Sequence	Sequence Name(s)	Sequence Description	Ratio	Fold Chang	P-value	Sequence	Sequence I	Accession #	Primary Sequence Name
YJL032W	YJL032W		55.54	55.54	5.57E-42	SGD	634272		YJL032W
YKL084W	YKL084W		52.88	52.88	0	SGD	638967		YKL084W
YKL070W	YKL070W		46.5	46.5	0	SGD	639074		YKL070W
YCR020C	PET18,HIT2	Transcription regulator; petite, una	41.1	41.1	0	SGD	638332		PET18
YML027W	YOX1	Homeodomain protein that binds I	38.04	38.04	0	SGD	635232		YOX1
YPL172C	COX10	Required for an essential posttran	35.13	35.13	0	SGD	637915		COX10
YPL241C	CIN2	involvement in microtubule functio	34.75	34.75	0	SGD	636603		CIN2
YHR056C	RSC30	RSC complex component; Null mu	33.47	33.47	0	SGD	635511		RSC30
YER106W	MAM1	monopolin, involved in chromoson	30.88	30.88	0	SGD	635147		MAM1
YHR054C	YHR054C		30.39	30.39	0	SGD	639336		YHR054C
YCL027C-A	ORF:YCL027C-A	BioProcess=biological_process ur	25.8	25.8	4.93E-18	SGD	970683		ORF:YCL027C-A
YOL149W	DCP1	Decapping protein involved in mR	24.7	24.7	1.84E-21	SGD	634445		DCP1
YJR129C	YJR129C		23.66	23.66	0	SGD	637800		YJR129C
YGR212W	YGR212W		18.04	18.04	0	SGD	636153		YGR212W
YPL153C	RAD53,LSD1,MEC2,S	Required for DNA damage-induce	17.23	17.23	0	SGD	634782		RAD53
YJL033W	HCA4,DBP4,ECM24	putative RNA helicase; RNA helica	16.95	16.95	0	SGD	634235		HCA4
YOL056W	GPM3	converts 3-phosphoglycerate to 2-	15.97	15.97	0	SGD	636612		GPM3
YDR356W	NUF1,SPC110,XCM1	may be involved in connecting nuc	14.32	14.32	0	SGD	634640		NUF1
YBR244W	GPX2,AMI1	Glutathione peroxidase paralogue	14.16	14.16	0	SGD	634399		GPX2
YMR177W	MMT1	Protein involved in mitochondrial i	14.14	14.14	0	SGD	637113		MMT1
YLR460C	YLR460C		13.98	13.98	0	SGD	638533		YLR460C
YKL086W	YKL086W		13.83	13.83	0	SGD	633310		YKL086W
YIL025C	YIL025C		13.3	13.3	0	SGD	637507		YIL025C
YBR073W	RDH54,TID1	genetic interaction with DMC1; he	13.06	13.06	0	SGD	637316		RDH54
YKR065C	YKR065C		12.93	12.93	0	SGD	637602		YKR065C
YBL034C	STU1	Suppressor of cold-sensitive tub2	12.06	12.06	0	SGD	635692		STU1
YOL123W	HRP1,NAB4,NAB5	Putative polyadenylated-RNA-binc	11.87	11.87	9.52E-38	SGD	637116		HRP1
YFR057W	YFR057W		11.83	11.83	6.01E-34	SGD	638201		YFR057W
YPR166C	MRP2	14 kDa mitochondrial ribosomal pr	11.71	11.71	0	SGD	633542		MRP2
YLR213C	CRR1	CRH-Related	11.21	11.21	0	SGD	636773		CRR1
YOR224C	RPB8	16-kDa RNA polymerase subunit (	11.01	11.01	0	SGD	634943		RPB8
YNL075W	IMP4	Interacts With Mpp10. Imp4p is a s	10.79	10.79	0	SGD	637692		IMP4
YOL151W	GRE2	induced by osmotic stress, similar	10.72	10.72	0	SGD	633862		GRE2
YDR256C	CTA1	catalase A; Null mutant is viable a	10.5	10.5	0	SGD	638660		CTA1
YJR136C	YJR136C		10.31	10.31	1.11E-18	SGD	637037		YJR136C
YCR020C-	MAK31,LSM9,SMX1	Like Sm protein, member of the S	10.29	10.29	0	SGD	634787		MAK31

YPL242C	IQG1,CYK1	Homolog of the mammalian IQGA	10.12	10.12	0	SGD	633508	IQG1
YLR077W	YLR077W		10.09	10.09	0	SGD	636242	YLR077W
YKR077W	YKR077W		9.98	9.98	7.82E-40	SGD	636028	YKR077W
YNL252C	MRPL17,YML30	mitochondrial ribosomal protein of	9.94	9.94	0	SGD	635952	MRPL17
YEL033W	YEL033W		9.85	9.85	9.33E-35	SGD	638229	YEL033W
YGR139W	YGR139W		9.82	9.82	1.35E-38	SGD	633307	YGR139W
YOR297C	TIM18	mitochondrial inner membrane tra	9.71	9.71	0	SGD	635824	TIM18
YLR111W	YLR111W		9.41	9.41	5.18E-42	SGD	634261	YLR111W
YBR008C	FLR1	Fluconazole Resistance 1; major f	9.37	9.37	0	SGD	639463	FLR1
YNL176C	YNL176C		9.35	9.35	0	SGD	636916	YNL176C
YBR250W	YBR250W		9.16	9.16	0	SGD	635338	YBR250W
YJL051W	YJL051W		9.11	9.11	0	SGD	636319	YJL051W
YEL053C	MAK10	Glucose-repressible protein; Null r	9.04	9.04	2.48E-32	SGD	634135	MAK10
YIL167W	YIL167W		9.01	9.01	0	SGD	634972	YIL167W
YOL157C	YOL157C		8.86	8.86	0	SGD	638005	YOL157C
YJL221C	FSP2	homology to maltase(alpha-D-gluc	8.85	8.85	0	SGD	637989	FSP2
YIL172C	YIL172C	putative alpha glucosidase	8.82	8.82	0	SGD	639489	YIL172C
YNL175C	NOP13	Nucleolar Protein 13	8.75	8.75	2.02E-37	SGD	636784	NOP13
Q0297	ORF:Q0297	BioProcess=biological_process ur	8.68	8.68	1.94E-35	SGD	970694	ORF:Q0297
YOL150C	YOL150C		8.52	8.52	6.41E-26	SGD	634857	YOL150C
YNL120C	YNL120C		8.43	8.43	0	SGD	634994	YNL120C
YBR099C	YBR099C		8.38	8.38	6.19E-32	SGD	638987	YBR099C
YML130C	ERO1	involved in protein disulfide bond f	8.23	8.23	0	SGD	637967	ERO1
YPR044C	YPR044C		8.15	8.15	5.84E-43	SGD	633570	YPR044C
YOL166C	YOL166C		8.14	8.14	0	SGD	639028	YOL166C
YBL023C	MCM2	Member of complex that acts at A	8.14	8.14	1.02E-08	SGD	637300	MCM2
YKL009W	MRT4	mRna turnover 4; Null mutant exh	8.12	8.12	0	SGD	635028	MRT4
YER104W	RTT105	same phenotype as RTT101, 102,	8.1	8.1	2.19E-16	SGD	633741	RTT105
YAL011W	YAL011W	possible mitochondrial transit pept	8.05	8.05	0	SGD	636917	YAL011W
Q0255	ORF:Q0255	BioProcess=biological_process ur	7.94	7.94	1.38E-31	SGD	970691	ORF:Q0255
YHR179W	OYE2	NAPDH dehydrogenase (old yello	7.8	7.8	1.98E-25	SGD	638531	OYE2
YBR247C	ENP1,MEG1	Essential nuclear protein; 57 kDa	7.76	7.76	0	SGD	637086	ENP1
Q0275	COX3,OXI2	Cytochrome-c oxidase subunit III,	7.63	7.63	3.29E-18	SGD	970692	COX3
Q0140	VAR1,VARI	Mitochondrial ribosomal protein er	7.61	7.61	5.48E-32	SGD	970800	VAR1
YCL050C	APA1,DTP1	diadenosine 5',5'''-P1,P4-tetrapho	7.58	7.58	0	SGD	638495	APA1
YML089C	YML089C		7.55	7.55	0	SGD	635721	YML089C
YBR119W	MUD1	U1 snRNP A protein; Null mutant i	7.36	7.36	6.95E-29	SGD	638429	MUD1

YPL201C	YPL201C		7.22	7.22	5.56E-39	SGD	634037	YPL201C
YJR156C	THI11	thiamine regulated gene, homolog	7.19	7.19	0	SGD	639311	THI11
YBR284W	YBR284W		7.19	7.19	1.22E-15	SGD	634229	YBR284W
YIL168W	SDL1	L-serine dehydratase	7.15	7.15	1.22E-22	SGD	639098	SDL1
YJL050W	MTR4,DOB1	Dead-box family helicase required	7.15	7.15	3.68E-21	SGD	633437	MTR4
YEL061C	CIN8,KSL2,SDS15	Kinesin-related protein involved in	7.07	7.07	1.66E-30	SGD	637361	CIN8
YOR006C	YOR006C		6.97	6.97	1.63E-13	SGD	638441	YOR006C
YPL187W	MF(ALPHA)1	mating factor alpha; Null mutant is	6.88	6.88	5.72E-35	SGD	635007	MF(ALPHA)1
YNL155W	YNL155W		6.87	6.87	0	SGD	637653	YNL155W
Q0045	COX1,OXI3	cytochrome-c oxidase subunit I; cy	6.86	6.86	0	SGD	970781	COX1
YGR209C	TRX2	thioredoxin; Null mutant is viable,	6.82	6.82	0	SGD	638175	TRX2
YDR355C	YDR355C		6.8	6.8	1.21E-39	SGD	634880	YDR355C
YGR160W	FYV13	Function required for Yeast Viabili	6.79	6.79	4.67E-23	SGD	637596	FYV13
YFL056C	AAD6	high degree of similarity with the A	6.74	6.74	0	SGD	638319	AAD6
Q0250	COX2,OXI1,OXII	subunit II of cytochrome c oxidase	6.68	6.68	7.66E-20	SGD	970706	COX2
YOR325W	YOR325W		6.65	6.65	3.79E-37	SGD	634982	YOR325W
YLR112W	YLR112W		6.61	6.61	0	SGD	638246	YLR112W
YKR071C	DRE2	Protein required for cell viability	6.61	6.61	0	SGD	639288	DRE2
YGR152C	RSR1,BUD1	Gtp-binding protein of the ras sup	6.52	6.52	0	SGD	633785	RSR1
YDL244W	THI13	Product of gene unknown	6.5	6.5	0	SGD	633863	THI13
YOL029C	YOL029C		6.5	6.5	0	SGD	635848	YOL029C
YJL096W	MRPL49	mitochondrial ribosomal protein of	6.48	6.48	0	SGD	634466	MRPL49
YOR305W	YOR305W		6.47	6.47	7.29E-37	SGD	639144	YOR305W
Q0010	ORF:Q0010	BioProcess=biological_process ur	6.43	6.43	1.19E-16	SGD	970777	ORF:Q0010
YHR180W	YHR180W		6.33	6.33	0	SGD	634415	YHR180W
YDR532C	KRE28	Killer toxin REsistant; K1 killer tox	6.27	6.27	1.70E-14	SGD	635216	KRE28
YLR215C	CDC123	Product of gene unknown	6.26	6.26	6.46E-17	SGD	639348	CDC123
YKL187C	YKL187C		6.21	6.21	1.76E-17	SGD	634147	YKL187C
Q0080	AAP1,ATP8	Subunit 8 of Mitochondrial ATP sy	6.13	6.13	7.63E-15	SGD	970798	AAP1
YDR353W	TRR1	Thioredoxin reductase; thioredoxi	6.09	6.09	8.00E-41	SGD	635131	TRR1
Q0182	ORF:Q0182	BioProcess=biological_process ur	6.02	6.02	2.80E-45	SGD	970803	ORF:Q0182
YOL028C	YAP7	basic leucine zipper (bZIP) transc	5.95	5.95	0	SGD	637665	YAP7
YLL063C	AYT1	Transacetylase	5.93	5.93	0	SGD	639432	AYT1
YMR290W	YMR290W-A		5.92	5.92	7.93E-35	SGD	635682	YMR290W-A
YBR007C	YBR007C		5.89	5.89	0	SGD	634150	YBR007C
YCL031C	RRP7	involved in rRNA processing; Null	5.85	5.85	0	SGD	634553	RRP7
YNR073C	YNR073C		5.74	5.74	2.29E-26	SGD	635299	YNR073C

Q0055	AI2	Mobile mitochondrial group II intro	5.68	5.68	0	SGD	970785	AI2
Q0160	SCEI	SCEI -DNA endonuclease in mito	5.68	5.68	1.12E-30	SGD	970819	SCEI
YDL242W	YDL242W		5.64	5.64	8.67E-31	SGD	635761	YDL242W
YOR226C	ISU2,NUA2	Iron-sulfur cluster nifU-like protein	5.62	5.62	1.22E-39	SGD	638278	ISU2
YDR132C	YDR132C		5.58	5.58	0	SGD	638574	YDR132C
YJL219W	HXT9	High-affinity hexose transporter; h	5.56	5.56	0	SGD	634112	HXT9
YPL192C	PRM3	pheromone-regulated membrane	5.5	5.5	0	SGD	634259	PRM3
Q0110	BI2	Mrna maturase encoded from part	5.49	5.49	9.70E-21	SGD	970805	BI2
YGL058W	RAD6,UBC2	Involved in DNA repair and sporul	5.48	5.48	3.51E-29	SGD	635789	RAD6
YHL030W	ECM29	ExtraCellular Mutant; A Tn3 insert	5.47	5.47	0	SGD	635702	ECM29
YNL332W	THI12	thiamine regulated gene, homolog	5.42	5.42	0	SGD	635939	THI12
YBL096C	YBL096C		5.4	5.4	1.93E-11	SGD	634291	YBL096C
YBR088C	POL30	Accessory factor for DNA polymer	5.37	5.37	1.89E-32	SGD	635087	POL30
YLR081W	GAL2	Galactose transport, also able to t	5.37	5.37	6.68E-15	SGD	637997	GAL2
Q0060	AI3	Mobile group I intron of mitochond	5.35	5.35	7.14E-31	SGD	970787	AI3
YNL072W	RNH35	RNase H(35), a 35 kDa ribonuclea	5.28	5.28	0	SGD	635160	RNH35
YKR070W	YKR070W		5.28	5.28	0	SGD	637789	YKR070W
YPL253C	VIK1	vegetative interaction with Kar3p;	5.28	5.28	1.51E-16	SGD	637177	VIK1
YIL140W	AXL2,BUD10,SRO4	involved in polarity establishment/	5.27	5.27	6.82E-36	SGD	634224	AXL2
Q0050	AI1	Mobile mitochondrial group II intro	5.25	5.25	0	SGD	970783	AI1
YBL067C	UBP13	similar to Ubp9p; ubiquitin carboxy	5.19	5.19	0	SGD	635409	UBP13
YHR052W	CIC1,NSA3	Core interacting component 1; rib	5.18	5.18	0	SGD	636690	CIC1
YJR044C	YJR044C		5.17	5.17	0	SGD	638213	YJR044C
YNL008C	ASI3	Amino acid Sensor-Independent (	5.17	5.17	0	SGD	638796	ASI3
Q0085	ATP6,OLI2,OLI4,PHO	Subunit 6 of mitochondrial ATP sy	5.06	5.06	5.34E-19	SGD	970822	ATP6
YML091C	RPM2	involved in processing of mitochor	5.05	5.05	1.36E-27	SGD	637400	RPM2
YEL070W	YEL070W		5.03	5.03	1.70E-30	SGD	637091	YEL070W
YBR098W	MMS4,SLX2	Product of gene unknown; null is s	5.03	5.03	1.29E-14	SGD	636099	MMS4
YFL058W	THI5	proposed biosynthetic enzyme inv	5.01	5.01	0	SGD	633843	THI5
YHR204W	MNL1,HTM1	mannosidase like	4.96	4.96	0	SGD	634748	MNL1
Q0105	COB,COB1,CYTB	Cytochrome b; cytochrome b; Null	4.94	4.94	6.35E-31	SGD	970802	COB
YHR157W	REC104	meiosis-specific recombination ge	4.94	4.94	4.70E-21	SGD	637583	REC104
YDL168W	SFA1	Long-chain alcohol dehydrogenas	4.86	4.86	0	SGD	638525	SFA1
YOR005C	DNL4,LIG4	DNA ligase IV homolog; ATP depe	4.83	4.83	0	SGD	638839	DNL4
YDL027C	YDL027C		4.83	4.83	2.30E-31	SGD	636774	YDL027C
Q0017	ORF:Q0017	BioProcess=biological_process ur	4.81	4.81	0	SGD	970779	ORF:Q0017
YAL012W	CYS3,CYI1,FUN35,ST	cystathionine gamma-lyase; Null r	4.81	4.81	5.75E-14	SGD	636678	CYS3

Q0120	BI4	Mitochondrial mRNA maturase bI4	4.75	4.75	8.60E-24	SGD	970814	BI4
YGR208W	SER2	phosphoserine phosphatase; serir	4.75	4.75	4.92E-16	SGD	634544	SER2
YDR172W	SUP35,GST1,PNM2,S	altered form creates [PSI] prion; tr	4.73	4.73	2.76E-09	SGD	634587	SUP35
YML007W	YAP1,PAR1,SNQ3	jun-like transcription factor; pleiotr	4.72	4.72	5.61E-45	SGD	634566	YAP1
Q0075	AI5_BETA	Intron of mitochondrial COX1, aI5·	4.67	4.67	9.00E-20	SGD	970796	AI5_BETA
YLR108C	YLR108C		4.66	4.66	0	SGD	638596	YLR108C
YGL230C	YGL230C		4.65	4.65	0	SGD	638238	YGL230C
YLR325C	RPL38	Homology to rat L38; ribosomal pr	4.65	4.65	1.73E-30	SGD	634209	RPL38
YOR051C	YOR051C		4.63	4.63	0	SGD	636794	YOR051C
YPL051W	ARL3	Similar to ADP-ribosylation factor;	4.62	4.62	3.36E-32	SGD	633751	ARL3
YKL110C	KTI12,TOT4	Protein involved in resistance to K	4.58	4.58	0	SGD	636655	KTI12
YJR158W	HXT16	hexose transporter; hexose perme	4.53	4.53	0	SGD	634051	HXT16
YBR066C	NRG2	homologue of NRG1; NRG1 homo	4.53	4.53	2.31E-38	SGD	636586	NRG2
YAL015C	NTG1,FUN33	endonuclase III like glycosylase in	4.49	4.49	3.90E-40	SGD	636723	NTG1
YPL170W	YPL170W		4.49	4.49	7.88E-26	SGD	633374	YPL170W
YCR098C	GIT1	permease involved in the uptake o	4.48	4.48	0	SGD	636859	GIT1
YBL035C	POL12	Required for DNA synthesis and c	4.45	4.45	0	SGD	634706	POL12
YLL056C	YLL056C		4.45	4.45	0	SGD	635150	YLL056C
YKL015W	PUT3	Positive regulator of PUT (proline	4.4	4.4	3.48E-26	SGD	634698	PUT3
YJL220W	YJL220W		4.4	4.4	5.13E-15	SGD	634320	YJL220W
YGL015C	YGL015C		4.39	4.39	1.99E-31	SGD	635725	YGL015C
YKR012C	YKR012C		4.38	4.38	0	SGD	633630	YKR012C
YNL233W	BNI4	bud neck involved; required to link	4.32	4.32	0	SGD	634651	BNI4
YIL024C	YIL024C		4.32	4.32	0	SGD	639075	YIL024C
YNL212W	VID27	Vacuole import and degradation; N	4.28	4.28	0	SGD	636260	VID27
YCR102C	YCR102C		4.26	4.26	3.67E-11	SGD	639273	YCR102C
YMR277W	FCP1	TFIIF interacting Component of C	4.22	4.22	5.16E-26	SGD	638046	FCP1
YGL113W	SLD3	synthetic lethality with dpb11-1, Sl	4.21	4.21	4.08E-34	SGD	634576	SLD3
YPR151C	YPR151C		4.19	4.19	0	SGD	639111	YPR151C
YJL057C	IKS1	ira1* kinase suppressor; serine/thr	4.19	4.19	4.73E-34	SGD	638737	IKS1
YDL020C	RPN4,SON1,UFD5	involved in ubiquitin degradation p	4.18	4.18	6.06E-23	SGD	636905	RPN4
YOR028C	CIN5,HAL6,YAP4	Protein involved in silencing; bZIP	4.14	4.14	0	SGD	634494	CIN5
YDL245C	HXT15	High-affinity hexose transporter; h	4.13	4.13	0	SGD	638016	HXT15
YNL076W	MKS1,LYS80	Pleiotropic regulatory factor involv	4.11	4.11	1.92E-28	SGD	639508	MKS1
YML088W	UFO1	F-box protein; Null mutant is viable	4.06	4.06	0	SGD	635478	UFO1
YPR125W	YPR125W		4.05	4.05	0	SGD	636163	YPR125W
YDL028C	MPS1,RPK1	Required for spindle pole body du	4.04	4.04	0	SGD	636299	MPS1

YKL003C	MRP17	Mitochondrial ribosomal protein M	4.03	4.03	0	SGD	638998	MRP17
YIL143C	SSL2,LOM3,RAD25	DNA helicase homolog, homolog (	4.03	4.03	1.93E-08	SGD	638785	SSL2
YJL030W	MAD2	spindle checkpoint complex subur	4.02	4.02	0	SGD	639105	MAD2
YER081W	SER3	catalyzes the first step in serine bi	4.02	4.02	0	SGD	639419	SER3
YER093C-	YER093C-A		3.99	3.99	9.54E-22	SGD	633386	YER093C-A
YCR019W	MAK32	Protein necessary for structural st	3.99	3.99	1.98E-16	SGD	639330	MAK32
YGR142W	BTN2	Gene/protein whose expression is	3.97	3.97	0	SGD	638550	BTN2
YHR079C-	SAE3	Involved in meiotic recombination	3.93	3.93	5.87E-18	SGD	970732	SAE3
YPR174C	YPR174C		3.92	3.92	1.25E-30	SGD	634469	YPR174C
YIL141W	YIL141W		3.92	3.92	1.32E-27	SGD	637518	YIL141W
YGL029W	CGR1	coiled-coil growth-regulated; coile	3.9	3.9	1.47E-40	SGD	635658	CGR1
YLL057C	YLL057C		3.89	3.89	2.78E-34	SGD	638549	YLL057C
YNR019W	ARE2,SAT1	Acyl-CoA cholesterol acyltransfera	3.88	3.88	0	SGD	637179	ARE2
YLR260W	LCB5	involved in sphingolipid biosynthes	3.88	3.88	2.64E-35	SGD	634571	LCB5
YOL156W	HXT11,LGT3	High-affinity hexose transporter; g	3.86	3.86	4.97E-12	SGD	636191	HXT11
YER185W	YER185W		3.84	3.84	4.90E-14	SGD	634549	YER185W
YNL275W	YNL275W		3.83	3.83	0	SGD	634124	YNL275W
YGR087C	PDC6	Third, minor isozyme of pyruvate (	3.83	3.83	8.86E-24	SGD	636193	PDC6
YDR528W	HLR1	LRE1 homolog; Null mutant is vial	3.8	3.8	3.28E-18	SGD	635263	HLR1
YOL057W	YOL057W		3.79	3.79	4.62E-21	SGD	634140	YOL057W
YGR214W	RPS0A,NAB1,NAB1A,	Homology to rat Sa; ribosomal pro	3.75	3.75	0	SGD	637047	RPS0A
YDR151C	CTH1	cysteine-three histidine; CCCH zir	3.73	3.73	5.79E-43	SGD	638431	CTH1
YOL065C	INP54	INositol polyphosphate 5-Phospha	3.71	3.71	6.72E-27	SGD	635217	INP54
YDR354W	TRP4	anthranilate phosphoribosyl transf	3.69	3.69	0	SGD	635173	TRP4
YPL255W	BBP1	Involved in mitotic cell cycle and n	3.66	3.66	0	SGD	635170	BBP1
YGR048W	UFD1	Ubiquitin fusion degradation prote	3.66	3.66	0	SGD	637838	UFD1
YDR257C	RMS1	Transcription regulator; null mutar	3.65	3.65	6.36E-20	SGD	637095	RMS1
YLR162W	YLR162W		3.65	3.65	2.48E-12	SGD	639035	YLR162W
YLL042C	APG10	Involved in autophagy, protein-cor	3.64	3.64	3.53E-31	SGD	636477	APG10
YDR042C	YDR042C		3.64	3.64	6.68E-22	SGD	637630	YDR042C
YHR084W	STE12	Involved in pheromone and pseud	3.63	3.63	0	SGD	637275	STE12
YPL251W	YPL251W		3.62	3.62	1.16E-06	SGD	634216	YPL251W
YHR014W	SPO13	Spo13 acts as a transcriptional ac	3.61	3.61	2.99E-14	SGD	639266	SPO13
YLR217W	YLR217W		3.58	3.58	3.92E-44	SGD	634834	YLR217W
YJR122W	CAF17	CCR4 associated factor; CCR4 tra	3.58	3.58	1.16E-35	SGD	635286	CAF17
YLR076C	YLR076C		3.57	3.57	1.47E-29	SGD	634253	YLR076C
YML087C	YML087C		3.55	3.55	0	SGD	636673	YML087C

YIR030C	DCG1	Product of gene unknown	3.54	3.54	5.12E-22	SGD	637682	DCG1
YCR105W	YCR105W	Alcohol dehydrogenase	3.53	3.53	0	SGD	639279	YCR105W
YDR061W	YDR061W		3.52	3.52	3.58E-13	SGD	636146	YDR061W
YDL241W	YDL241W		3.52	3.52	1.06E-09	SGD	637493	YDL241W
YCL044C	YCL044C		3.5	3.5	4.30E-37	SGD	637023	YCL044C
YER148W	SPT15,BTF1,TBP1,TF	TATA-binding protein (tfIId); TFIID	3.5	3.5	8.52E-33	SGD	639161	SPT15
YNL065W	AQR1	A(acids, azoles) Q(quinidine, quin	3.49	3.49	0	SGD	639491	AQR1
YMR067C	YMR067C		3.48	3.48	1.02E-29	SGD	638607	YMR067C
YGR211W	ZPR1	Involved in nucleolar function, sim	3.47	3.47	4.01E-35	SGD	637101	ZPR1
YML028W	TSA1,TPX1,ZRG14	antioxidant enzyme that provides	3.46	3.46	2.47E-40	SGD	633736	TSA1
YLR026C	SED5	Sed5p is a t-SNARE (soluble NSF	3.46	3.46	6.43E-26	SGD	637799	SED5
YKL043W	PHD1	protein similar to StuA of Aspergill	3.42	3.42	0	SGD	637779	PHD1
YBR184W	MEL1	alpha-galactosidase; lack of melib	3.42	3.42	8.80E-35	SGD	635403	MEL1
YNL108C	YNL108C		3.41	3.41	0	SGD	635879	YNL108C
YOR338W	YOR338W		3.41	3.41	1.12E-39	SGD	639278	YOR338W
YER050C	RSM18	protein similar to bacterial riboson	3.41	3.41	1.34E-16	SGD	635815	RSM18
YNL102W	POL1,CDC17,CRT5,H	Required for mitotic DNA synthesi	3.4	3.4	9.16E-17	SGD	638965	POL1
YFL016C	MDJ1	involved in protection against heat	3.38	3.38	0	SGD	635329	MDJ1
YNR074C	YNR074C		3.37	3.37	0	SGD	635237	YNR074C
YMR318C	YMR318C		3.37	3.37	3.10E-14	SGD	639280	YMR318C
YDR004W	RAD57	Required for X-ray damage repair	3.36	3.36	4.90E-43	SGD	639440	RAD57
YJR048W	CYC1	iso-1-cytochrome c; Cytochrome c	3.36	3.36	3.10E-31	SGD	634295	CYC1
YHR124W	NDT80	Meiosis-specific gene, mRNA is sp	3.35	3.35	3.92E-44	SGD	636907	NDT80
YPL124W	NIP29,LPH3,SPC29	Nuclear import protein; spindle po	3.34	3.34	2.44E-11	SGD	638348	NIP29
YGR223C	YGR223C		3.33	3.33	6.66E-41	SGD	633942	YGR223C
YNL123W	YNL123W		3.32	3.32	0	SGD	638836	YNL123W
YNR071C	YNR071C		3.31	3.31	0	SGD	637731	YNR071C
YPR048W	TAH18	Product of gene unknown; tah18-1	3.3	3.3	0	SGD	636911	TAH18
YNL333W	SNZ2	Snooze: stationary phase-induced	3.3	3.3	0	SGD	638392	SNZ2
YBR292C	YBR292C		3.3	3.3	0	SGD	639008	YBR292C
Q0130	OLI1,ATP9,OLI3	Subunit 9 of mitochondrial ATP sy	3.3	3.3	1.99E-14	SGD	970682	OLI1
YFR039C	YFR039C		3.28	3.28	2.14E-24	SGD	635345	YFR039C
YPL173W	MRPL40	Mitochondrial ribosomal protein M	3.27	3.27	0	SGD	634554	MRPL40
YDR523C	SPS1	dispensable for mitosis, involved i	3.27	3.27	1.41E-12	SGD	637082	SPS1
YNR064C	YNR064C		3.27	3.27	1.14E-09	SGD	637708	YNR064C
YPL107W	YPL107W		3.26	3.26	0	SGD	635886	YPL107W
YML047W-	ORF:YML047W-A	BioProcess=biological_process ur	3.26	3.26	2.06E-15	SGD	970725	ORF:YML047W-A

YER044C-	MEI4	Functions in early recombination;	3.24	3.24	1.07E-21	SGD	633465	MEI4
YBL033C	RIB1	First step in the riboflavin biosynth	3.23	3.23	0	SGD	635983	RIB1
YMR061W	RNA14	Protein with a role in mRNA stabil	3.23	3.23	7.67E-13	SGD	635459	RNA14
YNL231C	PDR16	involved in pleiotropic drug resista	3.21	3.21	0	SGD	633870	PDR16
YDL064W	UBC9	ubiquitin-conjugating enzyme; Nul	3.2	3.2	0	SGD	637637	UBC9
YAL010C	MDM10,FUN37	Mitochondrial outer membrane pro	3.2	3.2	5.44E-05	SGD	638631	MDM10
YNL135C	FPR1,FKB1,RBP1	FK506 binding protein, proline rota	3.18	3.18	1.54E-14	SGD	633543	FPR1
YOR266W	PNT1	Involved in targeting of proteins to	3.18	3.18	9.37E-14	SGD	635248	PNT1
YDR368W	YPR1	homologous to the aldo-keto redu	3.16	3.16	0	SGD	635121	YPR1
YDR218C	SPR28	Septin-related protein expressed d	3.16	3.16	1.42E-16	SGD	635247	SPR28
YBR018C	GAL7	galactose-1-phosphate uridyl trans	3.16	3.16	2.29E-13	SGD	633963	GAL7
YHR176W	YHR176W	Dimethylaniline monoxygenase	3.15	3.15	8.03E-35	SGD	633888	YHR176W
YIL066C	RNR3,DIN1,RIR3	Ribonucleotide reductase (ribonuc	3.13	3.13	0	SGD	638765	RNR3
YML092C	PRE8	proteasome component Y7	3.13	3.13	4.58E-38	SGD	637677	PRE8
YKR097W	PCK1,JPM2,PPC1	phosphoenolpyruvate carboxylkina	3.13	3.13	1.20E-09	SGD	636201	PCK1
YEL069C	HXT13	high-affinity hexose transporter; hi	3.12	3.12	8.94E-22	SGD	636209	HXT13
YNL251C	NRD1	RNA recognition motif-containing p	3.12	3.12	5.91E-19	SGD	638012	NRD1
YGL091C	NBP35	NBP35 encodes an essential evol	3.12	3.12	1.62E-06	SGD	636957	NBP35
YOR058C	ASE1	essential for anaphase spindle elo	3.11	3.11	0	SGD	637297	ASE1
YJL143W	TIM17,MIM17,MPI2,SN	Mitochondrial inner membrane pro	3.11	3.11	4.99E-25	SGD	634996	TIM17
YOR344C	TYE7,SGC1	may be involved in glycolytic gene	3.11	3.11	2.92E-22	SGD	639251	TYE7
YMR037C	MSN2	multicopy suppressor of snf1 muta	3.1	3.1	1.58E-21	SGD	638038	MSN2
YGR146C	YGR146C		3.09	3.09	6.97E-06	SGD	634461	YGR146C
YNL230C	ELA1	similar to mammalian elongin A, in	3.08	3.08	0	SGD	636737	ELA1
YHL024W	RIM4	Regulator of IMe2 expression; RN	3.08	3.08	1.66E-39	SGD	634155	RIM4
YLR064W	YLR064W		3.08	3.08	3.25E-11	SGD	637669	YLR064W
YNL077W	YNL077W		3.07	3.07	0	SGD	637119	YNL077W
YGR055W	MUP1	high affinity methionine permease	3.07	3.07	6.73E-24	SGD	636171	MUP1
YIL171W	HXT12	High level of sequence similarity to	3.06	3.06	0	SGD	638166	HXT12
YJL035C	TAD2	tRNA-specific adenosine-34 deam	3.06	3.06	6.35E-33	SGD	633792	TAD2
YOR361C	PRT1,CDC63,DNA26	translation initiation factor eIF3 su	3.06	3.06	2.91E-18	SGD	636264	PRT1
YGR059W	SPR3	a sporulation-specific homologue o	3.06	3.06	1.91E-09	SGD	637112	SPR3
Q0065	AI4	intron of mitochondrial COX1; I-Sc	3.04	3.04	0	SGD	970789	AI4
YKR067W	GPT2	Encodes a Glycerol-3-phosphate a	3.04	3.04	1.66E-33	SGD	633406	GPT2
YOR152C	YOR152C		3.03	3.03	7.81E-14	SGD	635105	YOR152C
YOL036W	YOL036W		3.02	3.02	0	SGD	634186	YOL036W
YPL108W	YPL108W		3.02	3.02	0	SGD	634395	YPL108W

YBR148W	YSW1	Spore-specific protein	3.02	3.02	0	SGD	636923	YSW1
YMR006C	PLB2	Phospholipase B 2; lysophospholi	3.02	3.02	2.04E-23	SGD	633380	PLB2
YNR075W	COS10	Protein with strong similarity to su	3.01	3.01	0	SGD	636036	COS10
YDL122W	UBP1	Ubiquitin-specific protease; ubiqui	3	3	0	SGD	634812	UBP1
YHL022C	SPO11	Dispensable for mitosis, premeioti	3	3	9.14E-22	SGD	636717	SPO11
YGR265W	YGR265W		2.99	2.99	1.15E-10	SGD	634936	YGR265W
YDR071C	YDR071C		2.98	2.98	0	SGD	639178	YDR071C
YLR457C	NBP1	Nap1p Binding Protein; Null mutar	2.98	2.98	2.09E-16	SGD	634518	NBP1
YCR020W	HTL1	High-Temperature Lethal; Null mu	2.98	2.98	2.21E-14	SGD	970797	HTL1
YAL068C	YAL068C		2.97	2.97	0	SGD	633395	YAL068C
YHR198C	YHR198C		2.97	2.97	0	SGD	636715	YHR198C
YIL026C	IRR1,SCC3	Irregular, involved in sister chroma	2.97	2.97	1.01E-33	SGD	635558	IRR1
YPL001W	HAT1	histone acetyltransferase; Null mu	2.97	2.97	1.06E-08	SGD	639338	HAT1
YBR255C-	ORF:YBR255C-A	BioProcess=biological_process ur	2.96	2.96	0	SGD	970700	ORF:YBR255C-A
YFR050C	PRE4	B-type subunit of proteasome, eul	2.95	2.95	8.31E-43	SGD	633713	PRE4
YAR053W	YAR053W	predicted membrane protein	2.95	2.95	2.67E-32	SGD	634207	YAR053W
YFL048C	EMP47	47 kDa type I transmembrane pro	2.95	2.95	1.21E-25	SGD	637877	EMP47
YLR073C	YLR073C		2.94	2.94	0	SGD	639170	YLR073C
YLR113W	HOG1,SSK3	osmoregulation; MAP kinase; Null	2.94	2.94	1.90E-22	SGD	637884	HOG1
YMR257C	PET111	translational activator of cytochror	2.93	2.93	4.36E-41	SGD	634245	PET111
YHL002W	YHL002W	SH3 domain	2.93	2.93	3.49E-20	SGD	639446	YHL002W
YAL007C	ERP2	Emp24p/Erv25p related protein 2;	2.93	2.93	6.98E-14	SGD	636524	ERP2
YBR167C	POP7,RPP2	Processing of Precursors; RNase	2.92	2.92	1.96E-23	SGD	634346	POP7
YDL098C	SNU23	23 kD U4/U6.U5 snRNP associate	2.92	2.92	2.98E-17	SGD	639106	SNU23
YDR157W	YDR157W		2.92	2.92	3.18E-15	SGD	634938	YDR157W
YOR333C	YOR333C		2.92	2.92	7.29E-05	SGD	634950	YOR333C
YJL058C	YJL058C		2.91	2.91	1.88E-13	SGD	636204	YJL058C
YDR131C	YDR131C		2.91	2.91	2.36E-11	SGD	636213	YDR131C
YGR151C	YGR151C		2.91	2.91	9.53E-10	SGD	633578	YGR151C
YLR297W	YLR297W		2.9	2.9	0	SGD	635711	YLR297W
YHR062C	RPP1	Ribonuclease P protein 1, require	2.9	2.9	2.82E-07	SGD	633808	RPP1
YKL082C	YKL082C		2.89	2.89	0	SGD	634005	YKL082C
YKL085W	MDH1	mitochondrial malate dehydrogena	2.89	2.89	3.69E-41	SGD	639300	MDH1
YLR042C	YLR042C		2.89	2.89	8.13E-28	SGD	638274	YLR042C
YML032C	RAD52	Required for X-ray damage repair	2.88	2.88	7.74E-20	SGD	636868	RAD52
YFR004W	RPN11,MPR1	Suppressor of mutant (ts on glyce	2.87	2.87	0	SGD	635144	RPN11
YOR214C	YOR214C		2.86	2.86	1.95E-11	SGD	634425	YOR214C

YIL170W	HXT12	High level of sequence similarity t	2.84	2.84	0	SGD	636160	HXT12
YOL162W	YOL162W		2.84	2.84	5.36E-08	SGD	638333	YOL162W
YPL202C	AFT2	Activator of Iron (Fe) Transcriptior	2.83	2.83	1.09E-14	SGD	638547	AFT2
YDR195W	REF2	RNA-binding protein involved in cl	2.83	2.83	1.99E-11	SGD	637154	REF2
YMR309C	NIP1	Protein required for nuclear impor	2.82	2.82	3.77E-13	SGD	634226	NIP1
YKL115C	YKL115C		2.81	2.81	0	SGD	639000	YKL115C
YMR266W	RSN1	overexpression Rescues sro7/sop	2.81	2.81	1.67E-19	SGD	637315	RSN1
YGR143W	SKN1	Involved in (1->6)-beta-glucan bio	2.81	2.81	2.57E-17	SGD	638077	SKN1
YDR449C	YDR449C		2.81	2.81	7.43E-08	SGD	639393	YDR449C
YMR172C-	YMR172C-A		2.8	2.8	4.05E-15	SGD	635745	YMR172C-A
YOL124C	YOL124C		2.8	2.8	1.39E-12	SGD	636047	YOL124C
YPR094W	YPR094W		2.79	2.79	0	SGD	638154	YPR094W
YFL017C	GNA1	involved in UDP-N-acetylglucosan	2.79	2.79	1.54E-30	SGD	638260	GNA1
YDR515W	SLF1,SRO99	Associates with translating riboso	2.79	2.79	1.92E-28	SGD	633996	SLF1
YNL183C	NPR1	protein kinase homolog; inactive a	2.78	2.78	9.10E-36	SGD	636375	NPR1
YFR010W	UBP6	deubiquitinating enzyme (putative)	2.78	2.78	4.80E-18	SGD	636871	UBP6
YLR168C	MSF1'	possibly involved in intramitochon	2.77	2.77	6.24E-29	SGD	634446	MSF1'
YCL029C	BIK1,ARM5,PAC14	Microtubule-associated protein re	2.77	2.77	5.48E-11	SGD	633931	BIK1
YKL087C	CYT2	links heme covalently to apocytoc	2.77	2.77	1.37E-09	SGD	636583	CYT2
YMR175W	SIP18	Salt-Induced Protein; Null mutant	2.76	2.76	7.89E-23	SGD	633396	SIP18
YOR309C	YOR309C		2.76	2.76	1.02E-16	SGD	635731	YOR309C
YKL054C	VID31	Vacuole import and degradation	2.76	2.76	2.98E-14	SGD	636221	VID31
YOR050C	YOR050C		2.76	2.76	6.26E-14	SGD	639024	YOR050C
YGL212W	VAM7,VPS43	Regulator of vacuolar morphogen	2.76	2.76	6.11E-12	SGD	638455	VAM7
YLL054C	YLL054C		2.75	2.75	0	SGD	634753	YLL054C
YKR101W	SIR1	repressor of silent mating loci; sile	2.75	2.75	1.19E-23	SGD	634630	SIR1
YML093W	YML093W		2.74	2.74	6.98E-36	SGD	637279	YML093W
YCR104W	PAU3	member of the seripauperin protei	2.74	2.74	4.77E-20	SGD	633615	PAU3
YFL059W	SNZ3	Snooze: stationary phase-induced	2.74	2.74	6.43E-11	SGD	634491	SNZ3
YOL079W	YOL079W		2.74	2.74	1.82E-09	SGD	639092	YOL079W
YNL188W	KAR1	involved in spindle pole body dupl	2.73	2.73	1.05E-37	SGD	637852	KAR1
YBL042C	FUI1	uridine permease; Null mutant is v	2.73	2.73	5.12E-15	SGD	637143	FUI1
YLR163C	MAS1,MIF1	mitochondrial processing protease	2.72	2.72	0	SGD	636105	MAS1
YNL335W	YNL335W		2.71	2.71	7.48E-19	SGD	634381	YNL335W
YKL107W	YKL107W		2.7	2.7	0	SGD	635158	YKL107W
YLR075W	RPL10,GRC5,QSR1	similar to members of the QM gen	2.7	2.7	3.44E-13	SGD	638296	RPL10
YJL197W	UBP12	ubiquitin carboxyl-terminal hydrola	2.69	2.69	0	SGD	635588	UBP12

YMR270C	RRN9	Upstream activation factor subunit	2.69	2.69	5.23E-27	SGD	639329	RRN9
YML077W	BET5	Bet5p/18kD component of TRAPF	2.69	2.69	3.26E-12	SGD	636467	BET5
YER054C	GIP2	Glc7-interacting protein, shares ho	2.68	2.68	0	SGD	637921	GIP2
YHL036W	MUP3	methionine uptake; very low affinit	2.68	2.68	8.79E-37	SGD	639464	MUP3
YEL072W	YEL072W		2.68	2.68	6.28E-19	SGD	636578	YEL072W
YMR004W	MVP1	Protein required for sorting protein	2.68	2.68	2.39E-09	SGD	637128	MVP1
YNR048W	YNR048W		2.67	2.67	3.13E-15	SGD	635228	YNR048W
YDR183W	PLP1	Phosducin-Like Protein; Null muta	2.66	2.66	5.03E-09	SGD	636497	PLP1
YHL029C	YHL029C		2.65	2.65	2.96E-34	SGD	635458	YHL029C
YFL061W	YFL061W		2.65	2.65	4.77E-33	SGD	634959	YFL061W
Q0115	BI3	Mitochondrial mRNA maturase bI3	2.65	2.65	9.24E-09	SGD	970809	BI3
YLR066W	SPC3	signal peptidase subunit; Null mut	2.65	2.65	6.42E-07	SGD	637549	SPC3
YCR018C-	ORF:YCR018C-A	BioProcess=biological_process un	2.64	2.64	2.82E-14	SGD	970824	ORF:YCR018C-A
YJR064W	CCT5,TCP5	Required for assembly of microtub	2.64	2.64	3.80E-14	SGD	634070	CCT5
YLR037C	DAN2	Delayed anaerobic gene; putative	2.63	2.63	9.61E-32	SGD	635733	DAN2
YLR151C	PCD1	peroxisomal nudix hydrolase activ	2.62	2.62	3.69E-26	SGD	637733	PCD1
YMR046W	ORF:YMR046W-A	BioProcess=biological_process un	2.62	2.62	2.36E-13	SGD	970695	ORF:YMR046W-A
YOL116W	MSN1,FUP1,HRB382,	multicopy supressor of snf1 and s	2.62	2.62	6.98E-13	SGD	635172	MSN1
YPR152C	YPR152C		2.61	2.61	2.58E-30	SGD	639406	YPR152C
YMR101C	SRT1	cis-prenyltransferase homologue;	2.61	2.61	6.77E-17	SGD	639308	SRT1
YAR008W	SEN34,FUN4	tRNA splicing endonuclease 34kD	2.6	2.6	2.40E-08	SGD	635903	SEN34
YGL116W	CDC20,PAC5	Required for onset of anaphase; a	2.59	2.59	8.22E-18	SGD	638712	CDC20
YOR208W	PTP2	protein tyrosine phosphatase; tyro	2.59	2.59	3.17E-12	SGD	634190	PTP2
YBL078C	AUT7,APG8,CVT5	Forms a protein complex with Aut	2.58	2.58	0	SGD	633586	AUT7
YKL205W	LOS1	Nuclear pore protein involved in p	2.58	2.58	0	SGD	638890	LOS1
YJR024C	YJR024C		2.58	2.58	3.24E-31	SGD	637650	YJR024C
YGR224W	AZR1	MFS-MDR	2.58	2.58	2.07E-09	SGD	636921	AZR1
YDR184C	ATC1	interacts with AIP3, localized to th	2.57	2.57	5.68E-26	SGD	635068	ATC1
YML116W	ATR1,SNQ1	aminotriazole resistance; very hyd	2.57	2.57	5.62E-14	SGD	639466	ATR1
YGL188C	YGL188C		2.57	2.57	1.45E-08	SGD	634790	YGL188C
YKL069W	YKL069W		2.55	2.55	0	SGD	635799	YKL069W
YKL042W	SPC42	involved in SPB duplication, may f	2.55	2.55	1.02E-27	SGD	633880	SPC42
YLR214W	FRE1	Ferric (and cupric) reductase; cup	2.55	2.55	3.62E-15	SGD	638732	FRE1
YGR291C	YGR291C		2.55	2.55	4.47E-15	SGD	634200	YGR291C
YOR310C	NOP58	57 kDa nucleolar protein involved	2.54	2.54	6.73E-19	SGD	636848	NOP58
YKL066W	YKL066W		2.54	2.54	4.11E-08	SGD	636377	YKL066W
YPR202W	YPR202W		2.54	2.54	7.66E-07	SGD	635947	YPR202W

YNL129W	YNL129W		2.53	2.53	0	SGD	633799	YNL129W
YOL140W	ARG8	Acetylornithine aminotransferase;	2.53	2.53	0	SGD	636757	ARG8
YJL103C	YJL103C		2.53	2.53	0	SGD	637145	YJL103C
YBR042C	YBR042C	Probable membrane-bound small	2.53	2.53	0	SGD	638502	YBR042C
YER143W	DDI1,VSM1	DNA Damage Inducible, binds to	2.53	2.53	2.78E-37	SGD	637826	DDI1
YKL083W	YKL083W		2.52	2.52	5.02E-18	SGD	633286	YKL083W
YGL215W	CLG1	cyclin-like protein that interacts wi	2.52	2.52	3.52E-09	SGD	639430	CLG1
YOL068C	HST1	Homolog of SIR2; Overexpressior	2.51	2.51	8.47E-41	SGD	635314	HST1
YGR249W	MGA1	Mga1p shows similarity to heat sh	2.51	2.51	1.91E-23	SGD	634040	MGA1
YNL151C	RPC31,ACP2,RPC8	31-kDa subunit of RNA polymeras	2.51	2.51	2.84E-12	SGD	635024	RPC31
YKR040C	YKR040C		2.51	2.51	2.88E-07	SGD	634396	YKR040C
YNR062C	YNR062C		2.51	2.51	3.98E-07	SGD	638430	YNR062C
YOR204W	DED1,SPP81	ATP-dependent RNA helicase of	2.51	2.51	6.68E-05	SGD	636886	DED1
YER179W	DMC1,ISC2	Disp. for double strand breaks, sy	2.5	2.5	1.17E-35	SGD	639345	DMC1
YMR179W	SPT21	involved in trascriptional regulatio	2.5	2.5	1.12E-32	SGD	636317	SPT21
YPL106C	SSE1,LPG3,MSI3	HSP70 family member, highly hon	2.5	2.5	5.69E-16	SGD	636217	SSE1
YBR100W	YBR100W		2.5	2.5	4.98E-14	SGD	635670	YBR100W
YPL239W	YAR1	YAR1 encodes a 200-amino-acid	2.5	2.5	9.42E-10	SGD	633732	YAR1
YBR243C	ALG7,TUR1	ER protein that transfers Glc-Nac-	2.49	2.49	3.18E-43	SGD	637875	ALG7
YER091C-	ORF:YER091C-A	BioProcess=biological_process ur	2.49	2.49	1.65E-34	SGD	970807	ORF:YER091C-A
YCL021W-	ORF:YCL021W-A	BioProcess=biological_process ur	2.49	2.49	1.87E-18	SGD	970801	ORF:YCL021W-A
YGL252C	RTG2	Protein involved in interorganelle	2.49	2.49	1.97E-08	SGD	634101	RTG2
YJL223C	PAU1	member of the seripauperin protei	2.49	2.49	9.31E-08	SGD	639047	PAU1
YOR304W	ISW2	has strong homology to Drosophil	2.48	2.48	2.48E-25	SGD	637390	ISW2
YLR312W-	MRPL15	Mitochondrial ribosomal protein M	2.48	2.48	7.97E-16	SGD	633350	MRPL15
YER042W	MXR1,MSRA	peptide Methionine sulfoXide Red	2.46	2.46	4.13E-41	SGD	633593	MXR1
YHR065C	RRP3	Required for maturation of the 35	2.46	2.46	9.01E-22	SGD	636144	RRP3
YPL279C	YPL279C		2.46	2.46	1.80E-12	SGD	637773	YPL279C
YPR065W	ROX1,REO1	The ROX1 gene encodes a heme-	2.46	2.46	2.75E-09	SGD	639342	ROX1
YHR205W	SCH9,KOM1	protein kinase involved in growth	2.45	2.45	3.13E-25	SGD	638108	SCH9
YKL223W	YKL223W		2.45	2.45	9.02E-25	SGD	638148	YKL223W
YKL106W	AAT1	aspartate aminotransferase, mitoc	2.45	2.45	2.53E-17	SGD	639355	AAT1
YGR062C	COX18	cytochrome oxidase gene 18; Null	2.45	2.45	1.36E-07	SGD	636967	COX18
YJL060W	YJL060W		2.44	2.44	0	SGD	633998	YJL060W
YER149C	PEA2,DFG9,PPF2	Pea2p is localized with Spa2p to	2.44	2.44	0	SGD	635265	PEA2
YDR331W	GPI8	Protein involved in the attachment	2.44	2.44	5.57E-37	SGD	638566	GPI8
YLR067C	PET309	Involved in expression of mitocho	2.44	2.44	3.72E-35	SGD	638809	PET309

YJR120W	YJR120W		2.44	2.44	3.15E-34	SGD	635680	YJR120W
YBR172C	SMY2	partial suppressor of myo2-66; Nu	2.44	2.44	6.74E-34	SGD	638074	SMY2
YDR002W	YRB1,CST20,HTN1,SI	Yeast Ran Binder #1, suppressor	2.44	2.44	5.88E-30	SGD	635847	YRB1
YIR012W	SQT1	Involved in a late step of 60S ribos	2.44	2.44	5.90E-24	SGD	633938	SQT1
YJR030C	YJR030C		2.44	2.44	1.23E-14	SGD	634191	YJR030C
YKL044W	YKL044W		2.44	2.44	8.78E-14	SGD	636325	YKL044W
YLR020C	YLR020C		2.44	2.44	1.72E-10	SGD	639484	YLR020C
YHR126C	YHR126C		2.44	2.44	4.61E-10	SGD	634328	YHR126C
YIL142W	CCT2,BIN3,TCP2	cytoplasmic chaperonin of the Cct	2.44	2.44	1.29E-07	SGD	637157	CCT2
YKL068W	NUP100,NSP100	Participates in nucleocytoplasmic	2.43	2.43	6.86E-33	SGD	634680	NUP100
YOL122C	SMF1,SBS1	Isolated as high copy suppressor	2.43	2.43	2.22E-10	SGD	637960	SMF1
YLR372W	SUR4,ELO3,SRE1,VB	Required for conversion of 24-carl	2.42	2.42	0	SGD	633875	SUR4
YNL036W	NCE103	involved in secretion of proteins th	2.42	2.42	0	SGD	634452	NCE103
YJL090C	DPB11	Part of the DNA polymerase II cor	2.42	2.42	7.74E-20	SGD	638079	DPB11
YOL106W	YOL106W		2.42	2.42	6.72E-04	SGD	637438	YOL106W
YJR070C	YJR070C		2.41	2.41	0	SGD	636646	YJR070C
YER012W	PRE1	Required for mitotic division and s	2.41	2.41	0	SGD	637616	PRE1
YLR313C	SPH1	SPa2-Homolog, protein involved i	2.41	2.41	2.73E-16	SGD	636890	SPH1
YMR325W	YMR325W		2.41	2.41	1.10E-15	SGD	633616	YMR325W
YNR034W	SOL1	Multicopy Suppressor Of los1; Nu	2.41	2.41	3.30E-09	SGD	638480	SOL1
YNR066C	YNR066C		2.4	2.4	0	SGD	633950	YNR066C
YPL212C	PUS1	Involved in tRNA biogenesis; tRN	2.4	2.4	0	SGD	634064	PUS1
YDR194C	MSS116	Mitochondrial RNA helicase of the	2.4	2.4	0	SGD	635479	MSS116
YGL260W	YGL260W		2.4	2.4	2.59E-30	SGD	634788	YGL260W
YHL046C	YHL046C		2.4	2.4	1.25E-10	SGD	635674	YHL046C
YGR039W	YGR039W		2.39	2.39	3.80E-32	SGD	634841	YGR039W
YLR223C	IFH1	Interacts with fork head protein. P	2.39	2.39	2.89E-26	SGD	637340	IFH1
YIL108W	YIL108W		2.39	2.39	4.56E-18	SGD	634709	YIL108W
YGL244W	RTF1,CSL3	Directly or indirectly regulates the	2.39	2.39	4.69E-17	SGD	637917	RTF1
YDL039C	PRM7	pheromone-regulated membrane	2.39	2.39	5.46E-16	SGD	637440	PRM7
YNL061W	NOP2,YNA1	May participate in nucleolar functi	2.39	2.39	3.06E-14	SGD	636935	NOP2
YDR213W	UPC2,MOX4	involved in sterol uptake; zinc fing	2.39	2.39	3.10E-11	SGD	638813	UPC2
YJR072C	YJR072C		2.39	2.39	1.48E-09	SGD	636748	YJR072C
YIL075C	RPN2,SEN3	involved in tRNA processing and	2.39	2.39	4.54E-08	SGD	634678	RPN2
YFR043C	YFR043C		2.39	2.39	5.83E-07	SGD	635095	YFR043C
YLR329W	REC102	Dispensable for mitotic recombina	2.38	2.38	5.75E-16	SGD	639134	REC102
YCR102W	ORF:YCR102W-A	BioProcess=biological_process ur	2.37	2.37	0	SGD	970817	ORF:YCR102W-A

YNR072W	HXT17	Hexose transporter; hexose transp	2.37	2.37	5.50E-38	SGD	639470	HXT17
YLR458W	YLR458W		2.37	2.37	1.30E-30	SGD	633629	YLR458W
YDR394W	RPT3,YNT1,YTA2	probable 26S protease subunit an	2.37	2.37	1.17E-27	SGD	637810	RPT3
YIL174W	YIL174W		2.37	2.37	1.41E-26	SGD	638103	YIL174W
YGL214W	YGL214W		2.37	2.37	1.39E-20	SGD	636535	YGL214W
YJL043W	YJL043W		2.37	2.37	2.20E-17	SGD	634432	YJL043W
YDL185C-A	ORF:YDL185C-A	BioProcess=biological_process ur	2.37	2.37	5.48E-05	SGD	970703	ORF:YDL185C-A
YLR205C	HMX1	Homology to heme oxygenases; N	2.36	2.36	1.68E-25	SGD	633800	HMX1
YLL046C	RNP1	ribonucleoprotein 1; RNA binding	2.36	2.36	1.86E-18	SGD	635885	RNP1
YOR082C	YOR082C		2.35	2.35	6.53E-31	SGD	633560	YOR082C
YBL022C	PIM1,LON1	mitochondrial ATP-dependent pro	2.35	2.35	2.22E-27	SGD	633494	PIM1
YDR488C	PAC11	Protein required in the absence of	2.35	2.35	1.06E-17	SGD	636904	PAC11
YNR051C	BRE5	protein of unknown function; null r	2.35	2.35	5.51E-16	SGD	636861	BRE5
YPL237W	SUI3	beta subunit of translation initiatio	2.35	2.35	2.26E-14	SGD	639203	SUI3
YNL211C	YNL211C		2.35	2.35	3.37E-11	SGD	634218	YNL211C
YNL064C	YDJ1,MAS5	yeast dnaJ homolog (nuclear enve	2.35	2.35	2.24E-08	SGD	638551	YDJ1
YJL218W	YJL218W		2.34	2.34	5.21E-22	SGD	637619	YJL218W
YDL167C	NRP1	asparagine-rich protein	2.34	2.34	6.45E-22	SGD	638049	NRP1
YPR136C	FYV15	Function required for Yeast Viabili	2.34	2.34	3.17E-17	SGD	637480	FYV15
YKL055C	OAR1	3-oxoacyl-[acyl-carrier-protein] rec	2.34	2.34	7.51E-12	SGD	635938	OAR1
YOR143C	THI80	Thiamin pyrophosphokinase; thiar	2.33	2.33	4.73E-35	SGD	636701	THI80
YPL091W	GLR1,LPG17	converts oxidized glutathine and N	2.33	2.33	1.02E-26	SGD	638638	GLR1
YBL109W	YBL109W		2.33	2.33	1.48E-12	SGD	633297	YBL109W
YDR426C	YDR426C		2.33	2.33	5.01E-08	SGD	633365	YDR426C
YMR014W	BUD22	Null mutant is viable, random bud	2.33	2.33	7.92E-07	SGD	637161	BUD22
YKR011C	TOS5	Hypothetical ORF	2.33	2.33	1.28E-06	SGD	633902	TOS5
YLL044W	YLL044W		2.33	2.33	1.68E-04	SGD	638237	YLL044W
YMR276W	DSK2	Required with RAD23 for duplicati	2.32	2.32	1.30E-32	SGD	636021	DSK2
YNR020C	YNR020C		2.32	2.32	2.11E-07	SGD	639231	YNR020C
YOL148C	SPT20,ADA5	Transcription factor; histone acety	2.31	2.31	0	SGD	637195	SPT20
YGL148W	ARO2	Chorismate synthase; chorismate	2.31	2.31	2.03E-40	SGD	638516	ARO2
YMR317W	YMR317W		2.31	2.31	2.57E-37	SGD	638871	YMR317W
YDL143W	CCT4,TCP4	cytoplasmic chaperonin subunit re	2.31	2.31	1.09E-19	SGD	636854	CCT4
YGL261C	YGL261C		2.31	2.31	1.10E-15	SGD	637531	YGL261C
YPL021W	ECM23,SRD2	ExtraCellular Mutant, similar to SF	2.31	2.31	1.29E-15	SGD	637563	ECM23
YDL202W	MRPL11	Mitochondrial ribosomal protein M	2.31	2.31	1.07E-13	SGD	633716	MRPL11
YJL209W	CBP1	Protein required for COB mRNA s	2.31	2.31	1.86E-13	SGD	637238	CBP1

YDR503C	LPP1	Lipid phosphate phosphatase; lipi	2.3	2.3	3.23E-16	SGD	639211	LPP1
YBL077W	YBL077W		2.3	2.3	1.37E-14	SGD	634945	YBL077W
YDR153C	YDR153C		2.3	2.3	7.31E-10	SGD	635254	YDR153C
YKL116C	PRR1	protein kinase	2.3	2.3	2.45E-07	SGD	638617	PRR1
YER006W	NUG1	NUclear GTPase; Nuclear GTPas	2.29	2.29	0	SGD	635324	NUG1
YGL217C	YGL217C		2.29	2.29	1.81E-25	SGD	639026	YGL217C
YJR091C	JSN1,PUF1	benomyl dependent tubulin mutan	2.29	2.29	7.14E-19	SGD	635599	JSN1
YDR173C	ARG82,ARGR3,IPK2	Regulator of arginine-responsive g	2.29	2.29	6.52E-17	SGD	637771	ARG82
YKL093W	MBR1	Involved in mitochondrial biogene	2.29	2.29	2.63E-16	SGD	633802	MBR1
YFR032C	YFR032C		2.29	2.29	1.12E-06	SGD	633812	YFR032C
YJL049W	YJL049W		2.29	2.29	2.73E-06	SGD	636114	YJL049W
YDR227W	SIR4,ASD1,STE9,UTH	regulator of silencing at HML, HMI	2.29	2.29	7.14E-06	SGD	638953	SIR4
YJR042W	NUP85,RAT9	Protein in nuclear pore complex, r	2.28	2.28	8.83E-41	SGD	633289	NUP85
YML043C	RRN11	rDNA transcription factor CF comp	2.28	2.28	4.19E-28	SGD	637130	RRN11
YPL261C	YPL261C		2.28	2.28	1.65E-27	SGD	634293	YPL261C
YGL038C	OCH1,NGD29	membrane-bound alpha-1,6-manr	2.28	2.28	7.10E-27	SGD	637072	OCH1
YPR137W	RRP9	Rrp9p is an ortholog of the human	2.28	2.28	2.38E-22	SGD	637998	RRP9
YFL055W	AGP3	General amino acid permease wit	2.28	2.28	1.68E-13	SGD	637985	AGP3
YOR267C	YOR267C		2.28	2.28	2.96E-11	SGD	636265	YOR267C
YDR453C	YDR453C		2.28	2.28	2.89E-10	SGD	635821	YDR453C
YDR034C-	ORF:YDR034C-A	BioProcess=biological_process ur	2.28	2.28	3.21E-10	SGD	970721	ORF:YDR034C-A
YFL034C-A	RPL22B	Homology to rat L22; ribosomal pr	2.28	2.28	1.69E-06	SGD	970761	RPL22B
YFR003C	YFR003C		2.27	2.27	9.42E-36	SGD	634999	YFR003C
YOR390W	YOR390W		2.27	2.27	1.98E-22	SGD	639322	YOR390W
YPL282C	YPL282C		2.27	2.27	7.40E-20	SGD	634992	YPL282C
YBR180W	DTR1	dityrosine transporter MFS-MDR;	2.27	2.27	2.25E-19	SGD	634048	DTR1
YOL154W	YOL154W		2.27	2.27	1.05E-14	SGD	637662	YOL154W
YOL035C	YOL035C		2.27	2.27	3.37E-10	SGD	638194	YOL035C
YLL028W	TPO1	Polyamine transport protein	2.27	2.27	2.33E-07	SGD	636257	TPO1
YFL020C	PAU5	member of the seripauperin protei	2.27	2.27	2.44E-05	SGD	637495	PAU5
YIL176C	YIL176C		2.26	2.26	5.01E-40	SGD	635757	YIL176C
YHR123W	EPT1	sn-1,2-diacylglycerol ethanolamin	2.26	2.26	2.01E-27	SGD	635281	EPT1
YHR143W	RPC10,RPB12	subunit of RNA polymerase II; RN	2.26	2.26	2.29E-27	SGD	633413	RPC10
YNL319W	YNL319W		2.26	2.26	3.18E-09	SGD	636378	YNL319W
YJL148W	RPA34	RNA polymerase I subunit, not sh	2.26	2.26	6.15E-08	SGD	636634	RPA34
YLR216C	CPR6	a cyclophilin related to the mamm	2.26	2.26	1.15E-05	SGD	637775	CPR6
YOL032W	YOL032W		2.25	2.25	8.16E-10	SGD	637664	YOL032W

YAL014C	YAL014C		2.24	2.24	0	SGD	639165	YAL014C
YAL009W	SPO7	dispensable for mitosis, but requir	2.24	2.24	2.42E-14	SGD	638360	SPO7
Q0070	AI5_ALPHA	Intron of mitochondrial COX1, aI5-	2.24	2.24	7.42E-04	SGD	970792	AI5_ALPHA
YML046W	PRP39	May function to facilitate or stabiliz	2.23	2.23	0	SGD	638703	PRP39
YDR036C	YDR036C		2.23	2.23	2.32E-20	SGD	637092	YDR036C
YFL064C	YFL064C		2.23	2.23	1.55E-16	SGD	637572	YFL064C
YBR029C	CDS1,CDG1	CDP-diacylglycerol synthase, CTF	2.23	2.23	2.48E-11	SGD	633973	CDS1
YDR333C	YDR333C		2.23	2.23	1.16E-08	SGD	634153	YDR333C
YBR301W	DAN3	delayed anaerobic gene; putative	2.22	2.22	1.45E-33	SGD	637530	DAN3
YGL057C	YGL057C		2.22	2.22	7.43E-12	SGD	637694	YGL057C
YOL115W	TRF4	TRF5 homolog, Involved in mitotic	2.22	2.22	1.45E-11	SGD	638008	TRF4
YNL184C	YNL184C		2.22	2.22	9.61E-07	SGD	634265	YNL184C
YGR215W	RSM27	mitochondrial ribosome small subu	2.22	2.22	1.55E-05	SGD	636407	RSM27
YER113C	YER113C		2.21	2.21	0	SGD	638052	YER113C
YGL122C	NAB2	nuclear polyadenylated RNA bindi	2.21	2.21	9.54E-16	SGD	636856	NAB2
YIR041W	YIR041W		2.21	2.21	8.19E-09	SGD	637524	YIR041W
YDL217C	TIM22	Mitochondrial inner membrane pro	2.21	2.21	1.53E-06	SGD	637592	TIM22
YFL017W-	SMX2,SNP2	snRNP G protein (the homologue	2.21	2.21	1.92E-06	SGD	970738	SMX2
YMR016C	SOK2	Protein that can when overexpress	2.21	2.21	2.23E-06	SGD	638075	SOK2
YHR184W	SSP1,SPO3	Involved in the control of meiotic n	2.21	2.21	5.50E-05	SGD	634049	SSP1
YNL232W	CSL4,SKI4	Represses the replication of doubl	2.2	2.2	2.26E-34	SGD	637690	CSL4
YNL174W	YNL174W		2.2	2.2	2.87E-28	SGD	633691	YNL174W
YKL011C	CCE1,mgt1	cruciform cutting endonuclease; N	2.2	2.2	2.49E-25	SGD	637772	CCE1
YML080W	DUS1	tRNA dihydrouridine synthase	2.2	2.2	1.17E-24	SGD	637036	DUS1
YGR113W	DAM1	Duo1 And Mps1 interacting. Local	2.2	2.2	2.53E-24	SGD	635976	DAM1
YML041C	YML041C		2.2	2.2	1.74E-11	SGD	635953	YML041C
YMR003W	YMR003W		2.2	2.2	6.95E-07	SGD	639103	YMR003W
YHR105W	YHR105W		2.2	2.2	4.25E-05	SGD	635045	YHR105W
YPL244C	HUT1	similar to UDP-galactose transpor	2.19	2.19	0	SGD	635904	HUT1
YBR012C	YBR012C		2.19	2.19	2.88E-39	SGD	634949	YBR012C
YPL252C	YAH1	Yeast Adrenodoxin Homologue 1,	2.19	2.19	1.45E-13	SGD	637516	YAH1
YBR074W	YBR074W	Homolog to aminopeptidase Y (S.	2.19	2.19	5.92E-12	SGD	637041	YBR074W
YIL030C	SSM4	Protein involved in mRNA turnove	2.19	2.19	1.01E-11	SGD	633485	SSM4
YJL097W	YJL097W		2.18	2.18	1.31E-32	SGD	634387	YJL097W
YDR420W	HKR1	cell surface protein that may regul	2.18	2.18	3.62E-29	SGD	637419	HKR1
YJL059W	YHC3,BTN1	Homolog of human CLN3; Null mu	2.18	2.18	2.66E-25	SGD	636755	YHC3
YHR217C	YHR217C		2.18	2.18	3.05E-08	SGD	633309	YHR217C

YBR135W	CKS1	subunit of the Cdc28 protein kinas	2.17	2.17	0	SGD	638267	CKS1
YKL224C	YKL224C		2.17	2.17	2.10E-44	SGD	635735	YKL224C
YBL108C-A	ORF:YBL108C-A	BioProcess=biological_process ur	2.17	2.17	4.02E-32	SGD	970780	ORF:YBL108C-A
YML009C-A	ORF:YML009C-A	BioProcess=biological_process ur	2.17	2.17	9.69E-19	SGD	970811	ORF:YML009C-A
YEL052W	AFG1	ATPase family gene; ATPase fam	2.16	2.16	6.11E-33	SGD	636849	AFG1
YIR040C	YIR040C		2.16	2.16	2.31E-32	SGD	634828	YIR040C
YNR077C	YNR077C		2.16	2.16	6.96E-29	SGD	638187	YNR077C
YDR189W	SLY1	Hydrophilic suppressor of ypt1 inv	2.16	2.16	1.37E-23	SGD	637250	SLY1
YLR381W	YLR381W		2.16	2.16	4.39E-18	SGD	634715	YLR381W
YDR080W	VPS41,CVT8,FET2,SV	vacuolar protein sorting; Null muta	2.16	2.16	8.42E-14	SGD	638803	VPS41
YKR105C	YKR105C		2.16	2.16	1.36E-04	SGD	637993	YKR105C
YGR238C	KEL2	protein containing kelch repeats, s	2.15	2.15	5.10E-27	SGD	634599	KEL2
YDR302W	GPI11	Glycosylphosphatidylinositol (GPI)	2.15	2.15	6.70E-23	SGD	634964	GPI11
YGR294W	YGR294W		2.15	2.15	1.91E-21	SGD	633655	YGR294W
YGR164W	YGR164W		2.15	2.15	1.46E-19	SGD	635656	YGR164W
YHL005C	YHL005C		2.15	2.15	2.70E-19	SGD	638984	YHL005C
YMR185W	YMR185W		2.15	2.15	1.22E-16	SGD	635530	YMR185W
YHR209W	YHR209W		2.15	2.15	4.53E-10	SGD	637691	YHR209W
YOL091W	SPO21,MPC70	sporulation defective; meiosis prot	2.15	2.15	9.43E-06	SGD	637149	SPO21
YAL069W	YAL069W		2.14	2.14	0	SGD	633339	YAL069W
YDR542W	YDR542W		2.14	2.14	0	SGD	633654	YDR542W
YBL041W	PRE7	proteasome subunit; Null mutant i	2.14	2.14	1.08E-43	SGD	633798	PRE7
YNL012W	SPO1	dispensable for mitosis, premeioti	2.14	2.14	8.71E-26	SGD	636903	SPO1
YGR153W	TOS10	Hypothetical ORF	2.14	2.14	7.31E-12	SGD	638299	TOS10
YOR020C	HSP10,CPN10	Homolog of E. coli GroES protein,	2.14	2.14	2.06E-11	SGD	636432	HSP10
YJR157W	YJR157W		2.13	2.13	3.54E-35	SGD	637532	YJR157W
YGR213C	RTA1	involved in 7-aminocholesterol res	2.13	2.13	6.81E-25	SGD	636636	RTA1
YJL028W	YJL028W		2.12	2.12	6.75E-30	SGD	637447	YJL028W
YLR009W	RLP24	Ribosomal Like Protein 24; part of	2.12	2.12	1.35E-25	SGD	637600	RLP24
YOL037C	YOL037C		2.12	2.12	9.48E-23	SGD	639052	YOL037C
YKL114C	APN1	major apurinic/apyrimidinic endon	2.12	2.12	1.31E-20	SGD	636009	APN1
YLL065W	GIN11	growth inhibitor; Inhibits growth wh	2.12	2.12	2.26E-19	SGD	639022	GIN11
YNL166C	BNI5	bud neck involved, localizes to mo	2.12	2.12	5.85E-19	SGD	637860	BNI5
YPL260W	YPL260W		2.12	2.12	6.71E-09	SGD	636125	YPL260W
YKL225W	YKL225W		2.11	2.11	1.73E-39	SGD	639039	YKL225W
YNL207W	YNL207W		2.11	2.11	8.39E-33	SGD	638558	YNL207W
YIL175W	YIL175W		2.11	2.11	2.33E-32	SGD	636433	YIL175W

YGR166W	KRE11,TRS65	Involved in biosynthetic pathway f	2.11	2.11	1.19E-26	SGD	639472	KRE11
YLR424W	YLR424W		2.11	2.11	2.60E-23	SGD	636228	YLR424W
YPR002C-	ORF:YPR002C-A	BioProcess=biological_process ur	2.11	2.11	5.17E-15	SGD	970708	ORF:YPR002C-A
YMR069W	YMR069W		2.11	2.11	3.49E-14	SGD	635932	YMR069W
YER056C-	RPL34A	Homology to rat L34; ribosomal pr	2.11	2.11	4.31E-12	SGD	633385	RPL34A
YLR212C	TUB4	spindle pole body component that	2.11	2.11	3.61E-10	SGD	637893	TUB4
YLL034C	YLL034C		2.11	2.11	1.14E-08	SGD	638771	YLL034C
YEL026W	SNU13	RNA binding protein (putative), sir	2.11	2.11	1.40E-07	SGD	635730	SNU13
YLR437C	YLR437C		2.11	2.11	3.46E-07	SGD	634922	YLR437C
YAL025C	MAK16	putative nuclear protein; nuclear p	2.11	2.11	3.35E-05	SGD	638401	MAK16
YIL078W	THS1	Threonyl-tRNA synthetase, cytopl	2.1	2.1	6.67E-29	SGD	638030	THS1
YFL063W	YFL063W		2.1	2.1	4.22E-20	SGD	638282	YFL063W
YOR394W	YOR394W		2.1	2.1	7.40E-17	SGD	638272	YOR394W
YAL004W	YAL004W		2.1	2.1	4.16E-14	SGD	634373	YAL004W
YBR049C	REB1,GRF2	DNA binding protein which binds s	2.1	2.1	4.92E-14	SGD	638126	REB1
YER070W	RNR1,CRT7,RIR1,SD	ribonucleotide reductase; ribonucl	2.1	2.1	2.41E-11	SGD	637262	RNR1
YAR070C	YAR070C	potential mitochondrial transit pep	2.1	2.1	3.32E-08	SGD	634891	YAR070C
YAL034W-	MTW1	Mis TWelve like (a Schizosacchar	2.1	2.1	8.16E-07	SGD	639268	MTW1
YER103W	SSA4	member of 70 kDa heat shock pro	2.1	2.1	3.63E-05	SGD	635424	SSA4
YKL198C	PTK1,KKT8,STK1	Putative serine/threonine protein k	2.09	2.09	0	SGD	634015	PTK1
YPL246C	YPL246C		2.09	2.09	4.53E-41	SGD	636547	YPL246C
YBR174C	YBR174C		2.09	2.09	4.86E-39	SGD	638142	YBR174C
YNL196C	SLZ1	sporulation-specific protein with a	2.09	2.09	9.49E-25	SGD	638456	SLZ1
YDR366C	YDR366C		2.09	2.09	7.98E-14	SGD	638236	YDR366C
YOR233W	KIN4,KIN31	protein kinase; Null mutant is viab	2.09	2.09	1.46E-13	SGD	636373	KIN4
YCL037C	SRO9	Associates with translating riboso	2.09	2.09	2.23E-11	SGD	636087	SRO9
YCL024W	KCC4	involved in septin organization; S.	2.09	2.09	4.78E-11	SGD	636320	KCC4
YBR166C	TYR1	Step of tyrosine biosynthesis path	2.09	2.09	4.27E-08	SGD	634043	TYR1
YGR145W	YGR145W		2.09	2.09	7.03E-07	SGD	634721	YGR145W
YDR180W	SCC2	Sister chromatid cohesion protein	2.09	2.09	2.22E-06	SGD	635636	SCC2
YKR066C	CCP1	Cytochrome-c peroxidase; cytoch	2.08	2.08	3.24E-28	SGD	633336	CCP1
YGR217W	CCH1	calcium channel; calcium channel	2.08	2.08	4.82E-25	SGD	637417	CCH1
YMR169C	ALD3	Expression induced in response t	2.08	2.08	9.88E-13	SGD	633415	ALD3
YLR222C	YLR222C		2.08	2.08	1.07E-12	SGD	634225	YLR222C
YMR041C	YMR041C		2.08	2.08	7.01E-12	SGD	639299	YMR041C
YLL064C	YLL064C		2.08	2.08	2.27E-08	SGD	633565	YLL064C
YER037W	PHM8	involved in phosphate metabolism	2.08	2.08	2.57E-07	SGD	634532	PHM8

YGR219W	YGR219W		2.08	2.08	2.09E-06	SGD	637459	YGR219W
YCL027W	FUS1	cell-surface protein required for ce	2.08	2.08	4.53E-06	SGD	635344	FUS1
YDR097C	MSH6,PMS3	Required for mismatch repair in m	2.08	2.08	1.53E-05	SGD	633472	MSH6
YBR040W	FIG1	Factor-Induced Gene 1: expressic	2.08	2.08	1.54E-05	SGD	638408	FIG1
YPL054W	LEE1	Product of gene unknown	2.08	2.08	7.78E-05	SGD	635078	LEE1
YGL157W	YGL157W		2.07	2.07	2.15E-34	SGD	637742	YGL157W
YNR076W	PAU6	member of the seripauperin protei	2.07	2.07	5.87E-29	SGD	639048	PAU6
YJL031C	BET4	catalyzes prenylation of Ypt1p (as	2.07	2.07	5.00E-28	SGD	639267	BET4
YFL012W	YFL012W		2.07	2.07	1.85E-26	SGD	634355	YFL012W
YBR070C	YBR070C	involved in osmotolerance	2.07	2.07	1.45E-17	SGD	636630	YBR070C
YMR301C	ATM1	mitochondrial ABC transporter prc	2.07	2.07	5.13E-08	SGD	637227	ATM1
YLR464W	YLR464W		2.07	2.07	5.17E-07	SGD	635072	YLR464W
YCL048W	YCL048W		2.07	2.07	1.33E-05	SGD	637914	YCL048W
YOL094C	RFC4	RFC is a DNA binding protein and	2.06	2.06	0	SGD	636977	RFC4
YDR263C	DIN7,DIN3	DNA-damage inducible gene	2.06	2.06	0	SGD	639369	DIN7
YAL037W	YAL037W		2.06	2.06	2.66E-44	SGD	637642	YAL037W
YHR107C	CDC12,CLA10,PSL7	involved in proper bud growth; 10	2.06	2.06	4.85E-21	SGD	637060	CDC12
YNR015W	SMM1	Suppressor of Mitochondrial Muta	2.06	2.06	3.40E-20	SGD	636749	SMM1
YEL076C-/	YEL076C-A		2.06	2.06	2.22E-18	SGD	633392	YEL076C-A
YIL079C	YIL079C		2.06	2.06	1.02E-14	SGD	636030	YIL079C
YDL235C	YPD1	Ypd1p is an intermediate protein b	2.06	2.06	2.30E-14	SGD	636460	YPD1
YNL132W	KRE33	Killer toxin REsistant; Heterozygou	2.06	2.06	1.50E-12	SGD	638846	KRE33
YNL028W	YNL028W		2.06	2.06	3.12E-11	SGD	634303	YNL028W
YNL189W	SRP1,KAP60,SCM1	karyopherin alpha homolog of 60 k	2.06	2.06	3.26E-08	SGD	639482	SRP1
YLR416C	YLR416C		2.06	2.06	3.17E-06	SGD	635707	YLR416C
YAL067C	SEO1	Suppressor of Sulfoxyde Ethionine	2.06	2.06	1.05E-05	SGD	638003	SEO1
YGL185C	YGL185C		2.06	2.06	2.00E-05	SGD	638530	YGL185C
YHR175W	CTR2	Putative low-affinity copper transp	2.05	2.05	1.42E-29	SGD	635804	CTR2
YCL022C	YCL022C		2.05	2.05	3.15E-29	SGD	633603	YCL022C
YGL078C	DBP3	ATP-dependent RNA helicase CA	2.05	2.05	7.45E-18	SGD	638672	DBP3
YGR084C	MRP13	35 kDa mitochondrial ribosomal su	2.05	2.05	5.95E-17	SGD	639296	MRP13
YPR135W	CTF4,CHL15,POB1	May function in DNA synthesis; DI	2.05	2.05	2.87E-16	SGD	635575	CTF4
YDR543C	YDR543C		2.05	2.05	3.28E-14	SGD	638195	YDR543C
YNL313C	YNL313C		2.05	2.05	1.31E-12	SGD	635482	YNL313C
YOR359W	YOR359W		2.05	2.05	2.10E-07	SGD	638657	YOR359W
YCL051W	LRE1	involved in laminarase resistance;	2.04	2.04	1.61E-29	SGD	637987	LRE1
YOL161C	YOL161C		2.04	2.04	3.00E-21	SGD	637450	YOL161C

YNL185C	MRPL19	mitochondrial ribosomal protein of	2.04	2.04	5.98E-20	SGD	636538	MRPL19
YNL073W	MSK1	mitochondrial lysine-tRNA synthet	2.04	2.04	2.07E-17	SGD	637996	MSK1
YGL224C	SDT1,SSM1	suppressor of deletion of TFIIS; nu	2.04	2.04	2.09E-12	SGD	637715	SDT1
YDR171W	HSP42	Similar to HSP26, expression is re	2.04	2.04	3.86E-11	SGD	633957	HSP42
YLR065C	YLR065C		2.04	2.04	3.41E-08	SGD	635798	YLR065C
YIR011C	STS1,DBF8,SSM5	restores protein transport when ov	2.04	2.04	2.57E-06	SGD	638498	STS1
YOR378W	YOR378W		2.04	2.04	6.27E-06	SGD	636898	YOR378W
YDL227C	HO	Homothallic switching; homothallic	2.04	2.04	7.82E-06	SGD	634102	HO
YJR023C	YJR023C		2.04	2.04	7.13E-05	SGD	634369	YJR023C
YPL238C	YPL238C		2.03	2.03	0	SGD	633626	YPL238C
YHR108W	GGA2	Golgi-localized, gamma-adaptin h	2.03	2.03	7.95E-21	SGD	636241	GGA2
YDR485C	YDR485C		2.03	2.03	1.32E-15	SGD	634243	YDR485C
YNL289W	PCL1,HCS26	G(sub)1 cyclin that associates with	2.03	2.03	5.90E-14	SGD	633820	PCL1
YKL102C	YKL102C		2.03	2.03	1.17E-12	SGD	634213	YKL102C
YDL139C	SCM3	Suppressor of chromosome misse	2.03	2.03	2.44E-11	SGD	639140	SCM3
YDR278C	YDR278C		2.03	2.03	7.73E-10	SGD	638141	YDR278C
YDR003W	YDR003W		2.03	2.03	1.48E-09	SGD	636512	YDR003W
YBR075W	YBR075W		2.03	2.03	1.33E-07	SGD	636106	YBR075W
YCR072C	YCR072C	regulatory protein	2.03	2.03	1.45E-07	SGD	635326	YCR072C
YGR206W	YGR206W		2.03	2.03	1.29E-06	SGD	634878	YGR206W
YHR061C	GIC1	Gtpase-interacting component 1; I	2.02	2.02	4.76E-44	SGD	634522	GIC1
YIL032C	YIL032C		2.02	2.02	2.72E-24	SGD	635760	YIL032C
YPR167C	MET16	3'phosphoadenylylsulfate reductas	2.02	2.02	5.30E-16	SGD	634497	MET16
YBL053W	YBL053W		2.02	2.02	2.03E-15	SGD	637491	YBL053W
YGR263C	YGR263C		2.02	2.02	1.29E-14	SGD	637051	YGR263C
YJL190C	RPS22A,RPS24	Homology to rat S15a; ribosomal p	2.02	2.02	1.33E-09	SGD	633624	RPS22A
YHL049C	YHL049C		2.02	2.02	4.69E-08	SGD	637655	YHL049C
YHR010W	RPL27A	Homology to mammalian L27; ribo	2.02	2.02	2.64E-07	SGD	638478	RPL27A
YHR049C-	YHR049C-A		2.02	2.02	2.58E-06	SGD	633444	YHR049C-A
YNR024W	YNR024W		2.02	2.02	6.60E-05	SGD	639128	YNR024W
YPL273W	SAM4	AdoMet-homocysteine methyltrans	2.01	2.01	4.41E-41	SGD	635127	SAM4
YJL111W	CCT7,TCP7	Required for assembly of microtub	2.01	2.01	1.09E-37	SGD	636141	CCT7
YIR020W-E	ORF:YIR020W-B	BioProcess=biological_process un	2.01	2.01	4.22E-31	SGD	970760	ORF:YIR020W-B
YPR118W	YPR118W		2.01	2.01	5.74E-19	SGD	635270	YPR118W
YFL066C	YFL066C		2.01	2.01	1.92E-11	SGD	637002	YFL066C
YDL026W	YDL026W		2.01	2.01	9.64E-11	SGD	634290	YDL026W
YML037C	YML037C		2.01	2.01	1.20E-08	SGD	633848	YML037C

YJR162C	YJR162C		2.01	2.01	1.84E-07	SGD	635649	YJR162C
YBR004C	YBR004C		2.01	2.01	3.68E-04	SGD	633952	YBR004C
YBR300C	YBR300C		2	2	8.14E-21	SGD	638255	YBR300C
YJR097W	YJR097W		2	2	9.98E-21	SGD	639072	YJR097W
YDR524C	AGE1,SAT1	ADP-ribosylation factor (ARF) GTI	2	2	9.20E-19	SGD	637071	AGE1
YOL104C	NDJ1,TAM1	Involved in meiotic chromosome s	2	2	1.16E-08	SGD	633854	NDJ1
YNL292W	PUS4	catalyzes formation of Psi55 (mod	2	2	1.53E-07	SGD	633356	PUS4
YDR486C	VPS60,MOS10	vacuolar protein sorting (putative);	2	2	1.83E-07	SGD	633715	VPS60
YDL115C	IWR1	Hypothetical ORF	0.5	-2	2.80E-45	SGD	639145	IWR1
YMR194C-	ORF:YMR194C-A	BioProcess=biological_process ur	0.5	-2	3.26E-16	SGD	970799	ORF:YMR194C-A
YNL165W	YNL165W		0.5	-2	1.56E-11	SGD	636766	YNL165W
YGR172C	YIP1	Golgi integral membrane protein, I	0.5	-2	6.57E-08	SGD	633793	YIP1
YDL015C	TSC13	ER protein involved in very long cl	0.5	-2.01	0	SGD	635155	TSC13
YDL017W	CDC7,LSD6,SAS1	Required for mitotic DNA synthesi	0.5	-2.01	1.96E-16	SGD	637114	CDC7
YBR149W	ARA1	D-arabinose dehydrogenase; Null	0.5	-2.01	9.12E-16	SGD	637729	ARA1
YDR284C	DPP1,ZRG1	contains a novel phosphatase sec	0.5	-2.01	1.04E-13	SGD	637759	DPP1
YMR235C	RNA1	Protein involved in RNA processin	0.5	-2.01	2.24E-13	SGD	635272	RNA1
YKL176C	LST4	involved in regulated secretion/rec	0.5	-2.01	3.65E-12	SGD	634808	LST4
YNL163C	RIA1	RIbosome Assembly; Null: quasi e	0.5	-2.01	5.27E-10	SGD	638928	RIA1
YOR371C	KRH2	Kelch Repeat Homologue. Homol	0.5	-2.01	3.18E-06	SGD	638776	KRH2
YNL288W	CAF40	Hypothetical ORF; Null mutant is v	0.5	-2.01	1.50E-05	SGD	639339	CAF40
YJL093C	TOK1,DUK1,YKC1,YC	outward-rectifier potassium chann	0.5	-2.01	3.31E-05	SGD	635470	TOK1
YPL235W	RVB2,TIH2,TIP49B	RUVB-like protein, TIP49b Homol	0.49	-2.02	1.95E-25	SGD	636100	RVB2
YLR178C	TFS1,DKA1	(putative) lipid binding protein, sup	0.49	-2.02	5.27E-25	SGD	636587	TFS1
YOR132W	VPS17,PEP21	Peripheral membrane protein requ	0.5	-2.02	3.81E-10	SGD	634020	VPS17
YMR258C	YMR258C		0.49	-2.02	1.14E-09	SGD	637918	YMR258C
YML001W	YPT7,AST4,VAM4	Gtp-binding protein of the rab fam	0.5	-2.02	6.53E-08	SGD	635841	YPT7
YML108W	YML108W		0.49	-2.03	1.74E-29	SGD	638174	YML108W
YGL126W	SCS3	Required for inositol prototrophy; r	0.49	-2.03	4.24E-23	SGD	635220	SCS3
YLR242C	ARV1	similar to Nup120p and C.elegans	0.49	-2.03	1.92E-10	SGD	635185	ARV1
YJL061W	NUP82,HRB187	Interacts with nuclear pore comple	0.49	-2.03	1.17E-07	SGD	634163	NUP82
YOR186W	YOR186W		0.49	-2.03	1.06E-06	SGD	636380	YOR186W
YFR044C	YFR044C		0.49	-2.03	6.28E-06	SGD	635311	YFR044C
YPR036W	VMA13,CLS11	vacuolar ATPase V1 domain subu	0.49	-2.03	7.55E-06	SGD	636148	VMA13
YMR103C	YMR103C		0.49	-2.03	1.39E-05	SGD	635675	YMR103C
YLR294C	YLR294C		0.49	-2.03	2.48E-05	SGD	636426	YLR294C
YEL024W	RIP1	oxidizes ubiquinol at center P in th	0.49	-2.04	3.56E-43	SGD	634389	RIP1

YDL067C	COX9	Plays role in cytochrome c oxidas	0.49	-2.04	9.97E-21	SGD	636365	COX9
YGR003W	YGR003W		0.49	-2.04	1.23E-17	SGD	636220	YGR003W
YBR271W	YBR271W		0.49	-2.04	5.07E-14	SGD	636790	YBR271W
YPL024W	NCE4	negative regulator of cts1 express	0.49	-2.04	3.34E-09	SGD	633783	NCE4
YDR293C	SSD1,CLA1,MCS1,RL	Product of gene unknown; Suppre	0.49	-2.04	1.66E-06	SGD	638919	SSD1
YHR079C	IRE1,ERN1	Involved in myo-inositol biosynthe	0.49	-2.04	2.71E-06	SGD	637337	IRE1
YIR032C	DAL3	ureidoglycolate hydrolase; Null mu	0.49	-2.04	4.52E-06	SGD	633671	DAL3
YMR247C	YMR247C		0.49	-2.05	0	SGD	635634	YMR247C
YGR266W	YGR266W		0.49	-2.05	0	SGD	638054	YGR266W
YDR381C-	ORF:YDR381C-A	BioProcess=biological_process ur	0.49	-2.05	9.70E-27	SGD	970769	ORF:YDR381C-A
YLR305C	STT4,BLM1	functions in the PKC1 protein kina	0.49	-2.05	1.10E-26	SGD	638974	STT4
YCR081W	SRB8,GIG1,NUT6,SSI	activation mediator subcomplex of	0.49	-2.05	6.29E-26	SGD	638898	SRB8
YDL111C	RRP42	Ribosomal RNA Processing; exos	0.49	-2.05	1.20E-25	SGD	633790	RRP42
YOL022C	YOL022C		0.49	-2.05	2.98E-23	SGD	635256	YOL022C
YER178W	PDA1	alpha subunit of pyruvate dehydro	0.49	-2.05	1.16E-21	SGD	633945	PDA1
YNL224C	YNL224C		0.49	-2.05	1.43E-19	SGD	634820	YNL224C
YPL064C	YPL064C		0.49	-2.05	6.97E-19	SGD	638389	YPL064C
YNL097C	PHO23	Involved in expression of PHO5; N	0.49	-2.05	2.26E-13	SGD	638427	PHO23
YHR077C	NMD2,IFS1,SUA1,UPF	Protein involved in decay of mRNA	0.49	-2.05	4.86E-13	SGD	633435	NMD2
YOL020W	TAT2,LTG3,SAB2,SCN	Tryptophan permease, high affinity	0.49	-2.05	4.44E-09	SGD	637988	TAT2
YLL010C	PSR1	Plasma membrane Sodium Respo	0.49	-2.05	2.03E-07	SGD	636786	PSR1
YDL040C	NAT1,AAA1	Required for entry into stationary p	0.49	-2.05	3.85E-06	SGD	637287	NAT1
YOR213C	SAS5	Involved in silencing at telomeres,	0.48	-2.06	3.99E-43	SGD	635870	SAS5
YDL125C	HNT1	Hint homolog, member of the histi	0.48	-2.06	2.69E-39	SGD	639176	HNT1
YDR479C	YDR479C		0.49	-2.06	5.05E-34	SGD	634074	YDR479C
YOL158C	ENB1,ARN4	Siderophore transporter for enterc	0.49	-2.06	1.53E-32	SGD	635439	ENB1
YIL096C	YIL096C		0.49	-2.06	5.76E-13	SGD	633851	YIL096C
YIL071C	PCI8,YIH1	Proteasome-COP9 signalosome-e	0.48	-2.06	1.74E-10	SGD	637878	PCI8
YNL297C	MON2	protein with similarity to N-termina	0.49	-2.06	8.25E-10	SGD	635633	MON2
YDL142C	CRD1,CLS1	Cardiolipin synthase; cardiolipin sy	0.48	-2.06	4.85E-09	SGD	633832	CRD1
YOL143C	RIB4	catalyzes synthesis of immediate p	0.48	-2.06	1.08E-05	SGD	637576	RIB4
YBR105C	VID24	also involved in vacuolar protein ta	0.48	-2.07	2.95E-36	SGD	633912	VID24
YDL231C	BRE4	contains several putative trans-me	0.48	-2.07	1.51E-24	SGD	633495	BRE4
YOL137W	YOL137W		0.48	-2.07	9.53E-23	SGD	638589	YOL137W
YLR083C	EMP70	identified as a 24 kDa cleavage pr	0.48	-2.07	4.36E-21	SGD	638753	EMP70
YLR278C	YLR278C		0.48	-2.07	5.68E-10	SGD	633513	YLR278C
YDL091C	YDL091C		0.48	-2.07	1.18E-08	SGD	637888	YDL091C

YOR040W	GLO4	Mitochondrial glyoxylase-II; glyoxy	0.48	-2.07	4.69E-08	SGD	639187	GLO4
YDR304C	CPR5,CYP5	Cyclophilin D, Peptidyl-prolyl cis-tr	0.48	-2.08	0	SGD	634465	CPR5
YNL323W	LEM3,BRE3	Product of gene unknown; null mu	0.48	-2.08	0	SGD	635198	LEM3
YHL047C	TAF1,ARN2	Siderophore transporter for triacet	0.48	-2.08	2.68E-39	SGD	637186	TAF1
YJL196C	ELO1	elongation enzyme 1, required for	0.48	-2.08	1.06E-26	SGD	636635	ELO1
YHL044W	YHL044W		0.48	-2.08	5.11E-17	SGD	638354	YHL044W
YKL023W	YKL023W		0.48	-2.08	3.64E-16	SGD	637718	YKL023W
YOR067C	ALG8	adds glucose to the dolichol-linke	0.48	-2.08	3.90E-16	SGD	634091	ALG8
YDR166C	SEC5	107 kDa component of the Exocys	0.48	-2.08	1.62E-10	SGD	634644	SEC5
YMR020W	FMS1	Multicopy suppressor of fenpropim	0.48	-2.08	1.22E-09	SGD	638680	FMS1
YNL032W	SIW14	Synthetic interaction with Whi2; ty	0.48	-2.08	2.38E-08	SGD	633834	SIW14
YAR035W	YAT1	Outer carnitine acetyltransferase,	0.48	-2.08	5.90E-06	SGD	635471	YAT1
YDR539W	YDR539W		0.48	-2.09	1.71E-27	SGD	638585	YDR539W
YBR221C	PDB1	beta subunit of pyruvate dehydrog	0.48	-2.09	1.72E-16	SGD	636041	PDB1
YNL294C	RIM21,PAL3	Regulator of IME2; Unknown func	0.48	-2.09	3.67E-14	SGD	635349	RIM21
YNL310C	YNL310C		0.48	-2.09	2.21E-10	SGD	639112	YNL310C
YGL251C	HFM1,MER3	C4 zinc finger DNA-binding protei	0.48	-2.09	3.35E-08	SGD	637306	HFM1
YOL072W	THP1	Null mutant is viable and shows tr	0.48	-2.1	0	SGD	639444	THP1
YDL223C	YDL223C		0.48	-2.1	5.81E-29	SGD	637360	YDL223C
YFL027C	GYP8	GAP for Ypt protein; GTPase-acti	0.48	-2.1	7.92E-18	SGD	636872	GYP8
YNL190W	YNL190W		0.48	-2.1	4.89E-16	SGD	637595	YNL190W
YIL119C	RPI1	inhibitor of ras; ras inhibitor; Null n	0.48	-2.1	2.55E-14	SGD	637029	RPI1
YKR027W	YKR027W		0.48	-2.1	7.84E-13	SGD	636263	YKR027W
YCR044C	PER1	Protein Processing in the ER	0.48	-2.1	3.12E-08	SGD	639281	PER1
YEL066W	HPA3	Histone and other Protein Acetyltr	0.48	-2.1	5.57E-05	SGD	635784	HPA3
YMR226C	YMR226C		0.47	-2.11	8.03E-15	SGD	639151	YMR226C
YML082W	YML082W		0.47	-2.11	1.96E-13	SGD	637176	YML082W
YDL145C	COP1,RET1,SEC33	alpha subunit of the coatamer con	0.47	-2.11	6.79E-12	SGD	637347	COP1
YLR417W	VPS36,GRD12,VAC3,	Defective in vacuolar protein sorti	0.47	-2.11	7.49E-11	SGD	636132	VPS36
YER187W-	KHS1	Killer toxin; killer toxin	0.47	-2.11	1.74E-06	SGD	970845	KHS1
YJR127C	ZMS1	Product of gene unknown	0.47	-2.11	2.61E-04	SGD	637471	ZMS1
YNL280C	ERG24	sterol C-14 reductase; Null mutan	0.47	-2.12	0	SGD	633372	ERG24
YCR036W	RBK1	ribokinase	0.47	-2.12	6.11E-30	SGD	633806	RBK1
YKL077W	YKL077W		0.47	-2.12	2.05E-26	SGD	636979	YKL077W
YDR483W	KRE2,MNT1	N-glycosylation; alpha-1,2-manno	0.47	-2.12	1.15E-25	SGD	637879	KRE2
YPL040C	ISM1	nuclear encoded mitochondrial isc	0.47	-2.12	2.35E-25	SGD	635537	ISM1
YPR098C	YPR098C		0.47	-2.12	6.04E-24	SGD	638169	YPR098C

YBR206W	YBR206W		0.47	-2.12	1.28E-19	SGD	638137	YBR206W
YIL150C	DNA43,MCM10	Protein required for S-phase (DNA	0.47	-2.12	2.14E-18	SGD	636248	DNA43
YMR009W	YMR009W		0.47	-2.12	5.80E-18	SGD	637553	YMR009W
YBL095W	YBL095W		0.47	-2.12	3.30E-17	SGD	633710	YBL095W
YIL091C	YIL091C		0.47	-2.12	3.41E-11	SGD	636225	YIL091C
YBR193C	MED8	Member of RNA Polymerase II tra	0.47	-2.12	4.02E-11	SGD	634450	MED8
YMR218C	TRS130	targeting complex (TRAPP) comp	0.47	-2.12	1.44E-10	SGD	633497	TRS130
YEL034W	HYP2,TIF51A	Translation initiation factor eIF-5A	0.47	-2.12	1.48E-10	SGD	638261	HYP2
YOR035C	SHE4	Required for mother cell-specific H	0.47	-2.12	1.50E-05	SGD	634800	SHE4
YJL215C	YJL215C		0.47	-2.12	5.39E-05	SGD	639049	YJL215C
YKR091W	SRL3	Suppressor of Rad53 null Lethality	0.47	-2.12	1.86E-04	SGD	638266	SRL3
YLR038C	COX12	essential during assembly for full	0.47	-2.13	0	SGD	638197	COX12
YDL215C	GDH2	NAD-dependent glutamate dehydr	0.47	-2.13	0	SGD	638891	GDH2
YNL227C	YNL227C		0.47	-2.13	1.60E-24	SGD	634100	YNL227C
YOR031W	CRS5	Metallothionein-like protein; metal	0.47	-2.13	1.61E-17	SGD	638198	CRS5
YBR054W	YRO2	Homolog to HSP30 heat shock pr	0.47	-2.13	5.35E-14	SGD	639307	YRO2
YJR084W	YJR084W		0.47	-2.13	5.56E-12	SGD	637020	YJR084W
YGL140C	YGL140C		0.47	-2.13	3.11E-11	SGD	637346	YGL140C
YML002W	YML002W		0.47	-2.13	4.87E-07	SGD	638045	YML002W
YML107C	YML107C		0.47	-2.14	0	SGD	636683	YML107C
YML128C	MSC1	Meiotic Sister-Chromatid recombi	0.47	-2.14	0	SGD	637127	MSC1
YDR466W	YDR466W		0.47	-2.14	4.32E-38	SGD	634665	YDR466W
YOR317W	FAA1	cellular lipid metabolism and prote	0.47	-2.14	1.88E-15	SGD	634708	FAA1
YNL169C	PSD1	converts phosphatidylserine to ph	0.47	-2.14	1.31E-09	SGD	638611	PSD1
YGL143C	MRF1	Mitochondrial polypeptide chain re	0.47	-2.14	1.74E-04	SGD	636778	MRF1
YDR435C	PPM1	carboxy methyl transferase for pro	0.47	-2.15	6.59E-44	SGD	638490	PPM1
YDR436W	PPZ2	serine-threonine phosphatase Z; N	0.46	-2.15	4.33E-24	SGD	636277	PPZ2
YOR251C	YOR251C		0.46	-2.15	3.78E-13	SGD	636665	YOR251C
YMR007W	YMR007W		0.47	-2.15	8.73E-11	SGD	635715	YMR007W
YOL087C	YOL087C		0.46	-2.15	6.47E-08	SGD	638873	YOL087C
YNL015W	PBI2	Proteinase inhibitor that inhibits pr	0.46	-2.15	3.38E-06	SGD	638188	PBI2
YGL258W-	ORF:YGL258W-A	BioProcess=biological_process ur	0.47	-2.15	1.57E-05	SGD	970697	ORF:YGL258W-A
YHR042W	NCP1,CPR1	NADP-cytochrome P450 reductas	0.47	-2.15	8.16E-05	SGD	634569	NCP1
YBR223C	TDP1	Tyrosine-DNA Phosphodiesterase	0.47	-2.15	5.73E-04	SGD	637977	TDP1
YGR008C	STF2	ATPase stabilizing factor	0.46	-2.16	4.52E-42	SGD	634883	STF2
YAL001C	TFC3,FUN24,TSV115	transcription factor tau (TFIIIC) su	0.46	-2.16	8.90E-17	SGD	638922	TFC3
YPL145C	KES1,LPI3,OSH4	Homologous to human oxysterol-b	0.46	-2.17	3.00E-31	SGD	633936	KES1

YIL090W	YIL090W		0.46	-2.17	3.55E-30	SGD	637081	YIL090W
YHR072W	ERG7	carries out complex cyclization ste	0.46	-2.17	1.97E-28	SGD	634151	ERG7
YGL196W	YGL196W		0.46	-2.17	1.23E-27	SGD	634414	YGL196W
YKL133C	YKL133C	probable purine nucleotide-bindin	0.46	-2.17	6.64E-26	SGD	639407	YKL133C
YDR103W	STE5,HMD3,NUL3	Protein of the pheromone pathwa	0.46	-2.17	7.14E-16	SGD	637304	STE5
YCR042C	TSM1,TAF150	TATA binding protein-associated f	0.46	-2.17	1.42E-13	SGD	638905	TSM1
YLR371W	ROM2	Gdp-GTP Exchange Protein (GEF	0.46	-2.17	3.23E-10	SGD	635625	ROM2
YOL130W	ALR1	aluminium resistance; ion transpo	0.46	-2.17	2.77E-09	SGD	637302	ALR1
YPL149W	APG5	Involved in autophagy; reduced vi	0.46	-2.17	7.44E-09	SGD	635925	APG5
YOR187W	TUF1	Translation elongation factor Tu, r	0.46	-2.18	4.30E-32	SGD	639364	TUF1
YJR155W	AAD10	high degree of similarity with the A	0.46	-2.18	3.94E-12	SGD	637760	AAD10
YPL087W	YDC1	Yeast dihydro-ceramidase; alkalin	0.46	-2.18	6.07E-05	SGD	638438	YDC1
YOR041C	YOR041C		0.46	-2.18	6.78E-05	SGD	634913	YOR041C
YGR168C	YGR168C		0.46	-2.19	1.01E-26	SGD	636754	YGR168C
YGL206C	CHC1,SWA5	presumed vesicle coat protein; Cl	0.46	-2.19	8.42E-21	SGD	633363	CHC1
YIL125W	KGD1,OGD1	alpha-ketoglutarate dehydrogenas	0.46	-2.19	9.42E-12	SGD	637309	KGD1
YLR179C	YLR179C		0.46	-2.19	1.02E-11	SGD	637598	YLR179C
YOL083W	YOL083W		0.46	-2.19	3.38E-10	SGD	637042	YOL083W
YNL168C	YNL168C		0.46	-2.2	0	SGD	636549	YNL168C
YBR068C	BAP2	contains 12 predicted transmembr	0.45	-2.2	8.20E-34	SGD	636883	BAP2
YOR292C	YOR292C		0.45	-2.2	6.80E-23	SGD	635142	YOR292C
YPR058W	YMC1	putative mitochondrial carrier prot	0.45	-2.21	1.07E-39	SGD	638385	YMC1
YCL041C	YCL041C		0.45	-2.21	2.99E-24	SGD	634976	YCL041C
YAL058W	CNE1,FUN48	Functions in endoplasmic reticulu	0.45	-2.21	6.41E-14	SGD	638642	CNE1
YDR119W	YDR119W		0.45	-2.21	2.71E-10	SGD	634168	YDR119W
YER125W	RSP5,MDP1,MUT2,NE	involved in ubiquitin-mediated pro	0.45	-2.21	1.43E-07	SGD	638111	RSP5
YNL317W	PFS2	Polyadenylation Factor I subunit 2	0.45	-2.22	0	SGD	639437	PFS2
YAL044W-	ORF:YAL044W-A	BioProcess=biological_process ur	0.45	-2.22	3.25E-43	SGD	970773	ORF:YAL044W-A
YLR352W	YLR352W		0.45	-2.22	2.10E-18	SGD	634746	YLR352W
YKR028W	SAP190	190 kDa protein that associates w	0.45	-2.22	5.58E-07	SGD	637354	SAP190
YMR153W	NUP53	Component of karyopherin dockin	0.45	-2.23	0	SGD	634029	NUP53
YNL144C	YNL144C		0.45	-2.23	4.31E-39	SGD	636287	YNL144C
YDR239C	YDR239C		0.45	-2.23	1.67E-32	SGD	633414	YDR239C
YMR029C	YMR029C		0.45	-2.23	1.18E-28	SGD	638615	YMR029C
YIL124W	AYR1	Subcellular location of Ayr1p: lipid	0.45	-2.23	7.13E-23	SGD	636670	AYR1
YCR011C	ADP1	Shows homology to ATP-depende	0.45	-2.23	3.13E-16	SGD	634685	ADP1
YER172C	BRR2,RSS1,SLT22,SN	RNA helicase-related protein requ	0.45	-2.23	1.51E-11	SGD	635700	BRR2

YLR358C	YLR358C		0.45	-2.23	1.26E-10	SGD	639061	YLR358C
YBR274W	CHK1	checkpoint kinase 1, homolog of tl	0.45	-2.23	9.71E-08	SGD	636873	CHK1
YML102W	CAC2	Involved in DNA-replication-linked	0.45	-2.23	3.61E-05	SGD	639404	CAC2
YPR026W	ATH1	Null mutant is viable, increased to	0.45	-2.24	9.27E-32	SGD	635555	ATH1
YJR062C	NTA1,DEA1	Removes amide group from N-ter	0.45	-2.24	5.04E-30	SGD	636093	NTA1
YER073W	ALD5	Utilizes NADP+ as the preferred c	0.45	-2.24	5.41E-26	SGD	635340	ALD5
YOR161C	YOR161C		0.45	-2.24	2.15E-20	SGD	634026	YOR161C
YMR162C	DNF3	Drs2 Neo1 Family; Potential amin	0.45	-2.24	7.55E-19	SGD	637377	DNF3
YLR098C	CHA4,SIL2,SIL3	Zinc-finger protein with Zn[2]-Cys[	0.45	-2.24	6.12E-10	SGD	634582	CHA4
YKL020C	SPT23	Dosage dependent suppressor of	0.45	-2.24	1.16E-08	SGD	635600	SPT23
YCR097W	HMRA1,A1,MATA1	silenced copy of A1, which encode	0.45	-2.24	2.26E-05	SGD	970838	HMRA1
YDR291W	YDR291W		0.44	-2.25	8.16E-27	SGD	635565	YDR291W
YOR329C	SCD5,FTB1	Multicopy suppressor of clathrin d	0.44	-2.25	2.80E-10	SGD	634654	SCD5
YNL020C	ARK1	actin regulating kinase; serine/thre	0.45	-2.25	3.62E-08	SGD	637202	ARK1
YHL042W	YHL042W		0.45	-2.25	5.52E-06	SGD	634410	YHL042W
YER033C	ZRG8	Zinc regulated gene	0.44	-2.26	7.68E-28	SGD	638893	ZRG8
YBR228W	SLX1		0.44	-2.26	3.60E-20	SGD	634548	SLX1
YAR019C	CDC15,LYT1	Required for mitosis and sporulati	0.44	-2.26	1.63E-16	SGD	635581	CDC15
YDR264C	AKR1	Negative regulator of pheromone	0.44	-2.26	1.30E-09	SGD	634754	AKR1
YBR117C	TKL2	transketolase, homologous to tkl1	0.44	-2.26	9.90E-09	SGD	638733	TKL2
YLR046C	YLR046C		0.44	-2.26	3.42E-08	SGD	633771	YLR046C
YKL221W	MCH2	monocarboxylate permease homo	0.44	-2.26	6.95E-08	SGD	639417	MCH2
YOR122C	PFY1,PRF1	profilin (actin-binding protein); pro	0.44	-2.26	1.08E-06	SGD	635822	PFY1
YPR117W	YPR117W		0.44	-2.26	2.80E-05	SGD	638955	YPR117W
YLR368W	YLR368W		0.44	-2.27	0	SGD	634113	YLR368W
YOR241W	MET7	METhionine requiring; folylpolyglu	0.44	-2.27	1.47E-27	SGD	636202	MET7
YML029W	USA1	Identified by its interaction with the	0.44	-2.27	2.83E-26	SGD	635510	USA1
YLL032C	YLL032C		0.44	-2.27	1.74E-23	SGD	634824	YLL032C
YLR133W	CKI1	choline kinase; Null mutant is viab	0.44	-2.27	1.15E-15	SGD	638009	CKI1
YPL268W	PLC1	Hydrolyzes phosphatidylinositol 4,	0.44	-2.27	1.71E-15	SGD	637284	PLC1
YCR037C	PHO87	May collaborate with Pho86p and	0.44	-2.27	1.24E-11	SGD	635523	PHO87
YOL008W	YOL008W		0.44	-2.27	2.10E-09	SGD	635826	YOL008W
YHR099W	TRA1	TRA1 is the homolog of the huma	0.44	-2.27	1.35E-07	SGD	633376	TRA1
YOR323C	PRO2	gamma-glutamyl phosphate reduc	0.44	-2.28	8.53E-42	SGD	636109	PRO2
YNL295W	YNL295W		0.44	-2.28	2.31E-39	SGD	636841	YNL295W
YER062C	HOR2,GPP2	RHR2 (GPP1) encodes another D	0.44	-2.28	1.71E-36	SGD	639138	HOR2
YPR053C	YPR053C		0.44	-2.28	9.08E-34	SGD	634987	YPR053C

YDR204W	COQ4	Involved in ubiquinone biosynthes	0.44	-2.28	7.22E-31	SGD	637752	COQ4
YBR102C	EXO84,USA3	exocyst complex component, hom	0.44	-2.28	4.70E-29	SGD	638026	EXO84
YER119C	YER119C	similar to amino acid transport pro	0.44	-2.28	4.24E-17	SGD	637812	YER119C
YIR022W	SEC11	signal peptidase subunit; Null mut	0.44	-2.28	1.95E-15	SGD	636531	SEC11
YBR222C	FAT2	Fatty acid transporter, very similar	0.44	-2.28	2.77E-12	SGD	634080	FAT2
YBR037C	SCO1,PET161	inner mitochondrial membrane pro	0.44	-2.28	1.94E-09	SGD	634493	SCO1
YDR242W	AMD2	putative amidase; amidase (putati	0.44	-2.28	1.89E-07	SGD	633407	AMD2
YMR088C	YMR088C		0.44	-2.29	1.02E-19	SGD	639471	YMR088C
YCR077C	PAT1,MRT1	Necessary for accurate chromoso	0.44	-2.29	3.79E-09	SGD	634198	PAT1
YEL071W	DLD3	D-lactate dehydrogenase	0.44	-2.29	9.75E-09	SGD	637094	DLD3
YDR307W	YDR307W		0.44	-2.29	2.34E-07	SGD	637220	YDR307W
YNL321W	YNL321W		0.43	-2.3	0	SGD	638829	YNL321W
YKL076C	YKL076C		0.44	-2.3	1.94E-07	SGD	637488	YKL076C
YER164W	CHD1	Sole S. cerevesiae member of CH	0.43	-2.3	8.99E-07	SGD	635637	CHD1
YBR094W	YBR094W		0.43	-2.3	4.50E-06	SGD	638083	YBR094W
YDR034C	LYS14	Transcriptional activator of lysine p	0.43	-2.31	1.90E-37	SGD	634180	LYS14
YOR298C-	MBF1	bridges the DNA-binding region of	0.43	-2.31	2.82E-34	SGD	970752	MBF1
YLR189C	UGT51	Udp-glycosyltransferase; UDP-glu	0.43	-2.31	1.29E-33	SGD	633490	UGT51
YLR342W	FKS1,CND1,CWH53,E	Required for viability of calcineurir	0.43	-2.31	7.46E-25	SGD	637405	FKS1
YIL113W	YIL113W		0.43	-2.31	1.54E-23	SGD	635825	YIL113W
YPR074C	TKL1	Transketolase 1; transketolase 1;	0.43	-2.31	3.17E-20	SGD	637246	TKL1
YDR525W	SNA2	Homology to PMP3/SNA1 (Sensiti	0.43	-2.31	1.37E-18	SGD	970734	SNA2
YER155C	BEM2,IPL2,SUP9,TSL	Protein with role in bud emergenc	0.43	-2.31	1.95E-17	SGD	633531	BEM2
YDR089W	YDR089W		0.43	-2.31	2.39E-10	SGD	635504	YDR089W
YJR051W	OSM1	osmotic growth protein; Null mutar	0.43	-2.31	1.38E-06	SGD	637076	OSM1
YHR135C	YCK1,CKI2	membrane-bound casein kinase I	0.43	-2.31	1.93E-05	SGD	636147	YCK1
YBR145W	ADH5	alcohol dehydrogenase isoenzym	0.43	-2.31	1.02E-04	SGD	635994	ADH5
YOR228C	YOR228C		0.43	-2.32	0	SGD	634488	YOR228C
YDR388W	RVS167	Involved in endocytosis; cytoskele	0.43	-2.32	5.84E-29	SGD	637103	RVS167
YML103C	NUP188	Localized at both the cytoplasmic	0.43	-2.32	2.97E-27	SGD	637406	NUP188
YBR183W	YPC1	Yeast Phyto-ceramidase; alkaline	0.43	-2.32	4.55E-24	SGD	636637	YPC1
YPR122W	AXL1,FUS5,STE22	determinant in axial budding patte	0.43	-2.32	3.22E-16	SGD	638867	AXL1
YDL112W	TRM3	Trna ribose methylase; tRNA (Gm	0.43	-2.32	9.62E-13	SGD	637411	TRM3
YHR001W	QCR10	8.5 kDa subunit of the ubiqunol-cy	0.43	-2.32	7.09E-07	SGD	633421	QCR10
YMR147W	YMR147W		0.43	-2.32	2.02E-04	SGD	635038	YMR147W
YGR191W	HIP1	histidine permease; requires supp	0.43	-2.33	0	SGD	635396	HIP1
YLR241W	YLR241W		0.43	-2.33	5.47E-42	SGD	634232	YLR241W

YOR303W	CPA1	Carbamoyl phosphate synthetase	0.43	-2.33	3.39E-11	SGD	636795	CPA1
YGR170W	PSD2	converts phosphatidylserine to ph	0.43	-2.33	5.60E-11	SGD	638887	PSD2
YHL019C	APM2	homologous to the medium chain	0.43	-2.33	1.10E-10	SGD	637194	APM2
YLR356W	YLR356W		0.43	-2.34	0	SGD	633735	YLR356W
YOR273C	TPO4	Polyamine transport protein	0.43	-2.34	3.97E-34	SGD	638799	TPO4
YOR014W	RTS1	B-type regulatory subunit of protei	0.43	-2.34	5.10E-33	SGD	634757	RTS1
YPL017C	YPL017C		0.43	-2.34	3.48E-21	SGD	638573	YPL017C
YDR283C	GCN2,AAS1	Derepression of GCN4 expressior	0.43	-2.34	3.91E-21	SGD	638914	GCN2
YLR454W	YLR454W		0.43	-2.34	1.13E-17	SGD	635699	YLR454W
YHR208W	BAT1,ECA39,TWT1	branched-chain amino acid transa	0.43	-2.35	7.43E-38	SGD	638460	BAT1
YBR056W	YBR056W	Homolog to glucan-1,3--glucosida	0.43	-2.35	2.43E-36	SGD	638643	YBR056W
YPL128C	TBF1,LPI16	TTAGGG repeat binding factor; le	0.43	-2.35	1.14E-13	SGD	639520	TBF1
YER080W	YER080W		0.43	-2.35	2.11E-10	SGD	635428	YER080W
YOR288C	MPD1	Disulfide isomerase related protei	0.43	-2.35	5.23E-07	SGD	636702	MPD1
YGL142C	GPI10	Involved in glycosyl phosphatidyl i	0.43	-2.35	5.90E-05	SGD	638725	GPI10
YDR298C	ATP5,OSC1	Subunit 5 of the mitochondrial ATI	0.42	-2.36	0	SGD	634970	ATP5
YML035C	AMD1,AMD3	putative alpha-mannosidase; alph	0.42	-2.36	0	SGD	636371	AMD1
YGL155W	CDC43,CAL1	may participate in a ras-like C-terr	0.42	-2.36	5.19E-40	SGD	636953	CDC43
YLR328W	YLR328W		0.42	-2.36	1.48E-38	SGD	635205	YLR328W
YDR474C	YDR474C		0.42	-2.36	8.80E-32	SGD	634073	YDR474C
YER047C	SAP1	interacts with Sin1p; AAA ATPase	0.42	-2.36	1.11E-24	SGD	635515	SAP1
YDR276C	PMP3,SNA1	plasma membrane protein involve	0.42	-2.36	5.36E-16	SGD	634221	PMP3
YPL120W	VPS30,APG6,VPT30	Required for sorting and delivery c	0.42	-2.36	2.35E-13	SGD	634057	VPS30
YKR031C	SPO14,PLD1	dispensable for mitosis, premeioti	0.42	-2.36	8.09E-13	SGD	637421	SPO14
YMR271C	URA10	Fifth step in pyrimidine bio5; orota	0.42	-2.36	8.78E-09	SGD	634464	URA10
YML072C	YML072C		0.42	-2.37	0	SGD	633522	YML072C
YKL168C	KKQ8	Serine/threonine protein kinase of	0.42	-2.37	8.35E-08	SGD	634193	KKQ8
YDR294C	DPL1	dihydrosphingosine phosphate lya	0.42	-2.37	1.91E-06	SGD	636238	DPL1
YLR180W	SAM1,ETH10	S-adenosylmethionine synthetase	0.42	-2.37	2.25E-06	SGD	635234	SAM1
YPL096W	PNG1	de-N-glycosylation enzyme; peptic	0.42	-2.37	6.12E-06	SGD	637807	PNG1
YML100W	TSL1	123 kD regulatory subunit of treha	0.42	-2.37	2.66E-05	SGD	637392	TSL1
YHR078W	YHR078W		0.42	-2.38	0	SGD	634019	YHR078W
YOR002W	ALG6	Required for glucosylation in the N	0.42	-2.38	0	SGD	637923	ALG6
YGL221C	NIF3	similar to Listeria monocytogenes	0.42	-2.38	3.98E-40	SGD	639200	NIF3
YOL133W	HRT1,RBX1,ROC1	High level expression Reduces Ty	0.42	-2.38	4.83E-29	SGD	639014	HRT1
YPR191W	QCR2,COR2,UCR2	40 kDa ubiquinol cytochrome-c re	0.42	-2.38	2.05E-16	SGD	639274	QCR2
YLR285W	YLR285W		0.42	-2.38	1.54E-07	SGD	638414	YLR285W

YIR036C	YIR036C		0.42	-2.38	1.26E-05	SGD	637660	YIR036C
YLR401C	YLR401C		0.42	-2.39	2.64E-30	SGD	638697	YLR401C
YOR332W	VMA4	vacuolar ATPase V1 domain subu	0.42	-2.39	7.14E-23	SGD	635015	VMA4
YLR398C	SKI2	blocks translation of non-poly(A) n	0.42	-2.39	5.00E-16	SGD	638879	SKI2
YMR152W	YIM1	Mitochondrial inner membrane pro	0.42	-2.39	2.04E-12	SGD	636027	YIM1
YLR425W	TUS1,SOP10	TOR Unique function Suppressor,	0.42	-2.4	0	SGD	637380	TUS1
YPL094C	SEC62,LPG14	membrane component of ER prote	0.42	-2.4	3.63E-38	SGD	635951	SEC62
YGL009C	LEU1	leucine biosynthesis; isopropylmal	0.42	-2.4	5.83E-38	SGD	634182	LEU1
YNL201C	YNL201C		0.42	-2.4	3.87E-34	SGD	635448	YNL201C
YNL268W	LYP1	lysine permease	0.42	-2.4	2.80E-25	SGD	636922	LYP1
YGL003C	CDH1,HCT1	CDC20 homolog 1; required for C	0.42	-2.4	1.45E-19	SGD	634068	CDH1
YOL082W	CVT19	Cytoplasm to Vacuole Targeting, I	0.42	-2.4	1.53E-14	SGD	635252	CVT19
YJL210W	PEX2,CRT1,PAS5	Required for peroxisome biogenes	0.42	-2.4	7.07E-05	SGD	633786	PEX2
YOR056C	YOR056C		0.41	-2.41	0	SGD	633972	YOR056C
YDR377W	ATP17	Subunit f of mitochondrial ATP syn	0.42	-2.41	0	SGD	638181	ATP17
YPL098C	YPL098C		0.42	-2.41	4.90E-27	SGD	635654	YPL098C
YPL022W	RAD1,LPB9	UV endonuclease; radiation sensit	0.42	-2.41	8.36E-09	SGD	638929	RAD1
YOR215C	YOR215C		0.42	-2.41	1.76E-08	SGD	639062	YOR215C
YGR270W	YTA7	Member of CDC48/PAS1/SEC18	0.42	-2.41	2.68E-08	SGD	637413	YTA7
YNR002C	FUN34	Highly homologous to Ycr010p an	0.41	-2.42	0	SGD	633761	FUN34
YBR263W	SHM1,SHMT1,TMP3	Serine hydroxymethyltransferase,	0.41	-2.42	0	SGD	637927	SHM1
YBR270C	YBR270C	Probable ATP/GTP-binding protei	0.41	-2.42	1.43E-29	SGD	636203	YBR270C
YGL162W	SUT1	Involved in sterol uptake; Null mut	0.41	-2.42	1.32E-26	SGD	638454	SUT1
YPL049C	DIG1,RST1	Down-regulator of Invasive Growth	0.41	-2.42	8.56E-06	SGD	633977	DIG1
YIL087C	YIL087C		0.41	-2.43	0	SGD	634403	YIL087C
YJL151C	SNA3	Homology to PMP3/SNA1 (Sensit	0.41	-2.43	5.92E-25	SGD	634353	SNA3
YBR216C	YBR216C		0.41	-2.43	1.09E-20	SGD	635414	YBR216C
YOR133W	EFT1	translation elongation factor 2 (EF	0.41	-2.43	4.32E-13	SGD	634622	EFT1
YHR122W	YHR122W		0.41	-2.43	9.49E-11	SGD	638357	YHR122W
YDR306C	YDR306C		0.41	-2.43	3.15E-07	SGD	636837	YDR306C
YJR039W	YJR039W		0.41	-2.44	5.08E-36	SGD	638888	YJR039W
YJL132W	YJL132W		0.41	-2.44	6.07E-33	SGD	638084	YJL132W
YKL060C	FBA1	aldolase; Null mutant is viable, lac	0.41	-2.44	6.69E-24	SGD	639349	FBA1
YKL174C	YKL174C	probable transport protein	0.41	-2.44	2.88E-11	SGD	637189	YKL174C
YER175C	TMT1,TAM1	Trans-aconitate Methyltransferase	0.41	-2.44	2.27E-04	SGD	638406	TMT1
YMR026C	PEX12,PAS11	C3HC4 zinc-binding integral perox	0.41	-2.45	0	SGD	638517	PEX12
YOL086C	ADH1,ADC1	Alcohol dehydrogenase; alcohol d	0.41	-2.45	1.23E-23	SGD	633922	ADH1

YMR056C	AAC1	minor species of mitochondrial AD	0.41	-2.45	4.95E-15	SGD	638383	AAC1
YEL060C	PRB1,CVT1	dispensable for haploidization and	0.41	-2.46	0	SGD	638721	PRB1
YGR070W	ROM1,SKC1	Gdp-GTP Exchange Protein (GEF	0.41	-2.46	5.11E-42	SGD	637387	ROM1
YNL025C	SSN8,GIG3,NUT9,SRI	Component of RNA polymerase II	0.41	-2.46	5.95E-29	SGD	636961	SSN8
YGR287C	YGR287C		0.41	-2.46	1.98E-16	SGD	634731	YGR287C
YHR028C	DAP2,DPP2	Dipeptidyl aminopeptidase B (DPA	0.4	-2.47	0	SGD	636369	DAP2
YJL141C	YAK1	Serine-threonine protein kinase; v	0.4	-2.47	0	SGD	636372	YAK1
YKR096W	YKR096W		0.41	-2.47	4.38E-34	SGD	635607	YKR096W
YNR067C	DSE4	Hypothetical ORF	0.4	-2.47	3.46E-15	SGD	635612	DSE4
YNL138W	SRV2,CAP	70-kDa adenylyl cyclase-associate	0.41	-2.47	1.23E-04	SGD	638655	SRV2
YMR129W	POM152	May be involved in duplication of r	0.4	-2.48	0	SGD	635585	POM152
YAR014C	BUD14	Null mutant is viable, random bude	0.4	-2.48	1.23E-35	SGD	634143	BUD14
YJR121W	ATP2	F(1)F(0)-ATPase complex beta su	0.4	-2.48	1.81E-24	SGD	638663	ATP2
YDL175C	YDL175C		0.4	-2.48	1.15E-08	SGD	633844	YDL175C
YBR043C	YBR043C		0.4	-2.49	1.29E-26	SGD	634585	YBR043C
YFL054C	YFL054C		0.4	-2.49	9.71E-05	SGD	634567	YFL054C
YMR221C	YMR221C		0.4	-2.49	3.77E-04	SGD	635366	YMR221C
YGR261C	APL6,YKS5	beta3-like subunit of the yeast AP-	0.4	-2.5	1.96E-40	SGD	638127	APL6
YNL091W	YNL091W		0.4	-2.5	4.74E-38	SGD	635604	YNL091W
YLR355C	ILV5	branched-chain amino acid biosyr	0.4	-2.5	7.06E-23	SGD	635210	ILV5
YOR184W	SER1,ADE9	phosphoserine transaminase; Null	0.4	-2.5	1.37E-17	SGD	636984	SER1
YPR114W	YPR114W		0.4	-2.5	8.78E-12	SGD	635119	YPR114W
YIR035C	YIR035C		0.4	-2.51	5.37E-18	SGD	635022	YIR035C
YPL162C	YPL162C		0.4	-2.51	1.53E-17	SGD	635893	YPL162C
YOR307C	SLY41	multicopy suppressor of ypt1 dele	0.4	-2.51	4.62E-15	SGD	633992	SLY41
YML117W	YML117W		0.4	-2.51	8.99E-12	SGD	637351	YML117W
YHR001W	OSH7	Oxysterol Binding Protein	0.4	-2.51	5.72E-08	SGD	636074	OSH7
YMR280C	CAT8,DIL1,MSP8	Zinc-cluster protein involved in act	0.4	-2.52	4.44E-34	SGD	635695	CAT8
YOR356W	YOR356W		0.4	-2.52	8.74E-28	SGD	635369	YOR356W
YHR074W	QNS1	Hypothetical ORF	0.4	-2.52	1.53E-09	SGD	636226	QNS1
YCR024C-	PMP1	May regulate plasma membrane H	0.4	-2.53	1.97E-40	SGD	636366	PMP1
YMR319C	FET4	Putative transmembrane low-affini	0.4	-2.53	1.91E-28	SGD	636124	FET4
YGR194C	XKS1	Xylulokinase; xylulokinase; Null m	0.39	-2.53	1.25E-23	SGD	634097	XKS1
YOR015W	YOR015W		0.4	-2.53	1.45E-13	SGD	633658	YOR015W
YPL219W	PCL8	PHO85 cyclin; cyclin; Null mutant	0.39	-2.53	1.65E-12	SGD	635304	PCL8
YOR065W	CYT1,CTC1	Cytochrome c1; cytochrome c1	0.4	-2.53	9.06E-12	SGD	634483	CYT1
YAL043C	PTA1,FUN39	pre-tRNA processing; Null mutant	0.4	-2.53	7.36E-10	SGD	636324	PTA1

YHR170W	NMD3,SRC5	putative Upf1p-interacting protein;	0.39	-2.54	0	SGD	635325	NMD3
YMR219W	ESC1	Establishes Silent Chromatin	0.39	-2.54	3.91E-36	SGD	638961	ESC1
YNL218W	MGS1	Maintenance of Genome Stability	0.39	-2.54	6.25E-20	SGD	636180	MGS1
YBR287W	YBR287W		0.39	-2.54	1.02E-17	SGD	636770	YBR287W
YIR007W	YIR007W		0.39	-2.54	6.45E-13	SGD	634805	YIR007W
YAL038W	CDC19,PYK1	Required for START A in the cell c	0.39	-2.54	6.41E-04	SGD	638587	CDC19
YGR138C	TPO2	Polyamine transport protein	0.39	-2.55	0	SGD	637206	TPO2
YIL112W	YIL112W		0.39	-2.55	1.07E-14	SGD	633463	YIL112W
YJL005W	CYR1,CDC35,HSR1,S	Required for START A of cell cycl	0.39	-2.55	3.13E-14	SGD	633592	CYR1
YKL091C	YKL091C		0.39	-2.55	1.50E-10	SGD	635140	YKL091C
YCR073W	SOL2	multicopy suppressor of los1-1; Nu	0.39	-2.56	0	SGD	634537	SOL2
YML120C	NDI1	NADH dehydrogenase (ubiquinon	0.39	-2.56	0	SGD	637111	NDI1
YCL049C	YCL049C		0.39	-2.56	1.33E-38	SGD	636970	YCL049C
YCL030C	HIS4	histidinol dehydrogenase; Null mu	0.39	-2.56	5.37E-34	SGD	636308	HIS4
YOL098C	YOL098C		0.39	-2.56	1.40E-21	SGD	635534	YOL098C
YMR237W	YMR237W		0.39	-2.56	3.96E-20	SGD	638090	YMR237W
YAR044W	OSH1	May be involved in ergosterol synt	0.39	-2.56	1.01E-17	SGD	635490	OSH1
YOR109W	INP53,SJL3,SOP2	Synaptojanin-like protein; inositol	0.39	-2.57	0	SGD	637391	INP53
YDL174C	DLD1	mitochondrial enzyme D-lactate fe	0.39	-2.57	0	SGD	639505	DLD1
YNL236W	SIN4,BEL2,GAL22,SD	involved in positive and negative r	0.39	-2.57	2.71E-41	SGD	635545	SIN4
YBR229C	ROT2,GLS2	Reversal of tor2 lethality. Involved	0.39	-2.57	2.16E-32	SGD	634679	ROT2
YKL197C	PEX1,PAS1	member of the AAA-protein family	0.39	-2.57	6.18E-25	SGD	638863	PEX1
YEL017C-A	PMP2	May regulate plasma membrane H	0.39	-2.57	3.22E-19	SGD	633397	PMP2
YMR256C	COX7	subunit VII of cytochrome c oxidas	0.39	-2.57	2.27E-05	SGD	634201	COX7
YKR018C	YKR018C		0.39	-2.57	4.92E-05	SGD	636224	YKR018C
YJL070C	YJL070C		0.39	-2.58	0	SGD	633293	YJL070C
YJL164C	TPK1,PKA1,SRA3	putative catalytic subunit of cAMP	0.39	-2.58	0	SGD	636740	TPK1
YBR158W	CST13,ICS4	Chromosome STability; Null muta	0.39	-2.58	9.94E-43	SGD	639478	CST13
YBR132C	AGP2	General amino acid permease wit	0.39	-2.58	4.73E-32	SGD	639486	AGP2
YGR127W	YGR127W		0.39	-2.58	1.12E-17	SGD	638442	YGR127W
YOL048C	YOL048C		0.39	-2.58	2.57E-09	SGD	634301	YOL048C
YNL104C	LEU4	leucine biosynthesis; alpha-isopro	0.39	-2.59	0	SGD	635434	LEU4
YBL105C	PKC1,CLY15,HPO2,S	Protein Kinase C; The null mutant	0.39	-2.59	3.38E-16	SGD	637403	PKC1
YDL066W	IDP1	Mitochondrial form of NADP-speci	0.39	-2.59	5.56E-12	SGD	636081	IDP1
YGL173C	KEM1,DST2,RAR5,SE	Kar1-1 nuclear-fusion-defect Enha	0.39	-2.59	1.43E-09	SGD	638901	KEM1
YGL032C	AGA2	adhesion subunit of a-agglutinin; a	0.39	-2.59	9.50E-06	SGD	638196	AGA2
YJL127C	SPT10,CRE1,SUD1	chromatin maintenance and trans	0.39	-2.59	1.37E-04	SGD	636878	SPT10

YDR385W	EFT2	translation elongation factor 2 (EF	0.38	-2.6	0	SGD	637270	EFT2
YKL010C	UFD4	Ubiquitin Fusion Degradation; Nul	0.38	-2.6	0	SGD	638949	UFD4
YLR090W	XDJ1	Homolog of E. coli DnaJ, closely r	0.38	-2.6	0	SGD	639425	XDJ1
YJL047C	RTT101	Regulator of Ty1 Transposition; N	0.38	-2.6	9.16E-35	SGD	637289	RTT101
YEL046C	GLY1	Threonine Aldolase; threonine ald	0.38	-2.6	9.59E-06	SGD	635168	GLY1
YMR154C	RIM13,CPL1	calpain-like protease involved in p	0.38	-2.61	0	SGD	636290	RIM13
YAL028W	YAL028W		0.38	-2.61	0	SGD	638653	YAL028W
YMR196W	YMR196W		0.38	-2.61	0	SGD	638876	YMR196W
YPL111W	CAR1,LPH15	arginase; Null mutant is viable but	0.38	-2.61	2.26E-27	SGD	637738	CAR1
YEL032W	MCM3	Member of complex that acts at A	0.38	-2.61	3.85E-12	SGD	637318	MCM3
YBR053C	YBR053C		0.38	-2.62	0	SGD	633883	YBR053C
YBR111C	YSA1,RMA2	Protein with weak homology to D.	0.38	-2.62	0	SGD	634444	YSA1
YKL100C	YKL100C		0.38	-2.62	6.73E-20	SGD	634117	YKL100C
YPL036W	PMA2	plasma membrane ATPase; Null r	0.38	-2.62	2.23E-14	SGD	637369	PMA2
YCL009C	ILV6	acetolactate synthase regulatory s	0.38	-2.62	1.27E-04	SGD	635071	ILV6
YAR023C	YAR023C	membrane protein	0.38	-2.62	6.94E-04	SGD	637585	YAR023C
YER166W	DNF1	Drs2 Neo1 Family; Potential amin	0.38	-2.63	0	SGD	633581	DNF1
YOR377W	ATF1	Alcohol acetyltransferase; alcohol	0.38	-2.63	1.15E-21	SGD	638614	ATF1
YLR120C	YPS1	Gpi-anchored aspartic protease (Y	0.38	-2.64	0	SGD	638000	YPS1
YOR264W	DSE3	Hypothetical ORF	0.38	-2.64	6.52E-41	SGD	636080	DSE3
YOL013C	HRD1,DER3	Ubiquitin-protein ligase for endopl	0.38	-2.64	2.49E-16	SGD	639526	HRD1
YIL111W	COX5B	Cytochrome-c oxidase chain Vb; c	0.38	-2.64	3.26E-16	SGD	637584	COX5B
YPL084W	BRO1,LPF2	BCK1-like resistance to osmotic s	0.38	-2.64	1.86E-12	SGD	635493	BRO1
YOR175C	YOR175C		0.38	-2.64	1.20E-09	SGD	638693	YOR175C
YOL089C	HAL9	involved in salt tolerance; contains	0.38	-2.65	0	SGD	637308	HAL9
YNR043W	MVD1,ERG19	involved in the polyisoprene biosy	0.38	-2.65	0	SGD	638503	MVD1
YGL137W	SEC27	Involved in endoplasmic-to-Golgi p	0.38	-2.65	1.35E-16	SGD	635578	SEC27
YGR043C	YGR043C		0.38	-2.65	1.11E-07	SGD	635908	YGR043C
YDL078C	MDH3	malate dehydrogenase; Null muta	0.38	-2.65	2.05E-06	SGD	633845	MDH3
YDR154C	YDR154C		0.38	-2.65	5.89E-04	SGD	639037	YDR154C
YJR109C	CPA2	carbamyl phosphate synthetase; N	0.38	-2.66	0	SGD	633480	CPA2
YJL082W	IML2	Similar to Ykr018p	0.38	-2.66	2.23E-28	SGD	634194	IML2
YML058W	SML1	Suppressor of mec lethality; Null r	0.38	-2.66	4.84E-15	SGD	634872	SML1
YER015W	FAA2,FAM1	acyl-CoA synthetase (long-chain f	0.38	-2.66	1.14E-08	SGD	634133	FAA2
YPR156C	TPO3	Polyamine transport protein	0.38	-2.66	6.56E-07	SGD	636926	TPO3
YBL099W	ATP1	mitochondrial F1F0-ATPase alpha	0.37	-2.67	0	SGD	634023	ATP1
YGL186C	YGL186C		0.37	-2.67	0	SGD	636168	YGL186C

YOR270C	VPH1	vacuolar ATPase V0 domain subu	0.37	-2.67	0	SGD	637271	VPH1
YDL237W	YDL237W		0.37	-2.67	1.16E-39	SGD	636681	YDL237W
YLR144C	ACF2	Identified as an activity necessary	0.37	-2.67	1.37E-25	SGD	636312	ACF2
YER061C	CEM1	homology with beta-keto-acyl synt	0.37	-2.67	7.67E-09	SGD	637816	CEM1
YFR029W	PTR3,SSY3	Regulator of expression of the PT	0.37	-2.68	4.53E-09	SGD	637215	PTR3
YDL022W	GPD1,DAR1,HOR1,O	glycerol-3-phosphate dehydrogen	0.37	-2.7	0	SGD	638523	GPD1
YDL204W	YDL204W		0.37	-2.7	1.73E-17	SGD	636679	YDL204W
YPR028W	YOP1,YIP2	Ypt Interacting Protein	0.37	-2.7	5.86E-16	SGD	634449	YOP1
YNR041C	COQ2	para hydroxybenzoate: polyprenyl	0.37	-2.7	3.62E-10	SGD	636037	COQ2
YMR216C	SKY1	SRPK1-like Kinase in Yeast (SRP	0.37	-2.7	2.54E-06	SGD	638086	SKY1
YGL156W	AMS1	vacuolar alpha mannosidase; alpl	0.37	-2.71	0	SGD	633499	AMS1
YGR183C	QCR9,UCR9	7.3 kDa subunit 9 of the ubiquinol	0.37	-2.71	7.85E-21	SGD	634349	QCR9
YOR350C	MNE1	similar to Lucilia illustris mitochon	0.37	-2.71	1.01E-14	SGD	638798	MNE1
YIL155C	GUT2	glycerol-3-phosphate dehydrogen	0.37	-2.71	8.45E-10	SGD	638727	GUT2
YDR397C	NCB2	Negative Cofactor B2 is the beta s	0.37	-2.71	3.55E-08	SGD	633599	NCB2
YGR201C	YGR201C		0.37	-2.71	3.52E-07	SGD	633767	YGR201C
YFL041W	FET5	ferrous iron transport; multicopper	0.37	-2.71	6.89E-06	SGD	637196	FET5
YMR316C-	YMR316C-B		0.37	-2.72	1.01E-17	SGD	634276	YMR316C-B
YOR136W	IDH2	NAD+-dependent isocitrate dehyd	0.37	-2.72	4.54E-10	SGD	633891	IDH2
YAL031C	FUN21	Function unknown now; Null muta	0.37	-2.73	5.12E-14	SGD	636316	FUN21
YDL024C	DIA3	involved in invasive and pseudohy	0.37	-2.73	1.07E-12	SGD	636101	DIA3
YFR016C	YFR016C		0.37	-2.73	1.25E-09	SGD	637398	YFR016C
YBL015W	ACH1	Mannose-containing glycoprotein	0.37	-2.74	0	SGD	636855	ACH1
YKL019W	RAM2	CAAX farnesyltransferase alpha s	0.36	-2.74	4.52E-42	SGD	636653	RAM2
YML075C	HMG1	3-hydroxy-3-methylglutaryl-coenzy	0.36	-2.74	1.05E-40	SGD	638862	HMG1
YOR178C	GAC1	Regulatory subunit for phosphopr	0.37	-2.74	2.54E-22	SGD	634179	GAC1
YNR018W	YNR018W		0.36	-2.74	2.09E-16	SGD	638379	YNR018W
YGL060W	YGL060W		0.36	-2.75	2.98E-27	SGD	637203	YGL060W
YLR001C	YLR001C		0.36	-2.75	7.22E-22	SGD	635505	YLR001C
YGR271W	SLH1	SKI2-like helicase; null mutant is	0.36	-2.75	4.94E-08	SGD	635701	SLH1
YLR082C	SRL2	Suppressor of Rad53 null Lethality	0.36	-2.75	7.52E-08	SGD	636745	SRL2
YDR406W	PDR15	similar to Pdr5p and Pdr10p; multi	0.36	-2.76	1.52E-33	SGD	638963	PDR15
YLR375W	STP3	Involved in pre-tRNA splicing and	0.36	-2.76	3.26E-13	SGD	636002	STP3
YER086W	ILV1,ISO1	threonine deaminase; Isoleucine-p	0.36	-2.76	8.75E-09	SGD	634107	ILV1
YFR021W	AUT10,NMR1	Required for cytoplasm to vacuole	0.36	-2.78	7.01E-45	SGD	635300	AUT10
YNL118C	DCP2,PSU1	Mrna Decapping. essential suppre	0.36	-2.78	6.20E-36	SGD	635529	DCP2
YPL076W	GPI2,GCR4	Required for synthesis of N-acetyl	0.36	-2.78	2.08E-26	SGD	639207	GPI2

YMR171C	YMR171C		0.36	-2.78	7.76E-22	SGD	639462	YMR171C
YGL007W	YGL007W		0.36	-2.78	5.86E-09	SGD	637490	YGL007W
YDR232W	HEM1	First enzyme in heme biosynthetic	0.36	-2.79	0	SGD	637975	HEM1
YMR264W	CUE1	Cue1p assembles with Ubc7p. Cu	0.36	-2.79	4.33E-11	SGD	639114	CUE1
YIL154C	IMP2'	Protein involved in nucleo-mitocho	0.36	-2.8	1.98E-11	SGD	639236	IMP2'
YKR019C	IRS4	Increased rDNA silencing; Null mu	0.36	-2.81	0	SGD	635375	IRS4
YLR093C	NYV1,MAM2	Synaptobrevin (v-SNARE) homolo	0.36	-2.81	6.83E-42	SGD	636570	NYV1
YLR361C	YLR361C		0.36	-2.81	2.86E-11	SGD	634123	YLR361C
YDR224C	HTB1,SPT12	Histone H2B (HTB1 and HTB2 co	0.36	-2.81	3.53E-08	SGD	633622	HTB1
YMR206W	YMR206W		0.36	-2.81	7.19E-05	SGD	636706	YMR206W
YPL262W	FUM1	Fumarase converts l-malate to fur	0.35	-2.82	0	SGD	635307	FUM1
YOL096C	COQ3	3,4-dihydroxy-5-hexaprenylbenzo	0.35	-2.82	2.35E-34	SGD	635190	COQ3
YHR018C	ARG4	argininosuccinate lyase; Arginine	0.35	-2.82	1.53E-27	SGD	636089	ARG4
YGR248W	SOL4	similar to SOL3	0.35	-2.82	4.71E-25	SGD	634500	SOL4
YDR392W	SPT3	Transcription factor; histone acety	0.35	-2.82	3.66E-11	SGD	633866	SPT3
YBL029C-A	ORF:YBL029C-A	BioProcess=biological_process ur	0.35	-2.82	1.93E-07	SGD	970681	ORF:YBL029C-A
YJL217W	YJL217W		0.35	-2.83	0	SGD	635819	YJL217W
YML116W-A	ORF:YML116W-A	BioProcess=biological_process ur	0.35	-2.83	1.50E-20	SGD	970714	ORF:YML116W-A
YCR023C	YCR023C	Membrane transporter	0.35	-2.84	0	SGD	635392	YCR023C
YDL185W	TFP1,CLS8,VMA1	Encodes a protein with three regic	0.35	-2.84	3.25E-29	SGD	635582	TFP1
YDR457W	TOM1	Temperature dependent Organiza	0.35	-2.84	6.67E-26	SGD	635626	TOM1
YKL220C	FRE2	Ferric reductase, similar to Fre1p;	0.35	-2.84	2.06E-19	SGD	638051	FRE2
YIL097W	FYV10	Function required for Yeast Viabili	0.35	-2.84	1.06E-07	SGD	638618	FYV10
YGR061C	ADE6	5'-phosphoribosylformyl glycinami	0.35	-2.84	1.22E-07	SGD	637429	ADE6
YPR113W	PIS1	phosphatidylinositol synthase; Nul	0.35	-2.85	0	SGD	636520	PIS1
YDR028C	REG1,HEX2,PZF240,S	The reg1 locus encodes a gene w	0.35	-2.85	1.50E-21	SGD	638833	REG1
YJL134W	LCB3,LBP1,YSR2	Protein involved in incorporation o	0.35	-2.85	7.78E-20	SGD	638564	LCB3
YDR009W	GAL3	Involved in galactose induction of	0.35	-2.85	5.56E-19	SGD	636843	GAL3
YDR391C	YDR391C		0.35	-2.85	2.15E-17	SGD	636590	YDR391C
YJR074W	MOG1	Required for nuclear-protein impo	0.35	-2.86	4.71E-27	SGD	634371	MOG1
YJR151C	DAN4	Delayed Anaerobic Gene; cell wal	0.35	-2.86	1.71E-24	SGD	638924	DAN4
YHR087W	YHR087W		0.35	-2.86	1.37E-23	SGD	635672	YHR087W
YGR032W	GSC2,FKS2	Highly similar to FKS1 (GSC1). G	0.35	-2.86	9.32E-21	SGD	638911	GSC2
YJL167W	ERG20,BOT3,FDS1,F	May be rate-limiting step in sterol	0.35	-2.86	1.29E-06	SGD	639301	ERG20
YJL016W	YJL016W		0.35	-2.87	0	SGD	639057	YJL016W
YPL231W	FAS2	Trifunctional enzyme; fatty acid sy	0.35	-2.87	7.60E-33	SGD	637418	FAS2
YPL221W	BOP1	bypass of PAM1	0.35	-2.87	8.72E-19	SGD	634230	BOP1

YNL031C	HHT2	Histone H3 (HHT1 and HHT2 cod	0.35	-2.87	7.91E-13	SGD	634350	HHT2
YNL329C	PEX6,PAS8	Required for peroxisome assembl	0.35	-2.88	0	SGD	637362	PEX6
YPL103C	YPL103C		0.35	-2.88	1.76E-20	SGD	637911	YPL103C
YLR354C	TAL1	Transaldolase, enzyme in the pen	0.35	-2.89	0	SGD	635992	TAL1
YAR027W	YAR027W	membrane protein	0.35	-2.89	3.78E-26	SGD	636632	YAR027W
YGL227W	VID30	vacuole import and degradation (\	0.35	-2.89	9.17E-06	SGD	637371	VID30
YDR070C	YDR070C		0.34	-2.9	1.40E-37	SGD	634217	YDR070C
YOR370C	MRS6,MSI4	protein of the TCD/MRS6 family o	0.34	-2.91	0	SGD	638649	MRS6
YMR278W	YMR278W		0.34	-2.91	0	SGD	638726	YMR278W
YOR086C	YOR086C		0.34	-2.91	1.49E-24	SGD	637401	YOR086C
YLR450W	HMG2	3-hydroxy-3-methylglutaryl-coenzy	0.34	-2.91	6.46E-20	SGD	634670	HMG2
YNL274C	YNL274C		0.34	-2.91	2.86E-19	SGD	633855	YNL274C
YHR093W	AHT1	the AHT1 DNA sequence is upstre	0.34	-2.91	1.11E-16	SGD	637566	AHT1
YMR021C	MAC1,CUA1	metal-binding transcriptional activa	0.34	-2.91	1.06E-15	SGD	637055	MAC1
YLL040C	VPS13,SOI1,VPT2	vacuolar Protein Sorting; Null mut	0.34	-2.91	4.41E-12	SGD	638954	VPS13
YPR196W	MAL63	zinc-finger transcription factor of tl	0.34	-2.91	1.59E-09	SGD	636085	MAL63
YNL066W	SUN4	Protein involved in the aging proce	0.34	-2.92	0	SGD	637022	SUN4
YKL209C	STE6	ABC transporter, glycoprotein, cor	0.34	-2.92	1.29E-35	SGD	635602	STE6
YGR289C	MAL11,AGT1	Part of MAL1 complex locus, encc	0.34	-2.92	1.73E-13	SGD	637205	MAL11
YGR065C	VHT1	vitamin H transporter; H+-biotin sy	0.34	-2.93	0	SGD	634099	VHT1
YPL083C	SEN54	Trna splicing endonuclease 54kDa	0.34	-2.94	0	SGD	633967	SEN54
YHR102W	KIC1,NRK1	Kinase that interacts with Cdc31p,	0.34	-2.94	6.11E-21	SGD	633436	KIC1
YIR016W	YIR016W		0.34	-2.94	8.33E-19	SGD	637675	YIR016W
YMR181C	YMR181C		0.34	-2.95	0	SGD	636471	YMR181C
YDL086W	YDL086W		0.34	-2.95	3.74E-41	SGD	635892	YDL086W
YJR073C	OPI3,PEM2	Second and third steps of methyla	0.34	-2.96	0	SGD	639181	OPI3
YMR160W	YMR160W		0.34	-2.96	1.00E-21	SGD	634744	YMR160W
YAR029W	YAR029W	membrane protein	0.34	-2.97	0	SGD	634219	YAR029W
YGR240C	PFK1	phosphofructokinase alpha subun	0.34	-2.98	0	SGD	637319	PFK1
YKL038W	RGT1	transcriptional repressor and activ	0.34	-2.98	0	SGD	637402	RGT1
YBR235W	YBR235W		0.34	-2.98	3.12E-27	SGD	637352	YBR235W
YIL136W	OM45	45-kDa mitochondrial outer memb	0.33	-2.99	3.22E-10	SGD	638506	OM45
YPL014W	YPL014W		0.33	-2.99	4.88E-10	SGD	638529	YPL014W
YIL047C	SYG1	Protein for which truncation and o	0.33	-3	0	SGD	635498	SYG1
YGL035C	MIG1,CAT4,SSN1,TD	Transcription factor involved in glu	0.33	-3	0	SGD	637132	MIG1
YDL085W	YDL085W		0.33	-3	4.90E-44	SGD	636128	YDL085W
YGR100W	MDR1,GYP2,MIC1	Mac1-dependent regulator; GTPa	0.33	-3	3.51E-11	SGD	634641	MDR1

YDR297W	SUR2,SYR2	Suppressor of rvs161 and rvs167	0.33	-3.01	0	SGD	639287	SUR2
YLR452C	SST2	Protein involved in desensitization	0.33	-3.01	8.13E-37	SGD	636282	SST2
YOR173W	YOR173W		0.33	-3.01	2.36E-17	SGD	638535	YOR173W
YBR298C	MAL31,MAL3T	Part of the complex locus MAL3, f	0.33	-3.01	2.34E-11	SGD	637190	MAL31
YKL022C	CDC16	a component of anaphase-promot	0.33	-3.02	4.56E-37	SGD	637255	CDC16
YPL270W	MDL2	ATP-binding cassette (ABC) trans	0.33	-3.02	1.70E-16	SGD	638124	MDL2
YJR016C	ILV3	catalyzes third step in common pa	0.33	-3.02	1.17E-15	SGD	634734	ILV3
YOR081C	YOR081C		0.33	-3.02	2.60E-10	SGD	634712	YOR081C
YBR140C	IRA1,GLC1,PPD1	Inhibitory regulator of the RAS-cA	0.33	-3.03	1.45E-12	SGD	638971	IRA1
YOR062C	YOR062C		0.33	-3.03	1.29E-10	SGD	635896	YOR062C
YDL155W	CLB3	Involved in mitotic induction and p	0.33	-3.04	6.42E-17	SGD	635261	CLB3
YNL330C	RPD3,REC3,SDI2,SD	Transcription modifier, required fo	0.33	-3.04	2.84E-14	SGD	633937	RPD3
YOL084W	PHM7	transcription is regulated by PHO	0.33	-3.05	1.49E-24	SGD	637311	PHM7
YLL006W	MMM1	Involved in mechanism by which r	0.33	-3.05	4.85E-08	SGD	638557	MMM1
YDR376W	ARH1	adrenodoxin oxidoreductase homo	0.33	-3.06	0	SGD	638575	ARH1
YOR070C	GYP1	Gtpase activating protein for Ypt1	0.33	-3.07	7.02E-32	SGD	638690	GYP1
YNL264C	PDR17,ISS1	involved in pleiotropic drug resista	0.33	-3.07	5.76E-31	SGD	637740	PDR17
YBR147W	YBR147W		0.33	-3.07	5.42E-25	SGD	636617	YBR147W
YPR091C	YPR091C		0.33	-3.07	3.59E-23	SGD	634819	YPR091C
YGL017W	ATE1	arginyl-tRNA-protein transferase;	0.33	-3.07	5.24E-18	SGD	637090	ATE1
YKR080W	MTD1	NAD-dependent 5,10-methylenete	0.32	-3.08	1.57E-42	SGD	634533	MTD1
YMR212C	EFR3	PHO _E_ighty _F_ive _R_equiring	0.32	-3.09	0	SGD	636311	EFR3
YOR042W	YOR042W		0.32	-3.09	0	SGD	636779	YOR042W
YGR175C	ERG1	Squalene monooxygenase; squale	0.32	-3.09	1.80E-17	SGD	637137	ERG1
YPL026C	SKS1,SHA3	multicopy suppressor of snf3 and	0.32	-3.09	2.78E-12	SGD	638627	SKS1
YFL031W	HAC1,ERN4,IRE15	Transcription factor that is require	0.32	-3.09	1.21E-06	SGD	633666	HAC1
YGL026C	TRP5	tryptophan synthetase; Null mutar	0.32	-3.1	0	SGD	636278	TRP5
YDR272W	GLO2	Cytoplasmic glyoxylase-II; glyoxyl	0.32	-3.1	8.02E-26	SGD	635941	GLO2
YMR232W	FUS2	Involved in cell fusion during matir	0.32	-3.1	1.85E-20	SGD	638794	FUS2
YDR178W	SDH4,ACN18	succinate dehydrogenase membra	0.32	-3.1	4.20E-15	SGD	637551	SDH4
YJR115W	YJR115W		0.32	-3.11	1.57E-11	SGD	635706	YJR115W
YGL121C	YGL121C		0.32	-3.11	4.48E-09	SGD	638989	YGL121C
YNR055C	HOL1	Putative ion transporter similar to	0.32	-3.12	3.11E-31	SGD	637991	HOL1
YGR288W	MAL13	Part of complex locus MAL1, nonf	0.32	-3.12	2.32E-09	SGD	636116	MAL13
YDL198C	YHM1	high copy suppressor of abf2 lack	0.32	-3.13	0	SGD	636598	YHM1
YGR236C	SPG1	Hypothetical ORF; Null mutant is	0.32	-3.13	0	SGD	639001	SPG1
YPL057C	SUR1,BCL21,CSG1,LI	Involved in maintenance of phosp	0.32	-3.14	3.17E-09	SGD	638528	SUR1

YKL151C	YKL151C		0.32	-3.15	2.80E-45	SGD	639298	YKL151C
YJL185C	YJL185C		0.32	-3.16	0	SGD	635942	YJL185C
YMR297W	PRC1,LBC1	dispensable for haploidization anc	0.32	-3.17	0	SGD	636889	PRC1
YDR498C	SEC20	membrane glycoprotein, sorted by	0.32	-3.17	1.04E-11	SGD	636991	SEC20
YMR203W	TOM40,ISP42,MOM38	Translocase of Outer Mitochondria	0.31	-3.18	0	SGD	635215	TOM40
YKL182W	FAS1	pentafunctional enzyme consisting	0.31	-3.19	0	SGD	637475	FAS1
YGR141W	YGR141W		0.31	-3.19	2.40E-24	SGD	639420	YGR141W
YBR139W	YBR139W	Probable serine-type carboxypept	0.31	-3.19	7.76E-17	SGD	635346	YBR139W
YMR243C	ZRC1,OSR1	Zinc- and cadmium-resistance pro	0.31	-3.2	1.09E-26	SGD	636120	ZRC1
YGL234W	ADE5,7	glycinamide ribotide synthetase ar	0.31	-3.21	0	SGD	634747	ADE5,7
YER053C	YER053C		0.31	-3.22	0	SGD	635148	YER053C
YPL181W	YPL181W		0.31	-3.22	0	SGD	637115	YPL181W
YLR087C	CSF1		0.31	-3.22	6.75E-11	SGD	637415	CSF1
YHR137W	ARO9	aromatic amino acid aminotransfe	0.31	-3.24	0	SGD	635359	ARO9
YFR022W	YFR022W		0.31	-3.24	4.23E-20	SGD	636222	YFR022W
YJL084C	YJL084C		0.31	-3.24	1.99E-12	SGD	634701	YJL084C
YML059C	YML059C		0.31	-3.26	1.01E-26	SGD	633520	YML059C
YOR203W	YOR203W		0.31	-3.26	4.80E-23	SGD	637454	YOR203W
YNL326C	YNL326C		0.31	-3.26	3.10E-18	SGD	639314	YNL326C
YMR302C	PRP12,RNA12,YME2	Integral membrane mitochondrial	0.31	-3.27	1.19E-34	SGD	634605	PRP12
YDL130W-	STF1,AIS2	ATPase stabilizing factor	0.31	-3.27	4.22E-34	SGD	970739	STF1
YJL142C	YJL142C		0.31	-3.28	3.47E-39	SGD	633608	YJL142C
YOL034W	YOL034W		0.3	-3.28	1.14E-17	SGD	638875	YOL034W
YFL026W	STE2	alpha-factor pheromone receptor,	0.3	-3.29	3.45E-18	SGD	639384	STE2
YLR130C	ZRT2	Low-affinity zinc transport protein;	0.3	-3.29	4.04E-15	SGD	637021	ZRT2
YBR151W	APD1	actin patches distal	0.3	-3.3	3.59E-17	SGD	636703	APD1
YDR517W	GRH1	Yeast (GR)ASP65 (H)omologue; r	0.3	-3.31	0	SGD	633959	GRH1
YHR143W	DSE2	Hypothetical ORF	0.3	-3.31	0	SGD	634529	DSE2
YPR106W	ISR1	Inhibition of staurosporine resistar	0.3	-3.31	9.02E-17	SGD	639376	ISR1
YGR243W	YGR243W		0.3	-3.32	0	SGD	638207	YGR243W
YDL048C	STP4	Involved in pre-tRNA splicing and	0.3	-3.32	4.19E-23	SGD	637131	STP4
YJR033C	RAV1	Regulator of (H+)-ATPase in vacu	0.3	-3.32	1.02E-21	SGD	633528	RAV1
YMR119W	ASI1	Amino acid Sensor-Independent (	0.3	-3.32	7.39E-14	SGD	635404	ASI1
YDL222C	YDL222C		0.3	-3.32	1.76E-09	SGD	638398	YDL222C
YGL018C	JAC1	may be involved in assembly/matu	0.3	-3.33	3.64E-15	SGD	635764	JAC1
YIL045W	PIG2	Interacts with Gsy2p; 30% identity	0.3	-3.34	4.05E-29	SGD	639468	PIG2
YOL025W	LAG2,ECM36	affects longevity; A Tn3 insertion i	0.3	-3.34	3.78E-11	SGD	634563	LAG2

YMR231W	PEP5,END1,VAM1,VP	peripheral vaculor membrane prot	0.3	-3.35	2.74E-34	SGD	635535	PEP5
YLR149C	YLR149C		0.3	-3.35	2.95E-23	SGD	634779	YLR149C
YOR179C	YOR179C		0.3	-3.35	7.21E-13	SGD	635793	YOR179C
YGR031W	YGR031W		0.3	-3.35	1.17E-09	SGD	633861	YGR031W
YNL305C	YNL305C		0.3	-3.36	2.01E-29	SGD	638457	YNL305C
YLL015W	BPT1	bile pigment transporter; ABC tran	0.3	-3.36	1.34E-28	SGD	635691	BPT1
YPL058C	PDR12	similar to Pdr5p; multidrug resistai	0.3	-3.37	6.08E-30	SGD	638948	PDR12
YLR359W	ADE13,BRA1,BRA8	Adenylosuccinate Lyase; adenylos	0.29	-3.4	1.61E-39	SGD	638582	ADE13
YBR203W	YBR203W		0.29	-3.4	3.02E-25	SGD	638853	YBR203W
YHR096C	HXT5	Member of superfamily of monosa	0.29	-3.42	1.94E-37	SGD	634730	HXT5
YHR002W	LEU5	mitochondrial carrier protein, invol	0.29	-3.44	3.86E-30	SGD	637840	LEU5
YER066W	YER066W		0.29	-3.44	4.47E-25	SGD	633678	YER066W
YGL012W	ERG4	Sterol C-24 reductase; sterol C-24	0.29	-3.44	6.70E-16	SGD	636150	ERG4
YDR074W	TPS2,HOG2,PFK3	Trehalose-6-phosphate phosphata	0.29	-3.45	0	SGD	637295	TPS2
YPL031C	PHO85	involved in phosphate and glycoge	0.29	-3.47	1.86E-15	SGD	635989	PHO85
YDR432W	NPL3,MTR13,MTS1,N	involved as a protein carrier in mR	0.29	-3.48	2.09E-13	SGD	637025	NPL3
YLR128W	YLR128W		0.29	-3.5	1.48E-19	SGD	634473	YLR128W
YDR043C	NRG1	involved in regulation of glucose r	0.29	-3.5	3.86E-16	SGD	636562	NRG1
YDR399W	HPT1,BRA6	enzyme involved in de novo purin	0.29	-3.5	6.66E-14	SGD	636585	HPT1
YER187W	YER187W	similar to killer toxin	0.29	-3.5	4.39E-12	SGD	636485	YER187W
YMR119W	YMR119W-A		0.29	-3.5	4.55E-08	SGD	637492	YMR119W-A
YOR125C	CAT5,COQ7	may encode a protein involved in	0.29	-3.51	1.65E-21	SGD	635878	CAT5
YMR304W	UBP15	putative deubiquitinating enzyme;	0.28	-3.52	1.96E-21	SGD	633488	UBP15
YKL062W	MSN4	multicopy suppressor of snf1 muta	0.28	-3.53	2.74E-17	SGD	638719	MSN4
YCR032W	BPH1	beige protein homologue 1; Null m	0.28	-3.54	0	SGD	633515	BPH1
YML110C	COQ5,DBI56	co-enzyme Q deficient; C-methyltr	0.28	-3.55	0	SGD	636609	COQ5
YHR162W	YHR162W		0.28	-3.55	0	SGD	637501	YHR162W
YGR149W	YGR149W		0.28	-3.56	0	SGD	639368	YGR149W
YBR001C	NTH2	hydrolyzes trehalose, may be inol	0.28	-3.56	2.38E-24	SGD	634751	NTH2
YPR161C	SGV1,BUR1	CDC28/cdc2 related protein kinas	0.28	-3.56	2.06E-09	SGD	635419	SGV1
YMR261C	TPS3	115 kD regulatory subunit of treha	0.28	-3.57	2.61E-10	SGD	637305	TPS3
YER024W	YAT2	The Yat2p protein shows significa	0.28	-3.58	0	SGD	635574	YAT2
YGL193C	YGL193C		0.28	-3.59	6.49E-37	SGD	634873	YGL193C
YDL239C	ADY3	Accumulation of dyads; Null: form	0.28	-3.61	2.25E-41	SGD	634164	ADY3
YKL150W	MCR1	NADH-cytochrome b5 reductase	0.28	-3.61	8.76E-13	SGD	638404	MCR1
YNL022C	YNL022C		0.28	-3.63	0	SGD	635290	YNL022C
YMR145C	YMR145C		0.28	-3.63	3.99E-31	SGD	636212	YMR145C

YDL128W	VCX1,HUM1,MNR1	Similar to sodium/calcium exchan	0.28	-3.63	1.79E-30	SGD	635199	VCX1
YGL248W	PDE1	3',5'-Cyclic-nucleotide phosphodie	0.28	-3.64	0	SGD	639341	PDE1
YKR058W	GLG1	self-glucosylating initiator of glyco	0.27	-3.65	6.64E-27	SGD	637088	GLG1
YIL009C-A	EST3	ever shorter telomeres; 20.5 kDa	0.27	-3.65	1.82E-07	SGD	970717	EST3
YAR028W	YAR028W	membrane protein	0.27	-3.66	8.02E-26	SGD	636633	YAR028W
YOL016C	CMK2	Calmodulin-dependent protein kin	0.27	-3.66	4.57E-20	SGD	636117	CMK2
YMR272C	SCS7,FAH1	Required for the hydroxylation of t	0.27	-3.69	0	SGD	636733	SCS7
YCL033C	YCL033C	Transcription regulator	0.27	-3.72	3.84E-16	SGD	633605	YCL033C
YJL186W	MNN5	mannan synthesis; golgi alpha-1,2	0.27	-3.73	0	SGD	636240	MNN5
YIL121W	YIL121W		0.27	-3.73	6.21E-43	SGD	636129	YIL121W
YBR126C	TPS1,BYP1,CIF1,FDP	Probable regulator of glucose influ	0.27	-3.74	1.37E-28	SGD	635318	TPS1
YJL163C	YJL163C		0.27	-3.74	1.08E-11	SGD	636214	YJL163C
YGL208W	SIP2,SPM2	Member of a family of proteins, in	0.27	-3.74	1.15E-10	SGD	636792	SIP2
YKL029C	MAE1	Mitochondrial malic enzyme; malic	0.27	-3.76	1.58E-32	SGD	635415	MAE1
YNR034W	ORF:YNR034W-A	BioProcess=biological_process ur	0.27	-3.76	6.72E-09	SGD	970744	ORF:YNR034W-A
YMR213W	CEF1	homolog of S. pombe cdc5+; prote	0.27	-3.77	1.57E-20	SGD	638004	CEF1
YLR058C	SHM2,SHMT2	serine hydroxymethyltransferase;	0.27	-3.77	5.16E-15	SGD	637895	SHM2
YML013W	YML013W		0.26	-3.78	8.83E-43	SGD	636182	YML013W
YOR285W	YOR285W		0.26	-3.79	0	SGD	636385	YOR285W
YMR083W	ADH3	alcohol dehydrogenase isoenzym	0.26	-3.8	0	SGD	636035	ADH3
YAR015W	ADE1	phosphoribosyl amino imidazolesu	0.26	-3.81	0	SGD	634502	ADE1
YKR049C	YKR049C		0.26	-3.83	0	SGD	636405	YKR049C
YBR116C	YBR116C		0.26	-3.86	2.00E-13	SGD	637571	YBR116C
YLR044C	PDC1	pyruvate decarboxylase; undetect	0.26	-3.87	3.07E-10	SGD	639519	PDC1
YKL034W	YKL034W		0.26	-3.89	2.13E-10	SGD	634187	YKL034W
YBR241C	YBR241C	Probable sugar transport protein	0.26	-3.9	0	SGD	636800	YBR241C
YAL061W	YAL061W		0.26	-3.91	2.51E-39	SGD	637054	YAL061W
YKR089C	YKR089C		0.26	-3.92	5.44E-38	SGD	634610	YKR089C
YLR240W	VPS34,END12,PEP15	phosphatidylinositol 3-kinase; tem	0.25	-3.93	1.67E-15	SGD	638764	VPS34
YNL115C	YNL115C		0.25	-3.94	0	SGD	635469	YNL115C
YPR184W	GDB1	Glycogen debranching enzyme, th	0.25	-3.94	0	SGD	635635	GDB1
YDL110C	YDL110C		0.25	-3.95	0	SGD	638283	YDL110C
YOR291W	YOR291W		0.25	-3.96	1.55E-40	SGD	633584	YOR291W
YDR046C	BAP3	branched-chain amino acid perme	0.25	-3.97	5.30E-26	SGD	635395	BAP3
YJL213W	YJL213W		0.25	-3.99	0	SGD	636955	YJL213W
YDL079C	MRK1	putative protein kinase with simila	0.25	-3.99	0	SGD	638017	MRK1
YNL328C	MDJ2	Protein of the mitochondrial inner	0.25	-3.99	1.26E-36	SGD	636394	MDJ2

YHR190W	ERG9	squalene synthetase; Null mutant	0.25	-3.99	9.90E-11	SGD	637862	ERG9
YBR086C	IST2	Similar to calcium and sodium cha	0.25	-4.02	3.33E-41	SGD	637330	IST2
YPL004C	YPL004C		0.24	-4.09	0	SGD	639241	YPL004C
YBR196C	PGI1,CDC30	Phosphoglucoisomerase; glucose	0.24	-4.11	0	SGD	634058	PGI1
YNL037C	IDH1	alpha-4-beta-4 subunit of mitocho	0.24	-4.13	5.53E-14	SGD	637768	IDH1
YBR067C	TIP1	cold- and heat-shock induced prot	0.24	-4.15	4.39E-10	SGD	633292	TIP1
YDR127W	ARO1	pentafunctional arom polypeptide	0.24	-4.17	0	SGD	635618	ARO1
YNR001C	CIT1,CS1,LYS6	citrate synthase. Nuclear encoded	0.24	-4.17	0	SGD	638640	CIT1
YPL265W	DIP5	dicarboxylic amino acid permease	0.24	-4.17	0	SGD	638713	DIP5
YLR258W	GSY2	Highly similar to GSY1. GSY2 is tl	0.24	-4.17	1.32E-40	SGD	638037	GSY2
YGR044C	RME1,CSP1	mediates cell type control of sporu	0.24	-4.18	0	SGD	635063	RME1
YER028C	YER028C		0.24	-4.18	6.05E-20	SGD	638520	YER028C
YJL198W	PHO90	Low-affinity phosphate transporte	0.24	-4.19	3.35E-43	SGD	635502	PHO90
YFR053C	HXK1	Glucose phosphorylation; hexokin	0.24	-4.2	0	SGD	638580	HXK1
YNL055C	POR1,OMP2	Outer mitochondrial membrane pc	0.24	-4.2	1.07E-38	SGD	633817	POR1
YPL092W	SSU1,LPG16	sensitive to sulfite; major facilitato	0.23	-4.27	3.71E-10	SGD	639426	SSU1
YER067W	YER067W		0.23	-4.28	0	SGD	634400	YER067W
YPL101W	ELP4,HAP1	ELongator Protein 4, 50kD subuni	0.23	-4.33	2.48E-34	SGD	639443	ELP4
YBL003C	HTA2,H2A2	Histone H2A (HTA1 and HTA2 co	0.23	-4.34	0	SGD	634354	HTA2
YMR019W	STB4	binds Sin3p in two-hybrid assay; N	0.23	-4.34	2.33E-22	SGD	634694	STB4
YOR120W	GCY1	Galactose-induced transcript, proc	0.23	-4.36	1.78E-15	SGD	634541	GCY1
YCR091W	KIN82	Putative serine/threonine protein k	0.23	-4.38	0	SGD	634764	KIN82
YNL045W	YNL045W		0.23	-4.4	1.22E-42	SGD	638736	YNL045W
YGL197W	MDS3	Mck1 Dosage Suppressor 3, nega	0.23	-4.41	0	SGD	638902	MDS3
YBR286W	APE3,APY1	Aminopeptidase yscIII; aminopept	0.23	-4.42	6.11E-15	SGD	637928	APE3
YOR347C	PYK2	Pyruvate kinase, glucose-represse	0.23	-4.43	4.04E-30	SGD	638681	PYK2
YOL153C	YOL153C		0.22	-4.44	4.65E-34	SGD	639509	YOL153C
YKL035W	UGP1	Uridinephosphoglucose pyrophosp	0.22	-4.46	0	SGD	635301	UGP1
YBR218C	PYC2	converts pyruvate to oxaloacetate	0.22	-4.49	0	SGD	635556	PYC2
YCL040W	GLK1,HOR3	Glucose phosphorylation; glucokir	0.22	-4.49	1.35E-06	SGD	638628	GLK1
YDL019C	OSH2	Oxysterol Binding Protein; Null mu	0.22	-4.5	0	SGD	637343	OSH2
YLR134W	PDC5	pyruvate decarboxylase; undetect	0.22	-4.54	0	SGD	639455	PDC5
YFR047C	YFR047C		0.22	-4.56	0	SGD	638394	YFR047C
YPL006W	NCR1	Niemann-Pick Type C homologou	0.22	-4.58	1.63E-19	SGD	633355	NCR1
YNR044W	AGA1	anchorage subunit of a-agglutinin;	0.22	-4.58	3.29E-15	SGD	636274	AGA1
YBR052C	YBR052C	Homolog to YCR004, obr1 (S. por	0.22	-4.62	1.58E-15	SGD	638337	YBR052C
YMR098C	YMR098C		0.22	-4.63	0	SGD	638695	YMR098C

YMR136W	GAT2	Product of gene unknown	0.21	-4.67	5.71E-28	SGD	636195	GAT2
YNR014W	YNR014W		0.21	-4.7	9.12E-26	SGD	636511	YNR014W
YDR277C	MTH1,BPC1,DGT1,HT	Negative regulator of HXT gene e	0.21	-4.72	7.31E-07	SGD	636046	MTH1
YNL194C	YNL194C		0.21	-4.77	0	SGD	635062	YNL194C
YFR017C	YFR017C		0.21	-4.77	0	SGD	637604	YFR017C
YMR105C	PGM2,GAL5	Phosphoglucomutase; phosphoglu	0.21	-4.81	1.45E-38	SGD	634096	PGM2
YAL044C	GCV3	H-protein subunit of the glycine cle	0.21	-4.81	2.98E-14	SGD	637586	GCV3
YGR066C	YGR066C		0.21	-4.84	2.56E-24	SGD	633809	YGR066C
YAL060W	BDH1	(2R,3R)-2,3-butanediol dehydroge	0.21	-4.86	0	SGD	638512	BDH1
YDR225W	HTA1,H2A1,SPT11	Histone H2A (HTA1 and HTA2 co	0.21	-4.86	3.70E-10	SGD	634827	HTA1
YLR348C	DIC1	mitochondrial dicarboxylate transp	0.21	-4.87	2.06E-28	SGD	635065	DIC1
YPR035W	GLN1	glutamine synthetase; Glutamine s	0.2	-4.89	3.55E-12	SGD	636007	GLN1
YLR152C	YLR152C		0.2	-4.94	2.99E-39	SGD	634738	YLR152C
YLR304C	ACO1,GLU1	Aconitase, mitochondrial; aconitas	0.2	-4.96	3.29E-17	SGD	638061	ACO1
YGR260W	TNA1	Transporter of Nicotinic Acid; high	0.2	-5.01	0	SGD	635348	TNA1
YMR096W	SNZ1	Snooze: stationary phase-induced	0.2	-5.06	0	SGD	635151	SNZ1
YFR015C	GSY1	Highly similar to GSY2. GSY2 is th	0.2	-5.12	1.32E-30	SGD	634141	GSY1
YBR230C	YBR230C		0.2	-5.12	1.69E-09	SGD	638286	YBR230C
YGL008C	PMA1	major regulator of cytoplasmic pH	0.19	-5.21	0	SGD	638812	PMA1
YJL078C	PRY3	Pathogen Related in Sc, contains	0.19	-5.26	2.34E-15	SGD	635486	PRY3
YMR095C	SNO1	SNZ1 proximal ORF, stationary ph	0.19	-5.29	0	SGD	635037	SNO1
YHL021C	YHL021C		0.19	-5.29	2.84E-40	SGD	636103	YHL021C
YMR291W	YMR291W		0.19	-5.31	0	SGD	634733	YMR291W
YKL185W	ASH1	Zinc-finger inhibitor of HO transcri	0.19	-5.37	0	SGD	636179	ASH1
YLR286C	CTS1	Endochitinase; endochitinase; Null	0.19	-5.4	3.27E-17	SGD	636194	CTS1
YJR148W	BAT2,TWT2	Branched-Chain Amino Acid Tran	0.18	-5.42	0	SGD	635238	BAT2
YPL082C	MOT1,BUR3,LPF4	involved in TBP (TATA-binding pr	0.18	-5.46	1.98E-15	SGD	635630	MOT1
YGR060W	ERG25	C-4 sterol methyl oxidase; Null mu	0.18	-5.5	2.10E-44	SGD	634482	ERG25
YMR008C	PLB1	Responsible for the production of	0.18	-5.52	0	SGD	638738	PLB1
YPL230W	USV1	Up in StarVation	0.18	-5.53	2.02E-20	SGD	637003	USV1
YPL274W	SAM3	S-adenosylMethionine Permease;	0.18	-5.6	0	SGD	638006	SAM3
YHR037W	PUT2	delta-1-pyrroline-5-carboxylate de	0.17	-5.76	0	SGD	636186	PUT2
YPL095C	YPL095C		0.17	-5.79	3.02E-38	SGD	636162	YPL095C
YHR094C	HXT1,HOR4	High-affinity hexose (glucose) tran	0.17	-5.79	1.41E-24	SGD	636189	HXT1
YMR205C	PFK2	phosphofructokinase beta subunit	0.17	-5.79	5.11E-15	SGD	634642	PFK2
YMR011W	HXT2	hexose transporter; high affinity he	0.17	-5.91	3.95E-18	SGD	636206	HXT2
YGL255W	ZRT1	High-affinity zinc transport protein	0.17	-5.92	9.98E-19	SGD	636996	ZRT1

YKL109W	HAP4	Regulates respiratory functions, e	0.17	-5.98	0	SGD	637933	HAP4
YDR380W	ARO10		0.17	-6.02	0	SGD	637201	ARO10
YMR189W	GCV2,GSD2	Glycine CleaVage system; glycine	0.16	-6.21	0	SGD	634671	GCV2
YMR195W	ICY1	Interacting with the cytoskeleton<l	0.16	-6.27	0	SGD	635714	ICY1
YMR250W	GAD1	glutamate decarboxylase	0.16	-6.37	0	SGD	637992	GAD1
YDR343C	HXT6	Repression of HXT6 expression b	0.16	-6.4	9.50E-19	SGD	634095	HXT6
YKR075C	YKR075C		0.15	-6.45	0	SGD	636593	YKR075C
YGL158W	RCK1	Serine/threonine protein kinase; N	0.15	-6.53	6.28E-26	SGD	637165	RCK1
YLR142W	PUT1	proline oxidase; inability to use pr	0.15	-6.54	0	SGD	639431	PUT1
YMR081C	ISF1,MBR3	May regulate NAM7 function, pos	0.15	-6.84	0	SGD	635974	ISF1
YDR342C	HXT7	Hexose transporter; hexose trans	0.14	-6.93	2.00E-06	SGD	638015	HXT7
YLR056W	ERG3,SYR1	C-5 sterol desaturase; Null mutan	0.14	-7	1.09E-26	SGD	633894	ERG3
YEL011W	GLC3,GHA1	Glycogen branching enzyme; 1,4-	0.14	-7.14	0	SGD	634770	GLC3
YMR120C	ADE17	AICAR transformylase/IMP cycloh	0.14	-7.18	0	SGD	633447	ADE17
YGL209W	MIG2,MLZ1	Involved in repression, along with	0.14	-7.26	2.49E-36	SGD	636992	MIG2
YDR345C	HXT3	Low-affinity glucose transporter; lo	0.13	-7.88	0	SGD	637964	HXT3
YNL327W	EGT2	cell-cycle regulation protein, may l	0.13	-7.95	3.53E-12	SGD	638897	EGT2
YLR089C	YLR089C		0.12	-8.03	7.15E-22	SGD	638019	YLR089C
YGL117W	YGL117W		0.12	-8.09	1.24E-39	SGD	635867	YGL117W
YDR019C	GCV1,GSD1	Required for metabolizing glycine	0.11	-9.06	4.46E-22	SGD	637033	GCV1
YHR092C	HXT4,LGT1,RAG1	hexose transporter; high affinity gl	0.11	-9.39	4.24E-33	SGD	637930	HXT4
YPR160W	GPH1	Releases glucose-1-phosphate fro	0.09	-11.25	0	SGD	637278	GPH1
YCR005C	CIT2	non-mitochondrial citrate synthase	0.09	-11.4	0	SGD	639424	CIT2