.38	-2.64	7.09E-11	SGD	638963	PDR15
YNL102W	POL1,CDC17,CRT5,HPR	Required for mitotic DNA s	3.88	3.88	2.02E-09	SGD	638965	POL1
YCR093W	CDC39,NOT1,ROS1,SMI	Required for Start B in mitc	2.17	2.17	1.32E-04	SGD	638973	CDC39
YGL088W	YGL088W		2.62	2.62	3.06E-20	SGD	638981	YGL088W
YOR200W	YOR200W		2.52	2.52	5.80E-08	SGD	638982	YOR200W
YBR099C	YBR099C		0.19	-5.36	1.62E-07	SGD	638987	YBR099C
YGL121C	YGL121C		0.39	-2.58	3.20E-07	SGD	638989	YGL121C
YLR379W	YLR379W		2.05	2.05	3.56E-12	SGD	638992	YLR379W
YGR236C	SPG1	Hypothetical ORF; Null mu	0.44	-2.26	3.53E-22	SGD	639001	SPG1
YEL003W	GIM4,PFD2	Prefoldin subunit 2, putativ	2.86	2.86	1.06E-05	SGD	639009	GIM4
YOL133W	HRT1,RBX1,ROC1	High level expression Redu	0.4	-2.49	4.19E-10	SGD	639014	HRT1
YJL202C	YJL202C		0.46	-2.2	8.72E-06	SGD	639023	YJL202C
YCL042W	YCL042W		2.45	2.45	5.41E-07	SGD	639034	YCL042W
YLR162W	YLR162W		9.21	9.21	9.01E-04	SGD	639035	YLR162W
YOR253W	YOR253W		2.13	2.13	4.47E-27	SGD	639053	YOR253W
YHR193C	EGD2	GAL4 enhancer protein, hc	2.09	2.09	2.58E-06	SGD	639055	EGD2
YDL192W	ARF1	implicated in signal transdu	3.32	3.32	0	SGD	639065	ARF1
YMR242C	RPL20A,RPL18A2	Homology to rat L18a; ribo	3.36	3.36	1.93E-33	SGD	639066	RPL20A
YML055W	SPC2,SPY1	subunit of signal peptidase	3.57	3.57	1.99E-12	SGD	639085	SPC2
YMR306C-	YMR306C-A		2.76	2.76	6.19E-09	SGD	639096	YMR306C-A
YBL107C	YBL107C		2.49	2.49	1.62E-04	SGD	639104	YBL107C
YLR292C	SEC72,SEC67,SIM2	protein involved in membra	2.92	2.92	2.53E-10	SGD	639107	SEC72
YDL130W	RPP1B,RPL44',RPLA3	Homology to rat P1, humar	3.43	3.43	1.25E-06	SGD	639110	RPP1B
YPR151C	YPR151C		0.48	-2.1	1.94E-30	SGD	639111	YPR151C
YGR267C	FOL2	First enzyme in biosyntheti	0.38	-2.61	0	SGD	639143	FOL2
YGR161C	YGR161C		0.31	-3.22	9.29E-05	SGD	639153	YGR161C
YPR015C	YPR015C		0.43	-2.3	3.26E-05	SGD	639156	YPR015C
YER174C	GRX4	Member of a glutaredoxin s	0.26	-3.92	2.50E-23	SGD	639158	GRX4
YML024W	RPS17A,RP51A,RPL51A	Homology to rat S17; ribos	3.37	3.37	1.02E-08	SGD	639173	RPS17A
YOR234C	RPL33B	Homology to rat L35a; ribo	3.37	3.37	0	SGD	639189	RPL33B
YOL127W	RPL25	Homology to E. coli L23 an	3.62	3.62	2.00E-13	SGD	639191	RPL25

YLL023C	YLL023C		0.43	-2.32	1.11E-22	SGD	639192	YLL023C
YMR039C	SUB1,TSP1	Suppressor of TFIIB mutati	2.15	2.15	1.85E-26	SGD	639197	SUB1
YDL083C	RPS16B	Homology to rat S16; ribos	3.41	3.41	7.98E-12	SGD	639201	RPS16B
YEL005C	VAB2,VAB31	Vac8p binding protein of 3:	0.47	-2.15	5.41E-04	SGD	639205	VAB2
YBR165W	UBS1	General positive regulator	0.38	-2.62	1.15E-07	SGD	639209	UBS1
YDL051W	LHP1,LAH1,YLA1	Protein homologous to hun	2.53	2.53	6.63E-33	SGD	639210	LHP1
YIL069C	RPS24B,RPS24EB	Homology to rat S24; ribos	4.08	4.08	3.07E-09	SGD	639214	RPS24B
YPL004C	YPL004C		0.34	-2.92	8.58E-22	SGD	639241	YPL004C
YDR450W	RPS18A	Homology to rat S18 and E	2.86	2.86	1.85E-05	SGD	639250	RPS18A
YBR191W	RPL21A,URP1	Homology to rat L21; ribos	4.04	4.04	7.42E-15	SGD	639252	RPL21A
YNL162W	RPL42A	Homology to rat L36a and	2.82	2.82	0	SGD	639262	RPL42A
YJL031C	BET4	catalyzes prenylation of Yp	2.46	2.46	1.27E-11	SGD	639267	BET4
YMR318C	YMR318C		3.14	3.14	1.76E-08	SGD	639280	YMR318C
YDL100C	YDL100C		3.56	3.56	0	SGD	639283	YDL100C
YJR105W	ADO1	adenosine kinase	2.05	2.05	5.55E-08	SGD	639295	ADO1
YKL151C	YKL151C		0.25	-3.99	1.67E-09	SGD	639298	YKL151C
YCR034W	FEN1,ELO2,GNS1,VBM2	Involved in synthesis of 1,3	3.83	3.83	1.07E-31	SGD	639304	FEN1
YBR054W	YRO2	Homolog to HSP30 heat sh	0.15	-6.82	1.62E-33	SGD	639307	YRO2
YOL120C	RPL18A,RP28A	Homology to rat ribosomal	3.98	3.98	7.94E-13	SGD	639315	RPL18A
YMR142C	RPL13B	Homology to rat L13; ribos	4.02	4.02	5.53E-11	SGD	639316	RPL13B
YDL055C	PSA1,MPG1,SRB1,VIG9	mannose-1-phosphate gua	4.23	4.23	8.33E-11	SGD	639332	PSA1
YGL248W	PDE1	3',5'-Cyclic-nucleotide phos	0.29	-3.41	0	SGD	639341	PDE1
YDR055W	PST1	Protoplasts-secreted; the g	2.41	2.41	1.06E-14	SGD	639359	PST1
YPR106W	ISR1	Inhibition of staurosporine	0.31	-3.22	2.51E-08	SGD	639376	ISR1
YFL026W	STE2	alpha-factor pheromone re	0.36	-2.78	2.37E-08	SGD	639384	STE2
YDL182W	LYS20	homocitrate synthase, high	0.11	-8.74	2.01E-26	SGD	639386	LYS20
YMR323W	YMR323W		0.27	-3.68	4.13E-06	SGD	639395	YMR323W
YGL219C	MMM2	Hypothetical ORF	0.44	-2.29	1.88E-10	SGD	639409	MMM2
YBR293W	YBR293W	Probable multidrug resistar	0.4	-2.5	7.61E-20	SGD	639416	YBR293W
YKL221W	MCH2	monocarboxylate permeas	0.43	-2.31	4.41E-06	SGD	639417	MCH2
YER081W	SER3	catalyzes the first step in s	0.31	-3.22	2.01E-15	SGD	639419	SER3
YCR005C	CIT2	non-mitochondrial citrate s	0.13	-7.72	2.23E-29	SGD	639424	CIT2
YPL092W	SSU1,LPG16	sensitive to sulfite; major fa	0.16	-6.22	1.16E-10	SGD	639426	SSU1
YLR142W	PUT1	proline oxidase; inability to	0.21	-4.83	1.24E-16	SGD	639431	PUT1
YLR231C	YLR231C		2.31	2.31	7.69E-05	SGD	639445	YLR231C
YPL256C	CLN2	role in cell cycle START; G	2.18	2.18	4.48E-38	SGD	639449	CLN2
YLR134W	PDC5	pyruvate decarboxylase; u	2.28	2.28	6.72E-05	SGD	639455	PDC5

YMR171C	YMR171C		0.49	-2.02	1.08E-04	SGD	639462	YMR171C
YBR008C	FLR1	Fluconazole Resistance 1;	0.5	-2.01	1.03E-08	SGD	639463	FLR1
YML116W	ATR1,SNQ1	aminotriazole resistance; v	0.27	-3.64	2.24E-14	SGD	639466	ATR1
YIL045W	PIG2	Interacts with Gsy2p; 30%	0.19	-5.14	2.01E-23	SGD	639468	PIG2
YOR023C	AHC1	Ada Histone acetyltransfer	0.49	-2.03	6.68E-28	SGD	639469	AHC1
YNR030W	ECM39	ExtraCellular Mutant; A Tn	2.75	2.75	7.34E-05	SGD	639477	ECM39
YNL065W	AQR1	A(acids, azoles) Q(quinidin	0.49	-2.06	4.07E-10	SGD	639491	AQR1
YDR144C	MKC7,YPS2	protease involved in protei	2.25	2.25	8.38E-06	SGD	639502	MKC7
YOL153C	YOL153C		0.38	-2.6	5.00E-40	SGD	639509	YOL153C
YLR267W	BOP2	bypass of PAM1	0.49	-2.05	8.58E-13	SGD	639515	BOP2
YER065C	ICL1	component of glyoxylate cy	0.31	-3.21	4.30E-35	SGD	639522	ICL1
YIR031C	DAL7,MLS2,MSL2	allantoin pathway; malate s	0.41	-2.47	9.31E-07	SGD	639524	DAL7
Q0130	OLI1,ATP9,OLI3	Subunit 9 of mitochondrial	4.29	4.29	1.54E-05	SGD	970682	OLI1
YML012C-	ORF:YML012C-A	BioProcess=biological_pro	2.39	2.39	9.52E-04	SGD	970687	ORF:YML012C-A
Q0297	ORF:Q0297	BioProcess=biological_pro	5.25	5.25	9.55E-05	SGD	970694	ORF:Q0297
YGL258W-	ORF:YGL258W-A	BioProcess=biological_pro	0.3	-3.39	8.41E-07	SGD	970697	ORF:YGL258W-A
YMR122W	ORF:YMR122W-A	BioProcess=biological_pro	3.09	3.09	6.27E-12	SGD	970702	ORF:YMR122W-A
Q0250	COX2,OXI1,OXII	subunit II of cytochrome c	4.06	4.06	2.57E-04	SGD	970706	COX2
YKL096W-	CWP2,LPR1	major constituent of the cel	3.07	3.07	1.62E-12	SGD	970707	CWP2
YIL009C-A	EST3	ever shorter telomeres; 20.	0.32	-3.08	1.03E-05	SGD	970717	EST3
YDR525W	SNA2	Homology to PMP3/SNA1	0.47	-2.11	4.43E-06	SGD	970734	SNA2
YAR002C-	ERP1	Emp24p/Erv25p related pr	4.38	4.38	3.12E-40	SGD	970735	ERP1
YDR363W	SEM1,HOD1	Suppressor of Exocyst Mut	2.03	2.03	3.44E-04	SGD	970742	SEM1
YNR034W	ORF:YNR034W-A	BioProcess=biological_pro	0.42	-2.39	8.34E-05	SGD	970744	ORF:YNR034W-A
YML058W	HUG1	Transcription of HUG1 is ir	3.35	3.35	1.27E-10	SGD	970746	HUG1
YFR032C-	RPL29	Homology to rat L29; ribos	2.91	2.91	1.26E-04	SGD	970749	RPL29
YDL133C-	RPL41B,MAK18,RPL47B	Homology to human L41; r	2.42	2.42	9.95E-04	SGD	970750	RPL41B
YOR298C-	MBF1	bridges the DNA-binding re	0.39	-2.6	1.21E-38	SGD	970752	MBF1
YMR013W	ORF:YMR013W-A	BioProcess=biological_pro	3.41	3.41	4.35E-05	SGD	970757	ORF:YMR013W-A
YBR058C-	TSC3	Involved in sphingolipid bio	2.04	2.04	7.55E-06	SGD	970766	TSC3
YDL114W-	ORF:YDL114W-A	BioProcess=biological_pro	0.44	-2.28	3.72E-13	SGD	970771	ORF:YDL114W-A
YPL249C-	RPL36B	Homology to rat L36; ribos	3.07	3.07	2.01E-05	SGD	970774	RPL36B
YLR149C-	ORF:YLR149C-A	BioProcess=biological_pro	2.89	2.89	3.33E-09	SGD	970775	ORF:YLR149C-A
Q0017	ORF:Q0017	BioProcess=biological_pro	2.7	2.7	5.05E-05	SGD	970779	ORF:Q0017
Q0045	COX1,OXI3	cytochrome-c oxidase subu	4.51	4.51	1.72E-06	SGD	970781	COX1
Q0050	AI1	Mobile mitochondrial group	5.36	5.36	0	SGD	970783	AI1
Q0055	AI2	Mobile mitochondrial group	3.99	3.99	0	SGD	970785	AI2

Q0060	AI3	Mobile group I intron of mit	3.54	3.54	4.51E-12	SGD	970787	AI3
YER087C-	SBH1	BioProcess=co-translationa	3.09	3.09	6.33E-05	SGD	970788	SBH1
Q0065	AI4	intron of mitochondrial CO	5.07	5.07	5.95E-16	SGD	970789	AI4
Q0070	AI5_ALPHA	Intron of mitochondrial CO	3.26	3.26	2.00E-04	SGD	970792	AI5_ALPHA
Q0075	AI5_BETA	Intron of mitochondrial CO	4.58	4.58	5.10E-14	SGD	970796	AI5_BETA
Q0140	VAR1,VARI	Mitochondrial ribosomal pr	3.16	3.16	4.01E-04	SGD	970800	VAR1
Q0105	COB,COB1,CYTB	Cytochrome b; cytochrome	5.91	5.91	2.64E-25	SGD	970802	COB
Q0182	ORF:Q0182	BioProcess=biological_pro	2.78	2.78	7.69E-06	SGD	970803	ORF:Q0182
Q0110	BI2	Mrna maturase encoded fr	6.1	6.1	1.23E-06	SGD	970805	BI2
Q0115	BI3	Mitochondrial mRNA matu	2.16	2.16	5.83E-04	SGD	970809	BI3
Q0120	BI4	Mitochondrial mRNA matu	7.39	7.39	2.83E-09	SGD	970814	BI4
Q0160	SCEI	SCEI -DNA endonuclease	4.63	4.63	1.07E-17	SGD	970819	SCEI
Q0085	ATP6,OLI2,OLI4,PHO1	Subunit 6 of mitochondrial	3.79	3.79	5.17E-05	SGD	970822	ATP6
YER053C-	ORF:YER053C-A	BioProcess=biological_pro	0.21	-4.74	2.36E-10	SGD	970826	ORF:YER053C-A
YPR133W-	TOM5,MOM8A	Translocase of the Outer M	2.15	2.15	6.16E-12	SGD	970830	TOM5