Summary of Supplementary Data

	Title	**Description**
1	Summary	Summary of Supplementary Data
2	C. albicans dataset	Fold changes for all *C. albicans* genes
3	C. albicans Venn Diagrams	Venn diagrams comparing the number of genes regulated by low, medium and high glucose
4	S. cerevisiae dataset	Fold changes for all *S. cerevisiae* genes [Yin *et al* .(2003) data re-analysed]
5	C. albicans vs S. cerevisiae	Comparison of fold changes for homologues in *C. albicans* and *S. cerevisiae*
6	Functions	Regulation of genes involved in central metabolism, stress and ribosome biogenesis
7	Mitochondrial Functions	Comparison of C. albicans and S. cerevisiae Mitochondrial Functions
8	PCR primers	PCR primers to generate gene-specific probes

Complete *C. albicans* dataset

Heatmap Scale

>=10	5.00	0.00	-5.00
9.62	4.62	-0.38	-5.38
9.23	4.23	-0.77	-5.77
8.85	3.85	-1.15	-6.15
8.46	3.46	-1.54	-6.54
8.08	3.08	-1.92	-6.92
7.69	2.69	-2.31	-7.31
7.31	2.31	-2.69	-7.69
6.92	1.92	-3.08	-8.08
6.54	1.54	-3.46	-8.46
6.15	1.15	-3.85	-8.85
5.77	0.77	-4.23	-9.23
5.38	0.38	-4.62	<=-10

Gene Name		Expression ratio Glucose Concentration (%)						
Systematic	**Common**	**0**	**0.01**	**0.1**	**1**	**Description**	***S. cerevisiae* homologue**	**orf19. Number**
CA1067	HXT62	1.3	45.4	34.6	42.5	sugar transporter	YDR345c	orf19.2023
CA1069	HXT5.3F	1.4	17.4	15.9	15.9	sugar transporter, 3-prime end		orf19.2021
CA0495	IPF20056	-1.0	12.8	8.1	13.5	unknown function	YER067w	orf19.2659
CA3707	TYE7	-1.1	16.4	15.0	11.4	Basic helix-loop-helix transcription factor by homology	YOR344c	orf19.4941
CA2474	PDC11	-1.1	9.2	6.4	9.7	Pyruvate decarboxylase (by homology)	YLR044c	orf19.2877
CA5788	RHR2	1.0	9.7	8.1	9.4	DL-glycerol phosphatase	YIL053w	orf19.5437
CA3112	PFK2	-1.0	9.6	8.3	8.5	6-phosphofructokinase, beta subunit	YMR205c	orf19.6540
CA0127	HXK2.3F	-1.1	9.5	9.7	7.9	hexokinase II, 3-prime end (by homology)	YGL253w	orf19.8176
CA4127	IPF6629	1.7	5.0	7.2	7.7	unknown function	YLR109w	orf19.2762
CA1579	GDH3	1.0	6.8	11.1	7.4	NADP-glutamate dehydrogenase (by homology)	YOR375c	orf19.4716
CA4570	IPF9550	-1.1	8.4	7.2	7.3	similar to Saccharomyces cerevisiae Osm1p osmotic gr	YJR051w	orf19.6882
CA4501	QDR1	1.0	8.1	13.2	7.0	putative antibiotic resistance proteins (by homology)	YIL120w	orf19.8138
CA1834	PFK1	-1.2	6.9	6.1	6.6	6-phosphofructokinase, alpha subunit	YGR240c	orf19.3967
CA2075	IFE2	-1.1	8.2	10.6	6.3	Unknown function		orf19.5288
CA0943	YHB1	-1.1	4.4	5.1	6.2	flavohemoglobin (by homology)	YGR234w	orf19.3707
CA2832	CRD1	1.0	6.8	7.7	5.9	Cu-transporting P1-type ATPase		orf19.4784
CA5066	TPS2	1.2	3.9	4.8	4.9	Threalose-6-phosphate phosphatase (by homology)	YDR074w	orf19.3038
CA3895	CDR4	1.0	4.2	6.8	4.8	Multidrug resistance protein		orf19.5079
CA4492	RNR22	-1.0	2.8	5.3	4.8	ribonucleoside-diphosphate reductase (by homology)		orf19.1868
CA1464	PYC2.EXON2	-1.2	5.4	6.4	4.6	Pyruvate carboxylase 2 (by homology)	YBR218c	orf19.789
CA4030	EBP4	1.0	4.4	6.0	4.4	NADPH dehydrogenase (by homology)	YHR179w	orf19.3433
CA3483	CDC19	-1.1	3.2	2.1	4.2	pyruvate kinase (by homology)	YAL038w ; Missing in array	orf19.3575
CA0302	MEP3	-1.0	3.0	4.3	4.0	low affinity high capacity ammonium permease (by hom	YPR138c	orf19.9181
CA4155	RNR21	1.2	2.9	2.7	4.0	ribonucleoside-diphosphate reductase (by homology)	YJL026w	orf19.5801
CA1678	IPF5185	1.6	4.2	5.6	3.9	putative cell wall protein (by homology)	YAR050w	orf19.3618
CA1070	HXT61	1.2	4.6	8.0	3.9	sugar transporter	YDR343c	orf19.2020
CA2225	SUR2	1.0	3.3	4.8	3.8	Hydroxylation of C-4 of the sphingoid moiety of ceramid	YDR297w	orf19.5818
CA0689	IPF14119	1.4	2.7	3.7	3.5	unknown function		orf19.12157

CA1564	GAD1	1.0	2.8	3.4	3.4	Glutamate decarboxylase (by homology)	YMR250w	orf19.1153
CA1330	IPF11713	1.5	2.8	3.4	3.4	unknown function		orf19.8744
CA3142	IPF9211.5F	1.3	3.6	3.9	3.3	unknown function, 3-prime end		orf19.3713
CA4707	PTR21	-1.0	2.6	3.4	3.2	peptide transporter	YKR093w	orf19.6937
CA3590	ARE2	1.2	2.2	3.6	3.0	acyl-CoA sterol acyltransferase-like (by homology)	YNR019w	orf19.2248
CA5467	GSY1	-1.0	2.3	2.7	3.0	UDP glucose--starch glucosyltransferase, glycogen syn	YFR015c	orf19.3278
CA2938	IPF8321	-1.0	2.4	3.1	3.0	similar to Saccharomyces cerevisiae Glg2p self-glucosy	YJL137c	orf19.3325
CA4633	NDH1	-1.2	3.1	3.7	2.9	Mitochondrial NADH dehydrogenase	YMR145c	orf19.339
CA2452	IPF9955	1.1	3.1	4.8	2.9	unknown function		orf19.10993
CA2021	IPF17283	1.1	2.8	2.3	2.9	unknown function	YCR061w	orf19.4907
CA4111	IPF3964	1.1	3.6	4.1	2.8	unknown function		orf19.675
CA4569	IPF9552	1.1	3.1	3.4	2.8	unknown function	YPR107c	orf19.6881
CA2520	IPF20104	1.2	2.7	3.9	2.7	alcohol dehydrogenase (by homology)	YMR318c	orf19.5517
CA5322	PRB1	1.3	1.9	3.2	2.7	Protease B, vacuolar (by homology)	YEL060c	orf19.7196
CA1199	IPF10404	1.0	3.4	5.8	2.7	unknown function	YBL049w	orf19.10876
CA3141	IPF9211.3F	1.4	2.6	4.9	2.7	unknown function, 3-prime end		orf19.3712
CA3160	ZRT2	1.2	2.7	3.8	2.6	zinc transport protein (by homology)	YLR130c	orf19.1585
CA1691	PGK1	1.0	2.5	2.4	2.5	Phosphoglycerate kinase	YCR012w	orf19.3651
CA5144	IPF1019	1.5	2.2	3.1	2.5	unknown function	YJR013w	orf19.4581
CA1315	URA2.5EOC	-1.0	2.6	3.2	2.5	multifunctional pyrimidine biosynthesis protein, 5-prime	YJL130c	orf19.9896
CA4199	UBC8	1.3	2.1	3.6	2.5	ubiquitin-conjugating enzyme (by homology)	YEL012w	orf19.4540
CA2214	IPF9939	1.1	2.8	4.2	2.5	similar to Saccharomyces cerevisiae Msn4p transcriptio	YKL062w	orf19.4752
CA5476	IPF8527	1.0	2.3	2.7	2.5	unknown function		orf19.5305
CA4611	IPF10727	-1.1	2.3	3.9	2.5	unknown function		orf19.3302
CA1688	COX15	-1.1	2.0	2.6	2.5	cytochrome oxidase assembly factor (by homology)	YER141w	orf19.3656
CA3030	IPF19968	1.1	2.1	2.5	2.4	putative cell wall protein of the PIR family	YKL164c	orf19.220
CA5494	IPF85	1.1	3.8	3.4	2.4	similar to Saccharomyces cerevisiae Tis11p tRNA-spec	YLR136c	orf19.5334
CA4951	IPF13607	1.1	2.2	3.6	2.4	unknown function	YJL108c	orf19.6527
11759.2		1.1	4.3	9.2	2.4			
CA2181	ECM331	1.1	2.5	2.8	2.4	Involved in cell wall biogenesis and architecture (by hon	YDR055w	orf19.4255
CA4516	IPF18207	-1.1	2.1	2.0	2.3	unknown function	YPL170w	orf19.489
CA3334	ALP1	1.4	1.8	2.3	2.3	amino-acid permease (by homology)		orf19.2337
CA4164	IPF9302	1.4	2.4	3.2	2.3	unknown function	YOR052c	orf19.13235
CA0887	IPF12383	1.1	2.3	2.3	2.3	unknown function	YIL003w	orf19.1387
CA2493	IPF7227	-1.0	2.0	2.4	2.3	putative fatty acid desaturase (by homology)		orf19.4048
CA0104	RBT4	1.4	2.2	2.9	2.2	repressed by TUP1 protein		orf19.13583
CA0576	NPR1	1.1	2.0	2.7	2.2	nitrogen permease reactivator protein (by homology)	YNL183c	orf19.6232
CA4671	GPM1	-1.1	2.2	1.9	2.2	phosphoglycerate mutase (by homology)	YKL152c	orf19.903
CA5950	TPI1	1.1	2.2	2.3	2.2	Triose phosphate isomerase	YDR050c	orf19.6745
CA5505	TPS3.3	-1.1	2.2	1.9	2.2	alpha,alpha-trehalose-phosphate synthase, regulatory s	YMR261c	orf19.5348
CA5892	GAP1	1.1	1.9	2.1	2.1	Glyceraldehyde-3-phosphate dehydrogenase	YGR192c	orf19.6814
CA4874	IPF1674	1.0	2.5	2.1	2.1	putative transcription initiation factor (by homology)	YNL108c	orf19.6559
CA3637	IPF9255	-1.1	2.5	3.1	2.1	unknown function	YGR017w	orf19.5136
CA4827	SMF2	-1.1	2.0	3.3	2.1	Manganese transporter (by homology)	YLR034c	orf19.2069
CA0824	GPD2	-1.1	1.9	2.2	2.1	Glycerol 3-phosphate dehydrogenase (by homology)		orf19.691
CA1964	IFR2	-1.0	2.3	2.4	2.1	unknown function		orf19.2396
CA4220	IPF8762	-1.0	1.8	3.5	2.1	unknown function		orf19.822
CA3365	ALG6	1.3	1.8	2.5	2.1	glucosyltransferase (by homology)	YOR002w	orf19.1843
CA5180	FBA1	-1.2	2.1	1.6	2.1	fructose-bisphosphate aldolase (by homology)	YKL060c	orf19.4618

CA5497	IPF776	-1.0	2.3	2.3	2.1	transcriptional activator (by homology)		orf19.5338
CA5142	IPF1022	1.4	1.6	2.4	2.1	similar to Saccharomyces cerevisiae Erv29p ER-Golgi t	YGR284c	orf19.4579
CA4657	IPF3094	1.1	2.2	2.6	2.1	4-nitrophenyl phosphatase (by homology)	YDL236w	orf19.4444
CA6066	CDR1	-1.1	2.0	1.6	2.0	multidrug resistance protein (by homology)	YOR153w	orf19.6000
CA0413	ALS12.3F	1.1	1.8	3.7	2.0	agglutinin-like protein, 3-prime end		orf19.2122
CA1356	IPF10138.5F	1.1	2.4	2.1	2.0	unknown function, 5-prime end	YNR018w	orf19.409
CA0875	ERG251	-1.0	1.8	1.8	2.0	C-4 sterol methyl oxidase (by homology)		orf19.12101
CA1339	IPF5330	1.5	2.3	2.9	2.0	unknown function		orf19.10952
CA4852	SCS7	1.1	1.7	4.1	2.0	Required for hydroxylation of ceramide (by homology)	YMR272c	orf19.3822
CA2782	IPF3806	1.0	1.6	2.1	2.0	unknown function	YNL157w	orf19.285
CA1525	AGP3	1.0	1.7	2.8	2.0	amino acid-permease (by homology)	YFL055w	orf19.3795
CA3923	ADH2	1.2	2.4	2.1	2.0	alcohol dehydrogenase I (by homology)	YOL086c	orf19.5113
CA1528	ALS4.3F	1.2	2.0	3.9	2.0	agglutinin-like protein, 3-prime end		orf19.4556
CA6000	FDH11.3	1.0	1.9	1.8	2.0	glutathione-dependent formaldehyde dehydrogenase, 3	YDL168w	orf19.7600
CA1353	ERG1	1.2	1.6	2.4	2.0	squalene epoxidase	YGR175c	orf19.406
CA5078	IPF15297	1.3	1.9	1.7	2.0	unknown function		orf19.3053
CA5985	IPF907	-1.2	1.9	1.9	2.0	unknown function		orf19.7583
CA4022	FRP6	1.1	1.7	2.9	2.0	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathwa		orf19.3441
CA2302	IPF6518	-1.0	1.9	1.8	1.9	unknown function		orf19.1691
CA4696	HTA1	1.5	1.7	1.6	1.9	Histone H2A (by homology)	YDR225w	orf19.6924
CA0183	CAP1	-1.0	1.8	2.2	1.9	transcriptional acivator (by homology)	YML007w	orf19.9191
CA1974	IPF10410	1.2	2.1	2.7	1.9	unknown function	YLR021w	orf19.5227
CA3305	RPL29	2.1	1.6	1.7	1.9	ribosomal protein, cytosolic(by homology)	YFR032ca	
CA2853	IPF17057	1.3	1.6	1.8	1.9	unknown function	YMR010w	orf19.1070
CA2761	IPF15013	-1.1	2.2	2.1	1.9	pyruvate decarboxylase regulatory protein (by homology)		orf19.13071
CA3200	IPF3439	1.2	1.4	2.0	1.9	unknown function	YDL054c	orf19.6180
CA4566	IPF19801	1.0	1.5	1.4	1.9	unknown function		orf19.6877
CA3988	IPF7145	1.1	1.5	1.8	1.9	unknown function	YDL072c	orf19.1564
CA1570	IPF7617	1.4	1.7	1.9	1.9	unknown function	YHR181w	orf19.1160
CA2545	RRP9	-1.1	-1.1	1.0	1.8	U3 small nucleolar ribonucleoprotein-associated protein	YPR137w	orf19.2830
CA4515	IPF16652	1.2	1.6	1.6	1.8	unknown function	YOR253w	orf19.490
CA6099	CDR2	1.0	2.0	2.2	1.8	Candida albicans drug resistance protein 2		orf19.5958
CA4424	PMT1	1.1	1.5	2.0	1.8	mannosyltransferase	YDL095w	orf19.5171
CA4314	PMT4	1.0	1.6	2.1	1.8	Mannosyltransferase (by homology)	YJR143c	orf19.4109
CA0311	DAK2.3EOC	-1.1	2.1	2.4	1.8	dihydroxyacetone kinase, 3-prime end (by homology)		
CA4016	GFA1	-1.2	1.8	1.8	1.8	glutamine:fructose-6-phosphate amidotransferase	YKL104c	orf19.1618
CA3639	IPF9251	1.0	1.9	1.9	1.8	unknown function	YOR363c	orf19.5133
CA2189	AOX2	1.0	1.7	2.9	1.8	alternative oxidase (by homology)		orf19.4773
CA2906	IPF15523	1.2	1.3	1.7	1.8	unknown function	YOR246c	orf19.4521
CA5558	IPF1969	1.6	1.6	1.9	1.8	unknown function	YPL225w	orf19.7322
CA5185	NHP6A	1.3	1.3	1.7	1.8	nonhistone chromosomal protein related to HMG1	YBR089ca	
CA3918	VTC2	1.0	1.5	1.9	1.8	putative polyphosphate synthetase (by homology)	YFL004w	orf19.4381
CA4919	TTR1	1.3	1.7	1.6	1.8	Glutaredoxin (by homology)	YDR513w	orf19.6059
CA0641	IPF15977	-1.0	1.8	2.0	1.8	unknown function		orf19.4698
CA4551	APT1	1.5	1.8	1.8	1.8	adenine phosphoribosyltransferase	YML022w	orf19.1448
CA3497	FEN11	1.5	1.6	2.1	1.8	Fatty acid elongase required for sphingolipid formation (	YCR034w	orf19.6343
CA5735	IPF2878	1.1	1.7	2.1	1.8	unknown function	YBR105c	orf19.7445
CA0431	IPF7927	-1.0	-1.0	-1.0	1.8	putative aldose reductase (by homology)	YDL124w	orf19.1340
CA2263	GPD1	-1.0	1.3	1.8	1.8	Glycerol-3-phosphate dehydrogenase (by homology)	YOL059w	orf19.1756

CA4762	IPF9647	1.2	1.4	1.6	1.8	similar to Saccharomyces cerevisiae Ost3p oligosaccha	YOR085w	orf19.3994
CA6057	IPF4959	1.3	2.0	2.8	1.8	D-xylulose reductase (by homology)	YDL246c	orf19.7676
CA1855	GLN1	-1.5	1.7	1.5	1.8	glutamate-ammonia ligase (by homology)	YPR035w	orf19.646
CA5418	IPF1580	1.1	1.5	1.7	1.7	unknown function	YNL190w	orf19.968
CA1355	IPF10138.3F	1.2	2.0	2.0	1.7	unknown function, 3-prime end		orf19.408
CA0616	PHO11	1.0	2.0	2.9	1.7	Secreted acid phosphatase	YBR092c	orf19.2619
CA1782	PHO84.3EOC	-1.1	1.4	1.4	1.7	Inorganic phosphate transport protein, 3-prime end (by	YML123c	orf19.1172
CA0083	PHO84	-1.1	1.6	1.3	1.7	high-affinity inorganic phosphate/H+ symporter by homology		orf19.655
CA4929	ENA22	-1.0	1.6	1.5	1.7	P-type ATPase involved in Na+ efflux (by homology)	YDR038c	orf19.6070
CA3329	IPF12162	1.1	2.0	2.1	1.7	Unknown function	YHR067w	orf19.2670
CA6151	IPF1853	1.1	1.6	1.6	1.7	unknown function		orf19.5890
CA4949	CDC34	1.2	1.6	2.5	1.7	Ubiquitin-conjugating enzyme (by homology)	YDR054c	orf19.6529
CA3559	PGI1	1.0	1.7	1.8	1.7	Glucose-6-phosphate isomerase	YBR196c	orf19.3888
CA0270	PRB2	1.1	1.5	2.2	1.7	Protease B, vacuolar (by homology)		orf19.9783
CA4571	RPL33.3	1.5	1.2	1.3	1.7	ribosomal protein L35a, 3-prime end	YPL143w	
CA0368	IPF11646	-1.0	2.0	2.3	1.7	unknown function		orf19.1353
CA2327	IPF4782	1.0	1.4	2.2	1.7	probable membrane protein (by homology)	YBR187w	orf19.11972
CA0171	IPF15957	1.6	1.4	2.1	1.7	unknown function		
CA5232	SUN42	1.5	1.4	1.6	1.7	Putative cell wall beta-glucosidase (by homology)		orf19.5032
CA6129	YRA1.EXON2	1.1	1.6	1.7	1.7	RNA annealing protein, exon 2 (by homology)	YDR381w	
CA5894	PMT2	1.2	1.6	1.7	1.7	O-D-mannosyltransferase (by homology)	YAL023c	orf19.6812
CA6010	TRX1	1.5	1.5	1.8	1.7	thioredoxin (by homology)	YLR043c	orf19.7611
CA3034	RPN12	1.2	1.3	1.5	1.7	26S proteasome regulatory subunit (by homology)	YFR052w	orf19.213
CA1957	IPF3887	1.0	1.4	2.4	1.6	similar to Saccharomyces cerevisiae Syg1p plasma me	YIL047c	orf19.768
CA2650	STV1	1.1	1.5	2.0	1.6	H+-ATPase V0 domain (by homology)		orf19.1190
CA0110	IPF17190	1.3	1.5	2.0	1.6	unknown function		orf19.11350
CA0950	IPF3737	1.4	1.4	2.0	1.6	similar to Saccharomyces cerevisiae Aps1p AP-1 comp	YLR170c	orf19.1012
CA2016	IPF3415	1.0	1.9	2.6	1.6	similar to Saccharomyces cerevisiae Yim1p mitochondr	YMR152w	orf19.8467
CA1423	IPF14247	1.3	1.5	1.6	1.6	unknown function	YDR233c	orf19.3799
CA5802	IPF4164	1.1	1.5	1.6	1.6	similar to Saccharomyces cerevisiae Vtc1p negative re	YER072w	orf19.5455
CA4897	TUB2.3	1.4	1.3	1.7	1.6	Beta-tubulin, 3-prime end	YFL037w	orf19.6034
CA2043	GSL21	1.1	1.4	1.6	1.6	1,3-beta-D-glucan synthase subunit	YLR342w	orf19.2929
CA2625	IPF10919	1.4	1.6	1.8	1.6	Similar to Flo1p (by homology)	YLR110c	orf19.12229
CA2638	GAP3	-1.1	1.5	1.8	1.6	General amino acid permease (by homology)		orf19.4304
CA2405	IPF3844	1.5	1.5	1.9	1.6	unknown function		orf19.301
CA4862	EFB1	1.2	1.4	1.6	1.6	translation elongation factor eEF1beta	YAL003w	orf19.3838
CA4436	IPF13868	1.2	1.9	2.5	1.6	unknown function	YNL191w	orf19.5159
CA3005	CC43	1.2	1.2	1.6	1.6	Cell Division Control -like (by homology)		orf19.13617
CA3899	DPM1	1.1	1.3	1.5	1.6	dolichol-phosphate (beta-D) mannosyltransferase 1 by	YPR183w	orf19.5073
CA5468	IFF7	1.1	1.6	2.2	1.6	unknown function		orf19.3279
CA4363	STE24	1.1	1.4	1.8	1.6	zinc metallo-protease by homology	YJR117w	orf19.5654
CA2438	IPF5505	1.1	1.6	1.9	1.6	unknown function		orf19.2198
CA0503	PMT6	-1.1	1.6	1.7	1.6	protein mannosyltransferase		orf19.3802
CA1772	ALG7	1.3	1.5	2.1	1.6	UDP-N-acetylglucosamine-1-phosphate transferase (by	YBR243c	orf19.2187
CA0202	IPF19126	1.2	1.5	1.8	1.6	putative aminoacid transporter (by homology)	YER119c	orf19.1210
CA1167	IPF16646	1.2	1.4	1.5	1.6	unknown function	YEL001c	orf19.1782
CA0988	PMI40	-1.0	1.4	1.9	1.6	mannose-6-phosphate isomerase (PHOSPHOMANNO	YER003c	orf19.8968
CA2056	URA5	1.2	1.5	1.5	1.6	Orotate phosphoribosyltransferase (by homology)	YML106w	orf19.2555
CA4882	IPF1651	1.1	1.8	1.7	1.6	purine nucleoside permease (by homology)		orf19.6570

CA3336	IPF19983	1.0	1.4	1.6	1.6	unknown function	YHR113w	orf19.2335
CA3372	HHF22	1.3	1.3	1.5	1.6	histone H4 (by homology)		orf19.1854
CA1333	MRF1	1.0	1.6	1.8	1.6	mitochondrial respiratory function protein (by homology)		orf19.8742
CA0938	COX12	1.4	1.2	1.5	1.6	cytochrome-c oxidase, subunit VIB (by homology)	YLR038c	
CA4764	GPI10	1.2	1.5	1.8	1.6	required for Glycosyl Phosphatdyl Inositol sy	YGL142c	orf19.3996
CA2769	IPF15870	1.5	1.5	1.4	1.6	unknown function		orf19.2685
CA2765	APA2	1.1	1.3	1.9	1.6	ATP adenylyltransferase II (by homology)	YDR530c	orf19.13075
CA5171	IPF6037	1.2	1.5	1.6	1.6	Similar to Legionella pneumophila sbpA	YAL049c	orf19.4609
CA3169	IPF7686	1.0	1.5	2.0	1.6	putative mitochondrial phosphate carrier protein (by hor	YER053c	orf19.1395
CA0601	MSN5.3F	-1.4	1.8	1.2	1.6	Importin-beta family member required for nuclear export of Pho4p and involved in phe		orf19.10182
CA5646	RPS28B.3	1.6	1.5	1.6	1.6	Ribosomal protein S28B (S33B) (YS27), 3-prime end (b	YLR264w	
CA4885	IPF1636	1.3	1.4	1.9	1.6	similar to Saccharomyces cerevisiae Tpo1p multidrug re	YLL028w	orf19.6577
CA0425	PPH21	1.2	1.3	1.7	1.6	protein ser/thr phosphatase PP2A-1 (by homology)	YDL188c	orf19.9252
CA3607	RTA2	1.0	1.4	2.0	1.5	Unknown function	YOR049c	orf19.24
CA2246	IPF7405	1.4	1.4	2.2	1.5	unknown function		orf19.4666
CA4534	RPS26A	1.7	1.3	1.3	1.5	ribosomal protein S26.e.A, cytosolic (by homology)	YGL189c	orf19.1470
CA4044	GAL7	-1.1	2.3	2.4	1.5	UDP-glucose-hexose-1-phosphate uridylyltransferase (I	YBR018c	orf19.3675
CA3527	IPF9934	1.2	1.6	2.4	1.5	unknown function	YGR149w	orf19.8603
CA1956	ERG3	1.4	1.4	1.6	1.5	C5,6 desaturase	YLR056w	orf19.767
CA2805	RNR1	1.1	1.6	2.0	1.5	ribonucleoside-diphosphate reductase (by homology)	YER070w	orf19.5779
CA3239	IPF10558	1.5	1.2	1.4	1.5	unknown function		
CA1230	SSA4	-1.1	1.5	1.6	1.5	cahsp70 mRNA for heat shock	YER103w	orf19.4980
CA2335	LYS21	1.0	1.7	2.0	1.5	homocitrate synthase (by homology)		orf19.11982
CA4749	IPF4481	1.2	1.4	1.8	1.5	unknown function		orf19.4831
CA5257	SNC2.EXON2	1.2	1.5	1.8	1.5	Strong similarity to synaptobrevin, exon 2 (by homology	YOR327c	
CA6092	RPL35.3	1.6	1.2	1.7	1.5	Ribosomal protein L35A, 3-prime end (by homology)	YDL191w	
CA5551	IPF5972	1.1	1.8	2.0	1.5	putative cysteine dioxygenase (by homology)		orf19.7314
CA0274	IPF15153	1.4	1.3	2.0	1.5	unknown function		orf19.13289
CA0958	SEC24	1.0	1.6	1.5	1.5	component of COPII coat of ER-Golgi vesicles(by homo	YIL109c	orf19.12194
CA4084	TPS1	-1.0	1.5	2.1	1.5	TREHALOSE-6-PHOSPHATE SYNTHASE	YBR126c	orf19.6640
CA2134	COX8	1.5	1.3	1.4	1.5	CYTOCHROME C OXIDASE (by homology)	YLR395c	orf19.5213
CA2932	NHX1	1.2	1.5	1.5	1.5	NA+-H+ antiporter	YDR456w	orf19.11677
CA2076	ERO1	-1.0	1.6	2.1	1.5	Required for protein disulfide bond formation in the ER (	YML130c	orf19.4871
CA2082	NTF2	1.8	1.3	1.7	1.5	nuclear transport factor (by homology)	YER009w	
CA5749	IPF2908	-1.4	1.3	1.2	1.5	unknown function	YBR238c	orf19.7459
CA0982	IPF7397	1.1	1.6	2.0	1.5	unknown function	YGR141w	orf19.1800
CA2393	RHO3	1.3	1.4	1.7	1.5	GTP-binding protein of the rho family	YIL118w	orf19.11018
CA1102	AKR1	1.1	1.3	1.6	1.5	ankyrin repeat-containing protein by homology	YDR264c	orf19.4950
CA3686	IPF4890	1.4	1.4	2.2	1.5	unknown function	YOL119c	orf19.13642
CA3382	HTA3	1.2	1.2	1.4	1.5	histone H2A F/Z variant (by homology)	YOL012c	orf19.327
CA0863	ITR2	1.1	1.3	2.3	1.5	Myo-inositol transporter (by homology)	YOL103w	orf19.3526
CA2696	IPF9169	1.0	1.3	1.9	1.5	similar to Saccharomyces cerevisiae Bur6p functional h	YER159c	orf19.2736
CA4986	SER33	-1.1	1.6	1.8	1.5	Phosphoglycerate dehydrogenase (by homology)	YIL074c	orf19.5263
CA1373	AGP1	1.4	1.7	1.2	1.5	asparagine and glutamine permease (by homology)	YDR508c	orf19.8784
CA2024	IPF9616	1.2	1.5	1.5	1.5	unknown function		orf19.4910
CA4822	DFG5	1.1	1.4	1.9	1.5	Required for filamentous growth (by homology)	YMR238w	orf19.2075
CA3874	ENO1	1.6	1.6	1.2	1.5	Enolase I (2-phosphoglycerate dehydratase)	YGR254w	orf19.395
CA5750	CHS21	1.0	1.1	1.6	1.5	Chitin synthase (by homology)		orf19.5384
CA0117	IPF19231	1.2	1.1	1.4	1.5	unknown function	YNL305c	orf19.916

CA2280	DUR1,2	-1.0	1.2	1.2	1.5	urea amidolyase (by homology)	YBR208c	orf19.780
CA0086	IPF16598	-1.0	1.4	1.3	1.5	unknown function	YBR042c	orf19.7781
CA1470	IPF17942	1.1	1.6	1.5	1.5	unknown function	YKL189w	orf19.8415
CA4823	ERC3	1.1	1.6	2.4	1.5	ethionine resistance protein (by homology)	YDR338c	orf19.2073
CA0892	PHO8.5	-1.1	1.3	1.6	1.5	repressible alkaline phosphatase, 5-prime end (by homo	YDR481c	orf19.4736
CA4739	IPF4498	1.4	1.2	2.1	1.5	unknown function	YMR071c	orf19.4845
CA0574	IPF15183	1.3	1.3	1.7	1.5	unknown function		orf19.9373
CA4921	IPF1416	1.0	1.5	1.8	1.5	unknown function	YPL103c	orf19.6061
CA4416	IPF11888	1.1	1.4	1.8	1.5	unknown function	YBL064c	orf19.5180
CA2861	HHT21	1.4	1.4	1.5	1.5	Histone H3	YNL031c	orf19.1061
CA0692	PGM2	-1.2	1.3	1.5	1.5	Phosphoglucomutase (by homology)	YMR105c	orf19.10359
CA1720	IPF15581	1.3	1.6	1.7	1.5	unknown function		orf19.12120
CA0697	VTC4	-1.0	1.4	1.9	1.5	putative polyphosphate synthetase (by homology)	YJL012c	orf19.3363
CA2659	NDH2	1.0	1.3	1.4	1.5	NADH dehydrogenase (by homology)		orf19.5713
CA1789	GAR1	1.3	1.5	1.4	1.5	Nucleolar rRNA processing protein (by homology)	YHR089c	orf19.1164
CA0526	BUB3	1.0	1.3	2.0	1.5	cell cycle arrest protein (by homology)	YOR026w	orf19.2655
CA4265	GAP6	1.0	1.4	1.8	1.5	General amino acid permease (by homology)		orf19.6659
CA1874	TPK2	1.1	1.5	1.7	1.5	cAMP-dependent protein kinase 2 (by homology)	YPL203w	orf19.2277
CA4873	IPF1674.3	1.0	1.4	1.4	1.5	putative transcription initiation factor, 3-prime end (by homology)		
CA0471	ECM22	1.1	1.6	2.2	1.4	putative protein involved in cell wall biogenesis (by homology)		orf19.2623
CA5546	TUB1.3	1.3	1.4	1.9	1.4	Alpha-1 tubulin, 3-prime end	YML085c	orf19.7308
CA2619	IPF9490	1.0	1.3	1.7	1.4	amino acid permease (by homology)		orf19.2810
CA5920	RPS12	1.4	1.1	1.3	1.4	acidic ribosomal protein S12 (by homology)	YOR369c	orf19.6785
CA1386	THR1	1.1	1.5	1.5	1.4	homoserine kinase	YHR025w	orf19.923
CA2937	RPS21B.3	1.9	1.3	1.4	1.4	ribosomal protein S21, 3-prime end	YJL136c	
CA5353	IML2	-1.1	1.7	1.7	1.4	unknown function	YKR018c	orf19.7229
CA0622	IPF14171	1.2	1.1	1.2	1.4	unknown function	YGR086c	orf19.3149
CA5691	DED1	1.3	1.6	1.9	1.4	RNA helicase (by homology)	YOR204w	orf19.7392
CA0038	CYC1	1.2	1.2	1.3	1.4	cytochrome-c isoform 1	YJR048w	orf19.1770
CA4227	SCH9	1.2	1.4	1.9	1.4	strong similarity to S.pombe sck1 protein kinase	YHR205w	orf19.829
CA1304	RPS13.3	1.5	1.3	1.3	1.4	ribosomal protein, 3-prime end (by homology)	YDR064w	
CA2186	IPF6881	-1.2	1.3	1.1	1.4	putative phosphatidyl synthase		orf19.4246
CA0367	TIM22	-1.1	1.5	1.7	1.4	Mitochondrial import inner membrane translocase subu	YDL217c	orf19.1352
CA2758	GLC3	-1.2	-1.0	1.2	1.4	1,4-glucan branching enzyme (by homology)	YEL011w	orf19.13067
CA2862	HHF21	1.2	1.2	1.2	1.4	histone H4	YNL030w	orf19.1059
CA4791	IPF3370	1.4	1.4	1.4	1.4	similar to Saccharomyces cerevisiae Pre1p 20S proteas	YER012w	orf19.4025
CA0056	IPF15839	1.6	1.4	1.7	1.4	unknown function		orf19.556
CA1508	IPF9977	1.4	1.3	2.0	1.4	unknown function	YLR064w	orf19.4525
CA4755	IPF11480	1.1	1.3	1.8	1.4	unknown function		orf19.4824
CA0722	ERK1	-1.0	1.2	1.5	1.4	mitogen-activated protein kinase (FUS3 homolog)	YGR040w	orf19.10404
CA5178	POL30	-1.0	1.3	1.6	1.4	Proliferating Cell Nuclear Antigen (by homology)	YBR088c	orf19.4616
CA4179	TOM20	1.2	1.1	1.5	1.4	mitochondrial outer membrane import recept	YGR082w	orf19.2953
CA5206	GPH1	1.0	-1.0	1.3	1.4	Glycogen phosphorylase (by homology)	YPR160w	orf19.7021
CA3828	SNQ2	-1.0	1.8	2.0	1.4	multidrug resistance protein (by homology)	YDR011w	orf19.5759
CA3689	RPS22A	1.9	1.2	1.2	1.4	ribosomal protein S15a.e.c10 (by homology)	YJL190c	orf19.6265
CA1914	IPF16564	1.4	1.4	1.3	1.4	putative mitochondrial ribosomal protein S12	YNR036c	orf19.2438
CA0688	PF10555.3EO	-1.3	1.3	1.2	1.4	unknown function, 3-prime end		orf19.12155
CA4484	HEM15	-1.1	1.4	1.4	1.4	ferrochelatase precursor (by homology)	YOR176w	orf19.1880
CA5352	IPF856	1.1	1.3	1.8	1.4	unknown function	YKR030w	orf19.7228

CA2490	MUM2	-1.0	1.4	1.8	1.4	ubiquitin C-terminal hydrolase (by homology)	YBR057c	orf19.4044
CA5082	SUA70	-1.2	1.4	1.6	1.4	TFIIB subunit (transcription initiation factor E)(by homolo	YPR086w	orf19.3059
CA5766	IPF1097	-1.3	1.4	1.4	1.4	serine/threonine protein kinase (by homology)	YOR267c	orf19.5408
CA0156	SCW1	1.5	1.3	1.3	1.4	glucanase (by homology)	YGR279c	orf19.9345
CA1288	KSP1	1.2	1.3	1.6	1.4	SERINE/THREONINE-PROTEIN KINASE by homology	YHR082c	orf19.4432
CA6154	IPF1848	1.5	1.2	1.7	1.4	similar to Saccharomyces cerevisiae Snu13p U4/U6.U5	YEL026w	orf19.5885
CA5704	CHA11	1.0	1.4	1.6	1.4	L-serine/L-threonine deaminase (by homology)	YCL064c	orf19.7404
CA1188	RPL30.3	1.9	1.3	1.4	1.4	RNA binding, 3-prime end (by homology)	YGL030w	
CA4854	RCE1	1.2	1.3	1.7	1.4	CAAX PRENYL PROTEASE 2 (by homology)	YMR274c	orf19.3825
CA5435	UFD4	-1.1	1.3	1.3	1.4	ubiquitin fusion degradation protein (by homology)	YKL010c	orf19.3237
CA0553	IPF16653	1.0	1.3	1.5	1.4	unknown function	YKR088c	orf19.5534
CA0828	IPF17186	1.3	1.2	1.1	1.4	unknown function	YDR533c	orf19.7882
CA1104	IPF18761	1.2	1.3	1.6	1.4	unknown function	YPR098c	
CA2738	STF2	1.1	1.2	1.3	1.4	ATP synthase regulatory factor (by homology)	YLR327c	
CA4148	IDH2	-1.0	1.4	1.4	1.4	Isocitrate dehydrogenase (NAD+) subunit 2, mitochondı	YOR136w	orf19.13213
CA2648	IPF9062	-1.2	1.5	1.3	1.4	unknown function	YOR032c	orf19.1187
CA2644	GRP2	-1.0	1.4	1.6	1.4	Reductase (by homology)		orf19.4309
CA1504	ARF3	1.2	1.3	1.5	1.4	GTP-binding protein of the ARF family (by homology)		orf19.1702
CA2344	SFT2	1.2	1.2	1.7	1.4	similar to Saccharomyces cerevisiae Sft2p suppressor (	YBL102w	orf19.2342
CA4124	IPF20008	1.1	1.3	1.3	1.4	unknown function		orf19.2767
CA2579	RPL34B.3	1.8	1.3	1.2	1.4	Ribosomal protein L34.e, 3-prime end (by homology)	YIL052c	
CA4266	IPF2283	-1.1	1.3	1.3	1.4	unknown function	YHR131c	orf19.6660
CA6011	CTM1	-1.0	1.4	2.0	1.4	cytochrome c methyltransferase (by homology)	YHR109w	orf19.7612
CA2023	RPL42.3	1.9	1.1	1.1	1.4	ribosomal protein L36a, 3-prime end (by homology)	YNL162w	
CA5046	YCK2	1.2	1.2	1.5	1.4	casein kinase I (by homology)	YNL154c	orf19.7001
CA2311	SSO2	1.3	1.2	1.5	1.4	syntaxin (by homology)	YMR183c	orf19.1376
CA0323	CDC95	1.1	1.6	1.6	1.4	translation initiation factor 6 (eIF6) (by homology)	YPR016c	orf19.9378
CA5543	IPF5988	1.3	1.2	1.8	1.4	unknown function		orf19.7305
CA2534	IPF12793	1.1	1.2	1.5	1.4	similar to Saccharomyces cerevisiae Gis2p containing s	YNL255c	orf19.3182
CA5170	PDC12.EXON2	1.0	1.3	1.7	1.4	Pyruvate decarboxylase I, exon 2 (by homology)		orf19.4608
CA0586	IPF13493	1.3	1.2	1.3	1.4	Unknown function		orf19.12529
CA3293	IPF5726	1.2	1.3	1.3	1.4	unknown function		orf19.6327
CA4866	IPF4083	-1.1	-1.0	-1.2	1.4	similar to Saccharomyces cerevisiae Sec66p ER proteir	YBR171w	orf19.3843
CA2314	IPF14545	1.0	1.3	1.4	1.4	unknown function	YCL034w	orf19.1381
CA1767	SIT4	1.1	1.3	1.6	1.4	Ser/thr protein phosphatase	YDL047w	orf19.5200
CA0081	IPF11379	1.0	1.3	1.4	1.4	unknown function		orf19.633
CA2834	IPF12093	1.1	1.3	1.6	1.4	unknown function		orf19.4786
CA3318	WBP1	-1.1	1.1	1.2	1.4	Oligosaccharyl transferase beta subunit (by homology)	YEL002c	orf19.2298
CA0684	IPF4450	1.1	1.5	1.7	1.4	unknown function		orf19.12173
CA3197	SEC61	-1.2	1.4	1.4	1.4	ER protein-translocation complex subunit	YLR378c	orf19.6176
CA0752	MNN22	-1.1	2.0	2.5	1.4	Golgi alpha-1,2-mannosyltransferase (by homology)		orf19.11284
CA2454	RPL23B.3	1.4	-1.0	1.1	1.4	ribosomal protein L23.e, 3-prime end (by homology)	YER117w	orf19.3504
CA2391	ADH5	-1.1	1.3	1.6	1.4	probable alcohol dehydrogenase (by homology)		orf19.2608
CA4088	HMO1	-1.2	1.1	1.2	1.4	High-mobility protein 1 by homology	YDR174w	orf19.6645
CA4587	IPF2223	-1.3	1.5	1.4	1.4	unknown function	YNL011c	orf19.6905
CA2612	GAA1	1.1	1.2	1.4	1.4	required for attachment of GPI anchor onto proteins by I	YLR088w	orf19.5693
CA4476	01-Apr	1.1	1.3	1.6	1.4	aspartyl protease	YPL154c	orf19.1891
CA5083	IPF9278	1.1	1.2	1.6	1.4	similar to Saccharomyces cerevisiae Swp1p oligosacch	YMR149w	orf19.3060
CA0122	SNF4	-1.0	1.3	1.3	1.4	Nuclear regulatory protein (by homology).	YGL115w	orf19.13191

CA3759	IPF13139	1.0	1.0	1.1	1.4	unknown function		orf19.2910
CA5941	IPF3486	1.2	1.3	1.9	1.4	unknown function	YGL198w	orf19.6756
CA3688	YIP3.3	1.3	1.2	1.6	1.3	protein of unknown function, 3-prime end (by homology	YNL044w	
CA1260	IPF3170	1.2	1.6	1.6	1.3	unknown function	YDR141c	orf19.3166
CA5003	MCD4	1.3	1.3	1.6	1.3	Sporulation protein (by homology)	YKL165c	orf19.5244
CA0559	GPX1	1.0	1.5	1.6	1.3	glutathione peroxidase (by homology)	YIR037w	orf19.86
CA0116	IPF17975	-1.1	1.1	1.1	1.3	unknown function		orf19.915
CA0489	IPF6960	1.2	1.3	1.8	1.3	unknown function		orf19.2636
CA4420	SSM4	1.1	1.2	1.3	1.3	involved in mRNA turnover by homology	YIL030c	orf19.5175
CA1298	RPL32	1.5	1.2	1.2	1.3	ribosomal protein L32	YBL092w	
CA5705	IPF2645	1.0	1.3	1.5	1.3	unknown function		orf19.7405
CA2833	PTC1	1.0	1.5	1.9	1.3	protein serine/threonine phosphatase 2c (by homology)	YDL006w	orf19.4785
CA1098	IPF12316	-1.2	1.4	1.4	1.3	unknown function		
CA5037	PRE3	1.0	1.3	1.5	1.3	20S proteasome subunit (beta1)(by homology)	YJL001w	orf19.6991
CA4603	IPF6230	1.6	1.1	1.6	1.3	unknown function	YDL015c	orf19.10803
CA0112	IPF17358	-1.0	1.2	1.5	1.3	unknown function	YLR023c	orf19.5754
CA3741	MRS4	1.1	1.2	1.3	1.3	RNA splicing protein and member of the mitochondrial c	YKR052c	orf19.2178
CA0883	SUN41	1.4	1.3	1.5	1.3	Putative cell wall beta-glucosidase (by homology)	YIL123w	orf19.3642
CA0188	IPF15442	1.1	1.4	1.7	1.3	unknown function	YJL171c	orf19.9467
CA2939	TIF1	1.2	1.2	1.4	1.3	translation initiation factor	YKR059w	orf19.3324
CA4765	ADH1	1.6	1.7	1.2	1.3	alcohol dehydrogenase (by homology)		orf19.3997
CA4391	ARR3	1.0	1.3	1.5	1.3	involved in arsenite transport (by homology)	YPR201w	orf19.3122
CA5537	CHS2	1.2	1.2	1.6	1.3	Chitin synthase	YNL192w	orf19.7298
CA0349	IPF19026	1.2	1.3	1.5	1.3	unknown function	YAL053w ; Missing in array	orf19.1813
CA5409	COF1	1.2	1.2	1.3	1.3	cofilin (by homology)	YLL050c	
CA1285	SKP1	1.4	1.1	1.1	1.3	kinetochore protein complex CBF3 by homology	YDR328c	orf19.11905
CA1216	EBP1	1.0	1.4	2.1	1.3	NADPH dehydrogenase		orf19.7772
CA1022	IPF4820	1.0	1.3	2.0	1.3	putativecomplex I intermediate associated protein CIA30 (by homology)		orf19.10861
CA4936	IPF8369	1.2	1.2	1.8	1.3	unknown function	YOR161c	orf19.13498
CA2001	IPF17074	-1.0	1.3	1.4	1.3	unknown function	YBR086c	orf19.2792
CA4425	ENA21.3	-1.1	1.2	1.1	1.3	P-type ATPase, 3-prime end (by homology)		orf19.5170
CA4863	IPF4089	-1.1	1.2	1.1	1.3	secretory aspartyl proteinase		orf19.3839
CA5407	IPF1548	-1.1	1.5	1.6	1.3	unknown function		orf19.951
CA5492	GCN1.3F	1.2	1.2	1.5	1.3	translational activator, 3-prime end (by homology)		orf19.5328
CA1898	IPF11998	-1.0	1.5	1.2	1.3	unknown function		orf19.10273
CA4610	IPF19802	1.1	1.3	1.4	1.3	similar to Saccharomyces cerevisiae Met30p involved ir	YIL046w	orf19.3301
CA5666	PUB1	1.3	1.3	1.4	1.3	Major polyadenylated RNA-binding protein (by homolog	YNL016w	orf19.7368
CA5550	SSU1	1.1	1.4	1.8	1.3	Sulfite sensitivity protein (by homology)	YPL092w	orf19.7313
CA1977	RPL25.3	1.6	1.2	1.2	1.3	ribosomal protein L23a, 3-prime end (by homology)	YOL127w	
CA2151	ERC2	1.1	1.2	1.5	1.3	ethionine resistance protein (by homology)		orf19.6023
CA5313	IPF2163	1.2	1.4	1.8	1.3	unknown function		orf19.7184
CA2198	PMM1	1.2	1.5	1.4	1.3	phosphomannomutase	YFL045c	orf19.2937
CA4217	IPF5809	-1.1	1.3	1.3	1.3	unknown function		orf19.816
CA6033	COQ2	1.2	1.2	1.6	1.3	para-hydroxybenzoate:polyprenyl transferase (by homo	YNR041c	orf19.7643
CA2734	RPL38	1.5	1.4	1.4	1.3	ribosomal protein L38 (by homology)	YLR325c	
CA0306	HEM3	1.3	1.2	1.5	1.3	porphobilinogen deaminase	YDL205c	orf19.1742
CA4972	MUP1	1.2	1.1	1.6	1.3	High affinity methionine permease (by homology)	YGR055w	orf19.5280
CA4263	IPF2277	1.1	1.2	2.0	1.3	unknown function		orf19.6656
CA2166	FEN12	1.4	1.4	1.5	1.3	Probable subunit of 1,3-beta-glucan synthase (by homology)		orf19.908

CA5986	INO1	1.0	1.5	2.1	1.3	myo-inositol-1-phosphate synthase	YJL153c	orf19.7585
CA4125	IPF20161	-1.1	1.1	1.2	1.3	unknown function		orf19.10281
CA2583	IPF9445	-1.0	1.2	1.5	1.3	unknown function		orf19.4372
CA5914	HHT3	1.1	1.2	1.4	1.3	histone H3		orf19.6791
CA2562	IPF19953	1.4	1.4	1.6	1.3	unknown function		orf19.5642
CA1094	YIP1	1.2	1.2	1.4	1.3	golgi membrane protein (by homology)	YGR172c	orf19.3951
CA2714	IFF2	1.5	1.4	1.9	1.3	unknown function		orf19.575
CA5507	TIF11	1.3	1.3	1.2	1.3	translation initiation factor eIF1a (by homology)	YMR260c	orf19.5351
CA0961	IPF18822	-1.0	1.2	1.4	1.3	unknown function		orf19.3720
CA3097	IPF6600	1.1	1.4	1.4	1.3	unknown function	YBR159w	orf19.3859
CA3125	IPF8921.5EOC	1.1	1.2	1.8	1.3	unknown function, 5-prime end		
CA4970	IPF4696	-1.1	1.7	1.4	1.3	unknown Function		orf19.5282
CA3879	CDC42	1.1	1.3	1.5	1.3	Cell Division Control	YLR229c	orf19.390
CA2859	IPF7056	1.1	1.3	1.9	1.3	unknown function	YBR004c	orf19.1063
CA0317	SSD1	1.1	1.2	1.5	1.3	Protein phosphatase (by homology)	YDR293c	orf19.3959
CA2117	SNG3	1.3	1.2	1.5	1.3	Drug transporter (by homology)		orf19.1333
CA5151	IPF1009	1.2	1.4	1.6	1.3	Weak similarity to S. cerevisiae RFX1	Missing in array	orf19.4590
CA3676	RBP1	1.4	1.1	1.4	1.3	rapamycin-binding protein	YNL135c	orf19.6452
CA3950	PTM1	1.1	1.1	1.3	1.3	Possibly involved in the TCA cycle (by homology)	YKL039w	orf19.9542
CA2615	CTA241.EXON	1.3	1.2	1.4	1.3	transcriptional activator, exon 1		orf19.5700
CA1016	IPF11142	-1.0	1.1	1.3	1.3	unknown function	YOR273c	orf19.473
CA0370	IPF13678	1.1	1.2	1.6	1.3	unknown function	YDR276c	
CA5143	IPF1020	1.2	1.4	1.3	1.3	Weak similarity to N. crassa hypothetical protein	YJR012c	orf19.4580
CA3848	IPF7940	1.1	1.1	1.7	1.3	unknown function		orf19.6608
CA0785	IPF14603	1.1	1.2	1.3	1.3	unknown function	YJR100c	orf19.11411
CA5661	KRE6	1.1	1.3	1.8	1.3	Glucan synthase subunit	YPR159w	orf19.7363
CA2564	IPF12127	-1.0	1.3	1.6	1.3	unknown function	YML066c	orf19.5644
CA4190	IPF7530	-1.0	1.2	1.6	1.3	ATP-binding-cassette protein (by homology to A.gambia	YOL075c	orf19.12006
CA4577	MKK2	-1.3	1.2	1.3	1.3	Protein kinase of MEK (by homology)	YPL140c	orf19.6889
CA5707	ERV25	1.1	1.4	1.3	1.3	Component of COPII-coated vesicles (by homology)	YML012w	orf19.7409
CA1679	IPF5180.3EOC	1.1	1.3	1.4	1.3	unknown function, 3-prime end		
CA1476	IPF10214	1.5	1.4	1.6	1.3	unknown function		orf19.1093
CA4669	IPF4537	1.2	1.3	1.7	1.3	putative permease (by homology)	YIL088c	orf19.905
CA3226	RPS27	1.4	-1.0	1.3	1.3	ribosomal protein S27 (by homology)	YKL156w	
CA6131	IPF4369	-1.0	1.2	1.4	1.3	similar to Saccharomyces cerevisiae Stp2p involved in pre-tRNA splicing (by homolog		orf19.5917
CA1536	SOK1	1.1	1.1	1.4	1.3	high copy suppressor of a cyclic AMP-dependent	YDR006c	orf19.451
CA0740	IPF3262.3	1.4	1.3	1.1	1.3	unknown function, 3-prime end	YBR173c	
CA2339	IPF13377	1.0	1.1	1.3	1.3	unknown function		orf19.2350
CA5949	IPF3498	1.1	1.1	1.2	1.3	unknown function	YDR051c	orf19.6747
CA1896	ERD2	1.1	1.3	1.4	1.3	ER lumen protein retaining receptor (by homology)	YBL040c	orf19.2756
CA4528	STT3	-1.2	1.2	1.4	1.3	oligosaccharyl transferase (by homology)	YGL022w	orf19.1478
CA4700	SAP9	-1.0	1.6	2.2	1.3	aspartyl proteinase 9 (by homology)	YLR120c	orf19.6928
CA3346	IPF13356	-1.1	1.3	1.4	1.3	molybdopterin biosynthesis (by homology)	YHR111w	orf19.2324
CA1883	IPF5479	-1.0	1.2	1.4	1.3	unknown function	YOR088w	orf19.2209
CA5460	IPF277	1.3	1.3	1.3	1.3	human IgE-dependent histamine-releasing factor homol	YKL056c	orf19.3268
CA0736	RPL20B	1.3	-1.1	1.2	1.3	ribosomal protein (by homology)	YOR312c	orf19.4632
CA4021	EBP2	1.1	1.4	1.4	1.3	NADPH dehydrogenase (by homology)		orf19.3442
CA2597	IFQ3	-1.0	1.4	1.3	1.3	unknown function		orf19.54
CA5203	RPS18	1.8	1.1	1.1	1.3	Ribosomal protein S18 (by homology)	YML026c	orf19.7018

CA2521	IPF4317	1.0	1.1	1.3	1.3	unknown function		orf19.5518
CA0581	IPF3181	1.3	1.3	1.4	1.3	similar to Saccharomyces cerevisiae Erp3p p24 protein	YDL018c	orf19.3558
CA5536	IPF2837	1.1	1.1	1.3	1.3	putative cystathionine gamma-synthase (by homology)	YHR112c	orf19.7297
CA1905	IPF7274	1.0	1.1	1.1	1.3	unknown function		orf19.2783
CA5016	IPF7561	-1.0	1.4	1.5	1.3	unknown function		orf19.6968
CA3385	DRS23	1.0	1.3	1.3	1.3	Membrane-spanning Ca-ATPase (by homology)		orf19.7955
CA1637	RPL43A.3	1.5	1.1	1.4	1.3	ribosomal protein, 3-prime end (by homology)	YPR043w	
CA2211	IPF13921	1.1	1.2	1.5	1.3	Unknown function		orf19.4749
CA2980	GOG5	1.1	1.1	1.4	1.3	GDP-mannose transporter (by homology)	YGL225w	orf19.1232
CA4204	HOL4	1.1	1.3	1.6	1.3	member of major facilitator superfamily multidrug-resistance protein subfamily 1 (by h		orf19.12021
CA3870	YPK1	-1.1	1.3	1.5	1.3	ser/thr-specific protein kinase (by homology)	YMR104c	orf19.399
CA0267	IPF12262	1.0	1.1	1.1	1.3	extracellular alpha-1,4-glucan (by homology)		orf19.9183
CA5488	IPF810	1.1	1.3	1.5	1.3	unknown function	YJL178c	orf19.5322
CA0969	IPF9132	1.4	1.5	1.6	1.3	unknown function	YPL184c	orf19.12987
CA2803	IPF11711	-1.1	1.3	1.3	1.3	ubiquitin-protein ligase (by homology)	YDR457w	orf19.5776
CA0256	IPF10309	-1.2	1.2	1.1	1.3	unknown function	YKL206c	orf19.2278
CA3579	HSH49	1.0	1.2	1.2	1.3	spliceosome-associated essential protein [Candida albi	YOR319w	orf19.2261
CA0066	IPF15051	1.3	1.2	1.3	1.3	unknown function		orf19.8843
CA5013	IPF13941	1.0	1.3	1.5	1.3	Unknown function		orf19.5234
CA4218	ACP1	1.2	-1.1	1.3	1.3	mitochondrial acyl carrier protein (by homology)	YKL192c	orf19.819
CA5275	IPF1760.3F	-1.1	1.1	1.4	1.3	unknown function, 3-prime end		orf19.12451
CA3836	IPF8179	1.2	1.3	1.4	1.3	putative esterase (by homology)	YJL068c	orf19.6596
CA5236	LCB2	1.2	1.1	1.4	1.3	Palmitoyl transferase (by homology)	YDR062w	orf19.5027
CA1673	PST2	1.1	1.3	1.4	1.3	1,4-benzoquinone reductase by homology	YDR032c	orf19.3612
CA6097	NCE102	1.3	1.3	1.5	1.3	secretion of proteins that lack classical secretory signal	YPR149w	orf19.5960
CA4617	STB5	1.1	1.2	1.5	1.3	SIN3 binding protein (by homology)	YHR178w	orf19.3308
CA0899	IPF4905	1.0	1.3	1.5	1.3	unknown function		orf19.411
CA4697	HTB1	1.1	1.3	1.5	1.3	Histone H2B (by homology)	YDR224c	orf19.6925
2566.2		1.0	1.3	1.6	1.3			
CA5919	IPF8926.3	1.2	1.2	1.5	1.2	unknown function, 3-prime end		orf19.6786
CA5811	IPF2690.5F	1.1	1.4	1.6	1.2	unknown function, 5-prime end		orf19.5469
CA3267	RPS620A	1.2	1.1	1.2	1.2	unknown function		orf19.6300
CA4477	IPF6459	-1.1	1.3	1.3	1.2	unknown function	YMR210w	orf19.1890
CA5034	OST1	1.1	1.3	1.4	1.2	oligosaccharyltransferase	YJL002c	orf19.6988
CA0881	IPF16965	-1.0	1.3	1.3	1.2	unknown function	YOR256c	orf19.8006
CA2756	IPF18418	-1.1	1.0	1.1	1.2	unknown function	YHR029c	orf19.13065
CA0362	TEF1	1.6	1.5	1.1	1.2	translation elongation factor eEF1 alpha-A chain	YPR080w	orf19.9009
CA4527	IPF4398	1.2	1.3	1.5	1.2	unknown function	YGL023c	orf19.9054
CA2473	CBF1	-1.2	1.4	1.2	1.2	putative centromere binding factor 1	YJR060w	orf19.2876
CA2903	IPF11725	1.1	1.5	1.3	1.2	unknown function		orf19.10979
CA6070	IPF4842	1.1	1.2	1.6	1.2	similar to Saccharomyces cerevisiae Rsg1p ras-related	YCR027c	orf19.5994
CA3341	RPS17.3	1.3	-1.0	1.2	1.2	Ribosomal protein S17, 3-prime end (by homology)	YDR447c	
CA1737	LYS12	-1.1	1.2	1.5	1.2	homo-isocitrate dehydrogenase (by homology)	YIL094c	orf19.2525
CA4105	SMT3	1.3	1.1	1.1	1.2	Ubiquitin-like protein (by homology)	YDR510w	orf19.670
CA1635	URA7	-1.1	1.3	1.5	1.2	CTP synthase 1 (by homology)	YBL039c	orf19.3941
CA4525	SEC22	1.0	1.2	1.3	1.2	synaptobrevin-type protein transport protein (by homolo	YLR268w	
CA4434	MRPL49	1.5	1.1	1.4	1.2	ribosomal protein mitochondrial	YJL096w	orf19.5161
CA3613	SPF1	1.0	1.1	1.2	1.2	P-type ATPase	YEL031w	orf19.30
CA3658	TGL1	-1.1	1.3	1.5	1.2	Triacylglycerol lipase (by homology)	YKL140w ; Missing in array	orf19.2050

CA1204	IPF14524	-1.1	1.1	1.3	1.2	unknown function	YGL160w	orf19.8486
CA5897	IPF2384	1.0	1.3	1.4	1.2	unknown function	YKL128c	orf19.6809
CA0558	GPX2	1.1	1.7	2.2	1.2	glutathione peroxidase (by homology)		orf19.85
CA3669	IPF19997	1.1	1.2	1.2	1.2	by homology to S. cerevisiae: U6 snRNA associated protein		
CA0403	IPF15224	-1.0	1.2	1.4	1.2	unknown function	YKL046c	orf19.1989
CA3035	VPS28	1.0	1.2	1.3	1.2	involved in vacuolar traffic (by homology)	YPL065w	orf19.212
CA5333	DOA4	-1.1	1.4	1.5	1.2	ubiquitin-specific isopeptidase (by homology)	YDR069c	orf19.7207
CA3230	EMP24	1.3	1.3	1.3	1.2	component of the COPII-coated vesicles (by homology)	YGL200c	orf19.6293
CA3411	IPF9413	1.1	1.1	1.3	1.2	unknown function	YGL215w	orf19.13565
CA4272	CUE1	1.1	1.1	1.1	1.2	Involved in ubiquitination and degradation at the ER sur	YMR264w	orf19.6668
CA5264	IPF1798	-1.3	1.3	-1.1	1.2	unknown function		orf19.4998
CA5025	AMI3	-1.1	1.2	1.3	1.2	protein required for normal mitochondrial structure (by h	YOL060c	orf19.6979
CA5076	IPF15301	1.3	-1.1	1.4	1.2	unknown function	YJR116w	orf19.3051
CA2156	IPF8535	-1.0	1.2	1.5	1.2	unknown function		orf19.5302
CA2645	YNK1	1.4	1.0	1.1	1.2	Nucleoside diphosphate kinase (by homology)	YKL067w	orf19.4311
CA1415	DBP2.EXON2	1.1	1.4	1.7	1.2	ATP-dependent RNA helicase of DEAD box family, exon 2 (by homology)		orf19.170
CA5187	TOA2	1.1	1.2	1.2	1.2	TFIIA subunit 13.5 kD (by homology)	YKL058w	orf19.4625
CA3987	ECM3	1.2	1.2	1.6	1.2	Involved in cell wall biogenesis and architecture (by hon	YOR092w	orf19.1563
CA5067	IPF3589	1.1	1.6	1.9	1.2	putative alcohol acyl transferase (by homology)	YBR177c	orf19.3040
CA2537	IPF20108	1.2	1.1	1.3	1.2	similar to Saccharomyces cerevisiae Sft2p suppressor of SED5 thermosensitive muta		orf19.3184
CA6002	IPF661	1.1	1.3	1.2	1.2	unknown function	YDR214w	orf19.7602
CA1880	IPF13316	1.1	1.3	1.4	1.2	unknown function	YNL010w	orf19.2269
CA1904	GRX5	1.2	-1.0	1.0	1.2	Glutaredoxin	YPL059w	orf19.10298
CA1790	IPF13971	1.1	1.2	1.6	1.2	unknown function	YNL042w	orf19.5204
CA5317	RPP1B	1.1	1.1	1.0	1.2	Acidic ribosomal protein L44 (by homology)		orf19.7188
CA1222	IPF14871	1.2	1.2	1.3	1.2	unknown function		orf19.4132
CA2855	GPM2	1.0	1.3	1.4	1.2	phosphoglycerate mutase (by homology)		orf19.1067
CA0913	IPF14810	1.2	1.1	1.3	1.2	unknown function	YER044c	orf19.9566
CA4621	IPF5753	-1.0	1.2	1.5	1.2	unknown function	YER080w	orf19.3312
CA3428	VPS21	-1.0	1.2	1.3	1.2	GTP-binding protein (by homology)		orf19.589
CA1662	RPL28.3F	1.3	-1.0	1.1	1.2	Ribosomal protein, 3-prime end (by homology)	YGL103w	
CA4618	IPF5757	-1.0	1.1	1.3	1.2	unknown function		orf19.3309
CA4809	IPF1162	-1.0	1.3	1.3	1.2	Cystathionine beta-lyase (by homology)	YGL184c	orf19.2092
CA3657	IPF7459	-1.0	1.2	1.5	1.2	unknown function		orf19.2049
CA5951	IPF3500	1.1	1.2	1.3	1.2	unknown function	YMR262w	orf19.6744
CA2955	IPF15201	-1.0	1.2	1.1	1.2	Unknown function		orf19.5857
CA1764	IPF7596	1.2	1.2	1.1	1.2	similar to Saccharomyces cerevisiae Ess1p peptidyl-prc	YJR017c	orf19.5196
CA2260	OST2	1.1	1.1	1.4	1.2	Oligosaccharyltransferase epsilon subunit	YOR103c	orf19.1761
CA1861	RAD32	1.0	1.2	1.2	1.2	DNA repair protein (by homology)	YDR419w	orf19.866
CA0700	SHR3	1.2	1.0	1.1	1.2	endoplasmatic reticulum membrane protein (by homolo	YDL212w	orf19.3366
CA1613	IPF19735	1.2	1.1	1.3	1.2	unknown function		orf19.3215
CA2631	IPF14389	1.1	1.1	1.1	1.2	ubiquinone oxidoreductase subunit NUIM (by homology)		orf19.4758
CA0109	IPF13723	1.0	1.1	1.5	1.2	unknown function		orf19.7892
CA5671	CTA4	1.0	1.2	1.2	1.2	Probable transcription factor	YAL051w	orf19.7374
CA0898	SSH1.3	1.1	-1.1	1.3	1.2	involved in co-translational pathway of protein transport	YBR283c	orf19.412
CA5890	FCR1	1.1	1.3	1.5	1.2	Zinc cluster transcription factor		orf19.6817
CA2669	PF17494.3EOC	1.0	1.2	1.4	1.2	unknown function, 3-prime end		
CA5276	IPF1759.53F	-1.2	-1.0	1.2	1.2	unknown function, similar to endochitinases, internal fragment		
CA4437	IPF13867	1.2	1.4	1.4	1.2	unknown function		orf19.5158

CA5793	IPF4192	-1.0	1.3	1.4	1.2	unknown function		orf19.5442
CA4366	SWI1	1.2	1.3	1.7	1.2	Transcription regulation by homology	YPL016w	orf19.5657
CA3917	IPF3273	1.2	1.2	1.2	1.2	similar to Saccharomyces cerevisiae Ret3p coatomer c	YPL010w	orf19.4382
CA2188	SSU81	1.2	1.2	1.4	1.2	protein involved in the HOG1 high-osmolarity signal trar	YER118c	orf19.4772
CA0161	RMS1	-1.0	1.2	1.4	1.2	(putative) transcriptional regulator (by homology)	YDR257c	orf19.10177
CA4830	ATP8.EXON2	1.5	1.1	1.3	1.2	F1F0-ATPase complex, Atp8 subunit, exon 2 (by homol	YML081ca	
CA3018	SAH1	1.4	1.1	1.2	1.2	S-adenosyl-L-homocysteine hydrolase by homology	YER043c	orf19.3911
CA5434	IPF199	1.1	-1.0	-1.1	1.2	F-actin capping protein alpha subunit (by homology)	YKL007w	orf19.3235
CA4799	RPN5.5F	1.0	1.2	1.1	1.2	subunit of the regulatory particle of the proteasome, 5-prime end (by homology)		orf19.4034
CA0386	IPF4065	1.0	1.2	1.3	1.2	unknown function	YHR087w	orf19.1862
CA3463	ALG8	1.2	1.2	1.5	1.2	glucosyltransferase (by homology)	YOR067c	orf19.1659
CA2607	MRPL38	1.3	1.3	1.3	1.2	ribosomal protein of the large subunit(L14), mitochondri	YKL170w	orf19.5684
CA1484	ARO4	-1.1	1.2	1.3	1.2	3-dehydro-deoxyphosphoheptonate aldolase, tyrosine-i	YBR249c	orf19.4060
CA5694	IPF3311	1.0	1.2	1.1	1.2	unknown function		orf19.7396
CA3553	IFA16.5	-1.0	1.2	1.1	1.2	unknown function, 5-prime end		orf19.3878
CA0322	RPS9B	1.4	1.1	1.1	1.2	Ribosomal protein	YPL081w	orf19.8459
CA0701	IPF10397	1.2	1.1	1.1	1.2	unknown function	Missing in array	
CA5904	IPF5944	1.1	1.1	1.5	1.2	Unknown function	YNL326c	orf19.6802
CA3565	MSC2	1.2	1.2	1.3	1.2	Probable membrane protein	YDR205w	orf19.3132
CA2124	IPF10490	1.0	1.2	1.4	1.2	unknown function		orf19.8049
CA5575	IPF19813	1.3	1.2	1.3	1.2	unknown function		orf19.7342
CA5307	IPF2172	-1.1	1.1	1.6	1.2	similar to Saccharomyces cerevisiae Kap120 nuclear tr	YPL125w	orf19.7177
CA5918	ERV14	1.3	1.2	1.5	1.2	membrane protein	YGL054c	orf19.6787
CA2178	IPF9282	1.1	1.3	1.5	1.2	unknown function	YOL019w	orf19.1510
CA3014	IPF11915	1.1	1.4	1.4	1.2	similar to Saccharomyces cerevisiae Pcl7p cyclin like pr	YIL050w	orf19.13605
CA2854	RPN4	1.0	1.3	1.4	1.2	26S proteasome subunit (by homology)	YDL020c	orf19.1069
CA3168	PRS3	1.1	1.2	1.4	1.2	ribose-phosphate pyrophosphokinase	YHL011c	orf19.1575
CA5349	IPF861	-1.2	1.1	1.2	1.2	unknown function	YKR017c	orf19.7224
CA4405	IPF8773	-1.1	1.2	1.5	1.2	putative cytochrome P450 (by homology)		orf19.3105
CA2673	IPF5849	1.3	1.2	1.6	1.2	unknown function		orf19.5496
CA5413	IPF1567	1.2	1.1	1.1	1.2	mitochondrial ribosomal protein L34 (by homology)	YDR115w	
CA0123	MXR1	1.0	1.2	1.2	1.2	methionine sulfoxide reductase	YER042w	orf19.9576
CA1020	IPF4824	-1.1	1.3	1.3	1.2	unknown function	YOR155c	orf19.10863
CA0010	IPF16036	1.1	1.2	1.3	1.2	similar to Saccharomyces cerevisiae Tim17p mitochond	YJL143w	orf19.7790
CA2752	IPF6238	-1.0	1.3	1.4	1.2	GAG protein of retrotransposon pCal		orf19.2374
CA0754	IPF15880	1.3	1.3	1.3	1.2	unknown function		orf19.3486
CA4466	VPH1	-1.1	-1.0	1.3	1.2	H+-ATPase V0 domain subunit (by homology)	YOR270c	orf19.6863
CA3673	IPF13667	1.2	1.2	1.4	1.2	unknown function	YHR122w	orf19.6455
CA3309	IPF8806	-1.1	1.4	1.5	1.2	6-phosphofructose-2-kinase (by homology)		orf19.9844
CA5891	IPF2400	-1.0	1.2	1.2	1.2	putative aldehyde reductase (by homology)	YJR096w	orf19.6816
CA1962	IPF14285	1.1	1.4	1.3	1.2	unknown function		orf19.2398
CA3984	HOM2	-1.3	1.3	1.3	1.2	Aspartate-semialdehyde dehydrogenase (by homology)	YDR158w	orf19.9132
CA3867	PHR2	1.1	1.1	1.4	1.2	pH-regulated protein 2	YMR307w	orf19.13500
CA5503	DSK2	1.0	1.3	1.2	1.2	ubiquitin-like protein (by homology)	YMR276w	orf19.5345
CA3880	CAF16	-1.0	1.2	1.2	1.2	ABC ATPase (by homology)	YFL028c	orf19.388
CA3075	IPF6105	1.1	1.2	1.6	1.2	similar to Saccharomyces cerevisiae Gua1p GMP synth	YMR217w	orf19.4813
CA0005	IPF14994	-1.0	1.2	1.2	1.2	unknown function	YJL066c	orf19.2414
CA3268	RPS620B	1.1	1.1	1.2	1.2	unknown function		orf19.6301
CA2115	IPF8030	1.2	1.3	1.4	1.2	unknown function	YBR272c	orf19.8911

CA0966	IPF9136.5EOC	1.0	1.2	1.3	1.2	potassium transporter, 5-prime end (by homology)		orf19.6249
CA2226	BET3.EXON2	1.2	1.2	1.3	1.2	targeting and fusion of ER to Golgi transport vesicles, e	YKR068c	orf19.5817
CA2866	RHO1	1.2	1.1	1.4	1.2	GTP-binding protein of the rho subfamily of ras-like prot	YPR165w	orf19.2843
CA2565	MET15	1.1	1.4	1.6	1.2	O-acetylhomoserine O-acetylserine sulphydrylase	YLR303w	orf19.5645
CA4890	PRE10	1.1	1.1	1.0	1.2	20S proteasome subunit C1 (by homology)	YOR362c	orf19.6582
CA3277	IPF6266	1.1	1.3	1.3	1.2	unknown function		orf19.6311
CA1907	ATP7	1.2	-1.1	1.1	1.2	F1F0-ATPase complex, FO D subunit (by homology)	YKL016c	orf19.2785
CA5112	IPF1341	-1.0	1.3	1.3	1.2	Similarity to mucin proteins (by homology)		orf19.6420
CA3878	IPF7289	-1.2	1.1	1.2	1.2	similar to Saccharomyces cerevisiae Upc2p RNA polym	YDR213w	orf19.391
CA1802	IPF11443	-1.0	1.0	-1.0	1.2	unknown function	YIR002c	orf19.2919
CA5077	YPT1	1.3	1.2	1.2	1.2	GTP-binding protein of the rab family (by homology)	YFL038c	orf19.3052
CA4807	PDR6	-1.2	1.1	1.2	1.2	Pleiotropic drug resistance regulatory protein (by homol	YGL016w	orf19.2094
CA3737	BLM3	-1.2	1.4	1.1	1.2	bleomycin resistance (by homology)	YFL007w	orf19.2182
CA1410	GAT1	-1.0	1.2	1.1	1.2	nitrogen regulation (by homology)	YFL021w	orf19.1275
CA0687	CPA2	-1.0	1.2	1.3	1.2	arginine-specific carbamoylphosphate (by homology)	YJR109c	orf19.3221
CA6135	CMK1	1.0	1.3	1.4	1.2	Ca2+/calmodulin-dependent ser/thr protein kinase (by homology)		orf19.5911
CA2108	RPL26A.3	1.1	-1.1	1.2	1.2	ribosomal protein, 3-prime end (by homology)	YLR344w	
CA3986	IPF7141	1.1	1.3	1.2	1.2	unknown function		orf19.1562
CA0375	CRH11	1.1	1.2	1.5	1.2	Probable membrane protein (by homology)	YGR189c	orf19.2706
CA3353	AUR1	1.3	1.2	1.6	1.2	aureobasidin-resistance protein	YKL004w	orf19.9500
CA4191	IPF7531	-1.0	1.3	1.3	1.2	unknown function	YER156c	orf19.12007
CA4103	IPF3980	1.1	1.4	1.2	1.2	unknown function	YLR183c	orf19.668
CA4362	ATP2	2.1	1.4	1.2	1.2	F1F0-ATPase complex, F1 beta subunit (by homology)	YJR121w	orf19.5653
CA2315	YEA4	1.0	1.2	1.2	1.2	Golgi uridine diphosphate-N-acetylglucosamine transpo	YEL004w	orf19.8962
CA0890	IPF11766	1.0	1.2	1.2	1.2	unknown function		orf19.4734
CA2007	GPI8	-1.1	1.1	1.1	1.2	essential for GPI anchor attachment (by homology)	YDR331w	orf19.2799
CA0605	UTR2	-1.1	1.0	-1.0	1.2	1,3-1,4-beta-glucanase (by homology)	YEL040w	orf19.9240
CA5962	ALO1	-1.2	1.1	1.3	1.2	D-arabinono-1,4-lactone oxidase (by homology)	YML086c	orf19.7551
CA4163	IPF9301	1.1	1.2	1.2	1.2	unknown function	YOR051c	orf19.5812
CA4923	IPF1413.3	1.2	1.2	1.1	1.2	unknown function, 3-prime end	YFR011c	
CA4722	SAC1	1.1	1.1	1.3	1.2	integral membrane protein localizing to the ER and Gol	YKL212w	orf19.12329
CA3159	PLC3	1.1	1.2	1.4	1.2	phosphatidylinositol phospholipase C		orf19.1586
5124.1		-1.0	1.2	1.3	1.2			
CA5084	IMP1	1.1	1.3	1.3	1.2	protease, mitochondrial (by homology)	YMR150c	orf19.3061
CA1760	PF17914.3EOC	1.3	1.1	1.4	1.2	unknown function	Missing in array	orf19.5124
CA5444	IPF230	-1.3	1.0	1.2	1.2	unknown function	YJL207c	orf19.3247
CA0376	QCR9	1.1	-1.0	1.1	1.2	ubiquinol--cytochrome-c reductase subunit 9(by homolo	YGR183c	
CA0262	IPF20054	-1.0	1.2	1.7	1.2	unknown function	YBR287w	orf19.1407
CA5789	IPF1143	-1.1	1.2	1.1	1.2	Probable zinc-finger protein	YER116c	orf19.5438
CA0512	VMA16	1.3	-1.0	1.4	1.2	H+-ATPase 23 KD subunit, vacuolar (by homology)	YHR026w	orf19.4954
CA1972	RPL27A	1.6	1.2	1.2	1.2	ribosomal protein L27	YHR010w	
CA1606	NCS1	1.1	1.1	1.0	1.2	Calcium binding protein (by homology)	YDR373w	orf19.4726
CA4206	IPF9079	1.1	1.1	1.3	1.2	Membrane transporter (by homology)	YCR023c	orf19.4550
CA5065	IPF3584	1.0	1.2	1.3	1.2	similar to Saccharomyces cerevisiae Pab1p mRNA poly	YER165w	orf19.3037
CA6155	IPF1846	1.1	1.2	1.4	1.2	unknown function	YJR041c	orf19.5884
CA2958	KRE9	1.0	1.1	1.3	1.2	cell wall synthesis protein	YJL174w	orf19.5861
CA5162	IPF982	1.0	1.1	1.1	1.2	Weakly similar to human dolichol-phosphate-mannose synthase		
CA2702	EMP70	1.2	1.2	1.5	1.2	Endosomal protein (by homology)	YLR083c	orf19.10260
CA5678	IPF1292	1.0	1.2	1.7	1.2	unknown function Hypothetical zinc-finger protein		orf19.7381

CA5717	CYP51	1.2	1.2	1.1	1.2	Cyclophilin - peptidylprolyl cis-trans isomerase or PPIas	YDR304c	orf19.7421
CA2931	IPF7841	-1.1	1.2	1.1	1.2	similar to Saccharomyces cerevisiae Ndc1p nuclear env	YML031w	orf19.4203
CA2367	SUI1	1.1	1.1	1.3	1.2	translation initiation factor 3 (eIF3) (by homology)	YNL244c	orf19.8867
CA3059	TRR1	-1.0	1.2	1.1	1.2	Thioredoxin reductase (by homology)	YDR353w	orf19.11766
CA2164	AXL2	1.2	1.1	1.2	1.2	similar to saccharomyces cerevisiae Axl2p required for	YIL140w	orf19.5292
CA1836	IPF5773	1.1	1.2	1.4	1.2	unknown function		orf19.3965
CA3834	PLB3	-1.1	1.3	1.3	1.2	phospholipase B (by homology)	YMR008c	orf19.6594
CA1837	IPF5776	1.1	1.2	1.3	1.2	ash2-trithorax family protein (by homology)	YLR015w	orf19.3964
CA4439	IPF13865	1.3	1.1	1.3	1.2	unknown function	YJL097w	orf19.5156
CA4274	LAP42	-1.1	-1.0	1.0	1.2	Aminopeptidase yscI precursor, vacuolar (by homology)		orf19.6671
CA0981	GAP4	1.0	1.1	1.9	1.2	general amino acid permease (by homology)		orf19.1799
CA2904	IPL1	-1.1	-1.0	-1.1	1.2	Ser/thr protein kinase (by homology)	YPL209c	orf19.3474
CA1935	IPF19936	1.0	1.2	1.3	1.2	unknown function	YGR203w	orf19.4185
CA1279	RSP5	-1.0	1.1	1.2	1.2	ubiquitin-protein ligase (by homology)	YER125w	orf19.3628
CA5742	FUN31	1.0	1.1	1.2	1.2	Serine/threonine kinase (by homology)	YAL017w	orf19.7451
CA1515	ECM21.3	-1.1	1.2	1.1	1.2	Involved in cell wall biogenesis and architecture (by hon	YBL101c	orf19.12351
CA0954	IPF13162	1.1	1.1	1.3	1.2	unknown function	YNL101w	orf19.1142
CA2216	IPF6235	-1.1	1.3	1.2	1.2	Candida albicans Tca2 retrotransposon		orf19.5372
CA3550	IPF13228	1.0	1.1	1.3	1.2	unknown function		orf19.3874
CA6103	SFP1	-1.0	1.3	1.4	1.2	zinc finger protein (by homology)	YLR403w	orf19.5953
CA3587	AAH1	1.1	1.3	1.2	1.2	adenosine deaminase (by homology)	YNL141w	orf19.2251
CA1761	IPF7602	1.0	1.2	1.5	1.2	oxidoreductase (by homology)		orf19.5193
CA1997	YCF1	-1.2	1.1	1.2	1.2	Glutathione S-conjugate transporter (by homology)	YDR135c	orf19.6478
CA5569	PRE8	1.1	1.0	1.1	1.2	20S proteasome subunit Y7 (by homology)	YML092c	orf19.7335
CA2185	IPF6880	1.0	1.0	1.2	1.2	unknown function		orf19.4247
CA4937	TFP3	1.0	1.1	1.4	1.2	H+-ATPase by homology	YPL234c	orf19.6538
CA0269	PUF2.EXON1	1.1	1.1	1.0	1.2	RNA-binding protein (by homology)		orf19.4263
CA2591	IPF18448.3	1.2	1.2	1.4	1.2	unknown function, 3-prime end		orf19.60
CA3122	IPF5356	1.0	1.1	1.3	1.2	unknown function	YDR262w	orf19.3004
CA2375	IPF15504	-1.0	-1.0	-1.1	1.2	unknown function	YGL138c	orf19.2211
CA2736	ATE1	-1.1	1.1	1.2	1.2	arginyl tRNA transferase (by homology)	YGL017w	orf19.2110
CA0531	UBC1	1.2	1.0	1.4	1.2	ubiquitin-conjugating enzyme by homology	YDR177w	orf19.8686
CA0070	IPF19295.3F	1.0	1.4	1.1	1.2	unknown function, 3-prime end		orf19.6469
CA4174	IPF4119.5	1.3	1.1	1.5	1.2	unknown function, 5-prime end		
CA2286	IPF5369	1.1	1.1	-1.0	1.2	unknown function	YKL069w	orf19.5553
CA2462	CDC16	1.2	1.1	1.2	1.2	subunit of anaphase-promoting complex (by homology)	YKL022c	orf19.1792
CA4602	IPF6231	1.1	1.1	1.1	1.2	unknown function	YCL033c	orf19.10802
CA3606	RTA3	-1.0	1.1	1.3	1.2	Unknown function		orf19.23
CA1211	IPF7031.3	1.2	1.0	1.3	1.2	unknown function, 3-prime end	YPR063c	
SCADH1		1.0	1.1	1.1	1.2			
CA3173	IPF14145	1.1	1.1	1.3	1.2	unknown function		orf19.1401
CA1566	DPP2	1.2	1.2	1.4	1.2	Diacylglycerol pyrophosphate phosphatase (by homology)		orf19.1155
CA3287	IPF14295	1.1	1.2	1.2	1.2	putative Sed1p-like cell surface protein (by homology)		orf19.6321
CA3766	IPF18298.3	-1.1	-1.2	1.1	1.2	unknown function, 3-prime end		orf19.2903
CA2550	IPF9099	-1.0	1.2	1.1	1.2	similar to Saccharomyces cerevisiae Aos1p activating e	YPR180w	orf19.2835
CA3181	IPF12241	1.1	1.2	1.2	1.2	unknown function		orf19.2132
CA3320	IPF6898	-1.2	1.1	1.1	1.2	similar to Saccharomyces cerevisiae Bub1p serine/thre	YGR188c	orf19.2678
CA3245	IPF19980	-1.1	1.0	1.2	1.2	putative lipase (by homology)	YJR107w	orf19.4678
CA2888	GIM5	1.1	1.2	1.2	1.2	Gim complex component (by homology)	YML094w	orf19.2471

CA4780	IPF3352	1.0	1.1	1.1	1.2	unknown function	YHR045w	orf19.4013
CA0044	IPF17347	-1.0	1.3	1.3	1.2	unknown function		orf19.6492
CA2609	IPF5457	1.2	1.1	1.3	1.2	similar to Saccharomyces cerevisiae sec28p epsilon-C	YIL076w	orf19.5689
CA0200	IPF15119	1.1	1.1	1.4	1.2	unknown function	YKL175w	orf19.9109
CA3084	IPF11625	1.1	-1.1	-1.1	1.2	unknown function		orf19.4149
CA0490	COS161	1.2	1.3	1.7	1.2	involved in manganese homeostasis (by homology)		orf19.2637
CA3387	MUP3	-1.0	1.2	1.4	1.2	Very low affinity methionine permease	YHL036w	orf19.7953
CA5508	IPF745	1.1	1.1	1.3	1.2	unknown function		orf19.5352
CA4536	COX13	1.2	-1.0	1.1	1.2	cytochrome-c oxidase chain VIa (by homology)	YGL191w	orf19.1467
CA0152	IPF16368.3F	-1.1	1.5	1.3	1.2	unknown function, 3-prime end		orf19.254
CA0971	IPF11428	1.2	-1.0	1.1	1.2	unknown function		orf19.6470
CA0644	IPF17131	-1.0	1.3	1.2	1.2	unknown function		orf19.69
CA0977	IPF18810	-1.0	1.3	1.3	1.2	unknown function	YNL215w	orf19.11087
CA0441	IPF12472	1.0	1.2	1.4	1.2	unknown function		orf19.13018
CA3792	UGA5	1.1	1.1	1.0	1.2	GABA-SPECIFIC TRANSPORT PROTEIN by homology to S. cerevisiae		orf19.5826
CA2680	MCI4	1.4	1.1	1.2	1.2	NADH dehydrogenase (ubiquinone)		orf19.2570
CA0603	IPF1709	1.1	1.0	1.4	1.2	unknown function	YDR100w	orf19.3076
CA3105	IPF12083	1.1	1.2	1.3	1.2	unknown function		orf19.6553
CA2240	CRD2	1.5	1.1	1.4	1.2	Cu-binding metallothionein		
CA2251	IPF12845	1.2	1.2	1.4	1.2	unknown function	YOR286w	orf19.2363
Mice G3PDH		1.0	1.1	1.3	1.2			
CA2318	ILV1	-1.1	1.2	1.3	1.2	Threonine dehydratase (by homology)	YER086w	orf19.5480
CA1625	IPF6156	-1.2	1.3	1.3	1.2	similar to C.elegans LIM homeobox protein		orf19.1034
CA5604	IPF549	1.1	1.2	1.7	1.2	unknown function	YOR390w	orf19.7095
CA3349	IPF19588	1.1	1.1	1.4	1.2	unknown function	YDR367w	
CA4130	IPF20009	1.1	1.1	1.1	1.2	Unknown function	YBR129c	orf19.11720
CA5714	IPF2431	1.1	1.1	-1.0	1.2	similar to Saccharomyces cerevisiae Tsa1p thiol-specifi	YML028w	orf19.7417
CA2135	COX9	1.4	1.1	1.4	1.2	CYTOCHROME C OXIDASE (by homology)	YDL067c	
CA2031	RPL10A	1.2	-1.0	1.1	1.2	L10A ribosomal protein	YPL220w	orf19.3465
CA0915	KAR2	-1.2	1.3	1.1	1.2	dnaK-type molecular chaperone (by homology)	YJL034w	orf19.9564
CA2951	SBP1	-1.0	1.1	1.2	1.2	RNA binding protein-like (by homology)	YHL034c	orf19.5854
CA3228	IPF9325	1.1	-1.0	1.0	1.2	unknown function		orf19.6288
CA2215	PFK26	-1.1	1.2	-1.1	1.2	6-phosphofructose-2-kinase (by homology)	YIL107c	orf19.4753
CA5383	ZORRO1B.3F	1.1	1.0	1.2	1.2	reverse transcriptase, 3-prime end (by homology)		orf19.7273
CA0896	SBA1	1.2	1.3	1.3	1.2	Hsp90 (Ninety) Associated Co-chaperone (by homolog	YKL117w	orf19.5749
CA5496	IPF779	1.1	1.2	1.3	1.2	E2 ubiquitin conjugating enzyme (by homology)		orf19.5337
CA2581	IPF9450	1.1	1.0	1.1	1.2	unknown function		orf19.4370
CA1980	YHM1	1.1	1.2	1.2	1.2	member of the mitochondrial carrier family (MCF) (by h	YDL198c	orf19.685
CA2038	IPF17510	-1.0	1.0	1.1	1.2	unknown function	YDL157c	orf19.11836
CA2739	MUQ1	1.2	1.1	1.2	1.2	choline phosphate cytidylyltransferase (by homology)	YGR007w	orf19.2107
CA6093	ARF22	-1.0	1.0	1.0	1.1	GTP-binding protein of the ARF family (by homology)	YDL137w	orf19.5964
COB		-1.0	-1.0	1.1	1.1			
CA1137	IFN1	-1.0	1.2	1.5	1.1	glycerophosphoinositol transporter (by homology)		orf19.1979
CA3943	IPF4751	1.0	1.0	1.1	1.1	unknown Function		orf19.1999
CA2999	MRPL8	1.0	1.2	1.2	1.1	mitochondrial 60s ribosomal subunit (by homology)	YJL063c	orf19.6129
CA2563	ECM7	1.0	1.2	1.4	1.1	cell wall biogenesis and architecture (by homology)	YLR443w	orf19.5643
CA1223	IPF14870	1.1	1.0	1.3	1.1	unknown function	YCL045c	orf19.4131
CA5038	QDR2	1.1	1.1	1.4	1.1	putative antibiotic resistance proteins (by homology)		orf19.6992
CA4216	IPF5806	-1.2	1.2	1.1	1.1	unknown function	YLR422w	orf19.8435

CA1875	RPB9	1.1	1.1	1.4	1.1	DNA-directed RNA polymerase II (by homology)	YGL070c	orf19.2276
CA3319	DRS25.3EOC	-1.2	1.4	1.1	1.1	Probable ATPase, 3-prime end (by homology)	YMR162c	orf19.2680
CA4932	IPF8374	1.0	1.2	1.2	1.1	unknown function	YLR205c	orf19.6073
CA5612	KAP114	-1.1	1.2	1.0	1.1	putative RAN-binding protein/importin (by homology)	YGL241w	orf19.7086
CA4898	IPF1461	1.1	1.2	1.3	1.1	putative NADH dehydrogenase (ubiquinone) (by homology)		orf19.6035
CA3422	IPF17289	-1.2	1.1	1.1	1.1	unknown function	YLR440c	orf19.13553
CA3809	KAP123	1.3	1.3	1.2	1.1	karyopherin-beta protein (by homology)	YER110c	orf19.2489
CA1431	FET34.3EOC	1.0	1.1	1.2	1.1	iron transport multicopper oxidase, 3-prime end (by homology)		orf19.1206
CA5385	ZORRO2B.3F	1.1	1.1	1.1	1.1	reverse transcriptase, 3-prime end (by homology)		orf19.7275
CA2630	COX5A	1.3	-1.1	1.4	1.1	cytochrome-c oxidase chain V.A precursor (by homolog	YNL052w	orf19.12223
CA0763	RPL11	1.4	1.0	-1.1	1.1	60S ribosomal protein (by homology)	YPR102c	orf19.2232
CA0908	MRPL31	1.3	1.1	1.2	1.1	Mitochondrial ribosomal protein	YKL138c	orf19.1485
CA1441	QCR8	1.5	1.0	1.1	1.1	ubiquinol-cytochrome-c reductase chain VIII (by homolo	YJL166w	
CA2373	CBF5	-1.2	-1.1	1.1	1.1	centromere/ microtubule binding protein	YLR175w	orf19.1833
CA3001	IPF8841	1.4	1.2	1.3	1.1	unknown function	YBR262c	orf19.6132
CA1753	IPF8245	-1.0	1.1	1.1	1.1	putative chitinase	YDR371w	orf19.1515
CA5581	RAD3	-1.2	1.2	1.2	1.1	DNA helicase/ATPase by homology	YER171w	orf19.7119
CA0316	ALS1.3EOC	1.2	1.3	1.4	1.1	agglutinin-like protein, 3-prime end		orf19.5741
CA2666	IPF16995	1.3	1.0	-1.0	1.1	unknown function	YBL095w	orf19.3548
CA2546	RPC31	1.0	-1.0	1.1	1.1	DNA-directed RNA polymerase III (by homology)	YNL151c	orf19.2831
CA0592	IPF8862	1.0	1.1	1.1	1.1	unknown function		orf19.12370
CA2345	HNT1	1.3	1.2	1.2	1.1	similarity to protein kinase C inhibitor-I (by homol	YDL125c	orf19.2341
CA1510	IPF9973	1.1	-1.0	1.1	1.1	similar to Saccharomyces cerevisiae Fau1p 5,10-methe	YER183c	orf19.4523
CA3656	IPF7456	1.0	1.1	1.2	1.1	unknown function	YOR289w	orf19.2047
CA2912	IPF11206	-1.0	1.1	1.2	1.1	unknown function		orf19.4515
CA2026	IPF9777	1.3	1.1	1.4	1.1	unknown function	YOL129w	orf19.10962
CA1791	IPF13967	-1.0	1.0	1.0	1.1	unknown function		orf19.5205
CA0569	CDC8	1.1	1.1	1.2	1.1	dTMP kinase (by homology)	YJR057w	orf19.8730
CA6141	RPL19A.3	1.6	1.4	1.1	1.1	Ribosomal protein L19.e, 3-prime end (by homology)	YBR084ca	orf19.5904
CA2303	TOS1	1.3	1.1	1.3	1.1	putative Anchor subunit of a-agglutinin (by homology)	YBR162c	orf19.1690
CA6150	IPF1857	-1.3	1.4	-1.1	1.1	similar to Saccharomyces cerevisiae Hul4p hect domair	YJR036c	orf19.5892
CA5804	IPF4160	1.1	1.2	1.3	1.1	unknown function	YGR178c	orf19.5459
CA5912	IPF5966	-1.0	1.1	1.1	1.1	unknown function		orf19.6793
CA2873	AQY1	1.0	1.1	1.3	1.1	similarity to plasma membrane and water channel prote	YPR192w	orf19.2849
CA4154	IPF20010	-1.0	1.1	-1.1	1.1	unknown function		orf19.5799
CA3876	APS3	1.1	1.2	1.1	1.1	AP-3 complex subunit, sigma3 subunit (by homology)	YJL024c	orf19.8023
CA6079	RPL18.EXON2	-1.0	1.1	1.1	1.1	Ribosomal Protein RPL18B (large subunit), exon 2 (by l	YOL120c	orf19.5982
CA1018	PF13479.3EOC	-1.1	1.0	1.0	1.1	unknown function, 3-prime end		orf19.3768
CA3571	IPF3264	-1.1	1.2	1.6	1.1	unknown function		orf19.10651
CA0721	IPF10429	1.1	1.0	1.2	1.1	unknown function	YMR295c	orf19.10405
CA1091	SPT4	1.1	-1.0	1.1	1.1	transcription elongation protein (by homology)	YGR063c	orf19.3947
CA4482	IPF9154	-1.0	1.3	1.2	1.1	similar to Saccharomyces cerevisiae Ycs4p subunit of c	YLR272c	orf19.1883
CA0972	CYP1	1.1	1.2	1.1	1.1	cyclophilin (peptidylprolyl isomerase), mitochondrial (by	YDR155c	orf19.6472
CA4829	IPF1210	-1.0	1.1	1.1	1.1	similar to Saccharomyces cerevisiae Nfu1p involved in l	YKL040c	orf19.2067
CA0822	EXG1	-1.0	1.1	1.2	1.1	glucan 1,3-beta-glucosidase	YLR300w	orf19.2990
CA5933	IPF2804	-1.0	1.2	1.4	1.1	unknown function	YLL038c	orf19.6770
CA4061	IPF5935	-1.0	1.1	1.2	1.1	Unknown function	YHR078w	orf19.438
CA3957	RBT2	1.0	1.0	1.2	1.1	Repressed by TUP1 protein 2		orf19.1415
CA0674	IPF19608	1.1	1.2	1.2	1.1	unknown function		orf19.8770

CA2288	IPF5376	1.0	1.0	1.0	1.1	unknown function		orf19.5557
CA1054	SAS3	1.1	1.1	1.2	1.1	silencing protein (by homology)	YBL052c	orf19.2540
CA3814	IPF4023	1.0	1.1	1.2	1.1	unknown function	YDR143c	orf19.2498
CA4225	RPL39.3	1.4	1.1	1.2	1.1	ribosomal protein L39, 3-prime end	YMR194w	
CA3347	ERP5	1.0	1.1	1.1	1.1	protein involved in membrane trafficking (by homology)	YHR110w	
CA6068	RPS19A.3	1.4	1.1	-1.0	1.1	ribosomal protein S19.e, 3-prime end (by homology)	YOL121c	
CA1728	WHI3	1.1	1.1	1.2	1.1	Putative RNA binding protein (by homology)	YNL197c	orf19.6494
CA0932	EPT1	1.4	1.1	1.3	1.1	alcohol phosphatidyl transferase (by homology)	YHR123w	orf19.3695
CA5886	IPF2417	1.1	1.1	1.2	1.1	unknown function	YLR128w	orf19.6822
CA2294	IPF19946	-1.1	1.2	1.1	1.1	similar to Saccharomyces cerevisiae Nbp35p nucleotide	YGL091c	orf19.747
CA5179	MAK3	1.1	1.1	1.2	1.1	N-acetyltransferase (by homology)	YPR051w	orf19.4617
CA2011	RPS31	1.2	1.1	-1.0	1.1	Ubiquitin fusion protein	YLR167w	orf19.3087
CA0189	IPF12201	1.4	1.1	1.3	1.1	Na+-nucleoside cotransporter (by homology)		orf19.11600
CA1460	HAM1	1.0	1.0	1.1	1.1	Controls 6-N-hydroxylaminopurine sensitivity and mutag	YJR069c	orf19.1108
CA4070	IPF2562	1.2	1.3	1.4	1.1	unknown function	YKL160w	orf19.6623
CA0125	IPF4119	1.1	1.2	1.2	1.1	unknown function		orf19.9578
CA4257	PRE6	1.0	1.1	1.1	1.1	20S proteasome subunit	YOL038w	
CA1169	PF16120.3EO(	1.2	1.1	1.4	1.1	unknown function, 3-prime end		orf19.2751
CA2508	BET5	-1.0	1.0	1.2	1.1	targeting and fusion of ER to Golgi transport vesicles (b	YML077w	orf19.302
CA5977	UBC4.3	1.3	1.1	1.1	1.1	E2 ubiquitin-conjugating enzyme, 3-prime end	YBR082c	orf19.7571
CA0145	IPF11449	-1.0	1.0	-1.0	1.1	unknown function		
CA0609	CDR11.3F	1.1	1.1	1.3	1.1	multidrug resistance protein, 3-prime end (by homology)		orf19.919
CA2172	IPF15377	-1.0	1.1	1.2	1.1	probable membrane protein involved in bipolar budding	YLR084c	orf19.3765
CA4300	HIS2	-1.0	1.2	1.2	1.1	Histidinol phosphatase (by homology)	YFR025c	orf19.6699
CA5954	IPF3508	-1.0	1.2	1.2	1.1	unknown function	YLL036c	orf19.6740
CA1894	PRE7.EXON1	1.0	1.1	1.2	1.1	putative subunit of 20S proteasome, exon 1 (by homolo	YBL041w	orf19.2755
CA2804	IPF19961	1.1	1.3	1.2	1.1	unknown function	YBR096w	orf19.5777
CA1100	IPF5681	-1.0	1.1	1.3	1.1	unknown function		orf19.12417
CA2285	IPF12629	-1.1	1.1	1.4	1.1	unknown function	YOL063c	orf19.5552
CA6112	IPF97	1.0	1.2	1.3	1.1	unknown function	YML067c	orf19.5941
CA5381	IPF5222	1.3	1.1	1.1	1.1	arylalkylamine n-acetyltransferase (by homology)	YDR071c	orf19.7269
CA3944	IPF4750	1.0	1.3	1.3	1.1	unknown Function		orf19.1998
CA5005	CDC62	1.0	1.0	1.1	1.1	Cell division control protein (by homology)		
CA0147	IPF9690	1.1	1.1	1.1	1.1	unknown function	YBR101c	orf19.11133
CA2020	IPF16901	1.1	1.0	1.1	1.1	unknown function		orf19.8462
CA1889	CBP6	1.1	1.1	1.1	1.1	Apo-cytochrome B pre-mRNA processing protein (by hc	YBR120c	
CA3110	LPI9	-1.0	1.3	1.1	1.1	Microtubule-associated protein (by homology)	YOR227w	orf19.6544
CA0567	RPS23	1.0	-1.1	-1.0	1.1	Ribosomal protein S23 (by homology)	YPR132w	orf19.13632
CA2292	VAC8	-1.1	1.2	1.0	1.1	required for vacuole inheritance and protein targe	YEL013w	orf19.745
CA4716	IPF8666	-1.0	1.1	1.1	1.1	unknown function	YDR295c	orf19.6952
CA1586	ODC1	1.1	1.1	1.2	1.1	Ornithine decarboxylase	YKL184w	orf19.6032
CA4430	IPF5577	-1.0	1.1	1.2	1.1	unknown function	YNR029c	orf19.5165
CA2217	POL0	-1.1	1.3	1.2	1.1	pol polyprotein, reverse transcripase		orf19.5373
CA1776	IPF14704	1.1	1.2	1.3	1.1	unknown function		orf19.1823
CA3045	IPF7297.3	1.2	1.0	1.1	1.1	similar to Saccharomyces cerevisiae Mlc1p myosin ((My	YGL106w	
CA5213	SSR1	1.4	1.2	1.5	1.1	Secretory Stress Response protein 1 (by homology)	YLR390wa	orf19.7030
CA3337	IPF13583	1.6	1.1	1.1	1.1	unknown function	YHR101c	orf19.2334
CA2296	SCL1	1.2	1.0	1.0	1.1	Proteasome subunit YC7alpha (by homology)	YGL011c	orf19.5378
CA4269	RPS25B	1.2	1.0	1.0	1.1	Cytosolic ribosomal protein (by homology)	YLR333c	orf19.6663

CA6122	RPP2B	1.1	1.1	1.2	1.1	acidic ribosomal protein (by homology)	YDR382w	orf19.5928
CA5173	CPS2.3F	-1.1	1.0	1.0	1.1	Carboxypeptidase YSCS precursor, 3-prime end (by homology)		
CA1101	IPF5678	-1.0	1.1	1.1	1.1	Unknown function		orf19.12415
CA5341	HSP10.3	1.1	1.0	1.0	1.1	10 kDa mitochondrial heat shock chaperonin, 3-prime e	YOR020c	
CA1600	CTR2	1.1	1.2	1.2	1.1	copper transport protein (by homology)	YHR175w	orf19.4720
CA0457	IPF15604	-1.2	1.1	1.0	1.1	transcription factor (by homology)	YFL031w	orf19.2432
CA2885	IPF7204	-1.0	1.2	1.4	1.1	unknown function		orf19.2475
CA2837	IPF8340	-1.0	-1.0	1.0	1.1	unknown function		orf19.4789
CA5024	IPF3009	-1.2	1.0	1.4	1.1	similar to Saccharomyces cerevisiae Gpi1p required for	YGR216c	orf19.6977
CA0219	YAP3	1.0	1.0	1.2	1.1	transcription factor of a fungal-specific family of bzip pro	YHL009c	orf19.3193
CA3685	IPF19540	1.2	-1.0	1.2	1.1	unknown function	YPL230w	orf19.723
CA4403	IPF8777	1.1	-1.0	1.0	1.1	unknown function		orf19.3107
CA5942	DLD2	1.0	1.2	1.3	1.1	D-lactate ferrycytochrome C oxidoreductase (by homolo	YDL174c	orf19.6755
CA5764	IPF20031	-1.1	1.1	1.1	1.1	similar to Saccharomyces cerevisiae Psr2p plasma mer	YLR019w	orf19.5406
CA1709	HOL2	1.1	-1.0	1.0	1.1	Multidrug-resistance protein subfamily 1 (by homology)	YNR055c ; Missing in array	orf19.4889
CA4964	IPF3920	1.3	1.0	1.2	1.1	unknown function		orf19.6509
CA3999	IPF10447	-1.0	1.1	1.1	1.1	unknown function		orf19.1637
CA3724	IPF6181	1.0	1.1	1.6	1.1	similar to Saccharomyces cerevisiae Fun 26p nucleosid	YAL022c	orf19.4174
CA5246	IPF19808	1.0	1.3	1.3	1.1	unknown function	A_A110	orf19.5016
CA2817	RPS16.3	1.2	1.1	1.1	1.1	ribosomal protein, 3-prime end	YMR143w	
CA1923	IPF9130	1.5	1.0	1.3	1.1	unknown function		orf19.5539
CA1593	MIG1	-1.0	1.3	1.1	1.1	transcriptional regulator	YGL035c	orf19.4318
CA0570	SVL3	1.1	1.1	1.1	1.1	Involved in vacuole function (by homology)	YPL032c	orf19.8732
CA4381	IPF20169	1.0	1.1	1.1	1.1	unknown function		orf19.5674
CA4576	IPF9425.3	1.0	1.2	1.3	1.1	unknown function, 3-prime end		orf19.6888
CA5690	OCH1	1.1	1.1	1.1	1.1	Alpha-1,6-mannosyltransferase (by homology)	YGL038c	orf19.7391
CA0037	IPF17652.3	-1.0	1.1	1.4	1.1	reverse transcriptase, 3-prime end (by homology)		orf19.6078
CA1029	TLG2	1.1	1.1	-1.0	1.1	Syntaxin family of t-SNAREs (by homology)	YOL018c	orf19.9112
CA6157	GEF1.5F	-1.1	1.2	1.1	1.1	Voltage-gated chloride channel protein, 5-prime end (by	YJR040w	orf19.5880
CA6062	IPF8307	-1.0	1.0	1.2	1.1	putative permease (by homology)		orf19.6005
CA5561	SCO1	1.0	1.0	1.1	1.1	Inner mitochondrial membrane protein (by homology)	YBR037c	orf19.7325
CA0541	IPF14574	1.1	1.1	1.2	1.1	unknown function	YMR132c	orf19.1083
CA4043	IPF5291	1.0	1.1	1.3	1.1	UDP-glucose 4-epimerase (by homology)		orf19.3674
CA0126	IPF4284	1.1	1.1	1.2	1.1	unknown function	YOL026c	orf19.8177
CA4625	IPF5742	-1.1	1.0	1.1	1.1	thioredoxin-like protein (by homology)		orf19.3319
CA1403	IPF14155	1.2	1.3	1.1	1.1	similar to Saccharomyces cerevisiae Rim4p involved in	YHL024w	orf19.3373
CA1719	ILV6	1.1	1.0	1.1	1.1	acetolactate synthase, regulatory subunit (by homology)	YCL009c	orf19.12119
CA4338	IPF3616	-1.0	1.0	1.0	1.1	Unknown function	YNR064c	orf19.6709
CA5601	IPF556	1.0	1.1	1.1	1.1	transcriptional regulator (by homology)	YKL070w	orf19.7098
CA1602	RTG1	1.1	1.1	1.1	1.1	basic helix-loop-helix transcription factor that reg	YOL067c	orf19.4722
CA1530	ALG2.5	-1.0	1.0	1.2	1.1	mannosyltransferase, 5-prime end (by homology)	YGL065c	orf19.1221
CA3469	MNT1	-1.2	1.1	1.2	1.1	Mannosyltransferase involved in n-linked and o-linked g	YOR099w	orf19.1665
CA4309	IPF2127.3	-1.0	1.1	1.1	1.1	unknown function, 3-prime end		orf19.4117
CA1629	NPI46	1.1	1.2	1.2	1.1	proline cis-trans isomerase (by homology)	YLR449w	orf19.1030
CA0271	IPF12897	-1.0	1.3	1.3	1.1	putative oxidoreductase (by homology)		orf19.9785
CA6037	ERC4	1.0	1.2	1.2	1.1	ethionine resistance protein (by homology)		orf19.7648
CA4631	VTI1	-1.0	1.2	1.2	1.1	v-SNARE involved in Golgi retrograde traffic (by homolo	YMR197c	orf19.337
CA4670	IPF4536	1.0	1.1	1.2	1.1	unknown function		orf19.904
CA0951	MNN6	-1.3	1.2	1.1	1.1	putative golgi alpha-1,2-mannosyltransferase (by homol	YBR015c	orf19.1011

CA1311	IPF14233	-1.0	1.1	-1.0	1.1	Putative transthyretin precursor (by homology)		orf19.3633
CA5843	IPF416	-1.1	1.2	1.3	1.1	unknown function	YLR328w	orf19.7499
CA0984	IPF7400	-1.0	1.1	1.0	1.1	unknown function	YER049w	orf19.1802
CA4068	IPF5922	1.1	1.1	1.1	1.1	unknown function		orf19.446
CA2883	IPF3790	-1.0	1.1	1.4	1.1	unknown function		orf19.5852
CA0829	SLC1	1.2	1.1	1.3	1.1	fatty acyltransferase (by homology)	YDL052c	orf19.250
CA3593	YPT71	1.2	1.1	1.0	1.1	GTP-binding protein of the RAB family (by homology)	YML001w	orf19.2245
CA0325	IPF15222	1.0	1.1	1.0	1.1	Unknown function		orf19.3781
CA4555	IPF17555.3	-1.0	1.1	1.0	1.1	unknown function, 3-prime end	YLR206w	orf19.9019
CA5614	IPF522	1.1	1.3	1.4	1.1	unknown function		orf19.7084
CA1887	IPF5496	1.2	1.1	1.3	1.1	unknown function	YPL264c	orf19.2204
CA2867	IPF11688	-1.1	1.2	1.1	1.1	similar to Saccharomyces cerevisiae Apl4p AP-1 compl	YPR029c	orf19.2844
CA0261	LYS22	-1.0	1.3	1.5	1.1	Homocitrate synthase (by homology)	YDL131w	orf19.8394
CA5654	IPF15543	-1.0	1.0	1.1	1.1	unknown function		orf19.7356
CA3736	IPF5533	1.3	1.5	1.2	1.1	ABC transporter (by homology)	YER036c	orf19.2183
CA1232	IPF11815	-1.1	1.0	1.3	1.1	similar to Saccharomyces cerevisiae Lys14 triacyglycerol lipase (by homology)		orf19.4982
CA0871	APE3	1.1	1.1	1.0	1.1	aminopeptidase (by homology)	YBR286w	orf19.3591
CA3683	PPZ1	1.1	1.2	1.3	1.1	ser/thr phosphatase required for normal osmoregulation	YML016c	orf19.726
CA5287	IPF1922	1.1	1.1	1.3	1.1	similar to multidrug resistance proteins		orf19.7148
CA3178	IPF19974	-1.0	1.1	1.1	1.1	unknown function		orf19.1406
CA5463	IPF284	1.0	1.1	1.3	1.1	unknown function		orf19.3272
CA1638	GRR1	1.0	1.2	1.2	1.1	Required for glucose repression and for glucose and ca	YJR090c	orf19.3944
CA3180	IPF12244	-1.1	1.1	1.3	1.1	unknown function	YKL034w	orf19.2131
CA0530	PF19633.3EOC	1.0	1.2	1.1	1.1	similar to Saccharomyces cerevisiae Cdc39p nuclear pr	YCR093w	orf19.8685
CA4567	IPF9555	1.0	1.2	1.1	1.1	unknown function	YAR008w	orf19.6879
CA0568	APS2	-1.1	1.0	1.1	1.1	AP-2 complex subunit, sigma2 subunit (by homology)	YJR058c	orf19.8729
CA3907	IPF3304	-1.1	1.1	1.1	1.1	similar to Saccharomyces cerevisiae Aip1p actin cytosk	YMR092c	orf19.11873
CA5211	IPF18125	1.0	1.1	1.1	1.1	similar to glutenin and glutamine-rich proteins		orf19.7028
CA3840	IPF12745	1.0	1.2	1.2	1.1	unknown function	YLR193c	orf19.6600
CA4041	GAL10	-1.4	1.5	1.2	1.1	UDP-glucose 4-epimerase by homology	YBR019c	orf19.3672
CA1111	RIB3	1.1	1.3	1.4	1.1	3,4-dihydroxy-2-butanone 4-phosphate synthase (by ho	YDR487c	orf19.12693
CA1062	IPF14165	1.6	-1.1	1.1	1.1	unknown function		orf19.4642
CA5854	IPF393	1.1	1.2	1.2	1.1	similar to Saccharomyces cerevisiae Nup192p nucleopo	YJL039c	orf19.7511
CA3437	IPF15925	1.0	1.2	1.3	1.1	unknown function		orf19.10505
CA1607	IPF14916	1.2	1.1	1.1	1.1	unknown function	YOL071w	orf19.4727
CA1944	IPF10645	1.2	1.1	1.1	1.1	unknown function	YOR154w	orf19.4738
CA4129	IPF6878	1.2	-1.0	1.0	1.1	unknown function	YLR118c	orf19.11723
CA0436	RBL2	1.0	1.1	1.1	1.1	Beta-tubulin binding protein (by homology)	YOR265w	
CA3323	IKI1	1.1	1.0	1.1	1.1	killer toxin insensitive protein	YHR187w	orf19.2676
CA0663	PUP2	1.2	1.3	1.3	1.1	20S proteasome subunit(alpha5) (by homology)	YGR253c	orf19.709
CA3570	NOP1	1.1	1.2	1.1	1.1	Fibrillarin	YDL014w	orf19.3138
CA3966	IPF9376	1.1	1.1	1.4	1.1	unknown function	YLR004c	orf19.1427
CA3773	IPF11153	-1.0	-1.1	1.0	1.1	unknown function	YDR416w	orf19.2893
CA5482	F14094.REPEA	-1.1	1.0	1.1	1.1	repeated protein (10 times) of unknown function		orf19.5315
CA3732	IPF11898	1.1	1.0	1.2	1.1	unknown function		orf19.4182
CA1168	IPF13017	1.1	1.3	1.2	1.1	unknown function		orf19.1785
CA0482	IPF14763	1.6	-1.2	1.1	1.1	delta-12 fatty acid desaturase (by homology)		orf19.7765
CA3217	DHH1	1.1	1.2	1.2	1.1	RNA helicase by homology	YDL160c	orf19.6197
CA4082	PTC4	-1.0	1.0	1.1	1.1	ser/thr protein phosphatase PP2C(by homology)	YBR125c	orf19.6638

1977.2		-1.0	-1.0	1.0	1.1			
CA2277	DRS21	1.1	1.1	1.1	1.1	Membrane-spanning Ca-ATPase (by homology)	YIL048w	orf19.783
CA0994	IPF10077	1.0	1.0	1.0	1.1	3-oxoacid CoA-transferase by homology		orf19.2281
CA3247	IPF15832	1.2	1.1	1.2	1.1	unknown function	YKL053ca	orf19.4676
CA5657	IPF14682	1.2	1.0	1.4	1.1	putative transcription factor (by homology)	YNL027w	orf19.7359
CA4655	IPF3098	1.1	1.0	1.5	1.1	Putative mannosyltransferase (by homology)	YNL219c	orf19.4442
CA5251	IPF1824	1.1	1.0	-1.1	1.1	unknown function	YPL269w	orf19.5011
CA1849	IPF19932	1.1	1.0	1.1	1.1	unknown function		orf19.640
CA0996	IPF10071	1.3	1.2	1.0	1.1	catabolic 3-dehydroquinase (by homology)		orf19.9823
CA4485	IPF9160	1.0	1.1	1.2	1.1	similar to Saccharomyces cerevisiae Med4ptranscriptio	YOR174w	orf19.1878
CA0631	IPF11698	1.0	1.1	1.3	1.1	similar to Saccharomyces cerevisiae Esbp6p probable r	YNL125c	orf19.11813
CA5278	CTA29.EXON2	1.2	1.1	1.1	1.1	Protein with putative transcription activation domain, exon 2		
CA3270	LYS5	-1.1	1.0	1.1	1.1	L-aminoadipate-semialdehyde dehydrogenase (by hom	YGL154c	orf19.6304
CA0775	IFK2	-1.1	1.1	1.2	1.1	probable monoxygenase (by homology)		orf19.856
CA0297	CDC53	-1.3	-1.2	-1.3	1.1	Cell division control protein (by homology)	YDL132w	orf19.1674
CA5358	IPF846	-1.1	1.3	1.1	1.1	WD-repeat protein, beta-transducin (by homology)	YMR102c	orf19.7235
CA4015	IPF12268	1.1	1.0	1.0	1.1	unknown function		
CA0124	RFC5	-1.0	1.1	1.0	1.1	DNA replication factor C (by homology)	YBR087w	orf19.9577
CA1768	IPF7585	1.1	1.0	1.0	1.1	unknown function	YER050c	orf19.5201
CA6005	PUP1	1.1	1.3	1.4	1.1	20S proteasom ebeta2 subunit (by homology)	YOR157c	orf19.7605
CA5911	IPF5965	-1.1	1.0	1.1	1.1	NADH-ubiquinone oxidoreductase (by homology)		orf19.6794
CA5853	LSM6	1.1	1.1	1.2	1.1	U6 snRNA-associated Sm-like protein (by homology)	YDR378c	
CA4042	TRS23	1.1	1.2	1.2	1.1	targeting and fusion of ER to golgi transport vesicles by	YDR246w	orf19.3673
CA6143	IPF1873	-1.1	1.2	1.2	1.1	putative GTP-binding protein (by homology)		orf19.5902
CA2102	IPF9363	-1.0	1.1	1.0	1.1	similar to Saccharomyces cerevisiae Yku80p componer	YMR106c	orf19.2383
CA2002	IPF16470	1.0	1.1	1.2	1.1	unknown function	YBL036c	orf19.2794
CA2587	RPS30.3	1.2	1.1	1.1	1.1	40S ribosomal protein S30, 3-prime end (by homology)	YOR182c	
CA2807	IPF11965	-1.2	1.3	1.1	1.1	unknown function	YOR022c	orf19.5782
CA5868	IPF351	1.1	1.2	1.2	1.1	unknown function	YMR090w	orf19.7531
CA3072	ERG12	-1.0	1.2	1.2	1.1	Mevalonate kinase (by homology)	YMR208w	orf19.4809
CA1553	IPF14081	1.1	1.2	1.4	1.1	unknown function		orf19.1714
CA3740	SIT1	1.1	1.2	1.6	1.1	Ferrioxamine B permease by homology	YHL040c	orf19.2179
CA2369	TBP1	1.1	1.2	1.1	1.1	TATA-binding protein (by homology)	YER148w	orf19.1837
CA5491	IPF798	1.1	1.1	1.1	1.1	transcriptional regulator (by homology)	YGL209w	orf19.5326
CA3646	IPF4128	1.1	1.0	1.2	1.1	unknown function		orf19.2037
CA0468	DIB1	1.0	1.0	1.1	1.1	Component of the U4/U6.U5 snRNP (by homology)	YPR082c	orf19.9531
CA1978	IPF9580	-1.1	-1.0	1.0	1.1	unknown function		orf19.687
CA5068	IPF3592	-1.0	1.2	1.2	1.1	unknown function	YGR068c	orf19.3041
CA4253	IPF4288	1.0	1.0	1.1	1.1	unknown function		
CA2489	IPF7217	-1.0	1.5	1.2	1.1	unknown function		orf19.11525
CA1372	IPF15844	1.0	1.0	1.1	1.1	similar to Saccharomyces cerevisiae Stp2p involved in p	YHR006w	orf19.4961
CA3120	IPF5358	1.0	1.0	1.2	1.1	unknown function	YDR357c	orf19.3007
CA4040	GAL1	-1.0	1.1	1.2	1.1	galactokinase	YDR009w	orf19.3670
CA4120	SOD1.3	1.1	1.1	1.1	1.1	Cu,Zn-superoxide dismutase, 3-prime end	YJR104c	
CA2283	MRT4	-1.0	1.1	1.1	1.1	required for mRNA decay (by homology)	YKL009w	orf19.12996
CA5091	ACF3	1.1	1.3	1.2	1.1	endo-1,3-beta-glucanase	YNR067c	orf19.10584
CA0357	FCY22	1.0	1.1	1.3	1.1	purine-cytosine permease (by homology)	YER060w	orf19.333
CA0604	VID21	-1.0	-1.0	-1.0	1.1	unknown function	YDR359c	orf19.3077
CA4589	BEL1.EXON2	1.1	1.1	1.2	1.1	protein of the 40S ribosomal subunit, exon 2 (by homology)		

CA0041	IPF10360	1.1	1.3	1.3	1.1	unknown function	YMR134w	orf19.3804
CA5042	IPF4514	-1.1	1.1	1.1	1.1	putative alpha-1,3-mannosyltransferase (by homology)		orf19.6996
CA2053	IPF11029	1.1	1.0	1.3	1.1	unknown function		orf19.5720
CA4643	PRE9	-1.0	1.0	1.0	1.1	20S proteasome subunit Y13 (alpha3) (by homology)	YGR135w	orf19.350
CA1643	IPF9347	-1.0	1.0	1.2	1.1	unknown function		orf19.1729
CA3522	IPF20134	1.1	-1.1	1.1	1.1	unknown function		orf19.994
CA4453	CHL4	1.0	1.1	1.1	1.1	chromosome segregation protein (by homology)	YDR254w	orf19.6851
CA5790	IPF1144	-1.0	1.1	1.1	1.1	unknown function		orf19.5439
CA5559	CBP1	-1.2	1.1	1.2	1.1	Corticosteroid binding protein		orf19.7323
CA5029	IPF2997	-1.0	1.0	1.0	1.1	unknown function		orf19.6983
CA5007	IPF12579	-1.0	1.0	1.0	1.1	putative phospholipase A2 (by homology)	YNL040w	orf19.5239
CA1090	COX18	-1.0	1.0	1.3	1.1	protein required for activity of mitochondrial cytochrome	YGR062c	orf19.3946
CA3556	IPF7764	1.0	1.0	1.1	1.1	unknown function		orf19.3885
CA4262	IPF2275	-1.0	-1.0	1.3	1.1	unknown function		orf19.6654
CA4081	IPF2523	1.0	1.2	1.1	1.1	unknown function		orf19.6637
CA2640	IPF2930	1.1	1.2	1.2	1.1	Suppressor of PAB1 (by homology)		
CA3431	FUN9	1.0	1.0	1.3	1.1	Protein involved in vesicular transport between the endc	YAL042w	orf19.586
CA0466	URA4	1.1	1.1	1.1	1.1	dihydrooratase (by homology)	YLR420w	orf19.1977
CA1418	IPF16124	1.1	1.1	1.4	1.1	zinc-finger containing protein (by homology)	YOR113w	orf19.173
CA3902	YVH1	1.1	1.0	1.1	1.1	protein tyrosine phosphatase (by homology)	YIR026c	orf19.4401
CA2092	RPL21A.3	1.1	-1.1	-1.1	1.1	Ribosomal protein, 3-prime end (by homology)	YBR191w	orf19.840
CA1483	YHC3	-1.1	1.1	1.1	1.1	involved in cellular pH homeostasis (by homology)	YJL059w	orf19.4059
CA1743	IPF12209	1.0	1.1	1.0	1.1	similar to Saccharomyces cerevisiae Eco1p involved in	YFR027w	orf19.5053
6532.2		1.0	1.1	1.2	1.1			
CA4561	IPF8031	1.0	1.5	1.5	1.1	unknown function	YLR126c	orf19.6872
CA5458	IPF274	-1.0	1.0	1.1	1.1	unknown function		orf19.3266
CA6118	IPF126	1.1	1.1	1.3	1.1	unknown function	YLR241w	orf19.5932
CA2693	IPF9173.5F	1.0	1.0	1.1	1.1	similar to Saccharomyces cerevisiae Vps30p involved ir	YPL120w	orf19.10247
CA1915	IPF16565	1.3	1.1	1.2	1.1	unknown function		orf19.2439
CA1252	RPN1	-1.1	1.1	1.1	1.1	26S proteasome regulatory subunit (by homology)	YHR027c	orf19.12421
CA2190	AOX1	-1.0	-1.0	1.1	1.1	alternative oxidase (by homology)		orf19.4774
CA4627	DUT1	1.2	1.0	1.0	1.1	dUTP pyrophosphatase	YBR252w	orf19.10832
CA1771	SEH1	1.0	1.0	1.1	1.1	nuclear pore protein (by homology)	YGL100w	orf19.2186
CA3087	SMD3	1.0	-1.0	1.0	1.1	core snRNP protein (by homology)	YLR147c	orf19.11622
CA4102	RPL37B	1.1	1.1	1.1	1.1	Ribosomal protein	YDR500c	
CA0997	IPF9998	1.1	1.0	1.2	1.1	unknown function		orf19.9824
CA1512	IPF15255	1.1	1.1	1.0	1.1	unknown function	YEL007w	orf19.4884
CA1213	VPS15.5F	1.0	1.0	-1.0	1.1	serine/threonine protein kinase, 5-prime end (by homolc	YBR097w	orf19.7776
CA3338	IPF13582	-1.1	1.1	-1.1	1.1	unknown function	YHR009c	orf19.2333
CA3285	IPF6280	1.0	1.1	1.0	1.1	unknown function	YJR085c	orf19.6318
CA4922	IPF1415	1.3	1.1	1.2	1.1	unknown function	YPL098c	orf19.6062
CA4678	IPF3670	-1.2	1.0	1.0	1.1	unknown function	YDR137w	orf19.894
CA5837	IPF426	1.1	-1.0	1.1	1.1	unknown function	YLL002w	orf19.7491
CA0942	IPF8619	-1.0	1.0	1.1	1.1	unknown function		orf19.3706
CA3730	IPF11900	1.1	1.1	1.1	1.1	unknown function	YLR292c	orf19.4180
CA0792	DIT2	1.1	1.1	1.1	1.1	putative cytochrome P450	YDR402c	orf19.554
CA0578	IPF9605	-1.1	1.1	1.0	1.1	similar to Saccharomyces cerevisiae Mih1p M-phase inc	YMR036c	orf19.3071
CA3489	IPF3195	1.0	1.1	1.1	1.1	unknown function		orf19.3567
CA5157	IPF993	-1.0	1.1	1.2	1.1	unknown function		orf19.4595

CA4514	IPF20016	-1.4	1.1	1.0	1.1	similar to Saccharomyces cerevisiae Sec63p ER proteir	YOR254c	orf19.491
CA1177	VMA7	1.1	1.0	1.1	1.1	vacuolar ATPase (by homology)	YGR020c	orf19.806
CA3089	IPF9825	-1.0	1.1	1.1	1.1	unknown function	YLR253w	
CA3746	ARA1	1.1	1.2	1.2	1.1	D-arabinose dehydrogenase (by homology)	YBR149w	orf19.2172
CA2710	IPF7403	1.1	1.1	1.2	1.1	unknown function	YMR069w	orf19.4664
CA2977	HOM3	-1.1	1.0	1.2	1.1	Aspartokinase (by homology)	YER052c	orf19.1235
CA5580	RVS161	1.1	1.0	1.0	1.1	cytoskeletal binding protein (by homology)	YCR009c	orf19.7124
CA0435	UGP1	-1.3	1.1	1.3	1.1	UTP--glucose-1-phosphate uridylyltransferase (by homc	YKL035w	orf19.9305
CA3095	CDC28	-1.1	1.0	1.1	1.1	CELL DIVISION CONTROL PROTEIN 28 -protein kinas	YBR160w	orf19.3856
CA0484	IPF19622	-1.0	1.1	-1.0	1.1	unknown function		orf19.7762
CA5303	IPF2180	1.0	1.1	1.3	1.1	unknown function		orf19.7170
CA2741	IPF10632	1.0	1.2	1.2	1.1	unknown function	YLR323c	orf19.2105
CA5697	IPF18076.3F	1.2	1.1	1.2	1.1	thiol-specific antioxidant-like protein, 3-prime end (by homology)		
CA1832	IPF17727	1.1	-1.0	1.3	1.1	unknown function		orf19.5190
CA5856	ALK2	1.0	1.0	1.1	1.1	n-alkane inducible cytochrome P-450 (by homology)		orf19.7513
CA1523	PAT1	-1.1	1.1	1.1	1.1	Topoisomerase II-associated protein (by homology)	YCR077c	orf19.3792
CA6166	CTP1	-1.0	1.0	1.2	1.1	Citrate transport protein (by homology)	YBR291c	orf19.13291
CA2425	IPF9907	1.1	1.1	1.5	1.1	similar to Saccharomyces cerevisiae Sed4 protein of the	YCR067c	orf19.10912
CA4726	IPF12255	1.1	1.2	1.2	1.1	unknown function	YDR084c	orf19.12326
CA1632	IPF10181	1.1	1.0	1.0	1.1	similar to Saccharomyces cerevisiae Rsm26p protein of	YJR101w	orf19.11420
CA4616	IPF5761	1.0	1.1	1.2	1.1	flavin-containing monooxigenase (by homology)	YHR176w	orf19.3307
CA0851	IPF16670	-1.0	1.1	1.2	1.1	unknown function	YOR242c	orf19.9313
CA0602	CTA22	1.2	1.1	1.1	1.1	Protein with putative transcription activation domain		orf19.3074
CA1359	IPF11842	1.0	1.1	1.2	1.1	unknown function		orf19.4405
CA0535	IPF15606	1.1	1.1	1.2	1.1	similar to Saccharomyces cerevisiae Erd1p required for	YDR414c	orf19.5065
CA0831	PF10493.5EOC	-1.0	1.1	1.1	1.1	unknown function, 5-prime end		orf19.7878
CA0387	PF10318.5EOC	-1.0	1.1	1.1	1.1	unknown function, 5-prime end		
CA1745	IPF10888	-1.0	-1.0	-1.0	1.1	unknown function		orf19.5051
CA3706	PSA2	-1.0	1.2	1.2	1.1	mannose-1-phosphate guanyltransferase by homology		orf19.4943
CA2543	IPF16925	1.0	1.0	1.1	1.1	unknown function	YNL148c	orf19.2828
CA5713	ALS6	1.0	1.0	1.0	1.1	agglutinin-like protein		orf19.7414
CA4056	IPF7721	-1.2	1.2	1.3	1.1	unknown function		orf19.431
CA6102	SPO70.5F	-1.0	-1.0	1.1	1.1	involved in meiosis and sporulation, 5-prime end	YGR225w	orf19.5954
CA1300	SLY41	1.0	-1.0	1.1	1.1	vesicular transport (by homology)	YOR307c	orf19.4199
CA5974	IPF930	-1.0	1.0	1.1	1.1	unknown function	YOR313c	orf19.7568
CA3896	IPF10339	1.1	-1.2	-1.1	1.1	unknown function		orf19.5077
CA5715	HNT2	1.1	1.1	1.2	1.1	Diadenosine polyphosphate hydrolase	YDR305c	orf19.7419
CA1669	IPF11393	1.3	-1.0	-1.2	1.1	unknown function	YBL090w	orf19.2852
CA1433	IPF12464	1.1	1.1	1.1	1.1	unknown function		
CA2210	MSL1	-1.0	1.0	1.2	1.1	U2 snRNA-associated protein (by homology)	YIR009w	orf19.4748
CA0417	UBC13	1.2	1.1	1.1	1.1	E2 ubiquitin-conjugating enzyme (by homology)	YDR092w	orf19.2225
CA2042	IPF14219	1.0	-1.0	1.1	1.1	probable membrane protein (by homology)	YOL107w	orf19.10445
CA5481	IPF19810	1.2	1.1	1.3	1.1	unknown function		orf19.12773
CA1132	F2710.REPEA	1.3	1.0	1.5	1.1	putative permease (by homology)		orf19.9705
CA3208	PSA1	-1.0	1.2	1.2	1.1	GDP-mannose pyrophosphorylase	YDL055c ; Missing in array	orf19.6190
CA3383	IPF8359	1.0	-1.0	1.0	1.1	unknown function		orf19.326
CA2029	SAR1.3	1.2	1.0	1.1	1.1	GTP-binding protein of the ARF family, 3-prime end (by	YPL218w	orf19.10966
CA2744	IPF10626	1.1	1.0	1.1	1.1	unknown function	YGL020c	orf19.2101
CA1541	BGL21	1.3	1.0	1.2	1.1	endo-beta-1,3-glucanase (by homology)	YGR282c	orf19.4565

CA0438	STE4.5EOC	-1.0	1.1	1.0	1.1	GTP-binding protein beta subunit of the pheromone pat	YOR212w	orf19.8419
CA2120	PUP3	1.0	1.1	1.2	1.1	PRCT yeast proteasome component (by homology)	YER094c	
CA5987	CHT3	1.3	1.2	1.3	1.1	chitinase 3 precursor	YLR286c	orf19.7586
CA4952	IPF13609	1.0	-1.0	1.1	1.1	unknown function	YPL246c	orf19.6526
CA2084	IPF3384.3F	1.2	1.1	1.3	1.1	similar to Saccharomyces cerevisiae Gpi13p phosphoryltransferase that adds phosph		orf19.833
CA5079	RPN3	-1.2	1.1	1.1	1.1	26S proteasome regulatory subunit (by homology)	YER021w	orf19.3054
CA1801	IPF11444	1.2	1.2	1.0	1.1	unknown function	YER007ca	orf19.2920
CA1654	IPF19660	-1.1	1.1	1.3	1.1	unknown function	YDR202c	orf19.5559
CA4251	IPF4291	-1.0	1.1	1.1	1.1	unknown function		orf19.540
CA1308	IPF8642	-1.0	-1.0	-1.0	1.1	unknown function		orf19.11450
CA4776	CNB1	1.1	1.1	1.0	1.1	Protein phosphatase, Calcineurin B (by homology)	YKL190w	orf19.4009
CA1865	IPF7646	-1.0	1.1	1.3	1.1	putative transcription factor (by homology)		orf19.861
CA3690	RPS14B	1.1	1.0	-1.1	1.1	ribosomal protein (by homology)	YJL191w	
CA5369	WSC4	1.0	1.2	1.2	1.1	Cell wall integrity by homology	YHL028w	orf19.7251
CA5893	IPF2392	1.1	1.1	1.1	1.1	unknown function		orf19.6813
CA2175	IPF8892	1.0	1.1	1.1	1.1	unknown function		orf19.3762
CA1416	DBP2.EXON1	1.0	1.3	1.4	1.1	ATP-dependent RNA helicase of DEAD box family, exo	YNL112w	orf19.171
CA2200	IPF8114	-1.0	-1.0	1.0	1.1	unknown function	YFL046w	orf19.2939
CA1467	IPF5082	1.0	1.2	1.2	1.1	similar to Saccharomyces cerevisiae Cak1p cdk-activati	YFL029c	orf19.8412
CA1010	GLT1.3EOC	-1.0	-1.1	-1.1	1.1	glutamate synthase (NAPDPH), 3-prime end (by homol	YDL171c	orf19.6257
CA3424	NOP10	-1.0	1.1	1.1	1.1	Nucleolar rRNA processing protein (by homology)	YHR072wa	
CA6003	IPF660	-1.0	-1.0	1.0	1.1	unknown function	YMR244ca	orf19.7603
CA3692	IPF4876	1.1	1.0	1.1	1.1	unknown function		orf19.6267
CA5255	ACT1	-1.1	-1.0	1.1	1.1	actin (by homology)	YFL039c	orf19.5007
CA0952	MNT3.3EOC	1.0	1.0	1.2	1.1	Putative mannosyltransferase, 3-prime end		
CA0963	IPF9143	1.0	1.1	1.1	1.1	similar to Saccharomyces cerevisiae Nat3p N-acetyltra	YPR131c	orf19.6246
CA5493	GCN1.5F	1.1	1.5	1.2	1.1	translational activator, 5-prime end (by homology)	YGL195w	orf19.5333
CA2245	IPF7409	1.0	1.0	1.1	1.1	unknown function		orf19.4668
CA1734	IPF4988	1.1	1.1	1.1	1.1	unknown function		orf19.2529
CA5535	IPF2839	-1.0	1.0	1.2	1.1	unknown function		orf19.7296
CA4800	IPF8796	-1.1	1.1	1.1	1.1	putative GPI-anchhored protein related to Phr1, Phr2 ar	YOL030w	orf19.4035
CA2777	THI6	1.0	1.1	1.0	1.1	thiamin-phosphate pyrophosphorylase and hydroxyethy	YPL214c	orf19.277
CA5767	IPF1098	1.1	1.1	-1.0	1.1	unknown function	YNL265c	orf19.5409
CA5448	ARC19.EXON2	1.1	1.1	1.2	1.1	subunit of the Arp2/3 complex involved in the control of	YKL013c	orf19.3251
CA2806	IPF11702	1.0	-1.0	1.1	1.1	unknown function	YIL067c	orf19.5780
CA4512	RPL15B	1.1	-1.0	-1.1	1.1	ribosomal protein L15.e.c13 (by homology)	YLR029c	orf19.8123
CA0926	IPF11335	-1.1	-1.0	1.3	1.1	Member of the phosphate permease	YNR013c	orf19.3663
CA2897	IPF14979	-1.2	-1.0	-1.0	1.1	similar to Saccharomyces cerevisiae Npy1p NADH pyro	YGL067w	orf19.3482
CA5347	IPF864	1.1	1.1	1.0	1.1	unknown function	YJL104w	orf19.7222
CA5186	HRT2	-1.0	1.1	1.2	1.1	Similar to ScHRT2 (by homology)	YMR027w	orf19.4624
CA1860	UTR4	-1.0	1.0	1.1	1.1	unknown function	YEL038w	orf19.9072
CA1783	IPF7635	1.0	1.0	1.0	1.1	unknown function		orf19.1171
CA0385	IPF4071	-1.2	1.0	-1.0	1.1	unknown function		orf19.1861
CA1395	IPF17558	1.1	1.0	1.1	1.1	unknown function		orf19.9332
CA3963	IPF11233	-1.1	1.0	1.1	1.1	similar to Saccharomyces cerevisiae Fzo1p required for	YBR179c	orf19.1422
CA4991	LCB4	-1.0	1.1	1.1	1.1	Sphingolipid long chain base kinase (by homology)	YOR171c	orf19.5257
CA2027	MCK1	1.1	1.1	1.5	1.1	ser/thr/tyr protein kinase (by homology)	YNL307c	orf19.10963
CA1117	ARP3	-1.1	1.2	1.1	1.1	actin related protein (by homology)	YJR065c	orf19.2289
CA2780	IPF3831	1.1	1.1	1.1	1.1	unknown function		orf19.281

CA1729	IPF8440	-1.0	1.1	1.0	1.1	similar to Saccharomyces cerevisiae Trs33p TRAPP su	YOR115c	orf19.6496
CA2408	IPF3833	1.0	1.0	1.0	1.1	unknown function		orf19.296
CA4934	CDC36	1.1	1.1	1.0	1.1	transcription factor (by homology)	YDL165w	orf19.6075
CA2435	IPF9483	1.1	1.1	1.2	1.1	probable permease (by homology)	YHR048w	orf19.10898
CA0695	IPF12601	1.2	1.0	-1.0	1.1	unknown function		orf19.3290
CA5039	GAP2	1.0	-1.0	1.2	1.1	general amino acid permease (by homology)	YKR039w	orf19.6993
CA0410	IPF15065	1.2	1.1	1.1	1.1	unknown function	YMR178w	orf19.13180
CA0597	IPF9704	1.1	-1.0	1.0	1.1	similar to Saccharomyces cerevisiae Tfa2p TFIIE subur	YKR062w	orf19.12345
CA2330	RIM2	-1.0	-1.1	1.2	1.1	mitochondrial carrier protein (by homology)	YBR192w	orf19.4499
CA5989	IPF692	1.1	1.0	1.2	1.1	unknown function		orf19.7589
CA1603	FAD1	1.1	1.1	1.1	1.1	flavin adenine dinucleotide (FAD) synthetase (by	YDL045c	orf19.4723
CA5821	PHO81	-1.1	1.0	1.1	1.1	Cyclin-dependent kinase inhibitor (by homology)	YGR233c	orf19.7475
CA1377	IPF18690	-1.3	1.6	-1.2	1.1	unknown function		orf19.461
CA0279	IPF10568	1.1	1.0	1.1	1.1	unknown function		orf19.1440
CA2795	IPF8407	-1.0	1.2	1.2	1.1	unknown function	YJL055w	orf19.1723
CA3651	MSS1	-1.1	-1.1	-1.0	1.1	Mitochondrial GTPase involved in expression of COX1 (	YMR023c	orf19.2042
CA3842	YKE2.3	1.1	-1.1	1.1	1.1	Gim complex component, 3-prime end (by homology)	YLR200w	
CA2434	IPF9484	1.0	1.1	1.2	1.1	unknown function		orf19.3396
CA1975	PLB1	-1.0	1.1	-1.0	1.1	phospholipase B		orf19.689
CA4230	IPF12481	-1.0	-1.0	-1.0	1.1	unknown function		orf19.513
CA5062	SEC62	1.0	1.1	1.3	1.1	subunit of ER protein-translocation complex (by homolo	YPL094c	orf19.3031
CA4630	IPF1537	1.0	1.1	1.1	1.1	putative adrenodoxin and ferrodoxin (by homolgy)	YPL252c	orf19.336
CA4994	IPF2033	1.0	1.0	1.1	1.1	unknown function		orf19.5254
CA2429	IPF9890	1.0	1.0	1.0	1.1	unknown function		orf19.3404
CA5049	IPF3714	-1.0	1.0	1.3	1.1	similar to Saccharomyces cerevisiae Cdc12p septin (by	YHR107c	orf19.3013
CA1815	IPF18606	-1.0	1.1	1.1	1.1	unknown function	YBR040w	orf19.138
CA3126	GCN4	-1.3	-1.1	-1.1	1.1	transcriptional activator	YEL009c	orf19.1358
CA5711	MUB1	1.0	-1.1	-1.1	1.1	Regulation of bud site selection (by homology)	YMR100w	orf19.7412
CA4422	LIP9.EXON2	1.0	1.1	1.1	1.1	secretory lipase 9, exon 2		orf19.5173
CA2539	IPF9188	-1.0	1.0	1.1	1.1	unknown function		orf19.3187
CA5231	IPF10422	1.1	1.1	1.0	1.1	Similar to APG12, component of the autophagic system	YBR217w	orf19.5033
CA0917	RAD16	-1.0	1.1	1.3	1.1	nucleotide excision repair protein (by homology)	YBR114w	orf19.2969
CA1511	IPF9972.3EOC	1.0	1.1	1.2	1.1	unknown function, 3-prime end	YMR073c	orf19.4522
CA4983	IPF2053	1.1	1.2	1.2	1.1	unknown function		orf19.5267
CA3129	OST4	-1.0	1.0	1.1	1.1	oligosaccharyltransferase subunit		
CA2902	HRR25	1.1	1.0	1.1	1.1	casein kinase I (by homology)	YPL204w	orf19.3476
CA0549	IPF14031	-1.0	1.0	1.2	1.1	putative secreted aspartic protease (by homology)		orf19.852
CA0344	IFF1.3EOC	1.1	1.2	1.2	1.1	Unknown function, 3-prime end	Missing in array	orf19.1346
CA4818	IPF1193	1.3	1.2	1.3	1.1	unknown function	YHL018w	orf19.2079
CA5320	IPF2147	1.0	1.1	-1.0	1.1	unknown function		orf19.7194
CA3544	BPT1.3F	1.1	1.3	1.2	1.1	membrane transporter of the ATP-binding cassette (ABC) superfamily, 3-prime end (b		orf19.6382
CA5373	IPF5243	1.1	1.0	1.1	1.1	snRNP (by homology)	YER146w	orf19.7256
CA2059	CDC4	1.1	1.3	1.2	1.1	CANAL CELL DIVISION CONTROL PROTEIN 4	YFL009w	orf19.2559
CA2572	IPF13766	-1.1	1.2	1.3	1.1	unknown function		orf19.6211
CA2144	IPF12802	1.0	-1.0	1.1	1.1	unknown function		orf19.2513
CA4153	DNLI	-1.0	-1.0	1.1	1.1	CANAL DNA LIGASE (POLYDEOXYRIBONUCLEOTID	YOR005c	orf19.5798
CA2361	IPF8950	-1.0	1.1	1.1	1.1	unknown function	YER004w	orf19.12363
CA4706	RAD53	1.0	1.0	1.0	1.1	protein kinase	YPL153c	orf19.6936
CA5389	IFA13	-1.0	1.0	1.1	1.1	unknown function		orf19.931

CA2611	IPF5453	-1.0	1.1	1.2	1.1	unknown function		orf19.5692
CA5720	UNG1	-1.0	1.0	1.1	1.1	Uracil-DNA glycosylase (by homology)	YML021c	orf19.7425
CA5585	CSA1	1.1	1.1	1.0	1.1	mycelial surface antigen by homology		orf19.7114
CA4867	IPF4080	-1.0	1.0	-1.0	1.1	similar to Saccharomyces cerevisiae Mrp8p ribosomal p	YKL142w	orf19.3844
CA3203	IPF3445	1.1	1.1	1.2	1.1	Unknown function	YJR135wa	orf19.6183
CA0557	HYR1.53	1.1	1.0	1.0	1.1	Hyphally regulated protein, internal fragment		
CA3936	COX17	1.0	1.1	1.1	1.1	cysteine-rich cytoplasmic protein(by homology)	YLL009c	
CA5672	IPF1271	-1.0	1.1	1.1	1.1	Small nuclear ribonucleoprotein (by homology)		orf19.7375
CA4018	MOG1	-1.0	1.0	-1.1	1.1	Ran-Binding Protein by homology	YJR074w	orf19.3446
CA0538	IPF10901	1.0	1.1	1.1	1.1	unknown function		orf19.2819
CA6146	IPF1863	1.1	-1.0	1.1	1.1	unknown function	YMR244w	orf19.5896
CA4222	GCD7	1.1	1.1	1.2	1.1	translation initiation factor eIF2b subunit (by homology)	YLR291c	orf19.825
CA5295	IPF1954	1.0	1.0	1.1	1.1	putative transporter (by homology)		orf19.7158
CA3157	IPF14456	1.0	1.1	1.0	1.1	unknown function	YBR269c	orf19.1588
CA5282	IPF1911	1.1	1.0	1.1	1.1	unknown function		orf19.7139
CA3610	IPF3854	1.0	1.1	1.0	1.1	unknown function		orf19.27
CA1963	IPF14040	1.1	1.3	1.6	1.1	probable transporter (by homology)		orf19.2397
CA5195	GRP8	-1.0	-1.0	1.0	1.1	Similarity to dihydroflavonol-4-reductases		orf19.7009
CA4985	IPF2050	1.1	1.0	1.1	1.1	similar to Saccharomyces cerevisiae Kip1p kinesin-relat	YBL063w	orf19.5265
CA2477	IPF16016	-1.1	1.2	1.1	1.1	unknown function		orf19.10399
CA5824	NTH1	-1.1	-1.0	1.4	1.1	Neutral trehalase	YDR001c	orf19.7479
CA1872	IPF6700	1.0	1.0	1.0	1.1	unknown function		orf19.2459
CA2389	IPF8500	-1.0	1.1	1.0	1.1	unknown function		orf19.2610
CA1934	YAP1802.3EOC	1.1	1.2	1.1	1.1	cytoskeletal adaptor, member of AP180 protein family, 3-prime end (by homology)		
CA3640	VPS24	-1.0	1.0	1.0	1.1	endosomal Vps protein complex subunit	YKL041w	orf19.2031
CA3600	SPC3	1.1	1.1	1.2	1.1	signal peptidase subunit (by homology)	YLR066w	orf19.4930
CA3635	IFA20	-1.0	1.1	1.3	1.1	unknown function		orf19.5139
CA2213	IPF16405	-1.0	-1.3	-1.1	1.1	similar to saccharomyces cerevisiae Rsm25p protein of	YIL093c	orf19.4751
CA4304	IPF6649	-1.0	-1.0	1.1	1.1	unknown function		orf19.6704
CA4240	NHP2	1.1	1.1	1.1	1.1	nucleolar rRNA processing protein (by homology)	YDL208w	orf19.526
CA5364	DCD1	1.1	1.0	1.0	1.1	deoxycytidylate deaminase (by homology)	YHR144c	orf19.7243
CA5312	IPF2165	1.1	1.0	1.1	1.1	unknown function	YGL231c	orf19.7183
CA1922	DIP52	1.1	1.1	1.1	1.1	Dicarboxylic amino acid permease (by homology)		orf19.2445
CA0853	IPF19640	-1.0	1.1	1.1	1.1	unknown function		orf19.9316
CA4104	IPF20157	-1.0	1.0	1.0	1.1	unknown function	YNL279w	orf19.669
CA2070	IPF6971.3	1.1	-1.0	-1.1	1.1	unknown function, 3-prime end		
CA5268	SEC18.3F	-1.0	-1.1	-1.0	1.1	vesicular fusion protein, 3-prime end (by homology)	YBR080c	orf19.4994
CA3325	IPF6890	1.0	-1.0	1.0	1.1	unknown function		orf19.2674
CA0804	BNA1	1.0	1.1	1.1	1.1	3-hydroxyanthranilic acid dioxygenase (by homology)	YJR025c	orf19.3515
CA0055	IPF12442	1.1	1.2	1.3	1.1	unknown function	YML052w	orf19.10917
CA3862	NSR1	1.2	1.1	1.1	1.1	nuclear localization sequence binding protein (by homol	YGR159c	orf19.6090
CA3777	IPF10432	1.0	1.1	1.0	1.1	unknown function	YEL044w	orf19.2889
CA0836	IPF12495.5F	-1.0	-1.1	1.0	1.1	unknown function, 5-prime end		orf19.9248
CA4855	IPF5830	-1.0	-1.0	-1.0	1.1	unknown function		orf19.3826
CA3314	IPF8812	-1.0	1.0	1.0	1.1	unknown function	YGR075c	orf19.2303
CA4384	DUR34	-1.0	1.0	1.1	1.1	Urea transport protein (by homology)		orf19.13122
CA2838	IPF8339	1.1	1.1	1.0	1.1	unknown function		orf19.4791
CA1165	IPF19902	-1.1	1.1	1.1	1.1	unknown function		orf19.10868
CA3564	IPF7817	-1.0	-1.0	1.0	1.1	putative NADH-dependent flavin oxidoreductase (by homology)		orf19.3131

CA0023	IPF6922	1.1	1.1	1.0	1.1	unknown function		orf19.3788
CA3521	IFA15	1.0	1.1	-1.0	1.1	unknown function		orf19.996
CA3889	TAD3	1.1	1.0	-1.0	1.1	tRNA-specific adenosine-34 deaminase subunit (by hon	YLR316c	orf19.5090
CA5122	IPF1308	-1.0	-1.0	-1.1	1.1	Similarity to ribosomal protein S13 (by homology)	YNL081c	orf19.6406
CA5807	RPS24	1.3	1.2	-1.1	1.1	ribosomal protein S24.e	YIL069c	orf19.5466
CA2275	BIO4	1.1	1.1	-1.0	1.1	dethiobiotin synthetase (by homology)	YNR057c	orf19.2590
CA0371	IPF19578	-1.0	-1.0	-1.0	1.1	unknown function		orf19.1087
CA1756	IPF14562	-1.0	-1.0	1.0	1.1	unknown function		orf19.5129
CA1595	IPF9544	1.2	1.0	1.2	1.1	unknown function	YNL156c	orf19.7905
CA2724	RPB7	1.3	1.1	1.2	1.1	DNA-directed RNA polymerase II,19KD subunit (by hon	YDR404c	orf19.10855
CA0259	SOL1	-1.2	-1.0	-1.0	1.1	multicopy suppressor of los1-1	YNR034w	orf19.1355
CA2864	IPF17234.3	1.1	1.0	1.1	1.1	unknown function, 3-prime end		orf19.1057
CA4734	TFA1	-1.0	-1.0	-1.1	1.1	Large subunit of transcription factor tfIIE	YKL028w	orf19.4851
CA0683	IPF14519	-1.0	1.0	1.0	1.1	unknown function		orf19.12172
CA0949	IPF10269	1.1	1.1	1.1	1.1	Gim complex component-like by homology	YNL153c	orf19.8859
CA1338	IPF5333	1.0	1.0	1.0	1.1	unknown function	YDR266c	orf19.10953
CA0246	F14452.REPEA	1.1	1.1	1.2	1.1	F1-ATPase epsilon subunit (by homology)		
CA3051	IPF13043	1.0	-1.0	1.1	1.1	unknown function	YGL050w	orf19.2408
CA5822	YRB1	-1.0	-1.1	-1.1	1.1	GTPase-activating protein (by homology)	YDR002w	orf19.7477
CA4902	SED5	1.0	-1.0	-1.1	1.1	Syntaxin (by homology)	YLR026c	orf19.6039
CA2083	IPF3384.5F	1.2	1.2	1.3	1.1	similar to Saccharomyces cerevisiae Gpi13p phosphory	YLL031c	orf19.832
CA4142	PRE4	-1.0	1.1	1.1	1.1	20S proteasome subunit(beta7) (by homology)	YFR050c	orf19.11705
CA5074	IPF3607	1.0	1.1	-1.0	1.1	putative serine/threonine protein kinase	YDR523c	orf19.3049
CA1913	ARC35	-1.2	-1.0	-1.1	1.1	subunit of the Arp2/3 complex involved in the control of	YNR035c	orf19.2437
CA4064	RPT1	-1.1	1.1	1.1	1.1	26S PROTEASE REGULATORY SUBUNIT 7 (by homo	YKL145w	orf19.441
CA1752	UBP14	-1.2	1.1	-1.0	1.1	Ubiquitin-specific protease (by homology)	YBR058c	orf19.1516
CA2104	IPF19939	1.1	1.0	-1.0	1.1	unknown function		orf19.9917
CA4689	IPF9020	1.0	1.2	1.1	1.1	unknown function		orf19.8495
CA2526	SEC20	-1.0	1.1	1.1	1.1	secretory pathway protein	YDR498c	orf19.5526
CA5308	PRE5	1.1	1.1	1.0	1.1	20S proteasome subunit alpha6 (by homology)	YMR314w	orf19.7178
CA3235	SNF8	-1.0	1.1	1.1	1.1	involved in glucose derepression (by homology)	YPL002c	orf19.6296
CA0866	IPF14775	1.0	1.0	-1.0	1.1	unknown function	YNR046w	orf19.3585
CA2914	IFA17.5F	-1.1	1.0	1.0	1.1	unknown function, 5-prime end		orf19.4512
CA1131	NAG2	1.0	1.1	1.2	1.1	N-acetyl-glucosamine-6-phosphate deacetylase		orf19.9704
CA4004	IPF4256	-1.0	-1.1	-1.1	1.1	unknown function		orf19.1632
CA4250	IPF4292	-1.0	1.0	1.0	1.1	bleomycin Hydrolase	YNL239w	orf19.539
CA1389	PLP2	-1.1	-1.1	1.2	1.1	Might regulate Ste4p in pheromone response (by homc	YOR281c	orf19.9338
CA0540	IPF10896	1.1	1.0	1.1	1.1	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 22K chain precursor (by homology)		orf19.2821
CA4187	IPF7524	1.0	1.0	1.0	1.1	unknown function	YLR065c	orf19.12003
CA0118	IPF16430.3	1.1	-1.1	-1.0	1.1	similar to Saccharomyces cerevisiae Qcr6p ubiquinol-cy	YFR033c	
CA1048	IPF15394	1.1	-1.0	1.0	1.1	unknown function	YDR469w	orf19.3899
CA4545	SSL1	-1.0	-1.0	1.1	1.1	TFIIH subunit (transcription initiation factor), factor B	YLR005w	orf19.1457
CA4938	IPF5166	-1.0	1.1	1.0	1.1	unknown function	YPL233w	orf19.6537
CA4641	IPF1505	1.0	1.1	1.2	1.1	similar to saccharomyces cerevisiae Kre6p glucan synthase subunit (by homology)		orf19.348
CA3841	IPF16640	1.0	1.1	1.0	1.1	unknown function		orf19.6601
CA3829	PPQ1	1.1	-1.0	1.1	1.1	phosphoprotein phosphatase (by homology)		orf19.5758
CA4756	LIP6	-1.0	1.1	1.2	1.1	Secretory lipase		orf19.4823
CA1190	CIP1	1.1	1.1	1.1	1.1	Cadmium induced protein (by homology)		orf19.7761
CA4654	IPF3101	-1.0	-1.0	-1.0	1.1	unknown function	YIL150c	orf19.4441

CA0172	IPF19154	-1.0	1.0	-1.0	1.1	unknown function		orf19.1126
CA2205	SEO2	1.0	1.0	1.0	1.1	suppressor of sulfoxyde ethionine resistance	YAL067c	orf19.8319
CA1250	IPF9626	1.0	1.1	1.1	1.1	unknown function		orf19.12424
CA4149	SMP3	1.0	1.1	1.1	1.1	Protein kinase C pathway protein	YOR149c	orf19.5792
CA0075	IFA24.3	1.0	1.0	1.0	1.1	unknown function, 3-prime end		orf19.9164
CA3784	IPF11229	1.0	-1.1	-1.1	1.1	similar to Saccharomyces cerevisiae Rrp7p involved in	YCL031c	orf19.5835
CA4499	IPF11316	-1.1	-1.0	1.1	1.1	unknown function	YNL129w	orf19.511
CA0459	HOL3	-1.0	-1.0	-1.0	1.1	member of major facilitator superfamily multidrug-resistance protein subfamily 1 (by h		orf19.2517
CA0788	IPF14107	1.1	1.1	1.0	1.1	unknown function		orf19.9985
CA3747	IPF10153	1.5	1.3	1.2	1.1	membrane transporter by homology	YOL084w	orf19.2170
CA0550	IPF14030	1.0	1.0	1.1	1.1	unknown function		orf19.851
CA5573	IPF2005	1.1	1.1	1.2	1.1	unknown function		
CA3793	IPF5701	1.1	1.0	1.1	1.1	unknown function	YER074wa	
CA3225	IPF9329	1.0	1.0	1.0	1.1	unknown function	YER128w	orf19.6286
CA4990	IPF2039	1.0	1.1	1.1	1.1	unknown function		orf19.5258
CA4719	DAL51	1.0	1.1	1.2	1.1	allantoate permease (by homology)	YJR152w	orf19.6956
CA3013	PET117	1.0	1.0	1.1	1.1	cytochrome c oxidase assembly factor (by homology)	YER058w	
CA1634	IPF10179	1.1	1.0	1.0	1.1	unknown function	YJR088c	orf19.11421
CA1584	IPF15824	1.0	-1.0	1.0	1.1	unknown function		orf19.6030
CA3786	UFD1	-1.1	1.2	1.1	1.1	Ubiquitin fusion degradation protein (by homology)	YGR048w	orf19.5833
CA5205	KEX1	-1.2	1.1	-1.0	1.1	Carboxypeptidase-alpha (by homology)	YGL203c	orf19.7020
CA1149	MET223	1.0	1.0	-1.0	1.1	protein ser/thr phosphatase (by homology)		orf19.99
CA3139	YHB3	-1.0	1.2	1.1	1.1	flavohemoglobin (by homology)		orf19.3710
CA1365	IPF11849	1.0	1.1	1.0	1.1	unknown function	YNL234w	orf19.4459
CA2558	RBT5	1.1	1.1	1.1	1.1	repressed by TUP1 protein 5		orf19.5636
CA1331	IPF11714	1.1	1.1	1.2	1.1	unknown function		
CA1148	CAN1	1.0	1.0	1.1	1.1	amino acid permease (by homology)		orf19.97
CA6041	RPO21	1.0	-1.0	-1.0	1.1	DNA-directed RNA polymerase II, 215 KD subunit (by h	YDL140c	orf19.7655
CA1651	RNH1.EXON2	1.1	1.2	1.2	1.1	Ribonuclease H, exon 2 (by homology)		orf19.5564
CA5603	IPF553	-1.0	1.1	1.1	1.1	unknown function	YLR001c	orf19.7096
CA2068	ARP1	1.1	1.0	1.1	1.1	centractin (by homology)	YHR129c	orf19.2641
CA5769	UBC12	-1.0	1.0	-1.1	1.1	E2 ubiquitin-conjugating enzyme (by homology)	YLR306w	orf19.5411
CA2363	IPF10590	1.0	1.1	-1.0	1.1	unknown function	YPR091c	orf19.1285
CA5018	IPF7558	-1.0	1.0	1.0	1.1	unknown function	YGR227w	orf19.6971
CA3938	IPF4764	1.1	1.2	1.1	1.1	unknown Function	YDR028c	orf19.9556
CA3873	IPF8825	1.0	1.0	-1.0	1.1	unknown function	YJR082c	orf19.396
CA6036	IPF585	1.1	-1.0	1.0	1.1	unknown function	YHR034c	orf19.7646
CA3082	IPF11627	-1.0	-1.0	1.0	1.1	unknown function		orf19.11627
CA3257	IFC1	-1.0	1.0	1.0	1.1	Unknown Function		orf19.3746
CA2836	ARG5,6	1.0	1.1	1.2	1.1	acetylglutamate kinase and acetylglutamyl-phosphate r	YER069w	orf19.4788
CA1417	IPF16126	1.2	1.1	1.4	1.1	similar to Saccharomyces cerevisiae Rpc19p DNA-dire	YNL113w	orf19.172
CA3391	PNP1	1.0	-1.0	1.0	1.1	Purine Nucleoside Phosphorylase (by homology)	YLR209c	orf19.7949
CA5399	KRE62.5F	-1.0	1.0	1.0	1.1	Glucan synthase subunit, 5-prime end (by homology)		orf19.942
CA2599	IPF11176	-1.0	-1.0	1.2	1.1	similar to Saccharomyces cerevisiae Mmt2p mitochond	YPL224c	orf19.52
CA0544	IPF3252	1.0	1.1	1.0	1.1	unknown function		orf19.2868
CA2784	IPF3810	1.2	-1.0	1.1	1.1	unknown function		orf19.287
CA0106	IPF16308	1.1	1.0	1.1	1.1	unknown function		orf19.11332
CA0850	IPF16671	1.1	1.0	1.2	1.1	unknown function		orf19.9312
CA2677	ATP14.EXON2	1.3	-1.0	-1.0	1.1	F1F0-ATPase complex, subunit h, exon 2 (by homology	YLR295c	

CA1851	SAP155	-1.0	1.0	1.1	1.1	Cell cycle protein, interacts with Sit4 (by homology)		orf19.642
CA4118	IPF11952	-1.3	-1.0	-1.3	1.1	similar to Saccharomyces cerevisiae Hos3p putative his	YPL116w	orf19.2772
CA5552	IPF5971	-1.0	1.1	1.1	1.1	unknown function		orf19.7316
CA2618	SNG2	1.0	1.1	1.1	1.1	drug transporter (by homology)		orf19.2812
CA1741	IPF12213	-1.0	-1.0	-1.1	1.1	unknown function		orf19.5057
CA1925	IPF18587	1.1	-1.0	1.0	1.1	putative methyltransferase (by homology)		orf19.8372
CA2258	IFR1	1.1	1.0	1.1	1.1	Unknown function		orf19.1763
CA3078	IPF19970	1.1	1.1	1.2	1.1	unknown function	YMR209c	orf19.4816
CA3108	IPF11826	1.1	1.1	1.1	1.1	unknown function	YOR228c	orf19.6550
CA1816	IPF7020	1.0	1.1	1.3	1.1	unknown function	YBR043c	orf19.136
CA5408	IPF1551	1.0	1.0	1.0	1.1	unknown function		orf19.952
CA0989	IPF11069	1.0	1.0	1.1	1.1	unknown function		orf19.1391
CA4753	IDH1.3	-1.1	1.0	-1.1	1.1	isocitrate dehydrogenase (NAD+) subunit1, mitochondri	YNL037c	orf19.4826
CA4825	IPF1205	-1.0	1.0	1.1	1.1	unknown function		orf19.2071
CA1653	STE23	-1.4	1.0	-1.2	1.1	protease involved in a-factor processing by homology	YLR389c	orf19.5561
CA4448	PHO85	1.1	1.1	1.2	1.1	Negative regulator of PHO system	YPL031c	orf19.6846
CA1660	DAP2	-1.0	-1.0	1.1	1.1	dipeptidyl aminopeptidase B (by homology)	YHR028c	orf19.4322
CA3123	RPL6.3	1.4	1.1	1.0	1.1	ribosomal protein, 3-prime end	YLR448w	
CA4020	IPF5324	-1.0	1.1	-1.0	1.1	putative transporter (by homology)		orf19.3444
CA0360	IPF2328	1.0	1.0	1.0	1.1	unknown function		orf19.8720
CA6142	IPF1879	1.1	-1.0	1.3	1.1	unknown function	YOR301w	orf19.5903
CA0711	VMA5	-1.4	1.1	-1.1	1.1	H+-ATPase V1 domain 42 KD subunit (by homology)	YKL080w	orf19.9712
CA4881	IPF1652	1.0	1.0	1.1	1.1	putative purine nucleoside permease (by homology)		orf19.6569
CA1494	IPF171	-1.0	-1.0	1.2	1.1	unknown function	YER113c	orf19.3228
CA4306	GYP7	-1.0	1.1	1.0	1.1	GTPase activating protein (by homology)	YDL234c	orf19.6706
CA0226	IPF16024	1.1	1.0	1.1	1.1	unknown function		orf19.1297
CA5555	SUC1	-1.0	1.0	1.0	1.1	Putative zinc finger protein Suc1	YFL052w	orf19.7319
CA3198	IPF3432	1.1	1.0	1.1	1.1	Unknown function		orf19.6177
CA5812	IPF2690.3F	1.0	1.1	1.2	1.1	unknown function, 3-prime end		orf19.5474
CA4619	IPF5756	-1.1	-1.0	-1.0	1.1	unknown function		orf19.3310
CA2553	IPF9096	1.1	-1.0	-1.0	1.1	probable mannosidase (by homology)		orf19.2838
CA2081	IPF9699	1.0	-1.0	-1.0	1.1	unknown function	YIR003w	orf19.4878
CA1158	IPF13275	-1.2	1.1	1.0	1.1	unknown function	YHR016c	orf19.4127
CA3965	IPF9375	-1.0	1.1	-1.0	1.1	unknown function		orf19.1426
CA3549	ARC40	1.1	-1.1	1.1	1.1	subunit of the Arp2/3 complex involved in the control of	YBR234c	orf19.3873
CA2044	IPF10668	1.0	1.0	-1.0	1.1	unknown function	YGR054w	orf19.10447
CA1206	HUB1	-1.1	-1.0	1.0	1.1	Ubiquitin-like modifier (by homology)	YNR032ca	
CA3696	IPF4868	-1.1	-1.1	-1.0	1.1	unknown function	YPR045c	orf19.13650
CA3709	IPF7880	-1.4	1.1	-1.1	1.1	unknown function	YNL297c	orf19.4939
CA4438	IPF13866	1.2	-1.0	1.1	1.1	unknown function		orf19.5157
CA5953	IPF3506	1.0	1.1	1.1	1.1	unknown function		orf19.6741
CA2000	IPF11796	1.0	1.1	1.1	1.1	unknown function	YJL021c	orf19.2791
CA3642	IPF4123	-1.1	1.0	1.1	1.1	unknown function		orf19.2033
CA2578	MMD1.3	1.6	-1.1	-1.2	1.1	Maintenance of mitochondrial DNA, 3-prime end (by hoı	YIL051c	
CA0803	IFL4	1.1	1.0	1.0	1.1	unknown function		orf19.3512
CA1687	IPF12275	-1.1	1.1	1.2	1.1	unknown function	YER140w	orf19.3658
CA5924	IPF2822	1.1	1.1	1.1	1.1	unknown function		orf19.6781
CA0654	IPF11550.3F	1.0	-1.1	1.0	1.1	Ca2+-transporting P-type ATPase, 3-prime end (by homology)		orf19.10084
CA0276	IPF15015	1.1	1.0	1.0	1.1	unknown function		orf19.13055

CA6081	IPF24	1.0	1.1	1.1	1.1	reductase (by homology)		orf19.5978
CA1773	VRP1	1.1	1.2	1.3	1.1	verprolin (by homology)	YLR337c	orf19.2190
CA1868	PF14501.3EOC	-1.0	1.0	-1.1	1.1	putative G-protein, -transducin type, 3-prime end (by ho	YBR281c	orf19.9992
CA5379	IPF5228.5	1.0	1.0	1.1	1.1	similar to Saccharomyces cerevisiae Sad1p snRNP ass	YFR005c	orf19.7265
CA5304	IPF2178	-1.0	1.0	1.0	1.1	unknown function		orf19.7173
CA0910	MRPL16	1.3	-1.0	-1.1	1.1	ribosomal protein	YBL038w	orf19.9569
CA5310	IPF2167	-1.1	1.0	-1.0	1.1	unknown function		orf19.7181
CA1187	QRI7	1.0	1.1	1.1	1.1	putative glycoprotease (by homology)	YKR038c	orf19.11267
CA0308	RHK1	1.0	-1.0	1.0	1.1	Mannosyltransferase (by homology)	YBL082c	orf19.8693
CA3783	IPF11226	1.0	1.0	1.0	1.1	unknown function	YMR289w	orf19.5837
CA5140	TIM10	1.2	1.2	1.1	1.1	Subunit of the Tim22-complex (by homology)	YHR004ca	
CA0369	IPF13675	1.0	1.0	1.0	1.1	unknown function		orf19.1656
CA4698	CDC25	1.1	1.0	1.2	1.1	cell division cycle protein	YLR310c	orf19.6926
CA1007	DLH1.3F	-1.0	1.0	1.1	1.1	meiotic recombination protein, 3-prime end	YER179w	orf19.3760
CA4963	IPF3919	-1.0	1.2	1.2	1.1	unknown function		orf19.6510
CA3249	GEF2	-1.0	1.0	1.4	1.1	Putative voltage-gated chloride channel protein (by homology)		orf19.11219
CA1235	IPF20079	1.1	1.0	1.1	1.1	unknown function	YMR074c	orf19.8332
CA4380	IPF12736	1.0	1.1	1.2	1.1	unknown function		orf19.5673
CA5877	IPF12082.3F	-1.0	1.1	1.0	1.1	bumetanide-sensitive Na-K-Cl cotransport protein, 3-prime end (by homology)		orf19.6832
CA4926	IPF1404	1.1	1.1	-1.0	1.1	unknown function		orf19.6065
CA2676	YHC1	-1.0	-1.0	1.0	1.1	SMALL NUCLEAR RIBONUCLEOPROTEIN C (by hom	YLR298c	orf19.5492
CA5221	MVP1.EXON1	-1.1	1.0	1.1	1.1	Required for vacuolar protein sorting, exon 1 (by homology)		orf19.7039
CA5519	RDH54	1.0	1.2	1.3	1.1	helicase required for mitotic diploid-specific recombinati	YBR073w	orf19.5367
CA2450	IPF2589	-1.1	1.0	1.1	1.1	unknown function		orf19.5508
CA5783	IPF1128	1.0	-1.1	-1.0	1.1	unknown function		orf19.5430
CA3403	IPF8650	-1.2	1.2	-1.1	1.1	RNA helicase (by homology)	YGR271w	orf19.3980
CA3845	IPF7944	-1.1	1.0	1.1	1.1	unknown function	YOR292c	orf19.6605
CA6124	ARG11	1.1	1.0	-1.0	1.1	mitochondrial amino acid transporter (by homology)	YOR130c	orf19.5926
CA0391	DDC1	1.0	1.0	1.0	1.1	DNA damage checkpoint protein, delays the cell cycle a	YPL194w	orf19.7875
CA0454	RPN6	-1.0	-1.1	-1.1	1.1	subunit of the regulatory particle of the proteasome (by	YDL097c	orf19.8879
CA2089	GNA1	-1.1	-1.0	1.0	1.1	Acetyltransferase	YFL017c ; Missing in array	orf19.837
CA0798	IPF13565	-1.0	1.0	-1.0	1.1	unknown function	YNL308c	orf19.9177
CA5514	IPF730	1.0	1.1	1.1	1.1	unknown function		orf19.5362
CA5071	IPF3597	1.2	1.1	1.3	1.1	similar to Saccharomyces cerevisiae Ald4p mitochondrial aldehyde dehydrogenase (b		orf19.3045
CA2877	TFB2	-1.0	1.1	1.1	1.1	Transcription/repair factor (by homology)	YPL122c	orf19.5846
CA4819	IPF1194	-1.1	1.2	-1.0	1.1	Similar to clathrin coat proteins	YHL019c	orf19.2078
CA0796	ALR1	1.0	-1.0	1.0	1.1	divalent cation transporter (by homology)	YOL130w	orf19.9175
CA3000	TSC1.5	1.1	1.1	1.1	1.1	3-ketosphinganine reductase, 5-prime end (by homolog	YBR265w	orf19.6131
CA4907	PSD1	-1.1	1.1	1.1	1.1	Phosphatidylserine decarboxylase 1 (by homology)	YNL169c	orf19.6045
CA1672	IPF5196	-1.1	-1.2	-1.0	1.1	unknown function		orf19.11094
CA2091	IPF3401	-1.0	1.1	1.2	1.1	unknown function	YLR143w	orf19.839
CA1827	IPF9520	1.1	1.1	1.1	1.1	unknown function		orf19.11740
CA2969	IPF19772	1.0	1.2	1.1	1.1	unknown function		orf19.5602
CA2242	IFQ1.5F	1.1	1.0	1.1	1.1	Unknown function, 5-prime end		orf19.4673
CA5846	IPF409	1.0	1.0	1.0	1.1	unknown function		orf19.7502
CA1012	PSD2.5F	1.0	1.1	1.1	1.1	phosphatidylserine decarboxylase 2, 5-prime end (by hc	YGR170w	orf19.11436
CA2097	IPF11489	1.1	1.1	1.0	1.1	unknown function	YKL108w	orf19.2389
CA3432	MRPL17	1.1	-1.0	1.2	1.1	ribosomal protein of the large subunit (YmL3	YNL252c	orf19.585
CA1120	IPF7666	1.0	1.0	-1.0	1.1	unknown function		orf19.4056

CA4565	VPS35	1.1	1.0	-1.0	1.1	Protein-sorting protein, vacuolar (by homology)	YJL154c	orf19.6875
CA0611	IPF17542	-1.1	1.0	-1.1	1.1	unknown function		orf19.13024
CA4935	VPS29	-1.0	1.1	-1.0	1.1	vacuolar protein sorting protein (by homology)	YHR012w	orf19.6076
CA4135	IPF20163	1.1	1.0	1.2	1.1	unknown function		orf19.4239
CA4778	IFJ1	-1.0	1.1	-1.0	1.1	Unknown function		orf19.4011
CA5196	IPF2338	-1.0	1.2	1.3	1.1	unknown function	YIL001w	orf19.7010
CA2992	RRS1	1.0	1.1	1.0	1.1	Regulator for ribosome synthesis (by homology)	YOR294w	orf19.6014
CA5277	CTA29.EXON1	1.1	1.0	1.1	1.1	Protein with putative transcription activation domain, exon 1		orf19.7127
CA4745	URA1	1.0	1.1	1.1	1.1	dihydroorotate dehydrogenase		orf19.4836
CA4833	IPF1216	-1.0	1.1	1.2	1.1	unknown function		orf19.2064
CA5733	IPF2873	1.0	1.0	1.0	1.1	unknown function		orf19.7443
CA0031	COX7	1.0	-1.0	1.0	1.1	Subunit VII of cytochrome c oxidase (by homology)	YMR256c	orf19.227
CA2276	HNM3	1.0	1.0	1.1	1.1	Choline permease (by homology)		orf19.2587
CA5921	IPF8930	1.0	-1.1	-1.2	1.1	unknown function		orf19.6784
CA5699	ALS7	1.1	1.1	1.2	1.1	agglutinin-like protein		orf19.7400
CA5782	IPF1127	1.0	-1.0	1.0	1.1	unknown function	YOR080w	orf19.5429
CA2771	RPB10	1.1	1.1	1.2	1.1	DNA-directed RNA polymerase II (by homology)	YOR210w	
CA5662	IPF1250	1.1	1.1	-1.0	1.1	Flavin-containing monooxygenase(by homology)		orf19.7364
CA5244	IPF3043	-1.0	-1.0	-1.0	1.1	unknown function		orf19.5019
CA5215	PPS1	1.0	1.1	1.0	1.1	protein tyrosine phosphatase (by homology)	YBR276c	orf19.7033
CA3447	YPT70	-1.0	1.0	1.1	1.1	GTP-binding protein (by homology)		orf19.2975
CA4759	IPF9655	-1.0	1.0	-1.0	1.1	unknown function		orf19.3988
CA4754	IPF11479	1.1	1.0	1.1	1.1	unknown function	YIL098c	orf19.4825
GSTTag		-1.0	-1.0	1.0	1.1			
CA5155	IPF995	1.1	-1.0	1.0	1.1	unknown function	YDR379ca	
CA2383	IPF18474	-1.0	1.1	1.1	1.1	unknown function		
CA3467	MNT2	1.0	-1.0	1.1	1.1	Alpha-1,2-mannosyltransferase (by homology)	YDR483w	orf19.1663
CA2778	MTR	-1.1	1.1	1.1	1.1	neutral amino acid permease-like by homology		orf19.278
CA2128	IPF4898	-1.1	1.0	-1.0	1.1	unknown function	YGR235c	orf19.415
CA5283	IPF1912	1.1	1.0	-1.2	1.1	putative catechol o-methyltransferase		orf19.7140
CA2887	IPF13631	-1.0	1.0	1.0	1.1	unknown function		orf19.2472
CA2013	CDC1	-1.1	1.2	1.1	1.1	Cell division control protein (by homology)	YDR182w	orf19.3083
CA0068	ARC18	1.2	1.1	1.1	1.1	subunit of the Arp2/3 complex involved in the control of	YLR370c	orf19.121
CA5248	IPF1828	-1.0	-1.1	-1.1	1.1	unknown function	YGL085w	orf19.5014
CA3594	IPF6076.3	1.0	1.0	1.1	1.1	unknown function, 3-prime end	YGL161c	orf19.4922
CA0657	IPF19877	1.0	1.1	1.0	1.1	putative cysteine synthase (by homology)	YGR012w	orf19.5574
CA1343	IPF14624	-1.1	-1.0	-1.1	1.1	unknown function		
CA2755	IFA12	1.1	1.1	1.1	1.1	unknown function		orf19.13064
CA0523	IPF4459	1.1	1.0	1.1	1.1	unknown function	YKR074w	orf19.11012
CA4750	IPF4477	-1.0	1.1	1.2	1.1	similar to Saccharomyces cerevisiae Doa1p involved in	YKL213c	orf19.4829
CA0170	IPF15959	-1.0	1.0	-1.0	1.1	unknown function		orf19.1105
CA4886	IPF1634	1.1	1.0	1.1	1.1	unknown function		orf19.6578
CA0716	DOG2	-1.0	1.2	1.1	1.1	2-deoxyglucose-6-phosphate phosphatase (by homolog	YHR044c	orf19.3392
CA2266	HEM1	-1.0	1.1	1.0	1.1	5-aminolevulinic acid synthase	YDR232w	orf19.10132
CA1161	GRX3	1.1	1.0	1.2	1.1	glutaredoxin-like protein	YDR098c	orf19.2727
CA5404	MET14	1.0	1.1	1.0	1.1	Adenylylsulfate kinase (by homology)	YKL001c	orf19.946
CA1812	IPF13879	1.0	1.1	1.0	1.1	unknown function		orf19.1120
CA0842	IPF15633	-1.1	1.0	-1.0	1.1	similar to Saccharomyces cerevisiae Bst1p egative regu	YFL025c	orf19.1053
CA2941	CVB1	-1.0	1.0	1.0	1.1	vacuole biogenesis component		orf19.1970

CA3743	IPF19998	1.0	1.1	1.2	1.1	unknown function	YNR074c	orf19.2175
CA0491	IPF18966	1.1	1.0	1.1	1.1	unknown function		
CA2596	IPF19546	1.4	-1.4	-1.0	1.1	unknown function	YOL002c	orf19.55
CA2133	IPF5866	-1.1	1.1	1.2	1.1	unknown function		orf19.5213
CA0212	IPF4325	1.0	1.1	1.1	1.1	unknown function		orf19.12969
CA3370	IPF4674	1.1	1.0	1.1	1.1	unknown Function	YIL087c	orf19.1852
CA2337	IPF13379	-1.0	-1.0	1.0	1.1	unknown function	YGR031w	orf19.2352
CA1902	OPT1	-1.0	1.1	1.1	1.1	oligopeptide transporter	YJL212c	orf19.2602
CA0447	IPF14275	-1.1	1.0	1.0	1.1	Probable ADP-ribosylation factors (by homology)	YPL051w	orf19.2297
CA1488	IPF17402	1.4	1.1	1.4	1.1	unknown function	YJL062w	orf19.4064
CA0944	IPF10280	1.0	1.0	1.0	1.1	unknown function		orf19.8852
CA2870	OPT2.53F	-1.0	1.0	1.0	1.1	Oligopeptide transporter, internal fragment (by homology)		
CA0677	IPF13095	-1.1	-1.1	-1.1	1.1	unknown function	YGL212w	orf19.8773
CA2617	IPF3539	1.1	-1.0	-1.0	1.1	unknown function	Missing in array	orf19.2813
CA2909	IPF11424	-1.1	-1.1	-1.1	1.1	unknown function	YPL150w	orf19.4518
CA2584	IPF9440	1.2	1.1	-1.0	1.1	similar to Saccharomyces cerevisiae Fmn1p riboflavin k	YDR236c	orf19.4373
CA2808	IPF11966	1.3	1.1	1.1	1.1	unknown function	YOR021c	orf19.5783
CA0620	IPF17998	-1.0	1.0	1.0	1.1	unknown function		orf19.3147
CA3805	IPF12403	1.0	1.1	1.2	1.1	unknown function	YDR415c	orf19.2484
CA4930	IPF8381	-1.2	1.0	1.1	1.1	similar to Saccharomyces cerevisiae Mdm20p involved	YOL076w	orf19.6071
CA3036	IPF13443	-1.0	1.1	1.1	1.1	unknown function		orf19.211
CA0340	IPF19859	1.1	1.1	1.0	1.1	unknown function		orf19.3375
CA1302	FCA1.3	1.1	1.0	1.1	1.1	cytosine deaminase, 3-prime end	YPR062w	
CA5554	IPF1960.5F	-1.1	1.1	1.0	1.1	putative transcriptional activator, 5-prime end		orf19.7318
CA2628	SIR22	1.0	-1.0	1.0	1.1	canal regulatory protein (by homology)	YOL068c	orf19.12225
CA3069	IPF6117	-1.0	1.1	1.2	1.1	unknown function	YMR266w	orf19.4805
CA4298	TIM9	1.1	1.1	1.1	1.1	Mitochondrial inner membrane translocase (by homolog	YEL020wa	orf19.6696
CA0600	MSN5.5F	-1.1	1.4	1.4	1.1	Importin-beta family member required for nuclear expor	YDR335w	orf19.2666
CA5984	CUS1	-1.1	1.0	1.0	1.1	spliceosome associated protein (by homology)	YMR240c	orf19.7581
CA4608	CCH1	-1.2	1.1	1.3	1.1	Calcium channel protein (by homology)	YGR217w	orf19.3298
CA2509	IPF1471	1.1	1.0	1.1	1.1	aminotriazole resistance protein (by homology)	YOR378w	orf19.304
CA3420	SMX4	1.1	1.1	1.0	1.1	U6 snRNA-associated Sm-like protein (by homology)	YLR438ca	
CA1619	IPF2067	1.1	-1.0	1.2	1.1	Required for mannosylation of sphingolipids (by homolo	YPL057c	orf19.11558
CA0076	IPF8866	1.2	1.1	1.2	1.1	unknown function		orf19.4906
CA5130	IFH2	1.0	1.0	-1.1	1.1	Dioxygenase (by homology)		orf19.13756
CA5405	MRP17	1.0	1.0	-1.0	1.1	Mitochondrial ribosomal protein (by homology)	YKL003c	orf19.947
CA3355	IPF11277	1.0	1.0	1.1	1.1	unknown function		orf19.9498
CA4451	ELC1	1.1	-1.0	1.0	1.1	Transcription elongation factor (by homology)	YPL046c	orf19.6849
CA3392	SEC13	-1.0	1.0	-1.1	1.1	Protein transport protein	YLR208w	orf19.316
CA2078	IPF13352	1.0	1.1	1.0	1.1	unknown function		orf19.4873
CA6083	IPF26	1.0	-1.0	1.0	1.1	unknown function	YPR152c	orf19.5976
CA3134	F11499.REPEA	1.0	1.1	1.0	1.1	unknown function		orf19.1365
CA1835	CRH12	-1.0	-1.0	1.0	1.1	Cell wall protein (by homology)		orf19.3966
CA2230	IPF10936	1.0	-1.1	1.0	1.1	unknown function		orf19.3928
CA4099	IPF3986	1.1	1.0	1.1	1.1	unknown function	YLR186w	orf19.665
CA1677	GTR1	1.0	1.0	1.0	1.1	GTP-binding protein by homology	YML121w	orf19.3617
CA0545	IPF3251	1.0	-1.0	-1.1	1.1	unknown function		orf19.2869
CA3506	IFA5	1.0	1.1	1.1	1.1	unknown function		orf19.6353
CA5198	LPA4	1.4	1.0	-1.1	1.1	Similar to ribosomal protein S16, mitochondrial (by hom	YPL013c	orf19.7012

CA1893	TIM13	1.0	1.1	1.1	1.1	subunit of mitochondrial protein import machinery-like b	YGR181w	orf19.2754
CA3088	IPF9826	-1.2	-1.1	1.1	1.1	unknown function	YLR256w	orf19.11621
CA4277	BTS1	-1.1	1.0	-1.0	1.1	Geranylgeranyl diphosphate synthase (by homology)	YPL069c	orf19.6674
CA1160	IPF10262	-1.0	1.1	1.0	1.1	unknown function	YKL051w	orf19.2726
CA4319	RPN10	1.0	1.1	1.1	1.1	Protein degradation (by homology)	YHR200w	orf19.4102
CA5429	CDC27	-1.0	1.1	-1.0	1.1	subunit of anaphase-promoting complex (by homology)	YBL084c	orf19.3231
CA2594	IPF12824	-1.0	1.0	1.0	1.1	unknown function	YJL072c	orf19.57
CA5644	IPF447	-1.0	1.0	1.0	1.1	unknown function	YNL110c	orf19.7050
CA3816	IPF4017	1.0	1.1	1.0	1.1	unknown function		orf19.2500
CA0305	INO80	-1.1	-1.0	-1.1	1.1	DNA helicase (by homology)	YGL150c	orf19.1734
CA0882	PHR3	1.1	1.0	1.1	1.1	surface glycoprotein (by homology)	YOL132w	orf19.8010
NAD1		1.0	1.0	1.0	1.1			
CA1888	IPF18594	1.0	1.0	1.1	1.1	unknown function		orf19.9748
CA3397	IPF13618	1.1	1.0	1.0	1.1	unknown function	YMR292w	orf19.3972
CA3020	IPF15492	1.1	1.0	1.0	1.1	unknown function		orf19.3908
CA0812	IPF3348	1.1	1.1	1.2	1.1	unknown function		orf19.1917
CA1624	IPF10055	1.0	1.1	1.2	1.1	unknown function		orf19.467
CA3779	IPF11221	1.0	1.0	1.0	1.1	unknown function		orf19.5841
CA1844	IFL5.3	1.0	1.0	-1.0	1.1	unknown function, 3-prime end		orf19.654
CA0293	IPF6624	1.0	1.1	1.1	1.1	unknown function	YDL222c	orf19.6489
CA2964	IPF13176.3	1.1	1.0	1.0	1.1	ornithine carbamoyltransferase, 3-prime end (by homol	YJL088w	orf19.5610
CA5361	NPL3	-1.1	1.2	1.2	1.1	nucleolar shuttling protein with an RNA recognition moti	YDR432w	orf19.7238
CA4533	COX4	1.2	1.1	1.3	1.1	cytochrome-c oxidase (by homology)	YGL187c	orf19.1471
CA0900	IPF12031	1.1	1.2	1.2	1.1	unknown function	YNR027w	orf19.3411
CA0745	MTF1	-1.1	-1.1	-1.0	1.1	RNA polymerase specific factor, mitochondrial (by hom	YMR228w	orf19.9104
CA4703	CLP1	-1.1	-1.1	1.0	1.1	probable cleaveage/polyadenylation factor	YOR250c	orf19.6931
CA0383	IPF16028	-1.1	1.0	1.2	1.1	unknown function		orf19.1841
CA6089	RDI1	1.2	-1.0	-1.0	1.1	Rho GDP dissociation inhibitor (by homology)	YDL135c	orf19.5968
CA5081	COQ6	-1.2	-1.0	1.0	1.1	monooxygenase (by homology)	YGR255c	orf19.3058
CA0873	BUL1	-1.3	-1.0	-1.2	1.1	Ubiquitin ligase binding protein	YMR275c	orf19.12099
CA0655	IPF11560.5F	1.1	1.1	1.1	1.1	Ca2+-transporting P-type ATPase, 5-prime end (by homology)		orf19.10085
CA5331	DUR33	-1.0	1.1	1.1	1.1	Urea transport protein (by homology)		orf19.7205
CA4254	IPF18234.3	-1.0	1.0	1.2	1.1	Unknown Function, 3-prime end		
CA2822	IPF14550	1.0	1.0	1.1	1.1	unknown function		orf19.1314
CA5610	PMR1	1.1	1.0	1.1	1.1	calcium/mangenease P-type ATPase	YGL167c	orf19.7089
CA5982	IPF915	1.0	1.1	-1.0	1.1	unknown function	YDR057w	orf19.7578
CA0178	CDC6	-1.0	1.0	1.1	1.1	Cell division control protein	YJL194w	orf19.12707
CA3910	IPF3293	-1.1	1.0	-1.0	1.1	unknown function	YBR163w	orf19.4392
CA1437	IPF7163	1.1	1.1	1.1	1.1	unknown function		orf19.1200
CA0326	IPF15220	1.0	-1.0	1.1	1.1	Unknown function	Missing in array	orf19.3780
CA0794	IPF15639	1.0	-1.0	1.0	1.1	unknown function	YCL038c	orf19.552
CA2247	IPF7404	1.1	-1.0	1.0	1.1	unknown function		orf19.12135
CA5906	IPF5949	-1.0	1.0	1.1	1.1	unknown function	YPL188w	orf19.6800
CA3875	IPF14430	-1.1	-1.1	-1.0	1.1	putative kynureninase (by homology)	YLR231c	orf19.8024
CA2316	IPF14542	-1.0	1.0	1.0	1.1	unknown function		orf19.8963
CA1426	ALS11.3F	1.1	1.1	1.1	1.1	agglutinin-like protein, 3-prime end		orf19.13168
CA1183	IPF14805	1.1	-1.0	1.1	1.1	acetyl-coenzyme A transporter(by homology)	YBR220c	orf19.11263
CA2241	IFQ1.3F	1.1	1.0	1.1	1.1	Unknown function, 3-prime end		orf19.4674
CA5656	IPF14683	-1.0	-1.1	-1.1	1.1	unknown function	YNL026w	orf19.7358

CA4646	IPF1495	1.1	1.1	1.0	1.1	unknown function		orf19.353
CA2812	TEM1	1.0	1.0	1.1	1.1	GTP-binding protein of the RAS superfamily	YML064c	orf19.10519
CA5238	MET3	-1.0	1.1	1.3	1.1	ATP sulfurylase	YJR010w	orf19.5025
CA2829	IFA7	1.0	1.1	1.1	1.1	unknown function		orf19.1326
CA0263	GLK1	-1.2	1.0	1.0	1.1	aldohexose specific glucokinase (by homology)	YCL040w	orf19.1408
CA1184	IPF14802	1.1	-1.1	1.3	1.1	unknown function	YCL057ca	
CA3768	IPF13467	1.0	1.0	-1.0	1.1	Putative peroxisomal 2,4-dienoyl-CoA reductase (by homology)		orf19.2899
CA3712	IPF7891	-1.0	1.1	-1.0	1.1	unknown function		orf19.4936
CA0777	IPF11777	-1.1	1.2	1.0	1.1	unknown function		orf19.4778
4511.1		-1.0	-1.1	-1.1	1.1			
CA0227	PHO23	-1.1	-1.1	-1.0	1.1	Involved in transcriptional regulation of PHO5 (by homo	YNL097c	orf19.9328
CA0517	HEM13	1.1	-1.0	1.0	1.1	by homology S. cerev.: coproporphyrinogen III oxidase	YDR044w ; Missing in array	orf19.2803
CA1502	RPS7A	-1.1	-1.1	-1.0	1.1	ribosomal protein (by homology)	YOR096w	orf19.9267
CA4538	IPF20018	1.2	1.3	1.3	1.1	unknown function		orf19.1465
CA0015	PHO87.5EOC	-1.0	1.1	1.0	1.1	Member of the phosphate permease family, 5-prime end (by homology)		orf19.9990
CA0045	IPF8985.5EOC	-1.0	1.0	1.1	1.1	unknown function, 5-prime end		orf19.1368
CA3853	MVD1.3	1.1	1.1	1.2	1.1	mevalonate pyrophosphate decarboxylase, 3-prime end	YNR043w	orf19.6105
CA3481	IPF3223	1.0	-1.0	1.1	1.1	unknown function		
CA0129	IPF10495	1.1	-1.0	-1.0	1.1	unknown function	YIL108w	orf19.246
CA0359	IPF17488.3F	-1.0	1.0	-1.0	1.1	unknown function, 3-prime end		orf19.1820
CA4792	HIS1	1.1	1.1	1.1	1.1	ATP phosphoribosyltransferase	YER055c	orf19.4026
CA5532	ARP2	-1.0	1.1	1.2	1.1	actin-like protein (by homology)	YDL029w	orf19.7292
CA0419	IPF19864	-1.0	-1.1	-1.1	1.1	unknown function	YGR080w	orf19.2228
CA2635	CKB22	1.0	1.1	1.1	1.1	Casein kinase II, beta subunit (by homology)	YOR039w	orf19.4297
CA0623	MSS4.3	-1.1	-1.1	1.1	1.1	phosphatidylinositol-4-phosphate 5-kinase, 3-prime end	YDR208w	orf19.3153
CA2749	IPF11465	-1.0	-1.1	-1.0	1.1	unknown function	YNL261w	orf19.2369
CA4535	CDC55	1.0	1.1	1.1	1.1	B subunit of protein phosphatase 2A (by homology)	YGL190c	orf19.1468
CA1107	IPF11271	1.1	1.0	1.1	1.1	by homology to S. cerevisiae: ATP19 subunit K of the	YOL077wa	
CA4828	IPF1209	-1.1	1.0	1.0	1.1	unknown function		orf19.2068
CA4162	MET1	1.0	-1.0	1.0	1.1	siroheme synthase (by homology)	YKR069w	orf19.5811
CA3445	IPF7325	1.0	-1.0	1.1	1.1	unknown function		orf19.2978
CA4219	SDS22	1.1	1.1	1.0	1.1	regulatory subunit for the mitotic function of type I protei	YKL193c	orf19.820
CA5028	IPF2998	1.0	1.0	1.0	1.1	unknown function	YJL131c	orf19.6982
CA4715	DPL1	1.1	1.1	1.1	1.1	dihydrosphingosine phosphate lyase (by homology)	YDR294c	orf19.6951
CA5043	FRP4	-1.0	1.0	1.0	1.1	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathway		orf19.6997
CA5477	IPF18101	1.0	1.1	1.1	1.1	unknown function		orf19.12766
CA4374	IPF5288	1.0	1.1	1.2	1.1	Unknown function	YMR041c	orf19.5665
CA5465	IPF285.3F	1.1	1.0	1.0	1.1	unknown function, 3-prime end		orf19.3274
CA2055	SAP4	1.0	-1.0	1.0	1.1	secreted aspartyl proteinase		orf19.5716
CA0016	CAN5.5	1.0	-1.0	-1.0	1.1	basic-amino-acid permease, 5-prime end (by homology)		
CA4686	IPF9015	-1.0	1.1	1.1	1.1	unknown function	YHR098c	orf19.880
CA3067	IPF15811	-1.0	1.0	1.1	1.1	unknown function		orf19.11756
CA2533	IPF12790	-1.1	-1.1	-1.0	1.1	inositol polyphosphate 5-phosphatase (by homology)	YOL065c	orf19.3180
CA4456	ATP1.EXON2	1.1	1.0	1.0	1.1	F1F0-ATPase complex, F1 alpha subunit, exon 2		
CA0028	IPF15345	1.0	1.0	-1.0	1.1	peptidyl-tRNA-hydrolase (by homology)		orf19.1502
CA2227	EBP7	1.1	1.1	1.1	1.1	NADPH DEHYDROGENASE by homology		orf19.5816
CA5036	CYP52	1.0	1.1	1.0	1.1	Peptidyl-prolyl cis-trans isomerase D (by homology)		orf19.6990
CA0947	CFL3	-1.0	1.0	1.1	1.1	ferric reductase-like protein		orf19.1270
CA3037	IPF13442	-1.0	1.0	1.1	1.1	unknown function	YPL066w	orf19.210

CA0291	IPF13328	1.0	-1.1	1.0	1.1	unknown function	YPL041c	orf19.1592
CA4343	IPF3630	1.0	1.1	1.1	1.0	unknown function	YHR049w	orf19.6717
CA2776	IPF10124	1.0	1.0	1.0	1.0	Alcohol acetyltransferase (by homology)	YGR212w	orf19.276
CA6067	DYN1	-1.0	1.2	1.2	1.0	dynein heavy chain, cytosolic (by homology)	YKR054c ; Missing in array	orf19.5999
CA0888	BET1	1.1	1.1	1.1	1.0	involved in ER-Golgi transport (by homology)	YIL004c	orf19.1386
CA3232	IPF17727.3	1.0	1.1	1.1	1.0	unknown function, 3-prime end		
CA3739	RPS10.3	1.4	-1.1	-1.1	1.0	ribosomal protein, 3-prime end (by homology)	YOR293w	
HumanG3PDH		1.0	-1.0	1.1	1.0			
CA2610	CDC11	-1.0	-1.0	1.0	1.0	septin by homology	YJR076c	orf19.5691
CA5722	IPF2446	1.0	1.0	1.1	1.0	unknown function	YML018c	orf19.7427
CA2352	FMT1	-1.0	1.0	1.1	1.0	Methionyl-tRNA Transformylase (by homology)	YBL013w	orf19.4418
CA0289	IPF13333	1.0	1.0	-1.0	1.0	unknown function		orf19.1590
CA1126	ECM18.3EOC	-1.0	-1.1	-1.1	1.0	cell wall biogenesis, 3-prime end (by homology)		orf19.3607
CA4604	MBF1	1.2	1.0	1.1	1.0	Multiprotein bridging factor mediates GCN4-dependent	YOR298ca	orf19.3294
CA2265	CMK2	-1.1	-1.1	-1.1	1.0	Ca2+/calmodulin-dependent ser/thr protein kinase, type	YOL016c	orf19.1754
CA2036	MSP1	1.0	-1.0	1.0	1.0	40 kDa putative membrane-spanning ATPase	YGR028w	orf19.4362
CA2954	IPF10685	-1.0	1.0	1.0	1.0	unknown function		orf19.5856
CA3430	IPF6382	1.0	-1.0	1.0	1.0	unknown function	YNL253w	orf19.587
CA2606	IPF5466	-1.0	1.0	1.0	1.0	unknown function	YHR140w	orf19.5683
CA4553	CYB1	-1.1	1.1	-1.0	1.0	G2/Mitotic-specific cyclin	YPR119w	orf19.1446
CA1537	IPF17483	1.0	1.1	1.1	1.0	unknown function		orf19.450
CA3379	IPF8350	1.1	1.1	-1.0	1.0	putative methyltransferase (by homology)	YDR140w	orf19.331
CA1947	IPF10637	1.0	1.0	-1.0	1.0	starvation protein -like (by homology)		orf19.12204
CA3643	IPF4124	1.0	-1.0	-1.0	1.0	unknown function	Missing in array	orf19.2034
CA5996	IPF673	1.0	-1.0	1.1	1.0	unknown function		orf19.7596
CA1664	ERV1.3	1.1	1.1	1.0	1.0	Mitochondrial biogenesis and regulation of cell cycle, 3-	YGR029w	
CA1996	SEC1	1.1	1.1	1.0	1.0	transport protein	YDR164c	orf19.6479
CA6020	SPT3	-1.0	-1.0	1.0	1.0	transcription factor	YDR392w	orf19.7622
CA2234	IPF10922	1.0	1.0	1.0	1.0	unknown function		orf19.3923
CA2588	IPF15098	1.1	1.0	1.1	1.0	Unknown function		orf19.4376
CA3552	IPF13231	1.0	1.1	1.1	1.0	unknown function		orf19.3877
CA5645	CYB5	1.6	-1.2	1.2	1.0	Cytochrome b5 (by homology)	YNL111c	orf19.7049
CA0252	SBP1.5EOC	-1.1	-1.0	1.3	1.0	RNA binding protein-like, 5-prime end (by homology)		orf19.13276
ATP6		1.0	-1.0	-1.0	1.0			
CA1328	RRP4	1.1	1.0	1.0	1.0	3 ->5 exoribonuclease required for 3 end formation of 5.8S rRNA (by homology)		orf19.1304
CA4973	IPF4703	1.1	1.0	1.1	1.0	unknown Function	YPR100w	orf19.5279
NAD4		1.0	-1.1	-1.0	1.0			
CA1534	MAP2	-1.1	-1.0	1.1	1.0	methionine aminopeptidase (by homology)	YBL091c	orf19.1214
CA5176	IPF6045	-1.0	-1.0	-1.0	1.0	unknown function	YPR049c	orf19.4614
CA5871	PIF2	1.0	1.1	1.4	1.0	DNA helicase (by homology)	YHR031c	orf19.7538
CA0845	IPF16314	-1.1	-1.2	-1.3	1.0	unknown function		orf19.7896
CA5337	APL1	-1.0	1.0	1.1	1.0	AP-2 complex subunit, beta2-adaptin (by homology)	YJR005w	orf19.7212
CA2898	IPF15646	1.0	1.0	1.1	1.0	putative ATP-dependent RNA helicase (by homology)	YGL064c	orf19.3481
CA2919	IFA18.3	1.0	1.0	1.1	1.0	unknown function, 3-prime end		orf19.4507
CA5374	DDI1	1.0	1.1	1.3	1.0	Response to DNA alkylation by homology	YER143w	orf19.7258
CA5818	ARG1	1.1	1.1	1.2	1.0	argininosuccinate synthetase (by homology)	YOL058w	orf19.7469
CA4816	IPF1183	-1.0	1.1	-1.0	1.0	putative aspartyl protease (by homology)		orf19.2082
CA5253	KEL3	-1.0	-1.0	-1.0	1.0	Kelch-repeat protein	YPL263c	orf19.5009
CA4586	GCN3	1.0	1.0	1.1	1.0	Translation initiation factor eIF2B alpha subunit (by hom	YKR026c	orf19.6904

CA5965	IPF961	1.0	-1.0	1.3	1.0	drug resistance protein (by homology)		orf19.7554
CA1519	RIM20	-1.1	-1.0	-1.0	1.0	Rim101 activating protein	YOR275c	orf19.4800
CA3662	IPF17021	-1.1	-1.0	-1.0	1.0	unknown function		orf19.6464
CA4814	SAS2	1.1	1.1	1.1	1.0	Zinc finger protein involved in silencing (by homology)	YMR127c	orf19.2087
CA4742	SHY1	1.1	-1.1	1.1	1.0	SURF homologue protein (by homology)	YGR112w	orf19.4841
CA1350	MCM2	-1.0	-1.0	-1.1	1.0	replication licensing factor (by homology)	YBL023c	orf19.4354
CA1147	KAP95	1.1	-1.0	1.2	1.0	karyopherin-beta protein (by homology)	YLR347c	orf19.11165
CA5553	IPF1960.3F	-1.0	1.1	-1.0	1.0	putative transcriptional activator, 3-prime end		orf19.7317
CA0421	IPF9047	-1.0	1.1	-1.0	1.0	unknown function	YPR094w	orf19.2230
CA0619	IPF18924	-1.1	-1.0	-1.0	1.0	unknown function		orf19.3146
CA2079	MNN3	-1.2	1.0	-1.0	1.0	Golgi alpha-1,2-mannosyltransferase (by homology)		orf19.4874
CA3505	IPF11372	1.0	-1.0	-1.0	1.0	unknown function		orf19.6351
CA0931	IPF3748	1.0	1.0	1.1	1.0	unknown function		orf19.562
CA0150	CDC123	-1.1	1.1	1.3	1.0	similar to Saccharomyces cerevisiae Cdc123p cell cycle	YLR215c	orf19.10236
CA3345	IPF13357	1.0	1.0	1.1	1.0	unknown function	YDR362c	orf19.2325
CA1290	IPF16212	-1.0	1.1	1.1	1.0	unknown function	YMR311c	orf19.2710
CA5360	IPF839	1.1	1.1	1.2	1.0	unknown function	YDR428c	orf19.7237
CA5129	ATS1	1.1	1.0	1.1	1.0	similar to Saccharomyces cerevisiae Ats1p suppressor	YAL020c	orf19.13757
CA3269	IPF12221	1.0	1.0	1.0	1.0	unknown function		orf19.6302
CA3668	DPP3	1.1	1.0	1.1	1.0	Diacylglycerol Pyrophosphate Phosphatase by homolog	YDR284c	orf19.6459
CA5855	ALK3	1.0	1.1	1.1	1.0	n-alkane inducible cytochrome P-450 (by homology)		orf19.7512
CA0142	CSL4	1.1	1.0	1.1	1.0	Involved in kinetochore-related function (by homology)	YNL232w	orf19.1026
CA4460	NSP49.5F	1.1	1.1	1.1	1.0	nuclear pore protein, 5-prime end (by homology)		orf19.6857
CA6050	IPF4939	1.0	1.0	1.1	1.0	similar to Saccharomyces cerevisiae Seo1p suppressor of sulfoxyde ethionine resista		orf19.7666
CA0860	IPF17272	-1.0	1.0	1.1	1.0	unknown function		orf19.3522
CA2476	IFF5	-1.0	-1.0	-1.0	1.0	unknown function		orf19.10397
CA3655	POT13	-1.1	1.2	1.1	1.0	Acetyl-CoA C-acyltransferase, peroxisomal (by homology)		orf19.2046
CA4282	IPF2319	-1.2	-1.0	-1.0	1.0	unknown function		orf19.6680
CA5394	IPF9400	1.1	1.0	1.0	1.0	unknown function		orf19.937
CA2850	CDC50	-1.0	-1.0	-1.0	1.0	cell division cycle mutant (by homology)	YCR094w	orf19.5735
CA4487	IPF4039	-1.0	1.0	-1.1	1.0	similar to Saccharomyces cerevisiae Nam8p recombina	YHR086w	orf19.1876
CA4180	EXG2	1.1	1.0	-1.0	1.0	glucan 1,3-beta-glucosidase-like by homology		orf19.2952
CA0718	IPF9782	-1.0	-1.1	1.0	1.0	unknown function	YPL060w	orf19.3455
CA4241	IPF8177	-1.0	-1.0	-1.0	1.0	unknown function		orf19.527
CA2891	IFS4	-1.0	-1.0	-1.0	1.0	Pirin protein (by homology)		orf19.2467
CA4592	IPF2215	1.1	1.0	-1.0	1.0	unknown function	YMR112c	orf19.6909
CA1234	IPF18732	-1.0	1.0	1.1	1.0	histidine-rich glycoprotein precursor (by homology)		orf19.8330
CA2142	MRPL33	1.0	1.1	1.0	1.0	ribosomal protein of the large subunit, mitochondrial (by	YMR286w	
CA2760	IPF13790	1.0	1.0	-1.1	1.0	Unknown function		orf19.13070
CA5177	IPF11101	1.0	1.0	1.1	1.0	Weak similarity to C. cerevisiae hypothetical protein (by	YBR095c	orf19.4615
CA4924	UBP6.3	-1.1	1.1	-1.0	1.0	Ubiquitin-specific protease, 3-prime end (by homology)	YFR010w	orf19.6063
CA4205	IFA10	1.0	1.1	1.1	1.0	unknown function		orf19.12024
CA4278	IPF2310	-1.0	-1.0	-1.1	1.0	unknown function		orf19.6675
CA5080	IPF9268.3	-1.0	1.1	1.1	1.0	similar to Saccharomyces cerevisiae Srb4p DNA-directe	YER022w	orf19.3055
CA3038	IPF13438	1.1	1.1	1.2	1.0	unknown function	YIL049w	orf19.209
CA2818	RPL13	1.3	-1.1	-1.2	1.0	Ribosomal protein	YDL082w	orf19.2994
CA2801	URA3	1.0	1.0	1.0	1.0	orotidine-5 -monophosphate decarboxylase [Candida al	YEL021w	orf19.1716
CA1559	IPF16533	1.0	1.0	1.0	1.0	unknown function		orf19.1708
CA2968	BMR1	1.0	1.1	1.0	1.0	benomyl/methothrexate resistance protein (by homolog	YBR008c	orf19.5604

CA1205	SSK2	1.1	1.1	1.0	1.0	MAP kinase kinase kinase of the high osmolarity	YNR031c	orf19.11257
CA4034	HSP31	1.0	1.1	1.1	1.0	heat shock protein (by homology)		orf19.11148
CA5757	IPF1067	-1.0	-1.1	-1.0	1.0	Putative glutamate decarboxylase (by homology)		orf19.5393
CA3128	IPF8914	1.0	1.1	1.0	1.0	unknown function	YNL213c	orf19.1360
CA2544	IPF16924	1.0	1.1	1.1	1.0	unknown function	YNL149c	orf19.2829
CA5109	UBC9	1.0	1.2	1.1	1.0	E2 ubiquitin-conjugating enzyme (by homology)	YDL064w	orf19.6424
CA1903	IPF2754	1.1	1.0	1.0	1.0	unknown function		
CA0546	IPF3250	1.0	1.1	1.0	1.0	unknown function		orf19.2870
CA5637	IPF472	-1.0	-1.0	1.1	1.0	unknown Function	YFR048w	orf19.7058
CA0921	IPF12992	1.1	1.1	1.2	1.0	unknown function	YPR139c	orf19.1043
CA3260	IPF7968	-1.1	1.0	1.0	1.0	unknown function		orf19.2693
CA6120	IPF132	1.0	1.1	-1.0	1.0	unknown function		orf19.5930
CA2421	IPF14998	1.0	1.1	1.1	1.0	unknown function	YDR200c	orf19.4471
CA0856	IFL1	1.1	1.1	-1.0	1.0	unknown function		orf19.11943
CA2946	IPF6296	1.0	1.1	1.0	1.0	putative methyltransferase (by homology)	YCR047c	orf19.1966
CA1030	ZRC1	-1.0	-1.0	1.2	1.0	Zinc and cadmium resistance protein (by homology)	YMR243c	orf19.9111
CA2928	SME1	1.0	1.1	-1.0	1.0	Nuclear ribonucleoprotein E	YOR159c	
CA5254	IPF1820	1.0	1.0	1.0	1.0	unknown function	YDR016c	
CA4396	IPF12294	-1.0	1.0	-1.1	1.0	unknown function		orf19.3115
CA6064	RPL81	1.2	1.0	-1.0	1.0	60S ribosomal protein L7a.e.B (by homology)	YLL045c	orf19.6002
CA0593	ARP6	1.0	-1.0	1.2	1.0	actin-related protein (by homology)	YLR085c	orf19.4904
CA3335	IPF8682	1.0	1.0	1.0	1.0	unknown function		orf19.2336
CA0144	IPF19195.3F	-1.0	1.0	1.0	1.0	putative amino acid or GABA permease, 3-prime end (b	YKL174c	orf19.151
CA0114	SSU72	-1.0	1.0	-1.0	1.0	suppressor of cs mutant of sua7(by homology)	YNL222w	orf19.9939
CA4889	IPF1629	1.0	1.1	1.1	1.0	unknown function	YOL003c	orf19.6581
CA2952	IPF19671	-1.0	1.0	1.0	1.0	unknown function		
CA0487	IPF13724	1.0	1.0	1.0	1.0	unknown function		orf19.259
CA2940	IPF8318	-1.0	-1.0	1.1	1.0	unknown function		orf19.3323
CA3835	RTA4	1.0	1.0	1.2	1.0	Protein involved in 7-aminocholesterol resistance (by homology)		orf19.6595
CA1401	TOM22	1.0	-1.0	1.0	1.0	mitochondrial outer membrane import receptor complex	YNL131w	orf19.3696
CA0920	IPF18833	1.0	1.1	1.2	1.0	unknown function		
CA3644	IPF4126	-1.0	-1.1	-1.0	1.0	unknown function		orf19.2035
CA0928	IPF19891	-1.1	1.0	1.0	1.0	unknown function		orf19.8192
CA2920	FET5	-1.1	1.2	-1.0	1.0	multicopy oxidase (by homology)		orf19.4215
CA1099	IPF12312	1.0	-1.0	-1.0	1.0	unknown function		orf19.12536
CA2973	F14452.REPEA	1.2	-1.0	1.2	1.0	F1-ATPase epsilon subunit (by homology)		
CA2960	IPF8590	1.1	1.0	1.0	1.0	unknown function		orf19.5863
CA0907	IPF19889	1.0	-1.0	1.1	1.0	Unknown Function		orf19.1484
CA3090	IPF18385	-1.0	-1.1	-1.1	1.0	unknown function	YLR068w	orf19.11619
CA2860	IPF7054	1.0	-1.0	1.0	1.0	unknown function		orf19.1062
CA1995	IPF6612	-1.2	1.0	1.1	1.0	unknown function	YML038c	orf19.6480
CA3156	IPF14455	-1.1	-1.1	-1.1	1.0	similar to Saccharomyces cerevisiae Rrn7p polymerase	YJL025w	orf19.1589
CA4580	IPF2233	1.1	1.0	1.1	1.0	unknown function		
CA4675	IPF3664	1.1	1.0	1.1	1.0	unknown function	YMR077c	orf19.897
CA1736	IPF4983	1.0	1.0	-1.1	1.0	unknown function	YNL035c	orf19.2527
CA5675	SIS2	-1.0	1.0	1.2	1.0	Involved in cell cycle-specific gene expression (by homc	YKR072c	orf19.7378
CA3223	SRP102	1.1	1.0	1.1	1.0	Signal recognition particle receptor (by homology)	YKL154w	orf19.6284
CA4186	PUT4	1.0	1.0	-1.0	1.0	proline permease		orf19.2945
CA5759	PET191.3	1.0	1.0	1.1	1.0	Assembly of cytochrome oxidase, 3-prime end (by hom	YJR034w	

CA1003	ATP20	1.4	-1.0	1.2	1.0	F1F0-ATPase complex, G subunit (by homology)	YPR020w	orf19.3757
CA3794	NCB2	-1.0	1.2	1.1	1.0	Transcriptional repressor by homology	YDR397c	orf19.5825
CA5624	IPF501	-1.0	-1.0	1.0	1.0	unknown function		orf19.7073
CA4055	YPT522	1.0	-1.0	1.0	1.0	GTP-binding protein of the rab family(by homology)	YBR264c	orf19.430
CA2868	IPF20118	1.0	1.1	1.1	1.0	unknown function		orf19.2846
CA3511	MMS2	1.0	1.0	1.2	1.0	ubiquitin-conjugating enzyme (by homology)	YGL087c	orf19.6358
CA0510	ETF1	-1.3	-1.1	-1.1	1.0	ETF-UBIQUINONE OXIDOREDUCTASE (by homology	YOR356w	orf19.10685
CA3206	IPF3454	-1.0	1.1	1.1	1.0	unknown function		orf19.6187
CA1309	IPF8627	1.0	-1.0	-1.0	1.0	unknown function		orf19.11452
CA1475	GLE2	-1.0	1.1	1.1	1.0	nuclear pore complex structure and function-like protein	YER107c	orf19.1095
CA4946	TOM71	1.1	1.0	1.1	1.0	Translocase of the outer mitochondrial membrane (by h	YNL070w	
CA5784	IPF1129	1.1	1.0	1.1	1.0	unknown function		orf19.5431
CA5008	IPF12577	1.1	1.1	1.2	1.0	unknown function		orf19.5238
CA3647	IPF4129	1.0	1.0	1.1	1.0	unknown function		orf19.2038
CA5913	RRD1	-1.0	1.0	-1.0	1.0	Phosphotyrosyl phosphatase activator involved in cell c	YIL153w	orf19.6792
CA5001	IPF2022	-1.0	1.0	1.1	1.0	unknown function		orf19.5246
CA0731	IPF7333	-1.0	1.1	1.1	1.0	unknown function	YNL023c	orf19.11206
CA2601	IPF11181	-1.1	-1.0	-1.0	1.0	unknown function	YML088w	orf19.50
CA3554	IPF7770	1.1	1.1	-1.0	1.0	unknown function	YOL053w	orf19.3881
CA2950	CLN2	1.1	-1.1	1.0	1.0	G1/S-SPECIFIC CYCLIN CLN2	YAL040c	orf19.9515
CA1171	IPF13264	1.0	-1.0	1.0	1.0	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type (by h		orf19.2748
CA2845	IPF10782	-1.1	1.1	1.2	1.0	unknown function	YDR539w	orf19.5730
CA5391	IPF18109	1.0	1.1	-1.0	1.0	unknown function		orf19.934
CA0250	IPF17661	-1.0	1.1	1.1	1.0	unknown function		orf19.1348
CA6111	IPF96	-1.0	-1.0	-1.0	1.0	C3HC4 type zinc finger protein (by homology)	YML068w	orf19.5942
CA4086	IPF5014	-1.0	-1.0	-1.0	1.0	unknown function	YNL263c	orf19.6642
CA4013	IPF4234	1.1	1.0	1.0	1.0	unknown function		orf19.1620
CA0520	IPF4466	1.0	1.0	-1.0	1.0	unknown function		orf19.3531
CA5634	IPF477	1.0	1.0	1.0	1.0	unknown function	YFR007w	orf19.7061
CA1481	RPB3	-1.0	1.1	1.1	1.0	DNA-directed RNA-polymerase II (by homology)	YIL021w	orf19.8832
CA0835	IPF12498.53F	-1.0	1.1	1.1	1.0	unknown function, internal fragment		
CA5350	IPF859	1.0	1.1	1.1	1.0	unknown function		orf19.7225
CA4431	ECM39	1.2	-1.0	1.1	1.0	cell wall biogenesis by homology	YNR030w	orf19.5164
CA0590	IPF13079	-1.1	-1.0	-1.0	1.0	unknown function	YDR336w	orf19.8756
CA2528	MOB1	1.0	1.0	-1.0	1.0	required for completion of mitosis	YIL106w	orf19.5528
CA0739	IPF18885	1.0	-1.0	1.1	1.0	similar to Saccharomyces cerevisiae Cdc91p cell divisi	YLR459w	orf19.11816
CA5502	IPF763	1.1	1.2	1.1	1.0	putative transcription factor with a Cys4- zinc finger (by	YKL185w	orf19.5343
CA2852	ALS5	1.0	1.1	1.1	1.0	agglutinin-like protein		orf19.5736
CA2642	FTI1	1.1	1.0	1.0	1.0	Rad52 inhibitor (by homology)	YKR035wa	orf19.4307
CA5267	IPF1787.5F	1.0	1.0	1.1	1.0	unknown function, 5-prime end		orf19.4995
CA1368	IPF15969	-1.0	1.0	1.0	1.0	unknown function		orf19.4965
CA0778	IPF12884	1.0	1.3	1.3	1.0	unknown function	YKR105c	orf19.4779
CA1412	IPF11854	-1.0	1.1	1.1	1.0	unknown function		orf19.1278
CA2713	IFF8	1.0	1.2	1.1	1.0	unknown function		orf19.570
CA3602	RPL14B.3	1.0	-1.0	-1.1	1.0	ribosomal protein L14B, 3-prime end (by homology)	YKL006w	
CA3310	PFS2	-1.0	1.0	1.2	1.0	Polyadenylation Factor I subunit (by homology)	YNL317w	orf19.2307
CA0656	IPF12470	-1.0	-1.0	-1.0	1.0	unknown function		orf19.5573
CA4032	IPF11081	-1.0	-1.0	1.0	1.0	unknown function		
CA0232	IFA1	1.1	1.0	1.1	1.0	Unknown function		orf19.156

CA5342	YPT521	-1.0	-1.0	1.0	1.0	GTP-binding protein of the rab/ypt family (by homology)	YKR014c	orf19.7216
CA1297	ACF2	1.0	-1.0	-1.1	1.0	endo-1,3-beta-glucanase	YLR144c	orf19.3417
CA5166	TYR1	1.0	1.0	-1.0	1.0	Prephenate dehydrogenase (NADP+) (by homology)	YBR166c	orf19.4605
CA3117	IPF5363	-1.1	1.0	-1.0	1.0	unknown function	YDR179wa	orf19.3009
CA0286	IPF14618	1.0	1.0	1.0	1.0	unknown function		orf19.6079
SCULP1		1.1	1.0	1.1	1.0			
CA3989	IPF7147	1.1	-1.0	1.0	1.0	unknown function	YLR401c	orf19.1565
CA5087	IPF20025	-1.1	1.0	-1.0	1.0	unknown function	YKL033w	orf19.3062
CA4395	EXM2	-1.1	1.0	1.1	1.0	EXit from Mitosis (by homology)	YDL087c	orf19.3116
CA5747	IPF2903	-1.0	1.1	1.1	1.0	unknown function		orf19.7456
CA6023	CDC33	1.1	1.0	1.1	1.0	translation initiation factor eIF4E, cap binding protein	YOL139c	orf19.7626
CA5452	SEC11	1.1	1.1	1.0	1.0	signal peptidase subunit (by homology)	YIR022w	orf19.3259
CA5895	ISA2	1.1	1.1	1.1	1.0	Mitochondrial protein required for iron metabolism (by h	YPR067w	orf19.6811
CA1080	IPF14710	-1.0	-1.1	1.0	1.0	unknown function	YKL162c	orf19.4820
CA2475	IPF3233	1.0	1.2	1.1	1.0	unknown function		orf19.2878
CA1251	IPF9624	1.1	-1.0	1.0	1.0	similar to Saccharomyces cerevisiae Ecm25p involved i	YJL201w	orf19.12423
CA2254	IPF15487	1.0	1.0	1.0	1.0	unknown function		orf19.1958
CA2233	IFJ3	1.0	-1.0	-1.0	1.0	unknown function		orf19.3924
CA0955	IPF13160	1.1	-1.0	1.0	1.0	unknown function		orf19.1140
CA3306	IPF11738	1.0	-1.0	-1.0	1.0	unknown function	YFR032c	orf19.2310
CA1663	IPF7309	-1.1	-1.0	1.0	1.0	unknown function	YGL101w	orf19.2864
CA3762	IPF13135	1.0	1.0	1.1	1.0	unknown function		orf19.2907
CA5600	IPF559	-1.1	-1.0	1.2	1.0	unknown function	YJR001w	orf19.7100
CA1717	IPF9315	1.1	1.2	1.2	1.0	putative CCAAT-binding factor subunit (by homology)		orf19.4647
CA1122	PMS1.3	-1.0	-1.1	-1.1	1.0	DNA mismatch repair protein, 3-prime end (by homolog	YNL082w	orf19.1605
CA5069	IPF3593	1.0	1.1	1.1	1.0	unknown function		orf19.3042
CA3510	MAD1	-1.0	1.0	-1.0	1.0	coiled-coil protein involved in the spindle-assembly chec	YGL086w	orf19.6357
CA4581	IPF2232	1.0	1.0	1.0	1.0	unknown function		orf19.6899
CA0215	IPF15350	1.1	1.0	1.0	1.0	putative zinc finger transcription factor (by homology)	YDR207c	orf19.2745
CA3315	IPF8814	1.0	1.0	1.2	1.0	unknown function		orf19.2302
CA3496	IPF17064	-1.0	1.0	1.0	1.0	unknown function		orf19.6342
CA4028	IPF7171.3F	1.0	-1.0	-1.1	1.0	unknown function, 3-prime end		orf19.3435
CA2819	RPA1	-1.0	1.0	-1.0	1.0	60S ribosomal protein	YDL081c	orf19.2992
CA1019	IPF13485	-1.1	-1.0	1.1	1.0	unknown function	YNR039c	orf19.3769
CA2143	IPF12803	-1.1	1.0	-1.0	1.0	unknown function		orf19.10048
CA2317	IPF13586	1.0	1.0	-1.1	1.0	unknown function		orf19.5479
CA1866	IPF7647	-1.0	-1.0	1.2	1.0	unknown function		orf19.860
CA4316	IPF2111	-1.0	1.0	1.0	1.0	unknown function	YJR141w	orf19.4106
CA1614	IPF18645	-1.1	-1.0	-1.0	1.0	unknown function		orf19.10728
CA3767	NUP60	-1.1	1.1	-1.0	1.0	Putative nuclear pore protein (by homology)	YAR002w	orf19.2901
CA0402	IPF15225	1.0	1.1	1.1	1.0	Sorting nexin-like protein (by homology)	YJL036w	orf19.1990
CA3577	IPF11106	1.1	-1.0	-1.0	1.0	unknown function		orf19.2263
CA5745	TAF60	-1.0	1.0	-1.0	1.0	TATA-binding protein-associated-factor (by homology)	YGL112c	orf19.7454
CA0973	IPF12662	1.3	1.1	1.2	1.0	unknown function		orf19.6474
CA3890	TERT2	-1.1	-1.0	-1.1	1.0	telomerase reverse transcriptase 2	YLR318w	orf19.5089
CA0837	IPF12495.3F	-1.0	-1.0	1.1	1.0	unknown function, 3-prime end		
CA2514	FUR4	1.0	1.1	1.1	1.0	Probable uracile or allantoin permease (by homology)	YIR028w	orf19.313
CA0690	IPF18901.3	1.0	1.1	1.0	1.0	unknown function, 3-prime end		
CA1941	IPF7998	-1.0	-1.0	-1.0	1.0	Ribosomal protein L24 (by homology)	YLR009w	orf19.4191

CA3363	FRE32	1.1	1.0	1.0	1.0	ferric reductase (by homology)	YOR381w	orf19.9488
CA0767	KEM1.3	-1.1	-1.0	-1.1	1.0	multifunctional nuclease, 3-prime end (by homology)	YGL173c	orf19.12434
CA3664	IPF11433.3F	1.1	-1.0	1.0	1.0	unknown function, 3-prime end	YKL207w	orf19.6462
CA1411	IPF11858	1.0	1.1	1.3	1.0	unknown function		orf19.1277
CA4573	IPF9431	1.0	1.1	1.2	1.0	unknown function	YJL091c	orf19.6884
CA3152	IPF4032	1.0	-1.0	-1.0	1.0	unknown function		orf19.6168
CA4375	IPF11309	1.1	-1.1	-1.1	1.0	unknown function	YMR039c	orf19.5666
CA3453	SEC23	-1.1	1.2	1.0	1.0	Component of COPII coat (by homology)	YPR181c	orf19.1254
CA3366	FRE43	-1.1	-1.0	1.2	1.0	ferric reductase-like (by homology)		orf19.9403
CA5334	SMK1	-1.0	1.1	-1.0	1.0	MAP kinase (by homology)	YPR054w	orf19.7208
CA5623	IPF502	1.0	1.0	-1.0	1.0	unknown function	YCL010c	orf19.7074
CA3672	IPF13669	1.0	-1.0	-1.0	1.0	unknown function		orf19.6456
CA0040	IPF15632	1.1	-1.0	1.0	1.0	unknown function		orf19.10973
CA4518	SPT14	-1.1	1.0	1.0	1.0	N-acetylglucosaminyl-phosphatidylinositol biosynthetic	YPL175w	orf19.487
CA4406	YDC1	1.1	1.0	1.3	1.0	alkaline dihydroceramidase (by homology)	YPL087w	orf19.3104
CA3282	IPF6272	1.0	1.0	-1.0	1.0	unknown function		orf19.6315
CA2759	ARP4	1.1	-1.0	1.1	1.0	actin-related protein (by homology)	YJL081c	orf19.13069
NAD3		1.1	1.0	-1.1	1.0			
CA4052	PF10231.EXON	1.0	-1.1	-1.2	1.0	similar to Saccharomyces cerevisiae Rif1p Rap1p-intera	YBR275c	orf19.427
CA3294	IPF5725	1.0	1.0	1.0	1.0	unknown function	YDR511w	orf19.6328
CA4261	PDX3	-1.1	1.0	-1.0	1.0	pyridoxamine-phosphate oxidase (by homology)	YBR035c	orf19.550
CA0884	CAN5	1.1	1.1	1.2	1.0	amino acid permease (by homology)		orf19.3641
CA0379	SSP120	1.0	1.0	-1.0	1.0	secretory protein (by homology)	YLR250w	orf19.3173
CA1953	IPF3899	1.1	1.0	1.0	1.0	similar to Saccharomyces cerevisiae Cbc2p small subu	YPL178w	orf19.763
CA5446	LAG1	1.3	-1.0	1.3	1.0	longevity-assurance protein (by homology)	YHL003c	orf19.3249
CA3954	YFH1	1.0	1.0	-1.0	1.0	Regulates mitochondrial iron accumulation (by homolog	YDL120w	orf19.1413
CA0789	ESP1	-1.0	1.0	1.1	1.0	Required for sister chromatid separation (by homology)	YGR098c	orf19.3356
CA3040	IPF7306	1.0	1.1	1.1	1.0	putative permease (by homology)	YBR241c	orf19.2425
CA2063	IPF7859	-1.0	-1.0	1.0	1.0	unknown function		orf19.2564
CA4915	IPF1427	-1.0	1.1	1.2	1.0	Similar to ubiquitination protein Bul1p (by homology)		orf19.6055
CA0242	IPF12047	1.1	-1.0	1.0	1.0	unknown function		orf19.3471
CA3614	IPF8878	-1.0	1.1	1.1	1.0	unknown function		orf19.31
CA5017	IPF7559	1.0	-1.0	1.1	1.0	unknown function		orf19.6970
CA5387	CTA24.3	-1.0	-1.1	-1.0	1.0	transcriptional activator, 3-prime end		
CA0696	HMT1	1.0	1.1	1.1	1.0	hnRNP methyltransferase (by homology)	YBR034c	orf19.3291
CA4906	MOB2	-1.0	1.1	1.1	1.0	Required for maintenance in ploidy	YFL034cb	orf19.6044
CA1360	IPF14598	1.1	-1.0	1.1	1.0	unknown function		orf19.4404
CA3470	IPF6310	1.1	1.0	1.0	1.0	unknown function		orf19.1666
CA1806	IPF6329	1.0	-1.0	1.0	1.0	unknown function		orf19.1113
CA2792	TRK1.3F	-1.0	-1.0	1.0	1.0	Potassium transporter, 3-prime end	Missing in array	orf19.602
CA3062	IPF2968	1.0	1.0	1.0	1.0	unknown function		orf19.11762
CA5908	IPF5960	-1.0	1.0	-1.0	1.0	unknown function		orf19.6797
CA1028	IPF6488	-1.1	1.0	-1.0	1.0	unknown function		orf19.1539
CA5706	IPF2649	1.0	1.1	-1.1	1.0	unknown function		orf19.7406
CA0478	YAE8	-1.0	1.0	-1.1	1.0	GTP-binding protein (by homology)	YAL048c	orf19.13437
CA0534	IPF15607	1.1	1.1	1.1	1.0	unknown function	YDR412w	orf19.5066
CA1231	IPF11817	-1.1	-1.0	1.0	1.0	unknown function	YDL206w	orf19.4981
CA0509	CDC24	-1.1	1.2	-1.0	1.0	GTP/GDP exchange factor for Cdc42p (by homology)	YAL041w	orf19.10684
CA0060	IPF13661	1.0	-1.1	-1.1	1.0	unknown function	YHR114w	orf19.1699

CA4727	IPF12253	1.1	1.0	-1.0	1.0	unknown function		
CA1049	TLG1	1.0	1.1	1.0	1.0	tSNARE that affects a Late Golgi compartment (by hom	YDR468c	orf19.3898
CA4249	IPF4293	1.0	1.1	1.1	1.0	similar to Saccharomyces cerevisiae Gpi2p N-acetylglu	YPL076w	orf19.538
CA0598	IPF9703	1.1	1.0	1.1	1.0	unknown function		orf19.12344
CA4977	IPF4710	-1.0	-1.1	-1.1	1.0	unknown Function	YLR181c	orf19.5275
CA0594	IPF8860	1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Gpi12p N-acetylgl	YMR281w	orf19.12368
CA3934	IPF17119	-1.1	1.0	-1.1	1.0	unknown function	YPR118w	orf19.2008
CA1245	IMH3.EXON2	1.0	-1.1	1.1	1.0	IMP dehydrogenase, exon 2	YLR432w	orf19.7689
CA1255	IPF9030	-1.0	-1.0	-1.0	1.0	unknown function	YGR277c	orf19.1776
CA1319	IPF3144	1.0	1.1	1.1	1.0	unknown function	YPR172w	orf19.4220
CA4365	PF5268.EXON	-1.0	1.1	1.0	1.0	choline monooxygenase, exon 1 (by homology)		orf19.5656
CA1162	IPF10258	-1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Rad24p cell cycle	YER173w	orf19.2728
CA2775	POP5	1.0	-1.0	1.0	1.0	subunit of RNase P- like by homology	YAL033w	orf19.275
CA0714	IPF9480	1.0	1.0	1.2	1.0	unknown function		orf19.3394
CA5560	THI13	1.0	-1.0	1.0	1.0	Pyrimidine precursor biosynthesis enzyme (by homolog	YDL244w	orf19.7324
CA4557	IPF8043	1.5	-1.1	1.1	1.0	unknown function		orf19.6867
CA4386	IPF12412	-1.0	1.1	1.0	1.0	unknown function		orf19.3125
CA1727	IPF8448	-1.0	1.0	1.1	1.0	unknown function		orf19.13846
CA5836	IPF428	1.1	1.0	1.2	1.0	transport protein (by homology)	YOL137w	orf19.7490
CA2763	DIC1.3	1.0	-1.1	-1.1	1.0	dicarboxylate carrier protein, 3-prime end (by homology	YLR348c	orf19.5628
CA3450	PDE2	-1.0	1.1	-1.0	1.0	Nucleotide phosphodiesterase	YOR360c	orf19.2972
CA4494	VMA1	1.1	1.0	1.0	1.0	vacuolar ATPase V1 domain subunit G	YHR039ca	orf19.1866
CA4215	SSY1	1.0	1.1	1.1	1.0	Regulator of transporters (by homology)	YDR160w	orf19.8434
CA5442	IPF18105.3F	-1.1	1.1	-1.1	1.0	unknown function, 3-prime end		orf19.3245
CA1960	IPF15232	1.0	1.0	-1.0	1.0	unknown function	YNL224c	orf19.2400
CA4133	IPF7010.3	1.0	1.1	1.1	1.0	unknown function, 3-prime end		orf19.4241
CA5533	IPF2846	1.0	1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Mps1p serine/thre	YDL028c	orf19.7293
CA3146	IPF9797	1.1	1.1	1.0	1.0	unknown function	YER093ca	orf19.6156
CA4197	IPF8057	1.0	-1.0	1.0	1.0	similar to Saccharomyces cerevisiae Rna15p componen	YGL044c	orf19.4538
CA1795	IPF11261	-1.1	-1.0	1.0	1.0	unknown function	YNL041c	orf19.5209
CA4122	PBI2	1.0	1.1	1.0	1.0	proteinase B inhibitor 2 (by homology)	YNL015w	orf19.2769
CA2465	IPF8726	1.0	-1.1	1.2	1.0	unknown function	YLL013c	orf19.1795
CA2037	IFF3	-1.0	-1.0	1.0	1.0	unknown function		orf19.11839
CA4258	IPF4279	-1.1	1.0	1.1	1.0	unknown function	YKL113c	orf19.547
CA1462	THI80	1.1	-1.0	1.0	1.0	Thiamin pyrophosphokinase (by homology)	YOR143c	orf19.8707
CA5345	FTR1	1.1	1.1	1.2	1.0	high affinity iron permease	YER145c	orf19.7219
CA3698	IPF4861	-1.0	1.0	1.0	1.0	unknown function		orf19.6274
CA6153	CUP5	1.0	1.0	1.1	1.0	Vacuolar H+-ATPase (by homology)		orf19.5886
CA4344	IPF3631	-1.1	1.0	1.0	1.0	unknown function		orf19.6718
CA3973	IPF6505	1.2	1.1	1.3	1.0	unknown function	YMR158w	orf19.1545
CA4341	IPF3624	-1.0	1.1	1.1	1.0	unknown function		orf19.6713
CA5115	IPF1331	1.0	1.0	1.0	1.0	unknown function	YNL080c	orf19.6416
CA0799	IPF14825	-1.0	-1.0	-1.0	1.0	unknown function		orf19.9178
CA2592	IPF18447	1.1	1.0	-1.0	1.0	putative zinc-finger protein (by homology)	YBR267w	orf19.59
CA3897	PFY1	1.2	-1.0	1.0	1.0	BINDS TO ACTIN	YOR122c	orf19.5076
CA4000	IPF4262	-1.0	1.0	1.1	1.0	similar to Saccharomyces cerevisiae Ste50p pheromone	YCL032w	orf19.1636
CA0855	AMYG1	1.0	1.0	1.0	1.0	glucoamylase		orf19.4899
CA3720	IFL3	-1.0	-1.0	1.0	1.0	Unknown function		orf19.11646
CA4851	IPF5818	1.1	1.0	1.0	1.0	unknown function		orf19.3821

CA3567	IPF7804.5F	-1.0	1.0	1.1	1.0	unknown function, 5-prime end		orf19.3134
CA0859	IPF14495.3	-1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Erf2p involved in p	YLR246w	orf19.11946
CA1509	IPF19920.3	-1.0	1.0	1.0	1.0	unknown function, 3-prime end		orf19.4524
CA0561	CIN4	-1.0	1.0	1.0	1.0	GTP-binding protein	YMR138w	orf19.2925
CA3137	IPF8976	-1.1	1.1	1.2	1.0	unknown function		orf19.8949
CA1698	IPF15681	1.0	1.0	1.1	1.0	unknown function		orf19.5045
CA2657	IPF8486	1.1	-1.0	1.1	1.0	unknown function		orf19.5710
CA5009	VPH2	-1.1	-1.1	-1.0	1.0	H+-ATPase assembly protein (by homology)	YKL119c	orf19.5237
CA4085	IPF5015	-1.1	1.1	1.0	1.0	unknown function		orf19.6641
CA4488	MEK1.3F	-1.0	1.0	1.0	1.0	serine/threonine protein kinase, 3-prime end	YOR351c	orf19.1875
CA5386	ZORRO2B.5F	1.0	1.0	-1.1	1.0	Putative gag protein, 5-prime end		orf19.7277
CA1316	IPF14587.3	1.1	-1.0	1.0	1.0	unknown function, 3-prime end		
CA4116	IDI1	1.2	-1.0	1.0	1.0	isopentenyl-diphosphate delta-isomerase (by homology	YPL117c	orf19.2775
CA3616	ASN1	-1.1	1.0	1.1	1.0	asparagine synthetase (by homology)	YPR145w	
CA3748	IPF7385	1.3	-1.0	1.2	1.0	unknown function		orf19.3430
CA5763	IFF10.5	1.0	1.1	-1.0	1.0	unknown function, 5-prime end		orf19.5404
CA1154	MET221	1.0	-1.0	-1.0	1.0	protein ser/thr phosphatase (by homology)	YOL064c	orf19.105
CA3343	IPF13360	-1.0	1.0	1.1	1.0	unknown function		orf19.2328
CA1730	IPF8439	1.0	1.1	1.0	1.0	unknown function	YDL115c	orf19.6498
CA1174	IPF14255	1.0	-1.0	-1.0	1.0	unknown function		orf19.4767
CA3130	TIM23	1.1	-1.0	1.0	1.0	mitochondrial inner membrane import translocase subu	YNR017w	orf19.1361
CA4520	CDC31	-1.0	1.0	1.0	1.0	spindle pole body component, centrin (by homology)	YOR257w	orf19.485
CA3145	CDC9	-1.1	1.0	1.1	1.0	DNA ligase (by homology)	YDL164c	orf19.6155
CA3250	IPF4716	1.1	1.1	1.3	1.0	unknown Function		orf19.11220
CA1936	PCT1	-1.2	1.0	-1.0	1.0	cholinephosphate cytidylyltransferase (by homology)	YGR202c	orf19.4186
CA5339	IPF885	1.1	1.0	1.1	1.0	glucan 1,3-beta-glucosidase (by homology)	YBR056w	orf19.7214
CA4601	IPF2195	-1.0	1.0	1.0	1.0	unknown function		orf19.6920
CA0034	IPF8016	1.1	1.0	1.0	1.0	unknown function		
CA6156	GEF1.3F	-1.1	1.2	1.0	1.0	Voltage-gated chloride channel protein, 3-prime end (by homology)		orf19.5881
CA1809	IPF6325	1.1	1.0	-1.0	1.0	unknown function		orf19.1116
CA2983	IPF18396	1.1	1.0	1.1	1.0	unknown function		orf19.8814
CA3991	VAM6.5F	-1.1	-1.0	-1.0	1.0	Vacuolar carboxypeptidase Y, 5-prime end (by homology)		orf19.1567
CA1108	IPF11273	1.0	-1.0	-1.0	1.0	unknown function		orf19.12696
CA6121	IPF33	1.0	1.0	1.0	1.0	unknown function		orf19.5929
CA4687	IPF9017	-1.0	-1.0	1.0	1.0	similar to Saccharomyces cerevisiae She4p required fo	YOR035c	orf19.879
CA3043	DOM34	-1.0	-1.0	-1.1	1.0	probable involvement in meiotic and mitotic divisi	YNL001w	orf19.2419
CA5903	IPF5942	1.1	1.1	1.1	1.0	transmembrane sugar transporter (by homology)	YPL244c	orf19.6803
CA3916	IPF3274	1.0	1.0	-1.0	1.0	Unknown function	YOR258w	orf19.4383
CA2790	IPF3562	1.1	1.0	1.0	1.0	Unknown function		orf19.604
CA2874	IPF4999	1.1	1.1	1.0	1.0	unknown function		orf19.5843
CA2346	SEF1	1.1	1.0	1.0	1.0	Putative transcription factor1	YBL066c	orf19.3753
CA6096	IPF56	1.0	1.0	-1.1	1.0	similar to Saccharomyces cerevisiae Nas6p subunit of 2	YGR232w	orf19.5961
CA0389	IPF14465	-1.0	-1.0	1.1	1.0	unknown function		orf19.1910
CA4144	IPF13340	-1.1	-1.1	1.0	1.0	unknown function	YOR164c	orf19.4228
CA2809	AMO1	1.0	1.0	1.1	1.0	amine oxidase (by homology)		orf19.5784
CA0228	IPT1	1.0	1.1	1.0	1.0	Mannosyl diphosphorylinositol ceramide (by homology)	YDR072c	orf19.12233
CA3745	MAF1	-1.0	-1.1	1.1	1.0	nuclear protein by homology	YDR005c	orf19.2173
Cox 2		1.0	1.0	-1.0	1.0			
CA3408	IPF9407	1.2	-1.1	-1.1	1.0	similar to Saccharomyces cerevisiae Arc15p subunit of	YIL062c	orf19.6151

CA5041	FRP7	1.1	-1.0	1.1	1.0	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathway		orf19.6995
CA1732	ECM42	1.0	1.0	1.1	1.0	Acetylornithine acetyltransferase (by homology)	YMR062c	orf19.6500
CA0686	IPF162	-1.2	-1.1	1.0	1.0	sulphate transporter (by homology)	YGR125w	orf19.3222
CA1829	IPF17177.3F	1.1	1.1	1.1	1.0	similar to Saccharomyces cerevisiae Srm1p regulator o	YGL097w	orf19.5184
CA3213	IPF8160	1.0	-1.0	-1.1	1.0	unknown function	YML003w	orf19.6205
CA3806	IPF9224	-1.1	1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Nup170p nuclear	YBL079w	orf19.2485
CA0214	SCT11	1.0	1.1	1.1	1.0	Suppresses a choline-transport mutant	YBL011w	orf19.1289
CA0092	IPF8268.3F	1.0	1.0	-1.0	1.0	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathway		orf19.1571
CA6016	IPF630	1.1	1.0	-1.1	1.0	unknown function	YOR145c	orf19.7618
CA2826	APL6	-1.0	1.0	1.1	1.0	AP-3 complex subunit, beta3-adaptin (by homology)	YGR261c	orf19.1323
CA3482	COQ5	1.1	1.0	-1.0	1.0	C-methyltransferase (by homology)	YML110c	orf19.3577
CA4871	IPF1680	-1.0	1.0	1.0	1.0	probable amidase	YDR242w	orf19.6557
CA2355	TPK1	1.0	-1.0	1.1	1.0	cAMP-dependent protein kinase 2 (by homology)		orf19.12357
CA2221	IPF9670	1.0	1.2	1.1	1.0	membrane transporter of the ATP-binding cassette (ABC) superfamily involved in met		orf19.5100
CA4293	IFA8	1.0	1.1	1.0	1.0	Unknown function		orf19.6690
CA3770	SOU2	1.1	1.1	1.1	1.0	Sorbitol utilization protein Sou2p [Candida albicans]		orf19.2897
CA3436	NRD1	-1.0	1.0	1.0	1.0	Involved in regulation of nuclear pre-mRNA abundance	YNL251c	orf19.581
CA4940	CRN1.3F	1.0	-1.0	1.1	1.0	actin-binding protein, 3-prime end (by homology)		orf19.6535
CA4283	IFJ4	-1.0	-1.0	1.0	1.0	Unknown function		orf19.6681
CA0705	IPF11804	-1.0	1.0	1.1	1.0	unknown function		orf19.10433
CA4137	CNA1	1.1	-1.0	1.0	1.0	cyclic nucleotide phosphodiesterase	YGL248w	orf19.4235
9290.2		-1.0	1.1	1.2	1.0			
CA0753	IPF10359	-1.0	-1.0	-1.0	1.0	unknown function	YMR135c	orf19.11287
CA0469	IPF18977	1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Smb1p associated	YER029c	orf19.2621
CA5031	IPF20023	1.0	1.0	1.1	1.0	similar to Saccharomyces cerevisiae Tea1p activator of	YOR337w	orf19.6985
CA4333	IPF2083	1.1	-1.0	1.0	1.0	unknown function	YNL056w	orf19.4086
CA2478	DAL52	-1.1	1.0	1.0	1.0	allantoate permease (by homology)		orf19.3208
CA4404	MET16	1.1	-1.0	-1.1	1.0	3 -phosphoadenylylsulfate reductase (by homology)	YPR167c	orf19.3106
CA2900	NIP7	1.2	1.1	1.0	1.0	required for efficient 60S ribosome subunit biogenesis (	YPL211w	orf19.3478
CA3406	IPF9711	1.0	1.1	-1.0	1.0	unknown function	YGR266w	orf19.3983
CA0235	HIS3	1.0	1.0	1.1	1.0	imidazole glycerol phosphate dehydratase	YOR202w	orf19.7813
CA0838	TFP1	-1.3	-1.1	1.1	1.0	vacuolar ATPase subunit (by homology)	YDL185w	orf19.9249
CA4642	IPF1500	-1.1	-1.0	1.0	1.0	similar to Saccharomyces cerevisiae Nca2p regulating	YPR155c	orf19.349
CA1799	IPF11446	1.0	1.0	1.1	1.0	unknown function		orf19.2922
CA0738	SEC16.3F	1.1	1.1	1.0	1.0	Multidomain vesicle coat protein, 3-prime end (by homology)		orf19.11819
CA0288	IPF14614	-1.0	1.1	-1.0	1.0	unknown function		
CA5563	PHO88	1.2	-1.0	-1.1	1.0	Involved in phosphate transport (by homology)	YBR106w	orf19.7327
CA3922	GRD19	-1.0	1.1	1.1	1.0	Probable golgi membrane protein-sorting protein (by ho	YOR357c	orf19.5114
CA1449	PF14730.5EOC	1.0	1.0	1.0	1.0	unknown function, 5-prime end		orf19.193
CA2472	IPF3239	1.0	1.0	-1.0	1.0	unknown function		orf19.2875
CA2766	IPF18416	1.0	1.0	-1.0	1.0	unknown function		orf19.13076
CA4290	IPF2617	-1.0	1.0	1.0	1.0	unknown function		orf19.6687
CA1351	PCL2	1.0	-1.1	1.0	1.0	G1/S specific cyclin	YDL127w	orf19.403
CA6086	PHB2	-1.0	-1.2	-1.3	1.0	Mitochondrial protein, prohibitin homolog (by homology)	YGR231c	orf19.5973
CA3398	IPF13621	1.0	1.0	-1.0	1.0	unknown function	YGR268c	orf19.3973
CA1800	IPF11445	-1.0	1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Pac2p involved in	YER007w	orf19.2921
CA4423	LIP9.EXON1	1.0	-1.1	-1.1	1.0	secretory lipase 9, exon 1		orf19.5172
CA3634	IFA25	1.0	1.0	1.1	1.0	unknown function		orf19.5140
CA3578	IPF11105	1.1	1.1	1.1	1.0	probable quinone oxidoreductase	YBR046c	orf19.2262

CA2268	IFU1.3F	1.0	-1.0	-1.0	1.0	Unknown function, 3-prime end		
CA2802	IPF11363	1.0	1.0	-1.0	1.0	unknown function		orf19.9283
CA4911	IPF1435	-1.1	-1.0	1.0	1.0	unknown function	YBR156c	orf19.6049
CA0218	IPF15294	-1.0	-1.0	-1.0	1.0	unknown function		orf19.6238
CA5785	TPT1	1.0	1.0	1.1	1.0	tRNA 2 -phosphotransferase (by homology)	YOL102c	orf19.5432
CA4777	PAN3	2.6	1.0	1.1	1.0	component of the Pab1p-dependent poly(A) ribo	YKL025c	orf19.4010
CA4053	IKS1	-1.0	-1.0	1.1	1.0	PROBABLE SERINE/THREONINE-PROTEIN KINASE	YJL057c	orf19.428
CA2942	IPF6291	-1.0	1.0	1.1	1.0	Secretory Stress Response protein (by homology)		orf19.1969
CA3856	IPF4641	1.1	1.1	1.1	1.0	similar to Saccharomyces cerevisiae Crd1p cardiolipin s	YDL142c	orf19.6100
CA4912	CNS1	1.0	-1.0	-1.1	1.0	Cyclophilin Seven Suppressor (by homology)	YBR155w	orf19.6052
CA0062	IPF19315.5F	-1.0	1.0	1.0	1.0	unknown function, 5-prime end	Missing in array	
CA1581	CWH41.3EOC	-1.1	-1.1	1.0	1.0	ER glucosidase I, 3-prime end (by homology)	YGL027c	orf19.4719
CA1495	IPF9686	-1.1	1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Sec8p Golgi - plas	YPR055w	orf19.3647
CA3769	IPF13465	1.1	-1.1	-1.0	1.0	Putative anion transport protein (by homology)	YNL275w	orf19.2898
CA3276	IPF6263	1.0	1.0	-1.0	1.0	unknown function		orf19.6310
CA1526	IPF13815	1.1	-1.1	1.2	1.0	unknown function		orf19.4553
CA4918	GLO1	1.0	-1.0	1.0	1.0	Glyoxalase I (by homology)	YML004c	orf19.6058
CA5599	IPF560	1.0	1.1	1.1	1.0	unknown function		orf19.7102
CA2118	IPF8024	1.0	-1.0	-1.0	1.0	unknown function		orf19.1334
CA1847	IPF11127	1.0	1.0	1.1	1.0	unknown function		orf19.639
CA1633	IPF10180	1.0	1.1	1.1	1.0	unknown function		orf19.11422
CA2995	IPF9113	1.0	1.1	1.1	1.0	unknown function	YER130c	orf19.6121
CA1568	IPF7615	1.1	-1.1	-1.1	1.0	unknown function		orf19.1158
CA0995	IPF10074	1.0	1.0	1.0	1.0	unknown function		orf19.9822
CA0682	IPF14514	1.0	1.0	-1.0	1.0	unknown function	YMR312w	orf19.12171
CA1646	IPF9336.3EOC	1.0	1.1	1.1	1.0	unknown function, 3-prime end		orf19.1725
CA0381	IPF16047	1.0	1.0	1.1	1.0	unknown function	YKR071c	orf19.2825
CA0266	IPF17773	-1.0	1.1	-1.0	1.0	unknown function		
CA1926	IPF13407	-1.0	1.1	1.0	1.0	Unknown function		orf19.8373
CA1535	IPF9515	1.2	1.0	1.2	1.0	similar to Saccharomyces cerevisiae Scs2p required for	YER120w	orf19.8800
CA1056	IPF17503	1.1	1.1	1.1	1.0	protein folding and stabilization (by homology)		orf19.2542
CA3115	ECM33.3	1.0	1.1	1.1	1.0	cell wall biogenesis, 3-prime end (by homology)	YBR078w	
CA2182	IPF6871	-1.0	-1.0	-1.1	1.0	unknown function		orf19.4253
CA1715	RPS21	1.0	1.0	-1.1	1.0	ribosomal protein (by homology)	YGL123w	orf19.3334
CA5619	IPF514	1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Bud3p budding pr	YCL014w ; Missing in array	orf19.7079
CA1841	CCA1	-1.0	1.0	1.1	1.0	tRNA nucleotidyltransferase (by homology)	YER168c	orf19.4705
CA1656	IPF16019	1.1	1.0	-1.0	1.0	unknown function	YOR308c	orf19.4326
CA0764	PRE2	-1.0	-1.0	-1.1	1.0	20S proteasome subunit (beta5)	YPR103w	orf19.2233
CA3164	IPF13187	1.0	-1.0	-1.0	1.0	unknown function		orf19.1580
CA2504	IPF6803.3F	1.0	-1.0	1.1	1.0	unknown function, 3-prime end		orf19.5593
CA3979	ENT3.3F	-1.1	1.1	1.1	1.0	putative endocytosis and cytoskeleton protein, 3-prime	YJR125c	orf19.1553
CA5133	IPF5129	1.1	1.0	1.1	1.0	unknown function		orf19.6392
CA3726	IPF6175	-1.1	-1.1	1.1	1.0	unknown function	YMR188c	orf19.4176
CA5089	MRPL27	1.1	1.0	1.0	1.0	ribosomal protein (by homology)	YBR282w	orf19.3064
CA0281	IPF10564.3	1.0	1.0	1.1	1.0	unknown function, 3-prime end		orf19.1438
CA3932	IPF20150	1.0	-1.0	1.0	1.0	unknown function		orf19.9561
CA0992	IPF11063	1.1	-1.0	1.0	1.0	unknown function	YCR090c	orf19.8972
CA1733	IPF3931	1.0	1.1	1.1	1.0	Unknown function		orf19.13854
CA5681	MNN9	1.0	1.0	1.0	1.0	Required for complex N-glycosylation	YPL050c	orf19.7383

CA5622	GBP2.3	1.1	1.0	1.3	1.0	single-strand telomeric DNA-binding protein, 3-prime en	YCL011c	orf19.7076
CA0769	IPF10967	1.1	1.0	1.0	1.0	unknown function		orf19.2826
CA2787	EFG1	1.1	1.1	1.1	1.0	Enhanced filamentous growth factor	YMR016c	orf19.8243
CA2496	IPF3468	1.0	1.1	1.1	1.0	unknown function		orf19.4055
CA3053	GTR2	-1.0	1.0	1.1	1.0	GTP-binding protein (by homology)	YGR163w	orf19.9944
CA5002	IPF2021	1.0	-1.0	1.0	1.0	unknown function		orf19.5245
CA0455	TCA5A	-1.0	1.0	-1.0	1.0	polyprotein of Tca5 retrotransposon		orf19.2427
CA2730	IPF10325	1.0	-1.0	-1.1	1.0	molybdopterin-converting factor by homology	YKL027w	orf19.9663
Human c Myc1		1.0	1.1	1.0	1.0			
CA1314	MAG1	-1.0	1.0	1.1	1.0	3-methyladenine DNA glycosylase (by homology)	YER142c	orf19.3639
CA4101	IPF3984	1.1	-1.0	1.0	1.0	unknown function		orf19.667
CA0483	SEC9	1.0	1.1	1.1	1.0	transport protein (by homology)	YGR009c	orf19.7764
CA0514	BEM1	1.0	1.1	1.1	1.0	bud emergence mediator (by homology)	YBR200w	orf19.4645
CA1363	IPF5556	-1.0	1.1	-1.0	1.0	acid phosphatase (by homology)		orf19.4424
CA2374	FCY23	1.1	-1.0	1.1	1.0	Putative purine-cytosine transport protein	YGL186c	orf19.9390
CA5948	IPF3496	-1.1	-1.1	-1.0	1.0	unknown function		orf19.6748
CA3440	IPF11328	-1.1	1.0	-1.0	1.0	unknown function		orf19.2985
CA5265	IPF1792	-1.1	-1.0	1.0	1.0	unknown function		orf19.4997
CA3324	IPF6893	1.0	1.0	-1.0	1.0	unknown function	YMR288w	orf19.2675
CA5777	IPF1118	-1.0	1.0	-1.0	1.0	unknown function		orf19.5422
CA1457	IPF8287	1.1	-1.0	-1.0	1.0	unknown function	YML050w	orf19.612
CA1393	IFO3	-1.1	-1.0	-1.1	1.0	Similar to Streptomyces coelicolor putative hydrolase		orf19.1766
CA6133	DUR35.3F	-1.0	-1.0	-1.1	1.0	Urea transport protein, 3-prime end (by homology)		orf19.5915
CA0296	IFA11	1.0	1.1	1.0	1.0	Unknown function		orf19.1596
CA4367	MNN10	1.1	-1.0	1.1	1.0	galactosyltransferase (by homology)	YDR245w	orf19.5658
CA1083	IPF1034	1.0	-1.0	1.0	1.0	Similarity to transcription factors		orf19.12042
CA0105	IPF17529.3	-1.1	-1.0	1.0	1.0	unknown function, 3-prime end		orf19.786
CA4287	IPF20011.3F	-1.0	1.1	1.1	1.0	similar to Saccharomyces cerevisiae Pnc1p pyrazinamidase and nicotinamidase, 3-prime end (by homolo		
CA5754	IPF1060	1.1	1.2	1.1	1.0	unknown function, Asn rich		orf19.5390
CA4701	IPF4214	1.0	1.0	1.1	1.0	unknown function	YER134c	orf19.6929
CA1419	IPF17296	-1.0	1.1	1.0	1.0	unknown function		orf19.175
CA5486	IPF813	-1.1	1.0	1.0	1.0	unknown function		orf19.5320
CA6001	IPF662	1.0	1.0	-1.1	1.0	unknown function	YGL136c	orf19.7601
CA5107	IPF1358	1.0	-1.0	1.0	1.0	unknown function		orf19.6431
CA2271	MRS2	-1.0	1.0	-1.0	1.0	Mitochondrial RNA splicing protein (by homology)	YOR334w	orf19.2597
CA0141	PF17520.53EO	-1.0	1.0	1.1	1.0	unknown function, internal fragment		orf19.1021
CA0901	IPF12033	-1.0	1.1	1.0	1.0	unknown function	YCR068w	orf19.3412
CA4957	IPF4588	-1.0	1.1	-1.0	1.0	putative aldehyde dehydrogenase (by homology)		orf19.6518
CA1257	IPF18725	-1.1	1.1	1.1	1.0	unknown function	YOR262w	orf19.10678
CA4526	MON1.3	-1.0	1.0	1.0	1.0	unknown function, 3-prime end	YGL124c	orf19.8109
CA4837	IPF1228	1.0	1.0	-1.0	1.0	unknown function		orf19.2059
CA1724	MRP10	1.0	1.0	1.0	1.0	Mitochondrial ribosomal protein (by homology)	YDL045wa	
CA5851	KIN2	1.0	1.1	1.0	1.0	ser/thr protein kinase (by homology)	YLR096w	orf19.7510
CA1336	PF5334.EXON	1.1	1.0	-1.0	1.0	unknown function, exon 2	YHR100c	
CA0946	IPF10277	1.0	1.1	1.1	1.0	unknown function	YER048wa	
CA4188	IPF7525	1.0	1.1	1.1	1.0	unknown function		orf19.4529
CA5289	NRG1	-1.0	1.1	-1.0	1.0	similar to transcriptional repressor Nrg1p/Nrg2p	YBR066c	orf19.7150
CA4704	RRD2	-1.0	1.0	1.1	1.0	hosphotyrosyl phosphatase activator	YPL152w	orf19.6933
CA1203	IPF3937	-1.1	1.2	1.2	1.0	Unknown function		orf19.8487

CA2797	IPF8404	1.0	1.0	-1.0	1.0	putative helicase (by homology)	YFR038w	orf19.1720
CA5030	IPF2988	1.0	1.0	1.2	1.0	unknown function		orf19.6984
CA2830	RBT1	1.1	-1.0	1.1	1.0	repressed by TUP1 protein 1		orf19.1327
CA0821	IPF16795	-1.0	1.0	1.1	1.0	glycerate/formate-dehydrogenase (by homology)	YNL274c	orf19.2989
CA2725	MRPL23A	1.0	-1.0	1.0	1.0	mitochondrial ribosomal protein L23 (by homology)	YOR150w	orf19.10856
CA2440	IPF7513	-1.0	-1.0	-1.0	1.0	unknown function	YGL110c	orf19.2196
CA4544	IPF6252	-1.0	-1.0	1.1	1.0	similar to Saccharomyces cerevisiae Tad2p tRNA-speci	YJL035c	orf19.1458
CA0610	CDR11.5F	1.1	1.2	-1.1	1.0	multidrug resistance protein, 5-prime end (by homology)		orf19.8533
CA3459	CGT1.3F	1.0	-1.1	-1.0	1.0	mRNA capping enzyme alpha subunit, 3-prime end	YGL130w	orf19.1261
CA1196	IPF10394	-1.0	1.1	1.1	1.0	unknown function		
CA3983	IPF7133.3	-1.0	1.1	1.1	1.0	unknown function, 3-prime end	YLR137w	orf19.9130
CA0720	IPF17932	1.1	-1.2	-1.0	1.0	unknown function	YBR175w	orf19.3457
CA5010	IPF13945	1.0	-1.0	-1.1	1.0	Unknown function		
CA1919	IPF7477	1.0	1.0	1.0	1.0	unknown function		orf19.2442
CA4454	IPF15160	-1.0	-1.0	1.0	1.0	unknown function	YEL072w	orf19.6852
CA0396	SNM1	1.1	1.0	1.0	1.0	RNA binding protein of RNase MRP (by homology)		orf19.1927
CA2177	ROD1	1.1	1.1	1.1	1.0	O-dinitrobenzene,calcium and zinc resistance protein (b	YFR022w	orf19.9084
CA0301	IPF19688	1.0	1.0	1.0	1.0	unknown function		orf19.1606
CA4676	HK1	-1.0	1.1	1.2	1.0	Histidine kinase		orf19.896
CA0273	IPF19066	-1.1	-1.2	-1.2	1.0	unknown function		orf19.1433
CA0053	IFA16	-1.0	1.0	-1.0	1.0	unknown function		orf19.380
CA3144	ASF1	1.1	1.1	1.0	1.0	anti-silencing protein (by homology)	YJL115w	orf19.3715
CA6160	IPF1835	1.0	1.1	1.1	1.0	unknown function		orf19.5876
CA1258	RPN8	-1.2	-1.0	-1.1	1.0	26S proteasome regulatory subunit (by homology)	YOR261c	orf19.10677
CA1576	HYR1	1.1	1.0	-1.0	1.0	hyphally regulated protein		orf19.12440
CA5743	IPF2895	-1.0	-1.0	-1.0	1.0	unknown function	YGL113w	orf19.7452
CA3491	RPC40	1.1	1.0	1.0	1.0	RNA polymerase (by homology)	YPR110c	orf19.3564
CA1116	CCT5	-1.3	-1.0	-1.1	1.0	T-complex protein 1, epsilon subunit (by homology)	YJR064w	orf19.2288
CA0935	IPF14203.5F	1.0	1.0	-1.0	1.0	similarity to several transaminases, 5-prime end (by hor	YFL030w	orf19.1079
CA4336	DDR48	-1.1	1.0	-1.2	1.0	stress protein (by homology)		orf19.4082
CA2158	ECM1	-1.0	-1.0	-1.1	1.0	involved in cell wall biosynthesis (by homology)	YAL059w	orf19.5299
CA4634	IPF1526	-1.0	1.0	-1.0	1.0	unknown function	YLR119w	orf19.340
CA6055	SMD1	1.0	-1.0	1.0	1.0	snRNA-associated protein (by homology)		orf19.7673
CA4539	IFQ4	-1.0	-1.0	1.1	1.0	Unknown function		orf19.1464
CA4622	IPF5751	-1.2	1.1	1.0	1.0	TRAPP subunit of 20 kDa involved in targeting and fusi	YBR254c	orf19.3314
CA0321	APL2	-1.2	-1.1	1.0	1.0	AP-1 complex subunit, beta1-adaptin (by homology)	YKL135c	orf19.7861
CA5593	IPF5615	1.0	1.0	1.0	1.0	unknown function	YJL122w	orf19.7107
CA0282	IPF17417	1.0	1.0	-1.0	1.0	Unknown function		orf19.12160
CA2418	MNT4	-1.0	1.0	-1.0	1.0	putative mannosyltransferase	YBR199w	orf19.4475
CA5464	IPF285.5F	1.0	1.0	1.0	1.0	unknown function, 5-prime end	YCR059c	orf19.3273
CA1670	IPF11392	1.1	1.2	1.1	1.0	unknown function		orf19.2851
CA2750	ATX1	1.1	1.0	1.1	1.0	antioxidant protein and metal homeostasis factor (by ho	YNL259c	
CA4445	IPF3530	-1.0	1.1	-1.1	1.0	unknown function		orf19.6843
CA0133	IPF3746	1.0	1.0	1.0	1.0	unknown function	YDR017c	orf19.1007
CA1474	IPF10208	1.0	-1.0	-1.0	1.0	chloride channel-like protein (by homology)		orf19.1096
CA2882	STE13	-1.0	-1.1	-1.1	1.0	type IV dipeptidyl aminopeptidase (by homology)	YOR219c	orf19.5851
CA4126	IPF6631	-1.0	-1.0	1.0	1.0	unknown function		orf19.2763
CA0233	URE2	1.0	1.0	1.0	1.0	Nitrogen catabolite repression regulator (by homology)	YNL229c	orf19.7794
CA5052	IPF3708	1.1	1.0	1.1	1.0	unknown function		orf19.3016

CA5748	IPF2905	1.0	1.1	-1.0	1.0	unknown function		orf19.7457
CA2445	IPF13885	1.1	1.0	1.1	1.0	unknown function		orf19.5503
CA3532	IPF13448	1.0	-1.0	1.0	1.0	similar to Saccharomyces Ptp1p protein tyrosine phospl	YDL230w	orf19.6365
CA0039	IPF3998	1.0	1.1	1.0	1.0	unknown function		orf19.8278
CA1469	IPF5078	-1.1	1.0	1.1	1.0	unknown function	YLR417w	orf19.8414
CA5395	IPF9401	-1.0	-1.0	1.1	1.0	unknown function		orf19.938
CA0342	IPF10470	-1.1	-1.0	1.0	1.0	unknown function	YJR003c	orf19.1789
CA4189	IPF7527	-1.0	-1.0	-1.0	1.0	unknown function		
CA5898	IPF2383	1.0	-1.1	1.0	1.0	unknown function		orf19.6808
CA4332	GLO2	-1.1	1.0	1.1	1.0	Glyoxalase II (hydroxyacylglutathione hydrolase) (by ho	YDR272w	orf19.4088
CA1543	IPF1043	1.0	1.0	-1.0	1.0	Similar to hydroxyquinol 1,2-dioxygenase		orf19.4567
CA2536	IPF20107	1.1	-1.0	1.0	1.0	unknown function	YOL111c	orf19.3183
CA2347	RAD51	1.1	1.2	1.3	1.0	DNA repair protein by homology	YER095w	orf19.3752
CA0825	PLB2	1.1	1.0	1.0	1.0	phospholipase B		orf19.8309
CA2681	SEC4	-1.0	1.0	1.3	1.0	GTP-binding protein	YFL005w	orf19.2571
CA3628	IPF18316.3F	-1.1	1.0	1.0	1.0	unknown function, 3-prime end		orf19.12611
CA0889	IPF11767	1.1	1.0	1.2	1.0	mitochondrial carrier protein (by homology)		orf19.4733
CA1751	ARO3.EXON2	-1.1	1.1	-1.0	1.0	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	YDR035w	orf19.1517
CA2072	IPF6970	1.0	1.0	1.0	1.0	unknown function	YKR085c	orf19.2639
CA3589	IPF10113	1.1	1.0	-1.1	1.0	unknown function	YNR020c	orf19.2249
CA2698	SUL1	-1.1	1.0	1.1	1.0	High-affinity sulfate transport protein (by homology)	YLR092w	orf19.10252
CA1546	IPF6671	-1.0	1.0	-1.0	1.0	unknown function	YLL005c	orf19.8891
CA0473	GRP1	-1.0	-1.0	-1.0	1.0	dihydroflavonol-4-reductases (by homology)		orf19.12245
CA1407	UAPC	1.0	1.0	1.0	1.0	purine permease (by homology)		orf19.2882
CA3344	IPF13359	-1.0	-1.0	-1.1	1.0	unknown function	YDR363w	orf19.2326
CA2071	IPF6971.53	1.0	1.0	1.1	1.0	unknown function, internal fragment	YNL147w	
CA0373	IPF7655.5EOC	1.0	1.1	1.0	1.0	unknown function, 5-prime end		
CA3492	IPF3189	1.0	1.1	1.1	1.0	unknown function		orf19.3563
CA5344	PRY2	1.1	1.0	1.2	1.0	putative pathogen related proteins (by homology)	YJL079c	orf19.7218
CA5300	IPF2189	1.0	1.0	1.0	1.0	unknown function		orf19.7165
CA4377	IPF11301	1.0	-1.0	1.0	1.0	unknown function		orf19.5669
CA4009	IPF4247	1.1	-1.0	1.0	1.0	unknown function		orf19.1625
CA3312	IPF8810	1.0	1.1	-1.0	1.0	unknown function	YEL003w	orf19.2305
CA4607	IPF6223	1.1	-1.0	1.1	1.0	unknown function	YGR215w	orf19.3297
CA1965	IPF14035	-1.1	1.0	-1.0	1.0	Similar to serine/threonine protein kinase (by homology)	YJL106w	orf19.2395
CA2015	IPF3416	1.0	-1.0	1.0	1.0	unknown function		orf19.8468
CA0335	IFA2	1.1	1.0	1.0	1.0	unknown function		orf19.7825
CA5375	IPF5239	1.1	1.1	1.1	1.0	similarity to aldose reductase (by homology)		orf19.7260
CA3967	IPF9377	1.0	-1.0	-1.0	1.0	unknown function		orf19.1428
CA5596	IPF564	-1.1	1.1	-1.1	1.0	unknown function		orf19.7104
CA6048	IPF4934	1.0	1.1	-1.0	1.0	unknown function	YCR087ca	orf19.7664
CA5520	IPF714	-1.0	-1.1	-1.1	1.0	unknown function	YDR049w	orf19.5368
CA4995	YAK1	1.0	-1.0	-1.0	1.0	Ser/thr protein kinase (by homology)		orf19.5253
CA0519	MRPL10.3	1.0	-1.0	1.0	1.0	ribosomal protein, 3-prime end (by homology)	YNL284c	orf19.11016
CA1611	SPO72	1.0	1.1	-1.0	1.0	required for sporulation (by homology)	YNL242w ; Missing in array	orf19.4119
CA5567	FCY24	-1.0	1.0	1.1	1.0	Putative purine-cytosine transport protein		orf19.7331
CA4813	DPB4	-1.0	1.1	-1.1	1.0	DNA-directed DNA polymerase epsilon, subunit D (by h	YDR121w	orf19.2088
CA3140	IPF9214	1.0	1.0	1.0	1.0	unknown function		orf19.3711
CA1636	IPF20086	1.0	1.1	1.1	1.0	unknown function	YJR102c	orf19.3942

CA0980	IPF17655	1.0	-1.1	1.0	1.0	unknown function		orf19.3600
CA6071	IPF4835	-1.0	-1.1	-1.0	1.0	zinc finger protein (by homology)		orf19.5992
CA5311	IPF2166	1.1	1.0	1.1	1.0	unknown function	YGL232w	orf19.7182
CA6022	IPF618	1.1	1.0	1.1	1.0	GPI-anchored cell surface protein (by homology)		orf19.7625
CA1229	MLH1	-1.0	1.0	-1.0	1.0	DNA mismatch repair protein (by homology)	YMR167w	orf19.4162
CA4945	FLX1	1.1	1.1	1.1	1.0	MITOCHONDRIAL FAD CARRIER by homology	YIL134w	orf19.6532
CA6015	ARD1	1.1	-1.0	-1.0	1.0	protein N-acetyltransferase subunit (by homology)	YHR013c	orf19.7617
CA2466	IPF8725	1.1	1.0	1.0	1.0	unknown function		
CA2148	AUT1	-1.0	1.0	1.0	1.0	similar to Saccharomyces cerevisiae Aut1p essential fo	YNR007c	orf19.6020
CA1241	LIP8	1.1	1.1	1.0	1.0	Secretory lipase		orf19.8925
CA5252	DIM1	1.0	-1.1	-1.0	1.0	rRNA (adenine-N6,N6-)-dimethyltransferase (by homol	YPL266w	orf19.5010
CA2420	SPC19	1.0	1.0	-1.0	1.0	spindle pole body protein (by homology)	YDR201w	orf19.4473
CA0467	TRX2	1.1	1.0	1.0	1.0	thioredoxin (by homology)		orf19.1976
CA4887	IPF1632	-1.0	1.0	1.0	1.0	unknown function		orf19.6579
CA0902	IPF12034	1.1	1.0	1.0	1.0	unknown function		orf19.3413
CA3058	IPF2955	1.1	-1.0	-1.1	1.0	unknown function		orf19.4292
CA5250	IPF1826	1.0	1.0	1.0	1.0	unknown function		orf19.5012
CA1843	IPF11364	1.0	1.0	-1.0	1.0	unknown function		orf19.635
CA4744	IPF4489	1.0	1.0	1.1	1.0	unknown function	YGR113w	orf19.4837
CA0499	IFA9	1.0	1.1	1.1	1.0	unknown function		orf19.2663
CA1383	IPF8422	-1.1	-1.0	1.0	1.0	unknown function	YML036w	orf19.927
CA0962	IPF9145	-1.2	1.0	1.1	1.0	unknown function		orf19.6245
CA2160	IPF15664	1.1	-1.0	1.0	1.0	unknown function	YIL157c	orf19.5296
CA5869	MIS12	1.0	-1.1	-1.0	1.0	mitochondrial C1-tetrahydrofolate synthase precursor (by homology)		orf19.7534
CA4207	YAT1	-1.1	-1.1	-1.0	1.0	carnitine acetyltransferase (by homology)	YAR035w	orf19.4551
CA5768	PAC1	1.0	1.1	1.0	1.0	Similarity to human LIS-1 protein (by homomology)	YOR269w	orf19.5410
CA0194	IPF16228	1.1	-1.0	1.1	1.0	unknown function	YGL224c	orf19.11404
CA4835	IPF1218	1.1	1.1	1.0	1.0	Similar to superoxide dismutase (by homology)		orf19.2062
CA6101	SPO70.3F	1.0	1.1	1.1	1.0	involved in meiosis and sporulation, 3-prime end		
CA3719	IPF6190	-1.0	1.1	-1.0	1.0	unknown function		orf19.11645
CA1492	IPF168	1.1	-1.0	1.1	1.0	unknown function	YDL046w	orf19.3226
CA4160	IPF9294	1.0	1.1	1.0	1.0	unknown function	YBR271w	orf19.5808
CA5070	IPF3594	1.1	-1.0	1.0	1.0	triglyceride lipase (by homology)	YDR058c	orf19.3043
CA2282	IPF14438	-1.0	1.0	1.1	1.0	unknown function		orf19.12995
CA3202	IPF3444.5F	-1.0	1.0	-1.0	1.0	unknown function, 5-prime end		orf19.6184
CA0927	IPF11332	-1.2	-1.0	-1.2	1.0	unknown function	YPL072w	orf19.3661
CA4357	IPF19800	-1.0	1.0	1.0	1.0	unknown function	YCR015c	orf19.6732
CA3962	IPF11234	1.0	1.0	1.0	1.0	similar to saccharomyces cerevisiae Dal3p ureidoglycol	YIR032c	orf19.1421
CA1823	IPF9522.5F	1.0	-1.0	1.1	1.0	septin, 5-prime end (by homology)		orf19.4267
CA2585	IPF9438	-1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Prp42p U1 snRNP	YDR235w	orf19.4374
CA1930	IPF3906.3	-1.0	1.0	1.0	1.0	unknown function, 3-prime end	YPR079w	orf19.758
CA2745	HIR1	-1.0	1.0	1.1	1.0	Histone transcription regulator (by homology)	YBL008w	orf19.9647
CA4151	SHE9	1.0	-1.1	-1.1	1.0	causes lethality when overexpressed	YDR393w	orf19.5796
CA2187	IPF11667	-1.0	-1.0	1.0	1.0	unknown function		orf19.4771
CA0516	IPF11526	-1.0	1.0	1.0	1.0	unknown function	Missing in array	orf19.2804
CA2814	IPF5607	1.1	-1.0	-1.0	1.0	unknown function	YLR435w	orf19.2998
CA5366	IPF823	1.1	-1.0	1.0	1.0	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltran	YDL033c	orf19.7245
CA6073	HRP1	1.1	1.0	1.1	1.0	Nuclear polyadenylated RNA-binding protein (by homol	YOL123w	orf19.5989
CA3760	ERG26	1.0	-1.0	-1.1	1.0	C-3 sterol dehydrogenase (C-4 decarboxylase) (by hom	YGL001c	orf19.2909

CA3291	IPF5730	-1.0	1.1	1.1	1.0	unknown function	YNL211c	
CA5146	YMC2	-1.0	-1.0	1.1	1.0	Carnitine/acylcarnitine translocase (by homology)		orf19.4583
CA5462	GSL23.3F	1.0	1.0	1.1	1.0	1,3-beta-D-glucan synthase subunit, 3-prime end	Missing in array	orf19.3270
CA3961	IPF11235	-1.0	-1.1	1.0	1.0	unknown function	YFR043c	orf19.1420
CA4763	IPF9645	-1.1	-1.0	-1.1	1.0	similar to Saccharomyces cerevisiae Rim13p calpain-lik	YMR154c	orf19.3995
CA0936	IPF16291	1.1	-1.0	1.1	1.0	unknown function		orf19.1080
CA4767	IPF13054	1.0	1.0	1.1	1.0	unknown function		orf19.3999
CA6152	NUP85	-1.1	1.2	-1.0	1.0	Nuclear pore protein (by homology)	YJR042w	orf19.5887
CA1531	RVS167	1.0	-1.0	1.0	1.0	(putative) cytoskeletal protein (by homology)	YDR388w	orf19.1220
CA0363	SPR3	1.1	1.1	1.0	1.0	sporulation-specific septin (by homology)		orf19.1524
CA6080	IPF21	-1.0	1.0	1.1	1.0	unknown function		orf19.5980
CA4464	IPF9828	-1.0	1.0	1.0	1.0	similar to Saccharomyces cerevisiae Apc5p component	YOR249c	orf19.6861
CA0013	MAK32	1.1	1.1	1.1	1.0	sugar kinase (by homology)	YCR019w	orf19.4548
CA5302	IPF20175	1.1	-1.0	1.0	1.0	unknown function		orf19.7167
CA5182	IPF11093	-1.0	-1.0	1.1	1.0	weak similarity to pig tubulin-tyrosine ligase	YBR094w	orf19.4621
CA1450	IPF6474	-1.0	-1.1	-1.0	1.0	unknown function		orf19.4414
CA0976	PEX17	1.0	1.1	1.1	1.0	Peroxisomal peripheral membrane protein (by homology)		orf19.11088
CA5598	IPF562	1.0	1.0	1.1	1.0	unknown function	YGR099w	orf19.7101
CA4637	IPF1514	1.0	1.1	1.0	1.0	unknown function		orf19.344
CA5324	IPF2140	-1.0	1.0	1.1	1.0	unknown function	YNL288w	orf19.7198
CA4321	KAR3.53	-1.0	-1.0	-1.0	1.0	Kinesin-related protein, internal fragment	YPR141c	orf19.4100
CA2309	IPF9875	1.1	1.1	1.0	1.0	unknown function		orf19.1374
CA1103	IPF5673	1.0	1.1	-1.0	1.0	similar to Saccharomyces cerevisiae Rex3p RNA exonu	YLR107w	orf19.12413
CA4588	BEL1.EXON1	1.3	1.0	1.1	1.0	protein of the 40S ribosomal subunit, exon 1 (by homolo	YMR116c	orf19.6906
CA5272	IPF1770	-1.1	-1.0	-1.1	1.0	unknown function		orf19.4988
CA2530	IPF12782	-1.1	1.0	-1.0	1.0	unknown function	YNL294c	orf19.3176
CA2235	MPD1	1.1	1.0	1.0	1.0	disulfide isomerase related protein (by homology)	YOR288c	orf19.3920
CA1217	IPF13909	-1.0	1.0	1.0	1.0	Unknown function		orf19.7770
CA3201	IPF3444.3F	1.0	1.0	1.0	1.0	unknown function, 3-prime end		orf19.6182
CA1310	IPF14232	1.0	-1.0	1.0	1.0	unknown function		orf19.11114
CA4275	MDJ1	1.0	1.0	1.0	1.0	Heat shock protein - chaperone (by homology)	YFL016c	orf19.6672
CA4045	ABP140	-1.0	-1.0	-1.0	1.0	putative methyltransferase (by homology)	YOR240w	orf19.3676
CA3925	IPF13257	1.0	1.0	1.1	1.0	unknown function		orf19.5110
CA5040	BAT22	-1.1	-1.1	1.1	1.0	branched chain amino acid aminotransferase (by homology)		orf19.6994
CA0844	CDC3	-1.0	-1.1	-1.1	1.0	Cell division control protein	YLR314c	orf19.8657
CA0366	IPF19017	1.0	1.0	1.0	1.0	unknown function	Missing in array	orf19.8931
CA4847	IPF6951	1.0	1.2	-1.0	1.0	similar to Saccharomyces cerevisiae Ubp11p ubiquitin (	YKR098c	orf19.3815
CA0067	IPF13904	1.2	1.1	1.1	1.0	farnesyl cysteine carboxyl-methyltransferase (by homology)		orf19.120
CA1864	IPF7644	-1.0	1.0	1.0	1.0	unknown function		orf19.862
CA5927	DRS22	-1.1	1.0	1.1	1.0	Membrane-spanning Ca-ATPase (by homology)	YAL026c	orf19.6778
CA4568	IPF9554	-1.1	1.1	-1.1	1.0	unknown function	YPR105c	orf19.6880
CA0231	RAD23	-1.2	-1.2	-1.3	1.0	nucleotide excision repair protein(ubiquitin-like protein)	YEL037c	orf19.1494
CA5931	ECM29.EXON1	-1.1	1.0	-1.1	1.0	Involved in cell wall biogenesis and architecture, exon 1 (by homology)		orf19.6772
CA4112	BIM1	-1.0	1.0	-1.0	1.0	microtubule-binding protein (by homology)	YER016w	orf19.676
CA5445	IPF232	1.0	1.0	1.0	1.0	unknown function		orf19.3248
CA6091	UFD2	-1.4	1.0	1.0	1.0	Ubiquitin fusion degradation protein 2 (by homology)	YDL190c	orf19.5965
CA4031	IPF11077	1.0	1.1	-1.0	1.0	membrane transporter (by homology)		orf19.3432
CA5995	IPF676	1.0	1.1	1.1	1.0	unknown function		orf19.7595
CA5736	OPI3	1.5	-1.0	1.2	1.0	Methylene-fatty-acyl-phospholipid synthase (by homolo	YJR073c	orf19.7446

CA3501	CDC40	-1.0	1.1	-1.0	1.0	cell division control protein (by homology)	YDR364c	orf19.6347
CA4500	IPF11319	-1.0	-1.0	-1.0	1.0	unknown function		orf19.8141
CA6028	IPF607	-1.0	1.0	-1.1	1.0	unknown function	YDL003w	orf19.7634
CA4688	NBN1	1.0	-1.0	1.0	1.0	involved in chromatin remodeling and possibly transcrip	YHR090c	orf19.878
CA4236	IPF8166	-1.0	1.0	1.0	1.0	unknown function	YBL025w	orf19.519
CA1507	HSP30	1.0	-1.0	1.0	1.0	heat shock protein (by homology)	YCR021c	orf19.4526
CA1440	RPL17B	1.0	-1.3	-1.1	1.0	RPL17B ribosomal protein L17.e	YJL177w	orf19.4490
CA4606	IPF6224	1.0	-1.0	1.1	1.0	unknown function		orf19.3296
CA2085	IPF3388	-1.0	1.1	1.1	1.0	unknown function	YHR204w	orf19.834
CA1237	IPF15784	1.0	-1.0	-1.1	1.0	unknown function		orf19.8334
CA0148	POP1	-1.0	-1.0	-1.0	1.0	protein component of ribonuclease P and ribonuclease I	YNL221c	orf19.2404
CA3680	IPF8395	-1.0	1.0	-1.0	1.0	unknown function		orf19.729
CA2152	IPF7899	1.0	1.0	-1.0	1.0	unknown function		orf19.6024
CA3937	IPF14686	-1.0	1.1	-1.0	1.0	unknown function	YPL162c	orf19.9557
CA2094	IPF11493	1.0	-1.0	1.1	1.0	unknown function		orf19.9929
CA4640	IPF1506	-1.0	1.0	-1.0	1.0	unknown function		orf19.347
CA4956	IPF4583	1.0	1.0	1.1	1.0	putative allantoate permease (by homology)	YIL166c	orf19.6520
CA5123	IPF1306	-1.0	-1.0	1.0	1.0	unknown function	YAL018c	orf19.6405
CA4955	IPF4580	1.0	-1.0	-1.0	1.0	putative allantoate permease (by homology)		orf19.6522
CA0179	DCP1	1.0	1.0	1.1	1.0	mRNA decapping enzyme (by homology)	YOL149w	orf19.423
CA4048	IPF9207	-1.0	-1.0	1.1	1.0	unknown function	YNL200c	orf19.11163
CA4612	PPM2	-1.1	-1.1	-1.1	1.0	carboxy methyl transferase	YOL141w	orf19.3303
CA1521	FTH1	1.0	1.0	-1.0	1.0	iron transporter	YBR207w	orf19.4802
CA1882	IPF19934	-1.0	1.0	-1.0	1.0	unknown function		orf19.9755
CA5576	PRP4	-1.0	1.0	1.0	1.0	pre-mRNA-processing U4/U6 small nuclear ribonucleop	YPR178w	orf19.7343
CA4276	HEX1	-1.0	-1.0	1.1	1.0	ß-N-acetylglucosaminidase		orf19.6673
CA3478	IPF3227	1.0	-1.0	-1.1	1.0	similar to Saccharomyces cerevisiae chromatin assemb	YBR195c	orf19.3581
CA4234	HAP3	1.1	-1.0	1.1	1.0	CCAAT-binding factor subunit (by homology)	YBL021c	orf19.517
CA2502	IPF20103	1.1	-1.1	1.0	1.0	unknown function		orf19.5588
CA0307	IPF4719	1.0	1.0	1.1	1.0	similar to Saccharomyces cerevisiae Kar4p regulatory p	YCL055w	orf19.3736
CA2556	FRE5	1.0	1.0	1.0	1.0	ferric reductase transmembrane component (by homology)		orf19.5634
CA1240	IPF14026	1.1	-1.1	-1.0	1.0	similar to Saccharomyces cerevisiae Rrn11p involved ir	YML043c	orf19.8337
CA0957	IPF14322	1.0	1.0	-1.0	1.0	unknown function	YNL051w	
CA1486	IPF10521	1.1	1.1	-1.0	1.0	unknown function		orf19.4062
CA2167	IPF4553	-1.1	1.1	-1.0	1.0	unknown function	YDL048c	orf19.909
CA1599	IPF11452	1.0	1.0	1.0	1.0	unknown function	YDR030c	orf19.7900
CA3735	IPF5534	1.0	-1.0	1.0	1.0	5-oxo-1,2,5-tricarboxilic-3-penten acid decarboxylase (by homology)		orf19.2184
CA4802	ILV3	2.8	1.0	1.0	1.0	dihydroxyacid dehydratase (by homology)	YJR016c	orf19.4040
CA3774	IPF10437	1.0	-1.0	1.0	1.0	budding protein-like (by homology)	YHR103w	orf19.2892
CA3313	IPF8811	-1.2	1.0	-1.1	1.0	unknown function		orf19.2304
CA1853	LYP1	1.4	1.0	1.3	1.0	lysine-specific high-affinity permease (by homology)		orf19.651
CA2088	IPF3394	-1.0	1.1	1.1	1.0	unknown function	YFL017wa	
CA4757	LIP10	1.1	-1.0	1.0	1.0	Secretory lipase		orf19.4822
CA5852	ATP17.3	1.2	1.1	1.1	1.0	F1F0-ATPase complex, F1 delta subunit f, 3-prime end	YDR377w	
CA5072	IPF3598	-1.2	1.0	1.1	1.0	similar to Saccharomyces cerevisiae Sip3p protein whic	YNL257c	orf19.3047
CA3772	VMA8	-1.0	-1.1	-1.0	1.0	CANAL VACUOLAR ATP SYNTHASE SUBUNIT D	YEL051w	orf19.2895
CA1278	IPF10835	1.0	1.1	1.1	1.0	unknown function	YER124c	orf19.3629
CA4202	IPF8047	1.1	1.1	1.1	1.0	unknown function		orf19.4544
CA3264	IPF5035	1.0	1.0	1.0	1.0	unknown function	YLL014w	orf19.2698

LacZ 5end		1.1	1.0	1.1	1.0			
CA2262	IPF6857	1.0	1.1	1.0	1.0	putative transcriptional regulator (unknown function)	YDR253c	orf19.1757
CA1055	IPF17504	-1.1	-1.1	-1.1	1.0	unknown function	YBL055c	orf19.2541
CA5825	IPF2489	1.0	1.1	1.1	1.0	unknown function		orf19.7480
CA0354	YAK1.5F	1.0	1.1	1.0	1.0	serine/threonine protein kinase, 5-prime end (by homology)		orf19.7788
CA1549	IPF8744	-1.2	1.1	1.1	1.0	unknown function	YKL005c	orf19.4278
CA5160	PHO89	1.1	-1.0	1.1	1.0	Na+-coupled phosphate transport (by homology)	YBR296c	orf19.4599
CA3394	IPF6747	-1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Stb2p involved Sir	YMR053c	orf19.7946
CA0790	IPF14193	1.2	1.0	1.1	1.0	unknown function	YHR059w	orf19.3357
CA4933	IPF8372	1.1	-1.1	-1.1	1.0	unknown function	YDL166c	orf19.6074
CA2653	IPF8472.3EOC	1.1	-1.0	1.1	1.0	unknown function, 3-prime end	YLR381w	orf19.5701
CA3103	IPF12086	1.0	-1.0	1.0	1.0	unknown function	YKL084w	orf19.13908
CA1798	IPF11448	1.1	-1.1	1.1	1.0	unknown function		orf19.2923
CA5306	NPT1	-1.0	-1.0	-1.1	1.0	Nicotinate phosphoribosyltransferase (by homology)	YOR209c	orf19.7176
CA6030	YHB2	1.0	1.0	1.1	1.0	flavohemoprotein (by homology)		orf19.7637
CA0797	IPF13564	1.0	1.0	-1.0	1.0	putative arylsulfatase (by homology)		orf19.1608
CA2229	IPF5682	-1.0	1.1	1.1	1.0	unknown function		orf19.5814
CA0536	PANC.3	1.0	-1.0	1.0	1.0	pantothenate synthetase, 3-prime end (by homology)	YIL145c ; Missing in array	orf19.2815
CA4789	IPF3366	1.1	1.0	1.0	1.0	Mitochondrial ribosomal protein (by homology)	YPR166c	orf19.4023
CA3638	IPF9252	-1.0	1.0	1.0	1.0	unknown function		orf19.5134
CA3629	IPF18316.5F	-1.0	-1.0	1.0	1.0	unknown function, 5-prime end		orf19.12610
CA0017	IPF17811	-1.0	1.3	1.1	1.0	unknown function		
CA3799	IPF7198	1.1	-1.0	1.0	1.0	unknown function		orf19.10015
CA1282	PF10171.EXON	1.1	-1.0	1.1	1.0	unknown function, exon 2		
KanMX		-1.0	1.1	1.1	1.0			
CA0051	IPF4443	1.0	-1.0	1.0	1.0	unknown function		orf19.12177
CA5831	MRPL6	1.1	-1.0	-1.1	1.0	ribosomal protein L6 precursor, mitochondrial (by homo	YHR147c	orf19.7486
CA1774	IPF7498	1.1	-1.0	-1.0	1.0	unknown function	YBR246w	orf19.2191
CA2517	IPF4311	-1.0	-1.0	1.0	1.0	unknown function		orf19.5514
CA5059	IPF3691	1.0	1.1	1.0	1.0	unknown function		orf19.3027
CA6074	IPF11	1.0	-1.0	-1.0	1.0	unknown function	YOL124c	orf19.5987
CA4410	TRP4	-1.0	-1.1	1.0	1.0	Anthranilate phosphoribosyltransferase	YDR354w	orf19.3099
CA2376	IPF15506	-1.1	-1.1	-1.1	1.0	unknown function	YGR042w	orf19.2213
CA3472	PF6305.EXON	1.1	1.1	-1.0	1.0	unknown function, exon 2	YLR218c	
CA2621	IPF9499	1.0	-1.0	1.0	1.0	probable transcription factor (by homology)		orf19.2808
CA5101	LCB1	-1.0	1.0	1.3	1.0	Serine C-palmitoyltransferase subunit (by homology)	YMR296c	orf19.6438
CA5216	IPF3069	1.0	-1.0	-1.1	1.0	unknown function		orf19.7034
CA3421	IPF19782	-1.0	-1.0	-1.1	1.0	unknown function		orf19.13554
CA1031	IPF17469	1.1	-1.0	-1.0	1.0	unknown function		orf19.3848
CA2934	IPF11515	1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Lcb3p sphingoid b	YJL134w	orf19.3329
CA3625	CYR1.3F	1.0	1.1	1.1	1.0	adenylate cyclase, 3-prime end	YJL005w	orf19.12617
CA2193	IPF14273	-1.0	-1.0	1.1	1.0	Probable ser/thr protein kinase (by homology)	YKL116c	orf19.11824
CA2087	IPF3393	-1.1	1.1	-1.0	1.0	unknown function		orf19.836
CA1648	IPF16662	1.0	1.0	1.0	1.0	unknown function	YBR257w	orf19.5567
CA5803	IPF4163	1.1	-1.0	1.1	1.0	unknown function	YKL047w	orf19.5457
CA1675	IPF5192	1.0	1.0	1.0	1.0	unknown function	YPL191c	orf19.3615
CA0238	PHA2.3	1.1	1.0	1.1	1.0	prephenate dehydratase, 3-prime end (by homology)	YNL316c	orf19.7864
CA2380	IPF4072	-1.1	-1.1	1.7	1.0	unknown function		orf19.2217
CA3116	LAB2	-1.0	-1.0	1.1	1.0	LIPOATE BIOSYNTHESIS PROTEIN by homology	YLR239c	orf19.3010

CA0337	IPF9867	-1.0	-1.0	1.0	1.0	unknown function		orf19.1370
CA5778	IPF1119	1.0	1.0	1.1	1.0	unknown function	YIL009ca	orf19.5423
CA1959	IFD2	1.0	1.1	1.1	1.0	putative oxidoreductase (by homology)	YPL088w	orf19.771
CA2147	IPF18533	1.0	-1.0	1.1	1.0	unknown function		orf19.2516
CA2872	APG13	-1.0	1.0	1.0	1.0	probable component of the autophagic system (by hom	YPR185w	orf19.2848
CA5833	IMP3	1.1	1.0	-1.0	1.0	U3 small nucleolar ribonucleoprotein (by homology)	YHR148w	orf19.7488
CA2963	GRP3	1.0	-1.0	1.0	1.0	dihydroflavonol-4-reductases (by homology)	YOL151w	orf19.5611
CA3671	IPF13933	1.0	-1.0	-1.0	1.0	unknown function	YBL086c	orf19.6457
CA0346	ROX1	1.1	1.0	-1.0	1.0	Possible heme-dependent transcriptional repressor (by	YPR065w	orf19.10341
CA4693	IPF3952	1.0	1.0	1.0	1.0	unknown function		orf19.872
CA5480	IPF8210	-1.0	1.0	-1.0	1.0	unknown function	YNL103w	orf19.5312
CA1429	IPF15123	1.1	1.0	1.0	1.0	unknown function		orf19.13171
CA1445	MRP51	1.1	-1.0	-1.0	1.0	Mitochondrial ribosomal protein of the small subunit (by	YPL118w	orf19.185
CA3781	IPF11224	-1.0	1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Pdr16p protein inv	YNL231c	orf19.5839
CA0284	IPF14657	1.0	-1.0	-1.1	1.0	unknown function		orf19.1441
CA0762	TAF67	-1.0	-1.0	-1.0	1.0	TFIID subunit (by homology)	YMR227c	orf19.9147
CA1681	IPF12676	1.1	1.0	1.0	1.0	unknown function	YOL086wa	orf19.4914
CA4478	IPF6461	1.1	1.0	-1.0	1.0	unknown function	YKR043c	orf19.1889
CA5734	IPF20029	1.1	1.0	1.0	1.0	unknown function	YOR352w	orf19.7444
CA1014	MES1	-1.1	1.0	1.1	1.0	methionyl-tRNA synthetase (by homology)	YGR264c	orf19.11437
CA0166	PF19161.53EO	1.0	-1.0	-1.0	1.0	unknown function, internal fragment	Missing in array	
CA0024	RPC31.5EOC	-1.0	1.0	1.0	1.0	DNA-directed RNA polymerase III, 5-prime end (by homology)		orf19.10349
CA3865	IPF4608	1.0	-1.0	-1.0	1.0	unknown Function		orf19.6084
CA0192	IPF15134	-1.1	-1.0	-1.0	1.0	Unknown function	YNL206c	orf19.1177
CA4998	IPF2026	-1.0	1.1	1.1	1.0	unknown function		orf19.5249
CA1432	APM3	1.0	1.1	-1.0	1.0	AP-3 complex subunit, mu3 subunit (by homology)	YBR288c	orf19.1204
CA0353	YAK1.3F	1.0	-1.0	1.0	1.0	serine/threonine protein kinase, 3-prime end (by homolo	YJL141c	orf19.147
CA1747	IPF10884	-1.0	-1.0	1.0	1.0	unknown function	YLR003c	orf19.5049
CA5100	IPF1372	-1.1	-1.0	1.0	1.0	unknown function	YNL008c	orf19.6440
CA4303	IFB1	-1.0	1.0	-1.1	1.0	unknown function		orf19.6703
CA1993	IPF6614	1.1	-1.0	1.0	1.0	unknown function		orf19.6482
CA0548	PHO87	-1.1	-1.0	1.1	1.0	Member of the phosphate permease family (by homolog	YCR037c	orf19.2454
CA1807	IPF6328	1.1	1.0	-1.0	1.0	unknown function	YML030w	orf19.1114
CA5932	UBI4	1.0	1.0	-1.0	1.0	Polyubiquitin	YLL039c	orf19.6771
CA5335	IPF894	-1.0	1.0	1.1	1.0	unknown function		orf19.7209
CA1004	IPF8901	-1.1	-1.1	1.2	1.0	unknown function	YDR105c	orf19.3758
CA3098	SIS1	-1.1	1.0	-1.1	1.0	heat shock protein (by homology)	YNL007c	orf19.3861
CA3620	IPF9063	1.1	1.1	1.2	1.0	similar to Saccharomyces cerevisiae Stb3p protein bind	YDR169c	orf19.203
CA0815	IPF16231	1.0	1.0	1.1	1.0	unknown function		orf19.1913
CA4540	SMP2	-1.1	-1.0	-1.1	1.0	Involved in plasmid maintenance, respiration and cell p	YMR165c	orf19.1462
CA1490	IPF165	1.1	-1.2	-1.0	1.0	unknown function		
CA4177	MGM101	-1.0	1.0	1.1	1.0	mitochondrial genome maintenance protein	YJR144w	orf19.2956
CA6077	IPF16	-1.0	-1.1	-1.0	1.0	unknown function	YOL073c	orf19.5984
CA2975	ARO9	1.0	1.1	1.1	1.0	aromatic amino acid aminotransferase II(by homology)	YHR137w	orf19.8822
CA0633	IPF16269	1.0	-1.0	1.0	1.0	unknown function	YGR278w	orf19.9340
CA1369	IPF15968	-1.0	-1.0	1.0	1.0	unknown function	YGL174w	orf19.4964
CA3884	IPF6367	1.0	1.0	1.0	1.0	unknown function	YPL247c	orf19.8014
CA2050	IPF11023	1.1	-1.0	-1.0	1.0	unknown function		orf19.13147
CA4628	IPF13704	1.1	1.0	-1.0	1.0	unknown function		

CA3649	IPF4132	-1.0	-1.0	-1.0	1.0	unknown function	YPR048w	orf19.2040
CA5966	IPF959	1.0	-1.0	1.0	1.0	unknown function		orf19.7556
CA5885	IPF2419	1.1	1.1	1.0	1.0	unknown function		orf19.6824
CA5209	MCM1	1.0	-1.0	1.2	1.0	Transcription factor of the MADS box (by homology)	YMR043w	orf19.7025
CA2551	IPF9098	1.1	1.0	1.0	1.0	unknown function		orf19.2836
CA3048	IPF14991	1.1	1.0	1.1	1.0	unknown function	YJR044c	orf19.9950
CA5574	IPF2007	1.0	1.0	-1.0	1.0	unknown function		orf19.7341
CA2407	ECM14	-1.1	1.1	1.1	1.0	carboxypeptidase involved in cell wall biogenesis and a	YHR132c	orf19.299
14432.2		-1.1	1.0	1.1	1.0			
CA1248	IPF3866	1.0	1.1	1.0	1.0	unknown function	YLR251w	orf19.7692
CA2820	HOL1	1.0	-1.1	1.0	1.0	member of major facilitator superfamily multidrug-resistance protein subfamily 1 by h		orf19.2991
CA3971	IPF6498	1.0	-1.0	-1.1	1.0	unknown function		orf19.1543
CA0780	CIRT1A	-1.0	-1.1	1.0	1.0	transposase		orf19.3492
CA3401	IPF8652	-1.0	-1.0	-1.1	1.0	putative GTP-binding protein (by homology)	YGR173w	orf19.3977
CA4786	IPF3362	1.0	-1.0	1.1	1.0	Unknown function	YBL046w	orf19.4019
CA4958	RAD14	-1.0	1.0	-1.0	1.0	nucleotide excision repair protein (by homology)	YMR201c	orf19.6517
CA4110	IPF3965	1.1	1.0	1.0	1.0	unknown function	YDL209c	orf19.674
CA5515	SAT2	-1.0	1.1	1.1	1.0	putative glycosyl-transferase involved in osmotolerance	YBR070c	orf19.5363
CA4982	NUT2	1.1	-1.0	1.0	1.0	Negative transcription regulator from artifical reporters (	YPR168w	orf19.5268
CA3358	IPF19984	1.1	1.2	1.1	1.0	similar to Saccharomyces cerevisiae Cat5p involved in	YOR125c	orf19.1940
CA1966	IFR4	1.0	1.0	1.1	1.0	unknown function	YNL134c	orf19.2394
CA5367	RIM101	1.1	1.0	1.1	1.0	Zn finger transcription factor homolog	YHL027w	orf19.7247
CA5760	IPF1072	1.0	1.1	1.1	1.0	unknown function	YGL005c	orf19.5397
CA2261	RAS1	-1.0	1.1	1.1	1.0	GTP-binding protein (by homology)	YNL098c	orf19.1760
CA2871	OPT2.3F	1.1	1.0	1.0	1.0	Oligopeptide transporter, 3-prime end (by homology)		orf19.2847
CA3189	IPF11607	1.0	1.1	1.1	1.0	unknown function	YPR003c	orf19.2149
CA4522	RPT4	-1.0	-1.1	-1.1	1.0	26S proteasome regulatory subunit (by homology)	YOR259c	orf19.482
CA6162	IPF1833	1.0	1.0	1.0	1.0	similar to opaque phase protein OP4 (by homology)		orf19.5874
CA2431	IPF12951	-1.0	1.1	1.0	1.0	unknown function	YDR486c	orf19.3401
CA5393	IPF9398	-1.0	1.0	-1.0	1.0	unknown function		orf19.936
CA5439	TAF25	-1.0	-1.0	-1.2	1.0	transcription initiation factor TFIID subunit (by homology	YDR167w	orf19.3242
CA3041	IPF7303	-1.0	1.0	-1.1	1.0	unknown function	YBR239c	orf19.2423
CA5928	IPF2815	1.0	1.0	1.0	1.0	unknown function		orf19.6777
CA5455	IPF263.3	1.0	1.0	1.1	1.0	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathway		orf19.3263
CA3439	IPF11329	1.0	1.0	1.1	1.0	unknown function		orf19.2986
CA0941	IPF8617	-1.1	1.0	-1.0	1.0	unknown function	YCR079w	orf19.3705
CA3928	GAL11	1.1	1.0	1.1	1.0	DNA-directed RNA polymerase II holoenzyme and Korn	YOL051w	orf19.5105
CA2614	CTA241.EXON	-1.0	-1.0	-1.0	1.0	transcriptional activator, exon 2		
CA0151	PF15923.5EO	1.1	-1.0	-1.0	1.0	unknown function, 5-prime end		orf19.177
CA3636	IFA21	-1.0	-1.1	-1.1	1.0	unknown function		orf19.12603
CA2639	IPF2932	-1.0	1.1	1.1	1.0	unknown function		orf19.4305
CA3998	IPF10443	1.0	-1.0	1.0	1.0	formamidase-like protein (by homology)		orf19.1641
CA6148	IPF1862.3F	1.1	1.0	-1.0	1.0	unknown function, 3-prime end	YEL023c	orf19.5894
CA6027	IPF609	-1.0	1.0	-1.0	1.0	unknown function		orf19.7632
CA1601	IPF15728	1.0	1.0	1.1	1.0	unknown function		orf19.4721
CA2145	IPF12800	-1.0	-1.1	-1.0	1.0	unknown function		orf19.2514
CA5847	CDA2	-1.0	1.0	-1.0	1.0	chitin deacetylase (by homology)	YLR308w	orf19.7503
CA5680	CAM1.EXON2	-1.1	1.2	1.2	1.0	translation elongation factor eEF1 gamma, exon 2 (by homology)		orf19.7382
CA1430	IPF14331	-1.0	-1.0	1.0	1.0	Probable extracellular alpha-1,4-glucan glucosidase (by homology)		orf19.3380

CA2014	IPF1717	1.0	1.1	1.1	1.0	similar to Saccharomyces cerevisiae Scc2p involved in	YDR180w	orf19.10592
CA5909	YSA1	1.1	1.0	1.1	1.0	sugar-nucleotide hydrolase (by homology)	YBR111c	orf19.6796
CA0074	IFD7	1.0	-1.0	-1.0	1.0	Putative aryl-alcohol dehydrogenase (by homology)		orf19.629
CA4893	IPF1621	-1.1	1.1	-1.0	1.0	unknown function	YAL046c	orf19.6585
CA4543	PPE1	-1.0	1.0	1.1	1.0	Ribosomal protein of the small subunit, mitochondrial (b	YHR075c	orf19.1459
CA4820	IPF1196	-1.0	-1.0	1.0	1.0	unknown function Hypothetical Zn(2)-Cys(6) zinc-finger protein (by homology)		orf19.2077
CA3641	IPF4122	1.0	-1.1	1.0	1.0	unknown function		orf19.2032
CA0806	IPF12567	1.0	1.0	1.0	1.0	unknown function	YOR223w	orf19.3517
CA1424	IPF9090	1.1	-1.0	1.0	1.0	unknown function		orf19.11282
CA0059	IPF17840	1.0	-1.0	1.2	1.0	unknown function		orf19.566
CA1166	IFO1	1.0	1.0	-1.0	1.0	Unknown function		orf19.1780
CA5765	SOF1	-1.1	-1.1	-1.1	1.0	Involved in 18S pre-rRNA production (by homology)	YLL011w	orf19.5407
CA5217	RFC2	1.1	1.0	1.0	1.0	Replication factor (by homology)	YJR068w	orf19.7035
CA1219	PRC2	1.0	1.0	-1.0	1.0	carboxypeptidase y precursor , serine-type protease (by homology)		orf19.4135
CA4519	IPF7088	-1.0	1.1	1.1	1.0	similar to Saccharomyces cerevisiae Nip100p myosin-lil	YPL174c	orf19.486
CA3389	IPF6754	1.0	-1.0	1.1	1.0	unknown function	YDR286c	orf19.7951
CA1979	IPF9577	-1.0	1.0	-1.0	1.0	unknown function	YNL193w	orf19.686
Int 3		1.0	1.0	1.0	1.0			
CA5975	SIK1	1.1	1.1	1.1	1.0	nucleolar protein involved in pre-rRNA processing (by h	YLR197w	orf19.7569
CA0032	IPF15248	-1.0	1.0	1.0	1.0	zinc finger protein (by homology)	YOL054w	orf19.229
CA1951	HEM14	1.1	-1.0	1.0	1.0	Mitochondrial protoporphyrinogen oxidase (by	YER014w	orf19.12209
CA5411	IPF1558	-1.0	1.0	-1.1	1.0	unknown function		orf19.955
Int 2		1.0	1.0	1.0	1.0			
CA6007	IPF650	-1.0	-1.0	-1.0	1.0	unknown function		orf19.7608
CA4299	IPF2598	1.0	1.0	-1.0	1.0	unknown function	YCR024c	orf19.6698
CA2794	IPF8408	1.1	1.1	1.0	1.0	unknown function		orf19.1724
CA0474	IPF12887	1.0	-1.0	1.0	1.0	Putative multidrug protein (by homology)		orf19.12244
CA5145	SKI6	1.1	1.0	1.0	1.0	3 ->5 exoribonuclease (by homology)		orf19.4582
CA2944	IPF6294	1.0	1.0	-1.0	1.0	unknown function		orf19.1968
CA0993	IPF11059	-1.0	-1.0	-1.0	1.0	unknown function		orf19.8973
CA5284	UFE1	-1.0	1.1	-1.1	1.0	Endoplasmic reticulum t-SNARE (by homology)	YOR075w	orf19.7141
CA3869	IPF8831	-1.0	-1.1	-1.2	1.0	unknown function		orf19.400
CA3475	BRO1	1.0	1.0	-1.0	1.0	required for normal response to nutrient limitatior	YPL084w	orf19.1670
CA0903	IPF4401	1.5	-1.0	-1.0	1.0	putative succinate dehydrogenase (by homology)	YMR118c	orf19.1480
CA5845	NAP1	1.1	1.1	1.0	1.0	nucleosome assembly protein (by homology)	YKR048c	orf19.7501
CA1992	F6617.REPEA	1.0	1.0	1.0	1.0	unknown function, repeated protein		orf19.6484
CA5829	ADE1	1.1	1.0	-1.0	1.0	phosphoribosyl-amidoimidazole-succinocarboxamide sy	YAR015w	orf19.7484
CA5092	IPF1394	1.0	-1.0	1.0	1.0	unknown function		orf19.6450
CA5451	SLN1	-1.1	-1.0	-1.0	1.0	Two-component signal transducer histidine kinase comp	YIL147c ; Missing in array	orf19.3256
CA5459	IPF276	-1.0	-1.0	-1.0	1.0	unknown function	YDR126w	orf19.3267
CA3106	IPF11821	1.1	1.0	1.1	1.0	unknown function	YPR037c	orf19.6552
CA2287	IPF5373	1.1	1.0	-1.0	1.0	unknown function		orf19.5555
CA5653	SSN8	1.0	-1.0	1.0	1.0	C-type cyclin associated with the Ssn3p cyclin-depende	YNL025c	orf19.7355
CA3449	IPF7320	1.0	-1.1	-1.0	1.0	unknown function	YOR359w	orf19.2973
CA1597	IPF9538	1.0	1.0	-1.0	1.0	unknown function		orf19.271
CA2279	DUR31	-1.0	1.0	1.0	1.0	Urea transport protein (by homology)	YHL016c	orf19.781
CA1542	ROT11	1.0	-1.0	-1.0	1.0	Putative membrane protein		orf19.4566
E coli 2		-1.0	-1.0	1.0	1.0			
CA3888	IPF12967	1.0	1.0	-1.0	1.0	unknown function		orf19.5092

CA2349	IFC3	1.0	1.1	1.0	1.0	Unknown function	YPR194c	orf19.3749
CA0380	IPF14109	1.5	-1.3	1.1	1.0	unknown function		orf19.2451
CA2220	NTG1	1.0	-1.1	1.1	1.0	endonuclease III-like glycosylase (by homology)	YOL043c	orf19.5098
CA3952	IPF6716	1.0	1.0	1.0	1.0	Phenylacetate 2-hydroxylase (by homology)		orf19.1411
CA0221	PUS4	1.0	-1.0	-1.0	1.0	pseudouridine synthase (by homology)	YNL292w	orf19.9509
CA5572	BGL22	-1.0	-1.0	-1.1	1.0	endo-beta-1,3-glucanase (by homology)		orf19.7339
CA4232	IPF12484	1.0	-1.1	1.0	1.0	unknown function	YER137c	orf19.515
CA1178	IPF5062	1.0	1.0	-1.0	1.0	unknown function	YGR021w	orf19.805
CA3434	CCP1	1.1	1.1	1.1	1.0	Cytochrome-c peroxidase precursor (by homology)	YKR066c	orf19.584
CA4483	IPF9156	-1.1	-1.1	1.0	1.0	unknown function	YOR175c	orf19.1881
CA4597	ATP11	1.0	-1.0	-1.0	1.0	F1F0-ATPase complex assembly protein (by homology)	YNL315c	orf19.6916
CA3025	IPF11503	1.0	1.1	1.1	1.0	unknown function		orf19.3902
CA4649	GPX4	1.0	1.2	1.3	1.0	glutathione peroxidase (by homology)		orf19.4436
CA5156	CLC1	1.2	-1.1	-1.2	1.0	clathrin light chain (by homology)	YGR167w	orf19.4594
CA3049	IPF14990	1.1	1.1	1.0	1.0	unknown function	YAL014c	orf19.9949
CA3275	IPF17068	-1.1	-1.0	-1.0	1.0	unknown function		orf19.6309
CA3621	IPF8942	-1.0	1.0	1.1	1.0	unknown function		orf19.204
CA1786	IPF7629	-1.0	-1.1	-1.1	1.0	unknown function		orf19.1168
CA1725	IPF15985	-1.0	1.0	1.0	1.0	unknown function		orf19.2650
CA1684	IPF6070	1.0	1.0	1.0	1.0	unknown function		orf19.4921
CA0614	IPF19700	1.2	-1.0	-1.0	1.0	unknown function		orf19.1600
CA0923	IPF12987	-1.0	-1.0	1.0	1.0	unknown function	YMR049c	orf19.1047
CA3830	SSF1	1.1	1.0	-1.0	1.0	mating protein (by homology)	YDR312w	orf19.6589
CA2660	SAP1	1.0	-1.0	1.1	1.0	secreted aspartyl proteinase		orf19.5714
CA3079	RAM2	1.0	-1.0	1.0	1.0	geranylgeranyltransferase type I alpha subunit	YKL019w	orf19.4817
CA0432	IPF7926	1.0	-1.0	-1.0	1.0	putative protein kinase (by homology)		orf19.1341
CA0857	SEN15	1.0	1.0	-1.0	1.0	tRNA splicing endonuclease delta subunit(by homology)		orf19.4464
CA5660	SKN1.3	1.0	1.0	1.0	1.0	Glucan synthase subunit, 3-prime end		orf19.7362
CA6158	IPF1839	1.0	-1.0	1.0	1.0	putative 1-Acyl dihydroxyacetone phosphate reductase (by homology)		orf19.5879
CA2523	IPF4319	1.0	1.1	1.0	1.0	unknown function		orf19.5520
CA1109	MRPS9	1.1	-1.0	-1.0	1.0	ribosomal protein S9 small subunit precursor	YBR146w	orf19.5230
CA2989	SIN3.EXON3	-1.2	1.0	-1.1	1.0	Histone deacetylase by homology	YOL004w	orf19.6011
CA2439	IPF7514	1.0	-1.0	-1.0	1.0	unknown function		orf19.2197
CA4271	SAP30	1.0	1.0	-1.0	1.0	Subunit of the histone deacetylase B complex (by homo	YMR263w	orf19.6667
CA5615	IPF520	-1.0	-1.0	1.1	1.0	unknown function	YCL016c	orf19.7083
CA0444	IPF17429.3F	-1.1	-1.1	-1.2	1.0	similar to Saccharomyces cerevisiae Sec5p required for	YDR166c	orf19.75
CA3788	IPF16445	-1.0	1.1	1.0	1.0	unknown function		orf19.5831
CA5208	IPF2361	-1.1	1.0	1.0	1.0	unknown function	YLR455w	orf19.7023
CA3753	IPF14743	-1.0	-1.1	-1.1	1.0	unknown function		orf19.3425
CA1876	IPF10301	-1.1	-1.2	-1.2	1.0	putative 60S ribosomal protein L7/L12 homolog, mitoch	YGL068w	orf19.2275
CA1777	IPF14706	-1.0	1.0	1.0	1.0	unknown function		orf19.1824
CA5810	IPF4137.3F	1.1	1.1	1.2	1.0	unknown function, 3-prime end		
CA1079	LIP1	1.1	-1.0	1.2	1.0	Secretory lipase		orf19.4821
CA2111	IPF13748	1.1	1.1	1.2	1.0	Unknown function	YJL184w	orf19.3688
CA0080	IPF11378	1.1	1.0	1.1	1.0	unknown function		orf19.632
CA5384	ZORRO1B.5F	1.0	1.1	1.0	1.0	reverse transcriptase, 5-prime end (by homology)		orf19.7274
CA4026	IPF7175	-1.0	1.1	1.0	1.0	unknown function		orf19.3437
CA3443	IPF11324	1.0	1.1	1.0	1.0	unknown function	YLR423c	orf19.2982
CA2646	IPF13089	1.2	1.0	1.1	1.0	unknown function	YNL116w	orf19.1185

CA5219	YAE1	1.0	-1.2	1.1	1.0	Essential protein	YJR067c	orf19.7037
CA0575	IPF15178	1.0	1.0	1.1	1.0	Unknown function		orf19.1808
CA1897	IPF12002	-1.1	1.1	1.2	1.0	unknown function		orf19.10271
CA5944	IPF3491	1.1	1.0	1.0	1.0	unknown function	YBR062c	orf19.6753
CA1233	IPF11814	1.0	1.0	-1.0	1.0	unknown function		orf19.4983
CA3704	IPF5671	-1.0	1.1	-1.0	1.0	unknown function		orf19.4946
CA6117	IPF122	1.0	-1.0	1.0	1.0	unknown function		orf19.5933
CA2800	IPF11366	-1.0	1.1	1.0	1.0	unknown function		orf19.1717
CA2604	IPF5469	-1.0	-1.0	1.1	1.0	unknown function		orf19.5681
CA3627	IPF18318	-1.2	-1.0	-1.1	1.0	unknown function	YLL007c	orf19.12613
CA0043	HRD1	-1.3	1.0	-1.1	1.0	Involved in degradation of Hmg2p	YOL013c	orf19.719
CA4200	CCL1	1.1	-1.0	-1.0	1.0	cyclin (by homology)	YPR025c	orf19.4542
CA3143	IPF8295	-1.0	1.0	1.0	1.0	unknown function		orf19.3714
CA1376	IPF7159	1.1	1.1	1.0	1.0	unknown function	YBL107c	orf19.8789
CA4989	IPF2041	1.1	1.1	1.0	1.0	unknown function		orf19.5259
CA4370	IPF5279	-1.2	1.1	-1.1	1.0	unknown function	YHR076w	orf19.5661
CA4652	IPF3105	-1.1	-1.0	1.1	1.0	Unknown function		orf19.4439
CA2863	IPF20117	1.0	1.0	1.0	1.0	unknown function	YLR421c	orf19.1058
CA4325	IPF2094	1.0	1.0	-1.1	1.0	unknown function		orf19.4094
CA1718	IPF9312	1.0	-1.1	1.1	1.0	unknown function		orf19.4649
CA3542	IPF5426	1.0	-1.0	-1.0	1.0	putative methyltransferase (by homology)	YML014w	orf19.6378
CA1157	PZF1	1.0	-1.0	1.0	1.0	TFIIIA (transcription initiation factor) (by homology)	YPR186c ; Missing in array	orf19.4125
CA4346	IPF3634	1.0	-1.0	1.1	1.0	unknown function	YDR090c	orf19.6720
CA2191	IPF9417	-1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Hsf1p heat shock	YGL073w	orf19.4775
CA3258	IFC2	-1.0	-1.0	1.0	1.0	Unknown Function		orf19.11233
CA0998	IPF12369	1.0	1.0	1.1	1.0	Putative dipeptidase (by homology)		orf19.11846
CA0191	PEX7	1.0	1.1	1.0	1.0	peroxisomal import protein (by homology)	YDR142c	orf19.89
CA0894	ORM1	-1.1	-1.0	1.1	1.0	unknown function	YGR038w	orf19.5751
CA4530	IME4	-1.0	1.0	1.0	1.0	positive transcription factor for IME2 (by homology)	YGL192w	orf19.1476
CA1482	IPF15575	1.0	-1.0	-1.0	1.0	unknown function		orf19.8831
CA2495	CTA24	-1.1	-1.0	-1.0	1.0	transcriptional regulation (by homology)		orf19.4054
CA2846	PAD1	1.0	-1.0	-1.0	1.0	phenylacrylic acid decarboxylase (by homology)	YDR538w	orf19.5731
CA4770	IPF9382.3	1.0	1.1	1.0	1.0	similar to Saccharomyces cerevisiae Dun1p protein kina	YDL101c	orf19.4002
CA3585	IFT1	1.1	-1.0	-1.2	1.0	unknown function		orf19.2253
CA4647	IPF1493	-1.0	-1.0	1.0	1.0	similarity to E.coli X-Pro aminopeptidase II (by homolog	YER078c	orf19.354
CA5571	IPF2001	1.0	-1.0	-1.1	1.0	unknown function		orf19.7337
CA5019	IPF7557	1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Smi1p involved in beta-1,3-glucan synthesis (by		orf19.6972
CA1952	IFP1	1.0	1.0	-1.1	1.0	Unknown function		orf19.762
CA0397	FRE31	1.0	-1.0	-1.0	1.0	Ferric reductase (by homology)	YNR060w	orf19.1930
CA2455	IPF12228	-1.2	1.1	-1.2	1.0	unknown function	YNL047c	orf19.3505
CA1270	IPF13504	-1.0	1.0	1.1	1.0	unknown function		orf19.10665
CA5220	MVP1.EXON2	1.1	1.0	-1.0	1.0	Required for vacuolar protein sorting, exon 2 (by homol	YMR004w	orf19.7038
CA0580	PF3184.EXON	1.1	1.0	-1.1	1.0	unknown function, exon 2	YGR165w	orf19.3559
CA5761	IFF11	1.1	-1.0	1.0	1.0	unknown function		orf19.5399
CA5419	PRS1	-1.1	-1.1	1.1	1.0	Ribose-phosphate pyrophosphokinase	YKL181w	orf19.969
CA2080	IPF9693	1.0	1.1	1.1	1.0	unknown function	YDR482c	orf19.4875
CA0486	IPF15540	1.0	-1.0	-1.0	1.0	unknown function		orf19.258
CA1259	IPF3174	-1.1	-1.0	-1.0	1.0	Farnesyl transferase (by homology)	YPL172c	orf19.10676
CA4036	IPF12042	-1.1	-1.1	-1.1	1.0	unknown function	YGR093w	orf19.3666

CA0113	AUT2	1.0	1.1	1.1	1.0	anchor protein mediateing attachment of autophagosom	YNL223w	orf19.9938
CA0522	IPF4463	1.1	1.0	1.1	1.0	unknown function		orf19.11013
CA4019	HOC1	1.0	-1.0	-1.0	1.0	GLYCOSYLTRANSFERASE by homology	YJR075w	orf19.3445
CA2201	BOS1	1.0	-1.0	-1.0	1.0	ER-to-Golgi v-SNARE (by homology)	YLR078c	orf19.2940
CA2095	IPF11492	1.0	-1.0	-1.0	1.0	unknown function		orf19.2392
CA1456	PF11835.3EOC	1.0	1.0	-1.0	1.0	unknown function		
CA0130	IPF4470	1.1	1.0	1.1	1.0	unknown function	YDR512c	orf19.3533
CA3588	SPE3	1.2	1.1	1.1	1.0	putrescine aminopropyltransferase by homology	YPR069c	orf19.2250
CA2569	IPF12117	1.3	-1.1	-1.0	1.0	unknown function		orf19.5648
CA1610	LAS1	1.0	1.1	1.1	1.0	cell morphogenesis, cytoskeletal regulation and bud for	YKR063c	orf19.4120
CA6104	IPF65	-1.0	1.0	-1.0	1.0	unknown function		orf19.5952
CA4598	IPF20019	1.0	1.1	-1.0	1.0	unknown function	YNL310c	orf19.6917
CA5181	TIM12	1.0	1.0	1.0	1.0	subunit of the TIM22-complex (by homology)	YBR091c	orf19.4620
CA2654	IPF8474	1.1	1.1	1.1	1.0	unknown function	YOR093c	orf19.5702
CA2351	IPF19947	1.1	1.0	1.2	1.0	unknown function	YBL014c	orf19.4420
CA5487	MET12	-1.1	1.2	1.1	1.0	methylenetetrahydrofolate reductase (by homology)	YPL023c	orf19.5321
CA0680	IPF14511.5F	-1.0	1.0	-1.0	1.0	unknown function, 5-prime end	YMR313c	orf19.12169
CA1461	IPF6338	1.1	1.0	1.1	1.0	unknown function		orf19.1109
CA0571	CDC43	-1.0	-1.1	-1.0	1.0	geranylgeranyltransferase I	YGL155w	orf19.9369
CA4969	IPF3930	1.1	-1.0	1.1	1.0	unknown function	YDL114w	orf19.6502
CA0064	IPF19308.3F	1.1	-1.1	-1.1	1.0	unknown function, 3-prime end	Missing in array	
CA4268	IPF2287	1.0	1.0	1.1	1.0	unknown function	YOL008w	orf19.6662
CA4850	CIRT2	-1.0	1.0	1.1	1.0	Transposase		orf19.3820
CA3188	IPF11610	1.0	-1.0	1.1	1.0	similar to Saccharomyces cerevisiae Hat2 subunit of the	YEL056w	orf19.2146
CA5973	IPF931	1.1	1.1	1.0	1.0	unknown function	YDR124w	orf19.7567
CA3021	IPF17640	1.0	-1.0	1.1	1.0	unknown function		orf19.3906
CA1630	RPP1	1.1	-1.0	-1.0	1.0	required for processing of tRNA and 35S rRNA (by hom	YHR062c	orf19.1029
CA3480	IPF3224	1.1	1.0	1.0	1.0	unknown function		orf19.3578
CA2049	IPF12982	1.1	1.0	1.0	1.0	unknown function		orf19.13148
CA4378	IPF11299	-1.0	1.1	1.1	1.0	unknown function	YCR030c	orf19.5671
CA3861	RIM8	1.0	-1.0	-1.0	1.0	regulator of PH response	YGL046w	orf19.6091
CA5674	IPF1274	1.0	1.0	1.1	1.0	similar to Saccharomyces cerevisiae Ase1p component	YOR058c	orf19.7377
CA5225	ACB1.EXON2	1.1	-1.0	1.0	1.0	acyl-coenzyme-A-binding protein, exon 2 (by homology)	YGR037c	
CA5163	TFC1	-1.0	1.0	-1.0	1.0	Transcription initiation factor TFIIIC 95 kD subunit (by h	YBR123c ; Missing in array	orf19.4601
CA1928	MRPL37	1.0	1.0	1.0	1.0	Mitochondrial ribosomal protein YmL37 (by homology)	YBR268w	orf19.755
CA1932	IPF3903	1.1	1.1	1.1	1.0	unknown function	YPL183wa	orf19.760
CA1033	MAD2	-1.0	-1.0	-1.1	1.0	spindle checkpoint complex subunit (by homology)	YJL030w	orf19.8642
CA0589	IPF13080	1.0	-1.0	1.0	1.0	unknown function		
CA3390	CAF17	1.1	-1.0	-1.1	1.0	Component of CCR4 transcriptional complex	YJR122w	
CA3162	HOL5.3F	1.0	1.0	1.0	1.0	member of major facilitator superfamily multidrug-resistance protein subfamily 1, 3-pri		orf19.1583
CA2746	IPF19766	-1.1	-1.0	1.0	1.0	unknown function		orf19.9646
CA6047	IPF4933	1.0	-1.1	-1.0	1.0	unknown function	YCR086w	orf19.7663
CA2402	IPF6437	1.0	1.0	1.0	1.0	unknown function		orf19.3543
CA0906	IPF4406	1.0	1.0	1.0	1.0	unknown function	YKL137w	orf19.1483
CA2409	IPF19948	1.2	-1.0	-1.0	1.0	unknown function	YHR134w	orf19.291
CA2799	IPF19769	-1.0	-1.0	-1.0	1.0	unknown function		orf19.1718
CA1940	IPF7999	1.2	1.1	1.3	1.0	unknown function	YLR008c	orf19.4190
CA2461	MAK11	-1.0	-1.1	-1.1	1.0	involved in cell growth and replication of M1 dsR	YKL021c	orf19.1791
CA1886	RHO2.3F	1.0	1.0	1.1	1.0	GTP-binding protein of the RHO subfamily, 3-prime end		

CA4465	IPF9829	1.1	1.0	1.1	1.0	unknown function	YHR197w	orf19.6862
CA3576	IPF11107	1.0	-1.0	1.0	1.0	probably stearoyl-CoA desaturase by homology to S. cerevisiae		orf19.2264
CA2857	SSA1	-1.4	1.0	-1.1	1.0	Heat shock protein of HSP70 family		orf19.1065
CA3530	IPF9926	1.0	1.0	1.2	1.0	alkaline phosphatase (by homology)		orf19.984
CA2168	IPF4558	1.0	1.1	-1.0	1.0	similar to Saccharomyces cerevisiae Prp3p splicing fact	YDR473c	orf19.910
CA1659	IPF11054	1.0	1.0	1.1	1.0	unknown function	YHR105w	orf19.4323
CA2395	IPF6425	1.0	-1.0	-1.0	1.0	unknown function	YOR320c	orf19.3536
CA5421	SKN7	1.0	1.0	1.1	1.0	Transcription factor (by homology)	YHR206w	orf19.971
CA5314	HAT2	1.0	-1.0	-1.0	1.0	Subunit of the major yeast histone acetyltransferase (by homology)		orf19.7185
CA1195	KAR5	-1.0	-1.0	-1.1	1.0	nuclear fusion protein-like (by homology)	YMR065w	orf19.7750
CA4730	IPF7737	1.0	1.0	1.1	1.0	unknown function		orf19.12320
13882.1		1.0	-1.0	-1.0	1.0			
CA2527	IPF4331	-1.0	1.1	-1.0	1.0	unknown function	YMR285c	orf19.5527
CA1136	IFN2	1.1	-1.0	1.1	1.0	glycerophosphoinositol transporter (by homology)		orf19.1980
CA0563	MNN11	-1.0	-1.1	-1.1	1.0	Mannosyltransferase complex component (by homolog	YJL183w	orf19.2927
CA4653	IPF3102	1.2	1.1	1.1	1.0	similar to Saccharomyces cerevisiae Sec34p required f	YER157w	orf19.4440
CA3972	IPF6504	1.1	1.0	-1.0	1.0	unknown function	YDL099w	orf19.9118
CA3279	IPF6268	1.1	1.0	1.0	1.0	unknown function		orf19.6313
CA0239	RPL9B	1.4	-1.3	1.1	1.0	RPL9B ribosomal protein L9 by homology	YNL067w	orf19.236
CA3859	IPF4632	-1.0	1.1	1.1	1.0	similar to Saccharomyces cerevisiae Vps53p subunit of	YJL029c	orf19.6094
CA4128	IPF6876	1.0	-1.0	-1.0	1.0	unknown function		orf19.11725
CA0372	IPF10062	1.1	1.0	-1.0	1.0	unknown function	YNR051c	orf19.1086
CA1194	MET222	1.0	1.0	1.1	1.0	protein ser/thr phosphatase (by homology)		orf19.7752
CA3931	IPF12719	1.0	1.1	1.0	1.0	unknown function		orf19.5103
CA4388	IPF12416.3	1.0	1.0	1.0	1.0	cytidine deaminase, 3-prime end (by homology)	YLR245c	
CA3259	IPF7970	-1.0	1.1	1.0	1.0	unknown function		orf19.10206
CA2943	MAK31	-1.0	-1.1	1.0	1.0	Involved in stability of L-A dsRNA-containing particles (	YCR020ca	
CA4472	IPF6444	1.1	-1.1	-1.1	1.0	putative methyltransferase (by homology)	YPL157w	orf19.1900
CA2329	IPF4784	-1.0	1.1	1.1	1.0	unknown Function		orf19.4498
CA0137	SEC232	-1.1	1.0	1.0	1.0	Component of COPII coat (by homology)		orf19.9206
CA2670	MAK16	1.0	-1.1	-1.0	1.0	nuclear viral propagation protein (by homology)	YAL025c	orf19.5500
CA2232	IPF10929	1.0	-1.0	-1.0	1.0	unknown function		orf19.3925
CA3586	IFT3	1.0	1.0	1.0	1.0	Unknown function		orf19.2252
CA4156	IPF10990	-1.1	-1.1	-1.0	1.0	unknown function	YOR006c	orf19.5802
CA5191	IPF19538	1.0	1.0	1.0	1.0	partially similar to Isocitrate dehydrogenase (NAD+) subunit 1		
CA3711	CHS3.3F	1.0	1.1	1.2	1.0	chitin-UDP acetyl-glucosaminyl transferase 3, 5-prime e	YBR023c	orf19.4937
CA0309	IPF16935	-1.0	1.0	-1.0	1.0	unknown function	YOL144w	orf19.1091
CA3592	IPF12900	1.0	1.0	1.0	1.0	unknown function	YPL199c	orf19.2246
CA5011	IPF13944	-1.0	-1.1	-1.0	1.0	unknown function	Missing in array	orf19.5236
CA1958	IFE1	1.0	1.1	-1.0	1.0	Unknown function	YAL061w	orf19.769
CA5741	IPF2891	1.1	1.1	1.0	1.0	unknown function		
CA4246	IPF4299	-1.0	1.1	1.0	1.0	unknown function		orf19.535
CA5677	IPF1286	1.0	1.1	1.1	1.0	unknown function		orf19.7380
CA2223	PLB5	-1.1	1.1	1.0	1.0	putative phospholipase B precursor		orf19.12568
CA3695	IPF4872.5F	1.0	-1.0	1.1	1.0	unknown function, 5-prime end		orf19.6270
CA5746	IPF2902	1.1	1.0	1.0	1.0	unknown function		orf19.7455
CA1220	IPF14985	-1.0	-1.1	1.0	1.0	unknown function	YDR459c	orf19.4134
CA3780	IPF11222	-1.0	1.0	-1.0	1.0	unknown function		orf19.5840
CA5165	ARL1	-1.0	-1.0	-1.0	1.0	GTP-binding protein of the ARF family (by homology)	YBR164c	orf19.4603

CA1163	IPF15357	-1.1	1.1	1.0	1.0	unknown function	YER169w	orf19.2730
CA0760	IPF11161.3	1.0	1.1	-1.0	1.0	unknown function, 3-prime end	YCR097w	orf19.3201
CA2040	IPF12946	1.1	-1.0	1.2	1.0	unknown function	YDL199c	orf19.4356
CA0723	PRI2	-1.1	-1.1	-1.0	1.0	DNA-directed DNA polymerase alpha , 58 KD subunit (	YKL045w	orf19.2885
CA4997	IPF2027	1.0	-1.1	-1.1	1.0	unknown function		orf19.5250
CA4984	IPF2052	1.2	1.0	1.3	1.0	unknown function		orf19.5266
CA3024	IPF11506	1.0	1.1	1.1	1.0	unknown function		orf19.3903
CA2017	IPF3414	-1.2	1.0	-1.1	1.0	putative serine/threonine protein kinase	YKL171w	orf19.846
CA2270	VMA4	1.0	-1.2	-1.1	1.0	H+-transporting ATPase E chain	YOR332w	orf19.2598
CA0820	IPF12138	-1.0	-1.2	-1.0	1.0	unknown function	YBR022w	orf19.1950
CA1060	IPF11460	1.0	1.1	-1.1	1.0	unknown function	YJL076w	orf19.267
CA4779	IPF3351	1.0	1.2	1.1	1.0	unknown function	YHR071w	orf19.4012
CA0595	IPF8856	1.0	1.0	1.0	1.0	unknown function		orf19.12367
CA3292	IPF5729	-1.0	-1.0	-1.0	1.0	unknown function		orf19.6326
CA5636	IPF473	1.0	-1.0	-1.0	1.0	unknown Function	YOR166c	orf19.7059
CA2695	IPF9070	1.0	-1.0	1.0	1.0	similar to Saccharomyces cerevisiae Sen2p tRNA splici	YLR105c	orf19.2735
CA4747	IPF4484	1.0	-1.0	-1.0	1.0	unknown function		orf19.4834
CA4623	CTA9	1.0	1.1	1.0	1.0	Putative transcriptional regulator		orf19.3315
CA5794	IPF4191	-1.0	-1.1	1.2	1.0	unknown function	YBL098w	orf19.5443
CA1690	FAT1	-1.1	-1.0	-1.1	1.0	very long-chain fatty acyl-CoA synthetase (by homology	YBR041w	orf19.3653
CA0876	VMA6	1.1	1.0	-1.0	1.0	H+-ATPase V0 domain 36 KD subunit,vacuolar (by hom	YLR447c	orf19.7996
CA0691	CIRT4A	-1.2	-1.1	1.0	1.0	Transposase (by homology)		orf19.10357
CA5376	GDI1	1.1	1.0	1.0	1.0	GDP dissociation inhibitor by homology	YER136w	orf19.7261
CA5882	RRP1	-1.0	-1.1	-1.1	1.0	Involved in processing rRNA precursor species to matu	YDR087c	orf19.6828
CA3751	IPF7378	-1.0	-1.0	-1.0	1.0	unknown function		orf19.3427
CA2557	IPF12101	-1.0	-1.0	1.0	1.0	mycelial surface antigen precursor (by homology to Candida gene CSA1)		orf19.5635
CA0437	DIT1	1.1	1.0	1.1	1.0	Spore wall maturation protein (by homology)	YDR403w	orf19.9308
CA0339	IPF13247	-1.0	-1.1	1.0	1.0	unknown function		orf19.3376
CA3959	IPF11236.3F	-1.1	-1.0	-1.1	1.0	similar to Saccharomyces cerevisiae Sec15p component of the exocyst complex, 3-pr		orf19.1418
CA1307	IPF13506.3	-1.0	-1.0	-1.0	1.0	unknown function, 3-prime end		
CA4228	IPF16057	1.1	1.0	1.0	1.0	unknown function	YHL025w	orf19.831
CA3826	IPF20148	1.0	1.1	1.0	1.0	unknown function		orf19.5762
CA3114	IPF18384	1.1	1.0	-1.0	1.0	unknown function		
CA4788	SDH42	1.0	-1.0	1.0	1.0	succinate dehydrogenase membrane anchor subunit for sdh2p (by homology)		orf19.4022
CA5999	IPF668	1.0	-1.0	1.0	1.0	unknown function	YDR398w	orf19.7599
CA4397	IPF14369	-1.0	1.0	1.1	1.0	unknown function	YLR165c	orf19.3114
CA0426	CFT1	-1.1	-1.0	-1.0	1.0	pre-mRNA 3 -end processing factor CF II (by homology	YDR301w	orf19.2760
CA1594	IPF11051	-1.0	-1.0	1.1	1.0	unknown function		orf19.4321
CA0424	IPF10795	1.0	1.1	1.2	1.0	putative transcription factor (by homology)		orf19.2356
CA5523	NIT2	1.1	-1.0	-1.0	1.0	Nitrilase (by homology)	YJL126w	orf19.7279
CA2005	IPF11802	1.0	-1.0	1.0	1.0	unknown function		orf19.2797
CA5141	CYT2	1.0	1.1	1.0	1.0	holocytochrome-c1 synthase (by homology)	YKL087c	orf19.4578
CA2774	TFC4	1.0	1.0	1.1	1.0	transcription factor IIIC chain TFC4- like by homology	YGR047c	orf19.274
CA4095	IPF4002	-1.0	-1.0	1.0	1.0	unknown function		orf19.660
CA1173	IPF14254	-1.0	-1.1	-1.1	1.0	unknown function		orf19.4768
CA0652	SHP1	-1.1	-1.1	-1.2	1.0	potential regulatory subunit for Glc7p (by homology)	YBL058w	orf19.10082
CA2737	IPF15423	-1.1	-1.0	-1.1	1.0	putative superoxide dismutase (by homology)		orf19.2108
CA4591	IPF2216	-1.0	-1.0	-1.0	1.0	putative folylpolyglutamate synthetase (by homology)	YMR113w	orf19.6908
CA0925	IPF17050	1.0	1.1	-1.0	1.0	unknown function		orf19.1049

CA1831	CHS1	1.0	1.0	1.2	1.0	Chitin synthase (by homology)	YBR038w ; Missing in array	orf19.5188
CA1906	IPF7271	-1.0	-1.0	1.1	1.0	unknown function		orf19.2784
CA3493	CDC7	-1.1	1.1	1.0	1.0	serine/threonine protein kinase (by homology)	YDL017w	orf19.3561
CA5513	RPC11	1.1	1.1	1.0	1.0	RNA polymerase III C11 subunit (by homology)	YDR045c	orf19.5360
CA4066	IPF5925	1.0	1.1	1.0	1.0	RNA-binding protein (by homology)		orf19.444
CA2982	CSE1.3F	1.0	-1.0	1.1	1.0	Importin-beta-like protein, 3-prime end (by homology)		orf19.8815
CA4680	AMD1	-1.3	1.1	-1.1	1.0	AMP deaminase (by homology)	YML035c	orf19.891
CA2446	IPF2582	-1.0	1.0	1.0	1.0	unknown function	YKL098w ; Missing in array	orf19.5504
CA3019	IPF15494	-1.0	-1.0	-1.0	1.0	putative ribonuclease (by homology)		orf19.3910
CA4049	PF10482.EXON	1.1	-1.0	-1.1	1.0	unknown function, exon 1		orf19.8054
CA0904	IPF4403	-1.1	-1.0	1.0	1.0	unknown function		orf19.1481
CA2295	HOS2	-1.1	1.0	-1.0	1.0	putative histone deacetylase (by homology)	YGL194c	orf19.5377
CA3471	IPF6308	-1.0	1.0	-1.0	1.0	unknown function		orf19.1667
CA0248	IPF7262	1.0	1.0	-1.0	1.0	unknown function		orf19.2789
CA0452	IPF13554	1.1	1.0	1.0	1.0	Hypothetical acidic protein		orf19.8881
CA0338	IPF13252	-1.0	1.0	1.0	1.0	unknown function		orf19.3378
CA1785	IPF7631	1.1	1.0	1.0	1.0	unknown function	YPR061c	orf19.1169
CA2705	NEM1	1.1	-1.1	-1.0	1.0	required for nuclear morphology (by homology)	YHR004c	orf19.4657
CA4695	IPF4229	-1.1	-1.0	1.1	1.0	unknown function	YML015c	orf19.6923
CA0220	ABZ1	1.0	-1.1	-1.0	1.0	para-aminobenzoate synthase (by homology)	YNR033w	orf19.1291
CA5504	TAF65	1.0	1.0	1.0	1.0	subunit of transcription factor TFIID (by homology)	YML114c	orf19.5346
CA1916	IPF16566.3	1.1	1.0	1.0	1.0	unknown function, 3-prime end	YHR001wa	
CA0330	BAT21	-1.1	-1.1	1.1	1.0	branched-chain amino acid transaminase (by homology	YJR148w	orf19.797
CA5979	IPF921	-1.0	-1.1	-1.0	1.0	BTB domain and Ankaryin repeat containing protein (by homology)		orf19.7574
CA5441	IPF227	1.0	-1.1	-1.2	1.0	unknown function	YHR116w	orf19.3244
CA2045	IPF8107	1.1	-1.0	-1.0	1.0	unknown function	YFL044c	orf19.10450
CA1327	IPF6680	1.0	-1.1	1.0	1.0	unknown function	YHR070w	orf19.1305
CA5260	RAD54	-1.0	1.1	1.0	1.0	DNA-dependent ATPase of the Snf2p family (by homolc	YGL163c	orf19.5004
CA0770	IPF10963	-1.2	-1.0	-1.2	1.0	similar to Saccharomyces cerevisiae Tid3p intercating	YIL144w	orf19.10345
CA1323	IPF6675	1.0	1.0	1.1	1.0	unknown function		orf19.1309
CA4548	IPF7862	1.0	1.0	1.1	1.0	unknown function		orf19.1450
CA4910	IPF1437	1.0	-1.0	1.1	1.0	unknown function		orf19.6048
CA0103	IPF17515	-1.1	1.1	1.5	1.0	unknown function		orf19.749
CA2422	IPF14997	-1.0	-1.0	-1.1	1.0	unknown function		orf19.11950
CA0295	IPF15033	1.0	1.0	1.1	1.0	unknown function	YDL091c	orf19.1595
CA2428	IPF9894.3	-1.0	1.0	1.1	1.0	unknown function, 3-prime end		orf19.3405
CA1454	ALG1	-1.0	-1.1	-1.1	1.0	beta-1,4-mannosyltransferase (by homology)	YBR110w	orf19.4410
CA1274	SAS10	-1.0	-1.0	-1.0	1.0	Involved in silencing (by homology)	YDL153c	orf19.2717
CA3958	COX11	1.1	1.1	1.3	1.0	cytochrome-c oxidase assembly protein by homology to	YPL132w	orf19.1416
CA6018	IPF627	1.1	1.0	-1.0	1.0	unknown function	YOR148c	orf19.7620
CA3540	PTC5	-1.2	-1.0	-1.0	1.0	Type 2C Protein Phosphatase by homology	YOR090c	orf19.6376
CA1141	IPF17322.5F	1.1	-1.0	-1.0	1.0	unknown function, 5-prime end		orf19.4069
CA0315	ALS9.5EOC	-1.0	-1.0	1.0	1.0	agglutinin-like protein, 5-prime end	Missing in array	orf19.5742
CA2665	CDC21	1.0	-1.1	1.0	1.0	thymidylate synthase (by homology)	YOR074c	orf19.3549
HumanActin		1.0	1.0	1.1	1.0			
CA3622	IPF12022	-1.0	1.0	1.1	1.0	extracellular alpha-1,4-glucan glucosidase (by homology)		orf19.7836
CA2136	VPS33	1.0	-1.0	-1.0	1.0	VACUOLAR PROTEIN SORTING (by homology)	YLR396c	orf19.5214
CA2516	IPF4301	1.0	1.0	1.1	1.0	unknown function	YAL032c	orf19.5513
CA5212	IPF3050	1.1	1.0	1.0	1.0	unknown function	YDL238c	orf19.7029

CA3833	IPF8192	1.0	1.0	1.2	1.0	unknown function		orf19.6592
CA6006	IPF652	1.0	-1.0	1.0	1.0	unknown function		orf19.7606
CA0078	CTA27	-1.0	1.0	-1.1	1.0	transcriptional activation		
CA5643	IPF448	1.0	-1.0	-1.0	1.0	unknown function	YOR111w	orf19.7051
CA6039	CKA1	-1.1	1.0	-1.0	1.0	casein kinase II, catalytic alpha chain (by homology)	YIL035c	orf19.7652
CA2397	CFL12	1.0	1.1	-1.0	1.0	Strong similarity to ferric reductase Fre2p (by homology)		orf19.3538
CA1641	NHP10.3F	1.1	1.0	-1.0	1.0	unknown function, 3-prime end	YDL002c	orf19.1731
CA1038	IPF6159	-1.1	-1.1	-1.1	1.0	unknown function	YML076c	orf19.8637
CA1114	IPF9995	1.0	1.1	1.2	1.0	unknown function	YJR070c	orf19.2286
CA0111	IPF16830	-1.0	1.0	1.0	1.0	similar to Saccharomyces cerevisiae Spo1p transcriptio	YNL012w	orf19.4151
CA3558	IPF7760	1.0	-1.0	-1.0	1.0	unknown function		orf19.3887
CA5901	IPF2374	1.0	1.0	-1.0	1.0	unknown function	YDR089w	orf19.6805
CA0463	IPF18979	1.0	1.1	1.0	1.0	unknown function		orf19.7797
CA4644	IPF1497	-1.0	1.0	-1.0	1.0	unknown function	YPR153w	orf19.351
CA1612	IFJ6	1.1	1.0	1.1	1.0	unknown function		orf19.3214
CA1159	IPF13423	1.0	1.0	-1.0	1.0	unknown function		orf19.4128
CA0096	IPF13409	-1.0	1.0	1.0	1.0	unknown function	YJL149w	orf19.751
CA6017	IPF629	-1.1	-1.1	-1.1	1.0	unknown function		orf19.7619
CA5762	IPF1084.3	1.1	1.1	1.1	1.0	unknown function, 3-prime end		orf19.5401
CA3340	ADA2	-1.1	-1.0	-1.1	1.0	general transcriptional adaptor or co-activator (by homo	YDR448w	orf19.2331
CA2849	POP2	-1.0	1.0	1.0	1.0	required for glucose derepression (by homology)	YNR052c	orf19.5734
CA3138	SAP2	1.0	1.0	1.0	1.0	aspartic protease		orf19.3708
CA4462	IPF17251	1.0	-1.0	1.1	1.0	unknown function		orf19.6859
CA4080	IPF2524	-1.0	-1.0	1.1	1.0	unknown function	YPR084w	orf19.6636
CA2224	UGA6.3EOC	1.0	1.0	1.2	1.0	GABA-specific transport protein, 3-prime end		
CA2370	APN2	-1.0	-1.0	-1.1	1.0	AP endonuclease, exonuclease III homologue (by homo	YBL019w	orf19.1836
CA2392	IPF15672	-1.0	1.0	1.1	1.0	unknown function		orf19.10138
CA3612	IPF3852	1.1	1.0	-1.0	1.0	unknown function	YJR046w	orf19.29
CA5368	IPF5257	1.0	-1.1	-1.0	1.0	unknown function		orf19.7250
CA1920	IPF7476	-1.2	-1.2	1.1	1.0	similar to Saccharomyces cerevisiae Rgd1p putative GT	YBR260c	orf19.2443
CA3207	IPF3456	-1.0	1.0	1.1	1.0	unknown function	YHR198c	orf19.6189
CA3351	IPF18347	1.0	1.0	-1.0	1.0	unknown function		orf19.9503
CA0735	IPF8995	1.1	-1.1	1.1	1.0	unknown function	YMR226c	orf19.4633
CA4600	IPF2199	1.1	1.0	1.0	1.0	unknown function		orf19.6919
CA5128	IPF5118	-1.0	1.0	-1.0	1.0	unknown function	YOL032w	orf19.13758
CA3791	IPF11212	1.0	1.0	1.0	1.0	similar to Saccharomyces cerevisiae Bub2 cell cycle arr	YMR055c	orf19.5827
CA4888	IPF1631	1.1	1.0	-1.1	1.0	unknown function		orf19.6580
CA5297	YAR1	1.1	1.1	-1.2	1.0	Ankyrin repeat-containing protein (by homology)	YPL239w	orf19.7160
COX3a		-1.1	-1.1	-1.1	1.0			
CA3653	IPF7451	1.0	1.0	1.0	1.0	unknown function		orf19.2044
CA4720	ECM18	1.0	1.2	1.0	1.0	Involved in cell wall biogenesis and architecture (by hom	YDR125c	orf19.6958
CA1826	UAP1	-1.2	-1.0	-1.1	1.0	UDP-N-acetylglucosamine pyrophosphorylase	YDL103c ; Missing in array	orf19.4265
CA4480	IPF6464	1.0	1.1	1.1	1.0	putative triacylglycerol lipase (by homology)	YLL012w	orf19.1887
CA1443	IPF4776	-1.1	-1.2	-1.1	1.0	unknown Function	YKL172w	orf19.4492
CA5117	IPF1323	-1.1	1.0	-1.0	1.0	unknown function		orf19.6414
CA3380	MSL5	1.0	-1.0	1.0	1.0	branch point bridging protein (by homology)	YLR116w	orf19.329
CA5055	IPF3701	1.0	1.0	1.0	1.0	unknown function	YMR114c	orf19.3021
CA5472	IPF16948	-1.0	1.1	-1.0	1.0	unknown function		orf19.3285
CA5045	IPF4510	-1.0	1.0	1.1	1.0	unknown function		orf19.6999

CA1939	IPF8000	1.0	1.0	1.1	1.0	unknown function		orf19.4189
CA4848	RTS2	1.1	1.1	1.1	1.0	Unknown function	YOR077w	orf19.3817
CA0014	IPF13368	1.0	-1.0	1.0	1.0	unknown function		orf19.11034
CA1334	IPF19912	1.0	1.1	-1.0	1.0	unknown function		orf19.8740
CA3255	IPF4729	1.1	1.0	-1.0	1.0	unknown Function		orf19.3743
CA5118	IPF1321	1.0	-1.1	1.0	1.0	unknown function		orf19.6413
CA0405	IPF19862.3F	-1.0	-1.0	1.0	1.0	unknown function, 3-prime end		orf19.12993
CA3373	SEO1	1.1	1.0	-1.0	1.0	suppressor of sulfoxyde ethionine resistance (by homology)		orf19.1855
CA2917	IPF16173.5F	1.0	1.0	1.1	1.0	Unknown function, 5-prime end		orf19.4509
CA6161	IPF1834	1.0	-1.1	-1.0	1.0	probable syntaxin (by homology)	YOR036w	orf19.5875
CA0217	MNN4	1.1	-1.0	1.1	1.0	regulates the mannosylphosphorylation (by homology)	YKL201c	orf19.849
CA5093	IPF1390	1.0	1.1	1.0	1.0	unknown function		orf19.6449
COX1		-1.1	1.0	-1.1	1.0			
CA5470	IPF300	-1.0	-1.0	-1.0	1.0	unknown function		orf19.3282
CA3396	IPF13617	1.1	-1.0	1.1	1.0	unknown function		orf19.3971
CA2918	IPF16173.3F	-1.0	-1.0	1.1	1.0	unknown function, 3-prime end		orf19.4508
CA0897	IPF4902	-1.1	1.0	-1.0	1.0	unknown function		orf19.8043
CA4139	THR4	-1.1	-1.1	-1.1	1.0	threonine synthase (by homology)	YCR053w	orf19.4233
CA1058	DOT6	1.1	-1.1	-1.0	1.0	involved in derepression of telomeric silencin	YER088c	orf19.2545
CA0968	SAP6	-1.0	1.0	-1.0	1.0	secreted aspartyl protease		orf19.12988
CA3317	URM1	1.0	1.1	1.0	1.0	ubiquitin like protein (by homology)	YIL008w	orf19.2299
CA1135	IMP2	-1.0	1.0	-1.0	1.0	mitochondrial inner membrane protease subunit (by hom	YMR035w	orf19.1981
Int 1		1.0	1.0	1.0	1.0			
CA2267	IFU1.5F	-1.1	-1.1	-1.1	1.0	Unknown function, 5-prime end	YNL126w	orf19.2600
Lux A		1.0	1.0	1.0	1.0			
CA2069	FUR1	1.0	1.1	1.1	1.0	Uracil phosphoribosyltransferase (by homology)	YHR128w	orf19.2640
CA2894	IFS2	-1.1	-1.0	-1.0	1.0	Unknown function		orf19.2462
CA4552	IPF7869	1.0	-1.0	-1.0	1.0	unknown function		orf19.1447
CA1726	IPF13021	-1.1	-1.0	-1.0	1.0	unknown function		orf19.2647
CA2321	MEC3	-1.0	1.0	-1.0	1.0	G2-specific checkpoint protein (by homology)	YLR288c	orf19.5485
CA3465	MRP1.3F	-1.0	-1.1	-1.1	1.0	Mitochondrial ribosomal protein of the small subunit, 3-p	YDR347w	
CA4383	IPF8573	-1.1	1.0	1.1	1.0	unknown function	YLR427w	orf19.13121
Int 4		1.0	1.0	1.0	1.0			
CA0390	DCG1	-1.0	-1.0	-1.1	1.0	involved in nitrogen-catabolite metabolism (by ho	YIR030c	orf19.244
CA2791	IMP4	1.0	1.0	1.0	1.0	Ribonucleoprotein (by homology)	YNL075w	orf19.603
CA2129	IPF4899	-1.0	-1.1	-1.1	1.0	unknown function	YKL155c	orf19.414
CA4100	IPF3985	-1.0	1.0	-1.1	1.0	unknown function	YDR499w	orf19.666
CA4503	SRV2	-1.0	-1.0	1.0	1.0	adenylate cyclase-associated protein homolog	YNL138w	orf19.505
CA1689	IPF13030	-1.1	1.0	-1.0	1.0	unknown function		orf19.3655
CA0937	IPF19892	1.1	1.1	1.0	1.0	unknown function		orf19.8683
CA2101	IPF9364	-1.0	-1.1	-1.1	1.0	unknown function	YMR097c	orf19.2384
CA1692	PF17055.3EOC	1.1	1.0	1.0	1.0	unknown function, 3-prime end	YDR425w	orf19.5036
CA2929	IPF7838	1.0	1.0	1.1	1.0	similar to Saccharomyces cerevisiae Mus81p involved in	YDR386w	orf19.4206
CA2783	IPF3808	-1.0	-1.0	-1.0	1.0	unknown function	YLL042c	orf19.286
CA0874	CPA1	-1.0	1.1	1.0	1.0	Arginine-specific carbamoylphosphate synthase, small (	YOR303w	orf19.12100
CA1739	IPF4976	1.1	1.0	1.1	1.0	unknown function		orf19.10057
CA1453	HOS1	-1.1	-1.1	-1.0	1.0	Putative histon deacetylase (by homology)	YPR068c	orf19.4411
CA2915	IFA17.3F	-1.0	1.0	1.1	1.0	unknown function, 3-prime end		orf19.4511
NAD5		-1.0	-1.0	-1.1	1.0			

CA4733	IPF7732	-1.0	-1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Hcm1p transcripti	YCR065w	orf19.4853
CA4376	IPF11307	-1.0	1.0	1.1	1.0	unknown function	YKL064w	orf19.5667
CA5380	IPF5224	1.1	1.1	1.1	1.0	unknown function		orf19.7267
CA2747	IPF11467	-1.0	1.0	1.0	1.0	unknown function	YNL260c	orf19.2367
CA2815	IPF5604	-1.0	1.0	-1.0	1.0	unknown function	YLR436c	orf19.2996
CA3811	PET112	-1.0	-1.0	-1.1	1.0	glutamyl-tRNA (GLN) amidotransferase subunit B (by h	YBL080c	orf19.2494
CA0911	IPF14814	1.0	-1.0	1.0	1.0	unknown function	YJR097w	orf19.9568
CA1908	APL3	-1.2	-1.1	-1.1	1.0	AP-2 complex subunit, alpha-adaptin (by homology)	YBL037w	orf19.2786
CA4368	PEX10.3	1.1	-1.0	-1.1	1.0	peroxisomal assembly protein, 3-prime end (by homolo	YDR265w	orf19.5660
CA1949	IPF14021	1.0	1.0	-1.0	1.0	dual specificity phosphatase (PTP/DSP) (by homology)	YJR110w	orf19.12206
CA2686	HST2	-1.1	1.0	-1.1	1.0	Transcription regulatory protein	YPL015c	orf19.2580
CA2236	IFA23	-1.1	-1.0	-1.1	1.0	unknown function		orf19.3919
CA6058	ATP16	1.0	-1.0	1.0	-1.0	F1F0-ATPase complex, F1 delta subunit	YDL004w	orf19.7678
CA3935	IPF14688	-1.2	-1.0	1.1	-1.0	unknown function	YDR027c	orf19.2007
CA0493	PRP39.3	1.0	-1.0	1.1	-1.0	pre-mRNA splicing factor, 3-prime end (by homology)	YML046w	orf19.1492
CA0206	IPF14089	-1.1	1.0	-1.1	-1.0	putative serine/threonine protein kinase		orf19.10297
CA4948	IPF5149	1.0	-1.1	1.0	-1.0	unknown function	Missing in array	orf19.6530
CA0205	DBF2	-1.1	-1.1	-1.2	-1.0	putative ser/thr protein kinase by homology	YGR092w	orf19.1223
CA4917	ECM31	1.0	-1.1	-1.0	-1.0	Involved in cell wall biogenesis and architecture (by hon	YBR176w	orf19.6057
CA1008	IPF14083	-1.1	-1.1	-1.1	-1.0	similarity to Saccharomyces cerevisiae carrier protein F	YPR128c ; Missing in array	orf19.6254
CA3843	IPF7947	-1.1	-1.0	1.1	-1.0	unknown function	YLR201c	orf19.6602
CA1093	MSM1	1.0	1.0	-1.0	-1.0	mitochondrial methionyl-tRNA synthetase	YGR171c	orf19.3950
CA5839	IPF423	1.0	1.0	-1.0	-1.0	unknown function	YLR320w	orf19.7494
CA1769	IPF7581	-1.1	1.0	-1.0	-1.0	unknown function		orf19.5203
CA2879	IPF3779	-1.0	1.1	-1.0	-1.0	unknown function		orf19.5848
CA3066	IPF15813	-1.0	-1.2	1.0	-1.0	unknown function	YLR223c	orf19.4281
CA1366	IPF11847	1.0	1.0	1.1	-1.0	unknown function	YNL233w	orf19.4457
CA2140	IPF19665	-1.5	-1.3	-1.2	-1.0	unknown function	YOR349w	orf19.10046
CA4093	IPF5002	-1.0	-1.0	-1.1	-1.0	GTP binding protein (by homology)	YHR168w	orf19.6653
CA2090	IPF3398.3	1.1	-1.0	1.0	-1.0	unknown function, 3-prime end		
CA3204	IPF3446	1.1	1.1	1.1	-1.0	Unknown function		orf19.6186
CA0236	MDM10	1.0	-1.0	-1.0	-1.0	Involved in mitochondrial morphology and inheritance (	YAL010c	orf19.7814
CA4315	PPX1	-1.1	-1.1	-1.1	-1.0	Exopolyphosphatase (by homology)	YHR201c	orf19.4107
CA6098	IPF61	-1.0	-1.2	-1.1	-1.0	unknown function	YDL148c	orf19.5959
CA3561	SLY1	-1.1	1.0	-1.1	-1.0	hydrophilic suppressor of YPT1 and member of the Sec	YDR189w	orf19.3128
CA2350	CWH41.5EOC	1.0	1.1	1.0	-1.0	ER glucosidase I, 5-prime end (by homology)		orf19.4421
CA0511	IPF13975	-1.1	1.1	1.0	-1.0	unknown function	YCL047c	orf19.4953
CA1626	STR2	-1.1	-1.0	1.1	-1.0	O-succinylhomoserine (thiol)-lyase (by homology)	YJR130c	orf19.1033
CA5565	QRI8	1.1	1.1	1.0	-1.0	E2 ubiquitin-conjugation enzyme (by homology)	YMR022w	orf19.7329
CA0195	IPF12688	1.2	1.0	1.1	-1.0	unknown function	YOR280c	orf19.11403
CA2174	IPF20096	-1.0	1.0	1.1	-1.0	unknown function		orf19.3763
CA3179	YLF2	-1.0	-1.0	-1.1	-1.0	GTP-binding protein	YHL014c	orf19.2128
CA0805	IPF12568	-1.1	1.0	1.0	-1.0	unknown function		orf19.3516
CA4165	IPF7774	-1.0	1.1	-1.0	-1.0	unknown function		orf19.10485
CA1420	RNT1	-1.1	-1.1	-1.1	-1.0	Ribonuclease III (by homology)	YMR239c	orf19.11277
CA5245	DUR32	1.1	1.1	1.1	-1.0	Urea transport protein (by homology)		orf19.5017
CA0097	IPF13290	-1.0	-1.1	-1.1	-1.0	unknown function		orf19.5314
CA2022	CBK1	1.0	1.2	-1.0	-1.0	serine/threonine protein kinase (by homology)	YNL161w	orf19.4909
CA5498	IPF772	-1.2	1.0	1.1	-1.0	unknown function	YPL249c	orf19.5340

CA1050	IPF19897	1.0	1.0	1.0	-1.0	unknown function		orf19.3897
CA0893	IPF13517	-1.1	-1.0	-1.0	-1.0	unknown function	YBR280c	orf19.5752
CA4978	IPF2065	1.0	1.1	-1.0	-1.0	unknown function	YLR187w	orf19.5274
CA3731	SPC2	1.1	1.1	1.1	-1.0	signal peptidase 18 kDa subunit (by homology)	YML055w	orf19.4181
CA0208	IPF19850	-1.0	-1.0	1.1	-1.0	unknown function		orf19.1227
CA5751	VPS8	-1.2	1.0	1.0	-1.0	Vacuolar sorting protein (by homology)	YAL002w	orf19.5387
CA1400	IPF8067	1.0	-1.0	-1.0	-1.0	unknown function	YNL127w	orf19.3697
CA2895	IFS1	-1.0	1.0	1.1	-1.0	Unknown function		orf19.2461
CA2893	IFS3	1.1	-1.0	1.1	-1.0	Unknown function		orf19.2463
CA2735	TFG2	1.1	-1.0	-1.1	-1.0	transcription initiation factor TFIIF middle subunit (by ho	YGR005c	orf19.2111
CA5781	IPF1126	-1.0	1.0	1.1	-1.0	unknown function	YOR079c	orf19.5428
CA4369	TIM11	1.1	-1.1	-1.1	-1.0	subunit e of mitochondrial F1F0-ATPase by homology		
CA2643	HSL1	1.0	1.0	-1.1	-1.0	Ser/thr protein kinase that interacts genetically with hist	YKL101w	orf19.4308
CA4702	IPF4213	-1.1	-1.1	-1.1	-1.0	unknown function		orf19.6930
CA1086	IPF1039	1.0	1.0	-1.0	-1.0	unknown function		orf19.12038
CA5175	IPF6041	1.1	1.1	1.0	-1.0	Similar to Legionella pneumophila sbpA		orf19.4612
CA4731	LIP3	1.0	1.0	-1.0	-1.0	Secretory lipase		orf19.4856
CA5332	IPF900.3	1.0	-1.0	1.0	-1.0	unknown function, , 3-prime end	YDR067c	orf19.7206
CA1105	IPF18760.3	1.1	1.0	1.1	-1.0	unknown function, 3-prime end		
CA3985	POB3	-1.3	-1.1	-1.0	-1.0	Binds DNA polymerase delta (by homology)	YML069w	orf19.1560
CA5945	IPF3492	-1.0	-1.0	-1.1	-1.0	unknown function	YDR041w	orf19.6752
CA2426	IPF9901	-1.1	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae rad18p DNA repai	YCR066w	orf19.3407
CA3417	FRE41	-1.0	-1.0	-1.0	-1.0	ferric reductase transmembrane component (by homology)		orf19.6138
CA4636	IPF1520	1.1	1.0	1.0	-1.0	unknown function		orf19.342
CA0513	IPF13972	-1.0	1.0	-1.0	-1.0	unknown function	YCL048w	orf19.4955
CA1577	KNS1	1.0	1.1	1.0	-1.0	Ser/thr protein kinase (by homology)	YLL019c	orf19.12446
CA4815	CDH1	-1.0	1.0	-1.0	-1.0	Substrate-specific activator of APC-dependent proteolys	YGL003c	orf19.2084
CA3252	IPF4722	1.0	-1.1	-1.1	-1.0	unknown Function		orf19.3738
CA0162	IPF19168	1.0	-1.0	-1.0	-1.0	unknown function		orf19.5616
CA5730	HST6	1.0	-1.0	-1.0	-1.0	ATP binding cassette protein	YKL209c	orf19.7440
CA2506	IPF6794	1.0	-1.0	1.1	-1.0	unknown function		orf19.5596
CA0502	IPF16761	1.0	1.0	1.0	-1.0	unknown function	YNL085w	orf19.2664
CA3374	IPF4683	-1.0	-1.1	1.0	-1.0	unknown Function	YIL084c	orf19.1856
CA2717	MSB3	1.0	1.1	1.0	-1.0	GTPase-activating protein for Sec4p (by homology)	YNL293w	orf19.8209
CA5285	HBS1.3F	-1.1	1.0	1.2	-1.0	Translation elongation factor eEF-1 alpha chain homolo	YKR084c	orf19.7144
CA4024	IPF7182	1.0	-1.0	-1.1	-1.0	unknown function		orf19.3439
CA0336	IPF9869	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.1371
CA2065	QCR2	1.0	-1.2	-1.2	-1.0	Ubiquinol--cytochrome-c reductase 40KD chain II (by ho	YPR191w	orf19.2644
CA1762	IPF20014	1.0	-1.0	-1.0	-1.0	oxidoreductase by homology	YIR035c	
CA4390	HOD1	1.1	1.1	1.2	-1.0	regulator of G2/M progression (by homology)		
CA1825	IPF9522.3F	1.2	-1.1	-1.0	-1.0	septin, 3-prime end (by homology)		orf19.4266
CA1040	IPF4010	1.0	-1.0	1.1	-1.0	unknown function		orf19.2503
CA2338	NIT3	1.1	-1.1	-1.0	-1.0	nitrilase (by homology)	YLR351c	orf19.2351
CA2590	PPH3.3B	1.0	-1.0	1.1	-1.0	protein serine/threonine phosphatase, 3-prime end (by homology)		orf19.4378
CA6116	TOP3	-1.0	-1.0	-1.1	-1.0	DNA topoisomerase III (by homology)	YLR234w	orf19.5934
CA0521	CKA2	1.0	-1.0	1.1	-1.0	casein kinase II alpha chain (by homology)	YOR061w	orf19.3530
CA2252	IPF12844	-1.0	-1.0	-1.0	-1.0	unknown function	YOR287c	orf19.9898
CA6069	IPF4847	-1.0	1.1	1.1	-1.0	unknown function	YOR197w	orf19.5995
CA4594	IPF2212	-1.1	-1.0	-1.2	-1.0	unknown function		orf19.6912

CA0930	ZORRO1A	-1.0	-1.2	-1.2	-1.0	Putative reverse transcriptase		orf19.559
CA2368	RPA190	-1.2	1.1	-1.1	-1.0	DNA-directed RNA polymerase I (by homology)	YOR341w	orf19.1839
CA4751	IPF11473	1.0	-1.0	-1.1	-1.0	unknown function		orf19.4828
CA0050	CTA25	-1.0	-1.1	-1.1	-1.0	transcriptional activation		orf19.362
CA2652	DNA2	-1.0	1.0	-1.1	-1.0	DNA helicase (by homology)	YHR164c	orf19.1192
CA1380	BCS1	-1.0	-1.1	-1.1	-1.0	mitochondrial protein of the CDC48/PAS1/SEC18 (AAA	YDR375c	orf19.458
CA4805	RAD5	-1.0	1.0	-1.0	-1.0	DNA helicase (by homology)	YLR032w	orf19.2097
CA2704	IPF12195	1.0	-1.0	1.0	-1.0	unknown function		orf19.4656
CA4394	IPF12297	-1.0	1.0	1.0	-1.0	mycelial surface antigen (by homology)		orf19.3117
CA6082	CEM1	-1.1	-1.1	-1.2	-1.0	3-oxoacyl-[acyl-carrier-protein]-synthase (by homology)	YER061c	orf19.5977
CA1053	SCW11.3EOC	1.1	1.2	1.3	-1.0	glucanase gene family member, 3-prime end (by homol	YGL028c	orf19.3893
CA3127	IPF8915	1.0	1.0	-1.0	-1.0	unknown function	YMR067c	orf19.1359
CA1811	MTR10	1.0	-1.0	-1.1	-1.0	Involved in nuclear protein import	YOR160w	orf19.1119
CA5626	IPF498	1.0	-1.0	-1.0	-1.0	unknown function		orf19.7071
CA5489	MDH12	1.2	-1.1	1.2	-1.0	mitochondrial malate dehydrogenase (by homology)	YDL078c	orf19.5323
CA0356	IPF2532	-1.0	1.1	1.0	-1.0	unknown function	YLR104w	orf19.13952
CA3831	VMA22	1.1	1.0	-1.0	-1.0	vacuolar ATPase assembly protein (by homology)	YHR060w	orf19.6590
CA5125	RPP2	1.1	1.0	-1.0	-1.0	acidic ribosomal protein by homology	YOL039w	
CA5207	IPF2359	-1.0	1.0	1.0	-1.0	unknown function		orf19.7022
CA3027	IPF20126	-1.0	-1.0	1.1	-1.0	putative chromosome segregation protein (by homology	YDR470c	orf19.11381
CA1852	885.REPEAT2.	1.0	1.1	1.0	-1.0	unknown function, 5-prime end		
CA2856	IPF7062	-1.0	-1.0	1.0	-1.0	unknown function	YPL067c	orf19.1066
CA4880	RHC18	1.0	-1.1	-1.0	-1.0	Recombination repair protein (by homology)	YLR383w	orf19.6568
CA1378	ERK2	-1.0	1.0	1.0	-1.0	mitogen-activated protein kinase (MAP kinase)		orf19.460
CA2500	FIG4	-1.0	-1.0	-1.0	-1.0	suppressor of sac1 mutation (by homology)	YNL325c	orf19.5586
CA4134	COS162	-1.0	1.0	1.0	-1.0	involved in manganese homeostasis (by homology)	YCR044c	orf19.4240
CA0494	RAD7	1.0	1.2	1.2	-1.0	nucleotide excision repair protein (by homology)	YJR052w	orf19.9070
CA3050	IPF13042	-1.1	-1.1	-1.1	-1.0	similar to Saccharomyces cerevisiaeImh1p involved in v	YLR309c	orf19.9948
CA4537	YNT2	1.1	-1.1	1.0	-1.0	suppressor of rna12/yme2 (by homology)	YLR059c	orf19.1466
CA4065	RPC25	1.1	-1.1	-1.0	-1.0	DNA-direcred RNA polymerase III (by homology)	YKL144c	orf19.443
CA3512	IPF11247	-1.0	1.0	1.1	-1.0	unknown function	YEL059ca	orf19.6359
CA6026	IPF610	-1.0	1.0	-1.0	-1.0	unknown function	YDR489w	orf19.7631
CA2381	YCK3.3F	-1.0	1.1	1.1	-1.0	casein kinase I, 3-prime end (by homology)		orf19.2221
CA0505	IPF11988.3	1.1	-1.0	1.0	-1.0	unknown function, 3-prime end		
CA1780	IPF14509	-1.0	-1.0	-1.1	-1.0	unknown function		orf19.1827
CA4931	IPF8378	1.0	1.0	-1.1	-1.0	unknown function		orf19.6072
CA5616	PET8	-1.0	1.1	1.2	-1.0	mitochondrial carrier protein (by homology)	YNL003c	orf19.7082
CA4167	IPF7778	-1.2	1.0	-1.0	-1.0	putative carboxymethylenebutenolidase (dienelactone h	YDL086w	orf19.2966
CA1381	IPF8420	1.1	1.1	1.0	-1.0	unknown function		orf19.929
CA3615	GIT1	-1.0	1.0	-1.0	-1.0	glycerophosphoinositol transporter (by homology)	YCR098c	orf19.34
CA1046	IPF11617	-1.0	1.0	-1.0	-1.0	unknown function	YOR298w	orf19.1647
CA1455	IPF15081	-1.0	1.0	-1.0	-1.0	phophodiesterase (by homology)	YCR026c	orf19.4409
CA1371	IPF19731	1.1	1.0	1.0	-1.0	unknown function	YLR145w	orf19.4962
CA3135	IPF8990	1.1	-1.0	1.0	-1.0	unknown function		orf19.1366
CA3076	IPF6101.3	1.0	-1.0	1.0	-1.0	unknown function, 3-prime end		orf19.4814
CA5500	IPF768	-1.1	1.0	-1.1	-1.0	unknown function	YHR202w	orf19.5342
CA2987	RPB11.3	1.0	-1.0	1.0	-1.0	DNA-directed RNA polymerase II subunit, 3-prime end (	YOL005c	
CA0676	IPF13097	-1.0	1.0	-1.0	-1.0	unknown function		orf19.8772
CA6019	IPF625	1.0	-1.0	-1.0	-1.0	unknown function	YOR144c	orf19.7621

CA2945	IMG1	1.1	1.1	1.0	-1.0	Ribosomal protein, mitochondrial (by homology)	YCR046c	orf19.1967
CA1299	PTK2	1.0	-1.0	-1.0	-1.0	serine /threonine protein kinase involved in polyamine u	YJR059w	orf19.3415
CA3068	LIP2	-1.0	1.0	1.1	-1.0	Secretory lipase		orf19.4804
CA3209	CTA2.5.3F	-1.1	1.1	1.0	-1.0	transcriptional activator, 3-prime end		
CA1078	SPR1	-1.0	-1.0	1.0	-1.0	exo-1,3-beta-glucanase precursor (by homology)		orf19.2237
CA1269	IPF19726	-1.2	-1.1	-1.0	-1.0	unknown function	YDL001w	orf19.10667
CA6043	RFC4	1.1	1.1	1.0	-1.0	DNA replication factor C (by homology)	YOL094c	orf19.7658
CA3032	IPF12319	-1.1	1.0	1.0	-1.0	unknown function		orf19.216
CA0351	RPB4.3F	-1.1	-1.0	-1.1	-1.0	DNA-directed RNA polymerase II, 32 kDa subunit, 3-pri	YJL140w	orf19.145
CA5968	IPF946	-1.0	1.0	-1.0	-1.0	unknown function		orf19.7561
CA1877	IPF10300	-1.0	1.0	1.0	-1.0	unknown function		orf19.2274
CA0618	UGT51	-1.0	1.0	1.0	-1.0	UDP-glucose:sterol glucosyltransferase	YLR189c	orf19.2616
CA4473	IPF6447	1.1	1.0	1.1	-1.0	unknown function		orf19.1897
CA1516	IPF16764	1.4	-1.0	-1.0	-1.0	unknown function		orf19.4796
CA4141	PTH2	-1.0	1.0	1.2	-1.0	proline transport helper		orf19.11706
CA4879	IPF1660	1.1	-1.0	1.0	-1.0	unknown function		orf19.6566
CA4609	ZPR1	1.0	1.0	-1.1	-1.0	Zinc finger protein (by homology)	YGR211w	orf19.3300
CA3839	IPF12744	-1.0	1.1	1.1	-1.0	unknown function		
CA2970	IPF14448	1.0	-1.0	1.0	-1.0	unknown function		orf19.5601
CA4784	IPF3359	1.1	-1.0	-1.0	-1.0	Unknown function		orf19.4017
CA5786	IPF1134	-1.0	-1.0	1.0	-1.0	unknown function	YDR493w	orf19.5433
CA4324	IPF2095	1.0	1.1	-1.0	-1.0	unknown function		orf19.4095
CA4992	IPF2036	1.1	1.0	1.1	-1.0	unknown function		orf19.5256
CA1556	END3	-1.1	-1.1	-1.0	-1.0	required for endocytosis and cytoskeletal organization (	YNL084c	orf19.1711
CA4355	IPF3649	1.0	1.1	-1.1	-1.0	unknown function	YCR016w	orf19.6730
CA2468	IPF8723	1.0	1.0	1.0	-1.0	unknown function		orf19.1797
CA4787	IPF3364	1.1	-1.0	-1.1	-1.0	Unknown function		orf19.4021
CA1249	SPE4	1.1	-1.0	-1.1	-1.0	spermine synthase (by homology)	YLR146c	orf19.4960
CA3666	IPF11435	1.0	-1.1	1.1	-1.0	unknown function	YDR231c	orf19.6461
CA2723	IPF4805	-1.1	-1.1	-1.1	-1.0	unknown Function	YDR409w	orf19.3345
CA2916	IFA4	-1.0	1.1	-1.1	-1.0	unknown function		orf19.4510
6672.2		-1.0	-1.0	-1.0	-1.0			
CA0498	CTA211.3F	-1.0	-1.1	-1.1	-1.0	transcriptional activator, 3-prime end (by homology)	Missing in array	orf19.2661
CA3575	IPF11108	-1.0	1.0	-1.1	-1.0	unknown function	YCR052w	orf19.2265
CA0751	IPF6286	-1.0	-1.1	-1.1	-1.0	unknown function		orf19.1971
CA2051	PXP5	1.0	1.0	1.1	-1.0	acyl-coenzyme A oxidase I precursor by homology to Candida tropicalis		orf19.5723
CA3231	IPF14348.3	1.1	1.0	-1.0	-1.0	unknown function, 3-prime end		
CA5630	IPF486	1.0	-1.0	-1.0	-1.0	unknown function	YOL146w	orf19.7065
CA1133	F2710.REPEA	1.2	-1.0	1.1	-1.0	putative permease (by homology)		orf19.9706
CA1685	IPF12270	1.0	1.0	1.0	-1.0	unknown function		orf19.3660
CA0694	IPF12603	1.0	-1.1	-1.0	-1.0	unknown function		orf19.3289
CA2343	IPF8671	-1.0	1.0	1.0	-1.0	unknown function	YCL008c	orf19.2343
CA5805	IPF4153	-1.2	1.0	1.2	-1.0	similar to Saccharomyces cerevisiae Sec6p protein inv	YIL068c	orf19.5463
CA0649	RFC3	1.1	1.0	1.0	-1.0	DNA replication factor C, 40 kDa subunit (by homology)	YNL290w	orf19.3211
CA3184	TSM1.5F	1.0	1.1	-1.1	-1.0	component of TFIID complex, 5-prime end (by homology)		orf19.2136
CA1787	IFH3	1.0	-1.0	-1.0	-1.0	Dioxygenase (by homology)	YLL057c	orf19.1167
CA2731	URIC	1.0	-1.1	-1.0	-1.0	uricase (urate oxidase) (by homology)		orf19.2114
CA5860	IPF376	1.0	-1.0	1.1	-1.0	transcriptional regulator (by homology)		orf19.7518
CA1066	IPF9001	-1.0	-1.0	1.1	-1.0	unknown function	YLR097c	orf19.12107

CA0599	IPF12428	1.1	-1.2	-1.1	-1.0	unknown function	YHR088w	orf19.10184
CA0427	IPF11995	-1.0	-1.0	1.2	-1.0	unknown function	YDR302w	orf19.2761
CA5414	IPF1568	1.0	-1.0	-1.1	-1.0	unknown function	YDR156w	orf19.962
CA5739	IPF2884	-1.0	-1.0	1.0	-1.0	unknown function	YMR211w	orf19.7449
CA3433	IPF6387.3	1.1	1.1	1.2	-1.0	unknown function, 3-prime end		
CA2554	CIRT4B	1.0	-1.1	-1.1	-1.0	probable transposase (by homology)		orf19.2839
CA0121	IPF17048	-1.0	-1.0	-1.1	-1.0	unknown function	YOR322c	orf19.983
CA5371	RPC10	-1.0	1.0	-1.0	-1.0	DNA-directed RNA polymerases small subunit by homo	YHR143wa	orf19.7255
CA5530	SPB8	1.1	-1.0	-1.1	-1.0	Suppressor of PAB1 (by homology)	YJL124c	orf19.7290
CA5952	IPF3503	1.1	-1.0	1.0	-1.0	similar to Saccharomyces cerevisiae Fcp1p TFIIF intera	YMR277w	orf19.6742
CA4011	IPF4240	-1.2	-1.2	-1.2	-1.0	similar to Saccharomyces cerevisiae Ycg1p condensin (	YDR325w	orf19.1622
CA3176	IPF11588	-1.0	-1.0	-1.0	-1.0	unknown function	YML080w	orf19.1404
CA0131	IPF13402	1.0	-1.0	1.0	-1.0	unknown function	YML071c	orf19.36
CA4550	DYN2.3	1.1	-1.0	1.1	-1.0	Dynein light chain 1, cytosolic, 3-prime end	YDR424c	
CA2153	IPF7900	-1.1	1.0	1.0	-1.0	unknown function	YGL047w	orf19.6025
CA4185	HNM4	1.0	1.1	1.1	-1.0	Choline permease-like (by homology)		orf19.2946
CA1985	IPF9591	1.0	-1.0	1.0	-1.0	unknown function	YGR053c	orf19.91
CA0177	IFL2	1.0	1.0	-1.1	-1.0	unknown function		orf19.8268
CA0742	IPF3259	1.0	-1.1	1.0	-1.0	unknown function		orf19.3142
CA3717	IPF6192	1.1	-1.1	-1.0	-1.0	unknown function	YPL108w	orf19.11643
CA4372	IPF5282	1.0	1.0	1.0	-1.0	unknown function	YMR034c	orf19.5663
CA0429	IPF14827	1.0	1.0	1.1	-1.0	unknown function		orf19.1611
CA3342	IPF13361	-1.0	-1.1	1.0	-1.0	unknown function	YDR449c	orf19.2330
CA0588	IPF13081	-1.0	1.0	-1.0	-1.0	unknown function		orf19.1162
CA5321	RAD6.3	1.1	-1.0	1.1	-1.0	Ubiquitin protein ligase, 3-prime end	YGL058w	orf19.7195
CA2323	SMD2	-1.0	1.0	1.0	-1.0	U1 snRNP protein of the Sm class protein (by homolog	YLR275w	
CA3533	IPF13450	1.1	1.0	1.0	-1.0	unknown function		orf19.6366
CA5627	IPF495	1.0	1.0	1.0	-1.0	unknown function	YBR261c	orf19.7069
CA0046	IPF14850	-1.0	-1.1	-1.1	-1.0	Hypothetical protein		orf19.9988
CA1686	IPF12272	-1.1	1.1	1.0	-1.0	unknown function	YER139c	orf19.3659
CA1444	KTR2	-1.0	1.1	1.2	-1.0	mannosyltransferase (by homology)	YKR061w	orf19.4494
CA1946	IPF19937	-1.1	1.0	-1.0	-1.0	putative peptidyl-tRNA hydrolases (by homology)	YHR189w	orf19.4740
CA4656	IPF3095	-1.1	-1.1	-1.0	-1.0	unknown function	YDL235c	orf19.4443
CA2586	IPF9435	1.0	-1.1	-1.0	-1.0	unknown function	YLR285w	orf19.4375
CA0707	IPF7711	-1.0	-1.1	1.0	-1.0	related to Neurospora crassa AP-1-like transcription factor (by homology)		orf19.8298
CA3099	LST8	1.1	1.0	1.1	-1.0	required for transport of permeases from the gol	YNL006w	orf19.3862
CA0704	IPF11806	-1.1	-1.0	1.1	-1.0	similar to Saccharomyces cerevisiae Ynd1p nucleoside	YER005w	orf19.2915
CA3303	FRE42	-1.0	1.0	1.0	-1.0	ferric reductase (by homology)		orf19.2312
CA4846	IPF6945.3F	1.0	1.1	-1.0	-1.0	unknown function, 3-prime end		orf19.3814
CA1413	MTR3	-1.1	-1.1	-1.0	-1.0	Involved in mRNA transport (by homology)	YGR158c	orf19.168
CA1642	NHP1.5F	-1.1	-1.0	-1.1	-1.0	unknown function, 5-prime end		orf19.1730
CA1567	IPF7613	1.1	1.0	-1.0	-1.0	unknown function		orf19.1156
CA1585	VPS27	-1.1	-1.0	1.1	-1.0	Vacuolar protein sorting (by homology)	YNR006w	orf19.6031
CA0793	IPF16273	1.0	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Dtr1p dityrosine tra	YBR180w	orf19.553
CA2412	IPF13755	1.1	1.1	1.1	-1.0	unknown function		orf19.4481
CA1573	IPF15087	-1.0	-1.0	-1.1	-1.0	unknown function	Missing in array	orf19.1653
CA5241	SMF3	1.0	1.0	1.1	-1.0	Probable manganese transporter (by homology)		orf19.5022
CA5210	IPF2373	1.1	-1.0	1.0	-1.0	unknown function		orf19.7027
CA1017	IPF11144	1.0	-1.0	1.1	-1.0	unknown function	YHR036w	orf19.8105

CA2281	HAT1	-1.0	1.0	-1.1	-1.0	histone acetyltransferase (by homology)	YPL001w	orf19.779
CA1087	MYO5	1.1	1.1	1.1	-1.0	Myosin I (by homology)	YMR109w	orf19.8357
CA1277	IPF10837	-1.0	-1.0	-1.0	-1.0	unknown function	YDR083w	orf19.3630
CA0157	IPF19178.3F	-1.0	-1.0	-1.0	-1.0	unknown function, 3-prime end	Missing in array	
CA3715	IPF6205	1.1	-1.0	-1.1	-1.0	unknown function	YJR014w	orf19.4164
CA5456	IPF267	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.3264
CA5665	UBP1	1.0	-1.1	-1.0	-1.0	Ubiquitin-specific protease (by homology)	YDL122w	orf19.7367
CA3729	IPF11901	1.0	-1.0	1.0	-1.0	unknown function		orf19.4179
CA0264	IPF8434	1.1	1.0	1.1	-1.0	unknown function		
CA1649	LAB1	1.0	-1.1	-1.0	-1.0	Lipoate biosynthesis by homology	YJL046w	orf19.5566
CA3877	CBP4	-1.0	-1.1	-1.1	-1.0	Ubiquinol--cytochrome-c reductase assembly factor (by	YGR174c	orf19.392
CA1153	IPF10455	1.0	1.0	1.1	-1.0	unknown function		orf19.104
CA5727	ECM15	1.1	1.1	1.0	-1.0	Involved in cell wall biogenesis and architecture (by hon	YBL001c	
CA4291	IPF2615	-1.0	1.0	1.0	-1.0	unknown function		orf19.6688
CA4950	IPF5143	-1.0	-1.0	1.1	-1.0	Unknown function		orf19.6528
CA2066	RPO26	1.2	1.1	1.0	-1.0	DNA-directed RNA polymerase I, II, III 18 KD subunit (b	YPR187w	orf19.2643
CA4729	VPS41.5F	-1.0	-1.0	-1.0	-1.0	required for the vacuolar assembly, 5-prime end (by homology)		orf19.12321
CA0661	APG7	-1.0	1.0	1.0	-1.0	component of the autophagic system (by homology)	YHR171w	orf19.8326
CA3378	RUB1	1.0	1.0	-1.0	-1.0	ubiquitin-like protein (by homology)		
CA5916	IPF19818	-1.0	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Nud1p cell cycle re	YOR373w	orf19.6789
CA4244	IPF4305	1.0	-1.0	-1.0	-1.0	unknown function		orf19.530
CA2325	IPF10977	1.0	-1.1	-1.0	-1.0	unknown function	YLR281c	orf19.5488
CA0940	IPF8616	1.1	1.0	1.0	-1.0	similar to Saccharomyces cerevisiae Rsm19p ribosoma	YNR037c	
CA1267	YSY6	1.1	1.1	1.2	-1.0	protein involved in the secretory pathway, by homology		
CA6035	BPL1	-1.1	1.0	1.0	-1.0	biotin holocarboxylase synthetase (by homology)	YDL141w	orf19.7645
CA6145	IPF1869	-1.2	-1.0	-1.2	-1.0	unknown function	YBL104c	orf19.5897
CA4109	IPF3967	-1.0	1.1	-1.0	-1.0	unknown function		orf19.673
CA0727	IPF7347	1.1	1.1	1.0	-1.0	unknown function	YIL027c	orf19.11214
CA3955	IPF6712.5F	-1.1	1.1	-1.2	-1.0	unknown function, 5-prime end		orf19.1414
CA2398	IPF6431	1.1	1.0	-1.0	-1.0	unknown function	YBR141c	orf19.3539
CA4379	MEP2	1.0	1.0	1.0	-1.0	high affinity low capacity ammonia (by homology)	YNL142w	orf19.5672
CA0465	IPF14113	-1.3	-1.0	-1.1	-1.0	unknown function	YIL130w	orf19.7800
CA6013	IPF635	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.7614
CA4108	IPF3968	1.0	-1.0	1.0	-1.0	similar to Saccharomyces cerevisiae pre-mRNA splicing	YDR243c	orf19.672
CA3804	RIM1	1.1	1.2	1.1	-1.0	telomere-binding protein (by homology)		orf19.2483
CA5214	IPF19807	-1.1	1.0	-1.0	-1.0	unknown function		orf19.7032
CA5012	IPF13943	1.0	-1.0	1.0	-1.0	Unknown function		orf19.5235
CA2684	IFU3	-1.0	1.0	1.0	-1.0	Unknown function	YLR063w	orf19.2575
CA5976	IPF928	-1.0	1.1	1.1	-1.0	zinc-finger transcription factor of the Zn(2)-Cys(6) binuc	YDL170w	orf19.7570
CA0840	IFD1	-1.0	-1.0	-1.1	-1.0	Putative aryl-alcohol dehydrogenase (by homology)		orf19.8650
CA1517	IPF11045	1.1	1.0	1.1	-1.0	unknown function	YMR212c	orf19.4798
CA4267	IPF2286	1.0	1.0	-1.0	-1.0	unknown function		orf19.6661
CA1265	IPF10510	-1.1	-1.2	-1.0	-1.0	unknown function	YKR065c	orf19.240
CA5054	IPF3704	-1.0	-1.0	-1.0	-1.0	unknown function	YNL218w	orf19.3019
CA2394	IPF6424	1.0	1.0	1.0	-1.0	unknown function		orf19.11019
CA3551	IPF13229	1.1	1.0	1.1	-1.0	unknown function	YDR520c	orf19.3876
CA2595	ARG2	-1.0	-1.0	-1.0	-1.0	acetylglutamate synthase (by homology)	YJL071w	orf19.56
CA5570	IPF1992	-1.0	1.0	1.0	-1.0	putative MFS transporter		orf19.7336
CA3913	IPF3283	1.0	-1.0	-1.1	-1.0	unknown function	YPL011c	orf19.4388

CA3166	IPF9634	-1.0	-1.0	1.0	-1.0	probable GATA zinc finger transcription factor (by homo	YMR136w	orf19.1577
CA3824	SKI8	-1.1	-1.1	-1.0	-1.0	antiviral protein-like (by homology)	YGL213c	orf19.5764
CA5595	IPF568	1.1	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Far1p cyclin-depe	YJL157c	orf19.7105
CA2106	IPF10714	-1.0	-1.1	-1.1	-1.0	similar to pH-regulated (PHR) proteins	YLR343w	orf19.3693
CA4692	COX6.3	1.0	-1.0	1.0	-1.0	cytochrome-c oxidase subunit VI, 3-prime end (by hom	YHR051w	
CA1991	F6617.REPEA	1.0	1.0	-1.1	-1.0	unknown function, repeated protein		orf19.13839
CA1115	RPA12	1.0	-1.0	-1.0	-1.0	DNA-directed RNA polymerase I (by homology)	YJR063w	orf19.2287
CA0165	IPF19165.3	1.0	1.0	-1.0	-1.0	unknown function, 3-prime end	Missing in array	
CA5641	GAC1	1.2	-1.1	1.0	-1.0	ser/thr phosphoprotein phosphatase 1, regulatory chain	YOR178c	orf19.7053
CA0533	IPF19872	1.0	-1.0	1.0	-1.0	unknown function	YHR081w	orf19.5067
CA3177	IPF11589	-1.1	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Pho13p 4-nitrophenylphosphatase		orf19.1405
CA4579	IPF2234	-1.0	1.0	1.0	-1.0	unknown function		orf19.6898
CA5354	FTR2	1.2	1.1	1.2	-1.0	high affinity iron permease		orf19.7231
CA0642	ERG25	1.5	-1.1	1.1	-1.0	C-4 sterol methyl oxidase	YGR060w	orf19.3732
CA2598	IPF13142	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.53
CA0285	IPF14392	-1.1	1.0	-1.0	-1.0	unknown function		orf19.1535
CA5149	HGH1	-1.1	-1.1	-1.1	-1.0	Similar to human HMG1 and HMG2 proteins (by homol	YGR187c	orf19.4587
CA3386	IPF6758	-1.0	1.0	-1.0	-1.0	unknown function		orf19.7954
CA2722	IPF4801	-1.1	-1.1	-1.1	-1.0	similar to Saccharomyces cerevisiae Vps17p vacuolar s	YOR132w	orf19.3344
CA2112	PFD1	1.0	1.1	-1.0	-1.0	Prefoldin subunit 1 (by homology)	YJL179w	orf19.3687
CA5649	CHS4	-1.2	-1.1	-1.2	-1.0	Chitin synthase regulatory factor	YBL061c ; Missing in array	orf19.7349
CA4615	IPF7955	1.0	1.0	1.0	-1.0	DNA binding protein (by homology)	YIL072w	orf19.3306
CA5613	IPF525	-1.0	1.2	-1.0	-1.0	unknown function		orf19.7085
CA1551	IPF8741.3F	-1.0	-1.1	-1.2	-1.0	unknown function, 3-prime end	YDR217c	orf19.4275
CA2953	MBP1	-1.1	-1.1	-1.1	-1.0	transcription factor (by homologgy)	YDL056w	orf19.5855
CA3591	IFT2	1.0	-1.0	-1.1	-1.0	unknown function		orf19.2247
CA2957	DAL53	1.0	-1.0	1.0	-1.0	allantoate permease (by homology)		orf19.5859
CA3908	IPF3301	1.0	-1.0	1.0	-1.0	unknown function		orf19.4394
CA2456	DBR1	-1.1	-1.0	-1.0	-1.0	lariat-debranching enzyme (by homology)	YKL149c	orf19.3506
CA1621	IFF6	1.1	1.0	1.0	-1.0	unknown function		orf19.11553
CA3548	IPF12179	1.0	-1.1	-1.0	-1.0	unknown function	YGR026w ; Missing in array	orf19.3872
CA5635	IPF474	-1.0	1.0	1.0	-1.0	unknown Function		orf19.7060
CA2875	MEI5	1.0	1.0	1.1	-1.0	meiotic protein (by homology)	YPL121c	orf19.5844
CA3107	GOS1	-1.0	1.0	1.0	-1.0	SNARE protein of Golgi compartment (by homology)	YHL031c	orf19.6551
CA0960	DPP1	1.0	1.0	1.2	-1.0	Diacylglycerol Pyrophosphate Phosphatase by homology		orf19.8271
CA1538	IDI1.3EOC	1.0	-1.0	-1.0	-1.0	Isopentenyl-diphosphate delta-isomerase, 3-prime end		orf19.4558
CA1186	IPF6930	1.0	-1.0	1.1	-1.0	unknown function		orf19.3785
CA0411	IPF17676	1.0	1.1	1.1	-1.0	similar to Saccharomyces cerevisiae Cst13p involved in	YBR158w	orf19.1507
CA5873	IPF331	1.1	1.0	-1.0	-1.0	GPI-anchored cell surface protein (by homology)		orf19.7542
CA0071	IPF19290.3	1.0	1.0	-1.0	-1.0	unknown function, 3-prime end	Missing in array	orf19.621
CA2740	IPF10633	1.1	1.0	1.1	-1.0	unknown function	YLR326w	orf19.2106
CA2518	CBP3	-1.0	1.0	-1.0	-1.0	involved in cytochrome-c reductase assembly (by homo	YPL215w	orf19.5515
CA5233	SSK1	1.1	1.0	-1.0	-1.0	Putative reponse regulator two-component phosphorela	YLR006c	orf19.5031
CA1015	IPF15547	1.0	1.0	1.1	-1.0	putative glutamyl-tRNA amidotransferase subunit A (by	YMR293c	orf19.11438
CA2949	IPF14506	1.0	-1.0	1.0	-1.0	unknown function		orf19.9516
CA3563	IPF7819	-1.0	1.0	1.0	-1.0	unknown function	YLR243w	orf19.3130
Empty		1.0	-1.0	1.0	-1.0			
CA0713	IFJ2	1.1	-1.1	-1.1	-1.0	Unknown function	YGR263c	orf19.2168
CA5336	IPF893	-1.0	1.1	1.0	-1.0	unknown function	YJR008w	orf19.7210

CA2993	IPF9118	1.0	-1.0	-1.0	-1.0	unknown function	YPR017c	orf19.6118
CA3357	IPF9562	-1.0	1.0	1.0	-1.0	similar to Saccharomyces cerevisiae Nuf2pspindle pole	YOL069w	orf19.1941
CA4781	IPF3355	-1.0	-1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Cdc1 cell cycle protein involved in ion homeosta		orf19.4014
CA0560	GPX3	1.1	-1.0	-1.0	-1.0	glutathione peroxidase (by homology)		orf19.87
CA0175	NPL4	-1.4	1.1	1.1	-1.0	nuclear protein localization factor and ER translocation (	YBR170c	orf19.9970
CA3761	IFR3	1.0	-1.0	1.1	-1.0	unknown function		orf19.2908
CA1722	TEF41	-1.0	-1.1	-1.0	-1.0	Probable translation elongation factor (by homology)		orf19.2652
CA4541	IPF6257	1.0	1.0	-1.0	-1.0	unknown function		orf19.1461
CA3703	IPF11945	1.1	-1.0	-1.1	-1.0	unknown function		orf19.6281
CA5752	IPF1055	-1.0	1.1	1.1	-1.0	unknown function	YAR003w	orf19.5388
CA4531	SLA1	1.1	1.2	1.2	-1.0	cytoskeleton assembly control protein	YBL007c	orf19.1474
CA0100	IPF11569	-1.0	-1.1	-1.0	-1.0	unknown function		orf19.7682
CA0331	ANC1	1.1	1.0	1.0	-1.0	TFIIF subunit, transcription initiation factor (by homolog	YPL129w	orf19.798
CA3158	IPF13131.3	1.0	1.0	1.1	-1.0	unknown function, 3-prime end	Missing in array	orf19.1587
CA1023	IPF4817	-1.0	-1.0	-1.1	-1.0	unknown Function		orf19.10860
CA1134	IPF2702	1.0	-1.0	1.1	-1.0	unknown function	YBR074w	orf19.2163
CA0430	PRC1	-1.0	-1.0	-1.0	-1.0	Carboxypeptidase Y precursor	YMR297w	orf19.1339
CA2499	SAP5	1.0	1.0	-1.0	-1.0	secreted aspartyl proteinase 5		orf19.5585
CA5841	IPF420	-1.0	-1.1	-1.1	-1.0	unknown function	YGR003w	orf19.7497
CA0666	FIP1	1.0	1.0	-1.0	-1.0	Component of pre-mRNA polyadenylation factor PF (by	YJR093c	orf19.11734
CA4741	IPF4496	-1.1	-1.0	-1.0	-1.0	unknown function	YLR047c	orf19.4843
CA4987	IPF2045	1.0	1.0	1.0	-1.0	unknown function		orf19.5262
CA3086	GLR1	-1.2	-1.0	1.0	-1.0	by similarity to S. cerev. and C. albicans:glutathione red	YPL091w	orf19.11623
CA3316	IPF8817	1.1	1.1	1.0	-1.0	putative proteasome subunit (by homology)	YIL007c	orf19.2301
CA5858	IPF380	1.0	1.0	1.0	-1.0	unknown function		orf19.7516
COX3b		1.0	-1.1	-1.1	-1.0			
CA0079	IPF14323	1.0	-1.0	1.0	-1.0	unknown function	YNL050c	orf19.4730
CA3413	IPF9239	-1.0	-1.0	-1.1	-1.0	unknown function		orf19.6142
CA4371	PEP7	-1.1	-1.0	-1.1	-1.0	vacuolar segregation protein by homology	YDR323c	orf19.5662
CA3595	IPF6079	1.0	-1.0	1.0	-1.0	putative permease (by homology)		orf19.4923
CA2372	IPF10335	-1.1	-1.1	-1.0	-1.0	unknown function		orf19.1834
CA1447	NRK1	1.3	-1.0	-1.1	-1.0	Cdc31p-interacting ser/thr protein kinase (by homology)	YHR102w	orf19.191
CA2387	IPF8504	-1.0	1.0	-1.0	-1.0	unknown function		orf19.2612
CA1744	IPF10889	1.1	1.0	1.0	-1.0	unknown function	YFR045w	orf19.5052
CA4317	IPF2109	1.0	-1.0	-1.2	-1.0	unknown function	YMR048w	orf19.4105
SCORC4		1.1	1.1	1.0	-1.0			
CA1810	FDH2	1.0	-1.0	-1.0	-1.0	Formate dehydrogenase (by homology)		orf19.1117
CA0450	IPF9353	-1.0	-1.1	-1.0	-1.0	unknown function	YMR123w	orf19.2378
CA4328	IPF2090	1.0	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Srb5p DNA-directe	YGR104c	orf19.4091
CA3976	SNU23	-1.0	1.1	1.1	-1.0	RNA binding zinc finger protein (by homology)	YDL098c ; Missing in array	orf19.1548
CA0912	RPA49	1.0	1.0	1.0	-1.0	DNA-directed RNA polymerase A (by homology)	YNL248c	orf19.9567
CA6132	DUR35.5F	1.0	1.0	1.0	-1.0	Urea transport protein, 5-prime end (by homology)		orf19.5916
CA3727	HIS5.3F	-1.1	-1.1	-1.0	-1.0	Histidinol-phosphate aminotransferase, 3-prime end (by	YIL116w	orf19.4177
CA2786	KRE5.3EOC	-1.1	-1.0	-1.1	-1.0	UDP-glucose:glycoprotein glucosyltransferase, 3-prime	YOR336w	orf19.290
CA1817	IPF7021	-1.2	-1.1	-1.2	-1.0	similar to Saccharomyces cerevisiae Exo84p exocyst pr	YBR102c	orf19.135
CA2430	IPF12950	1.1	-1.1	-1.1	-1.0	unknown function		orf19.3402
CA1326	IPF6679	-1.0	1.0	-1.0	-1.0	unknown function		orf19.1306
CA1590	IPF14665	-1.0	1.1	1.0	-1.0	unknown function	YFL027c	orf19.11790
CA2025	IPF9618	-1.0	-1.0	-1.1	-1.0	unknown function		orf19.4911

CA2077	IPF13353	1.1	1.0	-1.0	-1.0	unknown function		orf19.4872
CA5048	IPF20024	-1.0	-1.1	1.1	-1.0	unknown function	YDR421w	orf19.10530
CA1130	NAG1	-1.0	-1.0	-1.0	-1.0	Glucosamine-6-phosphate deaminase		orf19.9703
CA5998	IPF670	1.1	1.0	1.0	-1.0	unknown function	YOR023c	orf19.7598
CA4736	IPF4503	1.0	1.0	-1.1	-1.0	unknown function	YIR011c	orf19.4849
CA4900	IFP2	1.0	1.0	-1.0	-1.0	unknown function		orf19.6037
CA0671	GRP4	1.0	-1.0	1.0	-1.0	putative reductase (by homology)		orf19.10660
CA3280	IPF6269.3	1.0	-1.0	1.0	-1.0	unknown function, 3-prime end		
CA0635	IPF9036	1.0	1.0	1.1	-1.0	similar to Saccharomyces cerevisiae Rap1p DNA-bindir	YNL216w	orf19.9342
CA3582	IPF15466	1.0	1.0	1.0	-1.0	unknown function		orf19.2258
CA3849	IPF7938	-1.0	1.1	1.1	-1.0	similar to Saccharomyces cerevisiae Stu2p suppressor	YLR045c	orf19.6610
CA0552	IPF4343	-1.0	-1.0	1.0	-1.0	similar to Saccharomyces cerevisiae Vps9pvacuolar so	YML097c	orf19.5533
E coli 1		1.0	-1.0	-1.0	-1.0			
CA1645	PMC1	-1.1	-1.0	-1.0	-1.0	Ca2+-transporting P-type ATPase (by homology)	YGL006w	orf19.1727
CA4214	IPF5796	1.0	1.0	1.0	-1.0	unknown function		orf19.812
CA0772	UGA11.EXON2	-1.0	-1.1	-1.1	-1.0	4-aminobutyrate aminotransferase, exon 2 (by homology)		
CA5780	IPF1123	-1.0	-1.0	1.0	-1.0	unknown function	YKR089c	orf19.5426
CA4766	IPF13056	1.0	1.1	1.1	-1.0	unknown function		orf19.3998
CA5158	IPF992	-1.1	-1.0	1.0	-1.0	unknown function		orf19.4596
CA3787	HPT1	-1.2	-1.1	1.1	-1.0	hypoxanthine guanine phosphoribosy transferase(by ho	YDR399w	orf19.5832
CA3484	IPF3214	1.0	1.1	-1.0	-1.0	HSP-mitochondrial chaperone (by homology)	YNL328c	orf19.3574
CA5506	IPF748	-1.1	-1.0	1.1	-1.0	unknown function	YML112w	orf19.5350
CA1193	MSY1	1.0	-1.1	1.1	-1.0	tyrosyl-tRNA synthetase 8by homology	YPL097w	orf19.7756
CA3148	IPF9808	1.0	1.0	1.0	-1.0	similar to Saccharomyces cerevisiae cse4p with strong	YKL049c	orf19.6163
CA4824	HNM2	-1.0	1.1	-1.0	-1.0	Choline permease (by homology)	YGL077c	orf19.2072
CA4360	IPF6050	-1.0	-1.1	-1.0	-1.0	unknown function		orf19.6737
CA5116	TPM2.3	1.5	-1.1	-1.0	-1.0	Tropomyosin, 3-prime end	YIL138c	
CA0830	APL5	-1.0	-1.0	-1.0	-1.0	AP-3 complex subunit, gamma-adaptin (by homology)	YPL195w	orf19.7879
CA3541	IPF5425	1.1	1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Ppm1p carboxy m	YDR435c	orf19.6377
CA3237	SPB4	-1.0	1.0	-1.0	-1.0	ATP-dependent RNA helicase of DEAH box family (by h	YFL002c	orf19.6298
CA5447	IPF234	-1.0	-1.0	1.1	-1.0	similar to Saccharomyces cerevisiae Prp40p splicing fa	YKL012w	orf19.3250
CA6100	IPF66	1.1	1.2	-1.0	-1.0	unknown function	YPR154w	orf19.5956
CA5960	PMT5	1.1	1.0	1.1	-1.0	protein mannosyltransferase (by homology)		orf19.7549
CA1565	EGD1	1.1	-1.1	-1.3	-1.0	GAL4 DNA-binding enhancer protein (by homology)	YPL037c	orf19.1154
CA2692	IPF9173.3F	-1.0	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Vps30p involved in vacuolar protein sorting and		orf19.10246
CA2956	EGD2	1.2	1.1	-1.0	-1.0	Nascent polypeptide associated complex protein alpha	YHR193c	orf19.5858
CA1112	PF18758.5EO	1.0	1.0	1.1	-1.0	unknown function, 5-prime end		orf19.2282
CA5939	IPF3484	-1.1	-1.0	-1.0	-1.0	aldo/keto reductase (by homology)		orf19.6758
CA4563	IPF6566	1.1	-1.0	1.0	-1.0	unknown function	YBL071wa ; Missing in array	
CA4443	IPF3535	-1.0	1.0	1.1	-1.0	unknown function		orf19.6840
CA4440	IPF13864	-1.0	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Chs6p chitin biosy	YJL099w	orf19.5155
CA2299	IPF8222	-1.0	-1.0	1.0	-1.0	unknown function	YGL014w	orf19.5381
CA4801	APM1	-1.0	-1.1	-1.0	-1.0	AP-1 complex subunit, mu1 subunit (by homology)	YPL259c	orf19.4036
CA2542	IPF16067	1.1	1.1	1.1	-1.0	unknown function	YOL089c	orf19.3190
SCGPM1		1.0	1.1	-1.0	-1.0			
CA1119	IPF7669.3	1.0	1.1	-1.0	-1.0	unknown function, 3-prime end		
CA4025	SCJ1	-1.0	1.0	-1.0	-1.0	Mitochondrial and ER import protein (by homology)	YMR214w	orf19.3438
CA5988	IPF693	1.1	1.1	1.0	-1.0	unknown function	YOR305w	orf19.7588
CA3520	IPF6785	1.1	1.1	1.0	-1.0	unknown function		orf19.997

CA1674	PAF1	-1.2	-1.2	-1.2	-1.0	DNA-directed RNA polymerase II regulator by homolog	YBR279w	orf19.3613
CA1819	IPF16549	-1.0	-1.0	1.0	-1.0	Unknown function	YLR139c	orf19.4273
CA4861	IPF4094	1.0	1.1	-1.2	-1.0	unknown function	YGR001c	orf19.3836
CA5870	IPF345	-1.0	-1.0	-1.0	-1.0	FH1/FH2 involved in cytokinesis and polarity (by homology)		orf19.7537
CA0101	IPF10105	1.1	1.0	1.1	-1.0	RNA polymerase-like (by homology)	YOL135c	orf19.232
CA0737	EC16.53F.EO	-1.0	1.0	-1.0	-1.0	Multidomain vesicle coat protein, internal fragment (by homology)		
CA3102	RLP7	1.0	1.0	1.0	-1.0	ribosomal-like proteins	YNL002c	orf19.3867
CA2649	IPF9057	-1.1	1.2	-1.1	-1.0	unknown function		orf19.1189
CA1313	IPF14126	1.1	1.0	1.0	-1.0	unknown function		orf19.3638
CA0730	IPF7334	1.0	-1.0	-1.1	-1.0	unknown function	YOR004w	orf19.11208
CA0022	IPF19421	1.0	-1.1	1.0	-1.0	unknown function	Missing in array	orf19.162
CA1325	IPF6678	1.0	-1.0	1.1	-1.0	unknown function		orf19.1307
CA0222	IPF12141	1.0	-1.1	-1.1	-1.0	unknown function		orf19.9508
CA3802	AUT7.EXON2	1.1	1.0	1.2	-1.0	microtubule-associated protein essential for autophagy,	YBL078c	
CA2122	CPY1.3F	1.1	-1.0	1.0	-1.0	Carboxypeptidase Y precursor, 3-prime end		orf19.8919
CA0839	IPF12492	-1.0	1.1	1.0	-1.0	unknown function		
CA3395	IPF13616	-1.1	1.0	-1.0	-1.0	unknown function	YGR251w	orf19.3970
CA3504	IPF11369	-1.0	1.0	-1.0	-1.0	unknown function		orf19.6350
CA1937	MMM1	1.0	-1.0	-1.1	-1.0	mitochondrial outer membrane protein (by homology)	YLL006w	orf19.4187
CA2878	RET1	1.0	1.0	1.0	-1.0	DNA-directed RNA polymerase III (by homology)	YOR207c	orf19.5847
CA3393	IPF6748	-1.1	-1.0	-1.1	-1.0	unknown function	YMR052w	orf19.315
CA3605	IPF3865	1.2	-1.1	-1.1	-1.0	unknown function		orf19.22
CA2718	IPF7374	1.1	-1.0	1.0	-1.0	unknown function		orf19.10847
CA1945	MSS116	-1.0	-1.1	-1.0	-1.0	RNA helicase of the DEAD box family (by homology)	YDR194c	orf19.4739
CA3071	NUP188	1.0	1.0	1.1	-1.0	Nucleoporin	YML103c	orf19.4808
CA1485	IPF20082	1.0	1.0	-1.0	-1.0	unknown function	YOR238w	orf19.4061
CA6076	PAC10.3	1.1	1.0	-1.1	-1.0	Non-native Actin Binding Complex Component, 3-prime	YGR078c	orf19.5985
CA0648	IPF12399	1.1	1.1	1.1	-1.0	unknown function		orf19.3210
CA3911	IPF3292	1.0	1.0	-1.1	-1.0	unknown function		orf19.4391
CA4096	KRR1	1.1	-1.0	1.0	-1.0	involved in cell division and spore germination	YCL059c	orf19.661
CA1409	SPT16	-1.0	1.0	1.0	-1.0	general chromatin factor (by homology)	YGL207w	orf19.2884
CA0872	IPF13100	-1.0	1.0	1.0	-1.0	unknown function	YJL073w	orf19.3592
CA1628	HMG1	1.0	-1.1	-1.0	-1.0	3-hydroxy-3-methylglutaryl-coenzyme A red	YLR450w	orf19.1031
CA2603	IPF5471	1.0	1.0	-1.1	-1.0	unknown function		orf19.5680
CA1848	IPF11128	1.0	1.0	1.0	-1.0	unknown function	YMR225c	
CA5883	IPF2425	1.0	-1.0	-1.0	-1.0	unknown function	YDR088c	orf19.6827
CA5658	IPF1242	-1.0	1.0	1.0	-1.0	unknown function	YPL047w	orf19.7360
Pho4 BD		-1.0	-1.0	1.0	-1.0			
CA4318	IPF2106	1.1	1.0	-1.0	-1.0	unknown function		orf19.4104
CA1032	IPF19896	-1.0	1.0	-1.1	-1.0	unknown function		orf19.3852
CA4079	IPF2527	-1.0	1.0	1.0	-1.0	unknown function		orf19.6635
CA0880	IPF19542.3F	1.2	1.1	1.3	-1.0	unknown function, 3-prime end	YER163c	orf19.372
CA1652	RNH1.EXON1	1.2	-1.0	-1.0	-1.0	Ribonuclease H, exon 1 (by homology)	YMR234w	orf19.5563
CA3136	IPF8989	1.0	-1.0	1.0	-1.0	unknown function	YAL034wa	orf19.1367
CA1929	SAP7	1.1	1.0	1.1	-1.0	secreted aspartyl proteinase 7		orf19.8376
CA3193	IPF3418	-1.1	1.0	-1.1	-1.0	unknown function	YCL029c	orf19.6170
CA2411	IFI3.3	1.0	-1.0	-1.0	-1.0	Unknown function, 3-prime end		orf19.4483
CA2353	VPS13	1.1	1.0	1.0	-1.0	involved in regulating membrane traffic (by homology)	YLL040c	orf19.4416
CA1106	IPF11270	1.1	1.0	1.0	-1.0	unknown function	YOL077c	orf19.12697

CA4248	IPF4294	-1.0	1.0	1.0	-1.0	unknown function	YBR197c	orf19.537
CA0744	IPF14919	-1.1	-1.0	-1.1	-1.0	unknown function		orf19.9105
CA3700	IPF4859	-1.1	1.0	1.0	-1.0	unknown function		orf19.6276
CA1703	IPF7987	1.0	-1.1	1.0	-1.0	unknown function	YGR247w	orf19.703
CA4223	IPF8757	-1.2	-1.1	-1.0	-1.0	unknown function		orf19.826
CA1615	IPF14540	1.0	-1.0	1.0	-1.0	putative multidrug protein (by homology)	YJR124c ; Missing in array	orf19.3218
CA6024	IPF615	-1.2	-1.1	-1.0	-1.0	unknown function	YNL320w	orf19.7627
CA0761	IPF8267	-1.1	1.1	-1.1	-1.0	P-type ATPase	YOR291w	orf19.9146
CA5194	IPF11756	1.0	1.2	-1.1	-1.0	unknown function		orf19.7006
CA3513	IPF11246	1.1	1.0	-1.0	-1.0	unknown function		orf19.6360
CA3654	IPF7452	1.2	-1.0	1.2	-1.0	unknown function	YOR311c	orf19.2045
CA4212	HFM1	1.0	1.0	-1.0	-1.0	DNA/RNA helicase by homology	YGL251c	orf19.810
CA2272	RPA43	1.1	-1.0	-1.1	-1.0	DNA-directed RNA polymerase I, 36 KD subunit(by hon	YOR340c	orf19.2594
CA1361	PEP5	-1.0	-1.0	-1.0	-1.0	vacuolar biogenesis protein (by homology)	YMR231w	orf19.4403
CA4685	IPF9013	-1.2	1.1	-1.1	-1.0	unknown function	YOR030w	orf19.881
CA4556	IPF8044	-1.0	-1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Snp1p U1 small nu	YIL061c	orf19.6866
CA3023	IPF11508	1.0	1.0	1.0	-1.0	unknown function		orf19.3904
CA0093	19980.REPEA	1.0	1.0	-1.0	-1.0	putative lipase (by homology)		orf19.7747
CA3691	IPF4880	1.0	-1.0	-1.0	-1.0	unknown function		orf19.6266
CA0377	IPF14356	1.0	1.0	1.0	-1.0	unknown function	YLR022c	orf19.2708
CA2385	RSR1.3	-1.0	-1.1	-1.1	-1.0	GTP-binding protein, 3-prime end	YGR152c	orf19.2614
CA4858	IPF15927.3F	-1.0	1.0	1.0	-1.0	similar to Saccharomyces cerevisiae Tfc3p transcription	YGR280c	orf19.3831
CA0404	LYS14	-1.0	-1.0	-1.0	-1.0	transcription factor involved in lysine biosynthesis (by ho	YDR034c	orf19.5548
CA5035	IPF4531	-1.1	1.0	-1.0	-1.0	unknown function		orf19.6989
CA0591	ALS3.5EOC	1.1	1.0	1.0	-1.0	agglutinin-like protein, 5-prime end	YJR004c ; Missing in array	orf19.1816
CA3782	SER2	1.0	-1.1	-1.1	-1.0	phosphoserine phosphatase by homology to S. cerevisi	YGR208w	orf19.5838
CA0757	GAP7.3EOC	1.2	-1.0	1.0	-1.0	general amino-acid permease, 3-prime end		
CA1342	IPF11347	1.0	1.0	1.0	-1.0	unknown function		
CA5625	PEL1	-1.0	-1.0	-1.1	-1.0	CDP-diacylglycerol-serine-O-phosphatidyltransferase (b	YCL004w	orf19.7072
CA1001	IPF6006	1.0	1.0	-1.0	-1.0	unknown function		orf19.9065
CA2359	IPF8952	-1.1	-1.1	-1.1	-1.0	similar to Saccharomyces cerevisiae Rpa34p nonessen	YJL148w	orf19.4896
CA4017	PBN1	1.0	1.0	1.0	-1.0	protease by homology	YCL052c	orf19.3447
CA2753	IPF16806	-1.1	-1.0	-1.1	-1.0	unknown function	YPL181w	orf19.13062
CA6164	SNF5.5F	-1.0	-1.0	1.0	-1.0	Component of SWI/SNF transcription activator complex, 5-prime end (by homology)		orf19.5872
CA5896	TPD3	-1.3	-1.1	-1.2	-1.0	Ser/thr protein phosphatase (by homology)	YAL016w	orf19.6810
CA3543	IPF5428	1.0	1.1	-1.0	-1.0	unknown function		orf19.6379
CA0808	SUA71	1.0	1.0	1.0	-1.0	TFIIB subunit (transcription initiation factor E)(by homology)		orf19.3519
CA5351	IPF857	1.0	-1.0	1.0	-1.0	unknown function	YFR003c	orf19.7227
CA1096	IPF7578	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.4366
CA1808	GUK1	-1.1	-1.1	-1.0	-1.0	Guanylate kinase (by homology)	YDR454c	orf19.1115
CA4843	GYP1	-1.1	1.1	1.2	-1.0	GTPase activating protein (by homology)	YOR070c	orf19.3811
CA5469	IPF298	1.0	1.0	1.0	-1.0	unknown function	YER051w	orf19.3281
CA4399	PRA1	1.0	-1.0	1.1	-1.0	pH-regulated antigen	YOL154w	orf19.3111
CA5591	IPF5618	-1.1	-1.1	-1.3	-1.0	unknown function	YGL242c	orf19.7109
CA3569	IPF3268	-1.0	-1.1	1.0	-1.0	unknown function		orf19.3136
CA3517	IFA22	-1.1	-1.0	1.0	-1.0	Unknown function		orf19.1002
CA4714	IPF5912	-1.1	1.0	1.0	-1.0	unknown function	YDR352w	orf19.6950
CA0577	IPF16051	1.0	-1.0	1.0	-1.0	unknown function		orf19.3068
CA5771	IPF1104	-1.0	1.1	1.0	-1.0	similar to Saccharomyces cerevisiae Prp28p pre-mRNA	YPL151c	orf19.5413

CA4046	IPF9205	-1.0	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Apg5p involved in	YPL149w	orf19.3677
CA3699	IPF4860	1.1	1.0	-1.0	-1.0	similarity to ribosomal protein kinases (by homology)	YBR028c	orf19.6275
CA0650	IPF11566	-1.1	1.1	-1.0	-1.0	unknown function		orf19.11
CA4511	IPF8966	-1.0	1.0	-1.0	-1.0	unknown function	YNL124w	orf19.8124
CA5417	NUC1	1.0	1.0	1.1	-1.0	Nuclease, mitochondrial	YJL208c	orf19.967
CA0451	IPF13556	-1.0	-1.0	1.0	-1.0	unknown function		orf19.8882
CA5668	IPF1261	1.2	1.1	-1.0	-1.0	unknown function	YOL092w	orf19.7370
CA3905	IPF19792	1.1	1.0	1.0	-1.0	unknown function	YPR147c	orf19.11876
CA3684	IPF13613	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.725
CA0006	IPF2072	1.0	1.0	-1.0	-1.0	unknown function	YDR279w	orf19.11561
6100.2		1.0	-1.0	-1.1	-1.0			
CA4968	IPF3928	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.6503
CA1604	IPF13653	-1.0	1.1	-1.0	-1.0	unknown function	YDL043c	orf19.4724
CA0662	SPC97	-1.0	-1.1	1.1	-1.0	spindle pole body component (by homology)	YHR172w	orf19.708
CA1550	IPF8741.5F	1.1	-1.1	1.0	-1.0	unknown function, 5-prime end		orf19.4276
CA1335	TRA1	-1.1	1.2	-1.1	-1.0	phosphatidylinositol kinase by homology	YHR099w	orf19.3451
CA4497	IPF4064	-1.1	-1.0	-1.0	-1.0	unknown function		orf19.9419
CA5881	SSS1	1.0	1.0	1.0	-1.0	ER protein-translocase complex subunit (by homology)	YDR086c	
CA5020	IPF7556	-1.0	-1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Pim1p mitochondrial ATP-dependent protease (		orf19.6973
CA4419	IFA6	-1.1	1.0	1.0	-1.0	Unknown function		orf19.5177
CA4273	CAC2	-1.0	1.1	-1.0	-1.0	Chromatin assembly complex, subunit p60 (by homolog	YML102w	orf19.6670
CA1518	IPF11040	1.1	-1.0	-1.0	-1.0	similar to Schizosaccharomyces pombe cdc5 myb-relat	YMR213w	orf19.4799
CA5136	IPF5139	1.0	-1.0	1.0	-1.0	unknown function		orf19.13743
CA2328	MED8	-1.1	-1.1	1.1	-1.0	transcriptional regulation mediator (by homology)	YBR193c	orf19.11973
CA1788	USO1.3	1.2	1.2	1.1	-1.0	Cytoskeletal-related transport protein, Ca++ binding, 3-	YBL047c	orf19.1166
CA1968	IPF10864	-1.1	1.0	1.1	-1.0	similar to Saccharomyces cerevisiae Rex4p member of	YOL080c	orf19.5220
CA1082	IPF14797	1.0	-1.1	1.0	-1.0	unknown function		orf19.4818
CA1520	IPF11035	1.0	1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Mod5p tRNA isope	YOR274w	orf19.4801
CA2441	APM4	1.0	-1.0	1.1	-1.0	AP-2 complex subunit, mu2 subunit (by homology)	YOL062c	orf19.2194
CA5433	SFT1	1.0	1.0	-1.0	-1.0	SNARE-like protein (by homology)	YKL006ca	
CA3982	SAC3	-1.0	-1.1	-1.1	-1.0	Leucine permease transcriptional regulator	YDR159w	orf19.9129
CA3518	AMYG2	-1.0	-1.0	-1.0	-1.0	glucoamylase		orf19.8614
CA4651	IPF3121	-1.0	1.0	1.1	-1.0	unknown function	YGR044c	orf19.11918
CA3326	IPF6889	-1.0	-1.1	-1.1	-1.0	unknown function	YDR288w	orf19.2673
CA0058	IPF3770	-1.0	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Kar3p kinesin-related protein		
CA3170	IPF7685	1.0	-1.0	1.0	-1.0	putative GTPase activating protein (by homology)	YIL044c	orf19.1396
CA0507	IPF11989	-1.0	-1.0	1.0	-1.0	unknown function		orf19.3625
CA5647	RTF1.5EOC	1.0	1.0	-1.1	-1.0	Nuclear protein regulating DNA binding properties of TATA Binding Protein, 5-prime end (by homology)		
CA2132	IPF5865	-1.0	1.0	1.0	-1.0	unknown function	YLR394w	orf19.5212
CA2901	PUS1	1.1	-1.1	-1.0	-1.0	pseudouridine synthase 1 (by homology)	YPL212c ; Missing in array	orf19.3477
E coli 3		1.0	1.0	-1.0	-1.0			
CA2549	RPD31	-1.1	-1.0	-1.0	-1.0	histone deacetylase B (by homology)		orf19.2834
CA4231	SNP3	1.1	1.1	1.0	-1.0	snRNP-related protein (by homology)	YBL026w	orf19.514
CA1346	KRE2.3F	1.1	-1.1	-1.0	-1.0	secretory pathway protein, 3-prime end		
CA5579	IPF5661	1.0	1.1	1.2	-1.0	unknown function		orf19.7125
CA5226	RIM15	1.0	-1.2	-1.1	-1.0	Protein kinase involved in the RIM pathway (by homolo	YFL033c	orf19.7044
CA2149	IPF10761	1.0	1.0	1.0	-1.0	unknown function		orf19.6021
CA3195	IPF3426	-1.0	-1.1	-1.0	-1.0	unknown function	YOR047c	orf19.6173
CA1582	CLN21	-1.0	-1.0	-1.1	-1.0	G1 cyclin (by homology)	YMR199w	orf19.6028

CA1738	MGE1	1.1	1.0	1.1	-1.0	heat shock protein (by homology)	YOR232w	orf19.2524
CA3441	MST1	-1.1	-1.0	-1.1	-1.0	mitochondrial threonyl tRNA synthetase [Candida albica	YKL194c	orf19.2984
CA3948	RPN9	-1.2	-1.1	-1.0	-1.0	26S proteasome regulatory particle (by homology)	YDR427w	orf19.1993
Int 5		-1.0	-1.0	-1.0	-1.0			
CA2913	IPF11205	-1.0	-1.0	1.1	-1.0	unknown function		orf19.4513
CA4264	IPF2280	-1.1	-1.0	1.0	-1.0	unknown function		orf19.6658
CA5628	MAC1	-1.0	-1.0	1.0	-1.0	putative metal-binding transcriptional regulator (by homology)		orf19.7068
CA2511	IPF1474	1.0	1.0	-1.0	-1.0	myosin-like protein		orf19.306
CA3949	SIR21	-1.0	-1.0	-1.0	-1.0	regulatory protein (by homology)		orf19.9544
CA1200	IPF10223	1.0	1.1	1.1	-1.0	putative serine/threonine kinase	YJL187c	orf19.12331
CA3881	GCR3	-1.3	-1.0	-1.2	-1.0	Large subunit of the nuclear cap-binding protein comple	YMR125w ; Missing in array	orf19.387
CA1340	VPS4	-1.1	-1.0	-1.1	-1.0	vacuolar sorting protein by homology to S. cerevisiae	YPR173c	orf19.4339
CA2248	IPF11469	1.1	-1.0	-1.0	-1.0	unknown function		orf19.9902
CA2690	PTR2.EXON2	1.0	1.0	1.1	-1.0	Peptide transporter for di- and tripeptides, exon 2		
CA2743	CKB21	1.0	1.1	1.2	-1.0	Casein kinase II, beta subunit (by homology)	YGL019w	orf19.2102
CA3821	IPF6990	-1.0	-1.0	1.1	-1.0	unknown function	YGL114w	orf19.5770
CA5880	IPF12074	-1.0	-1.1	-1.1	-1.0	unknown function	YMR282c	orf19.6829
CA1895	PRE7.EXON2	-1.0	1.0	1.1	-1.0	subunit of 20S proteasome, exon 2 (by homology)		
CA0400	IPF7423.3EOC	-1.0	1.0	1.1	-1.0	similar to Saccharomyces cerevisiae Spo22 involved in sporulation, 3-prime end		orf19.6223
CA1076	IPF19721	1.0	1.0	1.0	-1.0	similar to Saccharomyces cerevisiae Lte1p GDP/GTP e	YAL024c	orf19.2239
CA1540	IPF1047	1.0	-1.0	1.0	-1.0	unknown function	YMR310c	orf19.4563
CA5139	IPF1027	-1.0	1.0	1.1	-1.0	unknown function	YOR371c	orf19.4577
CA2831	IPF15706	-1.1	-1.0	-1.0	-1.0	unknown function		orf19.4783
CA2575	SEC31	1.0	1.2	-1.0	-1.0	Component of the COPII coat of ER-golgi vesicles (by h	YDL195w	orf19.6217
CA3047	MSE1	-1.0	-1.0	-1.1	-1.0	Mitochondrial glutamyl-tRNA synthetase (by homology)	YOL033w	orf19.9953
CA5719	IPF2441	1.0	-1.0	-1.0	-1.0	unknown function	YER126c	orf19.7424
CA4398	ZRT1	1.0	1.0	-1.0	-1.0	high-affinity zinc transport protein (by homology)		orf19.3112
CA4402	MGT1	1.0	1.0	1.0	-1.0	O6-methylguanine DNA repair methyltransferase (by ho	YDL200c	orf19.3108
CA3311	IPF8809	-1.0	-1.1	-1.1	-1.0	unknown function	YMR009w	orf19.2306
CA4023	FRP5	-1.0	1.0	1.1	-1.0	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathway		orf19.3440
CA4596	MRE11	1.0	-1.0	-1.0	-1.0	DNA repair and meiotic recombination protein (by homo	YMR224c	orf19.6915
CA6008	IPF647	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.7609
CA4393	IPF12300	-1.0	1.0	-1.0	-1.0	unknown function		orf19.3120
CA4194	PTR3	-1.1	-1.0	-1.0	-1.0	transcriptional regulator (by homology)	YFR029w	orf19.4535
CA0020	IPF7046	1.1	1.0	-1.0	-1.0	unknown function	YHR052w	orf19.124
CA0257	IPF10079	1.1	1.1	1.0	-1.0	unknown function		orf19.2280
CA1696	ASM4	-1.1	-1.1	-1.1	-1.0	similar to Saccharmoyces cerevisiae Asm4p suppressoi	YDL088c	orf19.5040
CA1059	TRP2	-1.1	-1.0	-1.1	-1.0	anthranilate synthase component I (by homology)	YER090w	orf19.10080
CA2513	SNG1	1.0	1.0	1.0	-1.0	Involved in nitroguanidine resistance (by homology)	YGR197c	orf19.308
CA3723	DPH2	1.0	-1.0	-1.0	-1.0	Diphtheria toxin resistance protein (by homology)	YKL191w	orf19.4173
CA1292	SRB2.3	1.0	-1.0	1.1	-1.0	DNA-directed RNA polymerase II holoenzyme and Korn	YHR041c	
CA1399	IPF8069	1.0	1.1	1.0	-1.0	unknown function	YHR121w	orf19.3698
CA3026	11499.REPEA	1.1	-1.0	-1.0	-1.0	unknown function		orf19.11382
CA4327	IPF2091	1.1	-1.1	-1.0	-1.0	unknown function	YGR102c	orf19.4092
CA1804	TAF17	1.1	1.0	-1.0	-1.0	TFIID and SAGA subunit (by homology)	YMR236w	orf19.1111
CA2293	IPF9748	1.0	1.0	-1.0	-1.0	unknown function	YJL049w	orf19.746
CA0768	COX19	1.0	-1.0	1.0	-1.0	Protein required for cytochrome c oxidase activity (by h	YLL018ca	orf19.12432
CA5632	IPF480	-1.1	-1.1	-1.1	-1.0	unknown function	YGR024c	orf19.7063
CA5085	RPS22.EXON2	1.0	-1.0	1.0	-1.0	ribosomal protein S15a, exon 2 (by homology)		

CA2451	IFB2	-1.0	-1.1	-1.0	-1.0	unknown function		orf19.5509
CA0811	IPF17625	-1.0	1.0	1.0	-1.0	putative cell wall protein of the PIR family		orf19.1920
CA0275	NTA1	1.0	1.0	1.1	-1.0	Amino-terminal amidase (by homology)	YJR062c	orf19.8470
CA0496	IPF11644	-1.0	-1.0	1.0	-1.0	unknown function	YPR023c	orf19.2660
CA2624	ARG81.3EOC	1.1	1.0	1.0	-1.0	transcription factor possibly involved in arginine metabolism, 3-prime end (by homology)		
CA4310	IPF2125	1.0	1.0	1.0	-1.0	unknown function		orf19.4116
CA1711	POX18	1.0	-1.0	-1.0	-1.0	Lipid-transfer protein (by homology)		orf19.10841
CA2116	SNG4	1.0	-1.0	1.1	-1.0	Drug transporter (by homology)		orf19.1332
CA3328	IPF10564	-1.0	1.1	1.0	-1.0	unknown function		orf19.2671
CA5876	IPF12082.5F	-1.1	1.1	-1.3	-1.0	bumetanide-sensitive Na-K-Cl cotransport protein, 5-pri	YBR235w	orf19.6833
CA1499	IPF6521.3EOC	1.1	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Tao3p transcriptional activator, 3-prime end		
CA3721	IPF6186	-1.0	-1.0	-1.1	-1.0	unknown function	Missing in array	orf19.11647
CA2324	CDC46	1.0	1.0	1.0	-1.0	cell division control protein (by homology)	YLR274w	orf19.5487
CA4743	IPF4491	-1.0	-1.0	-1.1	-1.0	unknown function	YER083c	orf19.4839
CA0991	IPF11065	-1.0	-1.1	1.0	-1.0	unknown function	YIL006w	orf19.8971
CA4877	IPF1667	-1.1	-1.1	-1.1	-1.0	unknown function	YJR054w	orf19.6563
CA3815	CYP7	1.0	-1.0	1.0	-1.0	peptidyl-prolyl cis-trans isomerase cyp7 (ppiase)	YJR032w	orf19.2499
CA2379	IPF4073	-1.1	1.0	-1.2	-1.0	similar to Saccharomyces cerevisiae CaPds5p regulatio	YMR076c	orf19.2216
CA5150	FMS1	-1.0	1.0	1.1	-1.0	Similar to corticosteroid-binding protein CBP1 (by homo	YMR020w	orf19.4589
CA0628	IPF3878	-1.0	-1.0	1.0	-1.0	unknown function	YLR221c	orf19.773
CA3763	IPF13070	1.0	1.0	1.1	-1.0	unknown function		orf19.2906
CA2966	RPC34	1.1	1.0	-1.0	-1.0	DNA-directed RNA polymerase III (by homology)	YNR003c	orf19.5608
CA0049	IPF3908	-1.2	-1.0	-1.2	-1.0	unknown function	YPR090w	orf19.757
CA4281	IPF2314	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.6679
CA5753	FKH1	1.1	1.1	1.0	-1.0	Fork head protein type transcription factor	YNL068c	orf19.5389
CA1192	IPF11926	1.1	-1.0	-1.0	-1.0	unknown function		
CA0479	IPF16191	-1.0	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Rad59p recombina	YDL059c	orf19.2630
CA5710	OAC1	1.0	1.1	1.0	-1.0	Mitochondrial oxaloacetate transport protein (by homolo	YKL120w ; Missing in array	orf19.7411
CA4773	IPF3340	1.1	1.0	-1.0	-1.0	unknown function	YDR196c	orf19.4005
CA3969	IPF9379	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.1430
CA6056	IPF4955	1.1	-1.0	1.1	-1.0	similar to Saccharomyces cerevisiae Mrpl25p ribosomal	YGR076c	orf19.7675
CA3442	IPF11326	-1.1	-1.1	-1.1	-1.0	similar to Saccharomyces cerevisiae (by homology)	YLR418c	orf19.2983
CA3670	IPF13934	-1.1	1.0	1.0	-1.0	unknown function		orf19.6458
CA5432	EBP5	1.0	-1.1	-1.1	-1.0	NADPH dehydrogenase (by homology)	YPL171c	orf19.3234
CA0475	IPF2580	-1.0	-1.1	-1.2	-1.0	unknown function	YOR140w	orf19.8085
CA4092	DBP8	-1.0	-1.0	-1.0	-1.0	DEAD box protein ATP-dependent RNA helicase (by ho	YHR169w	orf19.6652
CA4876	RNH35	1.0	-1.0	-1.1	-1.0	RNase H (by homology)	YNL072w	orf19.6562
CA4245	IPF4303	1.0	-1.1	-1.1	-1.0	unknown function		orf19.532
CA2965	IPF13174	1.0	1.1	1.0	-1.0	unknown function		orf19.5609
CA0328	IPF15217.3F	-1.1	-1.0	1.1	-1.0	WD-repeat protein, 3-prime end (by homology)	YCR072c	orf19.3778
CA2491	IPF7221	1.1	-1.0	1.0	-1.0	unknown function		orf19.4046
CA2130	RPS27A	1.0	1.0	1.1	-1.0	ribosomal protein S27.e (by homology)		
CA5159	CAP2	1.1	1.0	-1.0	-1.0	F-actin capping protein, beta subunit (by homology)	YIL034c	orf19.4597
CA0303	IPF17507	1.0	1.0	-1.0	-1.0	putative glutathione S-transferase (by homology)		orf19.8339
CA2711	TFB3	1.0	-1.0	-1.0	-1.0	Transcription/repair factor (by homology)	YDR460w	orf19.8198
CA0332	FEN2	1.1	-1.2	-1.1	-1.0	allantoate permease transporter (by homology)	YCR028c	orf19.12981
CA3243	IPF7489	-1.1	-1.1	-1.1	-1.0	unknown function		orf19.4680
CA2332	IPF4792	-1.1	-1.1	-1.2	-1.0	unknown Function		orf19.11979
CA0251	IPF9146	1.0	-1.1	-1.1	-1.0	unknown function		orf19.13622

CA5620	IPF511	1.0	1.0	-1.0	-1.0	unknown function		orf19.7078
CA2487	PIK1	-1.0	1.0	-1.0	-1.0	phosphatidylinositol 4-kinase	YNL267w	orf19.10711
CA1228	IPF16081	-1.0	-1.1	-1.0	-1.0	unknown function	YDL105w	orf19.4161
CA5485	RAD1.53F	-1.0	1.1	-1.0	-1.0	UV endonuclease, component of the nucleotide excision repairosome, internal fragme		orf19.5319
CA2365	CKS1	1.1	-1.0	1.0	-1.0	cyclin-dependent kinases regulatory subunit (by homolo	YBR135w	orf19.1282
CA1892	IPF10197	-1.0	-1.0	1.0	-1.0	Similarity to transcription factors		orf19.2753
CA2707	IPF11003	-1.0	-1.1	-1.1	-1.0	by homology pre-mrna splicing factor	YJL203w	orf19.4659
CA4337	IPF2071	-1.1	-1.0	-1.1	-1.0	unknown function		orf19.4079
CA3812	GSL22	1.1	1.0	1.2	-1.0	1,3-beta-D-glucan synthase subunit		orf19.2495
CA3900	IPF10092	-1.0	1.1	-1.0	-1.0	unknown function	YDL167c	orf19.5071
CA4295	MNN7	-1.0	-1.0	-1.1	-1.0	putative Golgi alpha-1,2-mannosyltransferase (by homology)		orf19.6692
CA6113	IPF100.3	-1.0	1.0	-1.0	-1.0	zinc finger protein, 3-prime end (by homology)		orf19.5940
CA3555	IPF7766	1.0	-1.0	1.0	-1.0	unknown function		orf19.3884
CA4208	CHS5.5EOC	-1.0	-1.0	-1.0	-1.0	chitin biosynthesis, 5-prime end		
CA4329	VMA21	1.1	1.0	-1.0	-1.0	Vacuolar H+-ATPase assembly (by homology)	YGR105w	
CA5813	IPF2522	1.0	-1.0	1.0	-1.0	unknown function	YOL125w	orf19.7460
CA6144	PKC1	-1.1	-1.1	-1.1	-1.0	Ser/thr protein kinase C	YBL105c	orf19.5901
CA4896	IPF18160	1.1	1.0	1.0	-1.0	unknown function	YDR162c	orf19.6588
CA2492	IPF7224	-1.0	1.1	1.1	-1.0	putative telomere elongation protein (by homology)	YDR206w	orf19.4045
CA2694	IPF9171	-1.1	1.0	-1.0	-1.0	unknown function		orf19.10248
CA5910	IPF5964	1.0	-1.0	1.1	-1.0	unknown function		orf19.6795
CA6119	ARV1	-1.0	1.0	1.0	-1.0	involved in sterol uptake and distribution into the plasma	YLR242c	orf19.5931
CA3573	RFA2	-1.1	-1.0	-1.1	-1.0	DNA replication factor by homology to S. cerevisiae	YNL312w	orf19.2267
CA3460	CFL1	1.1	-1.0	1.1	-1.0	ferric reductase		orf19.1263
CA2936	IPF8326	1.0	-1.0	1.0	-1.0	similar to Saccharomyces cerevisiae Rnc1p endo-exonu	YKR056w	orf19.3327
CA4486	IPF9162	2.3	-1.1	-1.1	-1.0	unknown function	YLR271w	orf19.1877
CA1497	IPF9683	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.3644
CA2058	IPF7848	1.1	1.0	1.0	-1.0	unknown function		orf19.2558
CA2512	HFI1	-1.0	-1.0	-1.1	-1.0	Putative transcriptional coactivator (by homology)	YPL254w	orf19.307
CA0358	IPF17488.5F	-1.0	-1.1	-1.0	-1.0	unknown function, 5-prime end		orf19.1818
CA4614	IPF7952	-1.1	-1.0	1.1	-1.0	unknown function		orf19.3305
CA5438	IPF223	1.0	1.0	-1.2	-1.0	unknown function	YDR128w	orf19.3241
CA4737	SKI3	1.0	1.0	-1.0	-1.0	antiviral protein	YPR189w	orf19.4848
CA0365	IPF15177	-1.0	-1.0	-1.1	-1.0	Unknown function		orf19.750
CA3187	IPF17094	1.0	-1.0	-1.1	-1.0	unknown function	YPL183c	orf19.2143
CA2616	IPF3540	1.0	1.0	1.0	-1.0	unknown function		orf19.2814
CA4359	IPF6054	-1.0	-1.0	-1.1	-1.0	unnown function	YOR205c	orf19.6736
CA3738	IPF5526	1.1	-1.0	-1.0	-1.0	unknown function	YGR058w	orf19.2180
CA5299	IPF2190	1.0	1.0	1.0	-1.0	putative serine/threonine protein kinase (by homology)	YPL236c	orf19.7164
CA5670	IPF1266	-1.1	-1.1	-1.1	-1.0	Probable transcription factor		orf19.7372
CA1151	IPF10459	-1.0	1.0	1.0	-1.0	unknown function		orf19.102
CA3687	IPF4889	1.1	1.0	1.0	-1.0	unknown function		orf19.6264
CA2019	IPF3409	-1.1	-1.1	-1.1	-1.0	unknown function	YLR361c	orf19.8463
CA0155	RPT6	-1.1	1.0	-1.1	-1.0	26S proteasome regulatory subunit (by homology)	YGL048c	orf19.11075
CA3468	IPF6318	-1.0	-1.1	-1.1	-1.0	beta-glucosidase (by homology)		orf19.1664
LacZ 3end		-1.0	1.0	1.0	-1.0			
CA0158	F19178.5EOC3	1.0	-1.0	1.0	-1.0	unknown function, 3-prime end	Missing in array	orf19.1073
CA3693	IPF4874	-1.1	-1.1	-1.1	-1.0	unknown function	YBR007c	orf19.6268
CA2948	GDS1	-1.1	-1.1	-1.1	-1.0	nam9-1 suppressor (by homology)	YOR355w	orf19.1963

CA0732	IPF9000	1.0	1.0	-1.0	-1.0	unknown function		orf19.4636
CA0187	IPF15734	-1.0	1.0	-1.1	-1.0	unknown function		
CA2390	CET1	-1.0	-1.0	-1.0	-1.0	mRNA 5 -triphosphatase (capping enzyme, beta subuni	YPL228w ; Missing in array	orf19.2609
CA1838	IPF5777	1.1	1.1	1.1	-1.0	unknown function	YER182w	orf19.3963
CA2179	FAB1	-1.1	1.0	-1.3	-1.0	phosphatidylinositol 3-phosphate 5-kinase (by homology	YFR019w	orf19.9088
CA4774	IPF3341	-1.1	-1.0	-1.1	-1.0	Unknown function	YHR063c	orf19.4006
CA3538	ATP10	-1.1	-1.1	-1.2	-1.0	F1F0 ATPase complex assembly protein (by homology)	YLR393w	orf19.6374
CA0190	IPF14773	-1.1	1.0	-1.0	-1.0	unknown function	YBR005w	orf19.11070
CA0749	HAP5	-1.0	-1.0	-1.0	-1.0	CCAAT-binding factor subunit (by homology)	YOR358w	orf19.1973
CA4725	PET100	-1.0	1.0	1.0	-1.0	cytochrome-c oxidase assembly protein (by homology)	YDR079w	
CA2098	IPF11487	-1.0	-1.1	-1.1	-1.0	unknown function	YMR098c	orf19.2387
CA2222	CCR4	-1.0	1.0	-1.0	-1.0	glucose-repressible alcohol dehydrogenase	YAL021c	orf19.5101
CA2086	IPF3392	-1.1	1.1	1.1	-1.0	unknown function	YFL013c	orf19.835
CA2057	SEC65	1.1	-1.1	-1.1	-1.0	Recognition particle subunit (by homology)	YML105c	orf19.2557
CA5566	PET18	-1.0	1.0	1.0	-1.0	Putative transcriptional regulator (by homology)	YCR020c	orf19.7330
CA5589	IPF5621	-1.1	-1.1	-1.0	-1.0	unknown function	YIL065c	orf19.7111
CA3604	IPF12942	1.0	-1.1	-1.1	-1.0	delta-12 fatty acid desaturase (by homology)		orf19.4933
CA5422	IPF1588	1.0	1.0	-1.0	-1.0	unknown function	YBR228w	orf19.972
CA3785	IPF19788	-1.0	1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Sxm1p putative be	YDR395w	orf19.5834
CA0072	IPF19283.3F	-1.1	-1.0	-1.1	-1.0	unknown function, 3-prime end	Missing in array	orf19.625
CA5737	JEN1	1.0	1.0	-1.0	-1.0	Carboxylic acid transporter protein (by homology)	YKL217w	orf19.7447
CA5378	MPR1	1.1	1.0	1.1	-1.0	26S proteasome regulatory subunit by homology	YFR004w	orf19.7264
CA5874	CTA23	1.1	1.0	1.1	-1.0	transcriptional activation	Missing in array	orf19.7544
CA3803	IPF12407	1.1	1.0	-1.0	-1.0	unknown function		orf19.2481
CA1284	IPF10168.3	1.0	1.0	1.0	-1.0	unknown function, 3-prime end	YJR089w	orf19.8257
CA5401	FET35.3	-1.1	-1.0	-1.0	-1.0	Cell surface ferroxidase, high affinity, 3-prime end (by homology)		orf19.943
CA4035	IPF12040	1.0	-1.0	-1.1	-1.0	unknown function	YPL165c	orf19.3665
CA0090	UBP13	-1.1	1.0	-1.1	-1.0	ubiquitin carboxyl-terminal hydrolase (by homology)	YER098w	orf19.2026
CA2908	SUV3	-1.1	-1.1	-1.0	-1.0	ATP-dependent RNA helicase, mitochondrial (by homol	YPL029w	orf19.4519
CA4307	IPF20013	1.0	1.0	1.0	-1.0	Unknown function	YNL217w	orf19.6707
CA4352	IPF3642	1.0	1.1	-1.0	-1.0	Unknown function	YER161c	orf19.6726
CA3609	IPF3856	-1.1	-1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Png1P peptide:N-(	YPL096w	orf19.26
CA2464	IPF8727	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.1794
CA3705	MSH6	-1.1	1.0	1.0	-1.0	DNA mismatch repair protein by homology	YDR097c	orf19.4945
CA3930	LPT1.EXON2	1.1	-1.0	1.0	-1.0	protein-tyrosine-phosphatase, exon 2	YPR073c	orf19.5104
CA2358	IPF8953	1.0	-1.0	1.0	-1.0	unknown function		orf19.4895
CA3476	NUP2.3EOC	-1.0	-1.1	-1.1	-1.0	nucleoporine involved in nuclear protein export, 3-prime	YIL063c	orf19.3583
CA3742	IFM3	-1.1	-1.1	-1.1	-1.0	2-hydroxyacid dehydrogenase by homology, Glycerate-formate-dehydrogenases-like		orf19.2176
CA4195	CYS4	-1.2	-1.0	1.1	-1.0	cystathionine beta-synthase (by homology)	YGR155w	orf19.4536
CA4967	IPF3927	-1.1	-1.1	-1.1	-1.0	unknown function	YMR075w	orf19.6506
CA3749	IPF7389	1.0	-1.0	-1.0	-1.0	unknown function		orf19.3429
CA5201	IPF2349	-1.0	-1.2	-1.2	-1.0	similar to human sphingomyelin	YDR452w	orf19.7016
CA0651	ALK8	1.1	1.0	1.0	-1.0	n-alkane inducible cytochrome P-450 (by homology)		orf19.10
CA1210	IPF7030	-1.0	1.1	-1.0	-1.0	unknown function	YBR103w	orf19.7778
CA3233	MYO1	-1.1	-1.0	-1.1	-1.0	myosin-1 isoform (type II myosin) heavy chain (by hom	YHR023w	orf19.6294
CA2165	IPF17024	-1.0	-1.0	-1.1	-1.0	unknown function	YGL126w ; Missing in array	orf19.5291
CA2532	PRP9	-1.1	-1.0	-1.1	-1.0	pre-mRNA splicing factor (snRNA-associate	YDL030w	orf19.3178
CA5534	IPF2843	1.1	1.0	1.1	-1.0	unknown function	YOR329c	orf19.7295
CA5663	IPF1251	-1.0	-1.0	-1.0	-1.0	unknown function	YIL097w	orf19.7365

CA5454	IPF257.3	-1.1	1.0	-1.1	-1.0	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathway		orf19.3261
CA6012	HCR1	-1.0	1.0	-1.2	-1.0	putative translation initiation factor 3 subunit (by homolo	YLR192c	orf19.7613
CA3133	IPF16939	1.1	-1.0	1.1	-1.0	unknown function		orf19.1364
CA5000	IPF2023	-1.0	1.0	-1.1	-1.0	unknown function	YCR095c	orf19.5247
CA5047	IPF4504	1.1	-1.0	-1.1	-1.0	unknown function		orf19.7002
CA3970	IPF6497	-1.1	-1.0	-1.1	-1.0	unknown function	YDL013w	orf19.1542
CA5875	IPF324.3	1.0	1.1	1.0	-1.0	unknown function, , 3-prime end		orf19.7545
CA5192	HOK	1.0	1.1	1.1	-1.0	unknown function		orf19.7004
CA2576	IPF7432	1.1	1.0	1.1	-1.0	unknown function		orf19.6219
CA2360	IPF8951	1.0	1.0	1.0	-1.0	unknown function	YJL145w	orf19.4897
CA1998	IPF6605	-1.0	-1.0	-1.0	-1.0	unknown function	YDR165w	orf19.6477
CA0388	IPF14468	-1.0	1.0	1.2	-1.0	unknown function	YGR089w	orf19.1907
CA3854	IPF4649	1.0	1.1	1.2	-1.0	unknown Function	YIL036w	orf19.6102
CA2458	IPF12233	1.0	-1.1	-1.0	-1.0	unknown function	YKL151c	orf19.3508
CA4674	HEM2	1.1	-1.1	1.0	-1.0	Porphobilinogen synthase (by homology)	YGL040c	orf19.898
CA4916	IPF1425	-1.0	1.0	-1.0	-1.0	Hypothetical phosphoglycerate mutase (by homology)	YOR283w	orf19.6056
CA1358	NIF3	-1.0	-1.1	-1.1	-1.0	Ngg1p-interacting factor 3 (by homology)	YGL221c	orf19.4406
CA1296	IPF18712	-1.1	1.0	-1.0	-1.0	unknown function		
CA1480	HIS6	1.1	1.0	-1.1	-1.0	5 Pro-FAR isomerase	YIL020c	orf19.1249
CA3281	RPB8	1.0	-1.1	-1.0	-1.0	DNA-directed RNA polymerase I, II, III 16 KD subunit (b	YOR224c	orf19.6314
CA4558	GRP5	1.1	1.0	-1.0	-1.0	dihydroflavonol-4-reductases (by homology)		orf19.6868
CA4562	RPS8A	1.1	-1.0	-1.1	-1.0	ribosomal protein (by homology)	YER102w	orf19.6873
CA0063	IPF19310.3F	1.0	1.0	-1.0	-1.0	unknown function, 3-prime end	Missing in array	
CA3494	RPB5	1.1	1.0	1.1	-1.0	DNA-directed RNA polymerase I, II, III (by homology)	YBR154c	orf19.6340
CA0132	SPT10	-1.1	-1.0	1.1	-1.0	Transcription regulatory protein (by homology)	YJL127c	orf19.2361
CA4356	IPF3651	1.0	-1.0	-1.0	-1.0	unknown function		
CA1680	IPF15649	-1.0	-1.0	-1.0	-1.0	unknown function	YOL087c	orf19.4913
CA2231	IPF10934	1.0	1.0	1.0	-1.0	similar to Saccharomyces cerevisiae Rny1 ribonuclease	YPL123c	orf19.3926
CA4458	IPF8464	1.1	-1.0	-1.1	-1.0	unknown function		orf19.6855
CA5199	IPF2334	1.0	-1.0	-1.0	-1.0	unknown function		orf19.7013
CA4239	IPF8174	-1.1	1.0	-1.1	-1.0	unknown function		orf19.524
CA5806	IPF4149	1.0	-1.1	1.0	-1.0	unknown function	YKL095w	orf19.5465
CA0164	IPF11694	1.0	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Tna1p high affinity	YGR260w	orf19.4335
LexA BD		-1.0	-1.0	-1.0	-1.0			
CA4585	IPF2227	-1.1	-1.1	-1.1	-1.0	unknown function	YKR025w	orf19.6903
CA4624	IPF5747	-1.1	1.0	-1.0	-1.0	unknown function	YBR255w	orf19.3318
CA3502	IPF14485	-1.1	-1.0	-1.1	-1.0	unknown function		orf19.6348
CA5436	CTF18	-1.0	-1.0	-1.1	-1.0	chromosome transmission in mitosis and maintenance	YMR078c	orf19.3239
CA3975	IPF20152	1.0	1.0	-1.1	-1.0	unknown function	YMR156c	orf19.1547
CA0506	IPF11988	1.0	1.0	-1.1	-1.0	unknown function	YML096w	orf19.3626
CA1658	IPF19924	1.0	-1.0	-1.1	-1.0	unknown function		orf19.4324
CA0629	IPF3876	-1.0	-1.0	-1.1	-1.0	unknown function		orf19.775
CA0153	IPF16368.5F	-1.1	1.0	-1.2	-1.0	Unknown function, 5-prime end		orf19.255
CA4884	ALK6	-1.0	-1.0	1.0	-1.0	n-alkane inducible cytochrome P-450 (by homology)		orf19.6574
CA3410	IPF9411	-1.1	-1.1	-1.0	-1.0	unknown function	YER030w	orf19.6147
CA5583	IPF5644	-1.0	-1.0	-1.2	-1.0	unknown function	YOR123c	orf19.7116
CA1436	IPF7165	-1.1	-1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Dia4p seryl-tRNA	YHR011w	orf19.1201
CA0582	IPF3180	1.1	-1.0	-1.0	-1.0	unknown function	YDR437w	orf19.11041
CA1286	IPF5546	-1.0	-1.0	-1.1	-1.0	unknown function		orf19.11906

CA5994	IPF677	1.0	-1.0	1.0	-1.0	unknown function		orf19.7594
CA5121	IPF1310	-1.1	-1.1	-1.1	-1.0	unknown function	YLR387c	orf19.6407
CA2348	IPF12811	1.1	-1.1	-1.1	-1.0	putative serine/threonine kinase	YOR233w	orf19.3751
CA2986	CDC5	-1.0	1.1	1.0	-1.0	Cell-cycle protein kinase (by homology)	YMR001c	orf19.6010
CA0852	KIP2	-1.0	-1.1	-1.1	-1.0	Kinesin-related protein required for nuclear migration (b	YPL155c	orf19.9315
CA4213	IPF5795	-1.0	-1.1	-1.1	-1.0	unknown function	YLR283w	orf19.811
CA5693	GDA1	-1.1	-1.0	1.0	-1.0	Golgi guanosine diphosphatase (by homology)	YEL042w	orf19.7394
CA0572	IPF14864	-1.2	-1.1	-1.2	-1.0	unknown function	YDL119c	orf19.9370
CA1924	IPF9126	1.2	1.1	1.1	-1.0	unknown function	YOL105c	orf19.5537
CA5229	IPF10425	-1.0	1.0	-1.1	-1.0	unknown function	YBR215w	orf19.5035
CA4891	IPF1627	-1.0	1.0	1.0	-1.0	unknown function		orf19.6583
CA4865	IPF4085	-1.1	-1.0	1.0	-1.0	similar to Saccharomyces cerevisiae Apg1p essential fo	YGL180w	orf19.3841
CA5511	AKL1	-1.4	1.0	-1.1	-1.0	serine/threonine protein kinase (by homology)	YIL095w	orf19.5357
CA3031	IPF12324	1.0	1.0	-1.1	-1.0	unknown function	YPR013c	orf19.217
CA3694	IPF4872.3F	-1.0	1.0	-1.1	-1.0	unknown function, 3-prime end		orf19.6269
CA2127	IPF4897	-1.0	-1.0	1.0	-1.0	unknown function		orf19.416
CA4308	IPF6660	1.0	-1.0	-1.0	-1.0	unknown function		orf19.6708
CA4708	MEU1	-1.0	1.1	1.1	-1.0	regulator of ADH2 expression (by homology)	YLR017w	orf19.6938
CA0292	IPF19855	1.0	1.0	-1.0	-1.0	unknwon function		orf19.13841
CA5135	HSP104	1.1	-1.0	-1.1	-1.0	Heat shock protein (by homology)	YLL026w	orf19.13747
CA3844	IPF7945	-1.1	-1.0	1.0	-1.0	unknown function		orf19.6604
CA3887	IPF12964	-1.0	-1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Sfh1p subunit of th	YLR321c	orf19.5093
CA2626	PAN2	-1.0	1.0	1.0	-1.0	component of Pab1p-stimulated poly(A)(by homology)	YGL094c	orf19.4764
CA4181	HOM6	1.0	1.0	1.0	-1.0	homoserine dehydrogenase (by homology)	YJR139c	orf19.2951
CA5799	IPF4176	1.1	-1.0	1.0	-1.0	unknown function		orf19.5449
CA4849	IPF6954	1.0	-1.1	1.0	-1.0	unknown function		orf19.3818
CA2259	IPF6845	1.0	1.0	-1.0	-1.0	unknown function	YNL099c	orf19.1762
CA0625	IPF19637	1.1	1.0	-1.1	-1.0	unknown function		
CA4288	IPF6662	1.0	-1.0	1.0	-1.0	similar to Saccharomyces cerevisiae Isy1p pre-mRNA s	YJR050w	orf19.6685
CA3091	IPF9821.5F	-1.0	-1.0	1.0	-1.0	unknown function, 5-prime end		orf19.11618
CA3855	IPF4645	1.0	1.0	-1.0	-1.0	unknown Function	YER046w	orf19.6103
CA2274	BIO3	1.0	1.0	1.0	-1.0	DAPA aminotransferase (by homology)	YNR058w	orf19.2591
CA0630	IPF3875.5EOC	1.0	-1.0	1.0	-1.0	unknown function, 5-prime end		orf19.776
CA1236	YPT6	-1.1	-1.0	-1.1	-1.0	GTP-binding protein of the rab family (by homology)	YLR262c	orf19.8333
CA2139	PF15654.EXON	1.1	1.0	-1.0	-1.0	unknown function, exon 1		orf19.2509
CA5382	IPF5217	1.1	1.0	1.5	-1.0	unknown function		orf19.7270
CA3545	BPT1.5F	1.1	1.1	1.1	-1.0	membrane transporter of the ATP-binding cassette (ABC) superfamily, 5-prime end (b		orf19.6383
CA4297	IPF2603	1.0	-1.1	-1.0	-1.0	unknown function		orf19.6694
CA2967	IPF12513	-1.0	-1.1	-1.2	-1.0	unknown function	YJL084c	orf19.5605
CA4426	AMD21	1.1	1.0	-1.0	-1.0	amidase (by homology)		orf19.5169
CA3500	IPF14487	-1.1	1.0	1.0	-1.0	unknown function	YDR361c	orf19.6346
CA5835	IPF429	1.1	1.0	1.1	-1.0	unknown function	YGL220w	
CA5940	IPF3485	1.0	-1.2	-1.3	-1.0	aldo/keto reductase (by homology)	YOR120w	orf19.6757
CA3661	IPF17991	1.0	1.1	-1.2	-1.0	unknown function		orf19.6465
CA3236	DEG1	-1.1	-1.1	-1.0	-1.0	pseudouridine synthase (by homology)	YFL001w	orf19.6297
CA1781	IPF14508	1.0	-1.0	-1.0	-1.0	unknown function	YEL029c	orf19.1828
CA3427	IPF11865	1.1	-1.0	-1.1	-1.0	unknown function		orf19.590
CA0442	IFC4	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.2292
14652.2		1.0	1.0	-1.1	-1.0			

CA4444	IPF3533	1.0	1.1	1.2	-1.0	putative GDP/GTP exchange factor (by homology)	YLR425w	orf19.6842
CA3163	HOL5.5F	1.1	1.0	1.1	-1.0	member of major facilitator superfamily multidrug-resistance protein subfamily 1, 5-pri		orf19.1582
CA3096	IPF11551	-1.0	1.0	-1.0	-1.0	unknown function		orf19.3858
CA4668	ROM2	-1.0	1.0	1.2	-1.0	GDP/GTP exchange factor for Rho1p (by homology)	YLR371w	orf19.906
CA3332	GAG	-1.1	-1.1	-1.2	-1.0	GAG protein of pCal retrotransposon		orf19.2668
CA2793	TRK1.5F	1.0	1.1	1.1	-1.0	Potassium transporter, 5-prime end	YKR050w	orf19.8233
CA0350	SNU114	-1.0	-1.0	-1.0	-1.0	snRNP-specific protein (by homology)	YKL173w	orf19.7784
CA4007	LAP41	-1.0	-1.1	-1.1	-1.0	aminopeptidase yscI precursor (by homology)	YKL103c	orf19.1628
CA5905	RPD32	-1.3	-1.0	-1.1	-1.0	histone deacetylase B (by homology)	YNL330c	orf19.6801
CA5755	IPF1063	-1.1	-1.1	-1.1	-1.0	Spliceosomal protein SAP 130 (by homology)	YML049c	orf19.5391
CA1045	IPF11620	-1.1	-1.1	1.0	-1.0	similar to Saccharomyces cerevisiae Rad50p DNA repa	YNL250w	orf19.1648
CA5770	IPF1103	1.0	1.1	1.0	-1.0	unknown function	YKR004c	orf19.5412
CA3978	CPR3	1.1	-1.1	-1.2	-1.0	cyclophilin (peptidylprolyl isomerase),	mitochondrial (by homology)	orf19.1552
CA2930	IPF7840	1.0	-1.1	-1.1	-1.0	similar to Saccharomyces cerevisiae Pet123p ribosoma	YOR158w	orf19.4204
CA4740	IPF4497	1.0	-1.1	1.0	-1.0	unknown function	YIL079c	orf19.4844
CA1778	IPF13810.3	-1.1	-1.1	-1.1	-1.0	unknown function, 3-prime end		orf19.1825
CA3360	IPF9568	1.1	-1.1	-1.0	-1.0	unknown function		orf19.9493
CA0007	IPF12061	-1.0	1.1	-1.1	-1.0	unknown function		orf19.7807
CA0800	IPF14064	-1.1	-1.1	1.1	-1.0	similar to Saccharomyces cerevisiae Mcm21p involved	YDR318w	orf19.3494
CA3003	IPF15741	-1.2	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Cyk3p possibly inv	YDL117w	orf19.13620
CA3466	MRP1.5F	-1.1	-1.1	-1.1	-1.0	mitochondrial ribosomal protein of the small subunit, 5-prime end (by homology)		orf19.1662
CA5687	REV3.5F	-1.0	1.1	-1.0	-1.0	DNA-directed DNA polymerase zeta subunit, 5-prime er	YPL167c	orf19.7389
CA2961	URK1	1.0	1.1	1.1	-1.0	uridine kinase (by homology)	YNR012w	orf19.5864
CA5544	IPF5987	1.0	-1.1	-1.1	-1.0	unknown function	YPR127w	orf19.7306
CA5247	MYO2	-1.5	1.0	-1.1	-1.0	Myosin heavy chain (by homology)	YOR326w	orf19.5015
CA0085	IPF16201	-1.1	1.0	1.3	-1.0	unknown function		orf19.693
CA2762	IPF15012	1.0	1.0	-1.0	-1.0	pre mRNA splicing factor (by homology)	YBL032w	orf19.13072
CA2010	IPF1731	1.2	1.0	1.0	-1.0	unknown function	YDR184c	orf19.3088
CA1622	IPF10045	-1.0	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Taf61p TFIID and	YDR145w	orf19.470
CA0399	CDC45	-1.1	-1.0	1.0	-1.0	Chromosomal DNA replication initiation protein (by hom	YLR103c	orf19.1988
CA1387	ERG16	1.2	-1.2	-1.0	-1.0	cytochrome P450 lanosterol 14a-demethylase	YHR007c	orf19.922
CA5073	IPF3603	1.0	-1.0	-1.0	-1.0	unknown function		orf19.3048
CA0149	VPS34	-1.1	-1.0	-1.1	-1.0	1-phosphatidylinositol 3-kinase	YLR240w	orf19.6243
CA0159	TUB4.3	1.0	-1.0	-1.0	-1.0	gamma-tubulin, 3-prime end	YLR212c ;Missing in array	orf19.1238
CA0675	IPF13098	-1.1	-1.1	-1.1	-1.0	unknown function	YER152c	orf19.8771
CA0434	IPF13577	1.1	1.1	1.0	-1.0	unknown function		orf19.9303
CA1983	ILV5	-1.4	1.1	-1.1	-1.0	ketol-acid reducto-isomerase (by homology)	YLR355c	orf19.7733
CA4192	IPF7533	-1.1	-1.1	-1.0	-1.0	unknown function	YDR117c	orf19.4533
CA3557	IPF7763	-1.0	1.0	-1.0	-1.0	unknown function		orf19.3886
CA3863	LEU41	1.1	-1.0	-1.0	-1.0	2-isopropylmalalate synthase (by homology)	YNL104c	orf19.6086
CA2664	IPF13370	-1.1	-1.0	-1.0	-1.0	unknown function	YKR083c	orf19.3551
CA4629	IPF13709	-1.2	-1.1	-1.2	-1.0	unknown function		orf19.335
CA4260	IPF4276	1.1	-1.1	-1.1	-1.0	similar to Saccharomyces cerevisiae Mrpl32p putative n	YCR003w	orf19.549
CA6094	IPF53	1.0	-1.1	1.0	-1.0	unknown function	YDL193w	orf19.5963
CA5609	IPF538	1.1	-1.0	1.0	-1.0	unknown function		orf19.7091
CA3330	POL21.3	-1.1	-1.1	-1.2	-1.0	pol polyprotein, reverse transcripase (by homology)		orf19.2669
CA5773	DOT5	1.0	-1.0	-1.0	-1.0	Derepression of telomeric silencing (by homology)	YIL010w	orf19.5417
Luciferase		-1.0	1.0	1.1	-1.0			
CA1244	IPF12767	-1.0	1.0	-1.0	-1.0	unknown function		orf19.2624

CA2218	IPF18508	1.1	1.0	-1.1	-1.0	unknown function	Missing in array	orf19.5375
CA4358	IPF6067	-1.0	1.0	1.0	-1.0	putative transcription factor (by homology)		orf19.6734
CA5132	GTS1	1.0	1.0	1.0	-1.0	Transcription factor by homology	YGL181w	orf19.6393
CA1942	HCT5.3EOC	1.1	-1.0	1.0	-1.0			
CA3490	IPF3192	1.0	-1.1	1.0	-1.0	unknown function		orf19.3565
CA4074	IPF2557	1.2	-1.2	-1.1	-1.0	unknown function	YDR476c	orf19.6627
CA5315	CYB2	-1.1	1.0	1.1	-1.0	B-type cyclin	YLR210w	orf19.7186
CA2757	IPF19767	1.0	-1.0	1.0	-1.0	unknown function	YPR097w	orf19.13066
CA0057	IPF3767	1.1	-1.2	-1.2	-1.0	unknown function	YPR143w	
CA2494	HTS1	-1.1	-1.0	1.1	-1.0	histidine tRNA synthetase (by homology)	YPR033c	orf19.4051
CA5153	IPF1003	-1.0	-1.0	1.0	-1.0	unknown function		orf19.4592
CA2890	IPF13626	1.1	-1.0	1.0	-1.0	Putative methyltransferase (by homology)	YER175c	orf19.2468
CA4198	IPF8055	1.1	-1.1	-1.1	-1.0	unknown function		orf19.4539
CA1522	IPF6916	1.0	1.0	1.0	-1.0	unknown function		orf19.3791
CA2067	IPF6976	-1.0	1.0	-1.0	-1.0	unknown function		orf19.2642
CA1042	IPF18784	-1.0	-1.0	1.1	-1.0	unknown function		orf19.2506
CA3560	CZF1	-1.0	1.2	1.1	-1.0	canal zinc finger protein		orf19.3127
CA2433	IPF12959	1.0	1.1	-1.0	-1.0	unknown function	YDR485c	orf19.3399
CA5167	ERG8	-1.1	-1.1	-1.1	-1.0	Phosphomevalonate kinase (by homology)	YMR220w	orf19.4606
CA1713	IPF19743	1.0	-1.0	1.0	-1.0	unknown function	YDL231c	orf19.3332
CA5708	MRPL39	1.0	-1.0	1.0	-1.0	Mitochondrial 60S ribosomal protein (by homology)	YML009c	
CA5850	IPF404.3F	1.0	-1.0	1.0	-1.0	unknown function, 3-prime end		orf19.7507
CA5815	IPF2517	1.0	-1.0	-1.0	-1.0	putative protease (by homology)		orf19.7464
CA1591	IPF14663	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.11791
CA5840	EBP6	-1.1	1.0	1.0	-1.0	NADPH dehydrogenase (by homology)		orf19.7495
CA3205	IPF3448	-1.0	1.0	-1.0	-1.0	Unknown function		orf19.6185
CA6087	YHV1	-1.0	-1.1	-1.1	-1.0	unknown function	YHR151c	orf19.5971
CA5088	IPF9758	1.0	-1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Dpb3p DNA-direct	YBR278w	orf19.3063
CA2034	SGD1.3F	-1.0	1.1	1.0	-1.0	Involved in HOG pathway, 3-prime end (by homology)		
CA5983	IPF913	-1.1	1.1	1.1	-1.0	unknown function		orf19.7579
CA4913	CIS2	-1.0	1.0	-1.0	-1.0	Gamma-glutamyltransferase (by homology)	YLR299w	orf19.6053
CA5501	MTR2.3	1.0	-1.0	-1.1	-1.0	mRNA transport protein, 3-prime end (by homology)	YKL186c	
CA3426	IPF11869	-1.0	1.1	1.1	-1.0	unknown function	YNL092w	orf19.592
CA3368	IPF4671	-1.1	-1.1	1.1	-1.0	unknown Function	YIL091c	orf19.1849
CA4121	IPF7081	1.0	1.0	-1.0	-1.0	unknown function		orf19.2770
CA1215	VPS15.3F	-1.1	1.0	-1.0	-1.0	serine/threonine protein kinase, 3-prime end		orf19.7773
CA4853	IPF5823	1.0	1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Zds1p involved in	YMR273c	orf19.3823
CA4168	IPF7781	-1.1	1.0	-1.0	-1.0	putative pump-driving ATPase	YDL100c	orf19.2965
CA0210	IPF4328	1.1	-1.2	-1.1	-1.0	unknown function	YMR315w	orf19.12971
CA3327	NCP1	-1.1	-1.1	-1.1	-1.0	NADPH-cytochrome P450 reductase	YHR042w	orf19.2672
CA1142	IPF9459	1.1	-1.0	-1.1	-1.0	unknown function		orf19.4070
CA0047	PTC2	-1.1	-1.0	1.0	-1.0	Protein phosphatase type 2C (by homology)	YER089c	orf19.2538
CA5935	IPF2798	1.0	-1.1	-1.1	-1.0	unknown function	YNL175c	orf19.6766
CA0237	IPF13416	-1.0	-1.1	-1.2	-1.0	Unknown function	YAL011w	orf19.7818
CA4593	IPF2214	1.0	-1.0	1.0	-1.0	unknown function	YDR013w	orf19.6910
CA5943	IPF3490	1.0	-1.0	1.0	-1.0	unknown function		orf19.6754
CA2208	IPF17255	1.1	1.0	1.1	-1.0	similar to Saccharomyces cerevisiae Ste2p pheromone	YFL026w	orf19.696
CA1123	IPF19723	-1.2	-1.1	-1.3	-1.0	similar to Saccharomyces cerevisiae Bph1p involved in	YCR032w	orf19.6261
CA5980	IPF918	-1.1	-1.0	-1.0	-1.0	unknown function		orf19.7576

CA1862	NMD2	-1.0	1.0	-1.1	-1.0	Nonsense-mediated mRNA decay protein 2 (by homolo	YHR077c	orf19.864
CA4479	URH1	1.1	-1.0	-1.0	-1.0	Uridine ribohydrolase (by homology)	YDR400w	orf19.1888
CA3063	IPF2971	-1.1	-1.1	-1.1	-1.0	unknown function	YLR226w	orf19.4284
CA2396	IPF6428	-1.0	1.0	-1.0	-1.0	unknown function	YKL086w	orf19.3537
CA3457	IPF8521	1.0	-1.0	1.1	-1.0	unknown function	YPL213w	orf19.1260
CA1618	RRP45	-1.0	-1.2	-1.0	-1.0	Protein component of the exosome 3 -5 exoribonucleas	YDR280w	orf19.11559
CA6014	TRS31	1.0	-1.1	1.0	-1.0	targeting complex (TRAPP) component involved in ER t	YDR472w	orf19.7615
CA3852	TUP1	1.0	1.0	1.1	-1.0	general transcription repressor	YCR084c	orf19.6109
CA0298	PPT1	-1.1	-1.0	-1.0	-1.0	Protein ser/thr phosphatase	YGR123c	orf19.1673
CA0795	IPF15641	-1.0	-1.0	1.0	-1.0	unknown function		orf19.8186
CA1185	IPF19903	1.0	1.1	1.0	-1.0	unknown function		orf19.11264
CA3801	UGA4	-1.0	1.0	1.1	-1.0	GABA-specific transport protein	YDL210wi	orf19.10016
CA6063	IPF8311	-1.1	-1.1	-1.1	-1.0	unknown function	YLR094c	orf19.6003
CA1723	TEF4	1.0	1.1	1.1	-1.0	translation elongation factor eEF1 (by homology)	YPL048w	orf19.2651
CA4943	IPF5158	-1.0	-1.0	1.0	-1.0	unknown function		orf19.6534
CA0061	IPF19315.3F	1.0	-1.0	-1.0	-1.0	unknown function, 3-prime end	Missing in array	
CA4947	NUC2	-1.0	1.0	-1.1	-1.0	NADH-UBIQUINONE OXIDOREDUCTASE (by homolo	Missing in array	orf19.6531
CA5578	IPF12536	-1.0	-1.0	-1.0	-1.0	unknown function	YGR205w	orf19.7345
CA3701	IPF11936.3F	-1.0	-1.0	1.0	-1.0	unknown function, 5-prime end		orf19.13656
CA2377	MRPL7	1.0	1.0	-1.1	-1.0	Ribosomal protein of the large subunit, mitochondrial (b	YDR237w	orf19.2214
CA3308	PET127	-1.0	-1.1	-1.0	-1.0	component of mitochondrial translation (by hom	YOR017w	orf19.9845
CA4660	YMC1	1.0	-1.1	-1.1	-1.0	mitochondrial carrier protein (MCF) (by homology)	YPR058w	orf19.4447
CA4037	KIP31	-1.0	-1.0	-1.0	-1.0	kinesin-related protein required for nuclear migration (by homology)		orf19.3667
CA0771	IPF11977	-1.0	1.1	1.0	-1.0	asaprtic proteinase (by homology)		orf19.853
CA4662	LYS7	-1.0	-1.0	-1.0	-1.0	Copper chaperone for superoxide dismutase Sod1p (by	YMR038c	orf19.4449
CA3488	IPF3198	-1.1	-1.0	-1.0	-1.0	unknown function	YDL076c	orf19.3568
CA0965	IPF9139	1.0	1.1	1.2	-1.0	unknown function		orf19.6248
CA5137	IPF1032	1.0	1.0	1.1	-1.0	similar to probable membrane protein [S. cerevisiae]	YOR059c	orf19.4574
CA5830	MRPL9	1.1	-1.0	-1.2	-1.0	Mitochondrial ribosomal protein of the large subunit (by	YGR220c	orf19.7485
CA2922	FET31	-1.0	-1.0	-1.1	-1.0	cell surface ferroxidase (by homology)		orf19.11689
CA1668	IPF11396	-1.0	1.0	-1.0	-1.0	unknown function		orf19.2853
CA4965	IPF3921	1.0	1.0	-1.1	-1.0	unknown function	YGR057c	orf19.6508
CA2687	IFU6.3F	1.1	1.1	1.0	-1.0	Unknown function, 3-prime end		orf19.10113
CA5859	CHT1	1.0	-1.0	-1.0	-1.0	endochitinase 1 precursor		orf19.7517
CA3028	IPF18393	-1.0	-1.0	1.1	-1.0	unknown function		orf19.11380
CA2498	VPS181	-1.1	-1.1	-1.1	-1.0	vacuolar membrane protein	YLR148w	orf19.5584
CA5602	IPF554	1.1	1.0	-1.1	-1.0	RNA binding protein (by homology)		orf19.7097
CA6049	IPF4935	1.0	1.1	-1.0	-1.0	unknown function	YJL003w	orf19.7665
CA0529	SMC2	-1.0	1.0	-1.0	-1.0	chromosome segregation protein (by homology)	YFR031c	orf19.3623
CA5258	GCV3	1.0	-1.2	-1.1	-1.0	Glycine decarboxylase, subunit H (by homology)	YAL044c	orf19.5006
CA4758	PPR1	-1.0	1.0	-1.1	-1.0	transcription factor regulating pyrimidine pathway (by hc	YLR014c	orf19.3986
CA1487	GPT1	1.0	1.1	-1.0	-1.0	polyamine transporter		orf19.4063
CA5113	IPF20026	-1.1	-1.1	-1.2	-1.0	unknown function	YDL063c	orf19.6418
CA3044	IPF7298	1.0	-1.0	-1.2	-1.0	unknown function		orf19.2418
CA1074	PRORS.5F	-1.1	-1.1	-1.2	-1.0	prolyl-tRNA synthetase, 5-prime end		orf19.2532
CA3322	IPF6895.3F	-1.1	-1.0	-1.0	-1.0	unknown function, 3-prime end		
CA0019	IPF17799	-1.0	-1.0	-1.0	-1.0	unknown function	YBR151w	
CA4560	IPF8038	-1.1	1.1	-1.0	-1.0	unknown function	YMR124w	orf19.6871
CA3435	IPF6391	1.0	-1.1	-1.1	-1.0	similarity to mammalian indoleamine 2,3-dioxygenase (I	YJR078w	orf19.583

CA5102	CDC23	1.0	-1.0	1.0	-1.0	Subunit of anaphase-promoting complex (by homology)	YHR166c	orf19.6437
CA2841	IPF12981	1.1	-1.0	1.0	-1.0	unknown function		orf19.5727
CA0409	PHO80	-1.0	-1.0	-1.1	-1.0	Cyclin (by homology)	YOL001w	orf19.5755
CA1683	CIRT	-1.1	-1.1	-1.1	-1.0	Probable transposase		orf19.4919
CA5648	UBC6	-1.0	1.0	1.1	-1.0	E2 ubiquitin-conjugating enzyme (by homology)	YER100w	orf19.7347
CA5888	IPF2414	1.0	-1.0	-1.1	-1.0	unknown function		orf19.6820
CA0492	SNU71	1.0	-1.1	-1.1	-1.0	Associated with U1 snRNP (by homology)	YGR013w	orf19.9068
CA1306	CDC14.3	-1.1	-1.1	-1.1	-1.0	protein phosphatase, 3-prime end	YFR028c	orf19.4192
CA0725	IPF20063	1.0	-1.1	-1.1	-1.0	unknown function		orf19.1749
CA4925	IPF1408	1.0	-1.1	-1.1	-1.0	unknown function	YFR021w	orf19.6064
CA1500	IPF13221	-1.0	-1.0	-1.1	-1.0	unknown function	YOR091w	orf19.1697
CA5758	IPF1069	1.0	-1.0	1.1	-1.0	similar to Saccharomyces cerevisiae Rav1p involved in	YJR033c	orf19.5395
CA2785	MET13	-1.0	-1.0	1.0	-1.0	Methylene tetrahydrofolate reductase (by homology)	YGL125w	orf19.288
CA3182	LIP4	-1.0	1.0	1.1	-1.0	secretory lipase		orf19.2133
CA0948	IPF10270	-1.2	-1.2	-1.1	-1.0	unknown function	YGR111w	orf19.1272
CA5884	SLF1	-1.0	-1.0	-1.1	-1.0	Copper homeostasis protein (by homology)	YDR515w	orf19.6826
3692.2		-1.1	-1.1	-1.1	-1.0			
CA3611	IPF3853	-1.1	-1.1	-1.1	-1.0	unknown function	YGR096w	orf19.28
CA0094	IPF12819	1.0	1.0	1.0	-1.0	unknown function	YDR474c	orf19.3213
CA0814	IPF16233	1.0	1.1	1.1	-1.0	unknown function		orf19.1914
CA2701	PF14414.EXON	-1.0	-1.0	-1.1	-1.0	unknown function, exon 2		orf19.10255
CA3172	IPF7676	-1.1	1.0	1.0	-1.0	unknown function		orf19.1400
CA2709	IPF4828	1.1	1.0	1.0	-1.0	by homology to S. cerevisiae YEAST TRANSCRIPTION	YPL089c	orf19.4662
CA0703	IPF11807	-1.1	-1.0	-1.1	-1.0	unknown function		orf19.2914
CA0709	ZORRO2A.3F	1.0	1.1	1.0	-1.0	Reverse transcriptase, 3-prime end		orf19.3387
CA0138	INH1	1.1	-1.2	-1.1	-1.0	Inhibitor of mitochondrial ATPase		
CA2685	MSH4	-1.0	1.0	-1.1	-1.0	DNA mismatch repair protein	YFL003c	orf19.2579
CA3903	IPF14890	1.1	-1.0	-1.0	-1.0	unknown function		orf19.4400
CA0476	UBP2	-1.1	1.1	-1.0	-1.0	Ubiquitin-specific proteinase (by homology)	YOR124c	orf19.8088
CA0312	IPF6396	1.2	-1.0	1.1	-1.0	unknown function	YNL254c	orf19.8211
CA0329	IMG2	-1.0	1.0	-1.1	-1.0	Required for Integrity of Mitochondrial Genome (by hom	YCR071c	orf19.3777
CA2767	TOA1	-1.1	-1.1	-1.1	-1.0	transcription initiation factor IIA (by homology)	YOR194c	orf19.2682
CA2100	KTI12	-1.0	-1.1	-1.2	-1.0	involved in resistance to K.lactis killer toxin (by h	YKL110c	orf19.2385
CA2503	IPF6803.5F	-1.0	1.0	1.0	-1.0	unknown function, 5-prime end	YAL045c	orf19.5592
CA5370	IPF5248	1.0	1.0	-1.1	-1.0	unknown function	YPL005w	orf19.7254
CA2113	ATP12	-1.1	-1.1	-1.0	-1.0	F1F0-ATPase complex assembly protein (by homology)	YJL180c	orf19.3686
CA0203	MID1	-1.1	-1.1	-1.1	-1.0	involved in Ca2+ influx during mating (by homology)	YNL291c	orf19.10724
CA5305	IPF2175	-1.0	-1.0	-1.2	-1.0	similar to Saccharomyces cerevisiae Hlj1p dnaJ-type pr	YMR161w	orf19.7175
CA3697	IPF4866	1.0	1.1	1.1	-1.0	similar to Saccharomyces cerevisiae Yuh1p ubiquitin-sp	YJR099w	orf19.13651
CA3222	IPF15883	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.6283
CA0009	IPF11382	1.0	-1.0	1.0	-1.0	unknown function		orf19.8247
CA5597	IPF563	-1.0	-1.0	-1.0	-1.0	unknown function	YCL036w	orf19.7103
CA0364	IPF15983	-1.1	-1.1	-1.1	-1.0	unknown function	YLR363c	orf19.1525
CA0841	IPF15638	1.0	-1.1	-1.0	-1.0	unknown function		orf19.8652
CA3940	NIC96	-1.0	-1.0	-1.0	-1.0	nuclear pore protein (by homology)	YFR002w	orf19.9553
CA5590	TAD1	-1.0	-1.0	1.1	-1.0	Double-stranded rna specific adenosine deaminase by h	YGL243w	orf19.7110
CA3296	PF5723.EXON	1.1	-1.1	1.2	-1.0	cell surface GPI-anchored protein, exon 2 (by homology)		orf19.6336
CA4233	RFT1	1.2	-1.1	-1.0	-1.0	nuclear division protein (by homology)	YBL020w	orf19.516
CA2691	PTR2.EXON1	1.0	1.0	1.0	-1.0	Peptide transporter for di- and tripeptides, exon 1		orf19.2583

CA1731	IPF8437	-1.1	-1.2	-1.1	-1.0	putative DNA-directed RNA polymerase (by homology)		orf19.6499
CA5461	GSL23.5F	1.1	1.0	-1.0	-1.0	1,3-beta-D-glucan synthase subunit, 5-prime end		orf19.3269
CA1152	IPF10457	1.0	-1.0	-1.0	-1.0	nuclear fusion protein-like (by homology)		orf19.103
CA1263	IPF9880	1.0	1.2	1.1	-1.0	unknown function		orf19.1246
CA4415	HIK1.3EOC	-1.0	1.1	1.1	-1.0	histidine kinase, 3-prime end		
CA4033	IPF19795	1.1	1.1	1.0	-1.0	similar to Saccharomyces cerevisiae Mip1p DNA-directe	YOR330c	orf19.3431
CA5689	REV3.3F	-1.0	-1.0	1.0	-1.0	DNA-directed DNA polymerase zeta subunit, 3-prime end (by homology)		orf19.7390
CA0439	IPF12478	-1.1	-1.0	-1.1	-1.0	unknown function	YML034w	orf19.13015
CA1857	IPF15348	1.0	1.0	-1.0	-1.0	unknown function		orf19.9080
CA0639	FDH13.3F	1.0	1.0	1.0	-1.0	Putative formate dehydrogenase, 3-prime end (by homology)		
CA4960	IPF3912	1.3	1.1	1.4	-1.0	unknown function	YPL177c	orf19.6514
CA4345	IPF3633.3	-1.0	-1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Hir3p involved in c	YJR140c	orf19.6719
CA2876	RNR2	1.1	1.0	1.0	-1.0	Ribonucleotide reductase (by homology)		orf19.5845
CA1052	IPF15861	1.0	1.0	1.0	-1.0	unknown function		orf19.3894
CA1931	IPF3905	-1.3	1.0	-1.2	-1.0	similar to Saccharomyces cerevisiae Sec21p coatomer	YNL287w	orf19.759
CA0073	IPF19283.5F	1.0	-1.0	1.0	-1.0	unknown function, 5-prime end	Missing in array	
CA4071	IPF2561	1.1	1.0	1.1	-1.0	unknown function	YJL044c	orf19.6624
CA1422	IPF14248	1.0	-1.1	-1.1	-1.0	putative methyltransferase (by homology)	YDL201w	orf19.3798
CA1616	IPF14538	-1.1	-1.2	-1.4	-1.0	unknown function		orf19.3219
CA4279	DPH51	1.1	1.1	1.2	-1.0	Diphthamide methyltransferase (by homology)	YLR172c	orf19.6676
CA4280	IFJ5	-1.0	1.0	-1.0	-1.0	Unknown function		orf19.6678
CA3758	IPF8889	1.0	1.0	1.0	-1.0	putative arginase (by homology)		orf19.10922
CA6034	APC11	-1.2	-1.1	1.1	-1.0	subunit of the anaphase promoting complex (by homolo	YDL008w	orf19.7644
CA2183	IPF6872	1.0	-1.0	1.0	-1.0	serine/threonine protein kinase (by homology)	YGR262c	orf19.4252
CA0458	IPF15601	1.0	1.0	1.0	-1.0	unknown function		orf19.2433
CA1878	IPF10298	-1.1	1.1	-1.1	-1.0	unknown function	YPL202c	orf19.2272
CA5716	MED6	-1.0	1.0	-1.1	-1.0	RNA polymerase II transcriptional regulation mediator (	YHR058c	orf19.7420
CA1901	IPF14135	-1.0	-1.0	-1.1	-1.0	unknown function	YNL022c	orf19.2604
CA4768	IPF9385	1.0	-1.1	-1.1	-1.0	similar to Saccharomyces cerevisiae Pho2p homeobox-	YDL106c	orf19.4000
CA3283	IPF6274	-1.0	-1.1	-1.0	-1.0	unknown function	YMR221c	orf19.6316
CA0746	IPF14921	-1.0	1.1	-1.0	-1.0	unknown function		orf19.1527
CA1981	IPF9470	-1.1	-1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Pcf11p componen	YDR228c	orf19.684
CA5522	IPF708	-1.1	1.0	1.0	-1.0	unknown function	YBR075w	orf19.5370
CA2768	IPF17011	1.0	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Slk19p involved in	YOR195w ; Missing in array	orf19.2684
CA2427	IPF9898	-1.0	1.0	1.0	-1.0	probable formate dehydrogenase (by homology)	YHL008c	orf19.3406
CA1357	ARH1	-1.1	-1.2	-1.4	-1.0	adrenodoxin reductase and ferredoxin-NADP+ reductas	YDR376w	orf19.410
CA6065	SAP3	-1.0	-1.0	-1.0	-1.0	secreted aspartyl proteinase		orf19.6001
CA4584	IPF2228	-1.1	-1.2	-1.2	-1.0	similar to Saccharomyces cerevisiae Dbp7p RNA helica	YKR024c	orf19.6902
CA1850	IPF14630	1.0	-1.0	-1.1	-1.0	unknown function	YFR041c	orf19.641
CA1207	PPG1	-1.1	1.2	-1.0	-1.0	Phosphoprotein phosphatase PPG catalytic chain (by h	YNR032w	orf19.11256
CA4252	IPF4290	-1.0	1.0	-1.0	-1.0	unknown function		orf19.541
CA3444	IPF11323	-1.1	-1.1	-1.1	-1.0	unknown function	YLR424w	orf19.2980
CA3486	IPF3206	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.3572
CA0244	IPF19082	1.0	1.0	-1.1	-1.0	unknown function		
CA3377	CLF1	-1.0	-1.1	1.0	-1.0	pre-mRNA splicing factor (by homology)	YLR117c	orf19.7964
CA2844	IPF13158	1.0	-1.0	1.0	-1.0	unknown function		orf19.5729
CA5230	IPF10424	1.1	-1.1	-1.0	-1.0	unknown function	YBR216c	orf19.5034
CA1657	IPF16022	-1.1	1.0	-1.0	-1.0	unknown function		orf19.4325
CA0645	PF18917.5EO	1.0	1.1	-1.0	-1.0	unknown function, 5-prime end		

CA3100	IPF6594	-1.0	1.0	1.1	-1.0	unknown function		orf19.3863
CA0169	RBT7	-1.0	1.0	1.1	-1.0	repressed by TUP1		orf19.10196
CA1035	IFI2.3F	-1.1	-1.1	-1.2	-1.0	unknown function, 3-prime end		orf19.1038
CA1352	VCX1	1.1	-1.1	1.1	-1.0	Ca2+-transport by homology	YDL128w	orf19.405
CA6138	IPF4351	-1.1	-1.0	-1.1	-1.0	unknown function	YBR083w	orf19.5908
CA5014	IPF11120	-1.0	-1.1	-1.0	-1.0	similar to Saccharomyces cerevisiae Cki1p choline kina	YLR133w	orf19.6966
CA4645	IPF1496	-1.0	-1.0	-1.1	-1.0	unknown function		orf19.352
CA1631	IPF19582	1.0	1.0	-1.0	-1.0	unknown function	YNL230c	orf19.1028
CA1057	IPF17031	1.0	-1.0	-1.1	-1.0	unknown function	YBL057c	orf19.2544
CA2935	IPF11521	1.0	-1.2	-1.2	-1.0	unknown function	YMR172w	orf19.3328
CA3253	IPF4724	1.1	1.0	-1.0	-1.0	unknown Function	Missing in array	orf19.11225
CA5724	NUP116	-1.0	1.0	1.1	-1.0	nuclear pore protein (by homology)	YMR047c	orf19.7433
CA1529	SPC105	-1.1	-1.0	-1.1	-1.0	Spindle pole body protein (by homology)	YGL093w	orf19.4557
CA3599	IPF19785	-1.1	-1.0	-1.1	-1.0	unknown function	YLR067c	orf19.4929
CA4790	IPF3367	-1.1	-1.1	-1.2	-1.0	Riboflavin synthase (by homology)	YBR256c	orf19.4024
CA4682	IPF3687	1.0	1.1	-1.2	-1.0	similar to Saccharomyces cerevisiae Pan1p actin-cytosl	YIR006c	orf19.886
CA5301	IPF2186	1.1	1.0	1.0	-1.0	unknown function		orf19.7166
CA4170	IPF7784	-1.0	1.1	1.1	-1.0	unknown function		orf19.2963
CA2706	IPF11006	1.0	-1.0	-1.0	-1.0	unknown function		orf19.4658
CA1121	IPF6730	-1.2	1.0	-1.1	-1.0	Unknown function	YLR368w	orf19.1604
CA4798	RPN5.3F	-1.1	1.1	1.0	-1.0	subunit of the regulatory particle of the proteasome, 3-p	YDL147w	orf19.4032
CA1695	RRP42	1.0	-1.1	-1.1	-1.0	rRNA processing protein (by homology)	YDL111c	orf19.5039
CA0646	IPF19702	1.1	-1.1	-1.1	-1.0	unknown function		orf19.11806
CA3220	IPF10001	1.0	1.1	-1.0	-1.0	unknown function		orf19.6194
CA2444	IPF13883	-1.1	-1.0	-1.1	-1.0	Unknown function		orf19.5502
CA2161	IPF11876	1.0	1.5	-1.0	-1.0	unknown function		orf19.5295
CA4050	PF10482.EXON	1.1	-1.0	1.0	-1.0	unknown function, exon 2	YOL114c	orf19.425
CA1065	IPF9002	1.0	-1.1	-1.1	-1.0	unknown function		orf19.12108
CA4832	DAL2	-1.0	-1.0	-1.1	-1.0	Allantoinase	YIR029w	orf19.2065
CA3289	HPA3	1.0	1.0	1.1	-1.0	histone and other protein acetyltransferase(by homolog	YEL066w	orf19.6323
CA5712	IPF2657	-1.1	-1.0	1.0	-1.0	unknown function	YEL019c	orf19.7413
CA2535	NCE11	-1.0	-1.0	1.1	-1.0	involved in non-classical protein export pathway (by hor	YJL205ca	
CA0461	IPF4972	1.0	-1.0	1.1	-1.0	unknown function	YJR112w	orf19.2519
CA0922	IPF12991	1.0	-1.1	-1.1	-1.0	unknown function	YIR005w	orf19.1045
CA3083	IPF11262	-1.0	-1.1	-1.1	-1.0	unknown function	YDL010w	orf19.11626
CA2510	IPF1472	-1.0	-1.1	-1.0	-1.0	unknown function		orf19.305
CA1563	IPF13855	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.4713
CA1948	IPF14022	-1.0	-1.0	1.0	-1.0	ATPase family gene (by homology)		orf19.12205
CA2842	ALK5.3F	1.1	-1.1	-1.0	-1.0	n-alkane-inducible cytochrome P-450, 3-prime end		
CA3942	CHL1	1.0	1.0	-1.0	-1.0	protein of the DEAH box family (by homology)	YPL008w	orf19.2000
CA0975	IPF18811	-1.0	-1.1	-1.2	-1.0	unknown function		
CA5861	IPF373	1.1	1.0	1.0	-1.0	unknown function		orf19.7519
CA6031	PRO1	1.0	-1.1	-1.0	-1.0	glutamate 5-kinase (by homology)	YDR300c	orf19.7638
CA5400	KRE62.3F	-1.0	-1.0	-1.0	-1.0	Glucan synthase subunit, 3-prime end (by homology)		
CA1794	IPF18608.3F	-1.0	-1.0	-1.0	-1.0	unknown function, 3-prime end	YIL103w	orf19.5208
CA4182	IPF19797	1.1	-1.1	-1.3	-1.0	similar to Saccharomyces cerevisiae Iml1pinvolved in cl	YJR138w	orf19.10466
CA0964	IPF9141	-1.1	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Ctf4p DNA-directe	YPR135w	orf19.6247
CA2173	IPF18527	-1.1	-1.2	-1.2	-1.0	unknown function	YDR108w	orf19.3764
CA3960	IPF11236.5F	-1.0	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Sec15p componer	YGL233w	orf19.1419

CA3352	IPF16194	1.0	-1.0	-1.1	-1.0	unknown function	YMR099c	orf19.9501
CA2366	IPF10373	1.0	-1.0	1.0	-1.0	unknown function	YNL245c	orf19.1281
CA3006	IPF12152	1.1	-1.0	1.0	-1.0	Unknown function	YDL213c	orf19.13616
CA3744	RAD57	-1.0	-1.0	-1.0	-1.0	DNA-repair like protein	YDR004w	orf19.2174
CA2620	IPF9496	1.0	-1.1	-1.0	-1.0	carnitine O-acetyltransferase (by homology)	YER024w	orf19.2809
CA0918	IPF17881	-1.0	-1.0	1.1	-1.0	cyclin (by homology)	YJL006c	orf19.1041
CA6115	IPF112	-1.0	-1.1	-1.0	-1.0	unknown function		orf19.5935
CA2764	QCR7	1.1	-1.3	-1.3	-1.0	ubiquinol--cytochrome-c reductase subunit 7 (by homol	YDR529c	orf19.5629
CA5721	IPF2443	-1.1	-1.2	-1.1	-1.0	similar to Saccharomyces cerevisiae Ost6p N-oligosacc	YML019w	orf19.7426
CA3623	IPF15911	1.1	1.0	1.0	-1.0	unknown function	Missing in array	orf19.7838
CA4353	IPF3645	-1.1	-1.1	-1.0	-1.0	similar to Saccharomyces cerevisiae Rit1p initiator tRNA	YMR283c	orf19.6727
CA1002	ROK1.3	-1.0	1.0	1.1	-1.0	RNA helicase, 3-prime end	YGL171w	orf19.3756
CA4427	IPF5584	1.1	1.0	1.0	-1.0	unknown function	YOL022c	orf19.5168
CA2721	IPF4799	-1.1	-1.0	1.0	-1.0	unknown Function	YOR138c	orf19.3342
CA5224	IPF3081	1.0	1.1	1.0	-1.0	unknown function	YLR050c	orf19.7043
CA0869	IPF14772	-1.1	-1.0	1.0	-1.0	unknown function	YHL022c	orf19.3589
CA6114	SEN1	-1.0	-1.0	-1.2	-1.0	positive effector of tRNA-splicing endonuclease (by hom	YLR430w	orf19.5938
CA5917	IPF8923	1.2	-1.1	-1.0	-1.0	unknown function		orf19.6788
CA0867	PF14773.EXON	-1.0	-1.0	1.0	-1.0	unknown function, exon 2		orf19.3586
CA4988	RPN2	-1.3	1.1	-1.1	-1.0	Proteasome regulatory subunit (by homology)	YIL075c	orf19.5260
CA2715	CTF8	1.0	1.0	-1.0	-1.0	putative) kinetochore protein (by homology)	YHR191c	orf19.576
CA5343	RPL4B	-1.1	1.1	1.0	-1.0	Ribosomal protein L4B (by homology)	YDR012w	orf19.7217
CA4211	IPF5052	-1.0	-1.1	-1.1	-1.0	RNA-binding protein (by homology)	YOL041c	orf19.809
CA0422	IPF9046	1.0	-1.0	-1.1	-1.0	unknown function		orf19.2231
CA3581	IPF16143	1.0	-1.0	-1.1	-1.0	unknown function		orf19.2259
CA3725	TOK1.3	-1.1	-1.0	1.1	-1.0	Outward-rectifier potassium channel, 3-prime end (by h	YJL093c	orf19.4175
CA4976	IPF4708	1.0	-1.0	1.0	-1.0	unknown Function	YOL072w	orf19.5276
CA1202	DBP3	1.0	-1.1	-1.1	-1.0	ATP-dependent RNA helicase (HELICASE CA3) by hom	YGL078c	orf19.12334
CA0779	IPF20065	-1.0	1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Yku70p high-affinit	YMR284w	orf19.3491
CA4834	IPF1217	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.2063
CA5586	IPF5625	-1.0	-1.1	-1.1	-1.0	unknown function		orf19.7112
CA5667	IPF1259	-1.0	1.0	-1.0	-1.0	Conserved hypothetical protein	YML005w	orf19.7369
CA5484	RAD1.3F	-1.2	-1.1	1.1	-1.0	UV endonuclease, component of the nucleotide excision	YPL022w	orf19.5318
CA2463	IPF8730	-1.0	1.0	-1.0	-1.0	unknown function	YGR223c	orf19.1793
CA0500	IPF20058	-1.1	-1.1	-1.0	-1.0	unknown function	YOR252w	orf19.4793
CA1039	IPF4012	1.2	-1.1	1.0	-1.0	Unknown Function	YPL221w	orf19.2501
CA2253	IPF15485	-1.0	-1.1	-1.1	-1.0	unknown function	YHL013c	orf19.1959
CA2662	IPF17139	-1.0	1.1	1.1	-1.0	unknown function	YKR081c ; Missing in array	orf19.3553
CA2419	IPF14379	-1.0	1.1	-1.0	-1.0	unknown function	YNL155w	orf19.4474
CA1071	IPF16624	1.1	1.1	1.0	-1.0	unknown function	YBL051c	orf19.2534
CA0679	885.REPEAT1.	1.0	1.1	1.1	-1.0	unknown function, 5-prime end		
CA1967	IPF10866	1.0	1.1	1.2	-1.0	similar to Saccharomyces cerevisiae Ira2p GTPase-acti	YOL081w	orf19.5219
CA5453	IPF256	1.1	1.1	1.0	-1.0	control of gene expression (by homology)	YKL088w	orf19.3260
CA4392	IPF12303	1.0	1.0	1.0	-1.0	glutathione-S-transferase (by homology)		orf19.3121
CA2485	PAP12	-1.1	-1.0	-1.0	-1.0	poly(A) polymerase	Missing in array	orf19.10713
CA3810	IPF9230	-1.0	1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Ste3p pheromone	YKL178c	orf19.2492
CA3093	TOF1	-1.1	-1.0	-1.1	-1.0	Topoisomerase I interacting factor 1 (by homology)	YNL273w	orf19.11613
CA0858	IPF14493	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.4465
CA3919	IFC5	1.0	1.0	1.0	-1.0	unknown function		orf19.5121

CA3850	IPF7932	1.1	-1.2	-1.1	-1.0	similar to Saccharomyces cerevisiae Etf-beta electron-t	YGR207c	orf19.6612
CA5328	RER1	-1.1	-1.0	1.1	-1.0	Required for correct localization of Sec12p (by homolog	YCL001w	orf19.7202
CA1243	IPF7922	-1.0	-1.0	-1.0	-1.0	unknown function	YNL236w	orf19.8923
CA2255	CYC3	1.0	-1.1	1.0	-1.0	cytochrome C heme lyase	YAL039c	orf19.1957
CA5651	KIP3	-1.1	-1.1	-1.0	-1.0	Kinesin-related protein required for nuclear migration (b	YGL216w	orf19.7353
CA3597	BNI1	-1.1	-1.0	-1.2	-1.0	regulator of budding (by homology)	YNL271c	orf19.4927
CA4996	IPF2029	1.0	-1.0	-1.0	-1.0	unknown function		orf19.5251
CA0327	IPF15217.5F	-1.1	-1.0	-1.1	-1.0	WD-repeat protein, 5-prime end (by homology)		orf19.3779
CA3858	TRP1	-1.1	1.0	1.1	-1.0	phosphoribosylanthranilate isomerase	YDR007w	orf19.6096
CA1266	SAP8	1.0	-1.0	1.0	-1.0	aspartic protease		orf19.242
CA4812	IPF1171	1.0	-1.1	-1.0	-1.0	Putative synaptobrevin (by homology)	YLR093c	orf19.2089
CA0374	IFK3	-1.0	-1.0	-1.0	-1.0	Probable monooxygenase (by homology)		orf19.8477
CA6051	IPF4940	1.0	1.0	-1.0	-1.0	unknown function	YOR126c	orf19.7667
CA1170	IPF13268	-1.1	-1.0	-1.1	-1.0	unknown function	YDR132c	orf19.2749
CA4626	MRS7	-1.1	-1.1	-1.2	-1.0	suppressor splicing defects (by homology)	YOL027c	orf19.10831
CA2432	COQ3	1.1	1.0	1.1	-1.0	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase	YOL096c	orf19.3400
CA3085	IPF17086	-1.1	-1.1	-1.1	-1.0	unknown function		orf19.4148
CA2566	IPF12122	-1.1	1.0	1.0	-1.0	unknown function	YPL034w	orf19.5646
CA0801	CHC1	1.4	1.1	1.1	-1.0	clathrin heavy chain (by homology)	YGL206c	orf19.3496
CA4502	IPF10391	-1.0	1.1	-1.0	-1.0	Similar to dnaJ proteins	YNL064c	orf19.8136
CA6044	IPF4928	-1.0	-1.1	-1.1	-1.0	similar to Saccharomyces cerevisiae Sac2p suppressor	YDR484w	orf19.7660
CA5867	EPL1	1.0	-1.0	-1.0	-1.0	DNA-binding protein (by homology)	YFL024c ; Missing in array	orf19.7529
CA3278	RPS3	1.1	-1.2	-1.3	-1.0	Ribosomal protein S3.e (by homology)	YNL178w	orf19.6312
CA4760	IPF9652	1.0	1.0	-1.1	-1.0	unknown function	YJL011c ; Missing in array	orf19.3990
CA3461	CFL2	1.0	1.0	-1.1	-1.0	ferric reductase (by homology)		orf19.1264
CA3755	IPF17743	-1.0	-1.0	-1.2	-1.0	Unknown function	YBL093c	
CA0539	NUP57	1.0	-1.0	1.1	-1.0	nuclear pore protein (by homology)	YGR119c	orf19.2820
CA0624	IPF312	-1.1	-1.1	-1.1	-1.0	unknown function	YJR080c	orf19.3154
CA4738	IPF4500	-1.0	-1.0	-1.0	-1.0	putative GTP-binding protein (by homology)	YGR210c	orf19.4846
CA4691	IPF3958	1.1	-1.0	-1.0	-1.0	unknown function		orf19.874
CA5298	SUI3	-1.0	1.1	-1.0	-1.0	Translation initiation factor eIF2 beta subunit (by homolo	YPL237w	orf19.7161
CA5406	IPF1547	-1.1	-1.1	-1.1	-1.0	unknown function		orf19.949
CA5106	AFG2	1.0	-1.1	-1.0	-1.0	Member of the Sec18p, Pas1p, Cdc48p, TBP-1 family o	YLR397c	orf19.6432
CA1881	RCK2	-1.1	-1.1	-1.1	-1.0	Ca/calmodulin-dependent ser/thr protein kin	YLR248w	orf19.9808
CA4006	IPF4253	-1.1	-1.1	-1.1	-1.0	unknown function	YML017w	orf19.1630
CA2312	IPF16498	-1.1	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Arg82p arginine m	YDR173c	orf19.1377
CA3872	MRPL28	1.0	-1.0	-1.2	-1.0	mitochondrial ribosomal protein of the large subunit (by	YDR462w	orf19.397
CA3012	IPF14013	-1.0	-1.1	-1.1	-1.0	unknown function		orf19.6227
CA4794	SQT1	1.1	1.1	-1.0	-1.0	suppresses dominant-negative mutants of the rib	YIR012w	orf19.4029
CA5792	IPF4195	-1.0	-1.1	-1.1	-1.0	similar to Saccharomyces cerevisiae Ulp2p involved in	YIL031w	orf19.5441
CA1226	IPF15660	1.1	-1.0	1.0	-1.0	putative mitochondrial carrier (by homology)	YMR166c	orf19.4159
CA5547	IPF5981	-1.1	-1.1	-1.2	-1.0	similar to Saccharomyces cerevisiae Gin3p (by homolo	YML128c	orf19.7310
CA5410	IPF1557	-1.1	-1.1	-1.2	-1.0	similar to dnaJ proteins	YLR090w	orf19.954
CA1081	IPF14797.3	1.3	1.0	1.1	-1.0	unknown function, 3-prime end		
CA3891	BUD6	-1.1	-1.1	-1.1	-1.0	bud site selection protein (by homology)	YLR319c	orf19.5087
CA2155	IPF7903	-1.0	-1.0	-1.0	-1.0	unknown function	YPL255w	orf19.6027
CA3029	IPF13825	-1.3	1.0	-1.1	-1.0	similarity to serine/threonine protein kinases (by homolo	YNR047w	orf19.223
CA2927	RAD52	1.0	-1.0	1.0	-1.0	Nuclear ribonucleoprotein E	YML032c	orf19.4208
CA4087	IPF5013	-1.0	-1.1	-1.1	-1.0	similar to Saccharomyces cerevisiae Mct1p malonyl-Co	YOR221c	orf19.6643

CA0209	HAP2	1.0	1.1	1.0	-1.0	CCAAT-binding factor subunit (by homology)	YGL237c	orf19.1228
CA0423	IPF15273	-1.1	-1.1	-1.2	-1.0	unknown function		orf19.9381
CA4845	IPF6945.5F	-1.0	-1.0	-1.1	-1.0	unknown function, 5-prime end		orf19.3813
CA4859	IPF15927.5F	-1.1	-1.1	-1.2	-1.0	similar to Saccharomyces cerevisiae Tfc3p transcription	YAL001c	orf19.3833
CA5120	YDJ1	-1.1	-1.1	-1.1	-1.0	Mitochondrial and ER import protein (by homology)		orf19.6408
CA1294	MSH5.3F	1.0	-1.0	1.0	-1.0	Meiosis-specific protein, 3-prime end (by homology)	YDL154w	orf19.10228
CA4583	IPF2229	-1.1	-1.1	-1.0	-1.0	unknown function	YOR173w	orf19.6901
CA3776	IPF10435	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.2890
CA1976	IPF9582	1.1	-1.1	-1.2	-1.0	similar to Saccharomyces cerevisiae Mrps18p ribosoma	YNL306w	orf19.688
CA2886	IPF7207	-1.1	-1.0	-1.0	-1.0	unknown function	YML127w	orf19.2473
CA5271	IPF1777	-1.0	-1.1	-1.0	-1.0	similar to Saccharomyces cerevisiae Mpt5p multicopy s	YGL178w	orf19.4991
CA3568	IPF7804.3F	-1.1	-1.1	-1.2	-1.0	unknown function, 3-prime end	YML013w	orf19.3135
CA0758	PAP11	-1.1	-1.0	-1.0	-1.0	poly(A) polymerase by homology to S. cerevisiae	YKR002w	orf19.3197
CA3248	IPF15834	1.0	1.0	1.0	-1.0	unknown function		orf19.4675
CA5281	SPT6	1.1	1.1	-1.1	-1.0	Transcription elongation protein (by homology)	YGR116w	orf19.7136
CA0669	IPF5918	-1.1	-1.1	-1.1	-1.0	unknown function	YOR042w	orf19.448
CA1704	SOL3	1.1	-1.2	-1.3	-1.0	weak multicopy suppressor of los1-1 (by homology)	YHR163w	orf19.704
CA0861	CRK1.3F	-1.1	-1.1	-1.3	-1.0	Protein kinase, 3-prime end		orf19.3523
CA1318	IPF3147	-1.0	-1.1	-1.1	-1.0	Nuclear valosin-containing protein-like (by homology)	YLL034c	orf19.4219
CA5978	SPT7	-1.1	-1.1	-1.3	-1.0	transcription factor, member of the histone acetyltransfe	YBR081c	orf19.7572
CA5026	IPF3001	1.0	-1.0	-1.0	-1.0	serine/threonine protein kinase (by homology)		orf19.6980
CA5683	IPF3333	1.0	-1.0	-1.0	-1.0	unknown function	YPL054w	orf19.7385
CA4193	IPF7535	-1.1	1.1	1.1	-1.0	unknown function	YBR273c	orf19.4534
CA4559	IPF8041	1.2	-1.0	-1.1	-1.0	putative mitochondrial inner membrane protease (by homology)		orf19.6869
CA1870	PF16981.EXON	-1.1	-1.2	-1.2	-1.0	unknown function, exon 2		orf19.9994
CA2304	PRP43	-1.0	-1.0	-1.1	-1.0	RNA-dependent ATPase (by homology)	YGL120c	orf19.1687
CA3124	IPF5353.3	-1.1	1.2	-1.3	-1.0	unknown function, 3-prime end	YML072c	orf19.3003
CA5280	IPF1899	1.2	-1.0	1.0	-1.0	unknown function	YHL021c	orf19.7131
CA0243	BSD2	-1.1	-1.1	-1.1	-1.0	Metal homeostasis protein (by homology)	YBR290w	orf19.5869
CA2342	IPF13836	1.1	-1.1	1.0	-1.0	probable heat shock protein (by homology)		orf19.2344
CA2636	MSW1	-1.0	-1.0	1.0	-1.0	Mitochondrial tryptophanyl-tRNA synthetase (by homolo	YDR268w	orf19.4299
CA5700	IPF2630	-1.0	1.0	-1.1	-1.0	unknown function		
CA3218	IPF10005	1.0	-1.1	-1.1	-1.0	unknown function		orf19.6196
CA5095	ARF21	-1.1	-1.1	-1.0	-1.0	GTP-binding protein of the ARF family (by homology)		orf19.6447
CA5495	SGS1	1.0	1.1	-1.1	-1.0	ATP-dependent DNA helicase (by homology)	YMR190c	orf19.5335
CA3752	TIF51.3	1.2	-1.2	-1.2	-1.0	translation initiation factor eIF-5A, 3-prime end	YEL034w	orf19.3426
CA4051	PF10231.EXON	-1.1	-1.0	-1.1	-1.0	similar to Saccharomyces cerevisiae Rif1p Rap1p-interacting factor 1, exon 1 (by hom		orf19.426
CA1458	IPF6342	1.0	-1.0	1.0	-1.0	unknown function		orf19.1106
CA2567	SUB2.3F	-1.1	-1.1	1.0	-1.0	Involved in pre-mRNA splicing, 3-prime end (by homolo	YDL084w	orf19.5647
CA2362	IPF10595	1.0	-1.1	-1.0	-1.0	unknown function		orf19.1287
CA3080	IPF14634	-1.0	-1.0	-1.1	-1.0	APP-binding protein 1 (by homology)	YPL003w	orf19.4153
CA3947	IPF14768	-1.1	-1.0	-1.0	-1.0	unknown function		orf19.1994
CA3927	DIP2	-1.0	-1.1	-1.1	-1.0	beta transducin	YLR129w	orf19.5106
CA2006	IPF11801	-1.2	-1.1	-1.2	-1.0	unknown function	YDR332w	orf19.2798
CA5172	CPS2.5F	1.0	-1.0	-1.0	-1.0	Carboxypeptidase YSCS precursor, 5-prime end		orf19.4610
CA2655	IPF8477	1.1	-1.1	-1.0	-1.0	unknown function	YGR150c	orf19.5704
CA6123	RPS15.3	1.0	-1.2	-1.2	-1.0	40S ribosomal protein S15, 3-prime end (by homology)	YOL040c	orf19.5927
CA1208	IPF17195	-1.1	-1.0	-1.1	-1.0	unknown function		orf19.11255
CA3941	IPF4754	-1.0	-1.0	-1.1	-1.0	unknown Function		orf19.2001

CA0253	FIL1	1.0	1.0	-1.0	-1.0	Putative mitochondrial ribosome recycling factor (by hor	YHR038w	orf19.477
CA2552	ALG5	-1.0	-1.1	-1.1	-1.0	dolichol-P-glucose synthetase (by homology)	YPL227c	orf19.2837
CA5970	DPB2	-1.0	-1.0	-1.1	-1.0	DNA-directed DNA polymerase epsilon, subunit B (by h	YPR175w	orf19.7564
CA4047	IPF9206	-1.1	-1.0	1.0	-1.0	unknown function		orf19.3678
CA5577	IPF12537	1.0	-1.0	-1.0	-1.0	unknown function	YPR179c	orf19.7344
CA4694	IPF3950	-1.0	1.0	1.0	-1.0	unknown function		orf19.8490
CA1089	IPF13799	-1.1	-1.1	-1.1	-1.0	unknown function	YJR084w	orf19.3945
CA0401	RTA1	-1.0	-1.0	1.0	-1.0	unknown function		orf19.6224
CA5772	ESA1	-1.0	1.0	1.0	-1.0	Histone acetyltransferase (by homology)	YOR244w	orf19.5416
CA5958	PIB1	-1.1	1.0	-1.0	-1.0	phosphatidylinositol(3)-phosphate binding protein (by hc	YDR313c	orf19.7547
CA2880	IPF3781	-1.1	-1.0	1.0	-1.0	unknown function	YPL133c	orf19.5849
CA2052	IPF11027	-1.0	-1.0	-1.1	-1.0	unknown function	YDR026c	orf19.5722
CA2199	IPF8113	-1.3	-1.1	-1.1	-1.0	unknown function	YLR077w	orf19.2938
CA0734	IPF8996	1.1	-1.0	1.0	-1.0	unknown function	YGL211w	orf19.4634
CA5428	BOI2	-1.1	-1.1	-1.2	-1.0	budding protein (by homology)	YER114c	orf19.3230
CA4840	IPF1235	1.0	-1.0	-1.0	-1.0	unknown function		orf19.2054
CA2613	IPF5446	1.2	1.0	1.1	-1.0	putative ribosomal protein (by homology)	YDR116c	orf19.5698
CA0774	IPF11974	1.0	-1.0	1.0	-1.0	unknown function		orf19.855
CA1435	IPF7166	-1.0	-1.0	-1.0	-1.0	unknown function		orf19.1202
CA2641	IPF2929	1.1	1.1	1.0	-1.0	unknown function	YJR024c	orf19.4306
CA2305	MPA43	-1.1	-1.0	-1.1	-1.0	Unknown function	YNL249c	orf19.1686
CA1375	IPF7158	1.0	1.1	-1.0	-1.0	putative serine/threonine kinase	YDR466w	orf19.8787
CA2041	IPF12944	1.0	-1.0	-1.1	-1.0	unknown function		
CA2105	IPF10711	-1.1	-1.0	-1.1	-1.0	unknown function		orf19.3694
CA3503	IPF15890	-1.1	1.0	1.0	-1.0	cytoskeletal binding protein (by homology)		orf19.6349
CA2519	SRP72	-1.1	-1.1	-1.1	-1.0	signal recognition particle protein SRP72 (by homology	YPL210c	orf19.5516
CA2789	IPF3567	-1.0	-1.1	-1.2	-1.0	unknown function	YLR352w ; Missing in array	orf19.606
Human c Myc2		-1.1	-1.1	-1.0	-1.0			
CA4090	BRF1	-1.1	-1.1	-1.1	-1.0	TFIIIB subunit	YGR246c	orf19.6649
CA0556	IPF15920	-1.0	1.0	1.1	-1.0	zinc-finger containing protein (by homology)		orf19.4972
CA5866	IPF361	-1.1	1.0	-1.1	-1.0	unknown function	Missing in array	orf19.7527
CA4421	TAF19	-1.0	1.0	1.0	-1.0	TBP-associated factor by homology	YML098w	orf19.5174
CA2039	IPF12947	-1.0	-1.1	-1.0	-1.0	unknown function	YMR115w	orf19.11835
CA3920	SDS24	-1.0	-1.0	-1.1	-1.0	Similar to S. cerevisiae YBR214w which presents strong	YBR214w	orf19.5118
CA5702	PCH1	-1.3	1.1	-1.1	-1.0	Putative ATPase (by homology)	YDR440w	orf19.7402
CA2976	IPF14676	-1.2	-1.2	-1.1	-1.0	unknown function	YIL041w	orf19.8821
CA4681	IPF3679	-1.1	-1.1	-1.2	-1.0	similar to Saccharomyces cerevisiae Thi20p hydroxyme	YOL055c	orf19.889
CA0634	IPF16267	1.0	-1.1	-1.1	-1.0	unknown function	YER077c	orf19.1772
CA3196	IPF3428	-1.0	-1.1	-1.1	-1.0	unknown function	YLR051c	orf19.6175
CA3529	IPF9929	-1.0	-1.1	-1.2	-1.0	unknown function	YEL043w	orf19.8600
CA2028	IPF18561.3	-1.1	1.1	-1.1	-1.0	unknown function, , 3-prime end		
CA2816	IPF5601	-1.1	-1.0	-1.1	-1.0	unknown function	YKL183w	orf19.2995
CA1072	SBH1	-1.1	-1.0	-1.0	-1.0	involved in translocation into the ER (by homology)	YER087ca	
CA2501	IPF6812	1.0	-1.0	-1.0	-1.0	unknown function	YLR224w	orf19.5587
CA6054	IPF4952	1.0	-1.0	1.1	-1.0	unknown function	YDR411c	orf19.7672
CA1034	BET4.EXON2	-1.0	-1.0	-1.0	-1.0	alpha subunit of geranylgeranyl transferase type 2, exor	YJL031c	orf19.8641
CA5326	IPF2137	1.1	-1.1	-1.1	-1.0	unknown function		orf19.7200
CA3286	UBP3.3EOC	1.0	1.0	1.0	-1.0	Ubiquitin-specific proteinase, 3-prime end (by homology	YER151c	orf19.6319
CA4761	IPF9650	-1.2	-1.0	-1.2	-1.0	lipase family protein containing serine active site (by ho	YGL144c	orf19.3991

CA3405	IPF8644	1.0	1.0	1.0	-1.0	maltase (by homology)	YGR287c	orf19.3982
CA1025	IPF10184	1.1	1.0	-1.1	-1.0	unknown function	YPL110c	orf19.3936
CA4732	IPF7733	-1.1	-1.1	-1.0	-1.0	unknown function	YCR063w	orf19.4855
CA4172	IPF4432	-1.0	-1.1	-1.0	-1.0	unknown function		orf19.2961
CA4407	RPO31	1.1	-1.1	-1.2	-1.0	DNA-directed RNA polymerase III (by homology)	YOR116c	orf19.3103
CA4221	IPF8760	-1.1	1.1	1.0	-1.0	unknown function		orf19.823
CA5814	IPF2521	-1.0	1.0	-1.0	-1.0	putative protease (by homology)	YCR045c	orf19.7463
CA2341	IPF13838	-1.1	1.0	1.0	-1.0	unknown function	YPL222w	orf19.2346
CA1514	IPF7539	-1.1	1.0	-1.1	-1.0	unknown function		orf19.4886
NAD6		-1.0	-1.1	-1.1	-1.0			
CA5538	IPF2830	-1.1	-1.0	-1.1	-1.0	unknown function		orf19.7300
CA5608	IPF539	-1.1	-1.1	-1.2	-1.0	unknown function	YLR290c	orf19.7092
CA5398	SEC14	-1.0	-1.2	-1.1	-1.0	phosphatidylinositol(PI)/phosphatidylcholine(PC) transfe	YMR079w	orf19.941
CA2667	IPF16996	-1.2	-1.1	-1.1	-1.0	unknown function	YDR496c	orf19.3547
CA0647	IPF19706	1.0	-1.0	-1.0	-1.0	unknown function	Missing in array	orf19.4334
CA3951	VAC7.3	1.0	-1.1	-1.1	-1.0	Vacuolar protein, 3-prime end (by homology)	YNL054w	orf19.1409
CA2600	IPF11177	-1.3	-1.2	-1.4	-1.0	similar to Saccharomyces cerevisiae Clu1p translation i	YMR012w	orf19.51
CA1345	IPF6003	-1.3	1.0	1.1	-1.0	similar to Saccharomyces cerevisiae Msb2p multicopy s	YGR014w	orf19.1490
CA2257	SHR5	1.0	1.0	-1.0	-1.0	RAS suppressor (by homology)	YOL110w	orf19.1955
CA3995	PF11615.3EOC	-1.0	-1.0	-1.0	-1.0	RNA-binding protein (by homology)		
CA5457	TRM1	-1.1	-1.0	-1.1	-1.1	N2,N2-dimethylguanine tRNA methyltransferase (by ho	YDR120c	orf19.3265
CA2962	PRP2	-1.1	-1.1	-1.1	-1.1	RNA-dependent ATPase (by homology)	YNR011c	orf19.5865
CA1209	ARG8	-1.0	-1.0	-1.1	-1.1	acetylornithine aminotransferase (by homology)	YOL140w	orf19.11254
CA0543	IPF3255	-1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Vps5p involved in	YOR069w	orf19.2867
CA3055	HIR2	-1.2	-1.1	-1.1	-1.1	Histone transcription regulator (by homology)	YOR038c	orf19.11771
CA1026	PF19645.EXON	1.0	1.0	1.1	-1.1	unknown function, exon 1		orf19.3937
CA3254	IPF4728	1.0	1.0	-1.0	-1.1	unknown Function		orf19.11227
CA0784	YUH1.3	1.1	-1.0	-1.0	-1.1	Putative ubiquitin carboxyl-terminal hydrolase-like protein, 3-prime end (by homology)		orf19.3930
CA3523	IPF20135	-1.1	-1.0	-1.1	-1.1	unknown function		orf19.993
CA2448	PLC1	-1.1	-1.1	-1.1	-1.1	1-phosphatidylinositol-4,5-bisphosphate phosphodieste	YPL268w	orf19.5506
CA4899	IPF1460	-1.0	-1.0	1.0	-1.1	unknown function	YLR039c	orf19.6036
CA2357	IPF8957	-1.1	-1.0	-1.1	-1.1	unknown function	YER010c	orf19.4894
CA0414	IPF4068	-1.2	-1.1	-1.2	-1.1	reverse transcriptase		orf19.2164
CA0011	IPF17430	-1.0	-1.0	-1.2	-1.1	possible zinc protease (by homology)	YIL137c	orf19.73
CA5650	IPF7109	1.1	-1.0	-1.1	-1.1	unknown function	YNL208w	orf19.7350
CA3216	IPF13038	-1.1	-1.0	1.0	-1.1	unknown function	YKL018ca	
CA3299	IPF13777	-1.0	1.0	-1.0	-1.1	unknown function		orf19.2317
CA0001	IPF19501	1.1	1.0	1.0	-1.1	unknown function	Missing in array	
CA1391	IPF6151	-1.0	-1.0	-1.1	-1.1	unknown function		
CA4259	CDC10	-1.0	-1.0	-1.0	-1.1	cell division control protein	YCR002c	orf19.548
CA3388	IPF6755	-1.0	1.0	-1.0	-1.1	unknown function		orf19.320
CA2869	RPC82	-1.0	-1.1	-1.2	-1.1	DNA-directed RNA polymerase III, 82 KD subunit (by h	YPR190c	orf19.2847
CA1644	IPF9345	-1.0	-1.0	-1.1	-1.1	unknown function		orf19.1728
CA0440	IPF12473	-1.2	-1.2	-1.5	-1.1	unknown function	YML033w	orf19.5571
CA3151	IPF4033	-1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Ayr1p 1-acyldihyd	YIL124w	orf19.6167
CA5548	IPF5978	-1.0	-1.0	1.0	-1.1	unknown function		orf19.7311
CA5479	IPF8205	1.0	1.0	1.1	-1.1	unknown function		orf19.5311
CA4709	IPF5895	1.0	1.0	1.0	-1.1	unknown function	YOR245c	orf19.6941
CA0395	SEF11.5EOC	-1.2	-1.2	-1.2	-1.1	Putative transcription factor, 5-prime end (by homology)		orf19.1926

CA3295	PF5723.EXON	1.0	-1.2	-1.1	-1.1	cell surface GPI-anchored protein, exon 1 (by homology)		orf19.6329
CA5729	UBA1	-1.2	1.0	-1.2	-1.1	Ubiquitin-activating enzyme (by homology)	YKL210w	orf19.7438
CA4157	HYU1	-1.3	1.2	-1.1	-1.1	hydantoin utilization protein A (hyuA) homolog	YKL215c	orf19.5804
CA3356	IPF9560	-1.1	-1.1	-1.2	-1.1	unknown function		orf19.9497
CA3271	GLY2	-1.0	-1.1	-1.1	-1.1	L-threonine aldolase, low-specific	YEL046c	orf19.6305
CA0985	IPF4815	1.0	1.0	-1.0	-1.1	unknown Function		orf19.3351
CA4795	IPF3378	-1.1	-1.1	-1.0	-1.1	similar to Saccharomyces cerevisiae Pri1p DNA-directe	YIR008c	orf19.4030
CA0176	IPF11388	-1.1	-1.0	-1.1	-1.1	unknown function	YER041w	orf19.8267
CA4001	RPL12	-1.0	-1.0	-1.0	-1.1	ribosomal protein	YEL054c	orf19.1635
CA6165	SNF5.3F	-1.1	1.1	-1.0	-1.1	Component of SWI/SNF transcription activator complex	YBR289w	orf19.5871
CA2340	MNN5	-1.1	-1.0	-1.0	-1.1	Golgi alpha-1,2-mannosyltransferase (by homology)		orf19.2347
CA0990	IPF11068	-1.3	-1.1	-1.1	-1.1	unknown function	YIL005w	orf19.1392
CA2157	IPF8537	-1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Cne1p calnexin, in	YAL058w	orf19.5300
CA2907	IPF15525	1.0	-1.0	-1.1	-1.1	putative gluconokinase (by homology)	YDR248c	orf19.4520
CA5594	IPF19814	1.1	-1.0	-1.1	-1.1	folate hydrolase (by homology)	YJR126c	orf19.7106
CA1899	HDA1	-1.1	-1.0	-1.2	-1.1	Histone deacetylase (by homology)	YNL021w	orf19.2606
CA5584	SAC7	1.2	-1.1	-1.2	-1.1	GAP for RHO1 by homology	YDR389w	orf19.7115
CA3574	IPF19584	1.1	-1.0	-1.1	-1.1	unknown function	YFR013w ; Missing in array	orf19.2266
CA2354	IPF18480	1.0	1.0	-1.0	-1.1	unknown function		orf19.11893
CA1854	IPF12611	-1.0	1.0	1.0	-1.1	unknown function	YGL228w	orf19.649
CA0636	FDH4.3F	-1.0	-1.1	-1.2	-1.1	Formate dehydrogenase, 3-prime end (by homology)		
CA3790	IPF11215	-1.1	-1.0	-1.1	-1.1	unknown function	YKL074c	orf19.13250
CA4547	SRB9	-1.0	1.0	1.0	-1.1	DNA-directed RNA polymerase II holoenzyme and Srb1	YDR443c	orf19.1451
CA1617	IPF14536	1.0	-1.0	-1.0	-1.1	unknown function	YDR339c	orf19.3220
CA3261	TYS1	1.0	-1.0	1.0	-1.1	tyrosyl-tRNA synthetase by homology	YGR185c	orf19.2694
CA4062	IPF5933	1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Mhr1p involved in	YDR296w	orf19.439
CA0626	IPF3161	1.1	-1.1	-1.2	-1.1	Unknown function	YNR054c	orf19.3161
CA3674	PF19529.EXON	1.1	-1.0	1.0	-1.1	unknown function, exon 1		orf19.6454
CA0324	STT4	-1.0	-1.1	-1.0	-1.1	Phosphatidylinositol-4-kinase (by homology)	YLR305c	orf19.9377
CA5174	PRS4	1.2	1.1	1.1	-1.1	Ribose-phosphate pyrophosphokinase 3 (by homology)	YER099c	orf19.4611
CA3409	IPF9410	-1.0	-1.0	-1.1	-1.1	similar to Saccharomyces cerevisiae Nuf1p spindle pole	YDR356w	orf19.6148
CA2237	IPF10032.3F	1.0	-1.0	1.0	-1.1	unknown function, 3-prime end		orf19.3917
CA3515	MRPL15	-1.0	-1.1	-1.1	-1.1	mitochondrial ribosomal protein of the large subunit (by	YLR312wa	orf19.6363
CA2637	IPF19954	-1.0	-1.0	1.0	-1.1	unknown function		orf19.4301
CA1468	SRB10	-1.0	1.0	1.0	-1.1	cyclin-dependent kinase by homology	YPL042c	orf19.794
CA3764	IPF13072	1.0	-1.0	-1.0	-1.1	unknown function		orf19.2905
CA4493	IPF4055	-1.1	-1.0	1.0	-1.1	unknown function		orf19.1867
CA3454	PF10533.EXON	1.0	-1.2	-1.1	-1.1	unknown function, exon 1		orf19.1255
CA1665	RIB1	1.2	-1.0	1.0	-1.1	GTP cyclohydrolase II by homology to S.cerevisiae	YBL033c	orf19.2862
CA3064	IPF2973	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.4283
CA0234	IFA3	-1.1	-1.1	-1.1	-1.1	unknown function	YKR060w	orf19.7793
CA4868	IPF4078	1.0	-1.0	-1.0	-1.1	Unknown Function		orf19.3845
CA5330	IPF2130	1.1	1.0	-1.0	-1.1	similar to 2-nitropropane dioxygenases	YJR149w	orf19.7204
CA5420	IPF1583	1.0	-1.0	1.0	-1.1	unknown function	YLR412w	orf19.970
CA3838	LAS17	1.1	1.1	1.1	-1.1	actin assembly factor (by homology)	YOR181w	orf19.6598
CA4146	LEU3	1.0	1.0	-1.1	-1.1	Binds to UASs in promoters of LEU1, LEU2, LEU4, ILV	YLR451w	orf19.11700
CA2525	IPF4324.3	-1.0	-1.0	-1.0	-1.1	unknown function, 3-prime end		orf19.5522
CA3057	IPF2954	-1.0	-1.1	-1.0	-1.1	unknown function	YDR267c	orf19.4293
CA5774	IPF1113	1.0	1.0	1.1	-1.1	unknown function	YIL039w	orf19.5418

CA0077	IPF1239	-1.1	-1.1	-1.1	-1.1	unknown function		
CA2219	CAT8	1.0	-1.0	-1.1	-1.1	transcription factor involved in gluconeogenesis	YMR280c	orf19.12563
CA2926	UBA3	1.1	-1.0	1.0	-1.1	Ubiquitin-like protein activating enzyme	YPR066w	orf19.4209
CA4699	IPF4220	1.1	-1.0	1.0	-1.1	similar to Saccharomyces cerevisiae Pep8p involved in	YJL053w	orf19.6927
CA1332	IPF11716	1.0	-1.1	-1.1	-1.1	unknown function		orf19.1150
CA3056	IPF2953	-1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Cyc2p cytochrome	YOR037w	orf19.4294
CA5820	IPF2500	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.7473
CA0826	IPF19885	1.0	-1.0	1.0	-1.1	unknown function		orf19.8308
CA3718	POP7	-1.1	-1.1	1.0	-1.1	Nuclear RNase P subunit (by homology)	YBR167c	orf19.11644
CA1427	IPF9914	-1.0	1.0	-1.1	-1.1	alanyl-tRNA synthetase (by homology)	YOR335c	orf19.5746
CA0585	ADE5,7	1.0	-1.0	-1.0	-1.1	phosphoribosylamine-glycine ligase and phosphoribosy	YGL234w	orf19.12528
CA5431	IPF195	1.1	1.1	1.0	-1.1	unknown function	YHL002w	orf19.3233
CA1390	IPF17474	-1.0	1.1	1.1	-1.1	unknown function		orf19.1768
CA1583	ROT1	-1.1	-1.1	1.0	-1.1	Suppressor of TOR2 mutations (by homology)	YMR200w	orf19.6029
CA1272	CGR1	-1.1	-1.1	-1.1	-1.1	Cell growth protein (by homology)	YBR053c ; Missing in array	orf19.2722
CA5161	IPF983	-1.0	-1.2	-1.2	-1.1	unknown function	YPL107w	orf19.4600
CA5526	IPF2857	-1.1	-1.1	-1.2	-1.1	unknown function		orf19.7284
CA5279	SYS1	1.1	1.0	1.1	-1.1	Similar to ypt6 suppressor in S. cerevisae (by homology	YJL004c	orf19.7128
CA5926	PRO2	-1.1	-1.1	-1.1	-1.1	Proline biosynthetic enzyme (by homology)	YOR323c	orf19.6779
CA4334	IPF2082	-1.0	-1.0	-1.1	-1.1	unknown function		orf19.4085
CA1113	IPF9996	1.0	1.1	1.1	-1.1	unknown function		orf19.2285
CA1268	IPF14693	-1.1	-1.0	-1.3	-1.1	unknown function	YBL004w	orf19.3159
CA2672	EFH1	1.1	-1.0	-1.1	-1.1	Transcription regulator		orf19.5498
CA1273	CCT4	1.0	-1.1	-1.2	-1.1	Component of chaperonin-containing T-complex	YDL143w	orf19.2720
CA3464	DBP5	-1.2	-1.2	-1.2	-1.1	RNA helicase (by homology)	YOR046c	orf19.1661
CA4635	IPF1524	-1.0	-1.2	-1.1	-1.1	putative multidrug resistance protein (by homology)		orf19.341
CA4844	PDR13	-1.3	1.1	-1.0	-1.1	Drug resistance	YHR064c	orf19.3812
CA5607	STL2.5F	1.0	-1.1	-1.0	-1.1	sugar transporter, 5-prime end (by homology)		orf19.7093
CA0384	PCL1	1.0	-1.1	-1.1	-1.1	cyclin, G1/S-specific (by homology)	YNL289w	orf19.10172
CA3074	IPF6106	-1.0	-1.1	1.1	-1.1	similar to Bacillus halodurans holo-(acyl carrier protein) synthase		orf19.4812
CA5726	AAF1	1.0	1.1	1.0	-1.1	Adhesion and aggregation mediating surface antigen		orf19.7436
CA4014	CTK1	-1.1	-1.1	-1.1	-1.1	probable cell division protein kinase	YKL139w	orf19.1619
CA0765	IPF9040.3EOC	1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Fhl1p transcription	YPR104c	orf19.9778
CA4856	IPF15950	1.1	-1.1	1.0	-1.1	unknown function	YKR087c	orf19.3827
CA2467	IPF8724	1.0	-1.0	-1.0	-1.1	unknown function	YPL113c	orf19.1796
CA1088	IPF13319	1.0	-1.0	1.1	-1.1	unknown function		orf19.740
CA5148	TFG1	-1.1	-1.0	-1.0	-1.1	RNA pol.II transcription initiation factor TFIIF (by homol	YGR186w	orf19.4585
CA1994	IPF6613	-1.2	-1.1	-1.1	-1.1	unknown function	YDR349c	orf19.6481
CA2647	IPF13088	-1.0	-1.0	-1.1	-1.1	unknown function		orf19.1186
CA4417	LIP5	1.0	1.0	1.1	-1.1	Secretory lipase		orf19.5179
CA5517	IPF721.3F	1.1	-1.0	-1.1	-1.1	unknown function, 3-prime end		orf19.5365
CA0026	IPF16843	-1.1	-1.1	1.1	-1.1	unknown function	YGR127w	
CA3118	COQ4	-1.2	-1.2	-1.1	-1.1	ubiquinone biosynthesis	YDR204w	orf19.3008
CA3708	HIP1	1.2	-1.2	-1.0	-1.1	Histidine permease (by homology)		orf19.4940
CA4073	IPF2559.3	1.0	1.0	-1.1	-1.1	unknown function, 3-prime end		orf19.6626
CA3921	OLE1	-1.2	-1.3	-1.1	-1.1	Stearoyl-CoA desaturase (by homology)	YGL055w	orf19.5117
CA0865	IFM2	-1.1	-1.1	-1.2	-1.1	Glycerate-formate-dehydrogenases (by homology)		orf19.3584
CA0448	ALS10	1.1	1.0	1.2	-1.1	agglutinin like protein		orf19.2355
CA0678	IPF13094	-1.2	-1.2	1.0	-1.1	unknown function	YNL115c	orf19.8774

CA6032	IPF596	-1.1	1.0	1.0	-1.1	similar to Saccharomyces cerevisiae Vps3p vacuolar so	YDR495c	orf19.7642
CA5061	IPF8495	1.2	-1.1	-1.1	-1.1	unknown function		orf19.3030
CA0733	NIP1	-1.1	-1.1	-1.2	-1.1	translation initiation factor subunit	YMR309c	orf19.4635
CA2482	IPF9841	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.3204
CA4961	IPF3916	-1.1	-1.1	-1.2	-1.1	similar to Saccharomyces cerevisiae Exo70p 70 kDa ex	YJL085w	orf19.6512
CA1708	IPF7543	-1.0	-1.1	-1.2	-1.1	unknown function		orf19.4888
CA3660	IPF17794	1.1	1.1	-1.0	-1.1	unknown function		
CA4582	MDM12	-1.1	-1.0	-1.1	-1.1	Involved in mitochondrial inheritance (by homology)	YOL009c	orf19.6900
CA5483	IPF817	1.1	1.0	-1.1	-1.1	unknown function		orf19.5316
CA5450	IPF243	-1.1	-1.1	-1.2	-1.1	unknown function		orf19.3254
CA2703	IPF12193	-1.0	1.0	1.0	-1.1	unknown function	Missing in array	orf19.4655
CA3926	IPF16198	1.0	-1.0	-1.1	-1.1	possible regulatory protein	YPR072w	orf19.5107
CA4400	IPF14362	-1.1	-1.0	-1.1	-1.1	unknown function		orf19.3110
CA5696	IPF3309.3EOC	1.0	1.1	-1.0	-1.1	unknown function, 3-prime end		orf19.7398
CA4132	STE20	1.1	1.0	1.1	-1.1	serine/threonine-specific protein kinase	YHL007c	orf19.4242
CA5878	PRP5	-1.1	-1.1	-1.2	-1.1	pre-mRNA processing RNA-helicase (by homology)	YBR237w	orf19.6831
CA1714	NAB2	-1.2	-1.1	-1.2	-1.1	Nuclear poly(A)-RNA-binding protein (by homology)	YGL122c	orf19.3333
CA3547	ADE13	1.1	-1.2	-1.1	-1.1	adenylosuccinate lyase (by homology)	YLR359w ; Missing in array	orf19.3870
CA5684	IPF3331	1.2	1.1	1.1	-1.1	unknown function	YBR185c	orf19.7386
CA4387	MAP1	1.1	-1.0	-1.0	-1.1	methionine aminopeptidase, isoform 1 (by homology)	YLR244c	orf19.3124
CA6075	THI4	-1.0	1.0	1.0	-1.1	Thiazole biosynthetic enzyme precursor (by homology)	YGR144w	orf19.5986
CA3219	IPF10003	-1.1	1.0	-1.3	-1.1	similar to Saccharomyces cerevisiae Rnh70p ribonuclea	YGR276c	orf19.6195
CA4836	IPF1222	-1.1	-1.1	-1.1	-1.1	Similar to superoxide dismutase (by homology)		orf19.2060
CA3104	IPF12084	1.0	1.0	1.0	-1.1	unknown function	YOR220w	orf19.13907
CA2839	IPF8336	-1.1	-1.0	-1.2	-1.1	unknown function		orf19.4792
CA0508	IPF11991	-1.1	-1.1	-1.4	-1.1	similar to Saccharomyces cerevisiae Msu1p 3 -5 exonu	YMR287c	orf19.11107
CA3904	IPF14888	-1.1	-1.1	-1.1	-1.1	unknown function	YNL119w	orf19.11877
CA3263	UBR12	-1.2	1.0	-1.1	-1.1	ubiquitin-protein ligase by homology	YLR024c	orf19.2697
CA3795	IPF5699	1.1	-1.1	-1.0	-1.1	Abhydrolase by homology		orf19.5824
CA3215	HCS1	-1.1	-1.1	-1.2	-1.1	putative DNA helicase A (by homology)	YKL017c	orf19.6199
CA3681	IPF19787	-1.1	1.0	-1.0	-1.1	unknown function	YER093c	orf19.728
CA4161	IPF20164	1.0	-1.2	1.1	-1.1	putative kynurenine aminotransferase (by homology)	YJL060w	orf19.5809
CA2742	JAC1	-1.0	1.1	1.0	-1.1	molecular chaperone (by homology)	YGL018c	orf19.2104
CA5218	WHI2	-1.1	-1.1	-1.1	-1.1	Growth regulation factor (by homology)	YOR043w	orf19.7036
CA1221	IPF14872	1.0	-1.1	-1.2	-1.1	unknown function	YDR527w	orf19.4133
CA1749	IPF8257.3F	1.0	1.1	-1.1	-1.1	unknown function, 3-prime end		
CA1989	IPF16596	1.0	1.1	1.1	-1.1	unknown function		orf19.95
CA0999	IPF12368	-1.1	-1.0	-1.0	-1.1	unknown function		orf19.11847
CA6021	BFR2	1.0	-1.1	-1.1	-1.1	involved in protein transport steps at the Brefeldin A blo	YDR299w	orf19.7624
CA0136	IFH1	-1.0	-1.0	-1.0	-1.1	Dioxygenase (by homology)		orf19.9207
CA3509	PRP6	-1.1	-1.1	-1.1	-1.1	snRNP(U4/U6)-associated splicing factor (by homology)	YBR055c	orf19.6356
CA4785	IPF3361	1.2	-1.1	-1.1	-1.1	putative mitochondrial ribosomal protein S7 (by homolo	YJR113c	orf19.4018
CA2632	NAR1	1.1	-1.0	-1.0	-1.1	Yeast nuclear architecture related protein (by homology	YNL240c	orf19.4757
CA2754	VPS45	-1.0	1.1	1.0	-1.1	vacuolar protein sorting-associated protein (by homolog	YGL095c	orf19.13063
CA4508	NAM9	-1.1	-1.1	-1.2	-1.1	mitochondrial ribosomal protein	YNL137c	orf19.498
CA3847	IPF7942	-1.0	-1.1	-1.0	-1.1	NADH-ubiquinone oxidoreductase		orf19.6607
CA4097	GIN4	-1.1	-1.1	-1.0	-1.1	ser/thr protein kinase (by homology)	YDR507c	orf19.663
CA0759	IPF11167	-1.1	-1.1	-1.2	-1.1	unknown function	YKR003w	orf19.3198
CA3361	SNF1	-1.1	-1.1	-1.1	-1.1	serine/threonine protein kinase	YDR477w	orf19.9491

CA3974	IPF6507	1.0	-1.1	-1.1	-1.1	unknown function	YMR157c ; Missing in array	orf19.1546
CA5363	NCR1	-1.1	-1.1	-1.1	-1.1	Polytopic membrane protein involved in sterol homeosta	YPL006w	orf19.7242
CA4481	IPF9150	-1.1	-1.1	-1.2	-1.1	similar to Saccharomyces cerevisiae Mpt1p required for	YMR005w	orf19.9441
CA2212	IPF13919	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.4750
CA1289	ZUO1	-1.0	1.0	-1.0	-1.1	Zuotin, a putative Z-DNA binding (by homology)	YGR285c	orf19.10224
CA5827	IPF2485	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.7482
CA0198	IPF19685	-1.4	-1.5	-1.2	-1.1	unknown function	YHR097c	orf19.9227
CA6147	IPF1862.5F	-1.1	-1.0	-1.1	-1.1	unknown function, 5-prime end		orf19.5895
CA1856	IPF13689	-1.0	-1.1	-1.0	-1.1	unknown function		orf19.9081
CA1043	TOM6	1.0	-1.1	1.1	-1.1	mitochondrial outer membrane import receptor subunit (	YOR045w	orf19.9219
CA3004	KIN28	1.0	1.1	1.0	-1.1	cyclin-dependent ser/thr protein kinase (by homology)	YDL108w	orf19.13619
CA4735	IPF7726	-1.2	1.1	1.0	-1.1	unknown function	YPL260w	orf19.4850
CA2159	IPF19753	-1.1	-1.0	-1.1	-1.1	similar to Saccharomyces cerevisiae Tfb1p transcriptior	YDR311w	orf19.5297
CA5969	BET2	1.0	1.0	-1.0	-1.1	beta subunit of geranylgeranyl transferase type2	YPR176c	orf19.7563
CA4683	HSP78.3F	1.1	1.0	-1.0	-1.1	heat shock protein of clpb family of ATP-dependent proteases, mitochondrial, 3-prime		orf19.884
CA2555	IPF12105	-1.0	1.1	-1.0	-1.1	unknown function		orf19.5633
CA3618	THO1	-1.1	-1.0	-1.1	-1.1	suppressor of the hpr1 ts phenotype (by homology)	YER063w	orf19.200
CA2459	PF12234.5EOC	-1.1	1.0	-1.1	-1.1	unknown function, 5-prime end		orf19.3509
CA3807	IPF9225	-1.1	1.0	1.0	-1.1	unknown function	YDR020c	orf19.2487
CA1754	IPF16320	-1.3	-1.1	-1.2	-1.1	Unknown function	YCL039w	orf19.5131
CA2197	IPF8110	-1.1	-1.1	-1.3	-1.1	unknown function		orf19.2936
CA4721	CPP1	-1.1	-1.0	-1.1	-1.1	probable protein-tyrosine phosphatase	YNL053w	orf19.12330
CA3359	IPF9566	-1.0	-1.1	1.1	-1.1	unknown function	YDR374c	orf19.1939
CA3010	IPF14568	1.1	-1.1	-1.0	-1.1	unknown function	YGL246c	orf19.13610
CA0054	RIB4.3	1.2	-1.0	-1.0	-1.1	6,7-dimethyl-8-ribityllumazine synthase, 3-prime end (b	YOL143c	
CA6025	IPF614	-1.0	-1.1	-1.0	-1.1	unknown function	YOL138c	orf19.7629
CA2679	IFU5	1.1	1.0	1.1	-1.1	Unknown function	YFL010c	orf19.2568
CA3369	IPF4672	-1.0	-1.0	-1.0	-1.1	unknown Function	YNL032w	orf19.1850
CA0481	STE14	-1.0	1.0	-1.0	-1.1	farnesyl cystein carboxyl-methyltransferase (by hc	YDR410c	orf19.7766
CA5147	PHO12	-1.0	-1.0	-1.0	-1.1	Acid phosphatase, secreted (by homology)		orf19.4584
CA4797	PRP22	-1.0	-1.0	-1.1	-1.1	RNA-dependent ATPase (by homology)	YER013w	orf19.4033
CA5329	MRP7	-1.1	-1.2	-1.1	-1.1	Mitochondrial ribosomal protein YmL2 precursor (by hor	YNL005c	orf19.7203
CA4811	ECM16	-1.0	-1.1	-1.1	-1.1	RNA helicase (by homology)	YMR128w	orf19.2090
CA3448	YKT6	-1.1	-1.1	-1.1	-1.1	Endoplasmic Reticulum-Golgi transport (by homology)	YKL196c	orf19.2974
CA4284	DPH52.3EOC	-1.1	-1.0	1.0	-1.1	Diphthamide methyltransferase, 3-prime end (by homology)		orf19.6682
CA5348	IPF863	-1.1	-1.1	-1.1	-1.1	involved in inositol biosynthesis (by homology)	YBR030w	orf19.7223
CA5188	TAP42	-1.0	-1.0	1.1	-1.1	Component of the Tor signaling pathway (by homology)	YMR028w	orf19.4626
CA3632	DFR1	1.0	1.0	1.0	-1.1	dihydrofolate reductase	YOR236w	orf19.5142
CA1971	PKH2	1.0	1.0	-1.0	-1.1	Ser/Thr protein kinase(by homology)	YOL100w	orf19.5224
CA5168	IPF6032	1.0	1.0	1.1	-1.1	unknown function	Missing in array	orf19.4607
CA2779	IPF3836	1.1	-1.1	-1.2	-1.1	unknown function	YDL219w	orf19.279
CA5981	MSS51	-1.1	-1.1	-1.1	-1.1	involved in maturation of COX1 and COB mRNA (by ho	YLR203c	orf19.7577
CA0833	IPF12501	-1.1	-1.1	-1.0	-1.1	unknown function	YDL183c	orf19.9245
NAD2		1.1	-1.0	-1.1	-1.1			
CA1820	IPF9529	1.1	1.1	-1.0	-1.1	probable mannosyltransferase (by homology)		orf19.4270
CA1544	IPF1040	1.1	-1.0	-1.1	-1.1	Similar to transcriptional activators		orf19.4568
CA1479	IPF16428	1.1	-1.1	-1.2	-1.1	unknown function	YIL019w	orf19.1250
CA0002	DOC1	-1.0	-1.1	-1.0	-1.1	component of the anaphase promoting complex (by hor	YGL240w	orf19.12523
CA4979	IPF2062	1.0	-1.2	-1.1	-1.1	unknown function		orf19.5271

CA4226	IPF8752	-1.1	-1.2	-1.3	-1.1	similar to Saccharomyces cerevisiae Mrpl24p ribosomal	YMR193w	orf19.828
CA1262	MDR1	-1.0	-1.1	-1.0	-1.1	Mac1p interacting protein (by homology)	YGR100w	orf19.1244
CA4083	IPF5018	-1.1	-1.1	-1.0	-1.1	unknown function		orf19.6639
CA3846	IPF7943	1.0	1.0	1.0	-1.1	unknown function		orf19.6606
CA0029	PET56	-1.0	1.0	-1.1	-1.1	ribosomal RNA methylase (by homology)	YOR201c	orf19.182
CA3820	PBP2	-1.1	-1.1	-1.1	-1.1	PAB1 binding protein (by homology)	YBR233w	orf19.5771
CA1493	FTH2	-1.1	-1.2	-1.1	-1.1	iron transporter (by homology)		orf19.3227
CA5779	IPF1121	-1.1	-1.1	-1.1	-1.1	unknown function	YKR079c	orf19.5425
CA3400	JNM1	-1.0	-1.1	-1.0	-1.1	mitosis protein, involved in nuclear migration (by homolo	YMR294w	orf19.3976
CA0460	SEC17	-1.0	-1.0	1.0	-1.1	transport vesicle fusion protein (by homology)	YBL050w	orf19.2518
CA6059	CTA26	-1.0	-1.0	-1.2	-1.1	transcriptional activation		orf19.7680
CA3584	IPF15468	1.0	-1.0	-1.1	-1.1	unknown function	YCR051w	orf19.2256
CA0782	IPF16253	-1.0	-1.1	-1.0	-1.1	unknown function		orf19.11414
CA4980	IPF2059	-1.1	-1.2	-1.1	-1.1	unknown function		orf19.5270
CA1218	CDC20	-1.0	1.1	-1.2	-1.1	anaphase promoting complex subunit (by homology)	YGL116w	orf19.7769
CA2574	ATH1	-1.0	-1.1	-1.2	-1.1	acid trehalase, vacuolar	YPR026w	orf19.6214
CA1280	IPF10828	1.0	-1.0	-1.0	-1.1	unknown function		orf19.3627
CA1821	IPF9527	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.4269
CA3633	IFA19	-1.1	1.0	1.0	-1.1	unknown function		orf19.5141
CA3153	FRP2	1.1	-1.1	-1.1	-1.1	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathwa		orf19.6169
CA2921	IPF17037	1.1	1.1	1.0	-1.1	unknown function		orf19.4214
CA4771	IPF3336	-1.2	-1.0	-1.2	-1.1	unknown function	YGL145w	orf19.4003
CA3192	IPF11598	-1.0	-1.1	1.0	-1.1	by homology to S. cerv.:hexokinase I		orf19.2154
CA2137	ARP9	-1.1	-1.1	-1.1	-1.1	actin-related protein (by homology)	YMR033w	orf19.2507
CA3964	IPF9370	1.0	-1.1	-1.1	-1.1	unknown function	YMR155w	orf19.1424
CA2228	SCT12	-1.2	-1.2	-1.2	-1.1	Suppresses a choline-transport mutant		orf19.5815
CA6140	IPF1882	-1.0	-1.1	-1.0	-1.1	unknown function	YBL028c	orf19.5905
CA2096	IPF11491	1.1	-1.0	-1.2	-1.1	unknown function	YKR023w	orf19.2391
CA3339	IPF20131	1.0	1.0	1.0	-1.1	unknown function	YDR446w	orf19.2332
CA3167	IPF9632	-1.1	-1.2	-1.1	-1.1	unknown function	YHL010c	orf19.1576
CA1128	IPF5198	-1.1	-1.2	-1.1	-1.1	unknown function	YMR093w	orf19.3609
CA5127	CYS3	-1.1	1.3	1.2	-1.1	cystathionine gamma-lyase by homology	YAL012w	orf19.6402
CA1085	IPF1038	-1.0	1.0	1.0	-1.1	unknown function		orf19.4570
CA5664	IPF1252	-1.0	-1.0	-1.0	-1.1	Conserved hypothetical protein	YIL096c	orf19.7366
CA2994	IPF9116	-1.1	-1.0	-1.2	-1.1	unknown function		orf19.6119
CA2371	IPF10333	-1.0	-1.0	-1.1	-1.1	unknown function	YER149c	orf19.1835
CA5801	DAL1	1.0	1.1	1.1	-1.1	allantoinase	YIR027c	orf19.5454
CA3598	SEC2	-1.2	-1.1	-1.1	-1.1	GDP/GTP exchange factor (by homology)	YNL272c	orf19.12394
CA4012	GPA2	1.1	1.1	1.2	-1.1	nucleotide-binding regulatory protein GPA2	YER020w	orf19.1621
CA2925	IPF7827	1.0	-1.0	1.0	-1.1	unknown function	YGR110w	orf19.4210
CA0278	IPF15772	-1.0	1.0	-1.0	-1.1	unknown function		
CA0449	MOT2.3	1.1	-1.0	-1.0	-1.1	transcriptional repressor, 3-prime end (by homology)	YER068w	orf19.2379
CA5243	IPF3040	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.5020
CA0877	CNH1.5F	-1.1	1.0	-1.1	-1.1	Na+/H+ antiporter, 5-prime end (by homology)	YLR138w	orf19.8000
CA2727	IPF10318	1.1	-1.0	-1.1	-1.1	similar to Saccharomyces cerevisiae Ndt80p meiosis-sp	YHR124w	orf19.2119
CA4506	GCD10	-1.0	-1.1	-1.2	-1.1	translation initiation factor eIF3 RNA-binding subunit (by	YNL062c	orf19.500
CA1405	IPF19554.3F	-1.0	1.0	-1.1	-1.1	unknown function, 3-prime end		orf19.3371
CA4342	IPF3629	1.0	1.0	1.1	-1.1	RNA (guanine-N7-) methyltransferase	YBR236c	orf19.6716
CA2781	IPF3821	1.0	-1.0	-1.0	-1.1	unknown function		orf19.284

CA5959	SRB7	1.1	-1.1	-1.0	-1.1	DNA-directed RNA polymerase II holoenzyme and korn	YDR308c	orf19.7548
CA2207	IPF12169	1.0	-1.0	-1.0	-1.1	unknown function	YHR017w	orf19.8316
CA4677	HOG1	1.1	1.0	-1.0	-1.1	Ser/thr protein kinase of MAPK family	YLR113w	orf19.895
CA2484	IPF9846	-1.0	-1.0	-1.1	-1.1	unknown function		orf19.10714
GFPTag		1.0	1.0	1.0	-1.1			
CA2471	TOP2	-1.1	-1.1	-1.2	-1.1	Topoisomerase II	YNL088w	orf19.2873
CA5528	RPN7	-1.0	1.0	-1.1	-1.1	Subunit of the regulatory particle of the proteasome (by	YPR108w	orf19.7286
CA3456	IPF19986	-1.0	1.0	-1.3	-1.1	unknown function	YGL131c	orf19.1259
CA4147	ADE8	1.1	-1.1	-1.1	-1.1	Phosphoribosylglycinamide formyltransferase (GART)	YDR408c	orf19.13211
CA5642	INP52	-1.0	-1.1	-1.1	-1.1	phosphatidylinositol phosphate phosphatase (by homolo	YOR109w	orf19.7052
CA0254	IPF14968	1.0	-1.1	-1.1	-1.1	unknown function		orf19.3461
CA0729	IPF7338	-1.0	1.0	-1.1	-1.1	unknown function		orf19.11210
CA6085	IPF32	-1.0	1.0	-1.2	-1.1	similar to Saccharomyces cerevisiae Apg9p integral me	YDL149w	orf19.5974
CA5359	TIF35	1.0	-1.1	-1.3	-1.1	translation initiation factor eIF3, p33 subunit (by homolo	YDR429c	orf19.7236
CA1545	CDR3.5EOC	-1.1	1.0	-1.2	-1.1	ABC transporter, multidrug resistance protein, 5-prime end		orf19.1313
CA1845	IPF11123	1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Sdh2p succinate d	YLL041c	orf19.637
CA2629	IPF10911	1.1	-1.1	-1.1	-1.1	unknown function	YIL110w	orf19.12224
CA5541	IPF2827	-1.0	-1.1	1.0	-1.1	unknown function		orf19.7303
CA3362	IPF9789	-1.2	-1.1	-1.2	-1.1	unknown function	YDR479c	orf19.9489
CA0258	IPF17112	-1.1	-1.1	-1.2	-1.1	thiosulfate sulfurtransferase (by homology)	YOR251c	orf19.1356
CA4590	IPF2218	1.1	-1.1	1.0	-1.1	unknown function	YDL156w	orf19.6907
CA1394	IFO2	-1.2	-1.1	-1.1	-1.1	unknown function		orf19.9334
CA5197	IPF2342	-1.2	-1.0	-1.4	-1.1	unknown function	YPL012w	orf19.7011
CA2788	RAD26	1.1	-1.0	-1.2	-1.1	DNA repair and recombination protein (by homology)	YJR035w ; Missing in array	orf19.8240
CA4432	IPF5574	-1.1	-1.2	-1.3	-1.1	unknown function	YLL003w	orf19.5163
CA2336	PF13383.53EO	-1.1	-1.1	-1.2	-1.1	unknown function, internal fragment	YOR086c	orf19.2353
CA4452	IPF3514	1.0	1.1	1.0	-1.1	unknown function	YDR255c	orf19.6850
CA2004	POL12	-1.0	-1.1	-1.0	-1.1	DNA-directed DNA polymerase alpha (by homology)	YBL035c	orf19.2796
CA3132	IPF8904	1.0	1.0	-1.0	-1.1	unknown function	YOR338w	orf19.1363
CA1859	IPF19614	1.0	-1.0	-1.0	-1.1	putative transcription factor similar to positive activator of the proline utilisation pathwa		orf19.9073
CA1757	IPF14559.5F	-1.1	-1.0	-1.1	-1.1	unknown function, 5-prime end		orf19.5128
CA5864	IPF364	-1.0	-1.2	-1.2	-1.1	transaminase type I (by homology)		orf19.7522
CA0846	SMC3	-1.1	1.0	-1.1	-1.1	required for structural maintenance of chromosomes (b	YJL074c	orf19.7895
CA0334	IPF19562	-1.3	-1.1	-1.2	-1.1	unknown function		orf19.7824
CA3429	IPF6380	1.1	1.1	-1.0	-1.1	unknown function	YDR031w	orf19.588
CA2424	IPF18468	-1.2	-1.2	-1.2	-1.1	unknown function		orf19.11948
CA0986	IPF4814	-1.0	-1.0	-1.1	-1.1	similar to Saccharomyces cerevisiae Mrp20p ribosomal	YDR405w	orf19.3350
CA1224	IPF15662	-1.1	-1.0	-1.1	-1.1	unknown function		orf19.4156
CA3194	IPF3425	-1.1	-1.1	-1.1	-1.1	unknown function	YIL115c	orf19.6171
CA4229	IPF12480.5	-1.1	-1.0	-1.1	-1.1	unknown function, 5-prime end		
CA4690	IPF3959	-1.0	-1.0	-1.0	-1.1	unknown function		orf19.8494
CA0612	IPF17545	-1.1	-1.0	-1.1	-1.1	unknown function		orf19.5579
CA1374	MIP1	-1.2	1.0	1.1	-1.1	Mitochondrial intermediate peptidase (by homology)	YKL134c	orf19.1195
CA4322	IPF2097	-1.1	-1.0	-1.2	-1.1	unknown function		orf19.4097
CA5823	COQ1	-1.2	-1.2	-1.2	-1.1	Hexaprenyl pyrophosphate synthetase (by homology)	YBR003w	orf19.7478
CA2107	IPF10716	1.1	-1.1	-1.0	-1.1	unknown function	YGR033c	orf19.3691
CA6108	SEC7	-1.3	1.1	-1.3	-1.1	Guanine nucleotide exchange protein for ADP-robosyla	YDR170c	orf19.5947
CA5111	SSY5	-1.1	-1.0	-1.1	-1.1	Involved in sulfonylurea herbicide sensitivity (by homolo	YJL156c	orf19.6422
CA2688	IFU6.5F	-1.1	1.0	1.0	-1.1	Putative ortholog of S. cerevisiae Gre2p, 5-prime end		orf19.2581

CA6110	IPF91	1.0	-1.1	-1.2	-1.1	unknown function	YHR150w	orf19.5943
CA2249	POL2	-1.1	-1.1	-1.2	-1.1	DNA-directed DNA polymerase epsilon, catalytic subuni	YNL262w	orf19.2365
CA4507	IPF20015	1.1	1.0	-1.0	-1.1	unknown function	YNL063w	orf19.499
CA6137	IPF4356	-1.0	1.0	-1.1	-1.1	unknown function	YPR031w	orf19.5910
CA3002	PIF1	-1.0	-1.1	-1.1	-1.1	mitochondrial DNA helicase (by homology)	YML061c	orf19.6133
CA1676	ERG9	-1.4	1.0	-1.0	-1.1	farnesyl-diphosphate farnesyltransferase	YHR190w	orf19.3616
CA5134	IPF5131	-1.0	1.1	1.0	-1.1	unknown function		orf19.6391
CA4953	IPF4567.3	-1.0	-1.1	-1.1	-1.1	unknown function, 3-prime end		orf19.6525
CA3652	NBP35	-1.1	1.0	-1.1	-1.1	Nucleotide-binding protein (by homology).		orf19.2043
CA3101	IPF6593	-1.0	-1.2	-1.3	-1.1	similar to Saccharomyces cerevisiae Rfx1p DNA-bindin	YLR176c	orf19.3865
CA0583	GSH1.EXON2	-1.2	-1.1	-1.2	-1.1	gamma-glutamylcysteine synthetase, exon 2 (by homol	YJL101c	orf19.12526
CA0247	RIB21	-1.0	-1.0	-1.0	-1.1	DRAP deaminase (by homology)		orf19.2788
CA3956	IPF6712.3F	-1.1	1.1	-1.2	-1.1	unknown function, 3-prime end		
CA5266	IPF1787.3F	-1.1	1.0	1.1	-1.1	unknown function, 3-prime end	YBL029w	orf19.4996
CA3229	FUN30	1.0	-1.1	-1.3	-1.1	helicases of the Snf2/Rad54 family(by homology)	YAL019w	orf19.6291
CA1858	IPF15344	-1.1	1.0	-1.2	-1.1	unknown function		orf19.9076
CA4509	IPF8973	1.0	-1.1	-1.2	-1.1	unknown function	YNL136w	orf19.497
CA6053	IPF4949	1.0	-1.0	-1.0	-1.1	unknown function	YNL321w	orf19.7670
CA1005	LPG7	-1.0	-1.0	-1.1	-1.1	probable membrane protein (by homology)	YPL101w	orf19.3759
CA0319	IPF15244.3F	-1.0	-1.1	-1.2	-1.1	unknown function, 3-prime end		
CA0681	IPF14511.3F	-1.1	-1.0	-1.0	-1.1	unknown function, 3-prime end		orf19.12170
CA0983	CBR1	1.0	-1.1	-1.0	-1.1	Cytochrome-b5 reductase (by homology)	YIL043c	orf19.1801
CA2843	ALK5.5F	1.0	-1.0	-1.1	-1.1	n-alkane-inducible cytochrome P-450, 5-prime end		orf19.5728
CA5240	IPF3032	-1.2	-1.2	-1.1	-1.1	allantoate permease (by homology)		orf19.5023
CA1961	IPF14284	-1.1	-1.1	-1.1	-1.1	putative dnaJ-like protein (by homology)	YNL227c	orf19.2399
CA3150	IPF4035	1.1	-1.0	1.0	-1.1	unknown function		orf19.6166
CA2062	IPF7858	1.0	-1.1	-1.2	-1.1	similar to Saccharomyces cerevisiae Prp24p U4/U6 spli	YMR268c	orf19.2563
CA4123	AMS1	-1.2	-1.1	-1.1	-1.1	alpha-mannosidase (by homology)	YGL156w	orf19.2768
CA4098	IPF3988	1.0	-1.1	1.0	-1.1	unknown function		orf19.664
CA5631	GLN4	-1.0	-1.0	-1.1	-1.1	glutaminyl-tRNA synthetase (by homology)	YOR168w	orf19.7064
CA1047	IPF11615	-1.1	-1.0	-1.1	-1.1	RNA-binding proteins (by homology)	YPR112c	orf19.9215
CA1706	NMD3	-1.0	-1.0	1.1	-1.1	RNA binding (by homology)	YHR170w	orf19.706
CA1909	IPF20091	1.0	-1.1	-1.0	-1.1	unknown function		orf19.10303
CA5907	SSN6	-1.1	1.0	-1.3	-1.1	transcriptional repressor (by homology)	YBR112c	orf19.6798
CA4605	IPF6226	-1.0	-1.0	-1.0	-1.1	unknown function		orf19.3295
CA1900	ARK1	-1.2	-1.0	-1.1	-1.1	actin regulating serine/threonine kinase (by homology)		orf19.2605
CA2732	IPF10327	-1.0	-1.1	-1.0	-1.1	unknown function	YLR324w	orf19.2113
CA2437	PHO86	-1.0	-1.1	-1.1	-1.1	inorganic phospate transporter by homology	YJL117w	orf19.2199
CA0304	IPF12829	-1.0	-1.1	-1.1	-1.1	unknown function	YLL035w	orf19.8340
CA5692	UTR1	-1.1	-1.0	-1.0	-1.1	Associated with ferric reductase activity (by homology)	YJR049c	orf19.7393
CA1322	GCD11	-1.0	1.1	-1.1	-1.1	Translation initiation factor eIF2 (by homology)	YER025w	orf19.4223
CA3800	RPL7A.3	1.0	-1.1	-1.2	-1.1	60S Ribosomal Protein L7-A, 3-prime end	YPL198w	
CA3350	RPL18A.5	1.1	-1.0	1.0	-1.1	ribosomal protein S18.e, 5-prime end (by homology)		
CA2308	IPF9874.3	1.1	-1.0	1.1	-1.1	similar to Saccharomyces cerevisiae Inp51p phosphatid	YIL002c	orf19.8953
CA0069	F19295.5EOC	1.2	1.3	-1.4	-1.1	unknown function, internal fragment		orf19.6468
CA0084	NAB3	-1.1	-1.1	-1.2	-1.1	polyadenylated RNA-binding protein (by homology)	YPL190c	orf19.12976
CA3266	IPF5045	1.0	-1.1	-1.1	-1.1	unknown function	YMR171c	orf19.2703
CA3997	LOC1	-1.0	-1.1	-1.0	-1.1	putative double-stranded RNA-binding protein (by hom	YFR001w	orf19.1642
CA4063	SDH11	-1.1	-1.1	-1.1	-1.1	Succinate dehydrogenase (by homology)	YKL148c	orf19.440

CA3710	CHS3.5F	1.0	1.0	-1.3	-1.1	chitin-UDP acetyl-glucosaminyl transferase 3, 3-prime end		orf19.4938
CA2209	IPF18512	-1.0	-1.1	-1.1	-1.1	unknown function	YOR107w	orf19.695
CA4903	SNF7	1.0	-1.0	-1.1	-1.1	Class E Vps protein (by homology)	YLR025w	orf19.6040
CA3519	IPF6787	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.8613
CA0420	IPF9048	1.0	1.0	1.2	-1.1	unknown function	YPR093c	orf19.2229
CA1398	IPF19913	-1.1	-1.1	-1.0	-1.1	unknown function	YNL128w	orf19.3699
CA1927	YBN5	-1.0	-1.1	-1.1	-1.1	Putative purine nucleotide-binding protein (by homology	YBR025c	orf19.754
CA1478	IPF16426	-1.0	-1.1	-1.1	-1.1	similar to human BRRN1 (by homology)	YBL097w	orf19.1251
CA4091	IPF5005	-1.0	1.0	-1.1	-1.1	unknown function		orf19.6650
CA0408	SAC6.5F	-1.4	-1.1	-1.2	-1.1	actin filament bundling protein, fimbrin, 5-prime end (by	YDR129c	orf19.5544
CA2678	IPF5834	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.12946
CA4490	IPF4045	1.0	-1.1	-1.2	-1.1	unknown function		orf19.9428
CA0160	GAP7.5EOC	1.0	-1.1	1.0	-1.1	general amino acid permease, 5-prime end		orf19.10706
CA5842	LEU1	-1.6	-1.0	-1.2	-1.1	3-isopropylmalate dehydratase (by homology)	YGL009c	orf19.7498
CA2671	IPF5856	-1.1	-1.1	-1.2	-1.1	4-hydroxyphenylpyruvate dioxygenase (by homology)		orf19.5499
CA3412	IPF9238	1.0	-1.1	-1.2	-1.1	long chain fatty alcohol oxidase (by homology)		orf19.13562
CA0213	CDS1	1.0	-1.1	-1.1	-1.1	CDP-diacylglycerol synthase (by homology)	YBR029c	orf19.1279
CA4510	IPF8970	-1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Msh1p DNA mism	YHR120w	orf19.496
CA1608	TES12	1.1	-1.1	-1.0	-1.1	Thiosterase (by homology)	YJR019c	orf19.4122
CA1421	MRPL11	1.1	-1.3	-1.2	-1.1	Mitochondrial ribosomal protein (by komology)	YDL202w	orf19.11278
CA2770	CPS1	1.1	-1.1	-1.1	-1.1	Carboxypeptidase YSCS precursor, second fragment (b	YJL172w	orf19.2686
CA5961	IFA14	1.0	1.0	-1.0	-1.1	unknown function		orf19.7550
CA4944	MSK1	-1.1	-1.0	-1.0	-1.1	lysyl-tRNA synthetase by homology	YNL073w	orf19.6533
CA5521	HEM12	-1.1	-1.1	-1.2	-1.1	uroporphyrinogen decarboxylase (by homology)	YDR047w	orf19.5369
CA2378	GLE1	-1.1	-1.1	-1.1	-1.1	RNA export mediator (by homology)	YDL207w	orf19.2215
CA3452	IPF10541	-1.1	-1.1	-1.1	-1.1	unknown function	YFR034c	orf19.1253
CA5718	LCP5	-1.1	-1.1	-1.1	-1.1	Ngg1p interacting protein (by homology)	YER127w	orf19.7422
CA2751	IPF19558	-1.2	-1.0	-1.1	-1.1	unknown function	YNL258c	orf19.2370
CA1990	TOP1	1.0	-1.1	-1.1	-1.1	CANAL DNA TOPOISOMERASE I	YOL006c	orf19.7742
CA5294	IPF1952	-1.1	-1.2	-1.3	-1.1	unknown function		orf19.7157
CA1189	RPL24A	1.1	-1.3	-1.4	-1.1	ribosomal protein L24 (by homology)	YGL031c	orf19.11269
CA5617	SPL1	-1.1	-1.0	1.0	-1.1	tRNA splicing protein	YCL017c	orf19.7081
CA0843	IPF18853	-1.0	-1.1	-1.2	-1.1	unknown function	YLL023c	orf19.8656
CA2547	IPF14911	-1.2	-1.1	-1.2	-1.1	unknown function	YNL152w	orf19.2832
CA1740	SMI1	-1.2	-1.1	-1.2	-1.1	beta-1,3-glucan synthesis protein (by homology)	YGR229c	orf19.5058
CA4821	IPF1197	-1.0	-1.1	1.0	-1.1	unknown function	YMR130w	orf19.2076
CA4524	IPF7097	1.1	-1.1	1.0	-1.1	unknown function	YJR056c	orf19.480
CA1214	VPS15.53F	-1.1	-1.0	-1.2	-1.1	serine/threonine protein kinase, internal fragment		orf19.129
CA2835	IPF12091	-1.0	-1.0	-1.2	-1.1	Unknown function		orf19.4787
CA2924	FET33	1.0	-1.1	-1.0	-1.1	cell surface ferroxidase (by homology)	YMR058w	orf19.11687
CA3307	RPL2.3	1.0	1.0	-1.2	-1.1	ribosomal protein L8, 3-prime end (by homology)	YIL018w	
CA4171	IPF7785	1.0	1.0	1.1	-1.1	unknown function		orf19.2962
CA4175	F4425.REPEAT	-1.0	-1.0	1.1	-1.1	unknown function		orf19.2958
CA1999	IPF19513	-1.1	-1.1	-1.0	-1.1	unknown function	YLR114c	orf19.13830
CA3473	PF6305.EXON1	1.0	-1.1	-1.0	-1.1	unknown function, exon 1	YDL139c	orf19.1668
CA5879	IPF12076	1.1	-1.3	-1.2	-1.1	enoyl CoA hydratase (by homology)		orf19.6830
CA4002	IPF4258	-1.2	-1.1	-1.2	-1.1	unknown function		orf19.1634
CA5356	IRR1.5F	-1.1	-1.0	-1.2	-1.1	cohesin complex subunit, 5-prime end (by homology)	YIL026c	orf19.7233
CA5964	IPF963	-1.1	-1.2	-1.1	-1.1	unknown function		orf19.7553

CA3851	CTA21	1.1	1.0	-1.0	-1.1	transcriptional activation		orf19.6112
CA5740	IPF20030	1.0	1.0	-1.0	-1.1	unknown function	YNL166c	orf19.7450
CA6040	CPR6	-1.2	1.1	-1.3	-1.1	cyclophylin (by homology)	YLR216c	orf19.7654
CA2284	MIF2	-1.0	1.0	-1.1	-1.1	required for normal chromosome segregation and spind	YKL089w	orf19.5551
CA1287	IPF5545	-1.1	-1.1	-1.3	-1.1	unknown function	YDR330w	orf19.4430
CA3886	IPF12963	-1.2	1.0	1.0	-1.1	ubiquitin-mediated protein degradation (by homology)		orf19.5094
CA2991	IPF5088.3	1.0	1.0	1.0	-1.1	unknown function, 3-prime end	YMR233w	orf19.6013
CA2306	IPF6510	-1.0	1.0	-1.0	-1.1	unknown function		orf19.1685
CA3645	IPF4127	-1.0	-1.1	-1.1	-1.1	putative dimeric dihydrodiol dehydrogenase (by homology)		orf19.2036
CA0970	IPF10894	1.1	1.0	1.0	-1.1	unknown function	YGR120c	orf19.10340
CA0280	IPF10566	-1.1	-1.0	1.1	-1.1	unknown function	YDR315c	orf19.1439
CA5791	RPT2	-1.1	-1.2	-1.4	-1.1	26S proteasome regulatory subunit (by homology)	YDL007w	orf19.5440
CA2206	IPF12173	1.0	-1.1	1.0	-1.1	unknown function	YIL090w ; Missing in array	orf19.698
CA2486	IPF9851	-1.1	-1.1	-1.1	-1.1	unknown function	YCR040w	orf19.10712
CA0565	IPF13526	-1.0	-1.1	-1.1	-1.1	unknown function	YPR129w	orf19.6250
CA5703	IPF2463	1.0	1.0	-1.1	-1.1	unknown function	YML020w	orf19.7403
CA0566	IPF13522	1.0	-1.1	-1.1	-1.1	unknown function	YPR133c	orf19.6252
CA2984	PF12606.3EOC	-1.2	-1.1	-1.2	-1.1	unknown function, 3-prime end		
CA1138	IFN3	-1.0	-1.0	1.0	-1.1	glycerophosphoinositol transporter (by homology)		orf19.1978
CA0685	ADO1	1.1	-1.0	1.0	-1.1	adenosine kinase (by homology)	YJR105w	orf19.13037
CA3572	IPF18321	-1.0	1.0	-1.0	-1.1	unknown function	Missing in array	
CA3183	TSM1.3F	-1.0	1.0	-1.2	-1.1	component of TFIID complex, 3-prime end (by homolog	YCR042c	orf19.2135
CA3185	IPF13637	1.1	1.0	1.1	-1.1	unknown function		orf19.2137
CA3679	IPF20142	-1.0	1.0	-1.0	-1.1	unknown function	YFL047w	orf19.730
CA5466	PWP2	-1.0	1.1	-1.1	-1.1	periodic tryptophan protein (by homology)	YCR057c	orf19.3276
CA2905	IPF12049	-1.2	-1.1	-1.1	-1.1	unknown function	YGL066w	orf19.10977
CA4107	IPF3970	-1.1	-1.1	-1.1	-1.1	unknown function	YLR177w	orf19.671
CA5103	IPF1367	1.0	1.1	-1.0	-1.1	unknown function		orf19.6436
CA0525	MSB1	-1.0	1.0	1.1	-1.1	Morphogenesis-related protein (by homology)	YOR188w	orf19.8726
CA3113	IPF15737	-1.1	-1.0	-1.1	-1.1	simailar to Saccharomyces cerevisiae Rvb2p RuvB-like	YPL235w	orf19.13892
CA2633	KEX2	-1.3	-1.1	-1.4	-1.1	Kexin precursor (KEX2 protease)	YNL238w	orf19.4755
CA0348	IFK1	-1.0	1.0	-1.0	-1.1	probable monoxygenase (by homology)		orf19.9098
CA4872	SEC231	-1.2	-1.1	-1.2	-1.1	Component of COPII coat (by homology)		orf19.6558
CA3224	GLC7	-1.3	1.0	1.0	-1.1	Ser/thr phosphoprotein phosphatase 1 (by homology)	YER133w	orf19.6285
CA2531	RIB2	-1.2	-1.2	-1.2	-1.1	DRAP deaminase (by homology)	YOL066c	orf19.3177
CA1448	IPF14728	-1.1	1.0	-1.1	-1.1	unknown function		orf19.192
CA4908	IPF1445	-1.1	1.1	-1.2	-1.1	similar to Saccharomyces cerevisiae Apc1p subunit of a	YNL172w	orf19.6046
CA4974	IPF4704	1.0	-1.1	-1.2	-1.1	unknown Function	YJR111c	orf19.5278
CA1569	IPF7616	1.1	-1.1	-1.2	-1.1	putative homoserine O-acetyltransferase (by homology)		orf19.1159
CA0462	MRPS28	1.0	-1.1	-1.1	-1.1	ribosomal protein (by homology)	YDR337w	orf19.2520
CA3819	IPF6993	-1.0	-1.1	-1.1	-1.1	unknown function	YBR231c	orf19.5772
CA0802	IPF14060	-1.1	-1.1	-1.0	-1.1	unknown function		orf19.3498
CA3992	VAM6.3F	-1.3	-1.1	-1.4	-1.1	Vacuolar carboxypeptidase Y, 3-prime end (by homolog	YDL077c	orf19.1568
CA5819	IFF4	1.1	-1.1	-1.1	-1.1	Unknown function		orf19.7472
CA3823	IPF10651	-1.1	-1.0	-1.1	-1.1	unknown function	YJL061w	orf19.5765
CA1884	IPF5486	1.1	1.0	1.0	-1.1	unknown function		orf19.2208
CA1446	YAL011	-1.0	-1.1	-1.1	-1.1	mitochondrial transit peptide (by homology)		orf19.190
CA4435	SAP190	-1.3	-1.0	-1.3	-1.1	phosphatase associated protein by homology	YKR028w	orf19.5160
CA0743	RNA14.3EOC	-1.1	-1.0	-1.1	-1.1	component of pre-mRNA 3 -end processing factor CF I,	YMR061w	

CA4166	TIF34	-1.2	-1.2	-1.2	-1.1	Translation initiation factor eIF3, p39 subunit	YMR146c	orf19.2967
CA0230	TOM37	-1.1	-1.2	-1.2	-1.1	Mitochondrial outer membrane import receptor subunit (by homology)		orf19.1532
CA4094	IPF4004	-1.1	-1.1	-1.3	-1.1	unknown function	YCL061c	orf19.658
CA1354	GCD6	-1.0	-1.1	-1.2	-1.1	translation initiation factor- like protein	YDR211w	orf19.407
CA6045	IPF4929	-1.1	-1.0	-1.0	-1.1	similar to Saccharomyces cerevisiae Hmi1p mitochondr	YOL095c	orf19.7661
CA2605	SRP1	-1.0	1.0	1.2	-1.1	alpha importin by homology	YNL189w	orf19.5682
CA3756	IPF8884	-1.1	-1.0	-1.3	-1.1	unknown function	YLR454w	orf19.3422
CA1191	CAN2	-1.0	-1.3	-1.5	-1.1	amino acid permease (by homology)	YEL063c	orf19.111
CA5126	SLS1	1.0	1.0	-1.1	-1.1	Endoplasmic translocation machinery by homology	YOL031c ; Missing in array	orf19.6403
CA2121	IPF7930	-1.2	-1.2	-1.2	-1.1	unknown function	YJL123c	orf19.8918
CA0750	IPF6284	1.0	-1.1	-1.1	-1.1	unknown function	YHR207c	orf19.1972
CA3507	IPF11375	-1.2	-1.1	-1.2	-1.1	unknown function		orf19.6354
CA5057	IPF3695	-1.0	-1.2	-1.3	-1.1	similar to Saccharomyces cerevisiae Ngg1p general tra	YDR176w	orf19.3023
Gal4 BD		-1.0	-1.0	-1.1	-1.1			
CA1533	IPF9510	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.8803
CA0361	IPF2326	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.1124
CA4710	ORC3	-1.1	-1.1	-1.2	-1.1	Origin recognition complex (by homology)	YLL004w	orf19.6942
CA5064	CHD1	-1.2	-1.1	-1.3	-1.1	transcriptional regulator (by homology)	YER164w	orf19.3035
CA1571	SPO14.3EOC	-1.1	-1.0	-1.2	-1.1	phospholipase D, 3-prime end	Missing in array	
CA2307	PF18488.5EO	-1.0	1.0	-1.1	-1.1	unknown function, 5-prime end		
CA2892	IPF6688	-1.1	-1.0	-1.1	-1.1	unknown function		orf19.2465
CA1396	IPF8075	-1.1	1.1	-1.1	-1.1	unknown function	YLR392c	orf19.3701
CA3630	IPF8129	-1.2	-1.1	-1.1	-1.1	unknown function		orf19.12609
CA4058	IPF7717	-1.0	-1.0	-1.0	-1.1	unknown function	YGR166w	orf19.8063
CA4927	IPF1401	1.1	-1.2	-1.2	-1.1	similarity to aldehyde dehydrogenase (by homology)	YMR110c	orf19.6066
CA4224	IPF8755	-1.1	-1.1	-1.2	-1.1	unknown function		orf19.827
CA2483	IPF19758	-1.2	-1.3	-1.2	-1.1	unknown function	YJL204c	orf19.3203
CA1164	ARP8	-1.2	-1.1	-1.2	-1.1	actin-related protein (by homology)	YOR141c	orf19.10867
CA5318	OGG1	1.0	-1.0	1.1	-1.1	8-oxoguanine DNA glycosylase (by homology)	YML060w	orf19.7190
CA4470	IPF9717	-1.1	-1.1	-1.2	-1.1	unknown function	YPR144c	orf19.1902
CA4057	IPF7719	-1.1	-1.1	-1.1	-1.1	unknown function	YDR306c	orf19.432
CA1910	IPF7260	-1.1	-1.1	-1.1	-1.1	unknown function	YKL018w	orf19.10306
CA0382	IPF16030	-1.2	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Bud5p GDP/GTP	YCR038c	orf19.1842
CA5449	DAL81	-1.1	-1.2	-1.2	-1.1	Transcriptional activator for allantoin and GABA catabol	YIR023w	orf19.3252
CA3251	IPF4721	-1.2	-1.1	-1.2	-1.1	unknown Function		orf19.3737
CA4401	IPF8780	1.0	-1.0	-1.0	-1.1	unknown function		orf19.3109
CA3797	IPF5623	-1.2	-1.1	-1.0	-1.1	unknown function	YML002w	orf19.5821
CA5437	ERG27	1.1	-1.1	-1.2	-1.1	3-keto sterol reductase (by homology)	YLR100w	orf19.3240
CA4575	IPF9428	-1.0	-1.2	-1.1	-1.1	unknown function	YPL146c	orf19.6886
CA5202	YOX1	1.1	-1.1	-1.3	-1.1	Similar to homoeodomain protein (by homology)	YML027w	orf19.7017
CA2114	IPF13744	1.0	-1.0	-1.1	-1.1	protein involved in regulation of carbon metabolism (by	YNL201c	orf19.3685
CA1746	IPF10886	-1.1	-1.1	-1.2	-1.1	unknown function	YGL236c	orf19.5050
CA3477	IPF3229	1.0	-1.0	-1.1	-1.1	unknown function	YIL064w	orf19.3582
CA1092	YTA7	-1.1	-1.0	-1.2	-1.1	26S proteasome subunit (by homology)	YGR270w	orf19.3949
CA0766	IPF15335	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.12435
CA0849	HEM4	-1.0	1.0	1.1	-1.1	uroporphyrinogen III synthase	YOR278w	orf19.9311
CA0717	IPF9785	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.3453
CA3009	MRPL19	-1.0	-1.0	-1.1	-1.1	Ribosomal protein (by homology)	YNL185c	orf19.13611
CA0224	PRP31	-1.1	-1.1	1.0	-1.1	pre-mRNA splicing protein (by homology)	YGR091w	orf19.1296

CA1805	IPF6332	-1.2	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Bud7p chitin biosy	YOR299w	orf19.1112
CA4008	DYS1	-1.1	-1.1	-1.1	-1.1	deoxyhypusine synthase	YHR068w	orf19.1626
CA2889	IPF13628	-1.0	-1.0	-1.1	-1.1	putative DNA repair protein (by homology)	YML095c	orf19.2469
CA1341	IPF11344	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.4340
CA0182	IFI1	1.1	-1.0	-1.2	-1.1	unknown function		orf19.1130
CA1145	GCS1	-1.1	-1.0	-1.1	-1.1	ADP-ribosylation factor GTPase-activating protein (ARF	YDL226c	orf19.11167
CA1382	IPF8421	-1.0	1.0	-1.1	-1.1	unknown function		orf19.928
CA4347	IPF3636	-1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Rad4p excision re	YER162c	orf19.6722
CA0537	PRP16	-1.1	-1.1	-1.3	-1.1	RNA-dependent ATPase (by homology)	YKR086w	orf19.2818
CA1320	IPF3143	-1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Orc4p subunit of o	YPR162c	orf19.4221
CA5473	IPF16947	1.0	-1.3	-1.4	-1.1	unknown function	YDR221w	orf19.3286
CA5685	HPA1	-1.0	-1.0	-1.1	-1.1	RNA polymerase II-associated Histone acetyltransferas	YPL086c	orf19.7387
CA5190	IPF10155	1.0	-1.1	-1.0	-1.1	unknown function	YKL059c	orf19.4628
CA1513	MIR1	-1.0	-1.0	-1.0	-1.1	phosphate transport protein, mitochondrial (MCF) (by ho	YJR077c	orf19.4885
CA5509	IPF743	1.0	-1.0	-1.1	-1.1	unknown function		orf19.5353
CA1027	PF19645.EXON	1.0	-1.1	-1.1	-1.1	unknown function, exon 2	YPR040w	
CA0018	IPF19435	1.0	-1.1	1.0	-1.1	unknown function	Missing in array	
CA0551	CDC37	-1.0	-1.2	-1.3	-1.1	Cell division control protein (by homology)	YDR168w	orf19.5531
CA4409	IPF13151	-1.2	-1.1	-1.2	-1.1	unknown function		orf19.3100
CA0146	IPF9689	-1.1	-1.1	-1.2	-1.1	unknown function		orf19.11132
CA4247	TAF90	1.1	1.1	1.1	-1.1	Probable transcription-associated factor protein	YBR198c	orf19.536
CA5512	ORC2	-1.1	-1.0	-1.0	-1.1	origin recognition complex subunit 2 (by homology)	YBR060c	orf19.5358
CA5915	IPF10735	1.1	1.0	1.1	-1.1	similar to Saccharomyces cerevisiae Ngr1p negative gr	YBR212w	orf19.6790
CA2469	IPF7393	-1.0	-1.1	1.0	-1.1	unknown function		orf19.9364
CA3939	HNM1	1.7	-1.1	1.1	-1.1	Choline permease (by homology)		orf19.9554
CA2416	IFD4	1.1	-1.2	-1.3	-1.1	Putative aryl-alcohol dehydrogenase (by homology)		orf19.4477
CA5936	IPF2795	-1.2	-1.2	-1.2	-1.1	unknown function		orf19.6763
CA0817	IPF6339	1.1	-1.1	-1.1	-1.1	unknown function		orf19.10239
CA1125	RRP43	-1.0	-1.1	-1.1	-1.1	rRNA processing protein (by homology)	YCR035c	orf19.6259
CA2073	IPF6967	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.10161
CA1293	HCA4	-1.1	-1.2	-1.3	-1.1	Can suppress the U14 snoRNA rRNA processing functi	YJL033w	orf19.2712
CA2923	FET32	-1.1	-1.1	-1.1	-1.1	cell surface ferroxidase (by homology)		orf19.11688
CA5239	GND1	-1.1	-1.2	1.1	-1.1	6-phosphogluconate dehydrogenase	YHR183w ; Missing in array	orf19.5024
CA4408	CTA6.3	1.0	1.0	-1.1	-1.1	unknown function, 3-prime end		orf19.3102
CA3536	IPF5414	-1.0	-1.0	-1.0	-1.1	unknown function		orf19.6371
CA0587	SPO14.5EOC	-1.1	1.0	-1.5	-1.1	phospholipase D, 5-prime end	YKR031c	orf19.8753
CA5319	IPF2150	-1.2	-1.2	-1.3	-1.1	similar to protein involved in ER function	YKL124w	orf19.7193
CA6061	IPF8302	1.1	-1.1	-1.1	-1.1	unknown function		orf19.6007
CA2996	IPF9108	1.1	1.0	1.2	-1.1	similar to Saccharomyces cerevisiae Ace2p transcriptio	YLR131c	orf19.6124
CA0755	IPF14861	-1.0	-1.0	-1.0	-1.1	unknown function		orf19.3487
CA2384	MDL1	-1.1	-1.1	-1.1	-1.1	ATP-DEPENDENT PERMEASE	YLR188w	orf19.2615
CA5946	IPF3493	-1.0	-1.0	-1.0	-1.1	unknown function	YBR061c	orf19.6751
CA5817	IPF2511	1.0	-1.0	-1.1	-1.1	unknown function	YER064c	orf19.7468
CA4305	IPF6654	1.0	-1.0	1.0	-1.1	unknown function	YBL060w	orf19.6705
CA5887	IPF2415	-1.0	1.0	-1.1	-1.1	similar to Saccharomyces cerevisiae Apc2p component	YLR127c	orf19.6821
CA3348	RIO1	1.1	-1.1	-1.1	-1.1	unknown function	YOR119c	orf19.2320
CA1694	TRM3	-1.1	-1.2	-1.2	-1.1	2 -O-ribose methyltransferase (by homology)	YDL112w	orf19.5038
CA0959	SAM2	1.0	-1.0	-1.1	-1.1	S-adenosylmethionine synthetase 2	YDR502c	orf19.657
CA0485	IPF17574	-1.1	-1.1	-1.2	-1.1	Unknown function	YAR014c	orf19.11038

CA5849	IPF404.5F	-1.1	-1.1	-1.1	-1.1	unknown function, 5-prime end		orf19.7506
CA1321	IPF3141	-1.0	1.0	1.0	-1.1	similar to Saccharomyces cerevisiae Sst2p involved in c	YLR452c	orf19.4222
CA6042	IPF4924	1.0	1.0	-1.0	-1.1	unknown function	YNL282w	orf19.7657
CA3438	IPF11330	-1.2	-1.1	-1.2	-1.1	unknown function	YHR194w	orf19.2987
CA1305	IPF13508	-1.0	-1.0	-1.1	-1.1	unknown function	YDR063w	orf19.4193
CA5929	GCD2	-1.2	-1.1	-1.3	-1.1	Translation initiation factor eIF2B, 71 kDa (delta) subuni	YGR083c	orf19.6776
CA1580	TRP5	-1.0	-1.0	-1.1	-1.1	tryptophan synthase (by homology)	YGL026c	orf19.4718
CA4140	IPF11959	-1.1	-1.2	-1.0	-1.1	unknown function	YGR046w	orf19.4232
CA2979	ADE4	-1.3	-1.3	-1.2	-1.1	amidophosphoribosyltransferase (by homology)	YMR300c	orf19.1233
CA4256	IPF4282	-1.0	-1.2	-1.2	-1.1	unknown function	YIR015w	orf19.544
CA0035	PRC3	-1.1	-1.1	-1.0	-1.1	Carboxypeptidase Y precursor (by homology)	YBR139w	orf19.10011
CA4529	IPF4395	1.3	-1.2	1.1	-1.1	unknown function	YGL010w	orf19.1477
CA2184	IPF6874.3	-1.1	-1.0	-1.0	-1.1	unknown function, 3-prime end		orf19.4251
CA1212	IPF7033	-1.1	1.0	-1.0	-1.1	unknown function	YPR057w	orf19.7777
CA5673	IPF1272	-1.0	-1.1	-1.3	-1.1	unknown function		orf19.7376
CA5425	BDF1	-1.2	1.0	-1.1	-1.1	sporulation protein (by homology)	YLR399c	orf19.978
CA1984	IPF9592	-1.1	-1.1	-1.1	-1.1	unknown function	YFL042043c	orf19.7736
CA2046	IPF8108	-1.1	-1.1	-1.2	-1.1	unknown function	YLR074c	orf19.10451
CA2507	PF18459.3EOC	-1.0	-1.1	-1.0	-1.1	aldehyde dehydrogenase, 3-prime end (by homology)	Missing in array	
CA4131	IPF6886	1.0	-1.0	-1.0	-1.1	unknown function	YKL090w	orf19.11718
CA0953	PF13166.3EOC	-1.1	-1.2	-1.2	-1.1	unknown function, 3-prime end		orf19.1144
CA5900	IPF2379	-1.0	-1.1	-1.2	-1.1	unknown function		orf19.6806
CA4330	IPF2087	1.0	-1.1	1.1	-1.1	unknown function		orf19.4090
CA2074	IPF3733	1.0	1.0	-1.0	-1.1	unknown function		orf19.5287
CA4449	IPF3520	-1.0	-1.1	-1.1	-1.1	unknown function	YPL030w	orf19.6847
CA4138	IPF11954	-1.1	-1.1	-1.1	-1.1	unknown function	YCR054c	orf19.4234
CA5325	IPF2138	1.0	-1.0	-1.1	-1.1	unknown function	YBR137w	orf19.7199
CA3418	IPF12777	-1.0	-1.0	-1.1	-1.1	unknown function		orf19.6137
CA4059	PRD1	-1.3	-1.2	-1.2	-1.1	Proteinase (by homology)	YCL057w	orf19.8064
CA5838	IPF424	-1.1	-1.1	-1.1	-1.1	unknown function	YGR002c	orf19.7492
CA4340	IPF3621	-1.1	-1.1	-1.2	-1.1	unknown function	YJR134c	orf19.6712
CA5518	IPF721.5F	-1.0	-1.0	-1.2	-1.1	unknown function, 5-prime end	YMR259c	orf19.5366
CA3882	IPF7279	-1.0	-1.1	-1.2	-1.1	putative cobalamin-dependent homocysteine S-methyltr	YPL273w	orf19.386
CA2479	CCN1	-1.0	-1.1	-1.0	-1.1	G1 cyclin		orf19.3207
CA3871	IPF8828	-1.0	1.1	-1.1	-1.1	unknown function		orf19.398
CA2593	RRP6	-1.1	-1.2	-1.4	-1.1	involved in 5.8S rRNA processing (by homology)	YOR001w	orf19.58
CA3525	DJP1	1.0	-1.1	-1.2	-1.1	DnaJ-like protein involved in peroxisome biogenesis (by	YIR004w	orf19.8606
CA3733	IPF11897	1.0	-1.0	-1.0	-1.1	unknown function		orf19.11659
CA4901	IPF1457	-1.0	-1.2	-1.2	-1.1	putative transcription activator (by homology)		orf19.6038
CA4962	TRL1	-1.1	-1.1	-1.2	-1.1	tRNA ligase	YJL087c	orf19.6511
CA5731	IPF2870	-1.0	-1.0	-1.0	-1.1	unknown function		orf19.7441
CA3857	CCT8	1.0	-1.1	-1.1	-1.1	component of chaperonin-containing T-complex	YJL008c	orf19.6099
CA5872	IPF333	1.1	-1.1	1.0	-1.1	unknown function		orf19.7539
CA3924	TKL1	1.2	-1.2	-1.0	-1.1	transketolase 1	YPR074c	orf19.5112
CA2289	RBF1.3	-1.1	1.0	-1.1	-1.1	RPG-BOX-BINDING FACTOR, 3-prime end		orf19.13004
CA0008	IPF12110	1.1	-1.3	-1.3	-1.1	1,4-butanediol diacrylate esterase (by homology)		orf19.376
CA2689	IFU2	-1.1	-1.0	-1.2	-1.1	Unknown function	YPL009c	orf19.2582
CA0724	IPF13398	-1.2	-1.2	-1.2	-1.1	protein kinase (by homology)		orf19.7708
CA3354	IPF11281	-1.0	-1.1	-1.0	-1.1	similar to Saccharomyces cerevisiae Gpr1p G-protein c	YDL035c	orf19.9499

CA4806	IPF1155	-1.2	-1.0	-1.1	-1.1	Putative dipeptidase (by homology)	YLL029w	orf19.2095
CA0555	HYS2	-1.0	-1.1	-1.0	-1.1	DNA-directed DNA polymerase delta (by homology)	YJR006w	orf19.3960
CA5471	IPF302	-1.1	-1.1	-1.1	-1.1	short chain dehydrogenase/reductase (by homology)	YKL055c	orf19.3283
CA3092	IPF9821.3F	1.0	-1.1	-1.1	-1.1	unknown function, 3-prime end	YEL064c	orf19.11617
CA3535	IPF13458	-1.1	-1.1	-1.1	-1.1	unknown function	YNL207w	orf19.6369
CA4746	IPF4485	-1.0	-1.2	-1.2	-1.1	unknown function	YER082c	orf19.4835
CA0670	IPF5915	-1.2	1.1	-1.1	-1.1	phosphatidyl synthase (by homology)	YKR070w	orf19.449
CA0632	RPS5	1.2	-1.2	-1.2	-1.1	ribosomal protein S5.e (by homology)	YJR123w	orf19.11812
CA1735	IPF4986	-1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Tfc5p TFIIIB subu	YNL039w	orf19.2528
CA4173	FRS2	-1.1	-1.1	-1.0	-1.1	phenylalanine--tRNA ligase beta chain, cytos	YFL022c	orf19.2960
CA5372	MLH3	1.0	-1.0	-1.0	-1.1	DNA mismatch repair by homology	YPL164c	orf19.7257
CA2488	IPF17706	-1.1	-1.1	-1.1	-1.1	Unknown function		orf19.10708
CA4003	IPF4257	-1.1	-1.1	-1.2	-1.1	unknown function	YDR324c	orf19.1633
CA4941	CRN1.53F	1.0	-1.1	-1.2	-1.1	actin-binding protein, 5-prime end (by homology)	YLR429w	
CA4661	IPF6561	-1.1	-1.1	-1.0	-1.1	unknown function	YOR353c	orf19.4448
CA5051	IPF3709	-1.1	-1.0	-1.1	-1.1	unknown function	YDR101c	orf19.3015
CA0294	IPF16061	-1.0	-1.1	-1.0	-1.1	unknown function	YOR243c	orf19.9322
CA3262	UBR11.3	-1.1	1.0	-1.1	-1.1	ubiquitin-protein ligase, 3-prime end (by homology)	YGR184c	orf19.2695
CA1281	PF10171.EXON	1.1	-1.1	-1.1	-1.1	unknown function, exon 3		orf19.645
CA4089	IPF5009	-1.1	-1.1	-1.1	-1.1	unknown function	YGR245c	orf19.6648
CA5659	SEN54	1.0	-1.0	-1.1	-1.1	tRNA splicing endonuclease alpha subunit(by homology	YPL083c	orf19.7361
CA5204	YML6	-1.0	-1.2	-1.1	-1.1	Ribosomal protein, mitochondrial (by homology)	YML025c	orf19.7019
CA5618	LEU2	-1.2	-1.2	-1.3	-1.1	isopropyl malate dehydrogenase	YCL018w	orf19.7080
CA3462	IPF14959	-1.2	-1.1	-1.3	-1.1	similar to Saccharomyces cerevisiae Trs130p TRAPP s	YMR218c	orf19.1265
CA5403	IPF1542	-1.1	-1.0	-1.1	-1.1	unknown function	YKL002w	orf19.945
CA0658	IPF16505	1.1	-1.1	-1.1	-1.1	Unknown function	YPL112c	orf19.5575
CA0712	IPF13717	1.0	-1.1	-1.2	-1.1	unknown function	YKL082c	orf19.2167
CA5200	RPL10E	-1.2	-1.1	-1.1	-1.1	Ribosomal protein L10, cytosolic (by homology)	YLR340w	orf19.7015
CA0854	IPF8854	-1.3	-1.2	-1.3	-1.1	similar to Saccharomyces cerevisiae Mnn1p alpha-1,3-r	YER001w	orf19.4900
CA2541	IPF9191.3F	-1.2	-1.0	-1.1	-1.1	unknown function, 3-prime end		orf19.3188
CA5787	IPF1136	-1.1	-1.2	-1.2	-1.1	unknown function	YGR128c	orf19.5436
CA3912	IPF3288	1.0	-1.0	-1.0	-1.1	unknown function		orf19.4390
CA4546	SPT5	1.1	1.0	-1.0	-1.1	Transcription elongation protein	YML010w	orf19.1453
CA5775	ATP5	1.0	-1.2	-1.3	-1.1	F1F0-ATPase complex, OSCP subunit (by homology)	YDR298c	orf19.5419
CA5557	IPF1968	-1.2	-1.1	-1.2	-1.1	unknown function	YMR029c	orf19.7321
CA0453	IPF13552	-1.1	-1.1	-1.1	-1.1	putative methyltransferase (by homology)	YDR316w	orf19.8880
CA4075	IPF2555	1.0	-1.1	-1.1	-1.1	unknown function		orf19.6628
CA6088	HPR5	-1.2	-1.1	-1.2	-1.1	ATP-dependent DNA Helicase (by homology)	YJL092w	orf19.5970
CA0939	DBP6	-1.0	-1.1	-1.2	-1.1	RNA helicase required for 60S ribosomal subunit assem	YNR038w	orf19.3704
CA3678	IPF8392	-1.1	-1.2	-1.4	-1.1	unknown function	YLR080w	orf19.731
CA6038	LTV1	1.0	-1.1	-1.1	-1.1	low-temperature viability protein (by homology)	YKL143w	orf19.7650
CA4150	RPT3	-1.3	-1.0	-1.0	-1.1	26S proteasome regulatory subunit	YDR394w	orf19.5793
CA4119	BEM3	-1.0	-1.1	-1.0	-1.1	GTPase-activating protein for Cdc42p and Rho1p (by h	YPL115c	orf19.2771
CA1491	IPF166	-1.0	-1.1	-1.1	-1.1	unknown function	YCR017c	orf19.3225
CA0653	MET6	1.1	-1.3	-1.3	-1.1	BY HOMOLOGY TO S.CEREV.: 5-methyltetrahydropte	YER091c	orf19.10083
CA0052	IPF19567	1.0	-1.2	-1.1	-1.1	Unknown function	YHR085w	orf19.379
CA1176	CHS5	-1.0	-1.1	-1.3	-1.1	Chitin biosynthesis protein	YLR330w	orf19.807
CA4498	IPF11315	-1.1	-1.1	-1.3	-1.1	unknown function	YNL132w	orf19.8143
CA3996	IPF10440	-1.0	-1.2	1.1	-1.1	unknown function	YGR101w	orf19.1643

CA2126	IPF4896	1.0	-1.0	-1.1	-1.1	unknown function	YGR257c	orf19.417
CA5798	IPF4181	1.1	-1.1	-1.4	-1.1	putative permease (by homology)		orf19.5447
CA5738	LYS9	-1.0	-1.5	-1.3	-1.1	Lysine biosynthesis (by homology)	YNR050c	orf19.7448
CA3626	CYR1.5F	-1.1	1.1	-1.5	-1.1	adenylate cyclase, 5-prime end		orf19.12615
CA1796	IPF11259	-1.0	-1.0	1.0	-1.1	unknown function	YIL101c	orf19.5210
CA1037	MNS1	-1.1	-1.1	1.0	-1.1	Alpha1,2-mannosidase (by homology)	YJR131w	orf19.8638
CA0241	IPF15630	-1.1	-1.1	-1.2	-1.1	unknown function	YPL207w	orf19.3470
CA2300	PMA1	1.6	1.4	1.2	-1.1	plasma membrane H+-transporting ATPase 1	YGL008c	orf19.5383
CA5416	IPF1576	-1.0	-1.0	-1.0	-1.1	unknown function	YLR405w	orf19.966
CA5098	IPF1380	1.1	-1.0	-1.1	-1.1	delta3-cis-delta2-trans-enoyl-CoA isomerase (by homology)		orf19.6443
CA2911	MET7	-1.1	-1.1	-1.1	-1.1	folylpolyglutamate synthetase [Candida albicans]	YOR241w	orf19.4516
CA2515	IPF19759	1.0	-1.1	-1.1	-1.1	Unknown Function	YGL133w	orf19.5510
CA0229	IPF8147	-1.0	-1.1	-1.0	-1.1	unknown function		orf19.13580
CA0299	IPF3765	-1.1	-1.3	-1.1	-1.1	unknown function	YGR106c	orf19.1597
CA5227	IPF3087	1.1	-1.3	-1.2	-1.1	unknown function	YIR017c	orf19.7046
CA1697	IPF16758	-1.1	-1.2	-1.2	-1.1	unknown function		orf19.5043
CA1712	ABC1	-1.1	1.0	1.1	-1.1	ubiquinol--cytochrome-c reductase(by homology)	YGL119w	orf19.10842
CA3822	CUS2	-1.0	-1.0	-1.1	-1.1	cold sensitive U2 snRNA Suppressor(by homology)	YNL286w	orf19.5767
CA0260	IPF13683	1.1	-1.2	-1.2	-1.1	unknown function		orf19.2547
CA3953	IPF6714	1.0	-1.0	-1.0	-1.1			orf19.1412
CA3451	IPF7316	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.10488
CA1182	IPF19724	-1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Tbf1ptelomere rep	YPL128c	orf19.801
CA1471	ALS2.3FEOC	1.0	1.0	1.0	-1.1	agglutinin-like protein, 3-prime end	Missing in array	orf19.1098
CA0184	IPF19142	-1.3	-1.3	-1.4	-1.1	unknown function		orf19.11467
CA3508	RSA2	-1.1	-1.1	-1.2	-1.1	Involved in ribosome biogenesis (by homology)	YMR131c	orf19.6355
CA6109	IPF89.3	1.1	-1.1	-1.3	-1.1	unknown function, 3-prime end	YLR150w	
CA0174	PF11182.3EOC	-1.2	-1.0	-1.3	-1.1	unknown function, 3-prime end	YLR106c	
CA2273	BIO2	-1.1	-1.1	-1.1	-1.1	biotin synthetase (by homology)	YGR286c	orf19.2593
CA5956	VAN1	-1.2	-1.1	-1.1	-1.1	Vanadate resistance protein	YML115c	orf19.6738
CA1955	IPF3897.3F	-1.1	-1.1	-1.2	-1.1	unknown function, 3-prime end		orf19.765
CA0693	PF12606.5EOC	-1.1	-1.1	-1.2	-1.1	unknown function, 5-prime end	YNL123w	orf19.3288
CA0272	DPB11	-1.1	-1.3	-1.4	-1.1	DNA polymerase II complex (by homology)	YJL090c	orf19.1434
CA5863	IPF370	-1.0	-1.1	-1.0	-1.1	unknown function		orf19.7521
CA4914	IPF1428	-1.1	-1.2	-1.1	-1.1	Similar to ubiquitination protein Bul1p (by homology)		orf19.6054
CA0089	MRPL3	-1.0	-1.2	-1.0	-1.1	ribosomal protein of the large subunit, mitochondrial (by	YMR024w	orf19.5064
CA3722	PHO13	1.0	-1.1	-1.0	-1.1	4-nitrophenylphosphatase (by homology)		orf19.4172
CA3716	IPF6203	-1.1	-1.1	1.0	-1.1	unknown function		orf19.11642
CA0027	RCL1	-1.1	-1.1	-1.1	-1.1	RNA 3 -terminal phosphate cyclase (by homology)	YOL010w	orf19.1886
CA5756	IPF1065	1.0	-1.0	-1.0	-1.1	unknown function		orf19.5392
CA1623	STE7	-1.0	-1.0	-1.0	-1.1	MAP Kinase Kinase	YDL159w	orf19.469
CA4348	IPF3638	-1.1	-1.2	-1.3	-1.1	unknown function		orf19.6723
CA5475	IPF8532	-1.0	-1.0	-1.1	-1.1	unknown function	Missing in array	orf19.5303
CA0393	IPF12758.3F	1.1	-1.1	1.0	-1.1	unknown function, 3-prime end		
CA4523	GCD1	-1.2	-1.2	-1.3	-1.1	translation initiation factor eIF2bgamma (by homology)	YOR260w	orf19.481
CA0715	DBP9	-1.1	-1.2	-1.2	-1.1	dead box helicase	YLR276c	orf19.3393
CA1452	REV1	-1.1	1.0	-1.1	-1.1	DNA repair protein (by homology)	YOR346w	orf19.4412
CA0443	SPB1	1.1	-1.2	-1.2	-1.1	Putative methyltransferase by homology	YCL054w	orf19.7727
CA2990	IPF5092	-1.1	-1.1	-1.2	-1.1	unknown function	YOR296w	orf19.6012
CA5377	IPF5234	-1.0	-1.0	-1.0	-1.1	X-Pro dipeptidase (by homology)	YFR006w	orf19.7263

CA0672	GRP6	-1.1	-1.1	-1.1	-1.1	Putative reductase (by homology)		orf19.3151
CA2313	ERF3	-1.0	-1.0	-1.1	-1.1	translation release factor 3	YDR172w	orf19.1378
CA2627	IPF10916	1.1	-1.0	1.0	-1.1	unknown function	YAL008w	orf19.4763
CA1175	ARG81	-1.1	-1.1	-1.2	-1.1	transcription factor possibly involved in arginine metabo	YML099c	orf19.4766
CA0528	ANP1	-1.2	-1.1	-1.4	-1.1	Golgi mannosyltransferase (by homology)	YEL036c	orf19.3622
CA5291	LOS1	-1.4	-1.3	-1.3	-1.1	pre-tRNA splicing protein (by homology)	YKL205w	orf19.7153
CA1560	MET18	-1.0	-1.2	-1.2	-1.1	Involved in NER repair and RNA polymerase II transcrip	YIL128w	orf19.1706
CA1095	SMC1	-1.2	-1.1	-1.3	-1.1	Chromosomal ATPase family member (by homology)	YFL008w	orf19.4367
CA1921	IPF7475	1.2	-1.0	1.2	-1.1	similar to Saccharomyces cerevisiae Chs7p involved in	YHR142w	orf19.2444
CA2733	PRP18	-1.0	-1.1	-1.2	-1.1	U5 snRNA-associated protein (by homology)	YGR006w	orf19.2112
CA5412	IPF1566	-1.1	-1.1	-1.1	-1.1	unknown function	YLR087c	orf19.956
CA3419	IPF12778	1.1	-1.3	-1.3	-1.1	ribosomal protein, mitochondrial (by homology)	YLR439w	orf19.6136
CA4389	RPT5	-1.0	-1.0	-1.1	-1.1	26S proteasome regulatory subunit (by homology)	YOR117w	orf19.3123
CA0211	IPF4326	1.0	1.0	1.0	-1.1	unknown function		orf19.12970
CA5033	DNM1	-1.3	-1.2	-1.4	-1.1	Dynamin-related protein (by homology)	YLL001w	orf19.6987
CA0979	IPF19713	-1.1	-1.3	-1.3	-1.1	unknown function		orf19.3601
CA0318	FOL2	-1.0	-1.0	-1.1	-1.1	GTP cyclohydrolase (by homology)	YGR267c	orf19.3957
CA0416	IPF17492	1.0	-1.1	-1.1	-1.1	unknown function		orf19.1225
CA4718	IPF8661	-1.0	-1.2	-1.3	-1.1	unknown function	YOR056c	orf19.6955
CA0878	CNH1.3F	-1.0	1.2	-1.2	-1.1	Na+/H+ antiporter, 3-prime end (by homology)		orf19.8001
CA2194	RGR1	-1.3	-1.1	-1.3	-1.1	DNA-directed RNA polymerase II (by homology)	YLR071c	orf19.11825
CA3495	RIB7	-1.4	-1.1	-1.3	-1.1	HTP reductase (By homology)	YBR153w	orf19.6341
CA4176	F4425.REPEA	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.2957
CA4467	IPF9833	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.6864
CA4237	IPF6375	-1.1	-1.2	-1.1	-1.1	unknown function		orf19.520
CA3131	IPF8910	1.1	-1.0	-1.1	-1.1	unknown function	YNR015w	orf19.1362
CA1498	IPF12371	1.1	1.0	1.0	-1.1	extracellular alpha-1,4-glucan glucosidase (by homology)		orf19.3643
CA0488	SEC59	-1.1	-1.1	1.0	-1.1	Dolichol kinase (by homology)	YMR013c	orf19.261
CA2110	IPF13749.3F	-1.2	-1.3	-1.3	-1.1	unknown function, 3-prime end		orf19.3689
CA1671	IPF11391	-1.0	-1.1	-1.2	-1.1	unknown function		
CA4373	IPF5287	-1.1	-1.1	-1.1	-1.1	signal transduction protein (by homology)	YMR032w	orf19.5664
CA1140	IPF17322.3F	-1.1	-1.1	-1.3	-1.1	unknown function, 3-prime end		orf19.4068
CA2959	IPF8591	1.0	-1.0	-1.0	-1.1	putative arginase family member (by homolgy)		orf19.5862
CA5516	IPF726	1.1	1.0	-1.1	-1.1	rna binding protein (by homology)	YBR065c	orf19.5364
CA3562	IPF7823	-1.2	-1.2	-1.3	-1.1	similar to Saccharomyces cerevisiae Rvb1p RuvB-like p	YDR190c	orf19.3129
CA3256	IPF4730	-1.0	-1.0	-1.1	-1.1	unknown Function	YOR112w	orf19.11229
CA4468	TOR2.53EOC	1.1	1.3	-1.2	-1.1	phosphatidylinositol 3-kinase, internal fragment (by homology)		orf19.1905
CA1442	ERG20	-1.0	-1.1	-1.2	-1.1	farnesyl-pyrophosphate synthetase	YJL167w	orf19.4491
CA2356	IPF12282	-1.2	-1.1	-1.3	-1.1	unknown function		orf19.4893
CA4793	IPF3375	-1.0	-1.0	-1.1	-1.1	similar to Saccharomyces cerevisiae Rer2p cis-prenyltra	YBR002c	orf19.4028
CA0924	IFD5	-1.1	-1.1	-1.2	-1.1	Putative aryl-alcohol dehydrogenase (by homology)		orf19.1048
CA0154	CPH1	1.0	1.1	-1.1	-1.1	Transcription factor	YHR084w	orf19.4433
CA0378	IPF3178	-1.1	-1.2	-1.3	-1.1	Unknown function	YFL023w	orf19.3170
CA4595	GCN2	-1.2	-1.1	-1.1	-1.1	Ser/thr protein kinase (by homology)	YDR283c	orf19.6913
CA2326	NUBM	-1.3	-1.2	-1.1	-1.1	nucleotide-binding respiratory complex I subunit (by homology)		orf19.11971
CA5273	NUP49	-1.1	-1.1	-1.2	-1.1	nuclear pore protein (by homology)	YGL172w	orf19.4987
CA1077	IPF13694	-1.3	-1.2	-1.4	-1.1	unknown function		orf19.2238
CA5556	LIP7	-1.1	-1.2	-1.1	-1.1	Secretory lipase		orf19.7320
CA1303	TFB4	-1.1	-1.1	-1.1	-1.1	component of RNA polymerase transcription initiation TI	YPR056w	orf19.4194

CA4196	DST1	1.0	-1.0	-1.0	-1.1	RNA polymerase II elongation factor (by homology)	YGL043w	orf19.4537
CA0933	ATM1	-1.1	-1.0	-1.2	-1.1	ATP-binding cassette transporter (by homology)	YMR301c	orf19.8678
CA2573	SUI2	1.1	-1.1	-1.2	-1.1	translation initiation factor eIF2, alpha chain (by homolo	YJR007w	orf19.6213
CA1770	IPF12457	1.1	-1.2	1.0	-1.1	unknown function	YGL111w	orf19.2185
CA2773	MGM1	-1.1	-1.2	-1.1	-1.1	GTPase	YOR211c	orf19.2690
CA2436	IPF5500	-1.1	-1.1	-1.1	-1.1	unknown function	YKR044w	orf19.2200
CA0173	IPF6913	1.0	-1.1	-1.1	-1.1	unknown function		orf19.11273
CA1840	IFP3	-1.1	-1.1	-1.1	-1.1	Unknown Function		orf19.4707
CA4323	IPF2096	-1.1	-1.1	-1.2	-1.1	putative acyltransferase (by homology)	YPR140w	orf19.4096
CA1784	ARO7	-1.0	-1.2	-1.1	-1.1	chorismate mutase (by homology)	YPR060c	orf19.1170
CA1839	IPF4435	-1.2	-1.2	-1.1	-1.1	unknown function	YGR196c	orf19.4711
CA4679	IPF3674	-1.1	-1.1	-1.2	-1.1	unknown function		orf19.893
CA5723	APN1	-1.1	-1.1	-1.2	-1.1	AP endonuclease, exonuclease III homologue (by homo	YKL114c	orf19.7428
CA5357	RSC8	-1.0	-1.2	-1.2	-1.1	chromatin remodeling complex subunit (by homology)	YFR037c	orf19.7234
CA5800	IPF4175	1.1	-1.2	-1.1	-1.1	mitochondrial respiratory function (by homology)	YBR026c	orf19.5450
CA5744	IPF2898	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.7453
CA0355	IPF2535	-1.2	1.0	-1.3	-1.1	unknown function		orf19.13951
CA6134	MAK21	-1.1	-1.2	-1.2	-1.1	Ribosome biogenesis protein (by homology)	YDR060w	orf19.5912
CA2032	IPF13112	-1.1	-1.1	-1.2	-1.1	unknown function		orf19.3466
CA0702	IPF11812	-1.1	-1.2	-1.3	-1.1	unknown function	YER008c	orf19.10430
CA4971	IPF4697	-1.0	1.1	-1.6	-1.1	similar to Saccharomyces cerevisiae Scp160p required	YJL080c	orf19.5281
CA1384	IPF8423	-1.0	-1.1	-1.3	-1.1	similar to Saccharomyces cerevisiae Dhs1p exonucleas	YOR033c	orf19.926
CA4413	MSH2	-1.0	1.0	-1.1	-1.1	DNA mismatch repair protein (by homology)	YOL090w	orf19.3093
CA3663	IPF11432	-1.0	-1.1	-1.1	-1.1	unknown function	YJR072c	orf19.6463
CA2748	IPF11466	-1.0	-1.0	-1.1	-1.1	unknown function	YHR156c	orf19.2368
CA4463	PIS1	1.2	-1.1	-1.0	-1.1	CDP diacylglycerol--inositol 3-phosphatidyltransferase (	YPR113w	orf19.6860
CA1655	CCC2	-1.1	-1.2	-1.2	-1.1	putative copper-transporting ATPase (by homology)	YDR270w	orf19.4328
CA3274	IPF12227.3F	-1.3	-1.2	-1.3	-1.1	unknown function, 3-prime end		orf19.6308
CA5397	IPF9663	-1.2	-1.0	-1.2	-1.1	similar to Saccharomyces cerevisiae Bud2p GTPase-ac	YKL092c	orf19.940
CA0501	IPF16501	-1.0	-1.0	1.1	-1.1	unknown function		orf19.12259
CA4364	PF5268.EXON	1.0	1.0	1.0	-1.1	choline monooxygenase, exon 2 (by homology)		orf19.5655
CA4072	IPF2560	1.0	-1.1	-1.1	-1.1	unknown function	YNL246w	orf19.6625
CA3933	IPF18281	-1.0	-1.2	-1.3	-1.1	similar to Saccharomyces cerevisiae Pex12p peroxisom	YMR026c	orf19.9560
CA2012	SEC10	-1.1	-1.1	-1.0	-1.1	Required for exocytosis (by homology)	YLR166c	orf19.3086
CA2243	IPF7414	-1.0	-1.4	-1.4	-1.1	putative transcription factor (by homology)		orf19.4670
CA3832	IPF8193	-1.1	-1.1	-1.1	-1.1	unknown function	YLR151c	orf19.6591
CA0885	IPF12381	1.2	-1.3	-1.2	-1.1	unknown function	YIR001c	orf19.1389
CA2298	IPF8224	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.5380
CA2176	CDC54	-1.1	-1.0	-1.1	-1.1	cell division control protein (by homology)	YPR019w	orf19.11245
CA1987	IPF14895	1.3	-1.1	-1.2	-1.1	unknown function	YMR002w	orf19.7739
CA1198	IPF10399	1.1	-1.2	-1.1	-1.1	unknown function	YNL177c	orf19.10875
CA4447	IPF3523	-1.0	-1.1	-1.1	-1.1	unknown function		orf19.6845
CA4613	IPF7950	1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Rrp40p involved ir	YOL142w	orf19.3304
CA0554	HAS1	-1.2	-1.0	-1.1	-1.1	ATP-DEPENDENT RNA HELICASE (by homology)	YMR290c	orf19.11444
CA4382	IPF8576	-1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Ris1p DNA helicas	YOR191w	orf19.5675
CA4496	IPF4062	-1.4	-1.1	-1.2	-1.1	unknown function	YDR333c	orf19.9420
CA1918	IPF7479.5F	-1.1	-1.1	-1.2	-1.1	unknown function, 5-prime end		orf19.2441
1615.2		1.0	-1.0	-1.1	-1.1			
CA0787	IPF7472	-1.2	-1.4	-1.2	-1.1	unknown function	YJL100w	orf19.2447

CA2331	MOT1	-1.1	1.1	-1.3	-1.1	transcriptional accessory protein	YPL082c	orf19.4502
CA2481	MRPL36	-1.0	-1.2	-1.2	-1.1	ribosomal protein YmL36 precursor, mitochondrial (by h	YBR122c	orf19.3205
CA1548	IPF8746	-1.1	-1.1	-1.3	-1.1	putative alpha-1,3-mannosyltransferase (by homology)		orf19.4279
CA1201	IPF19906	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.4869
CA1917	IPF7479.3F	-1.2	-1.2	-1.3	-1.1	unknown function, 3-prime end		orf19.2440
CA4418	ERG5	1.1	-1.3	-1.2	-1.1	C-22 sterol desaturase by homology	YMR015c	orf19.5178
CA4717	IPF8663	-1.1	-1.1	-1.3	-1.1	Unknown function	YJL083w	orf19.6953
CA4469	TOR2.3F	1.1	1.1	-1.2	-1.1	phosphatidylinositol 3-kinase, 3-prime end (by homolog	YKL203c	orf19.1903
CA5934	IPF2802	-1.1	-1.2	-1.2	-1.1	unknown function	YHL029c	orf19.6769
CA4769	IPF9384	-1.1	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Mss2p serine/thre	YDL107w	orf19.4001
19812.1		1.1	-1.3	-1.4	-1.1			
CA3537	PSU1	-1.1	-1.1	-1.3	-1.1	suppressor of petit mutations by homology	YNL118c	orf19.6373
CA3407	IPF9406	-1.1	-1.1	-1.1	-1.1	unknown function		orf19.13571
CA1792	IPF13966	-1.1	-1.2	-1.1	-1.1	unknown function	YIL104c	orf19.5206
CA3234	MAS2	-1.1	-1.0	-1.1	-1.1	processing peptidase, catalytic 53kDa (alpha) subunit, r	YHR024c	orf19.6295
CA1524	SUR1	1.0	-1.0	-1.0	-1.1	Suppressor of ROK1	YJL056c	orf19.3794
CA4027	IPF7174	-1.1	-1.1	-1.0	-1.1	unknown function		orf19.3436
CA3190	IPF11603	-1.2	-1.0	-1.1	-1.1	unknown function	YPR004c	orf19.2150
CA2699	RLF2	1.0	-1.0	-1.0	-1.1	chromatin assembly complex, subunit p90 (by homolog	YPR018w	orf19.10253
CA3893	FUN11	-1.3	-1.1	-1.2	-1.1	putative GTP-binding protein (by homology)	YAL036c	orf19.5083
CA0120	IPF19593	-1.1	-1.2	-1.2	-1.1	similar to Saccharomyces cerevisiae Ulp1p Smt3-proce	YPL020c	
CA5050	BMH2	-1.3	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisae Bmh2p suppressor	YDR099w	orf19.3014
CA1666	SRP40	-1.2	-1.3	-1.2	-1.1	RNA I and II supressor (by homology)	YKR092c	orf19.2859
CA5606	STL2.3F	1.0	-1.1	-1.2	-1.1	sugar transporter, 3-prime end (by homology)		
CA2238	IPF10032.5F	-1.1	-1.1	-1.1	-1.1	unknown function, 5-prime end	YJR011c	orf19.3916
CA2460	LYS1.3EOC	-1.0	-1.1	-1.0	-1.1	Saccharopine dehydrogenase, 3-prime end		
CA0819	VPS1	-1.2	-1.1	-1.2	-1.1	member of the dynamin family of GTPases (by homolog	YKR001c	orf19.1949
CA4860	IPF19804	-1.0	-1.0	-1.2	-1.1	unknown Function		orf19.3835
CA1667	SSL2	-1.2	-1.1	-1.3	-1.1	by homology to S. cerevisiae: DNA helicase	YIL143c	orf19.2857
CA3648	MSF1	-1.1	-1.1	-1.1	-1.1	phenylalanine--tRNA ligase	YPR047w	orf19.2039
CA3109	IPF11829	1.2	-1.0	-1.1	-1.1	unknown function	YPL135w	orf19.6548
CA1912	SKY1	-1.1	-1.2	-1.1	-1.1	SRPK1 like protein kinase (by homology)	YMR216c	orf19.2436
CA0036	IPF19377	-1.2	-1.1	1.0	-1.1	unknown function		orf19.3336
CA3596	IPF6085	-1.1	-1.0	-1.1	-1.1	unknown function		orf19.4924
CA3677	SOU3	-1.1	-1.1	-1.2	-1.1	putative sorbitol utilization protein (by homology)		orf19.732
CA0673	AMO2	-1.1	-1.2	1.2	-1.1	amine oxidase (by homology)		orf19.3152
CA4455	IPF8454	1.0	-1.2	-1.4	-1.1	unknown function		orf19.6853
CA5415	SMC4	-1.0	-1.1	-1.3	-1.1	Stable Maintenance of Chromosomes (by homology)	YLR086w	orf19.964
CA5094	IPF1387	-1.0	-1.0	-1.1	-1.1	unknown function		orf19.6448
CA5104	IPF1364	1.4	-1.2	-1.2	-1.1	unknown function	YGR243w	orf19.6435
CA5490	KIN3	-1.1	-1.2	-1.2	-1.1	G2-specific serine/threonine protein kinase (by homolog	YAR018c	orf19.5325
CA2981	CSE1.5F	-1.4	-1.2	-1.3	-1.1	Importin-beta-like protein, 5-prime end (by homology)	YGL238w	orf19.1231
CA2848	PF10785.EXON	-1.1	-1.1	-1.2	-1.1	unknown function, exon 2		orf19.5733
CA4145	IPF3130	1.0	1.1	1.0	-1.1	unknown function		orf19.4227
CA4178	IPF4421	1.0	-1.1	-1.0	-1.1	unknown function		orf19.2954
CA3081	EFT3	-1.1	1.1	-1.1	-1.1	translation elongation factor 3	YNL014w	orf19.11629
CA3333	CDC48	-1.1	1.1	-1.1	-1.1	microsomal ATPase (by homology)	YDL126c	orf19.9876
CA1871	PF16981.EXON	-1.2	-1.2	-1.3	-1.1	unknown function, exon 1	YMR140w	orf19.9995
CA2449	ENP1	1.0	-1.1	-1.1	-1.1	Essential nuclear protein (by homology)	YBR247c	orf19.5507

CA3094	IPF11548	-1.3	-1.2	-1.1	-1.1	serine/threonine protein kinase (by homology)	YCR008w	orf19.11335
CA5925	MET8	-1.1	-1.3	-1.2	-1.1	Siroheme synthase (by homology)	YBR213w	orf19.6780
CA4895	IPF18161	-1.1	-1.3	-1.1	-1.1	unknown function	YDR152w	orf19.6587
CA0418	IPF9051.5EOC	-1.2	-1.1	-1.1	-1.1	unknown function, 5-prime end		orf19.2227
CA3906	IPF20149	-1.0	-1.2	-1.2	-1.1	unknown function	YKR016w	orf19.11874
CA3446	IPF7324	-1.1	-1.1	-1.2	-1.1	unknown function	YKL195w	orf19.2977
CA0287	IPF14615	-1.0	1.0	1.0	-1.1	unknown function		orf19.6080
CA4842	MTD1	1.1	-1.3	-1.2	-1.1	methylenetetrahydrofolate dehydrogenase	YKR080w	orf19.3810
CA3894	YIF2	-1.0	1.1	-1.0	-1.1	general translation factor eIF2 homolog (by homology)	YAL035w	orf19.5081
CA3301	IPF13782	-1.0	-1.1	-1.2	-1.1	unknown function	YGL029w	orf19.2314
CA0199	KAP104	-1.1	-1.1	-1.0	-1.1	karyopherin-beta protein (by homology)	YBR017c	orf19.3556
CA6125	IPF138	-1.2	-1.1	-1.0	-1.1	unknown function	YDL237w	orf19.5925
CA2334	ADH3	1.1	-1.1	-1.0	-1.1	probable alcohol dehydrogenase (by homology)		orf19.11981
CA5474	PF16944.3EOC	1.0	-1.4	-1.2	-1.1	unknown function, 3-prime end	YMR014w	orf19.3287
CA3246	IPF15830	-1.2	-1.2	-1.0	-1.1	unknown function	YML041c	orf19.4677
CA0180	SPT20	1.0	-1.0	-1.0	-1.1	transcription factor, member of the histone acetyltransfe	YOL148c	orf19.422
CA2400	SUP45	-1.3	-1.2	-1.0	-1.1	Translational release factor (by homology)	YBR143c	orf19.3541
CA3244	AGP2	-1.2	-1.1	-1.2	-1.1	amino-acid permease (by homology)	YBR132c	orf19.4679
CA1124	UBP12	-1.1	-1.1	-1.3	-1.1	ubiquitin C-terminal hydrolase (by homology)	YJL197w	orf19.6260
CA2099	IPF11484	1.0	-1.1	-1.2	-1.1	unknown function	YKL099c	orf19.2386
CA4429	DBF4	1.0	-1.1	-1.1	-1.1	regulatory subunit for Cdc7 by homology	YDR052c	orf19.5166
CA4975	IPF4706	1.0	-1.0	-1.1	-1.1	unknown Function	YGR072w	orf19.5277
CA0956	IPF14914	-1.1	-1.1	-1.2	-1.1	putative ankyrin (by homology)	YIL112w	orf19.12191
CA3866	IPF4606	-1.3	-1.3	-1.2	-1.1	unknown Function	YML048w	orf19.6082
CA1406	DOT4	1.1	-1.2	-1.2	-1.1	derepression of telomeric silencing (by homology)	YNL186w	orf19.3370
CA3968	IPF9378	-1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Soh1p suppressor	YGL127c	orf19.1429
CA2634	ZWF1	-1.6	-1.2	-1.2	-1.1	glucose-6-phosphate dehydrogenase (by homology)	YNL241c	orf19.12218
CA4517	MEX67	-1.2	-1.1	-1.3	-1.1	poly(A)+RNA binding protein involved in nuclear mRNA	YPL169c	orf19.488
CA4067	IPF5924	-1.1	-1.1	-1.1	-1.1	unknown function	YNR040w	orf19.445
CA0891	IPF11764	1.0	-1.2	-1.3	-1.1	unknown function	YGL159w	orf19.4735
CA4143	DDP1	-1.1	-1.3	-1.3	-1.1	diadenosine and diphosphoinositol polyphosphate phos	YOR163w	orf19.4229
CA5223	IPF3080	-1.2	-1.2	1.0	-1.1	unknown function (by homology)		orf19.7042
CA1197	IFG1	-1.0	-1.0	-1.0	-1.1	probable d-amino acid oxidase (by homology)		orf19.10873
CA4841	IPF10355	1.2	1.0	1.0	-1.1	unknown function	YKR099w	orf19.3809
CA0196	IPF15799	-1.1	-1.2	-1.1	-1.1	unknown function		orf19.1651
CA5338	IPF889	-1.0	1.1	1.0	-1.1	ATP-dependent RNA helicase (by homology)	YDR291w	orf19.7213
CA2047	RPL10	1.0	-1.3	-1.4	-1.1	Ribosomal protein L10 (by homology)	YLR075w	orf19.10452
CA4648	IPF9864	-1.3	-1.0	-1.1	-1.1	similar to Saccharomyces cerevisiae Stu1p mitotic spin	YBL034c	orf19.11914
CA4574	IPF9430	-1.1	-1.3	-1.2	-1.1	similar to Saccharomyces cerevisiae Spo7p meiotic pro	YAL009w	orf19.6885
CA0143	IPF19195.5F	-1.1	-1.0	-1.1	-1.1	putative amino acid or GABA permease, 5-prime end (by homology)		orf19.153
CA2103	ISM1	-1.1	-1.1	-1.3	-1.1	isoleucyl-tRNA synthetase (by homology)	YPL040c	orf19.9918
CA3331	POL.3	-1.1	1.0	-1.1	-1.1	Pol part of pCal retrotransposon		
CA2125	IPF4893	-1.1	1.0	-1.1	-1.1	unknown function	YHR186c	orf19.418
CA1402	ECE1	1.0	-1.1	-1.2	-1.1	Cell Elongation Protein		orf19.3374
CA0813	MPP10	1.0	-1.3	-1.3	-1.1	component of the U3 small nucleolar ribonucleoprotein	YJR002w	orf19.1915
CA0886	IPF12382	1.2	1.0	-1.0	-1.1	unknown function	YER002w	orf19.1388
CA3650	IPF4134	-1.3	1.0	-1.3	-1.1	unknown function	YKR008w	orf19.2041
CA5340	IPF883	1.0	-1.1	-1.1	-1.1	unknown function	YJL109c	orf19.7215
CA1064	PWP1	-1.0	-1.2	-1.3	-1.1	beta-transducin superfamily (by homology)	YLR196w	orf19.12110

CA1700	RAM1.5F	-1.1	-1.1	-1.2	-1.1	protein farnesyltransferase, beta subunit, 5-prime end (b	YDL090c	orf19.5046
CA5402	IFG3.3	-1.0	-1.3	-1.2	-1.1	probable d-amino acid oxidase, 3-prime end (by homology)		orf19.944
CA0916	LYS2	1.1	1.1	-1.0	-1.1	L-aminoadipate-semialdehyde dehydrogenase, large su	YBR115c	orf19.2970
CA1041	BMS1	-1.2	-1.3	-1.3	-1.1	probable membrane protein involved in bud site selectio	YPL217c	orf19.2504
CA5709	IPF2653	-1.3	-1.0	-1.5	-1.1	unknown function	YDR430c	orf19.7410
CA3977	IPF20153	1.1	-1.3	-1.2	-1.1	unknown function		orf19.1549
CA1009	IPF14084	1.0	-1.3	-1.2	-1.1	unknown function	YGR117c	orf19.6255
CA1155	JA2	-1.1	-1.3	-1.2	-1.1	ATP-dependent RNA helicases-like (by homology)	YKL078w	orf19.107
CA5499	RPS4A	1.0	-1.2	-1.3	-1.1	ribosomal protein S4	YJR145c	orf19.5341
CA1779	IPF14510	-1.0	-1.2	-1.1	-1.1	unknown function	YGL219c	orf19.1826
CA1950	IPF14019	1.0	-1.3	-1.3	-1.1	unknown function	YPR169w	orf19.12208
CA2278	IPF10806	-1.1	-1.2	-1.1	-1.1	unknown function	YBR204c	orf19.782
CA2401	LEM3	-1.1	-1.1	-1.2	-1.1	cell division cycle mutant (by homology)	YNL323w	orf19.3542
CA1370	TCI1	-1.2	-1.2	-1.2	-1.1	protein phosphatase Two C-Interacting protein (by homo	YDR161w	orf19.4963
CA0978	IPF16222	1.0	1.0	1.0	-1.1	unknown function	YDL233w	orf19.3603
CA5388	PET9	1.1	-1.1	1.0	-1.1	ADP/ATP carrier protein (by homology)	YBL030c	orf19.8545
CA1863	MRPL35	-1.2	-1.3	-1.4	-1.1	Ribosomal protein of the large subunit, mitochondrial (by	YDR322w	orf19.863
CA1814	TRA1.5EOC	-1.2	-1.0	-1.3	-1.1	ATM/Mec1/TOR1+2-related, 5-prime end (by homology)		orf19.139
CA4335	GAL83	-1.0	1.1	-1.1	-1.1	Glucose repression protein (by homology)	YER027c	orf19.4084
CA0201	IPF15116	-1.3	-1.4	-1.3	-1.1	Unknown function	YKL077w	orf19.9108
CA5922	MRS6	-1.2	-1.3	-1.5	-1.1	geranylgeranyltransferase regulatory subunit	YOR370c	orf19.6783
CA4894	IPF1617	-1.1	-1.2	-1.0	-1.1	unknown function		orf19.6586
CA3290	IPF5734	-1.4	1.1	-1.1	-1.1	unknown function	YNL212w	orf19.6324
CA3111	RPL5	-1.1	-1.1	-1.1	-1.1	ribosomal protein (by homology)	YPL131w	orf19.6541
CA4920	GCN20	-1.2	-1.1	-1.1	-1.1	Positive effector of Gcn2p (by homology)	YFR009w	orf19.6060
CA1647	IPF16663	-1.1	-1.1	-1.1	-1.1	unknown function	YKR020w	orf19.5568
CA6126	IPF143	-1.1	-1.1	-1.0	-1.1	unknown function		orf19.5924
CA4775	IPF3342	-1.1	-1.0	1.0	-1.1	Unknown function	YDR198c	orf19.4007
CA4599	IPF2200	-1.2	-1.1	-1.3	-1.1	Unknown function		orf19.6918
CA2683	IFU4	-1.2	-1.0	-1.2	-1.1	Unknown function	YFL034w	orf19.2574
CA5865	MKC1	-1.1	-1.2	-1.2	-1.1	ser/thr protein kinase of MAP kinase family	YHR030c	orf19.7523
CA5396	NAM7	-1.2	-1.1	-1.1	-1.1	nonsense-mediated mRNA decay protein (by homology	YMR080c	orf19.939
CA4114	IPF7704	-1.1	-1.2	-1.1	-1.1	unknown function		orf19.679
CA1969	IPF18579.3F	-1.0	1.0	-1.0	-1.2	unknown function, 3-prime end	YOL078w	orf19.5221
CA3402	IPF8651	-1.0	1.0	-1.0	-1.2	unknown function	YGR272c	orf19.3978
CA1970	IPF18579.5F	-1.1	1.0	-1.3	-1.2	unknown function, 5-prime end		orf19.5222
CA5290	IPF1943	-1.1	-1.1	-1.0	-1.2	similar to Aspergillus (Emericella) nidulans cysteine synthase (by homology)		orf19.7152
CA3796	SGT2	-1.2	-1.1	-1.3	-1.2	small glutamine-rich tetratricopeptide repeat containing	YOR007c	orf19.5823
CA0905	IPF4405	-1.1	-1.1	1.0	-1.2	unknown function		orf19.1482
CA2571	IPF13769	1.1	-1.2	-1.0	-1.2	unknown function	YKL221w	orf19.13590
CA4136	RET2	-1.5	-1.1	-1.2	-1.2	Coatomer complex delta chain (by homology)	YFR051c	orf19.4236
CA2256	IPF14757	-1.1	-1.2	-1.3	-1.2	unknown function	YOR354c	orf19.1956
CA0398	ARO2	-1.1	-1.2	-1.1	-1.2	chorismate synthase (by homology)	YGL148w	orf19.1986
CA5795	TIM44	-1.0	-1.1	-1.3	-1.2	mitochondrial inner membrane import receptor	YIL022w	orf19.5444
CA1710	CLA4	-1.1	-1.1	-1.1	-1.2	protein kinase homolog (by homology)	YNL298w	orf19.4890
CA2196	IPF18517.5F	-1.2	-1.2	-1.5	-1.2	unknown function, 5-prime end		orf19.11827
CA2798	IPF8402	-1.3	-1.4	-1.4	-1.2	similar to Saccharomyces cerevisiae Sga1p glucan 1,4-	YIL099w	orf19.1719
CA4354	IPF3647	-1.4	-1.1	-1.4	-1.2	unknown function		orf19.6729
CA3539	RPS22	-1.2	-1.3	-1.2	-1.2	ribosomal protein by homology	YHL015w	orf19.6375

CA1227	IPF16082	1.1	-1.2	-1.1	-1.2	unknown function	YDL104c	orf19.4160
CA2651	HRD3	-1.2	-1.2	-1.2	-1.2	involved in HMG-CoA reductase degradation (by homol	YLR207w	orf19.1191
CA1803	IPF16748	-1.1	-1.1	-1.2	-1.2	unknown function	YER006w	orf19.2917
CA4554	IPF7874	1.0	1.0	-1.0	-1.2	similar to Saccharomyces cerevisiae Esc4p involved in	YHR154w	orf19.1445
CA2811	RPS10	-1.2	-1.3	-1.4	-1.2	Ribosomal protein 10	YML063w	orf19.10520
CA3825	IPF10654	-1.1	-1.1	-1.1	-1.2	D-arabinitol dehydrogenase-like (by homology)		orf19.5763
CA2064	IPF13024	1.0	-1.1	-1.1	-1.2	unknown function		orf19.10169
CA1084	IPF1036	-1.0	-1.1	-1.0	-1.2	unknown function		orf19.4571
CA5531	GCD14	1.0	-1.0	-1.0	-1.2	Translational repressor of GCN4	YJL125c	orf19.7291
CA4826	IPF1206	-1.1	-1.1	-1.3	-1.2	unknown function	YLR033w	orf19.2070
CA4235	NCL1	-1.3	-1.3	-1.5	-1.2	Probable proliferating-cell nucleolar antigen (by homolo	YBL024w	orf19.518
CA3375	IPF4684	1.1	-1.2	-1.2	-1.2	unknown Function		orf19.1857
CA4433	BCK1	1.0	-1.2	-1.3	-1.2	serine/threonine protein kinase of the MEKK family (by	YJL095w	orf19.5162
CA3033	IPF13202	-1.1	-1.1	-1.2	-1.2	unknown function	YMR068w	orf19.215
CA1129	IPF5197	-1.0	-1.3	-1.3	-1.2	unknown function		orf19.3610
CA4471	MCM3	-1.3	-1.1	-1.3	-1.2	replication initiation protein (by homology)	YEL032w	orf19.1901
CA5545	IPF5986	1.2	-1.1	-1.1	-1.2	similar to cytochrome-b5- and nitrate reductases	YML125c	orf19.7307
CA2453	IPF9950	1.0	-1.1	-1.3	-1.2	unknown function	YKR090w	orf19.10995
CA5110	FBP26	-1.0	-1.1	-1.3	-1.2	Fructose-2,6-bisphosphatase (by homology)	YJL155c	orf19.6423
CA4296	IPF2605	-1.4	-1.2	-1.4	-1.2	unknown function	YOL098c	orf19.6693
CA4752	ADE12	-1.5	-1.3	-1.2	-1.2	adenylosuccinate synthetase (by homology)	YNL220w	orf19.4827
CA2828	IPF17026	1.0	-1.2	-1.2	-1.2	unknown function		orf19.1325
CA1554	GEA2.3F	-1.8	-1.2	-1.6	-1.2	GTP/GDP exchange factor, 3-prime end (by homology)	YEL022w	orf19.1713
CA3580	IPF16141	1.0	-1.0	-1.0	-1.2	unknown function	YHR040w	orf19.2260
CA1271	HIT1	-1.1	-1.1	-1.0	-1.2	required for growth at high temperature (by homology)	YJR055w	orf19.2723
CA5053	IPF3707	1.0	-1.0	1.0	-1.2	unknown function	YPL138c	orf19.3018
CA1362	PEX3	-1.0	-1.2	-1.4	-1.2	PEROXISOMAL MEMBRANE PROTEIN by homology	YDR329c	orf19.4426
CA3619	CDC47.5	-1.3	-1.2	-1.2	-1.2	cell division control protein, , 5-prime end (by homology	YBR202w	orf19.202
CA5633	RPA135	-1.0	1.2	-1.1	-1.2	DNA-directed RNA polymerase I, 135 KD subunit (by ho	YPR010c	orf19.7062
CA1627	SKO1.3	1.0	-1.1	-1.1	-1.2	Cre-binding bzip protein, 3-prime end (by homology)	YNL167c	orf19.1032
CA1434	SNI2	-1.1	-1.0	-1.2	-1.2	Sec9 interacting protein (by homology)	YBL106c	orf19.1203
CA5189	IPF10158	-1.3	-1.2	-1.4	-1.2	Weak similarity to ScNup12p	YKL057c	orf19.4627
CA0341	XKS1	-1.1	-1.3	-1.4	-1.2	xylulokinase (by homology)	YGR194c	orf19.1788
CA3583	IPF20137	-1.0	-1.2	-1.2	-1.2	unknown function	YNR021w	orf19.2257
CA0606	COP1	-1.2	-1.2	-1.3	-1.2	coatomer complex alpha chain of secretory pathway ve	YDL145c	orf19.9241
CA4999	IPF2024	-1.0	-1.1	-1.4	-1.2	unknown function	YNR049c	orf19.5248
CA0827	IPF18859	1.0	-1.3	-1.2	-1.2	unknown function	YGL080w	orf19.7884
CA4461	IPF8470	-1.1	-1.1	-1.3	-1.2	unknown function	YEL015w	orf19.6858
CA2674	IPF5846	-1.1	-1.1	-1.3	-1.2	unknown function		orf19.5495
CA2985	SET1	-1.1	-1.1	-1.4	-1.2	Chromatin regulatory protein (by homology)	YHR119w	orf19.6009
CA5639	DIP53.EXON2	1.0	-1.1	-1.1	-1.2	dicarboxylic amino acid permease, exon 2 (by homology)		orf19.7056
CA5270	SEC18.5F	-1.5	-1.1	-1.5	-1.2	vesicular fusion protein by homology, 5-prime end		orf19.4993
CA1011	SRP101	-1.2	1.1	-1.2	-1.2	signal recognition particle receptor, alpha ch	YDR292c	orf19.11434
CA6046	IPF4931	1.0	1.0	-1.1	-1.2	unknown function	YDR289c	orf19.7662
CA5440	SRP54	-1.2	-1.1	-1.1	-1.2	54 kD signal recognition particle subunit	YPR088c	orf19.3243
CA0268	PUF2.EXON2	-1.3	-1.1	-1.1	-1.2	RNA-binding protein, exon 2 (by homology)	YJR091c	orf19.4262
CA1312	IPF14241	-1.1	-1.1	-1.1	-1.2	unknown function		orf19.11117
CA0021	IPF19425	-1.1	-1.1	-1.0	-1.2	unknown function	Missing in array	orf19.161
CA5963	IPF966	-1.1	-1.2	-1.3	-1.2	unknown function	YML093w	orf19.7552

CA1392	IPF6149	-1.1	-1.1	-1.1	-1.2	similar to Saccharomyces cerevisiae Ubp8p deubiquina	YMR223w	orf19.1767
CA3425	IPF11873	-1.3	-1.1	-1.3	-1.2	similar to Saccharomyces cerevisiae Swa2p clathrin-bin	YDR320c	orf19.593
CA2386	ECM41.3	-1.1	-1.2	-1.2	-1.2	involved in cell wall biogenesis and architecture, 3-prim	YKR076w	orf19.2613
CA5234	IPF3014	-1.1	-1.3	-1.3	-1.2	weak similarity to S. cerevisiae DOS2 involved in genon	YDR068w	orf19.5030
CA1933	IPF18586	1.1	-1.1	-1.2	-1.2	Unknown function		orf19.8381
CA1818	IPF7023.3	-1.1	-1.1	-1.2	-1.2	unknown function, 3-prime end		orf19.134
CA0207	IPF18002	1.1	-1.1	-1.3	-1.2	Unknown function		orf19.1226
CA4313	IPF2121	-1.1	-1.2	-1.3	-1.2	unknown function		orf19.4110
CA0579	PF3184.EXON	-1.0	-1.2	-1.3	-1.2	unknown function, exon 1		orf19.3560
CA2824	IPF17888	-1.0	-1.3	-1.3	-1.2	unknown function	YOR385w	orf19.1318
CA2570	PRO3	1.1	-1.4	-1.6	-1.2	delta 1-pyrroline-5-carboxylate reductase (by homology)	YER023w	orf19.5650
CA0119	RMT2	-1.1	-1.0	-1.2	-1.2	N-delta-arginine methyltransferase (by homology)	YDR465c	orf19.920
CA3946	MNN2	-1.3	-1.4	-1.5	-1.2	Golgi alpha-1,2-mannosyltransferase (by homology)		orf19.9547
CA4320	ECM17	-1.1	1.2	-1.2	-1.2	Putative sulfite reductase (by homology)	YJR137c	orf19.4099
CA5776	RML2	-1.1	-1.2	-1.3	-1.2	Ribosomal L2 protein, mitochondrial (by homology)	YEL050c	orf19.5420
CA3898	UBA2	-1.3	-1.0	-1.2	-1.2	ubiquitin-activating -like enzyme by homology	YDR390c	orf19.5074
CA0719	IPF9779.5	1.0	-1.0	-1.1	-1.2	serine/threonine protein kinase, 5-prime end (by homology)		orf19.3456
CA1763	URA6	1.1	-1.2	-1.3	-1.2	Uridine-monophosphate kinase(by homology)	YKL024c	orf19.5195
CA5075	IPF3610	-1.1	-1.1	-1.1	-1.2	unknown function	YDR524c	orf19.3050
CA5235	IPF3015	-1.2	-1.3	-1.2	-1.2	Similar to E.coli modF and photorepair protein phrA	YDR061w	orf19.5029
CA4728	VPS41.3F	-1.2	-1.2	-1.3	-1.2	required for the vacuolar assembly, 3-prime end (by hor	YDR080w	orf19.12322
CA4242	SEC26	-1.3	-1.1	-1.5	-1.2	beta chain of secretory vesicles coatomer complex (by	YDR238c	orf19.528
CA5355	IRR1.3F	-1.2	-1.2	-1.2	-1.2	cohesin complex subunit, 3-prime end (by homology)		orf19.7232
CA3221	PF10000.5EOC	-1.2	-1.1	-1.4	-1.2	unknown function, 5-prime end	YGR274c	orf19.6193
CA3381	NPR2	-1.2	-1.2	-1.2	-1.2	nitrogen permease regulator (by homology)	YEL062w	orf19.328
CA4302	DED81	-1.2	-1.0	-1.3	-1.2	Asparaginyl-tRNA synthetase (by homology)	YHR019c	orf19.6702
CA2524	IPF4322	1.1	-1.2	-1.2	-1.2	unknown function	YLL027w	orf19.5521
CA0728	IPF7345	-1.2	-1.0	-1.2	-1.2	unknown function	YAL031c	orf19.11212
CA5392	IPF10571	-1.0	-1.2	-1.2	-1.2	Unknown function		orf19.935
CA1264	STH1	1.0	-1.0	-1.2	-1.2	helicase related protein by homology	YIL126w ; Missing in array	orf19.239
CA0562	PSO2	-1.1	-1.1	-1.2	-1.2	Interstrand crosslink repair protein (by homology)	YMR137c	orf19.2926
CA3868	CCT1	-1.2	-1.0	-1.1	-1.2	component of chaperonin-containing T-complex (by hor	YDR212w	orf19.401
CA1110	DIS3	-1.3	-1.1	-1.2	-1.2	3 --5 exoribonuclease required for 3 end formation of	YOL021c	orf19.5229
CA4705	IPF4206	-1.1	-1.2	-1.1	-1.2	unknown function		orf19.6934
CA3211	IPF19977	1.2	-1.1	-1.2	-1.2	unknown function		orf19.6192
CA1588	SPT8	-1.1	-1.3	-1.4	-1.2	transcriptional adaptor or co-activator (by homology)	YLR055c	orf19.11787
CA5930	ECM29.EXON2	-1.6	1.3	-1.5	-1.2	Involved in cell wall biogenesis and architecture, exon 2	YHL030w	orf19.6773
CA3617	IPF9069	1.1	-1.1	-1.0	-1.2	unknown function		orf19.199
CA1609	TES11	-1.0	-1.4	-1.4	-1.2	Thiosterase (by homology)		orf19.4121
CA1477	YME1	-1.2	-1.3	-1.3	-1.2	family of ATPases	YPR024w	orf19.1252
CA4010	MAK10.3	-1.2	-1.2	-1.3	-1.2	glucose-repressible protein, 3-prime end (by homology)	YEL053c	orf19.1624
CA4870	IPF19568	1.0	-1.1	-1.2	-1.2	unknown function		orf19.6556
CA3778	IPF10431	-1.3	-1.2	-1.2	-1.2	unknown function		orf19.2888
CA5138	IPF1031	-1.3	-1.2	-1.4	-1.2	Similar to aminoglycoside acetyltransferase regulator fr	YPL109c	orf19.4575
CA1275	RPC53	1.0	-1.3	-1.3	-1.2	DNA-directed RNA polymerase III (by homology)	YDL150w	orf19.2715
CA3885	IPF19790	-1.0	1.0	-1.2	-1.2	unknown function	YDL019c	orf19.5095
CA1256	UBP15	-1.5	-1.3	-1.4	-1.2	ubiquitin-specific protease (by homology)	YMR304w ; Missing in array	orf19.1777
CA0834	IPF12498.3F	-1.2	-1.4	-1.2	-1.2	unknown function, 3-prime end		orf19.1677
CA4289	IPF6665	-1.0	-1.3	-1.3	-1.2	unknown function	YGR145w	orf19.6686

CA0773	UGA11.EXON1	-1.0	-1.3	-1.3	-1.2	4-aminobutyrate aminotransferase, exon 1 (by homolog	YGR019w	orf19.854
CA2675	GSP1	-1.2	-1.3	-1.3	-1.2	GTP-binding protein (by homology)	YLR293c	orf19.5493
CA5063	IPF8493	1.1	-1.2	-1.1	-1.2	putative member of nontransporter group of ATP-bindin	YDR091c	orf19.3034
CA1986	IPF14899	-1.1	-1.2	-1.4	-1.2	unknown function	YFR016c	orf19.92
CA2560	PEX5	-1.1	-1.2	-1.2	-1.2	peroxisomal targeting signal receptor	YDR244w	orf19.5640
CA4238	PIM1	-1.0	-1.0	-1.1	-1.2	mitochondrial ATP-dependent protease (by homology)	YBL022c	orf19.522
CA5096	IPF1384	1.1	-1.2	-1.3	-1.2	similar to Saccharomyces cerevisiae Eci1p delta3-cis-d	YLR284c	orf19.6445
CA5365	IPF824	1.3	-1.3	-1.4	-1.2	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (by hon	YNL168c	orf19.7244
CA2403	IPF6438	1.0	-1.3	-1.3	-1.2	unknown function	YML131w	orf19.3544
CA5967	IPF955	-1.0	-1.0	-1.1	-1.2	member of the AAA ATPase family of proteins (by homo	YER047c	orf19.7558
CA4796	IPF3380	1.1	-1.1	-1.2	-1.2	unknown function	YIR007w	orf19.4031
CA5527	IPF2856	-1.1	-1.1	-1.1	-1.2	unknown function	YGR156w	orf19.7285
CA3240	IPF10559	-1.2	-1.2	-1.5	-1.2	myosin-like protein (by homology)	YKR095w	orf19.4683
CA4712	GTT1.3	1.0	-1.1	-1.2	-1.2	glutathione S-transferase, 3-prime end (by homology)	YIR038c	orf19.6947
CA4078	VMA2	-1.3	-1.2	-1.2	-1.2	H+-transporting ATPase (by homology)	YBR127c	orf19.6634
CA2497	TEL1.3EOC	1.0	-1.1	-1.3	-1.2	Putative phosphatidylinositol kinase involved in controlli	YBL088c	orf19.5580
CA2505	IPF6796	-1.3	-1.2	-1.6	-1.2	unknown function	YBR130c	orf19.5595
CA4521	MRPL40	-1.1	-1.3	-1.4	-1.2	Putative mitochondrial ribosomal protein (by homology)	YPL173w	orf19.484
CA0748	TFS1	1.1	-1.2	-1.3	-1.2	cdc25-dependent nutrient- and ammonia-response cell-	YLR178c	orf19.1974
CA0823	PF11987.3EOC	1.1	-1.1	-1.2	-1.2	unknown function, 3-prime end		orf19.692
CA4659	IPF17754	-1.2	-1.1	-1.1	-1.2	low affinity high capacity ammonium permease (by homology)		orf19.4446
CA5237	ZMS1	1.0	-1.2	-1.2	-1.2	Zinc Finger Protein C2H2 (by homology)	YML081w	orf19.5026
CA3065	IPF19775	-1.1	-1.1	-1.4	-1.2	unknown function		orf19.11758
CA2971	MDL2.5F	-1.2	-1.2	-1.2	-1.2	ATP-binding transporter, 5-prime end (by homology)		orf19.5600
CA2719	SOD2	1.2	-1.2	-1.3	-1.2	Manganese-superoxide dismutase	YHR008c	orf19.3340
CA1828	CDC22.3EOC	-1.1	-1.1	-1.3	-1.2	DNA Polymerase III, 3-prime end		
CA4532	IPF4386	-1.1	-1.2	-1.2	-1.2	unknown function		orf19.1473
CA0617	MET2	-1.0	-1.3	-1.3	-1.2	Homoserine O-acetyltransferase	YNL277w	orf19.2618
CA4673	IPF3661	1.0	-1.3	-1.4	-1.2	unknown function		orf19.899
CA5834	LRG1	-1.1	-1.2	-1.3	-1.2	GTPase-activating protein of the rho/rac family (by hom	YDL240w	orf19.7489
CA4817	POM152	-1.1	1.0	-1.3	-1.2	Nuclear pore membrane glycoprotein (by homology)	YMR129w	orf19.2081
CA1097	IPF7575	-1.1	-1.1	-1.2	-1.2	putative endo-exonuclease (by homology)		orf19.4365
CA5443	IPF18105.5F	-1.1	-1.1	-1.3	-1.2	unknown function, 3-prime end		orf19.3246
CA1459	IPF6340	-1.1	-1.1	-1.1	-1.2	unknown function		orf19.1107
CA0945	IPF10278	-1.2	-1.2	-1.5	-1.2	DNA-J - like protein (by homology)	YER048c	orf19.8853
CA1589	IPF16988	-1.1	-1.2	-1.3	-1.2	unknown function		orf19.11788
CA1404	IPF19554.5F	-1.1	-1.2	-1.4	-1.2	unknown function, 5-prime end	YDL216c	orf19.3372
CA2896	IPF14981	-1.2	-1.4	-1.5	-1.2	unknown function	YPL206c	orf19.3483
CA2457	MCR1	-1.1	-1.6	-1.5	-1.2	NADH-cytochrome-b5 reductase (by homology)	YKL150w	orf19.3507
CA2622	PER3.EXON2	-1.1	-1.3	-1.4	-1.2	peroxisomal import protein, exon 2 (by homology)		orf19.2806
CA3008	IPF12147	-1.1	-1.2	-1.0	-1.2	unknown function	YNL181w	orf19.13613
CA1364	IPF5561	-1.0	-1.1	-1.4	-1.2	unknown function		orf19.4423
CA3147	IPF9803	-1.1	-1.1	-1.3	-1.2	unknown function	YMR031c	orf19.6160
CA0181	NOT3	-1.0	-1.0	-1.1	-1.2	unknown function		orf19.2012
CA1179	IPF5064	-1.0	-1.5	-1.6	-1.2	ADP/ATP carrier protein (by homology)	YPR011c	orf19.804
CA5327	SLA2	-1.3	-1.2	-1.4	-1.2	Cytoskeleton assembly control protein	YNL243w	orf19.7201
CA2480	CCT7	-1.2	-1.1	-1.2	-1.2	component of chaperonin-containing T-complex (by hon	YJL111w	orf19.10718
CA5923	IFQ2	-1.2	-1.3	-1.3	-1.2	Unknown function		orf19.6782
CA1846	FDH12	-1.1	-1.2	-1.5	-1.2	Formate dehydrogenase (by homology)	YOR388c	orf19.638

CA2322	YSH1	-1.3	-1.1	-1.3	-1.2	component of pre-mRNA polyadenylation factor PF I (b	YLR277c	orf19.5486
CA4564	IPF6572	1.1	-1.1	1.1	-1.2	unknown function		orf19.6874
CA3073	IPF6108	-1.1	-1.2	-1.2	-1.2	putative tricarboxylate carrier (by homology)	YOR271c	orf19.4811
CA1253	FDH3.3F	-1.1	-1.2	-1.2	-1.2	formate dehydrogenase, 3-prime end (by homology)		orf19.1774
CA1349	PRP12	-1.2	1.1	-1.0	-1.2	involved in early maturation of pre-rRNA (by homology)	YMR302c	orf19.4351
CA3119	IPF5360.3	-1.1	-1.2	-1.1	-1.2	unknown function, 3-prime end		
CA4549	IPF7863	1.0	-1.2	-1.2	-1.2	unknown function	YNL335w	orf19.1449
CA3757	MAE1	-1.2	1.0	1.2	-1.2	mitochondrial malic enzyme (by homology)	YKL029c	orf19.3419
CA5032	IPF2982	-1.2	-1.1	-1.2	-1.2	unknown function		orf19.6986
CA1465	RIM11	-1.2	-1.3	-1.2	-1.2	Ser/thr protein kinase (by homology)		orf19.791
CA0277	RNH1	1.0	-1.1	-1.2	-1.2	ribonuclease H (by homology)		orf19.13057
CA0621	IPF17999	1.2	-1.1	-1.2	-1.2	unknown function		orf19.3148
CA1842	ARO1	1.1	-1.1	-1.0	-1.2	arom pentafunctional enzyme (by homology)	YDR127w	orf19.4704
CA6090	IPF44	-1.2	-1.2	-1.2	-1.2	unknown function	YDL189w	orf19.5967
CA1532	IPF9507	-1.2	-1.1	-1.4	-1.2	unknown function	YMR247c	orf19.8806
CA3321	IPF6896.5F	-1.2	-1.2	-1.3	-1.2	unknown function, 5-prime end	YHR188c	orf19.2677
CA2658	IPF8105	-1.0	-1.2	-1.2	-1.2	unknown function	YLR380w	orf19.5711
CA3007	IPF12148	-1.1	-1.3	-1.2	-1.2	Unknown function	YNL182c	orf19.13614
CA1682	CIRT3	-1.1	-1.1	-1.1	-1.2	Putative transposase		orf19.4918
CA3892	PSE1	-1.2	-1.0	-1.2	-1.2	karyopherin-beta protein (by homology)	YMR308c	orf19.5085
CA5728	IPF2471	-1.1	-1.5	-1.5	-1.2	maltose acetyltransferase	YJL218w	orf19.7437
CA2827	RAD2	-1.0	-1.1	-1.3	-1.2	structure-specific nuclease of the nucleotide	YGR258c	orf19.1324
CA0477	IPF13839	-1.1	-1.2	1.0	-1.2	unknown function		orf19.6017
CA1385	IPF8424	-1.3	-1.2	-1.3	-1.2	unknown function		orf19.925
CA1118	IPF9987	1.0	-1.0	-1.3	-1.2	similar to phosphatidylinositol kinase (by homology)		orf19.2290
CA2847	PF10785.EXON	-1.1	-1.3	-1.3	-1.2	unknown function, exon 1	YNR053c	orf19.5732
SCTEF1		-1.1	-1.1	-1.2	-1.2			
CA4491	SWR1	-1.1	-1.1	-1.6	-1.2	putative DNA helicase (by homology)	YDR334w	orf19.9427
CA1822	IPF9525	-1.3	-1.4	-1.5	-1.2	unknown function	YLR222c	orf19.4268
CA2333	ADH4	1.2	-1.2	-1.2	-1.2	probable alcohol dehydrogenase (by homology)		orf19.11980
CA2423	SDH41	-1.0	-1.5	-1.3	-1.2	succinate dehydrogenase membrane anchor subunit fo	YDR178w	orf19.11949
CA2154	ERG2	1.0	-1.3	-1.3	-1.2	C-8 sterol isomerase	YMR202w	orf19.6026
CA2988	SIN3.EXON2	-1.0	1.0	-1.1	-1.2	Histone deacetylase by homology		
CA5015	IPF11118	-1.1	-1.2	-1.5	-1.2	unknown function		orf19.6967
CA0532	IRE1	-1.1	-1.0	-1.0	-1.2	protein kinase (by homology)	YHR079c	orf19.5068
CA0283	IPF18034	-1.1	-1.1	-1.6	-1.2	Unknown function		
CA3302	IPF13784	1.0	-1.1	-1.0	-1.2	unknown function		orf19.2313
CA3165	FMI1	-1.4	-1.1	-1.4	-1.2	processing of pre-ribosomal RNA	YMR229c	orf19.1578
CA3608	IPF3857	-1.1	-1.2	-1.2	-1.2	unknown function	YOL093w	orf19.25
CA3052	DPS1	-1.3	-1.2	-1.2	-1.2	aspartyl-tRNA synthetase (by homology)	YLL018c ; Missing in array	orf19.9945
CA4578	RFC1	-1.0	-1.1	-1.3	-1.2	DNA replication factor C (by homology)	YOR217w	orf19.6891
CA5124	GSH2	-1.2	-1.2	-1.3	-1.2	Glutathione synthetase (by homology)	YOL049w	orf19.6404
CA5090	IFG4	-1.1	-1.4	-1.4	-1.2	probable d-amino acid oxidase (by homology)		orf19.3065
CA2589	KRE1	-1.0	-1.1	-1.1	-1.2	secretory pathway protein		orf19.4377
CA4620	IFD3	-1.1	-1.2	-1.3	-1.2	OXIDOREDUCTASE (by homology)		orf19.3311
CA5669	IPF1264	-1.0	1.0	-1.0	-1.2	unknown function, Asn rich		orf19.7371
CA0810	RRN3	1.2	-1.1	-1.2	-1.2	RNA polymerase I specific transcription fact	YKL125w	orf19.1923
CA2399	MAK5	-1.1	-1.2	-1.2	-1.2	ATP-dependent RNA helicase (by homology)	YBR142w	orf19.3540
CA1388	IPF16514	-1.1	-1.0	-1.2	-1.2	unknown function		orf19.921

CA5056	IPF3698	1.1	-1.3	-1.4	-1.2	similar to Saccharomyces cerevisiae Rsm24p mitochon	YDR175c	orf19.3022
CA2910	IPF11421	-1.2	-1.2	-1.3	-1.2	unknown function		orf19.4517
CA2146	IPF12799	-1.0	-1.2	-1.2	-1.2	unknown function		orf19.2515
CA5261	IPF1805	-1.3	-1.3	-1.4	-1.2	unknown function	YGL164c	orf19.5003
CA1261	IPF9887.3EOC	-1.4	1.1	-1.5	-1.2	unknown function, 3-prime end	YPR117w	orf19.1240
CA2170	IPF4563.3F	-1.1	1.3	-2.1	-1.2	similar to saccharomyces cerevisiae Tom1p E3 ubiqitin ligase required for G2/M trans		orf19.912
CA2716	IPF7353	-1.1	-1.3	-1.4	-1.2	unknown function	YDL057w	orf19.577
CA5323	IPF2142	-1.2	-1.3	-1.2	-1.2	unknown function	YLR002c	orf19.7197
CA3864	RPL16A	-1.0	-1.2	-1.4	-1.2	ribosomal protein (by homology)	YNL069c	orf19.6085
CA2364	MEC1	-1.2	-1.0	-1.2	-1.2	cell cycle checkpoint protein (by homology)	YBR136w	orf19.8870
CA3272	ALD4	-1.1	-1.2	-1.3	-1.2	aldehyde dehydrogenase, mitochondrial (by homology)		orf19.6306
CA1073	PRORS.3F	-1.1	-1.2	-1.3	-1.2	prolyl-tRNA synthetase, 3-prime end	YER087w	orf19.2533
CA4905	DLD1	-1.0	-1.3	-1.4	-1.2	D-lactate ferricytochrome C oxidoreductase (by homology)		orf19.6043
CA2548	IPF9101	1.5	-1.3	-1.3	-1.2	unknown function		orf19.2833
CA4339	IPF3618	-1.2	-1.3	-1.3	-1.2	Unknown function		orf19.6710
CA2202	SCW4	1.2	-1.3	-1.1	-1.2	cell wall glucanase (by homology)		orf19.2941
CA3860	KEL1	-1.0	-1.2	-1.4	-1.2	involved in cell fusion and morphology (by homology)	YGR238c	orf19.6092
CA4804	ARO8	-1.3	-1.2	-1.3	-1.2	aromatic amino acid aminotransferase I (by homology)	YGL202w	orf19.2098
CA1578	NUM11	-1.0	1.1	-1.4	-1.2	nuclear migration protein (by homology)	YDR150w	orf19.4715
CA4878	OXA1	-1.0	-1.2	-1.2	-1.2	Cytochrome oxidase biogenesis protein (by homology)	YER154w	orf19.6565
CA1501	IPF13217	-1.0	-1.2	-1.3	-1.2	unknown function	YNL094w	orf19.9265
CA2602	IPF5473	-1.0	1.0	-1.4	-1.2	unknown function		orf19.5679
CA4839	NPL6	1.0	-1.1	-1.1	-1.2	Nuclear protein localization factor (by homology)	YMR091c	orf19.2055
CA3524	LKH1.3	-1.3	-1.0	-1.1	-1.2	PROBABLE LEUKOTRIENE A-4 HYDROLASE (LTA-4	YNL045w	orf19.992
CA4939	IQG1	-1.3	-1.1	-1.4	-1.2	RAS GTPase-activating-like protein by homology	YPL242c	orf19.6536
CA1742	IPF12210	-1.1	-1.4	-1.3	-1.2	quinolinate phosphoribosyltransferase (by homology)	YFR047c	orf19.5054
CA1247	IPF3870	-1.5	1.0	-1.6	-1.2	similar to Saccharomyces cerevisiae Rts1p potential reg	YOR014w	orf19.20
CA3775	AFG1	-1.0	-1.5	-1.4	-1.2	ATPase family gene (by homology)	YEL052w	orf19.2891
CA1598	SES1	-1.5	-1.4	-1.4	-1.2	seryl-tRNA synthetase (by homology)	YDR023w	orf19.7901
CA3789	IPF11217	-1.4	-1.3	-1.6	-1.2	similar to Saccharomyces cerevisiae Lhs1p chaperone	YKL073w	orf19.13252
CA0573	PEX14	-1.2	-1.2	-1.4	-1.2	peroxisomal protein (by homology)	YGL153w	orf19.9371
CA0352	RPB4.5F	-1.0	-1.3	-1.4	-1.2	DNA-directed RNA polymerase II, 32 kDa subunit, 5-prime end (by homology)		orf19.146
CA1489	ATP3.3	1.2	-1.4	-1.2	-1.2	F1F0-ATPase complex, F1 gamma subunit, 3-prime en	YBR039w	orf19.10734
CA4115	IPF7706	-1.2	-1.3	-1.3	-1.2	putative plasma membrane phosphatase (by homology)	YPL063w	orf19.680
CA3046	IPF7295	-1.2	-1.2	-1.4	-1.2	unknown function	YOL034w	orf19.2417
CA2171	PEP1.3	-1.6	-1.1	-1.5	-1.2	Vacuolar protein sorting/targeting protein, 3-prime end	YBL017c	orf19.3767
CA0464	IPF14116	1.1	-1.5	-1.3	-1.2	unknown function	YOR084w	orf19.7798
CA4411	BRR2	-1.1	-1.1	-1.4	-1.2	RNA helicase-related protein (by homology)	YER172c	orf19.3098
CA1329	MRF2	-1.1	-1.4	-1.4	-1.2	peptide chain release factor, mitochondrial (I	YGL143c	orf19.1303
CA2018	STE11	-1.2	-1.1	-1.2	-1.2	ser/thr protein kinase of the MEKK family (by homology)	YLR362w	orf19.844
CA1505	POT1	1.1	-1.3	-1.5	-1.2	Acetyl-CoA C-acyltransferase, peroxisomal (by homology)		orf19.9271
CA3675	PF19529.EXON	-1.2	-1.3	-1.4	-1.2	unknown function, exon 2		orf19.6453
CA4724	PDC2	-1.1	-1.1	-1.1	-1.2	pyruvate decarboxylase regulator	YDR081c	orf19.12327
CA3487	IPF3203	-1.2	-1.4	-1.5	-1.2	unknown function	YLR407w	orf19.3569
CA2772	IPF20112	-1.1	-1.2	-1.4	-1.2	unknown function	YPL126w	orf19.2688
CA4810	IPF1164	-1.2	-1.2	-1.3	-1.2	Subunit NUHM of NADH:Ubiquinone Oxidoreductase (by homology)		orf19.2091
CA3161	IPF13121.3	1.2	-1.6	-1.2	-1.2	unknown function, 3-prime end		orf19.1584
CA2003	IPF16471	-1.2	-1.4	-1.5	-1.2	unknown function	YDL051w	orf19.2795
CA2729	NAT2	1.1	-1.2	-1.2	-1.2	N-acetyltransferase for N-terminal methionine (by homo	YGR147c	orf19.9664

CA0139	RUD3	-1.1	-1.3	-1.5	-1.2	Suppressor of uso1-1 transport defect (by homology)	YOR216c	orf19.14182
CA4666	IPF6542	-1.1	-1.3	-1.2	-1.2	unknown function	YNL164c	orf19.4455
CA1701	CFL11	1.1	-1.0	-1.0	-1.2	Ferric reductase (by homology)		orf19.701
CA4475	IPF6455	-1.2	-1.1	-1.4	-1.2	unknown function		orf19.1893
CA5249	PCM1	-1.2	-1.3	-1.3	-1.2	phosphoacetylglucosamine mutase (by homology)	YEL058w	orf19.5013
CA3070	PPA2	-1.1	-1.2	-1.2	-1.2	Mitochondrial inorganic pyrophosphatase	YMR267w	orf19.4807
CA5652	IPF19815	-1.0	-1.1	-1.3	-1.2	longevity-assurance protein (by homology)		orf19.7354
CA4959	HSP90	-1.2	-1.1	-1.5	-1.2	heat shock protein	YMR186w	orf19.6515
CA5228	RTF1.3EOC	-1.2	-1.3	-1.1	-1.2	Regulates DNA binding properties of TBP, 3-prime end	YGL244w	orf19.7047
CA0216	IPF11681	-1.2	-1.3	-1.6	-1.2	unknown function		orf19.1682
CA5549	ERG13	-1.1	-1.2	-1.2	-1.2	3-hydroxy-3-methylglutaryl coenzyme A synthase (by h	YML126c	orf19.7312
CA0665	INT1	-1.2	-1.0	-1.2	-1.2	integrin-like protein alpha chain	YJR092w	orf19.11733
CA5529	IPF2852	-1.2	-1.2	-1.5	-1.2	putative acetyl-coenzyme-A dehydrogenase		orf19.7288
CA4831	IPF1212	-1.1	-1.2	-1.0	-1.2	unknown function	YJR129c	orf19.2066
CA5844	PXA1	-1.1	-1.4	-1.4	-1.2	long chain fatty acid ABC transporter (by homology)	YPL147w	orf19.7500
CA0394	IPF12758.5F	1.3	-1.3	-1.4	-1.2	unknown function, 5-prime end		orf19.7966
CA1063	NMT1	-1.1	-1.2	-1.2	-1.2	N-myristoyltransferase	YLR195c	orf19.4641
CA3154	FUN34.5EOC	1.1	-1.3	-1.3	-1.2	unknown function, 5-prime end		
CA1466	IPF13324	-1.4	-1.3	-1.5	-1.2	unknown function		orf19.8411
CA5114	IPF1334	-1.0	-1.2	-1.4	-1.2	Conserved hypothetical protein	YDL060w	orf19.6417
CA5423	ROT2	-1.2	-1.2	-1.3	-1.2	Glucosidase II, catalytic subunit (by homology)	YBR229c	orf19.974
CA5611	SUA5	1.1	-1.2	-1.1	-1.2	translation initiation protein (by homology)	YGL169w	orf19.7088
CA3300	RTG3	-1.0	-1.2	-1.3	-1.2	Probable bHLH/zip transcription factor that regulates C	YBL103c	orf19.2315
CA5957	RRP3.3EOC	-1.2	-1.3	-1.3	-1.2	RNA-dependent ATPase, helicase,required for maturati	YHR065c	orf19.7546
CA2810	EFT2	-1.1	-1.0	-1.2	-1.2	translation elongation factor 2	YOR133w	orf19.5788
CA6159	IPF1837	-1.3	-1.3	-1.2	-1.2	unknown function	YOR377w	orf19.5877
CA2388	MCM6	-1.3	-1.1	-1.3	-1.2	component of MCM initiator complex involved in DNA re	YGL201c	orf19.2611
CA2700	F14414.EXON	-1.1	-1.2	-1.3	-1.2	unknown function, exon 1		orf19.10254
CA0786	IPF7473	-1.2	-1.4	-1.4	-1.2	unknown function	YDL144c	orf19.2446
CA2119	MTR4	-1.2	-1.3	-1.5	-1.2	RNA Helicase (by homology)	YJL050w	orf19.8915
CA3526	MRPS5	-1.0	-1.3	-1.3	-1.2	Probable ribosomal protein S5, mitochondrial (by homol	YBR251w	orf19.8604
CA3714	IPF16223	-1.3	-1.3	-1.6	-1.2	unknown function	YGR198w	orf19.11639
CA4723	IPF18177	1.1	-1.3	-1.2	-1.2	Unknown function	YKL094w	orf19.12328
CA3534	SSB1	-1.1	1.0	-1.1	-1.2	heat shock protein 70	YNL209w	orf19.6367
CA2825	HWP1	1.1	-1.1	-1.2	-1.3	Hyphal wall protein		orf19.1321
CA4361	IPF16104	-1.1	-1.1	-1.2	-1.3	unknown function	YJR119c	orf19.13096
CA4869	LYS4	-1.1	-1.1	-1.3	-1.3	homoaconitate hydratase	YDR234w	orf19.3846
CA2415	MSD1	-1.4	-1.2	-1.5	-1.3	Aspartyl-tRNA synthetase, mitochondrial.	YPL104w	orf19.4478
CA4076	IPF2542	-1.1	-1.3	-1.3	-1.3	putative neutral sphingomyelinase (by homology)	YER019w	orf19.6629
CA0756	IPF14859	1.1	-1.6	-1.6	-1.3	acyl-coenzyme-A dehydrogenase (by homology)		orf19.3488
CA4113	CHO1	1.4	-1.3	-1.2	-1.3	Phosphatidylserine synthase	YER026c	orf19.677
CA1150	RIM9	-1.1	-1.4	-1.6	-1.3	regulator for sporulation and invasive growth		orf19.101
CA1503	RKI1	1.1	-1.6	-1.4	-1.3	D-ribose-5-phosphate ketol-isomerase (by homology)	YOR095c	orf19.9268
CA2559	HIS4	-1.3	-1.2	-1.3	-1.3	Histidine biosynthesis trifunctional protein (phosphoribo	YCL030c	orf19.5639
CA4459	NSP49.3F	-1.2	-1.2	-1.3	-1.3	nucleoporin, 3-prime end (by homology)	YGL092w	orf19.6856
CA0025	IPF17945	-1.0	-1.4	-1.3	-1.3	unknown function		orf19.178
CA5524	IPF2861	-1.1	-1.3	-1.3	-1.3	putative pyruvate dehydrogenase kinase	YIL042c	orf19.7281
CA3304	RPL82	-1.1	-1.3	-1.5	-1.3	60S ribosomal protein L7a.e.B (by homology)		orf19.2311
CA3808	FAL1	-1.0	-1.1	-1.3	-1.3	ATP-dependent RNA helicase	YDR021w	orf19.2488

CA3498	RBK1	-1.1	-1.3	-1.4	-1.3	Ribokinase (by homology)	YCR036w	orf19.6344
CA2320	SER1	-1.1	-1.3	-1.3	-1.3	phosphoserine transaminase (by homology)	YOR184w	orf19.5484
CA1973	WRS1	-1.2	-1.3	-1.5	-1.3	tryptophan--tRNA ligase	YOL097c	orf19.5226
CA1044	RNA1	-1.2	-1.4	-1.4	-1.3	GTPase activating protein (by homology)	YMR235c	orf19.9218
CA2656	NAM2	-1.1	-1.3	-1.5	-1.3	mitochondrial leucine--tRNA ligase (by homology)	YLR382c	orf19.5705
CA1748	IPF8257	-1.2	-1.1	-1.6	-1.3	unknown function		orf19.1522
CA4572	KES1	-1.3	-1.2	-1.5	-1.3	involved in ergosterol biosynthesis (by homology)	YPL145c	orf19.6883
CA1869	IPF15822	-1.3	-1.6	-1.4	-1.3	unknown function		orf19.9993
CA0095	ALG11	-1.1	-1.4	-1.4	-1.3	required for asparagine-linked oligosaccharide assembl	YNL048w	orf19.3468
CA5099	PRP8	1.1	-1.1	-1.4	-1.3	U5 snRNP protein, pre-mRNA splicing factor (by homol	YHR165c	orf19.6442
CA4331	IPF2086	-1.1	-1.2	-1.5	-1.3	unknown function	YOR057w	orf19.4089
CA3273	IPF12227.5F	-1.2	-1.2	-1.4	-1.3	unknown function, 5-prime end		orf19.6307
CA6128	IPF152	-1.2	-1.3	-1.5	-1.3	unknown function	YOR129c	orf19.5919
CA1705	GCN5	1.1	-1.1	1.0	-1.3	Histone acetyltransferase (by homology)	YGR252w	orf19.705
CA4117	LAB5	-1.0	-1.5	-1.6	-1.3	lipoic acid synthase (by homology)	YOR196c	orf19.2774
CA0087	SMF11	-1.1	-1.2	-1.1	-1.3	manganese transporter (by homology)		orf19.4690
CA2406	AIP2	-1.2	-1.2	-1.3	-1.3	actin interacting protein 2 (by homology)	YDL178w	orf19.300
CA2821	CDR3.3EOC	1.1	-1.1	-1.2	-1.3	Opaque-specific ABC transporter, 3-prime end		
CA0504	IPF16466	-1.2	-1.1	-1.5	-1.3	unknown function	YKL014c	orf19.2778
CA3186	ILS1	-1.3	-1.0	-1.5	-1.3	isoleucyl-tRNA synthetase (by homology)	YBL076c	orf19.2138
CA0627	HSP12	1.5	-1.6	-1.8	-1.3	Heat shock protein (by homology)	YFL014w	orf19.3160
CA0862	CRK1.5F	-1.1	-1.1	-1.7	-1.3	Protein kinase, 5-prime end	YPR161c	orf19.3524
CA2881	RAD4	-1.1	-1.2	-1.3	-1.3	Excision repair protein (by homology)	YOR206w	orf19.5850
CA5021	YST1.EXON2	-1.1	-1.3	-1.3	-1.3	Ribosomal protein, exon 2	YGR214w	orf19.6975
CA1246	IMH3.EXON1	-1.3	-1.2	-1.1	-1.3	IMP dehydrogenase, exon 1		orf19.19
CA2250	MIS11	-1.0	-1.3	-1.3	-1.3	mitochondrial C1-tetrahydrofolate synthase precursor (b	YBR084w	orf19.2364
CA5222	IPF3079	-1.1	-1.2	-1.2	-1.3	similar to Saccharomyces cerevisiae Pta1p pre-tRNA pr	YAL043c	orf19.7041
CA3191	IPF11601	-1.1	-1.2	-1.0	-1.3	unknown function	YOR165w	orf19.2151
CA1750	IPF8252	-1.2	-1.2	-1.8	-1.3	unknown function		orf19.1519
CA0088	IPF7349	-1.3	-1.2	-1.6	-1.3	similar to Saccharomyces cerevisiae Fol1p dihydroneop	YNL256w	orf19.579
CA3414	IPF9240	1.1	-1.3	-1.4	-1.3	probable permease		orf19.6141
CA0870	IPP1	1.4	-1.1	-1.0	-1.3	inorganic pyrophosphatase (by homology)	YBR011c	orf19.3590
CA2319	GUF1	-1.2	-1.3	-1.3	-1.3	GTP-binding protein (by homology)	YLR289w	orf19.5483
CA2577	IPF7430	-1.1	-1.1	-1.3	-1.3	unknown function	YGR134w	orf19.6220
CA3284	ADE6	-1.2	-1.0	-1.3	-1.3	5 -phosphoribosylformyl glycinamidine synthetase (by h	YGR061c	orf19.6317
CA4450	IPF3518	-1.5	-1.2	-1.5	-1.3	similar to Saccharomyces cerevisiae Vps16p vacuolar s	YPL045w	orf19.6848
CA2413	IPF13756.5F	-1.5	-1.4	-1.7	-1.3	unknown function, 5-prime end		orf19.4480
CA2195	IPF18517.3F	-1.4	-1.2	-1.4	-1.3	unknown function, 3-prime end	YOL070c	orf19.11826
CA2030	IPF13116	-1.1	-1.3	-1.3	-1.3	unknown function	YGL099w	orf19.3463
CA6163	POL1	-1.2	-1.0	-1.3	-1.3	DNA-directed DNA polymerase alpha (by homology)	YNL102w	orf19.5873
CA5938	IPF3481	-1.2	-1.2	-1.6	-1.3	unknown function		orf19.6759
CA5006	IPF12584	1.1	-1.3	-1.4	-1.3	unknown function	YCR033w	orf19.5241
CA3367	IPF4667	-1.2	-1.9	-2.5	-1.3	unknown Function	YDR380w	orf19.9405
CA2712	SPE2	1.0	-1.2	-1.1	-1.3	by homology to S. cerevisiae adenosylmethionine deca	YOL052c	orf19.8199
CA5568	ELF1	-1.3	-1.2	-1.5	-1.3	Elongation-like factor	YPL226w	orf19.7332
CA5510	IPF741	-1.0	-1.1	-1.2	-1.3	unknown function	YNL313c	orf19.5356
CA3423	IPF3549	1.1	-1.3	-1.1	-1.3	unknown function		orf19.597
CA1587	CMP2	-1.2	-1.2	-1.5	-1.3	Calcineurin B, catalytic subunit (by homology)	YML057w	orf19.6033
CA1558	IPF15679	1.0	-1.5	-1.5	-1.3	lipid transfer protein (by homology)		orf19.1709

CA5242	PDX1	-1.3	-1.1	-1.4	-1.3	Pyruvate dehydrogenase complex protein X (by homolo	YGR193c	orf19.5021
CA0667	TIF5	-1.2	-1.4	-1.3	-1.3	Translation initiation factor eIF5 (by homology)	YPR041w	orf19.11737
CA1428	MRP4	-1.3	-1.5	-1.4	-1.3	Ribosomal protein of the small subunit mitochondrial (by	YHL004w	orf19.13170
CA1156	RLR1	-1.2	-1.2	-1.5	-1.3	hypothetical regulatory protein (by homology)	YNL139c	orf19.4123
CA5004	TRP3	-1.2	-1.2	-1.2	-1.3	Anthranilate synthase / indole glycerol phosphate synth	YKL211c	orf19.5243
CA0140	MDM1.3	-1.2	-1.3	-1.4	-1.3	intermediate filament protein, 3-prime end (by homolog	YML104c	orf19.10097
CA5796	GLO3	-1.2	-1.2	-1.4	-1.3	zinc finger protein	YER122c	orf19.5445
CA5582	ADK2	1.1	-1.6	-1.8	-1.3	adenylate kinase, mitochondrial (by homology)	YER170w	orf19.7118
CA5274	IPF1764	1.2	-1.5	-1.3	-1.3	similar to Saccharomyces cerevisiae Gup1p glycerol tra	YGL084c	orf19.4985
CA4039	SKS1	-1.5	-1.1	-1.5	-1.3	serine/threonine kinase by homology	YPL026c	orf19.3669
CA3214	PUT3	-1.1	-1.4	-1.4	-1.3	putative positive activator of the proline utilisation pathw	YKL015w	orf19.6203
CA0102	IPF16695	-1.3	-1.1	-1.5	-1.3	unknown function	YCR081w	orf19.736
CA4060	GRS1	-1.8	-1.4	-1.5	-1.3	glycine-tRNA ligase (by homology)	YBR121c	orf19.437
CA5424	IPF1598	-1.3	-1.3	-1.6	-1.3	unknown function	YDL074c	orf19.976
CA0864	CYT1	-1.3	-1.5	-1.4	-1.3	cytochrome-c1 (by homology)	YOR065w	orf19.3527
CA2720	IPF7366	-1.3	-1.2	-1.2	-1.3	Arginyl-tRNA synthetase	YDR341c	orf19.3341
CA5119	IPF1320	-1.4	-1.1	-1.4	-1.3	unknown function	YLR386w	orf19.6411
CA1242	IPF19908	1.1	-1.4	-1.4	-1.3	unknown function		orf19.1344
CA5105	PEX19	1.0	-1.4	-1.4	-1.3	Required for biogenesis of peroxisomes (by homology)	YDL065c	orf19.6434
CA0012	IPF19448	-1.2	-1.2	-1.2	-1.3	similar to Saccharomyces cerevisiae Lro1p lecithin chol	YNR008w	orf19.13439
CA2813	ORC1	-1.1	-1.2	-1.6	-1.3	Origin recognition complex protein 1	YML065w	orf19.10518
CA2291	IPF9740	-1.2	-1.4	-1.6	-1.3	oligo-1,4 -1,4-glucantransferase / amylo-1,6-glucosidas	YPR184w	orf19.744
CA0596	IPF9706	-1.0	-1.3	-1.5	-1.3	unknown function	YBR203w	orf19.12346
CA5605	SNF31	1.1	-1.4	-1.5	-1.3	high-affinity glucose transporter (by homology)		orf19.7094
CA1755	PDI1	-1.1	-1.2	-1.7	-1.3	protein disulfide-isomerase precursor (by homology)	YCL043c	orf19.5130
CA5701	ISW2	-1.2	-1.4	-1.4	-1.3	Chromatin remodeling complex (by homology)	YOR304w	orf19.7401
CA4385	CCT6	-1.4	-1.2	-1.4	-1.3	component of chaperonin-containing T-complex (zeta s	YDR188w	orf19.3126
CA0249	IPF19617	-1.1	-1.3	-1.4	-1.3	unknown function		orf19.1350
CA2708	RPS6A	-1.2	-1.5	-1.7	-1.3	ribosomal protein S6 (by homology)	YPL090c	orf19.4660
CA2697	IPF9167	-1.3	-1.2	-1.3	-1.3	unknown function	YDR109c	orf19.2737
CA4711	PHB1	-1.0	-1.3	-1.3	-1.3	Prohibitin, antiproliferative protein (by homology)	YGR132c	orf19.6944
CA1239	HSP60	-1.2	-1.3	-1.3	-1.3	Heat Shock Protein 60 (HSP60)	YLR259c	orf19.717
CA5682	NOG1	-1.3	-1.2	-1.4	-1.3	Nucleolar G-protein (by homology)	YPL093w	orf19.7384
CA3171	IPF7681	-1.0	-1.2	-1.4	-1.3	unknown function		orf19.1397
CA6052	IPF4942	-1.2	-1.5	-1.5	-1.3	similar to Saccharomyces cerevisiae Mal32p alpha-gluc	YBR299w	orf19.7668
CA4892	PRT1	-1.2	-1.3	-1.5	-1.3	Translation initiation factor eIF3 (by homology)	YOR361c	orf19.6584
CA5695	IPF3310	-1.1	-1.2	-1.5	-1.3	unknown function	YPR022c	orf19.7397
CA1291	IPF16752	-1.5	-1.2	-1.4	-1.3	unknown function	YGR200c	orf19.2711
CA5564	IPF1980	-1.2	-1.2	-1.5	-1.3	unknown function		orf19.7328
CA3909	CIT1.EXON2	-1.0	-1.0	-1.2	-1.3	Citrate synthase, exon 2	YNR001c	orf19.4393
CA2668	IPF17553	-1.2	-1.4	-1.5	-1.3	similar to Saccharomyces cerevisiae Pex2p peroxisoma	YJL210w	orf19.3546
CA1172	RGT1	-1.3	-1.4	-1.3	-1.3	Regulator of glucose-induced genes (by homology)	YKL038w	orf19.2747
CA2728	IPF10322	1.0	-1.5	-1.5	-1.3	putative mitochondrial carrier protein (by homology)	YHR002w	orf19.9665
CA5262	IPF1804	-1.3	-1.4	-1.5	-1.3	putative transcription factor (by homology)	YGL166w	orf19.5001
CA5292	IPF1948	-1.0	-1.4	-1.4	-1.3	unknown function	YJL069c	orf19.7154
CA5902	SRP68	-1.4	-1.6	-1.8	-1.3	SIGNAL RECOGNITION PARTICLE 68 (by homology)	YPL243w	orf19.6804
CA2141	IPF19664	-1.4	-1.3	-1.5	-1.3	unknown function		orf19.10047
CA5108	SKI2	-1.1	-1.2	-1.3	-1.3	Antiviral protein and putative helicase	YLR398c	orf19.6425
CA5621	FRE7	-1.0	-1.5	-1.4	-1.3	Ferric reductase transmembrane component (by homol	YOL152w	orf19.7077

CA5296	IPF1956	1.0	-1.3	-1.7	-1.3	unknown function	YMR185w	orf19.7159
CA0300	ERG24	1.1	-1.3	-1.3	-1.3	C-14 sterol reductase (by homology)	YNL280c	orf19.1598
CA4808	RFA1	-1.6	-1.2	-1.4	-1.3	DNA replication factor A, 69 KD subunit (by homology)	YAR007c	orf19.2093
CA3754	TIF3	-1.2	-1.1	-1.5	-1.3	translation initiation factor eIF4B (by homology)	YPR163c	orf19.3423
CA0919	POR1	1.6	-1.4	-1.3	-1.3	mitochondrial outer membrane porin (by homology)	YNL055c	orf19.1042
CA0706	IPF7715	-1.0	-1.1	-1.6	-1.3	unknown function		orf19.8300
CA3384	IPF8362	-1.2	-1.2	-1.7	-1.3	similar to Saccharomyces cerevisiae Cft2p involved in c	YLR115w	orf19.325
CA4312	IPF2122	-1.2	-1.3	-1.3	-1.3	similar to thiamin pyrophosphokinase	YJR142w	orf19.4112
CA2974	IPF12540	1.1	-1.5	-1.6	-1.3	unknown function		orf19.8824
CA4857	PHR1	-1.2	-1.4	-1.5	-1.3	GPI-anchored pH responsive glycosyl transferase		orf19.3829
CA4209	DEP1.3F	-1.5	-1.2	-1.8	-1.3	Regulator of phospholipid metabolism, 3-prime end (by	YAL013w	orf19.8427
CA2035	SGD1.5F	-1.2	-1.3	-1.4	-1.3	Involved in HOG pathway, 5-prime end	YLR336c	orf19.11841
CA1759	IPF14744	-1.2	-1.5	-1.5	-1.3	unknown function	YLR149c	orf19.5125
CA2682	FRS1	-1.3	-1.3	-1.4	-1.3	Phenylalanyl-tRNA synthetase	YLR060w	orf19.2573
CA4772	CCT3	-1.0	-1.4	-1.5	-1.3	Chaperonin (by homology)	YJL014w	orf19.4004
CA3042	ARC1	-1.1	-1.4	-1.6	-1.3	G4 nucleic acid binding protein (by homology)	YGL105w	orf19.2422
CA1324	IPF6676	1.4	-1.4	-1.2	-1.3	polytopic membrane protein involved in drug transport (	YBR293w	orf19.1308
CA0193	IPF6493	1.0	-1.2	-1.5	-1.3	unknown function		orf19.1541
CA5686	IPF3329	-1.1	-1.2	-1.3	-1.3	similar to Saccharomyces cerevisiae Pbs2p tyrosine pr	YJL128c	orf19.7388
CA1061	PF19720.3EOC	1.0	-1.2	-1.8	-1.3	unknown function, 3-prime end		orf19.12113
CA0470	YPT32	-1.1	-1.4	-1.6	-1.3	small GTP-binding protein essential for Golgi function (	YER031c	orf19.2622
CA0225	NUP84	-1.3	-1.3	-1.3	-1.3	nuclear pore protein (by homology)	YDL116w	orf19.1298
CA5309	IPF2170	-1.3	-1.3	-1.5	-1.3	similar to saccharomyces cerevisiae Ssc1pmitochondrial hsp70-type heat shock prote		orf19.7179
CA1283	PF10171.EXON	1.1	-1.1	-1.1	-1.3	unknown function, exon 1		orf19.644
CA0879	IPF19542.5F	1.2	-1.3	-1.4	-1.3	unknown function, 5-prime end		orf19.8003
CA1938	NMD5	-1.5	-1.3	-1.3	-1.3	putative Nam7p/Upf1p-interacting protein (by homolgy)	YJR132w	orf19.4188
CA6139	ADE2	-1.1	-1.1	-1.3	-1.3	phosphoribosylaminoimidazole carboxylase	YOR128c	orf19.5906
CA0480	IPF8610	1.0	-1.6	-1.5	-1.3	permease (by homology)		orf19.2633
CA5828	CRM1	-1.7	-1.3	-1.6	-1.3	Nuclear export factor	YGR218w	orf19.7483
CA5638	IPF470	-1.3	-1.2	-1.5	-1.3	putative glutamine-tRNA ligase (by homology)	YGL245w	orf19.7057
CA4658	IPF3092	-1.2	-1.8	-2.1	-1.3	unknown function		orf19.4445
CA1766	NOP4	-1.1	-1.3	-1.5	-1.4	Nucleolar protein	YPL043w	orf19.5198
CA1408	IPF10513	1.1	-1.6	-1.5	-1.4	unknown function		orf19.2883
CA3667	IPF16323	-1.4	-1.8	-2.1	-1.4	similar to Saccharomyces cerevisiae Pex1p peroxisoma	YKL197c	orf19.6460
CA2033	SEC27	-1.5	-1.3	-1.7	-1.4	coatomer complex beta chain (beta -cop) of secretory p	YGL137w	orf19.10971
CA0204	IKI3	-1.2	-1.3	-1.7	-1.4	killer toxin insensitive protein 3 (by homology)	YLR384c	orf19.1222
CA4169	RSC2	-1.3	-1.1	-1.4	-1.4	Member of RSC complex, which remodels the structure	YGR056w	orf19.2964
CA5184	PF11090.EXON	-1.2	-1.2	-1.5	-1.4	weak similarity to glutenin, exon 2		
CA4201	IPF8048	1.1	-1.5	-1.4	-1.4	probable succinate-semialdehyde dehydrogenase (by homology)		orf19.4543
CA2109	IPF13749.5F	-1.1	-1.4	-1.3	-1.4	unknown function, 5-prime end	YLR345w	orf19.3690
CA3601	IPF15618	-1.3	-1.3	-1.7	-1.4	cysteinyl-tRNA synthetase (by homology)	YNL247w	orf19.4931
CA2796	IPF8405	1.3	-1.4	-1.4	-1.4	similar to Saccharomyces cerevisiae Nce103p involved	YNL036w	orf19.1721
CA5362	IPF836.3	-1.2	-1.4	-1.5	-1.4	regulation of G-protein function, 3-prime end (by homol	YHR146w	orf19.7239
CA3631	TIM54	-1.1	-1.4	-1.4	-1.4	Translocase for the insertion of proteins into the mitoch	YJL054w	orf19.12608
CA4428	IFM1	-1.2	-1.3	-1.6	-1.4	translation initiation factor 2 by homology	YOL023w	orf19.5167
CA5316	MAM33	1.3	-1.5	-1.4	-1.4	Mitochondrial acidic matrix protein (by homology)	YIL070c	orf19.7187
CA4005	ERG6	1.2	-1.5	-1.4	-1.4	sterol transmethylase	YML008c	orf19.1631
CA2162	PDB1	-1.2	-1.8	-1.4	-1.4	pyruvate dehydrogenase (by homology)	YBR221c	orf19.5294
CA0003	IPF19484	-1.5	-1.4	-1.6	-1.4	putative zinc amino peptidase (by homology)		

CA1830	IPF17177.5F	-1.3	1.0	-1.2	-1.4	similar to Saccharomyces cerevisiae Srm1p regulator of chromosome condensation,		orf19.5185
CA5889	IPF2409	-1.1	-1.4	-1.7	-1.4	RNA-dependent ATPase (by homology)	YLR419w	orf19.6818
CA1557	IPF15677	-1.2	-1.4	-1.6	-1.4	probable NADH-ubiquinone oxidoreductase (by homology)		orf19.1710
CA3288	ARD8	1.1	-1.2	-1.1	-1.4	D-arabinitol dehydrogenase		orf19.6322
CA4783	IPF3358	-1.1	-1.3	-1.6	-1.4	ubiquinol-cytochrome-c reductase (by homology)	YBL045c	orf19.4016
CA5023	IPF7547	1.1	-1.4	-1.4	-1.4	unknown function	YJL163c	orf19.6976
CA0895	SHM2	-1.2	-1.5	-1.5	-1.4	Serine hydroxymethyltransferase precursor,	YLR058c	orf19.5750
CA3546	ACO1	1.2	1.1	-1.1	-1.4	aconitate hydratase (by homology)	YLR304c	orf19.6385
CA5027	IPF2999	-1.5	-1.3	-1.6	-1.4	unknown function	YKR051w	orf19.6981
CA4505	NOP2	-1.3	-1.1	-1.3	-1.4	nucleolar protein (by homology)	YNL061w	orf19.501
CA4684	HSP78.5F	-1.3	-1.1	-1.6	-1.4	heat shock protein of clpb family of ATP-dependent proteases, mitochondrial, 5-prime		orf19.882
CA0433	SHM1	-1.3	-1.4	-1.6	-1.4	Serine hydroxymethyltransferase precursor, mitochondr	YBR263w	orf19.1342
CA2442	PRS5	-1.1	-1.3	-1.3	-1.4	Phosphoribosylpyrophosphate synthetase (ribose-phos	YOL061w	orf19.2193
CA5947	KRS1	-1.4	-1.2	-1.4	-1.4	Lysyl-tRNA synthetase (by homology)	YDR037w	orf19.6749
CA0741	IPF3261	-1.1	-1.2	-1.4	-1.4	unknown function	YPL105c	orf19.3141
CA5164	MDH1	1.2	-1.4	-1.4	-1.4	Mitochondrial malate dehydrogenase precursor (by hom	YKL085w	orf19.4602
CA5183	PF11090.EXON	-1.2	-1.2	-1.9	-1.4	weak similarity to glutenin, exon 1	YKL054c	orf19.4622
CA4928	IPF1399	-1.2	-1.5	-1.4	-1.4	unknown function	YDR346c	orf19.6068
CA4542	IPF6255	-1.3	-1.4	-1.5	-1.4	unknown function	YHR074w	orf19.1460
CA4667	GAP5	1.1	-1.4	-1.2	-1.4	General amino acid permease (by homology)		orf19.4456
CA0446	IPF14282	1.2	1.0	-1.8	-1.4	Similar to mucin proteins (by homology)		orf19.2296
CA3901	IPF3282.3EOC	1.1	-1.7	-1.6	-1.4	hexose transporter, 3-prime end (by homology)		
CA0781	CAR1.3EOC	1.1	-1.4	-1.7	-1.4	arginase, 3-prime end (by homology)		orf19.11416
CA3016	IPF10027	-1.2	-1.4	-1.7	-1.4	unknown function		orf19.11396
CA1127	MSH3	-1.5	-1.5	-1.5	-1.4	DNA mismatch repair by homology	YCR092c	orf19.3608
CA1758	IPF14559.3F	-1.0	-1.4	-1.4	-1.4	unknown function, 3-prime end	YCL037c	orf19.5126
CA1592	IPF14662	1.6	-1.7	-1.4	-1.4	D-xylose reductase (by homology)	YHR104w	orf19.4317
CA1797	NUM12	-1.2	-1.0	-1.8	-1.4	nuclear migration protein (by homology)		orf19.2924
CA4864	IPF4087	-1.1	-1.4	-1.8	-1.4	similar to Saccharomyces cerevisiae Pak1p protein kin	YER129w	orf19.3840
CA3212	MEF2	-1.1	-1.4	-1.3	-1.4	translation elongation factor (by homology)	YJL102w	orf19.6208
CA2884	IPF7201	-1.4	-1.2	-1.9	-1.4	similar to Saccharomyces cerevisiae Ecm5p involved in	YMR176w	orf19.2476
CA3121	GGA1	-1.4	-1.3	-1.5	-1.4	Arf-binding protein	YHR108w	orf19.3006
CA0048	TIF4631	1.0	-1.2	-1.5	-1.4	mRNA cap-binding protein (by homology)	YGR162w	orf19.3599
CA1954	IPF3897.5F	-1.3	-1.1	-1.7	-1.4	unknown function, 5-prime end	YGL083w	orf19.764
CA2150	IPF19940	-1.2	-1.4	-1.4	-1.4	unknown function		orf19.6022
CA0987	RPB140	-1.2	-1.2	-1.9	-1.4	DNA-dependent RNA polymerase II RPB140	YOR151c	orf19.3349
CA2297	ERG4	1.5	-1.7	-1.2	-1.4	sterol C-24 reductase (by homology)	YGL012w	orf19.5379
CA0914	SRA1	-1.7	-1.4	-1.6	-1.4	cAMP dependent protein kinase, regulatory subunit (by	YIL033c	orf19.9565
CA0167	IPF19160	-1.6	-1.5	-1.9	-1.4	unknown function		orf19.1075
CA3061	IPF2965	-1.1	-1.5	-1.7	-1.4	unknown function		orf19.11763
CA0615	RPL3	-1.2	-1.3	-1.5	-1.4	60S large subunit ribosomal protein L3.e (by homology)	YOR063w	orf19.1601
CA0832	IPF14225	-1.1	-1.6	-1.5	-1.4	unknown function	YDL133w	orf19.9244
CA5288	IPF1928	-1.2	-1.4	-1.4	-1.4	unknown function	YMR258c	orf19.7149
CA1702	HEL1	-1.4	-1.3	-1.4	-1.4	DNA helicase I (by homology)	YER176w	orf19.702
CA5525	PEX13	1.0	-1.9	-1.7	-1.4	Peroxisome import protein - peroxin (by homology)	YLR191w	orf19.7282
CA0660	IPF16189.5F	-1.1	-1.4	-2.0	-1.4	panthotenate kinase, 5-prime end (by homology)	YDR531w	orf19.5577
CA2093	IPF3406	-1.2	-1.2	-1.4	-1.4	unknown function	YKL179c	orf19.841
CA2414	IPF13756.3F	-1.5	-1.5	-1.5	-1.4	unknown function, 3-prime end	YJL010c	orf19.4479
CA5937	IPF2784	-1.2	-1.2	-2.0	-1.4	unknown function	YER132c	orf19.6760

CA0445	IPF17429.5F	-1.6	-1.3	-1.8	-1.4	similar to Saccharomyces cerevisiae Sec5p required for exocytosis, 5-prime end		orf19.7725
CA1879	SMF12	-1.1	-1.5	-1.5	-1.4	manganese transporter (by homology)	YOL122c	orf19.2270
CA6060	IPF8301	-1.3	-1.3	-1.4	-1.4	unknown function	YLL032c	orf19.6008
CA0197	IPF9787	-1.3	-1.6	-1.9	-1.4	similar to Saccharomyces cerevisiae Hst3p silencing pr	YOR025w	orf19.1934
CA3750	IPF7377	-1.2	-1.4	-1.8	-1.4	unknown function		orf19.3428
CA3479	ATP4	-1.2	-1.4	-1.6	-1.4	F1F0-ATPase complex, F0 subunit B (by homology)	YPL078c	orf19.3579
CA4981	IPF2057	-1.2	-1.6	-1.7	-1.4	unknown function		orf19.5269
CA3265	ABP1	-1.2	-1.5	-1.6	-1.4	actin-binding protein (by homology)	YCR088w	orf19.2699
CA0343	LYS1.5EOC	-1.1	-1.3	-1.3	-1.4	saccharopine dehydrogenase, 5-prime end (by homolog	YIR034c	
CA4632	IPF1531	-1.2	-1.3	-1.8	-1.4	unknown function	YMR196w	orf19.338
CA4665	IPF6548	-1.3	-1.2	-1.6	-1.4	translation elongation factor eEF4 (by homology)	YNL163c	orf19.4451
CA4650	ISW1.3	-1.3	-1.4	-1.9	-1.4	ATPase component of a four subunit chromatin remode	YBR245c	orf19.11916
CA4457	ATP1.EXON3	-1.0	-1.4	-1.4	-1.4	F1F0-ATPase complex, F1 alpha subunit, exon 3	YBL099w	orf19.6854
CA0584	GSH1.EXON1	-1.9	-1.3	-2.1	-1.4	Gamma-glutamylcysteine synthetase, exon 1 (by homology)		orf19.12527
CA0524	CYT12	-1.1	-1.4	-1.3	-1.4	cytochrome-c1 (by homology)		orf19.11011
CA0108	HIK1.5EOC	-1.3	-1.1	-1.7	-1.4	histidine kinase, 5-prime end		orf19.5181
CA4495	IPF4059	-1.4	-1.5	-1.5	-1.4	aldehyde dehydrogenase (by homology)	YHR039c	orf19.1865
CA0223	VAS1	-1.6	-1.5	-1.8	-1.5	valyl-tRNA synthetase (by homology)	YGR094w	orf19.1295
CA0265	STI1	-1.6	-1.4	-1.6	-1.5	stress-induced protein (by homology)	YOR027w	orf19.10702
CA1873	IPF6696	1.2	-1.6	-1.8	-1.5	unknown function		orf19.9997
CA4326	IPF2093	-1.2	-1.3	-1.5	-1.5	nuclear protein of unknown function (by homology)	YGR103w	orf19.4093
CA3174	CCT2	-1.4	-1.2	-1.4	-1.5	chaperonin of the TCP1 ring complex,cytosolic (by hom	YIL142w	orf19.1402
CA2008	PF1742.3F.EO	-1.0	-1.4	-1.9	-1.5	unknown function, 3-prime end		
CA0747	SNF2	-1.3	-1.3	-1.8	-1.5	component of SWI/SNF global transcription activator co	YOR290c	orf19.9102
CA5955	IPF3510	-1.2	-1.3	-1.7	-1.5	unknown function	YMR278w	orf19.6739
CA0934	IPF14203.3F	-1.0	-1.5	-1.7	-1.5	similarity to several transaminases, 3-prime end (by homology)		orf19.1078
CA1699	RAM1.3F	-1.3	-1.4	-1.6	-1.5	protein farnesyltransferase, beta subunit, 3-prime end (by homology)		
CA4883	IPF1649	-1.6	-1.1	-2.0	-1.5	similar to Saccharomyces cerevisiae Bem2p GTPase-a	YER155c	orf19.6573
CA4054	TRF4	-1.2	-1.3	-1.4	-1.5	Topoisomerase I-related protein	YOL115w	orf19.429
CA4993	PXA2	1.0	-1.7	-1.8	-1.5	ABC transporter, peroxisomal (by homology)	YKL188c	orf19.5255
CA4294	ERC1	-1.0	-1.4	-1.6	-1.5	ethionine resistance protein (by homology)	YHR032w	orf19.6691
CA4875	LAT1	-1.4	-1.4	-1.7	-1.5	Dihydrolipoamide S-acetyltransferase (by homology)	YNL071w	orf19.6561
CA3175	IPF11587	-1.2	-1.6	-1.5	-1.5	unknown function	YNL083w	orf19.1403
CA4838	YTA12	-1.4	-1.3	-1.8	-1.5	Protease of the SEC18/CDC48/PAS1 family of ATPase	YMR089c	orf19.2057
CA6009	IPF643	-1.1	-1.5	-1.9	-1.5	similar to Saccharomyces cerevisiae Ptp3p protein tyros	YER075c	orf19.7610
CA1982	ADK1	-1.0	-1.4	-1.7	-1.5	adenylate kinase, cytosolic (by homology)	YDR226w	orf19.683
CA2060	CDC61.3F	-1.3	-1.2	-1.9	-1.5	Cytosolic leucyl-tRNA synthetase, 3-prime end		orf19.2560
CA3514	IPF11245	-1.3	-1.4	-2.1	-1.5	similar to Saccharomyces cerevisiae Spa2p involved in	YLL021w	orf19.6362
CA4904	RPO41	-1.2	-1.3	-1.9	-1.5	Mitochondrial DNA-directed RNA polymerase (by homo	YFL036w	orf19.6041
CA1793	IPF18608.5F	-1.2	-1.6	-1.7	-1.5	unknown function, 5-prime end		orf19.5207
CA5991	IPF690.3F	-1.4	-1.3	-1.6	-1.5	NADH dehydrogenase (ubiquinone) 78K chain precursor, 3-prime end (by homology)		orf19.7591
CA4954	TOM40	-1.3	-1.3	-1.4	-1.5	mitochondrial import receptor chain TOM40 (by homolog	YMR203w	orf19.6524
CA3499	RPG1	-1.5	-1.3	-1.9	-1.5	Translation initiation factor eIF3 (by homology)	YBR079c	orf19.6345
CA0245	POL5	-1.6	-1.5	-2.0	-1.5	DNA polymerase V (by homology)	YEL055c	orf19.13042
CA2608	THS1	-1.7	-1.3	-1.4	-1.5	threonyl tRNA synthetase by homology	YIL078w	orf19.5685
CA2899	IPF17681	-1.3	-1.5	-1.7	-1.5	similar to Saccharomyces cerevisiae Rsm23p involved i	YGL129c	orf19.3480
CA1620	MET10	-1.3	-1.6	-1.9	-1.5	Sulfite reductase flavin-binding subunit (by homology)	YFR030w	orf19.4076
CA4350	FUM12.53F	-1.1	-1.6	-2.2	-1.5	Fumarate hydratase, internal fragment (by homology)		
CA4412	PDA1	1.1	-1.0	-1.5	-1.5	Pyruvate dehydrogenase alpha chain (by homology)	YER178w	orf19.3097

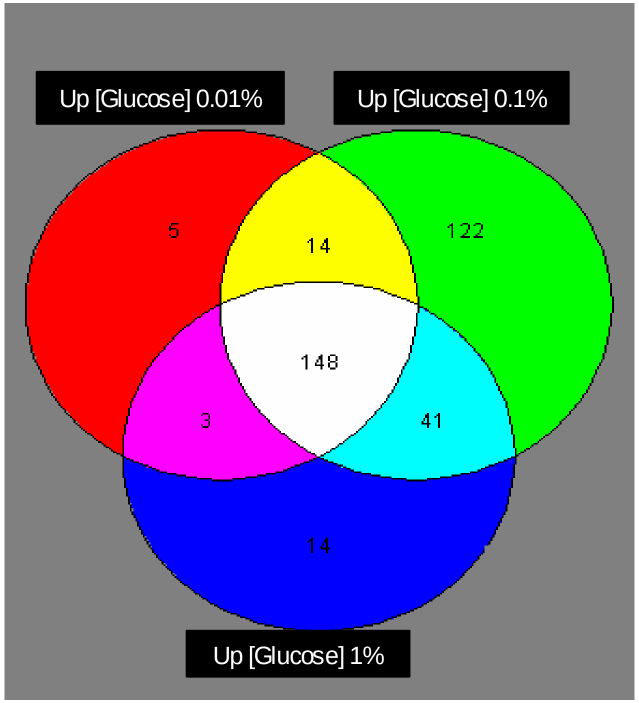
CA3474	AFG3	-1.3	-1.5	-1.8	-1.5	Member of the Sec18p, Pas1p, Cdc48p, TBP-1 family o	YER017c	orf19.1669
CA2009	IPF1732	1.3	-1.4	-1.4	-1.5	intramitochondrial protein sorting (by homology)	YLR168c	orf19.3089
CA2447	HIS7	-1.4	-1.6	-2.0	-1.5	Histidine biosynthesis	YBR248c	orf19.5505
CA1693	IPF17054	-1.0	-1.7	-1.8	-1.5	unknown function		orf19.5037
CA3771	SOU1	-1.0	-1.6	-1.7	-1.5	Sorbitol utilization protein Sou1p [Candida albicans]		orf19.2896
CA4210	DEP1.5F	-1.4	-1.3	-2.0	-1.5	Regulator of phospholipid metabolism, 5-prime end (by homology)		orf19.8428
CA4029	IPF7171.5F	-1.3	-1.5	-1.9	-1.5	unknown function, 5-prime end	YGR067c	orf19.3434
CA4504	ARP5	-1.3	-1.2	-1.8	-1.5	actin-related protein (by homology)	YNL059c	orf19.504
CA4713	CCC1	1.0	-1.7	-1.4	-1.5	Transmembrane Ca2+ transporter (by homology)	YLR220w	orf19.6948
CA5154	RGA2	-1.2	-1.2	-1.8	-1.5	rho-GTPase activating protein 2 (by homology)	YOR127w	orf19.4593
CA1911	SSE1	-1.5	-1.5	-1.7	-1.5	heat shock protein of HSP70 family (by homology)	YPL106c	orf19.2435
CA0163	AYR2	1.1	-1.7	-1.6	-1.5	1-acyl dihydroxyacetone phosphate reductase (by homology)		orf19.5615
CA6127	IPF149	-1.1	-1.7	-1.7	-1.5	peroxisomal membrane protein (by homology)		orf19.5921
CA2131	IDP1	1.1	-1.5	-1.9	-1.5	isocitrate dehydrogenase, cytosolic (by homology)		orf19.5211
CA3994	ERG7	-1.1	-1.5	-1.6	-1.5	lanosterol synthase	YHR072w	orf19.9143
CA6149	RIP1	-1.5	-1.5	-1.7	-1.5	Ubiquinol cytochrome-c reductase (by homology)	YEL024w	orf19.5893
CA4077	ACO2	-1.2	-1.1	-1.6	-1.6	aconitate hydratase (by homology)	YJL200c	orf19.6632
CA3990	IPF14782	1.1	-1.6	-1.9	-1.6	beta-transducin (by homology)	YLR409c	orf19.1566
CA5430	IPF191	1.3	-1.5	-1.5	-1.6	putative permease (by homology)		orf19.3232
CA1439	IPF19602	-1.6	-1.6	-1.9	-1.6	similar to Saccharomyces cerevisiae Swi3p transcriptio	YJL176c	orf19.4488
CA2972	MDL2.3F	-1.5	-1.3	-1.6	-1.6	ATP-binding transporter, 3-prime end (by homology)		orf19.5599
CA1024	CAR1	1.0	-1.7	-2.0	-1.6	arginase by homology	YPL111w	orf19.3934
CA5097	IPF1382	-1.1	-1.4	-1.2	-1.6	unknown function	YHL023c	orf19.6444
CA4243	IPF16491	-1.1	-1.3	-1.9	-1.6	unknown function		orf19.529
CA2538	NAT1	-1.6	-1.4	-1.8	-1.6	Protein N-acetyltransferase subunit (by homology)	YDL040c	orf19.3185
CA4966	IPF3923	-1.4	-1.3	-1.8	-1.6	unknown function		orf19.6507
CA4446	ICL1	-1.0	-1.9	-2.0	-1.6	Isocitrate lyase	YER065c	orf19.6844
CA2823	IPF14554	-1.3	-1.5	-1.8	-1.6	similar to Saccharomyces cerevisiae Osh3p oxysterol-b	YHR073w	orf19.1317
CA4301	IPF2593	-1.7	-1.3	-1.5	-1.6	amino acid-tRNA ligase homolog (by homology)	YHR020w	orf19.6701
CA0255	IPF16558.3	-1.0	-1.3	-1.9	-1.6	putative transcription initiation factor, 3-prime end (by homology)		orf19.735
CA3015	IPF10029	-1.4	-1.8	-1.8	-1.6	unknown function	YFR044c	orf19.11397
CA2169	IPF4563.5F	-1.3	1.3	-2.0	-1.6	similar to saccharomyces cerevisiae Tom1p E3 ubiqitin ligase required for G2/M trans		orf19.911
CA6029	DRS1	-1.0	-1.4	-1.9	-1.6	ATP dependent RNA helicase (by homology)	YLL008w	orf19.7635
CA1988	IPF19749	-1.1	-1.7	-1.8	-1.6	unknown function		orf19.94
CA2310	LEU42	-1.3	-2.8	-3.2	-1.6	2-isopropylmalalate synthase (by homology)		orf19.1375
CA3404	MAL31	1.0	-1.9	-2.4	-1.6	maltose permease (by homology)	YBR298c	orf19.3981
CA4474	SSC1	1.4	-1.1	-1.2	-1.6	Mitochondrial heat shock protein 70-related protein (by	YJR045c	orf19.1896
CA4909	TUF1	-1.1	-1.3	-1.3	-1.6	Translation elongation factor TU (by homology)	YOR187w	orf19.6047
CA2623	PER3.EXON1	-1.5	-1.9	-2.3	-1.6	peroxisomal import protein, exon 1 (by homology)		orf19.10323
CA1438	NOP58	-1.3	-1.3	-1.7	-1.6	nucleolar protein required for pre-18S rRNA processing	YOR310c	orf19.1199
CA4639	IPF1509	-1.1	-1.7	-1.9	-1.6	putative alanine transaminase (by homology)	YLR089c	orf19.346
CA0030	IPF17790	-1.5	-1.4	-1.8	-1.6	unknown function	YML091c	orf19.7710
CA2269	YOR100	1.2	-1.8	-2.0	-1.6	Putative mitochondrial carrier protein	YOR100c	orf19.2599
CA4513	ADE17	-1.3	-1.7	-1.8	-1.6	5-aminoimidazole-4-carboxamide ribotide transformylas	YMR120c	orf19.492
CA1344	IPF14623	1.1	-1.6	-1.8	-1.6	unknown function	YPR009w	orf19.4342
CA2244	AAT22	-1.1	-1.7	-2.1	-1.6	aspartate aminotransferase (by homology)		orf19.4669
CA5346	IPF867	-1.0	-1.5	-1.9	-1.6	unknown function	YKR029c	orf19.7221
CA5588	SOD22.3F	1.1	-1.8	-2.1	-1.6	superoxide dismutase, 3-prime end (by homology)		
CA4270	NUP2	-1.3	-1.6	-2.0	-1.6	Nuclear pore protein (by homology)	YLR335w	orf19.6665

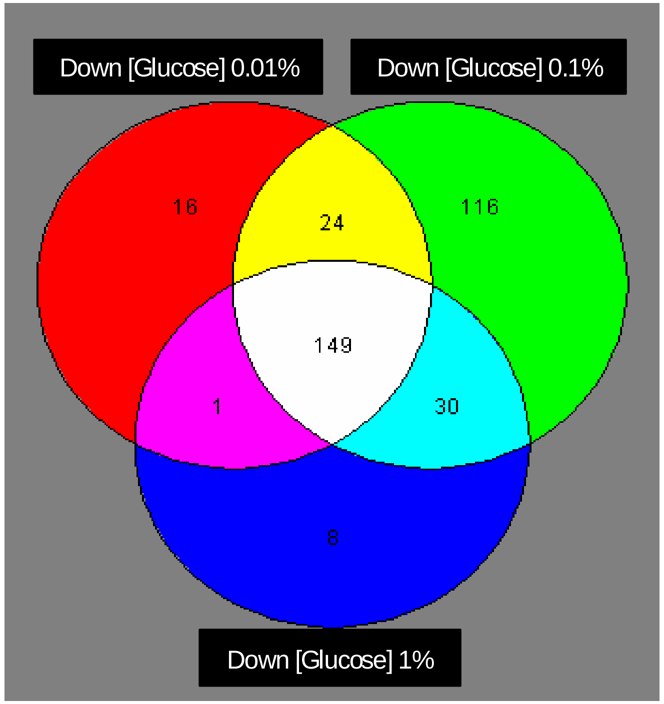
CA6095	SNF3	1.0	-1.7	-2.0	-1.6	High affinity glucose transport protein (by homology)	YDL194w	orf19.5962
CA1716	IPF17237	1.1	-1.4	-1.8	-1.6	unknown function		orf19.3335
CA5725	GLG2	1.1	-1.9	-2.2	-1.6	Self-glucosylating initiator of glycogen synthesis (by homology)		orf19.7434
CA2522	GCV1	-1.1	-2.0	-2.0	-1.6	glycine cleavage T protein (by homology)	YDR019c	orf19.5519
CA6072	DBP10	-1.3	-1.5	-2.1	-1.6	Putative ATP-dependent RNA helicase (by homology)	YDL031w	orf19.5991
CA0415	FRP3	1.4	-1.5	-1.6	-1.7	member of the FRP family of proteins related to Yarrowi	YCR010c	orf19.1224
CA6084	IPF29	-1.1	-1.7	-2.0	-1.7	zinc finger protein (by homology)		orf19.5975
CA1539	BFR1	-1.5	-1.7	-2.1	-1.7	Similar to Saccharomyces cerevisiae Bfr1p involved in t	YOR198c	orf19.4560
CA4203	SWI4	-1.3	-1.4	-1.9	-1.7	transcription factor (by homology)		orf19.12020
CA3993	IPF8275	-1.3	-1.4	-1.8	-1.7	unknown function	YGR090w	orf19.9142
CA3765	IPF18298	-1.8	-1.4	-2.4	-1.7	unknown function		orf19.2904
CA0791	LSC1	1.1	-1.9	-1.8	-1.7	succinate-CoA ligase / synthetase (by homology)	YOR142w	orf19.3358
CA0107	POL3.5EOC	-1.2	-1.4	-2.7	-1.7	DNA Polymerase III, 5-prime end	YDL102w	orf19.5183
CA5676	FAA22	-1.1	-2.1	-2.1	-1.7	Long-chain-fatty-acid--CoA ligase (by homology)		orf19.7379
CA2663	NUP133	-1.7	-1.5	-2.1	-1.7	nuclear pore protein (by homology)	YKR082w	orf19.3552
CA1238	IPF15781	-1.3	-2.0	-2.5	-1.7	unknown function		orf19.8335
CA1605	SWI6	-1.5	-1.6	-2.0	-1.7	Transcription factor (by homology)	YLR182w	orf19.4725
CA5899	IPF2382	-1.2	-1.8	-2.1	-1.7	unknown function		orf19.6807
CA2947	IPF6298	1.1	-1.9	-1.8	-1.7	unknown function		orf19.1964
CA4638	UGA2	-1.1	-1.6	-2.7	-1.8	succinate-semialdehyde dehydrogenase (NAD(P)+) (by	YBR006w	orf19.345
CA1051	CHT2	1.2	-1.8	-1.7	-1.8	chitinase 2 precursor		orf19.3895
2262.1		-1.1	-1.3	-1.7	-1.8			
CA2858	ACS2	-1.2	-1.8	-1.7	-1.8	acetyl-coenzyme-A synthetase (by homology)	YLR153c	orf19.1064
CA1367	IPF16755	-1.2	-2.1	-2.4	-1.8	unknown function	YPR021c	orf19.4966
CA5971	GNP2	1.1	-1.7	-1.8	-1.8	high affinity glutamine permease (by homology)		orf19.7565
CA4441	IPF2268.3	-1.1	-1.4	-1.7	-1.8	unknown function, 3-prime end		
CA4442	IPF3537	1.1	-2.1	-2.1	-1.8	unknown function		orf19.6838
CA3915	IPF3277	1.2	-2.0	-2.1	-1.8	unknown function		orf19.4384
CA2582	TAL1	-1.2	-1.8	-2.0	-1.8	transaldolase (by homology)	YLR354c	orf19.4371
CA3242	RAT1	-1.6	-1.7	-2.4	-1.8	5 -3 Exoribonuclease (by homology)	YOR048c	orf19.4681
CA1146	CWH8	1.5	-1.9	-1.6	-1.8	putative required protein for full levels of dolichol-linked	YGR036c	orf19.3682
CA5060	IPF3690	-1.2	-1.9	-2.1	-1.8	unknown function	YDR036c	orf19.3029
CA0848	ACS1	-1.0	-2.1	-2.0	-1.8	acetyl-coenzyme-A synthetase (by homology)	YAL054c	orf19.1743
CA3566	GUT2	1.1	-1.6	-1.6	-1.8	Glycerol-3-phosphate dehydrogenase, mitochondrial (b	YIL155c	orf19.3133
CA3528	GLY1	-1.2	-2.0	-2.2	-1.8	L-threonine aldolase		orf19.8601
CA4183	SNO1	-1.0	-2.2	-2.1	-1.8	hisH-like protein (by homology)	YMR095c	orf19.10465
CA3827	IPF10662	1.0	-1.6	-1.9	-1.9	unknown function		orf19.5760
CA3713	OPS4	1.2	-2.0	-3.3	-1.9	opaque - phase specific protein OP4, precursor (by homology)		orf19.4934
CA5426	FAS1	-1.2	-1.7	-2.0	-1.9	Fatty-acyl-CoA synthase, beta chain.	YKL182w	orf19.979
CA2061	CDC61.5F	-1.3	-1.3	-2.1	-1.9	Cytosolic leucyl-tRNA synthetase, 5-prime end	YPL160w	orf19.2562
CA3818	IPF6695	-1.5	-2.2	-2.5	-1.9	unknown function	YOL057w	orf19.5773
CA3017	IPF10021	-1.3	-2.0	-2.3	-1.9	unknown function	YER040w	orf19.11393
CA0929	GUT1	-1.0	-1.7	-1.9	-1.9	Glycerol kinase (by homology)	YHL032c	orf19.558
CA5259	OSM2	-1.2	-2.0	-1.7	-1.9	Osmotic growth protein (by homology)		orf19.5005
CA3813	FRP1	1.1	-1.8	-1.9	-1.9	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathway		orf19.2496
CA5797	IPF4182	1.0	-1.9	-2.6	-1.9	unknown function		orf19.5446
CA4663	IPF6554	-1.2	-1.9	-2.1	-1.9	unknown function	YJL103c	orf19.4450
CA1765	APE2	-1.3	-1.4	-2.0	-2.0	aminopeptidase yscII	YKL157w	orf19.5197
CA0428	ILV2	-1.5	-2.0	-2.5	-2.0	acetolactate synthase (by homology)	YMR108w	orf19.1613

CA3603	MEF1	-1.3	-1.8	-2.0	-2.0	mitochondrial translation elongation factor G (by homolc	YLR069c	orf19.4932
CA4672	IPF3659	-1.6	-1.5	-2.1	-2.0	similar to Saccharomyces cerevisiae Nsp1p nuclear po	YJL041w	orf19.900
CA1397	TOM72	-1.9	-1.9	-2.4	-2.0	mitochondrial import receptor (by homology)	YNL121c	orf19.3700
CA5629	CTR9	-1.5	-1.5	-2.9	-2.0	required for G1 cyclin expression (by homology)	YOL145c	orf19.7067
CA2470	SDH12	-1.2	-1.9	-1.8	-2.0	Succinate dehydrogenase (by homology)		orf19.10389
CA1075	IPF4991	-1.5	-2.7	-2.6	-2.0	putative membrane protein	Missing in array	orf19.2531
CA3149	KGD1	1.1	-2.0	-2.1	-2.0	2-oxoglutarate dehydrogenase	YIL125w	orf19.6165
CA4255	FUM11	-1.2	-2.0	-2.1	-2.0	fumarate hydratase	YPL262w	orf19.543
CA1000	IPF6011	1.1	-1.8	-2.1	-2.0	unknown function		orf19.9061
CA2998	LPD1	-1.3	-1.9	-2.6	-2.0	dihydrolipoamide dehydrogenase (by homology)	YFL018c	orf19.6127
CA6107	FAS2.3F	1.6	-1.2	-1.2	-2.1	fatty-acyl-CoA synthase, alpha chain, 3-prime end	YPL231w	orf19.5949
CA0098	IPF16479	-1.2	-2.1	-2.3	-2.1	unknown function	YDR365c	orf19.2319
CA3227	AAT21	-1.4	-2.1	-2.1	-2.1	aspartate aminotransferase (by homology)	YLR027c	orf19.6287
CA6106	FAS2.53F	-1.0	-1.3	-3.1	-2.1	fatty-acyl-CoA synthase, alpha chain, internal fragment		
CA1639	PF18641.EXON	-1.8	-1.8	-2.8	-2.1	unknown function, exon 1		orf19.1733
CA1891	IPF10196	-1.3	-2.4	-2.7	-2.2	unknown function	YDR216w	orf19.2752
CA0186	PLB4.3F	1.0	-2.5	-3.2	-2.2	phospholipase, 3-prime end (by homology)		orf19.9018
CA1640	PF18641.EXON	-2.3	-1.9	-2.9	-2.2	unknown function, exon 2		orf19.1732
CA5655	IPF18080	-1.5	-2.3	-2.5	-2.2	unknown function	YIL083c	orf19.7357
CA5992	FAA4	-1.1	-2.2	-2.5	-2.3	long-chain fatty acid--CoA ligase and synthetase 4 (by h	YMR246w	orf19.7592
CA1650	IPF5389	1.2	-2.5	-3.4	-2.3	3-hydroxyisobutyrate dehydrogenase by homology		orf19.5565
CA0783	ACR1	1.1	-3.3	-3.5	-2.3	Succinate-fumarate transporter (by homology)	YJR095w	orf19.3931
CA5990	IPF690.5F	-2.0	-1.7	-3.0	-2.3	NADH dehydrogenase (ubiquinone) 78K chain precursor, 5-prime end (by homology)		orf19.7590
CA4158	DLD3	-1.1	-2.7	-2.5	-2.3	D-lactate ferrycytochrome C oxidoreductase (by homology)		orf19.5805
CA3455	PF10533.EXON	-1.2	-2.2	-2.5	-2.3	unknown function, exon 2		orf19.1256
CA4803	PEX4	1.3	-2.5	-3.0	-2.4	E2 ubiquitin-conjugating enzyme -peroxin (by homology	YGR133w	orf19.4041
CA5263	CYB3	-1.2	-3.2	-2.7	-2.5	Lactate dehydrogenase cytochrome b2 (by homology)	YML054c	orf19.5000
CA5993	ASP1	-1.3	-2.5	-2.7	-2.5	L-asparaginase (by homology)	YDR321w	orf19.7593
CA0310	PEX11	1.6	-2.2	-2.0	-2.5	peroxisomal membrane protein - peroxin by homology	YOL147c	orf19.8690
CA1225	SPS20	1.0	-2.1	-2.2	-2.5	peroxisomal 2,4-dienoyl-CoA reductase (by homology)		orf19.4157
CA2204	DIP51.5F	1.7	-2.1	-1.8	-2.5	dicarboxylic amino acid permease, 5-prime end (by homology)		orf19.2943
CA2203	DIP51.3F	1.0	-2.4	-2.7	-2.6	dicarboxylic amino acid permease, 3-prime end (by hon	YPL265w	orf19.2942
CA1144	SPS19	1.1	-2.6	-3.6	-2.6	peroxisomal 2,4-dienoyl-CoA reductase (by homology)	YNL202w	orf19.11168
CA4351	FUM12.3F	-1.1	-2.8	-2.9	-2.6	Fumarate hydratase, 3-prime end (by homology)		orf19.6725
CA4311	FAA23	-1.2	-2.8	-3.0	-2.6	Long-chain-fatty-acid--CoA ligase (by homology)		orf19.4114
CA2997	KGD2	-1.4	-2.7	-3.2	-2.6	2-oxoglutarate dehydrogenase complex E2 component	YDR148c	orf19.6126
CA1301	YHM2	-1.4	-3.6	-4.4	-2.7	mtDNA stabilizing protein (by homology)	YMR241w	orf19.4197
CA4349	FUM12.5F	-1.2	-2.5	-3.0	-2.7	Fumarate hydratase, 5-prime end (by homology)		orf19.6724
CA1596	FAA21	-1.2	-3.0	-3.8	-2.7	long-chain-fatty-acid-CoA ligase (by homology)	YER015w	orf19.272
CA3945	CHA12	1.0	-3.2	-3.6	-2.7	L-serine/L-threonine deaminase (by homology)		orf19.9548
CA0664	LSC2.3EOC1	1.0	-2.7	-2.9	-2.7	succinate-CoA ligase beta subunit, 3-prime end (by hon	YGR244c	orf19.710
CA1414	CHO2	-1.7	-2.4	-2.8	-2.8	phosphatidylethanolamine N-methyltransferase (by hom	YGR157w	orf19.169
CA4184	SNZ1	-1.2	-3.6	-4.6	-2.8	stationary phase protein by homology	YMR096w	orf19.2947
CA1561	POT12	1.0	-2.8	-3.7	-2.8	peroxysomal 3-ketoacyl-CoA thiolase B (by homology)		orf19.1704
CA1775	GDH2	1.1	-2.9	-3.1	-2.8	NAD-specific glutamate dehydrogenase (NAD) (by hom	YDL215c	orf19.9738
CA6105	FAS2.5F	-1.1	-1.6	-4.0	-2.9	fatty-acyl-CoA synthase, alpha chain, 5-prime end		orf19.5951
CA3376	LSC2.3EOC2	-1.4	-2.4	-3.8	-2.9	succinate-CoA ligase beta subunit, 3-prime end (by homology)		
CA5848	IPF407	-1.1	-3.2	-4.3	-3.0	unknown function	YGR161c	orf19.7504
CA3485	IPF3213	-1.7	-3.2	-4.4	-3.0	similar to Saccharomyces cerevisiae Pex6p peroxisoma	YNL329c ; Missing in array	orf19.3573

CA1574	PXP2	-1.1	-3.1	-3.7	-3.0	acyl-CoA oxidase peroxisomal (by homology)		orf19.1655
CA3914	IPF3282	1.3	-3.1	-2.9	-3.0	hexose transporter (by homology)		orf19.4386
CA0807	IPF12564	-1.3	-3.5	-3.4	-3.0	ADP/ATP carrier proteins (by homology)	YPL134c	orf19.3518
CA0185	PLB4.5F	-1.1	-3.6	-4.3	-3.1	Phospholipase, 5-prime end (by homology)		orf19.9017
CA0643	IDP2	-1.1	-3.6	-4.8	-3.1	isocitrate dehydrogenase, cytosolic (by homology)	YLR174w	orf19.3733
CA5972	GNP1	1.3	-3.9	-5.5	-3.1	high affinity glutamine permease (by homology)		orf19.7566
CA0290	POT14	-1.2	-3.4	-2.9	-3.2	acetyl-CoA acetyltransferase (by homology)	YPL028w	orf19.1591
CA1496	CTR1	-1.1	-2.1	-2.2	-3.4	copper transport protein	YPR124w	orf19.3646
CA5293	FAA24	-1.3	-3.1	-5.0	-3.5	Long-chain-fatty-acid--CoA ligase (by homology)		orf19.7156
CA1506	HGT11	1.5	-2.3	-4.2	-3.6	hexose transporter	YFL040w	orf19.4527
CA5816	ACC1	-1.5	-3.4	-4.4	-3.6	acetyl-coenzyme-A carboxylase (by homology)	YNR016c	orf19.7466
CA3883	GCV2	-1.2	-3.7	-5.2	-3.7	Glycine decarboxylase P subunit	YMR189w	orf19.8015
CA1552	PUT1	-1.4	-4.0	-5.4	-3.7	proline oxidase (by homology)	YLR142w	orf19.4274
CA4159	ALD5	1.5	-3.3	-2.7	-3.7	aldehyde dehydrogenase (NAD+) (by homology)	YER073w	orf19.13228
CA4038	HGT12	1.4	-3.4	-5.4	-3.8	hexose transporter		orf19.3668
CA2561	CAR2	-1.2	-4.7	-4.7	-3.8	ornithine aminotransferase (by homology)	YLR438w	orf19.5641
CA1181	UGA12.5F	-1.4	-8.2	-11.9	-3.8	4-aminobutyrate aminotransferase (GABA transaminase), 5-prime end (by homology)		orf19.802
CA3416	FRE30.3	1.5	-1.9	-2.1	-3.9	Strong similarity to ferric reductase Fre2p, 3-prime end (by homology)		orf19.6139
CA1139	IPF9466	-1.7	-5.1	-6.8	-4.0	unknown function		orf19.4066
9601.2		1.2	-3.9	-4.2	-4.1			
CA0659	IPF16189.3F	-1.3	-3.9	-4.9	-4.2	panthotenate kinase, 3-prime end (by homology)		orf19.5576
CA0472	STL1	1.3	-3.9	-3.9	-4.3	sugar transporter (by homology)	YDR536w	orf19.13176
CA2661	AAT1	-1.1	-4.6	-4.9	-4.5	aspartate aminotransferase (by homology)		orf19.3554
CA5826	MDH11	-1.0	-5.0	-6.1	-4.6	Malate dehydrogenase (by homology)		orf19.7481
CA2290	IPF16300	-1.2	-5.1	-6.1	-4.7	putative aldehyde dehydrogenase (by homology)		orf19.742
CA4748	MLS1	-1.6	-4.2	-7.3	-4.8	malate synthase	YNL117w	orf19.4833
CA0345	ACH1	1.7	-4.0	-3.1	-5.5	acetyl-coenzyme-A hydrolase (by homology)	YBL015w	orf19.10681
CA3415	FRE30.53	-1.2	-3.7	-4.0	-5.7	Strong similarity to ferric reductase, internal fragment (by homology)		orf19.6140
CA1180	UGA12.3F	-1.8	-5.8	-9.6	-6.4	4-aminobutyrate aminotransferase (GABA transaminase), 3-prime end (by homology		orf19.803
CA2163	IPF11879	-1.5	-7.0	-7.4	-6.6	unknown function		orf19.5293
CA3241	IPF7493	1.1	-7.9	-15.9	-7.1	putative permease (by homology)		orf19.4682
CA3399	PUT2	-1.3	-8.3	-9.8	-7.1	1-pyrroline-5-carboxylate dehydrogenase (by homology	YHR037w	orf19.3974
CA3199	FBP1	-1.1	-6.2	-7.9	-7.2	Fructose-1,6-bisphosphatase	YLR377c	orf19.6178
CA5862	POT11	-1.2	-8.2	-10.0	-8.1	peroxysomal 3-ketoacyl-CoA thiolase A (by homology)	YIL160c	orf19.7520
CA1572	POX4	-1.0	-8.4	-11.0	-8.2	peroxisomal fatty acyl-CoA oxidase (by homology)	YGL205w	orf19.9221
CA3011	CTA1	1.0	-9.1	-7.2	-8.5	catalase A, peroxisomal(by homology)	YDR256c	orf19.6229
CA5152	CAT2	1.0	-7.2	-10.2	-10.3	carnitine O-acetyltransferase (by homology)	YML042w	orf19.4591
CA5478	JEN2	1.0	-12.4	-18.3	-15.8	carboxylic acid transporter protein (by homology)		orf19.12767
CA5857	PCK1	1.3	-11.5	-12.0	-19.3	phosphoenolpyruvate carboxykinase	YKR097w	orf19.7514

Venn diagrams comparing the number of genes regulated by low, medium and high glucose





Complete *S. cerevisiae* dataset

From Yin *et al.* (2003) *Molec. Microbiol.* 48, 713-724.

Heatmap Scale

>=10	5.00	0.00	-5.00
9.62	4.62	-0.38	-5.38
9.23	4.23	-0.77	-5.77
8.85	3.85	-1.15	-6.15
8.46	3.46	-1.54	-6.54
8.08	3.08	-1.92	-6.92
7.69	2.69	-2.31	-7.31
7.31	2.31	-2.69	-7.69
6.92	1.92	-3.08	-8.08
6.54	1.54	-3.46	-8.46
6.15	1.15	-3.85	-8.85
5.77	0.77	-4.23	-9.23
5.38	0.38	-4.62	<=-10

Gene Name		**Expression ratio Glucose Concentration (%)**			
Systematic	**Common**	**0.00**	**0.01**	**0.10**	**1.00**
YIL053W	RHR2	1.00	3.60	3.48	10.60
YDR345C	HXT3	1.00	8.70	11.38	9.05
YHR094C	HXT1	1.00	3.52	5.18	8.97
YCL030C	HIS4	1.00	1.55	2.87	6.80
YOL059W	GPD2	1.00	1.66	2.97	6.49
YHR174W	ENO2	1.00	2.43	3.88	6.29
YAR073W	IMD1	1.00	2.57	5.18	6.17
YER062C	HOR2	1.00	1.37	2.83	6.16
YER165W	PAB1	1.00	1.66	2.94	6.07
YMR011W	HXT2	1.00	3.03	14.99	5.47
YAL038W	CDC19	1.00	2.28	3.64	5.36
YPR156C	TPO3	1.00	1.07	1.23	5.27
YDR417C		1.00	2.53	3.30	5.20
YER102W	RPS8B	1.00	2.35	3.37	4.97
YLR044C	PDC1	1.00	1.88	3.71	4.90
YDL131W	LYS21	1.00	1.24	2.06	4.79
YEL026W	SNU13	1.00	1.96	2.05	4.76
YGL003C	CDH1	1.00	1.99	3.17	4.62
YKL060C	FBA1	1.00	2.04	3.72	4.61
YER081W	SER3	1.00	1.35	2.33	4.58
YMR217W	GUA1	1.00	1.87	3.22	4.57
YDL014W	NOP1	1.00	1.69	1.84	4.43
YKL029C	MAE1	1.00	1.22	1.75	4.38
YOL058W	ARG1	1.00	1.42	1.65	4.37
YCR031C	RPS14A	1.00	1.90	2.70	4.35
YPL220W	RPL1A	1.00	2.81	4.17	4.29
YPR035W	GLN1	1.00	1.09	1.57	4.28
YPL273W	SAM4	1.00	1.90	3.47	4.25
YPL131W	RPL5	1.00	1.50	3.22	4.23
YFL001W	DEG1	1.00	2.17	2.57	4.15
YGR254W	ENO1	1.00	1.80	2.73	4.15
YHL033C	RPL8A	1.00	1.58	2.36	4.14
YDR342C	HXT7	1.00	9.98	12.06	4.06
YDR418W	RPL12B	1.00	2.62	2.70	4.04
YLR300W	EXG1	1.00	1.41	1.83	4.04
YLR339C		1.00	1.84	3.82	3.91
YJR028W		1.00	1.72	3.20	3.88
YNL069C	RPL16B	1.00	1.63	2.90	3.86
YGR138C	TPO2	1.00	1.55	1.39	3.82

YDR037W	KRS1	1.00	1.35	1.60	3.81
YPL079W	RPL21B	1.00	2.21	2.55	3.77
YJR109C	CPA2	1.00	1.30	1.36	3.76
YGR148C	RPL24B	1.00	2.14	2.78	3.73
YKL180W	RPL17A	1.00	2.11	2.67	3.72
YGL135W	RPL1B	1.00	1.89	2.39	3.72
YHR216W	IMD2	1.00	1.74	2.67	3.71
YDR050C	TPI1	1.00	1.79	2.27	3.69
YPR080W	TEF1	1.00	1.74	2.86	3.65
YDL048C	STP4	1.00	1.08	1.40	3.65
YDR046C	BAP3	1.00	1.15	1.39	3.63
YHR203C	RPS4B	1.00	1.72	2.25	3.58
YER055C	HIS1	1.00	1.64	1.20	3.57
YDL191W	RPL35A	1.00	2.34	2.56	3.55
YOR133W	EFT1	1.00	1.23	2.48	3.55
YDL083C	RPS16B	1.00	1.92	2.57	3.53
YEL071W	DLD3	1.00	1.63	2.77	3.53
YPR132W	RPS23B	1.00	2.10	2.84	3.52
YHR082C	KSP1	1.00	1.73	2.16	3.51
YPR145W	ASN1	1.00	1.00	2.28	3.50
YPR163C	TIF3	1.00	1.60	2.89	3.49
YHR208W	BAT1	1.00	1.47	2.29	3.49
YGR175C	ERG1	1.00	1.01	1.51	3.47
YCR012W	PGK1	1.00	1.98	2.87	3.46
YNL190W		1.00	1.12	1.60	3.44
YOR369C	RPS12	1.00	2.50	3.59	3.36
YER006W		1.00	1.63	2.47	3.36
YPL090C	RPS6A	1.00	1.86	2.32	3.35
YGL117W		1.00	1.42	2.03	3.35
YKR042W	UTH1	1.00	1.04	1.96	3.34
YOR204W	DED1	1.00	1.11	2.42	3.33
YOL039W	RPP2A	1.00	2.26	2.84	3.31
YMR305C	SCW10	1.00	1.49	2.23	3.30
YDR447C	RPS17B	1.00	-1.31	3.07	3.29
YDR343C	HXT6	1.00	7.07	10.25	3.28
YDR406W	PDR15	1.00	2.17	2.26	3.28
YBR054W	YRO2	1.00	1.52	1.37	3.27
YLR150W	STM1	1.00	1.87	2.76	3.24
YLR340W	RPP0	1.00	1.66	2.61	3.24
YOR344C	TYE7	1.00	1.37	2.21	3.24
YNL162W	RPL42A	1.00	2.45	2.57	3.23
YOR096W	RPS7A	1.00	1.75	2.48	3.22
YMR121C	RPL15B	1.00	2.01	2.48	3.21
YMR242C	RPL20A	1.00	2.03	2.75	3.20
YLR075W	RPL10	1.00	1.97	2.55	3.20
YDR233C		1.00	1.68	2.55	3.17
YDR450W	RPS18A	1.00	2.09	2.36	3.16
YOR167C	RPS28A	1.00	2.59	3.26	3.13
YIL133C	RPL16A	1.00	2.55	3.23	3.13
YLL044W		1.00	1.62	2.31	3.11
YJR125C	ENT3	1.00	1.54	2.45	3.10
YHR093W	AHT1	1.00	1.16	1.66	3.10
YKL181W	PRS1	1.00	1.82	2.31	3.09
YBR249C	ARO4	1.00	1.67	2.39	3.09
YDR382W	RPP2B	1.00	2.48	3.21	3.08
YLL045C	RPL8B	1.00	1.74	2.35	3.08
YMR108W	ILV2	1.00	1.35	2.45	3.08
YHR046C		1.00	-1.06	1.26	3.08
YOR310C	NOP58	1.00	1.68	2.28	3.07
YPL226W	NEW1	1.00	1.04	1.71	3.06
YNL178W	RPS3	1.00	1.83	2.66	3.05

YHR179W	OYE2	1.00	1.02	1.63	3.05
YLR432W	IMD3	1.00	1.48	2.07	3.04
YDR025W	RPS11A	1.00	1.46	2.03	3.04
YFR031C	SMC2	1.00	1.52	2.11	3.02
YOR063W	RPL3	1.00	1.82	2.94	3.01
YDR012W	RPL4B	1.00	1.78	2.70	3.01
YML063W	RPS1B	1.00	1.65	1.80	3.00
YGR204W	ADE3	1.00	-1.05	1.93	2.97
YML123C	PHO84	1.00	-1.05	1.67	2.97
YLR441C	RPS1A	1.00	1.84	2.46	2.96
YPR073C	LTP1	1.00	1.58	2.35	2.96
YBR189W	RPS9B	1.00	1.17	1.58	2.93
YGR159C	NSR1	1.00	1.20	1.46	2.92
YGL147C	RPL9A	1.00	1.70	2.33	2.90
YBR118W	TEF2	1.00	1.45	2.09	2.90
YDR502C	SAM2	1.00	1.79	2.34	2.89
YPL198W	RPL7B	1.00	1.39	2.47	2.89
YFL026W	STE2	1.00	1.07	1.48	2.89
YDR035W	ARO3	1.00	1.41	1.90	2.87
YGR260W	TNA1	1.00	1.07	1.19	2.86
YNL301C	RPL18B	1.00	1.78	2.41	2.84
YGL148W	ARO2	1.00	1.63	1.84	2.84
YHR018C	ARG4	1.00	1.13	1.59	2.84
YOL040C	RPS15	1.00	1.92	2.13	2.82
YER156C		1.00	1.48	2.13	2.80
YER110C	KAP123	1.00	-1.03	1.57	2.80
YPL106C	SSE1	1.00	1.15	2.01	2.79
YCL023C		1.00	-1.01	1.74	2.79
YGR034W	RPL26B	1.00	1.82	2.18	2.78
YER036C	KRE30	1.00	1.07	1.42	2.78
YGL102C		1.00	2.04	1.98	2.77
YDR158W	HOM2	1.00	1.77	2.29	2.77
YFR023W	PES4	1.00	1.54	2.04	2.77
YBL039C	URA7	1.00	1.37	2.16	2.74
YNL165W		1.00	1.17	2.03	2.73
YLR076C		1.00	1.46	2.15	2.72
YPL250C	ICY2	1.00	-1.10	2.03	2.72
YDR489W		1.00	1.64	2.12	2.71
YKL030W		1.00	1.04	1.60	2.71
YDL081C	RPP1A	1.00	2.39	2.70	2.70
YER016W	BIM1	1.00	1.50	1.73	2.70
YLR367W	RPS22B	1.00	1.64	2.40	2.69
YDR234W	LYS4	1.00	1.35	1.86	2.69
YPL093W	NOG1	1.00	1.32	1.70	2.69
YLR134W	PDC5	1.00	-1.16	2.39	2.68
YOL121C	RPS19A	1.00	1.85	1.93	2.66
YGL234W	ADE5,7	1.00	1.22	1.48	2.66
YIL069C	RPS24B	1.00	1.90	1.86	2.65
YML045W		1.00	1.57	3.42	2.65
YDR341C		1.00	1.30	1.75	2.65
YMR205C	PFK2	1.00	1.21	2.10	2.65
YPR110C	RPC40	1.00	1.51	1.96	2.61
YCL018W	LEU2	1.00	1.35	2.46	2.61
YDR432W	NPL3	1.00	1.27	1.95	2.61
YIL052C	RPL34B	1.00	1.98	2.19	2.60
YLR197W	SIK1	1.00	1.68	2.30	2.60
YGR027C	RPS25A	1.00	1.61	1.80	2.60
YOR293W	RPS10A	1.00	1.60	2.18	2.60
YEL054C	RPL12A	1.00	-2.26	1.77	2.60
YDR163W		1.00	6.63	7.50	2.59
YMR321C		1.00	1.69	2.63	2.59

YHL001W	RPL14B	1.00	-1.08	1.72	2.59
YGR191W	HIP1	1.00	1.27	1.58	2.58
YGL026C	TRP5	1.00	1.05	1.92	2.58
YDR454C	GUK1	1.00	1.74	2.01	2.57
YDL051W	LHP1	1.00	1.64	2.10	2.57
YDR442W		1.00	1.19	1.49	2.57
YDL061C	RPS29B	1.00	1.73	1.89	2.56
YDL208W	NHP2	1.00	1.66	1.94	2.56
YOL109W	ZEO1	1.00	1.24	3.07	2.56
YHR186C		1.00	1.15	1.85	2.56
YGR124W	ASN2	1.00	-1.26	1.87	2.56
YER074W	RPS24A	1.00	2.21	2.21	2.54
YGL030W	RPL30	1.00	1.37	2.42	2.54
YNL066W	SUN4	1.00	1.23	1.82	2.54
YJL223C	PAU1	1.00	1.07	1.34	2.54
YER025W	GCD11	1.00	1.24	1.77	2.53
YCR013C		1.00	1.88	2.43	2.52
YIL041W		1.00	1.60	1.59	2.52
YPR010C	RPA135	1.00	1.01	1.69	2.52
YJL136C	RPS21B	1.00	2.44	2.39	2.51
YER117W	RPL23B	1.00	1.85	1.97	2.51
YDL097C	RPN6	1.00	1.28	1.70	2.49
YOL130W	ALR1	1.00	1.05	1.49	2.49
YDR385W	EFT2	1.00	-1.06	1.77	2.49
YNR053C		1.00	1.25	1.56	2.48
YLR264W	RPS28B	1.00	1.99	1.65	2.47
YGR214W	RPS0A	1.00	1.48	1.62	2.46
YKL006W	RPL14A	1.00	1.81	1.72	2.45
YGL255W	ZRT1	1.00	1.16	1.27	2.45
YPL075W	GCR1	1.00	1.31	1.81	2.44
YNL061W	NOP2	1.00	1.25	2.02	2.44
YGL158W	RCK1	1.00	1.42	2.66	2.43
YMR300C	ADE4	1.00	1.10	1.14	2.43
YMR307W	GAS1	1.00	1.09	2.27	2.43
YER073W	ALD5	1.00	1.18	1.17	2.42
YEL072W		1.00	1.10	1.78	2.42
YAR071W	PHO11	1.00	1.01	1.02	2.42
YEL037C	RAD23	1.00	1.36	1.61	2.41
YOR317W	FAA1	1.00	1.67	2.53	2.40
YOL086C	ADH1	1.00	1.55	2.24	2.40
YNL067W	RPL9B	1.00	1.54	2.37	2.40
YGL078C	DBP3	1.00	-1.01	1.50	2.40
YER052C	HOM3	1.00	-1.18	1.37	2.40
YLR054C		1.00	1.51	1.93	2.39
YFL002C	SPB4	1.00	1.25	1.57	2.39
YGL009C	LEU1	1.00	1.22	2.44	2.39
YIR012W	SQT1	1.00	1.42	1.49	2.38
YKR059W	TIF1	1.00	1.24	1.71	2.38
YPR113W	PIS1	1.00	1.63	1.91	2.37
YER056C	FCY2	1.00	1.10	1.51	2.37
YJL026W	RNR2	1.00	1.26	1.82	2.36
YDL130W	RPP1B	1.00	2.25	2.17	2.35
YER131W	RPS26B	1.00	1.71	2.12	2.35
YCR034W	FEN1	1.00	1.48	1.89	2.35
YLR048W	RPS0B	1.00	1.24	1.55	2.35
YHR150W		1.00	1.14	1.67	2.35
YLR293C	GSP1	1.00	1.24	1.66	2.34
YOL077C	BRX1	1.00	1.65	2.16	2.33
YFL031W	HAC1	1.00	1.32	3.02	2.33
YLR167W	RPS31	1.00	2.05	2.41	2.32
YKL056C		1.00	1.37	1.57	2.32

YLR342W	FKS1	1.00	-1.13	1.62	2.32
YJR064W	CCT5	1.00	1.05	1.66	2.31
YDL037C		1.00	-1.27	1.19	2.31
YOR247W	SRL1	1.00	1.73	2.61	2.29
YDR366C		1.00	1.72	2.08	2.29
YLR448W	RPL6B	1.00	1.61	2.42	2.29
YBR105C	VID24	1.00	1.60	2.18	2.29
YJL014W	CCT3	1.00	1.30	1.78	2.29
YNL209W	SSB2	1.00	1.25	1.53	2.29
YDL213C	FYV14	1.00	1.05	1.63	2.29
YJL138C	TIF2	1.00	1.50	1.74	2.28
YNL064C	YDJ1	1.00	1.12	1.62	2.28
YHR141C	RPL42B	1.00	2.01	2.12	2.27
YPL238C		1.00	1.48	1.70	2.26
YLR344W	RPL26A	1.00	1.79	2.13	2.25
YDL143W	CCT4	1.00	1.29	1.59	2.25
YBR191W	RPL21A	1.00	1.13	1.15	2.25
YOR312C	RPL20B	1.00	1.76	2.09	2.24
YLR250W	SSP120	1.00	1.37	2.04	2.24
YGL103W	RPL28	1.00	1.80	1.79	2.23
YNL002C	RLP7	1.00	1.08	1.85	2.23
YOL107W		1.00	-1.03	1.73	2.23
YJL052W	TDH1	1.00	1.62	2.20	2.22
YFR055W		1.00	1.19	1.31	2.22
YGR044C	RME1	1.00	1.24	1.52	2.21
YAR007C	RFA1	1.00	1.21	1.44	2.21
YEL009C	GCN4	1.00	1.16	2.03	2.21
YPR036W	VMA13	1.00	1.00	1.90	2.21
YLR185W	RPL37A	1.00	1.95	2.38	2.20
YGL123W	RPS2	1.00	1.20	1.42	2.20
YEL046C	GLY1	1.00	-1.12	1.52	2.20
YDL050C		1.00	1.48	2.15	2.19
YNL145W	MFA2	1.00	1.17	1.75	2.19
YER049W		1.00	1.04	1.32	2.19
YGR264C	MES1	1.00	-1.18	1.46	2.19
YGR149W		1.00	1.59	2.02	2.18
YMR046C		1.00	1.56	2.52	2.18
YPR198W	SGE1	1.00	-1.14	1.92	2.17
YKL048C	ELM1	1.00	1.70	1.66	2.16
YLR273C	PIG1	1.00	1.34	1.72	2.16
YJR145C	RPS4A	1.00	1.32	1.25	2.16
YBL072C	RPS8A	1.00	1.15	1.35	2.15
YLR067C	PET309	1.00	1.13	1.69	2.15
YDL153C	SAS10	1.00	1.66	2.03	2.14
YLR062C	BUD28	1.00	1.39	1.48	2.14
YHR053C	CUP1-1	1.00	1.49	3.59	2.13
YML126C	ERG13	1.00	1.27	1.79	2.13
YOR001W	RRP6	1.00	1.21	1.79	2.13
YKL081W	TEF4	1.00	1.17	1.70	2.13
YCL009C	ILV6	1.00	1.09	1.38	2.13
YPL143W	RPL33A	1.00	1.03	1.67	2.13
YCL059C	KRR1	1.00	1.42	1.90	2.12
YJL148W	RPA34	1.00	1.37	1.47	2.12
YEL040W	UTR2	1.00	-1.24	-1.05	2.12
YGR118W	RPS23A	1.00	1.79	1.99	2.11
YHR215W	PHO12	1.00	1.20	1.12	2.11
YJR105W	ADO1	1.00	1.19	1.76	2.11
YER150W	SPI1	1.00	2.15	2.92	2.10
YHR010W	RPL27A	1.00	1.60	1.93	2.10
YKR081C		1.00	1.31	1.42	2.10
YOL092W		1.00	1.33	1.61	2.09

YDL167C	NRP1	1.00	1.20	1.41	2.09
YHR219W		1.00	1.60	1.92	2.08
YMR290C	HAS1	1.00	1.26	1.90	2.08
YMR309C	NIP1	1.00	1.17	1.65	2.08
YPL081W	RPS9A	1.00	1.51	1.85	2.07
YDR072C	IPT1	1.00	1.46	1.99	2.07
YDL025C		1.00	1.15	1.25	2.07
YHR115C		1.00	1.15	1.48	2.07
YBL027W	RPL19B	1.00	-1.10	1.41	2.07
YPL267W		1.00	1.31	1.39	2.06
YGL001C	ERG26	1.00	1.24	1.86	2.06
YER120W	SCS2	1.00	1.21	1.76	2.06
YHR218W		1.00	1.10	2.10	2.06
YDL060W	TSR1	1.00	1.00	1.40	2.06
YDR166C	SEC5	1.00	1.86	1.63	2.05
YKL152C	GPM1	1.00	1.50	1.80	2.05
YJR029W		1.00	1.39	2.06	2.05
YOR335C	ALA1	1.00	1.32	1.87	2.05
YLR007W		1.00	1.27	1.63	2.05
YLR355C	ILV5	1.00	-1.08	1.09	2.05
YDR134C		1.00	1.54	2.11	2.04
YMR038C	LYS7	1.00	1.29	1.70	2.04
YNL160W	YGP1	1.00	1.25	1.77	2.04
YMR246W	FAA4	1.00	1.07	1.37	2.04
YMR296C	LCB1	1.00	-1.05	1.40	2.04
YNL110C		1.00	1.54	1.65	2.03
YNL308C	KRI1	1.00	1.35	1.87	2.03
YDR232W	HEM1	1.00	1.24	1.33	2.03
YIL116W	HIS5	1.00	1.08	1.20	2.03
YLR056W	ERG3	1.00	-1.15	1.77	2.03
YOR341W	RPA190	1.00	-1.46	1.43	2.03
YOL105C	WSC3	1.00	1.27	1.57	2.02
YNR043W	MVD1	1.00	1.22	1.79	2.02
YLR175W	CBF5	1.00	1.20	1.39	2.02
YNL154C	YCK2	1.00	1.16	1.76	2.02
YGL055W	OLE1	1.00	-2.03	1.92	2.02
YLR110C	CCW12	1.00	1.68	2.02	2.01
YEL003W	GIM4	1.00	1.50	1.36	2.01
YER130C		1.00	1.06	-1.11	2.01
YNL075W	IMP4	1.00	1.47	1.50	2.00
YEL023C		1.00	-1.13	1.15	2.00
YIL148W	RPL40A	1.00	2.19	2.62	1.99
YPL028W	ERG10	1.00	1.52	2.54	1.99
YGL202W	ARO8	1.00	1.28	1.47	1.99
YNL141W	AAH1	1.00	-1.01	1.41	1.99
YNL132W	KRE33	1.00	-1.04	1.66	1.99
YIL142W	CCT2	1.00	1.33	1.80	1.98
YKL153W		1.00	1.21	1.66	1.98
YAL003W	EFB1	1.00	1.18	1.09	1.98
YMR195W	ICY1	1.00	1.18	2.49	1.98
YDR002W	YRB1	1.00	1.33	1.64	1.97
YHR007C	ERG11	1.00	1.29	1.48	1.97
YKL143W	LTV1	1.00	1.27	1.66	1.97
YKL051W		1.00	1.26	1.21	1.97
YLR019W	PSR2	1.00	1.17	1.38	1.97
YDL226C	GCS1	1.00	1.10	1.26	1.97
YGR137W		1.00	1.06	1.38	1.97
YGL008C	PMA1	1.00	-2.31	-1.47	1.97
YNL031C	HHT2	1.00	2.32	2.27	1.96
YKR094C	RPL40B	1.00	2.03	2.59	1.96
YDR176W	NGG1	1.00	1.72	1.69	1.96

YOR224C	RPB8	1.00	1.57	1.52	1.96
YPL043W	NOP4	1.00	1.24	1.70	1.96
YLR372W	SUR4	1.00	1.23	1.53	1.96
YNL112W	DBP2	1.00	1.17	1.08	1.96
YGL108C		1.00	1.10	1.42	1.96
YOR342C		1.00	1.08	1.75	1.96
YPL026C	SKS1	1.00	1.01	1.29	1.96
YLR180W	SAM1	1.00	-1.11	1.46	1.96
YDL038C		1.00	-1.20	-1.05	1.96
YMR131C	RRB1	1.00	1.05	1.47	1.95
YML059C		1.00	-1.05	1.57	1.95
YOL142W	RRP40	1.00	1.40	1.64	1.94
YPR088C	SRP54	1.00	1.24	1.76	1.94
YDR429C	TIF35	1.00	1.22	1.64	1.94
YHR068W	DYS1	1.00	1.09	1.25	1.94
YML040W		1.00	-1.06	2.20	1.94
YNL333W	SNZ2	1.00	1.77	1.73	1.93
YDL111C	RRP42	1.00	1.40	1.28	1.93
YGR285C	ZUO1	1.00	1.35	1.50	1.93
YDR120C	TRM1	1.00	1.24	1.87	1.93
YGL120C	PRP43	1.00	1.17	1.32	1.93
YGR085C	RPL11B	1.00	1.59	2.08	1.92
YIL094C	LYS12	1.00	1.44	1.88	1.92
YKR013W	PRY2	1.00	1.36	1.56	1.92
YBR167C	POP7	1.00	1.33	1.36	1.92
YGL204C		1.00	1.27	1.43	1.92
YLR029C	RPL15A	1.00	1.12	1.23	1.92
YML022W	APT1	1.00	1.06	1.59	1.92
YEL047C		1.00	-1.06	1.29	1.92
YLR249W	YEF3	1.00	-1.37	-1.01	1.92
YOR375C	GDH1	1.00	1.44	2.45	1.91
YMR303C	ADH2	1.00	1.41	1.94	1.91
YMR208W	ERG12	1.00	1.40	1.55	1.91
YER148W	SPT15	1.00	1.34	1.66	1.91
YJR007W	SUI2	1.00	1.23	1.55	1.91
YOR272W	YTM1	1.00	1.21	1.62	1.91
YDR036C		1.00	1.17	1.52	1.91
YGL230C		1.00	1.17	1.22	1.91
YBR181C	RPS6B	1.00	1.07	1.02	1.91
YCL037C	SRO9	1.00	1.22	1.25	1.90
YGR192C	TDH3	1.00	-1.15	1.40	1.90
YOR271C		1.00	-1.27	1.16	1.90
YDR064W	RPS13	1.00	1.28	1.07	1.89
YLR296W		1.00	1.25	1.73	1.89
YDR055W	PST1	1.00	1.07	2.07	1.89
YPL169C	MEX67	1.00	1.06	1.54	1.89
YHR025W	THR1	1.00	-1.16	1.22	1.89
YLR061W	RPL22A	1.00	1.70	1.70	1.88
YOL030W		1.00	1.62	1.78	1.88
YPR086W	SUA7	1.00	1.42	1.71	1.88
YOL011W	PLB3	1.00	1.35	1.38	1.88
YNL007C	SIS1	1.00	1.31	1.24	1.88
YJR100C		1.00	-1.14	1.78	1.88
YPL037C	EGD1	1.00	1.25	1.45	1.87
YKL024C	URA6	1.00	1.21	1.36	1.87
YPR033C	HTS1	1.00	1.20	1.65	1.87
YLR333C	RPS25B	1.00	1.19	1.35	1.87
YOL127W	RPL25	1.00	1.40	1.48	1.86
YML106W	URA5	1.00	1.39	1.72	1.86
YLR286C	CTS1	1.00	1.27	2.29	1.86
YLR194C		1.00	1.21	1.48	1.86

YLR169W		1.00	1.12	1.44	1.86
YAL012W	CYS3	1.00	-1.01	1.73	1.86
YNL167C	SKO1	1.00	-1.05	1.51	1.86
YGR160W	FYV13	1.00	-1.25	1.00	1.86
YMR202W	ERG2	1.00	-1.83	1.20	1.86
YLR341W	SPO77	1.00	1.50	1.55	1.85
YNL096C	RPS7B	1.00	1.43	1.91	1.85
YGR234W	YHB1	1.00	1.35	1.93	1.85
YNL010W		1.00	1.28	1.12	1.85
YLR229C	CDC42	1.00	1.26	1.49	1.85
YJR090C	GRR1	1.00	1.19	1.43	1.85
YLR196W	PWP1	1.00	1.13	1.42	1.85
YDR277C	MTH1	1.00	1.59	2.45	1.84
YOR182C	RPS30B	1.00	1.38	1.75	1.84
YGL189C	RPS26A	1.00	1.31	1.77	1.84
YPL239W	YAR1	1.00	1.18	1.73	1.84
YHR042W	NCP1	1.00	1.16	1.53	1.84
YDR420W	HKR1	1.00	-1.08	1.22	1.84
YER043C	SAH1	1.00	-1.10	1.44	1.84
YPR043W	RPL43A	1.00	2.15	2.39	1.83
YDR076W	RAD55	1.00	1.27	1.59	1.83
YCL025C	AGP1	1.00	1.14	1.84	1.83
YML074C	NPI46	1.00	1.13	1.84	1.83
YOL136C	PFK27	1.00	-1.03	1.62	1.83
YCR021C	HSP30	1.00	-1.10	1.47	1.83
YEL002C	WBP1	1.00	1.24	1.56	1.82
YDL031W	DBP10	1.00	1.08	1.30	1.82
YDR346C		1.00	-1.15	1.34	1.82
YFL045C	SEC53	1.00	-1.39	1.70	1.82
YDL082W	RPL13A	1.00	1.39	1.62	1.81
YMR318C		1.00	1.36	1.78	1.81
YDR087C	RRP1	1.00	1.26	1.63	1.81
YIL117C	PRM5	1.00	1.19	1.31	1.81
YGL245W		1.00	1.18	1.60	1.81
YOR048C	RAT1	1.00	1.12	1.72	1.81
YGR123C	PPT1	1.00	1.03	1.21	1.81
YKR057W	RPS21A	1.00	1.61	1.64	1.80
YDR190C	RVB1	1.00	1.34	1.77	1.80
YOR331C		1.00	1.18	1.69	1.80
YHR162W		1.00	1.03	1.28	1.80
YNR051C	BRE5	1.00	-1.07	1.14	1.80
YPR102C	RPL11A	1.00	1.44	1.71	1.79
YDR324C		1.00	1.33	1.35	1.79
YFL039C	ACT1	1.00	1.17	1.59	1.79
YPL049C	DIG1	1.00	1.14	1.53	1.79
YLL018C	DPS1	1.00	1.13	1.65	1.79
YDL036C		1.00	1.07	1.29	1.79
YNL182C		1.00	1.05	1.31	1.79
YKL035W	UGP1	1.00	2.09	2.31	1.78
YOR248W	TOS11	1.00	1.61	2.60	1.78
YKL009W	MRT4	1.00	1.36	1.31	1.78
YPR187W	RPO26	1.00	1.31	1.14	1.78
YOL021C	DIS3	1.00	1.16	1.29	1.78
YGR282C	BGL2	1.00	1.14	1.27	1.78
YGR155W	CYS4	1.00	1.05	1.46	1.78
YOR243C		1.00	-1.03	1.10	1.78
YMR308C	PSE1	1.00	-1.05	1.48	1.78
YNL186W	UBP10	1.00	-1.06	1.38	1.78
YMR212C	EFR3	1.00	-1.08	1.45	1.78
YOR071C		1.00	-1.08	1.29	1.78
YHR021C	RPS27B	1.00	1.25	1.26	1.77

YGR279C	SCW4	1.00	1.23	1.62	1.77
YLR060W	FRS1	1.00	1.16	1.69	1.77
YFL064C		1.00	1.10	1.62	1.77
YML081W		1.00	1.04	1.32	1.77
YIL074C	SER33	1.00	-1.07	1.59	1.77
YDR381W	YRA1	1.00	1.65	2.01	1.76
YLR168C	MSF1'	1.00	1.49	1.67	1.76
YNL058C		1.00	1.34	1.94	1.76
YBL036C		1.00	1.30	1.41	1.76
YHL011C	PRS3	1.00	1.28	1.56	1.76
YJR009C	TDH2	1.00	1.24	1.61	1.76
YOR361C	PRT1	1.00	1.20	1.47	1.76
YFR001W	LOC1	1.00	1.02	1.47	1.76
YLR413W		1.00	-1.08	1.12	1.76
YGR054W		1.00	-1.33	1.54	1.76
YHR026W	PPA1	1.00	1.25	1.61	1.75
YPR183W	DPM1	1.00	1.19	1.75	1.75
YOR145C		1.00	1.09	1.36	1.75
YHR071W	PCL5	1.00	-1.02	1.30	1.75
YMR298W		1.00	-1.06	1.45	1.75
YDL227C	HO	1.00	-1.57	-1.11	1.75
YMR243C	ZRC1	1.00	1.47	1.37	1.74
YGR056W	RSC1	1.00	1.20	1.46	1.74
YMR272C	SCS7	1.00	1.03	1.33	1.74
YGR142W	BTN2	1.00	-1.02	2.47	1.74
YBR079C	RPG1	1.00	-1.24	1.59	1.74
YGL133W	ITC1	1.00	-1.49	1.39	1.74
YIL078W	THS1	1.00	1.27	1.56	1.73
YPR142C		1.00	1.14	1.50	1.73
YLR100W	ERG27	1.00	1.13	1.68	1.73
YNL268W	LYP1	1.00	1.12	1.67	1.73
YPL279C		1.00	-1.11	1.13	1.73
YOR178C	GAC1	1.00	1.50	2.48	1.72
YEL034W	HYP2	1.00	1.47	1.81	1.72
YBR082C	UBC4	1.00	1.07	1.66	1.72
YDR049W		1.00	-1.03	1.21	1.72
YLR359W	ADE13	1.00	-1.11	1.12	1.72
YGL037C	PNC1	1.00	1.58	2.34	1.71
YOR309C		1.00	1.47	1.68	1.71
YPL145C	KES1	1.00	1.24	1.79	1.71
YDR143C	SAN1	1.00	1.15	1.26	1.71
YPL263C	KEL3	1.00	1.05	1.44	1.71
YOR209C	NPT1	1.00	1.01	1.32	1.71
YKR043C		1.00	-1.09	1.12	1.71
YOR283W		1.00	-1.30	1.26	1.71
YDR339C		1.00	1.39	1.52	1.70
YOR117W	RPT5	1.00	1.12	1.49	1.70
YNL269W		1.00	1.02	1.54	1.70
YOR047C	STD1	1.00	-1.13	1.11	1.70
YHR020W		1.00	-1.16	1.39	1.70
YBR104W	YMC2	1.00	1.71	1.94	1.69
YKL156W	RPS27A	1.00	1.44	1.40	1.69
YJR122W	CAF17	1.00	1.17	1.29	1.69
YMR220W	ERG8	1.00	1.12	1.54	1.69
YDR501W	PLM2	1.00	1.08	1.21	1.69
YMR216C	SKY1	1.00	-1.04	1.65	1.69
YGR208W	SER2	1.00	1.33	1.11	1.68
YOL139C	CDC33	1.00	1.32	1.56	1.68
YOR323C	PRO2	1.00	1.15	1.37	1.68
YNL085W	MKT1	1.00	1.13	1.55	1.68
YPL190C	NAB3	1.00	1.10	1.71	1.68

YPR048W	TAH18	1.00	-1.04	1.47	1.68
YIR035C		1.00	-1.26	1.16	1.68
YBR196C	PGI1	1.00	-1.45	1.12	1.68
YGR117C		1.00	1.47	1.45	1.67
YOR056C		1.00	1.27	1.63	1.67
YGL029W	CGR1	1.00	1.21	1.04	1.67
YGL160W		1.00	1.10	1.03	1.67
YHR064C	PDR13	1.00	1.02	1.56	1.67
YBR093C	PHO5	1.00	-1.09	-1.09	1.67
YGL031C	RPL24A	1.00	1.37	1.56	1.66
YNL255C	GIS2	1.00	1.32	1.76	1.66
YDL176W		1.00	1.29	1.53	1.66
YNL114C		1.00	1.26	1.13	1.66
YER123W	YCK3	1.00	1.17	1.35	1.66
YLR147C	SMD3	1.00	1.16	1.32	1.66
YER112W	LSM4	1.00	1.15	1.31	1.66
YGL098W		1.00	1.11	1.24	1.66
YDR062W	LCB2	1.00	1.03	1.18	1.66
YGL028C	SCW11	1.00	1.02	1.18	1.66
YJL012C	VTC4	1.00	-1.24	1.12	1.66
YHR217C		1.00	-1.28	1.23	1.66
YHR092C	HXT4	1.00	-1.37	1.41	1.66
YER029C	SMB1	1.00	1.60	2.17	1.65
YEL015W		1.00	1.42	1.30	1.65
YJL191W	RPS14B	1.00	1.24	1.44	1.65
YNL109W		1.00	1.24	1.35	1.65
YER090W	TRP2	1.00	1.23	1.57	1.65
YER038C	KRE29	1.00	1.20	1.25	1.65
YHR170W	NMD3	1.00	1.12	1.32	1.65
YBR261C		1.00	1.11	1.23	1.65
YDL203C		1.00	1.06	1.17	1.65
YKL182W	FAS1	1.00	1.05	1.50	1.65
YNL119W		1.00	1.02	1.41	1.65
YOL061W	PRS5	1.00	1.00	1.16	1.65
YOR184W	SER1	1.00	1.00	1.31	1.65
YML058W	SML1	1.00	1.68	2.23	1.64
YBR256C	RIB5	1.00	1.53	1.32	1.64
YDR084C		1.00	1.29	1.78	1.64
YLR065C		1.00	1.28	1.19	1.64
YCR047C	BUD23	1.00	1.23	1.28	1.64
YHR072W	ERG7	1.00	1.14	1.48	1.64
YER133W	GLC7	1.00	1.04	1.45	1.64
YKL212W	SAC1	1.00	-1.07	1.26	1.64
YOR338W		1.00	-1.10	1.00	1.64
YCR059C	YIH1	1.00	1.36	1.20	1.63
YLR074C	BUD20	1.00	1.35	1.74	1.63
YOL064C	MET22	1.00	1.13	1.15	1.63
YLR325C	RPL38	1.00	1.12	1.30	1.63
YMR051C		1.00	1.04	1.97	1.63
YNL175C	NOP13	1.00	1.02	1.42	1.63
YJL177W	RPL17B	1.00	-1.04	1.46	1.63
YGL122C	NAB2	1.00	-1.05	1.07	1.63
YIL047C	SYG1	1.00	-1.13	-1.02	1.63
YDL049C	KNH1	1.00	-1.46	1.15	1.63
YNL180C	RHO5	1.00	1.46	1.58	1.62
YDR487C	RIB3	1.00	1.34	1.29	1.62
YJR070C		1.00	1.21	1.41	1.62
YOR222W	ODC2	1.00	1.18	1.22	1.62
YGR079W		1.00	1.17	1.13	1.62
YGR081C		1.00	1.11	1.21	1.62
YDL039C	PRM7	1.00	1.10	-1.07	1.62

YBR048W	RPS11B	1.00	1.09	1.19	1.62
YJR147W	HMS2	1.00	1.03	1.25	1.62
YNL187W		1.00	-1.09	1.32	1.62
YPL014W		1.00	-1.09	1.32	1.62
YHL015W	RPS20	1.00	1.14	2.10	1.61
YIR034C	LYS1	1.00	1.10	1.13	1.61
YOL022C		1.00	1.10	1.55	1.61
YNR052C	POP2	1.00	1.09	1.26	1.61
YJR027W		1.00	1.07	1.41	1.61
YJR111C		1.00	1.06	1.03	1.61
YDL136W	RPL35B	1.00	1.00	1.18	1.61
YDR013W		1.00	-1.04	1.16	1.61
YDR069C	DOA4	1.00	-1.07	1.07	1.61
YNL047C		1.00	-1.08	1.46	1.61
YOR267C		1.00	-1.41	1.00	1.61
YDR369C	XRS2	1.00	1.52	2.40	1.60
YLR113W	HOG1	1.00	1.32	1.67	1.60
YOR332W	VMA4	1.00	1.28	1.64	1.60
YPR143W		1.00	1.21	1.58	1.60
YLL051C	FRE6	1.00	1.20	1.48	1.60
YML010W	SPT5	1.00	1.11	1.46	1.60
YNL174W		1.00	-1.04	1.45	1.60
YDL212W	SHR3	1.00	1.45	1.53	1.59
YOR277C		1.00	1.43	1.25	1.59
YDR312W	SSF2	1.00	1.20	1.23	1.59
YEL058W	PCM1	1.00	1.20	1.51	1.59
YLR222C		1.00	1.19	1.23	1.59
YNL302C	RPS19B	1.00	1.17	1.10	1.59
YIL048W	NEO1	1.00	1.14	1.28	1.59
YGL105W	ARC1	1.00	1.13	1.60	1.59
YLR447C	VMA6	1.00	1.13	1.32	1.59
YPR062W	FCY1	1.00	1.11	1.42	1.59
YNL201C		1.00	1.10	1.19	1.59
YDR165W		1.00	1.05	1.61	1.59
YNL221C	POP1	1.00	1.03	1.04	1.59
YPL146C		1.00	1.03	1.58	1.59
YER100W	UBC6	1.00	1.02	1.17	1.59
YBR195C	MSI1	1.00	-1.06	-1.14	1.59
YNL087W		1.00	-1.06	1.44	1.59
YOR092W	ECM3	1.00	-1.06	-1.05	1.59
YIL119C	RPI1	1.00	-1.14	-1.07	1.59
YCR005C	CIT2	1.00	-1.43	-1.02	1.59
YPR041W	TIF5	1.00	1.29	1.28	1.58
YBL002W	HTB2	1.00	1.27	1.45	1.58
YLR307W	CDA1	1.00	1.09	1.52	1.58
YLR017W	MEU1	1.00	1.07	1.40	1.58
YMR100W	MUB1	1.00	1.04	1.17	1.58
YJL200C		1.00	-1.04	1.15	1.58
YEL042W	GDA1	1.00	-1.21	1.58	1.58
YLL024C	SSA2	1.00	-1.35	-1.11	1.58
YDR516C		1.00	1.62	2.47	1.57
YDR274C		1.00	1.50	1.78	1.57
YPR165W	RHO1	1.00	1.45	1.57	1.57
YBR286W	APE3	1.00	1.41	1.78	1.57
YNL062C	GCD10	1.00	1.21	1.83	1.57
YBR238C		1.00	1.11	1.36	1.57
YDR051C		1.00	1.10	1.21	1.57
YOR130C	ORT1	1.00	1.10	1.15	1.57
YHR193C	EGD2	1.00	1.09	1.40	1.57
YPR084W		1.00	1.06	1.30	1.57
YHR196W		1.00	-1.06	1.15	1.57

YOR206W	NOC2	1.00	-1.35	1.22	1.57
YDR370C		1.00	1.50	1.51	1.56
YDL224C	WHI4	1.00	1.49	1.39	1.56
YMR235C	RNA1	1.00	1.23	1.18	1.56
YPL117C	IDI1	1.00	1.20	1.75	1.56
YMR101C	SRT1	1.00	1.19	3.24	1.56
YOR311C	HSD1	1.00	1.19	1.23	1.56
YLR378C	SEC61	1.00	1.02	1.37	1.56
YCL020W		1.00	-1.01	1.60	1.56
YKL149C	DBR1	1.00	1.50	1.33	1.55
YDR430C		1.00	1.36	1.21	1.55
YGL076C	RPL7A	1.00	1.30	1.71	1.55
YDR344C		1.00	1.23	1.57	1.55
YIL123W	SIM1	1.00	1.07	1.53	1.55
YOR197W		1.00	1.07	1.33	1.55
YDL095W	PMT1	1.00	-1.06	1.46	1.55
YGL157W		1.00	-1.25	1.07	1.55
YEL043W		1.00	-1.33	1.15	1.55
YBR287W		1.00	1.30	1.29	1.54
YCR092C	MSH3	1.00	1.23	1.50	1.54
YLR207W	HRD3	1.00	1.15	1.52	1.54
YOR153W	PDR5	1.00	-1.16	1.63	1.54
YKL211C	TRP3	1.00	-1.18	-1.03	1.54
YLL039C	UBI4	1.00	1.65	1.83	1.53
YPR118W		1.00	1.29	1.16	1.53
YBR127C	VMA2	1.00	1.22	1.36	1.53
YNL192W	CHS1	1.00	1.14	1.34	1.53
YDR441C	APT2	1.00	1.12	1.14	1.53
YAR015W	ADE1	1.00	1.11	-1.13	1.53
YLR329W	REC102	1.00	1.06	1.28	1.53
YGL025C	PGD1	1.00	1.05	1.29	1.53
YPL259C	APM1	1.00	1.02	1.42	1.53
YOL097C	WRS1	1.00	-1.14	1.11	1.53
YPL019C	VTC3	1.00	-1.15	1.06	1.53
YCR053W	THR4	1.00	-1.41	1.14	1.53
YGR240C	PFK1	1.00	-1.94	-1.05	1.53
YOR089C	VPS21	1.00	1.45	1.66	1.52
YDL147W	RPN5	1.00	1.24	1.73	1.52
YDR354W	TRP4	1.00	1.18	1.20	1.52
YMR226C		1.00	1.09	1.31	1.52
YNR018W		1.00	1.07	1.24	1.52
YNL074C	MLF3	1.00	1.06	1.52	1.52
YPR159W	KRE6	1.00	-1.01	1.24	1.52
YBR031W	RPL4A	1.00	-1.02	1.05	1.52
YBR049C	REB1	1.00	-1.12	-1.02	1.52
YHR014W	SPO13	1.00	-1.16	1.12	1.52
YDR220C		1.00	-1.19	-1.19	1.52
YHL045W		1.00	-1.26	1.11	1.52
YNL298W	CLA4	1.00	1.31	1.41	1.51
YDR212W	TCP1	1.00	1.23	1.36	1.51
YDL236W	PHO13	1.00	1.15	1.39	1.51
YNL220W	ADE12	1.00	-1.09	1.14	1.51
YKL059C		1.00	-1.18	1.64	1.51
YOR177C	MPC54	1.00	-1.22	1.26	1.51
YBR025C		1.00	-1.26	1.39	1.51
YMR215W		1.00	-1.31	1.37	1.51
YOR298W		1.00	-1.46	1.27	1.51
YJL188C	BUD19	1.00	-2.00	1.26	1.51
YGL036W	MTC2	1.00	1.49	1.42	1.50
YDL070W	BDF2	1.00	1.32	1.61	1.50
YPL086C	ELP3	1.00	1.32	1.60	1.50

YOR085W	OST3	1.00	1.28	1.83	1.50
YOR154W		1.00	1.28	1.92	1.50
YAL040C	CLN3	1.00	1.17	1.16	1.50
YER124C		1.00	1.17	1.39	1.50
YDR500C	RPL37B	1.00	1.15	1.30	1.50
YDR539W		1.00	1.13	1.11	1.50
YLR403W	SFP1	1.00	1.11	1.30	1.50
YDR404C	RPB7	1.00	1.05	1.02	1.50
YGL022W	STT3	1.00	1.04	1.22	1.50
YNL327W	EGT2	1.00	-1.10	1.71	1.50
YJL158C	CIS3	1.00	-1.26	1.52	1.50
YGR066C		1.00	-1.27	1.03	1.50
YGL259W	YPS5	1.00	-1.28	-1.18	1.50
YOR132W	VPS17	1.00	1.22	1.36	1.49
YBR061C		1.00	1.12	1.17	1.49
YDR335W	MSN5	1.00	1.12	1.28	1.49
YGL099W	KRE35	1.00	1.11	1.07	1.49
YIL161W		1.00	1.11	1.11	1.49
YDR157W		1.00	1.09	1.04	1.49
YOL007C	CSI2	1.00	1.07	1.14	1.49
YDR477W	SNF1	1.00	1.06	1.34	1.49
YNL238W	KEX2	1.00	1.04	1.08	1.49
YPL044C		1.00	1.02	1.29	1.49
YBR263W	SHM1	1.00	-1.08	1.33	1.49
YNL153C	GIM3	1.00	-1.12	1.33	1.49
YDL132W	CDC53	1.00	-1.17	1.11	1.49
YOR329C	SCD5	1.00	-1.19	1.32	1.49
YLR018C	POM34	1.00	-1.29	1.17	1.49
YMR229C	RRP5	1.00	-1.29	1.24	1.49
YDL023C		1.00	2.31	2.86	1.48
YDL002C	NHP10	1.00	1.40	1.30	1.48
YMR260C	TIF11	1.00	1.23	1.39	1.48
YNL155W		1.00	1.17	1.58	1.48
YHR004C	NEM1	1.00	1.10	1.27	1.48
YMR275C	BUL1	1.00	1.07	1.24	1.48
YKR048C	NAP1	1.00	1.01	1.18	1.48
YFR040W	SAP155	1.00	-1.03	1.41	1.48
YOR007C	SGT2	1.00	-1.03	1.15	1.48
YDR186C		1.00	-1.09	1.48	1.48
YMR112C	MED11	1.00	-1.14	-1.01	1.48
YML075C	HMG1	1.00	-1.31	1.05	1.48
YFR042W		1.00	1.38	1.66	1.47
YBR005W		1.00	1.30	1.18	1.47
YDL168W	SFA1	1.00	1.28	1.54	1.47
YDR145W	TAF61	1.00	1.15	1.45	1.47
YHR019C	DED81	1.00	1.13	1.50	1.47
YMR200W	ROT1	1.00	1.13	1.27	1.47
YCR072C		1.00	1.10	1.02	1.47
YPR087W		1.00	1.10	1.30	1.47
YFL066C		1.00	1.06	1.72	1.47
YOR160W	MTR10	1.00	1.04	1.23	1.47
YMR311C	GLC8	1.00	1.03	1.53	1.47
YIL016W	SNL1	1.00	1.01	1.11	1.47
YML053C		1.00	1.01	3.00	1.47
YNL118C	DCP2	1.00	-1.02	1.34	1.47
YML127W	RSC9	1.00	-1.07	1.28	1.47
YCL011C	GBP2	1.00	-1.11	1.09	1.47
YNL057W		1.00	-1.12	1.51	1.47
YJL111W	CCT7	1.00	-1.13	1.49	1.47
YER069W	ARG5,6	1.00	-1.14	-1.06	1.47
YPL142C		1.00	-2.67	1.22	1.47

YOR088W		1.00	1.51	1.39	1.46
YFR050C	PRE4	1.00	1.27	1.62	1.46
YHR084W	STE12	1.00	1.25	1.14	1.46
YNL281W	HCH1	1.00	1.19	1.14	1.46
YGL225W	GOG5	1.00	1.09	-1.01	1.46
YIL060W		1.00	1.06	1.77	1.46
YLR345W		1.00	1.01	1.29	1.46
YLR051C		1.00	-1.01	1.20	1.46
YDL198C	YHM1	1.00	-1.04	-1.06	1.46
YNL084C	END3	1.00	-1.05	1.35	1.46
YDR188W	CCT6	1.00	-1.09	1.13	1.46
YLR182W	SWI6	1.00	-1.20	1.60	1.46
YOR108W		1.00	-1.26	1.46	1.46
YDR535C		1.00	-1.29	-1.21	1.46
YDR253C	MET32	1.00	-1.98	1.22	1.46
YDR458C		1.00	-2.67	1.27	1.46
YDL022W	GPD1	1.00	2.32	2.32	1.45
YBL037W	APL3	1.00	1.49	1.49	1.45
YBR074W		1.00	1.42	1.85	1.45
YDL015C	TSC13	1.00	1.41	1.68	1.45
YCL034W	LSB5	1.00	1.28	1.29	1.45
YOL006C	TOP1	1.00	1.21	1.16	1.45
YNR076W	PAU6	1.00	1.20	1.36	1.45
YNR055C	HOL1	1.00	1.17	1.20	1.45
YLR073C		1.00	1.13	1.23	1.45
YGL012W	ERG4	1.00	1.12	1.14	1.45
YDR361C	BCP1	1.00	1.06	1.53	1.45
YER064C		1.00	1.05	1.20	1.45
YOR168W	GLN4	1.00	-1.04	1.58	1.45
YMR317W		1.00	-1.07	1.46	1.45
YPL092W	SSU1	1.00	-1.07	-1.10	1.45
YDR427W	RPN9	1.00	-1.09	1.41	1.45
YIR030C	DCG1	1.00	-1.09	1.12	1.45
YDR033W	MRH1	1.00	-1.10	1.08	1.45
YAL036C	FUN11	1.00	-1.14	1.03	1.45
YDR301W	CFT1	1.00	-1.14	1.09	1.45
YDL182W	LYS20	1.00	-1.22	-1.01	1.45
YDR162C	NBP2	1.00	-1.29	1.09	1.45
YDL055C	PSA1	1.00	-1.46	1.65	1.45
YPL199C		1.00	1.30	1.38	1.44
YJL174W	KRE9	1.00	1.25	1.20	1.44
YNL244C	SUI1	1.00	1.23	1.09	1.44
YLR435W		1.00	1.22	1.22	1.44
YCR023C		1.00	1.21	1.25	1.44
YDR023W	SES1	1.00	1.18	1.41	1.44
YJR072C		1.00	1.17	1.39	1.44
YCR057C	PWP2	1.00	1.14	-1.02	1.44
YKR038C		1.00	1.14	1.32	1.44
YDR349C	YPS7	1.00	1.07	1.21	1.44
YKL120W	OAC1	1.00	1.07	1.16	1.44
YJL190C	RPS22A	1.00	1.05	1.19	1.44
YNL263C	YIF1	1.00	1.04	1.35	1.44
YPR157W		1.00	1.01	1.49	1.44
YOR259C	RPT4	1.00	-1.01	1.44	1.44
YJL130C	URA2	1.00	-1.03	1.30	1.44
YPL052W		1.00	-1.04	2.16	1.44
YLR464W		1.00	-1.17	1.15	1.44
YMR123W	PKR1	1.00	-1.25	-1.05	1.44
YCL019W		1.00	-1.27	1.19	1.44
YLR390W	ECM19	1.00	1.18	1.40	1.44
YLR160C	ASP3-4	1.00	2.01	1.93	1.43

YDL192W	ARF1	1.00	1.50	1.18	1.43
YBL083C		1.00	1.25	1.41	1.43
YPR037C	ERV2	1.00	1.23	1.33	1.43
YDL100C		1.00	1.20	1.56	1.43
YIL143C	SSL2	1.00	1.20	1.14	1.43
YER015W	FAA2	1.00	1.13	1.08	1.43
YDR524C	AGE1	1.00	1.12	1.25	1.43
YFR034C	PHO4	1.00	1.11	1.26	1.43
YHR200W	RPN10	1.00	1.05	1.26	1.43
YBR002C	RER2	1.00	1.03	1.09	1.43
YOL160W		1.00	1.01	1.08	1.43
YGR049W	SCM4	1.00	-1.01	1.35	1.43
YOR390W		1.00	-1.02	1.22	1.43
YOR119C	RIO1	1.00	-1.07	1.28	1.43
YGR113W	DAM1	1.00	-1.12	1.17	1.43
YLR144C	ACF2	1.00	-1.12	-1.02	1.43
YOR260W	GCD1	1.00	-1.19	1.49	1.43
YHR060W	VMA22	1.00	-1.21	1.07	1.43
YER103W	SSA4	1.00	-1.54	-1.06	1.43
YJL147C		1.00	1.27	1.39	1.42
YOR261C	RPN8	1.00	1.27	1.76	1.42
YLR319C	BUD6	1.00	1.23	1.23	1.42
YOR346W	REV1	1.00	1.20	1.57	1.42
YIL144W	TID3	1.00	1.16	1.08	1.42
YML088W	UFO1	1.00	1.16	1.26	1.42
YDL109C		1.00	1.14	1.30	1.42
YIL145C	PAN6	1.00	1.04	1.08	1.42
YLR114C	EFR4	1.00	1.04	1.27	1.42
YLR381W		1.00	1.00	1.31	1.42
YJR075W	HOC1	1.00	-1.01	1.13	1.42
YAL026C	DRS2	1.00	-1.04	1.11	1.42
YPR169W		1.00	-1.07	1.34	1.42
YMR049C	ERB1	1.00	-1.09	1.06	1.42
YLR388W	RPS29A	1.00	-1.13	1.16	1.42
YFR039C		1.00	-1.14	1.24	1.42
YMR265C		1.00	-1.19	1.35	1.42
YOL141W	PPM2	1.00	-1.46	1.18	1.42
YOR107W	RGS2	1.00	-2.01	1.10	1.42
YAR029W		1.00	1.29	1.38	1.41
YLR354C	TAL1	1.00	1.21	1.19	1.41
YOL123W	HRP1	1.00	1.20	1.48	1.41
YDL207W	GLE1	1.00	1.18	1.35	1.41
YFL021W	GAT1	1.00	1.14	1.30	1.41
YDL110C		1.00	1.13	1.07	1.41
YPL149W	APG5	1.00	1.12	1.40	1.41
YOR022C		1.00	1.06	1.14	1.41
YPL176C		1.00	1.01	1.12	1.41
YOR276W	CAF20	1.00	1.00	1.10	1.41
YML099C	ARG81	1.00	-1.04	1.31	1.41
YDL035C	GPR1	1.00	-1.05	1.16	1.41
YML082W		1.00	-1.12	1.12	1.41
YJL098W	SAP185	1.00	-1.13	1.05	1.41
YJL050W	MTR4	1.00	-1.14	1.09	1.41
YNL001W	DOM34	1.00	-1.16	1.30	1.41
YEL018W		1.00	-1.25	1.10	1.41
YMR291W		1.00	1.65	2.09	1.40
YJL060W		1.00	1.38	1.08	1.40
YDR118W	APC4	1.00	1.34	1.50	1.40
YDL013W	HEX3	1.00	1.24	1.09	1.40
YPL091W	GLR1	1.00	1.23	1.45	1.40
YIR042C		1.00	1.21	1.20	1.40

YNL004W	HRB1	1.00	1.20	1.46	1.40
YGL150C	INO80	1.00	1.15	1.31	1.40
YLR172C	DPH5	1.00	1.12	1.26	1.40
YOR337W	TEA1	1.00	1.07	-1.19	1.40
YHR161C	YAP1801	1.00	1.06	1.52	1.40
YOR330C	MIP1	1.00	1.05	1.32	1.40
YFR037C	RSC8	1.00	-1.01	1.25	1.40
YIL128W	MET18	1.00	-1.01	1.31	1.40
YNR015W	SMM1	1.00	-1.01	1.27	1.40
YPR174C		1.00	-1.02	1.16	1.40
YJL171C		1.00	-1.08	1.19	1.40
YLR086W	SMC4	1.00	-1.08	1.33	1.40
YGR190C		1.00	-1.09	1.27	1.40
YGL213C	SKI8	1.00	-1.10	1.14	1.40
YNL082W	PMS1	1.00	-2.21	1.16	1.40
YGR241C	YAP1802	1.00	1.23	1.32	1.39
YFL020C	PAU5	1.00	1.21	1.31	1.39
YHR055C	CUP1-2	1.00	1.21	2.33	1.39
YDL241W		1.00	1.17	1.34	1.39
YMR014W	BUD22	1.00	1.12	1.43	1.39
YIL127C		1.00	1.11	1.22	1.39
YPR167C	MET16	1.00	1.10	1.07	1.39
YPL137C		1.00	1.05	-1.01	1.39
YPR204W		1.00	1.00	1.28	1.39
YML076C		1.00	-1.09	1.23	1.39
YGL253W	HXK2	1.00	-1.11	1.42	1.39
YDL119C		1.00	-1.31	-1.16	1.39
YFL022C	FRS2	1.00	-1.31	1.00	1.39
YMR214W	SCJ1	1.00	-1.41	1.15	1.39
YGL023C	PIB2	1.00	-1.42	1.17	1.39
YGR185C	TYS1	1.00	-1.48	1.11	1.39
YGL011C	SCL1	1.00	-1.53	1.20	1.39
YDL124W		1.00	1.53	1.55	1.38
YIL062C	ARC15	1.00	1.45	1.58	1.38
YCR045C		1.00	1.42	1.35	1.38
YDL012C		1.00	1.30	1.17	1.38
YGL198W		1.00	1.26	1.12	1.38
YKR045C		1.00	1.26	1.15	1.38
YAL037W		1.00	1.25	1.19	1.38
YDR408C	ADE8	1.00	1.14	1.10	1.38
YDR223W		1.00	1.13	1.47	1.38
YER101C	AST2	1.00	1.07	1.11	1.38
YOL095C	HMI1	1.00	1.04	1.19	1.38
YEL053C	MAK10	1.00	-1.04	-1.02	1.38
YDL071C		1.00	-1.05	1.19	1.38
YLR424W		1.00	-1.10	1.32	1.38
YNL091W		1.00	-1.11	1.36	1.38
YEL001C		1.00	-1.13	-1.02	1.38
YOR270C	VPH1	1.00	-1.13	1.25	1.38
YPR066W	UBA3	1.00	-1.13	1.25	1.38
YGR211W	ZPR1	1.00	-1.18	1.22	1.38
YGL228W	SHE10	1.00	-1.19	1.18	1.38
YHR003C		1.00	-1.27	1.17	1.38
YOR165W		1.00	-1.33	1.09	1.38
YKL172W	EBP2	1.00	-1.54	-1.21	1.38
YAL005C	SSA1	1.00	-1.97	-1.57	1.38
YDL024C	DIA3	1.00	1.96	1.89	1.37
YDL155W	CLB3	1.00	1.28	1.34	1.37
YIL140W	AXL2	1.00	1.26	1.49	1.37
YMR130W		1.00	1.22	1.20	1.37
YDR211W	GCD6	1.00	1.20	1.39	1.37

YEL027W	CUP5	1.00	1.19	-1.04	1.37
YOL145C	CTR9	1.00	1.19	1.33	1.37
YBR156C	SLI15	1.00	1.17	1.32	1.37
YGR143W	SKN1	1.00	1.13	1.27	1.37
YOL038W	PRE6	1.00	1.13	1.44	1.37
YOL093W		1.00	1.13	1.23	1.37
YAL015C	NTG1	1.00	1.12	1.17	1.37
YPR121W	THI22	1.00	1.10	1.41	1.37
YPR137W	RRP9	1.00	1.10	-1.01	1.37
YBL011W	SCT1	1.00	1.09	1.29	1.37
YGL111W		1.00	1.09	1.20	1.37
YOL049W	GSH2	1.00	1.08	1.24	1.37
YMR211W		1.00	1.04	1.16	1.37
YGL209W	MIG2	1.00	1.03	1.13	1.37
YHR159W		1.00	-1.02	1.09	1.37
YMR310C		1.00	-1.15	1.22	1.37
YPL012W	RRP12	1.00	-1.17	1.04	1.37
YBR292C		1.00	-1.20	-1.14	1.37
YNL189W	SRP1	1.00	-1.21	1.14	1.37
YMR113W	FOL3	1.00	-1.36	2.18	1.37
YMR179W	SPT21	1.00	-1.42	-1.10	1.37
YFL065C		1.00	-1.46	1.09	1.37
YPL160W	CDC60	1.00	-1.52	-1.09	1.37
YGR168C		1.00	-1.74	1.06	1.37
YDR471W	RPL27B	1.00	1.62	1.73	1.36
YIL152W		1.00	1.48	2.15	1.36
YLR262C	YPT6	1.00	1.26	1.17	1.36
YGL016W	KAP122	1.00	1.19	1.13	1.36
YGL159W		1.00	1.19	1.27	1.36
YBR155W	CNS1	1.00	1.15	1.11	1.36
YLR099C	ICT1	1.00	1.15	1.34	1.36
YIL043C	CBR1	1.00	1.14	1.31	1.36
YKR023W		1.00	1.12	1.28	1.36
YOR171C	LCB4	1.00	1.10	1.20	1.36
YLR023C		1.00	1.07	1.44	1.36
YOL137W		1.00	1.02	1.12	1.36
YIL173W	VTH1	1.00	-1.01	1.26	1.36
YJL116C	NCA3	1.00	-1.01	1.25	1.36
YCR016W		1.00	-1.09	1.22	1.36
YGR229C	SMI1	1.00	-1.11	1.39	1.36
YNR065C		1.00	-1.13	1.08	1.36
YMR055C	BUB2	1.00	-1.17	1.32	1.36
YGR065C	VHT1	1.00	-1.18	-1.07	1.36
YDL121C		1.00	-1.32	-1.19	1.36
YFL054C		1.00	1.50	1.41	1.35
YDL086W		1.00	1.28	1.51	1.35
YPL065W	VPS28	1.00	1.22	1.26	1.35
YLR379W		1.00	1.20	1.56	1.35
YLR263W	RED1	1.00	1.16	1.26	1.35
YML115C	VAN1	1.00	1.13	1.35	1.35
YFR009W	GCN20	1.00	1.11	1.36	1.35
YIR026C	YVH1	1.00	1.08	1.08	1.35
YJR114W		1.00	1.08	1.16	1.35
YKR027W		1.00	1.07	1.26	1.35
YER151C	UBP3	1.00	1.06	1.13	1.35
YER113C		1.00	1.05	1.13	1.35
YLR005W	SSL1	1.00	1.05	-1.01	1.35
YGL110C		1.00	1.01	1.07	1.35
YNR026C	SEC12	1.00	-1.02	1.08	1.35
YDL001W		1.00	-1.03	1.06	1.35
YMR037C	MSN2	1.00	-1.03	1.22	1.35

YEL013W	VAC8	1.00	-1.05	1.15	1.35
YOL019W	TOS7	1.00	-1.09	1.04	1.35
YOL068C	HST1	1.00	-1.11	1.14	1.35
YDR399W	HPT1	1.00	-1.13	-1.28	1.35
YHL046C		1.00	-1.21	1.01	1.35
YHR128W	FUR1	1.00	-1.28	1.23	1.35
YPL083C	SEN54	1.00	-1.35	1.21	1.35
YLR161W		1.00	-1.36	1.09	1.35
YER061C	CEM1	1.00	-1.57	1.01	1.35
YLR179C		1.00	1.40	1.27	1.34
YCL049C		1.00	1.20	1.16	1.34
YML080W	DUS1	1.00	1.18	1.09	1.34
YLR373C	VID22	1.00	1.16	1.15	1.34
YGL242C		1.00	1.15	1.24	1.34
YJR126C		1.00	1.14	1.24	1.34
YPL240C	HSP82	1.00	1.12	1.71	1.34
YGR150C		1.00	1.11	1.24	1.34
YBL087C	RPL23A	1.00	1.08	-1.12	1.34
YKR039W	GAP1	1.00	1.08	1.08	1.34
YNL163C	RIA1	1.00	1.08	-1.26	1.34
YPL084W	BRO1	1.00	1.05	1.14	1.34
YMR316W	DIA1	1.00	1.03	1.09	1.34
YLR463C		1.00	1.01	1.61	1.34
YLR291C	GCD7	1.00	-1.01	1.21	1.34
YOR072W		1.00	-1.02	1.36	1.34
YDR106W	ARP10	1.00	-1.16	1.28	1.34
YGL021W	ALK1	1.00	-1.16	1.07	1.34
YER047C	SAP1	1.00	-1.20	-1.19	1.34
YLR255C		1.00	-1.26	1.12	1.34
YKR064W		1.00	1.76	1.72	1.33
YBR228W	SLX1	1.00	1.27	1.32	1.33
YJR018W		1.00	1.25	1.25	1.33
YOL080C	REX4	1.00	1.23	1.01	1.33
YOL159C		1.00	1.22	1.32	1.33
YDR105C		1.00	1.21	1.42	1.33
YER145C	FTR1	1.00	1.20	1.08	1.33
YGL254W	FZF1	1.00	1.18	1.13	1.33
YHR194W		1.00	1.18	1.25	1.33
YER189W		1.00	1.16	1.38	1.33
YJL029C	VPS53	1.00	1.16	1.14	1.33
YOL094C	RFC4	1.00	1.16	1.18	1.33
YNL250W	RAD50	1.00	1.12	1.34	1.33
YOR034C	AKR2	1.00	1.12	1.24	1.33
YML132W	COS3	1.00	1.07	1.68	1.33
YCR002C	CDC10	1.00	1.06	1.54	1.33
YPR085C		1.00	1.06	1.04	1.33
YJL001W	PRE3	1.00	1.05	1.29	1.33
YJL076W	NET1	1.00	1.05	1.14	1.33
YJL198W	PHO90	1.00	1.05	1.37	1.33
YMR020W	FMS1	1.00	1.05	1.15	1.33
YPL126W	NAN1	1.00	1.04	1.14	1.33
YPL179W	PPQ1	1.00	1.03	1.54	1.33
YBL113C		1.00	1.02	1.14	1.33
YLR089C		1.00	-1.05	1.18	1.33
YFR036W	CDC26	1.00	-1.11	1.08	1.33
YDR187C		1.00	-1.12	1.00	1.33
YLR083C	EMP70	1.00	-1.15	-1.01	1.33
YGR130C		1.00	-1.16	1.34	1.33
YEL051W	VMA8	1.00	-1.24	1.61	1.33
YOR303W	CPA1	1.00	-1.44	-1.30	1.33
YGR253C	PUP2	1.00	-1.65	-1.05	1.33

YOR015W		1.00	1.44	1.61	1.32
YHR104W	GRE3	1.00	1.38	1.60	1.32
YPL053C	KTR6	1.00	1.29	1.38	1.32
YGR245C	SDA1	1.00	1.25	1.68	1.32
YBR042C		1.00	1.24	1.32	1.32
YER177W	BMH1	1.00	1.21	1.43	1.32
YOL031C		1.00	1.18	1.40	1.32
YOR098C	NUP1	1.00	1.14	1.31	1.32
YCR106W		1.00	1.12	1.39	1.32
YPL050C	MNN9	1.00	1.12	1.25	1.32
YHR175W	CTR2	1.00	1.11	1.29	1.32
YGL195W	GCN1	1.00	1.07	-1.01	1.32
YMR154C	RIM13	1.00	1.04	1.07	1.32
YOL144W	NOP8	1.00	1.04	1.46	1.32
YPL243W	SRP68	1.00	1.03	1.30	1.32
YLR219W	MSC3	1.00	1.02	1.27	1.32
YPR050C		1.00	1.02	1.15	1.32
YDL084W	SUB2	1.00	-1.03	1.24	1.32
YDR357C		1.00	-1.03	1.36	1.32
YMR227C	TAF67	1.00	-1.05	1.11	1.32
YLR198C		1.00	-1.08	1.38	1.32
YPL184C		1.00	-1.10	1.06	1.32
YGR276C	RNH70	1.00	-1.11	1.27	1.32
YOR059C		1.00	-1.11	1.31	1.32
YGR036C	CAX4	1.00	-1.14	1.09	1.32
YEL075C		1.00	-1.16	1.33	1.32
YGR288W	MAL13	1.00	-1.16	1.14	1.32
YHR081W		1.00	-1.52	1.02	1.32
YDL066W	IDP1	1.00	-1.96	-1.11	1.32
YJL189W	RPL39	1.00	1.54	2.03	1.31
YHR192W		1.00	1.26	1.26	1.31
YPL159C		1.00	1.22	1.39	1.31
YPL088W		1.00	1.21	1.31	1.31
YAR030C		1.00	1.20	1.38	1.31
YNL158W		1.00	1.19	1.40	1.31
YHL016C	DUR3	1.00	1.18	1.77	1.31
YPL122C	TFB2	1.00	1.17	1.23	1.31
YBR063C		1.00	1.14	1.22	1.31
YIL038C	NOT3	1.00	1.13	1.26	1.31
YCR048W	ARE1	1.00	1.11	1.09	1.31
YNL113W	RPC19	1.00	1.09	1.00	1.31
YNR024W		1.00	1.08	1.20	1.31
YDR503C	LPP1	1.00	1.07	1.13	1.31
YLR330W	CHS5	1.00	1.06	1.19	1.31
YKR105C		1.00	1.03	1.11	1.31
YNR012W	URK1	1.00	1.03	1.15	1.31
YNL179C		1.00	1.01	1.35	1.31
YNL279W	PRM1	1.00	-1.02	1.33	1.31
YHR089C	GAR1	1.00	-1.06	1.07	1.31
YJL034W	KAR2	1.00	-1.06	1.09	1.31
YER136W	GDI1	1.00	-1.08	1.34	1.31
YOR060C		1.00	-1.16	1.01	1.31
YOR294W	RRS1	1.00	-1.19	1.00	1.31
YKL106W	AAT1	1.00	-1.27	-1.19	1.31
YLL033W		1.00	1.42	1.42	1.30
YBR274W	CHK1	1.00	1.25	1.28	1.30
YLR158C	ASP3-3	1.00	1.19	1.29	1.30
YER088C	DOT6	1.00	1.14	1.56	1.30
YCL002C		1.00	1.13	1.17	1.30
YLR078C	BOS1	1.00	1.13	1.23	1.30
YDL006W	PTC1	1.00	1.12	1.15	1.30

YJL065C		1.00	1.12	1.25	1.30
YOR370C	MRS6	1.00	1.10	1.49	1.30
YOL020W	TAT2	1.00	1.07	1.10	1.30
YGR043C		1.00	1.06	1.06	1.30
YDL003W	MCD1	1.00	1.04	1.19	1.30
YER046W	SPO73	1.00	1.00	1.00	1.30
YOR146W		1.00	1.00	1.27	1.30
YIR020C		1.00	-1.01	1.33	1.30
YOL067C	RTG1	1.00	-1.01	1.16	1.30
YLR102C	APC9	1.00	-1.02	1.66	1.30
YKL184W	SPE1	1.00	-1.05	1.07	1.30
YPL095C		1.00	-1.06	1.18	1.30
YLR467W	YRF1-5	1.00	-1.07	1.36	1.30
YPL001W	HAT1	1.00	-1.10	1.22	1.30
YJL109C		1.00	-1.12	-1.02	1.30
YMR044W	IOC4	1.00	-1.12	1.09	1.30
YEL035C	UTR5	1.00	-1.15	-1.17	1.30
YBR141C		1.00	-1.17	-1.09	1.30
YDR360W		1.00	-1.18	1.13	1.30
YLR244C	MAP1	1.00	-1.18	1.10	1.30
YDR331W	GPI8	1.00	-1.23	1.01	1.30
YGR091W	PRP31	1.00	-1.28	1.12	1.30
YLR272C	YCS4	1.00	-1.40	1.12	1.30
YOL166C		1.00	-1.54	-1.18	1.30
YBR084W	MIS1	1.00	-1.61	-1.28	1.30
YCL007C	CWH36	1.00	1.35	1.40	1.29
YJL151C	SNA3	1.00	1.31	1.24	1.29
YDL188C	PPH22	1.00	1.27	1.19	1.29
YJL044C	GYP6	1.00	1.23	1.20	1.29
YOR305W		1.00	1.20	1.17	1.29
YER159C	BUR6	1.00	1.16	1.09	1.29
YPR101W	SNT309	1.00	1.13	1.30	1.29
YIL025C		1.00	1.11	1.08	1.29
YDR222W		1.00	1.10	1.39	1.29
YLL026W	HSP104	1.00	1.07	1.22	1.29
YOR203W		1.00	1.06	1.20	1.29
YER078C		1.00	1.05	1.12	1.29
YOR210W	RPB10	1.00	1.03	1.09	1.29
YLR190W		1.00	-1.01	1.03	1.29
YNL285W		1.00	-1.02	1.17	1.29
YLR452C	SST2	1.00	-1.03	-1.02	1.29
YJL073W	JEM1	1.00	-1.04	1.00	1.29
YFL042C		1.00	-1.05	1.06	1.29
YHR108W	GGA2	1.00	-1.05	1.33	1.29
YLR006C	SSK1	1.00	-1.05	1.11	1.29
YOL028C	YAP7	1.00	-1.05	1.13	1.29
YJL042W	MHP1	1.00	-1.13	-1.40	1.29
YLR236C		1.00	-1.15	-1.14	1.29
YPL163C	SVS1	1.00	-1.15	1.18	1.29
YDL122W	UBP1	1.00	-1.18	-1.13	1.29
YMR295C		1.00	-1.19	1.02	1.29
YHR169W	DBP8	1.00	-1.22	-1.28	1.29
YKL001C	MET14	1.00	-1.39	1.01	1.29
YOR189W	IES4	1.00	-1.46	1.01	1.29
YLR257W		1.00	1.43	1.58	1.28
YBR064W		1.00	1.41	1.28	1.28
YDR171W	HSP42	1.00	1.40	1.85	1.28
YBR123C	TFC1	1.00	1.39	1.36	1.28
YEL038W	UTR4	1.00	1.37	1.51	1.28
YOL106W		1.00	1.28	1.84	1.28
YPR176C	BET2	1.00	1.28	1.34	1.28

YDR202C	RAV2	1.00	1.22	1.25	1.28
YOR384W	FRE5	1.00	1.22	1.13	1.28
YGR058W		1.00	1.21	1.30	1.28
YJL055W		1.00	1.16	1.22	1.28
YBR133C	HSL7	1.00	1.15	1.15	1.28
YDR488C	PAC11	1.00	1.15	1.85	1.28
YBR135W	CKS1	1.00	1.14	1.24	1.28
YIL132C	CSM2	1.00	1.14	-1.08	1.28
YFL027C	GYP8	1.00	1.13	1.28	1.28
YML011C		1.00	1.13	1.34	1.28
YDR478W	SNM1	1.00	1.12	1.16	1.28
YIR011C	STS1	1.00	1.11	1.33	1.28
YMR269W		1.00	1.10	1.30	1.28
YEL025C	SRI1	1.00	1.08	1.04	1.28
YDL160C	DHH1	1.00	1.06	1.37	1.28
YBL024W	NCL1	1.00	1.05	1.10	1.28
YOR251C		1.00	1.05	1.22	1.28
YOR360C	PDE2	1.00	1.05	-1.07	1.28
YDL201W		1.00	1.03	1.02	1.28
YER019W	ISC1	1.00	1.03	1.29	1.28
YGL113W	SLD3	1.00	1.03	1.06	1.28
YGL241W	KAP114	1.00	1.03	1.18	1.28
YER176W	ECM32	1.00	1.00	1.18	1.28
YDR040C	ENA1	1.00	-1.02	1.13	1.28
YOL037C		1.00	-1.03	1.32	1.28
YBR239C		1.00	-1.04	1.15	1.28
YHR027C	RPN1	1.00	-1.04	1.36	1.28
YKL068W	NUP100	1.00	-1.04	-1.13	1.28
YLR347C	KAP95	1.00	-1.07	1.07	1.28
YBR142W	MAK5	1.00	-1.08	1.06	1.28
YLR002C	NOC3	1.00	-1.09	1.06	1.28
YKR072C	SIS2	1.00	-1.17	1.09	1.28
YOR068C		1.00	-1.18	1.66	1.28
YER086W	ILV1	1.00	-1.24	-1.18	1.28
YBL081W		1.00	-1.31	-1.09	1.28
YFL009W	CDC4	1.00	-1.35	1.10	1.28
YKL096W	CWP1	1.00	1.45	1.43	1.27
YHR183W	GND1	1.00	1.51	1.12	1.27
YLR332W	MID2	1.00	1.34	1.40	1.27
YBR203W		1.00	1.32	1.24	1.27
YBL085W	BOI1	1.00	1.26	1.43	1.27
YBL063W	KIP1	1.00	1.23	1.47	1.27
YFL062W	COS4	1.00	1.23	1.35	1.27
YPL232W	SSO1	1.00	1.18	1.54	1.27
YNL275W		1.00	1.12	1.02	1.27
YAL002W	VPS8	1.00	1.10	1.12	1.27
YDR109C		1.00	1.08	1.23	1.27
YDR474C		1.00	1.08	1.15	1.27
YDR071C		1.00	1.07	1.47	1.27
YNL217W		1.00	1.07	1.00	1.27
YPL244C	HUT1	1.00	1.06	1.27	1.27
YIL153W	RRD1	1.00	1.05	1.25	1.27
YPL011C	TAF47	1.00	1.02	1.06	1.27
YOL036W		1.00	-1.03	1.16	1.27
YDL117W	CYK3	1.00	-1.09	1.16	1.27
YIL091C		1.00	-1.10	1.00	1.27
YDR300C	PRO1	1.00	-1.37	1.08	1.27
YPL119C	DBP1	1.00	-1.46	1.16	1.27
YNL135C	FPR1	1.00	1.52	1.53	1.26
YDR169C	STB3	1.00	1.25	1.23	1.26
YPL158C		1.00	1.18	1.46	1.26

YGR158C	MTR3	1.00	1.17	1.10	1.26
YDL152W		1.00	1.15	1.46	1.26
YMR036C	MIH1	1.00	1.14	1.11	1.26
YJL069C		1.00	1.12	-1.09	1.26
YNR046W		1.00	1.10	1.13	1.26
YGR144W	THI4	1.00	1.09	1.01	1.26
YMR039C	SUB1	1.00	1.07	1.24	1.26
YNL307C	MCK1	1.00	1.06	1.31	1.26
YOL070C		1.00	1.06	1.24	1.26
YDR407C	TRS120	1.00	1.05	1.12	1.26
YOR355W	GDS1	1.00	1.04	1.70	1.26
YDR348C		1.00	1.03	1.17	1.26
YJL123C		1.00	1.03	1.45	1.26
YPR058W	YMC1	1.00	1.01	1.06	1.26
YIR041W		1.00	1.00	1.19	1.26
YLR412W		1.00	-1.01	1.20	1.26
YJL088W	ARG3	1.00	-1.02	1.05	1.26
YPR061C		1.00	-1.03	1.12	1.26
YDR481C	PHO8	1.00	-1.04	1.11	1.26
YKL095W	YJU2	1.00	-1.04	1.05	1.26
YLR241W		1.00	-1.04	1.01	1.26
YHL050C		1.00	-1.07	1.28	1.26
YDR412W		1.00	-1.09	1.13	1.26
YPL136W		1.00	-1.11	1.01	1.26
YGR112W	SHY1	1.00	-1.12	1.11	1.26
YNL166C	BNI5	1.00	-1.14	1.16	1.26
YLR261C		1.00	-1.15	1.07	1.26
YFL028C	CAF16	1.00	-1.29	1.21	1.26
YML125C		1.00	-1.32	-1.17	1.26
YJL080C	SCP160	1.00	-1.44	1.17	1.26
YLR252W		1.00	-1.51	1.03	1.26
YML109W	ZDS2	1.00	-1.51	1.21	1.26
YLR457C	NBP1	1.00	-2.10	1.05	1.26
YDR133C		1.00	1.66	1.91	1.25
YBR030W		1.00	1.24	1.28	1.25
YAL014C		1.00	1.21	1.27	1.25
YGL137W	SEC27	1.00	1.21	1.45	1.25
YML048W	GSF2	1.00	1.20	1.48	1.25
YDL040C	NAT1	1.00	1.13	1.24	1.25
YDR281C	PHM6	1.00	1.13	1.14	1.25
YGL101W		1.00	1.13	1.06	1.25
YGL248W	PDE1	1.00	1.13	1.02	1.25
YOR157C	PUP1	1.00	1.11	1.44	1.25
YEL049W	PAU2	1.00	1.09	-1.02	1.25
YDR400W	URH1	1.00	1.08	1.21	1.25
YIL108W		1.00	1.06	1.09	1.25
YDR394W	RPT3	1.00	1.05	1.32	1.25
YDL170W	UGA3	1.00	1.04	1.14	1.25
YDL179W	PCL9	1.00	1.04	1.35	1.25
YPR199C	ARR1	1.00	1.03	1.26	1.25
YDL073W		1.00	1.00	1.11	1.25
YKL062W	MSN4	1.00	-1.01	1.18	1.25
YPR063C		1.00	-1.01	1.38	1.25
YDR326C		1.00	-1.02	1.10	1.25
YLR063W		1.00	-1.02	1.08	1.25
YGR249W	MGA1	1.00	-1.03	1.19	1.25
YPL202C	AFT2	1.00	-1.04	1.25	1.25
YPL274W	SAM3	1.00	-1.05	1.11	1.25
YJR026W		1.00	-1.06	1.20	1.25
YKR036C	CAF4	1.00	-1.07	-1.11	1.25
YFL037W	TUB2	1.00	-1.08	1.29	1.25

YOR027W	STI1	1.00	-1.13	1.52	1.25
YOR014W	RTS1	1.00	-1.20	1.14	1.25
YDL150W	RPC53	1.00	-1.25	1.14	1.25
YHR023W	MYO1	1.00	-1.25	1.03	1.25
YBR177C	EHT1	1.00	-1.26	1.01	1.25
YLR285W		1.00	-1.30	1.10	1.25
YER126C	KRE32	1.00	-1.31	-1.05	1.25
YKL209C	STE6	1.00	-1.32	1.07	1.25
YOR051C		1.00	-1.41	1.14	1.25
YBR253W	SRB6	1.00	1.32	1.26	1.24
YKL144C	RPC25	1.00	1.32	1.34	1.24
YNL227C		1.00	1.26	1.31	1.24
YIL005W		1.00	1.18	1.06	1.24
YNL156C		1.00	1.18	1.66	1.24
YOL075C		1.00	1.17	1.23	1.24
YPL015C	HST2	1.00	1.17	1.55	1.24
YBR169C	SSE2	1.00	1.15	-1.01	1.24
YOR179C		1.00	1.14	1.29	1.24
YLR221C	RSA3	1.00	1.11	1.23	1.24
YPR108W	RPN7	1.00	1.09	1.47	1.24
YIL037C	PRM2	1.00	1.07	1.04	1.24
YKL004W	AUR1	1.00	1.06	1.04	1.24
YDR315C	IPK1	1.00	1.04	1.24	1.24
YHR035W		1.00	1.03	1.06	1.24
YCR077C	PAT1	1.00	-1.01	-1.07	1.24
YGR135W	PRE9	1.00	-1.02	-1.06	1.24
YER057C	HMF1	1.00	-1.03	-1.06	1.24
YPR162C	ORC4	1.00	-1.03	1.19	1.24
YAL013W	DEP1	1.00	-1.06	1.13	1.24
YGL229C	SAP4	1.00	-1.06	1.11	1.24
YPR024W	YME1	1.00	-1.07	1.49	1.24
YBL104C		1.00	-1.10	1.05	1.24
YDR014W		1.00	-1.10	-1.02	1.24
YOL025W	LAG2	1.00	-1.11	1.06	1.24
YEL004W	YEA4	1.00	-1.16	-1.19	1.24
YGL240W	DOC1	1.00	-1.17	1.08	1.24
YGL218W		1.00	-1.20	1.09	1.24
YCR051W		1.00	-1.35	-1.02	1.24
YBR298C	MAL31	1.00	1.50	1.25	1.23
YGR106C		1.00	1.50	1.42	1.23
YKL061W		1.00	1.34	1.23	1.23
YDR505C	PSP1	1.00	1.23	1.33	1.23
YHR083W		1.00	1.22	1.15	1.23
YKL052C	ASK1	1.00	1.20	1.08	1.23
YCR035C	RRP43	1.00	1.18	1.07	1.23
YBR250W		1.00	1.17	1.22	1.23
YOL001W	PHO80	1.00	1.12	1.37	1.23
YIL015W	BAR1	1.00	1.08	1.28	1.23
YOL104C	NDJ1	1.00	1.08	1.13	1.23
YDL123W	SNA4	1.00	1.07	-1.09	1.23
YER028C		1.00	1.07	-1.06	1.23
YPL237W	SUI3	1.00	1.07	1.11	1.23
YKL131W		1.00	1.06	1.17	1.23
YMR124W		1.00	1.05	1.33	1.23
YER169W	RPH1	1.00	1.04	1.03	1.23
YGR218W	CRM1	1.00	1.04	1.15	1.23
YOR234C	RPL33B	1.00	1.02	1.16	1.23
YPL268W	PLC1	1.00	1.02	1.15	1.23
YHR078W		1.00	1.01	1.10	1.23
YNL256W	FOL1	1.00	1.01	1.15	1.23
YHR117W	TOM71	1.00	1.00	1.25	1.23

YOL076W	MDM20	1.00	-1.01	1.07	1.23
YDL190C	UFD2	1.00	-1.02	1.04	1.23
YOL158C	ENB1	1.00	-1.04	1.05	1.23
YOR351C	MEK1	1.00	-1.05	1.16	1.23
YGL129C	RSM23	1.00	-1.06	-1.09	1.23
YOR112W		1.00	-1.06	1.20	1.23
YOR383C	FIT3	1.00	-1.06	1.01	1.23
YLR366W		1.00	-1.09	1.07	1.23
YML064C	TEM1	1.00	-1.09	1.73	1.23
YPL188W	POS5	1.00	-1.13	-1.04	1.23
YOR287C		1.00	-1.14	1.00	1.23
YKR061W	KTR2	1.00	-1.15	1.02	1.23
YIL104C		1.00	-1.17	1.30	1.23
YJL008C	CCT8	1.00	-1.17	1.24	1.23
YHL009C	YAP3	1.00	-1.20	-1.03	1.23
YMR010W		1.00	-1.24	-1.08	1.23
YNL083W		1.00	-1.29	1.20	1.23
YLR064W		1.00	-1.33	1.13	1.23
YJL122W		1.00	-1.40	1.17	1.23
YBR131W	CCZ1	1.00	1.31	1.38	1.22
YBL049W		1.00	1.30	1.54	1.22
YDR006C	SOK1	1.00	1.26	1.32	1.22
YJL196C	ELO1	1.00	1.25	1.24	1.22
YHR073W	OSH3	1.00	1.24	1.26	1.22
YOL143C	RIB4	1.00	1.20	1.40	1.22
YBR178W		1.00	1.19	1.36	1.22
YBR242W		1.00	1.18	1.20	1.22
YLR374C		1.00	1.18	1.05	1.22
YJL037W		1.00	1.17	1.22	1.22
YFR006W		1.00	1.16	1.56	1.22
YLL043W	FPS1	1.00	1.15	1.28	1.22
YGR268C		1.00	1.14	1.25	1.22
YPL260W		1.00	1.14	1.55	1.22
YKL214C		1.00	1.13	1.00	1.22
YJL121C	RPE1	1.00	1.11	1.20	1.22
YFL068W		1.00	1.10	1.52	1.22
YBR240C	THI2	1.00	1.08	1.17	1.22
YBR179C	FZO1	1.00	1.07	-1.10	1.22
YDR545W	YRF1-1	1.00	1.07	1.26	1.22
YER122C	GLO3	1.00	1.07	1.05	1.22
YNL313C		1.00	1.07	1.21	1.22
YLR225C		1.00	1.06	1.11	1.22
YOL063C		1.00	1.05	1.19	1.22
YHR063C	PAN5	1.00	1.04	1.22	1.22
YKR028W	SAP190	1.00	1.04	1.12	1.22
YKR092C	SRP40	1.00	1.04	1.30	1.22
YLR034C	SMF3	1.00	1.03	1.04	1.22
YMR241W	YHM2	1.00	1.02	-1.04	1.22
YDR526C		1.00	1.01	1.09	1.22
YAL053W		1.00	1.00	1.00	1.22
YJL063C	MRPL8	1.00	1.00	1.33	1.22
YOR208W	PTP2	1.00	1.00	-1.02	1.22
YKL046C		1.00	-1.02	1.01	1.22
YMR319C	FET4	1.00	-1.04	1.15	1.22
YPR119W	CLB2	1.00	-1.05	-1.10	1.22
YNL013C		1.00	-1.14	1.14	1.22
YDR161W	TCI1	1.00	-1.16	1.18	1.22
YMR043W	MCM1	1.00	-1.24	1.12	1.22
YDR519W	FKB2	1.00	-1.30	1.06	1.22
YGR090W		1.00	-1.33	-1.22	1.22
YDR463W	STP1	1.00	-1.41	-1.24	1.22

YBL046W		1.00	-1.61	-1.36	1.22
YOR201C	PET56	1.00	-1.66	-1.11	1.22
YLR243W		1.00	-1.75	-1.11	1.22
YER070W	RNR1	1.00	-2.21	-1.20	1.22
YFR053C	HXK1	1.00	3.11	5.00	1.21
YOR044W		1.00	1.33	-1.02	1.21
YAL051W	OAF1	1.00	1.32	1.37	1.21
YBL088C	TEL1	1.00	1.27	1.43	1.21
YBL095W		1.00	1.27	1.22	1.21
YBR036C	CSG2	1.00	1.27	1.27	1.21
YOR169C		1.00	1.27	1.75	1.21
YDL112W	TRM3	1.00	1.25	1.02	1.21
YDL088C	ASM4	1.00	1.24	1.33	1.21
YBR160W	CDC28	1.00	1.23	1.30	1.21
YFR002W	NIC96	1.00	1.22	1.30	1.21
YBR146W	MRPS9	1.00	1.20	1.39	1.21
YGR151C		1.00	1.20	1.29	1.21
YCL051W	LRE1	1.00	1.18	1.09	1.21
YGL256W	ADH4	1.00	1.14	1.18	1.21
YML023C		1.00	1.14	1.21	1.21
YKR007W		1.00	1.11	1.22	1.21
YMR016C	SOK2	1.00	1.10	1.29	1.21
YNL226W		1.00	1.10	1.28	1.21
YOR353C		1.00	1.10	1.36	1.21
YDR121W	DPB4	1.00	1.08	1.22	1.21
YCR001W		1.00	1.07	1.41	1.21
YPL120W	VPS30	1.00	1.07	1.26	1.21
YIL109C	SEC24	1.00	1.06	1.48	1.21
YDR439W	LRS4	1.00	1.03	1.11	1.21
YIL177C		1.00	1.03	1.45	1.21
YHL026C		1.00	1.01	1.33	1.21
YPR114W		1.00	-1.01	1.17	1.21
YDR309C	GIC2	1.00	-1.02	1.01	1.21
YAL025C	MAK16	1.00	-1.05	1.03	1.21
YHL039W		1.00	-1.05	1.07	1.21
YJL212C	OPT1	1.00	-1.05	1.01	1.21
YBR062C		1.00	-1.07	1.10	1.21
YMR192W		1.00	-1.09	1.12	1.21
YMR093W		1.00	-1.13	-1.10	1.21
YDR077W	SED1	1.00	-1.16	1.19	1.21
YPR112C	MRD1	1.00	-1.24	1.04	1.21
YHR009C		1.00	-1.29	-1.40	1.21
YHR030C	SLT2	1.00	-1.29	1.02	1.21
YDR321W	ASP1	1.00	-1.37	-1.08	1.21
YHR005C	GPA1	1.00	-1.37	1.08	1.21
YOL117W		1.00	-1.42	1.23	1.21
YOR200W		1.00	-2.00	-1.16	1.21
YBL047C	EDE1	1.00	1.37	1.27	1.20
YKL150W	MCR1	1.00	1.25	1.29	1.20
YLR351C	NIT3	1.00	1.22	1.16	1.20
YHR040W		1.00	1.20	1.21	1.20
YCR014C	POL4	1.00	1.19	1.12	1.20
YDR001C	NTH1	1.00	1.17	1.48	1.20
YBL028C		1.00	1.16	1.17	1.20
YER004W		1.00	1.15	1.21	1.20
YMR127C	SAS2	1.00	1.15	1.13	1.20
YDR005C	MAF1	1.00	1.14	1.19	1.20
YER168C	CCA1	1.00	1.13	1.32	1.20
YMR191W		1.00	1.11	1.46	1.20
YJR024C		1.00	1.08	1.19	1.20
YGL073W	HSF1	1.00	1.06	1.30	1.20

YGL196W		1.00	1.03	-1.07	1.20
YNL225C	CNM67	1.00	1.03	1.13	1.20
YDL099W		1.00	1.02	-1.04	1.20
YMR153W	NUP53	1.00	1.01	1.11	1.20
YOR111W		1.00	1.01	1.11	1.20
YLR238W		1.00	1.00	1.10	1.20
YOR109W	INP53	1.00	-1.01	-1.01	1.20
YPL089C	RLM1	1.00	-1.01	1.20	1.20
YDR258C	HSP78	1.00	-1.02	1.17	1.20
YNR013C	PHO91	1.00	-1.02	1.07	1.20
YGR126W		1.00	-1.03	-1.08	1.20
YGL114W		1.00	-1.05	1.09	1.20
YDL054C		1.00	-1.06	1.14	1.20
YGL044C	RNA15	1.00	-1.06	1.14	1.20
YOL118C		1.00	-1.06	1.16	1.20
YMR213W	CEF1	1.00	-1.08	1.07	1.20
YNR044W	AGA1	1.00	-1.09	-1.06	1.20
YMR238W	DFG5	1.00	-1.11	1.03	1.20
YPR007C	SPO69	1.00	-1.11	1.33	1.20
YJR065C	ARP3	1.00	-1.17	1.03	1.20
YLL008W	DRS1	1.00	-1.20	1.07	1.20
YPL161C	BEM4	1.00	-1.23	-1.07	1.20
YLR052W	IES3	1.00	-1.24	-1.03	1.20
YLR129W	DIP2	1.00	-1.24	-1.13	1.20
YNL183C	NPR1	1.00	-1.28	1.13	1.20
YBR266C		1.00	-1.37	1.09	1.20
YJR143C	PMT4	1.00	-1.52	-1.01	1.20
YBL084C	CDC27	1.00	1.31	1.43	1.19
YKR066C	CCP1	1.00	1.29	1.53	1.19
YHL047C	TAF1	1.00	1.28	1.22	1.19
YDR538W	PAD1	1.00	1.25	1.19	1.19
YGR037C	ACB1	1.00	1.24	1.27	1.19
YOR389W		1.00	1.24	1.09	1.19
YJL059W	YHC3	1.00	1.19	1.03	1.19
YAL027W		1.00	1.16	1.10	1.19
YNL157W		1.00	1.15	1.24	1.19
YBR161W		1.00	1.14	1.14	1.19
YOR372C	NDD1	1.00	1.12	1.21	1.19
YPR075C	OPY2	1.00	1.12	1.23	1.19
YBR076W	ECM8	1.00	1.09	1.07	1.19
YML051W	GAL80	1.00	1.09	1.13	1.19
YOR307C	SLY41	1.00	1.03	1.09	1.19
YLR170C	APS1	1.00	1.02	1.20	1.19
YLR321C	SFH1	1.00	1.01	-1.01	1.19
YGL070C	RPB9	1.00	1.00	1.07	1.19
YMR148W		1.00	-1.01	1.26	1.19
YOR297C	TIM18	1.00	-1.02	1.17	1.19
YMR197C	VTI1	1.00	-1.03	1.15	1.19
YDR465C	RMT2	1.00	-1.04	1.04	1.19
YOL072W	THP1	1.00	-1.04	-1.05	1.19
YDL239C	ADY3	1.00	-1.05	1.00	1.19
YJL165C	HAL5	1.00	-1.06	1.26	1.19
YHR206W	SKN7	1.00	-1.07	-1.14	1.19
YER158C		1.00	-1.09	1.20	1.19
YNL188W	KAR1	1.00	-1.15	1.03	1.19
YNL339C	YRF1-6	1.00	-1.15	1.32	1.19
YLR458W		1.00	-1.24	2.36	1.19
YIL061C	SNP1	1.00	-1.25	1.04	1.19
YPL282C		1.00	-1.26	-1.16	1.19
YHL049C		1.00	-1.37	1.31	1.19
YGR265W		1.00	-1.39	-1.08	1.19

YJL159W	HSP150	1.00	-1.46	-1.04	1.19
YPR072W	NOT5	1.00	-1.62	1.42	1.19
YHR049W		1.00	-1.88	-1.12	1.19
YCR024C		1.00	1.15	1.01	1.19
YMR015C	ERG5	1.00	1.46	1.77	1.18
YDR063W		1.00	1.37	1.24	1.18
YBL003C	HTA2	1.00	1.29	1.14	1.18
YCR061W		1.00	1.24	1.25	1.18
YDR174W	HMO1	1.00	1.24	1.53	1.18
YDR067C		1.00	1.20	1.33	1.18
YBR065C	ECM2	1.00	1.14	1.28	1.18
YLR369W	SSQ1	1.00	1.13	1.04	1.18
YOL013C	HRD1	1.00	1.13	1.34	1.18
YER068W	MOT2	1.00	1.12	1.17	1.18
YIL139C	REV7	1.00	1.12	1.08	1.18
YBR202W	CDC47	1.00	1.08	1.10	1.18
YLR297W		1.00	1.07	1.02	1.18
YAR008W	SEN34	1.00	1.06	1.20	1.18
YPL182C		1.00	1.06	1.28	1.18
YPL129W	ANC1	1.00	1.05	1.29	1.18
YHR144C	DCD1	1.00	1.04	1.86	1.18
YLR246W	ERF2	1.00	1.01	1.14	1.18
YPL101W	TOT7	1.00	1.00	1.22	1.18
YDR184C	ATC1	1.00	-1.01	-1.09	1.18
YBL105C	PKC1	1.00	-1.02	1.17	1.18
YOR101W	RAS1	1.00	-1.05	1.08	1.18
YPR051W	MAK3	1.00	-1.05	-1.08	1.18
YPL066W		1.00	-1.06	1.24	1.18
YDR527W		1.00	-1.07	-1.06	1.18
YER164W	CHD1	1.00	-1.08	1.27	1.18
YHR197W		1.00	-1.09	1.09	1.18
YDL216C	RRI1	1.00	-1.10	-1.08	1.18
YNL181W		1.00	-1.10	1.20	1.18
YLR136C	TIS11	1.00	-1.11	1.00	1.18
YDL007W	RPT2	1.00	-1.12	1.51	1.18
YNL282W	POP3	1.00	-1.12	1.05	1.18
YOR131C		1.00	-1.12	1.22	1.18
YGR125W		1.00	-1.15	1.07	1.18
YKL114C	APN1	1.00	-1.15	-1.04	1.18
YJL051W		1.00	-1.18	1.03	1.18
YKL077W		1.00	-1.23	1.10	1.18
YLL048C	YBT1	1.00	-1.23	-1.13	1.18
YOR316C	COT1	1.00	-1.23	-1.11	1.18
YNL169C	PSD1	1.00	-1.24	1.00	1.18
YCL031C	RRP7	1.00	-1.26	-1.01	1.18
YER132C	PMD1	1.00	-1.27	1.03	1.18
YLR465C		1.00	-1.31	1.45	1.18
YPL214C	THI6	1.00	-1.35	-1.01	1.18
YNR031C	SSK2	1.00	-1.37	-1.14	1.18
YNL177C		1.00	-1.45	1.02	1.18
YCL043C	PDI1	1.00	-1.76	-1.07	1.18
YJL146W	IDS2	1.00	-1.76	1.28	1.18
YBR119W	MUD1	1.00	1.34	1.19	1.17
YDR333C		1.00	1.30	1.17	1.17
YDL205C	HEM3	1.00	1.27	1.06	1.17
YER175C	TMT1	1.00	1.27	1.46	1.17
YBL050W	SEC17	1.00	1.23	1.25	1.17
YBR215W	HPC2	1.00	1.23	1.11	1.17
YDL108W	KIN28	1.00	1.23	1.28	1.17
YDR099W	BMH2	1.00	1.21	1.41	1.17
YBR043C		1.00	1.18	1.17	1.17

YDR226W	ADK1	1.00	1.18	1.35	1.17
YFL052W		1.00	1.18	1.32	1.17
YGL017W	ATE1	1.00	1.17	1.09	1.17
YKL175W	ZRT3	1.00	1.15	1.20	1.17
YBR038W	CHS2	1.00	1.14	1.09	1.17
YJR031C	GEA1	1.00	1.13	1.19	1.17
YKR089C		1.00	1.13	1.20	1.17
YCR044C	PER1	1.00	1.12	1.04	1.17
YDR126W	PSL10	1.00	1.12	1.12	1.17
YGL244W	RTF1	1.00	1.12	1.14	1.17
YOR078W	BUD21	1.00	1.12	1.14	1.17
YCL027W	FUS1	1.00	1.09	1.07	1.17
YBL023C	MCM2	1.00	1.08	-1.05	1.17
YNL103W	MET4	1.00	1.07	1.09	1.17
YGR083C	GCD2	1.00	1.05	1.15	1.17
YKR098C	UBP11	1.00	1.05	1.11	1.17
YBR231C	AOR1	1.00	1.04	1.06	1.17
YHR146W	CRP1	1.00	1.04	1.18	1.17
YBR015C	MNN2	1.00	1.03	-1.22	1.17
YBR140C	IRA1	1.00	1.01	1.04	1.17
YKL188C	PXA2	1.00	1.00	1.01	1.17
YOR110W	TFC7	1.00	1.00	1.17	1.17
YDR373W	FRQ1	1.00	-1.01	1.33	1.17
YJL108C	PRM10	1.00	-1.03	1.13	1.17
YNL322C	KRE1	1.00	-1.03	1.39	1.17
YDL047W	SIT4	1.00	-1.04	1.08	1.17
YNL014W	HEF3	1.00	-1.04	1.89	1.17
YPL251W		1.00	-1.04	1.04	1.17
YIL036W	CST6	1.00	-1.07	1.14	1.17
YER031C	YPT31	1.00	-1.10	1.14	1.17
YKL167C	MRP49	1.00	-1.10	-1.09	1.17
YMR147W		1.00	-1.11	1.17	1.17
YBR148W	YSW1	1.00	-1.12	1.09	1.17
YBR162C	TOS1	1.00	-1.15	-1.39	1.17
YMR219W	ESC1	1.00	-1.15	1.24	1.17
YHR037W	PUT2	1.00	-1.21	-1.17	1.17
YDR269C		1.00	-1.25	-1.20	1.17
YIR018W	YAP5	1.00	-1.26	-1.02	1.17
YOR074C	CDC21	1.00	-1.26	1.63	1.17
YIL151C		1.00	-1.36	1.08	1.17
YJR146W		1.00	-1.36	-1.04	1.17
YPL278C		1.00	-1.43	-1.25	1.17
YOR191W	RIS1	1.00	-1.49	1.01	1.17
YNR029C		1.00	-1.66	1.07	1.17
YLR039C	RIC1	1.00	-1.67	-1.10	1.17
YNL129W		1.00	-1.72	-1.20	1.17
YOR295W	UAF30	1.00	-1.80	-1.03	1.17
YER190W	YRF1-2	1.00	1.39	1.21	1.16
YBR206W		1.00	1.37	1.23	1.16
YBR041W	FAT1	1.00	1.30	1.18	1.16
YLL064C		1.00	1.29	1.13	1.16
YDR479C		1.00	1.24	1.30	1.16
YJL064W		1.00	1.19	1.12	1.16
YKL110C	KTI12	1.00	1.18	1.02	1.16
YKR014C	YPT52	1.00	1.14	1.36	1.16
YLR208W	SEC13	1.00	1.14	1.14	1.16
YDR255C		1.00	1.12	1.19	1.16
YLR171W		1.00	1.12	1.06	1.16
YDL087C	LUC7	1.00	1.10	1.10	1.16
YDL217C	TIM22	1.00	1.10	1.05	1.16
YPL228W	CET1	1.00	1.10	1.11	1.16

YGL206C	CHC1	1.00	1.09	1.14	1.16
YMR023C	MSS1	1.00	1.09	1.50	1.16
YBR171W	SEC66	1.00	1.07	1.06	1.16
YHR041C	SRB2	1.00	1.06	1.06	1.16
YER077C		1.00	1.05	1.16	1.16
YFL067W		1.00	1.04	1.66	1.16
YGR157W	CHO2	1.00	1.04	1.10	1.16
YGL134W	PCL10	1.00	1.02	1.06	1.16
YPR175W	DPB2	1.00	1.02	1.18	1.16
YMR091C	NPL6	1.00	1.01	1.22	1.16
YDR017C	KCS1	1.00	1.00	1.04	1.16
YKL176C	LST4	1.00	-1.01	1.04	1.16
YJR130C	STR2	1.00	-1.03	-1.04	1.16
YHR133C		1.00	-1.04	1.12	1.16
YMR314W	PRE5	1.00	-1.04	1.18	1.16
YBR226C		1.00	-1.05	1.07	1.16
YLR274W	CDC46	1.00	-1.06	1.12	1.16
YDR290W		1.00	-1.08	1.14	1.16
YGL216W	KIP3	1.00	-1.10	-1.07	1.16
YML001W	YPT7	1.00	-1.10	1.12	1.16
YLL011W	SOF1	1.00	-1.12	-1.07	1.16
YOR377W	ATF1	1.00	-1.13	1.23	1.16
YLR041W		1.00	-1.15	1.14	1.16
YMR096W	SNZ1	1.00	-1.15	-1.14	1.16
YNR054C		1.00	-1.17	1.01	1.16
YGR055W	MUP1	1.00	-1.18	-1.10	1.16
YDR448W	ADA2	1.00	-1.19	1.10	1.16
YLR138W	NHA1	1.00	-1.20	1.03	1.16
YBR248C	HIS7	1.00	-1.21	-1.17	1.16
YMR129W	POM152	1.00	-1.25	1.04	1.16
YGL239C		1.00	-1.29	-1.28	1.16
YMR218C	TRS130	1.00	-1.30	-1.06	1.16
YDR353W	TRR1	1.00	-1.80	1.18	1.16
YHR143W		1.00	-1.18	1.14	1.16
YOR159C	SME1	1.00	1.25	1.06	1.15
YOR097C		1.00	1.21	1.26	1.15
YBR275C	RIF1	1.00	1.20	1.02	1.15
YOR103C	OST2	1.00	1.20	1.10	1.15
YGL231C		1.00	1.18	1.18	1.15
YBR085W	AAC3	1.00	1.17	1.17	1.15
YJR113C	RSM7	1.00	1.17	1.05	1.15
YOL052C	SPE2	1.00	1.11	1.59	1.15
YBR265W	TSC10	1.00	1.10	-1.04	1.15
YER017C	AFG3	1.00	1.10	1.17	1.15
YER035W	EDC2	1.00	1.10	1.20	1.15
YFL010C		1.00	1.10	1.15	1.15
YMR259C		1.00	1.10	1.08	1.15
YJL149W		1.00	1.09	1.02	1.15
YGL167C	PMR1	1.00	1.07	-1.02	1.15
YGL051W		1.00	1.05	1.16	1.15
YDR192C	NUP42	1.00	1.04	1.10	1.15
YER009W	NTF2	1.00	1.04	-1.11	1.15
YFL047W	RGD2	1.00	1.04	1.25	1.15
YBL020W	RFT1	1.00	1.03	1.00	1.15
YBR144C		1.00	1.03	-1.01	1.15
YOR322C		1.00	1.03	1.08	1.15
YKL104C	GFA1	1.00	1.02	1.19	1.15
YLR343W		1.00	1.02	1.18	1.15
YOL005C	RPB11	1.00	1.01	-1.05	1.15
YGR114C		1.00	1.00	1.05	1.15
YNL191W		1.00	-1.02	1.02	1.15

YPL030W		1.00	-1.02	-1.17	1.15
YER135C		1.00	-1.03	1.06	1.15
YGR057C	LST7	1.00	-1.03	-1.02	1.15
YDR142C	PEX7	1.00	-1.04	-1.09	1.15
YKL025C	PAN3	1.00	-1.06	1.04	1.15
YIL035C	CKA1	1.00	-1.08	1.00	1.15
YBR075W		1.00	-1.10	1.05	1.15
YNL071W	LAT1	1.00	-1.11	1.15	1.15
YKL145W	RPT1	1.00	-1.12	1.17	1.15
YMR032W	HOF1	1.00	-1.13	1.08	1.15
YOR223W		1.00	-1.13	1.37	1.15
YGR246C	BRF1	1.00	-1.18	1.19	1.15
YOR376W		1.00	-1.18	1.01	1.15
YNL073W	MSK1	1.00	-1.19	1.04	1.15
YPL067C		1.00	-1.19	-1.04	1.15
YOR371C	GPE1	1.00	-1.24	-1.19	1.15
YOR166C		1.00	-1.25	1.23	1.15
YML071C	DOR1	1.00	-1.31	1.10	1.15
YFR052W	RPN12	1.00	-1.35	1.09	1.15
YDL096C		1.00	-1.36	1.16	1.15
YGL252C	RTG2	1.00	-1.44	1.01	1.15
YDR297W	SUR2	1.00	-1.50	-1.12	1.15
YHR032W		1.00	-1.67	-1.29	1.15
YGL109W		1.00	-1.68	-1.04	1.15
YOR299W	BUD7	1.00	-1.70	-1.29	1.15
YPR181C	SEC23	1.00	-1.83	-1.21	1.15
YHR039C	MSC7	1.00	1.02	1.09	1.14
YJR008W		1.00	1.63	1.27	1.14
YLR157C	ASP3-2	1.00	1.44	1.68	1.14
YBL012C		1.00	1.22	1.10	1.14
YBL073W		1.00	1.22	1.11	1.14
YGL179C	TOS3	1.00	1.18	1.01	1.14
YNL240C	NAR1	1.00	1.17	1.20	1.14
YOR327C	SNC2	1.00	1.17	1.30	1.14
YLR079W	SIC1	1.00	1.15	1.29	1.14
YAR033W		1.00	1.14	1.18	1.14
YHR189W		1.00	1.14	1.03	1.14
YDR443C	SSN2	1.00	1.13	1.23	1.14
YNR025C		1.00	1.12	1.10	1.14
YPL256C	CLN2	1.00	1.12	1.07	1.14
YAL048C		1.00	1.10	-1.01	1.14
YDR039C	ENA2	1.00	1.07	1.02	1.14
YGL112C	TAF60	1.00	1.07	1.18	1.14
YDR434W	GPI17	1.00	1.06	1.22	1.14
YGL100W	SEH1	1.00	1.06	-1.11	1.14
YNL219C	ALG9	1.00	1.06	1.18	1.14
YPL108W		1.00	1.06	1.04	1.14
YNR004W		1.00	1.03	1.19	1.14
YGL205W	POX1	1.00	1.01	1.12	1.14
YLR128W		1.00	1.01	1.06	1.14
YNL027W	CRZ1	1.00	1.01	1.08	1.14
YDL166C		1.00	-1.03	1.00	1.14
YPR090W		1.00	-1.03	1.19	1.14
YDR257C	RMS1	1.00	-1.04	-1.18	1.14
YOR181W	LAS17	1.00	-1.04	1.06	1.14
YNL234W		1.00	-1.05	1.07	1.14
YPR138C	MEP3	1.00	-1.05	1.24	1.14
YBR198C	TAF90	1.00	-1.06	1.12	1.14
YDR179C		1.00	-1.06	1.03	1.14
YEL029C	BUD16	1.00	-1.09	-1.12	1.14
YLR040C		1.00	-1.10	1.05	1.14

YDR152W		1.00	-1.13	1.00	1.14
YOL016C	CMK2	1.00	-1.14	1.16	1.14
YOR021C		1.00	-1.21	-1.02	1.14
YDR177W	UBC1	1.00	-1.23	1.11	1.14
YPR049C	CVT9	1.00	-1.23	1.04	1.14
YLR192C	HCR1	1.00	-1.24	-1.01	1.14
YOR304W	ISW2	1.00	-1.24	-1.04	1.14
YDR320C	SWA2	1.00	-1.30	1.13	1.14
YJL194W	CDC6	1.00	-1.31	-1.04	1.14
YOR116C	RPO31	1.00	-1.34	-1.09	1.14
YAL023C	PMT2	1.00	-1.35	-1.23	1.14
YPL201C		1.00	-1.40	-1.27	1.14
YGR180C	RNR4	1.00	-1.41	1.07	1.14
YLR466W	YRF1-4	1.00	-1.42	1.11	1.14
YGL006W	PMC1	1.00	-1.44	-1.13	1.14
YOR083W		1.00	-1.45	-1.05	1.14
YDR229W		1.00	-1.47	-1.25	1.14
YBL005W	PDR3	1.00	-1.44	-1.16	1.14
YFL048C	EMP47	1.00	1.45	1.17	1.13
YNL335W		1.00	1.43	1.27	1.13
YBL062W		1.00	1.32	1.20	1.13
YOR220W		1.00	1.30	1.54	1.13
YOL153C		1.00	1.28	1.29	1.13
YBR134W		1.00	1.26	1.17	1.13
YDL178W	AIP2	1.00	1.24	1.39	1.13
YER027C	GAL83	1.00	1.23	1.14	1.13
YDL125C	HNT1	1.00	1.19	1.30	1.13
YIL175W		1.00	1.19	1.01	1.13
YIR022W	SEC11	1.00	1.16	1.24	1.13
YOL079W		1.00	1.16	-1.02	1.13
YEL016C		1.00	1.15	1.03	1.13
YBR254C	TRS20	1.00	1.14	1.09	1.13
YPL218W	SAR1	1.00	1.13	1.26	1.13
YDL184C	RPL41A	1.00	1.12	1.09	1.13
YLR137W		1.00	1.12	1.16	1.13
YBR227C	MCX1	1.00	1.10	1.26	1.13
YDL193W		1.00	1.10	1.02	1.13
YDR336W		1.00	1.10	1.30	1.13
YOL089C	HAL9	1.00	1.09	1.07	1.13
YPL211W	NIP7	1.00	1.09	-1.14	1.13
YCR037C	PHO87	1.00	1.08	1.01	1.13
YDL072C		1.00	1.07	1.08	1.13
YBR300C		1.00	1.06	1.14	1.13
YOR035C	SHE4	1.00	1.05	1.18	1.13
YOL088C	MPD2	1.00	1.04	1.25	1.13
YIL083C		1.00	1.03	1.05	1.13
YDR164C	SEC1	1.00	1.02	1.26	1.13
YLR353W	BUD8	1.00	1.02	1.05	1.13
YDR108W	GSG1	1.00	1.01	1.07	1.13
YDR362C	TFC6	1.00	1.01	1.12	1.13
YNR038W	DBP6	1.00	1.01	1.04	1.13
YPR029C	APL4	1.00	1.01	1.12	1.13
YGL013C	PDR1	1.00	1.00	1.13	1.13
YGR259C		1.00	1.00	-1.03	1.13
YPR180W	AOS1	1.00	-1.02	1.18	1.13
YPL002C	SNF8	1.00	-1.04	1.14	1.13
YNR037C	RSM19	1.00	-1.05	1.02	1.13
YOL051W	GAL11	1.00	-1.05	1.27	1.13
YJL041W	NSP1	1.00	-1.06	1.02	1.13
YJR078W		1.00	-1.06	-1.10	1.13
YJR117W	STE24	1.00	-1.06	1.08	1.13

YFR029W	PTR3	1.00	-1.07	1.04	1.13
YOR156C	NFI1	1.00	-1.11	1.01	1.13
YPL046C	ELC1	1.00	-1.11	1.76	1.13
YGR267C	FOL2	1.00	-1.12	-1.04	1.13
YNL086W		1.00	-1.13	1.16	1.13
YPL207W		1.00	-1.19	1.15	1.13
YKL015W	PUT3	1.00	-1.22	1.03	1.13
YPR173C	VPS4	1.00	-1.22	-1.08	1.13
YLR055C	SPT8	1.00	-1.25	1.05	1.13
YNL104C	LEU4	1.00	-1.35	-1.18	1.13
YGL169W	SUA5	1.00	-1.37	1.00	1.13
YGL132W		1.00	-1.39	-1.17	1.13
YBL048W		1.00	1.60	1.20	1.12
YNL030W	HHF2	1.00	1.49	1.53	1.12
YER044C	ERG28	1.00	1.40	1.39	1.12
YBL074C	AAR2	1.00	1.36	1.54	1.12
YFL011W	HXT10	1.00	1.31	1.17	1.12
YPL023C	MET12	1.00	1.30	1.20	1.12
YDR160W	SSY1	1.00	1.23	1.14	1.12
YBR098W	MMS4	1.00	1.21	1.33	1.12
YIL057C		1.00	1.21	1.45	1.12
YJR019C	TES1	1.00	1.20	1.03	1.12
YNL270C	ALP1	1.00	1.20	1.13	1.12
YPL234C	TFP3	1.00	1.19	1.21	1.12
YOL035C		1.00	1.18	1.17	1.12
YOR026W	BUB3	1.00	1.17	1.25	1.12
YGL125W	MET13	1.00	1.16	1.32	1.12
YGL185C		1.00	1.16	1.20	1.12
YMR132C		1.00	1.13	1.10	1.12
YNL206C	RTT106	1.00	1.13	1.07	1.12
YBL077W		1.00	1.12	1.09	1.12
YBR087W	RFC5	1.00	1.12	1.10	1.12
YPR103W	PRE2	1.00	1.11	1.02	1.12
YDL098C	SNU23	1.00	1.10	1.07	1.12
YLR184W		1.00	1.09	-1.09	1.12
YOR352W		1.00	1.07	1.19	1.12
YDL127W	PCL2	1.00	1.05	1.09	1.12
YJR102C	VPS25	1.00	1.05	1.29	1.12
YDL120W	YFH1	1.00	1.04	1.13	1.12
YER075C	PTP3	1.00	1.04	1.02	1.12
YOL060C	AMI3	1.00	1.03	1.07	1.12
YCR091W	KIN82	1.00	1.00	1.01	1.12
YLR317W	KRE34	1.00	1.00	1.01	1.12
YGL233W	SEC15	1.00	-1.01	-1.04	1.12
YHR006W	STP2	1.00	-1.02	-1.04	1.12
YDR367W		1.00	-1.03	-1.04	1.12
YDR047W	HEM12	1.00	-1.04	1.06	1.12
YGL050W		1.00	-1.04	-1.02	1.12
YDL126C	CDC48	1.00	-1.05	1.41	1.12
YHR188C	GPI16	1.00	-1.06	1.09	1.12
YPL254W	HFI1	1.00	-1.06	-1.13	1.12
YML117W		1.00	-1.07	1.44	1.12
YKL147C		1.00	-1.10	1.13	1.12
YLL056C		1.00	-1.10	-1.03	1.12
YOR365C		1.00	-1.12	1.09	1.12
YDL103C	QRI1	1.00	-1.13	1.02	1.12
YER072W	VTC1	1.00	-1.13	-1.11	1.12
YJL048C		1.00	-1.15	1.12	1.12
YLR331C		1.00	-1.15	1.06	1.12
YPR203W		1.00	-1.17	1.33	1.12
YLR101C		1.00	-1.18	1.21	1.12

YNL280C	ERG24	1.00	-1.18	1.08	1.12
YPR144C		1.00	-1.18	1.12	1.12
YNL078W	JIP1	1.00	-1.23	1.16	1.12
YOR046C	DBP5	1.00	-1.24	-1.03	1.12
YPR177C		1.00	-1.25	1.10	1.12
YGL227W	VID30	1.00	-1.26	-1.06	1.12
YOR227W		1.00	-1.29	1.15	1.12
YDR266C		1.00	-1.30	-1.08	1.12
YOR173W		1.00	-1.32	-1.32	1.12
YOR202W	HIS3	1.00	-1.32	-1.20	1.12
YPL071C		1.00	-1.41	-1.07	1.12
YOR387C		1.00	-1.42	-1.05	1.12
YGR162W	TIF4631	1.00	-1.43	1.05	1.12
YPR059C		1.00	-1.59	1.01	1.12
YDR172W	SUP35	1.00	-1.77	-1.08	1.12
YGR078C	PAC10	1.00	-1.86	-1.10	1.12
YPL036W	PMA2	1.00	-1.87	-1.48	1.12
YGR025W		1.00	-2.05	-1.07	1.12
YJR124C		1.00	-2.27	-1.04	1.12
YMR034C		1.00	1.29	1.34	1.11
YEL073C		1.00	1.26	1.36	1.11
YCL001W	RER1	1.00	1.23	1.20	1.11
YGL087C	MMS2	1.00	1.23	1.35	1.11
YIL042C		1.00	1.23	1.04	1.11
YGR063C	SPT4	1.00	1.15	-1.05	1.11
YOL050C		1.00	1.14	1.32	1.11
YKL064W	MNR2	1.00	1.13	1.21	1.11
YBR089W		1.00	1.12	1.17	1.11
YDR444W		1.00	1.10	-1.02	1.11
YGR261C	APL6	1.00	1.10	1.00	1.11
YCL017C	NFS1	1.00	1.09	1.18	1.11
YDR081C	PDC2	1.00	1.06	1.08	1.11
YBR255W		1.00	1.05	1.03	1.11
YCR101C		1.00	1.04	1.17	1.11
YLR440C		1.00	1.04	1.09	1.11
YML038C	YMD8	1.00	1.04	1.04	1.11
YMR073C		1.00	1.04	1.07	1.11
YMR180C	CTL1	1.00	1.04	1.25	1.11
YOL085C		1.00	1.04	-1.05	1.11
YFL017C	GNA1	1.00	1.03	1.07	1.11
YDR090C		1.00	1.02	-1.04	1.11
YGR210C		1.00	1.00	1.27	1.11
YPR161C	SGV1	1.00	-1.02	1.01	1.11
YDR267C		1.00	-1.03	1.23	1.11
YGR080W	TWF1	1.00	-1.03	-1.06	1.11
YDR515W	SLF1	1.00	-1.05	-1.23	1.11
YDR263C	DIN7	1.00	-1.06	1.15	1.11
YIL110W		1.00	-1.06	1.05	1.11
YLR328W		1.00	-1.07	1.10	1.11
YER045C	ACA1	1.00	-1.09	1.06	1.11
YJR043C	POL32	1.00	-1.09	1.00	1.11
YDR405W	MRP20	1.00	-1.13	-1.04	1.11
YNR030W	ECM39	1.00	-1.14	1.00	1.11
YDR496C	PUF6	1.00	-1.18	-1.10	1.11
YMR274C	RCE1	1.00	-1.23	1.04	1.11
YMR125W	STO1	1.00	-1.39	1.02	1.11
YCR052W	RSC6	1.00	-1.40	1.00	1.11
YDR065W		1.00	-1.40	1.16	1.11
YML087C		1.00	-1.48	-1.17	1.11
YDR293C	SSD1	1.00	-1.68	-1.30	1.11
YOR296W		1.00	-1.72	1.00	1.11

YGL097W	SRM1	1.00	-1.76	-1.10	1.11
YEL055C	POL5	1.00	-1.77	-1.11	1.11
YJR076C	CDC11	1.00	-2.03	1.11	1.11
YOR155C		1.00	1.39	1.56	1.10
YFR010W	UBP6	1.00	1.30	1.43	1.10
YGR257C		1.00	1.23	1.07	1.10
YDR457W	TOM1	1.00	1.22	1.11	1.10
YJL047C	RTT101	1.00	1.21	1.19	1.10
YGR255C	COQ6	1.00	1.19	1.09	1.10
YDR466W		1.00	1.18	1.15	1.10
YMR183C	SSO2	1.00	1.14	1.28	1.10
YCR069W	SCC3	1.00	1.13	1.25	1.10
YKR099W	BAS1	1.00	1.12	1.21	1.10
YNL063W		1.00	1.12	1.12	1.10
YNR049C	MSO1	1.00	1.12	1.07	1.10
YBR097W	VPS15	1.00	1.11	-1.04	1.10
YNL207W		1.00	1.11	1.13	1.10
YBR040W	FIG1	1.00	1.07	1.07	1.10
YDL156W		1.00	1.07	1.15	1.10
YGL223C	TFI1	1.00	1.06	1.09	1.10
YAR031W	PRM9	1.00	1.05	1.14	1.10
YMR092C	AIP1	1.00	1.04	1.51	1.10
YNL273W	TOF1	1.00	1.04	-1.03	1.10
YOL135C	MED7	1.00	1.04	1.07	1.10
YDL046W		1.00	1.03	1.09	1.10
YBL041W	PRE7	1.00	1.02	1.06	1.10
YCR081W	SRB8	1.00	1.02	1.00	1.10
YER005W	YND1	1.00	1.02	1.58	1.10
YNL101W		1.00	1.02	1.19	1.10
YPL252C	YAH1	1.00	1.02	-1.06	1.10
YLR015W	BRE2	1.00	1.01	-1.11	1.10
YLR091W		1.00	1.01	1.07	1.10
YLR248W	RCK2	1.00	1.00	1.43	1.10
YFR020W		1.00	-1.01	1.07	1.10
YHL012W		1.00	-1.01	-1.06	1.10
YNR035C	ARC35	1.00	-1.01	1.10	1.10
YNL331C	AAD14	1.00	-1.02	1.20	1.10
YJL085W	EXO70	1.00	-1.03	1.02	1.10
YGL059W		1.00	-1.04	-1.05	1.10
YGR128C		1.00	-1.04	-1.07	1.10
YIL121W		1.00	-1.04	1.00	1.10
YHR048W		1.00	-1.05	1.11	1.10
YGR193C	PDX1	1.00	-1.06	1.08	1.10
YHL027W	RIM101	1.00	-1.06	1.22	1.10
YJR161C	COS5	1.00	-1.06	1.25	1.10
YML077W	BET5	1.00	-1.06	1.01	1.10
YMR315W		1.00	-1.07	1.17	1.10
YEL005C	VAB2	1.00	-1.08	-1.04	1.10
YNR039C	ZRG17	1.00	-1.08	-1.09	1.10
YOR380W		1.00	-1.08	1.09	1.10
YHR107C	CDC12	1.00	-1.10	1.06	1.10
YIL130W		1.00	-1.10	1.13	1.10
YNL319W		1.00	-1.10	1.15	1.10
YPR025C	CCL1	1.00	-1.11	1.09	1.10
YDL018C	ERP3	1.00	-1.12	1.03	1.10
YIL023C		1.00	-1.13	-1.06	1.10
YOL103W	ITR2	1.00	-1.13	1.07	1.10
YMR264W	CUE1	1.00	-1.14	1.03	1.10
YML121W	GTR1	1.00	-1.15	1.11	1.10
YPL157W		1.00	-1.15	1.10	1.10
YDR504C		1.00	-1.16	-1.06	1.10

YDR451C	YHP1	1.00	-1.17	-1.21	1.10
YOR211C	MGM1	1.00	-1.17	1.07	1.10
YOR099W	KTR1	1.00	-1.18	-1.07	1.10
YER020W	GPA2	1.00	-1.20	1.14	1.10
YOL045W		1.00	-1.20	1.05	1.10
YHR062C	RPP1	1.00	-1.22	1.15	1.10
YCR030C		1.00	-1.23	-1.03	1.10
YOR017W	PET127	1.00	-1.25	1.08	1.10
YGR136W	LSB1	1.00	-1.26	-1.03	1.10
YLR320W		1.00	-1.26	1.02	1.10
YMR221C		1.00	-1.26	1.07	1.10
YDR224C	HTB1	1.00	-1.27	1.31	1.10
YGL035C	MIG1	1.00	-1.29	1.36	1.10
YLR139C	SLS1	1.00	-1.33	-1.04	1.10
YDL148C	NOP14	1.00	-1.40	-1.36	1.10
YLR022C		1.00	-1.44	-1.07	1.10
YAR002W	NUP60	1.00	-1.54	-1.17	1.10
YGL145W	TIP20	1.00	-1.63	-1.07	1.10
YGR042W		1.00	-1.73	-1.03	1.10
YDR018C		1.00	1.38	1.37	1.09
YOL010W	RCL1	1.00	1.33	1.05	1.09
YLR368W		1.00	1.27	1.26	1.09
YDL242W		1.00	1.11	1.06	1.09
YPL229W		1.00	1.10	1.25	1.09
YPR185W	APG13	1.00	1.10	1.19	1.09
YAR003W	SWD1	1.00	1.09	1.11	1.09
YML079W		1.00	1.09	-1.12	1.09
YBR243C	ALG7	1.00	1.07	1.20	1.09
YPL178W	CBC2	1.00	1.07	1.10	1.09
YEL061C	CIN8	1.00	1.06	1.11	1.09
YGL139W		1.00	1.04	-1.07	1.09
YOR183W	FYV12	1.00	1.04	1.00	1.09
YBR047W		1.00	1.03	1.02	1.09
YAL047C	SPC72	1.00	1.02	1.02	1.09
YBL068W	PRS4	1.00	1.01	1.11	1.09
YEL064C		1.00	1.00	-1.04	1.09
YJL124C	LSM1	1.00	-1.01	1.15	1.09
YNL276C		1.00	-1.01	1.06	1.09
YLR224W		1.00	-1.04	-1.06	1.09
YBR004C		1.00	-1.05	-1.10	1.09
YDL062W		1.00	-1.06	-1.02	1.09
YNL080C		1.00	-1.06	1.04	1.09
YGL207W	SPT16	1.00	-1.07	1.03	1.09
YHR054C		1.00	-1.07	1.49	1.09
YPR136C	FYV15	1.00	-1.07	-1.10	1.09
YCR033W		1.00	-1.08	-1.15	1.09
YOL087C		1.00	-1.08	1.09	1.09
YDR139C	RUB1	1.00	-1.09	-1.03	1.09
YER003C	PMI40	1.00	-1.09	1.28	1.09
YDR264C	AKR1	1.00	-1.11	-1.02	1.09
YDR221W		1.00	-1.12	-1.03	1.09
YLR218C		1.00	-1.12	1.05	1.09
YNL095C		1.00	-1.14	-1.04	1.09
YCL016C	DCC1	1.00	-1.15	-1.29	1.09
YHR149C		1.00	-1.15	-1.05	1.09
YOR008C	SLG1	1.00	-1.15	-1.12	1.09
YDL240W	LRG1	1.00	-1.16	-1.12	1.09
YHR077C	NMD2	1.00	-1.23	-1.24	1.09
YHR127W	HSN1	1.00	-1.23	1.02	1.09
YNL048W	ALG11	1.00	-1.23	1.08	1.09
YMR289W		1.00	-1.29	1.24	1.09

YCL054W	SPB1	1.00	-1.45	-1.24	1.09
YOL165C	AAD15	1.00	-1.49	1.04	1.09
YAL035W	FUN12	1.00	-1.59	-1.37	1.09
YJL110C	GZF3	1.00	-2.09	1.26	1.09
YBR276C	PPS1	1.00	1.47	-1.05	1.08
YDR468C	TLG1	1.00	1.34	1.22	1.08
YBR108W		1.00	1.28	-1.01	1.08
YNR034W	SOL1	1.00	1.28	1.38	1.08
YBL025W	RRN10	1.00	1.22	1.15	1.08
YBL032W		1.00	1.21	1.21	1.08
YBR012C		1.00	1.18	1.22	1.08
YDR201W	SPC19	1.00	1.17	1.13	1.08
YCR100C		1.00	1.16	1.00	1.08
YMR027W	HRT2	1.00	1.14	1.35	1.08
YGL015C		1.00	1.13	-1.03	1.08
YLR155C	ASP3-1	1.00	1.12	1.51	1.08
YLR275W	SMD2	1.00	1.12	-1.01	1.08
YCR099C		1.00	1.10	1.21	1.08
YGL027C	CWH41	1.00	1.08	1.21	1.08
YHR074W	QNS1	1.00	1.08	1.47	1.08
YMR001C	CDC5	1.00	1.08	1.15	1.08
YCR008W	SAT4	1.00	1.04	1.21	1.08
YLR299W	ECM38	1.00	1.04	1.10	1.08
YDR313C	PIB1	1.00	1.03	1.07	1.08
YHR187W	IKI1	1.00	1.03	1.10	1.08
YIL079C		1.00	1.03	-1.06	1.08
YLL034C		1.00	1.03	1.15	1.08
YLR462W		1.00	1.03	1.54	1.08
YOR241W	MET7	1.00	1.03	-1.01	1.08
YDR540C		1.00	1.02	-1.05	1.08
YEL022W	GEA2	1.00	1.02	1.12	1.08
YIR033W	MGA2	1.00	1.02	1.10	1.08
YCL014W	BUD3	1.00	1.01	-1.14	1.08
YPL135W	ISU1	1.00	1.00	1.13	1.08
YPR022C		1.00	1.00	-1.08	1.08
YMR133W	REC114	1.00	-1.01	1.05	1.08
YDR038C	ENA5	1.00	-1.04	1.07	1.08
YJR069C	HAM1	1.00	-1.04	-1.13	1.08
YNL326C		1.00	-1.04	1.11	1.08
YOR123C	LEO1	1.00	-1.04	1.21	1.08
YHR101C	BIG1	1.00	-1.05	-1.05	1.08
YOL115W	TRF4	1.00	-1.06	-1.09	1.08
YDL075W	RPL31A	1.00	-1.07	-1.26	1.08
YKR030W		1.00	-1.07	-1.06	1.08
YNL168C		1.00	-1.08	1.08	1.08
YMR171C		1.00	-1.10	1.03	1.08
YOR069W	VPS5	1.00	-1.10	-1.03	1.08
YDR261C	EXG2	1.00	-1.11	1.03	1.08
YCR019W	MAK32	1.00	-1.13	-1.15	1.08
YGR048W	UFD1	1.00	-1.15	-1.02	1.08
YHR065C	RRP3	1.00	-1.17	1.17	1.08
YOR212W	STE4	1.00	-1.17	1.04	1.08
YLR336C	SGD1	1.00	-1.20	1.02	1.08
YGR213C	RTA1	1.00	-1.21	-1.24	1.08
YNR003C	RPC34	1.00	-1.24	-1.06	1.08
YDR097C	MSH6	1.00	-1.27	-1.15	1.08
YDR319C		1.00	-1.28	-1.24	1.08
YGR275W	RTT102	1.00	-1.32	-1.29	1.08
YIL150C	DNA43	1.00	-1.33	1.31	1.08
YOR095C	RKI1	1.00	-1.42	-1.05	1.08
YAL007C	ERP2	1.00	-1.47	-1.31	1.08

YBR143C	SUP45	1.00	-1.50	-1.14	1.08
YOR199W		1.00	-1.70	-1.21	1.08
YGL054C	ERV14	1.00	-1.80	1.20	1.08
YDR173C	ARG82	1.00	1.46	1.13	1.07
YLR242C	ARV1	1.00	1.36	1.34	1.07
YCR063W	BUD31	1.00	1.33	-1.11	1.07
YER048C	CAJ1	1.00	1.33	1.21	1.07
YPR053C		1.00	1.24	1.38	1.07
YKL036C		1.00	1.22	1.30	1.07
YCR083W	TRX3	1.00	1.18	1.11	1.07
YPL034W		1.00	1.18	1.03	1.07
YCL066W	HMLALPHA1	1.00	1.14	-1.02	1.07
YPR081C		1.00	1.11	1.11	1.07
YNL214W	PEX17	1.00	1.10	1.09	1.07
YGL164C		1.00	1.08	1.31	1.07
YHL024W	RIM4	1.00	1.08	1.07	1.07
YLR453C	RIF2	1.00	1.08	1.08	1.07
YIL176C		1.00	1.07	-1.01	1.07
YDR311W	TFB1	1.00	1.06	1.00	1.07
YKL164C	PIR1	1.00	1.05	1.24	1.07
YDR497C	ITR1	1.00	1.04	1.13	1.07
YKR046C		1.00	1.04	-1.03	1.07
YDR338C		1.00	1.02	1.00	1.07
YHR113W		1.00	1.02	-1.08	1.07
YKR051W		1.00	1.01	-1.01	1.07
YMR270C	RRN9	1.00	1.01	1.11	1.07
YDL080C	THI3	1.00	-1.02	-1.09	1.07
YNL228W		1.00	-1.02	1.13	1.07
YGL063W	PUS2	1.00	-1.03	1.13	1.07
YOR023C	AHC1	1.00	-1.03	1.04	1.07
YLR014C	PPR1	1.00	-1.04	-1.15	1.07
YLR287C		1.00	-1.04	1.13	1.07
YDR299W	BFR2	1.00	-1.05	-1.03	1.07
YDR409W	SIZ1	1.00	-1.05	-1.05	1.07
YFR043C		1.00	-1.05	1.05	1.07
YOR354C	MSC6	1.00	-1.05	1.16	1.07
YNL003C	PET8	1.00	-1.06	1.01	1.07
YDR138W	HPR1	1.00	-1.07	-1.02	1.07
YIL014W	MNT3	1.00	-1.07	1.07	1.07
YOR388C	FDH1	1.00	-1.07	-1.10	1.07
YBR158W	CST13	1.00	-1.08	-1.04	1.07
YGL018C	JAC1	1.00	-1.08	1.15	1.07
YMR223W	UBP8	1.00	-1.08	1.00	1.07
YFR030W	MET10	1.00	-1.09	1.24	1.07
YIL044C	AGE2	1.00	-1.10	1.06	1.07
YKL021C	MAK11	1.00	-1.10	1.10	1.07
YDL128W	VCX1	1.00	-1.11	1.04	1.07
YGR119C	NUP57	1.00	-1.13	-1.02	1.07
YCL055W	KAR4	1.00	-1.14	-1.08	1.07
YPR034W	ARP7	1.00	-1.14	1.04	1.07
YLR310C	CDC25	1.00	-1.15	1.08	1.07
YDR317W		1.00	-1.20	1.07	1.07
YOR325W		1.00	-1.21	-1.17	1.07
YDR480W	DIG2	1.00	-1.23	1.02	1.07
YFR025C	HIS2	1.00	-1.25	1.06	1.07
YOR016C	ERP4	1.00	-1.25	-1.19	1.07
YBL034C	STU1	1.00	-1.27	-1.19	1.07
YBR175W	SWD3	1.00	-1.32	-1.17	1.07
YER037W	PHM8	1.00	-1.33	-1.34	1.07
YJL062W	LAS21	1.00	-1.36	1.08	1.07
YBR106W	PHO88	1.00	-1.53	-1.04	1.07

YGL048C	RPT6	1.00	-1.54	-1.07	1.07
YBL069W	AST1	1.00	-1.62	-1.25	1.07
YJR101W	RSM26	1.00	1.50	-1.01	1.06
YHR090C	YNG2	1.00	1.45	1.04	1.06
YIL004C	BET1	1.00	1.26	1.10	1.06
YBR137W		1.00	1.25	1.10	1.06
YNR056C	BIO5	1.00	1.24	1.08	1.06
YMR021C	MAC1	1.00	1.19	1.13	1.06
YEL033W		1.00	1.18	1.40	1.06
YMR155W		1.00	1.18	1.15	1.06
YMR185W		1.00	1.16	1.14	1.06
YEL060C	PRB1	1.00	1.14	1.30	1.06
YLR356W		1.00	1.14	1.12	1.06
YGR206W		1.00	1.13	1.13	1.06
YOL062C	APM4	1.00	1.13	1.06	1.06
YBL103C	RTG3	1.00	1.11	1.02	1.06
YHR114W	BZZ1	1.00	1.11	1.17	1.06
YOL017W		1.00	1.11	1.07	1.06
YBL013W	FMT1	1.00	1.10	1.00	1.06
YDL034W		1.00	1.07	1.11	1.06
YBR264C	YPT10	1.00	1.06	-1.02	1.06
YIL049W	DFG10	1.00	1.06	1.20	1.06
YLR081W	GAL2	1.00	1.06	1.13	1.06
YPR012W		1.00	1.06	1.63	1.06
YBR029C	CDS1	1.00	1.05	1.01	1.06
YCR015C		1.00	1.05	1.05	1.06
YGR069W		1.00	1.05	-1.09	1.06
YHR142W	CHS7	1.00	1.03	1.20	1.06
YFL044C		1.00	1.02	1.15	1.06
YLR193C		1.00	1.02	1.03	1.06
YPL235W	RVB2	1.00	1.02	1.09	1.06
YIL103W		1.00	1.01	1.17	1.06
YMR005W	MPT1	1.00	1.00	1.08	1.06
YNL232W	CSL4	1.00	1.00	1.30	1.06
YAL033W	POP5	1.00	-1.01	1.07	1.06
YGR146C		1.00	-1.01	1.06	1.06
YNL320W		1.00	-1.02	1.01	1.06
YPL227C	ALG5	1.00	-1.02	1.13	1.06
YLR231C		1.00	-1.03	1.14	1.06
YBR204C		1.00	-1.04	-1.10	1.06
YDR314C		1.00	-1.04	1.02	1.06
YJL049W		1.00	-1.05	1.03	1.06
YPR006C	ICL2	1.00	-1.05	1.12	1.06
YCR067C	SED4	1.00	-1.06	1.04	1.06
YNL287W	SEC21	1.00	-1.08	1.16	1.06
YDR322W	MRPL35	1.00	-1.09	-1.09	1.06
YNR027W	BUD17	1.00	-1.09	-1.05	1.06
YNR028W	CPR8	1.00	-1.09	1.07	1.06
YAR014C	BUD14	1.00	-1.10	1.16	1.06
YGL038C	OCH1	1.00	-1.11	-1.35	1.06
YLR003C		1.00	-1.11	1.02	1.06
YNR021W		1.00	-1.11	1.14	1.06
YKR071C	DRE2	1.00	-1.12	1.13	1.06
YLR253W		1.00	-1.12	1.03	1.06
YBL101C	ECM21	1.00	-1.14	1.13	1.06
YNL213C		1.00	-1.14	1.06	1.06
YBR166C	TYR1	1.00	-1.15	-1.11	1.06
YER021W	RPN3	1.00	-1.17	1.16	1.06
YOR198C	BFR1	1.00	-1.18	1.02	1.06
YPL076W	GPI2	1.00	-1.19	1.12	1.06
YHR148W	IMP3	1.00	-1.22	-1.14	1.06

YGR266W		1.00	-1.24	-1.01	1.06
YLR127C	APC2	1.00	-1.31	-1.09	1.06
YMR262W		1.00	-1.31	1.03	1.06
YBR101C		1.00	-1.32	-1.02	1.06
YLR228C	ECM22	1.00	-1.35	1.04	1.06
YHR163W	SOL3	1.00	-1.38	-1.18	1.06
YPL107W		1.00	-1.40	1.08	1.06
YNL072W	RNH35	1.00	-1.41	-1.01	1.06
YLR068W	FYV7	1.00	-1.48	-1.20	1.06
YNL088W	TOP2	1.00	-1.51	-1.06	1.06
YJR046W	TAH11	1.00	-1.52	-1.28	1.06
YHR172W	SPC97	1.00	-1.57	-1.30	1.06
YNL038W	GPI15	1.00	-1.57	-1.31	1.06
YHR116W		1.00	-1.70	-1.04	1.06
YBR007C		1.00	-1.82	-1.21	1.06
YBR217W	APG12	1.00	1.36	1.12	1.05
YHL021C		1.00	1.36	1.64	1.05
YBR006W	UGA2	1.00	1.27	-1.13	1.05
YBR229C	ROT2	1.00	1.20	1.10	1.05
YPR044C		1.00	1.13	-1.05	1.05
YCL063W		1.00	1.12	1.08	1.05
YGL219C	MMM2	1.00	1.12	1.22	1.05
YNL267W	PIK1	1.00	1.12	-1.06	1.05
YNL050C		1.00	1.09	1.14	1.05
YPR023C	EAF3	1.00	1.09	1.17	1.05
YER157W	SEC34	1.00	1.06	1.16	1.05
YKL050C		1.00	1.06	-1.03	1.05
YBR050C	REG2	1.00	1.04	1.28	1.05
YGL220W		1.00	1.03	1.20	1.05
YNL253W		1.00	1.03	1.21	1.05
YCL076W		1.00	1.02	-1.03	1.05
YGR139W		1.00	1.02	1.07	1.05
YLR173W		1.00	1.02	1.00	1.05
YOL073C		1.00	1.02	-1.02	1.05
YNL303W		1.00	1.01	1.17	1.05
YDR337W	MRPS28	1.00	-1.01	-1.15	1.05
YLR298C	YHC1	1.00	-1.01	1.16	1.05
YPR171W		1.00	-1.02	1.04	1.05
YPR018W	RLF2	1.00	-1.03	-1.03	1.05
YER034W		1.00	-1.04	-1.13	1.05
YLR021W		1.00	-1.05	1.06	1.05
YLR260W	LCB5	1.00	-1.05	1.07	1.05
YPR178W	PRP4	1.00	-1.05	1.17	1.05
YBR152W	SPP381	1.00	-1.06	1.07	1.05
YDL105W	QRI2	1.00	-1.06	-1.04	1.05
YDR523C	SPS1	1.00	-1.06	-1.09	1.05
YHL025W	SNF6	1.00	-1.06	1.25	1.05
YPL162C		1.00	-1.06	1.01	1.05
YJL218W		1.00	-1.07	1.05	1.05
YGR012W		1.00	-1.08	-1.05	1.05
YBR247C	ENP1	1.00	-1.09	-1.08	1.05
YCL008C	STP22	1.00	-1.09	1.03	1.05
YPR013C		1.00	-1.12	1.00	1.05
YFL041W	FET5	1.00	-1.13	-1.06	1.05
YOR090C	PTC5	1.00	-1.13	1.14	1.05
YOR186W		1.00	-1.13	-1.17	1.05
YDR318W	MCM21	1.00	-1.14	1.05	1.05
YGR287C		1.00	-1.14	-1.20	1.05
YGR277C		1.00	-1.18	1.06	1.05
YJL015C		1.00	-1.18	-1.12	1.05
YKL074C	MUD2	1.00	-1.19	-1.08	1.05

YDR416W	SYF1	1.00	-1.20	-1.21	1.05
YHR045W		1.00	-1.20	-1.05	1.05
YBL092W	RPL32	1.00	-1.21	-1.52	1.05
YJL061W	NUP82	1.00	-1.21	-1.23	1.05
YIL030C	SSM4	1.00	-1.23	1.01	1.05
YKL215C		1.00	-1.23	-1.11	1.05
YOL129W		1.00	-1.24	1.14	1.05
YIL085C	KTR7	1.00	-1.30	-1.03	1.05
YDL195W	SEC31	1.00	-1.39	-1.13	1.05
YLR205C	HMX1	1.00	-1.40	1.08	1.05
YLR223C	IFH1	1.00	-1.54	-1.24	1.05
YBL038W	MRPL16	1.00	-1.57	-1.69	1.05
YDR422C	SIP1	1.00	-1.58	-1.11	1.05
YOL119C		1.00	-1.81	-1.21	1.05
YBR053C		1.00	1.25	1.09	1.04
YBR199W	KTR4	1.00	1.17	1.10	1.04
YGL064C		1.00	1.16	-1.02	1.04
YPL064C		1.00	1.16	1.06	1.04
YDL146W		1.00	1.15	1.09	1.04
YHR044C	DOG1	1.00	1.15	1.36	1.04
YBR077C		1.00	1.14	1.17	1.04
YDL106C	PHO2	1.00	1.14	1.18	1.04
YBR017C	KAP104	1.00	1.13	1.12	1.04
YDR393W	SHE9	1.00	1.12	1.09	1.04
YHR066W	SSF1	1.00	1.12	1.02	1.04
YDR004W	RAD57	1.00	1.11	1.15	1.04
YGL149W		1.00	1.07	1.02	1.04
YDR027C	LUV1	1.00	1.06	-1.02	1.04
YFR008W		1.00	1.05	1.36	1.04
YLR251W		1.00	1.05	1.16	1.04
YFR032C		1.00	1.03	-1.10	1.04
YIL002C	INP51	1.00	1.02	-1.02	1.04
YGL243W	TAD1	1.00	1.01	-1.03	1.04
YNL332W	THI12	1.00	1.00	1.05	1.04
YCL029C	BIK1	1.00	-1.01	-1.08	1.04
YDR512C		1.00	-1.01	1.09	1.04
YBR096W		1.00	-1.03	1.05	1.04
YHR154W	ESC4	1.00	-1.03	1.39	1.04
YJL135W		1.00	-1.03	-1.05	1.04
YOR250C	CLP1	1.00	-1.03	1.05	1.04
YBL026W	LSM2	1.00	-1.04	-1.27	1.04
YGL142C	GPI10	1.00	-1.04	-1.22	1.04
YPL241C	CIN2	1.00	-1.04	1.23	1.04
YDL020C	RPN4	1.00	-1.06	1.10	1.04
YLL031C	GPI13	1.00	-1.07	-1.04	1.04
YPL013C		1.00	-1.09	-1.03	1.04
YIL021W	RPB3	1.00	-1.10	1.04	1.04
YEL006W		1.00	-1.12	1.04	1.04
YNL203C		1.00	-1.12	-1.39	1.04
YPL048W	CAM1	1.00	-1.12	1.10	1.04
YNR067C		1.00	-1.13	-1.18	1.04
YDL210W	UGA4	1.00	-1.15	-1.20	1.04
YIL095W	PRK1	1.00	-1.15	-1.02	1.04
YKL216W	URA1	1.00	-1.15	1.13	1.04
YJL016W		1.00	-1.16	-1.15	1.04
YPR120C	CLB5	1.00	-1.18	-1.01	1.04
YGR115C		1.00	-1.21	1.03	1.04
YDL144C		1.00	-1.22	-1.20	1.04
YDR210W		1.00	-1.22	-1.10	1.04
YGR147C	NAT2	1.00	-1.24	-1.24	1.04
YDR475C		1.00	-1.25	-1.16	1.04

YGL203C	KEX1	1.00	-1.25	-1.21	1.04
YGR272C		1.00	-1.26	-1.13	1.04
YMR251W		1.00	-1.27	-1.06	1.04
YGL172W	NUP49	1.00	-1.28	-1.09	1.04
YGL210W	YPT32	1.00	-1.29	-1.20	1.04
YOR195W	SLK19	1.00	-1.30	-1.11	1.04
YHR105W		1.00	-1.36	-1.12	1.04
YLR232W		1.00	-1.41	-1.04	1.04
YOR205C		1.00	-1.42	-1.12	1.04
YAL004W		1.00	-1.52	-1.76	1.04
YFL006W		1.00	-1.59	-1.10	1.04
YDR091C	RLI1	1.00	-1.75	-1.13	1.04
YJR049C	UTR1	1.00	-1.76	-1.38	1.04
YDL169C	UGX2	1.00	1.45	1.24	1.03
YGR178C	PBP1	1.00	1.34	1.36	1.03
YJL161W		1.00	1.24	1.19	1.03
YMR279C		1.00	1.24	1.08	1.03
YBR052C		1.00	1.18	1.13	1.03
YGR278W		1.00	1.18	1.13	1.03
YHL002W		1.00	1.18	1.11	1.03
YFR057W		1.00	1.17	1.09	1.03
YDR003W		1.00	1.16	1.16	1.03
YGR141W		1.00	1.16	1.06	1.03
YNL018C		1.00	1.12	1.01	1.03
YMR024W	MRPL3	1.00	1.09	1.06	1.03
YPL139C	UME1	1.00	1.06	-1.08	1.03
YBR257W	POP4	1.00	1.05	1.19	1.03
YBR288C	APM3	1.00	1.05	-1.02	1.03
YER185W		1.00	1.05	-1.01	1.03
YOR279C		1.00	1.05	1.14	1.03
YGL136C		1.00	1.04	1.13	1.03
YDR325W	YCG1	1.00	1.03	1.00	1.03
YGR205W		1.00	1.03	1.14	1.03
YMR004W	MVP1	1.00	1.03	1.02	1.03
YIL114C	POR2	1.00	1.02	-1.07	1.03
YOR308C	SNU66	1.00	1.02	1.00	1.03
YLR077W		1.00	1.00	-1.12	1.03
YGR040W	KSS1	1.00	-1.01	-1.03	1.03
YBL082C	RHK1	1.00	-1.02	-1.08	1.03
YGR127W		1.00	-1.02	-1.06	1.03
YHR131C		1.00	-1.02	-1.24	1.03
YNR040W		1.00	-1.02	1.04	1.03
YPL177C	CUP9	1.00	-1.02	1.09	1.03
YDL017W	CDC7	1.00	-1.04	1.06	1.03
YKR021W		1.00	-1.04	-1.11	1.03
YMR009W		1.00	-1.06	1.24	1.03
YNR064C		1.00	-1.06	1.14	1.03
YLL014W		1.00	-1.07	1.06	1.03
YDR034C	LYS14	1.00	-1.08	-1.02	1.03
YPR179C	PLO1	1.00	-1.08	1.09	1.03
YIL027C	KRE27	1.00	-1.10	1.10	1.03
YOL155C		1.00	-1.11	1.45	1.03
YPR089W		1.00	-1.13	1.06	1.03
YNL283C	WSC2	1.00	-1.14	-1.05	1.03
YPR186C	PZF1	1.00	-1.16	-1.04	1.03
YBR154C	RPB5	1.00	-1.18	-1.32	1.03
YKL032C	IXR1	1.00	-1.18	1.29	1.03
YDR137W	RGP1	1.00	-1.19	1.19	1.03
YNR007C	AUT1	1.00	-1.19	1.22	1.03
YDL237W		1.00	-1.20	1.09	1.03
YHL028W	WSC4	1.00	-1.20	1.02	1.03

YBR271W		1.00	-1.21	-1.24	1.03
YNL249C	MPA43	1.00	-1.21	1.08	1.03
YLR183C	TOS4	1.00	-1.23	-1.11	1.03
YAL019W	FUN30	1.00	-1.25	-1.04	1.03
YOL066C	RIB2	1.00	-1.25	-1.18	1.03
YBR172C	SMY2	1.00	-1.26	-1.14	1.03
YDR469W	SDC1	1.00	-1.26	-1.16	1.03
YNL237W	YTP1	1.00	-1.27	-1.10	1.03
YDR351W	SBE2	1.00	-1.28	-1.03	1.03
YCL048W		1.00	-1.30	-1.06	1.03
YDR130C	FIN1	1.00	-1.31	1.03	1.03
YJL143W	TIM17	1.00	-1.31	-1.33	1.03
YNR023W	SNF12	1.00	-1.38	-1.05	1.03
YLR088W	GAA1	1.00	-1.44	-1.08	1.03
YLR401C		1.00	-1.51	1.02	1.03
YDR334W	SWR1	1.00	-1.52	-1.35	1.03
YBR267W		1.00	-1.54	-1.32	1.03
YFL023W	FYV11	1.00	-1.58	-1.22	1.03
YLR130C	ZRT2	1.00	-1.59	-1.26	1.03
YHL043W	ECM34	1.00	-1.60	-1.23	1.03
YPL265W	DIP5	1.00	-1.66	-1.32	1.03
YGR252W	GCN5	1.00	-1.82	-1.11	1.03
YEL045C		1.00	-1.97	-1.71	1.03
YJR136C		1.00	-2.19	1.04	1.03
YIL162W	SUC2	1.00	3.37	4.15	1.02
YCL052C	PBN1	1.00	1.42	1.68	1.02
YHR178W	STB5	1.00	1.24	-1.02	1.02
YOL032W		1.00	1.21	1.54	1.02
YBR136W	MEC1	1.00	1.16	1.14	1.02
YNL006W	LST8	1.00	1.15	1.06	1.02
YOL096C	COQ3	1.00	1.15	1.06	1.02
YOR122C	PFY1	1.00	1.12	1.21	1.02
YBL052C	SAS3	1.00	1.11	1.04	1.02
YBR224W		1.00	1.11	1.25	1.02
YHR207C		1.00	1.11	1.16	1.02
YCL069W		1.00	1.10	1.00	1.02
YBR302C	COS2	1.00	1.09	-1.03	1.02
YDL164C	CDC9	1.00	1.09	1.11	1.02
YDR350C	TCM10	1.00	1.09	1.02	1.02
YMR301C	ATM1	1.00	1.08	1.31	1.02
YNL136W		1.00	1.08	1.05	1.02
YDR252W	BTT1	1.00	1.04	-1.07	1.02
YJL082W	IML2	1.00	1.04	1.00	1.02
YNL093W	YPT53	1.00	1.04	1.30	1.02
YPL242C	IQG1	1.00	1.04	1.08	1.02
YPR129W	SCD6	1.00	1.04	1.08	1.02
YBR192W	RIM2	1.00	1.03	-1.11	1.02
YHR132C	ECM14	1.00	1.03	1.06	1.02
YJL090C	DPB11	1.00	1.03	-1.17	1.02
YGL095C	VPS45	1.00	1.02	1.21	1.02
YJL003W		1.00	1.02	1.05	1.02
YJL031C	BET4	1.00	1.02	1.05	1.02
YNL325C	FIG4	1.00	1.02	1.21	1.02
YKL177W		1.00	1.01	-1.09	1.02
YFL012W		1.00	1.00	-1.05	1.02
YJL100W	LSB6	1.00	1.00	1.09	1.02
YCR104W	PAU3	1.00	-1.01	-1.01	1.02
YNR005C		1.00	-1.01	1.14	1.02
YDR419W	RAD30	1.00	-1.02	-1.21	1.02
YGL124C	MON1	1.00	-1.03	1.16	1.02
YIR021W	MRS1	1.00	-1.03	1.04	1.02

YNL079C	TPM1	1.00	-1.03	1.18	1.02
YDR289C	RTT103	1.00	-1.04	1.02	1.02
YGR280C		1.00	-1.04	1.13	1.02
YNR032W	PPG1	1.00	-1.04	-1.05	1.02
YDL063C		1.00	-1.05	-1.06	1.02
YPL270W	MDL2	1.00	-1.05	1.04	1.02
YEL020C		1.00	-1.06	-1.10	1.02
YCL067C	HMLALPHA2	1.00	-1.07	1.14	1.02
YDR052C	DBF4	1.00	-1.07	1.05	1.02
YDR392W	SPT3	1.00	-1.07	-1.06	1.02
YDR499W	LCD1	1.00	-1.07	-1.09	1.02
YGR101W		1.00	-1.08	-1.04	1.02
YGR223C		1.00	-1.09	1.52	1.02
YLR032W	RAD5	1.00	-1.10	1.04	1.02
YBR159W		1.00	-1.12	-1.06	1.02
YDR332W		1.00	-1.12	1.06	1.02
YML113W	DAT1	1.00	-1.13	-1.06	1.02
YNL042W	BOP3	1.00	-1.13	-1.05	1.02
YDR083W	RRP8	1.00	-1.15	1.05	1.02
YDR528W	HLR1	1.00	-1.15	-1.05	1.02
YHL044W		1.00	-1.16	-1.12	1.02
YDR544C		1.00	-1.17	-1.10	1.02
YAR062W		1.00	-1.19	-1.03	1.02
YCL010C		1.00	-1.19	-1.02	1.02
YDL165W	CDC36	1.00	-1.19	-1.06	1.02
YIL149C	MLP2	1.00	-1.19	-1.02	1.02
YAL065C		1.00	-1.20	1.09	1.02
YCR022C		1.00	-1.20	1.02	1.02
YIR031C	DAL7	1.00	-1.21	-1.02	1.02
YBR145W	ADH5	1.00	-1.24	-1.11	1.02
YDR363W	ESC2	1.00	-1.24	-1.02	1.02
YGL168W		1.00	-1.24	-1.05	1.02
YKL155C	RSM22	1.00	-1.24	-1.05	1.02
YDR256C	CTA1	1.00	-1.25	-1.09	1.02
YPL221W	BOP1	1.00	-1.26	-1.23	1.02
YDR135C	YCF1	1.00	-1.28	-1.08	1.02
YJR002W	MPP10	1.00	-1.30	1.13	1.02
YNL105W		1.00	-1.32	-1.11	1.02
YMR136W	GAT2	1.00	-1.33	-1.01	1.02
YLR371W	ROM2	1.00	-1.34	-1.20	1.02
YDL196W		1.00	-1.37	-1.24	1.02
YMR312W	TOT6	1.00	-1.37	-1.04	1.02
YLR338W	KRE21	1.00	-1.49	-1.33	1.02
YOR011W	AUS1	1.00	-1.49	-1.13	1.02
YMR105C	PGM2	1.00	3.13	3.33	1.01
YDR476C		1.00	1.57	2.18	1.01
YNR060W	FRE4	1.00	1.34	1.02	1.01
YNL147W	LSM7	1.00	1.32	1.20	1.01
YMR022W	QRI8	1.00	1.16	1.22	1.01
YER050C	RSM18	1.00	1.13	1.15	1.01
YNL277W	MET2	1.00	1.10	-1.06	1.01
YOR253W		1.00	1.10	-1.02	1.01
YFR004W	RPN11	1.00	1.07	1.31	1.01
YOR379C		1.00	1.07	1.00	1.01
YDR438W		1.00	1.06	1.00	1.01
YHL038C	CBP2	1.00	1.06	1.01	1.01
YAR018C	KIN3	1.00	1.05	1.02	1.01
YKL037W		1.00	1.04	1.05	1.01
YML057W	CMP2	1.00	1.04	1.06	1.01
YNL044W	YIP3	1.00	1.04	-1.07	1.01
YDR129C	SAC6	1.00	1.03	1.52	1.01

YEL074W		1.00	1.03	1.10	1.01
YPR139C		1.00	1.03	1.03	1.01
YOL091W	SPO21	1.00	1.02	-1.20	1.01
YKL206C		1.00	1.00	1.15	1.01
YML098W	TAF19	1.00	1.00	1.09	1.01
YPL195W	APL5	1.00	1.00	1.11	1.01
YIL063C	YRB2	1.00	-1.01	-1.05	1.01
YNR075W	COS10	1.00	-1.01	-1.06	1.01
YBL098W		1.00	-1.02	1.00	1.01
YDR541C		1.00	-1.02	-1.03	1.01
YDR193W		1.00	-1.03	1.01	1.01
YNL289W	PCL1	1.00	-1.03	1.14	1.01
YBR034C	HMT1	1.00	-1.04	-1.28	1.01
YGR189C	CRH1	1.00	-1.04	-1.10	1.01
YOR246C		1.00	-1.04	-1.09	1.01
YNL019C		1.00	-1.05	1.07	1.01
YNL295W		1.00	-1.06	1.04	1.01
YJL220W		1.00	-1.07	-1.01	1.01
YNL229C	URE2	1.00	-1.07	-1.06	1.01
YDR024W	FYV1	1.00	-1.09	-1.02	1.01
YER115C	SPR6	1.00	-1.10	-1.02	1.01
YGL127C	SOH1	1.00	-1.10	-1.17	1.01
YNL278W	CAF120	1.00	-1.10	-1.10	1.01
YOL026C		1.00	-1.10	1.02	1.01
YPL272C		1.00	-1.10	-1.02	1.01
YJL084C		1.00	-1.11	-1.16	1.01
YJL117W	PHO86	1.00	-1.11	-1.08	1.01
YIR008C	PRI1	1.00	-1.12	1.15	1.01
YOR345C		1.00	-1.12	-1.03	1.01
YBL016W	FUS3	1.00	-1.13	-1.10	1.01
YLR357W	RSC2	1.00	-1.14	-1.32	1.01
YNL204C	SPS18	1.00	-1.14	1.05	1.01
YJL125C	GCD14	1.00	-1.15	1.12	1.01
YBR183W	YPC1	1.00	-1.16	-1.12	1.01
YIL092W		1.00	-1.16	-1.09	1.01
YNL124W		1.00	-1.16	-1.15	1.01
YHR210C		1.00	-1.17	1.01	1.01
YJL099W	CHS6	1.00	-1.18	-1.06	1.01
YHR029C		1.00	-1.19	-1.05	1.01
YIR019C	MUC1	1.00	-1.19	1.11	1.01
YDR390C	UBA2	1.00	-1.20	1.06	1.01
YPL156C	PRM4	1.00	-1.20	1.06	1.01
YFL013C	IES1	1.00	-1.23	-1.03	1.01
YNL266W		1.00	-1.31	-1.06	1.01
YDR146C	SWI5	1.00	-1.37	-1.08	1.01
YOR151C	RPB2	1.00	-1.44	1.03	1.01
YDR167W	TAF25	1.00	-1.46	-1.12	1.01
YOR118W		1.00	-1.46	-1.14	1.01
YPL191C		1.00	-1.55	1.08	1.01
YCR020C	PET18	1.00	1.01	-1.02	1.01
YBL031W	SHE1	1.00	1.27	1.14	1.00
YDR455C		1.00	1.19	1.27	1.00
YJR011C		1.00	1.19	1.13	1.00
YPL277C		1.00	1.16	1.12	1.00
YMR088C		1.00	1.13	1.05	1.00
YNL239W	LAP3	1.00	1.13	1.10	1.00
YPR093C		1.00	1.13	1.08	1.00
YGL154C	LYS5	1.00	1.12	1.11	1.00
YNR069C		1.00	1.10	1.15	1.00
YDR431W		1.00	1.09	1.00	1.00
YBR236C	ABD1	1.00	1.08	1.02	1.00

YJR013W		1.00	1.08	-1.01	1.00
YOL156W	HXT11	1.00	1.08	1.17	1.00
YLR393W	ATP10	1.00	1.06	1.03	1.00
YBR070C		1.00	1.05	1.03	1.00
YPL194W	DDC1	1.00	1.04	1.06	1.00
YAL010C	MDM10	1.00	1.03	1.02	1.00
YBL086C		1.00	1.03	1.03	1.00
YBR046C	ZTA1	1.00	1.03	-1.09	1.00
YJL162C		1.00	1.01	1.00	1.00
YPL124W	NIP29	1.00	1.01	-1.09	1.00
YLR125W		1.00	-1.01	-1.01	1.00
YOR278W	HEM4	1.00	-1.02	1.13	1.00
YMR255W	GFD1	1.00	-1.03	1.00	1.00
YFR046C		1.00	-1.05	-1.14	1.00
YKR060W		1.00	-1.05	-1.17	1.00
YNL159C	ASI2	1.00	-1.05	1.10	1.00
YPR079W	MRL1	1.00	-1.05	-1.06	1.00
YDR396W		1.00	-1.06	-1.05	1.00
YGL151W	NUT1	1.00	-1.06	-1.12	1.00
YGR286C	BIO2	1.00	-1.07	-1.06	1.00
YOR128C	ADE2	1.00	-1.07	1.04	1.00
YBL109W		1.00	-1.08	-1.10	1.00
YDR015C		1.00	-1.08	-1.06	1.00
YDR352W		1.00	-1.09	1.31	1.00
YDR428C		1.00	-1.09	-1.06	1.00
YDR011W	SNQ2	1.00	-1.12	-1.28	1.00
YER155C	BEM2	1.00	-1.12	-1.14	1.00
YHR086W	NAM8	1.00	-1.12	-1.30	1.00
YOR236W	DFR1	1.00	-1.12	-1.17	1.00
YPL060W	LPE10	1.00	-1.12	1.05	1.00
YOR306C		1.00	-1.13	-1.28	1.00
YLL047W		1.00	-1.14	-1.11	1.00
YPL102C	KRE24	1.00	-1.14	1.01	1.00
YJL013C	MAD3	1.00	-1.15	1.26	1.00
YOL138C		1.00	-1.15	-1.03	1.00
YOR149C	SMP3	1.00	-1.16	-1.04	1.00
YLR159W		1.00	-1.17	-1.04	1.00
YOR091W		1.00	-1.17	1.00	1.00
YGR121C	MEP1	1.00	-1.18	-1.26	1.00
YLR096W	KIN2	1.00	-1.18	-1.22	1.00
YDR280W	RRP45	1.00	-1.19	1.10	1.00
YNL123W		1.00	-1.19	-1.02	1.00
YPR077C		1.00	-1.20	1.03	1.00
YOR226C	ISU2	1.00	-1.21	-1.28	1.00
YFR028C	CDC14	1.00	-1.24	-1.02	1.00
YER187W		1.00	-1.26	-1.18	1.00
YMR186W	HSC82	1.00	-1.26	1.14	1.00
YOR104W	PIN2	1.00	-1.26	-1.27	1.00
YAL029C	MYO4	1.00	-1.29	-1.17	1.00
YMR122C		1.00	-1.29	-1.13	1.00
YML008C	ERG6	1.00	-1.31	1.04	1.00
YGL246C	RAI1	1.00	-1.32	-1.13	1.00
YGL042C		1.00	-1.33	-1.01	1.00
YJL179W	PFD1	1.00	-1.33	-1.52	1.00
YDR410C	STE14	1.00	-1.36	1.01	1.00
YGR013W	SNU71	1.00	-1.40	-1.13	1.00
YHR155W		1.00	-1.40	-1.08	1.00
YBR187W		1.00	-1.42	-1.30	1.00
YLR313C	SPH1	1.00	-1.42	-1.22	1.00
YLR151C	PCD1	1.00	-1.87	-1.27	1.00
YJR016C	ILV3	1.00	-1.94	-1.33	1.00

YDR279W		1.00	1.40	1.39	-1.01
YHL048W	COS8	1.00	1.27	1.19	-1.01
YDR100W		1.00	1.24	1.06	-1.01
YDL202W	MRPL11	1.00	1.23	1.18	-1.01
YBL035C	POL12	1.00	1.22	1.04	-1.01
YJR115W		1.00	1.19	1.21	-1.01
YGR052W		1.00	1.18	1.12	-1.01
YNL215W	IES2	1.00	1.18	-1.05	-1.01
YJL140W	RPB4	1.00	1.17	1.05	-1.01
YMR134W		1.00	1.17	1.18	-1.01
YGR195W	SKI6	1.00	1.16	1.12	-1.01
YGL146C		1.00	1.15	1.03	-1.01
YCR026C		1.00	1.14	-1.02	-1.01
YKR003W	OSH6	1.00	1.14	1.28	-1.01
YOL044W	PEX15	1.00	1.14	-1.07	-1.01
YDR380W	ARO10	1.00	1.13	1.29	-1.01
YGL033W	HOP2	1.00	1.13	1.27	-1.01
YPL215W	CBP3	1.00	1.13	1.13	-1.01
YDR328C	SKP1	1.00	1.12	1.37	-1.01
YBR019C	GAL10	1.00	1.11	1.02	-1.01
YDR066C		1.00	1.11	1.03	-1.01
YDR110W	FOB1	1.00	1.10	1.12	-1.01
YGL034C		1.00	1.09	1.42	-1.01
YLR311C		1.00	1.07	1.01	-1.01
YCR086W	CSM1	1.00	1.05	-1.13	-1.01
YKL040C	NFU1	1.00	1.05	-1.02	-1.01
YBR039W	ATP3	1.00	1.04	-1.25	-1.01
YAL031C	FUN21	1.00	1.03	1.08	-1.01
YIL106W	MOB1	1.00	1.03	1.12	-1.01
YPL018W	CTF19	1.00	1.03	-1.07	-1.01
YDL133W		1.00	1.02	-1.15	-1.01
YPL068C		1.00	1.02	-1.11	-1.01
YGL232W		1.00	1.01	-1.08	-1.01
YPL233W		1.00	1.01	-1.11	-1.01
YJR106W	ECM27	1.00	1.00	1.12	-1.01
YPL042C	SSN3	1.00	1.00	-1.03	-1.01
YIL012W		1.00	-1.01	-1.04	-1.01
YML047C	PRM6	1.00	-1.01	-1.06	-1.01
YPR094W		1.00	-1.01	-1.02	-1.01
YLR254C		1.00	-1.03	-1.11	-1.01
YOR262W		1.00	-1.03	1.31	-1.01
YPL063W		1.00	-1.03	1.12	-1.01
YJL219W	HXT9	1.00	-1.04	1.05	-1.01
YKL223W		1.00	-1.04	-1.01	-1.01
YMR138W	CIN4	1.00	-1.04	1.01	-1.01
YOR273C	TPO4	1.00	-1.04	1.09	-1.01
YCR085W		1.00	-1.05	-1.08	-1.01
YJR091C	JSN1	1.00	-1.06	-1.05	-1.01
YBL057C		1.00	-1.07	-1.07	-1.01
YBR099C		1.00	-1.07	1.00	-1.01
YMR128W	ECM16	1.00	-1.07	-1.08	-1.01
YER039C	HVG1	1.00	-1.08	-1.02	-1.01
YMR239C	RNT1	1.00	-1.08	1.11	-1.01
YBR055C	PRP6	1.00	-1.09	-1.10	-1.01
YLR239C	LIP2	1.00	-1.09	-1.15	-1.01
YML083C		1.00	-1.10	1.00	-1.01
YBR100W		1.00	-1.11	-1.21	-1.01
YPL255W	BBP1	1.00	-1.11	-1.07	-1.01
YBR252W	DUT1	1.00	-1.12	-1.12	-1.01
YDR098C	GRX3	1.00	-1.12	-1.15	-1.01
YJL097W		1.00	-1.12	-1.07	-1.01

YNL297C	MON2	1.00	-1.13	-1.11	-1.01
YER140W		1.00	-1.15	-1.01	-1.01
YKL042W	SPC42	1.00	-1.15	-1.12	-1.01
YML130C	ERO1	1.00	-1.16	-1.15	-1.01
YLL063C	AYT1	1.00	-1.20	-1.01	-1.01
YOR193W		1.00	-1.22	-1.09	-1.01
YAL011W		1.00	-1.24	-1.14	-1.01
YAL016W	TPD3	1.00	-1.25	-1.28	-1.01
YHR205W	SCH9	1.00	-1.27	-1.03	-1.01
YKL218C	SRY1	1.00	-1.27	-1.17	-1.01
YPR009W		1.00	-1.28	-1.03	-1.01
YKL126W	YPK1	1.00	-1.29	-1.03	-1.01
YLR301W		1.00	-1.29	-1.43	-1.01
YDR227W	SIR4	1.00	-1.32	-1.06	-1.01
YKR050W	TRK2	1.00	-1.35	-1.10	-1.01
YPL072W	UBP16	1.00	-1.35	-1.12	-1.01
YHR069C	RRP4	1.00	-1.40	-1.08	-1.01
YLR148W	PEP3	1.00	-1.41	-1.15	-1.01
YLR131C	ACE2	1.00	-1.45	-1.26	-1.01
YPR060C	ARO7	1.00	-1.45	-1.09	-1.01
YAL059W	ECM1	1.00	-1.46	-1.34	-1.01
YLR240W	VPS34	1.00	-1.53	-1.18	-1.01
YBR013C		1.00	-1.59	-1.27	-1.01
YFR021W	AUT10	1.00	-1.60	-1.39	-1.01
YGR103W	RRP13	1.00	-1.74	-1.22	-1.01
YJL206C		1.00	-1.74	1.18	-1.01
YBR107C	IML3	1.00	-1.88	-1.53	-1.01
YBR214W	SDS24	1.00	1.36	1.09	-1.02
YHL034C	SBP1	1.00	1.27	1.28	-1.02
YPL022W	RAD1	1.00	1.20	-1.05	-1.02
YKL098W		1.00	1.19	-1.01	-1.02
YAR027W		1.00	1.17	1.31	-1.02
YLR394W	CST9	1.00	1.16	-1.04	-1.02
YCR025C		1.00	1.13	-1.03	-1.02
YPL164C	MLH3	1.00	1.11	1.06	-1.02
YML101C		1.00	1.10	1.02	-1.02
YKR022C		1.00	1.09	1.13	-1.02
YIL154C	IMP2'	1.00	1.04	1.16	-1.02
YMR111C		1.00	1.04	-1.15	-1.02
YGL053W	PRM8	1.00	1.03	1.33	-1.02
YHR013C	ARD1	1.00	1.03	-1.02	-1.02
YIL040W		1.00	1.03	-1.04	-1.02
YLR080W		1.00	1.03	-1.03	-1.02
YBR157C	ICS2	1.00	1.02	1.00	-1.02
YGL058W	RAD6	1.00	1.02	-1.19	-1.02
YOR265W	RBL2	1.00	1.02	1.06	-1.02
YGR051C		1.00	1.00	1.00	-1.02
YJL017W		1.00	1.00	-1.20	-1.02
YLR166C	SEC10	1.00	1.00	1.02	-1.02
YNL035C		1.00	1.00	-1.01	-1.02
YOL014W		1.00	1.00	1.04	-1.02
YBR174C		1.00	-1.01	-1.03	-1.02
YDL011C		1.00	-1.01	1.01	-1.02
YMR145C		1.00	-1.02	1.23	-1.02
YOL029C		1.00	-1.02	1.06	-1.02
YFL049W		1.00	-1.03	1.05	-1.02
YOR221C	MCT1	1.00	-1.03	-1.03	-1.02
YDR456W	NHX1	1.00	-1.04	1.09	-1.02
YGR028W	MSP1	1.00	-1.05	-1.02	-1.02
YGR274C	TAF145	1.00	-1.05	-1.11	-1.02
YGL212W	VAM7	1.00	-1.06	-1.15	-1.02

YMR126C		1.00	-1.06	-1.02	-1.02
YOR318C		1.00	-1.06	1.00	-1.02
YPR111W	DBF20	1.00	-1.06	-1.11	-1.02
YHR017W	YSC83	1.00	-1.07	-1.05	-1.02
YLR230W		1.00	-1.07	1.03	-1.02
YLR226W	BUR2	1.00	-1.08	-1.25	-1.02
YPR105C	COD1	1.00	-1.08	-1.05	-1.02
YBR290W	BSD2	1.00	-1.10	-1.15	-1.02
YBR232C		1.00	-1.11	1.05	-1.02
YNL296W	KRE25	1.00	-1.11	1.03	-1.02
YDL171C	GLT1	1.00	-1.12	-1.05	-1.02
YCR102C		1.00	-1.13	-1.09	-1.02
YMR172W	HOT1	1.00	-1.13	-1.13	-1.02
YNL286W	CUS2	1.00	-1.13	-1.08	-1.02
YJL033W	HCA4	1.00	-1.14	1.10	-1.02
YNL176C		1.00	-1.14	-1.20	-1.02
YDR140W	FYV9	1.00	-1.16	-1.09	-1.02
YPR040W	SDF1	1.00	-1.17	1.08	-1.02
YDL248W	COS7	1.00	-1.18	-1.12	-1.02
YIL137C		1.00	-1.18	-1.02	-1.02
YLR030W		1.00	-1.18	-1.03	-1.02
YML093W		1.00	-1.19	-1.12	-1.02
YBL080C	PET112	1.00	-1.21	-1.22	-1.02
YDR492W		1.00	-1.21	-1.10	-1.02
YKL179C		1.00	-1.22	1.08	-1.02
YNL243W	SLA2	1.00	-1.22	-1.15	-1.02
YOR037W	CYC2	1.00	-1.22	-1.02	-1.02
YDR132C		1.00	-1.23	-1.02	-1.02
YER127W	LCP5	1.00	-1.23	-1.34	-1.02
YKL174C		1.00	-1.23	-1.07	-1.02
YDR075W	PPH3	1.00	-1.24	-1.10	-1.02
YDR144C	MKC7	1.00	-1.25	-1.40	-1.02
YMR109W	MYO5	1.00	-1.26	-1.23	-1.02
YOR292C		1.00	-1.26	-1.13	-1.02
YOL004W	SIN3	1.00	-1.27	-1.14	-1.02
YHR160C	PEX18	1.00	-1.28	-1.28	-1.02
YBL076C	ILS1	1.00	-1.29	-1.14	-1.02
YER092W	IES5	1.00	-1.30	-1.23	-1.02
YJL054W	TIM54	1.00	-1.35	-1.32	-1.02
YCL047C		1.00	-1.38	1.06	-1.02
YBR283C	SSH1	1.00	-1.39	-1.28	-1.02
YJL128C	PBS2	1.00	-1.39	-1.10	-1.02
YGL140C		1.00	-1.42	-1.16	-1.02
YER089C	PTC2	1.00	-1.44	-1.14	-1.02
YJR052W	RAD7	1.00	-1.45	1.10	-1.02
YLR402W		1.00	-1.45	-1.08	-1.02
YFR024C		1.00	-1.46	-1.14	-1.02
YPL041C		1.00	-1.57	-1.09	-1.02
YJR089W	BIR1	1.00	-1.60	-1.04	-1.02
YDR254W	CHL4	1.00	-1.62	-1.05	-1.02
YBL111C		1.00	-1.84	-1.15	-1.02
YHR139C	SPS100	1.00	-1.92	-1.30	-1.02
YMR031C		1.00	1.50	1.46	-1.03
YNL241C	ZWF1	1.00	1.50	1.64	-1.03
YDL134C	PPH21	1.00	1.28	1.24	-1.03
YGL208W	SIP2	1.00	1.27	1.13	-1.03
YAL034C	FUN19	1.00	1.26	1.25	-1.03
YHR016C	YSC84	1.00	1.26	1.07	-1.03
YBR111C	YSA1	1.00	1.17	1.44	-1.03
YPL141C		1.00	1.17	1.35	-1.03
YBL089W		1.00	1.16	1.20	-1.03

YKL043W	PHD1	1.00	1.16	-1.03	-1.03
YBR251W	MRPS5	1.00	1.14	1.12	-1.03
YLL038C	ENT4	1.00	1.12	1.05	-1.03
YLR093C	NYV1	1.00	1.12	1.06	-1.03
YGR152C	RSR1	1.00	1.09	1.05	-1.03
YOR036W	PEP12	1.00	1.09	1.26	-1.03
YBR182C	SMP1	1.00	1.07	-1.02	-1.03
YGL072C		1.00	1.06	1.02	-1.03
YDL219W		1.00	1.05	-1.01	-1.03
YGL192W	IME4	1.00	1.05	1.22	-1.03
YBL071C		1.00	1.04	-1.01	-1.03
YCR089W	FIG2	1.00	1.04	1.02	-1.03
YBL059W		1.00	1.03	1.03	-1.03
YNL210W	MER1	1.00	1.03	-1.06	-1.03
YFR054C		1.00	1.02	-1.33	-1.03
YGR171C	MSM1	1.00	1.02	-1.04	-1.03
YPL210C	SRP72	1.00	1.02	1.06	-1.03
YDR517W	GRH1	1.00	-1.01	1.31	-1.03
YLR361C		1.00	-1.02	1.33	-1.03
YNL032W	SIW14	1.00	-1.02	1.03	-1.03
YGL045W		1.00	-1.03	1.02	-1.03
YML069W	POB3	1.00	-1.03	1.14	-1.03
YMR094W	CTF13	1.00	-1.03	-1.16	-1.03
YDL247W		1.00	-1.04	1.05	-1.03
YBR138C	HDR1	1.00	-1.05	-1.10	-1.03
YIR017C	MET28	1.00	-1.07	-1.08	-1.03
YAR042W	SWH1	1.00	-1.08	-1.07	-1.03
YMR245W		1.00	-1.08	-1.01	-1.03
YHL036W	MUP3	1.00	-1.11	1.28	-1.03
YBR225W		1.00	-1.12	-1.35	-1.03
YJR116W		1.00	-1.13	-1.15	-1.03
YGR129W	SYF2	1.00	-1.14	-1.26	-1.03
YCL004W	PGS1	1.00	-1.15	-1.10	-1.03
YDR423C	CAD1	1.00	-1.15	1.13	-1.03
YHR190W	ERG9	1.00	-1.15	-1.02	-1.03
YIL090W		1.00	-1.15	-1.17	-1.03
YJR131W	MNS1	1.00	-1.15	-1.06	-1.03
YGR203W		1.00	-1.16	1.03	-1.03
YBR170C	NPL4	1.00	-1.17	-1.22	-1.03
YGR064W		1.00	-1.17	-1.13	-1.03
YMR236W	TAF17	1.00	-1.17	-1.04	-1.03
YKL017C	HCS1	1.00	-1.20	-1.12	-1.03
YOL002C		1.00	-1.21	-1.07	-1.03
YOL090W	MSH2	1.00	-1.22	-1.21	-1.03
YGR041W	BUD9	1.00	-1.23	-1.23	-1.03
YML021C	UNG1	1.00	-1.24	-1.21	-1.03
YLR111W		1.00	-1.25	1.00	-1.03
YBR278W	DPB3	1.00	-1.28	-1.24	-1.03
YPR154W	PIN3	1.00	-1.28	-1.04	-1.03
YPL197C		1.00	-1.29	1.19	-1.03
YGL020C		1.00	-1.33	-1.14	-1.03
YHR185C	PFS1	1.00	-1.34	-1.12	-1.03
YNL049C	SFB2	1.00	-1.34	-1.06	-1.03
YGL186C		1.00	-1.42	-1.18	-1.03
YDL225W	SHS1	1.00	-1.45	1.00	-1.03
YPL025C		1.00	-1.45	-1.14	-1.03
YOR301W	RAX1	1.00	-1.47	-1.21	-1.03
YNR019W	ARE2	1.00	-1.49	-1.23	-1.03
YGR217W	CCH1	1.00	-1.51	-1.32	-1.03
YPL183C		1.00	-1.53	-1.38	-1.03
YLR082C	SRL2	1.00	-1.54	-1.29	-1.03

YPR170C		1.00	-1.73	-1.18	-1.03
YGR001C		1.00	-1.94	-1.19	-1.03
YPL275W		1.00	1.34	-1.13	-1.04
YNL205C		1.00	1.33	-1.03	-1.04
YNL202W	SPS19	1.00	1.24	1.16	-1.04
YEL041W		1.00	1.21	-1.04	-1.04
YGR231C	PHB2	1.00	1.21	1.12	-1.04
YBR086C	IST2	1.00	1.19	1.03	-1.04
YDR082W	STN1	1.00	1.19	1.05	-1.04
YIL138C	TPM2	1.00	1.19	1.27	-1.04
YIL080W		1.00	1.16	1.14	-1.04
YBR289W	SNF5	1.00	1.14	1.16	-1.04
YGR046W		1.00	1.13	1.10	-1.04
YIR043C		1.00	1.07	1.20	-1.04
YGR050C		1.00	1.06	-1.19	-1.04
YCR042C	TSM1	1.00	1.04	1.06	-1.04
YPL087W	YDC1	1.00	1.04	1.09	-1.04
YBR080C	SEC18	1.00	1.03	1.04	-1.04
YDL206W		1.00	1.03	-1.07	-1.04
YDR259C	YAP6	1.00	1.03	1.12	-1.04
YOR148C	SPP2	1.00	1.03	1.09	-1.04
YLL054C		1.00	1.02	-1.27	-1.04
YIL050W	PCL7	1.00	1.01	1.16	-1.04
YJL209W	CBP1	1.00	-1.02	-1.07	-1.04
YLR028C	ADE16	1.00	-1.02	1.03	-1.04
YGR196C	FYV8	1.00	-1.03	-1.09	-1.04
YNR057C	BIO4	1.00	-1.03	1.03	-1.04
YCL046W		1.00	-1.04	-1.07	-1.04
YHL010C		1.00	-1.04	-1.05	-1.04
YOR368W	RAD17	1.00	-1.04	-1.08	-1.04
YEL017W		1.00	-1.05	1.09	-1.04
YNL328C	MDJ2	1.00	-1.05	-1.01	-1.04
YNR058W	BIO3	1.00	-1.06	-1.20	-1.04
YOR313C	SPS4	1.00	-1.06	-1.15	-1.04
YHL037C		1.00	-1.07	1.25	-1.04
YLR337C	VRP1	1.00	-1.09	-1.08	-1.04
YGR140W	CBF2	1.00	-1.10	-1.24	-1.04
YLL030C		1.00	-1.11	-1.15	-1.04
YOL124C		1.00	-1.11	-1.10	-1.04
YDR486C	VPS60	1.00	-1.12	-1.15	-1.04
YHR015W	MIP6	1.00	-1.12	1.00	-1.04
YJL187C	SWE1	1.00	-1.12	-1.07	-1.04
YNL254C		1.00	-1.12	-1.02	-1.04
YMR035W	IMP2	1.00	-1.13	-1.07	-1.04
YMR137C	PSO2	1.00	-1.13	-1.14	-1.04
YJL027C		1.00	-1.14	1.04	-1.04
YJL167W	ERG20	1.00	-1.14	1.00	-1.04
YBL075C	SSA3	1.00	-1.15	-1.09	-1.04
YNL016W	PUB1	1.00	-1.15	-1.14	-1.04
YDR303C	RSC3	1.00	-1.16	1.02	-1.04
YIL165C		1.00	-1.16	-1.03	-1.04
YJR140C	HIR3	1.00	-1.17	-1.08	-1.04
YLR187W		1.00	-1.17	-1.46	-1.04
YGR024C		1.00	-1.18	1.01	-1.04
YNL059C	ARP5	1.00	-1.18	1.14	-1.04
YPL096W	PNG1	1.00	-1.18	-1.07	-1.04
YJR088C		1.00	-1.19	-1.04	-1.04
YCR090C		1.00	-1.20	-1.16	-1.04
YHR050W	SMF2	1.00	-1.20	1.03	-1.04
YNL212W	VID27	1.00	-1.20	-1.01	-1.04
YDR270W	CCC2	1.00	-1.21	-1.08	-1.04

YDL175C		1.00	-1.25	-1.19	-1.04
YDR073W	SNF11	1.00	-1.26	-1.10	-1.04
YGR251W		1.00	-1.26	-1.40	-1.04
YOR280C		1.00	-1.26	-1.17	-1.04
YLL021W	SPA2	1.00	-1.27	-1.07	-1.04
YPL155C	KIP2	1.00	-1.35	1.06	-1.04
YGL144C		1.00	-1.36	-1.44	-1.04
YOR018W	ROD1	1.00	-1.36	-1.13	-1.04
YML014W		1.00	-1.38	-1.60	-1.04
YER098W	UBP9	1.00	-1.40	-1.31	-1.04
YPL175W	SPT14	1.00	-1.49	-1.35	-1.04
YLR199C		1.00	-1.50	-1.23	-1.04
YPL021W	ECM23	1.00	-1.50	-1.26	-1.04
YDR294C	DPL1	1.00	-1.54	-1.31	-1.04
YJR148W	BAT2	1.00	-1.70	-1.01	-1.04
YKL207W		1.00	-1.75	-1.01	-1.04
YMR263W	SAP30	1.00	2.21	1.41	-1.05
YAL060W	BDH1	1.00	1.70	1.54	-1.05
YFR045W		1.00	1.15	1.00	-1.05
YOR367W	SCP1	1.00	1.15	1.07	-1.05
YGR172C	YIP1	1.00	1.14	1.02	-1.05
YNL126W	SPC98	1.00	1.14	1.08	-1.05
YBL108W		1.00	1.12	-1.10	-1.05
YDR467C		1.00	1.10	1.07	-1.05
YDL045C	FAD1	1.00	1.07	-1.06	-1.05
YHR067W		1.00	1.07	1.00	-1.05
YBL096C		1.00	1.06	-1.10	-1.05
YNL235C		1.00	1.06	-1.03	-1.05
YKL146W		1.00	1.05	1.19	-1.05
YMR041C		1.00	1.05	-1.02	-1.05
YOL149W	DCP1	1.00	1.05	-1.02	-1.05
YJL046W		1.00	1.03	-1.05	-1.05
YML019W	OST6	1.00	1.03	1.10	-1.05
YNL314W	DAL82	1.00	1.03	1.07	-1.05
YGL261C		1.00	1.02	-1.15	-1.05
YGR096W		1.00	1.02	-1.02	-1.05
YAR020C	PAU7	1.00	1.00	-1.01	-1.05
YCL061C	MRC1	1.00	1.00	1.06	-1.05
YER174C	GRX4	1.00	1.00	1.41	-1.05
YGR071C		1.00	1.00	-1.21	-1.05
YLR164W		1.00	-1.01	-1.05	-1.05
YDR185C		1.00	-1.02	1.00	-1.05
YIR013C	GAT4	1.00	-1.02	-1.11	-1.05
YGL082W		1.00	-1.03	1.10	-1.05
YJR139C	HOM6	1.00	-1.03	1.02	-1.05
YNR020C		1.00	-1.03	-1.11	-1.05
YPR019W	CDC54	1.00	-1.03	-1.09	-1.05
YCR065W	HCM1	1.00	-1.05	-1.36	-1.05
YJL009W		1.00	-1.05	1.02	-1.05
YJL032W		1.00	-1.05	-1.03	-1.05
YMR012W	CLU1	1.00	-1.07	1.08	-1.05
YKL063C		1.00	-1.08	-1.13	-1.05
YBR213W	MET8	1.00	-1.09	1.02	-1.05
YHR011W	DIA4	1.00	-1.09	-1.09	-1.05
YGR221C	TOS2	1.00	-1.10	1.01	-1.05
YBR008C	FLR1	1.00	-1.11	-1.10	-1.05
YIL082W		1.00	-1.13	-1.11	-1.05
YLR115W	CFT2	1.00	-1.13	-1.19	-1.05
YBR057C	MUM2	1.00	-1.14	-1.15	-1.05
YGL128C		1.00	-1.14	-1.19	-1.05
YFR005C	SAD1	1.00	-1.15	-1.08	-1.05

YJL077C	ICS3	1.00	-1.15	-1.06	-1.05
YKL186C	MTR2	1.00	-1.15	-1.19	-1.05
YBR188C	NTC20	1.00	-1.16	-1.10	-1.05
YGL074C		1.00	-1.18	-1.04	-1.05
YHR134W	WSS1	1.00	-1.18	1.00	-1.05
YDR206W	EBS1	1.00	-1.19	-1.16	-1.05
YDR275W		1.00	-1.19	-1.15	-1.05
YKR078W		1.00	-1.19	1.01	-1.05
YIR009W	MSL1	1.00	-1.21	-1.09	-1.05
YLR216C	CPR6	1.00	-1.21	1.10	-1.05
YDL161W	ENT1	1.00	-1.22	1.05	-1.05
YPR091C		1.00	-1.23	1.08	-1.05
YBR246W		1.00	-1.24	-1.16	-1.05
YHR214W		1.00	-1.27	1.18	-1.05
YDR026C		1.00	-1.28	-1.25	-1.05
YER076C		1.00	-1.28	-1.17	-1.05
YIR040C		1.00	-1.33	-1.13	-1.05
YCL022C		1.00	-1.36	-1.15	-1.05
YEL032W	MCM3	1.00	-1.39	-1.32	-1.05
YDL177C		1.00	-1.44	-1.36	-1.05
YJR071W		1.00	-1.44	-1.08	-1.05
YFL004W	VTC2	1.00	-1.45	-1.08	-1.05
YNL262W	POL2	1.00	-1.45	1.08	-1.05
YOR004W		1.00	-1.71	-1.35	-1.05
YGL193C		1.00	-1.91	-1.31	-1.05
YCR006C		1.00	1.33	1.11	-1.06
YLR066W	SPC3	1.00	1.33	1.08	-1.06
YLR043C	TRX1	1.00	1.30	1.10	-1.06
YDL064W	UBC9	1.00	1.28	1.20	-1.06
YDL027C		1.00	1.26	1.09	-1.06
YKL065C	YET1	1.00	1.26	1.25	-1.06
YBR295W	PCA1	1.00	1.15	1.13	-1.06
YGR105W	VMA21	1.00	1.12	-1.12	-1.06
YBR035C	PDX3	1.00	1.10	-1.10	-1.06
YJL217W		1.00	1.08	1.18	-1.06
YOR357C	GRD19	1.00	1.08	-1.14	-1.06
YBR277C		1.00	1.05	1.03	-1.06
YGL115W	SNF4	1.00	1.05	-1.07	-1.06
YBL056W	PTC3	1.00	1.01	-1.03	-1.06
YBR194W		1.00	1.01	-1.13	-1.06
YGR122W		1.00	1.01	1.03	-1.06
YMR104C	YPK2	1.00	1.01	1.27	-1.06
YGR170W	PSD2	1.00	1.00	1.00	-1.06
YOR286W		1.00	1.00	-1.07	-1.06
YHR176W		1.00	-1.01	-1.22	-1.06
YJL006C	CTK2	1.00	-1.01	-1.15	-1.06
YJR084W		1.00	-1.01	-1.09	-1.06
YNL299W	TRF5	1.00	-1.01	-1.18	-1.06
YDL185W	TFP1	1.00	-1.02	1.08	-1.06
YNL288W	CAF40	1.00	-1.02	-1.13	-1.06
YOR129C		1.00	-1.02	-1.03	-1.06
YCL058C	FYV5	1.00	-1.03	-1.25	-1.06
YHR151C		1.00	-1.03	-1.15	-1.06
YOR244W	ESA1	1.00	-1.04	1.09	-1.06
YJR062C	NTA1	1.00	-1.06	-1.02	-1.06
YNR010W	CSE2	1.00	-1.06	-1.02	-1.06
YBR150C	TBS1	1.00	-1.07	-1.08	-1.06
YDL235C	YPD1	1.00	-1.07	-1.11	-1.06
YML032C	RAD52	1.00	-1.07	-1.15	-1.06
YDL157C		1.00	-1.08	-1.16	-1.06
YHR166C	CDC23	1.00	-1.08	1.13	-1.06

YJL038C		1.00	-1.08	-1.09	-1.06
YPL280W		1.00	-1.09	-1.12	-1.06
YGR233C	PHO81	1.00	-1.10	1.14	-1.06
YKL028W	TFA1	1.00	-1.10	-1.12	-1.06
YCL039W		1.00	-1.11	-1.26	-1.06
YDR094W		1.00	-1.11	1.10	-1.06
YGL221C	NIF3	1.00	-1.11	-1.04	-1.06
YDR249C		1.00	-1.12	-1.07	-1.06
YLR387C		1.00	-1.13	-1.05	-1.06
YDR251W	PAM1	1.00	-1.14	-1.12	-1.06
YGR154C		1.00	-1.14	-1.03	-1.06
YOR289W		1.00	-1.14	-1.14	-1.06
YPL032C	SVL3	1.00	-1.14	1.01	-1.06
YPL269W	KAR9	1.00	-1.14	-1.12	-1.06
YGL039W		1.00	-1.15	-1.22	-1.06
YGL126W	SCS3	1.00	-1.15	-1.16	-1.06
YBR193C	MED8	1.00	-1.16	-1.42	-1.06
YKR056W	RNC1	1.00	-1.16	-1.16	-1.06
YDR307W		1.00	-1.17	-1.02	-1.06
YOR005C	DNL4	1.00	-1.17	-1.02	-1.06
YLR420W	URA4	1.00	-1.18	-1.13	-1.06
YNL185C	MRPL19	1.00	-1.20	1.01	-1.06
YKL125W	RRN3	1.00	-1.21	-1.10	-1.06
YOR039W	CKB2	1.00	-1.22	-1.15	-1.06
YER188W		1.00	-1.23	-1.19	-1.06
YER008C	SEC3	1.00	-1.25	-1.14	-1.06
YDR061W		1.00	-1.26	-1.24	-1.06
YPL038W	MET31	1.00	-1.26	-1.01	-1.06
YBR044C	TCM62	1.00	-1.28	1.01	-1.06
YDR537C		1.00	-1.28	-1.24	-1.06
YEL021W	URA3	1.00	-1.30	-1.36	-1.06
YDL189W		1.00	-1.31	-1.05	-1.06
YDL245C	HXT15	1.00	-1.34	1.00	-1.06
YJL056C	ZAP1	1.00	-1.34	-1.42	-1.06
YPL085W	SEC16	1.00	-1.37	-1.18	-1.06
YJL204C		1.00	-1.39	-1.09	-1.06
YMR078C	CTF18	1.00	-1.40	-1.04	-1.06
YMR210W		1.00	-1.43	-1.06	-1.06
YER107C	GLE2	1.00	-1.50	-1.23	-1.06
YHR111W		1.00	-1.62	-1.31	-1.06
YLR135W	SLX4	1.00	-1.67	-1.39	-1.06
YLR035C	MLH2	1.00	-1.69	-1.27	-1.06
YBL004W		1.00	-1.71	-1.61	-1.06
YGL049C	TIF4632	1.00	1.68	1.85	-1.07
YER154W	OXA1	1.00	1.54	1.65	-1.07
YHR043C	DOG2	1.00	1.34	1.38	-1.07
YGL106W	MLC1	1.00	1.17	1.12	-1.07
YMR297W	PRC1	1.00	1.15	1.27	-1.07
YNR009W		1.00	1.13	-1.08	-1.07
YMR029C		1.00	1.12	1.19	-1.07
YFL053W	DAK2	1.00	1.11	1.03	-1.07
YDR074W	TPS2	1.00	1.09	-1.06	-1.07
YOL043C	NTG2	1.00	1.08	1.11	-1.07
YMR063W	RIM9	1.00	1.07	-1.16	-1.07
YDR379W	RGA2	1.00	1.05	-1.13	-1.07
YEL024W	RIP1	1.00	1.05	1.17	-1.07
YBL042C	FUI1	1.00	1.04	-1.16	-1.07
YDR514C		1.00	1.04	-1.14	-1.07
YLR414C		1.00	1.04	1.16	-1.07
YBR129C	OPY1	1.00	1.02	-1.06	-1.07
YGR153W	TOS10	1.00	1.02	-1.05	-1.07

YKL075C		1.00	1.02	1.05	-1.07
YML068W		1.00	1.02	1.10	-1.07
YGL046W		1.00	1.01	1.09	-1.07
YJR119C		1.00	1.01	-1.10	-1.07
YNR041C	COQ2	1.00	1.01	-1.14	-1.07
YJL106W	IME2	1.00	1.00	-1.17	-1.07
YGR207C		1.00	-1.03	1.12	-1.07
YPR015C		1.00	-1.03	-1.01	-1.07
YIR028W	DAL4	1.00	-1.04	-1.04	-1.07
YKL053W		1.00	-1.04	-1.13	-1.07
YPL257W		1.00	-1.04	1.05	-1.07
YHR028C	DAP2	1.00	-1.05	-1.05	-1.07
YMR150C	IMP1	1.00	-1.06	-1.13	-1.07
YPR038W		1.00	-1.07	1.00	-1.07
YFL034W		1.00	-1.08	1.16	-1.07
YGR026W		1.00	-1.08	1.07	-1.07
YHR052W		1.00	-1.08	-1.13	-1.07
YOR144C	EFD1	1.00	-1.08	-1.10	-1.07
YGL014W	PUF4	1.00	-1.09	-1.25	-1.07
YIL072W	HOP1	1.00	-1.10	-1.15	-1.07
YNL248C	RPA49	1.00	-1.10	-1.05	-1.07
YDR191W	HST4	1.00	-1.11	-1.08	-1.07
YNL309W	STB1	1.00	-1.11	-1.21	-1.07
YBR066C	NRG2	1.00	-1.12	-1.25	-1.07
YCR105W		1.00	-1.12	-1.10	-1.07
YDR181C	SAS4	1.00	-1.12	1.09	-1.07
YER097W		1.00	-1.12	1.04	-1.07
YGR033C		1.00	-1.13	-1.13	-1.07
YOL084W	PHM7	1.00	-1.13	1.05	-1.07
YOR100C	CRC1	1.00	-1.13	-1.07	-1.07
YFR056C		1.00	-1.14	-1.08	-1.07
YGR163W	GTR2	1.00	-1.14	-1.10	-1.07
YJL053W	PEP8	1.00	-1.15	-1.10	-1.07
YNR011C	PRP2	1.00	-1.16	-1.20	-1.07
YBR285W		1.00	-1.18	-1.21	-1.07
YHR156C		1.00	-1.18	1.03	-1.07
YLR126C		1.00	-1.20	-1.15	-1.07
YNL170W		1.00	-1.20	1.14	-1.07
YNL236W	SIN4	1.00	-1.20	-1.20	-1.07
YDR199W		1.00	-1.21	-1.14	-1.07
YNL247W		1.00	-1.22	-1.11	-1.07
YER172C	BRR2	1.00	-1.24	-1.18	-1.07
YOR334W	MRS2	1.00	-1.24	-1.26	-1.07
YPR133C	IWS1	1.00	-1.24	-1.12	-1.07
YJL086C		1.00	-1.25	-1.11	-1.07
YGL005C	COD5	1.00	-1.28	-1.12	-1.07
YGR133W	PEX4	1.00	-1.31	-1.27	-1.07
YLR071C	RGR1	1.00	-1.31	-1.16	-1.07
YDR159W	SAC3	1.00	-1.35	-1.35	-1.07
YEL063C	CAN1	1.00	-1.35	-1.17	-1.07
YGL086W	MAD1	1.00	-1.36	-1.17	-1.07
YOR114W		1.00	-1.36	-1.19	-1.07
YJR059W	PTK2	1.00	-1.39	-1.15	-1.07
YDR228C	PCF11	1.00	-1.41	-1.14	-1.07
YDR302W	GPI11	1.00	-1.45	-1.02	-1.07
YLR143W		1.00	-1.48	-1.38	-1.07
YGL217C		1.00	-1.50	-1.15	-1.07
YJR017C	ESS1	1.00	-1.50	-1.09	-1.07
YEL036C	ANP1	1.00	-1.51	-1.01	-1.07
YLR266C		1.00	-1.55	-1.26	-1.07
YOR143C	THI80	1.00	-1.77	-1.49	-1.07

YGR225W	AMA1	1.00	-2.35	-1.55	-1.07
YKL099C		1.00	1.38	1.08	-1.08
YPR028W	YIP2	1.00	1.29	1.39	-1.08
YDR532C	KRE28	1.00	1.23	1.07	-1.08
YBR122C	MRPL36	1.00	1.12	-1.06	-1.08
YKR068C	BET3	1.00	1.11	1.02	-1.08
YMR232W	FUS2	1.00	1.10	-1.01	-1.08
YDR007W	TRP1	1.00	1.09	1.03	-1.08
YBR014C		1.00	1.06	1.00	-1.08
YMR151W	YIM2	1.00	1.06	-1.19	-1.08
YDL090C	RAM1	1.00	-1.01	-1.04	-1.08
YDL092W	SRP14	1.00	-1.01	-1.03	-1.08
YDR278C		1.00	-1.01	1.01	-1.08
YER147C	SCC4	1.00	-1.01	-1.05	-1.08
YDR287W		1.00	-1.02	-1.06	-1.08
YER116C	SLX8	1.00	-1.02	-1.03	-1.08
YMR224C	MRE11	1.00	-1.02	-1.15	-1.08
YNL312W	RFA2	1.00	-1.02	-1.07	-1.08
YPR054W	SMK1	1.00	-1.02	-1.09	-1.08
YCR007C		1.00	-1.03	-1.05	-1.08
YDR460W	TFB3	1.00	-1.04	-1.02	-1.08
YDR542W		1.00	-1.04	1.09	-1.08
YIL096C		1.00	-1.04	-1.28	-1.08
YNL231C	PDR16	1.00	-1.04	-1.05	-1.08
YPR116W		1.00	-1.04	1.04	-1.08
YMR234W	RNH1	1.00	-1.05	1.06	-1.08
YPL073C		1.00	-1.05	-1.14	-1.08
YBR058C	UBP14	1.00	-1.07	-1.06	-1.08
YMR095C	SNO1	1.00	-1.07	1.13	-1.08
YKR017C		1.00	-1.08	-1.19	-1.08
YOL054W		1.00	-1.09	1.00	-1.08
YBR173C	UMP1	1.00	-1.10	1.07	-1.08
YER007W	PAC2	1.00	-1.11	-1.03	-1.08
YOR025W	HST3	1.00	-1.11	-1.06	-1.08
YGR093W		1.00	-1.12	-1.06	-1.08
YIL105C		1.00	-1.12	-1.06	-1.08
YNL334C	SNO2	1.00	-1.12	1.08	-1.08
YDL026W		1.00	-1.13	-1.21	-1.08
YDL180W		1.00	-1.13	1.02	-1.08
YGR009C	SEC9	1.00	-1.15	1.00	-1.08
YNL293W	MSB3	1.00	-1.16	-1.10	-1.08
YPL144W		1.00	-1.16	1.02	-1.08
YHL013C		1.00	-1.17	1.17	-1.08
YIL147C	SLN1	1.00	-1.17	-1.20	-1.08
YLR031W		1.00	-1.17	-1.05	-1.08
YOR386W	PHR1	1.00	-1.17	-1.02	-1.08
YGR200C	ELP2	1.00	-1.18	-1.14	-1.08
YHR120W	MSH1	1.00	-1.18	-1.17	-1.08
YOR003W	YSP3	1.00	-1.18	-1.19	-1.08
YKL187C		1.00	-1.19	-1.11	-1.08
YLR124W		1.00	-1.21	-1.09	-1.08
YDR141C	DOP1	1.00	-1.22	-1.19	-1.08
YGR134W	CAF130	1.00	-1.22	-1.38	-1.08
YLR421C	RPN13	1.00	-1.24	-1.01	-1.08
YJL087C	TRL1	1.00	-1.25	-1.17	-1.08
YHR088W	RPF1	1.00	-1.26	-1.16	-1.08
YGL214W		1.00	-1.27	-1.25	-1.08
YIL024C		1.00	-1.28	-1.05	-1.08
YIL171W	HXT12	1.00	-1.28	-1.24	-1.08
YER018C	SPC25	1.00	-1.29	-1.24	-1.08
YIL054W	FYV2	1.00	-1.31	-1.30	-1.08

YJL127C	SPT10	1.00	-1.31	-1.14	-1.08
YOR006C		1.00	-1.35	1.02	-1.08
YOR094W	ARF3	1.00	-1.40	-1.30	-1.08
YGR067C		1.00	-1.45	-1.19	-1.08
YMR017W	SPO20	1.00	-1.46	-1.07	-1.08
YDR531W		1.00	-1.48	-1.25	-1.08
YDR041W	RSM10	1.00	-1.49	-1.07	-1.08
YEL019C	MMS21	1.00	-1.50	-1.24	-1.08
YLR094C	GIS3	1.00	-1.52	-1.28	-1.08
YLR123C		1.00	-1.53	-1.07	-1.08
YLR278C		1.00	-1.62	-1.39	-1.08
YDR119W		1.00	-1.63	-1.17	-1.08
YNR048W		1.00	-1.78	-1.76	-1.08
YPL283C	YRF1-7	1.00	-1.81	-1.11	-1.08
YLR118C		1.00	-2.15	-1.31	-1.08
YPL230W	USV1	1.00	1.62	1.53	-1.09
YPR196W		1.00	1.26	1.16	-1.09
YEL039C	CYC7	1.00	1.24	1.39	-1.09
YJL005W	CYR1	1.00	1.14	-1.12	-1.09
YBL044W		1.00	1.12	-1.03	-1.09
YDR453C		1.00	1.12	1.30	-1.09
YGL010W		1.00	1.11	-1.19	-1.09
YBR259W		1.00	1.09	-1.06	-1.09
YGR038W	ORM1	1.00	1.08	1.08	-1.09
YIL159W	BNR1	1.00	1.08	-1.15	-1.09
YAL024C	LTE1	1.00	1.03	-1.03	-1.09
YLR227C	ADY4	1.00	1.03	-1.25	-1.09
YML062C	MFT1	1.00	1.02	-1.09	-1.09
YPL140C	MKK2	1.00	1.02	-1.03	-1.09
YHR177W		1.00	1.01	-1.15	-1.09
YJR068W	RFC2	1.00	1.01	1.07	-1.09
YPR146C		1.00	1.01	1.03	-1.09
YDR180W	SCC2	1.00	1.00	-1.03	-1.09
YIL073C	SPO22	1.00	1.00	-1.13	-1.09
YBR016W		1.00	-1.01	-1.04	-1.09
YNL224C		1.00	-1.02	-1.18	-1.09
YPR117W		1.00	-1.02	-1.14	-1.09
YPR126C		1.00	-1.02	1.01	-1.09
YDL114W		1.00	-1.04	-1.02	-1.09
YJR128W		1.00	-1.04	-1.17	-1.09
YLR189C	UGT51	1.00	-1.05	-1.11	-1.09
YKR106W		1.00	-1.06	-1.02	-1.09
YLR042C		1.00	-1.06	-1.09	-1.09
YOR077W	RTS2	1.00	-1.06	-1.10	-1.09
YBL007C	SLA1	1.00	-1.07	-1.18	-1.09
YJL103C		1.00	-1.07	-1.03	-1.09
YMR103C		1.00	-1.07	1.00	-1.09
YOR170W		1.00	-1.07	1.01	-1.09
YOR174W	MED4	1.00	-1.07	-1.13	-1.09
YPL020C	ULP1	1.00	-1.07	-1.07	-1.09
YMR075W		1.00	-1.08	-1.02	-1.09
YPL103C		1.00	-1.08	-1.02	-1.09
YDR506C		1.00	-1.09	1.24	-1.09
YLR001C		1.00	-1.09	-1.16	-1.09
YER051W		1.00	-1.10	-1.23	-1.09
YGL060W		1.00	-1.10	-1.13	-1.09
YBR102C	EXO84	1.00	-1.12	-1.03	-1.09
YGR059W	SPR3	1.00	-1.12	-1.13	-1.09
YNR050C	LYS9	1.00	-1.12	-1.16	-1.09
YDR116C		1.00	-1.14	-1.19	-1.09
YDR189W	SLY1	1.00	-1.14	-1.06	-1.09

YMR030W		1.00	-1.14	1.07	-1.09
YOL133W	HRT1	1.00	-1.14	-1.15	-1.09
YOR033C	EXO1	1.00	-1.14	-1.04	-1.09
YJL089W	SIP4	1.00	-1.16	-1.14	-1.09
YKL189W	HYM1	1.00	-1.16	-1.22	-1.09
YLR349W		1.00	-1.16	-1.11	-1.09
YPL045W	VPS16	1.00	-1.16	-1.09	-1.09
YGL251C	HFM1	1.00	-1.17	-1.21	-1.09
YJR041C		1.00	-1.17	-1.20	-1.09
YKL088W		1.00	-1.17	-1.08	-1.09
YAL043C	PTA1	1.00	-1.18	-1.13	-1.09
YJL197W	UBP12	1.00	-1.18	-1.16	-1.09
YOL012C	HTZ1	1.00	-1.18	-1.21	-1.09
YBL008W	HIR1	1.00	-1.19	-1.14	-1.09
YDR080W	VPS41	1.00	-1.20	-1.14	-1.09
YNL092W		1.00	-1.20	-1.12	-1.09
YCR073C	SSK22	1.00	-1.21	-1.24	-1.09
YDR305C	HNT2	1.00	-1.21	-1.35	-1.09
YNL108C		1.00	-1.21	-1.37	-1.09
YKL031W		1.00	-1.22	-1.27	-1.09
YGL024W		1.00	-1.23	-1.13	-1.09
YPL174C	NIP100	1.00	-1.23	-1.13	-1.09
YEL028W		1.00	-1.27	-1.35	-1.09
YIL164C	NIT1	1.00	-1.29	-1.21	-1.09
YBR180W	DTR1	1.00	-1.30	-1.43	-1.09
YOR066W		1.00	-1.31	-1.25	-1.09
YIR032C	DAL3	1.00	-1.32	-1.27	-1.09
YDL116W	NUP84	1.00	-1.38	1.10	-1.09
YDR364C	CDC40	1.00	-1.44	-1.18	-1.09
YLR318W	EST2	1.00	-1.62	-1.28	-1.09
YNL161W	CBK1	1.00	-1.66	-1.27	-1.09
YOR013W		1.00	-1.71	-1.28	-1.09
YNL065W	AQR1	1.00	-2.06	-1.45	-1.09
YNL098C	RAS2	1.00	1.39	1.74	-1.10
YGL079W		1.00	1.36	-1.06	-1.10
YMR152W	YIM1	1.00	1.19	1.11	-1.10
YPL003W	ULA1	1.00	1.12	-1.04	-1.10
YLR392C		1.00	1.10	1.01	-1.10
YEL069C	HXT13	1.00	1.09	1.01	-1.10
YMR276W	DSK2	1.00	1.09	1.16	-1.10
YIL156W	UBP7	1.00	1.07	-1.23	-1.10
YIL093C	RSM25	1.00	1.06	-1.12	-1.10
YLR145W		1.00	1.06	-1.06	-1.10
YDR089W		1.00	1.05	-1.08	-1.10
YDR355C		1.00	1.05	-1.06	-1.10
YLR177W		1.00	1.05	1.40	-1.10
YIR010W		1.00	1.04	1.12	-1.10
YGL052W		1.00	1.03	-1.09	-1.10
YPL069C	BTS1	1.00	1.03	-1.14	-1.10
YAL030W	SNC1	1.00	1.01	1.02	-1.10
YNR008W	LRO1	1.00	1.01	-1.27	-1.10
YGL141W	HUL5	1.00	1.00	-1.12	-1.10
YGR131W		1.00	1.00	-1.09	-1.10
YBR088C	POL30	1.00	-1.02	-1.13	-1.10
YKL091C		1.00	-1.02	-1.09	-1.10
YDL129W		1.00	-1.03	-1.15	-1.10
YLR449W	FPR4	1.00	-1.03	1.11	-1.10
YKL005C		1.00	-1.04	-1.22	-1.10
YNL317W	PFS2	1.00	-1.04	-1.08	-1.10
YLL025W		1.00	-1.05	-1.10	-1.10
YOR076C	SKI7	1.00	-1.06	1.03	-1.10

YJL083W		1.00	-1.07	-1.25	-1.10
YDR030C	RAD28	1.00	-1.08	-1.13	-1.10
YHR024C	MAS2	1.00	-1.08	-1.16	-1.10
YBR095C		1.00	-1.09	1.01	-1.10
YBL065W		1.00	-1.10	-1.01	-1.10
YPL029W	SUV3	1.00	-1.10	-1.30	-1.10
YPR201W	ARR3	1.00	-1.11	-1.07	-1.10
YJR021C	REC107	1.00	-1.12	-1.17	-1.10
YPR194C	OPT2	1.00	-1.12	1.05	-1.10
YAR060C		1.00	-1.13	-1.03	-1.10
YKR008W	RSC4	1.00	-1.13	-1.16	-1.10
YAL001C	TFC3	1.00	-1.15	-1.20	-1.10
YDL159W	STE7	1.00	-1.15	1.06	-1.10
YCR049C		1.00	-1.16	-1.16	-1.10
YOR213C	SAS5	1.00	-1.17	-1.13	-1.10
YDL209C		1.00	-1.19	-1.18	-1.10
YPL181W		1.00	-1.19	-1.22	-1.10
YPR083W		1.00	-1.19	1.01	-1.10
YNR066C		1.00	-1.22	-1.27	-1.10
YOL081W	IRA2	1.00	-1.22	-1.36	-1.10
YBR272C	HSM3	1.00	-1.24	-1.22	-1.10
YGL182C		1.00	-1.25	-1.13	-1.10
YJL213W		1.00	-1.25	-1.07	-1.10
YPL082C	MOT1	1.00	-1.25	-1.05	-1.10
YKL165C	MCD4	1.00	-1.26	-1.30	-1.10
YAR023C		1.00	-1.27	-1.12	-1.10
YMR204C		1.00	-1.27	-1.01	-1.10
YHR181W		1.00	-1.28	-1.21	-1.10
YMR177W	MMT1	1.00	-1.30	-1.37	-1.10
YIL026C	IRR1	1.00	-1.31	-1.26	-1.10
YOR363C	PIP2	1.00	-1.31	-1.12	-1.10
YIL013C	PDR11	1.00	-1.32	1.04	-1.10
YDR198C		1.00	-1.45	-1.10	-1.10
YER024W	YAT2	1.00	-1.48	-1.55	-1.10
YDR413C		1.00	-1.52	-1.19	-1.10
YHR204W	HTM1	1.00	-1.53	-1.30	-1.10
YDR292C	SRP101	1.00	-1.91	-1.52	-1.10
YDL102W	CDC2	1.00	1.27	-1.12	-1.11
YDL033C		1.00	1.20	-1.22	-1.11
YPL024W	NCE4	1.00	1.20	1.12	-1.11
YCL038C		1.00	1.17	-1.11	-1.11
YDL218W		1.00	1.12	1.16	-1.11
YDR424C	DYN2	1.00	1.12	1.01	-1.11
YNL005C	MRP7	1.00	1.11	1.04	-1.11
YGR289C	MAL11	1.00	1.09	1.13	-1.11
YPL010W	RET3	1.00	1.09	1.08	-1.11
YEL012W	UBC8	1.00	1.08	-1.01	-1.11
YMR325W		1.00	1.06	-1.04	-1.11
YDR028C	REG1	1.00	1.04	-1.01	-1.11
YGL085W		1.00	1.04	1.06	-1.11
YIR005W	IST3	1.00	1.03	1.03	-1.11
YNL230C	ELA1	1.00	1.02	1.02	-1.11
YOR216C	RUD3	1.00	1.02	-1.05	-1.11
YGL263W	COS12	1.00	1.01	-1.12	-1.11
YNL116W		1.00	1.01	-1.13	-1.11
YBL010C		1.00	1.00	1.08	-1.11
YDR323C	PEP7	1.00	1.00	-1.04	-1.11
YHR012W	VPS29	1.00	1.00	-1.11	-1.11
YBR164C	ARL1	1.00	-1.01	-1.03	-1.11
YLR165C	PUS5	1.00	-1.01	-1.10	-1.11
YPL187W	MF(ALPHA)1	1.00	-1.01	-1.33	-1.11

YBL060W		1.00	-1.02	-1.14	-1.11
YNL252C	MRPL17	1.00	-1.02	1.09	-1.11
YMR054W	STV1	1.00	-1.03	-1.24	-1.11
YMR066W	SOV1	1.00	-1.03	-1.07	-1.11
YNL046W		1.00	-1.03	1.13	-1.11
YDL028C	MPS1	1.00	-1.04	-1.07	-1.11
YBR009C	HHF1	1.00	-1.05	1.02	-1.11
YMR026C	PEX12	1.00	-1.05	1.01	-1.11
YLR033W	RSC58	1.00	-1.06	1.02	-1.11
YMR278W		1.00	-1.06	-1.02	-1.11
YPR078C		1.00	-1.06	-1.24	-1.11
YOL015W		1.00	-1.08	-1.13	-1.11
YPL208W		1.00	-1.08	1.06	-1.11
YPR031W		1.00	-1.08	-1.07	-1.11
YBL051C	PIN4	1.00	-1.09	-1.13	-1.11
YGR007W	MUQ1	1.00	-1.09	-1.11	-1.11
YHR153C	SPO16	1.00	-1.10	1.15	-1.11
YKL168C	KKQ8	1.00	-1.10	-1.06	-1.11
YDR378C	LSM6	1.00	-1.13	-1.09	-1.11
YEL056W	HAT2	1.00	-1.13	-1.04	-1.11
YML070W	DAK1	1.00	-1.13	1.16	-1.11
YLL017W		1.00	-1.14	-1.16	-1.11
YBR244W	GPX2	1.00	-1.16	-1.05	-1.11
YDR048C		1.00	-1.16	-1.19	-1.11
YLR350W		1.00	-1.16	1.21	-1.11
YBR270C		1.00	-1.18	-1.14	-1.11
YNL081C		1.00	-1.18	-1.08	-1.11
YER014W	HEM14	1.00	-1.19	-1.11	-1.11
YGR169C		1.00	-1.19	-1.21	-1.11
YDR525W		1.00	-1.20	-1.06	-1.11
YML078W	CPR3	1.00	-1.21	1.07	-1.11
YMR299C		1.00	-1.22	-1.15	-1.11
YOR106W	VAM3	1.00	-1.23	-1.05	-1.11
YNL090W	RHO2	1.00	-1.24	-1.28	-1.11
YLR380W	CSR1	1.00	-1.26	-1.29	-1.11
YPL128C	TBF1	1.00	-1.27	-1.11	-1.11
YDL008W	APC11	1.00	-1.28	-1.20	-1.11
YJR006W	HYS2	1.00	-1.29	-1.03	-1.11
YAR064W		1.00	-1.30	-1.11	-1.11
YFL008W	SMC1	1.00	-1.30	-1.31	-1.11
YGR097W	ASK10	1.00	-1.31	-1.21	-1.11
YOL018C	TLG2	1.00	-1.33	-1.29	-1.11
YKL190W	CNB1	1.00	-1.35	-1.32	-1.11
YGR132C	PHB1	1.00	-1.37	-1.14	-1.11
YKL071W		1.00	-1.37	-1.08	-1.11
YGL121C		1.00	-1.43	-1.42	-1.11
YJR092W	BUD4	1.00	-1.45	-1.19	-1.11
YBL097W	BRN1	1.00	-1.46	-1.81	-1.11
YJR160C		1.00	-1.50	-1.15	-1.11
YAL008W	FUN14	1.00	-1.64	-1.42	-1.11
YHR099W	TRA1	1.00	-1.83	-1.54	-1.11
YOR012W		1.00	-1.97	-1.33	-1.11
YHR079C	IRE1	1.00	-1.26	-1.23	-1.11
YDR096W	GIS1	1.00	1.47	1.49	-1.12
YEL052W	AFG1	1.00	1.16	1.15	-1.12
YNR074C		1.00	1.14	1.03	-1.12
YGL041C		1.00	1.13	1.03	-1.12
YPR011C		1.00	1.13	-1.13	-1.12
YOL146W		1.00	1.11	-1.03	-1.12
YDL085W		1.00	1.09	-1.05	-1.12
YPL203W	TPK2	1.00	1.09	1.28	-1.12

YJL150W		1.00	1.06	-1.24	-1.12
YHL003C	LAG1	1.00	1.05	-1.13	-1.12
YLR085C	ARP6	1.00	1.04	1.03	-1.12
YNR071C		1.00	1.04	-1.05	-1.12
YAL066W		1.00	1.02	-1.12	-1.12
YOR073W		1.00	1.02	1.11	-1.12
YGR222W	PET54	1.00	1.00	-1.04	-1.12
YKL198C	PTK1	1.00	-1.02	-1.07	-1.12
YFL029C	CAK1	1.00	-1.03	-1.05	-1.12
YKL117W	SBA1	1.00	-1.03	1.16	-1.12
YDL068W		1.00	-1.04	-1.08	-1.12
YPL245W		1.00	-1.08	-1.21	-1.12
YJL018W		1.00	-1.09	-1.07	-1.12
YLR212C	TUB4	1.00	-1.11	-1.09	-1.12
YOL009C	MDM12	1.00	-1.11	1.00	-1.12
YBL019W	APN2	1.00	-1.13	-1.15	-1.12
YOR288C	MPD1	1.00	-1.13	-1.03	-1.12
YOR385W		1.00	-1.13	1.21	-1.12
YDR358W	GGA1	1.00	-1.14	-1.16	-1.12
YIL003W	DRE3	1.00	-1.14	-1.06	-1.12
YOR381W	FRE3	1.00	-1.14	-1.12	-1.12
YPR064W		1.00	-1.14	1.02	-1.12
YPL055C		1.00	-1.15	-1.06	-1.12
YOL157C		1.00	-1.16	1.03	-1.12
YGR145W		1.00	-1.17	-1.29	-1.12
YKR075C		1.00	-1.17	1.22	-1.12
YOR364W		1.00	-1.17	-1.05	-1.12
YFR027W	ECO1	1.00	-1.18	-1.21	-1.12
YER109C	FLO8	1.00	-1.19	-1.21	-1.12
YDR155C	CPH1	1.00	-1.20	-1.21	-1.12
YER032W	FIR1	1.00	-1.20	-1.04	-1.12
YDR485C		1.00	-1.21	-1.16	-1.12
YGR047C	TFC4	1.00	-1.23	-1.23	-1.12
YNL321W		1.00	-1.23	-1.27	-1.12
YDL142C	CRD1	1.00	-1.25	-1.09	-1.12
YOR067C	ALG8	1.00	-1.26	-1.11	-1.12
YBR190W		1.00	-1.28	-1.21	-1.12
YLR181C		1.00	-1.28	-1.20	-1.12
YNL022C		1.00	-1.28	-1.06	-1.12
YNL216W	RAP1	1.00	-1.29	-1.36	-1.12
YEL077C		1.00	-1.30	-1.03	-1.12
YHL029C		1.00	-1.30	-1.23	-1.12
YNR068C		1.00	-1.31	-1.36	-1.12
YLR053C		1.00	-1.33	-1.23	-1.12
YAL064W		1.00	-1.34	-1.25	-1.12
YLR397C	AFG2	1.00	-1.34	-1.40	-1.12
YJR154W		1.00	-1.36	-1.36	-1.12
YHR138C		1.00	-1.37	-1.27	-1.12
YHL031C	GOS1	1.00	-1.39	-1.12	-1.12
YMR106C	YKU80	1.00	-1.39	-1.16	-1.12
YKL011C	CCE1	1.00	-1.42	-1.09	-1.12
YFL003C	MSH4	1.00	-1.44	-1.36	-1.12
YLR308W	CDA2	1.00	-1.45	-1.12	-1.12
YLL001W	DNM1	1.00	-1.46	-1.30	-1.12
YCL045C		1.00	-1.50	-1.24	-1.12
YFL038C	YPT1	1.00	-1.50	-1.13	-1.12
YGR263C		1.00	-1.50	-1.30	-1.12
YAL020C	ATS1	1.00	-1.51	-1.41	-1.12
YDL141W	BPL1	1.00	-1.51	-1.15	-1.12
YHL007C	STE20	1.00	-1.51	-1.49	-1.12
YLR284C	ECI1	1.00	-1.51	-1.19	-1.12

YDR461W	MFA1	1.00	-1.69	-1.92	-1.12
YOR284W		1.00	-1.70	-1.35	-1.12
YLR446W		1.00	-1.77	1.27	-1.12
YBR126C	TPS1	1.00	1.64	1.42	-1.13
YFR015C	GSY1	1.00	1.46	2.26	-1.13
YKL109W	HAP4	1.00	1.21	1.29	-1.13
YBR284W		1.00	1.09	-1.04	-1.13
YFR044C		1.00	1.07	1.06	-1.13
YAR047C		1.00	1.05	-1.20	-1.13
YLR314C	CDC3	1.00	1.03	1.06	-1.13
YKR037C	SPC34	1.00	1.02	1.14	-1.13
YDR522C	SPS2	1.00	1.01	-1.06	-1.13
YDL029W	ARP2	1.00	-1.01	1.23	-1.13
YDL199C		1.00	-1.01	1.06	-1.13
YML102W	CAC2	1.00	-1.02	1.00	-1.13
YCR079W		1.00	-1.03	-1.07	-1.13
YJR012C		1.00	-1.03	-1.15	-1.13
YMR118C		1.00	-1.03	-1.06	-1.13
YOL034W		1.00	-1.03	-1.08	-1.13
YIL163C		1.00	-1.04	-1.13	-1.13
YLR309C	IMH1	1.00	-1.06	1.14	-1.13
YGR242W		1.00	-1.07	-1.03	-1.13
YOL065C	INP54	1.00	-1.07	-1.01	-1.13
YOL125W		1.00	-1.07	-1.22	-1.13
YMR203W	TOM40	1.00	-1.09	-1.02	-1.13
YER012W	PRE1	1.00	-1.13	-1.03	-1.13
YKL161C		1.00	-1.13	-1.10	-1.13
YNR033W	ABZ1	1.00	-1.13	-1.10	-1.13
YBR163W	DEM1	1.00	-1.14	-1.06	-1.13
YPL172C	COX10	1.00	-1.15	-1.10	-1.13
YBR124W		1.00	-1.17	-1.12	-1.13
YFL032W		1.00	-1.17	-1.18	-1.13
YKL019W	RAM2	1.00	-1.18	-1.04	-1.13
YPR092W		1.00	-1.18	-1.16	-1.13
YER149C	PEA2	1.00	-1.20	-1.03	-1.13
YOL132W		1.00	-1.21	-1.29	-1.13
YOL100W	PKH2	1.00	-1.22	-1.01	-1.13
YNL026W		1.00	-1.25	-1.10	-1.13
YMR089C	YTA12	1.00	-1.27	1.22	-1.13
YHR213W		1.00	-1.28	-1.19	-1.13
YPR153W		1.00	-1.30	-1.10	-1.13
YFL057C		1.00	-1.32	-1.15	-1.13
YNL068C	FKH2	1.00	-1.36	-1.25	-1.13
YDR020C		1.00	-1.38	-1.25	-1.13
YPL217C	BMS1	1.00	-1.40	-1.25	-1.13
YGR006W	PRP18	1.00	-1.44	-1.35	-1.13
YOR009W	TIR4	1.00	-1.45	-1.33	-1.13
YDR101C		1.00	-1.46	-1.53	-1.13
YDR128W		1.00	-1.48	-1.24	-1.13
YBL107C		1.00	-1.49	-1.43	-1.13
YJR123W	RPS5	1.00	-1.55	-1.39	-1.13
YLR087C	CSF1	1.00	-1.57	-1.31	-1.13
YKL169C		1.00	-1.59	-1.46	-1.13
YGR186W	TFG1	1.00	-1.67	-1.07	-1.13
YDR513W	TTR1	1.00	1.37	1.16	-1.14
YJL074C	SMC3	1.00	1.34	1.54	-1.14
YMR173W	DDR48	1.00	1.32	1.12	-1.14
YNL304W	YPT11	1.00	1.24	1.03	-1.14
YOL048C		1.00	1.21	1.27	-1.14
YGR082W	TOM20	1.00	1.15	1.07	-1.14
YIL068C	SEC6	1.00	1.15	-1.05	-1.14

YOR152C		1.00	1.15	-1.05	-1.14
YDR225W	HTA1	1.00	1.11	1.26	-1.14
YPL100W		1.00	1.09	1.07	-1.14
YDR231C	COX20	1.00	1.06	-1.10	-1.14
YLL029W		1.00	1.05	1.03	-1.14
YDR426C		1.00	1.04	-1.12	-1.14
YCL057W	PRD1	1.00	1.03	1.02	-1.14
YKR032W		1.00	1.01	-1.01	-1.14
YAL039C	CYC3	1.00	-1.01	1.10	-1.14
YOL003C		1.00	-1.01	-1.08	-1.14
YDR285W	ZIP1	1.00	-1.02	-1.18	-1.14
YER167W	BCK2	1.00	-1.02	1.01	-1.14
YNL272C	SEC2	1.00	-1.02	-1.10	-1.14
YPR134W	MSS18	1.00	-1.02	-1.06	-1.14
YJL113W		1.00	-1.04	1.10	-1.14
YNL265C	IST1	1.00	-1.05	-1.01	-1.14
YDL089W		1.00	-1.06	-1.35	-1.14
YOR087W		1.00	-1.06	1.11	-1.14
YJR053W	BFA1	1.00	-1.08	1.01	-1.14
YPR095C	SYT1	1.00	-1.09	-1.29	-1.14
YPR127W		1.00	-1.11	1.05	-1.14
YDR276C	PMP3	1.00	-1.13	-1.05	-1.14
YKR047W		1.00	-1.13	-1.17	-1.14
YER104W	RTT105	1.00	-1.15	-1.22	-1.14
YLR176C	RFX1	1.00	-1.15	-1.27	-1.14
YLR195C	NMT1	1.00	-1.16	1.04	-1.14
YPL051W	ARL3	1.00	-1.16	-1.14	-1.14
YPL224C	MMT2	1.00	-1.16	-1.02	-1.14
YKL195W		1.00	-1.17	-1.22	-1.14
YNL323W	LEM3	1.00	-1.17	1.16	-1.14
YDR372C		1.00	-1.18	-1.23	-1.14
YJR014W		1.00	-1.18	-1.09	-1.14
YPL168W		1.00	-1.18	-1.17	-1.14
YKR091W	SRL3	1.00	-1.20	-1.05	-1.14
YKL191W	DPH2	1.00	-1.21	-1.18	-1.14
YNL311C		1.00	-1.21	-1.24	-1.14
YKR019C	IRS4	1.00	-1.24	-1.13	-1.14
YJL079C	PRY1	1.00	-1.25	-1.12	-1.14
YIL056W		1.00	-1.26	-1.13	-1.14
YDR085C	AFR1	1.00	-1.28	-1.08	-1.14
YDR395W	SXM1	1.00	-1.28	1.04	-1.14
YGL194C	HOS2	1.00	-1.34	-1.26	-1.14
YDR068W	DOS2	1.00	-1.36	-1.06	-1.14
YPR055W	SEC8	1.00	-1.37	-1.23	-1.14
YIL059C		1.00	-1.38	-1.32	-1.14
YKL166C	TPK3	1.00	-1.40	-1.45	-1.14
YLL062C	MHT1	1.00	-1.40	-1.08	-1.14
YJR058C	APS2	1.00	-1.45	-1.09	-1.14
YHR001W	OSH7	1.00	-1.49	-1.48	-1.14
YGL215W	CLG1	1.00	-1.50	-1.44	-1.14
YDL043C	PRP11	1.00	-1.55	1.06	-1.14
YJR137C	ECM17	1.00	-1.56	-1.07	-1.14
YHR209W		1.00	-1.66	-1.37	-1.14
YPR190C	RPC82	1.00	-1.70	-1.23	-1.14
YDL151C	FYV3	1.00	1.25	1.04	-1.15
YNR073C		1.00	1.21	1.08	-1.15
YPL138C	SPP1	1.00	1.21	1.10	-1.15
YIL033C	BCY1	1.00	1.20	1.34	-1.15
YGL260W		1.00	1.16	1.03	-1.15
YER125W	RSP5	1.00	1.13	1.01	-1.15
YLL005C	SPO75	1.00	1.13	1.03	-1.15

YKL026C	GPX1	1.00	1.11	-1.04	-1.15
YPR130C		1.00	1.11	-1.01	-1.15
YBR071W		1.00	1.07	1.21	-1.15
YJL072C		1.00	1.06	-1.18	-1.15
YKL072W	STB6	1.00	1.03	-1.02	-1.15
YBL040C	ERD2	1.00	-1.01	-1.11	-1.15
YNL040W		1.00	-1.01	-1.04	-1.15
YNL198C		1.00	-1.01	-1.03	-1.15
YER094C	PUP3	1.00	-1.02	-1.08	-1.15
YPR188C	MLC2	1.00	-1.02	-1.13	-1.15
YBR092C	PHO3	1.00	-1.04	-1.23	-1.15
YGL004C		1.00	-1.04	-1.20	-1.15
YLR431C		1.00	-1.04	-1.13	-1.15
YOR264W		1.00	-1.04	1.25	-1.15
YPL253C	VIK1	1.00	-1.05	1.00	-1.15
YPL271W	ATP15	1.00	-1.05	1.20	-1.15
YOL116W	MSN1	1.00	-1.06	-1.12	-1.15
YNL053W	MSG5	1.00	-1.07	-1.12	-1.15
YBL094C		1.00	-1.08	-1.17	-1.15
YMR167W	MLH1	1.00	-1.12	-1.06	-1.15
YDR022C	CIS1	1.00	-1.13	-1.12	-1.15
YFL061W		1.00	-1.13	-1.06	-1.15
YGL235W		1.00	-1.13	-1.28	-1.15
YGR062C	COX18	1.00	-1.13	-1.22	-1.15
YLL007C		1.00	-1.13	-1.21	-1.15
YPL115C	BEM3	1.00	-1.13	-1.16	-1.15
YDR230W		1.00	-1.14	-1.19	-1.15
YJL154C	VPS35	1.00	-1.14	-1.05	-1.15
YDL010W		1.00	-1.15	-1.19	-1.15
YIR025W	MND2	1.00	-1.15	-1.07	-1.15
YJR055W	HIT1	1.00	-1.15	-1.15	-1.15
YBL006C		1.00	-1.17	-1.24	-1.15
YHL020C	OPI1	1.00	-1.19	-1.08	-1.15
YHR036W		1.00	-1.20	-1.19	-1.15
YGL056C	SDS23	1.00	-1.21	1.03	-1.15
YML072C		1.00	-1.22	-1.31	-1.15
YOL057W		1.00	-1.22	-1.09	-1.15
YDL154W	MSH5	1.00	-1.23	-1.29	-1.15
YOR238W		1.00	-1.24	-1.27	-1.15
YBL033C	RIB1	1.00	-1.26	-1.15	-1.15
YER186C		1.00	-1.26	1.23	-1.15
YFR035C		1.00	-1.28	-1.23	-1.15
YGR197C	SNG1	1.00	-1.29	-1.13	-1.15
YHR047C	AAP1'	1.00	-1.29	-1.17	-1.15
YHR140W		1.00	-1.30	-1.25	-1.15
YNL056W		1.00	-1.35	-1.14	-1.15
YLR188W	MDL1	1.00	-1.38	-1.22	-1.15
YER173W	RAD24	1.00	-1.41	-1.26	-1.15
YLR156W		1.00	-1.42	-1.18	-1.15
YFR022W		1.00	-1.45	-1.39	-1.15
YLR256W	HAP1	1.00	-1.45	-1.36	-1.15
YGR161C		1.00	-1.52	-1.28	-1.15
YPR125W		1.00	-1.53	-1.75	-1.15
YHR184W	SSP1	1.00	-1.55	-1.40	-1.15
YKL173W	SNU114	1.00	-1.71	-1.27	-1.15
YMR313C		1.00	-1.72	-1.32	-1.15
YBR222C	FAT2	1.00	-1.75	-1.83	-1.15
YDR045C	RPC11	1.00	-1.78	-1.30	-1.15
YDL215C	GDH2	1.00	-1.87	-1.56	-1.15
YKL082C		1.00	-1.89	-1.36	-1.15
YDR111C		1.00	-2.14	-1.56	-1.15

YHR070W	TRM5	1.00	-2.34	-1.24	-1.15
YOR302W		1.00	-2.58	-1.74	-1.15
YMR170C	ALD2	1.00	3.83	2.23	-1.16
YER058W	PET117	1.00	1.21	-1.09	-1.16
YGR010W		1.00	1.17	-1.12	-1.16
YLL006W	MMM1	1.00	1.11	-1.04	-1.16
YKL127W	PGM1	1.00	1.09	1.29	-1.16
YJL152W		1.00	1.07	-1.09	-1.16
YOR249C	APC5	1.00	1.04	1.06	-1.16
YMR064W	AEP1	1.00	1.02	1.01	-1.16
YER079W		1.00	1.00	1.21	-1.16
YBL102W	SFT2	1.00	-1.01	-1.16	-1.16
YGR084C	MRP13	1.00	-1.01	-1.32	-1.16
YHL004W	MRP4	1.00	-1.01	-1.16	-1.16
YNL292W	PUS4	1.00	-1.01	-1.12	-1.16
YNL033W		1.00	-1.03	-1.12	-1.16
YGR073C		1.00	-1.04	1.03	-1.16
YIL009W	FAA3	1.00	-1.04	-1.08	-1.16
YCR066W	RAD18	1.00	-1.07	-1.14	-1.16
YLR103C	CDC45	1.00	-1.07	-1.18	-1.16
YBR112C	CYC8	1.00	-1.08	-1.11	-1.16
YOR366W		1.00	-1.08	-1.17	-1.16
YGL152C		1.00	-1.09	-1.14	-1.16
YPL132W	COX11	1.00	-1.09	-1.03	-1.16
YKL136W		1.00	-1.13	-1.19	-1.16
YNL193W		1.00	-1.13	-1.08	-1.16
YJL004C	SYS1	1.00	-1.14	-1.21	-1.16
YLR370C	ARC18	1.00	-1.14	-1.23	-1.16
YPL205C		1.00	-1.14	-1.12	-1.16
YDR534C	FIT1	1.00	-1.15	-1.20	-1.16
YGL247W		1.00	-1.16	-1.20	-1.16
YGR227W	DIE2	1.00	-1.16	-1.31	-1.16
YDL104C	QRI7	1.00	-1.21	-1.05	-1.16
YHL023C		1.00	-1.21	-1.13	-1.16
YMR163C		1.00	-1.21	-1.19	-1.16
YGR005C	TFG2	1.00	-1.22	-1.06	-1.16
YKL199C	YKT9	1.00	-1.24	-1.16	-1.16
YNL099C		1.00	-1.24	-1.21	-1.16
YKL213C	DOA1	1.00	-1.25	-1.05	-1.16
YOR050C		1.00	-1.25	-1.21	-1.16
YLR016C		1.00	-1.28	-1.13	-1.16
YNR042W		1.00	-1.28	-1.28	-1.16
YDR058C	TGL2	1.00	-1.29	-1.28	-1.16
YPR164W	KIM3	1.00	-1.31	-1.28	-1.16
YGR094W	VAS1	1.00	-1.32	-1.38	-1.16
YNL164C		1.00	-1.32	-1.32	-1.16
YPR074C	TKL1	1.00	-1.32	-1.08	-1.16
YER143W	DDI1	1.00	-1.33	1.06	-1.16
YPL105C		1.00	-1.35	-1.11	-1.16
YML108W		1.00	-1.37	-1.35	-1.16
YBL106C	SRO77	1.00	-1.41	-1.36	-1.16
YBR121C	GRS1	1.00	-1.44	-1.33	-1.16
YNL111C	CYB5	1.00	-1.48	-1.02	-1.16
YOL120C	RPL18A	1.00	-1.53	-1.49	-1.16
YOL131W		1.00	-1.64	-1.41	-1.16
YOR190W	SPR1	1.00	-1.73	-1.19	-1.16
YDR508C	GNP1	1.00	-1.81	-1.10	-1.16
YBR078W	ECM33	1.00	-2.07	-1.95	-1.16
YNL261W	ORC5	1.00	-2.12	-1.26	-1.16
YPR155C	NCA2	1.00	1.10	1.14	-1.17
YNL316C	PHA2	1.00	1.02	-1.04	-1.17

YMR283C	RIT1	1.00	1.00	-1.16	-1.17
YMR304W	UBP15	1.00	1.00	1.09	-1.17
YHL006C	SHU1	1.00	-1.02	-1.32	-1.17
YBR027C		1.00	-1.03	-1.23	-1.17
YGL153W	PEX14	1.00	-1.03	-1.23	-1.17
YCR084C	TUP1	1.00	-1.04	1.33	-1.17
YHR145C		1.00	-1.05	1.17	-1.17
YPR166C	MRP2	1.00	-1.05	-1.15	-1.17
YHR191C	CTF8	1.00	-1.07	-1.25	-1.17
YLR445W		1.00	-1.07	-1.21	-1.17
YNL329C	PEX6	1.00	-1.08	-1.07	-1.17
YBL091C	MAP2	1.00	-1.09	-1.22	-1.17
YNR072W	HXT17	1.00	-1.09	-1.16	-1.17
YOR336W	KRE5	1.00	-1.09	-1.16	-1.17
YBL061C	SKT5	1.00	-1.11	-1.19	-1.17
YHL022C	SPO11	1.00	-1.11	-1.07	-1.17
YMR003W		1.00	-1.11	1.08	-1.17
YGR209C	TRX2	1.00	-1.13	1.04	-1.17
YOR020C	HSP10	1.00	-1.13	-1.16	-1.17
YCL036W		1.00	-1.14	-1.16	-1.17
YCL065W		1.00	-1.14	-1.19	-1.17
YGL199C		1.00	-1.14	-1.27	-1.17
YOL056W	GPM3	1.00	-1.15	-1.32	-1.17
YOR263C		1.00	-1.15	1.32	-1.17
YGL066W		1.00	-1.17	-1.19	-1.17
YJR022W	LSM8	1.00	-1.18	-1.22	-1.17
YMR040W		1.00	-1.18	-1.02	-1.17
YPL204W	HRR25	1.00	-1.18	-1.19	-1.17
YPR076W		1.00	-1.20	-1.09	-1.17
YGL238W	CSE1	1.00	-1.22	-1.41	-1.17
YGL116W	CDC20	1.00	-1.24	-1.23	-1.17
YKL139W	CTK1	1.00	-1.25	-1.29	-1.17
YMR018W		1.00	-1.25	-1.12	-1.17
YBR068C	BAP2	1.00	-1.26	-1.13	-1.17
YKR082W	NUP133	1.00	-1.26	-1.11	-1.17
YOR252W		1.00	-1.26	-1.24	-1.17
YDL030W	PRP9	1.00	-1.27	-1.23	-1.17
YHR075C	PPE1	1.00	-1.27	-1.16	-1.17
YER022W	SRB4	1.00	-1.28	-1.20	-1.17
YMR240C	CUS1	1.00	-1.29	-1.28	-1.17
YLR389C	STE23	1.00	-1.31	1.08	-1.17
YBR125C	PTC4	1.00	-1.33	-1.42	-1.17
YHR168W		1.00	-1.33	-1.35	-1.17
YOL154W		1.00	-1.33	-1.06	-1.17
YBR073W	RDH54	1.00	-1.35	-1.42	-1.17
YDR092W	UBC13	1.00	-1.35	-1.28	-1.17
YHR095W		1.00	-1.35	-1.38	-1.17
YCR068W	CVT17	1.00	-1.36	-1.21	-1.17
YJR030C		1.00	-1.37	-1.21	-1.17
YPR008W	HAA1	1.00	-1.37	-1.17	-1.17
YBR110W	ALG1	1.00	-1.41	-1.48	-1.17
YGL211W		1.00	-1.42	-1.21	-1.17
YDR347W	MRP1	1.00	-1.52	-1.54	-1.17
YKL034W		1.00	-1.53	-1.25	-1.17
YJL157C	FAR1	1.00	-1.71	-1.40	-1.17
YGR283C		1.00	-1.72	-1.34	-1.17
YKL201C	MNN4	1.00	-1.81	-1.56	-1.17
YBR165W	UBS1	1.00	-2.10	-2.13	-1.17
YDL021W	GPM2	1.00	1.08	1.22	-1.18
YJL057C	IKS1	1.00	1.03	-1.05	-1.18
YKL111C		1.00	1.02	1.08	-1.18

YIL141W		1.00	1.01	-1.14	-1.18
YPL165C		1.00	1.01	-1.02	-1.18
YNR061C		1.00	1.00	-1.08	-1.18
YGL184C	STR3	1.00	-1.01	-1.24	-1.18
YLR348C	DIC1	1.00	-1.03	-1.01	-1.18
YKR034W	DAL80	1.00	-1.04	-1.13	-1.18
YPL258C	THI21	1.00	-1.04	-1.12	-1.18
YBR051W		1.00	-1.06	1.12	-1.18
YHR057C	CYP2	1.00	-1.06	-1.20	-1.18
YDL183C		1.00	-1.07	-1.21	-1.18
YIL135C		1.00	-1.09	-1.19	-1.18
YLR004C		1.00	-1.09	-1.02	-1.18
YBR059C	AKL1	1.00	-1.10	-1.10	-1.18
YNR022C		1.00	-1.11	-1.15	-1.18
YCR011C	ADP1	1.00	-1.12	-1.26	-1.18
YER042W	MXR1	1.00	-1.13	1.05	-1.18
YML112W	CTK3	1.00	-1.13	-1.12	-1.18
YCR003W	MRPL32	1.00	-1.14	-1.11	-1.18
YKL097C		1.00	-1.14	-1.08	-1.18
YGR295C	COS6	1.00	-1.15	1.05	-1.18
YBL053W		1.00	-1.16	-1.15	-1.18
YDL194W	SNF3	1.00	-1.16	-1.08	-1.18
YGL093W	SPC105	1.00	-1.16	-1.12	-1.18
YDR445C		1.00	-1.17	-1.24	-1.18
YHR061C	GIC1	1.00	-1.17	-1.17	-1.18
YNR077C		1.00	-1.17	-1.26	-1.18
YPL125W	KAP120	1.00	-1.17	-1.06	-1.18
YER013W	PRP22	1.00	-1.18	-1.31	-1.18
YBR020W	GAL1	1.00	-1.20	-1.15	-1.18
YPR027C		1.00	-1.20	-1.09	-1.18
YJR001W		1.00	-1.22	-1.11	-1.18
YIL058W		1.00	-1.23	-1.23	-1.18
YML065W	ORC1	1.00	-1.23	-1.10	-1.18
YOR196C	LIP5	1.00	-1.23	-1.24	-1.18
YBR205W	KTR3	1.00	-1.24	-1.45	-1.18
YMR277W	FCP1	1.00	-1.25	1.08	-1.18
YDR437W		1.00	-1.26	-1.25	-1.18
YPR182W	SMX3	1.00	-1.26	-1.27	-1.18
YBR069C	TAT1	1.00	-1.28	-1.31	-1.18
YMR102C		1.00	-1.28	-1.16	-1.18
YGR029W	ERV1	1.00	-1.29	-1.36	-1.18
YEL008W		1.00	-1.32	-1.20	-1.18
YGR258C	RAD2	1.00	-1.32	-1.25	-1.18
YNL294C		1.00	-1.34	-1.31	-1.18
YDL091C		1.00	-1.36	-1.29	-1.18
YPR096C		1.00	-1.40	-1.33	-1.18
YPL151C	PRP46	1.00	-1.42	-1.33	-1.18
YBR147W		1.00	-1.49	-1.47	-1.18
YLL061W	MMP1	1.00	-1.49	-1.08	-1.18
YGL002W	ERP6	1.00	-1.50	-1.45	-1.18
YKR074W		1.00	-1.50	-1.11	-1.18
YBR081C	SPT7	1.00	-1.55	-1.46	-1.18
YJL222W	VTH2	1.00	-1.55	-1.35	-1.18
YDR217C	RAD9	1.00	-1.57	-1.32	-1.18
YJL170C	ASG7	1.00	-2.00	-1.24	-1.18
YHR080C		1.00	-2.12	-1.53	-1.18
YGR088W	CTT1	1.00	1.96	1.21	-1.19
YHR106W	TRR2	1.00	1.11	1.29	-1.19
YDL065C	PEX19	1.00	1.10	1.00	-1.19
YML004C	GLO1	1.00	1.09	1.14	-1.19
YGR232W	NAS6	1.00	1.06	-1.26	-1.19

YAL046C		1.00	1.01	-1.22	-1.19
YPL192C	PRM3	1.00	1.00	-1.19	-1.19
YNL222W	SSU72	1.00	-1.01	1.01	-1.19
YOR075W	UFE1	1.00	-1.01	1.10	-1.19
YNL245C		1.00	-1.02	-1.04	-1.19
YKR015C		1.00	-1.04	-1.13	-1.19
YNL127W		1.00	-1.04	1.05	-1.19
YDL093W	PMT5	1.00	-1.05	-1.15	-1.19
YPL098C		1.00	-1.05	-1.05	-1.19
YOR229W	WTM2	1.00	-1.06	-1.14	-1.19
YER111C	SWI4	1.00	-1.09	-1.16	-1.19
YLR362W	STE11	1.00	-1.10	-1.06	-1.19
YML114C	TAF65	1.00	-1.13	-1.17	-1.19
YER121W		1.00	-1.14	-1.08	-1.19
YDR044W	HEM13	1.00	-1.15	1.00	-1.19
YBR201W	DER1	1.00	-1.18	-1.21	-1.19
YBR297W	MAL33	1.00	-1.18	-1.11	-1.19
YHR130C		1.00	-1.19	-1.15	-1.19
YNL021W	HDA1	1.00	-1.19	-1.27	-1.19
YAR044W	OSH1	1.00	-1.20	-1.26	-1.19
YBR056W		1.00	-1.20	-1.18	-1.19
YCR054C	CTR86	1.00	-1.21	-1.25	-1.19
YLR036C		1.00	-1.21	-1.15	-1.19
YBL022C	PIM1	1.00	-1.22	-1.23	-1.19
YML119W		1.00	-1.24	-1.26	-1.19
YDL074C	BRE1	1.00	-1.25	-1.32	-1.19
YDL197C	ASF2	1.00	-1.25	-1.02	-1.19
YMR182C	RGM1	1.00	-1.27	-1.13	-1.19
YBR011C	IPP1	1.00	-1.31	-1.33	-1.19
YDR397C	NCB2	1.00	-1.32	-1.36	-1.19
YPL062W		1.00	-1.37	-1.03	-1.19
YKL033W		1.00	-1.40	-1.16	-1.19
YLR265C	NEJ1	1.00	-1.40	-1.41	-1.19
YBR001C	NTH2	1.00	-1.43	-1.28	-1.19
YJL208C	NUC1	1.00	-1.43	-1.12	-1.19
YJR155W	AAD10	1.00	-1.47	-1.29	-1.19
YOL152W	FRE7	1.00	-1.49	-1.17	-1.19
YOR300W		1.00	-1.51	-1.23	-1.19
YOR043W	WHI2	1.00	-1.53	-1.22	-1.19
YLR098C	CHA4	1.00	-1.54	-1.32	-1.19
YHL018W		1.00	-1.60	-1.51	-1.19
YHR091C	MSR1	1.00	-1.67	-1.44	-1.19
YHR201C	PPX1	1.00	-1.77	-1.47	-1.19
YOR161C		1.00	2.00	1.17	-1.20
YKL193C	SDS22	1.00	1.40	1.09	-1.20
YDR533C		1.00	1.22	-1.21	-1.20
YGR089W		1.00	1.17	-1.18	-1.20
YER059W	PCL6	1.00	1.07	-1.06	-1.20
YIL172C		1.00	1.06	-1.04	-1.20
YNL122C		1.00	1.05	-1.03	-1.20
YGR179C	OKP1	1.00	1.04	-1.21	-1.20
YIL051C	MMF1	1.00	1.04	-1.17	-1.20
YJL185C		1.00	1.04	-1.16	-1.20
YNL336W	COS1	1.00	-1.01	1.00	-1.20
YJL195C		1.00	-1.02	-1.23	-1.20
YPL056C		1.00	-1.02	-1.11	-1.20
YBR299W	MAL32	1.00	-1.05	1.06	-1.20
YJR057W	CDC8	1.00	-1.06	-1.08	-1.20
YKR063C	LAS1	1.00	-1.07	-1.09	-1.20
YIL001W		1.00	-1.11	1.06	-1.20
YLR383W	RHC18	1.00	-1.12	-1.24	-1.20

YNR014W		1.00	-1.12	-1.18	-1.20
YDL057W		1.00	-1.13	-1.31	-1.20
YOR135C		1.00	-1.13	-1.03	-1.20
YGL107C		1.00	-1.14	-1.33	-1.20
YKL132C	RMA1	1.00	-1.14	-1.08	-1.20
YNL246W		1.00	-1.15	-1.10	-1.20
YEL062W	NPR2	1.00	-1.16	-1.01	-1.20
YGL084C	GUP1	1.00	-1.16	-1.02	-1.20
YOL024W		1.00	-1.16	-1.13	-1.20
YHR165C	PRP8	1.00	-1.17	-1.10	-1.20
YOR172W		1.00	-1.17	-1.12	-1.20
YPR107C	YTH1	1.00	-1.17	-1.07	-1.20
YLR461W	PAU4	1.00	-1.18	-1.12	-1.20
YNL041C	TFI2	1.00	-1.18	-1.14	-1.20
YMR114C		1.00	-1.19	1.02	-1.20
YIR029W	DAL2	1.00	-1.22	-1.14	-1.20
YBR091C	MRS5	1.00	-1.23	-1.22	-1.20
YJL030W	MAD2	1.00	-1.25	-1.31	-1.20
YGL226W		1.00	-1.28	-1.41	-1.20
YML105C	SEC65	1.00	-1.30	-1.16	-1.20
YOR057W	SGT1	1.00	-1.30	-1.36	-1.20
YNL251C	NRD1	1.00	-1.31	-1.07	-1.20
YER066W		1.00	-1.32	-1.19	-1.20
YKR020W		1.00	-1.32	-1.23	-1.20
YLR237W	THI7	1.00	-1.32	-1.27	-1.20
YJL002C	OST1	1.00	-1.36	-1.25	-1.20
YLR277C	YSH1	1.00	-1.36	-1.37	-1.20
YHL017W		1.00	-1.38	-1.43	-1.20
YBL009W		1.00	-1.44	-1.29	-1.20
YMR119W	ASI1	1.00	-1.48	-1.10	-1.20
YLR117C	CLF1	1.00	-1.55	-1.49	-1.20
YKR073C		1.00	-1.60	-1.15	-1.20
YFR051C	RET2	1.00	-1.74	1.14	-1.20
YCR039C	MATALPHA2	1.00	-1.79	-2.16	-1.20
YBR197C		1.00	-1.92	-2.04	-1.20
YBR130C	SHE3	1.00	-2.15	-2.02	-1.20
YIL101C	XBP1	1.00	1.17	-1.01	-1.21
YAR069C		1.00	1.06	-1.14	-1.21
YER139C		1.00	1.05	-1.09	-1.21
YPR026W	ATH1	1.00	1.02	-1.18	-1.21
YNR063W		1.00	1.01	-1.09	-1.21
YIL008W	URM1	1.00	1.00	-1.19	-1.21
YDR124W		1.00	-1.03	-1.11	-1.21
YDR273W		1.00	-1.04	-1.17	-1.21
YER178W	PDA1	1.00	-1.05	1.12	-1.21
YHR182W		1.00	-1.05	-1.43	-1.21
YPL264C		1.00	-1.05	-1.23	-1.21
YBR273C		1.00	-1.09	-1.17	-1.21
YIL017C	VID28	1.00	-1.09	-1.14	-1.21
YLL013C	PUF3	1.00	-1.09	-1.22	-1.21
YOL162W		1.00	-1.11	-1.12	-1.21
YER096W	SHC1	1.00	-1.12	-1.10	-1.21
YJL039C	NUP192	1.00	-1.12	-1.11	-1.21
YPR158W		1.00	-1.12	-1.18	-1.21
YBR260C	RGD1	1.00	-1.15	-1.14	-1.21
YMR320W		1.00	-1.15	-1.15	-1.21
YCR041W		1.00	-1.16	-1.07	-1.21
YOR269W	PAC1	1.00	-1.16	-1.19	-1.21
YFR026C		1.00	-1.17	-1.29	-1.21
YPL039W		1.00	-1.17	-1.31	-1.21
YCR095C		1.00	-1.19	-1.08	-1.21

YER163C		1.00	-1.19	-1.11	-1.21
YIR044C		1.00	-1.21	-1.14	-1.21
YJL071W	ARG2	1.00	-1.21	-1.31	-1.21
YJL114W		1.00	-1.21	-1.22	-1.21
YBR072W	HSP26	1.00	-1.22	-1.08	-1.21
YKL027W		1.00	-1.24	-1.34	-1.21
YNL008C	ASI3	1.00	-1.25	-1.28	-1.21
YOR274W	MOD5	1.00	-1.26	-1.24	-1.21
YMR068W		1.00	-1.27	1.12	-1.21
YDR411C		1.00	-1.30	1.12	-1.21
YHR212C		1.00	-1.30	-1.20	-1.21
YMR288W	HSH155	1.00	-1.30	-1.34	-1.21
YNL106C	INP52	1.00	-1.30	-1.14	-1.21
YDL243C	AAD4	1.00	-1.31	-1.29	-1.21
YDR182W	CDC1	1.00	-1.31	-1.08	-1.21
YLL020C		1.00	-1.31	-1.11	-1.21
YHL030W	ECM29	1.00	-1.33	-1.40	-1.21
YLL060C	GTT2	1.00	-1.33	-1.21	-1.21
YLR210W	CLB4	1.00	-1.33	-1.26	-1.21
YDL059C	RAD59	1.00	-1.34	-1.25	-1.21
YIR023W	DAL81	1.00	-1.34	-1.22	-1.21
YIL028W		1.00	-1.35	-1.28	-1.21
YDR288W		1.00	-1.36	-1.12	-1.21
YKL210W	UBA1	1.00	-1.40	-1.05	-1.21
YER023W	PRO3	1.00	-1.43	-1.21	-1.21
YMR067C		1.00	-1.44	1.08	-1.21
YER063W	THO1	1.00	-1.45	-1.12	-1.21
YKL014C		1.00	-1.45	-1.30	-1.21
YPR168W	NUT2	1.00	-1.46	-1.15	-1.21
YKL116C	PRR1	1.00	-1.47	-1.34	-1.21
YHR103W	SBE22	1.00	-1.48	-1.36	-1.21
YKL078W		1.00	-1.49	-1.40	-1.21
YGL197W	MDS3	1.00	-1.50	-1.76	-1.21
YLR326W		1.00	-1.50	-1.46	-1.21
YMR042W	ARG80	1.00	-1.51	-1.48	-1.21
YDR053W		1.00	-1.54	-1.36	-1.21
YML089C		1.00	-1.58	-1.16	-1.21
YOR164C		1.00	-1.61	-1.09	-1.21
YLL012W		1.00	-1.66	-1.46	-1.21
YGR035C		1.00	-1.76	-1.38	-1.21
YDR112W		1.00	-2.33	-1.74	-1.21
YDR205W	MSC2	1.00	-2.36	-1.69	-1.21
YIL045W	PIG2	1.00	1.17	1.27	-1.22
YOR052C		1.00	1.12	1.12	-1.22
YGR167W	CLC1	1.00	1.01	-1.04	-1.22
YMR326C		1.00	-1.04	-1.03	-1.22
YPR131C	NAT3	1.00	-1.04	-1.07	-1.22
YDR436W	PPZ2	1.00	-1.05	-1.04	-1.22
YIL107C	PFK26	1.00	-1.07	-1.14	-1.22
YEL066W	HPA3	1.00	-1.08	-1.08	-1.22
YOL108C	INO4	1.00	-1.09	-1.08	-1.22
YLR132C		1.00	-1.10	-1.11	-1.22
YMR115W		1.00	-1.10	-1.11	-1.22
YPL213W	LEA1	1.00	-1.11	-1.16	-1.22
YDR250C		1.00	-1.12	-1.02	-1.22
YJL075C		1.00	-1.12	1.11	-1.22
YML110C	COQ5	1.00	-1.12	1.10	-1.22
YHR031C	RRM3	1.00	-1.16	-1.07	-1.22
YPL196W	OXR1	1.00	-1.17	1.06	-1.22
YPR082C	DIB1	1.00	-1.18	-1.07	-1.22
YCR018C	SRD1	1.00	-1.19	-1.17	-1.22

YNL260C		1.00	-1.20	-1.27	-1.22
YKR058W	GLG1	1.00	-1.21	-1.23	-1.22
YBL014C	RRN6	1.00	-1.22	-1.58	-1.22
YGL032C	AGA2	1.00	-1.22	-1.18	-1.22
YDR057W		1.00	-1.25	-1.17	-1.22
YNL029C	KTR5	1.00	-1.25	-1.41	-1.22
YIR007W		1.00	-1.26	-1.15	-1.22
YLR133W	CKI1	1.00	-1.32	-1.02	-1.22
YBR010W	HHT1	1.00	-1.33	-1.31	-1.22
YDL137W	ARF2	1.00	-1.34	1.19	-1.22
YDR415C		1.00	-1.37	-1.18	-1.22
YLL010C	PSR1	1.00	-1.42	-1.39	-1.22
YAL009W	SPO7	1.00	-1.46	-1.52	-1.22
YOR326W	MYO2	1.00	-1.48	-1.11	-1.22
YHR136C	SPL2	1.00	-1.50	-1.36	-1.22
YJL036W	SNX4	1.00	-1.53	-1.21	-1.22
YLL036C	PRP19	1.00	-1.56	-1.60	-1.22
YDR151C	CTH1	1.00	-1.66	-1.40	-1.22
YMR028W	TAP42	1.00	-1.66	-1.42	-1.22
YKL012W	PRP40	1.00	-1.72	-1.13	-1.22
YPR057W	BRR1	1.00	-1.74	-1.16	-1.22
YPL180W	SHD7	1.00	-1.82	-1.40	-1.22
YOL140W	ARG8	1.00	-2.01	-1.25	-1.22
YDR459C		1.00	-2.06	-1.41	-1.22
YGR102C		1.00	-3.34	-1.41	-1.22
YCR097W	A1	1.00	-1.04	-1.16	-1.23
YHR157W	REC104	1.00	1.25	1.01	-1.23
YJL141C	YAK1	1.00	1.16	1.55	-1.23
YGL180W	APG1	1.00	1.01	-1.33	-1.23
YDL076C		1.00	1.00	-1.02	-1.23
YDL214C	PRR2	1.00	1.00	-1.27	-1.23
YGL249W	ZIP2	1.00	1.00	-1.14	-1.23
YBR083W	TEC1	1.00	-1.02	-1.11	-1.23
YOL069W	NUF2	1.00	-1.02	-1.08	-1.23
YPL031C	PHO85	1.00	-1.04	1.06	-1.23
YLL065W	GIN11	1.00	-1.05	-1.12	-1.23
YPL017C		1.00	-1.07	-1.17	-1.23
YCR060W		1.00	-1.09	-1.10	-1.23
YIL067C		1.00	-1.10	-1.20	-1.23
YHR102W	KIC1	1.00	-1.11	-1.30	-1.23
YAR053W		1.00	-1.12	-1.31	-1.23
YHL005C		1.00	-1.12	-1.26	-1.23
YKL041W	VPS24	1.00	-1.13	-1.16	-1.23
YAR028W		1.00	-1.14	-1.03	-1.23
YNR062C		1.00	-1.15	-1.22	-1.23
YMR206W		1.00	-1.17	-1.22	-1.23
YNL233W	BNI4	1.00	-1.18	-1.10	-1.23
YHL040C	ARN1	1.00	-1.20	-1.32	-1.23
YJL010C		1.00	-1.20	-1.39	-1.23
YNL107W	YAF9	1.00	-1.20	-1.29	-1.23
YBR060C	ORC2	1.00	-1.21	-1.23	-1.23
YLR360W	VPS38	1.00	-1.21	-1.21	-1.23
YDR402C	DIT2	1.00	-1.23	-1.14	-1.23
YDR473C	PRP3	1.00	-1.23	-1.28	-1.23
YKL112W	ABF1	1.00	-1.23	-1.01	-1.23
YNR017W	MAS6	1.00	-1.23	-1.07	-1.23
YGR262C	BUD32	1.00	-1.24	-1.12	-1.23
YOR321W	PMT3	1.00	-1.24	-1.09	-1.23
YHR152W	SPO12	1.00	-1.25	-1.33	-1.23
YKL157W	APE2	1.00	-1.26	-1.19	-1.23
YJR003C		1.00	-1.27	-1.25	-1.23

YBR094W		1.00	-1.30	-1.18	-1.23
YDR495C	VPS3	1.00	-1.30	-1.44	-1.23
YAL042W	ERV46	1.00	-1.31	-1.37	-1.23
YHR058C	MED6	1.00	-1.31	-1.13	-1.23
YNL148C	ALF1	1.00	-1.31	-1.20	-1.23
YJL186W	MNN5	1.00	-1.32	-1.30	-1.23
YLR027C	AAT2	1.00	-1.33	-1.16	-1.23
YEL007W	TOS9	1.00	-1.34	-1.34	-1.23
YNL290W	RFC3	1.00	-1.35	-1.38	-1.23
YDL053C		1.00	-1.37	-1.41	-1.23
YMR080C	NAM7	1.00	-1.37	-1.21	-1.23
YMR247C		1.00	-1.37	-1.33	-1.23
YGL224C		1.00	-1.41	-1.30	-1.23
YBR200W	BEM1	1.00	-1.42	-1.12	-1.23
YER001W	MNN1	1.00	-1.52	-1.57	-1.23
YDR449C		1.00	-1.56	-1.66	-1.23
YPL109C		1.00	-1.57	-1.29	-1.23
YOR194C	TOA1	1.00	-1.58	-1.14	-1.23
YFL046W		1.00	-1.63	-1.40	-1.23
YMR146C	TIF34	1.00	-1.65	-1.42	-1.23
YDR359C	VID21	1.00	-1.77	-1.64	-1.23
YOR225W		1.00	-1.98	-1.52	-1.23
YAL045C		1.00	-2.15	-1.68	-1.23
YHR096C	HXT5	1.00	1.47	1.46	-1.24
YDR464W	SPP41	1.00	1.12	1.16	-1.24
YMR165C	SMP2	1.00	1.08	-1.08	-1.24
YOL151W	GRE2	1.00	1.06	1.02	-1.24
YMR189W	GCV2	1.00	1.03	-1.19	-1.24
YOR382W	FIT2	1.00	1.02	-1.07	-1.24
YOL147C	PEX11	1.00	1.01	1.02	-1.24
YPL206C		1.00	1.01	-1.13	-1.24
YFL016C	MDJ1	1.00	1.00	1.06	-1.24
YJL023C	PET130	1.00	-1.01	-1.11	-1.24
YOR192C		1.00	-1.02	1.13	-1.24
YCL056C		1.00	-1.04	-1.47	-1.24
YNL330C	RPD3	1.00	-1.05	-1.06	-1.24
YBR282W	MRPL27	1.00	-1.08	-1.21	-1.24
YML084W		1.00	-1.08	-1.19	-1.24
YDL211C		1.00	-1.09	-1.19	-1.24
YGR220C	MRPL9	1.00	-1.09	-1.29	-1.24
YMR231W	PEP5	1.00	-1.09	1.00	-1.24
YER183C	FAU1	1.00	-1.12	-1.20	-1.24
YJR020W		1.00	-1.15	-1.24	-1.24
YLR209C	PNP1	1.00	-1.15	-1.04	-1.24
YJL101C	GSH1	1.00	-1.16	-1.34	-1.24
YOR275C		1.00	-1.16	-1.18	-1.24
YIR014W		1.00	-1.17	-1.09	-1.24
YJR149W		1.00	-1.18	-1.24	-1.24
YDL163W		1.00	-1.19	-1.01	-1.24
YIL115C	NUP159	1.00	-1.19	-1.21	-1.24
YML066C	SMA2	1.00	-1.20	-1.20	-1.24
YOL008W		1.00	-1.20	-1.08	-1.24
YDR122W	KIN1	1.00	-1.22	-1.12	-1.24
YEL030W	ECM10	1.00	-1.24	-1.16	-1.24
YHR076W		1.00	-1.24	-1.24	-1.24
YOR319W	HSH49	1.00	-1.24	-1.23	-1.24
YGR116W	SPT6	1.00	-1.26	-1.20	-1.24
YBL055C		1.00	-1.27	-1.66	-1.24
YGL077C	HNM1	1.00	-1.27	-1.22	-1.24
YPR152C		1.00	-1.27	-1.15	-1.24
YGL176C		1.00	-1.30	-1.14	-1.24

YLL066C		1.00	-1.30	-1.37	-1.24
YDL232W	OST4	1.00	-1.31	-1.20	-1.24
YIL046W	MET30	1.00	-1.32	-1.27	-1.24
YLR294C		1.00	-1.35	-1.15	-1.24
YGL130W	CEG1	1.00	-1.37	-1.40	-1.24
YIL122W		1.00	-1.40	-1.33	-1.24
YGL083W	SCY1	1.00	-1.41	-1.17	-1.24
YGR215W	RSM27	1.00	-1.41	-1.31	-1.24
YGL096W	TOS8	1.00	-1.49	-1.46	-1.24
YKR096W		1.00	-1.52	-1.41	-1.24
YFL007W	BLM3	1.00	-1.53	-1.44	-1.24
YNL070W	TOM7	1.00	-1.64	-1.13	-1.24
YBL058W	SHP1	1.00	-2.15	-1.98	-1.24
YKR025W	RPC37	1.00	-2.18	-1.23	-1.24
YPL111W	CAR1	1.00	1.20	1.30	-1.25
YHR051W	COX6	1.00	1.15	1.08	-1.25
YMR322C		1.00	1.13	-1.16	-1.25
YPR046W	MCM16	1.00	1.13	-1.01	-1.25
YGL190C	CDC55	1.00	1.05	-1.16	-1.25
YAL017W	FUN31	1.00	1.04	-1.25	-1.25
YGL040C	HEM2	1.00	1.04	1.03	-1.25
YCR096C	A2	1.00	1.03	-1.12	-1.25
YMR267W	PPA2	1.00	1.02	-1.16	-1.25
YDR284C	DPP1	1.00	1.00	-1.10	-1.25
YHR158C	KEL1	1.00	-1.05	-1.14	-1.25
YDR268W	MSW1	1.00	-1.06	-1.20	-1.25
YGR011W		1.00	-1.06	-1.24	-1.25
YBR139W		1.00	-1.07	-1.18	-1.25
YGR237C		1.00	-1.07	1.02	-1.25
YGL250W		1.00	-1.08	-1.19	-1.25
YOL047C		1.00	-1.08	-1.15	-1.25
YER095W	RAD51	1.00	-1.10	-1.18	-1.25
YGL262W		1.00	-1.10	-1.30	-1.25
YBR269C		1.00	-1.12	-1.16	-1.25
YPR195C		1.00	-1.12	-1.10	-1.25
YIL120W	QDR1	1.00	-1.14	-1.30	-1.25
YOR134W	BAG7	1.00	-1.14	-1.22	-1.25
YDL069C	CBS1	1.00	-1.16	-1.39	-1.25
YPR032W	SRO7	1.00	-1.16	-1.24	-1.25
YBR186W	PCH2	1.00	-1.17	-1.33	-1.25
YDL077C	VAM6	1.00	-1.18	-1.25	-1.25
YDL200C	MGT1	1.00	-1.18	-1.18	-1.25
YLR119W	SRN2	1.00	-1.21	-1.14	-1.25
YBR024W	SCO2	1.00	-1.22	-1.23	-1.25
YPL033C		1.00	-1.22	-1.22	-1.25
YBR233W	PBP2	1.00	-1.27	-1.27	-1.25
YAR010C		1.00	-1.31	-1.38	-1.25
YDR490C	PKH1	1.00	-1.34	-1.31	-1.25
YPL266W	DIM1	1.00	-1.34	-1.24	-1.25
YPL225W		1.00	-1.36	-1.17	-1.25
YOR058C	ASE1	1.00	-1.37	-1.40	-1.25
YBR185C	MBA1	1.00	-1.40	-1.51	-1.25
YDL138W	RGT2	1.00	-1.43	-1.54	-1.25
YKL107W		1.00	-1.52	-1.22	-1.25
YGR072W	UPF3	1.00	-1.54	-1.53	-1.25
YAL022C	FUN26	1.00	-1.57	-1.45	-1.25
YDR209C		1.00	-1.62	-1.37	-1.25
YOL161C		1.00	-1.70	-1.39	-1.25
YGR018C		1.00	-2.00	-1.27	-1.25
YKL151C		1.00	1.29	1.31	-1.26
YDL079C	MRK1	1.00	1.28	1.52	-1.26

YLR149C		1.00	1.19	1.15	-1.26
YDL230W	PTP1	1.00	1.12	-1.02	-1.26
YJR107W		1.00	1.02	1.05	-1.26
YOL053W		1.00	1.01	1.02	-1.26
YMR099C		1.00	1.00	-1.03	-1.26
YLL046C	RNP1	1.00	-1.03	-1.25	-1.26
YIL170W	HXT12	1.00	-1.04	-1.10	-1.26
YOL042W	NGL1	1.00	-1.05	-1.06	-1.26
YOR081C		1.00	-1.07	-1.10	-1.26
YBR212W	NGR1	1.00	-1.13	-1.27	-1.26
YJR086W	STE18	1.00	-1.14	-1.22	-1.26
YGR100W	MDR1	1.00	-1.15	-1.19	-1.26
YIR004W	DJP1	1.00	-1.17	-1.18	-1.26
YGL173C	KEM1	1.00	-1.18	-1.29	-1.26
YHL019C	APM2	1.00	-1.19	-1.31	-1.26
YOR266W	PNT1	1.00	-1.21	-1.22	-1.26
YGR273C		1.00	-1.22	-1.35	-1.26
YJR032W	CPR7	1.00	-1.24	-1.25	-1.26
YJR044C		1.00	-1.24	-1.05	-1.26
YHR119W	SET1	1.00	-1.26	-1.17	-1.26
YMR323W		1.00	-1.28	-1.08	-1.26
YLR108C		1.00	-1.29	-1.09	-1.26
YDR200C		1.00	-1.30	-1.18	-1.26
YER011W	TIR1	1.00	-1.30	-1.46	-1.26
YLR268W	SEC22	1.00	-1.31	-1.22	-1.26
YOR291W		1.00	-1.31	-1.52	-1.26
YPL007C	TFC8	1.00	-1.31	-1.14	-1.26
YML041C		1.00	-1.32	-1.15	-1.26
YDL009C		1.00	-1.33	-1.29	-1.26
YDR170C	SEC7	1.00	-1.34	-1.58	-1.26
YFL063W		1.00	-1.36	-1.22	-1.26
YFR019W	FAB1	1.00	-1.36	-1.34	-1.26
YOR084W		1.00	-1.40	-1.04	-1.26
YDR021W	FAL1	1.00	-1.41	-1.24	-1.26
YGR184C	UBR1	1.00	-1.41	-1.41	-1.26
YGR296W	YRF1-3	1.00	-1.42	-1.54	-1.26
YMR302C	PRP12	1.00	-1.43	-1.18	-1.26
YML031W	NDC1	1.00	-1.56	-1.43	-1.26
YGL171W	ROK1	1.00	-1.60	-1.38	-1.26
YJL211C		1.00	-1.60	-1.53	-1.26
YOR290C	SNF2	1.00	-1.60	-1.40	-1.26
YJL203W	PRP21	1.00	-1.66	-1.40	-1.26
YBR223C		1.00	-1.67	-1.53	-1.26
YBR153W	RIB7	1.00	-1.68	-1.37	-1.26
YBR296C	PHO89	1.00	-1.75	1.03	-1.26
YGR216C	GPI1	1.00	-1.92	-1.19	-1.26
YDR543C		1.00	-1.99	-1.38	-1.26
YMR056C	AAC1	1.00	1.28	1.11	-1.27
YLR258W	GSY2	1.00	1.26	1.06	-1.27
YNL259C	ATX1	1.00	1.00	-1.41	-1.27
YPL173W	MRPL40	1.00	1.00	-1.20	-1.27
YPL148C	PPT2	1.00	-1.01	-1.03	-1.27
YMR098C		1.00	-1.02	-1.01	-1.27
YBR219C		1.00	-1.04	-1.30	-1.27
YBR268W	MRPL37	1.00	-1.04	-1.03	-1.27
YOL163W		1.00	-1.05	-1.37	-1.27
YPL080C		1.00	-1.05	-1.20	-1.27
YDL094C		1.00	-1.09	-1.11	-1.27
YER184C		1.00	-1.11	-1.12	-1.27
YGR164W		1.00	-1.13	-1.25	-1.27
YJL221C	FSP2	1.00	-1.14	-1.21	-1.27

YLR411W	CTR3	1.00	-1.14	-1.31	-1.27
YLR211C		1.00	-1.16	-1.15	-1.27
YML006C	GIS4	1.00	-1.17	-1.27	-1.27
YDR340W		1.00	-1.18	1.19	-1.27
YIL112W		1.00	-1.18	-1.03	-1.27
YIL131C	FKH1	1.00	-1.20	-1.60	-1.27
YLR025W	SNF7	1.00	-1.21	-1.12	-1.27
YGL119W	ABC1	1.00	-1.22	-1.23	-1.27
YPL133C		1.00	-1.26	-1.31	-1.27
YIR001C	SGN1	1.00	-1.29	-1.44	-1.27
YKR079C		1.00	-1.31	-1.20	-1.27
YPL276W		1.00	-1.32	-1.51	-1.27
YLR396C	VPS33	1.00	-1.33	-1.41	-1.27
YNL152W		1.00	-1.33	-1.37	-1.27
YJL028W		1.00	-1.36	-1.46	-1.27
YDR482C		1.00	-1.37	-1.46	-1.27
YDR330W		1.00	-1.38	-1.07	-1.27
YDR507C	GIN4	1.00	-1.38	1.04	-1.27
YMR244W		1.00	-1.39	-1.24	-1.27
YPL057C	SUR1	1.00	-1.39	1.33	-1.27
YGR120C	SEC35	1.00	-1.40	-1.25	-1.27
YDL118W		1.00	-1.41	-1.34	-1.27
YDR010C		1.00	-1.41	-1.34	-1.27
YOR217W	RFC1	1.00	-1.41	-1.12	-1.27
YJR061W		1.00	-1.43	-1.33	-1.27
YKL105C		1.00	-1.43	-1.42	-1.27
YLR456W		1.00	-1.45	-1.55	-1.27
YMR144W		1.00	-1.48	-1.36	-1.27
YHR202W		1.00	-1.49	-1.47	-1.27
YJR040W	GEF1	1.00	-1.60	-1.08	-1.27
YDL115C	IWR1	1.00	-1.66	-1.25	-1.27
YPR104C	FHL1	1.00	-1.70	-1.37	-1.27
YLR416C		1.00	-1.75	-1.66	-1.27
YLR011W	LOT6	1.00	-1.76	-1.72	-1.27
YPL167C	REV3	1.00	-1.77	-1.46	-1.27
YPL246C		1.00	-2.14	-1.64	-1.27
YPR197C		1.00	-2.16	-1.49	-1.27
YJL182C		1.00	-2.39	-1.14	-1.27
YNL036W	NCE103	1.00	2.32	1.03	-1.28
YER144C	UBP5	1.00	1.77	1.95	-1.28
YMR193W	MRPL24	1.00	1.05	-1.02	-1.28
YBL067C	UBP13	1.00	1.03	-1.13	-1.28
YDR306C		1.00	1.01	-1.15	-1.28
YML020W		1.00	-1.02	-1.15	-1.28
YAR070C		1.00	-1.04	-1.29	-1.28
YNL146W		1.00	-1.05	-1.18	-1.28
YPL130W	SPO19	1.00	-1.06	-1.07	-1.28
YBR018C	GAL7	1.00	-1.10	-1.18	-1.28
YDL113C		1.00	-1.10	-1.16	-1.28
YJR025C	BNA1	1.00	-1.14	-1.04	-1.28
YKR054C	DYN1	1.00	-1.14	-1.25	-1.28
YLL067C		1.00	-1.16	-1.29	-1.28
YPR065W	ROX1	1.00	-1.17	-1.27	-1.28
YPR109W		1.00	-1.18	-1.18	-1.28
YPR039W		1.00	-1.19	-1.18	-1.28
YGR212W		1.00	-1.20	-1.42	-1.28
YOL111C		1.00	-1.21	-1.16	-1.28
YIL011W	TIR3	1.00	-1.22	-1.31	-1.28
YPR017C	DSS4	1.00	-1.22	-1.37	-1.28
YHR022C		1.00	-1.23	-1.35	-1.28
YGR108W	CLB1	1.00	-1.26	-1.51	-1.28

YBR033W		1.00	-1.33	-1.48	-1.28
YHR167W	THP2	1.00	-1.33	-1.29	-1.28
YBR216C		1.00	-1.34	-1.60	-1.28
YOR010C	TIR2	1.00	-1.34	-1.24	-1.28
YER060W	FCY21	1.00	-1.35	1.04	-1.28
YOR121C		1.00	-1.39	-1.40	-1.28
YKL222C		1.00	-1.42	-1.23	-1.28
YKL008C	LAC1	1.00	-1.43	-1.54	-1.28
YKL010C	UFD4	1.00	-1.43	-1.40	-1.28
YOL164W		1.00	-1.43	-1.34	-1.28
YPR172W		1.00	-1.47	-1.65	-1.28
YOR239W	ABP140	1.00	-1.48	1.23	-1.28
YOR061W	CKA2	1.00	-1.57	-1.41	-1.28
YOR115C	TRS33	1.00	-1.59	-1.35	-1.28
YJR047C	ANB1	1.00	-1.62	-1.10	-1.28
YCR017C	CWH43	1.00	-1.79	-1.83	-1.28
YPL231W	FAS2	1.00	-2.28	-1.59	-1.28
YKL192C	ACP1	1.00	1.07	-1.09	-1.29
YLR070C		1.00	1.03	-1.22	-1.29
YPR160W	GPH1	1.00	1.02	-1.27	-1.29
YGR111W		1.00	1.01	-1.02	-1.29
YLR312C		1.00	1.01	-1.19	-1.29
YOR028C	CIN5	1.00	-1.02	-1.21	-1.29
YDR421W	ARO80	1.00	-1.04	1.03	-1.29
YPR147C		1.00	-1.06	-1.43	-1.29
YEL070W		1.00	-1.07	-1.09	-1.29
YMR013C	SEC59	1.00	-1.09	-1.12	-1.29
YNL338W		1.00	-1.09	-1.29	-1.29
YDL231C	BRE4	1.00	-1.10	-1.23	-1.29
YER010C		1.00	-1.10	-1.24	-1.29
YPL152W	RRD2	1.00	-1.10	-1.14	-1.29
YML100W	TSL1	1.00	-1.11	-1.16	-1.29
YDR403W	DIT1	1.00	-1.13	-1.03	-1.29
YGR177C	ATF2	1.00	-1.14	-1.27	-1.29
YHR123W	EPT1	1.00	-1.16	-1.46	-1.29
YIL102C		1.00	-1.16	-1.29	-1.29
YEL031W	SPF1	1.00	-1.18	-1.30	-1.29
YGL161C		1.00	-1.18	-1.15	-1.29
YNL043C		1.00	-1.19	-1.19	-1.29
YKL084W		1.00	-1.20	-1.32	-1.29
YLR090W	XDJ1	1.00	-1.21	-1.36	-1.29
YDR213W	UPC2	1.00	-1.23	-1.40	-1.29
YJL104W	MIA1	1.00	-1.23	-1.32	-1.29
YJL139C	YUR1	1.00	-1.23	-1.23	-1.29
YKR104W		1.00	-1.24	-1.26	-1.29
YOR024W		1.00	-1.26	-1.26	-1.29
YOR158W	PET123	1.00	-1.31	-1.19	-1.29
YPL112C		1.00	-1.31	-1.24	-1.29
YAL058W	CNE1	1.00	-1.32	-1.29	-1.29
YOL128C		1.00	-1.32	-1.31	-1.29
YLR220W	CCC1	1.00	-1.34	-1.14	-1.29
YDL041W	KRE26	1.00	-1.36	-1.39	-1.29
YDR265W	PEX10	1.00	-1.38	-1.49	-1.29
YJL045W		1.00	-1.39	-1.57	-1.29
YOL078W		1.00	-1.40	-1.36	-1.29
YLR217W		1.00	-1.42	-1.09	-1.29
YNL144C		1.00	-1.43	1.36	-1.29
YPR200C	ARR2	1.00	-1.44	-1.37	-1.29
YGR284C	ERV29	1.00	-1.47	-1.41	-1.29
YLR276C	DBP9	1.00	-1.47	-1.37	-1.29
YDL221W		1.00	-1.54	-1.20	-1.29

YNL094W		1.00	-1.58	-1.18	-1.29
YOR218C		1.00	-1.63	-1.20	-1.29
YHR002W		1.00	-1.65	-1.25	-1.29
YHR122W		1.00	-1.65	-1.51	-1.29
YJL225C		1.00	-1.82	-1.19	-1.29
YMR008C	PLB1	1.00	-1.82	-1.66	-1.29
YKR024C	DBP7	1.00	-1.87	-1.46	-1.29
YOR049C		1.00	-1.89	-1.44	-1.29
YBR090C		1.00	-1.38	-1.35	-1.29
YDR070C		1.00	1.07	-1.04	-1.30
YOR347C	PYK2	1.00	1.07	1.28	-1.30
YGR165W		1.00	1.06	-1.23	-1.30
YPL166W		1.00	1.04	-1.12	-1.30
YKL039W	PTM1	1.00	-1.09	-1.37	-1.30
YLL003W	SFI1	1.00	-1.09	-1.12	-1.30
YMR228W	MTF1	1.00	-1.09	-1.33	-1.30
YLR282C		1.00	-1.10	-1.37	-1.30
YIL010W	DOT5	1.00	-1.11	-1.19	-1.30
YER087W		1.00	-1.13	-1.34	-1.30
YPR192W	AQY1	1.00	-1.13	-1.14	-1.30
YLR204W	QRI5	1.00	-1.16	-1.02	-1.30
YOR127W	RGA1	1.00	-1.16	-1.43	-1.30
YNL257C	SIP3	1.00	-1.18	-1.20	-1.30
YNL140C		1.00	-1.21	-1.17	-1.30
YBR237W	PRP5	1.00	-1.22	-1.40	-1.30
YDR123C	INO2	1.00	-1.23	-1.13	-1.30
YDL052C	SLC1	1.00	-1.25	-1.40	-1.30
YLR442C	SIR3	1.00	-1.25	-1.31	-1.30
YLR095C	IOC2	1.00	-1.26	-1.39	-1.30
YDR521W		1.00	-1.27	-1.19	-1.30
YDR391C		1.00	-1.28	-1.38	-1.30
YIL020C	HIS6	1.00	-1.32	-1.26	-1.30
YDR029W		1.00	-1.33	-1.34	-1.30
YNL143C		1.00	-1.34	-1.09	-1.30
YNL337W		1.00	-1.35	-1.33	-1.30
YBR211C	AME1	1.00	-1.36	-1.44	-1.30
YDR102C		1.00	-1.45	-1.47	-1.30
YMR253C		1.00	-1.53	-1.71	-1.30
YMR076C	PDS5	1.00	-1.58	-1.24	-1.30
YBR168W		1.00	-1.60	-1.58	-1.30
YBR176W	ECM31	1.00	-1.73	-1.49	-1.30
YDR125C	ECM18	1.00	-1.79	-1.58	-1.30
YMR222C		1.00	-1.83	-1.40	-1.30
YGL043W	DST1	1.00	-1.94	-1.64	-1.30
YDR131C		1.00	-2.08	-1.83	-1.30
YNL195C		1.00	1.45	-1.09	-1.31
YKR077W		1.00	1.14	-1.02	-1.31
YOR320C		1.00	1.10	1.08	-1.31
YOR053W		1.00	1.06	1.28	-1.31
YJR079W		1.00	1.03	1.00	-1.31
YOR175C		1.00	1.02	-1.12	-1.31
YEL050C	RML2	1.00	1.00	-1.31	-1.31
YOR393W	ERR1	1.00	-1.03	1.08	-1.31
YLR376C		1.00	-1.04	-1.17	-1.31
YOL023W	IFM1	1.00	-1.05	-1.18	-1.31
YFL015C		1.00	-1.08	-1.21	-1.31
YPL219W	PCL8	1.00	-1.08	-1.24	-1.31
YER170W	ADK2	1.00	-1.12	-1.22	-1.31
YDL186W		1.00	-1.13	-1.49	-1.31
YLR316C	TAD3	1.00	-1.13	-1.14	-1.31
YGR269W		1.00	-1.16	-1.06	-1.31

YKL159C	RCN1	1.00	-1.17	-1.28	-1.31
YOL099C		1.00	-1.20	-1.22	-1.31
YPL123C	RNY1	1.00	-1.20	-1.19	-1.31
YNL310C		1.00	-1.21	-1.30	-1.31
YDR518W	EUG1	1.00	-1.22	-1.15	-1.31
YOR356W		1.00	-1.22	-1.05	-1.31
YGL200C	EMP24	1.00	-1.23	-1.28	-1.31
YNR047W		1.00	-1.25	-1.24	-1.31
YGL104C		1.00	-1.27	-1.24	-1.31
YGL258W		1.00	-1.30	-1.38	-1.31
YHR124W	NDT80	1.00	-1.31	-1.52	-1.31
YJL043W		1.00	-1.32	-1.40	-1.31
YGR092W	DBF2	1.00	-1.33	-1.38	-1.31
YHL014C	YLF2	1.00	-1.34	-1.28	-1.31
YLL022C	HIF1	1.00	-1.34	-1.31	-1.31
YNL102W	POL1	1.00	-1.34	-1.31	-1.31
YOR002W	ALG6	1.00	-1.35	-1.28	-1.31
YNL218W	MGS1	1.00	-1.38	-1.65	-1.31
YGR226C		1.00	-1.39	-1.51	-1.31
YHR135C	YCK1	1.00	-1.43	-1.28	-1.31
YDR452W	PHM5	1.00	-1.44	-1.29	-1.31
YIL129C	TAO3	1.00	-1.48	-1.36	-1.31
YER153C	PET122	1.00	-1.49	-1.36	-1.31
YBR113W		1.00	-1.53	-1.24	-1.31
YBR291C	CTP1	1.00	-1.62	-1.54	-1.31
YGL067W	NPY1	1.00	-1.62	-1.43	-1.31
YKL023W		1.00	-1.65	-1.40	-1.31
YKR084C	HBS1	1.00	-1.77	-1.55	-1.31
YKL129C	MYO3	1.00	-1.94	-1.51	-1.31
YOR340C	RPA43	1.00	-2.21	-2.02	-1.31
YBR037C	SCO1	1.00	-2.39	-2.10	-1.31
YMR081C	ISF1	1.00	1.38	2.37	-1.32
YHR008C	SOD2	1.00	1.14	1.08	-1.32
YKL205W	LOS1	1.00	1.07	-1.14	-1.32
YLR109W	AHP1	1.00	-1.03	-1.09	-1.32
YMR077C	VPS20	1.00	-1.04	-1.22	-1.32
YDR304C	CYP5	1.00	-1.05	-1.04	-1.32
YFL036W	RPO41	1.00	-1.09	-1.25	-1.32
YAL028W		1.00	-1.12	-1.34	-1.32
YMR258C		1.00	-1.12	-1.21	-1.32
YHR171W	APG7	1.00	-1.14	-1.24	-1.32
YIL032C		1.00	-1.20	-1.17	-1.32
YPR193C	HPA2	1.00	-1.21	-1.20	-1.32
YHR129C	ARP1	1.00	-1.24	-1.32	-1.32
YDR446W	ECM11	1.00	-1.27	-1.41	-1.32
YKL197C	PEX1	1.00	-1.32	-1.18	-1.32
YML005W		1.00	-1.33	-1.35	-1.32
YMR065W	KAR5	1.00	-1.33	-1.39	-1.32
YGR107W		1.00	-1.34	-1.34	-1.32
YPR115W		1.00	-1.34	-1.30	-1.32
YDR472W	TRS31	1.00	-1.39	-1.64	-1.32
YHL008C		1.00	-1.39	-1.26	-1.32
YHR100C		1.00	-1.41	-1.52	-1.32
YKR052C	MRS4	1.00	-1.43	-1.28	-1.32
YOR231W	MKK1	1.00	-1.44	-1.25	-1.32
YGR032W	GSC2	1.00	-1.47	-1.56	-1.32
YOR062C		1.00	-1.50	-1.24	-1.32
YMR237W		1.00	-1.51	-1.30	-1.32
YKL020C	SPT23	1.00	-1.55	-1.33	-1.32
YML046W	PRP39	1.00	-1.59	-1.51	-1.32
YIL075C	RPN2	1.00	-1.64	-1.40	-1.32

YCL035C	GRX1	1.00	-1.67	-1.28	-1.32
YLR104W		1.00	-1.83	-1.40	-1.32
YHR173C		1.00	-1.85	-1.69	-1.32
YBL001C	ECM15	1.00	-1.95	-1.40	-1.32
YGR228W		1.00	-2.01	-1.31	-1.32
YNL305C		1.00	1.24	1.19	-1.33
YHL035C		1.00	1.06	1.08	-1.33
YLL004W	ORC3	1.00	1.00	-1.22	-1.33
YKR065C		1.00	-1.01	-1.28	-1.33
YNL258C		1.00	-1.10	-1.15	-1.33
YCL044C		1.00	-1.15	-1.31	-1.33
YCR036W	RBK1	1.00	-1.15	-1.38	-1.33
YMR196W		1.00	-1.15	-1.25	-1.33
YKR018C		1.00	-1.17	-1.27	-1.33
YOR392W		1.00	-1.17	-1.30	-1.33
YGR219W		1.00	-1.18	-1.26	-1.33
YGL131C		1.00	-1.20	-1.29	-1.33
YHL041W		1.00	-1.22	-1.34	-1.33
YBL021C	HAP3	1.00	-1.30	-1.40	-1.33
YJL199C		1.00	-1.33	-1.56	-1.33
YJR129C		1.00	-1.33	-1.28	-1.33
YNR006W	VPS27	1.00	-1.34	-1.39	-1.33
YOR032C	HMS1	1.00	-1.34	-1.21	-1.33
YDL005C	MED2	1.00	-1.35	-1.20	-1.33
YIL134W	FLX1	1.00	-1.35	-1.32	-1.33
YLL015W	BPT1	1.00	-1.36	-1.34	-1.33
YPL008W	CHL1	1.00	-1.36	-1.23	-1.33
YJL105W		1.00	-1.37	-1.47	-1.33
YLL053C		1.00	-1.37	-1.45	-1.33
YMR025W		1.00	-1.37	-1.09	-1.33
YHR211W	FLO5	1.00	-1.38	-1.25	-1.33
YJL126W	NIT2	1.00	-1.38	-1.22	-1.33
YLR267W	BOP2	1.00	-1.38	-1.13	-1.33
YHR199C		1.00	-1.40	-1.40	-1.33
YGR271W	SLH1	1.00	-1.42	-1.48	-1.33
YOR093C		1.00	-1.43	-1.56	-1.33
YGR270W	YTA7	1.00	-1.47	-1.60	-1.33
YLR279W		1.00	-1.51	-1.46	-1.33
YPL212C	PUS1	1.00	-1.55	-1.47	-1.33
YFL058W	THI5	1.00	-1.75	-1.37	-1.33
YLR434C		1.00	-1.86	-1.07	-1.33
YDR043C	NRG1	1.00	-2.12	-1.19	-1.33
YJR023C		1.00	1.04	-1.27	-1.34
YMR140W		1.00	1.04	1.06	-1.34
YLR050C		1.00	-1.03	-1.36	-1.34
YOR232W	MGE1	1.00	-1.03	-1.26	-1.34
YKL219W	COS9	1.00	-1.04	-1.25	-1.34
YKR087C		1.00	-1.09	-1.12	-1.34
YNL223W	AUT2	1.00	-1.11	-1.22	-1.34
YGR022C		1.00	-1.12	-1.10	-1.34
YLR422W		1.00	-1.12	-1.21	-1.34
YMR176W	ECM5	1.00	-1.15	-1.15	-1.34
YPL097W	MSY1	1.00	-1.15	-1.31	-1.34
YLR363C	NMD4	1.00	-1.17	-1.47	-1.34
YOL033W	MSE1	1.00	-1.17	-1.15	-1.34
YGL138C		1.00	-1.18	-1.57	-1.34
YPL261C		1.00	-1.18	-1.14	-1.34
YGR188C	BUB1	1.00	-1.19	-1.30	-1.34
YDR291W		1.00	-1.20	-1.28	-1.34
YGL222C	EDC1	1.00	-1.21	-1.45	-1.34
YBR258C	SHG1	1.00	-1.29	-1.43	-1.34

YDR374C		1.00	-1.31	-1.52	-1.34
YKL022C	CDC16	1.00	-1.33	-1.37	-1.34
YJR077C	MIR1	1.00	-1.34	-1.24	-1.34
YOL027C		1.00	-1.34	-1.34	-1.34
YPL113C		1.00	-1.34	-1.33	-1.34
YMR285C	NGL2	1.00	-1.35	-1.31	-1.34
YMR159C	APG16	1.00	-1.38	-1.23	-1.34
YKL124W	SSH4	1.00	-1.40	-1.24	-1.34
YBL093C	ROX3	1.00	-1.43	-1.28	-1.34
YOR141C	ARP8	1.00	-1.43	-1.36	-1.34
YIL118W	RHO3	1.00	-1.45	-1.41	-1.34
YJR103W	URA8	1.00	-1.48	-1.50	-1.34
YCR046C	IMG1	1.00	-1.49	-1.51	-1.34
YMR161W	HLJ1	1.00	-1.50	-1.69	-1.34
YGL065C	ALG2	1.00	-1.53	-1.07	-1.34
YNL089C		1.00	-1.61	-1.54	-1.34
YLR200W	YKE2	1.00	-1.65	-1.51	-1.34
YOR235W		1.00	-1.70	-1.26	-1.34
YLR009W		1.00	-2.16	-1.53	-1.34
YDR365C		1.00	-2.55	-1.44	-1.34
YNL052W	COX5A	1.00	1.29	1.40	-1.35
YPL281C	ERR2	1.00	1.05	1.05	-1.35
YBR003W	COQ1	1.00	-1.04	-1.05	-1.35
YCR009C	RVS161	1.00	-1.04	-1.32	-1.35
YCR075C	ERS1	1.00	-1.05	-1.32	-1.35
YDL246C		1.00	-1.14	-1.12	-1.35
YML030W		1.00	-1.14	-1.19	-1.35
YLR283W		1.00	-1.16	-1.28	-1.35
YPL104W	MSD1	1.00	-1.16	-1.25	-1.35
YJR080C		1.00	-1.17	-1.11	-1.35
YBR120C	CBP6	1.00	-1.19	-1.37	-1.35
YKR101W	SIR1	1.00	-1.19	-1.25	-1.35
YJR033C	RAV1	1.00	-1.21	-1.48	-1.35
YNL017C		1.00	-1.22	-1.38	-1.35
YJR010W	MET3	1.00	-1.27	-1.52	-1.35
YNR070W		1.00	-1.28	-1.30	-1.35
YGR292W	MAL12	1.00	-1.29	-1.47	-1.35
YGL178W	MPT5	1.00	-1.33	-1.05	-1.35
YKL089W	MIF2	1.00	-1.35	-1.42	-1.35
YOR140W	SFL1	1.00	-1.37	-1.40	-1.35
YOR256C		1.00	-1.37	-1.28	-1.35
YJL201W	ECM25	1.00	-1.39	-1.37	-1.35
YDL145C	COP1	1.00	-1.40	-1.51	-1.35
YDR440W	DOT1	1.00	-1.44	-1.17	-1.35
YJL183W	MNN11	1.00	-1.44	-1.22	-1.35
YLR105C	SEN2	1.00	-1.45	-1.51	-1.35
YPR135W	CTF4	1.00	-1.45	-1.38	-1.35
YDR329C	PEX3	1.00	-1.54	-1.03	-1.35
YCL050C	APA1	1.00	-1.58	-5.80	-1.35
YBR281C		1.00	-1.61	-1.65	-1.35
YGR239C	PEX21	1.00	-1.61	-1.45	-1.35
YLR271W		1.00	-1.68	-1.57	-1.35
YDR147W	EKI1	1.00	-1.70	-1.48	-1.35
YAL018C		1.00	-1.74	-2.14	-1.35
YIL169C		1.00	-2.13	-1.22	-1.35
YJL134W	LCB3	1.00	-2.26	-1.22	-1.35
YPL247C		1.00	1.16	-1.09	-1.36
YGL061C	DUO1	1.00	1.09	1.11	-1.36
YDR272W	GLO2	1.00	1.02	-1.20	-1.36
YFR041C		1.00	1.01	1.01	-1.36
YPL116W	HOS3	1.00	-1.03	-1.24	-1.36

YKL170W	MRPL38	1.00	-1.05	-1.13	-1.36
YGL091C	NBP35	1.00	-1.07	-1.03	-1.36
YIR038C	GTT1	1.00	-1.09	-1.22	-1.36
YDR088C	SLU7	1.00	-1.12	-1.12	-1.36
YOR147W		1.00	-1.18	1.01	-1.36
YJL011C		1.00	-1.19	-1.21	-1.36
YKR049C		1.00	-1.20	-1.26	-1.36
YLL032C		1.00	-1.32	-1.41	-1.36
YPL099C		1.00	-1.33	-1.04	-1.36
YOR070C	GYP1	1.00	-1.35	-1.22	-1.36
YFR018C		1.00	-1.44	-1.09	-1.36
YGR230W	BNS1	1.00	-1.47	-1.28	-1.36
YOL113W	SKM1	1.00	-1.49	-1.32	-1.36
YNL300W	TOS6	1.00	-1.52	-1.66	-1.36
YBR245C	ISW1	1.00	-1.55	-1.42	-1.36
YHL042W		1.00	-1.56	-1.47	-1.36
YIL018W	RPL2B	1.00	-1.61	-1.47	-1.36
YKR044W		1.00	-1.85	-1.60	-1.36
YOR113W	AZF1	1.00	-2.09	-1.31	-1.36
YOR242C	SSP2	1.00	-1.03	-1.29	-1.37
YNR045W	PET494	1.00	-1.04	-1.29	-1.37
YOR176W	HEM15	1.00	-1.10	-1.09	-1.37
YPL249C	GYP5	1.00	-1.10	-1.34	-1.37
YML118W	NGL3	1.00	-1.14	-1.08	-1.37
YPR106W	ISR1	1.00	-1.17	-1.03	-1.37
YMR135C		1.00	-1.20	-1.20	-1.37
YPR005C	HAL1	1.00	-1.20	-1.22	-1.37
YOR040W	GLO4	1.00	-1.21	-1.28	-1.37
YOR314W		1.00	-1.22	-1.34	-1.37
YIL006W		1.00	-1.24	-1.31	-1.37
YJL216C		1.00	-1.25	-1.23	-1.37
YHR118C	ORC6	1.00	-1.26	-1.18	-1.37
YJR082C		1.00	-1.29	-1.27	-1.37
YBL029W		1.00	-1.33	-1.46	-1.37
YCL073C		1.00	-1.33	-1.30	-1.37
YJR153W	PGU1	1.00	-1.33	-1.29	-1.37
YDR282C		1.00	-1.36	-1.32	-1.37
YDL058W	USO1	1.00	-1.38	-1.37	-1.37
YOR126C	IAH1	1.00	-1.38	-1.24	-1.37
YPL077C		1.00	-1.38	-1.43	-1.37
YLR410W	VIP1	1.00	-1.39	-1.36	-1.37
YMR019W	STB4	1.00	-1.39	-1.33	-1.37
YIL071C	PCI8	1.00	-1.40	-1.29	-1.37
YER083C		1.00	-1.41	-1.42	-1.37
YBL079W	NUP170	1.00	-1.43	-1.31	-1.37
YNL291C	MID1	1.00	-1.44	-1.31	-1.37
YHR112C		1.00	-1.45	-1.41	-1.37
YDR511W	ACN9	1.00	-1.46	-1.61	-1.37
YGR020C	VMA7	1.00	-1.46	-1.56	-1.37
YOR185C	GSP2	1.00	-1.48	-1.28	-1.37
YAR050W	FLO1	1.00	-1.49	-1.13	-1.37
YER137C		1.00	-1.49	-1.36	-1.37
YDR042C		1.00	-1.51	-1.25	-1.37
YGL163C	RAD54	1.00	-1.51	-1.53	-1.37
YOR214C		1.00	-1.51	-1.27	-1.37
YDR262W		1.00	-1.54	-1.24	-1.37
YCR028C	FEN2	1.00	-1.65	-1.76	-1.37
YGL118C		1.00	-1.66	-1.35	-1.37
YDR079W	PET100	1.00	-1.74	-1.32	-1.37
YKL225W		1.00	-1.84	-1.69	-1.37
YDR398W		1.00	-1.89	-1.78	-1.37

YNL142W	MEP2	1.00	-1.90	-1.45	-1.37
YKL083W		1.00	-2.07	-1.35	-1.37
YBL112C		1.00	-2.08	-1.30	-1.37
YDL238C		1.00	-2.11	-1.78	-1.37
YDL204W		1.00	1.44	1.11	-1.38
YEL059W		1.00	1.29	1.85	-1.38
YBL078C	AUT7	1.00	1.12	-1.21	-1.38
YNR036C		1.00	1.03	1.02	-1.38
YKL100C		1.00	-1.01	-1.04	-1.38
YPR141C	KAR3	1.00	-1.04	-1.17	-1.38
YDL139C	SCM3	1.00	-1.05	-1.39	-1.38
YGR077C	PEX8	1.00	-1.07	-1.45	-1.38
YDR509W		1.00	-1.12	1.11	-1.38
YLR191W	PEX13	1.00	-1.13	-1.34	-1.38
YDL187C		1.00	-1.16	-1.41	-1.38
YLR290C		1.00	-1.19	-1.21	-1.38
YPR042C	PUF2	1.00	-1.20	-1.36	-1.38
YCR064C		1.00	-1.22	-1.28	-1.38
YDR156W	RPA14	1.00	-1.22	-1.09	-1.38
YLL058W		1.00	-1.25	-1.47	-1.38
YOR358W	HAP5	1.00	-1.25	-1.35	-1.38
YIL113W		1.00	-1.26	-1.24	-1.38
YOL041C	NOP12	1.00	-1.26	-1.32	-1.38
YOR080W	DIA2	1.00	-1.27	-1.29	-1.38
YGL201C	MCM6	1.00	-1.32	-1.24	-1.38
YDL173W		1.00	-1.33	-1.33	-1.38
YKL101W	HSL1	1.00	-1.34	-1.43	-1.38
YOR378W		1.00	-1.37	-1.31	-1.38
YGR235C		1.00	-1.39	-1.01	-1.38
YGR281W	YOR1	1.00	-1.40	-1.48	-1.38
YIL029C		1.00	-1.44	-1.29	-1.38
YLR382C	NAM2	1.00	-1.45	-1.24	-1.38
YPL009C		1.00	-1.52	-1.30	-1.38
YDR484W	SAC2	1.00	-1.57	-1.40	-1.38
YNL020C	ARK1	1.00	-1.58	-1.41	-1.38
YDR056C		1.00	-1.59	-1.45	-1.38
YOR105W		1.00	-1.64	-1.43	-1.38
YOR219C	STE13	1.00	-1.68	-1.26	-1.38
YLR323C		1.00	-1.73	-1.58	-1.38
YLR140W		1.00	-1.77	-1.61	-1.38
YDR433W	KRE22	1.00	-1.79	-1.66	-1.38
YDL140C	RPO21	1.00	-1.83	-1.70	-1.38
YMR110C		1.00	1.17	1.07	-1.39
YPR148C		1.00	1.14	1.20	-1.39
YGR087C	PDC6	1.00	1.07	1.38	-1.39
YOL150C		1.00	-1.03	-1.24	-1.39
YDR368W	YPR1	1.00	-1.07	-1.13	-1.39
YNL125C	ESBP6	1.00	-1.09	-1.29	-1.39
YGR016W		1.00	-1.11	-1.29	-1.39
YKR055W	RHO4	1.00	-1.11	-1.23	-1.39
YIL158W		1.00	-1.13	-1.25	-1.39
YLR072W		1.00	-1.15	-1.21	-1.39
YGR109C	CLB6	1.00	-1.16	-1.24	-1.39
YNL097C	PHO23	1.00	-1.18	-1.35	-1.39
YML097C	VPS9	1.00	-1.21	-1.28	-1.39
YBR294W	SUL1	1.00	-1.23	-1.21	-1.39
YKL185W	ASH1	1.00	-1.30	-1.23	-1.39
YER119C		1.00	-1.31	-1.35	-1.39
YML012W	ERV25	1.00	-1.32	-1.30	-1.39
YGR053C		1.00	-1.37	-1.30	-1.39
YNL324W		1.00	-1.37	-1.45	-1.39

YDR386W	MUS81	1.00	-1.38	-1.39	-1.39
YKL171W		1.00	-1.43	-1.18	-1.39
YKL038W	RGT1	1.00	-1.47	-1.38	-1.39
YLR450W	HMG2	1.00	-1.48	-1.37	-1.39
YIL084C	SDS3	1.00	-1.52	-1.41	-1.39
YJL178C		1.00	-1.53	-1.45	-1.39
YDL233W		1.00	-1.59	-1.17	-1.39
YDR388W	RVS167	1.00	-1.79	-1.46	-1.39
YFL050C	ALR2	1.00	-1.84	-1.28	-1.39
YDR384C		1.00	-2.64	-1.95	-1.39
YNL315C	ATP11	1.00	-1.09	-1.23	-1.40
YIL100W		1.00	-1.10	-1.39	-1.40
YKL196C	YKT6	1.00	-1.13	-1.26	-1.40
YBR241C		1.00	-1.15	-1.33	-1.40
YDR031W		1.00	-1.16	-1.46	-1.40
YBR128C	APG14	1.00	-1.23	-1.32	-1.40
YLR288C	MEC3	1.00	-1.25	-1.25	-1.40
YDR113C	PDS1	1.00	-1.29	-1.28	-1.40
YIL019W		1.00	-1.29	-1.25	-1.40
YMR268C	PRP24	1.00	-1.33	-1.25	-1.40
YPR122W	AXL1	1.00	-1.34	-1.37	-1.40
YDR493W		1.00	-1.40	-1.47	-1.40
YIL167W		1.00	-1.40	-1.42	-1.40
YCR098C	GIT1	1.00	-1.42	-1.68	-1.40
YLR026C	SED5	1.00	-1.42	-1.47	-1.40
YNL024C		1.00	-1.42	-1.47	-1.40
YPR189W	SKI3	1.00	-1.50	-1.60	-1.40
YBR109C	CMD1	1.00	-1.53	-1.86	-1.40
YCR043C		1.00	-1.54	-1.35	-1.40
YJL024C	APS3	1.00	-1.64	-1.42	-1.40
YPR068C	HOS1	1.00	-1.68	-1.58	-1.40
YBR207W	FTH1	1.00	-1.69	-1.74	-1.40
YNL120C		1.00	-1.69	-1.63	-1.40
YKL054C	VID31	1.00	-1.72	-1.59	-1.40
YJR051W	OSM1	1.00	-3.40	-1.65	-1.40
YPR124W	CTR1	1.00	1.05	-1.03	-1.41
YKL138C	MRPL31	1.00	1.02	-1.10	-1.41
YOL082W	CVT19	1.00	-1.01	-1.16	-1.41
YBL054W		1.00	-1.03	-1.26	-1.41
YLR270W		1.00	-1.07	-1.30	-1.41
YPL110C		1.00	-1.08	-1.16	-1.41
YJL164C	TPK1	1.00	-1.11	-1.09	-1.41
YBR028C		1.00	-1.18	-1.45	-1.41
YJR034W	PET191	1.00	-1.20	-1.39	-1.41
YBR022W		1.00	-1.23	-1.47	-1.41
YJL022W		1.00	-1.26	-1.19	-1.41
YJL107C		1.00	-1.28	-1.40	-1.41
YKR070W		1.00	-1.31	-1.24	-1.41
YML055W	SPC2	1.00	-1.31	-1.20	-1.41
YIL022W	TIM44	1.00	-1.33	-1.27	-1.41
YDR494W	RCT1	1.00	-1.37	-1.34	-1.41
YGL071W	RCS1	1.00	-1.40	-1.37	-1.41
YER002W		1.00	-1.44	-1.31	-1.41
YJL184W		1.00	-1.44	-1.42	-1.41
YOR245C	DGA1	1.00	-1.44	-1.40	-1.41
YHR085W		1.00	-1.45	-1.65	-1.41
YAR035W	YAT1	1.00	-1.50	-1.57	-1.41
YDR208W	MSS4	1.00	-1.52	-1.52	-1.41
YLR235C		1.00	-1.56	-1.49	-1.41
YDR107C		1.00	-1.59	-1.52	-1.41
YGR294W		1.00	-1.67	-1.32	-1.41

YDR194C	MSS116	1.00	-1.68	-1.71	-1.41
YJL025W	RRN7	1.00	-1.70	-1.63	-1.41
YGR250C		1.00	-1.99	-1.45	-1.41
YBL070C		1.00	-2.36	-2.24	-1.41
YBR184W		1.00	-3.16	-2.25	-1.41
YPL004C		1.00	1.70	1.94	-1.42
YGR236C	SPG1	1.00	1.48	-1.02	-1.42
YPL193W	RSA1	1.00	1.16	1.00	-1.42
YPR052C	NHP6A	1.00	1.03	1.03	-1.42
YCL033C		1.00	-1.03	-1.35	-1.42
YCR107W	AAD3	1.00	-1.04	-1.11	-1.42
YMR157C		1.00	-1.07	-1.24	-1.42
YIL098C	FMC1	1.00	-1.11	-1.21	-1.42
YMR293C		1.00	-1.15	-1.49	-1.42
YDR491C		1.00	-1.22	-1.09	-1.42
YLR295C	ATP14	1.00	-1.24	-1.07	-1.42
YNL121C	TOM70	1.00	-1.26	-1.41	-1.42
YER099C	PRS2	1.00	-1.28	-1.76	-1.42
YLR020C		1.00	-1.29	-1.54	-1.42
YDL032W		1.00	-1.33	-1.57	-1.42
YKL092C	BUD2	1.00	-1.37	-1.38	-1.42
YDR060W		1.00	-1.40	-1.35	-1.42
YJL058C		1.00	-1.41	-1.31	-1.42
YHR195W	NVJ1	1.00	-1.43	-1.61	-1.42
YJR133W	XPT1	1.00	-1.47	-1.70	-1.42
YBR235W		1.00	-1.48	-1.43	-1.42
YPR067W	ISA2	1.00	-1.58	-1.36	-1.42
YJR037W		1.00	-1.70	-1.83	-1.42
YDR008C		1.00	-1.71	-1.57	-1.42
YAL056W	GPE2	1.00	-1.73	-1.77	-1.42
YDR483W	KRE2	1.00	-1.74	-1.44	-1.42
YHR110W	ERP5	1.00	-1.76	-1.59	-1.42
YMR158W		1.00	-1.82	-1.41	-1.42
YER105C	NUP157	1.00	-1.99	-1.47	-1.42
YOR237W	HES1	1.00	-2.01	-1.51	-1.42
YNL171C		1.00	-2.04	-1.54	-1.42
YNL077W		1.00	-2.06	-1.68	-1.42
YCL042W		1.00	1.38	-1.11	-1.43
YHR126C		1.00	1.10	-1.24	-1.43
YIL157C		1.00	-1.07	-1.21	-1.43
YJR108W	ABM1	1.00	-1.11	-1.20	-1.43
YPL114W		1.00	-1.14	-1.31	-1.43
YOL114C		1.00	-1.15	-1.26	-1.43
YCR076C		1.00	-1.16	-1.17	-1.43
YMR257C	PET111	1.00	-1.17	-1.44	-1.43
YER128W		1.00	-1.18	-1.27	-1.43
YLR417W	VPS36	1.00	-1.18	-1.48	-1.43
YBR114W	RAD16	1.00	-1.20	-1.29	-1.43
YPL189W	GUP2	1.00	-1.31	-1.31	-1.43
YML090W		1.00	-1.38	-1.51	-1.43
YER142C	MAG1	1.00	-1.40	-1.34	-1.43
YGR187C	HGH1	1.00	-1.46	-1.55	-1.43
YKL183W	LOT5	1.00	-1.47	-1.48	-1.43
YOR254C	SEC63	1.00	-1.48	-1.63	-1.43
YER053C		1.00	-1.50	-1.54	-1.43
YPL027W	SMA1	1.00	-1.54	-1.30	-1.43
YOR102W		1.00	-1.90	-1.70	-1.43
YGL047W		1.00	-1.91	-1.55	-1.43
YJR099W	YUH1	1.00	-2.16	-1.54	-1.43
YER138C		1.00	-2.19	-2.21	-1.43
YJL133W	MRS3	1.00	-2.19	-1.35	-1.43

YEL048C		1.00	1.08	1.32	-1.44
YHR198C		1.00	-1.04	-1.24	-1.44
YNL200C		1.00	-1.04	-1.09	-1.44
YMR281W	GPI12	1.00	-1.13	-1.18	-1.44
YJR118C	ILM1	1.00	-1.14	-1.34	-1.44
YCL024W	KCC4	1.00	-1.17	-1.20	-1.44
YOR343C		1.00	-1.21	-1.32	-1.44
YIL146C	ECM37	1.00	-1.25	-1.28	-1.44
YLR084C	RAX2	1.00	-1.25	-1.34	-1.44
YPL150W		1.00	-1.25	-1.36	-1.44
YBL066C	SEF1	1.00	-1.32	-1.44	-1.44
YJL132W		1.00	-1.34	-1.36	-1.44
YLR430W	SEN1	1.00	-1.34	-1.36	-1.44
YOR258W	HNT3	1.00	-1.35	-1.15	-1.44
YLR234W	TOP3	1.00	-1.36	-1.39	-1.44
YBR045C	GIP1	1.00	-1.40	-1.50	-1.44
YJR083C		1.00	-1.48	-1.35	-1.44
YJL007C		1.00	-1.55	-1.47	-1.44
YOR086C		1.00	-1.57	-1.28	-1.44
YDR295C	PLO2	1.00	-1.62	-1.77	-1.44
YNL196C	SLZ1	1.00	-1.66	-1.69	-1.44
YEL076C		1.00	-1.75	-1.43	-1.44
YGR019W	UGA1	1.00	-1.82	-1.25	-1.44
YER067W		1.00	1.76	2.80	-1.45
YGR248W	SOL4	1.00	1.58	1.02	-1.45
YBL090W	MRP21	1.00	1.03	-1.11	-1.45
YKL194C	MST1	1.00	-1.10	-1.19	-1.45
YNL045W		1.00	-1.11	-1.10	-1.45
YMR139W	RIM11	1.00	-1.14	-1.19	-1.45
YOR281C	PLP2	1.00	-1.21	-1.67	-1.45
YNL137C	NAM9	1.00	-1.27	-1.24	-1.45
YNL318C	HXT14	1.00	-1.29	-1.34	-1.45
YDR104C	SPO71	1.00	-1.31	-1.36	-1.45
YOR064C	YNG1	1.00	-1.32	-1.56	-1.45
YDL019C	OSH2	1.00	-1.33	-1.16	-1.45
YMR168C	CEP3	1.00	-1.34	-1.71	-1.45
YJL120W		1.00	-1.37	-1.43	-1.45
YFR007W		1.00	-1.41	-1.32	-1.45
YGR291C		1.00	-1.57	-1.53	-1.45
YLR280C		1.00	-1.63	-1.37	-1.45
YDL244W	THI13	1.00	-1.81	-1.35	-1.45
YCR038C	BUD5	1.00	-1.88	-1.71	-1.45
YJR005W	APL1	1.00	-2.11	-1.63	-1.45
YER118C	SHO1	1.00	-2.12	-1.54	-1.45
YDR414C	ERD1	1.00	-2.38	-1.50	-1.45
YJL142C		1.00	1.10	1.12	-1.46
YIL055C		1.00	1.03	-1.21	-1.46
YPR056W	TFB4	1.00	-1.05	-1.18	-1.46
YHR097C		1.00	-1.06	1.08	-1.46
YLR203C	MSS51	1.00	-1.07	-1.26	-1.46
YOR054C		1.00	-1.09	-1.16	-1.46
YOR328W	PDR10	1.00	-1.10	-1.32	-1.46
YGR290W		1.00	-1.24	-1.22	-1.46
YER180C	ISC10	1.00	-1.25	-1.36	-1.46
YLR399C	BDF1	1.00	-1.26	-1.50	-1.46
YGR045C		1.00	-1.31	-1.26	-1.46
YGL155W	CDC43	1.00	-1.34	-1.27	-1.46
YPR021C		1.00	-1.34	-1.31	-1.46
YJR097W		1.00	-1.36	-1.45	-1.46
YPL121C	MEI5	1.00	-1.38	-1.34	-1.46
YKR029C		1.00	-1.39	-1.38	-1.46

YBR208C	DUR1,2	1.00	-1.42	-1.90	-1.46
YIL065C	FIS1	1.00	-1.42	-1.40	-1.46
YHR056C	RSC30	1.00	-1.43	-1.29	-1.46
YNL011C		1.00	-1.43	-1.37	-1.46
YKL119C	VPH2	1.00	-1.47	-1.51	-1.46
YKR041W		1.00	-1.50	-1.45	-1.46
YIL031W	ULP2	1.00	-1.51	-1.34	-1.46
YLR047C		1.00	-1.52	-1.65	-1.46
YDR327W		1.00	-1.79	-1.13	-1.46
YER082C	KRE31	1.00	-1.80	-1.83	-1.46
YKL047W		1.00	-2.01	-1.65	-1.46
YNL264C	PDR17	1.00	-2.01	-1.87	-1.46
YER040W	GLN3	1.00	-2.08	-1.90	-1.46
YLR395C	COX8	1.00	-1.05	-1.19	-1.47
YHR164C	DNA2	1.00	-1.09	-1.19	-1.47
YFL024C	EPL1	1.00	-1.15	-1.43	-1.47
YLR423C	APG17	1.00	-1.15	-1.20	-1.47
YKL137W		1.00	-1.18	-1.25	-1.47
YAR019C	CDC15	1.00	-1.24	-1.32	-1.47
YHR137W	ARO9	1.00	-1.34	-1.31	-1.47
YOR124C	UBP2	1.00	-1.37	-1.42	-1.47
YDR316W		1.00	-1.49	-1.48	-1.47
YOR138C		1.00	-1.54	-1.34	-1.47
YBR293W		1.00	-1.76	-2.24	-1.47
YKL178C	STE3	1.00	-1.77	-1.36	-1.47
YNL076W	MKS1	1.00	-1.86	-1.72	-1.47
YDR059C	UBC5	1.00	-2.10	-1.64	-1.47
YJR063W	RPA12	1.00	-2.10	-1.71	-1.47
YKL058W	TOA2	1.00	-2.31	-1.91	-1.47
YDR371W		1.00	-1.11	1.07	-1.48
YCL064C	CHA1	1.00	-1.13	-1.34	-1.48
YOR324C		1.00	-1.18	-1.41	-1.48
YDR016C	DAD1	1.00	-1.19	-1.35	-1.48
YIL088C		1.00	-1.24	-1.19	-1.48
YCR032W	BPH1	1.00	-1.27	-1.43	-1.48
YGL088W		1.00	-1.27	-1.31	-1.48
YJL102W	MEF2	1.00	-1.28	-1.41	-1.48
YDR498C	SEC20	1.00	-1.29	-1.47	-1.48
YGR247W		1.00	-1.30	-1.17	-1.48
YMR178W		1.00	-1.33	-1.28	-1.48
YGR023W	MTL1	1.00	-1.41	-1.14	-1.48
YPR045C		1.00	-1.46	-1.45	-1.48
YAR068W		1.00	-1.47	-1.62	-1.48
YMR047C	NUP116	1.00	-1.48	-1.62	-1.48
YEL065W	SIT1	1.00	-1.68	-1.39	-1.48
YKL057C	NUP120	1.00	-1.71	-1.66	-1.48
YLR116W	MSL5	1.00	-2.00	-1.46	-1.48
YNL194C		1.00	1.40	1.23	-1.49
YPR001W	CIT3	1.00	-1.08	-1.42	-1.49
YJL068C		1.00	-1.16	-1.13	-1.49
YLL059C		1.00	-1.20	-1.49	-1.49
YIL070C	MAM33	1.00	-1.22	-1.16	-1.49
YMR141C		1.00	-1.22	-1.27	-1.49
YER030W		1.00	-1.27	-1.05	-1.49
YGR238C	KEL2	1.00	-1.30	-1.29	-1.49
YJR045C	SSC1	1.00	-1.30	-1.23	-1.49
YPR003C		1.00	-1.32	-1.34	-1.49
YDR214W		1.00	-1.33	-1.44	-1.49
YIL007C		1.00	-1.35	-1.52	-1.49
YER071C		1.00	-1.39	-1.48	-1.49
YKL073W	LHS1	1.00	-1.39	-1.50	-1.49

YLL002W	REM50	1.00	-1.40	-1.26	-1.49
YLR008C		1.00	-1.42	-1.63	-1.49
YCR094W	CDC50	1.00	-1.44	-1.75	-1.49
YML092C	PRE8	1.00	-1.47	-1.79	-1.49
YDR283C	GCN2	1.00	-1.50	-1.77	-1.49
YIL174W		1.00	-1.53	-1.36	-1.49
YDL149W	APG9	1.00	-1.57	-1.36	-1.49
YPL170W		1.00	-1.57	-1.63	-1.49
YGR031W		1.00	-1.65	-1.38	-1.49
YGR030C	POP6	1.00	-1.71	-1.76	-1.49
YGR017W		1.00	-1.72	-1.44	-1.49
YGR198W		1.00	-1.81	-1.27	-1.49
YNL012W	SPO1	1.00	-1.88	-1.60	-1.49
YNL172W	APC1	1.00	-2.48	-1.90	-1.49
YIL160C	POT1	1.00	1.15	-1.23	-1.50
YKL163W	PIR3	1.00	1.10	1.30	-1.50
YCR071C	IMG2	1.00	1.02	-1.04	-1.50
YIR037W	HYR1	1.00	-1.06	-1.20	-1.50
YJL070C		1.00	-1.10	-1.24	-1.50
YJL095W	BCK1	1.00	-1.12	-1.46	-1.50
YMR162C		1.00	-1.19	-1.49	-1.50
YOR373W	NUD1	1.00	-1.20	-1.44	-1.50
YIL066C	RNR3	1.00	-1.30	-1.54	-1.50
YBR023C	CHS3	1.00	-1.36	-1.67	-1.50
YPL005W		1.00	-1.39	-1.56	-1.50
YJL156C	SSY5	1.00	-1.42	-1.63	-1.50
YKL203C	TOR2	1.00	-1.46	-1.38	-1.50
YKL007W	CAP1	1.00	-1.48	-1.29	-1.50
YLR451W	LEU3	1.00	-1.50	-1.86	-1.50
YIR002C	MPH1	1.00	-1.54	-1.30	-1.50
YDR435C	PPM1	1.00	-1.61	-1.40	-1.50
YLL037W		1.00	-1.85	-1.67	-1.50
YKL202W		1.00	-1.93	-1.78	-1.50
YDR425W		1.00	-2.02	-1.60	-1.50
YEL014C		1.00	1.08	-1.07	-1.51
YER134C		1.00	1.05	1.11	-1.51
YNL284C	MRPL10	1.00	-1.01	-1.31	-1.51
YOR055W		1.00	-1.13	-1.17	-1.51
YAL049C		1.00	-1.17	-1.13	-1.51
YOR394W		1.00	-1.21	-1.17	-1.51
YPR140W		1.00	-1.21	-1.12	-1.51
YJR067C	YAE1	1.00	-1.23	-1.45	-1.51
YER162C	RAD4	1.00	-1.35	-1.31	-1.51
YJR060W	CBF1	1.00	-1.35	-1.47	-1.51
YLR013W	GAT3	1.00	-1.39	-1.66	-1.51
YDR009W	GAL3	1.00	-1.40	-1.41	-1.51
YOR137C		1.00	-1.43	-1.42	-1.51
YLR406C	RPL31B	1.00	-1.45	-1.47	-1.51
YOL101C		1.00	-1.47	-1.47	-1.51
YDR207C	UME6	1.00	-1.55	-1.77	-1.51
YLR141W	RRN5	1.00	-1.57	-1.55	-1.51
YGR199W	PMT6	1.00	-1.62	-1.96	-1.51
YFR047C		1.00	-1.63	-1.59	-1.51
YLR107W	REX3	1.00	-1.83	-1.58	-1.51
YGR173W		1.00	-1.87	-1.69	-1.51
YDR204W	COQ4	1.00	-2.61	-1.83	-1.51
YOR120W	GCY1	1.00	1.03	-1.13	-1.52
YJL067W		1.00	-1.07	-1.35	-1.52
YNL128W	TEP1	1.00	-1.17	-1.33	-1.52
YAL062W	GDH3	1.00	-1.19	-1.27	-1.52
YDL107W	MSS2	1.00	-1.22	-1.36	-1.52

YMR187C		1.00	-1.22	-1.42	-1.52
YGL094C	PAN2	1.00	-1.25	-1.25	-1.52
YGL165C		1.00	-1.33	-1.35	-1.52
YOR315W		1.00	-1.35	-1.60	-1.52
YLR146C	SPE4	1.00	-1.36	-1.50	-1.52
YOR041C		1.00	-1.36	-1.26	-1.52
YNL139C	RLR1	1.00	-1.37	-1.27	-1.52
YKL204W	EAP1	1.00	-1.44	-1.23	-1.52
YOR255W		1.00	-1.44	-1.31	-1.52
YKL221W		1.00	-1.49	-1.50	-1.52
YFL051C		1.00	-1.52	-1.37	-1.52
YBL017C	PEP1	1.00	-1.56	-1.61	-1.52
YCR040W	MATALPHA1	1.00	-1.56	-1.78	-1.52
YOR180C	DCI1	1.00	-1.56	-1.38	-1.52
YCL074W		1.00	-1.59	-1.38	-1.52
YAR009C		1.00	-1.60	-1.15	-1.52
YDR154C		1.00	-1.60	-1.56	-1.52
YLL019C	KNS1	1.00	-1.60	-1.12	-1.52
YDR195W	REF2	1.00	-1.63	-1.81	-1.52
YLR306W	UBC12	1.00	-1.64	-1.33	-1.52
YDR383C		1.00	-1.65	-1.36	-1.52
YDR093W		1.00	-1.69	-1.66	-1.52
YOL148C	SPT20	1.00	-1.72	-1.61	-1.52
YGR224W	AZR1	1.00	-1.74	-1.78	-1.52
YLR012C		1.00	-1.74	-1.73	-1.52
YNL197C	WHI3	1.00	-1.99	-1.95	-1.52
YKR026C	GCN3	1.00	-2.14	-1.76	-1.52
YDR387C		1.00	-2.16	-1.93	-1.52
YAL041W	CDC24	1.00	-2.29	-1.50	-1.52
YDR086C	SSS1	1.00	1.04	-1.17	-1.53
YPL236C		1.00	-1.20	-1.35	-1.53
YPL118W	MRP51	1.00	-1.21	-1.41	-1.53
YIL111W	COX5B	1.00	-1.24	-1.15	-1.53
YKL003C	MRP17	1.00	-1.25	-1.41	-1.53
YIL097W	FYV10	1.00	-1.26	-1.38	-1.53
YOR257W	CDC31	1.00	-1.27	-1.39	-1.53
YJL096W	MRPL49	1.00	-1.32	-1.40	-1.53
YMR287C	MSU1	1.00	-1.33	-1.19	-1.53
YCR087W		1.00	-1.43	-1.64	-1.53
YMR057C		1.00	-1.43	-1.60	-1.53
YNL199C	GCR2	1.00	-1.45	-1.46	-1.53
YDR308C	SRB7	1.00	-1.47	-1.78	-1.53
YIR015W	RPR2	1.00	-1.48	-1.52	-1.53
YKL123W		1.00	-1.50	-1.45	-1.53
YMR052W	FAR3	1.00	-1.54	-1.37	-1.53
YMR190C	SGS1	1.00	-1.60	-1.53	-1.53
YDR117C		1.00	-1.63	-1.48	-1.53
YOL134C		1.00	-1.63	-1.62	-1.53
YDR127W	ARO1	1.00	-1.75	-1.89	-1.53
YKR093W	PTR2	1.00	-1.88	-2.01	-1.53
YPR184W	GDB1	1.00	1.71	1.21	-1.54
YBR117C	TKL2	1.00	1.30	-1.37	-1.54
YDL004W	ATP16	1.00	1.21	1.01	-1.54
YLR202C		1.00	-1.16	-1.43	-1.54
YPR070W	MED1	1.00	-1.16	-1.38	-1.54
YDL234C	GYP7	1.00	-1.23	-1.08	-1.54
YFR013W	IOC3	1.00	-1.26	-1.49	-1.54
YJL112W	MDV1	1.00	-1.28	-1.39	-1.54
YGR015C		1.00	-1.31	-1.44	-1.54
YGR194C	XKS1	1.00	-1.35	-1.61	-1.54
YIL064W		1.00	-1.39	-1.65	-1.54

YLR142W	PUT1	1.00	-1.47	-1.38	-1.54
YNL028W		1.00	-1.61	-1.55	-1.54
YJR093C	FIP1	1.00	-1.66	-1.64	-1.54
YOR282W		1.00	-1.81	-1.64	-1.54
YDR215C		1.00	-2.49	-2.23	-1.54
YDR510W	SMT3	1.00	-2.64	-1.59	-1.54
YEL011W	GLC3	1.00	1.52	2.17	-1.55
YPL061W	ALD6	1.00	1.46	2.22	-1.55
YGR183C	QCR9	1.00	1.05	1.21	-1.55
YKR076W	ECM4	1.00	-1.13	-1.11	-1.55
YER182W		1.00	-1.16	-1.28	-1.55
YPL216W		1.00	-1.28	-1.37	-1.55
YIL089W		1.00	-1.29	-1.44	-1.55
YNL023C	FAP1	1.00	-1.35	-1.46	-1.55
YLR305C	STT4	1.00	-1.49	-1.44	-1.55
YBR151W	APD1	1.00	-1.65	-1.60	-1.55
YMR160W		1.00	-1.94	-2.10	-1.55
YMR209C		1.00	-2.10	-1.88	-1.55
YMR261C	TPS3	1.00	-1.07	-1.30	-1.56
YEL067C		1.00	-1.19	-1.29	-1.56
YIR027C	DAL1	1.00	-1.19	-1.29	-1.56
YKL121W		1.00	-1.27	-1.20	-1.56
YLR122C		1.00	-1.27	-1.58	-1.56
YDR203W		1.00	-1.28	-1.13	-1.56
YDR219C		1.00	-1.34	-1.41	-1.56
YDR462W	MRPL28	1.00	-1.35	-1.30	-1.56
YKR062W	TFA2	1.00	-1.35	-1.32	-1.56
YLR206W	ENT2	1.00	-1.37	-1.22	-1.56
YGL075C	MPS2	1.00	-1.46	-1.40	-1.56
YOR285W		1.00	1.23	1.10	-1.57
YBR026C	MRF1'	1.00	1.02	-1.44	-1.57
YNL009W	IDP3	1.00	-1.01	-1.23	-1.57
YAL055W	PEX22	1.00	-1.04	-1.43	-1.57
YFL019C		1.00	-1.12	-1.21	-1.57
YJR096W		1.00	-1.23	-1.48	-1.57
YGL143C	MRF1	1.00	-1.28	-1.33	-1.57
YIR003W		1.00	-1.32	-1.22	-1.57
YLR433C	CNA1	1.00	-1.36	-1.37	-1.57
YKR088C		1.00	-1.44	-1.23	-1.57
YOL071W		1.00	-1.66	-1.48	-1.57
YOR188W	MSB1	1.00	-1.66	-1.50	-1.57
YKR053C	YSR3	1.00	-1.86	-1.57	-1.57
YGR256W	GND2	1.00	1.23	-1.10	-1.58
YCL028W	RNQ1	1.00	1.11	-1.33	-1.58
YDL172C		1.00	-1.10	-1.18	-1.58
YGR156W	PTI1	1.00	-1.16	-1.40	-1.58
YIL087C		1.00	-1.20	-1.19	-1.58
YGL237C	HAP2	1.00	-1.26	-1.24	-1.58
YGR021W		1.00	-1.30	-1.32	-1.58
YKL108W	SLD2	1.00	-1.30	-1.28	-1.58
YGR039W		1.00	-1.37	-1.59	-1.58
YLR364W		1.00	-1.41	-1.68	-1.58
YML043C	RRN11	1.00	-1.47	-1.11	-1.58
YKL102C		1.00	-1.50	-1.61	-1.58
YLR092W	SUL2	1.00	-1.55	-1.69	-1.58
YJL153C	INO1	1.00	-1.60	-1.72	-1.58
YMR156C	TPP1	1.00	-1.68	-1.44	-1.58
YKL115C		1.00	-1.99	-1.69	-1.58
YNL184C		1.00	-2.24	-2.00	-1.58
YJR039W		1.00	-2.29	-1.89	-1.58
YGR070W	ROM1	1.00	-1.06	-1.52	-1.59

YMR284W	YKU70	1.00	-1.22	-1.44	-1.59
YJR074W	MOG1	1.00	-1.25	-1.58	-1.59
YOR163W	DDP1	1.00	-1.26	-1.26	-1.59
YOR333C		1.00	-1.26	-1.57	-1.59
YLR097C		1.00	-1.28	-1.47	-1.59
YDR136C		1.00	-1.30	-1.46	-1.59
YLL027W	ISA1	1.00	-1.30	-1.40	-1.59
YMR048W	CSM3	1.00	-1.38	-1.46	-1.59
YMR282C	AEP2	1.00	-1.43	-1.40	-1.59
YMR071C		1.00	-1.70	-1.38	-1.59
YHR034C		1.00	-1.84	-1.74	-1.59
YLR426W		1.00	-1.85	-1.71	-1.59
YFR033C	QCR6	1.00	1.28	1.12	-1.60
YKL016C	ATP7	1.00	1.22	1.16	-1.60
YNL211C		1.00	-1.13	-1.22	-1.60
YGR004W		1.00	-1.24	-1.12	-1.60
YJR132W	NMD5	1.00	-1.26	-1.19	-1.60
YKR010C	TOF2	1.00	-1.27	-1.67	-1.60
YJR151C	DAN4	1.00	-1.33	-1.62	-1.60
YOR125C	CAT5	1.00	-1.35	-1.39	-1.60
YOR150W	MRPL23	1.00	-1.35	-1.40	-1.60
YJL094C	KHA1	1.00	-1.37	-1.44	-1.60
YGR099W	TEL2	1.00	-1.39	-1.49	-1.60
YBR234C	ARC40	1.00	-1.41	-1.60	-1.60
YGR060W	ERG25	1.00	-1.41	-1.28	-1.60
YKL113C	RAD27	1.00	-1.48	-1.47	-1.60
YDR296W	MHR1	1.00	-1.49	-1.45	-1.60
YJL137C	GLG2	1.00	-1.52	-1.64	-1.60
YER152C		1.00	-1.55	-1.18	-1.60
YDR054C	CDC34	1.00	-1.70	-1.39	-1.60
YJR159W	SOR1	1.00	-1.80	-1.76	-1.60
YGL257C	MNT2	1.00	-1.81	-1.97	-1.60
YBR067C	TIP1	1.00	-2.15	-1.94	-1.60
YKL224C		1.00	-2.47	-2.00	-1.60
YNR016C	ACC1	1.00	-3.04	-1.83	-1.60
YER171W	RAD3	1.00	-1.28	-1.44	-1.61
YER141W	COX15	1.00	-1.41	-1.41	-1.61
YBR210W		1.00	-1.46	-1.59	-1.61
YIL168W	SDL1	1.00	-1.49	-1.60	-1.61
YDR175C	RSM24	1.00	-1.51	-1.49	-1.61
YPR016C	TIF6	1.00	-1.52	-1.71	-1.61
YJR156C	THI11	1.00	-1.55	-1.60	-1.61
YIL126W	STH1	1.00	-1.57	-1.71	-1.61
YNL173C	MDG1	1.00	-1.64	-1.34	-1.61
YCL041C		1.00	-1.75	-1.49	-1.61
YKR002W	PAP1	1.00	-1.79	-1.98	-1.61
YHR121W		1.00	-1.91	-1.51	-1.61
YJL181W		1.00	-2.05	-2.05	-1.61
YJR142W		1.00	-2.23	-1.63	-1.61
YKL118W		1.00	-2.51	-1.83	-1.61
YDL181W	INH1	1.00	1.04	1.01	-1.62
YDR196C		1.00	-1.13	-1.18	-1.62
YDL016C		1.00	-1.30	-1.49	-1.62
YER091C	MET6	1.00	-1.31	1.14	-1.62
YBR209W		1.00	-1.32	-1.67	-1.62
YMR266W	RSN1	1.00	-1.34	-1.62	-1.62
YJL176C	SWI3	1.00	-1.35	-1.67	-1.62
YJL081C	ARP4	1.00	-1.36	-1.38	-1.62
YPL200W	CSM4	1.00	-1.39	-1.64	-1.62
YER085C		1.00	-1.48	-1.79	-1.62
YIR036C		1.00	-1.50	-1.27	-1.62

YFL056C	AAD6	1.00	-1.60	-1.26	-1.62
YML061C	PIF1	1.00	-1.62	-1.74	-1.62
YMR233W		1.00	-1.62	-1.48	-1.62
YLR024C	UBR2	1.00	-1.64	-1.69	-1.62
YDL135C	RDI1	1.00	-1.69	-1.38	-1.62
YLR384C	IKI3	1.00	-1.69	-1.97	-1.62
YDR168W	CDC37	1.00	-1.79	-1.38	-1.62
YCL032W	STE50	1.00	-1.90	-1.89	-1.62
YOR339C	UBC11	1.00	-2.03	-2.00	-1.62
YHR109W	CTM1	1.00	-2.30	-1.60	-1.62
YJL145W		1.00	-2.45	-1.73	-1.62
YPR149W	NCE102	1.00	1.27	1.03	-1.63
YDL044C	MTF2	1.00	1.26	-1.39	-1.63
YAL063C	FLO9	1.00	-1.06	-1.15	-1.63
YPL153C	RAD53	1.00	-1.16	-1.44	-1.63
YNL133C	FYV6	1.00	-1.17	-1.55	-1.63
YOR142W	LSC1	1.00	-1.38	-1.40	-1.63
YJL202C		1.00	-1.40	-1.53	-1.63
YJL215C		1.00	-1.48	-1.65	-1.63
YJR087W		1.00	-1.51	-1.58	-1.63
YOR038C	HIR2	1.00	-1.55	-1.71	-1.63
YDR095C		1.00	-1.62	-1.51	-1.63
YOL110W	SHR5	1.00	-1.72	-1.69	-1.63
YLR289W	GUF1	1.00	-1.73	-1.47	-1.63
YKL087C	CYT2	1.00	-1.77	-1.56	-1.63
YML122C		1.00	-1.78	-1.50	-1.63
YER054C	GIP2	1.00	-2.00	-1.73	-1.63
YKR040C		1.00	-2.27	-1.85	-1.63
YKR067W	GPT2	1.00	1.03	-1.27	-1.64
YJL163C		1.00	-1.30	-1.44	-1.64
YKR090W		1.00	-1.40	-1.51	-1.64
YPR047W	MSF1	1.00	-1.40	-1.36	-1.64
YIL099W	SGA1	1.00	-1.51	-1.61	-1.64
YOR359W		1.00	-1.59	-1.61	-1.64
YPR097W		1.00	-1.67	-1.68	-1.64
YDR103W	STE5	1.00	-1.70	-1.90	-1.64
YMR070W	MOT3	1.00	-1.72	-1.75	-1.64
YKR012C		1.00	-1.78	-1.68	-1.64
YLR400W		1.00	-1.79	-1.44	-1.64
YER033C	ZRG8	1.00	-1.81	-1.89	-1.64
YDR150W	NUM1	1.00	-2.02	-1.78	-1.64
YHR038W	FIL1	1.00	-2.05	-1.54	-1.64
YNL130C	CPT1	1.00	1.06	-1.21	-1.65
YMR083W	ADH3	1.00	-1.15	-1.15	-1.65
YLR315W		1.00	-1.29	-1.65	-1.65
YJL214W	HXT8	1.00	-1.32	-1.37	-1.65
YML034W	SRC1	1.00	-1.41	-1.41	-1.65
YKL220C	FRE2	1.00	-1.56	-1.54	-1.65
YML027W	YOX1	1.00	-1.58	-1.66	-1.65
YBR280C		1.00	-1.61	-1.97	-1.65
YOR029W		1.00	-1.74	-1.61	-1.65
YGR068C		1.00	-1.75	-1.68	-1.65
YLR046C		1.00	-1.78	-1.79	-1.65
YOR233W	KIN4	1.00	-1.80	-1.77	-1.65
YLR322W		1.00	-1.81	-2.03	-1.65
YLR037C	DAN2	1.00	-1.85	-1.63	-1.65
YEL044W	IES6	1.00	-2.44	-2.06	-1.65
YFR016C		1.00	1.00	-1.26	-1.66
YNL055C	POR1	1.00	-1.10	-1.18	-1.66
YNL274C		1.00	-1.11	-1.35	-1.66
YPL222W		1.00	-1.24	-1.35	-1.66

YOR082C		1.00	-1.50	-1.56	-1.66
YBR132C	AGP2	1.00	-1.51	-1.53	-1.66
YFR048W		1.00	-1.56	-1.70	-1.66
YGR293C		1.00	-1.56	-1.57	-1.66
YHR098C	SFB3	1.00	-1.74	-1.91	-1.66
YGR181W	TIM13	1.00	-2.06	-1.77	-1.66
YCR004C	YCP4	1.00	1.31	1.02	-1.67
YLR049C		1.00	1.31	1.42	-1.67
YFR017C		1.00	1.13	1.14	-1.67
YPL209C	IPL1	1.00	-1.10	-1.54	-1.67
YCR010C	ADY2	1.00	-1.14	-1.55	-1.67
YER026C	CHO1	1.00	-1.14	-1.24	-1.67
YDR019C	GCV1	1.00	-1.25	-1.58	-1.67
YPR202W		1.00	-1.38	-1.39	-1.67
YER179W	DMC1	1.00	-1.40	-1.41	-1.67
YML116W	ATR1	1.00	-1.48	-1.34	-1.67
YJR157W		1.00	-1.49	-1.47	-1.67
YKR080W	MTD1	1.00	-1.50	-1.73	-1.67
YLR415C		1.00	-1.57	-1.71	-1.67
YDR470C	UGO1	1.00	-1.91	-1.81	-1.67
YEL010W		1.00	-1.91	-1.82	-1.67
YKL049C	CSE4	1.00	-1.91	-1.53	-1.67
YJR104C	SOD1	1.00	1.20	1.34	-1.68
YFL040W		1.00	-1.01	1.47	-1.68
YPR020W	ATP20	1.00	-1.18	-1.38	-1.68
YML037C		1.00	-1.34	-1.89	-1.68
YMR149W	SWP1	1.00	-1.38	-1.39	-1.68
YJL168C	SET2	1.00	-1.55	-1.93	-1.68
YKR031C	SPO14	1.00	-1.55	-1.57	-1.68
YMR074C		1.00	-1.56	-1.60	-1.68
YDR153C		1.00	-1.61	-1.29	-1.68
YMR058W	FET3	1.00	-1.66	-1.90	-1.68
YBR220C		1.00	-1.78	-1.65	-1.68
YLR324W		1.00	-1.86	-1.53	-1.68
YDR078C		1.00	-1.93	-1.87	-1.68
YMR250W	GAD1	1.00	1.48	1.02	-1.69
YNL242W	APG2	1.00	1.09	-1.28	-1.69
YGR174C	CBP4	1.00	-1.03	-1.26	-1.69
YPL127C	HHO1	1.00	-1.16	-1.41	-1.69
YBR149W	ARA1	1.00	-1.21	-1.41	-1.69
YLL016W	SDC25	1.00	-1.21	-1.57	-1.69
YKL002W	DID4	1.00	-1.38	-1.50	-1.69
YJR094C	IME1	1.00	-1.41	-1.68	-1.69
YLR112W		1.00	-1.42	-1.45	-1.69
YCL075W		1.00	-1.52	-1.68	-1.69
YAL021C	CCR4	1.00	-1.78	-1.95	-1.69
YLR106C		1.00	-1.86	-1.88	-1.69
YML002W		1.00	-1.86	-1.51	-1.69
YKL080W	VMA5	1.00	-1.93	-1.98	-1.69
YGR014W	MSB2	1.00	-2.11	-1.77	-1.69
YKL128C	PMU1	1.00	-2.24	-2.24	-1.69
YHR087W		1.00	1.82	1.44	-1.70
YAL061W		1.00	1.07	-1.31	-1.70
YDL078C	MDH3	1.00	-1.02	-1.23	-1.70
YPL147W	PXA1	1.00	-1.07	-1.39	-1.70
YMR181C		1.00	-1.08	-1.36	-1.70
YPR123C		1.00	-1.23	-1.29	-1.70
YPL006W	NCR1	1.00	-1.27	-1.82	-1.70
YJR150C	DAN1	1.00	-1.31	-1.65	-1.70
YGL236C	MTO1	1.00	-1.37	-1.69	-1.70
YDL101C	DUN1	1.00	-1.40	-1.40	-1.70

YDR149C		1.00	-1.52	-1.29	-1.70
YIL076W	SEC28	1.00	-1.58	-1.24	-1.70
YLR405W		1.00	-1.61	-1.91	-1.70
YMR306W	FKS3	1.00	-1.80	-1.93	-1.70
YDR183W	PLP1	1.00	-1.85	-1.76	-1.70
YFR038W		1.00	-2.29	-1.79	-1.70
YCR027C	RSG1	1.00	-3.12	-2.46	-1.70
YML054C	CYB2	1.00	1.10	1.19	-1.71
YOR065W	CYT1	1.00	1.01	1.36	-1.71
YJL173C	RFA3	1.00	-1.19	-1.25	-1.71
YHR147C	MRPL6	1.00	-1.22	-1.55	-1.71
YIR024C	GIF1	1.00	-1.53	-1.64	-1.71
YKR100C		1.00	-1.57	-1.49	-1.71
YLR247C		1.00	-1.59	-1.71	-1.71
YCL005W		1.00	-1.67	-1.74	-1.71
YLR437C		1.00	-1.73	-1.76	-1.71
YLR365W		1.00	-1.82	-1.95	-1.71
YKL094W	YJU3	1.00	-2.79	-1.96	-1.71
YNL115C		1.00	-1.06	-1.39	-1.72
YDR530C	APA2	1.00	-1.21	-1.20	-1.72
YNL306W	MRPS18	1.00	-1.26	-1.52	-1.72
YDR376W	ARH1	1.00	-1.29	-1.48	-1.72
YPL186C		1.00	-1.29	1.03	-1.72
YLR292C	SEC72	1.00	-1.53	-1.84	-1.72
YKR069W	MET1	1.00	-1.60	-1.76	-1.72
YDL042C	SIR2	1.00	-1.71	-1.70	-1.72
YMR007W		1.00	-1.78	-1.74	-1.72
YJR015W		1.00	-2.08	-1.72	-1.72
YDR401W		1.00	-2.53	-1.86	-1.72
YBR116C		1.00	1.96	-1.29	-1.73
YIR016W		1.00	-1.04	-1.14	-1.73
YER114C	BOI2	1.00	-1.21	-1.53	-1.73
YMR072W	ABF2	1.00	-1.34	-1.44	-1.73
YGR075C	PRP38	1.00	-1.46	-1.54	-1.73
YJL119C		1.00	-1.78	-1.85	-1.73
YJL019W		1.00	-1.91	-1.54	-1.73
YKL154W	SRP102	1.00	-2.80	-2.00	-1.73
YGR243W		1.00	1.66	1.52	-1.74
YMR188C		1.00	-1.15	-1.38	-1.74
YER146W	LSM5	1.00	-1.17	-1.04	-1.74
YKR016W		1.00	-1.21	-1.07	-1.74
YPR014C		1.00	-1.37	-1.67	-1.74
YOR228C		1.00	-1.43	-1.67	-1.74
YKL208W	CBT1	1.00	-1.53	-1.62	-1.74
YJL020C	BBC1	1.00	-1.54	-1.61	-1.74
YDR375C	BCS1	1.00	-1.59	-1.82	-1.74
YMR069W		1.00	-1.59	-1.48	-1.74
YCL068C		1.00	-1.63	-1.88	-1.74
YLR059C	REX2	1.00	-1.64	-1.86	-1.74
YJR152W	DAL5	1.00	-1.68	-1.54	-1.74
YNL039W	TFC5	1.00	-1.71	-1.98	-1.74
YBR279W	PAF1	1.00	-2.90	-2.67	-1.74
YGR086C		1.00	1.21	1.29	-1.75
YDR298C	ATP5	1.00	-1.03	1.04	-1.75
YGR008C	STF2	1.00	-1.30	-1.21	-1.75
YJL115W	ASF1	1.00	-1.37	-1.38	-1.75
YNL138W	SRV2	1.00	-1.37	-1.44	-1.75
YJL118W		1.00	-1.39	-1.65	-1.75
YMR059W	SEN15	1.00	-1.44	-2.00	-1.75
YDL162C		1.00	-1.49	-1.61	-1.75
YFL025C	BST1	1.00	-1.49	-1.81	-1.75

YLR418C	CDC73	1.00	-1.59	-1.70	-1.75
YOR030W	DFG16	1.00	-1.78	-1.71	-1.75
YKR004C	ECM9	1.00	-1.92	-1.65	-1.75
YOL122C	SMF1	1.00	-2.06	-1.88	-1.75
YDR032C	PST2	1.00	1.11	-1.17	-1.76
YPR030W	CSR2	1.00	-1.08	-1.03	-1.76
YDR218C	SPR28	1.00	-1.34	-1.23	-1.76
YLR419W		1.00	-1.45	-1.37	-1.76
YGR104C	SRB5	1.00	-1.50	-2.04	-1.76
YJL093C	TOK1	1.00	-1.50	-1.68	-1.76
YPL171C	OYE3	1.00	-1.70	-1.88	-1.76
YML104C	MDM1	1.00	-1.73	-1.35	-1.76
YOR350C	MNE1	1.00	-2.01	-1.34	-1.76
YOL098C		1.00	-2.02	-2.13	-1.76
YBL018C	POP8	1.00	-2.19	-1.85	-1.76
YGL170C	SPO74	1.00	-2.41	-1.98	-1.76
YGL081W		1.00	-1.31	-1.42	-1.77
YHR125W		1.00	-1.49	-1.88	-1.77
YMR164C	MSS11	1.00	-1.52	-1.45	-1.77
YLR404W		1.00	-1.59	-1.55	-1.77
YMR082C		1.00	-1.65	-1.95	-1.77
YLR058C	SHM2	1.00	-2.22	-2.56	-1.77
YDR520C		1.00	-2.29	-1.89	-1.77
YDL067C	COX9	1.00	-1.14	-1.39	-1.78
YKL162C		1.00	-1.20	-1.54	-1.78
YPL016W	SWI1	1.00	-1.26	-1.74	-1.78
YOR230W	WTM1	1.00	-1.44	-1.20	-1.78
YLR408C		1.00	-1.57	-1.92	-1.78
YNR059W	MNT4	1.00	-1.77	-2.26	-1.78
YNL051W	COD4	1.00	-2.09	-1.65	-1.78
YKL070W		1.00	-2.76	-2.19	-1.78
YJL210W	PEX2	1.00	1.13	1.02	-1.79
YJL131C		1.00	-1.23	-1.46	-1.79
YER080W		1.00	-1.27	-1.11	-1.79
YGL156W	AMS1	1.00	-1.28	-1.69	-1.79
YLR438W	CAR2	1.00	-1.33	-1.44	-1.79
YMR294W	JNM1	1.00	-1.33	-1.61	-1.79
YPL054W	LEE1	1.00	1.03	-1.21	-1.80
YLL028W	TPO1	1.00	-1.30	-1.67	-1.80
YKR006C	MRPL13	1.00	-1.48	-1.84	-1.80
YGL089C	MF(ALPHA)2	1.00	-1.54	-1.50	-1.80
YLR375W	STP3	1.00	-1.55	-1.86	-1.80
YML013W		1.00	-1.58	-2.03	-1.80
YOL102C	TPT1	1.00	-1.62	-1.70	-1.80
YLR443W	ECM7	1.00	-1.88	-1.52	-1.80
YJR135C	MCM22	1.00	-2.17	-2.02	-1.80
YPR069C	SPE3	1.00	-2.43	-2.21	-1.80
YGR061C	ADE6	1.00	-2.66	-3.54	-1.80
YCL040W	GLK1	1.00	1.63	1.04	-1.81
YKL103C	LAP4	1.00	1.05	-1.09	-1.81
YGL080W		1.00	-1.09	1.00	-1.81
YGL068W		1.00	-1.10	-1.51	-1.81
YJR085C		1.00	-1.31	-1.32	-1.81
YBR021W	FUR4	1.00	-1.39	-1.93	-1.81
YKL086W		1.00	-1.43	-1.68	-1.81
YMR280C	CAT8	1.00	-1.45	-1.14	-1.81
YOR215C		1.00	-1.50	-1.48	-1.81
YLR386W		1.00	-1.66	-1.57	-1.81
YLR186W	EMG1	1.00	-1.72	-2.04	-1.81
YMR002W		1.00	-1.78	-1.72	-1.81
YFR003C		1.00	-1.11	-1.07	-1.82

YML091C	RPM2	1.00	-1.24	-1.22	-1.82
YDL056W	MBP1	1.00	-1.30	-1.64	-1.82
YER129W	PAK1	1.00	-1.38	-1.90	-1.82
YLR436C	ECM30	1.00	-1.57	-1.30	-1.82
YML120C	NDI1	1.00	-1.66	-1.02	-1.82
YJL092W	HPR5	1.00	-1.69	-1.73	-1.82
YER084W		1.00	-2.10	-2.16	-1.82
YGL181W	GTS1	1.00	-3.37	-2.11	-1.82
YOR045W	TOM6	1.00	1.05	-1.15	-1.83
YMR053C	STB2	1.00	-1.54	-1.60	-1.83
YKL090W		1.00	-1.72	-1.82	-1.83
YGL175C	SAE2	1.00	-2.06	-2.00	-1.83
YDR271C		1.00	-2.16	-2.14	-1.83
YKL045W	PRI2	1.00	-2.18	-1.81	-1.83
YNL134C		1.00	1.00	-1.07	-1.84
YER093C		1.00	-1.42	-1.81	-1.84
YOR139C		1.00	-1.52	-1.82	-1.84
YCR082W		1.00	-1.72	-1.74	-1.84
YGL162W	SUT1	1.00	-1.79	-1.83	-1.84
YJL129C	TRK1	1.00	-2.13	-2.08	-1.84
YJR112W	NNF1	1.00	-2.44	-1.86	-1.84
YGL069C		1.00	-1.18	-1.57	-1.85
YGL090W	LIF1	1.00	-1.43	-1.58	-1.85
YDR115W		1.00	-1.56	-1.70	-1.85
YOL112W	MSB4	1.00	-1.67	-1.60	-1.85
YMR207C	HFA1	1.00	-2.25	-2.27	-1.85
YMR271C	URA10	1.00	-2.81	-2.06	-1.85
YDR197W	CBS2	1.00	-1.31	-1.55	-1.86
YKL013C	ARC19	1.00	-1.42	-1.45	-1.86
YJR162C		1.00	-2.04	-1.79	-1.86
YMR198W	CIK1	1.00	-2.51	-1.91	-1.86
YPL078C	ATP4	1.00	-1.01	-1.07	-1.87
YGR110W		1.00	-1.08	-1.38	-1.87
YOR349W	CIN1	1.00	-1.34	-1.25	-1.87
YBR230C		1.00	-1.39	-1.60	-1.87
YJL091C		1.00	-1.63	-1.98	-1.87
YPR128C	ANT1	1.00	-1.73	-1.99	-1.87
YGL188C		1.00	-1.76	-1.75	-1.87
YIL039W		1.00	-1.88	-2.00	-1.87
YPL058C	PDR12	1.00	-1.91	-2.00	-1.87
YOR391C		1.00	-1.40	-1.51	-1.88
YGL092W	NUP145	1.00	-1.43	-1.32	-1.88
YKR001C	VPS1	1.00	-2.03	-1.68	-1.88
YEL068C		1.00	-2.37	-2.63	-1.88
YGL187C	COX4	1.00	1.06	-1.02	-1.89
YML050W		1.00	-1.45	-1.84	-1.89
YML029W		1.00	-1.52	-1.76	-1.89
YBL043W	ECM13	1.00	-1.67	-2.06	-1.89
YJL160C		1.00	-1.81	-1.93	-1.89
YJR056C		1.00	-2.10	-1.87	-1.89
YFR011C		1.00	-1.20	-1.29	-1.90
YLR038C	COX12	1.00	-1.38	-1.30	-1.90
YJR098C		1.00	-1.73	-1.97	-1.90
YAL067C	SEO1	1.00	-1.76	-1.88	-1.90
YIL124W	AYR1	1.00	-1.14	-1.22	-1.91
YLR269C		1.00	-1.51	-1.73	-1.91
YML096W		1.00	-1.91	-1.62	-1.91
YLR429W	CRN1	1.00	-1.47	-1.41	-1.92
YML095C	RAD10	1.00	-1.53	-1.72	-1.92
YLR425W	TUS1	1.00	-1.89	-1.81	-1.92
YLR045C	STU2	1.00	-2.31	-2.19	-1.92

YJL169W		1.00	-2.63	-2.58	-1.92
YOR042W		1.00	-1.36	-1.26	-1.93
YIL077C		1.00	-1.45	-1.46	-1.93
YML015C	TAF40	1.00	-1.53	-1.95	-1.93
YLR281C		1.00	-1.72	-2.03	-1.93
YML111W	BUL2	1.00	-1.98	-1.93	-1.93
YLL023C		1.00	-2.40	-2.24	-1.93
YDR114C		1.00	-2.84	-2.37	-1.93
YER181C		1.00	-1.30	-1.43	-1.94
YDL220C	CDC13	1.00	-1.40	-2.10	-1.94
YLR259C	HSP60	1.00	-1.44	-1.41	-1.94
YMR087W		1.00	-1.53	-1.76	-1.94
YPL047W		1.00	-1.56	-1.32	-1.94
YAR061W		1.00	-1.61	-2.04	-1.94
YBL064C		1.00	-1.66	-1.96	-1.94
YLL035W	GRC3	1.00	-1.78	-1.85	-1.94
YJL175W		1.00	-1.80	-1.83	-1.94
YNL100W		1.00	-1.85	-1.61	-1.94
YPL035C		1.00	-2.66	-2.37	-1.94
YML131W		1.00	-1.28	-1.37	-1.95
YMR107W		1.00	1.59	1.70	-1.96
YKR005C		1.00	-1.33	-1.62	-1.96
YLR163C	MAS1	1.00	-1.65	-2.36	-1.96
YGR002C		1.00	-1.92	-2.04	-1.96
YML016C	PPZ1	1.00	-2.00	-1.86	-1.96
YJR038C		1.00	-2.05	-2.36	-1.96
YJL192C		1.00	-2.07	-2.03	-1.96
YGR095C	RRP46	1.00	-3.43	-2.24	-1.96
YPR191W	QCR2	1.00	-1.24	-1.30	-1.97
YOR187W	TUF1	1.00	-1.33	-1.32	-1.97
YMR184W		1.00	-1.38	-1.41	-1.97
YPR098C		1.00	-1.47	-1.67	-1.97
YDR310C	SUM1	1.00	-1.70	-1.82	-1.97
YLL052C	AQY2	1.00	-1.72	-1.81	-1.97
YIL086C		1.00	-1.89	-1.78	-1.97
YKR083C	DAD2	1.00	-2.06	-2.21	-1.97
YML028W	TSA1	1.00	-1.26	-1.21	-1.98
YBL100C		1.00	-1.47	-1.29	-1.98
YCR088W	ABP1	1.00	-1.51	-1.57	-1.98
YOR079C	ATX2	1.00	-2.12	-2.04	-1.98
YFR049W	YMR31	1.00	-1.06	-1.17	-1.99
YFR012W		1.00	-1.62	-1.98	-1.99
YLR444C		1.00	-1.68	-1.71	-1.99
YPL185W		1.00	-1.89	-1.78	-1.99
YNL054W	VAC7	1.00	-2.54	-2.45	-1.99
YKR009C	FOX2	1.00	1.25	-1.67	-2.00
YER166W		1.00	1.01	-1.05	-2.00
YGR201C		1.00	-1.46	-1.69	-2.00
YJL207C		1.00	-1.84	-1.90	-2.00
YDL174C	DLD1	1.00	-1.98	-2.56	-2.00
YHR059W	FYV4	1.00	-2.23	-1.97	-2.00
YOL083W		1.00	-3.41	-2.00	-2.00
YJL193W		1.00	-2.30	-2.08	-2.01
YJR144W	MGM101	1.00	-2.36	-2.30	-2.01
YLR352W		1.00	-1.52	-1.70	-2.02
YML018C		1.00	-1.90	-2.43	-2.02
YJR110W		1.00	-2.05	-2.01	-2.02
YAL044C	GCV3	1.00	-1.48	-2.04	-2.03
YDR389W	SAC7	1.00	-1.62	-1.74	-2.03
YBR221C	PDB1	1.00	-1.96	-2.63	-2.03
YKR085C	MRPL20	1.00	-2.00	-2.04	-2.03

YMR061W	RNA14	1.00	-2.02	-1.89	-2.03
YLR154C		1.00	-2.03	-2.20	-2.03
YBL099W	ATP1	1.00	-3.33	-4.00	-2.03
YPR151C		1.00	-1.11	1.00	-2.04
YIR006C	PAN1	1.00	-1.80	-1.96	-2.04
YBR262C		1.00	-2.61	-2.26	-2.04
YLR010C	TEN1	1.00	-2.01	-1.90	-2.05
YKR035C		1.00	-1.27	-1.33	-2.06
YPL154C	PEP4	1.00	-1.30	-1.46	-2.06
YMR090W		1.00	-1.63	-1.25	-2.06
YDR216W	ADR1	1.00	-1.72	-1.68	-2.06
YPR150W		1.00	-1.96	-1.49	-2.06
YLR335W	NUP2	1.00	-2.26	-2.72	-2.06
YNL149C		1.00	-4.44	-2.09	-2.06
YNL150W		1.00	-1.42	-1.52	-2.07
YLR407W		1.00	-1.94	-2.12	-2.07
YLR302C		1.00	-1.96	-1.96	-2.07
YKL018W	SWD2	1.00	-2.22	-1.86	-2.07
YGR003W		1.00	-1.28	-1.33	-2.08
YDR286C		1.00	-1.79	-1.73	-2.08
YJR134C	SGM1	1.00	-1.98	-2.51	-2.08
YKL079W	SMY1	1.00	-2.43	-2.25	-2.08
YDR377W	ATP17	1.00	-1.15	-1.09	-2.09
YPL059W	GRX5	1.00	-1.42	-1.68	-2.09
YGL183C	MND1	1.00	-1.97	-2.45	-2.09
YPL094C	SEC62	1.00	-2.08	-1.79	-2.09
YDL223C		1.00	1.62	-1.44	-2.10
YGR202C	PCT1	1.00	-1.47	-1.52	-2.10
YKL122C	SRP21	1.00	-1.58	-1.71	-2.10
YML129C	COX14	1.00	-1.60	-1.61	-2.10
YLR439W	MRPL4	1.00	-1.74	-2.07	-2.10
YLR409C		1.00	-2.18	-2.10	-2.10
YLR459W	CDC91	1.00	-1.26	-1.23	-2.11
YML042W	CAT2	1.00	-1.28	-1.77	-2.11
YPR099C		1.00	-1.53	-1.80	-2.11
YBR218C	PYC2	1.00	-2.35	-2.39	-2.11
YLR153C	ACS2	1.00	-2.85	-2.56	-2.11
YOR268C		1.00	-1.71	-2.09	-2.12
YJR158W	HXT16	1.00	-1.87	-2.08	-2.12
YOR031W	CRS5	1.00	-2.01	-1.96	-2.12
YDL228C		1.00	-2.04	-6.79	-2.12
YML060W	OGG1	1.00	-2.06	-2.00	-2.12
YML103C	NUP188	1.00	-2.15	-2.08	-2.12
YDL222C		1.00	2.20	1.50	-2.13
YFL018C	LPD1	1.00	-1.85	-2.10	-2.13
YMR252C		1.00	-2.06	-1.88	-2.13
YAL032C	PRP45	1.00	-1.76	-2.22	-2.14
YMR086W		1.00	-1.02	-1.49	-2.15
YGL166W	CUP2	1.00	-1.22	-1.47	-2.15
YKL148C	SDH1	1.00	-1.32	-1.52	-2.15
YGR074W	SMD1	1.00	-1.49	-1.72	-2.15
YKR011C	TOS5	1.00	-1.57	-1.90	-2.15
YLR428C		1.00	-1.93	-2.04	-2.15
YML035C	AMD1	1.00	-2.04	-2.12	-2.15
YDR260C	SWM1	1.00	-2.42	-2.11	-2.15
YGL174W	BUD13	1.00	-2.73	-2.47	-2.15
YJR042W	NUP85	1.00	-1.86	-2.21	-2.16
YLR162W		1.00	-1.48	-4.26	-2.17
YKR033C		1.00	-1.66	-1.62	-2.17
YGR182C		1.00	-1.30	-1.52	-2.18
YKL067W	YNK1	1.00	-1.42	-1.53	-2.18

YDL158C		1.00	-1.32	-1.54	-2.19
YKL160W		1.00	-1.51	-1.71	-2.19
YPR100W		1.00	-2.33	-1.75	-2.19
YGL057C		1.00	-1.85	-2.08	-2.20
YDR178W	SDH4	1.00	-1.54	-1.24	-2.21
YLL009C	COX17	1.00	-1.93	-2.19	-2.21
YLL057C		1.00	-1.49	-1.78	-2.22
YKL135C	APL2	1.00	-1.70	-1.56	-2.22
YLR178C	TFS1	1.00	1.10	-1.24	-2.23
YNL131W	TOM22	1.00	-1.32	-1.72	-2.23
YKL134C	01-Oct	1.00	-1.65	-1.76	-2.23
YJR050W	ISY1	1.00	-1.89	-2.33	-2.23
YMR199W	CLN1	1.00	-2.36	-2.78	-2.23
YFR014C	CMK1	1.00	-1.29	-1.14	-2.24
YKR095W	MLP1	1.00	-1.66	-2.07	-2.24
YJR054W		1.00	-1.68	-1.86	-2.24
YOR162C	YRR1	1.00	-2.09	-2.30	-2.24
YNL271C	BNI1	1.00	-2.74	-2.51	-2.24
YER041W	YEN1	1.00	-1.33	-1.04	-2.25
YPL262W	FUM1	1.00	-1.54	-1.64	-2.25
YLR213C	CRR1	1.00	-2.26	-2.25	-2.26
YLR385C		1.00	-2.17	-2.24	-2.27
YLR427W		1.00	-2.29	-2.64	-2.27
YJR048W	CYC1	1.00	-1.51	-1.52	-2.28
YLR233C	EST1	1.00	-2.52	-2.89	-2.28
YJL155C	FBP26	1.00	-1.85	-2.09	-2.29
YJR004C	SAG1	1.00	-2.61	-2.29	-2.30
YOR136W	IDH2	1.00	-1.63	-1.58	-2.31
YJR141W		1.00	-1.80	-1.90	-2.31
YJL180C	ATP12	1.00	-1.96	-2.51	-2.31
YJR127C	ZMS1	1.00	-1.96	-2.21	-2.31
YNL015W	PBI2	1.00	-1.20	-1.72	-2.33
YFL033C	RIM15	1.00	-2.25	-2.52	-2.33
YOR207C	RET1	1.00	-2.73	-2.57	-2.34
YGL191W	COX13	1.00	-1.18	-1.50	-2.35
YLL042C	APG10	1.00	-1.71	-2.05	-2.35
YJR138W	IML1	1.00	-2.05	-2.11	-2.35
YLR398C	SKI2	1.00	-1.97	-1.90	-2.36
YJL078C	PRY3	1.00	-2.79	-2.85	-2.37
YLR460C		1.00	-1.35	-1.43	-2.38
YFL059W	SNZ3	1.00	-1.69	-2.19	-2.39
YBL045C	COR1	1.00	-1.82	-1.94	-2.39
YLR455W		1.00	-1.47	-2.26	-2.40
YHL032C	GUT1	1.00	-1.88	-2.34	-2.40
YKL140W	TGL1	1.00	-1.48	-1.88	-2.41
YKL076C		1.00	-2.04	-2.20	-2.41
YNL208W		1.00	-1.17	-1.51	-2.42
YNL151C	RPC31	1.00	-1.56	-1.83	-2.42
YGL062W	PYC1	1.00	-1.67	-1.73	-2.42
YNL034W		1.00	-1.88	-1.97	-2.42
YJR073C	OPI3	1.00	-1.89	-1.78	-2.44
YFL055W	AGP3	1.00	-1.48	-1.76	-2.46
YER106W	MAM1	1.00	-1.52	-1.99	-2.46
YKL141W	SDH3	1.00	-1.51	-1.59	-2.47
YML128C	MSC1	1.00	1.73	1.01	-2.48
YJL166W	QCR8	1.00	-1.50	-1.35	-2.48
YCR093W	CDC39	1.00	-2.04	-3.16	-2.48
YBR032W		1.00	-2.11	-2.33	-2.48
YEL057C		1.00	-2.29	-2.54	-2.48
YKL044W		1.00	-2.29	-2.61	-2.48
YLR152C		1.00	-2.50	-3.03	-2.48

YBR301W	DAN3	1.00	-1.29	-2.27	-2.50
YKL066W		1.00	-1.93	-2.40	-2.50
YKL069W		1.00	-2.32	-2.41	-2.51
YOL055C	THI20	1.00	-3.05	-2.01	-2.53
YPL223C	GRE1	1.00	-1.14	-2.03	-2.54
YLR215C	CDC123	1.00	-2.14	-2.43	-2.54
YMR097C		1.00	-2.85	-2.22	-2.54
YLR069C	MEF1	1.00	-2.26	-5.68	-2.56
YHR180W		1.00	-2.33	-2.24	-2.56
YER160C		1.00	-2.86	-3.66	-2.56
YDR529C	QCR7	1.00	-1.02	1.10	-2.57
YKL133C		1.00	-1.66	-1.70	-2.57
YPR004C		1.00	-2.20	-2.71	-2.57
YGL177W		1.00	-1.50	-1.62	-2.58
YJL035C	TAD2	1.00	-2.21	-2.17	-2.58
YKL093W	MBR1	1.00	-2.31	-2.23	-2.58
YKR102W	FLO10	1.00	-1.62	-2.10	-2.61
YML007W	YAP1	1.00	-2.05	-2.14	-2.61
YNL025C	SSN8	1.00	-3.73	-2.66	-2.62
YJR035W	RAD26	1.00	-1.82	-1.95	-2.64
YGR098C	ESP1	1.00	-2.03	-2.72	-2.64
YLR454W		1.00	1.11	-1.83	-2.66
YGR244C	LSC2	1.00	1.06	-1.28	-2.66
YJL172W	CPS1	1.00	-1.82	-1.86	-2.66
YPR002W	PDH1	1.00	-1.84	-2.38	-2.66
YML049C	RSE1	1.00	-2.43	-3.13	-2.66
YLR334C		1.00	-2.57	-4.48	-2.67
YLR121C	YPS3	1.00	-2.59	-2.27	-2.67
YPL040C	ISM1	1.00	-2.60	-2.78	-2.68
YDR148C	KGD2	1.00	-1.89	-1.63	-2.69
YLL055W		1.00	-2.00	-2.12	-2.70
YIL034C	CAP2	1.00	-2.21	-2.24	-2.70
YLL041C	SDH2	1.00	-1.10	-1.31	-2.71
YPL134C	ODC1	1.00	-1.55	-1.60	-2.71
YER161C	SPT2	1.00	-2.60	-2.42	-2.71
YJR121W	ATP2	1.00	-1.44	-1.41	-2.73
YLL040C	VPS13	1.00	-2.20	-2.49	-2.75
YOR348C	PUT4	1.00	-1.39	-1.57	-2.76
YKL130C	SHE2	1.00	-2.95	-2.38	-2.76
YPL074W	YTA6	1.00	-2.31	-2.62	-2.83
YLL050C	COF1	1.00	-2.33	-2.52	-2.87
YLR057W		1.00	-2.44	-5.86	-2.87
YKL142W	MRP8	1.00	-2.38	-1.82	-2.89
YLR201C		1.00	-2.76	-2.60	-2.89
YNL037C	IDH1	1.00	-1.27	-1.73	-2.90
YOR362C	PRE10	1.00	-1.84	-1.99	-2.90
YML107C		1.00	-2.63	-4.07	-2.90
YCR050C		1.00	-3.65	-3.23	-2.91
YJR036C	HUL4	1.00	-1.76	-1.93	-2.92
YBR115C	LYS2	1.00	-3.11	-5.29	-2.92
YIR039C	YPS6	1.00	-1.81	-2.07	-2.93
YDR536W	STL1	1.00	-1.44	-2.33	-2.95
YGR176W		1.00	-1.28	-1.54	-2.97
YKL085W	MDH1	1.00	-1.34	-1.49	-3.05
YLR346C		1.00	-2.74	-7.08	-3.06
YFL060C	SNO3	1.00	-2.75	-2.53	-3.06
YDL229W	SSB1	1.00	-3.37	-6.47	-3.06
YJR066W	TOR1	1.00	-1.74	-2.88	-3.10
YLR214W	FRE1	1.00	-2.21	-2.93	-3.11
YPL248C	GAL4	1.00	-2.22	-2.62	-3.15
YIL166C		1.00	-2.85	-2.79	-3.15

YKR103W		1.00	-1.42	-1.80	-3.16
YLR358C		1.00	-3.10	-3.23	-3.16
YFL030W		1.00	-1.52	-1.41	-3.17
YPL070W		1.00	-1.44	-2.42	-3.18
YLR245C	CDD1	1.00	-2.68	-7.36	-3.20
YLR377C	FBP1	1.00	-3.19	-3.81	-3.28
YNL117W	MLS1	1.00	-3.68	-3.79	-3.29
YML003W		1.00	-3.40	-3.09	-3.30
YGL019W	CKB1	1.00	-1.26	-1.95	-3.31
YKR086W	PRP16	1.00	-3.05	-2.83	-3.38
YDR356W	NUF1	1.00	-3.61	-4.20	-3.38
YOR019W		1.00	-2.90	-2.75	-3.42
YFL005W	SEC4	1.00	-1.71	-2.15	-3.50
YPR071W		1.00	-1.82	-2.81	-3.53
YIL125W	KGD1	1.00	-2.46	-2.06	-3.55
YOL046C		1.00	-2.52	-2.94	-3.56
YLR327C		1.00	2.03	2.26	-3.59
YJL144W		1.00	-2.86	-3.39	-3.63
YAL054C	ACS1	1.00	-3.36	-3.54	-3.69
YBR103W	SIF2	1.00	-1.95	-2.99	-3.70
YHR033W		1.00	-2.92	-3.93	-3.75
YKL055C	OAR1	1.00	-2.56	-2.80	-3.78
YGL007W		1.00	-1.68	-2.28	-3.89
YLL049W		1.00	-3.21	-2.69	-3.99
YGR076C	MRPL25	1.00	-2.97	-5.75	-4.03
YJR120W		1.00	-2.06	-2.10	-4.04
YNR002C	FUN34	1.00	-1.42	-2.33	-4.05
YJL066C	MPM1	1.00	-2.17	-3.10	-4.18
YBL030C	PET9	1.00	-2.05	-2.74	-4.38
YKL217W	JEN1	1.00	-1.60	-1.72	-4.48
YOL126C	MDH2	1.00	-2.52	-2.75	-4.48
YLR120C	YPS1	1.00	-3.24	-3.64	-4.58
YER065C	ICL1	1.00	-4.38	-5.31	-4.82
YJR095W	SFC1	1.00	-4.30	-4.56	-4.90
YGR166W	KRE11	1.00	-3.62	-7.44	-5.07
YIL155C	GUT2	1.00	-1.79	-2.82	-5.09
YBL015W	ACH1	1.00	-3.40	-3.86	-5.13
YLR303W	MET17	1.00	-3.21	-3.62	-5.30
YNR001C	CIT1	1.00	-1.99	-2.43	-5.77
YKR097W	PCK1	1.00	-7.98	-4.80	-5.98
YIL136W	OM45	1.00	-1.62	-2.37	-6.32
YLR174W	IDP2	1.00	-4.51	-7.46	-7.84
YLR304C	ACO1	1.00	-2.82	-3.76	-8.85
YFL014W	HSP12	1.00	-1.26	-2.07	-9.47
YOR374W	ALD4	1.00	1.34	-1.80	-9.91
YAL034W-A	MTW1				
YAL035C-A					
YAL043C-A	KRE23				
YAL044W-A					
YAL058C-A	KRE20				
YAL064C-A					
YAL064W-B					
YAL068C					
YAL069W					
YAR002C-A	ERP1				
YAR066W					
YAR075W					
YBL005W-A					
YBL005W-B					
YBL029C-A					
YBL059C-A					

YBL071W-A	
YBL091C-A	
YBL101W-A	
YBL101W-B	
YBL107W-A	
YBL108C-A	
YBR012W-A	
YBR012W-B	
YBR058C-A	TSC3
YBR084C-A	RPL19A
YBR085C-A	
YBR089C-A	NHP6B
YBR103C-A	
YBR162W-A	YSY6
YBR191W-A	
YBR233W-A	
YBR255C-A	
YCL001W-A	
YCL001W-B	
YCL021W-A	
YCL026C-A	FRM2
YCL027C-A	
YCL057C-A	
YCR018C-A	
YCR020C-A	MAK31
YCR020W-B	HTL1
YCR024C-A	PMP1
YCR028C-A	RIM1
YCR038W-A	
YCR073W-A	SOL2
YCR087C-A	
YCR097W-A	
YCR102W-A	
YDL045W-A	MRP10
YDL085C-A	
YDL114W-A	
YDL130W-A	STF1
YDL133C-A	RPL41B
YDL159W-A	
YDL185C-A	
YDL240C-A	
YDL247W-A	
YDR034C-A	
YDR034C-C	
YDR034C-D	
YDR034W-B	
YDR079C-A	
YDR098C-A	
YDR098C-B	
YDR170W-A	
YDR179W-A	
YDR210W-A	
YDR210W-B	
YDR210W-C	
YDR210W-D	
YDR235W	PRP42
YDR236C	FMN1
YDR237W	MRPL7
YDR238C	SEC26
YDR239C	
YDR240C	SNU56

YDR241W	BUD26
YDR242W	AMD2
YDR243C	PRP28
YDR244W	PEX5
YDR245W	MNN10
YDR246W	TRS23
YDR247W	
YDR248C	
YDR261C-C	
YDR261C-D	
YDR261W-A	
YDR261W-B	
YDR316W-A	
YDR316W-B	
YDR320C-A	
YDR322C-A	TIM11
YDR363W-A	SEM1
YDR365W-A	
YDR365W-B	
YDR379C-A	
YDR381C-A	
YDR525W-A	SNA2
YEL017C-A	PMP2
YEL020W-A	TIM9
YEL059C-A	SOM1
YEL076C-A	
YEL076W-C	
YER007C-A	
YER014C-A	BUD25
YER019C-A	SBH2
YER039C-A	
YER044C-A	MEI4
YER048W-A	
YER053C-A	
YER056C-A	RPL34A
YER060W-A	FCY22
YER066C-A	
YER074W-A	
YER087C-A	SBH1
YER091C-A	
YER093C-A	
YER119C-A	
YER137C-A	
YER138W-A	
YER159C-A	
YER187W-A	KHS1
YFL002W-A	
YFL002W-B	
YFL010W-A	AUA1
YFL013W-A	
YFL017W-A	SMX2
YFL034C-A	RPL22B
YFL034C-B	MOB2
YFR012W-A	
YFR024C-A	LSB3
YFR031C-A	RPL2A
YFR032C-A	RPL29
YGL226C-A	OST5
YGL258W-A	
YGR027W-A	
YGR027W-B	

YGR038C-A	
YGR038C-B	
YGR109W-A	
YGR109W-B	
YGR122C-A	
YGR161C-C	
YGR161C-D	
YGR161W-A	
YGR161W-B	
YGR271C-A	
YHL009W-A	
YHL009W-B	
YHR001W-A	QCR10
YHR005C-A	MRS11
YHR021W-A	ECM12
YHR039C-A	VMA10
YHR049C-A	
YHR072W-A	NOP10
YHR079C-A	SAE3
YHR132W-A	
YHR139C-A	
YHR143W-A	RPC10
YHR214C-B	
YHR214C-C	
YHR214W-A	
YIL009C-A	EST3
YIL015C-A	
YIL082W-A	
YIR020W-B	
YJL012C-A	
YJL052C-A	
YJL062W-A	
YJL127W-A	
YJL156W-A	
YJL205C-A	NCE101
YJR010C-A	SPC1
YJR094W-A	RPL43B
YJR135W-A	TIM8
YKL003W-A	
YKL006C-A	SFT1
YKL018C-A	
YKL033W-A	
YKL053C-A	
YKL096W-A	CWP2
YKL106C-A	
YKL162C-A	
YKL165C-A	
YKR035W-A	DID2
YLL018C-A	COX19
YLR035C-A	
YLR099W-A	
YLR149C-A	
YLR157C-A	
YLR157C-B	
YLR227W-A	
YLR227W-B	
YLR256W-A	
YLR262C-A	
YLR287C-A	RPS30A
YLR312W-A	MRPL15
YLR363W-A	

YLR390W-A	CCW14
YLR410W-A	
YLR410W-B	
YLR438C-A	LSM3
YML007C-A	
YML009C	MRPL39
YML010C-B	
YML010W-A	
YML013C-A	
YML017W	PSP2
YML024W	RPS17A
YML025C	
YML026C	RPS18B
YML035C-A	
YML036W	
YML039W	
YML045W-A	
YML048W-A	
YML052W	SUR7
YML056C	IMD4
YML058C-A	
YML058W-A	HUG1
YML067C	ERV41
YML073C	RPL6A
YML081C-A	ATP18
YML085C	TUB1
YML086C	ALO1
YML094W	GIM5
YML095C-A	
YML100W-A	
YML102C-A	
YML117W-A	
YML124C	TUB3
YML133C	
YMR006C	PLB2
YMR013W-A	
YMR031W-A	
YMR033W	ARP9
YMR045C	
YMR046W-A	
YMR050C	
YMR052C-A	
YMR060C	TOM37
YMR062C	ECM40
YMR075C-A	
YMR079W	SEC14
YMR084W	
YMR085W	
YMR086C-A	
YMR116C	ASC1
YMR117C	SPC24
YMR119W-A	
YMR120C	ADE17
YMR122W-A	
YMR135W-A	
YMR142C	RPL13B
YMR143W	RPS16A
YMR153C-A	
YMR158C-B	
YMR158W-A	
YMR166C	

YMR169C	ALD3
YMR172C-A	
YMR173W-A	
YMR174C	PAI3
YMR175W	SIP18
YMR193C-A	
YMR194C-A	
YMR194W	RPL36A
YMR201C	RAD14
YMR225C	MRPL44
YMR230W	RPS10B
YMR244C-A	
YMR251W-A	HOR7
YMR254C	
YMR256C	COX7
YMR273C	ZDS1
YMR286W	MRPL33
YMR290W-A	
YMR292W	GOT1
YMR294W-A	
YMR304C-A	
YMR306C-A	
YMR316C-A	
YMR316C-B	
YMR324C	
YNL054W-A	
YNL054W-B	
YNL067W-A	
YNL162W-A	
YNL284C-A	
YNL284C-B	
YNR001W-A	
YNR032C-A	HUB1
YNR034W-A	
YOL013W-A	
YOL052C-A	DDR2
YOL077W-A	ATP19
YOL086W-A	
YOL103W-A	
YOL103W-B	
YOL159C-A	
YOR008C-A	KIM1
YOR008W-B	
YOR142W-A	
YOR142W-B	
YOR192C-A	
YOR192C-B	
YOR298C-A	MBF1
YOR304C-A	
YOR314W-A	
YOR343C-A	
YOR343C-B	
YOR396W	
YPL060C-A	
YPL183W-A	
YPL249C-A	RPL36B
YPL257W-A	
YPL257W-B	
YPR002C-A	
YPR016W-A	
YPR074W-A	

YPR133W-A	TOM5
YPR137C-A	
YPR137C-B	
YPR158C-C	
YPR158C-D	
YPR158W-A	
YPR158W-B	

Comparison of *C. albicans* and *S. cerevisiae* homologues

Candida dataset			**Expression Ratio**				***Saccharomyces dataset***		**Expression Ratio**				
***C. albicans* gene**			**Glucose Concentration (%)**				***S.cerevisiae* gene homolo**		**GlucoseConcentration(%)**				
Systematic	**orf19 Number**	**Common**	**0**	**0.01**	**0.1**	**1**	**Systematic**	**Common**	**0.0**	**0.0**	**0.1**	**1.0**	**Description**
CA0002	orf19.12523	*DOC1*	-1.0	-1.1	-1.0	-1.1	YGL240W	*DOC1*	1.0	-1.2	1.1	1.2	component of the anaphase promoting complex (by homology)
CA0005	orf19.2414	*IPF14994*	-1.0	1.2	1.2	1.2	YJL066C	*MPM1*	1.0	-2.2	-3.1	-4.2	unknown function
CA0006	orf19.11561	*IPF2072*	1.0	1.0	-1.0	-1.0	YDR279W		1.0	1.4	1.4	-1.0	unknown function
CA0010	orf19.7790	*IPF16036*	1.1	1.2	1.3	1.2	YJL143W	*TIM17*	1.0	-1.3	-1.3	1.0	similar to Saccharomyces cerevisiae Tim17p mitochondrial inner membra
CA0011	orf19.73	*IPF17430*	-1.0	-1.0	-1.2	-1.1	YIL137C		1.0	-1.2	-1.0	-1.0	possible zinc protease (by homology)
CA0012	orf19.13439	*IPF19448*	-1.2	-1.2	-1.2	-1.3	YNR008W	*LRO1*	1.0	1.0	-1.3	-1.1	similar to Saccharomyces cerevisiae Lro1p lecithin cholesterol acyltransf
CA0013	orf19.4548	*MAK32*	1.1	1.1	1.1	1.0	YCR019W	*MAK32*	1.0	-1.1	-1.1	1.1	sugar kinase (by homology)
CA0019		*IPF17799*	-1.0	-1.0	-1.0	-1.0	YBR151W	*APD1*	1.0	-1.7	-1.6	-1.6	unknown function
CA0020	orf19.124	*IPF7046*	1.1	1.0	-1.0	-1.0	YHR052W		1.0	-1.1	-1.1	-1.1	unknown function
CA0026		*IPF16843*	-1.1	-1.1	1.1	-1.1	YGR127W		1.0	-1.0	-1.1	1.0	unknown function
CA0027	orf19.1886	*RCL1*	-1.1	-1.1	-1.1	-1.1	YOL010W	*RCL1*	1.0	1.3	1.1	1.1	RNA 3 -terminal phosphate cyclase (by homology)
CA0029	orf19.182	*PET56*	-1.0	1.0	-1.1	-1.1	YOR201C	*PET56*	1.0	-1.7	-1.1	1.2	ribosomal RNA methylase (by homology)
CA0030	orf19.7710	*IPF17790*	-1.5	-1.4	-1.8	-1.6	YML091C	*RPM2*	1.0	-1.2	-1.2	-1.8	unknown function
CA0031	orf19.227	*COX7*	1.0	-1.0	1.0	1.1	YMR256C	*COX7*					Subunit VII of cytochrome c oxidase (by homology)
CA0032	orf19.229	*IPF15248*	-1.0	1.0	1.0	1.0	YOL054W		1.0	-1.1	1.0	-1.1	zinc finger protein (by homology)
CA0035	orf19.10011	*PRC3*	-1.1	-1.1	-1.0	-1.1	YBR139W		1.0	-1.1	-1.2	-1.3	Carboxypeptidase Y precursor (by homology)
CA0038	orf19.1770	*CYC1*	1.2	1.2	1.3	1.4	YJR048W	*CYC1*	1.0	-1.5	-1.5	-2.3	cytochrome-c isoform 1
CA0041	orf19.3804	*IPF10360*	1.1	1.3	1.3	1.1	YMR134W		1.0	1.2	1.2	-1.0	unknown function
CA0043	orf19.719	*HRD1*	-1.3	1.0	-1.1	1.0	YOL013C	*HRD1*	1.0	1.1	1.3	1.2	Involved in degradation of Hmg2p
CA0047	orf19.2538	*PTC2*	-1.1	-1.0	1.0	-1.0	YER089C	*PTC2*	1.0	-1.4	-1.1	-1.0	Protein phosphatase type 2C (by homology)
CA0048	orf19.3599	*TIF4631*	1.0	-1.2	-1.5	-1.4	YGR162W	*TIF4631*	1.0	-1.4	1.1	1.1	mRNA cap-binding protein (by homology)
CA0049	orf19.757	*IPF3908*	-1.2	-1.0	-1.2	-1.0	YPR090W		1.0	-1.0	1.2	1.1	unknown function
CA0052	orf19.379	*IPF19567*	1.0	-1.2	-1.1	-1.1	YHR085W		1.0	-1.4	-1.7	-1.4	Unknown function
CA0054		*RIB4.3*	1.2	-1.0	-1.0	-1.1	YOL143C	*RIB4*	1.0	1.2	1.4	1.2	6,7-dimethyl-8-ribityllumazine synthase, 3-prime end (by homology)
CA0055	orf19.10917	*IPF12442*	1.1	1.2	1.3	1.1	YML052W	*SUR7*					unknown function
CA0057		*IPF3767*	1.1	-1.2	-1.2	-1.0	YPR143W		1.0	1.2	1.6	1.6	unknown function
CA0060	orf19.1699	*IPF13661*	1.0	-1.1	-1.1	1.0	YHR114W	*BZZ1*	1.0	1.1	1.2	1.1	unknown function
CA0068	orf19.121	*ARC18*	1.2	1.1	1.1	1.1	YLR370C	*ARC18*	1.0	-1.1	-1.2	-1.2	subunit of the Arp2/3 complex involved in the control of actin polymerizat
CA0079	orf19.4730	*IPF14323*	1.0	-1.0	1.0	-1.0	YNL050C		1.0	1.1	1.1	1.1	unknown function
CA0084	orf19.12976	*NAB3*	-1.1	-1.1	-1.2	-1.1	YPL190C	*NAB3*	1.0	1.1	1.7	1.7	polyadenylated RNA-binding protein (by homology)
CA0086	orf19.7781	*IPF16598*	-1.0	1.4	1.3	1.5	YBR042C		1.0	1.2	1.3	1.3	unknown function
CA0088	orf19.579	*IPF7349*	-1.3	-1.2	-1.6	-1.3	YNL256W	*FOL1*	1.0	1.0	1.2	1.2	similar to Saccharomyces cerevisiae Fol1p dihydroneopterin aldolase, di
CA0089	orf19.5064	*MRPL3*	-1.0	-1.2	-1.0	-1.1	YMR024W	*MRPL3*	1.0	1.1	1.1	1.0	ribosomal protein of the large subunit, mitochondrial (by homology)
CA0090	orf19.2026	*UBP13*	-1.1	1.0	-1.1	-1.0	YER098W	*UBP9*	1.0	-1.4	-1.3	-1.0	ubiquitin carboxyl-terminal hydrolase (by homology)
CA0094	orf19.3213	*IPF12819*	1.0	1.0	1.0	-1.0	YDR474C		1.0	1.1	1.2	1.3	unknown function
CA0095	orf19.3468	*ALG11*	-1.1	-1.4	-1.4	-1.3	YNL048W	*ALG11*	1.0	-1.2	1.1	1.1	required for asparagine-linked oligosaccharide assembly (by homology)
CA0096	orf19.751	*IPF13409*	-1.0	1.0	1.0	1.0	YJL149W		1.0	1.1	1.0	1.2	unknown function
CA0098	orf19.2319	*IPF16479*	-1.2	-2.1	-2.3	-2.1	YDR365C		1.0	-2.5	-1.4	-1.3	unknown function
CA0101	orf19.232	*IPF10105*	1.1	1.0	1.1	-1.0	YOL135C	*MED7*	1.0	1.0	1.1	1.1	RNA polymerase-like (by homology)
CA0102	orf19.736	*IPF16695*	-1.3	-1.1	-1.5	-1.3	YCR081W	*SRB8*	1.0	1.0	1.0	1.1	unknown function
CA0107	orf19.5183	*POL3.5EOC*	-1.2	-1.4	-2.7	-1.7	YDL102W	*CDC2*	1.0	1.3	-1.1	-1.1	DNA Polymerase III, 5-prime end
CA0111	orf19.4151	*IPF16830*	-1.0	1.0	1.0	1.0	YNL012W	*SPO1*	1.0	-1.9	-1.6	-1.5	similar to Saccharomyces cerevisiae Spo1p transcriptional regulator invo
CA0112	orf19.5754	*IPF17358*	-1.0	1.2	1.5	1.3	YLR023C		1.0	1.1	1.4	1.4	unknown function
CA0113	orf19.9938	*AUT2*	1.0	1.1	1.1	1.0	YNL223W	*AUT2*	1.0	-1.1	-1.2	-1.3	anchor protein mediateing attachment of autophagosomes to microtubul
CA0114	orf19.9939	*SSU72*	-1.0	1.0	-1.0	1.0	YNL222W	*SSU72*	1.0	-1.0	1.0	-1.2	suppressor of cs mutant of sua7(by homology)
CA0117	orf19.916	*IPF19231*	1.2	1.1	1.4	1.5	YNL305C		1.0	1.2	1.2	-1.3	unknown function
CA0118		*IPF16430.3*	1.1	-1.1	-1.0	1.1	YFR033C	*QCR6*	1.0	1.3	1.1	-1.6	similar to Saccharomyces cerevisiae Qcr6p ubiquinol-cytochrome-c redu
CA0119	orf19.920	*RMT2*	-1.1	-1.0	-1.2	-1.2	YDR465C	*RMT2*	1.0	-1.0	1.0	1.2	N-delta-arginine methyltransferase (by homology)
CA0120		*IPF19593*	-1.1	-1.2	-1.2	-1.1	YPL020C	*ULP1*	1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Ulp1p Smt3-processing enzyme (by
CA0121	orf19.983	*IPF17048*	-1.0	-1.0	-1.1	-1.0	YOR322C		1.0	1.0	1.1	1.2	unknown function
CA0122	orf19.13191	*SNF4*	-1.0	1.3	1.3	1.4	YGL115W	*SNF4*	1.0	1.1	-1.1	-1.1	Nuclear regulatory protein (by homology).
CA0123	orf19.9576	*MXR1*	1.0	1.2	1.2	1.2	YER042W	*MXR1*	1.0	-1.1	1.1	-1.2	methionine sulfoxide reductase
CA0124	orf19.9577	*RFC5*	-1.0	1.1	1.0	1.1	YBR087W	*RFC5*	1.0	1.1	1.1	1.1	DNA replication factor C (by homology)
CA0126	orf19.8177	*IPF4284*	1.1	1.1	1.2	1.1	YOL026C		1.0	-1.1	1.0	1.0	unknown function
CA0127	orf19.8176	*HXK2.3F*	-1.1	9.5	9.7	7.9	YGL253W	*HXK2*	1.0	-1.1	1.4	1.4	hexokinase II, 3-prime end (by homology)

CA0129	orf19.246	*IPF10495*	1.1	-1.0	-1.0	1.1	YIL108W		1.0	1.1	1.1	1.3	unknown function
CA0130	orf19.3533	*IPF4470*	1.1	1.0	1.1	1.0	YDR512C		1.0	-1.0	1.1	1.0	unknown function
CA0131	orf19.36	*IPF13402*	1.0	-1.0	1.0	-1.0	YML071C	*DOR1*	1.0	-1.3	1.1	1.2	unknown function
CA0132	orf19.2361	*SPT10*	-1.1	-1.0	1.1	-1.0	YJL127C	*SPT10*	1.0	-1.3	-1.1	-1.1	Transcription regulatory protein (by homology)
CA0133	orf19.1007	*IPF3746*	1.0	1.0	1.0	1.0	YDR017C	*KCS1*	1.0	1.0	1.0	1.2	unknown function
CA0139	orf19.14182	*RUD3*	-1.1	-1.3	-1.5	-1.2	YOR216C	*RUD3*	1.0	1.0	-1.1	-1.1	Suppressor of uso1-1 transport defect (by homology)
CA0140	orf19.10097	*MDM1.3*	-1.2	-1.3	-1.4	-1.3	YML104C	*MDM1*	1.0	-1.7	-1.4	-1.8	intermediate filament protein, 3-prime end (by homology)
CA0142	orf19.1026	*CSL4*	1.1	1.0	1.1	1.0	YNL232W	*CSL4*	1.0	1.0	1.3	1.1	Involved in kinetochore-related function (by homology)
CA0144	orf19.151	*IPF19195.3F*	-1.0	1.0	1.0	1.0	YKL174C		1.0	-1.2	-1.1	-1.0	putative amino acid or GABA permease, 3-prime end (by homology)
CA0147	orf19.11133	*IPF9690*	1.1	1.1	1.1	1.1	YBR101C		1.0	-1.3	-1.0	1.1	unknown function
CA0148	orf19.2404	*POP1*	-1.0	-1.0	-1.0	1.0	YNL221C	*POP1*	1.0	1.0	1.0	1.6	protein component of ribonuclease P and ribonuclease MRP (by homolog
CA0149	orf19.6243	*VPS34*	-1.1	-1.0	-1.1	-1.0	YLR240W	*VPS34*	1.0	-1.5	-1.2	-1.0	1-phosphatidylinositol 3-kinase
CA0150	orf19.10236	*CDC123*	-1.1	1.1	1.3	1.0	YLR215C	*CDC123*	1.0	-2.1	-2.4	-2.5	similar to Saccharomyces cerevisiae Cdc123p cell cycle regulator (by ho
CA0154	orf19.4433	*CPH1*	1.0	1.1	-1.1	-1.1	YHR084W	*STE12*	1.0	1.3	1.1	1.5	Transcription factor
CA0155	orf19.11075	*RPT6*	-1.1	1.0	-1.1	-1.0	YGL048C	*RPT6*	1.0	-1.5	-1.1	1.1	26S proteasome regulatory subunit (by homology)
CA0156	orf19.9345	*SCW1*	1.5	1.3	1.3	1.4	YGR279C	*SCW4*	1.0	1.2	1.6	1.8	glucanase (by homology)
CA0161	orf19.10177	*RMS1*	-1.0	1.2	1.4	1.2	YDR257C	*RMS1*	1.0	-1.0	-1.2	1.1	(putative) transcriptional regulator (by homology)
CA0164	orf19.4335	*IPF11694*	1.0	1.0	-1.0	-1.0	YGR260W	*TNA1*	1.0	1.1	1.2	2.9	similar to Saccharomyces cerevisiae Tna1p high affinity nicotinic acid pla
CA0174		*IPF11182.3EO*	-1.2	-1.0	-1.3	-1.1	YLR106C		1.0	-1.9	-1.9	-1.7	unknown function, 3-prime end
CA0175	orf19.9970	*NPL4*	-1.4	1.1	1.1	-1.0	YBR170C	*NPL4*	1.0	-1.2	-1.2	-1.0	nuclear protein localization factor and ER translocation component (by h
CA0176	orf19.8267	*IPF11388*	-1.1	-1.0	-1.1	-1.1	YER041W	*YEN1*	1.0	-1.3	-1.0	-2.3	unknown function
CA0178	orf19.12707	*CDC6*	-1.0	1.0	1.1	1.1	YJL194W	*CDC6*	1.0	-1.3	-1.0	1.1	Cell division control protein
CA0179	orf19.423	*DCP1*	1.0	1.0	1.1	1.0	YOL149W	*DCP1*	1.0	1.1	-1.0	-1.1	mRNA decapping enzyme (by homology)
CA0180	orf19.422	*SPT20*	1.0	-1.0	-1.0	-1.1	YOL148C	*SPT20*	1.0	-1.7	-1.6	-1.5	transcription factor, member of the histone acetyltransferase SAGA
CA0183	orf19.9191	*CAP1*	-1.0	1.8	2.2	1.9	YML007W	*YAP1*	1.0	-2.1	-2.1	-2.6	transcriptional acivator (by homology)
CA0188	orf19.9467	*IPF15442*	1.1	1.4	1.7	1.3	YJL171C		1.0	-1.1	1.2	1.4	unknown function
CA0190	orf19.11070	*IPF14773*	-1.1	1.0	-1.0	-1.0	YBR005W		1.0	1.3	1.2	1.5	unknown function
CA0191	orf19.89	*PEX7*	1.0	1.1	1.0	1.0	YDR142C	*PEX7*	1.0	-1.0	-1.1	1.2	peroxisomal import protein (by homology)
CA0192	orf19.1177	*IPF15134*	-1.1	-1.0	-1.0	1.0	YNL206C	*RTT106*	1.0	1.1	1.1	1.1	Unknown function
CA0194	orf19.11404	*IPF16228*	1.1	-1.0	1.1	1.0	YGL224C		1.0	-1.4	-1.3	-1.2	unknown function
CA0195	orf19.11403	*IPF12688*	1.2	1.0	1.1	-1.0	YOR280C		1.0	-1.3	-1.2	-1.0	unknown function
CA0197	orf19.1934	*IPF9787*	-1.3	-1.6	-1.9	-1.4	YOR025W	*HST3*	1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Hst3p silencing protein (by homolog
CA0198	orf19.9227	*IPF19685*	-1.4	-1.5	-1.2	-1.1	YHR097C		1.0	-1.1	1.1	-1.5	unknown function
CA0199	orf19.3556	*KAP104*	-1.1	-1.1	-1.0	-1.1	YBR017C	*KAP104*	1.0	1.1	1.1	1.0	karyopherin-beta protein (by homology)
CA0200	orf19.9109	*IPF15119*	1.1	1.1	1.4	1.2	YKL175W	*ZRT3*	1.0	1.2	1.2	1.2	unknown function
CA0201	orf19.9108	*IPF15116*	-1.3	-1.4	-1.3	-1.1	YKL077W		1.0	-1.2	1.1	1.2	Unknown function
CA0202	orf19.1210	*IPF19126*	1.2	1.5	1.8	1.6	YER119C		1.0	-1.3	-1.4	-1.4	putative aminoacid transporter (by homology)
CA0203	orf19.10724	*MID1*	-1.1	-1.1	-1.1	-1.0	YNL291C	*MID1*	1.0	-1.4	-1.3	-1.4	involved in Ca2+ influx during mating (by homology)
CA0204	orf19.1222	*IKI3*	-1.2	-1.3	-1.7	-1.4	YLR384C	*IKI3*	1.0	-1.7	-2.0	-1.6	killer toxin insensitive protein 3 (by homology)
CA0205	orf19.1223	*DBF2*	-1.1	-1.1	-1.2	-1.0	YGR092W	*DBF2*	1.0	-1.3	-1.4	-1.3	putative ser/thr protein kinase by homology
CA0209	orf19.1228	*HAP2*	1.0	1.1	1.0	-1.0	YGL237C	*HAP2*	1.0	-1.3	-1.2	-1.6	CCAAT-binding factor subunit (by homology)
CA0210	orf19.12971	*IPF4328*	1.1	-1.2	-1.1	-1.0	YMR315W		1.0	-1.1	1.2	1.1	unknown function
CA0213	orf19.1279	*CDS1*	1.0	-1.1	-1.1	-1.1	YBR029C	*CDS1*	1.0	1.1	1.0	1.1	CDP-diacylglycerol synthase (by homology)
CA0214	orf19.1289	*SCT11*	1.0	1.1	1.1	1.0	YBL011W	*SCT1*	1.0	1.1	1.3	1.4	Suppresses a choline-transport mutant
CA0215	orf19.2745	*IPF15350*	1.1	1.0	1.0	1.0	YDR207C	*UME6*	1.0	-1.6	-1.8	-1.5	putative zinc finger transcription factor (by homology)
CA0217	orf19.849	*MNN4*	1.1	-1.0	1.1	1.0	YKL201C	*MNN4*	1.0	-1.8	-1.6	-1.2	regulates the mannosylphosphorylation (by homology)
CA0219	orf19.3193	*YAP3*	1.0	1.0	1.2	1.1	YHL009C	*YAP3*	1.0	-1.2	-1.0	1.2	transcription factor of a fungal-specific family of bzip proteins (by homolog
CA0220	orf19.1291	*ABZ1*	1.0	-1.1	-1.0	1.0	YNR033W	*ABZ1*	1.0	-1.1	-1.1	-1.1	para-aminobenzoate synthase (by homology)
CA0221	orf19.9509	*PUS4*	1.0	-1.0	-1.0	1.0	YNL292W	*PUS4*	1.0	-1.0	-1.1	-1.2	pseudouridine synthase (by homology)
CA0223	orf19.1295	*VAS1*	-1.6	-1.5	-1.8	-1.5	YGR094W	*VAS1*	1.0	-1.3	-1.4	-1.2	valyl-tRNA synthetase (by homology)
CA0224	orf19.1296	*PRP31*	-1.1	-1.1	1.0	-1.1	YGR091W	*PRP31*	1.0	-1.3	1.1	1.3	pre-mRNA splicing protein (by homology)
CA0225	orf19.1298	*NUP84*	-1.3	-1.3	-1.3	-1.3	YDL116W	*NUP84*	1.0	-1.4	1.1	-1.1	nuclear pore protein (by homology)
CA0227	orf19.9328	*PHO23*	-1.1	-1.1	-1.0	1.1	YNL097C	*PHO23*	1.0	-1.2	-1.4	-1.4	Involved in transcriptional regulation of PHO5 (by homology)
CA0228	orf19.12233	*IPT1*	1.0	1.1	1.0	1.0	YDR072C	*IPT1*	1.0	1.5	2.0	2.1	Mannosyl diphosphorylinositol ceramide (by homology)
CA0231	orf19.1494	*RAD23*	-1.2	-1.2	-1.3	1.0	YEL037C	*RAD23*	1.0	1.4	1.6	2.4	nucleotide excision repair protein(ubiquitin-like protein) (by homology)
CA0233	orf19.7794	*URE2*	1.0	1.0	1.0	1.0	YNL229C	*URE2*	1.0	-1.1	-1.1	1.0	Nitrogen catabolite repression regulator (by homology)
CA0234	orf19.7793	*IFA3*	-1.1	-1.1	-1.1	-1.1	YKR060W		1.0	-1.1	-1.2	1.0	unknown function
CA0235	orf19.7813	*HIS3*	1.0	1.0	1.1	1.0	YOR202W	*HIS3*	1.0	-1.3	-1.2	1.1	imidazole glycerol phosphate dehydratase
CA0236	orf19.7814	*MDM10*	1.0	-1.0	-1.0	-1.0	YAL010C	*MDM10*	1.0	1.0	1.0	1.0	Involved in mitochondrial morphology and inheritance (by homology)
CA0237	orf19.7818	*IPF13416*	-1.0	-1.1	-1.2	-1.0	YAL011W		1.0	-1.2	-1.1	-1.0	Unknown function
CA0238	orf19.7864	*PHA2.3*	1.1	1.0	1.1	1.0	YNL316C	*PHA2*	1.0	1.0	-1.0	-1.2	prephenate dehydratase, 3-prime end (by homology)

CA0239	orf19.236	*RPL9B*	1.4	-1.3	1.1	1.0	YNL067W	*RPL9B*	1.0	1.5	2.4	2.4	RPL9B ribosomal protein L9 by homology
CA0241	orf19.3470	*IPF15630*	-1.1	-1.1	-1.2	-1.1	YPL207W		1.0	-1.2	1.2	1.1	unknown function
CA0243	orf19.5869	*BSD2*	-1.1	-1.1	-1.1	-1.0	YBR290W	*BSD2*	1.0	-1.1	-1.1	-1.0	Metal homeostasis protein (by homology)
CA0245	orf19.13042	*POL5*	-1.6	-1.5	-2.0	-1.5	YEL055C	*POL5*	1.0	-1.8	-1.1	1.1	DNA polymerase V (by homology)
CA0253	orf19.477	*FIL1*	1.0	1.0	-1.0	-1.0	YHR038W	*FIL1*	1.0	-2.1	-1.5	-1.6	Putative mitochondrial ribosome recycling factor (by homology)
CA0256	orf19.2278	*IPF10309*	-1.2	1.2	1.1	1.3	YKL206C		1.0	1.0	1.2	1.0	unknown function
CA0258	orf19.1356	*IPF17112*	-1.1	-1.1	-1.2	-1.1	YOR251C		1.0	1.1	1.2	1.3	thiosulfate sulfurtransferase (by homology)
CA0259	orf19.1355	*SOL1*	-1.2	-1.0	-1.0	1.1	YNR034W	*SOL1*	1.0	1.3	1.4	1.1	multicopy suppressor of los1-1
CA0261	orf19.8394	*LYS22*	-1.0	1.3	1.5	1.1	YDL131W	*LYS21*	1.0	1.2	2.1	4.8	Homocitrate synthase (by homology)
CA0262	orf19.1407	*IPF20054*	-1.0	1.2	1.7	1.2	YBR287W		1.0	1.3	1.3	1.5	unknown function
CA0263	orf19.1408	*GLK1*	-1.2	1.0	1.0	1.1	YCL040W	*GLK1*	1.0	1.6	1.0	-1.8	aldohexose specific glucokinase (by homology)
CA0265	orf19.10702	*STI1*	-1.6	-1.4	-1.6	-1.5	YOR027W	*STI1*	1.0	-1.1	1.5	1.3	stress-induced protein (by homology)
CA0268	orf19.4262	*PUF2.EXON2*	-1.3	-1.1	-1.1	-1.2	YJR091C	*JSN1*	1.0	-1.1	-1.1	-1.0	RNA-binding protein, exon 2 (by homology)
CA0272	orf19.1434	*DPB11*	-1.1	-1.3	-1.4	-1.1	YJL090C	*DPB11*	1.0	1.0	-1.2	1.0	DNA polymerase II complex (by homology)
CA0275	orf19.8470	*NTA1*	1.0	1.0	1.1	-1.0	YJR062C	*NTA1*	1.0	-1.1	-1.0	-1.1	Amino-terminal amidase (by homology)
CA0280	orf19.1439	*IPF10566*	-1.1	-1.0	1.1	-1.1	YDR315C	*IPK1*	1.0	1.0	1.2	1.2	unknown function
CA0290	orf19.1591	*POT14*	-1.2	-3.4	-2.9	-3.2	YPL028W	*ERG10*	1.0	1.5	2.5	2.0	acetyl-CoA acetyltransferase (by homology)
CA0291	orf19.1592	*IPF13328*	1.0	-1.1	1.0	1.1	YPL041C		1.0	-1.6	-1.1	-1.0	unknown function
CA0293	orf19.6489	*IPF6624*	1.0	1.1	1.1	1.1	YDL222C		1.0	2.2	1.5	-2.1	unknown function
CA0294	orf19.9322	*IPF16061*	-1.0	-1.1	-1.0	-1.1	YOR243C		1.0	-1.0	1.1	1.8	unknown function
CA0295	orf19.1595	*IPF15033*	1.0	1.0	1.1	1.0	YDL091C		1.0	-1.4	-1.3	-1.2	unknown function
CA0297	orf19.1674	*CDC53*	-1.3	-1.2	-1.3	1.1	YDL132W	*CDC53*	1.0	-1.2	1.1	1.5	Cell division control protein (by homology)
CA0298	orf19.1673	*PPT1*	-1.1	-1.0	-1.0	-1.0	YGR123C	*PPT1*	1.0	1.0	1.2	1.8	Protein ser/thr phosphatase
CA0299	orf19.1597	*IPF3765*	-1.1	-1.3	-1.1	-1.1	YGR106C		1.0	1.5	1.4	1.2	unknown function
CA0300	orf19.1598	*ERG24*	1.1	-1.3	-1.3	-1.3	YNL280C	*ERG24*	1.0	-1.2	1.1	1.1	C-14 sterol reductase (by homology)
CA0302	orf19.9181	*MEP3*	-1.0	3.0	4.3	4.0	YPR138C	*MEP3*	1.0	-1.1	1.2	1.1	low affinity high capacity ammonium permease (by homology)
CA0304	orf19.8340	*IPF12829*	-1.0	-1.1	-1.1	-1.1	YLL035W	*GRC3*	1.0	-1.8	-1.9	-1.9	unknown function
CA0305	orf19.1734	*INO80*	-1.1	-1.0	-1.1	1.1	YGL150C	*INO80*	1.0	1.2	1.3	1.4	DNA helicase (by homology)
CA0306	orf19.1742	*HEM3*	1.3	1.2	1.5	1.3	YDL205C	*HEM3*	1.0	1.3	1.1	1.2	porphobilinogen deaminase
CA0307	orf19.3736	*IPF4719*	1.0	1.0	1.1	1.0	YCL055W	*KAR4*	1.0	-1.1	-1.1	1.1	similar to Saccharomyces cerevisiae Kar4p regulatory protein required fo
CA0308	orf19.8693	*RHK1*	1.0	-1.0	1.0	1.1	YBL082C	*RHK1*	1.0	-1.0	-1.1	1.0	Mannosyltransferase (by homology)
CA0309	orf19.1091	*IPF16935*	-1.0	1.0	-1.0	1.0	YOL144W	*NOP8*	1.0	1.0	1.5	1.3	unknown function
CA0310	orf19.8690	*PEX11*	1.6	-2.2	-2.0	-2.5	YOL147C	*PEX11*	1.0	1.0	1.0	-1.2	peroxisomal membrane protein - peroxin by homology
CA0312	orf19.8211	*IPF6396*	1.2	-1.0	1.1	-1.0	YNL254C		1.0	-1.1	-1.0	-1.0	unknown function
CA0317	orf19.3959	*SSD1*	1.1	1.2	1.5	1.3	YDR293C	*SSD1*	1.0	-1.7	-1.3	1.1	Protein phosphatase (by homology)
CA0318	orf19.3957	*FOL2*	-1.0	-1.0	-1.1	-1.1	YGR267C	*FOL2*	1.0	-1.1	-1.0	1.1	GTP cyclohydrolase (by homology)
CA0321	orf19.7861	*APL2*	-1.2	-1.1	1.0	1.0	YKL135C	*APL2*	1.0	-1.7	-1.6	-2.2	AP-1 complex subunit, beta1-adaptin (by homology)
CA0322	orf19.8459	*RPS9B*	1.4	1.1	1.1	1.2	YPL081W	*RPS9A*	1.0	1.5	1.9	2.1	Ribosomal protein
CA0323	orf19.9378	*CDC95*	1.1	1.6	1.6	1.4	YPR016C	*TIF6*	1.0	-1.5	-1.7	-1.6	translation initiation factor 6 (eIF6) (by homology)
CA0324	orf19.9377	*STT4*	-1.0	-1.1	-1.0	-1.1	YLR305C	*STT4*	1.0	-1.5	-1.4	-1.6	Phosphatidylinositol-4-kinase (by homology)
CA0328	orf19.3778	*IPF15217.3F*	-1.1	-1.0	1.1	-1.0	YCR072C		1.0	1.1	1.0	1.5	WD-repeat protein, 3-prime end (by homology)
CA0329	orf19.3777	*IMG2*	-1.0	1.0	-1.1	-1.0	YCR071C	*IMG2*	1.0	1.0	-1.0	-1.5	Required for Integrity of Mitochondrial Genome (by homology)
CA0330	orf19.797	*BAT21*	-1.1	-1.1	1.1	1.0	YJR148W	*BAT2*	1.0	-1.7	-1.0	-1.0	branched-chain amino acid transaminase (by homology)
CA0331	orf19.798	*ANC1*	1.1	1.0	1.0	-1.0	YPL129W	*ANC1*	1.0	1.1	1.3	1.2	TFIIF subunit, transcription initiation factor (by homology)
CA0332	orf19.12981	*FEN2*	1.1	-1.2	-1.1	-1.0	YCR028C	*FEN2*	1.0	-1.7	-1.8	-1.4	allantoate permease transporter (by homology)
CA0341	orf19.1788	*XKS1*	-1.1	-1.3	-1.4	-1.2	YGR194C	*XKS1*	1.0	-1.4	-1.6	-1.5	xylulokinase (by homology)
CA0342	orf19.1789	*IPF10470*	-1.1	-1.0	1.0	1.0	YJR003C		1.0	-1.3	-1.3	-1.2	unknown function
CA0343		*LYS1.5EOC*	-1.1	-1.3	-1.3	-1.4	YIR034C	*LYS1*	1.0	1.1	1.1	1.6	saccharopine dehydrogenase, 5-prime end (by homology)
CA0345	orf19.10681	*ACH1*	1.7	-4.0	-3.1	-5.5	YBL015W	*ACH1*	1.0	-3.4	-3.9	-5.1	acetyl-coenzyme-A hydrolase (by homology)
CA0346	orf19.10341	*ROX1*	1.1	1.0	-1.0	1.0	YPR065W	*ROX1*	1.0	-1.2	-1.3	-1.3	Possible heme-dependent transcriptional repressor (by homology)
CA0349	orf19.1813	*IPF19026*	1.2	1.3	1.5	1.3	YAL053W		1.0	1.0	1.0	1.2	unknown function
CA0350	orf19.7784	*SNU114*	-1.0	-1.0	-1.0	-1.0	YKL173W	*SNU114*	1.0	-1.7	-1.3	-1.1	snRNP-specific protein (by homology)
CA0351	orf19.145	*RPB4.3F*	-1.1	-1.0	-1.1	-1.0	YJL140W	*RPB4*	1.0	1.2	1.1	-1.0	DNA-directed RNA polymerase II, 32 kDa subunit, 3-prime end (by homo
CA0353	orf19.147	*YAK1.3F*	1.0	-1.0	1.0	1.0	YJL141C	*YAK1*	1.0	1.2	1.6	-1.2	serine/threonine protein kinase, 3-prime end (by homology)
CA0356	orf19.13952	*IPF2532*	-1.0	1.1	1.0	-1.0	YLR104W		1.0	-1.8	-1.4	-1.3	unknown function
CA0357	orf19.333	*FCY22*	1.0	1.1	1.3	1.1	YER060W	*FCY21*	1.0	-1.4	1.0	-1.3	purine-cytosine permease (by homology)
CA0362	orf19.9009	*TEF1*	1.6	1.5	1.1	1.2	YPR080W	*TEF1*	1.0	1.7	2.9	3.7	translation elongation factor eEF1 alpha-A chain
CA0364	orf19.1525	*IPF15983*	-1.1	-1.1	-1.1	-1.0	YLR363C	*NMD4*	1.0	-1.2	-1.5	-1.3	unknown function
CA0367	orf19.1352	*TIM22*	-1.1	1.5	1.7	1.4	YDL217C	*TIM22*	1.0	1.1	1.1	1.2	Mitochondrial import inner membrane translocase subunit (by homology)
CA0370		*IPF13678*	1.1	1.2	1.6	1.3	YDR276C	*PMP3*	1.0	-1.1	-1.1	-1.1	unknown function
CA0372	orf19.1086	*IPF10062*	1.1	1.0	-1.0	1.0	YNR051C	*BRE5*	1.0	-1.1	1.1	1.8	unknown function

CA0375	orf19.2706	*CRH11*	1.1	1.2	1.5	1.2	YGR189C	*CRH1*	1.0	-1.0	-1.1	1.0	Probable membrane protein (by homology)
CA0376		*QCR9*	1.1	-1.0	1.1	1.2	YGR183C	*QCR9*	1.0	1.1	1.2	-1.6	ubiquinol--cytochrome-c reductase subunit 9(by homology)
CA0377	orf19.2708	*IPF14356*	1.0	1.0	1.0	-1.0	YLR022C		1.0	-1.4	-1.1	1.1	unknown function
CA0378	orf19.3170	*IPF3178*	-1.1	-1.2	-1.3	-1.1	YFL023W	*FYV11*	1.0	-1.6	-1.2	1.0	Unknown function
CA0379	orf19.3173	*SSP120*	1.0	1.0	-1.0	1.0	YLR250W	*SSP120*	1.0	1.4	2.0	2.2	secretory protein (by homology)
CA0381	orf19.2825	*IPF16047*	1.0	1.0	1.1	1.0	YKR071C	*DRE2*	1.0	-1.1	1.1	1.1	unknown function
CA0382	orf19.1842	*IPF16030*	-1.2	-1.1	-1.1	-1.1	YCR038C	*BUD5*	1.0	-1.9	-1.7	-1.4	similar to Saccharomyces cerevisiae Bud5p GDP/GTP exchange factor f
CA0384	orf19.10172	*PCL1*	1.0	-1.1	-1.1	-1.1	YNL289W	*PCL1*	1.0	-1.0	1.1	1.0	cyclin, G1/S-specific (by homology)
CA0386	orf19.1862	*IPF4065*	1.0	1.2	1.3	1.2	YHR087W		1.0	1.8	1.4	-1.7	unknown function
CA0388	orf19.1907	*IPF14468*	-1.0	1.0	1.2	-1.0	YGR089W		1.0	1.2	-1.2	-1.2	unknown function
CA0390	orf19.244	*DCG1*	-1.0	-1.0	-1.1	1.0	YIR030C	*DCG1*	1.0	-1.1	1.1	1.5	involved in nitrogen-catabolite metabolism (by homology)
CA0391	orf19.7875	*DDC1*	1.0	1.0	1.0	1.1	YPL194W	*DDC1*	1.0	1.0	1.1	1.0	DNA damage checkpoint protein, delays the cell cycle at the G1/S bound
CA0397	orf19.1930	*FRE31*	1.0	-1.0	-1.0	1.0	YNR060W	*FRE4*	1.0	1.3	1.0	1.0	Ferric reductase (by homology)
CA0398	orf19.1986	*ARO2*	-1.1	-1.2	-1.1	-1.2	YGL148W	*ARO2*	1.0	1.6	1.8	2.8	chorismate synthase (by homology)
CA0399	orf19.1988	*CDC45*	-1.1	-1.0	1.0	-1.0	YLR103C	*CDC45*	1.0	-1.1	-1.2	-1.2	Chromosomal DNA replication initiation protein (by homology)
CA0402	orf19.1990	*IPF15225*	1.0	1.1	1.1	1.0	YJL036W	*SNX4*	1.0	-1.5	-1.2	-1.2	Sorting nexin-like protein (by homology)
CA0403	orf19.1989	*IPF15224*	-1.0	1.2	1.4	1.2	YKL046C		1.0	-1.0	1.0	1.2	unknown function
CA0404	orf19.5548	*LYS14*	-1.0	-1.0	-1.0	-1.0	YDR034C	*LYS14*	1.0	-1.1	-1.0	1.0	transcription factor involved in lysine biosynthesis (by homology)
CA0408	orf19.5544	*SAC6.5F*	-1.4	-1.1	-1.2	-1.1	YDR129C	*SAC6*	1.0	1.0	1.5	1.0	actin filament bundling protein, fimbrin, 5-prime end (by homology)
CA0409	orf19.5755	*PHO80*	-1.0	-1.0	-1.1	-1.0	YOL001W	*PHO80*	1.0	1.1	1.4	1.2	Cyclin (by homology)
CA0410	orf19.13180	*IPF15065*	1.2	1.1	1.1	1.1	YMR178W		1.0	-1.3	-1.3	-1.5	unknown function
CA0411	orf19.1507	*IPF17676*	1.0	1.1	1.1	-1.0	YBR158W	*CST13*	1.0	-1.1	-1.0	1.1	similar to Saccharomyces cerevisiae Cst13p involved in chromosome sta
CA0415	orf19.1224	*FRP3*	1.4	-1.5	-1.6	-1.7	YCR010C	*ADY2*	1.0	-1.1	-1.6	-1.7	member of the FRP family of proteins related to Yarrowia lipolytica glyox
CA0417	orf19.2225	*UBC13*	1.2	1.1	1.1	1.1	YDR092W	*UBC13*	1.0	-1.4	-1.3	-1.2	E2 ubiquitin-conjugating enzyme (by homology)
CA0419	orf19.2228	*IPF19864*	-1.0	-1.1	-1.1	1.1	YGR080W	*TWF1*	1.0	-1.0	-1.1	1.1	unknown function
CA0420	orf19.2229	*IPF9048*	1.0	1.0	1.2	-1.1	YPR093C		1.0	1.1	1.1	1.0	unknown function
CA0421	orf19.2230	*IPF9047*	-1.0	1.1	-1.0	1.0	YPR094W		1.0	-1.0	-1.0	-1.0	unknown function
CA0425	orf19.9252	*PPH21*	1.2	1.3	1.7	1.6	YDL188C	*PPH22*	1.0	1.3	1.2	1.3	protein ser/thr phosphatase PP2A-1 (by homology)
CA0426	orf19.2760	*CFT1*	-1.1	-1.0	-1.0	1.0	YDR301W	*CFT1*	1.0	-1.1	1.1	1.5	pre-mRNA 3 -end processing factor CF II (by homology)
CA0427	orf19.2761	*IPF11995*	-1.0	-1.0	1.2	-1.0	YDR302W	*GPI11*	1.0	-1.4	-1.0	-1.1	unknown function
CA0428	orf19.1613	*ILV2*	-1.5	-2.0	-2.5	-2.0	YMR108W	*ILV2*	1.0	1.4	2.5	3.1	acetolactate synthase (by homology)
CA0430	orf19.1339	*PRC1*	-1.0	-1.0	-1.0	-1.0	YMR297W	*PRC1*	1.0	1.2	1.3	-1.1	Carboxypeptidase Y precursor
CA0431	orf19.1340	*IPF7927*	-1.0	-1.0	-1.0	1.8	YDL124W		1.0	1.5	1.6	1.4	putative aldose reductase (by homology)
CA0433	orf19.1342	*SHM1*	-1.3	-1.4	-1.6	-1.4	YBR263W	*SHM1*	1.0	-1.1	1.3	1.5	Serine hydroxymethyltransferase precursor, mitochondrial (by homology)
CA0435	orf19.9305	*UGP1*	-1.3	1.1	1.3	1.1	YKL035W	*UGP1*	1.0	2.1	2.3	1.8	UTP--glucose-1-phosphate uridylyltransferase (by homology)
CA0436		*RBL2*	1.0	1.1	1.1	1.1	YOR265W	*RBL2*	1.0	1.0	1.1	-1.0	Beta-tubulin binding protein (by homology)
CA0437	orf19.9308	*DIT1*	1.1	1.0	1.1	1.0	YDR403W	*DIT1*	1.0	-1.1	-1.0	-1.3	Spore wall maturation protein (by homology)
CA0438	orf19.8419	*STE4.5EOC*	-1.0	1.1	1.0	1.1	YOR212W	*STE4*	1.0	-1.2	1.0	1.1	GTP-binding protein beta subunit of the pheromone pathway, 5-prime en
CA0439	orf19.13015	*IPF12478*	-1.1	-1.0	-1.1	-1.0	YML034W	*SRC1*	1.0	-1.4	-1.4	-1.7	unknown function
CA0443	orf19.7727	*SPB1*	1.1	-1.2	-1.2	-1.1	YCL054W	*SPB1*	1.0	-1.4	-1.2	1.1	Putative methyltransferase by homology
CA0444	orf19.75	*IPF17429.3F*	-1.1	-1.1	-1.2	1.0	YDR166C	*SEC5*	1.0	1.9	1.6	2.1	similar to Saccharomyces cerevisiae Sec5p required for exocytosis, 3-pri
CA0447	orf19.2297	*IPF14275*	-1.1	1.0	1.0	1.1	YPL051W	*ARL3*	1.0	-1.2	-1.1	-1.1	Probable ADP-ribosylation factors (by homology)
CA0449	orf19.2379	*MOT2.3*	1.1	-1.0	-1.0	-1.1	YER068W	*MOT2*	1.0	1.1	1.2	1.2	transcriptional repressor, 3-prime end (by homology)
CA0450	orf19.2378	*IPF9353*	-1.0	-1.1	-1.0	-1.0	YMR123W	*PKR1*	1.0	-1.3	-1.1	1.4	unknown function
CA0453	orf19.8880	*IPF13552*	-1.1	-1.1	-1.1	-1.1	YDR316W		1.0	-1.5	-1.5	-1.5	putative methyltransferase (by homology)
CA0454	orf19.8879	*RPN6*	-1.0	-1.1	-1.1	1.1	YDL097C	*RPN6*	1.0	1.3	1.7	2.5	subunit of the regulatory particle of the proteasome (by homology)
CA0457	orf19.2432	*IPF15604*	-1.2	1.1	1.0	1.1	YFL031W	*HAC1*	1.0	1.3	3.0	2.3	transcription factor (by homology)
CA0460	orf19.2518	*SEC17*	-1.0	-1.0	1.0	-1.1	YBL050W	*SEC17*	1.0	1.2	1.3	1.2	transport vesicle fusion protein (by homology)
CA0461	orf19.2519	*IPF4972*	1.0	-1.0	1.1	-1.0	YJR112W	*NNF1*	1.0	-2.4	-1.9	-1.8	unknown function
CA0462	orf19.2520	*MRPS28*	1.0	-1.1	-1.1	-1.1	YDR337W	*MRPS28*	1.0	-1.0	-1.1	1.1	ribosomal protein (by homology)
CA0464	orf19.7798	*IPF14116*	1.1	-1.5	-1.3	-1.2	YOR084W		1.0	-1.4	-1.0	-1.3	unknown function
CA0465	orf19.7800	*IPF14113*	-1.3	-1.0	-1.1	-1.0	YIL130W		1.0	-1.1	1.1	1.1	unknown function
CA0466	orf19.1977	*URA4*	1.1	1.1	1.1	1.1	YLR420W	*URA4*	1.0	-1.2	-1.1	-1.1	dihydroorotase (by homology)
CA0468	orf19.9531	*DIB1*	1.0	1.0	1.1	1.1	YPR082C	*DIB1*	1.0	-1.2	-1.1	-1.2	Component of the U4/U6.U5 snRNP (by homology)
CA0469	orf19.2621	*IPF18977*	1.0	-1.0	-1.0	1.0	YER029C	*SMB1*	1.0	1.6	2.2	1.7	similar to Saccharomyces cerevisiae Smb1p associated with U1 snRNP a
CA0470	orf19.2622	*YPT32*	-1.1	-1.4	-1.6	-1.3	YER031C	*YPT31*	1.0	-1.1	1.1	1.2	small GTP-binding protein essential for Golgi function (by homology)
CA0472	orf19.13176	*STL1*	1.3	-3.9	-3.9	-4.3	YDR536W	*STL1*	1.0	-1.4	-2.3	-3.0	sugar transporter (by homology)
CA0475	orf19.8085	*IPF2580*	-1.0	-1.1	-1.2	-1.0	YOR140W	*SFL1*	1.0	-1.4	-1.4	-1.4	unknown function
CA0476	orf19.8088	*UBP2*	-1.1	1.1	-1.0	-1.0	YOR124C	*UBP2*	1.0	-1.4	-1.4	-1.5	Ubiquitin-specific proteinase (by homology)
CA0478	orf19.13437	*YAE8*	-1.0	1.0	-1.1	1.0	YAL048C		1.0	1.1	-1.0	1.1	GTP-binding protein (by homology)
CA0479	orf19.2630	*IPF16191*	-1.0	-1.0	-1.0	-1.0	YDL059C	*RAD59*	1.0	-1.3	-1.3	-1.2	similar to Saccharomyces cerevisiae Rad59p recombination and DNA re

CA0481	orf19.7766	*STE14*	-1.0	1.0	-1.0	-1.1	YDR410C	*STE14*	1.0	-1.4	1.0	1.0	farnesyl cystein carboxyl-methyltransferase (by homology)
CA0483	orf19.7764	*SEC9*	1.0	1.1	1.1	1.0	YGR009C	*SEC9*	1.0	-1.1	1.0	-1.1	transport protein (by homology)
CA0485	orf19.11038	*IPF17574*	-1.1	-1.1	-1.2	-1.1	YAR014C	*BUD14*	1.0	-1.1	1.2	1.1	Unknown function
CA0488	orf19.261	*SEC59*	-1.1	-1.1	1.0	-1.1	YMR013C	*SEC59*	1.0	-1.1	-1.1	-1.3	Dolichol kinase (by homology)
CA0492	orf19.9068	*SNU71*	1.0	-1.1	-1.1	-1.0	YGR013W	*SNU71*	1.0	-1.4	-1.1	1.0	Associated with U1 snRNP (by homology)
CA0493	orf19.1492	*PRP39.3*	1.0	-1.0	1.1	-1.0	YML046W	*PRP39*	1.0	-1.6	-1.5	-1.3	pre-mRNA splicing factor, 3-prime end (by homology)
CA0494	orf19.9070	*RAD7*	1.0	1.2	1.2	-1.0	YJR052W	*RAD7*	1.0	-1.4	1.1	-1.0	nucleotide excision repair protein (by homology)
CA0495	orf19.2659	*IPF20056*	-1.0	12.8	8.1	13.5	YER067W		1.0	1.8	2.8	-1.4	unknown function
CA0496	orf19.2660	*IPF11644*	-1.0	-1.0	1.0	-1.0	YPR023C	*EAF3*	1.0	1.1	1.2	1.1	unknown function
CA0500	orf19.4793	*IPF20058*	-1.1	-1.1	-1.0	-1.0	YOR252W		1.0	-1.3	-1.2	-1.2	unknown function
CA0502	orf19.2664	*IPF16761*	1.0	1.0	1.0	-1.0	YNL085W	*MKT1*	1.0	1.1	1.6	1.7	unknown function
CA0504	orf19.2778	*IPF16466*	-1.2	-1.1	-1.5	-1.3	YKL014C		1.0	-1.4	-1.3	-1.2	unknown function
CA0506	orf19.3626	*IPF11988*	1.0	1.0	-1.1	-1.0	YML096W		1.0	-1.9	-1.6	-1.9	unknown function
CA0508	orf19.11107	*IPF11991*	-1.1	-1.1	-1.4	-1.1	YMR287C	*MSU1*	1.0	-1.3	-1.2	-1.5	similar to Saccharomyces cerevisiae Msu1p 3 -5 exonuclease for RNA 3
CA0509	orf19.10684	*CDC24*	-1.1	1.2	-1.0	1.0	YAL041W	*CDC24*	1.0	-2.3	-1.5	-1.5	GTP/GDP exchange factor for Cdc42p (by homology)
CA0510	orf19.10685	*ETF1*	-1.3	-1.1	-1.1	1.0	YOR356W		1.0	-1.2	-1.1	-1.3	ETF-UBIQUINONE OXIDOREDUCTASE (by homology)
CA0511	orf19.4953	*IPF13975*	-1.1	1.1	1.0	-1.0	YCL047C		1.0	-1.4	1.1	-1.0	unknown function
CA0512	orf19.4954	*VMA16*	1.3	-1.0	1.4	1.2	YHR026W	*PPA1*	1.0	1.3	1.6	1.8	H+-ATPase 23 KD subunit, vacuolar (by homology)
CA0513	orf19.4955	*IPF13972*	-1.0	1.0	-1.0	-1.0	YCL048W		1.0	-1.3	-1.1	1.0	unknown function
CA0514	orf19.4645	*BEM1*	1.0	1.1	1.1	1.0	YBR200W	*BEM1*	1.0	-1.4	-1.1	-1.2	bud emergence mediator (by homology)
CA0517	orf19.2803	*HEM13*	1.1	-1.0	1.0	1.1	YDR044W	*HEM13*	1.0	-1.1	1.0	-1.2	by homology S. cerev.: coproporphyrinogen III oxidase
CA0519	orf19.11016	*MRPL10.3*	1.0	-1.0	1.0	1.0	YNL284C	*MRPL10*	1.0	-1.0	-1.3	-1.5	ribosomal protein, 3-prime end (by homology)
CA0521	orf19.3530	*CKA2*	1.0	-1.0	1.1	-1.0	YOR061W	*CKA2*	1.0	-1.6	-1.4	-1.3	casein kinase II alpha chain (by homology)
CA0523	orf19.11012	*IPF4459*	1.1	1.0	1.1	1.1	YKR074W		1.0	-1.5	-1.1	-1.2	unknown function
CA0525	orf19.8726	*MSB1*	-1.0	1.0	1.1	-1.1	YOR188W	*MSB1*	1.0	-1.7	-1.5	-1.6	Morphogenesis-related protein (by homology)
CA0526	orf19.2655	*BUB3*	1.0	1.3	2.0	1.5	YOR026W	*BUB3*	1.0	1.2	1.3	1.1	cell cycle arrest protein (by homology)
CA0528	orf19.3622	*ANP1*	-1.2	-1.1	-1.4	-1.1	YEL036C	*ANP1*	1.0	-1.5	-1.0	-1.1	Golgi mannosyltransferase (by homology)
CA0529	orf19.3623	*SMC2*	-1.0	1.0	-1.0	-1.0	YFR031C	*SMC2*	1.0	1.5	2.1	3.0	chromosome segregation protein (by homology)
CA0530	orf19.8685	*F19633.3EO*	1.0	1.2	1.1	1.1	YCR093W	*CDC39*	1.0	-2.0	-3.2	-2.5	similar to Saccharomyces cerevisiae Cdc39p nuclear protein involved in
CA0531	orf19.8686	*UBC1*	1.2	1.0	1.4	1.2	YDR177W	*UBC1*	1.0	-1.2	1.1	1.1	ubiquitin-conjugating enzyme by homology
CA0532	orf19.5068	*IRE1*	-1.1	-1.0	-1.0	-1.2	YHR079C	*IRE1*	1.0	-1.3	-1.2	-1.1	protein kinase (by homology)
CA0533	orf19.5067	*IPF19872*	1.0	-1.0	1.0	-1.0	YHR081W		1.0	-1.5	1.0	1.3	unknown function
CA0534	orf19.5066	*IPF15607*	1.1	1.1	1.1	1.0	YDR412W		1.0	-1.1	1.1	1.3	unknown function
CA0535	orf19.5065	*IPF15606*	1.1	1.1	1.2	1.1	YDR414C	*ERD1*	1.0	-2.4	-1.5	-1.4	similar to Saccharomyces cerevisiae Erd1p required for retention of lumi
CA0536	orf19.2815	*PANC.3*	1.0	-1.0	1.0	1.0	YIL145C	*PAN6*	1.0	1.0	1.1	1.4	pantothenate synthetase, 3-prime end (by homology)
CA0537	orf19.2818	*PRP16*	-1.1	-1.1	-1.3	-1.1	YKR086W	*PRP16*	1.0	-3.0	-2.8	-3.4	RNA-dependent ATPase (by homology)
CA0539	orf19.2820	*NUP57*	1.0	-1.0	1.1	-1.0	YGR119C	*NUP57*	1.0	-1.1	-1.0	1.1	nuclear pore protein (by homology)
CA0541	orf19.1083	*IPF14574*	1.1	1.1	1.2	1.1	YMR132C		1.0	1.1	1.1	1.1	unknown function
CA0543	orf19.2867	*IPF3255*	-1.1	-1.1	-1.1	-1.1	YOR069W	*VPS5*	1.0	-1.1	-1.0	1.1	similar to Saccharomyces cerevisiae Vps5p involved in Golgi retention a
CA0548	orf19.2454	*PHO87*	-1.1	-1.0	1.1	1.0	YCR037C	*PHO87*	1.0	1.1	1.0	1.1	Member of the phosphate permease family (by homology)
CA0551	orf19.5531	*CDC37*	-1.0	-1.2	-1.3	-1.1	YDR168W	*CDC37*	1.0	-1.8	-1.4	-1.6	Cell division control protein (by homology)
CA0552	orf19.5533	*IPF4343*	-1.0	-1.0	1.0	-1.0	YML097C	*VPS9*	1.0	-1.2	-1.3	-1.4	similar to Saccharomyces cerevisiae Vps9pvacuolar sorting protein
CA0553	orf19.5534	*IPF16653*	1.0	1.3	1.5	1.4	YKR088C		1.0	-1.4	-1.2	-1.6	unknown function
CA0554	orf19.11444	*HAS1*	-1.2	-1.0	-1.1	-1.1	YMR290C	*HAS1*	1.0	1.3	1.9	2.1	ATP-DEPENDENT RNA HELICASE (by homology)
CA0555	orf19.3960	*HYS2*	-1.0	-1.1	-1.0	-1.1	YJR006W	*HYS2*	1.0	-1.3	-1.0	-1.1	DNA-directed DNA polymerase delta (by homology)
CA0559	orf19.86	*GPX1*	1.0	1.5	1.6	1.3	YIR037W	*HYR1*	1.0	-1.1	-1.2	-1.5	glutathione peroxidase (by homology)
CA0561	orf19.2925	*CIN4*	-1.0	1.0	1.0	1.0	YMR138W	*CIN4*	1.0	-1.0	1.0	-1.0	GTP-binding protein
CA0562	orf19.2926	*PSO2*	-1.1	-1.1	-1.2	-1.2	YMR137C	*PSO2*	1.0	-1.1	-1.1	-1.0	Interstrand crosslink repair protein (by homology)
CA0563	orf19.2927	*MNN11*	-1.0	-1.1	-1.1	1.0	YJL183W	*MNN11*	1.0	-1.4	-1.2	-1.4	Mannosyltransferase complex component (by homology)
CA0565	orf19.6250	*IPF13526*	-1.0	-1.1	-1.1	-1.1	YPR129W	*SCD6*	1.0	1.0	1.1	1.0	unknown function
CA0566	orf19.6252	*IPF13522*	1.0	-1.1	-1.1	-1.1	YPR133C	*IWS1*	1.0	-1.2	-1.1	-1.1	unknown function
CA0567	orf19.13632	*RPS23*	1.0	-1.1	-1.0	1.1	YPR132W	*RPS23B*	1.0	2.1	2.8	3.5	Ribosomal protein S23 (by homology)
CA0568	orf19.8729	*APS2*	-1.1	1.0	1.1	1.1	YJR058C	*APS2*	1.0	-1.4	-1.1	-1.1	AP-2 complex subunit, sigma2 subunit (by homology)
CA0569	orf19.8730	*CDC8*	1.1	1.1	1.2	1.1	YJR057W	*CDC8*	1.0	-1.1	-1.1	-1.2	dTMP kinase (by homology)
CA0570	orf19.8732	*SVL3*	1.1	1.1	1.1	1.1	YPL032C	*SVL3*	1.0	-1.1	1.0	-1.1	Involved in vacuole function (by homology)
CA0571	orf19.9369	*CDC43*	-1.0	-1.1	-1.0	1.0	YGL155W	*CDC43*	1.0	-1.3	-1.3	-1.5	geranylgeranyltransferase I
CA0572	orf19.9370	*IPF14864*	-1.2	-1.1	-1.2	-1.0	YDL119C		1.0	-1.3	-1.2	1.4	unknown function
CA0573	orf19.9371	*PEX14*	-1.2	-1.2	-1.4	-1.2	YGL153W	*PEX14*	1.0	-1.0	-1.2	-1.2	peroxisomal protein (by homology)
CA0576	orf19.6232	*NPR1*	1.1	2.0	2.7	2.2	YNL183C	*NPR1*	1.0	-1.3	1.1	1.2	nitrogen permease reactivator protein (by homology)
CA0578	orf19.3071	*IPF9605*	-1.1	1.1	1.0	1.1	YMR036C	*MIH1*	1.0	1.1	1.1	1.3	similar to Saccharomyces cerevisiae Mih1p M-phase inducing protein tyr
CA0580	orf19.3559	*F3184.EXON*	1.1	1.0	-1.1	1.0	YGR165W		1.0	1.1	-1.2	-1.3	unknown function, exon 2

CA0581	orf19.3558	*IPF3181*	1.3	1.3	1.4	1.3	YDL018C	*ERP3*	1.0	-1.1	1.0	1.1	similar to Saccharomyces cerevisiae Erp3p p24 protein involved in memb
CA0582	orf19.11041	*IPF3180*	1.1	-1.0	-1.0	-1.0	YDR437W		1.0	-1.3	-1.3	-1.2	unknown function
CA0583	orf19.12526	*GSH1.EXON2*	-1.2	-1.1	-1.2	-1.1	YJL101C	*GSH1*	1.0	-1.2	-1.3	-1.2	gamma-glutamylcysteine synthetase, exon 2 (by homology)
CA0585	orf19.12528	*ADE5,7*	1.0	-1.0	-1.0	-1.1	YGL234W	*ADE5,7*	1.0	1.2	1.5	2.7	phosphoribosylamine-glycine ligase and phosphoribosylformylglycinamid
CA0587	orf19.8753	*SPO14.5EOC*	-1.1	1.0	-1.5	-1.1	YKR031C	*SPO14*	1.0	-1.6	-1.6	-1.7	phospholipase D, 5-prime end
CA0590	orf19.8756	*IPF13079*	-1.1	-1.0	-1.0	1.0	YDR336W		1.0	1.1	1.3	1.1	unknown function
CA0591	orf19.1816	*ALS3.5EOC*	1.1	1.0	1.0	-1.0	YJR004C	*SAG1*	1.0	-2.6	-2.3	-2.3	agglutinin-like protein, 5-prime end
CA0593	orf19.4904	*ARP6*	1.0	-1.0	1.2	1.0	YLR085C	*ARP6*	1.0	1.0	1.0	-1.1	actin-related protein (by homology)
CA0594	orf19.12368	*IPF8860*	1.0	-1.0	-1.0	1.0	YMR281W	*GPI12*	1.0	-1.1	-1.2	-1.4	similar to Saccharomyces cerevisiae Gpi12p N-acetylglucosaminyl phosp
CA0596	orf19.12346	*IPF9706*	-1.0	-1.3	-1.5	-1.3	YBR203W		1.0	1.3	1.2	1.3	unknown function
CA0597	orf19.12345	*IPF9704*	1.1	-1.0	1.0	1.1	YKR062W	*TFA2*	1.0	-1.4	-1.3	-1.6	similar to Saccharomyces cerevisiae Tfa2p TFIIE subunit (transcription ir
CA0599	orf19.10184	*IPF12428*	1.1	-1.2	-1.1	-1.0	YHR088W	*RPF1*	1.0	-1.3	-1.2	-1.1	unknown function
CA0600	orf19.2666	*MSN5.5F*	-1.1	1.4	1.4	1.1	YDR335W	*MSN5*	1.0	1.1	1.3	1.5	Importin-beta family member required for nuclear export of Pho4p and in
CA0603	orf19.3076	*IPF1709*	1.1	1.0	1.4	1.2	YDR100W		1.0	1.2	1.1	-1.0	unknown function
CA0604	orf19.3077	*VID21*	-1.0	-1.0	-1.0	1.1	YDR359C	*VID21*	1.0	-1.8	-1.6	-1.2	unknown function
CA0605	orf19.9240	*UTR2*	-1.1	1.0	-1.0	1.2	YEL040W	*UTR2*	1.0	-1.2	-1.1	2.1	1,3-1,4-beta-glucanase (by homology)
CA0606	orf19.9241	*COP1*	-1.2	-1.2	-1.3	-1.2	YDL145C	*COP1*	1.0	-1.4	-1.5	-1.4	coatomer complex alpha chain of secretory pathway vesicles (by homolo
CA0615	orf19.1601	*RPL3*	-1.2	-1.3	-1.5	-1.4	YOR063W	*RPL3*	1.0	1.8	2.9	3.0	60S large subunit ribosomal protein L3.e (by homology)
CA0616	orf19.2619	*PHO11*	1.0	2.0	2.9	1.7	YBR092C	*PHO3*	1.0	-1.0	-1.2	-1.1	Secreted acid phosphatase
CA0617	orf19.2618	*MET2*	-1.0	-1.3	-1.3	-1.2	YNL277W	*MET2*	1.0	1.1	-1.1	1.0	Homoserine O-acetyltransferase
CA0618	orf19.2616	*UGT51*	-1.0	1.0	1.0	-1.0	YLR189C	*UGT51*	1.0	-1.1	-1.1	-1.1	UDP-glucose:sterol glucosyltransferase
CA0622	orf19.3149	*IPF14171*	1.2	1.1	1.2	1.4	YGR086C		1.0	1.2	1.3	-1.7	unknown function
CA0623	orf19.3153	*MSS4.3*	-1.1	-1.1	1.1	1.1	YDR208W	*MSS4*	1.0	-1.5	-1.5	-1.4	phosphatidylinositol-4-phosphate 5-kinase, 3-prime end (by homology)
CA0624	orf19.3154	*IPF312*	-1.1	-1.1	-1.1	-1.0	YJR080C		1.0	-1.2	-1.1	-1.4	unknown function
CA0626	orf19.3161	*IPF3161*	1.1	-1.1	-1.2	-1.1	YNR054C		1.0	-1.2	1.0	1.2	Unknown function
CA0627	orf19.3160	*HSP12*	1.5	-1.6	-1.8	-1.3	YFL014W	*HSP12*	1.0	-1.3	-2.1	-9.5	Heat shock protein (by homology)
CA0628	orf19.773	*IPF3878*	-1.0	-1.0	1.0	-1.0	YLR221C	*RSA3*	1.0	1.1	1.2	1.2	unknown function
CA0631	orf19.11813	*IPF11698*	1.0	1.1	1.3	1.1	YNL125C	*ESBP6*	1.0	-1.1	-1.3	-1.4	similar to Saccharomyces cerevisiae Esbp6p probable monocarboxylate
CA0632	orf19.11812	*RPS5*	1.2	-1.2	-1.2	-1.1	YJR123W	*RPS5*	1.0	-1.6	-1.4	-1.1	ribosomal protein S5.e (by homology)
CA0633	orf19.9340	*IPF16269*	1.0	-1.0	1.0	1.0	YGR278W		1.0	1.2	1.1	1.0	unknown function
CA0634	orf19.1772	*IPF16267*	1.0	-1.1	-1.1	-1.0	YER077C		1.0	1.1	1.2	1.2	unknown function
CA0635	orf19.9342	*IPF9036*	1.0	1.0	1.1	-1.0	YNL216W	*RAP1*	1.0	-1.3	-1.4	-1.1	similar to Saccharomyces cerevisiae Rap1p DNA-binding protein with rep
CA0642	orf19.3732	*ERG25*	1.5	-1.1	1.1	-1.0	YGR060W	*ERG25*	1.0	-1.4	-1.3	-1.6	C-4 sterol methyl oxidase
CA0643	orf19.3733	*IDP2*	-1.1	-3.6	-4.8	-3.1	YLR174W	*IDP2*	1.0	-4.5	-7.5	-7.8	isocitrate dehydrogenase, cytosolic (by homology)
CA0649	orf19.3211	*RFC3*	1.1	1.0	1.0	-1.0	YNL290W	*RFC3*	1.0	-1.4	-1.4	-1.2	DNA replication factor C, 40 kDa subunit (by homology)
CA0652	orf19.10082	*SHP1*	-1.1	-1.1	-1.2	1.0	YBL058W	*SHP1*	1.0	-2.1	-2.0	-1.2	potential regulatory subunit for Glc7p (by homology)
CA0653	orf19.10083	*MET6*	1.1	-1.3	-1.3	-1.1	YER091C	*MET6*	1.0	-1.3	1.1	-1.6	BY HOMOLOGY TO S.CEREV.: 5-methyltetrahydropteroyltriglutamate-h
CA0657	orf19.5574	*IPF19877*	1.0	1.1	1.0	1.1	YGR012W		1.0	-1.1	-1.1	1.1	putative cysteine synthase (by homology)
CA0658	orf19.5575	*IPF16505*	1.1	-1.1	-1.1	-1.1	YPL112C		1.0	-1.3	-1.2	-1.3	Unknown function
CA0660	orf19.5577	*IPF16189.5F*	-1.1	-1.4	-2.0	-1.4	YDR531W		1.0	-1.5	-1.3	-1.1	panthotenate kinase, 5-prime end (by homology)
CA0661	orf19.8326	*APG7*	-1.0	1.0	1.0	-1.0	YHR171W	*APG7*	1.0	-1.1	-1.2	-1.3	component of the autophagic system (by homology)
CA0662	orf19.708	*SPC97*	-1.0	-1.1	1.1	-1.0	YHR172W	*SPC97*	1.0	-1.6	-1.3	1.1	spindle pole body component (by homology)
CA0663	orf19.709	*PUP2*	1.2	1.3	1.3	1.1	YGR253C	*PUP2*	1.0	-1.7	-1.1	1.3	20S proteasome subunit(alpha5) (by homology)
CA0664	orf19.710	*LSC2.3EOC1*	1.0	-2.7	-2.9	-2.7	YGR244C	*LSC2*	1.0	1.1	-1.3	-2.7	succinate-CoA ligase beta subunit, 3-prime end (by homology)
CA0665	orf19.11733	*INT1*	-1.2	-1.0	-1.2	-1.2	YJR092W	*BUD4*	1.0	-1.4	-1.2	-1.1	integrin-like protein alpha chain
CA0666	orf19.11734	*FIP1*	1.0	1.0	-1.0	-1.0	YJR093C	*FIP1*	1.0	-1.7	-1.6	-1.5	Component of pre-mRNA polyadenylation factor PF (by homology)
CA0667	orf19.11737	*TIF5*	-1.2	-1.4	-1.3	-1.3	YPR041W	*TIF5*	1.0	1.3	1.3	1.6	Translation initiation factor eIF5 (by homology)
CA0669	orf19.448	*IPF5918*	-1.1	-1.1	-1.1	-1.0	YOR042W		1.0	-1.4	-1.3	-1.9	unknown function
CA0670	orf19.449	*IPF5915*	-1.2	1.1	-1.1	-1.1	YKR070W		1.0	-1.3	-1.2	-1.4	phosphatidyl synthase (by homology)
CA0675	orf19.8771	*IPF13098*	-1.1	-1.1	-1.1	-1.0	YER152C		1.0	-1.6	-1.2	-1.6	unknown function
CA0677	orf19.8773	*IPF13095*	-1.1	-1.1	-1.1	1.1	YGL212W	*VAM7*	1.0	-1.1	-1.1	-1.0	unknown function
CA0678	orf19.8774	*IPF13094*	-1.2	-1.2	1.0	-1.1	YNL115C		1.0	-1.1	-1.4	-1.7	unknown function
CA0680	orf19.12169	*IPF14511.5F*	-1.0	1.0	-1.0	1.0	YMR313C		1.0	-1.7	-1.3	-1.1	unknown function, 5-prime end
CA0682	orf19.12171	*IPF14514*	1.0	1.0	-1.0	1.0	YMR312W	*TOT6*	1.0	-1.4	-1.0	1.0	unknown function
CA0685	orf19.13037	*ADO1*	1.1	-1.0	1.0	-1.1	YJR105W	*ADO1*	1.0	1.2	1.8	2.1	adenosine kinase (by homology)
CA0686	orf19.3222	*IPF162*	-1.2	-1.1	1.0	1.0	YGR125W		1.0	-1.1	1.1	1.2	sulphate transporter (by homology)
CA0687	orf19.3221	*CPA2*	-1.0	1.2	1.3	1.2	YJR109C	*CPA2*	1.0	1.3	1.4	3.8	arginine-specific carbamoylphosphate (by homology)
CA0692	orf19.10359	*PGM2*	-1.2	1.3	1.5	1.5	YMR105C	*PGM2*	1.0	3.1	3.3	1.0	Phosphoglucomutase (by homology)
CA0693	orf19.3288	*PF12606.5EO*	-1.1	-1.1	-1.2	-1.1	YNL123W		1.0	-1.2	-1.0	1.0	unknown function, 5-prime end
CA0696	orf19.3291	*HMT1*	1.0	1.1	1.1	1.0	YBR034C	*HMT1*	1.0	-1.0	-1.3	1.0	hnRNP methyltransferase (by homology)
CA0697	orf19.3363	*VTC4*	-1.0	1.4	1.9	1.5	YJL012C	*VTC4*	1.0	-1.2	1.1	1.7	putative polyphosphate synthetase (by homology)

CA0700	orf19.3366	*SHR3*	1.2	1.0	1.1	1.2	YDL212W	*SHR3*	1.0	1.5	1.5	1.6	endoplasmatic reticulum membrane protein (by homology)
CA0702	orf19.10430	*IPF11812*	-1.1	-1.2	-1.3	-1.1	YER008C	*SEC3*	1.0	-1.3	-1.1	-1.1	unknown function
CA0704	orf19.2915	*IPF11806*	-1.1	-1.0	1.1	-1.0	YER005W	*YND1*	1.0	1.0	1.6	1.1	similar to Saccharomyces cerevisiae Ynd1p nucleoside diphosphatase (
CA0711	orf19.9712	*VMA5*	-1.4	1.1	-1.1	1.1	YKL080W	*VMA5*	1.0	-1.9	-2.0	-1.7	H+-ATPase V1 domain 42 KD subunit (by homology)
CA0712	orf19.2167	*IPF13717*	1.0	-1.1	-1.2	-1.1	YKL082C		1.0	-1.9	-1.4	-1.1	unknown function
CA0713	orf19.2168	*IFJ2*	1.1	-1.1	-1.1	-1.0	YGR263C		1.0	-1.5	-1.3	-1.1	Unknown function
CA0715	orf19.3393	*DBP9*	-1.1	-1.2	-1.2	-1.1	YLR276C	*DBP9*	1.0	-1.5	-1.4	-1.3	dead box helicase
CA0716	orf19.3392	*DOG2*	-1.0	1.2	1.1	1.1	YHR044C	*DOG1*	1.0	1.2	1.4	1.0	2-deoxyglucose-6-phosphate phosphatase (by homology)
CA0718	orf19.3455	*IPF9782*	-1.0	-1.1	1.0	1.0	YPL060W	*LPE10*	1.0	-1.1	1.1	1.0	unknown function
CA0720	orf19.3457	*IPF17932*	1.1	-1.2	-1.0	1.0	YBR175W	*SWD3*	1.0	-1.3	-1.2	1.1	unknown function
CA0721	orf19.10405	*IPF10429*	1.1	1.0	1.2	1.1	YMR295C		1.0	-1.2	1.0	1.3	unknown function
CA0722	orf19.10404	*ERK1*	-1.0	1.2	1.5	1.4	YGR040W	*KSS1*	1.0	-1.0	-1.0	1.0	mitogen-activated protein kinase (FUS3 homolog)
CA0723	orf19.2885	*PRI2*	-1.1	-1.1	-1.0	1.0	YKL045W	*PRI2*	1.0	-2.2	-1.8	-1.8	DNA-directed DNA polymerase alpha , 58 KD subunit (DNA primase) (by
CA0727	orf19.11214	*IPF7347*	1.1	1.1	1.0	-1.0	YIL027C	*KRE27*	1.0	-1.1	1.1	1.0	unknown function
CA0728	orf19.11212	*IPF7345*	-1.2	-1.0	-1.2	-1.2	YAL031C	*FUN21*	1.0	1.0	1.1	-1.0	unknown function
CA0730	orf19.11208	*IPF7334*	1.0	-1.0	-1.1	-1.0	YOR004W		1.0	-1.7	-1.4	-1.1	unknown function
CA0731	orf19.11206	*IPF7333*	-1.0	1.1	1.1	1.0	YNL023C	*FAP1*	1.0	-1.4	-1.5	-1.6	unknown function
CA0733	orf19.4635	*NIP1*	-1.1	-1.1	-1.2	-1.1	YMR309C	*NIP1*	1.0	1.2	1.7	2.1	translation initiation factor subunit
CA0734	orf19.4634	*IPF8996*	1.1	-1.0	1.0	-1.0	YGL211W		1.0	-1.4	-1.2	-1.2	unknown function
CA0735	orf19.4633	*IPF8995*	1.1	-1.1	1.1	1.0	YMR226C		1.0	1.1	1.3	1.5	unknown function
CA0736	orf19.4632	*RPL20B*	1.3	-1.1	1.2	1.3	YOR312C	*RPL20B*	1.0	1.8	2.1	2.2	ribosomal protein (by homology)
CA0739	orf19.11816	*IPF18885*	1.0	-1.0	1.1	1.0	YLR459W	*CDC91*	1.0	-1.3	-1.2	-2.1	similar to Saccharomyces cerevisiae Cdc91p cell division control protein
CA0740		*IPF3262.3*	1.4	1.3	1.1	1.3	YBR173C	*UMP1*	1.0	-1.1	1.1	-1.1	unknown function, 3-prime end
CA0741	orf19.3141	*IPF3261*	-1.1	-1.2	-1.4	-1.4	YPL105C		1.0	-1.4	-1.1	-1.2	unknown function
CA0743		*RNA14.3EOC*	-1.1	-1.0	-1.1	-1.1	YMR061W	*RNA14*	1.0	-2.0	-1.9	-2.0	component of pre-mRNA 3 -end processing factor CF I, 3-prime end (by
CA0745	orf19.9104	*MTF1*	-1.1	-1.1	-1.0	1.1	YMR228W	*MTF1*	1.0	-1.1	-1.3	-1.3	RNA polymerase specific factor, mitochondrial (by homology)
CA0747	orf19.9102	*SNF2*	-1.3	-1.3	-1.8	-1.5	YOR290C	*SNF2*	1.0	-1.6	-1.4	-1.3	component of SWI/SNF global transcription activator complex (by homol
CA0748	orf19.1974	*TFS1*	1.1	-1.2	-1.3	-1.2	YLR178C	*TFS1*	1.0	1.1	-1.2	-2.2	cdc25-dependent nutrient- and ammonia-response cell-cycle regulator (b
CA0749	orf19.1973	*HAP5*	-1.0	-1.0	-1.0	-1.0	YOR358W	*HAP5*	1.0	-1.3	-1.4	-1.4	CCAAT-binding factor subunit (by homology)
CA0750	orf19.1972	*IPF6284*	1.0	-1.1	-1.1	-1.1	YHR207C		1.0	1.1	1.2	1.0	unknown function
CA0753	orf19.11287	*IPF10359*	-1.0	-1.0	-1.0	1.0	YMR135C		1.0	-1.2	-1.2	-1.4	unknown function
CA0758	orf19.3197	*PAP11*	-1.1	-1.0	-1.0	-1.0	YKR002W	*PAP1*	1.0	-1.8	-2.0	-1.6	poly(A) polymerase by homology to S. cerevisiae
CA0759	orf19.3198	*IPF11167*	-1.1	-1.1	-1.2	-1.1	YKR003W	*OSH6*	1.0	1.1	1.3	-1.0	unknown function
CA0760	orf19.3201	*IPF11161.3*	1.0	1.1	-1.0	1.0	YCR097W	*A1*	1.0	-1.0	-1.2	-1.2	unknown function, 3-prime end
CA0761	orf19.9146	*IPF8267*	-1.1	1.1	-1.1	-1.0	YOR291W		1.0	-1.3	-1.5	-1.3	P-type ATPase
CA0762	orf19.9147	*TAF67*	-1.0	-1.0	-1.0	1.0	YMR227C	*TAF67*	1.0	-1.1	1.1	1.3	TFIID subunit (by homology)
CA0763	orf19.2232	*RPL11*	1.4	1.0	-1.1	1.1	YPR102C	*RPL11A*	1.0	1.4	1.7	1.8	60S ribosomal protein (by homology)
CA0764	orf19.2233	*PRE2*	-1.0	-1.0	-1.1	1.0	YPR103W	*PRE2*	1.0	1.1	1.0	1.1	20S proteasome subunit (beta5)
CA0765	orf19.9778	*PF9040.3EOC*	1.1	-1.1	-1.1	-1.1	YPR104C	*FHL1*	1.0	-1.7	-1.4	-1.3	similar to Saccharomyces cerevisiae Fhl1p transcriptional activator of the
CA0767	orf19.12434	*KEM1.3*	-1.1	-1.0	-1.1	1.0	YGL173C	*KEM1*	1.0	-1.2	-1.3	-1.3	multifunctional nuclease, 3-prime end (by homology)
CA0770	orf19.10345	*IPF10963*	-1.2	-1.0	-1.2	1.0	YIL144W	*TID3*	1.0	1.2	1.1	1.4	similar to Saccharomyces cerevisiae Tid3p intercating Dcm1p (by homol
CA0773	orf19.854	*GA11.EXON*	-1.0	-1.3	-1.3	-1.2	YGR019W	*UGA1*	1.0	-1.8	-1.3	-1.4	4-aminobutyrate aminotransferase, exon 1 (by homology)
CA0778	orf19.4779	*IPF12884*	1.0	1.3	1.3	1.0	YKR105C		1.0	1.0	1.1	1.3	unknown function
CA0779	orf19.3491	*IPF20065*	-1.0	1.0	-1.0	-1.0	YMR284W	*YKU70*	1.0	-1.2	-1.4	-1.6	similar to Saccharomyces cerevisiae Yku70p high-affinity DNA-binding p
CA0783	orf19.3931	*ACR1*	1.1	-3.3	-3.5	-2.3	YJR095W	*SFC1*	1.0	-4.3	-4.6	-4.9	Succinate-fumarate transporter (by homology)
CA0785	orf19.11411	*IPF14603*	1.1	1.2	1.3	1.3	YJR100C		1.0	-1.1	1.8	1.9	unknown function
CA0786	orf19.2446	*IPF7473*	-1.2	-1.4	-1.4	-1.2	YDL144C		1.0	-1.2	-1.2	1.0	unknown function
CA0787	orf19.2447	*IPF7472*	-1.2	-1.4	-1.2	-1.1	YJL100W	*LSB6*	1.0	1.0	1.1	1.0	unknown function
CA0789	orf19.3356	*ESP1*	-1.0	1.0	1.1	1.0	YGR098C	*ESP1*	1.0	-2.0	-2.7	-2.6	Required for sister chromatid separation (by homology)
CA0790	orf19.3357	*IPF14193*	1.2	1.0	1.1	1.0	YHR059W	*FYV4*	1.0	-2.2	-2.0	-2.0	unknown function
CA0791	orf19.3358	*LSC1*	1.1	-1.9	-1.8	-1.7	YOR142W	*LSC1*	1.0	-1.4	-1.4	-1.6	succinate-CoA ligase / synthetase (by homology)
CA0792	orf19.554	*DIT2*	1.1	1.1	1.1	1.1	YDR402C	*DIT2*	1.0	-1.2	-1.1	-1.2	putative cytochrome P450
CA0793	orf19.553	*IPF16273*	1.0	-1.0	-1.0	-1.0	YBR180W	*DTR1*	1.0	-1.3	-1.4	-1.1	similar to Saccharomyces cerevisiae Dtr1p dityrosine transporter (by hom
CA0794	orf19.552	*IPF15639*	1.0	-1.0	1.0	1.1	YCL038C		1.0	1.2	-1.1	-1.1	unknown function
CA0796	orf19.9175	*ALR1*	1.0	-1.0	1.0	1.1	YOL130W	*ALR1*	1.0	1.1	1.5	2.5	divalent cation transporter (by homology)
CA0798	orf19.9177	*IPF13565*	-1.0	1.0	-1.0	1.1	YNL308C	*KRI1*	1.0	1.4	1.9	2.0	unknown function
CA0800	orf19.3494	*IPF14064*	-1.1	-1.1	1.1	-1.0	YDR318W	*MCM21*	1.0	-1.1	1.1	1.1	similar to Saccharomyces cerevisiae Mcm21p involved in minichromoson
CA0801	orf19.3496	*CHC1*	1.4	1.1	1.1	-1.0	YGL206C	*CHC1*	1.0	1.1	1.1	1.2	clathrin heavy chain (by homology)
CA0804	orf19.3515	*BNA1*	1.0	1.1	1.1	1.1	YJR025C	*BNA1*	1.0	-1.1	-1.0	-1.3	3-hydroxyanthranilic acid dioxygenase (by homology)
CA0806	orf19.3517	*IPF12567*	1.0	1.0	1.0	1.0	YOR223W		1.0	-1.1	1.4	1.2	unknown function
CA0807	orf19.3518	*IPF12564*	-1.3	-3.5	-3.4	-3.0	YPL134C	*ODC1*	1.0	-1.6	-1.6	-2.7	ADP/ATP carrier proteins (by homology)

CA0810	orf19.1923	*RRN3*	1.2	-1.1	-1.2	-1.2	YKL125W	*RRN3*	1.0	-1.2	-1.1	-1.1	RNA polymerase I specific transcription factor (by homology)
CA0813	orf19.1915	*MPP10*	1.0	-1.3	-1.3	-1.1	YJR002W	*MPP10*	1.0	-1.3	1.1	1.0	component of the U3 small nucleolar ribonucleoprotein (by homology)
CA0819	orf19.1949	*VPS1*	-1.2	-1.1	-1.2	-1.1	YKR001C	*VPS1*	1.0	-2.0	-1.7	-1.9	member of the dynamin family of GTPases (by homology)
CA0820	orf19.1950	*IPF12138*	-1.0	-1.2	-1.0	1.0	YBR022W		1.0	-1.2	-1.5	-1.4	unknown function
CA0821	orf19.2989	*IPF16795*	-1.0	1.0	1.1	1.0	YNL274C		1.0	-1.1	-1.4	-1.7	glycerate/formate-dehydrogenase (by homology)
CA0822	orf19.2990	*EXG1*	-1.0	1.1	1.2	1.1	YLR300W	*EXG1*	1.0	1.4	1.8	4.0	glucan 1,3-beta-glucosidase
CA0827	orf19.7884	*IPF18859*	1.0	-1.3	-1.2	-1.2	YGL080W		1.0	-1.1	1.0	-1.8	unknown function
CA0828	orf19.7882	*IPF17186*	1.3	1.2	1.1	1.4	YDR533C		1.0	1.2	-1.2	-1.2	unknown function
CA0829	orf19.250	*SLC1*	1.2	1.1	1.3	1.1	YDL052C	*SLC1*	1.0	-1.3	-1.4	-1.3	fatty acyltransferase (by homology)
CA0830	orf19.7879	*APL5*	-1.0	-1.0	-1.0	-1.0	YPL195W	*APL5*	1.0	1.0	1.1	1.0	AP-3 complex subunit, gamma-adaptin (by homology)
CA0832	orf19.9244	*IPF14225*	-1.1	-1.6	-1.5	-1.4	YDL133W		1.0	1.0	-1.1	-1.0	unknown function
CA0833	orf19.9245	*IPF12501*	-1.1	-1.1	-1.0	-1.1	YDL183C		1.0	-1.1	-1.2	-1.2	unknown function
CA0838	orf19.9249	*TFP1*	-1.3	-1.1	1.1	1.0	YDL185W	*TFP1*	1.0	-1.0	1.1	-1.1	vacuolar ATPase subunit (by homology)
CA0842	orf19.1053	*IPF15633*	-1.1	1.0	-1.0	1.1	YFL025C	*BST1*	1.0	-1.5	-1.8	-1.7	similar to Saccharomyces cerevisiae Bst1p egative regulator of COPII ve
CA0843	orf19.8656	*IPF18853*	-1.0	-1.1	-1.2	-1.1	YLL023C		1.0	-2.4	-2.2	-1.9	unknown function
CA0844	orf19.8657	*CDC3*	-1.0	-1.1	-1.1	1.0	YLR314C	*CDC3*	1.0	1.0	1.1	-1.1	Cell division control protein
CA0846	orf19.7895	*SMC3*	-1.1	1.0	-1.1	-1.1	YJL074C	*SMC3*	1.0	1.3	1.5	-1.1	required for structural maintenance of chromosomes (by homology)
CA0848	orf19.1743	*ACS1*	-1.0	-2.1	-2.0	-1.8	YAL054C	*ACS1*	1.0	-3.4	-3.5	-3.7	acetyl-coenzyme-A synthetase (by homology)
CA0849	orf19.9311	*HEM4*	-1.0	1.0	1.1	-1.1	YOR278W	*HEM4*	1.0	-1.0	1.1	1.0	uroporphyrinogen III synthase
CA0851	orf19.9313	*IPF16670*	-1.0	1.1	1.2	1.1	YOR242C	*SSP2*	1.0	-1.0	-1.3	-1.4	unknown function
CA0852	orf19.9315	*KIP2*	-1.0	-1.1	-1.1	-1.0	YPL155C	*KIP2*	1.0	-1.4	1.1	-1.0	Kinesin-related protein required for nuclear migration (by homology)
CA0854	orf19.4900	*IPF8854*	-1.3	-1.2	-1.3	-1.1	YER001W	*MNN1*	1.0	-1.5	-1.6	-1.2	similar to Saccharomyces cerevisiae Mnn1p alpha-1,3-mannosyltransfera
CA0859	orf19.11946	*IPF14495.3*	-1.0	-1.0	-1.0	1.0	YLR246W	*ERF2*	1.0	1.0	1.1	1.2	similar to Saccharomyces cerevisiae Erf2p involved in palmitoylation and
CA0862	orf19.3524	*CRK1.5F*	-1.1	-1.1	-1.7	-1.3	YPR161C	*SGV1*	1.0	-1.0	1.0	1.1	Protein kinase, 5-prime end
CA0863	orf19.3526	*ITR2*	1.1	1.3	2.3	1.5	YOL103W	*ITR2*	1.0	-1.1	1.1	1.1	Myo-inositol transporter (by homology)
CA0864	orf19.3527	*CYT1*	-1.3	-1.5	-1.4	-1.3	YOR065W	*CYT1*	1.0	1.0	1.4	-1.7	cytochrome-c1 (by homology)
CA0866	orf19.3585	*IPF14775*	1.0	1.0	-1.0	1.1	YNR046W		1.0	1.1	1.1	1.3	unknown function
CA0869	orf19.3589	*IPF14772*	-1.1	-1.0	1.0	-1.0	YHL022C	*SPO11*	1.0	-1.1	-1.1	-1.2	unknown function
CA0870	orf19.3590	*IPP1*	1.4	-1.1	-1.0	-1.3	YBR011C	*IPP1*	1.0	-1.3	-1.3	-1.2	inorganic pyrophosphatase (by homology)
CA0871	orf19.3591	*APE3*	1.1	1.1	1.0	1.1	YBR286W	*APE3*	1.0	1.4	1.8	1.6	aminopeptidase (by homology)
CA0872	orf19.3592	*IPF13100*	-1.0	1.0	1.0	-1.0	YJL073W	*JEM1*	1.0	-1.0	1.0	1.3	unknown function
CA0873	orf19.12099	*BUL1*	-1.3	-1.0	-1.2	1.1	YMR275C	*BUL1*	1.0	1.1	1.2	1.5	Ubiquitin ligase binding protein
CA0874	orf19.12100	*CPA1*	-1.0	1.1	1.0	1.0	YOR303W	*CPA1*	1.0	-1.4	-1.3	1.3	Arginine-specific carbamoylphosphate synthase, small chain
CA0876	orf19.7996	*VMA6*	1.1	1.0	-1.0	1.0	YLR447C	*VMA6*	1.0	1.1	1.3	1.6	H+-ATPase V0 domain 36 KD subunit,vacuolar (by homology)
CA0877	orf19.8000	*CNH1.5F*	-1.1	1.0	-1.1	-1.1	YLR138W	*NHA1*	1.0	-1.2	1.0	1.2	Na+/H+ antiporter, 5-prime end (by homology)
CA0880	orf19.372	*IPF19542.3F*	1.2	1.1	1.3	-1.0	YER163C		1.0	-1.2	-1.1	-1.2	unknown function, 3-prime end
CA0881	orf19.8006	*IPF16965*	-1.0	1.3	1.3	1.2	YOR256C		1.0	-1.4	-1.3	-1.4	unknown function
CA0882	orf19.8010	*PHR3*	1.1	1.0	1.1	1.1	YOL132W		1.0	-1.2	-1.3	-1.1	surface glycoprotein (by homology)
CA0883	orf19.3642	*SUN41*	1.4	1.3	1.5	1.3	YIL123W	*SIM1*	1.0	1.1	1.5	1.6	Putative cell wall beta-glucosidase (by homology)
CA0885	orf19.1389	*IPF12381*	1.2	-1.3	-1.2	-1.1	YIR001C	*SGN1*	1.0	-1.3	-1.4	-1.3	unknown function
CA0886	orf19.1388	*IPF12382*	1.2	1.0	-1.0	-1.1	YER002W		1.0	-1.4	-1.3	-1.4	unknown function
CA0887	orf19.1387	*IPF12383*	1.1	2.3	2.3	2.3	YIL003W	*DRE3*	1.0	-1.1	-1.1	-1.1	unknown function
CA0888	orf19.1386	*BET1*	1.1	1.1	1.1	1.0	YIL004C	*BET1*	1.0	1.3	1.1	1.1	involved in ER-Golgi transport (by homology)
CA0891	orf19.4735	*IPF11764*	1.0	-1.2	-1.3	-1.1	YGL159W		1.0	1.2	1.3	1.4	unknown function
CA0892	orf19.4736	*PHO8.5*	-1.1	1.3	1.6	1.5	YDR481C	*PHO8*	1.0	-1.0	1.1	1.3	repressible alkaline phosphatase, 5-prime end (by homology)
CA0893	orf19.5752	*IPF13517*	-1.1	-1.0	-1.0	-1.0	YBR280C		1.0	-1.6	-2.0	-1.7	unknown function
CA0894	orf19.5751	*ORM1*	-1.1	-1.0	1.1	1.0	YGR038W	*ORM1*	1.0	1.1	1.1	-1.1	unknown function
CA0895	orf19.5750	*SHM2*	-1.2	-1.5	-1.5	-1.4	YLR058C	*SHM2*	1.0	-2.2	-2.6	-1.8	Serine hydroxymethyltransferase precursor,
CA0896	orf19.5749	*SBA1*	1.2	1.3	1.3	1.2	YKL117W	*SBA1*	1.0	-1.0	1.2	-1.1	Hsp90 (Ninety) Associated Co-chaperone (by homology)
CA0898	orf19.412	*SSH1.3*	1.1	-1.1	1.3	1.2	YBR283C	*SSH1*	1.0	-1.4	-1.3	-1.0	involved in co-translational pathway of protein transport, 3-prime end (by
CA0900	orf19.3411	*IPF12031*	1.1	1.2	1.2	1.1	YNR027W	*BUD17*	1.0	-1.1	-1.1	1.1	unknown function
CA0901	orf19.3412	*IPF12033*	-1.0	1.1	1.0	1.0	YCR068W	*CVT17*	1.0	-1.4	-1.2	-1.2	unknown function
CA0903	orf19.1480	*IPF4401*	1.5	-1.0	-1.0	1.0	YMR118C		1.0	-1.0	-1.1	-1.1	putative succinate dehydrogenase (by homology)
CA0906	orf19.1483	*IPF4406*	1.0	1.0	1.0	1.0	YKL137W		1.0	-1.2	-1.3	-1.5	unknown function
CA0908	orf19.1485	*MRPL31*	1.3	1.1	1.2	1.1	YKL138C	*MRPL31*	1.0	1.0	-1.1	-1.4	Mitochondrial ribosomal protein
CA0910	orf19.9569	*MRPL16*	1.3	-1.0	-1.1	1.1	YBL038W	*MRPL16*	1.0	-1.6	-1.7	1.1	ribosomal protein
CA0911	orf19.9568	*IPF14814*	1.0	-1.0	1.0	1.0	YJR097W		1.0	-1.4	-1.4	-1.5	unknown function
CA0912	orf19.9567	*RPA49*	1.0	1.0	1.0	-1.0	YNL248C	*RPA49*	1.0	-1.1	-1.1	-1.1	DNA-directed RNA polymerase A (by homology)
CA0913	orf19.9566	*IPF14810*	1.2	1.1	1.3	1.2	YER044C	*ERG28*	1.0	1.4	1.4	1.1	unknown function
CA0914	orf19.9565	*SRA1*	-1.7	-1.4	-1.6	-1.4	YIL033C	*BCY1*	1.0	1.2	1.3	-1.1	cAMP dependent protein kinase, regulatory subunit (by homology)
CA0915	orf19.9564	*KAR2*	-1.2	1.3	1.1	1.2	YJL034W	*KAR2*	1.0	-1.1	1.1	1.3	dnaK-type molecular chaperone (by homology)

CA0916	orf19.2970	*LYS2*	1.1	1.1	-1.0	-1.1	YBR115C	*LYS2*	1.0	-3.1	-5.3	-2.9	L-aminoadipate-semialdehyde dehydrogenase, large subunit
CA0917	orf19.2969	*RAD16*	-1.0	1.1	1.3	1.1	YBR114W	*RAD16*	1.0	-1.2	-1.3	-1.4	nucleotide excision repair protein (by homology)
CA0918	orf19.1041	*IPF17881*	-1.0	-1.0	1.1	-1.0	YJL006C	*CTK2*	1.0	-1.0	-1.1	-1.1	cyclin (by homology)
CA0919	orf19.1042	*POR1*	1.6	-1.4	-1.3	-1.3	YNL055C	*POR1*	1.0	-1.1	-1.2	-1.7	mitochondrial outer membrane porin (by homology)
CA0921	orf19.1043	*IPF12992*	1.1	1.1	1.2	1.0	YPR139C		1.0	1.0	1.0	1.0	unknown function
CA0922	orf19.1045	*IPF12991*	1.0	-1.1	-1.1	-1.0	YIR005W	*IST3*	1.0	1.0	1.0	-1.1	unknown function
CA0923	orf19.1047	*IPF12987*	-1.0	-1.0	1.0	1.0	YMR049C	*ERB1*	1.0	-1.1	1.1	1.4	unknown function
CA0926	orf19.3663	*IPF11335*	-1.1	-1.0	1.3	1.1	YNR013C	*PHO91*	1.0	-1.0	1.1	1.2	Member of the phosphate permease family (by hom
CA0927	orf19.3661	*IPF11332*	-1.2	-1.0	-1.2	1.0	YPL072W	*UBP16*	1.0	-1.4	-1.1	-1.0	unknown function
CA0929	orf19.558	*GUT1*	-1.0	-1.7	-1.9	-1.9	YHL032C	*GUT1*	1.0	-1.9	-2.3	-2.4	Glycerol kinase (by homology)
CA0932	orf19.3695	*EPT1*	1.4	1.1	1.3	1.1	YHR123W	*EPT1*	1.0	-1.2	-1.5	-1.3	alcohol phosphatidyl transferase (by homology)
CA0933	orf19.8678	*ATM1*	-1.1	-1.0	-1.2	-1.1	YMR301C	*ATM1*	1.0	1.1	1.3	1.0	ATP-binding cassette transporter (by homology)
CA0935	orf19.1079	*IPF14203.5F*	1.0	1.0	-1.0	1.0	YFL030W		1.0	-1.5	-1.4	-3.2	similarity to several transaminases, 5-prime end (by homology)
CA0938		*COX12*	1.4	1.2	1.5	1.6	YLR038C	*COX12*	1.0	-1.4	-1.3	-1.9	cytochrome-c oxidase, subunit VIB (by homology)
CA0939	orf19.3704	*DBP6*	-1.0	-1.1	-1.2	-1.1	YNR038W	*DBP6*	1.0	1.0	1.0	1.1	RNA helicase required for 60S ribosomal subunit assembly (by homolog
CA0940		*IPF8616*	1.1	1.0	1.0	-1.0	YNR037C	*RSM19*	1.0	-1.1	1.0	1.1	similar to Saccharomyces cerevisiae Rsm19p ribosomal protein (by hom
CA0941	orf19.3705	*IPF8617*	-1.1	1.0	-1.0	1.0	YCR079W		1.0	-1.0	-1.1	-1.1	unknown function
CA0943	orf19.3707	*YHB1*	-1.1	4.4	5.1	6.2	YGR234W	*YHB1*	1.0	1.4	1.9	1.9	flavohemoglobin (by homology)
CA0945	orf19.8853	*IPF10278*	-1.2	-1.2	-1.5	-1.2	YER048C	*CAJ1*	1.0	1.3	1.2	1.1	DNA-J - like protein (by homology)
CA0948	orf19.1272	*IPF10270*	-1.2	-1.2	-1.1	-1.0	YGR111W		1.0	1.0	-1.0	-1.3	unknown function
CA0949	orf19.8859	*IPF10269*	1.1	1.1	1.1	1.1	YNL153C	*GIM3*	1.0	-1.1	1.3	1.5	Gim complex component-like by homology
CA0950	orf19.1012	*IPF3737*	1.4	1.4	2.0	1.6	YLR170C	*APS1*	1.0	1.0	1.2	1.2	similar to Saccharomyces cerevisiae Aps1p AP-1 complex subunit, sigm
CA0951	orf19.1011	*MNN6*	-1.3	1.2	1.1	1.1	YBR015C	*MNN2*	1.0	1.0	-1.2	1.2	putative golgi alpha-1,2-mannosyltransferase (by homology)
CA0954	orf19.1142	*IPF13162*	1.1	1.1	1.3	1.2	YNL101W		1.0	1.0	1.2	1.1	unknown function
CA0956	orf19.12191	*IPF14914*	-1.1	-1.1	-1.2	-1.1	YIL112W		1.0	-1.2	-1.0	-1.3	putative ankyrin (by homology)
CA0957		*IPF14322*	1.0	1.0	-1.0	1.0	YNL051W	*COD4*	1.0	-2.1	-1.7	-1.8	unknown function
CA0958	orf19.12194	*SEC24*	1.0	1.6	1.5	1.5	YIL109C	*SEC24*	1.0	1.1	1.5	1.2	component of COPII coat of ER-Golgi vesicles(by homology)
CA0959	orf19.657	*SAM2*	1.0	-1.0	-1.1	-1.1	YDR502C	*SAM2*	1.0	1.8	2.3	2.9	S-adenosylmethionine synthetase 2
CA0963	orf19.6246	*IPF9143*	1.0	1.1	1.1	1.1	YPR131C	*NAT3*	1.0	-1.0	-1.1	-1.2	similar to Saccharomyces cerevisiae Nat3p N-acetyltransferase (by hom
CA0964	orf19.6247	*IPF9141*	-1.1	1.0	-1.0	-1.0	YPR135W	*CTF4*	1.0	-1.4	-1.4	-1.4	similar to Saccharomyces cerevisiae Ctf4p DNA-directed DNA polymera
CA0969	orf19.12987	*IPF9132*	1.4	1.5	1.6	1.3	YPL184C		1.0	-1.1	1.1	1.3	unknown function
CA0970	orf19.10340	*IPF10894*	1.1	1.0	1.0	-1.1	YGR120C	*SEC35*	1.0	-1.4	-1.3	-1.3	unknown function
CA0972	orf19.6472	*CYP1*	1.1	1.2	1.1	1.1	YDR155C	*CPH1*	1.0	-1.2	-1.2	-1.1	cyclophilin (peptidylprolyl isomerase), mitochondrial (by homology)
CA0977	orf19.11087	*IPF18810*	-1.0	1.3	1.3	1.2	YNL215W	*IES2*	1.0	1.2	-1.1	-1.0	unknown function
CA0978	orf19.3603	*IPF16222*	1.0	1.0	1.0	-1.1	YDL233W		1.0	-1.6	-1.2	-1.4	unknown function
CA0982	orf19.1800	*IPF7397*	1.1	1.6	2.0	1.5	YGR141W		1.0	1.2	1.1	1.0	unknown function
CA0983	orf19.1801	*CBR1*	1.0	-1.1	-1.0	-1.1	YIL043C	*CBR1*	1.0	1.1	1.3	1.4	Cytochrome-b5 reductase (by homology)
CA0984	orf19.1802	*IPF7400*	-1.0	1.1	1.0	1.1	YER049W		1.0	1.0	1.3	2.2	unknown function
CA0986	orf19.3350	*IPF4814*	-1.0	-1.0	-1.1	-1.1	YDR405W	*MRP20*	1.0	-1.1	-1.0	1.1	similar to Saccharomyces cerevisiae Mrp20p ribosomal protein of the lar
CA0987	orf19.3349	*RPB140*	-1.2	-1.2	-1.9	-1.4	YOR151C	*RPB2*	1.0	-1.4	1.0	1.0	DNA-dependent RNA polymerase II RPB140
CA0988	orf19.8968	*PMI40*	-1.0	1.4	1.9	1.6	YER003C	*PMI40*	1.0	-1.1	1.3	1.1	mannose-6-phosphate isomerase (PHOSPHOMANNOSE ISOMERASE)
CA0990	orf19.1392	*IPF11068*	-1.3	-1.1	-1.1	-1.1	YIL005W		1.0	1.2	1.1	1.2	unknown function
CA0991	orf19.8971	*IPF11065*	-1.0	-1.1	1.0	-1.0	YIL006W		1.0	-1.2	-1.3	-1.4	unknown function
CA0992	orf19.8972	*IPF11063*	1.1	-1.0	1.0	1.0	YCR090C		1.0	-1.2	-1.2	-1.0	unknown function
CA1002	orf19.3756	*ROK1.3*	-1.0	1.0	1.1	-1.0	YGL171W	*ROK1*	1.0	-1.6	-1.4	-1.3	RNA helicase, 3-prime end
CA1003	orf19.3757	*ATP20*	1.4	-1.0	1.2	1.0	YPR020W	*ATP20*	1.0	-1.2	-1.4	-1.7	F1F0-ATPase complex, G subunit (by homology)
CA1004	orf19.3758	*IPF8901*	-1.1	-1.1	1.2	1.0	YDR105C		1.0	1.2	1.4	1.3	unknown function
CA1005	orf19.3759	*LPG7*	-1.0	-1.0	-1.1	-1.1	YPL101W	*TOT7*	1.0	1.0	1.2	1.2	probable membrane protein (by homology)
CA1007	orf19.3760	*DLH1.3F*	-1.0	1.0	1.1	1.1	YER179W	*DMC1*	1.0	-1.4	-1.4	-1.7	meiotic recombination protein, 3-prime end
CA1008	orf19.6254	*IPF14083*	-1.1	-1.1	-1.1	-1.0	YPR128C	*ANT1*	1.0	-1.7	-2.0	-1.9	similarity to Saccharomyces cerevisiae carrier protein Flx1p (by homolog
CA1009	orf19.6255	*IPF14084*	1.0	-1.3	-1.2	-1.1	YGR117C		1.0	1.5	1.5	1.7	unknown function
CA1010	orf19.6257	*GLT1.3EOC*	-1.0	-1.1	-1.1	1.1	YDL171C	*GLT1*	1.0	-1.1	-1.1	-1.0	glutamate synthase (NAPDPH), 3-prime end (by homology)
CA1011	orf19.11434	*SRP101*	-1.2	1.1	-1.2	-1.2	YDR292C	*SRP101*	1.0	-1.9	-1.5	-1.1	signal recognition particle receptor, alpha chain (by homology
CA1012	orf19.11436	*PSD2.5F*	1.0	1.1	1.1	1.1	YGR170W	*PSD2*	1.0	1.0	1.0	-1.1	phosphatidylserine decarboxylase 2, 5-prime end (by homology)
CA1014	orf19.11437	*MES1*	-1.1	1.0	1.1	1.0	YGR264C	*MES1*	1.0	-1.2	1.5	2.2	methionyl-tRNA synthetase (by homology)
CA1015	orf19.11438	*IPF15547*	1.0	1.0	1.1	-1.0	YMR293C		1.0	-1.1	-1.5	-1.4	putative glutamyl-tRNA amidotransferase subunit A (by homology)
CA1016	orf19.473	*IPF11142*	-1.0	1.1	1.3	1.3	YOR273C	*TPO4*	1.0	-1.0	1.1	-1.0	unknown function
CA1017	orf19.8105	*IPF11144*	1.0	-1.0	1.1	-1.0	YHR036W		1.0	-1.2	-1.2	-1.1	unknown function
CA1019	orf19.3769	*IPF13485*	-1.1	-1.0	1.1	1.0	YNR039C	*ZRG17*	1.0	-1.1	-1.1	1.1	unknown function
CA1020	orf19.10863	*IPF4824*	-1.1	1.3	1.3	1.2	YOR155C		1.0	1.4	1.6	1.1	unknown function
CA1024	orf19.3934	*CAR1*	1.0	-1.7	-2.0	-1.6	YPL111W	*CAR1*	1.0	1.2	1.3	-1.3	arginase by homology

CA1025	orf19.3936	*IPF10184*	1.1	1.0	-1.1	-1.0	YPL110C		1.0	-1.1	-1.2	-1.4	unknown function
CA1027		*IPF19645.EXON*	1.0	-1.1	-1.1	-1.1	YPR040W	*SDF1*	1.0	-1.2	1.1	-1.0	unknown function, exon 2
CA1029	orf19.9112	*TLG2*	1.1	1.1	-1.0	1.1	YOL018C	*TLG2*	1.0	-1.3	-1.3	-1.1	Syntaxin family of t-SNAREs (by homology)
CA1030	orf19.9111	*ZRC1*	-1.0	-1.0	1.2	1.0	YMR243C	*ZRC1*	1.0	1.5	1.4	1.7	Zinc and cadmium resistance protein (by homology)
CA1033	orf19.8642	*MAD2*	-1.0	-1.0	-1.1	1.0	YJL030W	*MAD2*	1.0	-1.3	-1.3	-1.2	spindle checkpoint complex subunit (by homology)
CA1034	orf19.8641	*3ET4.EXON2*	-1.0	-1.0	-1.0	-1.0	YJL031C	*BET4*	1.0	1.0	1.1	1.0	alpha subunit of geranylgeranyl transferase type 2, exon 2
CA1037	orf19.8638	*MNS1*	-1.1	-1.1	1.0	-1.1	YJR131W	*MNS1*	1.0	-1.1	-1.1	-1.0	Alpha1,2-mannosidase (by homology)
CA1038	orf19.8637	*IPF6159*	-1.1	-1.1	-1.1	1.0	YML076C		1.0	-1.1	1.2	1.4	unknown function
CA1039	orf19.2501	*IPF4012*	1.2	-1.1	1.0	-1.0	YPL221W	*BOP1*	1.0	-1.3	-1.2	1.0	Unknown Function
CA1041	orf19.2504	*BMS1*	-1.2	-1.3	-1.3	-1.1	YPL217C	*BMS1*	1.0	-1.4	-1.3	-1.1	probable membrane protein involved in bud site selection (by homology)
CA1043	orf19.9219	*TOM6*	1.0	-1.1	1.1	-1.1	YOR045W	*TOM6*	1.0	1.1	-1.1	-1.8	mitochondrial outer membrane import receptor subunit (by homology)
CA1044	orf19.9218	*RNA1*	-1.2	-1.4	-1.4	-1.3	YMR235C	*RNA1*	1.0	1.2	1.2	1.6	GTPase activating protein (by homology)
CA1045	orf19.1648	*IPF11620*	-1.1	-1.1	1.0	-1.0	YNL250W	*RAD50*	1.0	1.1	1.3	1.3	similar to Saccharomyces cerevisiae Rad50p DNA repair protein (by hor
CA1046	orf19.1647	*IPF11617*	-1.0	1.0	-1.0	-1.0	YOR298W		1.0	-1.5	1.3	1.5	unknown function
CA1047	orf19.9215	*IPF11615*	-1.1	-1.0	-1.1	-1.1	YPR112C	*MRD1*	1.0	-1.2	1.0	1.2	RNA-binding proteins (by homology)
CA1048	orf19.3899	*IPF15394*	1.1	-1.0	1.0	1.1	YDR469W	*SDC1*	1.0	-1.3	-1.2	1.0	unknown function
CA1049	orf19.3898	*TLG1*	1.0	1.1	1.0	1.0	YDR468C	*TLG1*	1.0	1.3	1.2	1.1	tSNARE that affects a Late Golgi compartment (by homology)
CA1053	orf19.3893	*SCW11.3EOC*	1.1	1.2	1.3	-1.0	YGL028C	*SCW11*	1.0	1.0	1.2	1.7	glucanase gene family member, 3-prime end (by homology)
CA1054	orf19.2540	*SAS3*	1.1	1.1	1.2	1.1	YBL052C	*SAS3*	1.0	1.1	1.0	1.0	silencing protein (by homology)
CA1055	orf19.2541	*IPF17504*	-1.1	-1.1	-1.1	1.0	YBL055C		1.0	-1.3	-1.7	-1.2	unknown function
CA1057	orf19.2544	*IPF17031*	1.0	-1.0	-1.1	-1.0	YBL057C		1.0	-1.1	-1.1	-1.0	unknown function
CA1058	orf19.2545	*DOT6*	1.1	-1.1	-1.0	1.0	YER088C	*DOT6*	1.0	1.1	1.6	1.3	involved in derepression of telomeric silencing (by homology)
CA1059	orf19.10080	*TRP2*	-1.1	-1.0	-1.1	-1.0	YER090W	*TRP2*	1.0	1.2	1.6	1.7	anthranilate synthase component I (by homology)
CA1060	orf19.267	*IPF11460*	1.0	1.1	-1.1	1.0	YJL076W	*NET1*	1.0	1.1	1.1	1.3	unknown function
CA1063	orf19.4641	*NMT1*	-1.1	-1.2	-1.2	-1.2	YLR195C	*NMT1*	1.0	-1.2	1.0	-1.1	N-myristoyltransferase
CA1064	orf19.12110	*PWP1*	-1.0	-1.2	-1.3	-1.1	YLR196W	*PWP1*	1.0	1.1	1.4	1.9	beta-transducin superfamily (by homology)
CA1066	orf19.12107	*IPF9001*	-1.0	-1.0	1.1	-1.0	YLR097C		1.0	-1.3	-1.5	-1.6	unknown function
CA1067	orf19.2023	*HXT62*	1.3	45.4	34.6	42.5	YDR345C	*HXT3*	1.0	8.7	11.4	9.1	sugar transporter
CA1070	orf19.2020	*HXT61*	1.2	4.6	8.0	3.9	YDR343C	*HXT6*	1.0	7.1	10.3	3.3	sugar transporter
CA1071	orf19.2534	*IPF16624*	1.1	1.1	1.0	-1.0	YBL051C	*PIN4*	1.0	-1.1	-1.1	-1.1	unknown function
CA1073	orf19.2533	*PRORS.3F*	-1.1	-1.2	-1.3	-1.2	YER087W		1.0	-1.1	-1.3	-1.3	prolyl-tRNA synthetase, 3-prime end
CA1076	orf19.2239	*IPF19721*	1.0	1.0	1.0	-1.0	YAL024C	*LTE1*	1.0	1.0	-1.0	-1.1	similar to Saccharomyces cerevisiae Lte1p GDP/GTP exchange factor
CA1080	orf19.4820	*IPF14710*	-1.0	-1.1	1.0	1.0	YKL162C		1.0	-1.2	-1.5	-1.8	unknown function
CA1087	orf19.8357	*MYO5*	1.1	1.1	1.1	-1.0	YMR109W	*MYO5*	1.0	-1.3	-1.2	-1.0	Myosin I (by homology)
CA1089	orf19.3945	*IPF13799*	-1.1	-1.1	-1.1	-1.0	YJR084W		1.0	-1.0	-1.1	-1.1	unknown function
CA1090	orf19.3946	*COX18*	-1.0	1.0	1.3	1.1	YGR062C	*COX18*	1.0	-1.1	-1.2	-1.1	protein required for activity of mitochondrial cytochrome oxidase (by hom
CA1091	orf19.3947	*SPT4*	1.1	-1.0	1.1	1.1	YGR063C	*SPT4*	1.0	1.2	-1.1	1.1	transcription elongation protein (by homology)
CA1092	orf19.3949	*YTA7*	-1.1	-1.0	-1.2	-1.1	YGR270W	*YTA7*	1.0	-1.5	-1.6	-1.3	26S proteasome subunit (by homology)
CA1093	orf19.3950	*MSM1*	1.0	1.0	-1.0	-1.0	YGR171C	*MSM1*	1.0	1.0	-1.0	-1.0	mitochondrial methionyl-tRNA synthetase
CA1094	orf19.3951	*YIP1*	1.2	1.2	1.4	1.3	YGR172C	*YIP1*	1.0	1.1	1.0	-1.1	golgi membrane protein (by homology)
CA1095	orf19.4367	*SMC1*	-1.2	-1.1	-1.3	-1.1	YFL008W	*SMC1*	1.0	-1.3	-1.3	-1.1	Chromosomal ATPase family member (by homology)
CA1102	orf19.4950	*AKR1*	1.1	1.3	1.6	1.5	YDR264C	*AKR1*	1.0	-1.1	-1.0	1.1	ankyrin repeat-containing protein by homology
CA1103	orf19.12413	*IPF5673*	1.0	1.1	-1.0	1.0	YLR107W	*REX3*	1.0	-1.8	-1.6	-1.5	similar to Saccharomyces cerevisiae Rex3p RNA exonuclease (by homol
CA1104		*IPF18761*	1.2	1.3	1.6	1.4	YPR098C		1.0	-1.5	-1.7	-2.0	unknown function
CA1106	orf19.12697	*IPF11270*	1.1	1.0	1.0	-1.0	YOL077C	*BRX1*	1.0	1.7	2.2	2.3	unknown function
CA1109	orf19.5230	*MRPS9*	1.1	-1.0	-1.0	1.0	YBR146W	*MRPS9*	1.0	1.2	1.4	1.2	ribosomal protein S9 small subunit precursor
CA1110	orf19.5229	*DIS3*	-1.3	-1.1	-1.2	-1.2	YOL021C	*DIS3*	1.0	1.2	1.3	1.8	3 --5 exoribonuclease required for 3 end formation of 5.8S rRNA (by hor
CA1111	orf19.12693	*RIB3*	1.1	1.3	1.4	1.1	YDR487C	*RIB3*	1.0	1.3	1.3	1.6	3,4-dihydroxy-2-butanone 4-phosphate synthase (by homology)
CA1114	orf19.2286	*IPF9995*	1.0	1.1	1.2	1.0	YJR070C		1.0	1.2	1.4	1.6	unknown function
CA1115	orf19.2287	*RPA12*	1.0	-1.0	-1.0	-1.0	YJR063W	*RPA12*	1.0	-2.1	-1.7	-1.5	DNA-directed RNA polymerase I (by homology)
CA1116	orf19.2288	*CCT5*	-1.3	-1.0	-1.1	1.0	YJR064W	*CCT5*	1.0	1.1	1.7	2.3	T-complex protein 1, epsilon subunit (by homology)
CA1117	orf19.2289	*ARP3*	-1.1	1.2	1.1	1.1	YJR065C	*ARP3*	1.0	-1.2	1.0	1.2	actin related protein (by homology)
CA1121	orf19.1604	*IPF6730*	-1.2	1.0	-1.1	-1.0	YLR368W		1.0	1.3	1.3	1.1	Unknown function
CA1122	orf19.1605	*PMS1.3*	-1.0	-1.1	-1.1	1.0	YNL082W	*PMS1*	1.0	-2.2	1.2	1.4	DNA mismatch repair protein, 3-prime end (by homology)
CA1123	orf19.6261	*IPF19723*	-1.2	-1.1	-1.3	-1.0	YCR032W	*BPH1*	1.0	-1.3	-1.4	-1.5	similar to Saccharomyces cerevisiae Bph1p involved in acetic acid expor
CA1124	orf19.6260	*UBP12*	-1.1	-1.1	-1.3	-1.1	YJL197W	*UBP12*	1.0	-1.2	-1.2	-1.1	ubiquitin C-terminal hydrolase (by homology)
CA1125	orf19.6259	*RRP43*	-1.0	-1.1	-1.1	-1.1	YCR035C	*RRP43*	1.0	1.2	1.1	1.2	rRNA processing protein (by homology)
CA1127	orf19.3608	*MSH3*	-1.5	-1.5	-1.5	-1.4	YCR092C	*MSH3*	1.0	1.2	1.5	1.5	DNA mismatch repair by homology
CA1128	orf19.3609	*IPF5198*	-1.1	-1.2	-1.1	-1.1	YMR093W		1.0	-1.1	-1.1	1.2	unknown function
CA1134	orf19.2163	*IPF2702*	1.0	-1.0	1.1	-1.0	YBR074W		1.0	1.4	1.9	1.5	unknown function
CA1135	orf19.1981	*IMP2*	-1.0	1.0	-1.0	1.0	YMR035W	*IMP2*	1.0	-1.1	-1.1	-1.0	mitochondrial inner membrane protease subunit (by homology)

CA1144	orf19.11168	*SPS19*	1.1	-2.6	-3.6	-2.6	YNL202W	*SPS19*	1.0	1.2	1.2	-1.0	peroxisomal 2,4-dienoyl-CoA reductase (by homology)
CA1145	orf19.11167	*GCS1*	-1.1	-1.0	-1.1	-1.1	YDL226C	*GCS1*	1.0	1.1	1.3	2.0	ADP-ribosylation factor GTPase-activating protein (ARF-GAP) (by homol
CA1146	orf19.3682	*CWH8*	1.5	-1.9	-1.6	-1.8	YGR036C	*CAX4*	1.0	-1.1	1.1	1.3	putative required protein for full levels of dolichol-linked oligosaccharides
CA1147	orf19.11165	*KAP95*	1.1	-1.0	1.2	1.0	YLR347C	*KAP95*	1.0	-1.1	1.1	1.3	karyopherin-beta protein (by homology)
CA1154	orf19.105	*MET221*	1.0	-1.0	-1.0	1.0	YOL064C	*MET22*	1.0	1.1	1.2	1.6	protein ser/thr phosphatase (by homology)
CA1155	orf19.107	*JA2*	-1.1	-1.3	-1.2	-1.1	YKL078W		1.0	-1.5	-1.4	-1.2	ATP-dependent RNA helicases-like (by homology)
CA1156	orf19.4123	*RLR1*	-1.2	-1.2	-1.5	-1.3	YNL139C	*RLR1*	1.0	-1.4	-1.3	-1.5	hypothetical regulatory protein (by homology)
CA1157	orf19.4125	*PZF1*	1.0	-1.0	1.0	1.0	YPR186C	*PZF1*	1.0	-1.2	-1.0	1.0	TFIIIA (transcription initiation factor) (by homology)
CA1158	orf19.4127	*IPF13275*	-1.2	1.1	1.0	1.1	YHR016C	*YSC84*	1.0	1.3	1.1	-1.0	unknown function
CA1160	orf19.2726	*IPF10262*	-1.0	1.1	1.0	1.1	YKL051W		1.0	1.3	1.2	2.0	unknown function
CA1161	orf19.2727	*GRX3*	1.1	1.0	1.2	1.1	YDR098C	*GRX3*	1.0	-1.1	-1.1	-1.0	glutaredoxin-like protein
CA1162	orf19.2728	*IPF10258*	-1.0	-1.0	-1.0	1.0	YER173W	*RAD24*	1.0	-1.4	-1.3	-1.1	similar to Saccharomyces cerevisiae Rad24p cell cycle checkpoint protei
CA1163	orf19.2730	*IPF15357*	-1.1	1.1	1.0	1.0	YER169W	*RPH1*	1.0	1.0	1.0	1.2	unknown function
CA1164	orf19.10867	*ARP8*	-1.2	-1.1	-1.2	-1.1	YOR141C	*ARP8*	1.0	-1.4	-1.4	-1.3	actin-related protein (by homology)
CA1167	orf19.1782	*IPF16646*	1.2	1.4	1.5	1.6	YEL001C		1.0	-1.1	-1.0	1.4	unknown function
CA1170	orf19.2749	*IPF13268*	-1.1	-1.0	-1.1	-1.0	YDR132C		1.0	-1.2	-1.0	-1.0	unknown function
CA1172	orf19.2747	*RGT1*	-1.3	-1.4	-1.3	-1.3	YKL038W	*RGT1*	1.0	-1.5	-1.4	-1.4	Regulator of glucose-induced genes (by homology)
CA1175	orf19.4766	*ARG81*	-1.1	-1.1	-1.2	-1.1	YML099C	*ARG81*	1.0	-1.0	1.3	1.4	transcription factor possibly involved in arginine metabolism, 3-prime end
CA1176	orf19.807	*CHS5*	-1.0	-1.1	-1.3	-1.1	YLR330W	*CHS5*	1.0	1.1	1.2	1.3	Chitin biosynthesis protein
CA1177	orf19.806	*VMA7*	1.1	1.0	1.1	1.1	YGR020C	*VMA7*	1.0	-1.5	-1.6	-1.4	vacuolar ATPase (by homology)
CA1178	orf19.805	*IPF5062*	1.0	1.0	-1.0	1.0	YGR021W		1.0	-1.3	-1.3	-1.6	unknown function
CA1179	orf19.804	*IPF5064*	-1.0	-1.5	-1.6	-1.2	YPR011C		1.0	1.1	-1.1	-1.1	ADP/ATP carrier protein (by homology)
CA1182	orf19.801	*IPF19724*	-1.1	-1.1	-1.1	-1.1	YPL128C	*TBF1*	1.0	-1.3	-1.1	-1.1	similar to Saccharomyces cerevisiae Tbf1ptelomere repeat-binding facto
CA1183	orf19.11263	*IPF14805*	1.1	-1.0	1.1	1.1	YBR220C		1.0	-1.8	-1.7	-1.7	acetyl-coenzyme A transporter(by homology)
CA1187	orf19.11267	*QRI7*	1.0	1.1	1.1	1.1	YKR038C		1.0	1.1	1.3	1.4	putative glycoprotease (by homology)
CA1188		*RPL30.3*	1.9	1.3	1.4	1.4	YGL030W	*RPL30*	1.0	1.4	2.4	2.5	RNA binding, 3-prime end (by homology)
CA1189	orf19.11269	*RPL24A*	1.1	-1.3	-1.4	-1.1	YGL031C	*RPL24A*	1.0	1.4	1.6	1.7	ribosomal protein L24 (by homology)
CA1191	orf19.111	*CAN2*	-1.0	-1.3	-1.5	-1.1	YEL063C	*CAN1*	1.0	-1.4	-1.2	-1.1	amino acid permease (by homology)
CA1193	orf19.7756	*MSY1*	1.0	-1.1	1.1	-1.0	YPL097W	*MSY1*	1.0	-1.1	-1.3	-1.3	tyrosyl-tRNA synthetase 8by homology
CA1195	orf19.7750	*KAR5*	-1.0	-1.0	-1.1	1.0	YMR065W	*KAR5*	1.0	-1.3	-1.4	-1.3	nuclear fusion protein-like (by homology)
CA1198	orf19.10875	*IPF10399*	1.1	-1.2	-1.1	-1.1	YNL177C		1.0	-1.4	1.0	1.2	unknown function
CA1199	orf19.10876	*IPF10404*	1.0	3.4	5.8	2.7	YBL049W		1.0	1.3	1.5	1.2	unknown function
CA1200	orf19.12331	*IPF10223*	1.0	1.1	1.1	-1.0	YJL187C	*SWE1*	1.0	-1.1	-1.1	-1.0	putative serine/threonine kinase
CA1202	orf19.12334	*DBP3*	1.0	-1.1	-1.1	-1.0	YGL078C	*DBP3*	1.0	-1.0	1.5	2.4	ATP-dependent RNA helicase (HELICASE CA3) by homology
CA1204	orf19.8486	*IPF14524*	-1.1	1.1	1.3	1.2	YGL160W		1.0	1.1	1.0	1.7	unknown function
CA1205	orf19.11257	*SSK2*	1.1	1.1	1.0	1.0	YNR031C	*SSK2*	1.0	-1.4	-1.1	1.2	MAP kinase kinase kinase of the high osmolarity
CA1207	orf19.11256	*PPG1*	-1.1	1.2	-1.0	-1.0	YNR032W	*PPG1*	1.0	-1.0	-1.1	1.0	Phosphoprotein phosphatase PPG catalytic chain (by homology)
CA1209	orf19.11254	*ARG8*	-1.0	-1.0	-1.1	-1.1	YOL140W	*ARG8*	1.0	-2.0	-1.3	-1.2	acetylornithine aminotransferase (by homology)
CA1210	orf19.7778	*IPF7030*	-1.0	1.1	-1.0	-1.0	YBR103W	*SIF2*	1.0	-2.0	-3.0	-3.7	unknown function
CA1211		*IPF7031.3*	1.2	1.0	1.3	1.2	YPR063C		1.0	-1.0	1.4	1.3	unknown function, 3-prime end
CA1212	orf19.7777	*IPF7033*	-1.1	1.0	-1.0	-1.1	YPR057W	*BRR1*	1.0	-1.7	-1.2	-1.2	unknown function
CA1213	orf19.7776	*VPS15.5F*	1.0	1.0	-1.0	1.1	YBR097W	*VPS15*	1.0	1.1	-1.0	1.1	serine/threonine protein kinase, 5-prime end (by homology)
CA1218	orf19.7769	*CDC20*	-1.0	1.1	-1.2	-1.1	YGL116W	*CDC20*	1.0	-1.2	-1.2	-1.2	anaphase promoting complex subunit (by homology)
CA1220	orf19.4134	*IPF14985*	-1.0	-1.1	1.0	1.0	YDR459C		1.0	-2.1	-1.4	-1.2	unknown function
CA1221	orf19.4133	*IPF14872*	1.0	-1.1	-1.2	-1.1	YDR527W		1.0	-1.1	-1.1	1.2	unknown function
CA1223	orf19.4131	*IPF14870*	1.1	1.0	1.3	1.1	YCL045C		1.0	-1.5	-1.2	-1.1	unknown function
CA1226	orf19.4159	*IPF15660*	1.1	-1.0	1.0	-1.0	YMR166C						putative mitochondrial carrier (by homology)
CA1227	orf19.4160	*IPF16082*	1.1	-1.2	-1.1	-1.2	YDL104C	*QRI7*	1.0	-1.2	-1.1	-1.2	unknown function
CA1228	orf19.4161	*IPF16081*	-1.0	-1.1	-1.0	-1.0	YDL105W	*QRI2*	1.0	-1.1	-1.0	1.1	unknown function
CA1229	orf19.4162	*MLH1*	-1.0	1.0	-1.0	1.0	YMR167W	*MLH1*	1.0	-1.1	-1.1	-1.1	DNA mismatch repair protein (by homology)
CA1230	orf19.4980	*SSA4*	-1.1	1.5	1.6	1.5	YER103W	*SSA4*	1.0	-1.5	-1.1	1.4	cahsp70 mRNA for heat shock
CA1231	orf19.4981	*IPF11817*	-1.1	-1.0	1.0	1.0	YDL206W		1.0	1.0	-1.1	-1.0	unknown function
CA1235	orf19.8332	*IPF20079*	1.1	1.0	1.1	1.1	YMR074C		1.0	-1.6	-1.6	-1.7	unknown function
CA1236	orf19.8333	*YPT6*	-1.1	-1.0	-1.1	-1.0	YLR262C	*YPT6*	1.0	1.3	1.2	1.4	GTP-binding protein of the rab family (by homology)
CA1239	orf19.717	*HSP60*	-1.2	-1.3	-1.3	-1.3	YLR259C	*HSP60*	1.0	-1.4	-1.4	-1.9	Heat Shock Protein 60 (HSP60)
CA1240	orf19.8337	*IPF14026*	1.1	-1.1	-1.0	1.0	YML043C	*RRN11*	1.0	-1.5	-1.1	-1.6	similar to Saccharomyces cerevisiae Rrn11p involved in RNA polymeras
CA1243	orf19.8923	*IPF7922*	-1.0	-1.0	-1.0	-1.0	YNL236W	*SIN4*	1.0	-1.2	-1.2	-1.1	unknown function
CA1245	orf19.7689	*MH3.EXON2*	1.0	-1.1	1.1	1.0	YLR432W	*IMD3*	1.0	1.5	2.1	3.0	IMP dehydrogenase, exon 2
CA1247	orf19.20	*IPF3870*	-1.5	1.0	-1.6	-1.2	YOR014W	*RTS1*	1.0	-1.2	1.1	1.3	similar to Saccharomyces cerevisiae Rts1p potential regulatory subunit o
CA1248	orf19.7692	*IPF3866*	1.0	1.1	1.0	1.0	YLR251W		1.0	1.1	1.2	1.0	unknown function
CA1249	orf19.4960	*SPE4*	1.1	-1.0	-1.1	-1.0	YLR146C	*SPE4*	1.0	-1.4	-1.5	-1.5	spermine synthase (by homology)

CA1251	orf19.12423	*IPF9624*	1.1	-1.0	1.0	1.0	YJL201W	*ECM25*	1.0	-1.4	-1.4	-1.4	similar to Saccharomyces cerevisiae Ecm25p involved in cell wall biogen
CA1252	orf19.12421	*RPN1*	-1.1	1.1	1.1	1.1	YHR027C	*RPN1*	1.0	-1.0	1.4	1.3	26S proteasome regulatory subunit (by homology)
CA1255	orf19.1776	*IPF9030*	-1.0	-1.0	-1.0	1.0	YGR277C		1.0	-1.2	1.1	1.1	unknown function
CA1256	orf19.1777	*UBP15*	-1.5	-1.3	-1.4	-1.2	YMR304W	*UBP15*	1.0	1.0	1.1	-1.2	ubiquitin-specific protease (by homology)
CA1257	orf19.10678	*IPF18725*	-1.1	1.1	1.1	1.0	YOR262W		1.0	-1.0	1.3	-1.0	unknown function
CA1258	orf19.10677	*RPN8*	-1.2	-1.0	-1.1	1.0	YOR261C	*RPN8*	1.0	1.3	1.8	1.4	26S proteasome regulatory subunit (by homology)
CA1259	orf19.10676	*IPF3174*	-1.1	-1.0	-1.0	1.0	YPL172C	*COX10*	1.0	-1.1	-1.1	-1.1	Farnesyl transferase (by homology)
CA1260	orf19.3166	*IPF3170*	1.2	1.6	1.6	1.3	YDR141C	*DOP1*	1.0	-1.2	-1.2	-1.1	unknown function
CA1261	orf19.1240	*PF9887.3EOC*	-1.4	1.1	-1.5	-1.2	YPR117W		1.0	-1.0	-1.1	-1.1	unknown function, 3-prime end
CA1262	orf19.1244	*MDR1*	-1.0	-1.1	-1.0	-1.1	YGR100W	*MDR1*	1.0	-1.1	-1.2	-1.3	Mac1p interacting protein (by homology)
CA1264	orf19.239	*STH1*	1.0	-1.0	-1.2	-1.2	YIL126W	*STH1*	1.0	-1.6	-1.7	-1.6	helicase related protein by homology
CA1265	orf19.240	*IPF10510*	-1.1	-1.2	-1.0	-1.0	YKR065C		1.0	-1.0	-1.3	-1.3	unknown function
CA1268	orf19.3159	*IPF14693*	-1.1	-1.0	-1.3	-1.1	YBL004W		1.0	-1.7	-1.6	-1.1	unknown function
CA1269	orf19.10667	*IPF19726*	-1.2	-1.1	-1.0	-1.0	YDL001W		1.0	-1.0	1.1	1.4	unknown function
CA1271	orf19.2723	*HIT1*	-1.1	-1.1	-1.0	-1.2	YJR055W	*HIT1*	1.0	-1.1	-1.1	-1.1	required for growth at high temperature (by homology)
CA1272	orf19.2722	*CGR1*	-1.1	-1.1	-1.1	-1.1	YBR053C		1.0	1.3	1.1	1.0	Cell growth protein (by homology)
CA1273	orf19.2720	*CCT4*	1.0	-1.1	-1.2	-1.1	YDL143W	*CCT4*	1.0	1.3	1.6	2.3	Component of chaperonin-containing T-complex
CA1274	orf19.2717	*SAS10*	-1.0	-1.0	-1.0	1.0	YDL153C	*SAS10*	1.0	1.7	2.0	2.1	Involved in silencing (by homology)
CA1275	orf19.2715	*RPC53*	1.0	-1.3	-1.3	-1.2	YDL150W	*RPC53*	1.0	-1.3	1.1	1.3	DNA-directed RNA polymerase III (by homology)
CA1277	orf19.3630	*IPF10837*	-1.0	-1.0	-1.0	-1.0	YDR083W	*RRP8*	1.0	-1.1	1.1	1.0	unknown function
CA1278	orf19.3629	*IPF10835*	1.0	1.1	1.1	1.0	YER124C		1.0	1.2	1.4	1.5	unknown function
CA1279	orf19.3628	*RSP5*	-1.0	1.1	1.2	1.2	YER125W	*RSP5*	1.0	1.1	1.0	-1.1	ubiquitin-protein ligase (by homology)
CA1284	orf19.8257	*IPF10168.3*	1.0	1.0	1.0	-1.0	YJR089W	*BIR1*	1.0	-1.6	-1.0	-1.0	unknown function, 3-prime end
CA1285	orf19.11905	*SKP1*	1.4	1.1	1.1	1.3	YDR328C	*SKP1*	1.0	1.1	1.4	-1.0	kinetochore protein complex CBF3 by homology
CA1287	orf19.4430	*IPF5545*	-1.1	-1.1	-1.3	-1.1	YDR330W		1.0	-1.4	-1.1	-1.3	unknown function
CA1288	orf19.4432	*KSP1*	1.2	1.3	1.6	1.4	YHR082C	*KSP1*	1.0	1.7	2.2	3.5	SERINE/THREONINE-PROTEIN KINASE by homology
CA1289	orf19.10224	*ZUO1*	-1.0	1.0	-1.0	-1.1	YGR285C	*ZUO1*	1.0	1.4	1.5	1.9	Zuotin, a putative Z-DNA binding (by homology)
CA1290	orf19.2710	*IPF16212*	-1.0	1.1	1.1	1.0	YMR311C	*GLC8*	1.0	1.0	1.5	1.5	unknown function
CA1291	orf19.2711	*IPF16752*	-1.5	-1.2	-1.4	-1.3	YGR200C	*ELP2*	1.0	-1.2	-1.1	-1.1	unknown function
CA1292		*SRB2.3*	1.0	-1.0	1.1	-1.0	YHR041C	*SRB2*	1.0	1.1	1.1	1.2	DNA-directed RNA polymerase II holoenzyme and Kornberg s mediator (
CA1293	orf19.2712	*HCA4*	-1.1	-1.2	-1.3	-1.1	YJL033W	*HCA4*	1.0	-1.1	1.1	-1.0	Can suppress the U14 snoRNA rRNA processing function
CA1294	orf19.10228	*MSH5.3F*	1.0	-1.0	1.0	-1.0	YDL154W	*MSH5*	1.0	-1.2	-1.3	-1.1	Meiosis-specific protein, 3-prime end (by homology)
CA1297	orf19.3417	*ACF2*	1.0	-1.0	-1.1	1.0	YLR144C	*ACF2*	1.0	-1.1	-1.0	1.4	endo-1,3-beta-glucanase
CA1298		*RPL32*	1.5	1.2	1.2	1.3	YBL092W	*RPL32*	1.0	-1.2	-1.5	1.1	ribosomal protein L32
CA1299	orf19.3415	*PTK2*	1.0	-1.0	-1.0	-1.0	YJR059W	*PTK2*	1.0	-1.4	-1.1	-1.1	serine /threonine protein kinase involved in polyamine uptake (by homolo
CA1300	orf19.4199	*SLY41*	1.0	-1.0	1.1	1.1	YOR307C	*SLY41*	1.0	1.0	1.1	1.2	vesicular transport (by homology)
CA1301	orf19.4197	*YHM2*	-1.4	-3.6	-4.4	-2.7	YMR241W	*YHM2*	1.0	1.0	-1.0	1.2	mtDNA stabilizing protein (by homology)
CA1302		*FCA1.3*	1.1	1.0	1.1	1.1	YPR062W	*FCY1*	1.0	1.1	1.4	1.6	cytosine deaminase, 3-prime end
CA1303	orf19.4194	*TFB4*	-1.1	-1.1	-1.1	-1.1	YPR056W	*TFB4*	1.0	-1.1	-1.2	-1.5	component of RNA polymerase transcription initiation TFIIH factor (by ho
CA1304		*RPS13.3*	1.5	1.3	1.3	1.4	YDR064W	*RPS13*	1.0	1.3	1.1	1.9	ribosomal protein, 3-prime end (by homology)
CA1305	orf19.4193	*IPF13508*	-1.0	-1.0	-1.1	-1.1	YDR063W		1.0	1.4	1.2	1.2	unknown function
CA1306	orf19.4192	*CDC14.3*	-1.1	-1.1	-1.1	-1.0	YFR028C	*CDC14*	1.0	-1.2	-1.0	1.0	protein phosphatase, 3-prime end
CA1314	orf19.3639	*MAG1*	-1.0	1.0	1.1	1.0	YER142C	*MAG1*	1.0	-1.4	-1.3	-1.4	3-methyladenine DNA glycosylase (by homology)
CA1315	orf19.9896	*URA2.5EOC*	-1.0	2.6	3.2	2.5	YJL130C	*URA2*	1.0	-1.0	1.3	1.4	multifunctional pyrimidine biosynthesis protein, 5-prime end (by homolog
CA1318	orf19.4219	*IPF3147*	-1.0	-1.1	-1.1	-1.0	YLL034C		1.0	1.0	1.2	1.1	Nuclear valosin-containing protein-like (by homology)
CA1319	orf19.4220	*IPF3144*	1.0	1.1	1.1	1.0	YPR172W		1.0	-1.5	-1.7	-1.3	unknown function
CA1320	orf19.4221	*IPF3143*	-1.0	-1.1	-1.1	-1.1	YPR162C	*ORC4*	1.0	-1.0	1.2	1.2	similar to Saccharomyces cerevisiae Orc4p subunit of origin recognition (
CA1321	orf19.4222	*IPF3141*	-1.0	1.0	1.0	-1.1	YLR452C	*SST2*	1.0	-1.0	-1.0	1.3	similar to Saccharomyces cerevisiae Sst2p involved in desensitization to
CA1322	orf19.4223	*GCD11*	-1.0	1.1	-1.1	-1.1	YER025W	*GCD11*	1.0	1.2	1.8	2.5	Translation initiation factor eIF2 (by homology)
CA1324	orf19.1308	*IPF6676*	1.4	-1.4	-1.2	-1.3	YBR293W		1.0	-1.8	-2.2	-1.5	polytopic membrane protein involved in drug transport (by homology)
CA1327	orf19.1305	*IPF6680*	1.0	-1.1	1.0	1.0	YHR070W	*TRM5*	1.0	-2.3	-1.2	-1.1	unknown function
CA1329	orf19.1303	*MRF2*	-1.1	-1.4	-1.4	-1.2	YGL143C	*MRF1*	1.0	-1.3	-1.3	-1.6	peptide chain release factor, mitochondrial (by homology)
CA1335	orf19.3451	*TRA1*	-1.1	1.2	-1.1	-1.0	YHR099W	*TRA1*	1.0	-1.8	-1.5	-1.1	phosphatidylinositol kinase by homology
CA1336		*IPF5334.EXON*	1.1	1.0	-1.0	1.0	YHR100C		1.0	-1.4	-1.5	-1.3	unknown function, exon 2
CA1338	orf19.10953	*IPF5333*	1.0	1.0	1.0	1.1	YDR266C		1.0	-1.3	-1.1	1.1	unknown function
CA1340	orf19.4339	*VPS4*	-1.1	-1.0	-1.1	-1.0	YPR173C	*VPS4*	1.0	-1.2	-1.1	1.1	vacuolar sorting protein by homology to S. cerevisiae
CA1344	orf19.4342	*IPF14623*	1.1	-1.6	-1.8	-1.6	YPR009W		1.0	-1.3	-1.0	-1.0	unknown function
CA1345	orf19.1490	*IPF6003*	-1.3	1.0	1.1	-1.0	YGR014W	*MSB2*	1.0	-2.1	-1.8	-1.7	similar to Saccharomyces cerevisiae Msb2p multicopy suppressor of a C
CA1349	orf19.4351	*PRP12*	-1.2	1.1	-1.0	-1.2	YMR302C	*PRP12*	1.0	-1.4	-1.2	-1.3	involved in early maturation of pre-rRNA (by homology)
CA1350	orf19.4354	*MCM2*	-1.0	-1.0	-1.1	1.0	YBL023C	*MCM2*	1.0	1.1	-1.1	1.2	replication licensing factor (by homology)
CA1351	orf19.403	*PCL2*	1.0	-1.1	1.0	1.0	YDL127W	*PCL2*	1.0	1.1	1.1	1.1	G1/S specific cyclin

CA1352	orf19.405	*VCX1*	1.1	-1.1	1.1	-1.0	YDL128W	*VCX1*	1.0	-1.1	1.0	1.1	Ca2+-transport by homology
CA1353	orf19.406	*ERG1*	1.2	1.6	2.4	2.0	YGR175C	*ERG1*	1.0	1.0	1.5	3.5	squalene epoxidase
CA1354	orf19.407	*GCD6*	-1.0	-1.1	-1.2	-1.1	YDR211W	*GCD6*	1.0	1.2	1.4	1.4	translation initiation factor- like protein
CA1356	orf19.409	*IPF10138.5F*	1.1	2.4	2.1	2.0	YNR018W		1.0	1.1	1.2	1.5	unknown function, 5-prime end
CA1357	orf19.410	*ARH1*	-1.1	-1.2	-1.4	-1.0	YDR376W	*ARH1*	1.0	-1.3	-1.5	-1.7	adrenodoxin reductase and ferredoxin-NADP+ reductase (by homology)
CA1358	orf19.4406	*NIF3*	-1.0	-1.1	-1.1	-1.0	YGL221C	*NIF3*	1.0	-1.1	-1.0	-1.1	Ngg1p-interacting factor 3 (by homology)
CA1361	orf19.4403	*PEP5*	-1.0	-1.0	-1.0	-1.0	YMR231W	*PEP5*	1.0	-1.1	1.0	-1.2	vacuolar biogenesis protein (by homology)
CA1362	orf19.4426	*PEX3*	-1.0	-1.2	-1.4	-1.2	YDR329C	*PEX3*	1.0	-1.5	-1.0	-1.4	PEROXISOMAL MEMBRANE PROTEIN by homology
CA1365	orf19.4459	*IPF11849*	1.0	1.1	1.0	1.1	YNL234W		1.0	-1.1	1.1	1.1	unknown function
CA1366	orf19.4457	*IPF11847*	1.0	1.0	1.1	-1.0	YNL233W	*BNI4*	1.0	-1.2	-1.1	-1.2	unknown function
CA1367	orf19.4966	*IPF16755*	-1.2	-2.1	-2.4	-1.8	YPR021C		1.0	-1.3	-1.3	-1.5	unknown function
CA1369	orf19.4964	*IPF15968*	-1.0	-1.0	1.0	1.0	YGL174W	*BUD13*	1.0	-2.7	-2.5	-2.1	unknown function
CA1370	orf19.4963	*TCI1*	-1.2	-1.2	-1.2	-1.1	YDR161W	*TCI1*	1.0	-1.2	1.2	1.2	protein phosphatase Two C-Interacting protein (by homology)
CA1371	orf19.4962	*IPF19731*	1.1	1.0	1.0	-1.0	YLR145W		1.0	1.1	-1.1	-1.1	unknown function
CA1372	orf19.4961	*IPF15844*	1.0	1.0	1.1	1.1	YHR006W	*STP2*	1.0	-1.0	-1.0	1.1	similar to Saccharomyces cerevisiae Stp2p involved in pre-tRNA splicing
CA1373	orf19.8784	*AGP1*	1.4	1.7	1.2	1.5	YDR508C	*GNP1*	1.0	-1.8	-1.1	-1.2	asparagine and glutamine permease (by homology)
CA1374	orf19.1195	*MIP1*	-1.2	1.0	1.1	-1.1	YKL134C	*01-Oct*	1.0	-1.7	-1.8	-2.2	Mitochondrial intermediate peptidase (by homology)
CA1375	orf19.8787	*IPF7158*	1.0	1.1	-1.0	-1.0	YDR466W		1.0	1.2	1.2	1.1	putative serine/threonine kinase
CA1376	orf19.8789	*IPF7159*	1.1	1.1	1.0	1.0	YBL107C		1.0	-1.5	-1.4	-1.1	unknown function
CA1380	orf19.458	*BCS1*	-1.0	-1.1	-1.1	-1.0	YDR375C	*BCS1*	1.0	-1.6	-1.8	-1.7	mitochondrial protein of the CDC48/PAS1/SEC18 (AAA) family of ATPas
CA1383	orf19.927	*IPF8422*	-1.1	-1.0	1.0	1.0	YML036W						unknown function
CA1384	orf19.926	*IPF8423*	-1.0	-1.1	-1.3	-1.1	YOR033C	*EXO1*	1.0	-1.1	-1.0	-1.1	similar to Saccharomyces cerevisiae Dhs1p exonuclease (by homology)
CA1386	orf19.923	*THR1*	1.1	1.5	1.5	1.4	YHR025W	*THR1*	1.0	-1.2	1.2	1.9	homoserine kinase
CA1387	orf19.922	*ERG16*	1.2	-1.2	-1.0	-1.0	YHR007C	*ERG11*	1.0	1.3	1.5	2.0	cytochrome P450 lanosterol 14a-demethylase
CA1389	orf19.9338	*PLP2*	-1.1	-1.1	1.2	1.1	YOR281C	*PLP2*	1.0	-1.2	-1.7	-1.4	Might regulate Ste4p in pheromone response (by homology)
CA1392	orf19.1767	*IPF6149*	-1.1	-1.1	-1.1	-1.2	YMR223W	*UBP8*	1.0	-1.1	1.0	1.1	similar to Saccharomyces cerevisiae Ubp8p deubiquinating enzyme (by h
CA1396	orf19.3701	*IPF8075*	-1.1	1.1	-1.1	-1.1	YLR392C		1.0	1.1	1.0	-1.1	unknown function
CA1397	orf19.3700	*TOM72*	-1.9	-1.9	-2.4	-2.0	YNL121C	*TOM70*	1.0	-1.3	-1.4	-1.4	mitochondrial import receptor (by homology)
CA1398	orf19.3699	*IPF19913*	-1.1	-1.1	-1.0	-1.1	YNL128W	*TEP1*	1.0	-1.2	-1.3	-1.5	unknown function
CA1399	orf19.3698	*IPF8069*	1.0	1.1	1.0	-1.0	YHR121W		1.0	-1.9	-1.5	-1.6	unknown function
CA1400	orf19.3697	*IPF8067*	1.0	-1.0	-1.0	-1.0	YNL127W		1.0	-1.0	1.1	-1.2	unknown function
CA1401	orf19.3696	*TOM22*	1.0	-1.0	1.0	1.0	YNL131W	*TOM22*	1.0	-1.3	-1.7	-2.2	mitochondrial outer membrane import receptor complex subunit (by homo
CA1403	orf19.3373	*IPF14155*	1.2	1.3	1.1	1.1	YHL024W	*RIM4*	1.0	1.1	1.1	1.1	similar to Saccharomyces cerevisiae Rim4p involved in sporulation (by ho
CA1404	orf19.3372	*IPF19554.5F*	-1.1	-1.2	-1.4	-1.2	YDL216C	*RRI1*	1.0	-1.1	-1.1	1.2	unknown function, 5-prime end
CA1406	orf19.3370	*DOT4*	1.1	-1.2	-1.2	-1.1	YNL186W	*UBP10*	1.0	-1.1	1.4	1.8	derepression of telomeric silencing (by homology)
CA1409	orf19.2884	*SPT16*	-1.0	1.0	1.0	-1.0	YGL207W	*SPT16*	1.0	-1.1	1.0	1.1	general chromatin factor (by homology)
CA1410	orf19.1275	*GAT1*	-1.0	1.2	1.1	1.2	YFL021W	*GAT1*	1.0	1.1	1.3	1.4	nitrogen regulation (by homology)
CA1413	orf19.168	*MTR3*	-1.1	-1.1	-1.0	-1.0	YGR158C	*MTR3*	1.0	1.2	1.1	1.3	Involved in mRNA transport (by homology)
CA1414	orf19.169	*CHO2*	-1.7	-2.4	-2.8	-2.8	YGR157W	*CHO2*	1.0	1.0	1.1	1.2	phosphatidylethanolamine N-methyltransferase (by homology)
CA1416	orf19.171	*DBP2.EXON1*	1.0	1.3	1.4	1.1	YNL112W	*DBP2*	1.0	1.2	1.1	2.0	ATP-dependent RNA helicase of DEAD box family, exon 1 (by homology
CA1417	orf19.172	*IPF16126*	1.2	1.1	1.4	1.1	YNL113W	*RPC19*	1.0	1.1	1.0	1.3	similar to Saccharomyces cerevisiae Rpc19p DNA-directed RNA polymer
CA1418	orf19.173	*IPF16124*	1.1	1.1	1.4	1.1	YOR113W	*AZF1*	1.0	-2.1	-1.3	-1.4	zinc-finger containing protein (by homology)
CA1420	orf19.11277	*RNT1*	-1.1	-1.1	-1.1	-1.0	YMR239C	*RNT1*	1.0	-1.1	1.1	-1.0	Ribonuclease III (by homology)
CA1421	orf19.11278	*MRPL11*	1.1	-1.3	-1.2	-1.1	YDL202W	*MRPL11*	1.0	1.2	1.2	-1.0	Mitochondrial ribosomal protein (by komology)
CA1422	orf19.3798	*IPF14248*	1.0	-1.1	-1.1	-1.0	YDL201W		1.0	1.0	1.0	1.3	putative methyltransferase (by homology)
CA1423	orf19.3799	*IPF14247*	1.3	1.5	1.6	1.6	YDR233C		1.0	1.7	2.6	3.2	unknown function
CA1427	orf19.5746	*IPF9914*	-1.0	1.0	-1.1	-1.1	YOR335C	*ALA1*	1.0	1.3	1.9	2.1	alanyl-tRNA synthetase (by homology)
CA1428	orf19.13170	*MRP4*	-1.3	-1.5	-1.4	-1.3	YHL004W	*MRP4*	1.0	-1.0	-1.2	-1.2	Ribosomal protein of the small subunit mitochondrial (by homology)
CA1432	orf19.1204	*APM3*	1.0	1.1	-1.0	1.0	YBR288C	*APM3*	1.0	1.1	-1.0	1.0	AP-3 complex subunit, mu3 subunit (by homology)
CA1434	orf19.1203	*SNI2*	-1.1	-1.0	-1.2	-1.2	YBL106C	*SRO77*	1.0	-1.4	-1.4	-1.2	Sec9 interacting protein (by homology)
CA1436	orf19.1201	*IPF7165*	-1.1	-1.0	-1.1	-1.0	YHR011W	*DIA4*	1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Dia4p seryl-tRNA synthetase (by ho
CA1438	orf19.1199	*NOP58*	-1.3	-1.3	-1.7	-1.6	YOR310C	*NOP58*	1.0	1.7	2.3	3.1	nucleolar protein required for pre-18S rRNA processing
CA1439	orf19.4488	*IPF19602*	-1.6	-1.6	-1.9	-1.6	YJL176C	*SWI3*	1.0	-1.4	-1.7	-1.6	similar to Saccharomyces cerevisiae Swi3p transcription regulatory prote
CA1440	orf19.4490	*RPL17B*	1.0	-1.3	-1.1	1.0	YJL177W	*RPL17B*	1.0	-1.0	1.5	1.6	RPL17B ribosomal protein L17.e
CA1441		*QCR8*	1.5	1.0	1.1	1.1	YJL166W	*QCR8*	1.0	-1.5	-1.4	-2.5	ubiquinol-cytochrome-c reductase chain VIII (by homology)
CA1442	orf19.4491	*ERG20*	-1.0	-1.1	-1.2	-1.1	YJL167W	*ERG20*	1.0	-1.1	1.0	-1.0	farnesyl-pyrophosphate synthetase
CA1443	orf19.4492	*IPF4776*	-1.1	-1.2	-1.1	1.0	YKL172W	*EBP2*	1.0	-1.5	-1.2	1.4	unknown Function
CA1444	orf19.4494	*KTR2*	-1.0	1.1	1.2	-1.0	YKR061W	*KTR2*	1.0	-1.1	1.0	1.2	mannosyltransferase (by homology)
CA1445	orf19.185	*MRP51*	1.1	-1.0	-1.0	1.0	YPL118W	*MRP51*	1.0	-1.2	-1.4	-1.5	Mitochondrial ribosomal protein of the small subunit (by homology)
CA1447	orf19.191	*NRK1*	1.3	-1.0	-1.1	-1.0	YHR102W	*KIC1*	1.0	-1.1	-1.3	-1.2	Cdc31p-interacting ser/thr protein kinase (by homology)
CA1452	orf19.4412	*REV1*	-1.1	1.0	-1.1	-1.1	YOR346W	*REV1*	1.0	1.2	1.6	1.4	DNA repair protein (by homology)

CA1453	orf19.4411	*HOS1*	-1.1	-1.1	-1.0	1.0	YPR068C	*HOS1*	1.0	-1.7	-1.6	-1.4	Putative histon deacetylase (by homology)
CA1454	orf19.4410	*ALG1*	-1.0	-1.1	-1.1	1.0	YBR110W	*ALG1*	1.0	-1.4	-1.5	-1.2	beta-1,4-mannosyltransferase (by homology)
CA1455	orf19.4409	*IPF15081*	-1.0	1.0	-1.0	-1.0	YCR026C		1.0	1.1	-1.0	-1.0	phophodiesterase (by homology)
CA1457	orf19.612	*IPF8287*	1.1	-1.0	-1.0	1.0	YML050W		1.0	-1.4	-1.8	-1.9	unknown function
CA1460	orf19.1108	*HAM1*	1.0	1.0	1.1	1.1	YJR069C	*HAM1*	1.0	-1.0	-1.1	1.1	Controls 6-N-hydroxylaminopurine sensitivity and mutagenesis (by homo
CA1462	orf19.8707	*THI80*	1.1	-1.0	1.0	1.0	YOR143C	*THI80*	1.0	-1.8	-1.5	-1.1	Thiamin pyrophosphokinase (by homology)
CA1464	orf19.789	*PYC2.EXON2*	-1.2	5.4	6.4	4.6	YBR218C	*PYC2*	1.0	-2.4	-2.4	-2.1	Pyruvate carboxylase 2 (by homology)
CA1467	orf19.8412	*IPF5082*	1.0	1.2	1.2	1.1	YFL029C	*CAK1*	1.0	-1.0	-1.1	-1.1	similar to Saccharomyces cerevisiae Cak1p cdk-activating protein kinase
CA1468	orf19.794	*SRB10*	-1.0	1.0	1.0	-1.1	YPL042C	*SSN3*	1.0	1.0	-1.0	-1.0	cyclin-dependent kinase by homology
CA1469	orf19.8414	*IPF5078*	-1.1	1.0	1.1	1.0	YLR417W	*VPS36*	1.0	-1.2	-1.5	-1.4	unknown function
CA1470	orf19.8415	*IPF17942*	1.1	1.6	1.5	1.5	YKL189W	*HYM1*	1.0	-1.2	-1.2	-1.1	unknown function
CA1475	orf19.1095	*GLE2*	-1.0	1.1	1.1	1.0	YER107C	*GLE2*	1.0	-1.5	-1.2	-1.1	nuclear pore complex structure and function-like protein (by homology)
CA1477	orf19.1252	*YME1*	-1.2	-1.3	-1.3	-1.2	YPR024W	*YME1*	1.0	-1.1	1.5	1.2	family of ATPases
CA1478	orf19.1251	*IPF16426*	-1.0	-1.1	-1.1	-1.1	YBL097W	*BRN1*	1.0	-1.5	-1.8	-1.1	similar to human BRRN1 (by homology)
CA1479	orf19.1250	*IPF16428*	1.1	-1.1	-1.2	-1.1	YIL019W		1.0	-1.3	-1.3	-1.4	unknown function
CA1480	orf19.1249	*HIS6*	1.1	1.0	-1.1	-1.0	YIL020C	*HIS6*	1.0	-1.3	-1.3	-1.3	5 Pro-FAR isomerase
CA1481	orf19.8832	*RPB3*	-1.0	1.1	1.1	1.0	YIL021W	*RPB3*	1.0	-1.1	1.0	1.0	DNA-directed RNA-polymerase II (by homology)
CA1483	orf19.4059	*YHC3*	-1.1	1.1	1.1	1.1	YJL059W	*YHC3*	1.0	1.2	1.0	1.2	involved in cellular pH homeostasis (by homology)
CA1484	orf19.4060	*ARO4*	-1.1	1.2	1.3	1.2	YBR249C	*ARO4*	1.0	1.7	2.4	3.1	3-dehydro-deoxyphosphoheptonate aldolase, tyrosine-inhibited (by homo
CA1485	orf19.4061	*IPF20082*	1.0	1.0	-1.0	-1.0	YOR238W		1.0	-1.2	-1.3	-1.1	unknown function
CA1488	orf19.4064	*IPF17402*	1.4	1.1	1.4	1.1	YJL062W	*LAS21*	1.0	-1.4	1.1	1.1	unknown function
CA1489	orf19.10734	*ATP3.3*	1.2	-1.4	-1.2	-1.2	YBR039W	*ATP3*	1.0	1.0	-1.3	-1.0	F1F0-ATPase complex, F1 gamma subunit, 3-prime end (by homology)
CA1491	orf19.3225	*IPF166*	-1.0	-1.1	-1.1	-1.1	YCR017C	*CWH43*	1.0	-1.8	-1.8	-1.3	unknown function
CA1492	orf19.3226	*IPF168*	1.1	-1.0	1.1	1.0	YDL046W		1.0	1.0	1.1	1.1	unknown function
CA1494	orf19.3228	*IPF171*	-1.0	-1.0	1.2	1.1	YER113C		1.0	1.1	1.1	1.4	unknown function
CA1495	orf19.3647	*IPF9686*	-1.1	1.0	-1.0	1.0	YPR055W	*SEC8*	1.0	-1.4	-1.2	-1.1	similar to Saccharomyces cerevisiae Sec8p Golgi - plasma membrane pr
CA1496	orf19.3646	*CTR1*	-1.1	-2.1	-2.2	-3.4	YPR124W	*CTR1*	1.0	1.1	-1.0	-1.4	copper transport protein
CA1500	orf19.1697	*IPF13221*	-1.0	-1.0	-1.1	-1.0	YOR091W		1.0	-1.2	1.0	1.0	unknown function
CA1501	orf19.9265	*IPF13217*	-1.0	-1.2	-1.3	-1.2	YNL094W		1.0	-1.6	-1.2	-1.3	unknown function
CA1502	orf19.9267	*RPS7A*	-1.1	-1.1	-1.0	1.1	YOR096W	*RPS7A*	1.0	1.8	2.5	3.2	ribosomal protein (by homology)
CA1503	orf19.9268	*RKI1*	1.1	-1.6	-1.4	-1.3	YOR095C	*RKI1*	1.0	-1.4	-1.1	1.1	D-ribose-5-phosphate ketol-isomerase (by homology)
CA1506	orf19.4527	*HGT11*	1.5	-2.3	-4.2	-3.6	YFL040W		1.0	-1.0	1.5	-1.7	hexose transporter
CA1507	orf19.4526	*HSP30*	1.0	-1.0	1.0	1.0	YCR021C	*HSP30*	1.0	-1.1	1.5	1.8	heat shock protein (by homology)
CA1508	orf19.4525	*IPF9977*	1.4	1.3	2.0	1.4	YLR064W		1.0	-1.3	1.1	1.2	unknown function
CA1510	orf19.4523	*IPF9973*	1.1	-1.0	1.1	1.1	YER183C	*FAU1*	1.0	-1.1	-1.2	-1.2	similar to Saccharomyces cerevisiae Fau1p 5,10-methenyltetrahydrofola
CA1511	orf19.4522	*PF9972.3EO*	1.0	1.1	1.2	1.1	YMR073C		1.0	1.0	1.1	1.1	unknown function, 3-prime end
CA1512	orf19.4884	*IPF15255*	1.1	1.1	1.0	1.1	YEL007W	*TOS9*	1.0	-1.3	-1.3	-1.2	unknown function
CA1513	orf19.4885	*MIR1*	-1.0	-1.0	-1.0	-1.1	YJR077C	*MIR1*	1.0	-1.3	-1.2	-1.3	phosphate transport protein, mitochondrial (MCF) (by homology)
CA1515	orf19.12351	*ECM21.3*	-1.1	1.2	1.1	1.2	YBL101C	*ECM21*	1.0	-1.1	1.1	1.1	Involved in cell wall biogenesis and architecture (by homology)
CA1517	orf19.4798	*IPF11045*	1.1	1.0	1.1	-1.0	YMR212C	*EFR3*	1.0	-1.1	1.5	1.8	unknown function
CA1518	orf19.4799	*IPF11040*	1.1	-1.0	-1.0	-1.0	YMR213W	*CEF1*	1.0	-1.1	1.1	1.2	similar to Schizosaccharomyces pombe cdc5 myb-related protein require
CA1519	orf19.4800	*RIM20*	-1.1	-1.0	-1.0	1.0	YOR275C		1.0	-1.2	-1.2	-1.2	Rim101 activating protein
CA1520	orf19.4801	*IPF11035*	1.0	1.0	-1.1	-1.0	YOR274W	*MOD5*	1.0	-1.3	-1.2	-1.2	similar to Saccharomyces cerevisiae Mod5p tRNA isopentenyltransferas
CA1521	orf19.4802	*FTH1*	1.0	1.0	-1.0	1.0	YBR207W	*FTH1*	1.0	-1.7	-1.7	-1.4	iron transporter
CA1523	orf19.3792	*PAT1*	-1.1	1.1	1.1	1.1	YCR077C	*PAT1*	1.0	-1.0	-1.1	1.2	Topoisomerase II-associated protein (by homology)
CA1524	orf19.3794	*SUR1*	1.0	-1.0	-1.0	-1.1	YJL056C	*ZAP1*	1.0	-1.3	-1.4	-1.1	Suppressor of ROK1
CA1525	orf19.3795	*AGP3*	1.0	1.7	2.8	2.0	YFL055W	*AGP3*	1.0	-1.5	-1.8	-2.5	amino acid-permease (by homology)
CA1529	orf19.4557	*SPC105*	-1.1	-1.0	-1.1	-1.0	YGL093W	*SPC105*	1.0	-1.2	-1.1	-1.2	Spindle pole body protein (by homology)
CA1530	orf19.1221	*ALG2.5*	-1.0	1.0	1.2	1.1	YGL065C	*ALG2*	1.0	-1.5	-1.1	-1.3	mannosyltransferase, 5-prime end (by homology)
CA1531	orf19.1220	*RVS167*	1.0	-1.0	1.0	1.0	YDR388W	*RVS167*	1.0	-1.8	-1.5	-1.4	(putative) cytoskeletal protein (by homology)
CA1532	orf19.8806	*IPF9507*	-1.2	-1.1	-1.4	-1.2	YMR247C		1.0	-1.4	-1.3	-1.2	unknown function
CA1534	orf19.1214	*MAP2*	-1.1	-1.0	1.1	1.0	YBL091C	*MAP2*	1.0	-1.1	-1.2	-1.2	methionine aminopeptidase (by homology)
CA1535	orf19.8800	*IPF9515*	1.2	1.0	1.2	1.0	YER120W	*SCS2*	1.0	1.2	1.8	2.1	similar to Saccharomyces cerevisiae Scs2p required for inositol metaboli
CA1536	orf19.451	*SOK1*	1.1	1.1	1.4	1.3	YDR006C	*SOK1*	1.0	1.3	1.3	1.2	high copy suppressor of a cyclic AMP-dependent protein kinase
CA1539	orf19.4560	*BFR1*	-1.5	-1.7	-2.1	-1.7	YOR198C	*BFR1*	1.0	-1.2	1.0	1.1	Similar to Saccharomyces cerevisiae Bfr1p involved in the maintenance
CA1540	orf19.4563	*IPF1047*	1.0	-1.0	1.0	-1.0	YMR310C		1.0	-1.1	1.2	1.4	unknown function
CA1541	orf19.4565	*BGL21*	1.3	1.0	1.2	1.1	YGR282C	*BGL2*	1.0	1.1	1.3	1.8	endo-beta-1,3-glucanase (by homology)
CA1546	orf19.8891	*IPF6671*	-1.0	1.0	-1.0	1.0	YLL005C	*SPO75*	1.0	1.1	1.0	-1.1	unknown function
CA1549	orf19.4278	*IPF8744*	-1.2	1.1	1.1	1.0	YKL005C		1.0	-1.0	-1.2	-1.1	unknown function
CA1551	orf19.4275	*IPF8741.3F*	-1.0	-1.1	-1.2	-1.0	YDR217C	*RAD9*	1.0	-1.6	-1.3	-1.2	unknown function, 3-prime end
CA1552	orf19.4274	*PUT1*	-1.4	-4.0	-5.4	-3.7	YLR142W	*PUT1*	1.0	-1.5	-1.4	-1.5	proline oxidase (by homology)

CA1554	orf19.1713	*GEA2.3F*	-1.8	-1.2	-1.6	-1.2	YEL022W	*GEA2*	1.0	1.0	1.1	1.1	GTP/GDP exchange factor, 3-prime end (by homology)
CA1556	orf19.1711	*END3*	-1.1	-1.1	-1.0	-1.0	YNL084C	*END3*	1.0	-1.1	1.4	1.5	required for endocytosis and cytoskeletal organization (by homology)
CA1560	orf19.1706	*MET18*	-1.0	-1.2	-1.2	-1.1	YIL128W	*MET18*	1.0	-1.0	1.3	1.4	Involved in NER repair and RNA polymerase II transcription (by homolog
CA1564	orf19.1153	*GAD1*	1.0	2.8	3.4	3.4	YMR250W	*GAD1*	1.0	1.5	1.0	-1.7	Glutamate decarboxylase (by homology)
CA1565	orf19.1154	*EGD1*	1.1	-1.1	-1.3	-1.0	YPL037C	*EGD1*	1.0	1.3	1.5	1.9	GAL4 DNA-binding enhancer protein (by homology)
CA1570	orf19.1160	*IPF7617*	1.4	1.7	1.9	1.9	YHR181W		1.0	-1.3	-1.2	-1.1	unknown function
CA1572	orf19.9221	*POX4*	-1.0	-8.4	-11.0	-8.2	YGL205W	*POX1*	1.0	1.0	1.1	1.1	peroxisomal fatty acyl-CoA oxidase (by homology)
CA1577	orf19.12446	*KNS1*	1.0	1.1	1.0	-1.0	YLL019C	*KNS1*	1.0	-1.6	-1.1	-1.5	Ser/thr protein kinase (by homology)
CA1578	orf19.4715	*NUM11*	-1.0	1.1	-1.4	-1.2	YDR150W	*NUM1*	1.0	-2.0	-1.8	-1.6	nuclear migration protein (by homology)
CA1579	orf19.4716	*GDH3*	1.0	6.8	11.1	7.4	YOR375C	*GDH1*	1.0	1.4	2.5	1.9	NADP-glutamate dehydrogenase (by homology)
CA1580	orf19.4718	*TRP5*	-1.0	-1.0	-1.1	-1.1	YGL026C	*TRP5*	1.0	1.1	1.9	2.6	tryptophan synthase (by homology)
CA1581	orf19.4719	*CWH41.3EOC*	-1.1	-1.1	1.0	1.0	YGL027C	*CWH41*	1.0	1.1	1.2	1.1	ER glucosidase I, 3-prime end (by homology)
CA1582	orf19.6028	*CLN21*	-1.0	-1.0	-1.1	-1.0	YMR199W	*CLN1*	1.0	-2.4	-2.8	-2.2	G1 cyclin (by homology)
CA1583	orf19.6029	*ROT1*	-1.1	-1.1	1.0	-1.1	YMR200W	*ROT1*	1.0	1.1	1.3	1.5	Suppressor of TOR2 mutations (by homology)
CA1585	orf19.6031	*VPS27*	-1.1	-1.0	1.1	-1.0	YNR006W	*VPS27*	1.0	-1.3	-1.4	-1.3	Vacuolar protein sorting (by homology)
CA1586	orf19.6032	*ODC1*	1.1	1.1	1.2	1.1	YKL184W	*SPE1*	1.0	-1.1	1.1	1.3	Ornithine decarboxylase
CA1587	orf19.6033	*CMP2*	-1.2	-1.2	-1.5	-1.3	YML057W	*CMP2*	1.0	1.0	1.1	1.0	Calcineurin B, catalytic subunit (by homology)
CA1588	orf19.11787	*SPT8*	-1.1	-1.3	-1.4	-1.2	YLR055C	*SPT8*	1.0	-1.3	1.1	1.1	transcriptional adaptor or co-activator (by homology)
CA1590	orf19.11790	*IPF14665*	-1.0	1.1	1.0	-1.0	YFL027C	*GYP8*	1.0	1.1	1.3	1.3	unknown function
CA1592	orf19.4317	*IPF14662*	1.6	-1.7	-1.4	-1.4	YHR104W	*GRE3*	1.0	1.4	1.6	1.3	D-xylose reductase (by homology)
CA1593	orf19.4318	*MIG1*	-1.0	1.3	1.1	1.1	YGL035C	*MIG1*	1.0	-1.3	1.4	1.1	transcriptional regulator
CA1595	orf19.7905	*IPF9544*	1.2	1.0	1.2	1.1	YNL156C		1.0	1.2	1.7	1.2	unknown function
CA1596	orf19.272	*FAA21*	-1.2	-3.0	-3.8	-2.7	YER015W	*FAA2*	1.0	1.1	1.1	1.4	long-chain-fatty-acid-CoA ligase (by homology)
CA1598	orf19.7901	*SES1*	-1.5	-1.4	-1.4	-1.2	YDR023W	*SES1*	1.0	1.2	1.4	1.4	seryl-tRNA synthetase (by homology)
CA1599	orf19.7900	*IPF11452*	1.0	1.0	1.0	1.0	YDR030C	*RAD28*	1.0	-1.1	-1.1	-1.1	unknown function
CA1600	orf19.4720	*CTR2*	1.1	1.2	1.2	1.1	YHR175W	*CTR2*	1.0	1.1	1.3	1.3	copper transport protein (by homology)
CA1602	orf19.4722	*RTG1*	1.1	1.1	1.1	1.1	YOL067C	*RTG1*	1.0	-1.0	1.2	1.3	basic helix-loop-helix transcription factor that regulates CIT2 gene
CA1603	orf19.4723	*FAD1*	1.1	1.1	1.1	1.1	YDL045C	*FAD1*	1.0	1.1	-1.1	-1.1	flavin adenine dinucleotide (FAD) synthetase (by homology)
CA1604	orf19.4724	*IPF13653*	-1.0	1.1	-1.0	-1.0	YDL043C	*PRP11*	1.0	-1.6	1.1	-1.1	unknown function
CA1605	orf19.4725	*SWI6*	-1.5	-1.6	-2.0	-1.7	YLR182W	*SWI6*	1.0	-1.2	1.6	1.5	Transcription factor (by homology)
CA1606	orf19.4726	*NCS1*	1.1	1.1	1.0	1.2	YDR373W	*FRQ1*	1.0	-1.0	1.3	1.2	Calcium binding protein (by homology)
CA1607	orf19.4727	*IPF14916*	1.2	1.1	1.1	1.1	YOL071W		1.0	-1.7	-1.5	-1.6	unknown function
CA1608	orf19.4122	*TES12*	1.1	-1.1	-1.0	-1.1	YJR019C	*TES1*	1.0	1.2	1.0	1.1	Thiosterase (by homology)
CA1610	orf19.4120	*LAS1*	1.0	1.1	1.1	1.0	YKR063C	*LAS1*	1.0	-1.1	-1.1	-1.2	cell morphogenesis, cytoskeletal regulation and bud formation (by homol
CA1611	orf19.4119	*SPO72*	1.0	1.1	-1.0	1.0	YNL242W	*APG2*	1.0	1.1	-1.3	-1.7	required for sporulation (by homology)
CA1615	orf19.3218	*IPF14540*	1.0	-1.0	1.0	-1.0	YJR124C		1.0	-2.3	-1.0	1.1	putative multidrug protein (by homology)
CA1617	orf19.3220	*IPF14536*	1.0	-1.0	-1.0	-1.1	YDR339C		1.0	1.4	1.5	1.7	unknown function
CA1618	orf19.11559	*RRP45*	-1.0	-1.2	-1.0	-1.0	YDR280W	*RRP45*	1.0	-1.2	1.1	1.0	Protein component of the exosome 3 -5 exoribonuclease complex (by h
CA1619	orf19.11558	*IPF2067*	1.1	-1.0	1.2	1.1	YPL057C	*SUR1*	1.0	-1.4	1.3	-1.3	Required for mannosylation of sphingolipids (by homology)
CA1620	orf19.4076	*MET10*	-1.3	-1.6	-1.9	-1.5	YFR030W	*MET10*	1.0	-1.1	1.2	1.1	Sulfite reductase flavin-binding subunit (by homology)
CA1622	orf19.470	*IPF10045*	-1.0	-1.0	-1.0	-1.0	YDR145W	*TAF61*	1.0	1.2	1.5	1.5	similar to Saccharomyces cerevisiae Taf61p TFIID and SAGA subunit (b
CA1623	orf19.469	*STE7*	-1.0	-1.0	-1.0	-1.1	YDL159W	*STE7*	1.0	-1.1	1.1	-1.1	MAP Kinase Kinase
CA1626	orf19.1033	*STR2*	-1.1	-1.0	1.1	-1.0	YJR130C	*STR2*	1.0	-1.0	-1.0	1.2	O-succinylhomoserine (thiol)-lyase (by homology)
CA1627	orf19.1032	*SKO1.3*	1.0	-1.1	-1.1	-1.2	YNL167C	*SKO1*	1.0	-1.1	1.5	1.9	Cre-binding bzip protein, 3-prime end (by homology)
CA1628	orf19.1031	*HMG1*	1.0	-1.1	-1.0	-1.0	YLR450W	*HMG2*	1.0	-1.5	-1.4	-1.4	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 (by hom
CA1629	orf19.1030	*NPI46*	1.1	1.2	1.2	1.1	YLR449W	*FPR4*	1.0	-1.0	1.1	-1.1	proline cis-trans isomerase (by homology)
CA1630	orf19.1029	*RPP1*	1.1	-1.0	-1.0	1.0	YHR062C	*RPP1*	1.0	-1.2	1.2	1.1	required for processing of tRNA and 35S rRNA (by homology)
CA1631	orf19.1028	*IPF19582*	1.0	1.0	-1.0	-1.0	YNL230C	*ELA1*	1.0	1.0	1.0	-1.1	unknown function
CA1632	orf19.11420	*IPF10181*	1.1	1.0	1.0	1.1	YJR101W	*RSM26*	1.0	1.5	-1.0	1.1	similar to Saccharomyces cerevisiae Rsm26p protein of the small subuni
CA1634	orf19.11421	*IPF10179*	1.1	1.0	1.0	1.1	YJR088C		1.0	-1.2	-1.0	-1.0	unknown function
CA1635	orf19.3941	*URA7*	-1.1	1.3	1.5	1.2	YBL039C	*URA7*	1.0	1.4	2.2	2.7	CTP synthase 1 (by homology)
CA1636	orf19.3942	*IPF20086*	1.0	1.1	1.1	1.0	YJR102C	*VPS25*	1.0	1.1	1.3	1.1	unknown function
CA1637		*RPL43A.3*	1.5	1.1	1.4	1.3	YPR043W	*RPL43A*	1.0	2.2	2.4	1.8	ribosomal protein, 3-prime end (by homology)
CA1638	orf19.3944	*GRR1*	1.0	1.2	1.2	1.1	YJR090C	*GRR1*	1.0	1.2	1.4	1.9	Required for glucose repression and for glucose and cation transport (by
CA1641	orf19.1731	*NHP10.3F*	1.1	1.0	-1.0	1.0	YDL002C	*NHP10*	1.0	1.4	1.3	1.5	unknown function, 3-prime end
CA1645	orf19.1727	*PMC1*	-1.1	-1.0	-1.0	-1.0	YGL006W	*PMC1*	1.0	-1.4	-1.1	1.1	Ca2+-transporting P-type ATPase (by homology)
CA1647	orf19.5568	*IPF16663*	-1.1	-1.1	-1.1	-1.1	YKR020W		1.0	-1.3	-1.2	-1.2	unknown function
CA1648	orf19.5567	*IPF16662*	1.0	1.0	1.0	1.0	YBR257W	*POP4*	1.0	1.1	1.2	1.0	unknown function
CA1649	orf19.5566	*LAB1*	1.0	-1.1	-1.0	-1.0	YJL046W		1.0	1.0	-1.1	-1.1	Lipoate biosynthesis by homology
CA1652	orf19.5563	*RNH1.EXON1*	1.2	-1.0	-1.0	-1.0	YMR234W	*RNH1*	1.0	-1.1	1.1	-1.1	Ribonuclease H, exon 1 (by homology)
CA1653	orf19.5561	*STE23*	-1.4	1.0	-1.2	1.1	YLR389C	*STE23*	1.0	-1.3	1.1	-1.2	protease involved in a-factor processing by homology

CA1654	orf19.5559	*IPF19660*	-1.1	1.1	1.3	1.1	YDR202C	*RAV2*	1.0	1.2	1.3	1.3	unknown function
CA1655	orf19.4328	*CCC2*	-1.1	-1.2	-1.2	-1.1	YDR270W	*CCC2*	1.0	-1.2	-1.1	-1.0	putative copper-transporting ATPase (by homology)
CA1656	orf19.4326	*IPF16019*	1.1	1.0	-1.0	1.0	YOR308C	*SNU66*	1.0	1.0	1.0	1.0	unknown function
CA1659	orf19.4323	*IPF11054*	1.0	1.0	1.1	1.0	YHR105W		1.0	-1.4	-1.1	1.0	unknown function
CA1660	orf19.4322	*DAP2*	-1.0	-1.0	1.1	1.1	YHR028C	*DAP2*	1.0	-1.1	-1.1	-1.1	dipeptidyl aminopeptidase B (by homology)
CA1662		*RPL28.3F*	1.3	-1.0	1.1	1.2	YGL103W	*RPL28*	1.0	1.8	1.8	2.2	Ribosomal protein, 3-prime end (by homology)
CA1663	orf19.2864	*IPF7309*	-1.1	-1.0	1.0	1.0	YGL101W		1.0	1.1	1.1	1.3	unknown function
CA1664		*ERV1.3*	1.1	1.1	1.0	1.0	YGR029W	*ERV1*	1.0	-1.3	-1.4	-1.2	Mitochondrial biogenesis and regulation of cell cycle, 3-prime end (by ho
CA1665	orf19.2862	*RIB1*	1.2	-1.0	1.0	-1.1	YBL033C	*RIB1*	1.0	-1.3	-1.1	-1.1	GTP cyclohydrolase II by homology to S.cerevisiae
CA1666	orf19.2859	*SRP40*	-1.2	-1.3	-1.2	-1.1	YKR092C	*SRP40*	1.0	1.0	1.3	1.2	RNA I and II supressor (by homology)
CA1667	orf19.2857	*SSL2*	-1.2	-1.1	-1.3	-1.1	YIL143C	*SSL2*	1.0	1.2	1.1	1.4	by homology to S. cerevisiae: DNA helicase
CA1669	orf19.2852	*IPF11393*	1.3	-1.0	-1.2	1.1	YBL090W	*MRP21*	1.0	1.0	-1.1	-1.4	unknown function
CA1673	orf19.3612	*PST2*	1.1	1.3	1.4	1.3	YDR032C	*PST2*	1.0	1.1	-1.2	-1.8	1,4-benzoquinone reductase by homology
CA1674	orf19.3613	*PAF1*	-1.2	-1.2	-1.2	-1.0	YBR279W	*PAF1*	1.0	-2.9	-2.7	-1.7	DNA-directed RNA polymerase II regulator by homology
CA1675	orf19.3615	*IPF5192*	1.0	1.0	1.0	1.0	YPL191C		1.0	-1.6	1.1	1.0	unknown function
CA1676	orf19.3616	*ERG9*	-1.4	1.0	-1.0	-1.1	YHR190W	*ERG9*	1.0	-1.1	-1.0	-1.0	farnesyl-diphosphate farnesyltransferase
CA1677	orf19.3617	*GTR1*	1.0	1.0	1.0	1.1	YML121W	*GTR1*	1.0	-1.1	1.1	1.1	GTP-binding protein by homology
CA1678	orf19.3618	*IPF5185*	1.6	4.2	5.6	3.9	YAR050W	*FLO1*	1.0	-1.5	-1.1	-1.4	putative cell wall protein (by homology)
CA1680	orf19.4913	*IPF15649*	-1.0	-1.0	-1.0	-1.0	YOL087C		1.0	-1.1	1.1	1.1	unknown function
CA1686	orf19.3659	*IPF12272*	-1.1	1.1	1.0	-1.0	YER139C		1.0	1.1	-1.1	-1.2	unknown function
CA1687	orf19.3658	*IPF12275*	-1.1	1.1	1.2	1.1	YER140W		1.0	-1.1	-1.0	-1.0	unknown function
CA1688	orf19.3656	*COX15*	-1.1	2.0	2.6	2.5	YER141W	*COX15*	1.0	-1.4	-1.4	-1.6	cytochrome oxidase assembly factor (by homology)
CA1690	orf19.3653	*FAT1*	-1.1	-1.0	-1.1	1.0	YBR041W	*FAT1*	1.0	1.3	1.2	1.2	very long-chain fatty acyl-CoA synthetase (by homology)
CA1691	orf19.3651	*PGK1*	1.0	2.5	2.4	2.5	YCR012W	*PGK1*	1.0	2.0	2.9	3.5	Phosphoglycerate kinase
CA1692	orf19.5036	*PF17055.3EO*	1.1	1.0	1.0	1.0	YDR425W		1.0	-2.0	-1.6	-1.5	unknown function, 3-prime end
CA1694	orf19.5038	*TRM3*	-1.1	-1.2	-1.2	-1.1	YDL112W	*TRM3*	1.0	1.3	1.0	1.2	2 -O-ribose methyltransferase (by homology)
CA1695	orf19.5039	*RRP42*	1.0	-1.1	-1.1	-1.0	YDL111C	*RRP42*	1.0	1.4	1.3	1.9	rRNA processing protein (by homology)
CA1696	orf19.5040	*ASM4*	-1.1	-1.1	-1.1	-1.0	YDL088C	*ASM4*	1.0	1.2	1.3	1.2	similar to Saccharmoyces cerevisiae Asm4p suppressor of temperature-s
CA1700	orf19.5046	*RAM1.5F*	-1.1	-1.1	-1.2	-1.1	YDL090C	*RAM1*	1.0	-1.0	-1.0	-1.1	protein farnesyltransferase, beta subunit, 5-prime end (by homology)
CA1702	orf19.702	*HEL1*	-1.4	-1.3	-1.4	-1.4	YER176W	*ECM32*	1.0	1.0	1.2	1.3	DNA helicase I (by homology)
CA1703	orf19.703	*IPF7987*	1.0	-1.1	1.0	-1.0	YGR247W		1.0	-1.3	-1.2	-1.5	unknown function
CA1704	orf19.704	*SOL3*	1.1	-1.2	-1.3	-1.0	YHR163W	*SOL3*	1.0	-1.4	-1.2	1.1	weak multicopy suppressor of los1-1 (by homology)
CA1705	orf19.705	*GCN5*	1.1	-1.1	1.0	-1.3	YGR252W	*GCN5*	1.0	-1.8	-1.1	1.0	Histone acetyltransferase (by homology)
CA1706	orf19.706	*NMD3*	-1.0	-1.0	1.1	-1.1	YHR170W	*NMD3*	1.0	1.1	1.3	1.7	RNA binding (by homology)
CA1709	orf19.4889	*HOL2*	1.1	-1.0	1.0	1.1	YNR055C	*HOL1*	1.0	1.2	1.2	1.5	Multidrug-resistance protein subfamily 1 (by homology)
CA1710	orf19.4890	*CLA4*	-1.1	-1.1	-1.1	-1.2	YNL298W	*CLA4*	1.0	1.3	1.4	1.5	protein kinase homolog (by homology)
CA1712	orf19.10842	*ABC1*	-1.1	1.0	1.1	-1.1	YGL119W	*ABC1*	1.0	-1.2	-1.2	-1.3	ubiquinol--cytochrome-c reductase(by homology)
CA1713	orf19.3332	*IPF19743*	1.0	-1.0	1.0	-1.0	YDL231C	*BRE4*	1.0	-1.1	-1.2	-1.3	unknown function
CA1714	orf19.3333	*NAB2*	-1.2	-1.1	-1.2	-1.1	YGL122C	*NAB2*	1.0	-1.1	1.1	1.6	Nuclear poly(A)-RNA-binding protein (by homology)
CA1715	orf19.3334	*RPS21*	1.0	1.0	-1.1	1.0	YGL123W	*RPS2*	1.0	1.2	1.4	2.2	ribosomal protein (by homology)
CA1719	orf19.12119	*ILV6*	1.1	1.0	1.1	1.1	YCL009C	*ILV6*	1.0	1.1	1.4	2.1	acetolactate synthase, regulatory subunit (by homology)
CA1723	orf19.2651	*TEF4*	1.0	1.1	1.1	-1.0	YPL048W	*CAM1*	1.0	-1.1	1.1	1.0	translation elongation factor eEF1 (by homology)
CA1728	orf19.6494	*WHI3*	1.1	1.1	1.2	1.1	YNL197C	*WHI3*	1.0	-2.0	-2.0	-1.5	Putative RNA binding protein (by homology)
CA1729	orf19.6496	*IPF8440*	-1.0	1.1	1.0	1.1	YOR115C	*TRS33*	1.0	-1.6	-1.4	-1.3	similar to Saccharomyces cerevisiae Trs33p TRAPP subunit of 33 kDa in
CA1730	orf19.6498	*IPF8439*	1.0	1.1	1.0	1.0	YDL115C	*IWR1*	1.0	-1.7	-1.3	-1.3	unknown function
CA1732	orf19.6500	*ECM42*	1.0	1.0	1.1	1.0	YMR062C	*ECM40*					Acetylornithine acetyltransferase (by homology)
CA1735	orf19.2528	*IPF4986*	-1.1	-1.1	-1.1	-1.1	YNL039W	*TFC5*	1.0	-1.7	-2.0	-1.7	similar to Saccharomyces cerevisiae Tfc5p TFIIIB subunit, 90 kD (by hom
CA1736	orf19.2527	*IPF4983*	1.0	1.0	-1.1	1.0	YNL035C		1.0	1.0	-1.0	-1.0	unknown function
CA1737	orf19.2525	*LYS12*	-1.1	1.2	1.5	1.2	YIL094C	*LYS12*	1.0	1.4	1.9	1.9	homo-isocitrate dehydrogenase (by homology)
CA1738	orf19.2524	*MGE1*	1.1	1.0	1.1	-1.0	YOR232W	*MGE1*	1.0	-1.0	-1.3	-1.3	heat shock protein (by homology)
CA1740	orf19.5058	*SMI1*	-1.2	-1.1	-1.2	-1.1	YGR229C	*SMI1*	1.0	-1.1	1.4	1.4	beta-1,3-glucan synthesis protein (by homology)
CA1742	orf19.5054	*IPF12210*	-1.1	-1.4	-1.3	-1.2	YFR047C		1.0	-1.6	-1.6	-1.5	quinolinate phosphoribosyltransferase (by homology)
CA1743	orf19.5053	*IPF12209*	1.0	1.1	1.0	1.1	YFR027W	*ECO1*	1.0	-1.2	-1.2	-1.1	similar to Saccharomyces cerevisiae Eco1p involved in sister chromatid
CA1744	orf19.5052	*IPF10889*	1.1	1.0	1.0	-1.0	YFR045W		1.0	1.2	1.0	-1.1	unknown function
CA1746	orf19.5050	*IPF10886*	-1.1	-1.1	-1.2	-1.1	YGL236C	*MTO1*	1.0	-1.4	-1.7	-1.7	unknown function
CA1747	orf19.5049	*IPF10884*	-1.0	-1.0	1.0	1.0	YLR003C		1.0	-1.1	1.0	1.1	unknown function
CA1751	orf19.1517	*ARO3.EXON2*	-1.1	1.1	-1.0	1.0	YDR035W	*ARO3*	1.0	1.4	1.9	2.9	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase, exon 2 (by hom
CA1752	orf19.1516	*UBP14*	-1.2	1.1	-1.0	1.1	YBR058C	*UBP14*	1.0	-1.1	-1.1	-1.1	Ubiquitin-specific protease (by homology)
CA1753	orf19.1515	*IPF8245*	-1.0	1.1	1.1	1.1	YDR371W		1.0	-1.1	1.1	-1.5	putative chitinase
CA1754	orf19.5131	*IPF16320*	-1.3	-1.1	-1.2	-1.1	YCL039W		1.0	-1.1	-1.3	-1.1	Unknown function
CA1755	orf19.5130	*PDI1*	-1.1	-1.2	-1.7	-1.3	YCL043C	*PDI1*	1.0	-1.8	-1.1	1.2	protein disulfide-isomerase precursor (by homology)

CA1758	orf19.5126	*IPF14559.3F*	-1.0	-1.4	-1.4	-1.4	YCL037C	*SRO9*	1.0	1.2	1.3	1.9	unknown function, 3-prime end
CA1759	orf19.5125	*IPF14744*	-1.2	-1.5	-1.5	-1.3	YLR149C		1.0	1.2	1.2	-1.3	unknown function
CA1762		*IPF20014*	1.0	-1.0	-1.0	-1.0	YIR035C		1.0	-1.3	1.2	1.7	oxidoreductase by homology
CA1763	orf19.5195	*URA6*	1.1	-1.2	-1.3	-1.2	YKL024C	*URA6*	1.0	1.2	1.4	1.9	Uridine-monophosphate kinase(by homology)
CA1764	orf19.5196	*IPF7596*	1.2	1.2	1.1	1.2	YJR017C	*ESS1*	1.0	-1.5	-1.1	-1.1	similar to Saccharomyces cerevisiae Ess1p peptidyl-prolyl cis/trans isom
CA1765	orf19.5197	*APE2*	-1.3	-1.4	-2.0	-2.0	YKL157W	*APE2*	1.0	-1.3	-1.2	-1.2	aminopeptidase yscII
CA1766	orf19.5198	*NOP4*	-1.1	-1.3	-1.5	-1.4	YPL043W	*NOP4*	1.0	1.2	1.7	2.0	Nucleolar protein
CA1767	orf19.5200	*SIT4*	1.1	1.3	1.6	1.4	YDL047W	*SIT4*	1.0	-1.0	1.1	1.2	Ser/thr protein phosphatase
CA1768	orf19.5201	*IPF7585*	1.1	1.0	1.0	1.1	YER050C	*RSM18*	1.0	1.1	1.2	1.0	unknown function
CA1770	orf19.2185	*IPF12457*	1.1	-1.2	1.0	-1.1	YGL111W		1.0	1.1	1.2	1.4	unknown function
CA1771	orf19.2186	*SEH1*	1.0	1.0	1.1	1.1	YGL100W	*SEH1*	1.0	1.1	-1.1	1.1	nuclear pore protein (by homology)
CA1772	orf19.2187	*ALG7*	1.3	1.5	2.1	1.6	YBR243C	*ALG7*	1.0	1.1	1.2	1.1	UDP-N-acetylglucosamine-1-phosphate transferase (by homology)
CA1773	orf19.2190	*VRP1*	1.1	1.2	1.3	1.1	YLR337C	*VRP1*	1.0	-1.1	-1.1	-1.0	verprolin (by homology)
CA1774	orf19.2191	*IPF7498*	1.1	-1.0	-1.0	1.0	YBR246W		1.0	-1.2	-1.2	-1.1	unknown function
CA1775	orf19.9738	*GDH2*	1.1	-2.9	-3.1	-2.8	YDL215C	*GDH2*	1.0	-1.9	-1.6	-1.1	NAD-specific glutamate dehydrogenase (NAD) (by homology)
CA1779	orf19.1826	*IPF14510*	-1.0	-1.2	-1.1	-1.1	YGL219C	*MMM2*	1.0	1.1	1.2	1.1	unknown function
CA1781	orf19.1828	*IPF14508*	1.0	-1.0	-1.0	-1.0	YEL029C	*BUD16*	1.0	-1.1	-1.1	1.1	unknown function
CA1782	orf19.1172	*HO84.3EOC*	-1.1	1.4	1.4	1.7	YML123C	*PHO84*	1.0	-1.1	1.7	3.0	Inorganic phosphate transport protein, 3-prime end (by homology)
CA1784	orf19.1170	*ARO7*	-1.0	-1.2	-1.1	-1.1	YPR060C	*ARO7*	1.0	-1.4	-1.1	-1.0	chorismate mutase (by homology)
CA1785	orf19.1169	*IPF7631*	1.1	1.0	1.0	1.0	YPR061C		1.0	-1.0	1.1	1.3	unknown function
CA1787	orf19.1167	*IFH3*	1.0	-1.0	-1.0	-1.0	YLL057C		1.0	-1.5	-1.8	-2.2	Dioxygenase (by homology)
CA1788	orf19.1166	*USO1.3*	1.2	1.2	1.1	-1.0	YBL047C	*EDE1*	1.0	1.4	1.3	1.2	Cytoskeletal-related transport protein, Ca++ binding, 3-prime end (by ho
CA1789	orf19.1164	*GAR1*	1.3	1.5	1.4	1.5	YHR089C	*GAR1*	1.0	-1.1	1.1	1.3	Nucleolar rRNA processing protein (by homology)
CA1790	orf19.5204	*IPF13971*	1.1	1.2	1.6	1.2	YNL042W	*BOP3*	1.0	-1.1	-1.1	1.0	unknown function
CA1792	orf19.5206	*IPF13966*	-1.1	-1.2	-1.1	-1.1	YIL104C		1.0	-1.2	1.3	1.2	unknown function
CA1794	orf19.5208	*IPF18608.3F*	-1.0	-1.0	-1.0	-1.0	YIL103W		1.0	1.0	1.2	1.1	unknown function, 3-prime end
CA1795	orf19.5209	*IPF11261*	-1.1	-1.0	1.0	1.0	YNL041C	*TFI2*	1.0	-1.2	-1.1	-1.2	unknown function
CA1796	orf19.5210	*IPF11259*	-1.0	-1.0	1.0	-1.1	YIL101C	*XBP1*	1.0	1.2	-1.0	-1.2	unknown function
CA1800	orf19.2921	*IPF11445*	-1.0	1.0	-1.0	1.0	YER007W	*PAC2*	1.0	-1.1	-1.0	-1.1	similar to Saccharomyces cerevisiae Pac2p involved in the stabilization o
CA1802	orf19.2919	*IPF11443*	-1.0	1.0	-1.0	1.2	YIR002C	*MPH1*	1.0	-1.5	-1.3	-1.5	unknown function
CA1803	orf19.2917	*IPF16748*	-1.1	-1.1	-1.2	-1.2	YER006W		1.0	1.6	2.5	3.4	unknown function
CA1804	orf19.1111	*TAF17*	1.1	1.0	-1.0	-1.0	YMR236W	*TAF17*	1.0	-1.2	-1.0	-1.0	TFIID and SAGA subunit (by homology)
CA1805	orf19.1112	*IPF6332*	-1.2	-1.1	-1.1	-1.1	YOR299W	*BUD7*	1.0	-1.7	-1.3	1.2	similar to Saccharomyces cerevisiae Bud7p chitin biosynthesis protein in
CA1807	orf19.1114	*IPF6328*	1.1	1.0	-1.0	1.0	YML030W		1.0	-1.1	-1.2	-1.4	unknown function
CA1808	orf19.1115	*GUK1*	-1.1	-1.1	-1.0	-1.0	YDR454C	*GUK1*	1.0	1.7	2.0	2.6	Guanylate kinase (by homology)
CA1811	orf19.1119	*MTR10*	1.0	-1.0	-1.1	-1.0	YOR160W	*MTR10*	1.0	1.0	1.2	1.5	Involved in nuclear protein import
CA1815	orf19.138	*IPF18606*	-1.0	1.1	1.1	1.1	YBR040W	*FIG1*	1.0	1.1	1.1	1.1	unknown function
CA1816	orf19.136	*IPF7020*	1.0	1.1	1.3	1.1	YBR043C		1.0	1.2	1.2	1.2	unknown function
CA1817	orf19.135	*IPF7021*	-1.2	-1.1	-1.2	-1.0	YBR102C	*EXO84*	1.0	-1.1	-1.0	-1.1	similar to Saccharomyces cerevisiae Exo84p exocyst protein essential fo
CA1819	orf19.4273	*IPF16549*	-1.0	-1.0	1.0	-1.0	YLR139C	*SLS1*	1.0	-1.3	-1.0	1.1	Unknown function
CA1822	orf19.4268	*IPF9525*	-1.3	-1.4	-1.5	-1.2	YLR222C		1.0	1.2	1.2	1.6	unknown function
CA1826	orf19.4265	*UAP1*	-1.2	-1.0	-1.1	1.0	YDL103C	*QRI1*	1.0	-1.1	1.0	1.1	UDP-N-acetylglucosamine pyrophosphorylase
CA1829	orf19.5184	*IPF17177.3F*	1.1	1.1	1.1	1.0	YGL097W	*SRM1*	1.0	-1.8	-1.1	1.1	similar to Saccharomyces cerevisiae Srm1p regulator of chromosome co
CA1831	orf19.5188	*CHS1*	1.0	1.0	1.2	1.0	YBR038W	*CHS2*	1.0	1.1	1.1	1.2	Chitin synthase (by homology)
CA1834	orf19.3967	*PFK1*	-1.2	6.9	6.1	6.6	YGR240C	*PFK1*	1.0	-1.9	-1.1	1.5	6-phosphofructokinase, alpha subunit
CA1837	orf19.3964	*IPF5776*	1.1	1.2	1.3	1.2	YLR015W	*BRE2*	1.0	1.0	-1.1	1.1	ash2-trithorax family protein (by homology)
CA1838	orf19.3963	*IPF5777*	1.1	1.1	1.1	-1.0	YER182W		1.0	-1.2	-1.3	-1.6	unknown function
CA1839	orf19.4711	*IPF4435*	-1.2	-1.2	-1.1	-1.1	YGR196C	*FYV8*	1.0	-1.0	-1.1	-1.0	unknown function
CA1841	orf19.4705	*CCA1*	-1.0	1.0	1.1	1.0	YER168C	*CCA1*	1.0	1.1	1.3	1.2	tRNA nucleotidyltransferase (by homology)
CA1842	orf19.4704	*ARO1*	1.1	-1.1	-1.0	-1.2	YDR127W	*ARO1*	1.0	-1.7	-1.9	-1.5	arom pentafunctional enzyme (by homology)
CA1845	orf19.637	*IPF11123*	1.1	-1.1	-1.1	-1.1	YLL041C	*SDH2*	1.0	-1.1	-1.3	-2.7	similar to Saccharomyces cerevisiae Sdh2p succinate dehydrogenase irc
CA1846	orf19.638	*FDH12*	-1.1	-1.2	-1.5	-1.2	YOR388C	*FDH1*	1.0	-1.1	-1.1	1.1	Formate dehydrogenase (by homology)
CA1848		*IPF11128*	1.0	1.0	1.0	-1.0	YMR225C	*MRPL44*					unknown function
CA1850	orf19.641	*IPF14630*	1.0	-1.0	-1.1	-1.0	YFR041C		1.0	1.0	1.0	-1.4	unknown function
CA1854	orf19.649	*IPF12611*	-1.0	1.0	1.0	-1.1	YGL228W	*SHE10*	1.0	-1.2	1.2	1.4	unknown function
CA1855	orf19.646	*GLN1*	-1.5	1.7	1.5	1.8	YPR035W	*GLN1*	1.0	1.1	1.6	4.3	glutamate-ammonia ligase (by homology)
CA1860	orf19.9072	*UTR4*	-1.0	1.0	1.1	1.1	YEL038W	*UTR4*	1.0	1.4	1.5	1.3	unknown function
CA1861	orf19.866	*RAD32*	1.0	1.2	1.2	1.2	YDR419W	*RAD30*	1.0	-1.0	-1.2	1.0	DNA repair protein (by homology)
CA1862	orf19.864	*NMD2*	-1.0	1.0	-1.1	-1.0	YHR077C	*NMD2*	1.0	-1.2	-1.2	1.1	Nonsense-mediated mRNA decay protein 2 (by homology)
CA1863	orf19.863	*MRPL35*	-1.2	-1.3	-1.4	-1.1	YDR322W	*MRPL35*	1.0	-1.1	-1.1	1.1	Ribosomal protein of the large subunit, mitochondrial (by homology)
CA1868	orf19.9992	*F14501.3EO*	-1.0	1.0	-1.1	1.1	YBR281C		1.0	-1.6	-1.7	-1.4	putative G-protein, -transducin type, 3-prime end (by homology)

CA1871	orf19.9995	*16981.EXON*	-1.2	-1.2	-1.3	-1.1	YMR140W		1.0	1.0	1.1	-1.3	unknown function, exon 1
CA1874	orf19.2277	*TPK2*	1.1	1.5	1.7	1.5	YPL203W	*TPK2*	1.0	1.1	1.3	-1.1	cAMP-dependent protein kinase 2 (by homology)
CA1875	orf19.2276	*RPB9*	1.1	1.1	1.4	1.1	YGL070C	*RPB9*	1.0	1.0	1.1	1.2	DNA-directed RNA polymerase II (by homology)
CA1876	orf19.2275	*IPF10301*	-1.1	-1.2	-1.2	1.0	YGL068W		1.0	-1.1	-1.5	-1.8	putative 60S ribosomal protein L7/L12 homolog, mitochondrial precursor
CA1878	orf19.2272	*IPF10298*	-1.1	1.1	-1.1	-1.0	YPL202C	*AFT2*	1.0	-1.0	1.3	1.3	unknown function
CA1879	orf19.2270	*SMF12*	-1.1	-1.5	-1.5	-1.4	YOL122C	*SMF1*	1.0	-2.1	-1.9	-1.7	manganese transporter (by homology)
CA1880	orf19.2269	*IPF13316*	1.1	1.3	1.4	1.2	YNL010W		1.0	1.3	1.1	1.9	unknown function
CA1881	orf19.9808	*RCK2*	-1.1	-1.1	-1.1	-1.0	YLR248W	*RCK2*	1.0	1.0	1.4	1.1	Ca/calmodulin-dependent ser/thr protein kinase (by homology
CA1883	orf19.2209	*IPF5479*	-1.0	1.2	1.4	1.3	YOR088W		1.0	1.5	1.4	1.5	unknown function
CA1887	orf19.2204	*IPF5496*	1.2	1.1	1.3	1.1	YPL264C		1.0	-1.1	-1.2	-1.2	unknown function
CA1889		*CBP6*	1.1	1.1	1.1	1.1	YBR120C	*CBP6*	1.0	-1.2	-1.4	-1.4	Apo-cytochrome B pre-mRNA processing protein (by homology)
CA1891	orf19.2752	*IPF10196*	-1.3	-2.4	-2.7	-2.2	YDR216W	*ADR1*	1.0	-1.7	-1.7	-2.1	unknown function
CA1893	orf19.2754	*TIM13*	1.0	1.1	1.1	1.1	YGR181W	*TIM13*	1.0	-2.1	-1.8	-1.7	subunit of mitochondrial protein import machinery-like by homology
CA1894	orf19.2755	*RE7.EXON1*	1.0	1.1	1.2	1.1	YBL041W	*PRE7*	1.0	1.0	1.1	1.1	putative subunit of 20S proteasome, exon 1 (by homology)
CA1896	orf19.2756	*ERD2*	1.1	1.3	1.4	1.3	YBL040C	*ERD2*	1.0	-1.0	-1.1	-1.1	ER lumen protein retaining receptor (by homology)
CA1899	orf19.2606	*HDA1*	-1.1	-1.0	-1.2	-1.1	YNL021W	*HDA1*	1.0	-1.2	-1.3	-1.2	Histone deacetylase (by homology)
CA1901	orf19.2604	*IPF14135*	-1.0	-1.0	-1.1	-1.0	YNL022C		1.0	-1.3	-1.1	-1.1	unknown function
CA1902	orf19.2602	*OPT1*	-1.0	1.1	1.1	1.1	YJL212C	*OPT1*	1.0	-1.1	1.0	1.2	oligopeptide transporter
CA1904	orf19.10298	*GRX5*	1.2	-1.0	1.0	1.2	YPL059W	*GRX5*	1.0	-1.4	-1.7	-2.1	Glutaredoxin
CA1907	orf19.2785	*ATP7*	1.2	-1.1	1.1	1.2	YKL016C	*ATP7*	1.0	1.2	1.2	-1.6	F1F0-ATPase complex, FO D subunit (by homology)
CA1908	orf19.2786	*APL3*	-1.2	-1.1	-1.1	1.0	YBL037W	*APL3*	1.0	1.5	1.5	1.5	AP-2 complex subunit, alpha-adaptin (by homology)
CA1910	orf19.10306	*IPF7260*	-1.1	-1.1	-1.1	-1.1	YKL018W	*SWD2*	1.0	-2.2	-1.9	-2.1	unknown function
CA1911	orf19.2435	*SSE1*	-1.5	-1.5	-1.7	-1.5	YPL106C	*SSE1*	1.0	1.2	2.0	2.8	heat shock protein of HSP70 family (by homology)
CA1912	orf19.2436	*SKY1*	-1.1	-1.2	-1.1	-1.1	YMR216C	*SKY1*	1.0	-1.0	1.7	1.7	SRPK1 like protein kinase (by homology)
CA1913	orf19.2437	*ARC35*	-1.2	-1.0	-1.1	1.1	YNR035C	*ARC35*	1.0	-1.0	1.1	1.1	subunit of the Arp2/3 complex involved in the control of actin polymerizat
CA1914	orf19.2438	*IPF16564*	1.4	1.4	1.3	1.4	YNR036C		1.0	1.0	1.0	-1.4	putative mitochondrial ribosomal protein S12
CA1916		*IPF16566.3*	1.1	1.0	1.0	1.0	YHR001W	*OSH7*	1.0	-1.5	-1.5	-1.1	unknown function, 3-prime end
CA1920	orf19.2443	*IPF7476*	-1.2	-1.2	1.1	1.0	YBR260C	*RGD1*	1.0	-1.1	-1.1	-1.2	similar to Saccharomyces cerevisiae Rgd1p putative GTPase activating
CA1921	orf19.2444	*IPF7475*	1.2	-1.0	1.2	-1.1	YHR142W	*CHS7*	1.0	1.0	1.2	1.1	similar to Saccharomyces cerevisiae Chs7p involved in control of protein
CA1924	orf19.5537	*IPF9126*	1.2	1.1	1.1	-1.0	YOL105C	*WSC3*	1.0	1.3	1.6	2.0	unknown function
CA1927	orf19.754	*YBN5*	-1.0	-1.1	-1.1	-1.1	YBR025C		1.0	-1.3	1.4	1.5	Putative purine nucleotide-binding protein (by homology)
CA1928	orf19.755	*MRPL37*	1.0	1.0	1.0	1.0	YBR268W	*MRPL37*	1.0	-1.0	-1.0	-1.3	Mitochondrial ribosomal protein YmL37 (by homology)
CA1930	orf19.758	*IPF3906.3*	-1.0	1.0	1.0	1.0	YPR079W	*MRL1*	1.0	-1.1	-1.1	1.0	unknown function, 3-prime end
CA1931	orf19.759	*IPF3905*	-1.3	1.0	-1.2	-1.0	YNL287W	*SEC21*	1.0	-1.1	1.2	1.1	similar to Saccharomyces cerevisiae Sec21p coatomer complex gamma
CA1935	orf19.4185	*IPF19936*	1.0	1.2	1.3	1.2	YGR203W		1.0	-1.2	1.0	-1.0	unknown function
CA1936	orf19.4186	*PCT1*	-1.2	1.0	-1.0	1.0	YGR202C	*PCT1*	1.0	-1.5	-1.5	-2.1	cholinephosphate cytidylyltransferase (by homology)
CA1937	orf19.4187	*MMM1*	1.0	-1.0	-1.1	-1.0	YLL006W	*MMM1*	1.0	1.1	-1.0	-1.2	mitochondrial outer membrane protein (by homology)
CA1938	orf19.4188	*NMD5*	-1.5	-1.3	-1.3	-1.3	YJR132W	*NMD5*	1.0	-1.3	-1.2	-1.6	putative Nam7p/Upf1p-interacting protein (by homolgy)
CA1940	orf19.4190	*IPF7999*	1.2	1.1	1.3	1.0	YLR008C		1.0	-1.4	-1.6	-1.5	unknown function
CA1941	orf19.4191	*IPF7998*	-1.0	-1.0	-1.0	1.0	YLR009W		1.0	-2.2	-1.5	-1.3	Ribosomal protein L24 (by homology)
CA1944	orf19.4738	*IPF10645*	1.2	1.1	1.1	1.1	YOR154W		1.0	1.3	1.9	1.5	unknown function
CA1945	orf19.4739	*MSS116*	-1.0	-1.1	-1.0	-1.0	YDR194C	*MSS116*	1.0	-1.7	-1.7	-1.4	RNA helicase of the DEAD box family (by homology)
CA1946	orf19.4740	*IPF19937*	-1.1	1.0	-1.0	-1.0	YHR189W		1.0	1.1	1.0	1.1	putative peptidyl-tRNA hydrolases (by homology)
CA1949	orf19.12206	*IPF14021*	1.0	1.0	-1.0	1.0	YJR110W		1.0	-2.1	-2.0	-2.0	dual specificity phosphatase (PTP/DSP) (by homology)
CA1950	orf19.12208	*IPF14019*	1.0	-1.3	-1.3	-1.1	YPR169W		1.0	-1.1	1.3	1.4	unknown function
CA1951	orf19.12209	*HEM14*	1.1	-1.0	1.0	1.0	YER014W	*HEM14*	1.0	-1.2	-1.1	-1.1	Mitochondrial protoporphyrinogen oxidase (by
CA1953	orf19.763	*IPF3899*	1.1	1.0	1.0	1.0	YPL178W	*CBC2*	1.0	1.1	1.1	1.1	similar to Saccharomyces cerevisiae Cbc2p small subunit of the nuclear
CA1954	orf19.764	*IPF3897.5F*	-1.3	-1.1	-1.7	-1.4	YGL083W	*SCY1*	1.0	-1.4	-1.2	-1.2	unknown function, 5-prime end
CA1956	orf19.767	*ERG3*	1.4	1.4	1.6	1.5	YLR056W	*ERG3*	1.0	-1.1	1.8	2.0	C5,6 desaturase
CA1957	orf19.768	*IPF3887*	1.0	1.4	2.4	1.6	YIL047C	*SYG1*	1.0	-1.1	-1.0	1.6	similar to Saccharomyces cerevisiae Syg1p plasma membrane protein o
CA1958	orf19.769	*IFE1*	1.0	1.1	-1.0	1.0	YAL061W		1.0	1.1	-1.3	-1.7	Unknown function
CA1959	orf19.771	*IFD2*	1.0	1.1	1.1	1.0	YPL088W		1.0	1.2	1.3	1.3	putative oxidoreductase (by homology)
CA1960	orf19.2400	*IPF15232*	1.0	1.0	-1.0	1.0	YNL224C		1.0	-1.0	-1.2	-1.1	unknown function
CA1961	orf19.2399	*IPF14284*	-1.1	-1.1	-1.1	-1.1	YNL227C		1.0	1.3	1.3	1.2	putative dnaJ-like protein (by homology)
CA1965	orf19.2395	*IPF14035*	-1.1	1.0	-1.0	1.0	YJL106W	*IME2*	1.0	1.0	-1.2	-1.1	Similar to serine/threonine protein kinase (by homology)
CA1966	orf19.2394	*IFR4*	1.0	1.0	1.1	1.0	YNL134C		1.0	1.0	-1.1	-1.8	unknown function
CA1967	orf19.5219	*IPF10866*	1.0	1.1	1.2	-1.0	YOL081W	*IRA2*	1.0	-1.2	-1.4	-1.1	similar to Saccharomyces cerevisiae Ira2p GTPase-activating protein for
CA1968	orf19.5220	*IPF10864*	-1.1	1.0	1.1	-1.0	YOL080C	*REX4*	1.0	1.2	1.0	1.3	similar to Saccharomyces cerevisiae Rex4p member of the 3-prime to 5-
CA1969	orf19.5221	*IPF18579.3F*	-1.0	1.0	-1.0	-1.2	YOL078W		1.0	-1.4	-1.4	-1.3	unknown function, 3-prime end
CA1971	orf19.5224	*PKH2*	1.0	1.0	-1.0	-1.1	YOL100W	*PKH2*	1.0	-1.2	-1.0	-1.1	Ser/Thr protein kinase(by homology)
CA1972		*RPL27A*	1.6	1.2	1.2	1.2	YHR010W	*RPL27A*	1.0	1.6	1.9	2.1	ribosomal protein L27

CA1973	orf19.5226	*WRS1*	-1.2	-1.3	-1.5	-1.3	YOL097C	*WRS1*	1.0	-1.1	1.1	1.5	tryptophan--tRNA ligase
CA1974	orf19.5227	*IPF10410*	1.2	2.1	2.7	1.9	YLR021W		1.0	-1.1	1.1	1.1	unknown function
CA1976	orf19.688	*IPF9582*	1.1	-1.1	-1.2	-1.0	YNL306W	*MRPS18*	1.0	-1.3	-1.5	-1.7	similar to Saccharomyces cerevisiae Mrps18p ribosomal protein of the sr
CA1977		*RPL25.3*	1.6	1.2	1.2	1.3	YOL127W	*RPL25*	1.0	1.4	1.5	1.9	ribosomal protein L23a, 3-prime end (by homology)
CA1979	orf19.686	*IPF9577*	-1.0	1.0	-1.0	1.0	YNL193W		1.0	-1.1	-1.1	-1.2	unknown function
CA1980	orf19.685	*YHM1*	1.1	1.2	1.2	1.2	YDL198C	*YHM1*	1.0	-1.0	-1.1	1.5	member of the mitochondrial carrier family (MCF) (by homology)
CA1981	orf19.684	*IPF9470*	-1.1	-1.0	-1.1	-1.0	YDR228C	*PCF11*	1.0	-1.4	-1.1	-1.1	similar to Saccharomyces cerevisiae Pcf11p component of pre-mRNA 3
CA1982	orf19.683	*ADK1*	-1.0	-1.4	-1.7	-1.5	YDR226W	*ADK1*	1.0	1.2	1.4	1.2	adenylate kinase, cytosolic (by homology)
CA1983	orf19.7733	*ILV5*	-1.4	1.1	-1.1	-1.0	YLR355C	*ILV5*	1.0	-1.1	1.1	2.1	ketol-acid reducto-isomerase (by homology)
CA1984	orf19.7736	*IPF9592*	-1.1	-1.1	-1.1	-1.1	YFL042C		1.0	-1.1	1.1	1.3	unknown function
CA1985	orf19.91	*IPF9591*	1.0	-1.0	1.0	-1.0	YGR053C		1.0	-1.4	-1.3	-1.4	unknown function
CA1986	orf19.92	*IPF14899*	-1.1	-1.2	-1.4	-1.2	YFR016C		1.0	1.0	-1.3	-1.7	unknown function
CA1987	orf19.7739	*IPF14895*	1.3	-1.1	-1.2	-1.1	YMR002W		1.0	-1.8	-1.7	-1.8	unknown function
CA1990	orf19.7742	*TOP1*	1.0	-1.1	-1.1	-1.1	YOL006C	*TOP1*	1.0	1.2	1.2	1.5	CANAL DNA TOPOISOMERASE I
CA1994	orf19.6481	*IPF6613*	-1.2	-1.1	-1.1	-1.1	YDR349C	*YPS7*	1.0	1.1	1.2	1.4	unknown function
CA1995	orf19.6480	*IPF6612*	-1.2	1.0	1.1	1.0	YML038C	*YMD8*	1.0	1.0	1.0	1.1	unknown function
CA1996	orf19.6479	*SEC1*	1.1	1.1	1.0	1.0	YDR164C	*SEC1*	1.0	1.0	1.3	1.1	transport protein
CA1997	orf19.6478	*YCF1*	-1.2	1.1	1.2	1.2	YDR135C	*YCF1*	1.0	-1.3	-1.1	1.0	Glutathione S-conjugate transporter (by homology)
CA1998	orf19.6477	*IPF6605*	-1.0	-1.0	-1.0	-1.0	YDR165W		1.0	1.1	1.6	1.6	unknown function
CA1999	orf19.13830	*IPF19513*	-1.1	-1.1	-1.0	-1.1	YLR114C	*EFR4*	1.0	1.0	1.3	1.4	unknown function
CA2001	orf19.2792	*IPF17074*	-1.0	1.3	1.4	1.3	YBR086C	*IST2*	1.0	1.2	1.0	-1.0	unknown function
CA2002	orf19.2794	*IPF16470*	1.0	1.1	1.2	1.1	YBL036C		1.0	1.3	1.4	1.8	unknown function
CA2003	orf19.2795	*IPF16471*	-1.2	-1.4	-1.5	-1.2	YDL051W	*LHP1*	1.0	1.6	2.1	2.6	unknown function
CA2004	orf19.2796	*POL12*	-1.0	-1.1	-1.0	-1.1	YBL035C	*POL12*	1.0	1.2	1.0	-1.0	DNA-directed DNA polymerase alpha (by homology)
CA2006	orf19.2798	*IPF11801*	-1.2	-1.1	-1.2	-1.0	YDR332W		1.0	-1.1	1.1	1.0	unknown function
CA2007	orf19.2799	*GPI8*	-1.1	1.1	1.1	1.2	YDR331W	*GPI8*	1.0	-1.2	1.0	1.3	essential for GPI anchor attachment (by homology)
CA2009	orf19.3089	*IPF1732*	1.3	-1.4	-1.4	-1.5	YLR168C	*MSF1'*	1.0	1.5	1.7	1.8	intramitochondrial protein sorting (by homology)
CA2010	orf19.3088	*IPF1731*	1.2	1.0	1.0	-1.0	YDR184C	*ATC1*	1.0	-1.0	-1.1	1.2	unknown function
CA2011	orf19.3087	*RPS31*	1.2	1.1	-1.0	1.1	YLR167W	*RPS31*	1.0	2.1	2.4	2.3	Ubiquitin fusion protein
CA2012	orf19.3086	*SEC10*	-1.1	-1.1	-1.0	-1.1	YLR166C	*SEC10*	1.0	1.0	1.0	-1.0	Required for exocytosis (by homology)
CA2013	orf19.3083	*CDC1*	-1.1	1.2	1.1	1.1	YDR182W	*CDC1*	1.0	-1.3	-1.1	-1.2	Cell division control protein (by homology)
CA2014	orf19.10592	*IPF1717*	1.0	1.1	1.1	1.0	YDR180W	*SCC2*	1.0	1.0	-1.0	-1.1	similar to Saccharomyces cerevisiae Scc2p involved in sister chromatid
CA2016	orf19.8467	*IPF3415*	1.0	1.9	2.6	1.6	YMR152W	*YIM1*	1.0	1.2	1.1	-1.1	similar to Saccharomyces cerevisiae Yim1p mitochondrial inner membra
CA2017	orf19.846	*IPF3414*	-1.2	1.0	-1.1	1.0	YKL171W		1.0	-1.4	-1.2	-1.4	putative serine/threonine protein kinase
CA2018	orf19.844	*STE11*	-1.2	-1.1	-1.2	-1.2	YLR362W	*STE11*	1.0	-1.1	-1.1	-1.2	ser/thr protein kinase of the MEKK family (by homology)
CA2019	orf19.8463	*IPF3409*	-1.1	-1.1	-1.1	-1.0	YLR361C		1.0	-1.0	1.3	-1.0	unknown function
CA2021	orf19.4907	*IPF17283*	1.1	2.8	2.3	2.9	YCR061W		1.0	1.2	1.3	1.2	unknown function
CA2022	orf19.4909	*CBK1*	1.0	1.2	-1.0	-1.0	YNL161W	*CBK1*	1.0	-1.7	-1.3	-1.1	serine/threonine protein kinase (by homology)
CA2023		*RPL42.3*	1.9	1.1	1.1	1.4	YNL162W	*RPL42A*	1.0	2.5	2.6	3.2	ribosomal protein L36a, 3-prime end (by homology)
CA2026	orf19.10962	*IPF9777*	1.3	1.1	1.4	1.1	YOL129W		1.0	-1.2	1.1	1.1	unknown function
CA2027	orf19.10963	*MCK1*	1.1	1.1	1.5	1.1	YNL307C	*MCK1*	1.0	1.1	1.3	1.3	ser/thr/tyr protein kinase (by homology)
CA2029	orf19.10966	*SAR1.3*	1.2	1.0	1.1	1.1	YPL218W	*SAR1*	1.0	1.1	1.3	1.1	GTP-binding protein of the ARF family, 3-prime end (by homology)
CA2030	orf19.3463	*IPF13116*	-1.1	-1.3	-1.3	-1.3	YGL099W	*KRE35*	1.0	1.1	1.1	1.5	unknown function
CA2031	orf19.3465	*RPL10A*	1.2	-1.0	1.1	1.2	YPL220W	*RPL1A*	1.0	2.8	4.2	4.3	L10A ribosomal protein
CA2033	orf19.10971	*SEC27*	-1.5	-1.3	-1.7	-1.4	YGL137W	*SEC27*	1.0	1.2	1.5	1.3	coatomer complex beta chain (beta -cop) of secretory pathway vesicles
CA2035	orf19.11841	*SGD1.5F*	-1.2	-1.3	-1.4	-1.3	YLR336C	*SGD1*	1.0	-1.2	1.0	1.1	Involved in HOG pathway, 5-prime end
CA2036	orf19.4362	*MSP1*	1.0	-1.0	1.0	1.0	YGR028W	*MSP1*	1.0	-1.1	-1.0	-1.0	40 kDa putative membrane-spanning ATPase
CA2038	orf19.11836	*IPF17510*	-1.0	1.0	1.1	1.2	YDL157C		1.0	-1.1	-1.2	-1.1	unknown function
CA2039	orf19.11835	*IPF12947*	-1.0	-1.1	-1.0	-1.0	YMR115W		1.0	-1.1	-1.1	-1.2	unknown function
CA2040	orf19.4356	*IPF12946*	1.1	-1.0	1.2	1.0	YDL199C		1.0	-1.0	1.1	-1.1	unknown function
CA2042	orf19.10445	*IPF14219*	1.0	-1.0	1.1	1.1	YOL107W		1.0	-1.0	1.7	2.2	probable membrane protein (by homology)
CA2043	orf19.2929	*GSL21*	1.1	1.4	1.6	1.6	YLR342W	*FKS1*	1.0	-1.1	1.6	2.3	1,3-beta-D-glucan synthase subunit
CA2044	orf19.10447	*IPF10668*	1.0	1.0	-1.0	1.1	YGR054W		1.0	-1.3	1.5	1.8	unknown function
CA2045	orf19.10450	*IPF8107*	1.1	-1.0	-1.0	1.0	YFL044C		1.0	1.0	1.2	1.1	unknown function
CA2046	orf19.10451	*IPF8108*	-1.1	-1.1	-1.2	-1.1	YLR074C	*BUD20*	1.0	1.4	1.7	1.6	unknown function
CA2047	orf19.10452	*RPL10*	1.0	-1.3	-1.4	-1.1	YLR075W	*RPL10*	1.0	2.0	2.6	3.2	Ribosomal protein L10 (by homology)
CA2052	orf19.5722	*IPF11027*	-1.0	-1.0	-1.1	-1.0	YDR026C		1.0	-1.3	-1.3	-1.1	unknown function
CA2056	orf19.2555	*URA5*	1.2	1.5	1.5	1.6	YML106W	*URA5*	1.0	1.4	1.7	1.9	Orotate phosphoribosyltransferase (by homology)
CA2057	orf19.2557	*SEC65*	1.1	-1.1	-1.1	-1.0	YML105C	*SEC65*	1.0	-1.3	-1.2	-1.2	Recognition particle subunit (by homology)
CA2059	orf19.2559	*CDC4*	1.1	1.3	1.2	1.1	YFL009W	*CDC4*	1.0	-1.4	1.1	1.3	CANAL CELL DIVISION CONTROL PROTEIN 4
CA2061	orf19.2562	*CDC61.5F*	-1.3	-1.3	-2.1	-1.9	YPL160W	*CDC60*	1.0	-1.5	-1.1	1.4	Cytosolic leucyl-tRNA synthetase, 5-prime end

CA2062	orf19.2563	*IPF7858*	1.0	-1.1	-1.2	-1.1	YMR268C	*PRP24*	1.0	-1.3	-1.3	-1.4	similar to Saccharomyces cerevisiae Prp24p U4/U6 splicing factor (by ho
CA2065	orf19.2644	*QCR2*	1.0	-1.2	-1.2	-1.0	YPR191W	*QCR2*	1.0	-1.2	-1.3	-2.0	Ubiquinol--cytochrome-c reductase 40KD chain II (by homology)
CA2066	orf19.2643	*RPO26*	1.2	1.1	1.0	-1.0	YPR187W	*RPO26*	1.0	1.3	1.1	1.8	DNA-directed RNA polymerase I, II, III 18 KD subunit (by homology)
CA2068	orf19.2641	*ARP1*	1.1	1.0	1.1	1.1	YHR129C	*ARP1*	1.0	-1.2	-1.3	-1.3	centractin (by homology)
CA2069	orf19.2640	*FUR1*	1.0	1.1	1.1	1.0	YHR128W	*FUR1*	1.0	-1.3	1.2	1.4	Uracil phosphoribosyltransferase (by homology)
CA2071		*IPF6971.53*	1.0	1.0	1.1	1.0	YNL147W	*LSM7*	1.0	1.3	1.2	1.0	unknown function, internal fragment
CA2072	orf19.2639	*IPF6970*	1.0	1.0	1.0	1.0	YKR085C	*MRPL20*	1.0	-2.0	-2.0	-2.0	unknown function
CA2076	orf19.4871	*ERO1*	-1.0	1.6	2.1	1.5	YML130C	*ERO1*	1.0	-1.2	-1.1	-1.0	Required for protein disulfide bond formation in the ER (by homology)
CA2080	orf19.4875	*IPF9693*	1.0	1.1	1.1	1.0	YDR482C		1.0	-1.4	-1.5	-1.3	unknown function
CA2081	orf19.4878	*IPF9699*	1.0	-1.0	-1.0	1.1	YIR003W		1.0	-1.3	-1.2	-1.6	unknown function
CA2082		*NTF2*	1.8	1.3	1.7	1.5	YER009W	*NTF2*	1.0	1.0	-1.1	1.2	nuclear transport factor (by homology)
CA2083	orf19.832	*IPF3384.5F*	1.2	1.2	1.3	1.1	YLL031C	*GPI13*	1.0	-1.1	-1.0	1.0	similar to Saccharomyces cerevisiae Gpi13p phosphoryltransferase that
CA2085	orf19.834	*IPF3388*	-1.0	1.1	1.1	1.0	YHR204W	*HTM1*	1.0	-1.5	-1.3	-1.1	unknown function
CA2086	orf19.835	*IPF3392*	-1.1	1.1	1.1	-1.0	YFL013C	*IES1*	1.0	-1.2	-1.0	1.0	unknown function
CA2089	orf19.837	*GNA1*	-1.1	-1.0	1.0	1.1	YFL017C	*GNA1*	1.0	1.0	1.1	1.1	Acetyltransferase
CA2091	orf19.839	*IPF3401*	-1.0	1.1	1.2	1.1	YLR143W		1.0	-1.5	-1.4	-1.1	unknown function
CA2092	orf19.840	*RPL21A.3*	1.1	-1.1	-1.1	1.1	YBR191W	*RPL21A*	1.0	1.1	1.2	2.3	Ribosomal protein, 3-prime end (by homology)
CA2093	orf19.841	*IPF3406*	-1.2	-1.2	-1.4	-1.4	YKL179C		1.0	-1.2	1.1	-1.0	unknown function
CA2096	orf19.2391	*IPF11491*	1.1	-1.0	-1.2	-1.1	YKR023W		1.0	1.1	1.3	1.4	unknown function
CA2097	orf19.2389	*IPF11489*	1.1	1.1	1.0	1.1	YKL108W	*SLD2*	1.0	-1.3	-1.3	-1.6	unknown function
CA2098	orf19.2387	*IPF11487*	-1.0	-1.1	-1.1	-1.0	YMR098C		1.0	-1.0	-1.0	-1.3	unknown function
CA2099	orf19.2386	*IPF11484*	1.0	-1.1	-1.2	-1.1	YKL099C		1.0	1.4	1.1	-1.1	unknown function
CA2100	orf19.2385	*KTI12*	-1.0	-1.1	-1.2	-1.0	YKL110C	*KTI12*	1.0	1.2	1.0	1.2	involved in resistance to K.lactis killer toxin (by homology)
CA2101	orf19.2384	*IPF9364*	-1.0	-1.1	-1.1	1.0	YMR097C		1.0	-2.8	-2.2	-2.5	unknown function
CA2102	orf19.2383	*IPF9363*	-1.0	1.1	1.0	1.1	YMR106C	*YKU80*	1.0	-1.4	-1.2	-1.1	similar to Saccharomyces cerevisiae Yku80p component of DNA end-joi
CA2103	orf19.9918	*ISM1*	-1.1	-1.1	-1.3	-1.1	YPL040C	*ISM1*	1.0	-2.6	-2.8	-2.7	isoleucyl-tRNA synthetase (by homology)
CA2106	orf19.3693	*IPF10714*	-1.0	-1.1	-1.1	-1.0	YLR343W		1.0	1.0	1.2	1.2	similar to pH-regulated (PHR) proteins
CA2107	orf19.3691	*IPF10716*	1.1	-1.1	-1.0	-1.1	YGR033C		1.0	-1.1	-1.1	-1.1	unknown function
CA2108		*RPL26A.3*	1.1	-1.1	1.2	1.2	YLR344W	*RPL26A*	1.0	1.8	2.1	2.3	ribosomal protein, 3-prime end (by homology)
CA2109	orf19.3690	*IPF13749.5F*	-1.1	-1.4	-1.3	-1.4	YLR345W		1.0	1.0	1.3	1.5	unknown function, 5-prime end
CA2111	orf19.3688	*IPF13748*	1.1	1.1	1.2	1.0	YJL184W		1.0	-1.4	-1.4	-1.4	Unknown function
CA2112	orf19.3687	*PFD1*	1.0	1.1	-1.0	-1.0	YJL179W	*PFD1*	1.0	-1.3	-1.5	1.0	Prefoldin subunit 1 (by homology)
CA2113	orf19.3686	*ATP12*	-1.1	-1.1	-1.0	-1.0	YJL180C	*ATP12*	1.0	-2.0	-2.5	-2.3	F1F0-ATPase complex assembly protein (by homology)
CA2114	orf19.3685	*IPF13744*	1.0	-1.0	-1.1	-1.1	YNL201C		1.0	1.1	1.2	1.6	protein involved in regulation of carbon metabolism (by homology)
CA2115	orf19.8911	*IPF8030*	1.2	1.3	1.4	1.2	YBR272C	*HSM3*	1.0	-1.2	-1.2	-1.1	unknown function
CA2119	orf19.8915	*MTR4*	-1.2	-1.3	-1.5	-1.2	YJL050W	*MTR4*	1.0	-1.1	1.1	1.4	RNA Helicase (by homology)
CA2120		*PUP3*	1.0	1.1	1.2	1.1	YER094C	*PUP3*	1.0	-1.0	-1.1	-1.1	PRCT yeast proteasome component (by homology)
CA2121	orf19.8918	*IPF7930*	-1.2	-1.2	-1.2	-1.1	YJL123C		1.0	1.0	1.5	1.3	unknown function
CA2125	orf19.418	*IPF4893*	-1.1	1.0	-1.1	-1.1	YHR186C		1.0	1.2	1.9	2.6	unknown function
CA2126	orf19.417	*IPF4896*	1.0	-1.0	-1.1	-1.1	YGR257C		1.0	1.2	1.1	1.1	unknown function
CA2128	orf19.415	*IPF4898*	-1.1	1.0	-1.0	1.1	YGR235C		1.0	-1.4	-1.0	-1.4	unknown function
CA2129	orf19.414	*IPF4899*	-1.0	-1.1	-1.1	1.0	YKL155C	*RSM22*	1.0	-1.2	-1.1	1.0	unknown function
CA2132	orf19.5212	*IPF5865*	-1.0	1.0	1.0	-1.0	YLR394W	*CST9*	1.0	1.2	-1.0	-1.0	unknown function
CA2134	orf19.5213	*COX8*	1.5	1.3	1.4	1.5	YLR395C	*COX8*	1.0	-1.1	-1.2	-1.5	CYTOCHROME C OXIDASE (by homology)
CA2135		*COX9*	1.4	1.1	1.4	1.2	YDL067C	*COX9*	1.0	-1.1	-1.4	-1.8	CYTOCHROME C OXIDASE (by homology)
CA2136	orf19.5214	*VPS33*	1.0	-1.0	-1.0	1.0	YLR396C	*VPS33*	1.0	-1.3	-1.4	-1.3	VACUOLAR PROTEIN SORTING (by homology)
CA2137	orf19.2507	*ARP9*	-1.1	-1.1	-1.1	-1.1	YMR033W	*ARP9*					actin-related protein (by homology)
CA2140	orf19.10046	*IPF19665*	-1.5	-1.3	-1.2	-1.0	YOR349W	*CIN1*	1.0	-1.3	-1.3	-1.9	unknown function
CA2142		*MRPL33*	1.0	1.1	1.0	1.0	YMR286W	*MRPL33*					ribosomal protein of the large subunit, mitochondrial (by homology)
CA2148	orf19.6020	*AUT1*	-1.0	1.0	1.0	1.0	YNR007C	*AUT1*	1.0	-1.2	1.2	1.0	similar to Saccharomyces cerevisiae Aut1p essential for autophagocytosi
CA2153	orf19.6025	*IPF7900*	-1.1	1.0	1.0	-1.0	YGL047W		1.0	-1.9	-1.6	-1.4	unknown function
CA2154	orf19.6026	*ERG2*	1.0	-1.3	-1.3	-1.2	YMR202W	*ERG2*	1.0	-1.8	1.2	1.9	C-8 sterol isomerase
CA2155	orf19.6027	*IPF7903*	-1.0	-1.0	-1.0	-1.0	YPL255W	*BBP1*	1.0	-1.1	-1.1	-1.0	unknown function
CA2157	orf19.5300	*IPF8537*	-1.1	-1.1	-1.1	-1.1	YAL058W	*CNE1*	1.0	-1.3	-1.3	-1.3	similar to Saccharomyces cerevisiae Cne1p calnexin, involved in regulati
CA2158	orf19.5299	*ECM1*	-1.0	-1.0	-1.1	1.0	YAL059W	*ECM1*	1.0	-1.5	-1.3	-1.0	involved in cell wall biosynthesis (by homology)
CA2159	orf19.5297	*IPF19753*	-1.1	-1.0	-1.1	-1.1	YDR311W	*TFB1*	1.0	1.1	1.0	1.1	similar to Saccharomyces cerevisiae Tfb1p transcription initiation factor (
CA2160	orf19.5296	*IPF15664*	1.1	-1.0	1.0	1.0	YIL157C		1.0	-1.1	-1.2	-1.4	unknown function
CA2162	orf19.5294	*PDB1*	-1.2	-1.8	-1.4	-1.4	YBR221C	*PDB1*	1.0	-2.0	-2.6	-2.0	pyruvate dehydrogenase (by homology)
CA2164	orf19.5292	*AXL2*	1.2	1.1	1.2	1.2	YIL140W	*AXL2*	1.0	1.3	1.5	1.4	similar to saccharomyces cerevisiae Axl2p required for axial pattern of bu
CA2165	orf19.5291	*IPF17024*	-1.0	-1.0	-1.1	-1.0	YGL126W	*SCS3*	1.0	-1.1	-1.2	-1.1	unknown function
CA2167	orf19.909	*IPF4553*	-1.1	1.1	-1.0	1.0	YDL048C	*STP4*	1.0	1.1	1.4	3.7	unknown function

CA2168	orf19.910	*IPF4558*	1.0	1.1	-1.0	1.0	YDR473C	*PRP3*	1.0	-1.2	-1.3	-1.2	similar to Saccharomyces cerevisiae Prp3p splicing factor (by homology)
CA2171	orf19.3767	*PEP1.3*	-1.6	-1.1	-1.5	-1.2	YBL017C	*PEP1*	1.0	-1.6	-1.6	-1.5	Vacuolar protein sorting/targeting protein, 3-prime end (by homology)
CA2172	orf19.3765	*IPF15377*	-1.0	1.1	1.2	1.1	YLR084C	*RAX2*	1.0	-1.3	-1.3	-1.4	probable membrane protein involved in bipolar budding (by homology)
CA2173	orf19.3764	*IPF18527*	-1.1	-1.2	-1.2	-1.0	YDR108W	*GSG1*	1.0	1.0	1.1	1.1	unknown function
CA2176	orf19.11245	*CDC54*	-1.1	-1.0	-1.1	-1.1	YPR019W	*CDC54*	1.0	-1.0	-1.1	-1.1	cell division control protein (by homology)
CA2177	orf19.9084	*ROD1*	1.1	1.1	1.1	1.0	YFR022W		1.0	-1.4	-1.4	-1.1	O-dinitrobenzene,calcium and zinc resistance protein (by homology)
CA2178	orf19.1510	*IPF9282*	1.1	1.3	1.5	1.2	YOL019W	*TOS7*	1.0	-1.1	1.0	1.4	unknown function
CA2179	orf19.9088	*FAB1*	-1.1	1.0	-1.3	-1.0	YFR019W	*FAB1*	1.0	-1.4	-1.3	-1.3	phosphatidylinositol 3-phosphate 5-kinase (by homology)
CA2181	orf19.4255	*ECM331*	1.1	2.5	2.8	2.4	YDR055W	*PST1*	1.0	1.1	2.1	1.9	Involved in cell wall biogenesis and architecture (by homology)
CA2183	orf19.4252	*IPF6872*	1.0	-1.0	1.0	-1.0	YGR262C	*BUD32*	1.0	-1.2	-1.1	-1.2	serine/threonine protein kinase (by homology)
CA2188	orf19.4772	*SSU81*	1.2	1.2	1.4	1.2	YER118C	*SHO1*	1.0	-2.1	-1.5	-1.4	protein involved in the HOG1 high-osmolarity signal transduction pathwa
CA2191	orf19.4775	*IPF9417*	-1.0	-1.0	-1.0	1.0	YGL073W	*HSF1*	1.0	1.1	1.3	1.2	similar to Saccharomyces cerevisiae Hsf1p heat shock transcription facto
CA2193	orf19.11824	*IPF14273*	-1.0	-1.0	1.1	1.0	YKL116C	*PRR1*	1.0	-1.5	-1.3	-1.2	Probable ser/thr protein kinase (by homology)
CA2194	orf19.11825	*RGR1*	-1.3	-1.1	-1.3	-1.1	YLR071C	*RGR1*	1.0	-1.3	-1.2	-1.1	DNA-directed RNA polymerase II (by homology)
CA2195	orf19.11826	*IPF18517.3F*	-1.4	-1.2	-1.4	-1.3	YOL070C		1.0	1.1	1.2	1.3	unknown function, 3-prime end
CA2198	orf19.2937	*PMM1*	1.2	1.5	1.4	1.3	YFL045C	*SEC53*	1.0	-1.4	1.7	1.8	phosphomannomutase
CA2199	orf19.2938	*IPF8113*	-1.3	-1.1	-1.1	-1.0	YLR077W		1.0	1.0	-1.1	1.0	unknown function
CA2200	orf19.2939	*IPF8114*	-1.0	-1.0	1.0	1.1	YFL046W		1.0	-1.6	-1.4	-1.2	unknown function
CA2201	orf19.2940	*BOS1*	1.0	-1.0	-1.0	1.0	YLR078C	*BOS1*	1.0	1.1	1.2	1.3	ER-to-Golgi v-SNARE (by homology)
CA2203	orf19.2942	*DIP51.3F*	1.0	-2.4	-2.7	-2.6	YPL265W	*DIP5*	1.0	-1.7	-1.3	1.0	dicarboxylic amino acid permease, 3-prime end (by homology)
CA2205	orf19.8319	*SEO2*	1.0	1.0	1.0	1.1	YAL067C	*SEO1*	1.0	-1.8	-1.9	-1.9	suppressor of sulfoxyde ethionine resistance
CA2206	orf19.698	*IPF12173*	1.0	-1.1	1.0	-1.1	YIL090W		1.0	-1.1	-1.2	-1.0	unknown function
CA2207	orf19.8316	*IPF12169*	1.0	-1.0	-1.0	-1.1	YHR017W	*YSC83*	1.0	-1.1	-1.1	-1.0	unknown function
CA2208	orf19.696	*IPF17255*	1.1	1.0	1.1	-1.0	YFL026W	*STE2*	1.0	1.1	1.5	2.9	similar to Saccharomyces cerevisiae Ste2p pheromone alpha-factor rece
CA2209	orf19.695	*IPF18512*	-1.0	-1.1	-1.1	-1.1	YOR107W	*RGS2*	1.0	-2.0	1.1	1.4	unknown function
CA2210	orf19.4748	*MSL1*	-1.0	1.0	1.2	1.1	YIR009W	*MSL1*	1.0	-1.2	-1.1	-1.1	U2 snRNA-associated protein (by homology)
CA2213	orf19.4751	*IPF16405*	-1.0	-1.3	-1.1	1.1	YIL093C	*RSM25*	1.0	1.1	-1.1	-1.1	similar to saccharomyces cerevisiae Rsm25p protein of the small subunit
CA2214	orf19.4752	*IPF9939*	1.1	2.8	4.2	2.5	YKL062W	*MSN4*	1.0	-1.0	1.2	1.3	similar to Saccharomyces cerevisiae Msn4p transcriptional activator (by h
CA2215	orf19.4753	*PFK26*	-1.1	1.2	-1.1	1.2	YIL107C	*PFK26*	1.0	-1.1	-1.1	-1.2	6-phosphofructose-2-kinase (by homology)
CA2219	orf19.12563	*CAT8*	1.0	-1.0	-1.1	-1.1	YMR280C	*CAT8*	1.0	-1.4	-1.1	-1.8	transcription factor involved in gluconeogenesis (by homology)
CA2220	orf19.5098	*NTG1*	1.0	-1.1	1.1	1.0	YOL043C	*NTG2*	1.0	1.1	1.1	-1.1	endonuclease III-like glycosylase (by homology)
CA2222	orf19.5101	*CCR4*	-1.0	1.0	-1.0	-1.0	YAL021C	*CCR4*	1.0	-1.8	-2.0	-1.7	glucose-repressible alcohol dehydrogenase transcriptional eff
CA2225	orf19.5818	*SUR2*	1.0	3.3	4.8	3.8	YDR297W	*SUR2*	1.0	-1.5	-1.1	1.2	Hydroxylation of C-4 of the sphingoid moiety of ceramide by homology
CA2226	orf19.5817	*BET3.EXON2*	1.2	1.2	1.3	1.2	YKR068C	*BET3*	1.0	1.1	1.0	-1.1	targeting and fusion of ER to Golgi transport vesicles, exon 2 (by homolo
CA2231	orf19.3926	*IPF10934*	1.0	1.0	1.0	-1.0	YPL123C	*RNY1*	1.0	-1.2	-1.2	-1.3	similar to Saccharomyces cerevisiae Rny1 ribonuclease from the T2 fami
CA2235	orf19.3920	*MPD1*	1.1	1.0	1.0	1.0	YOR288C	*MPD1*	1.0	-1.1	-1.0	-1.1	disulfide isomerase related protein (by homology)
CA2238	orf19.3916	*IPF10032.5F*	-1.1	-1.1	-1.1	-1.1	YJR011C		1.0	1.2	1.1	1.0	unknown function, 5-prime end
CA2249	orf19.2365	*POL2*	-1.1	-1.1	-1.2	-1.1	YNL262W	*POL2*	1.0	-1.4	1.1	-1.1	DNA-directed DNA polymerase epsilon, catalytic subunit A (by homology
CA2250	orf19.2364	*MIS11*	-1.0	-1.3	-1.3	-1.3	YBR084W	*MIS1*	1.0	-1.6	-1.3	1.3	mitochondrial C1-tetrahydrofolate synthase precursor (by homology)
CA2251	orf19.2363	*IPF12845*	1.2	1.2	1.4	1.2	YOR286W		1.0	1.0	-1.1	-1.1	unknown function
CA2252	orf19.9898	*IPF12844*	-1.0	-1.0	-1.0	-1.0	YOR287C		1.0	-1.1	1.0	1.2	unknown function
CA2253	orf19.1959	*IPF15485*	-1.0	-1.1	-1.1	-1.0	YHL013C		1.0	-1.2	1.2	-1.1	unknown function
CA2255	orf19.1957	*CYC3*	1.0	-1.1	1.0	-1.0	YAL039C	*CYC3*	1.0	-1.0	1.1	-1.1	cytochrome C heme lyase
CA2256	orf19.1956	*IPF14757*	-1.1	-1.2	-1.3	-1.2	YOR354C	*MSC6*	1.0	-1.1	1.2	1.1	unknown function
CA2257	orf19.1955	*SHR5*	1.0	1.0	-1.0	-1.0	YOL110W	*SHR5*	1.0	-1.7	-1.7	-1.6	RAS suppressor (by homology)
CA2259	orf19.1762	*IPF6845*	1.0	1.0	-1.0	-1.0	YNL099C		1.0	-1.2	-1.2	-1.2	unknown function
CA2260	orf19.1761	*OST2*	1.1	1.1	1.4	1.2	YOR103C	*OST2*	1.0	1.2	1.1	1.2	Oligosaccharyltransferase epsilon subunit
CA2261	orf19.1760	*RAS1*	-1.0	1.1	1.1	1.0	YNL098C	*RAS2*	1.0	1.4	1.7	-1.1	GTP-binding protein (by homology)
CA2262	orf19.1757	*IPF6857*	1.0	1.1	1.0	1.0	YDR253C	*MET32*	1.0	-2.0	1.2	1.5	putative transcriptional regulator (unknown function)
CA2263	orf19.1756	*GPD1*	-1.0	1.3	1.8	1.8	YOL059W	*GPD2*	1.0	1.7	3.0	6.5	Glycerol-3-phosphate dehydrogenase (by homology)
CA2265	orf19.1754	*CMK2*	-1.1	-1.1	-1.1	1.0	YOL016C	*CMK2*	1.0	-1.1	1.2	1.1	Ca2+/calmodulin-dependent ser/thr protein kinase, type II (by homology)
CA2266	orf19.10132	*HEM1*	-1.0	1.1	1.0	1.1	YDR232W	*HEM1*	1.0	1.2	1.3	2.0	5-aminolevulinic acid synthase
CA2267	orf19.2600	*IFU1.5F*	-1.1	-1.1	-1.1	1.0	YNL126W	*SPC98*	1.0	1.1	1.1	-1.1	Unknown function, 5-prime end
CA2269	orf19.2599	*YOR100*	1.2	-1.8	-2.0	-1.6	YOR100C	*CRC1*	1.0	-1.1	-1.1	-1.1	Putative mitochondrial carrier protein
CA2270	orf19.2598	*VMA4*	1.0	-1.2	-1.1	1.0	YOR332W	*VMA4*	1.0	1.3	1.6	1.6	H+-transporting ATPase E chain
CA2271	orf19.2597	*MRS2*	-1.0	1.0	-1.0	1.0	YOR334W	*MRS2*	1.0	-1.2	-1.3	-1.1	Mitochondrial RNA splicing protein (by homology)
CA2272	orf19.2594	*RPA43*	1.1	-1.0	-1.1	-1.0	YOR340C	*RPA43*	1.0	-2.2	-2.0	-1.3	DNA-directed RNA polymerase I, 36 KD subunit(by homology)
CA2273	orf19.2593	*BIO2*	-1.1	-1.1	-1.1	-1.1	YGR286C	*BIO2*	1.0	-1.1	-1.1	1.0	biotin synthetase (by homology)
CA2274	orf19.2591	*BIO3*	1.0	1.0	1.0	-1.0	YNR058W	*BIO3*	1.0	-1.1	-1.2	-1.0	DAPA aminotransferase (by homology)
CA2275	orf19.2590	*BIO4*	1.1	1.1	-1.0	1.1	YNR057C	*BIO4*	1.0	-1.0	1.0	-1.0	dethiobiotin synthetase (by homology)
CA2277	orf19.783	*DRS21*	1.1	1.1	1.1	1.1	YIL048W	*NEO1*	1.0	1.1	1.3	1.6	Membrane-spanning Ca-ATPase (by homology)

CA2278	orf19.782	*IPF10806*	-1.1	-1.2	-1.1	-1.1	YBR204C		1.0	-1.0	-1.1	1.1	unknown function
CA2279	orf19.781	*DUR31*	-1.0	1.0	1.0	1.0	YHL016C	*DUR3*	1.0	1.2	1.8	1.3	Urea transport protein (by homology)
CA2280	orf19.780	*DUR1,2*	-1.0	1.2	1.2	1.5	YBR208C	*DUR1,2*	1.0	-1.4	-1.9	-1.5	urea amidolyase (by homology)
CA2281	orf19.779	*HAT1*	-1.0	1.0	-1.1	-1.0	YPL001W	*HAT1*	1.0	-1.1	1.2	1.3	histone acetyltransferase (by homology)
CA2283	orf19.12996	*MRT4*	-1.0	1.1	1.1	1.1	YKL009W	*MRT4*	1.0	1.4	1.3	1.8	required for mRNA decay (by homology)
CA2284	orf19.5551	*MIF2*	-1.0	1.0	-1.1	-1.1	YKL089W	*MIF2*	1.0	-1.4	-1.4	-1.4	required for normal chromosome segregation and spindle integrity (by ho
CA2285	orf19.5552	*IPF12629*	-1.1	1.1	1.4	1.1	YOL063C		1.0	1.1	1.2	1.2	unknown function
CA2286	orf19.5553	*IPF5369*	1.1	1.1	-1.0	1.2	YKL069W		1.0	-2.3	-2.4	-2.5	unknown function
CA2291	orf19.744	*IPF9740*	-1.2	-1.4	-1.6	-1.3	YPR184W	*GDB1*	1.0	1.7	1.2	-1.5	oligo-1,4 -1,4-glucantransferase / amylo-1,6-glucosidase (by homology)
CA2292	orf19.745	*VAC8*	-1.1	1.2	1.0	1.1	YEL013W	*VAC8*	1.0	-1.1	1.2	1.4	required for vacuole inheritance and protein targeting from the cyto
CA2293	orf19.746	*IPF9748*	1.0	1.0	-1.0	-1.0	YJL049W		1.0	-1.1	1.0	1.1	unknown function
CA2294	orf19.747	*IPF19946*	-1.1	1.2	1.1	1.1	YGL091C	*NBP35*	1.0	-1.1	-1.0	-1.4	similar to Saccharomyces cerevisiae Nbp35p nucleotide-binding protein
CA2295	orf19.5377	*HOS2*	-1.1	1.0	-1.0	1.0	YGL194C	*HOS2*	1.0	-1.3	-1.3	-1.1	putative histone deacetylase (by homology)
CA2296	orf19.5378	*SCL1*	1.2	1.0	1.0	1.1	YGL011C	*SCL1*	1.0	-1.5	1.2	1.4	Proteasome subunit YC7alpha (by homology)
CA2297	orf19.5379	*ERG4*	1.5	-1.7	-1.2	-1.4	YGL012W	*ERG4*	1.0	1.1	1.1	1.5	sterol C-24 reductase (by homology)
CA2299	orf19.5381	*IPF8222*	-1.0	-1.0	1.0	-1.0	YGL014W	*PUF4*	1.0	-1.1	-1.3	-1.1	unknown function
CA2300	orf19.5383	*PMA1*	1.6	1.4	1.2	-1.1	YGL008C	*PMA1*	1.0	-2.3	-1.5	2.0	plasma membrane H+-transporting ATPase 1
CA2303	orf19.1690	*TOS1*	1.3	1.1	1.3	1.1	YBR162C	*TOS1*	1.0	-1.1	-1.4	1.2	putative Anchor subunit of a-agglutinin (by homology)
CA2304	orf19.1687	*PRP43*	-1.0	-1.0	-1.1	-1.0	YGL120C	*PRP43*	1.0	1.2	1.3	1.9	RNA-dependent ATPase (by homology)
CA2305	orf19.1686	*MPA43*	-1.1	-1.0	-1.1	-1.0	YNL249C	*MPA43*	1.0	-1.2	1.1	1.0	Unknown function
CA2308	orf19.8953	*IPF9874.3*	1.1	-1.0	1.1	-1.1	YIL002C	*INP51*	1.0	1.0	-1.0	1.0	similar to Saccharomyces cerevisiae Inp51p phosphatidylinositol phospha
CA2311	orf19.1376	*SSO2*	1.3	1.2	1.5	1.4	YMR183C	*SSO2*	1.0	1.1	1.3	1.1	syntaxin (by homology)
CA2312	orf19.1377	*IPF16498*	-1.1	-1.0	-1.0	-1.0	YDR173C	*ARG82*	1.0	1.5	1.1	1.1	similar to Saccharomyces cerevisiae Arg82p arginine metabolism transcr
CA2313	orf19.1378	*ERF3*	-1.0	-1.0	-1.1	-1.1	YDR172W	*SUP35*	1.0	-1.8	-1.1	1.1	translation release factor 3
CA2314	orf19.1381	*IPF14545*	1.0	1.3	1.4	1.4	YCL034W	*LSB5*	1.0	1.3	1.3	1.5	unknown function
CA2315	orf19.8962	*YEA4*	1.0	1.2	1.2	1.2	YEL004W	*YEA4*	1.0	-1.2	-1.2	1.2	Golgi uridine diphosphate-N-acetylglucosamine transporter (by homology
CA2318	orf19.5480	*ILV1*	-1.1	1.2	1.3	1.2	YER086W	*ILV1*	1.0	-1.2	-1.2	1.3	Threonine dehydratase (by homology)
CA2319	orf19.5483	*GUF1*	-1.2	-1.3	-1.3	-1.3	YLR289W	*GUF1*	1.0	-1.7	-1.5	-1.6	GTP-binding protein (by homology)
CA2320	orf19.5484	*SER1*	-1.1	-1.3	-1.3	-1.3	YOR184W	*SER1*	1.0	1.0	1.3	1.7	phosphoserine transaminase (by homology)
CA2321	orf19.5485	*MEC3*	-1.0	1.0	-1.0	1.0	YLR288C	*MEC3*	1.0	-1.3	-1.3	-1.4	G2-specific checkpoint protein (by homology)
CA2322	orf19.5486	*YSH1*	-1.3	-1.1	-1.3	-1.2	YLR277C	*YSH1*	1.0	-1.4	-1.4	-1.2	component of pre-mRNA polyadenylation factor PF I (by homology)
CA2323		*SMD2*	-1.0	1.0	1.0	-1.0	YLR275W	*SMD2*	1.0	1.1	-1.0	1.1	U1 snRNP protein of the Sm class protein (by homology)
CA2324	orf19.5487	*CDC46*	1.0	1.0	1.0	-1.0	YLR274W	*CDC46*	1.0	-1.1	1.1	1.2	cell division control protein (by homology)
CA2325	orf19.5488	*IPF10977*	1.0	-1.1	-1.0	-1.0	YLR281C		1.0	-1.7	-2.0	-1.9	unknown function
CA2327	orf19.11972	*IPF4782*	1.0	1.4	2.2	1.7	YBR187W		1.0	-1.4	-1.3	1.0	probable membrane protein (by homology)
CA2328	orf19.11973	*MED8*	-1.1	-1.1	1.1	-1.0	YBR193C	*MED8*	1.0	-1.2	-1.4	-1.1	transcriptional regulation mediator (by homology)
CA2330	orf19.4499	*RIM2*	-1.0	-1.1	1.2	1.1	YBR192W	*RIM2*	1.0	1.0	-1.1	1.0	mitochondrial carrier protein (by homology)
CA2331	orf19.4502	*MOT1*	-1.1	1.1	-1.3	-1.1	YPL082C	*MOT1*	1.0	-1.3	-1.1	-1.1	transcriptional accessory protein
CA2336	orf19.2353	*F13383.53EC*	-1.1	-1.1	-1.2	-1.1	YOR086C		1.0	-1.6	-1.3	-1.4	unknown function, internal fragment
CA2337	orf19.2352	*IPF13379*	-1.0	-1.0	1.0	1.1	YGR031W		1.0	-1.7	-1.4	-1.5	unknown function
CA2338	orf19.2351	*NIT3*	1.1	-1.1	-1.0	-1.0	YLR351C	*NIT3*	1.0	1.2	1.2	1.2	nitrilase (by homology)
CA2341	orf19.2346	*IPF13838*	-1.1	1.0	1.0	-1.0	YPL222W		1.0	-1.2	-1.4	-1.7	unknown function
CA2343	orf19.2343	*IPF8671*	-1.0	1.0	1.0	-1.0	YCL008C	*STP22*	1.0	-1.1	1.0	1.1	unknown function
CA2344	orf19.2342	*SFT2*	1.2	1.2	1.7	1.4	YBL102W	*SFT2*	1.0	-1.0	-1.2	-1.2	similar to Saccharomyces cerevisiae Sft2p suppressor of SED5 thermose
CA2345	orf19.2341	*HNT1*	1.3	1.2	1.2	1.1	YDL125C	*HNT1*	1.0	1.2	1.3	1.1	similarity to protein kinase C inhibitor-I (by homology)
CA2346	orf19.3753	*SEF1*	1.1	1.0	1.0	1.0	YBL066C	*SEF1*	1.0	-1.3	-1.4	-1.4	Putative transcription factor1
CA2347	orf19.3752	*RAD51*	1.1	1.2	1.3	1.0	YER095W	*RAD51*	1.0	-1.1	-1.2	-1.3	DNA repair protein by homology
CA2348	orf19.3751	*IPF12811*	1.1	-1.1	-1.1	-1.0	YOR233W	*KIN4*	1.0	-1.8	-1.8	-1.7	putative serine/threonine kinase
CA2349	orf19.3749	*IFC3*	1.0	1.1	1.0	1.0	YPR194C	*OPT2*	1.0	-1.1	1.1	-1.1	Unknown function
CA2351	orf19.4420	*IPF19947*	1.1	1.0	1.2	1.0	YBL014C	*RRN6*	1.0	-1.2	-1.6	-1.2	unknown function
CA2352	orf19.4418	*FMT1*	-1.0	1.0	1.1	1.0	YBL013W	*FMT1*	1.0	1.1	1.0	1.1	Methionyl-tRNA Transformylase (by homology)
CA2353	orf19.4416	*VPS13*	1.1	1.0	1.0	-1.0	YLL040C	*VPS13*	1.0	-2.2	-2.5	-2.7	involved in regulating membrane traffic (by homology)
CA2357	orf19.4894	*IPF8957*	-1.1	-1.0	-1.1	-1.1	YER010C		1.0	-1.1	-1.2	-1.3	unknown function
CA2359	orf19.4896	*IPF8952*	-1.1	-1.1	-1.1	-1.0	YJL148W	*RPA34*	1.0	1.4	1.5	2.1	similar to Saccharomyces cerevisiae Rpa34p nonessential component of
CA2360	orf19.4897	*IPF8951*	1.0	1.0	1.0	-1.0	YJL145W		1.0	-2.5	-1.7	-1.6	unknown function
CA2361	orf19.12363	*IPF8950*	-1.0	1.1	1.1	1.1	YER004W		1.0	1.2	1.2	1.2	unknown function
CA2363	orf19.1285	*IPF10590*	1.0	1.1	-1.0	1.1	YPR091C		1.0	-1.2	1.1	-1.1	unknown function
CA2364	orf19.8870	*MEC1*	-1.2	-1.0	-1.2	-1.2	YBR136W	*MEC1*	1.0	1.2	1.1	1.0	cell cycle checkpoint protein (by homology)
CA2365	orf19.1282	*CKS1*	1.1	-1.0	1.0	-1.0	YBR135W	*CKS1*	1.0	1.1	1.2	1.3	cyclin-dependent kinases regulatory subunit (by homology)
CA2366	orf19.1281	*IPF10373*	1.0	-1.0	1.0	-1.0	YNL245C		1.0	-1.0	-1.0	-1.2	unknown function
CA2367	orf19.8867	*SUI1*	1.1	1.1	1.3	1.2	YNL244C	*SUI1*	1.0	1.2	1.1	1.4	translation initiation factor 3 (eIF3) (by homology)

CA2368	orf19.1839	*RPA190*	-1.2	1.1	-1.1	-1.0	YOR341W	*RPA190*	1.0	-1.5	1.4	2.0	DNA-directed RNA polymerase I (by homology)
CA2369	orf19.1837	*TBP1*	1.1	1.2	1.1	1.1	YER148W	*SPT15*	1.0	1.3	1.7	1.9	TATA-binding protein (by homology)
CA2370	orf19.1836	*APN2*	-1.0	-1.0	-1.1	1.0	YBL019W	*APN2*	1.0	-1.1	-1.1	-1.1	AP endonuclease, exonuclease III homologue (by homology)
CA2371	orf19.1835	*IPF10333*	-1.0	-1.0	-1.1	-1.1	YER149C	*PEA2*	1.0	-1.2	-1.0	-1.1	unknown function
CA2373	orf19.1833	*CBF5*	-1.2	-1.1	1.1	1.1	YLR175W	*CBF5*	1.0	1.2	1.4	2.0	centromere/ microtubule binding protein
CA2374	orf19.9390	*FCY23*	1.1	-1.0	1.1	1.0	YGL186C		1.0	-1.4	-1.2	-1.0	Putative purine-cytosine transport protein
CA2375	orf19.2211	*IPF15504*	-1.0	-1.0	-1.1	1.2	YGL138C		1.0	-1.2	-1.6	-1.3	unknown function
CA2376	orf19.2213	*IPF15506*	-1.1	-1.1	-1.1	1.0	YGR042W		1.0	-1.7	-1.0	1.1	unknown function
CA2377	orf19.2214	*MRPL7*	1.0	1.0	-1.1	-1.0	YDR237W	*MRPL7*					Ribosomal protein of the large subunit, mitochondrial (by homology)
CA2378	orf19.2215	*GLE1*	-1.1	-1.1	-1.1	-1.1	YDL207W	*GLE1*	1.0	1.2	1.4	1.4	RNA export mediator (by homology)
CA2379	orf19.2216	*IPF4073*	-1.1	1.0	-1.2	-1.0	YMR076C	*PDS5*	1.0	-1.6	-1.2	-1.3	similar to Saccharomyces cerevisiae CaPds5p regulation of dissociation
CA2384	orf19.2615	*MDL1*	-1.1	-1.1	-1.1	-1.1	YLR188W	*MDL1*	1.0	-1.4	-1.2	-1.1	ATP-DEPENDENT PERMEASE
CA2385	orf19.2614	*RSR1.3*	-1.0	-1.1	-1.1	-1.0	YGR152C	*RSR1*	1.0	1.1	1.1	-1.0	GTP-binding protein, 3-prime end
CA2386	orf19.2613	*ECM41.3*	-1.1	-1.2	-1.2	-1.2	YKR076W	*ECM4*	1.0	-1.1	-1.1	-1.6	involved in cell wall biogenesis and architecture, 3-prime end (by homolo
CA2388	orf19.2611	*MCM6*	-1.3	-1.1	-1.3	-1.2	YGL201C	*MCM6*	1.0	-1.3	-1.2	-1.4	component of MCM initiator complex involved in DNA replication (by hom
CA2390	orf19.2609	*CET1*	-1.0	-1.0	-1.0	-1.0	YPL228W	*CET1*	1.0	1.1	1.1	1.2	mRNA 5 -triphosphatase (capping enzyme, beta subunit)
CA2393	orf19.11018	*RHO3*	1.3	1.4	1.7	1.5	YIL118W	*RHO3*	1.0	-1.4	-1.4	-1.3	GTP-binding protein of the rho family
CA2395	orf19.3536	*IPF6425*	1.0	-1.0	-1.0	1.0	YOR320C		1.0	1.1	1.1	-1.3	unknown function
CA2396	orf19.3537	*IPF6428*	-1.0	1.0	-1.0	-1.0	YKL086W		1.0	-1.4	-1.7	-1.8	unknown function
CA2398	orf19.3539	*IPF6431*	1.1	1.0	-1.0	-1.0	YBR141C		1.0	-1.2	-1.1	1.3	unknown function
CA2399	orf19.3540	*MAK5*	-1.1	-1.2	-1.2	-1.2	YBR142W	*MAK5*	1.0	-1.1	1.1	1.3	ATP-dependent RNA helicase (by homology)
CA2400	orf19.3541	*SUP45*	-1.3	-1.2	-1.0	-1.1	YBR143C	*SUP45*	1.0	-1.5	-1.1	1.1	Translational release factor (by homology)
CA2401	orf19.3542	*LEM3*	-1.1	-1.1	-1.2	-1.1	YNL323W	*LEM3*	1.0	-1.2	1.2	-1.1	cell division cycle mutant (by homology)
CA2403	orf19.3544	*IPF6438*	1.0	-1.3	-1.3	-1.2	YML131W		1.0	-1.3	-1.4	-2.0	unknown function
CA2406	orf19.300	*AIP2*	-1.2	-1.2	-1.3	-1.3	YDL178W	*AIP2*	1.0	1.2	1.4	1.1	actin interacting protein 2 (by homology)
CA2407	orf19.299	*ECM14*	-1.1	1.1	1.1	1.0	YHR132C	*ECM14*	1.0	1.0	1.1	1.0	carboxypeptidase involved in cell wall biogenesis and architecture (by ho
CA2409	orf19.291	*IPF19948*	1.2	-1.0	-1.0	1.0	YHR134W	*WSS1*	1.0	-1.2	1.0	-1.1	unknown function
CA2414	orf19.4479	*IPF13756.3F*	-1.5	-1.5	-1.5	-1.4	YJL010C		1.0	-1.2	-1.4	-1.2	unknown function, 3-prime end
CA2415	orf19.4478	*MSD1*	-1.4	-1.2	-1.5	-1.3	YPL104W	*MSD1*	1.0	-1.2	-1.3	-1.4	Aspartyl-tRNA synthetase, mitochondrial.
CA2418	orf19.4475	*MNT4*	-1.0	1.0	-1.0	1.0	YBR199W	*KTR4*	1.0	1.2	1.1	1.0	putative mannosyltransferase
CA2419	orf19.4474	*IPF14379*	-1.0	1.1	-1.0	-1.0	YNL155W		1.0	1.2	1.6	1.5	unknown function
CA2420	orf19.4473	*SPC19*	1.0	1.0	-1.0	1.0	YDR201W	*SPC19*	1.0	1.2	1.1	1.1	spindle pole body protein (by homology)
CA2421	orf19.4471	*IPF14998*	1.0	1.1	1.1	1.0	YDR200C		1.0	-1.3	-1.2	-1.3	unknown function
CA2423	orf19.11949	*SDH41*	-1.0	-1.5	-1.3	-1.2	YDR178W	*SDH4*	1.0	-1.5	-1.2	-2.2	succinate dehydrogenase membrane anchor subunit for sdh2p (by homo
CA2425	orf19.10912	*IPF9907*	1.1	1.1	1.5	1.1	YCR067C	*SED4*	1.0	-1.1	1.0	1.1	similar to Saccharomyces cerevisiae Sed4 protein of the endoplamic retic
CA2426	orf19.3407	*IPF9901*	-1.1	1.0	-1.0	-1.0	YCR066W	*RAD18*	1.0	-1.1	-1.1	-1.2	similar to Saccharomyces cerevisiae rad18p DNA repair protein (by hom
CA2427	orf19.3406	*IPF9898*	-1.0	1.0	1.0	-1.0	YHL008C		1.0	-1.4	-1.3	-1.3	probable formate dehydrogenase (by homology)
CA2431	orf19.3401	*IPF12951*	-1.0	1.1	1.0	1.0	YDR486C	*VPS60*	1.0	-1.1	-1.1	-1.0	unknown function
CA2432	orf19.3400	*COQ3*	1.1	1.0	1.1	-1.0	YOL096C	*COQ3*	1.0	1.2	1.1	1.0	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
CA2433	orf19.3399	*IPF12959*	1.0	1.1	-1.0	-1.0	YDR485C		1.0	-1.2	-1.2	-1.1	unknown function
CA2435	orf19.10898	*IPF9483*	1.1	1.1	1.2	1.1	YHR048W		1.0	-1.1	1.1	1.1	probable permease (by homology)
CA2436	orf19.2200	*IPF5500*	-1.1	-1.1	-1.1	-1.1	YKR044W		1.0	-1.9	-1.6	-1.4	unknown function
CA2437	orf19.2199	*PHO86*	-1.0	-1.1	-1.1	-1.1	YJL117W	*PHO86*	1.0	-1.1	-1.1	1.0	inorganic phospate transporter by homology
CA2440	orf19.2196	*IPF7513*	-1.0	-1.0	-1.0	1.0	YGL110C		1.0	1.0	1.1	1.4	unknown function
CA2441	orf19.2194	*APM4*	1.0	-1.0	1.1	-1.0	YOL062C	*APM4*	1.0	1.1	1.1	1.1	AP-2 complex subunit, mu2 subunit (by homology)
CA2442	orf19.2193	*PRS5*	-1.1	-1.3	-1.3	-1.4	YOL061W	*PRS5*	1.0	1.0	1.2	1.7	Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyrophosp
CA2446	orf19.5504	*IPF2582*	-1.0	1.0	1.0	1.0	YKL098W		1.0	1.2	-1.0	-1.0	unknown function
CA2447	orf19.5505	*HIS7*	-1.4	-1.6	-2.0	-1.5	YBR248C	*HIS7*	1.0	-1.2	-1.2	1.2	Histidine biosynthesis
CA2448	orf19.5506	*PLC1*	-1.1	-1.1	-1.1	-1.1	YPL268W	*PLC1*	1.0	1.0	1.2	1.2	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
CA2449	orf19.5507	*ENP1*	1.0	-1.1	-1.1	-1.1	YBR247C	*ENP1*	1.0	-1.1	-1.1	1.1	Essential nuclear protein (by homology)
CA2453	orf19.10995	*IPF9950*	1.0	-1.1	-1.3	-1.2	YKR090W		1.0	-1.4	-1.5	-1.6	unknown function
CA2454	orf19.3504	*RPL23B.3*	1.4	-1.0	1.1	1.4	YER117W	*RPL23B*	1.0	1.9	2.0	2.5	ribosomal protein L23.e, 3-prime end (by homology)
CA2455	orf19.3505	*IPF12228*	-1.2	1.1	-1.2	1.0	YNL047C		1.0	-1.1	1.5	1.6	unknown function
CA2456	orf19.3506	*DBR1*	-1.1	-1.0	-1.0	-1.0	YKL149C	*DBR1*	1.0	1.5	1.3	1.6	lariat-debranching enzyme (by homology)
CA2457	orf19.3507	*MCR1*	-1.1	-1.6	-1.5	-1.2	YKL150W	*MCR1*	1.0	1.3	1.3	1.2	NADH-cytochrome-b5 reductase (by homology)
CA2458	orf19.3508	*IPF12233*	1.0	-1.1	-1.0	-1.0	YKL151C		1.0	1.3	1.3	-1.3	unknown function
CA2461	orf19.1791	*MAK11*	-1.0	-1.1	-1.1	1.0	YKL021C	*MAK11*	1.0	-1.1	1.1	1.1	involved in cell growth and replication of M1 dsRNA virus (by hom
CA2462	orf19.1792	*CDC16*	1.2	1.1	1.2	1.2	YKL022C	*CDC16*	1.0	-1.3	-1.4	-1.3	subunit of anaphase-promoting complex (by homology)
CA2463	orf19.1793	*IPF8730*	-1.0	1.0	-1.0	-1.0	YGR223C		1.0	-1.1	1.5	1.0	unknown function
CA2465	orf19.1795	*IPF8726*	1.0	-1.1	1.2	1.0	YLL013C	*PUF3*	1.0	-1.1	-1.2	-1.2	unknown function
CA2467	orf19.1796	*IPF8724*	1.0	-1.0	-1.0	-1.1	YPL113C		1.0	-1.3	-1.3	-1.3	unknown function

CA2471	orf19.2873	*TOP2*	-1.1	-1.1	-1.2	-1.1	YNL088W	*TOP2*	1.0	-1.5	-1.1	1.1	Topoisomerase II
CA2473	orf19.2876	*CBF1*	-1.2	1.4	1.2	1.2	YJR060W	*CBF1*	1.0	-1.4	-1.5	-1.5	putative centromere binding factor 1
CA2474	orf19.2877	*PDC11*	-1.1	9.2	6.4	9.7	YLR044C	*PDC1*	1.0	1.9	3.7	4.9	Pyruvate decarboxylase (by homology)
CA2480	orf19.10718	*CCT7*	-1.2	-1.1	-1.2	-1.2	YJL111W	*CCT7*	1.0	-1.1	1.5	1.5	component of chaperonin-containing T-complex (by homology)
CA2481	orf19.3205	*MRPL36*	-1.0	-1.2	-1.2	-1.1	YBR122C	*MRPL36*	1.0	1.1	-1.1	-1.1	ribosomal protein YmL36 precursor, mitochondrial (by homology)
CA2483	orf19.3203	*IPF19758*	-1.2	-1.3	-1.2	-1.1	YJL204C		1.0	-1.4	-1.1	-1.1	unknown function
CA2486	orf19.10712	*IPF9851*	-1.1	-1.1	-1.1	-1.1	YCR040W	*MATALPHA1*	1.0	-1.6	-1.8	-1.5	unknown function
CA2487	orf19.10711	*PIK1*	-1.0	1.0	-1.0	-1.0	YNL267W	*PIK1*	1.0	1.1	-1.1	1.1	phosphatidylinositol 4-kinase
CA2490	orf19.4044	*MUM2*	-1.0	1.4	1.8	1.4	YBR057C	*MUM2*	1.0	-1.1	-1.1	-1.1	ubiquitin C-terminal hydrolase (by homology)
CA2492	orf19.4045	*IPF7224*	-1.0	1.1	1.1	-1.0	YDR206W	*EBS1*	1.0	-1.2	-1.2	-1.1	putative telomere elongation protein (by homology)
CA2494	orf19.4051	*HTS1*	-1.1	-1.0	1.1	-1.0	YPR033C	*HTS1*	1.0	1.2	1.7	1.9	histidine tRNA synthetase (by homology)
CA2497	orf19.5580	*TEL1.3EOC*	1.0	-1.1	-1.3	-1.2	YBL088C	*TEL1*	1.0	1.3	1.4	1.2	Putative phosphatidylinositol kinase involved in controlling telomere leng
CA2498	orf19.5584	*VPS181*	-1.1	-1.1	-1.1	-1.0	YLR148W	*PEP3*	1.0	-1.4	-1.1	-1.0	vacuolar membrane protein
CA2500	orf19.5586	*FIG4*	-1.0	-1.0	-1.0	-1.0	YNL325C	*FIG4*	1.0	1.0	1.2	1.0	suppressor of sac1 mutation (by homology)
CA2501	orf19.5587	*IPF6812*	1.0	-1.0	-1.0	-1.0	YLR224W		1.0	-1.0	-1.1	1.1	unknown function
CA2503	orf19.5592	*IPF6803.5F*	-1.0	1.0	1.0	-1.0	YAL045C		1.0	-2.1	-1.7	-1.2	unknown function, 5-prime end
CA2505	orf19.5595	*IPF6796*	-1.3	-1.2	-1.6	-1.2	YBR130C	*SHE3*	1.0	-2.1	-2.0	-1.2	unknown function
CA2508	orf19.302	*BET5*	-1.0	1.0	1.2	1.1	YML077W	*BET5*	1.0	-1.1	1.0	1.1	targeting and fusion of ER to Golgi transport vesicles (by homology)
CA2509	orf19.304	*IPF1471*	1.1	1.0	1.1	1.1	YOR378W		1.0	-1.4	-1.3	-1.4	aminotriazole resistance protein (by homology)
CA2512	orf19.307	*HFI1*	-1.0	-1.0	-1.1	-1.0	YPL254W	*HFI1*	1.0	-1.1	-1.1	1.1	Putative transcriptional coactivator (by homology)
CA2513	orf19.308	*SNG1*	1.0	1.0	1.0	-1.0	YGR197C	*SNG1*	1.0	-1.3	-1.1	-1.1	Involved in nitroguanidine resistance (by homology)
CA2514	orf19.313	*FUR4*	1.0	1.1	1.1	1.0	YIR028W	*DAL4*	1.0	-1.0	-1.0	-1.1	Probable uracile or allantoin permease (by homology)
CA2515	orf19.5510	*IPF19759*	1.0	-1.1	-1.1	-1.1	YGL133W	*ITC1*	1.0	-1.5	1.4	1.7	Unknown Function
CA2516	orf19.5513	*IPF4301*	1.0	1.0	1.1	1.0	YAL032C	*PRP45*	1.0	-1.8	-2.2	-2.1	unknown function
CA2518	orf19.5515	*CBP3*	-1.0	1.0	-1.0	-1.0	YPL215W	*CBP3*	1.0	1.1	1.1	-1.0	involved in cytochrome-c reductase assembly (by homology)
CA2519	orf19.5516	*SRP72*	-1.1	-1.1	-1.1	-1.0	YPL210C	*SRP72*	1.0	1.0	1.1	-1.0	signal recognition particle protein SRP72 (by homology)
CA2520	orf19.5517	*IPF20104*	1.2	2.7	3.9	2.7	YMR318C		1.0	1.4	1.8	1.8	alcohol dehydrogenase (by homology)
CA2522	orf19.5519	*GCV1*	-1.1	-2.0	-2.0	-1.6	YDR019C	*GCV1*	1.0	-1.3	-1.6	-1.7	glycine cleavage T protein (by homology)
CA2524	orf19.5521	*IPF4322*	1.1	-1.2	-1.2	-1.2	YLL027W	*ISA1*	1.0	-1.3	-1.4	-1.6	unknown function
CA2526	orf19.5526	*SEC20*	-1.0	1.1	1.1	1.1	YDR498C	*SEC20*	1.0	-1.3	-1.5	-1.5	secretory pathway protein
CA2527	orf19.5527	*IPF4331*	-1.0	1.1	-1.0	1.0	YMR285C	*NGL2*	1.0	-1.4	-1.3	-1.3	unknown function
CA2528	orf19.5528	*MOB1*	1.0	1.0	-1.0	1.0	YIL106W	*MOB1*	1.0	1.0	1.1	-1.0	required for completion of mitosis
CA2530	orf19.3176	*IPF12782*	-1.1	1.0	-1.0	1.0	YNL294C		1.0	-1.3	-1.3	-1.2	unknown function
CA2531	orf19.3177	*RIB2*	-1.2	-1.2	-1.2	-1.1	YOL066C	*RIB2*	1.0	-1.3	-1.2	1.0	DRAP deaminase (by homology)
CA2532	orf19.3178	*PRP9*	-1.1	-1.0	-1.1	-1.0	YDL030W	*PRP9*	1.0	-1.3	-1.2	-1.2	pre-mRNA splicing factor (snRNA-associated protein) (by ho
CA2533	orf19.3180	*IPF12790*	-1.1	-1.1	-1.0	1.1	YOL065C	*INP54*	1.0	-1.1	-1.0	-1.1	inositol polyphosphate 5-phosphatase (by homology)
CA2534	orf19.3182	*IPF12793*	1.1	1.2	1.5	1.4	YNL255C	*GIS2*	1.0	1.3	1.8	1.7	similar to Saccharomyces cerevisiae Gis2p containing seven zinc finger
CA2536	orf19.3183	*IPF20107*	1.1	-1.0	1.0	1.0	YOL111C		1.0	-1.2	-1.2	-1.3	unknown function
CA2538	orf19.3185	*NAT1*	-1.6	-1.4	-1.8	-1.6	YDL040C	*NAT1*	1.0	1.1	1.2	1.3	Protein N-acetyltransferase subunit (by homology)
CA2542	orf19.3190	*IPF16067*	1.1	1.1	1.1	-1.0	YOL089C	*HAL9*	1.0	1.1	1.1	1.1	unknown function
CA2543	orf19.2828	*IPF16925*	1.0	1.0	1.1	1.1	YNL148C	*ALF1*	1.0	-1.3	-1.2	-1.2	unknown function
CA2544	orf19.2829	*IPF16924*	1.0	1.1	1.1	1.0	YNL149C		1.0	-4.4	-2.1	-2.1	unknown function
CA2545	orf19.2830	*RRP9*	-1.1	-1.1	1.0	1.8	YPR137W	*RRP9*	1.0	1.1	-1.0	1.4	U3 small nucleolar ribonucleoprotein-associated protein involved in pre-ri
CA2546	orf19.2831	*RPC31*	1.0	-1.0	1.1	1.1	YNL151C	*RPC31*	1.0	-1.6	-1.8	-2.4	DNA-directed RNA polymerase III (by homology)
CA2547	orf19.2832	*IPF14911*	-1.2	-1.1	-1.2	-1.1	YNL152W		1.0	-1.3	-1.4	-1.3	unknown function
CA2550	orf19.2835	*IPF9099*	-1.0	1.2	1.1	1.2	YPR180W	*AOS1*	1.0	-1.0	1.2	1.1	similar to Saccharomyces cerevisiae Aos1p activating enzyme for Smt3 (
CA2552	orf19.2837	*ALG5*	-1.0	-1.1	-1.1	-1.0	YPL227C	*ALG5*	1.0	-1.0	1.1	1.1	dolichol-P-glucose synthetase (by homology)
CA2559	orf19.5639	*HIS4*	-1.3	-1.2	-1.3	-1.3	YCL030C	*HIS4*	1.0	1.6	2.9	6.8	Histidine biosynthesis trifunctional protein (phosphoribosyl-AMP cyclohy
CA2560	orf19.5640	*PEX5*	-1.1	-1.2	-1.2	-1.2	YDR244W	*PEX5*					peroxisomal targeting signal receptor
CA2561	orf19.5641	*CAR2*	-1.2	-4.7	-4.7	-3.8	YLR438W	*CAR2*	1.0	-1.3	-1.4	-1.8	ornithine aminotransferase (by homology)
CA2563	orf19.5643	*ECM7*	1.0	1.2	1.4	1.1	YLR443W	*ECM7*	1.0	-1.9	-1.5	-1.8	cell wall biogenesis and architecture (by homology)
CA2564	orf19.5644	*IPF12127*	-1.0	1.3	1.6	1.3	YML066C	*SMA2*	1.0	-1.2	-1.2	-1.2	unknown function
CA2565	orf19.5645	*MET15*	1.1	1.4	1.6	1.2	YLR303W	*MET17*	1.0	-3.2	-3.6	-5.3	O-acetylhomoserine O-acetylserine sulphydrylase
CA2566	orf19.5646	*IPF12122*	-1.1	1.0	1.0	-1.0	YPL034W		1.0	1.2	1.0	1.1	unknown function
CA2567	orf19.5647	*SUB2.3F*	-1.1	-1.1	1.0	-1.0	YDL084W	*SUB2*	1.0	-1.0	1.2	1.3	Involved in pre-mRNA splicing, 3-prime end (by homology)
CA2570	orf19.5650	*PRO3*	1.1	-1.4	-1.6	-1.2	YER023W	*PRO3*	1.0	-1.4	-1.2	-1.2	delta 1-pyrroline-5-carboxylate reductase (by homology)
CA2571	orf19.13590	*IPF13769*	1.1	-1.2	-1.0	-1.2	YKL221W		1.0	-1.5	-1.5	-1.5	unknown function
CA2573	orf19.6213	*SUI2*	1.1	-1.1	-1.2	-1.1	YJR007W	*SUI2*	1.0	1.2	1.6	1.9	translation initiation factor eIF2, alpha chain (by homology)
CA2574	orf19.6214	*ATH1*	-1.0	-1.1	-1.2	-1.1	YPR026W	*ATH1*	1.0	1.0	-1.2	-1.2	acid trehalase, vacuolar
CA2575	orf19.6217	*SEC31*	1.0	1.2	-1.0	-1.0	YDL195W	*SEC31*	1.0	-1.4	-1.1	1.1	Component of the COPII coat of ER-golgi vesicles (by homology).
CA2577	orf19.6220	*IPF7430*	-1.1	-1.1	-1.3	-1.3	YGR134W	*CAF130*	1.0	-1.2	-1.4	-1.1	unknown function

CA2578		*MMD1.3*	1.6	-1.1	-1.2	1.1	YIL051C	*MMF1*	1.0	1.0	-1.2	-1.2	Maintenance of mitochondrial DNA, 3-prime end (by homology)
CA2579		*RPL34B.3*	1.8	1.3	1.2	1.4	YIL052C	*RPL34B*	1.0	2.0	2.2	2.6	Ribosomal protein L34.e, 3-prime end (by homology)
CA2582	orf19.4371	*TAL1*	-1.2	-1.8	-2.0	-1.8	YLR354C	*TAL1*	1.0	1.2	1.2	1.4	transaldolase (by homology)
CA2584	orf19.4373	*IPF9440*	1.2	1.1	-1.0	1.1	YDR236C	*FMN1*					similar to Saccharomyces cerevisiae Fmn1p riboflavin kinase (by homolo
CA2585	orf19.4374	*IPF9438*	-1.0	-1.0	-1.0	1.0	YDR235W	*PRP42*					similar to Saccharomyces cerevisiae Prp42p U1 snRNP associated prote
CA2586	orf19.4375	*IPF9435*	1.0	-1.1	-1.0	-1.0	YLR285W		1.0	-1.3	1.1	1.3	unknown function
CA2587		*RPS30.3*	1.2	1.1	1.1	1.1	YOR182C	*RPS30B*	1.0	1.4	1.8	1.8	40S ribosomal protein S30, 3-prime end (by homology)
CA2592	orf19.59	*IPF18447*	1.1	1.0	-1.0	1.0	YBR267W		1.0	-1.5	-1.3	1.0	putative zinc-finger protein (by homology)
CA2593	orf19.58	*RRP6*	-1.1	-1.2	-1.4	-1.1	YOR001W	*RRP6*	1.0	1.2	1.8	2.1	involved in 5.8S rRNA processing (by homology)
CA2594	orf19.57	*IPF12824*	-1.0	1.0	1.0	1.1	YJL072C		1.0	1.1	-1.2	-1.1	unknown function
CA2595	orf19.56	*ARG2*	-1.0	-1.0	-1.0	-1.0	YJL071W	*ARG2*	1.0	-1.2	-1.3	-1.2	acetylglutamate synthase (by homology)
CA2596	orf19.55	*IPF19546*	1.4	-1.4	-1.0	1.1	YOL002C		1.0	-1.2	-1.1	-1.0	unknown function
CA2599	orf19.52	*IPF11176*	-1.0	-1.0	1.2	1.1	YPL224C	*MMT2*	1.0	-1.2	-1.0	-1.1	similar to Saccharomyces cerevisiae Mmt2p mitochondrial iron transporte
CA2600	orf19.51	*IPF11177*	-1.3	-1.2	-1.4	-1.0	YMR012W	*CLU1*	1.0	-1.1	1.1	-1.1	similar to Saccharomyces cerevisiae Clu1p translation initiation factor eIF
CA2601	orf19.50	*IPF11181*	-1.1	-1.0	-1.0	1.0	YML088W	*UFO1*	1.0	1.2	1.3	1.4	unknown function
CA2605	orf19.5682	*SRP1*	-1.0	1.0	1.2	-1.1	YNL189W	*SRP1*	1.0	-1.2	1.1	1.4	alpha importin by homology
CA2606	orf19.5683	*IPF5466*	-1.0	1.0	1.0	1.0	YHR140W		1.0	-1.3	-1.3	-1.1	unknown function
CA2607	orf19.5684	*MRPL38*	1.3	1.3	1.3	1.2	YKL170W	*MRPL38*	1.0	-1.1	-1.1	-1.4	ribosomal protein of the large subunit(L14), mitochondrial, by homology
CA2608	orf19.5685	*THS1*	-1.7	-1.3	-1.4	-1.5	YIL078W	*THS1*	1.0	1.3	1.6	1.7	threonyl tRNA synthetase by homology
CA2609	orf19.5689	*IPF5457*	1.2	1.1	1.3	1.2	YIL076W	*SEC28*	1.0	-1.6	-1.2	-1.7	similar to Saccharomyces cerevisiae sec28p epsilon-COP coatomer subu
CA2610	orf19.5691	*CDC11*	-1.0	-1.0	1.0	1.0	YJR076C	*CDC11*	1.0	-2.0	1.1	1.1	septin by homology
CA2612	orf19.5693	*GAA1*	1.1	1.2	1.4	1.4	YLR088W	*GAA1*	1.0	-1.4	-1.1	1.0	required for attachment of GPI anchor onto proteins by homology
CA2613	orf19.5698	*IPF5446*	1.2	1.0	1.1	-1.0	YDR116C		1.0	-1.1	-1.2	-1.1	putative ribosomal protein (by homology)
CA2620	orf19.2809	*IPF9496*	1.0	-1.1	-1.0	-1.0	YER024W	*YAT2*	1.0	-1.5	-1.6	-1.1	carnitine O-acetyltransferase (by homology)
CA2625	orf19.12229	*IPF10919*	1.4	1.6	1.8	1.6	YLR110C	*CCW12*	1.0	1.7	2.0	2.0	Similar to Flo1p (by homology)
CA2626	orf19.4764	*PAN2*	-1.0	1.0	1.0	-1.0	YGL094C	*PAN2*	1.0	-1.3	-1.3	-1.5	component of Pab1p-stimulated poly(A)(by homology)
CA2627	orf19.4763	*IPF10916*	1.1	-1.0	1.0	-1.1	YAL008W	*FUN14*	1.0	-1.6	-1.4	-1.1	unknown function
CA2628	orf19.12225	*SIR22*	1.0	-1.0	1.0	1.1	YOL068C	*HST1*	1.0	-1.1	1.1	1.4	canal regulatory protein (by homology)
CA2629	orf19.12224	*IPF10911*	1.1	-1.1	-1.1	-1.1	YIL110W		1.0	-1.1	1.1	1.1	unknown function
CA2630	orf19.12223	*COX5A*	1.3	-1.1	1.4	1.1	YNL052W	*COX5A*	1.0	1.3	1.4	-1.4	cytochrome-c oxidase chain V.A precursor (by homology)
CA2632	orf19.4757	*NAR1*	1.1	-1.0	-1.0	-1.1	YNL240C	*NAR1*	1.0	1.2	1.2	1.1	Yeast nuclear architecture related protein (by homology)
CA2633	orf19.4755	*KEX2*	-1.3	-1.1	-1.4	-1.1	YNL238W	*KEX2*	1.0	1.0	1.1	1.5	Kexin precursor (KEX2 protease)
CA2634	orf19.12218	*ZWF1*	-1.6	-1.2	-1.2	-1.1	YNL241C	*ZWF1*	1.0	1.5	1.6	-1.0	glucose-6-phosphate dehydrogenase (by homology)
CA2635	orf19.4297	*CKB22*	1.0	1.1	1.1	1.1	YOR039W	*CKB2*	1.0	-1.2	-1.1	-1.1	Casein kinase II, beta subunit (by homology)
CA2636	orf19.4299	*MSW1*	-1.0	-1.0	1.0	-1.0	YDR268W	*MSW1*	1.0	-1.1	-1.2	-1.3	Mitochondrial tryptophanyl-tRNA synthetase (by homology)
CA2641	orf19.4306	*IPF2929*	1.1	1.1	1.0	-1.0	YJR024C		1.0	1.1	1.2	1.2	unknown function
CA2643	orf19.4308	*HSL1*	1.0	1.0	-1.1	-1.0	YKL101W	*HSL1*	1.0	-1.3	-1.4	-1.4	Ser/thr protein kinase that interacts genetically with histone mutations (by
CA2645	orf19.4311	*YNK1*	1.4	1.0	1.1	1.2	YKL067W	*YNK1*	1.0	-1.4	-1.5	-2.2	Nucleoside diphosphate kinase (by homology)
CA2646	orf19.1185	*IPF13089*	1.2	1.0	1.1	1.0	YNL116W		1.0	1.0	-1.1	-1.1	unknown function
CA2648	orf19.1187	*IPF9062*	-1.2	1.5	1.3	1.4	YOR032C	*HMS1*	1.0	-1.3	-1.2	-1.3	unknown function
CA2651	orf19.1191	*HRD3*	-1.2	-1.2	-1.2	-1.2	YLR207W	*HRD3*	1.0	1.2	1.5	1.5	involved in HMG-CoA reductase degradation (by homology)
CA2652	orf19.1192	*DNA2*	-1.0	1.0	-1.1	-1.0	YHR164C	*DNA2*	1.0	-1.1	-1.2	-1.5	DNA helicase (by homology)
CA2653	orf19.5701	*PF8472.3EO*	1.1	-1.0	1.1	1.0	YLR381W		1.0	1.0	1.3	1.4	unknown function, 3-prime end
CA2654	orf19.5702	*IPF8474*	1.1	1.1	1.1	1.0	YOR093C		1.0	-1.4	-1.6	-1.3	unknown function
CA2655	orf19.5704	*IPF8477*	1.1	-1.1	-1.0	-1.0	YGR150C		1.0	1.1	1.2	1.3	unknown function
CA2656	orf19.5705	*NAM2*	-1.1	-1.3	-1.5	-1.3	YLR382C	*NAM2*	1.0	-1.4	-1.2	-1.4	mitochondrial leucine--tRNA ligase (by homology)
CA2658	orf19.5711	*IPF8105*	-1.0	-1.2	-1.2	-1.2	YLR380W	*CSR1*	1.0	-1.3	-1.3	-1.1	unknown function
CA2662	orf19.3553	*IPF17139*	-1.0	1.1	1.1	-1.0	YKR081C		1.0	1.3	1.4	2.1	unknown function
CA2663	orf19.3552	*NUP133*	-1.7	-1.5	-2.1	-1.7	YKR082W	*NUP133*	1.0	-1.3	-1.1	-1.2	nuclear pore protein (by homology)
CA2664	orf19.3551	*IPF13370*	-1.1	-1.0	-1.0	-1.0	YKR083C	*DAD2*	1.0	-2.1	-2.2	-2.0	unknown function
CA2665	orf19.3549	*CDC21*	1.0	-1.1	1.0	1.0	YOR074C	*CDC21*	1.0	-1.3	1.6	1.2	thymidylate synthase (by homology)
CA2666	orf19.3548	*IPF16995*	1.3	1.0	-1.0	1.1	YBL095W		1.0	1.3	1.2	1.2	unknown function
CA2667	orf19.3547	*IPF16996*	-1.2	-1.1	-1.1	-1.0	YDR496C	*PUF6*	1.0	-1.2	-1.1	1.1	unknown function
CA2668	orf19.3546	*IPF17553*	-1.2	-1.4	-1.5	-1.3	YJL210W	*PEX2*	1.0	1.1	1.0	-1.8	similar to Saccharomyces cerevisiae Pex2p peroxisomal protein (by hom
CA2670	orf19.5500	*MAK16*	1.0	-1.1	-1.0	1.0	YAL025C	*MAK16*	1.0	-1.1	1.0	1.2	nuclear viral propagation protein (by homology)
CA2675	orf19.5493	*GSP1*	-1.2	-1.3	-1.3	-1.2	YLR293C	*GSP1*	1.0	1.2	1.7	2.3	GTP-binding protein (by homology)
CA2676	orf19.5492	*YHC1*	-1.0	-1.0	1.0	1.1	YLR298C	*YHC1*	1.0	-1.0	1.2	1.1	SMALL NUCLEAR RIBONUCLEOPROTEIN C (by homology)
CA2677		*ATP14.EXON*	1.3	-1.0	-1.0	1.1	YLR295C	*ATP14*	1.0	-1.2	-1.1	-1.4	F1F0-ATPase complex, subunit h, exon 2 (by homology)
CA2679	orf19.2568	*IFU5*	1.1	1.0	1.1	-1.1	YFL010C		1.0	1.1	1.2	1.2	Unknown function
CA2681	orf19.2571	*SEC4*	-1.0	1.0	1.3	1.0	YFL005W	*SEC4*	1.0	-1.7	-2.1	-3.5	GTP-binding protein
CA2682	orf19.2573	*FRS1*	-1.3	-1.3	-1.4	-1.3	YLR060W	*FRS1*	1.0	1.2	1.7	1.8	Phenylalanyl-tRNA synthetase

CA2683	orf19.2574	*IFU4*	-1.2	-1.0	-1.2	-1.1	YFL034W		1.0	-1.1	1.2	-1.1	Unknown function
CA2684	orf19.2575	*IFU3*	-1.0	1.0	1.0	-1.0	YLR063W		1.0	-1.0	1.1	1.3	Unknown function
CA2685	orf19.2579	*MSH4*	-1.0	1.0	-1.1	-1.0	YFL003C	*MSH4*	1.0	-1.4	-1.4	-1.1	DNA mismatch repair protein
CA2686	orf19.2580	*HST2*	-1.1	1.0	-1.1	1.0	YPL015C	*HST2*	1.0	1.2	1.6	1.2	Transcription regulatory protein
CA2689	orf19.2582	*IFU2*	-1.1	-1.0	-1.2	-1.1	YPL009C		1.0	-1.5	-1.3	-1.4	Unknown function
CA2693	orf19.10247	*IPF9173.5F*	1.0	1.0	1.1	1.1	YPL120W	*VPS30*	1.0	1.1	1.3	1.2	similar to Saccharomyces cerevisiae Vps30p involved in vacuolar protein
CA2695	orf19.2735	*IPF9070*	1.0	-1.0	1.0	1.0	YLR105C	*SEN2*	1.0	-1.4	-1.5	-1.4	similar to Saccharomyces cerevisiae Sen2p tRNA splicing endonuclease
CA2696	orf19.2736	*IPF9169*	1.0	1.3	1.9	1.5	YER159C	*BUR6*	1.0	1.2	1.1	1.3	similar to Saccharomyces cerevisiae Bur6p functional homolog of human
CA2697	orf19.2737	*IPF9167*	-1.3	-1.2	-1.3	-1.3	YDR109C		1.0	1.1	1.2	1.3	unknown function
CA2698	orf19.10252	*SUL1*	-1.1	1.0	1.1	1.0	YLR092W	*SUL2*	1.0	-1.6	-1.7	-1.6	High-affinity sulfate transport protein (by homology)
CA2699	orf19.10253	*RLF2*	1.0	-1.0	-1.0	-1.1	YPR018W	*RLF2*	1.0	-1.0	-1.0	1.1	chromatin assembly complex, subunit p90 (by homology)
CA2702	orf19.10260	*EMP70*	1.2	1.2	1.5	1.2	YLR083C	*EMP70*	1.0	-1.1	-1.0	1.3	Endosomal protein (by homology)
CA2705	orf19.4657	*NEM1*	1.1	-1.1	-1.0	1.0	YHR004C	*NEM1*	1.0	1.1	1.3	1.5	required for nuclear morphology (by homology)
CA2707	orf19.4659	*IPF11003*	-1.0	-1.1	-1.1	-1.0	YJL203W	*PRP21*	1.0	-1.7	-1.4	-1.3	by homology pre-mrna splicing factor
CA2708	orf19.4660	*RPS6A*	-1.2	-1.5	-1.7	-1.3	YPL090C	*RPS6A*	1.0	1.9	2.3	3.4	ribosomal protein S6 (by homology)
CA2709	orf19.4662	*IPF4828*	1.1	1.0	1.0	-1.0	YPL089C	*RLM1*	1.0	-1.0	1.2	1.2	by homology to S. cerevisiae YEAST TRANSCRIPTION FACTOR RLM1
CA2710	orf19.4664	*IPF7403*	1.1	1.1	1.2	1.1	YMR069W		1.0	-1.6	-1.5	-1.7	unknown function
CA2711	orf19.8198	*TFB3*	1.0	-1.0	-1.0	-1.0	YDR460W	*TFB3*	1.0	-1.0	-1.0	-1.1	Transcription/repair factor (by homology)
CA2712	orf19.8199	*SPE2*	1.0	-1.2	-1.1	-1.3	YOL052C	*SPE2*	1.0	1.1	1.6	1.2	by homology to S. cerevisiae adenosylmethionine decarboxylase precurs
CA2715	orf19.576	*CTF8*	1.0	1.0	-1.0	-1.0	YHR191C	*CTF8*	1.0	-1.1	-1.3	-1.2	putative) kinetochore protein (by homology)
CA2716	orf19.577	*IPF7353*	-1.1	-1.3	-1.4	-1.2	YDL057W		1.0	-1.1	-1.3	-1.2	unknown function
CA2717	orf19.8209	*MSB3*	1.0	1.1	1.0	-1.0	YNL293W	*MSB3*	1.0	-1.2	-1.1	-1.1	GTPase-activating protein for Sec4p (by homology)
CA2719	orf19.3340	*SOD2*	1.2	-1.2	-1.3	-1.2	YHR008C	*SOD2*	1.0	1.1	1.1	-1.3	Manganese-superoxide dismutase
CA2720	orf19.3341	*IPF7366*	-1.3	-1.2	-1.2	-1.3	YDR341C		1.0	1.3	1.8	2.7	Arginyl-tRNA synthetase
CA2721	orf19.3342	*IPF4799*	-1.1	-1.0	1.0	-1.0	YOR138C		1.0	-1.5	-1.3	-1.5	unknown Function
CA2722	orf19.3344	*IPF4801*	-1.1	-1.1	-1.1	-1.0	YOR132W	*VPS17*	1.0	1.2	1.4	1.5	similar to Saccharomyces cerevisiae Vps17p vacuolar sorting protein (by
CA2723	orf19.3345	*IPF4805*	-1.1	-1.1	-1.1	-1.0	YDR409W	*SIZ1*	1.0	-1.1	-1.1	1.1	unknown Function
CA2724	orf19.10855	*RPB7*	1.3	1.1	1.2	1.1	YDR404C	*RPB7*	1.0	1.1	1.0	1.5	DNA-directed RNA polymerase II,19KD subunit (by homology)
CA2725	orf19.10856	*MRPL23A*	1.0	-1.0	1.0	1.0	YOR150W	*MRPL23*	1.0	-1.4	-1.4	-1.6	mitochondrial ribosomal protein L23 (by homology)
CA2727	orf19.2119	*IPF10318*	1.1	-1.0	-1.1	-1.1	YHR124W	*NDT80*	1.0	-1.3	-1.5	-1.3	similar to Saccharomyces cerevisiae Ndt80p meiosis-specific protein (by
CA2728	orf19.9665	*IPF10322*	1.0	-1.5	-1.5	-1.3	YHR002W		1.0	-1.7	-1.3	-1.3	putative mitochondrial carrier protein (by homology)
CA2729	orf19.9664	*NAT2*	1.1	-1.2	-1.2	-1.2	YGR147C	*NAT2*	1.0	-1.2	-1.2	1.0	N-acetyltransferase for N-terminal methionine (by homology)
CA2730	orf19.9663	*IPF10325*	1.0	-1.0	-1.1	1.0	YKL027W		1.0	-1.2	-1.3	-1.2	molybdopterin-converting factor by homology
CA2732	orf19.2113	*IPF10327*	-1.0	-1.1	-1.0	-1.1	YLR324W		1.0	-1.9	-1.5	-1.7	unknown function
CA2733	orf19.2112	*PRP18*	-1.0	-1.1	-1.2	-1.1	YGR006W	*PRP18*	1.0	-1.4	-1.4	-1.1	U5 snRNA-associated protein (by homology)
CA2734		*RPL38*	1.5	1.4	1.4	1.3	YLR325C	*RPL38*	1.0	1.1	1.3	1.6	ribosomal protein L38 (by homology)
CA2735	orf19.2111	*TFG2*	1.1	-1.0	-1.1	-1.0	YGR005C	*TFG2*	1.0	-1.2	-1.1	-1.2	transcription initiation factor TFIIF middle subunit (by homology)
CA2736	orf19.2110	*ATE1*	-1.1	1.1	1.2	1.2	YGL017W	*ATE1*	1.0	1.2	1.1	1.2	arginyl tRNA transferase (by homology)
CA2738		*STF2*	1.1	1.2	1.3	1.4	YLR327C		1.0	2.0	2.3	-3.6	ATP synthase regulatory factor (by homology)
CA2739	orf19.2107	*MUQ1*	1.2	1.1	1.2	1.2	YGR007W	*MUQ1*	1.0	-1.1	-1.1	-1.1	choline phosphate cytidylyltransferase (by homology)
CA2740	orf19.2106	*IPF10633*	1.1	1.0	1.1	-1.0	YLR326W		1.0	-1.5	-1.5	-1.2	unknown function
CA2741	orf19.2105	*IPF10632*	1.0	1.2	1.2	1.1	YLR323C		1.0	-1.7	-1.6	-1.4	unknown function
CA2742	orf19.2104	*JAC1*	-1.0	1.1	1.0	-1.1	YGL018C	*JAC1*	1.0	-1.1	1.2	1.1	molecular chaperone (by homology)
CA2743	orf19.2102	*CKB21*	1.0	1.1	1.2	-1.0	YGL019W	*CKB1*	1.0	-1.3	-2.0	-3.3	Casein kinase II, beta subunit (by homology)
CA2744	orf19.2101	*IPF10626*	1.1	1.0	1.1	1.1	YGL020C		1.0	-1.3	-1.1	-1.0	unknown function
CA2745	orf19.9647	*HIR1*	-1.0	1.0	1.1	1.0	YBL008W	*HIR1*	1.0	-1.2	-1.1	-1.1	Histone transcription regulator (by homology)
CA2747	orf19.2367	*IPF11467*	-1.0	1.0	1.0	1.0	YNL260C		1.0	-1.2	-1.3	-1.2	unknown function
CA2748	orf19.2368	*IPF11466*	-1.0	-1.0	-1.1	-1.1	YHR156C		1.0	-1.2	1.0	-1.1	unknown function
CA2749	orf19.2369	*IPF11465*	-1.0	-1.1	-1.0	1.1	YNL261W	*ORC5*	1.0	-2.1	-1.3	-1.2	unknown function
CA2750		*ATX1*	1.1	1.0	1.1	1.0	YNL259C	*ATX1*	1.0	1.0	-1.4	-1.3	antioxidant protein and metal homeostasis factor (by homology to S. cere
CA2751	orf19.2370	*IPF19558*	-1.2	-1.0	-1.1	-1.1	YNL258C		1.0	-1.1	-1.1	-1.3	unknown function
CA2753	orf19.13062	*IPF16806*	-1.1	-1.0	-1.1	-1.0	YPL181W		1.0	-1.2	-1.2	-1.1	unknown function
CA2754	orf19.13063	*VPS45*	-1.0	1.1	1.0	-1.1	YGL095C	*VPS45*	1.0	1.0	1.2	1.0	vacuolar protein sorting-associated protein (by homology)
CA2756	orf19.13065	*IPF18418*	-1.1	1.0	1.1	1.2	YHR029C		1.0	-1.2	-1.1	1.0	unknown function
CA2757	orf19.13066	*IPF19767*	1.0	-1.0	1.0	-1.0	YPR097W		1.0	-1.7	-1.7	-1.6	unknown function
CA2758	orf19.13067	*GLC3*	-1.2	-1.0	1.2	1.4	YEL011W	*GLC3*	1.0	1.5	2.2	-1.6	1,4-glucan branching enzyme (by homology)
CA2759	orf19.13069	*ARP4*	1.1	-1.0	1.1	1.0	YJL081C	*ARP4*	1.0	-1.4	-1.4	-1.6	actin-related protein (by homology)
CA2762	orf19.13072	*IPF15012*	1.0	1.0	-1.0	-1.0	YBL032W		1.0	1.2	1.2	1.1	pre mRNA splicing factor (by homology)
CA2763	orf19.5628	*DIC1.3*	1.0	-1.1	-1.1	1.0	YLR348C	*DIC1*	1.0	-1.0	-1.0	-1.2	dicarboxylate carrier protein, 3-prime end (by homology)
CA2764	orf19.5629	*QCR7*	1.1	-1.3	-1.3	-1.0	YDR529C	*QCR7*	1.0	-1.0	1.1	-2.6	ubiquinol--cytochrome-c reductase subunit 7 (by homology)
CA2765	orf19.13075	*APA2*	1.1	1.3	1.9	1.6	YDR530C	*APA2*	1.0	-1.2	-1.2	-1.7	ATP adenylyltransferase II (by homology)

CA2767	orf19.2682	*TOA1*	-1.1	-1.1	-1.1	-1.0	YOR194C	*TOA1*	1.0	-1.6	-1.1	-1.2	transcription initiation factor IIA (by homology)
CA2768	orf19.2684	*IPF17011*	1.0	1.0	-1.0	-1.0	YOR195W	*SLK19*	1.0	-1.3	-1.1	1.0	similar to Saccharomyces cerevisiae Slk19p involved in control of spindle
CA2770	orf19.2686	*CPS1*	1.1	-1.1	-1.1	-1.1	YJL172W	*CPS1*	1.0	-1.8	-1.9	-2.7	Carboxypeptidase YSCS precursor, second fragment (by homology)
CA2771		*RPB10*	1.1	1.1	1.2	1.1	YOR210W	*RPB10*	1.0	1.0	1.1	1.3	DNA-directed RNA polymerase II (by homology)
CA2772	orf19.2688	*IPF20112*	-1.1	-1.2	-1.4	-1.2	YPL126W	*NAN1*	1.0	1.0	1.1	1.3	unknown function
CA2773	orf19.2690	*MGM1*	-1.1	-1.2	-1.1	-1.1	YOR211C	*MGM1*	1.0	-1.2	1.1	1.1	GTPase
CA2774	orf19.274	*TFC4*	1.0	1.0	1.1	1.0	YGR047C	*TFC4*	1.0	-1.2	-1.2	-1.1	transcription factor IIIC chain TFC4- like by homology
CA2775	orf19.275	*POP5*	1.0	-1.0	1.0	1.0	YAL033W	*POP5*	1.0	-1.0	1.1	1.1	subunit of RNase P- like by homology
CA2776	orf19.276	*IPF10124*	1.0	1.0	1.0	1.0	YGR212W		1.0	-1.2	-1.4	-1.3	Alcohol acetyltransferase (by homology)
CA2777	orf19.277	*THI6*	1.0	1.1	1.0	1.1	YPL214C	*THI6*	1.0	-1.4	-1.0	1.2	thiamin-phosphate pyrophosphorylase and hydroxyethylthiazole kinase-li
CA2779	orf19.279	*IPF3836*	1.1	-1.1	-1.2	-1.1	YDL219W		1.0	1.1	-1.0	-1.0	unknown function
CA2782	orf19.285	*IPF3806*	1.0	1.6	2.1	2.0	YNL157W		1.0	1.2	1.2	1.2	unknown function
CA2783	orf19.286	*IPF3808*	-1.0	-1.0	-1.0	1.0	YLL042C	*APG10*	1.0	-1.7	-2.1	-2.4	unknown function
CA2785	orf19.288	*MET13*	-1.0	-1.0	1.0	-1.0	YGL125W	*MET13*	1.0	1.2	1.3	1.1	Methylene tetrahydrofolate reductase (by homology)
CA2786	orf19.290	*KRE5.3EOC*	-1.1	-1.0	-1.1	-1.0	YOR336W	*KRE5*	1.0	-1.1	-1.2	-1.2	UDP-glucose:glycoprotein glucosyltransferase, 3-prime end (by homolog
CA2787	orf19.8243	*EFG1*	1.1	1.1	1.1	1.0	YMR016C	*SOK2*	1.0	1.1	1.3	1.2	Enhanced filamentous growth factor
CA2788	orf19.8240	*RAD26*	1.1	-1.0	-1.2	-1.1	YJR035W	*RAD26*	1.0	-1.8	-2.0	-2.6	DNA repair and recombination protein (by homology)
CA2789	orf19.606	*IPF3567*	-1.0	-1.1	-1.2	-1.0	YLR352W		1.0	-1.5	-1.7	-2.0	unknown function
CA2791	orf19.603	*IMP4*	1.0	1.0	1.0	1.0	YNL075W	*IMP4*	1.0	1.5	1.5	2.0	Ribonucleoprotein (by homology)
CA2793	orf19.8233	*TRK1.5F*	1.0	1.1	1.1	-1.0	YKR050W	*TRK2*	1.0	-1.4	-1.1	-1.0	Potassium transporter, 5-prime end
CA2795	orf19.1723	*IPF8407*	-1.0	1.2	1.2	1.1	YJL055W		1.0	1.2	1.2	1.3	unknown function
CA2796	orf19.1721	*IPF8405*	1.3	-1.4	-1.4	-1.4	YNL036W	*NCE103*	1.0	2.3	1.0	-1.3	similar to Saccharomyces cerevisiae Nce103p involved in non-classical p
CA2797	orf19.1720	*IPF8404*	1.0	1.0	-1.0	1.0	YFR038W		1.0	-2.3	-1.8	-1.7	putative helicase (by homology)
CA2798	orf19.1719	*IPF8402*	-1.3	-1.4	-1.4	-1.2	YIL099W	*SGA1*	1.0	-1.5	-1.6	-1.6	similar to Saccharomyces cerevisiae Sga1p glucan 1,4-alpha-glucosidas
CA2801	orf19.1716	*URA3*	1.0	1.0	1.0	1.0	YEL021W	*URA3*	1.0	-1.3	-1.4	-1.1	orotidine-5 -monophosphate decarboxylase [Candida albicans]
CA2803	orf19.5776	*IPF11711*	-1.1	1.3	1.3	1.3	YDR457W	*TOM1*	1.0	1.2	1.1	1.1	ubiquitin-protein ligase (by homology)
CA2804	orf19.5777	*IPF19961*	1.1	1.3	1.2	1.1	YBR096W		1.0	-1.0	1.1	1.0	unknown function
CA2805	orf19.5779	*RNR1*	1.1	1.6	2.0	1.5	YER070W	*RNR1*	1.0	-2.2	-1.2	1.2	ribonucleoside-diphosphate reductase (by homology)
CA2806	orf19.5780	*IPF11702*	1.0	-1.0	1.1	1.1	YIL067C		1.0	-1.1	-1.2	-1.2	unknown function
CA2807	orf19.5782	*IPF11965*	-1.2	1.3	1.1	1.1	YOR022C		1.0	1.1	1.1	1.4	unknown function
CA2808	orf19.5783	*IPF11966*	1.3	1.1	1.1	1.1	YOR021C		1.0	-1.2	-1.0	1.1	unknown function
CA2810	orf19.5788	*EFT2*	-1.1	-1.0	-1.2	-1.2	YOR133W	*EFT1*	1.0	1.2	2.5	3.6	translation elongation factor 2
CA2811	orf19.10520	*RPS10*	-1.2	-1.3	-1.4	-1.2	YML063W	*RPS1B*	1.0	1.7	1.8	3.0	Ribosomal protein 10
CA2812	orf19.10519	*TEM1*	1.0	1.0	1.1	1.1	YML064C	*TEM1*	1.0	-1.1	1.7	1.2	GTP-binding protein of the RAS superfamily
CA2813	orf19.10518	*ORC1*	-1.1	-1.2	-1.6	-1.3	YML065W	*ORC1*	1.0	-1.2	-1.1	-1.2	Origin recognition complex protein 1
CA2814	orf19.2998	*IPF5607*	1.1	-1.0	-1.0	1.0	YLR435W		1.0	1.2	1.2	1.4	unknown function
CA2815	orf19.2996	*IPF5604*	-1.0	1.0	-1.0	1.0	YLR436C	*ECM30*	1.0	-1.6	-1.3	-1.8	unknown function
CA2816	orf19.2995	*IPF5601*	-1.1	-1.0	-1.1	-1.0	YKL183W	*LOT5*	1.0	-1.5	-1.5	-1.4	unknown function
CA2817		*RPS16.3*	1.2	1.1	1.1	1.1	YMR143W	*RPS16A*					ribosomal protein, 3-prime end
CA2818	orf19.2994	*RPL13*	1.3	-1.1	-1.2	1.0	YDL082W	*RPL13A*	1.0	1.4	1.6	1.8	Ribosomal protein
CA2819	orf19.2992	*RPA1*	-1.0	1.0	-1.0	1.0	YDL081C	*RPP1A*	1.0	2.4	2.7	2.7	60S ribosomal protein
CA2823	orf19.1317	*IPF14554*	-1.3	-1.5	-1.8	-1.6	YHR073W	*OSH3*	1.0	1.2	1.3	1.2	similar to Saccharomyces cerevisiae Osh3p oxysterol-binding protein (by
CA2824	orf19.1318	*IPF17888*	-1.0	-1.3	-1.3	-1.2	YOR385W		1.0	-1.1	1.2	-1.1	unknown function
CA2826	orf19.1323	*APL6*	-1.0	1.0	1.1	1.0	YGR261C	*APL6*	1.0	1.1	1.0	1.1	AP-3 complex subunit, beta3-adaptin (by homology)
CA2827	orf19.1324	*RAD2*	-1.0	-1.1	-1.3	-1.2	YGR258C	*RAD2*	1.0	-1.3	-1.3	-1.2	structure-specific nuclease of the nucleotide excision repairos
CA2833	orf19.4785	*PTC1*	1.0	1.5	1.9	1.3	YDL006W	*PTC1*	1.0	1.1	1.2	1.3	protein serine/threonine phosphatase 2c (by homology)
CA2836	orf19.4788	*ARG5,6*	1.0	1.1	1.2	1.1	YER069W	*ARG5,6*	1.0	-1.1	-1.1	1.5	acetylglutamate kinase and acetylglutamyl-phosphate reductase
CA2845	orf19.5730	*IPF10782*	-1.1	1.1	1.2	1.0	YDR539W		1.0	1.1	1.1	1.5	unknown function
CA2846	orf19.5731	*PAD1*	1.0	-1.0	-1.0	1.0	YDR538W	*PAD1*	1.0	1.3	1.2	1.2	phenylacrylic acid decarboxylase (by homology)
CA2847	orf19.5732	*F10785.EXON*	-1.1	-1.3	-1.3	-1.2	YNR053C		1.0	1.3	1.6	2.5	unknown function, exon 1
CA2849	orf19.5734	*POP2*	-1.0	1.0	1.0	1.0	YNR052C	*POP2*	1.0	1.1	1.3	1.6	required for glucose derepression (by homology)
CA2850	orf19.5735	*CDC50*	-1.0	-1.0	-1.0	1.0	YCR094W	*CDC50*	1.0	-1.4	-1.7	-1.5	cell division cycle mutant (by homology)
CA2853	orf19.1070	*IPF17057*	1.3	1.6	1.8	1.9	YMR010W		1.0	-1.2	-1.1	1.2	unknown function
CA2854	orf19.1069	*RPN4*	1.0	1.3	1.4	1.2	YDL020C	*RPN4*	1.0	-1.1	1.1	1.0	26S proteasome subunit (by homology)
CA2856	orf19.1066	*IPF7062*	-1.0	-1.0	1.0	-1.0	YPL067C		1.0	-1.2	-1.0	1.2	unknown function
CA2858	orf19.1064	*ACS2*	-1.2	-1.8	-1.7	-1.8	YLR153C	*ACS2*	1.0	-2.8	-2.6	-2.1	acetyl-coenzyme-A synthetase (by homology)
CA2859	orf19.1063	*IPF7056*	1.1	1.3	1.9	1.3	YBR004C		1.0	-1.1	-1.1	1.1	unknown function
CA2861	orf19.1061	*HHT21*	1.4	1.4	1.5	1.5	YNL031C	*HHT2*	1.0	2.3	2.3	2.0	Histone H3
CA2862	orf19.1059	*HHF21*	1.2	1.2	1.2	1.4	YNL030W	*HHF2*	1.0	1.5	1.5	1.1	histone H4
CA2863	orf19.1058	*IPF20117*	1.0	1.0	1.0	1.0	YLR421C	*RPN13*	1.0	-1.2	-1.0	-1.1	unknown function
CA2866	orf19.2843	*RHO1*	1.2	1.1	1.4	1.2	YPR165W	*RHO1*	1.0	1.5	1.6	1.6	GTP-binding protein of the rho subfamily of ras-like proteins (by homolog

CA2867	orf19.2844	*IPF11688*	-1.1	1.2	1.1	1.1	YPR029C	*APL4*	1.0	1.0	1.1	1.1	similar to Saccharomyces cerevisiae Apl4p AP-1 complex subunit, gamm
CA2869	orf19.2847	*RPC82*	-1.0	-1.1	-1.2	-1.1	YPR190C	*RPC82*	1.0	-1.7	-1.2	-1.1	DNA-directed RNA polymerase III, 82 KD subunit (by homology)
CA2872	orf19.2848	*APG13*	-1.0	1.0	1.0	1.0	YPR185W	*APG13*	1.0	1.1	1.2	1.1	probable component of the autophagic system (by homology)
CA2873	orf19.2849	*AQY1*	1.0	1.1	1.3	1.1	YPR192W	*AQY1*	1.0	-1.1	-1.1	-1.3	similarity to plasma membrane and water channel proteins (aquaporin-lik
CA2875	orf19.5844	*MEI5*	1.0	1.0	1.1	-1.0	YPL121C	*MEI5*	1.0	-1.4	-1.3	-1.5	meiotic protein (by homology)
CA2877	orf19.5846	*TFB2*	-1.0	1.1	1.1	1.1	YPL122C	*TFB2*	1.0	1.2	1.2	1.3	Transcription/repair factor (by homology)
CA2878	orf19.5847	*RET1*	1.0	1.0	1.0	-1.0	YOR207C	*RET1*	1.0	-2.7	-2.6	-2.3	DNA-directed RNA polymerase III (by homology)
CA2880	orf19.5849	*IPF3781*	-1.1	-1.0	1.0	-1.0	YPL133C		1.0	-1.3	-1.3	-1.3	unknown function
CA2881	orf19.5850	*RAD4*	-1.1	-1.2	-1.3	-1.3	YOR206W	*NOC2*	1.0	-1.4	1.2	1.6	Excision repair protein (by homology)
CA2882	orf19.5851	*STE13*	-1.0	-1.1	-1.1	1.0	YOR219C	*STE13*	1.0	-1.7	-1.3	-1.4	type IV dipeptidyl aminopeptidase (by homology)
CA2884	orf19.2476	*IPF7201*	-1.4	-1.2	-1.9	-1.4	YMR176W	*ECM5*	1.0	-1.1	-1.1	-1.3	similar to Saccharomyces cerevisiae Ecm5p involved in cell wall biogene
CA2886	orf19.2473	*IPF7207*	-1.1	-1.0	-1.0	-1.0	YML127W	*RSC9*	1.0	-1.1	1.3	1.5	unknown function
CA2888	orf19.2471	*GIM5*	1.1	1.2	1.2	1.2	YML094W	*GIM5*					Gim complex component (by homology)
CA2889	orf19.2469	*IPF13628*	-1.0	-1.0	-1.1	-1.1	YML095C	*RAD10*	1.0	-1.5	-1.7	-1.9	putative DNA repair protein (by homology)
CA2890	orf19.2468	*IPF13626*	1.1	-1.0	1.0	-1.0	YER175C	*TMT1*	1.0	1.3	1.5	1.2	Putative methyltransferase (by homology)
CA2896	orf19.3483	*IPF14981*	-1.2	-1.4	-1.5	-1.2	YPL206C		1.0	1.0	-1.1	-1.2	unknown function
CA2897	orf19.3482	*IPF14979*	-1.2	-1.0	-1.0	1.1	YGL067W	*NPY1*	1.0	-1.6	-1.4	-1.3	similar to Saccharomyces cerevisiae Npy1p NADH pyrophosphatase (by
CA2898	orf19.3481	*IPF15646*	1.0	1.0	1.1	1.0	YGL064C		1.0	1.2	-1.0	1.0	putative ATP-dependent RNA helicase (by homology)
CA2899	orf19.3480	*IPF17681*	-1.3	-1.5	-1.7	-1.5	YGL129C	*RSM23*	1.0	-1.1	-1.1	1.2	similar to Saccharomyces cerevisiae Rsm23p involved in mitochondrial fu
CA2900	orf19.3478	*NIP7*	1.2	1.1	1.0	1.0	YPL211W	*NIP7*	1.0	1.1	-1.1	1.1	required for efficient 60S ribosome subunit biogenesis (by homology)
CA2901	orf19.3477	*PUS1*	1.1	-1.1	-1.0	-1.0	YPL212C	*PUS1*	1.0	-1.6	-1.5	-1.3	pseudouridine synthase 1 (by homology)
CA2902	orf19.3476	*HRR25*	1.1	1.0	1.1	1.1	YPL204W	*HRR25*	1.0	-1.2	-1.2	-1.2	casein kinase I (by homology)
CA2904	orf19.3474	*IPL1*	-1.1	-1.0	-1.1	1.2	YPL209C	*IPL1*	1.0	-1.1	-1.5	-1.7	Ser/thr protein kinase (by homology)
CA2905	orf19.10977	*IPF12049*	-1.2	-1.1	-1.1	-1.1	YGL066W		1.0	-1.2	-1.2	-1.2	unknown function
CA2906	orf19.4521	*IPF15523*	1.2	1.3	1.7	1.8	YOR246C		1.0	-1.0	-1.1	1.0	unknown function
CA2907	orf19.4520	*IPF15525*	1.0	-1.0	-1.1	-1.1	YDR248C						putative gluconokinase (by homology)
CA2908	orf19.4519	*SUV3*	-1.1	-1.1	-1.0	-1.0	YPL029W	*SUV3*	1.0	-1.1	-1.3	-1.1	ATP-dependent RNA helicase, mitochondrial (by homology)
CA2909	orf19.4518	*IPF11424*	-1.1	-1.1	-1.1	1.1	YPL150W		1.0	-1.3	-1.4	-1.4	unknown function
CA2911	orf19.4516	*MET7*	-1.1	-1.1	-1.1	-1.1	YOR241W	*MET7*	1.0	1.0	-1.0	1.1	folylpolyglutamate synthetase [Candida albicans]
CA2924	orf19.11687	*FET33*	1.0	-1.1	-1.0	-1.1	YMR058W	*FET3*	1.0	-1.7	-1.9	-1.7	cell surface ferroxidase (by homology)
CA2925	orf19.4210	*IPF7827*	1.0	-1.0	1.0	-1.1	YGR110W		1.0	-1.1	-1.4	-1.9	unknown function
CA2926	orf19.4209	*UBA3*	1.1	-1.0	1.0	-1.1	YPR066W	*UBA3*	1.0	-1.1	1.3	1.4	Ubiquitin-like protein activating enzyme
CA2927	orf19.4208	*RAD52*	1.0	-1.0	1.0	-1.0	YML032C	*RAD52*	1.0	-1.1	-1.1	-1.1	Nuclear ribonucleoprotein E
CA2928		*SME1*	1.0	1.1	-1.0	1.0	YOR159C	*SME1*	1.0	1.3	1.1	1.2	Nuclear ribonucleoprotein E
CA2929	orf19.4206	*IPF7838*	1.0	1.0	1.1	1.0	YDR386W	*MUS81*	1.0	-1.4	-1.4	-1.4	similar to Saccharomyces cerevisiae Mus81p involved in DNA repair, inte
CA2930	orf19.4204	*IPF7840*	1.0	-1.1	-1.1	-1.0	YOR158W	*PET123*	1.0	-1.3	-1.2	-1.3	similar to Saccharomyces cerevisiae Pet123p ribosomal protein, mitocho
CA2931	orf19.4203	*IPF7841*	-1.1	1.2	1.1	1.2	YML031W	*NDC1*	1.0	-1.6	-1.4	-1.3	similar to Saccharomyces cerevisiae Ndc1p nuclear envelope protein (by
CA2932	orf19.11677	*NHX1*	1.2	1.5	1.5	1.5	YDR456W	*NHX1*	1.0	-1.0	1.1	-1.0	NA+-H+ antiporter
CA2934	orf19.3329	*IPF11515*	1.0	-1.0	-1.0	1.0	YJL134W	*LCB3*	1.0	-2.3	-1.2	-1.4	similar to Saccharomyces cerevisiae Lcb3p sphingoid base-phosphate pl
CA2935	orf19.3328	*IPF11521*	1.0	-1.2	-1.2	-1.0	YMR172W	*HOT1*	1.0	-1.1	-1.1	-1.0	unknown function
CA2936	orf19.3327	*IPF8326*	1.0	-1.0	1.0	-1.0	YKR056W	*RNC1*	1.0	-1.2	-1.2	-1.1	similar to Saccharomyces cerevisiae Rnc1p endo-exonuclease (by homo
CA2937		*RPS21B.3*	1.9	1.3	1.4	1.4	YJL136C	*RPS21B*	1.0	2.4	2.4	2.5	ribosomal protein S21, 3-prime end
CA2938	orf19.3325	*IPF8321*	-1.0	2.4	3.1	3.0	YJL137C	*GLG2*	1.0	-1.5	-1.6	-1.6	similar to Saccharomyces cerevisiae Glg2p self-glucosylating initiator of g
CA2939	orf19.3324	*TIF1*	1.2	1.2	1.4	1.3	YKR059W	*TIF1*	1.0	1.2	1.7	2.4	translation initiation factor
CA2945	orf19.1967	*IMG1*	1.1	1.1	1.0	-1.0	YCR046C	*IMG1*	1.0	-1.5	-1.5	-1.3	Ribosomal protein, mitochondrial (by homology)
CA2946	orf19.1966	*IPF6296*	1.0	1.1	1.0	1.0	YCR047C	*BUD23*	1.0	1.2	1.3	1.6	putative methyltransferase (by homology)
CA2948	orf19.1963	*GDS1*	-1.1	-1.1	-1.1	-1.0	YOR355W	*GDS1*	1.0	1.0	1.7	1.3	nam9-1 suppressor (by homology)
CA2950	orf19.9515	*CLN2*	1.1	-1.1	1.0	1.0	YAL040C	*CLN3*	1.0	1.2	1.2	1.5	G1/S-SPECIFIC CYCLIN CLN2
CA2951	orf19.5854	*SBP1*	-1.0	1.1	1.2	1.2	YHL034C	*SBP1*	1.0	1.3	1.3	-1.0	RNA binding protein-like (by homology)
CA2953	orf19.5855	*MBP1*	-1.1	-1.1	-1.1	-1.0	YDL056W	*MBP1*	1.0	-1.3	-1.6	-1.8	transcription factor (by homologgy)
CA2956	orf19.5858	*EGD2*	1.2	1.1	-1.0	-1.0	YHR193C	*EGD2*	1.0	1.1	1.4	1.6	Nascent polypeptide associated complex protein alpha subunit (by homo
CA2958	orf19.5861	*KRE9*	1.0	1.1	1.3	1.2	YJL174W	*KRE9*	1.0	1.3	1.2	1.4	cell wall synthesis protein
CA2961	orf19.5864	*URK1*	1.0	1.1	1.1	-1.0	YNR012W	*URK1*	1.0	1.0	1.2	1.3	uridine kinase (by homology)
CA2962	orf19.5865	*PRP2*	-1.1	-1.1	-1.1	-1.1	YNR011C	*PRP2*	1.0	-1.2	-1.2	-1.1	RNA-dependent ATPase (by homology)
CA2963	orf19.5611	*GRP3*	1.0	-1.0	1.0	1.0	YOL151W	*GRE2*	1.0	1.1	1.0	-1.2	dihydroflavonol-4-reductases (by homology)
CA2964	orf19.5610	*IPF13176.3*	1.1	1.0	1.0	1.1	YJL088W	*ARG3*	1.0	-1.0	1.1	1.3	ornithine carbamoyltransferase, 3-prime end (by homology)
CA2966	orf19.5608	*RPC34*	1.1	1.0	-1.0	-1.0	YNR003C	*RPC34*	1.0	-1.2	-1.1	1.1	DNA-directed RNA polymerase III (by homology)
CA2967	orf19.5605	*IPF12513*	-1.0	-1.1	-1.2	-1.0	YJL084C		1.0	-1.1	-1.2	1.0	unknown function
CA2968	orf19.5604	*BMR1*	1.0	1.1	1.0	1.0	YBR008C	*FLR1*	1.0	-1.1	-1.1	-1.1	benomyl/methothrexate resistance protein (by homology)
CA2975	orf19.8822	*ARO9*	1.0	1.1	1.1	1.0	YHR137W	*ARO9*	1.0	-1.3	-1.3	-1.5	aromatic amino acid aminotransferase II(by homology)
CA2976	orf19.8821	*IPF14676*	-1.2	-1.2	-1.1	-1.0	YIL041W		1.0	1.6	1.6	2.5	unknown function

CA2977	orf19.1235	*HOM3*	-1.1	1.0	1.2	1.1	YER052C	*HOM3*	1.0	-1.2	1.4	2.4	Aspartokinase (by homology)
CA2979	orf19.1233	*ADE4*	-1.3	-1.3	-1.2	-1.1	YMR300C	*ADE4*	1.0	1.1	1.1	2.4	amidophosphoribosyltransferase (by homology)
CA2980	orf19.1232	*GOG5*	1.1	1.1	1.4	1.3	YGL225W	*GOG5*	1.0	1.1	-1.0	1.5	GDP-mannose transporter (by homology)
CA2981	orf19.1231	*CSE1.5F*	-1.4	-1.2	-1.3	-1.1	YGL238W	*CSE1*	1.0	-1.2	-1.4	-1.2	Importin-beta-like protein, 5-prime end (by homology)
CA2985	orf19.6009	*SET1*	-1.1	-1.1	-1.4	-1.2	YHR119W	*SET1*	1.0	-1.3	-1.2	-1.3	Chromatin regulatory protein (by homology)
CA2986	orf19.6010	*CDC5*	-1.0	1.1	1.0	-1.0	YMR001C	*CDC5*	1.0	1.1	1.2	1.1	Cell-cycle protein kinase (by homology)
CA2987		*RPB11.3*	1.0	-1.0	1.0	-1.0	YOL005C	*RPB11*	1.0	1.0	-1.1	1.2	DNA-directed RNA polymerase II subunit, 3-prime end (by homology)
CA2989	orf19.6011	*SIN3.EXON3*	-1.2	1.0	-1.1	1.0	YOL004W	*SIN3*	1.0	-1.3	-1.1	-1.0	Histone deacetylase by homology
CA2990	orf19.6012	*IPF5092*	-1.1	-1.1	-1.2	-1.1	YOR296W		1.0	-1.7	1.0	1.1	unknown function
CA2991	orf19.6013	*IPF5088.3*	1.0	1.0	1.0	-1.1	YMR233W		1.0	-1.6	-1.5	-1.6	unknown function, 3-prime end
CA2992	orf19.6014	*RRS1*	1.0	1.1	1.0	1.1	YOR294W	*RRS1*	1.0	-1.2	1.0	1.3	Regulator for ribosome synthesis (by homology)
CA2993	orf19.6118	*IPF9118*	1.0	-1.0	-1.0	-1.0	YPR017C	*DSS4*	1.0	-1.2	-1.4	-1.3	unknown function
CA2995	orf19.6121	*IPF9113*	1.0	1.1	1.1	1.0	YER130C		1.0	1.1	-1.1	2.0	unknown function
CA2996	orf19.6124	*IPF9108*	1.1	1.0	1.2	-1.1	YLR131C	*ACE2*	1.0	-1.4	-1.3	-1.0	similar to Saccharomyces cerevisiae Ace2p transcription factor (by homo
CA2997	orf19.6126	*KGD2*	-1.4	-2.7	-3.2	-2.6	YDR148C	*KGD2*	1.0	-1.9	-1.6	-2.7	2-oxoglutarate dehydrogenase complex E2 component (by homology)
CA2998	orf19.6127	*LPD1*	-1.3	-1.9	-2.6	-2.0	YFL018C	*LPD1*	1.0	-1.9	-2.1	-2.1	dihydrolipoamide dehydrogenase (by homology)
CA2999	orf19.6129	*MRPL8*	1.0	1.2	1.2	1.1	YJL063C	*MRPL8*	1.0	1.0	1.3	1.2	mitochondrial 60s ribosomal subunit (by homology)
CA3000	orf19.6131	*TSC1.5*	1.1	1.1	1.1	1.1	YBR265W	*TSC10*	1.0	1.1	-1.0	1.2	3-ketosphinganine reductase, 5-prime end (by homology)
CA3001	orf19.6132	*IPF8841*	1.4	1.2	1.3	1.1	YBR262C		1.0	-2.6	-2.3	-2.0	unknown function
CA3002	orf19.6133	*PIF1*	-1.0	-1.1	-1.1	-1.1	YML061C	*PIF1*	1.0	-1.6	-1.7	-1.6	mitochondrial DNA helicase (by homology)
CA3003	orf19.13620	*IPF15741*	-1.2	1.0	-1.0	-1.0	YDL117W	*CYK3*	1.0	-1.1	1.2	1.3	similar to Saccharomyces cerevisiae Cyk3p possibly involved in cytokine
CA3004	orf19.13619	*KIN28*	1.0	1.1	1.0	-1.1	YDL108W	*KIN28*	1.0	1.2	1.3	1.2	cyclin-dependent ser/thr protein kinase (by homology)
CA3006	orf19.13616	*IPF12152*	1.1	-1.0	1.0	-1.0	YDL213C	*FYV14*	1.0	1.1	1.6	2.3	Unknown function
CA3007	orf19.13614	*IPF12148*	-1.1	-1.3	-1.2	-1.2	YNL182C		1.0	1.1	1.3	1.8	Unknown function
CA3008	orf19.13613	*IPF12147*	-1.1	-1.2	-1.0	-1.2	YNL181W		1.0	-1.1	1.2	1.2	unknown function
CA3009	orf19.13611	*MRPL19*	-1.0	-1.0	-1.1	-1.1	YNL185C	*MRPL19*	1.0	-1.2	1.0	-1.1	Ribosomal protein (by homology)
CA3010	orf19.13610	*IPF14568*	1.1	-1.1	-1.0	-1.1	YGL246C	*RAI1*	1.0	-1.3	-1.1	1.0	unknown function
CA3011	orf19.6229	*CTA1*	1.0	-9.1	-7.2	-8.5	YDR256C	*CTA1*	1.0	-1.3	-1.1	1.0	catalase A, peroxisomal(by homology)
CA3013		*PET117*	1.0	1.0	1.1	1.1	YER058W	*PET117*	1.0	1.2	-1.1	-1.2	cytochrome c oxidase assembly factor (by homology)
CA3014	orf19.13605	*IPF11915*	1.1	1.4	1.4	1.2	YIL050W	*PCL7*	1.0	1.0	1.2	-1.0	similar to Saccharomyces cerevisiae Pcl7p cyclin like protein interacting
CA3015	orf19.11397	*IPF10029*	-1.4	-1.8	-1.8	-1.6	YFR044C		1.0	1.1	1.1	-1.1	unknown function
CA3017	orf19.11393	*IPF10021*	-1.3	-2.0	-2.3	-1.9	YER040W	*GLN3*	1.0	-2.1	-1.9	-1.5	unknown function
CA3018	orf19.3911	*SAH1*	1.4	1.1	1.2	1.2	YER043C	*SAH1*	1.0	-1.1	1.4	1.8	S-adenosyl-L-homocysteine hydrolase by homology
CA3027	orf19.11381	*IPF20126*	-1.0	-1.0	1.1	-1.0	YDR470C	*UGO1*	1.0	-1.9	-1.8	-1.7	putative chromosome segregation protein (by homology)
CA3029	orf19.223	*IPF13825*	-1.3	1.0	-1.1	-1.0	YNR047W		1.0	-1.3	-1.2	-1.3	similarity to serine/threonine protein kinases (by homology)
CA3030	orf19.220	*IPF19968*	1.1	2.1	2.5	2.4	YKL164C	*PIR1*	1.0	1.1	1.2	1.1	putative cell wall protein of the PIR family
CA3031	orf19.217	*IPF12324*	1.0	1.0	-1.1	-1.0	YPR013C		1.0	-1.1	1.0	1.1	unknown function
CA3033	orf19.215	*IPF13202*	-1.1	-1.1	-1.2	-1.2	YMR068W		1.0	-1.3	1.1	-1.2	unknown function
CA3034	orf19.213	*RPN12*	1.2	1.3	1.5	1.7	YFR052W	*RPN12*	1.0	-1.4	1.1	1.2	26S proteasome regulatory subunit (by homology)
CA3035	orf19.212	*VPS28*	1.0	1.2	1.3	1.2	YPL065W	*VPS28*	1.0	1.2	1.3	1.4	involved in vacuolar traffic (by homology)
CA3037	orf19.210	*IPF13442*	-1.0	1.0	1.1	1.1	YPL066W		1.0	-1.1	1.2	1.2	unknown function
CA3038	orf19.209	*IPF13438*	1.1	1.1	1.2	1.0	YIL049W	*DFG10*	1.0	1.1	1.2	1.1	unknown function
CA3040	orf19.2425	*IPF7306*	1.0	1.1	1.1	1.0	YBR241C		1.0	-1.1	-1.3	-1.4	putative permease (by homology)
CA3041	orf19.2423	*IPF7303*	-1.0	1.0	-1.1	1.0	YBR239C		1.0	-1.0	1.2	1.3	unknown function
CA3042	orf19.2422	*ARC1*	-1.1	-1.4	-1.6	-1.3	YGL105W	*ARC1*	1.0	1.1	1.6	1.6	G4 nucleic acid binding protein (by homology)
CA3043	orf19.2419	*DOM34*	-1.0	-1.0	-1.1	1.0	YNL001W	*DOM34*	1.0	-1.2	1.3	1.4	probable involvement in meiotic and mitotic divisions (by homolog
CA3045		*IPF7297.3*	1.2	1.0	1.1	1.1	YGL106W	*MLC1*	1.0	1.2	1.1	-1.1	similar to Saccharomyces cerevisiae Mlc1p myosin ((Myo2p) light chain,
CA3046	orf19.2417	*IPF7295*	-1.2	-1.2	-1.4	-1.2	YOL034W		1.0	-1.0	-1.1	-1.1	unknown function
CA3047	orf19.9953	*MSE1*	-1.0	-1.0	-1.1	-1.0	YOL033W	*MSE1*	1.0	-1.2	-1.1	-1.3	Mitochondrial glutamyl-tRNA synthetase (by homology)
CA3048	orf19.9950	*IPF14991*	1.1	1.0	1.1	1.0	YJR044C		1.0	-1.2	-1.1	-1.3	unknown function
CA3049	orf19.9949	*IPF14990*	1.1	1.1	1.0	1.0	YAL014C		1.0	1.2	1.3	1.3	unknown function
CA3050	orf19.9948	*IPF13042*	-1.1	-1.1	-1.1	-1.0	YLR309C	*IMH1*	1.0	-1.1	1.1	-1.1	similar to Saccharomyces cerevisiaeImh1p involved in vesicular transpor
CA3051	orf19.2408	*IPF13043*	1.0	-1.0	1.1	1.1	YGL050W		1.0	-1.0	-1.0	1.1	unknown function
CA3052	orf19.9945	*DPS1*	-1.3	-1.2	-1.2	-1.2	YLL018C	*DPS1*	1.0	1.1	1.7	1.8	aspartyl-tRNA synthetase (by homology)
CA3053	orf19.9944	*GTR2*	-1.0	1.0	1.1	1.0	YGR163W	*GTR2*	1.0	-1.1	-1.1	-1.1	GTP-binding protein (by homology)
CA3055	orf19.11771	*HIR2*	-1.2	-1.1	-1.1	-1.1	YOR038C	*HIR2*	1.0	-1.6	-1.7	-1.6	Histone transcription regulator (by homology)
CA3056	orf19.4294	*IPF2953*	-1.1	-1.1	-1.1	-1.1	YOR037W	*CYC2*	1.0	-1.2	-1.0	-1.0	similar to Saccharomyces cerevisiae Cyc2p cytochrome-c mitochondrial
CA3057	orf19.4293	*IPF2954*	-1.0	-1.1	-1.0	-1.1	YDR267C		1.0	-1.0	1.2	1.1	unknown function
CA3059	orf19.11766	*TRR1*	-1.0	1.2	1.1	1.2	YDR353W	*TRR1*	1.0	-1.8	1.2	1.2	Thioredoxin reductase (by homology)
CA3063	orf19.4284	*IPF2971*	-1.1	-1.1	-1.1	-1.0	YLR226W	*BUR2*	1.0	-1.1	-1.3	-1.0	unknown function
CA3066	orf19.4281	*IPF15813*	-1.0	-1.2	1.0	-1.0	YLR223C	*IFH1*	1.0	-1.5	-1.2	1.1	unknown function

CA3069	orf19.4805	*IPF6117*	-1.0	1.1	1.2	1.1	YMR266W	*RSN1*	1.0	-1.3	-1.6	-1.6	unknown function
CA3070	orf19.4807	*PPA2*	-1.1	-1.2	-1.2	-1.2	YMR267W	*PPA2*	1.0	1.0	-1.2	-1.3	Mitochondrial inorganic pyrophosphatase
CA3071	orf19.4808	*NUP188*	1.0	1.0	1.1	-1.0	YML103C	*NUP188*	1.0	-2.1	-2.1	-2.1	Nucleoporin
CA3072	orf19.4809	*ERG12*	-1.0	1.2	1.2	1.1	YMR208W	*ERG12*	1.0	1.4	1.6	1.9	Mevalonate kinase (by homology)
CA3073	orf19.4811	*IPF6108*	-1.1	-1.2	-1.2	-1.2	YOR271C		1.0	-1.3	1.2	1.9	putative tricarboxylate carrier (by homology)
CA3075	orf19.4813	*IPF6105*	1.1	1.2	1.6	1.2	YMR217W	*GUA1*	1.0	1.9	3.2	4.6	similar to Saccharomyces cerevisiae Gua1p GMP synthase (glutamine-h
CA3078	orf19.4816	*IPF19970*	1.1	1.1	1.2	1.1	YMR209C		1.0	-2.1	-1.9	-1.6	unknown function
CA3079	orf19.4817	*RAM2*	1.0	-1.0	1.0	1.0	YKL019W	*RAM2*	1.0	-1.2	-1.0	-1.1	geranylgeranyltransferase type I alpha subunit
CA3080	orf19.4153	*IPF14634*	-1.0	-1.0	-1.1	-1.0	YPL003W	*ULA1*	1.0	1.1	-1.0	-1.1	APP-binding protein 1 (by homology)
CA3081	orf19.11629	*EFT3*	-1.1	1.1	-1.1	-1.1	YNL014W	*HEF3*	1.0	-1.0	1.9	1.2	translation elongation factor 3
CA3083	orf19.11626	*IPF11262*	-1.0	-1.1	-1.1	-1.0	YDL010W		1.0	-1.1	-1.2	-1.1	unknown function
CA3086	orf19.11623	*GLR1*	-1.2	-1.0	1.0	-1.0	YPL091W	*GLR1*	1.0	1.2	1.5	1.4	by similarity to S. cerev. and C. albicans:glutathione reductase
CA3087	orf19.11622	*SMD3*	1.0	-1.0	1.0	1.1	YLR147C	*SMD3*	1.0	1.2	1.3	1.7	core snRNP protein (by homology)
CA3088	orf19.11621	*IPF9826*	-1.2	-1.1	1.1	1.1	YLR256W	*HAP1*	1.0	-1.4	-1.4	-1.1	unknown function
CA3089		*IPF9825*	-1.0	1.1	1.1	1.1	YLR253W		1.0	-1.1	1.0	1.1	unknown function
CA3090	orf19.11619	*IPF18385*	-1.0	-1.1	-1.1	1.0	YLR068W	*FYV7*	1.0	-1.5	-1.2	1.1	unknown function
CA3092	orf19.11617	*IPF9821.3F*	1.0	-1.1	-1.1	-1.1	YEL064C		1.0	1.0	-1.0	1.1	unknown function, 3-prime end
CA3093	orf19.11613	*TOF1*	-1.1	-1.0	-1.1	-1.0	YNL273W	*TOF1*	1.0	1.0	-1.0	1.1	Topoisomerase I interacting factor 1 (by homology)
CA3094	orf19.11335	*IPF11548*	-1.3	-1.2	-1.1	-1.1	YCR008W	*SAT4*	1.0	1.0	1.2	1.1	serine/threonine protein kinase (by homology)
CA3095	orf19.3856	*CDC28*	-1.1	1.0	1.1	1.1	YBR160W	*CDC28*	1.0	1.2	1.3	1.2	CELL DIVISION CONTROL PROTEIN 28 -protein kinase
CA3097	orf19.3859	*IPF6600*	1.1	1.4	1.4	1.3	YBR159W		1.0	-1.1	-1.1	1.0	unknown function
CA3098	orf19.3861	*SIS1*	-1.1	1.0	-1.1	1.0	YNL007C	*SIS1*	1.0	1.3	1.2	1.9	heat shock protein (by homology)
CA3099	orf19.3862	*LST8*	1.1	1.0	1.1	-1.0	YNL006W	*LST8*	1.0	1.2	1.1	1.0	required for transport of permeases from the golgi to the plasma m
CA3101	orf19.3865	*IPF6593*	-1.0	-1.2	-1.3	-1.1	YLR176C	*RFX1*	1.0	-1.1	-1.3	-1.1	similar to Saccharomyces cerevisiae Rfx1p DNA-binding protein (by hom
CA3102	orf19.3867	*RLP7*	1.0	1.0	1.0	-1.0	YNL002C	*RLP7*	1.0	1.1	1.9	2.2	ribosomal-like proteins
CA3103	orf19.13908	*IPF12086*	1.0	-1.0	1.0	1.0	YKL084W		1.0	-1.2	-1.3	-1.3	unknown function
CA3104	orf19.13907	*IPF12084*	1.0	1.0	1.0	-1.1	YOR220W		1.0	1.3	1.5	1.1	unknown function
CA3106	orf19.6552	*IPF11821*	1.1	1.0	1.1	1.0	YPR037C	*ERV2*	1.0	1.2	1.3	1.4	unknown function
CA3107	orf19.6551	*GOS1*	-1.0	1.0	1.0	-1.0	YHL031C	*GOS1*	1.0	-1.4	-1.1	-1.1	SNARE protein of Golgi compartment (by homology)
CA3108	orf19.6550	*IPF11826*	1.1	1.1	1.1	1.1	YOR228C		1.0	-1.4	-1.7	-1.7	unknown function
CA3109	orf19.6548	*IPF11829*	1.2	-1.0	-1.1	-1.1	YPL135W	*ISU1*	1.0	1.0	1.1	1.1	unknown function
CA3110	orf19.6544	*LPI9*	-1.0	1.3	1.1	1.1	YOR227W		1.0	-1.3	1.2	1.1	Microtubule-associated protein (by homology)
CA3111	orf19.6541	*RPL5*	-1.1	-1.1	-1.1	-1.1	YPL131W	*RPL5*	1.0	1.5	3.2	4.2	ribosomal protein (by homology)
CA3112	orf19.6540	*PFK2*	-1.0	9.6	8.3	8.5	YMR205C	*PFK2*	1.0	1.2	2.1	2.7	6-phosphofructokinase, beta subunit
CA3113	orf19.13892	*IPF15737*	-1.1	-1.0	-1.1	-1.1	YPL235W	*RVB2*	1.0	1.0	1.1	1.1	simailar to Saccharomyces cerevisiae Rvb2p RuvB-like protein (by homo
CA3115		*ECM33.3*	1.0	1.1	1.1	1.0	YBR078W	*ECM33*	1.0	-2.1	-2.0	-1.2	cell wall biogenesis, 3-prime end (by homology)
CA3116	orf19.3010	*LAB2*	-1.0	-1.0	1.1	1.0	YLR239C	*LIP2*	1.0	-1.1	-1.1	-1.0	LIPOATE BIOSYNTHESIS PROTEIN by homology
CA3118	orf19.3008	*COQ4*	-1.2	-1.2	-1.1	-1.1	YDR204W	*COQ4*	1.0	-2.6	-1.8	-1.5	ubiquinone biosynthesis
CA3120	orf19.3007	*IPF5358*	1.0	1.0	1.2	1.1	YDR357C		1.0	-1.0	1.4	1.3	unknown function
CA3121	orf19.3006	*GGA1*	-1.4	-1.3	-1.5	-1.4	YHR108W	*GGA2*	1.0	-1.1	1.3	1.3	Arf-binding protein
CA3122	orf19.3004	*IPF5356*	1.0	1.1	1.3	1.2	YDR262W		1.0	-1.5	-1.2	-1.4	unknown function
CA3123		*RPL6.3*	1.4	1.1	1.0	1.1	YLR448W	*RPL6B*	1.0	1.6	2.4	2.3	ribosomal protein, 3-prime end
CA3124	orf19.3003	*IPF5353.3*	-1.1	1.2	-1.3	-1.0	YML072C		1.0	-1.2	-1.3	-1.1	unknown function, 3-prime end
CA3126	orf19.1358	*GCN4*	-1.3	-1.1	-1.1	1.1	YEL009C	*GCN4*	1.0	1.2	2.0	2.2	transcriptional activator
CA3127	orf19.1359	*IPF8915*	1.0	1.0	-1.0	-1.0	YMR067C		1.0	-1.4	1.1	-1.2	unknown function
CA3128	orf19.1360	*IPF8914*	1.0	1.1	1.0	1.0	YNL213C		1.0	-1.1	1.1	1.1	unknown function
CA3130	orf19.1361	*TIM23*	1.1	-1.0	1.0	1.0	YNR017W	*MAS6*	1.0	-1.2	-1.1	-1.2	mitochondrial inner membrane import translocase subunit (by homology)
CA3131	orf19.1362	*IPF8910*	1.1	-1.0	-1.1	-1.1	YNR015W	*SMM1*	1.0	-1.0	1.3	1.4	unknown function
CA3132	orf19.1363	*IPF8904*	1.0	1.0	-1.0	-1.1	YOR338W		1.0	-1.1	1.0	1.6	unknown function
CA3144	orf19.3715	*ASF1*	1.1	1.1	1.0	1.0	YJL115W	*ASF1*	1.0	-1.4	-1.4	-1.7	anti-silencing protein (by homology)
CA3145	orf19.6155	*CDC9*	-1.1	1.0	1.1	1.0	YDL164C	*CDC9*	1.0	1.1	1.1	1.0	DNA ligase (by homology)
CA3147	orf19.6160	*IPF9803*	-1.1	-1.1	-1.3	-1.2	YMR031C		1.0	1.5	1.5	-1.0	unknown function
CA3148	orf19.6163	*IPF9808*	1.0	1.0	1.0	-1.0	YKL049C	*CSE4*	1.0	-1.9	-1.5	-1.7	similar to Saccharomyces cerevisiae cse4p with strong similarity to histor
CA3149	orf19.6165	*KGD1*	1.1	-2.0	-2.1	-2.0	YIL125W	*KGD1*	1.0	-2.5	-2.1	-3.6	2-oxoglutarate dehydrogenase
CA3151	orf19.6167	*IPF4033*	-1.0	-1.1	-1.1	-1.1	YIL124W	*AYR1*	1.0	-1.1	-1.2	-1.9	similar to Saccharomyces cerevisiae Ayr1p 1-acyldihydroxyacetone-phos
CA3156	orf19.1589	*IPF14455*	-1.1	-1.1	-1.1	1.0	YJL025W	*RRN7*	1.0	-1.7	-1.6	-1.4	similar to Saccharomyces cerevisiae Rrn7p polymerase I specific transcr
CA3157	orf19.1588	*IPF14456*	1.0	1.1	1.0	1.1	YBR269C		1.0	-1.1	-1.2	-1.3	unknown function
CA3160	orf19.1585	*ZRT2*	1.2	2.7	3.8	2.6	YLR130C	*ZRT2*	1.0	-1.6	-1.3	1.0	zinc transport protein (by homology)
CA3165	orf19.1578	*FMI1*	-1.4	-1.1	-1.4	-1.2	YMR229C	*RRP5*	1.0	-1.3	1.2	1.5	processing of pre-ribosomal RNA
CA3166	orf19.1577	*IPF9634*	-1.0	-1.0	1.0	-1.0	YMR136W	*GAT2*	1.0	-1.3	-1.0	1.0	probable GATA zinc finger transcription factor (by homology)
CA3167	orf19.1576	*IPF9632*	-1.1	-1.2	-1.1	-1.1	YHL010C		1.0	-1.0	-1.1	-1.0	unknown function

CA3168	orf19.1575	*PRS3*	1.1	1.2	1.4	1.2	YHL011C	*PRS3*	1.0	1.3	1.6	1.8	ribose-phosphate pyrophosphokinase
CA3169	orf19.1395	*IPF7686*	1.0	1.5	2.0	1.6	YER053C		1.0	-1.5	-1.5	-1.4	putative mitochondrial phosphate carrier protein (by homology)
CA3170	orf19.1396	*IPF7685*	1.0	-1.0	1.0	-1.0	YIL044C	*AGE2*	1.0	-1.1	1.1	1.1	putative GTPase activating protein (by homology)
CA3174	orf19.1402	*CCT2*	-1.4	-1.2	-1.4	-1.5	YIL142W	*CCT2*	1.0	1.3	1.8	2.0	chaperonin of the TCP1 ring complex,cytosolic (by homology to S. cerev.
CA3175	orf19.1403	*IPF11587*	-1.2	-1.6	-1.5	-1.5	YNL083W		1.0	-1.3	1.2	1.2	unknown function
CA3176	orf19.1404	*IPF11588*	-1.0	-1.0	-1.0	-1.0	YML080W	*DUS1*	1.0	1.2	1.1	1.3	unknown function
CA3179	orf19.2128	*YLF2*	-1.0	-1.0	-1.1	-1.0	YHL014C	*YLF2*	1.0	-1.3	-1.3	-1.3	GTP-binding protein
CA3180	orf19.2131	*IPF12244*	-1.1	1.1	1.3	1.1	YKL034W		1.0	-1.5	-1.3	-1.2	unknown function
CA3183	orf19.2135	*TSM1.3F*	-1.0	1.0	-1.2	-1.1	YCR042C	*TSM1*	1.0	1.0	1.1	-1.0	component of TFIID complex, 3-prime end (by homology)
CA3186	orf19.2138	*ILS1*	-1.3	-1.0	-1.5	-1.3	YBL076C	*ILS1*	1.0	-1.3	-1.1	-1.0	isoleucyl-tRNA synthetase (by homology)
CA3187	orf19.2143	*IPF17094*	1.0	-1.0	-1.1	-1.0	YPL183C		1.0	-1.5	-1.4	-1.0	unknown function
CA3188	orf19.2146	*IPF11610*	1.0	-1.0	1.1	1.0	YEL056W	*HAT2*	1.0	-1.1	-1.0	-1.1	similar to Saccharomyces cerevisiae Hat2 subunit of the major yeast hist
CA3189	orf19.2149	*IPF11607*	1.0	1.1	1.1	1.0	YPR003C		1.0	-1.3	-1.3	-1.5	unknown function
CA3190	orf19.2150	*IPF11603*	-1.2	-1.0	-1.1	-1.1	YPR004C		1.0	-2.2	-2.7	-2.6	unknown function
CA3191	orf19.2151	*IPF11601*	-1.1	-1.2	-1.0	-1.3	YOR165W		1.0	-1.3	1.1	1.4	unknown function
CA3193	orf19.6170	*IPF3418*	-1.1	1.0	-1.1	-1.0	YCL029C	*BIK1*	1.0	-1.0	-1.1	1.0	unknown function
CA3194	orf19.6171	*IPF3425*	-1.1	-1.1	-1.1	-1.1	YIL115C	*NUP159*	1.0	-1.2	-1.2	-1.2	unknown function
CA3195	orf19.6173	*IPF3426*	-1.0	-1.1	-1.0	-1.0	YOR047C	*STD1*	1.0	-1.1	1.1	1.7	unknown function
CA3196	orf19.6175	*IPF3428*	-1.0	-1.1	-1.1	-1.0	YLR051C		1.0	-1.0	1.2	1.5	unknown function
CA3197	orf19.6176	*SEC61*	-1.2	1.4	1.4	1.4	YLR378C	*SEC61*	1.0	1.0	1.4	1.6	ER protein-translocation complex subunit
CA3199	orf19.6178	*FBP1*	-1.1	-6.2	-7.9	-7.2	YLR377C	*FBP1*	1.0	-3.2	-3.8	-3.3	Fructose-1,6-bisphosphatase
CA3200	orf19.6180	*IPF3439*	1.2	1.4	2.0	1.9	YDL054C		1.0	-1.1	1.1	1.2	unknown function
CA3207	orf19.6189	*IPF3456*	-1.0	1.0	1.1	1.0	YHR198C		1.0	-1.0	-1.2	-1.4	unknown function
CA3208	orf19.6190	*PSA1*	-1.0	1.2	1.2	1.1	YDL055C	*PSA1*	1.0	-1.5	1.7	1.5	GDP-mannose pyrophosphorylase
CA3212	orf19.6208	*MEF2*	-1.1	-1.4	-1.3	-1.4	YJL102W	*MEF2*	1.0	-1.3	-1.4	-1.5	translation elongation factor (by homology)
CA3213	orf19.6205	*IPF8160*	1.0	-1.0	-1.1	1.0	YML003W		1.0	-3.4	-3.1	-3.3	unknown function
CA3214	orf19.6203	*PUT3*	-1.1	-1.4	-1.4	-1.3	YKL015W	*PUT3*	1.0	-1.2	1.0	1.1	putative positive activator of the proline utilisation pathway
CA3215	orf19.6199	*HCS1*	-1.1	-1.1	-1.2	-1.1	YKL017C	*HCS1*	1.0	-1.2	-1.1	-1.0	putative DNA helicase A (by homology)
CA3217	orf19.6197	*DHH1*	1.1	1.2	1.2	1.1	YDL160C	*DHH1*	1.0	1.1	1.4	1.3	RNA helicase by homology
CA3219	orf19.6195	*IPF10003*	-1.1	1.0	-1.3	-1.1	YGR276C	*RNH70*	1.0	-1.1	1.3	1.3	similar to Saccharomyces cerevisiae Rnh70p ribonuclease H (by homolo
CA3221	orf19.6193	*'F10000.5EO*	-1.2	-1.1	-1.4	-1.2	YGR274C	*TAF145*	1.0	-1.1	-1.1	-1.0	unknown function, 5-prime end
CA3223	orf19.6284	*SRP102*	1.1	1.0	1.1	1.0	YKL154W	*SRP102*	1.0	-2.8	-2.0	-1.7	Signal recognition particle receptor (by homology)
CA3224	orf19.6285	*GLC7*	-1.3	1.0	1.0	-1.1	YER133W	*GLC7*	1.0	1.0	1.5	1.6	Ser/thr phosphoprotein phosphatase 1 (by homology)
CA3225	orf19.6286	*IPF9329*	1.0	1.0	1.0	1.1	YER128W		1.0	-1.2	-1.3	-1.4	unknown function
CA3226		*RPS27*	1.4	-1.0	1.3	1.3	YKL156W	*RPS27A*	1.0	1.4	1.4	1.7	ribosomal protein S27 (by homology)
CA3227	orf19.6287	*AAT21*	-1.4	-2.1	-2.1	-2.1	YLR027C	*AAT2*	1.0	-1.3	-1.2	-1.2	aspartate aminotransferase (by homology)
CA3229	orf19.6291	*FUN30*	1.0	-1.1	-1.3	-1.1	YAL019W	*FUN30*	1.0	-1.3	-1.0	1.0	helicases of the Snf2/Rad54 family(by homology)
CA3230	orf19.6293	*EMP24*	1.3	1.3	1.3	1.2	YGL200C	*EMP24*	1.0	-1.2	-1.3	-1.3	component of the COPII-coated vesicles (by homology)
CA3233	orf19.6294	*MYO1*	-1.1	-1.0	-1.1	-1.0	YHR023W	*MYO1*	1.0	-1.3	1.0	1.3	myosin-1 isoform (type II myosin) heavy chain (by homology)
CA3234	orf19.6295	*MAS2*	-1.1	-1.0	-1.1	-1.1	YHR024C	*MAS2*	1.0	-1.1	-1.2	-1.1	processing peptidase, catalytic 53kDa (alpha) subunit, mitochondrial (by
CA3235	orf19.6296	*SNF8*	-1.0	1.1	1.1	1.1	YPL002C	*SNF8*	1.0	-1.0	1.1	1.1	involved in glucose derepression (by homology)
CA3236	orf19.6297	*DEG1*	-1.1	-1.1	-1.0	-1.0	YFL001W	*DEG1*	1.0	2.2	2.6	4.2	pseudouridine synthase (by homology)
CA3237	orf19.6298	*SPB4*	-1.0	1.0	-1.0	-1.0	YFL002C	*SPB4*	1.0	1.3	1.6	2.4	ATP-dependent RNA helicase of DEAH box family (by homology)
CA3240	orf19.4683	*IPF10559*	-1.2	-1.2	-1.5	-1.2	YKR095W	*MLP1*	1.0	-1.7	-2.1	-2.2	myosin-like protein (by homology)
CA3242	orf19.4681	*RAT1*	-1.6	-1.7	-2.4	-1.8	YOR048C	*RAT1*	1.0	1.1	1.7	1.8	5 -3 Exoribonuclease (by homology)
CA3244	orf19.4679	*AGP2*	-1.2	-1.1	-1.2	-1.1	YBR132C	*AGP2*	1.0	-1.5	-1.5	-1.7	amino-acid permease (by homology)
CA3245	orf19.4678	*IPF19980*	-1.1	1.0	1.2	1.2	YJR107W		1.0	1.0	1.1	-1.3	putative lipase (by homology)
CA3246	orf19.4677	*IPF15830*	-1.2	-1.2	-1.0	-1.1	YML041C		1.0	-1.3	-1.1	-1.3	unknown function
CA3256	orf19.11229	*IPF4730*	-1.0	-1.0	-1.1	-1.1	YOR112W		1.0	-1.1	1.2	1.2	unknown Function
CA3261	orf19.2694	*TYS1*	1.0	-1.0	1.0	-1.1	YGR185C	*TYS1*	1.0	-1.5	1.1	1.4	tyrosyl-tRNA synthetase by homology
CA3262	orf19.2695	*UBR11.3*	-1.1	1.0	-1.1	-1.1	YGR184C	*UBR1*	1.0	-1.4	-1.4	-1.3	ubiquitin-protein ligase, 3-prime end (by homology)
CA3263	orf19.2697	*UBR12*	-1.2	1.0	-1.1	-1.1	YLR024C	*UBR2*	1.0	-1.6	-1.7	-1.6	ubiquitin-protein ligase by homology
CA3264	orf19.2698	*IPF5035*	1.0	1.0	1.0	1.0	YLL014W		1.0	-1.1	1.1	1.0	unknown function
CA3265	orf19.2699	*ABP1*	-1.2	-1.5	-1.6	-1.4	YCR088W	*ABP1*	1.0	-1.5	-1.6	-2.0	actin-binding protein (by homology)
CA3266	orf19.2703	*IPF5045*	1.0	-1.1	-1.1	-1.1	YMR171C		1.0	-1.1	1.0	1.1	unknown function
CA3270	orf19.6304	*LYS5*	-1.1	1.0	1.1	1.1	YGL154C	*LYS5*	1.0	1.1	1.1	1.0	L-aminoadipate-semialdehyde dehydrogenase (by homology)
CA3271	orf19.6305	*GLY2*	-1.0	-1.1	-1.1	-1.1	YEL046C	*GLY1*	1.0	-1.1	1.5	2.2	L-threonine aldolase, low-specific
CA3278	orf19.6312	*RPS3*	1.1	-1.2	-1.3	-1.0	YNL178W	*RPS3*	1.0	1.8	2.7	3.1	Ribosomal protein S3.e (by homology)
CA3281	orf19.6314	*RPB8*	1.0	-1.1	-1.0	-1.0	YOR224C	*RPB8*	1.0	1.6	1.5	2.0	DNA-directed RNA polymerase I, II, III 16 KD subunit (by homology)
CA3283	orf19.6316	*IPF6274*	-1.0	-1.1	-1.0	-1.0	YMR221C		1.0	-1.3	1.1	1.1	unknown function
CA3284	orf19.6317	*ADE6*	-1.2	-1.0	-1.3	-1.3	YGR061C	*ADE6*	1.0	-2.7	-3.5	-1.8	5 -phosphoribosylformyl glycinamidine synthetase (by homology)

CA3285	orf19.6318	*IPF6280*	1.0	1.1	1.0	1.1	YJR085C		1.0	-1.3	-1.3	-1.8	unknown function
CA3286	orf19.6319	*UBP3.3EOC*	1.0	1.0	1.0	-1.0	YER151C	*UBP3*	1.0	1.1	1.1	1.4	Ubiquitin-specific proteinase, 3-prime end (by homology)
CA3289	orf19.6323	*HPA3*	1.0	1.0	1.1	-1.0	YEL066W	*HPA3*	1.0	-1.1	-1.1	-1.2	histone and other protein acetyltransferase(by homology)
CA3290	orf19.6324	*IPF5734*	-1.4	1.1	-1.1	-1.1	YNL212W	*VID27*	1.0	-1.2	-1.0	-1.0	unknown function
CA3291		*IPF5730*	-1.0	1.1	1.1	1.0	YNL211C		1.0	-1.1	-1.2	-1.6	unknown function
CA3294	orf19.6328	*IPF5725*	1.0	1.0	1.0	1.0	YDR511W	*ACN9*	1.0	-1.5	-1.6	-1.4	unknown function
CA3300	orf19.2315	*RTG3*	-1.0	-1.2	-1.3	-1.2	YBL103C	*RTG3*	1.0	1.1	1.0	1.1	Probable bHLH/zip transcription factor that regulates CIT2 gene expressi
CA3301	orf19.2314	*IPF13782*	-1.0	-1.1	-1.2	-1.1	YGL029W	*CGR1*	1.0	1.2	1.0	1.7	unknown function
CA3306	orf19.2310	*IPF11738*	1.0	-1.0	-1.0	1.0	YFR032C		1.0	1.0	-1.1	1.0	unknown function
CA3307		*RPL2.3*	1.0	1.0	-1.2	-1.1	YIL018W	*RPL2B*	1.0	-1.6	-1.5	-1.4	ribosomal protein L8, 3-prime end (by homology)
CA3308	orf19.9845	*PET127*	-1.0	-1.1	-1.0	-1.0	YOR017W	*PET127*	1.0	-1.3	1.1	1.1	component of mitochondrial translation (by homology)
CA3310	orf19.2307	*PFS2*	-1.0	1.0	1.2	1.0	YNL317W	*PFS2*	1.0	-1.0	-1.1	-1.1	Polyadenylation Factor I subunit (by homology)
CA3311	orf19.2306	*IPF8809*	-1.0	-1.1	-1.1	-1.0	YMR009W		1.0	-1.1	1.2	1.0	unknown function
CA3312	orf19.2305	*IPF8810*	1.0	1.1	-1.0	1.0	YEL003W	*GIM4*	1.0	1.5	1.4	2.0	unknown function
CA3314	orf19.2303	*IPF8812*	-1.0	1.0	1.0	1.1	YGR075C	*PRP38*	1.0	-1.5	-1.5	-1.7	unknown function
CA3316	orf19.2301	*IPF8817*	1.1	1.1	1.0	-1.0	YIL007C		1.0	-1.4	-1.5	-1.5	putative proteasome subunit (by homology)
CA3317	orf19.2299	*URM1*	1.0	1.1	1.0	1.0	YIL008W	*URM1*	1.0	1.0	-1.2	-1.2	ubiquitin like protein (by homology)
CA3318	orf19.2298	*WBP1*	-1.1	1.1	1.2	1.4	YEL002C	*WBP1*	1.0	1.2	1.6	1.8	Oligosaccharyl transferase beta subunit (by homology)
CA3319	orf19.2680	*RS25.3EOC*	-1.2	1.4	1.1	1.1	YMR162C		1.0	-1.2	-1.5	-1.5	Probable ATPase, 3-prime end (by homology)
CA3320	orf19.2678	*IPF6898*	-1.2	1.1	1.1	1.2	YGR188C	*BUB1*	1.0	-1.2	-1.3	-1.3	similar to Saccharomyces cerevisiae Bub1p serine/threonine kinase (by
CA3321	orf19.2677	*IPF6896.5F*	-1.2	-1.2	-1.3	-1.2	YHR188C	*GPI16*	1.0	-1.1	1.1	1.1	unknown function, 5-prime end
CA3323	orf19.2676	*IKI1*	1.1	1.0	1.1	1.1	YHR187W	*IKI1*	1.0	1.0	1.1	1.1	killer toxin insensitive protein
CA3324	orf19.2675	*IPF6893*	1.0	1.0	-1.0	1.0	YMR288W	*HSH155*	1.0	-1.3	-1.3	-1.2	unknown function
CA3326	orf19.2673	*IPF6889*	-1.0	-1.1	-1.1	-1.0	YDR288W		1.0	-1.4	-1.1	-1.2	unknown function
CA3327	orf19.2672	*NCP1*	-1.1	-1.1	-1.1	-1.0	YHR042W	*NCP1*	1.0	1.2	1.5	1.8	NADPH-cytochrome P450 reductase
CA3329	orf19.2670	*IPF12162*	1.1	2.0	2.1	1.7	YHR067W		1.0	1.1	1.0	-1.1	Unknown function
CA3333	orf19.9876	*CDC48*	-1.1	1.1	-1.1	-1.1	YDL126C	*CDC48*	1.0	-1.1	1.4	1.1	microsomal ATPase (by homology)
CA3336	orf19.2335	*IPF19983*	1.0	1.4	1.6	1.6	YHR113W		1.0	1.0	-1.1	1.1	unknown function
CA3337	orf19.2334	*IPF13583*	1.6	1.1	1.1	1.1	YHR101C	*BIG1*	1.0	-1.1	-1.1	1.1	unknown function
CA3338	orf19.2333	*IPF13582*	-1.1	1.1	-1.1	1.1	YHR009C		1.0	-1.3	-1.4	1.2	unknown function
CA3339	orf19.2332	*IPF20131*	1.0	1.0	1.0	-1.1	YDR446W	*ECM11*	1.0	-1.3	-1.4	-1.3	unknown function
CA3340	orf19.2331	*ADA2*	-1.1	-1.0	-1.1	1.0	YDR448W	*ADA2*	1.0	-1.2	1.1	1.2	general transcriptional adaptor or co-activator (by homology)
CA3341		*RPS17.3*	1.3	-1.0	1.2	1.2	YDR447C	*RPS17B*	1.0	-1.3	3.1	3.3	Ribosomal protein S17, 3-prime end (by homology)
CA3342	orf19.2330	*IPF13361*	-1.0	-1.1	1.0	-1.0	YDR449C		1.0	-1.6	-1.7	-1.2	unknown function
CA3344	orf19.2326	*IPF13359*	-1.0	-1.0	-1.1	1.0	YDR363W	*ESC2*	1.0	-1.2	-1.0	1.0	unknown function
CA3345	orf19.2325	*IPF13357*	1.0	1.0	1.1	1.0	YDR362C	*TFC6*	1.0	1.0	1.1	1.1	unknown function
CA3346	orf19.2324	*IPF13356*	-1.1	1.3	1.4	1.3	YHR111W		1.0	-1.6	-1.3	-1.1	molybdopterin biosynthesis (by homology)
CA3347		*ERP5*	1.0	1.1	1.1	1.1	YHR110W	*ERP5*	1.0	-1.8	-1.6	-1.4	protein involved in membrane trafficking (by homology)
CA3348	orf19.2320	*RIO1*	1.1	-1.1	-1.1	-1.1	YOR119C	*RIO1*	1.0	-1.1	1.3	1.4	unknown function
CA3349		*IPF19588*	1.1	1.1	1.4	1.2	YDR367W		1.0	-1.0	-1.0	1.1	unknown function
CA3352	orf19.9501	*IPF16194*	1.0	-1.0	-1.1	-1.0	YMR099C		1.0	1.0	-1.0	-1.3	unknown function
CA3353	orf19.9500	*AUR1*	1.3	1.2	1.6	1.2	YKL004W	*AUR1*	1.0	1.1	1.0	1.2	aureobasidin-resistance protein
CA3354	orf19.9499	*IPF11281*	-1.0	-1.1	-1.0	-1.1	YDL035C	*GPR1*	1.0	-1.1	1.2	1.4	similar to Saccharomyces cerevisiae Gpr1p G-protein coupled receptor (
CA3357	orf19.1941	*IPF9562*	-1.0	1.0	1.0	-1.0	YOL069W	*NUF2*	1.0	-1.0	-1.1	-1.2	similar to Saccharomyces cerevisiae Nuf2pspindle pole body protein
CA3358	orf19.1940	*IPF19984*	1.1	1.2	1.1	1.0	YOR125C	*CAT5*	1.0	-1.4	-1.4	-1.6	similar to Saccharomyces cerevisiae Cat5p involved in coenzyme Q (ubi
CA3359	orf19.1939	*IPF9566*	-1.0	-1.1	1.1	-1.1	YDR374C		1.0	-1.3	-1.5	-1.3	unknown function
CA3361	orf19.9491	*SNF1*	-1.1	-1.1	-1.1	-1.1	YDR477W	*SNF1*	1.0	1.1	1.3	1.5	serine/threonine protein kinase
CA3362	orf19.9489	*IPF9789*	-1.2	-1.1	-1.2	-1.1	YDR479C		1.0	1.2	1.3	1.2	unknown function
CA3363	orf19.9488	*FRE32*	1.1	1.0	1.0	1.0	YOR381W	*FRE3*	1.0	-1.1	-1.1	-1.1	ferric reductase (by homology)
CA3365	orf19.1843	*ALG6*	1.3	1.8	2.5	2.1	YOR002W	*ALG6*	1.0	-1.4	-1.3	-1.3	glucosyltransferase (by homology)
CA3367	orf19.9405	*IPF4667*	-1.2	-1.9	-2.5	-1.3	YDR380W	*ARO10*	1.0	1.1	1.3	-1.0	unknown Function
CA3368	orf19.1849	*IPF4671*	-1.1	-1.1	1.1	-1.0	YIL091C		1.0	-1.1	1.0	1.3	unknown Function
CA3369	orf19.1850	*IPF4672*	-1.0	-1.0	-1.0	-1.1	YNL032W	*SIW14*	1.0	-1.0	1.0	-1.0	unknown Function
CA3370	orf19.1852	*IPF4674*	1.1	1.0	1.1	1.1	YIL087C		1.0	-1.2	-1.2	-1.6	unknown Function
CA3374	orf19.1856	*IPF4683*	-1.0	-1.1	1.0	-1.0	YIL084C	*SDS3*	1.0	-1.5	-1.4	-1.4	unknown Function
CA3377	orf19.7964	*CLF1*	-1.0	-1.1	1.0	-1.0	YLR117C	*CLF1*	1.0	-1.6	-1.5	-1.2	pre-mRNA splicing factor (by homology)
CA3379	orf19.331	*IPF8350*	1.1	1.1	-1.0	1.0	YDR140W	*FYV9*	1.0	-1.2	-1.1	-1.0	putative methyltransferase (by homology)
CA3380	orf19.329	*MSL5*	1.0	-1.0	1.0	1.0	YLR116W	*MSL5*	1.0	-2.0	-1.5	-1.5	branch point bridging protein (by homology)
CA3381	orf19.328	*NPR2*	-1.2	-1.2	-1.2	-1.2	YEL062W	*NPR2*	1.0	-1.2	-1.0	-1.2	nitrogen permease regulator (by homology)
CA3382	orf19.327	*HTA3*	1.2	1.2	1.4	1.5	YOL012C	*HTZ1*	1.0	-1.2	-1.2	-1.1	histone H2A F/Z variant (by homology)
CA3384	orf19.325	*IPF8362*	-1.2	-1.2	-1.7	-1.3	YLR115W	*CFT2*	1.0	-1.1	-1.2	-1.1	similar to Saccharomyces cerevisiae Cft2p involved in cleavage and poly

CA3387	orf19.7953	*MUP3*	-1.0	1.2	1.4	1.2	YHL036W	*MUP3*	1.0	-1.1	1.3	-1.0	Very low affinity methionine permease
CA3389	orf19.7951	*IPF6754*	1.0	-1.0	1.1	1.0	YDR286C		1.0	-1.8	-1.7	-2.1	unknown function
CA3390		*CAF17*	1.1	-1.0	-1.1	1.0	YJR122W	*CAF17*	1.0	1.2	1.3	1.7	Component of CCR4 transcriptional complex
CA3391	orf19.7949	*PNP1*	1.0	-1.0	1.0	1.1	YLR209C	*PNP1*	1.0	-1.1	-1.0	-1.2	Purine Nucleoside Phosphorylase (by homology)
CA3392	orf19.316	*SEC13*	-1.0	1.0	-1.1	1.1	YLR208W	*SEC13*	1.0	1.1	1.1	1.2	Protein transport protein
CA3393	orf19.315	*IPF6748*	-1.1	-1.0	-1.1	-1.0	YMR052W	*FAR3*	1.0	-1.5	-1.4	-1.5	unknown function
CA3394	orf19.7946	*IPF6747*	-1.0	-1.0	-1.0	1.0	YMR053C	*STB2*	1.0	-1.5	-1.6	-1.8	similar to Saccharomyces cerevisiae Stb2p involved Sin3p binding (by ho
CA3395	orf19.3970	*IPF13616*	-1.1	1.0	-1.0	-1.0	YGR251W		1.0	-1.3	-1.4	-1.0	unknown function
CA3397	orf19.3972	*IPF13618*	1.1	1.0	1.0	1.1	YMR292W	*GOT1*					unknown function
CA3398	orf19.3973	*IPF13621*	1.0	1.0	-1.0	1.0	YGR268C		1.0	1.1	1.3	1.2	unknown function
CA3399	orf19.3974	*PUT2*	-1.3	-8.3	-9.8	-7.1	YHR037W	*PUT2*	1.0	-1.2	-1.2	1.2	1-pyrroline-5-carboxylate dehydrogenase (by homology)
CA3400	orf19.3976	*JNM1*	-1.0	-1.1	-1.0	-1.1	YMR294W	*JNM1*	1.0	-1.3	-1.6	-1.8	mitosis protein, involved in nuclear migration (by homology)
CA3401	orf19.3977	*IPF8652*	-1.0	-1.0	-1.1	1.0	YGR173W		1.0	-1.9	-1.7	-1.5	putative GTP-binding protein (by homology)
CA3402	orf19.3978	*IPF8651*	-1.0	1.0	-1.0	-1.2	YGR272C		1.0	-1.3	-1.1	1.0	unknown function
CA3403	orf19.3980	*IPF8650*	-1.2	1.2	-1.1	1.1	YGR271W	*SLH1*	1.0	-1.4	-1.5	-1.3	RNA helicase (by homology)
CA3404	orf19.3981	*MAL31*	1.0	-1.9	-2.4	-1.6	YBR298C	*MAL31*	1.0	1.5	1.3	1.2	maltose permease (by homology)
CA3405	orf19.3982	*IPF8644*	1.0	1.0	1.0	-1.0	YGR287C		1.0	-1.1	-1.2	1.1	maltase (by homology)
CA3406	orf19.3983	*IPF9711*	1.0	1.1	-1.0	1.0	YGR266W		1.0	-1.2	-1.0	1.1	unknown function
CA3408	orf19.6151	*IPF9407*	1.2	-1.1	-1.1	1.0	YIL062C	*ARC15*	1.0	1.5	1.6	1.4	similar to Saccharomyces cerevisiae Arc15p subunit of the ARP2/3 comp
CA3409	orf19.6148	*IPF9410*	-1.0	-1.0	-1.1	-1.1	YDR356W	*NUF1*	1.0	-3.6	-4.2	-3.4	similar to Saccharomyces cerevisiae Nuf1p spindle pole body componen
CA3410	orf19.6147	*IPF9411*	-1.1	-1.1	-1.0	-1.0	YER030W		1.0	-1.3	-1.1	-1.5	unknown function
CA3411	orf19.13565	*IPF9413*	1.1	1.1	1.3	1.2	YGL215W	*CLG1*	1.0	-1.5	-1.4	-1.1	unknown function
CA3419	orf19.6136	*IPF12778*	1.1	-1.3	-1.3	-1.1	YLR439W	*MRPL4*	1.0	-1.7	-2.1	-2.1	ribosomal protein, mitochondrial (by homology)
CA3422	orf19.13553	*IPF17289*	-1.2	1.1	1.1	1.1	YLR440C		1.0	1.0	1.1	1.1	unknown function
CA3425	orf19.593	*IPF11873*	-1.3	-1.1	-1.3	-1.2	YDR320C	*SWA2*	1.0	-1.3	1.1	1.1	similar to Saccharomyces cerevisiae Swa2p clathrin-binding protein requ
CA3426	orf19.592	*IPF11869*	-1.0	1.1	1.1	-1.0	YNL092W		1.0	-1.2	-1.1	-1.1	unknown function
CA3429	orf19.588	*IPF6380*	1.1	1.1	-1.0	-1.1	YDR031W		1.0	-1.2	-1.5	-1.4	unknown function
CA3430	orf19.587	*IPF6382*	1.0	-1.0	1.0	1.0	YNL253W		1.0	1.0	1.2	1.1	unknown function
CA3431	orf19.586	*FUN9*	1.0	1.0	1.3	1.1	YAL042W	*ERV46*	1.0	-1.3	-1.4	-1.2	Protein involved in vesicular transport between the endoplasmic reticulun
CA3432	orf19.585	*MRPL17*	1.1	-1.0	1.2	1.1	YNL252C	*MRPL17*	1.0	-1.0	1.1	-1.1	ribosomal protein of the large subunit (YmL30), mitochondrial
CA3434	orf19.584	*CCP1*	1.1	1.1	1.1	1.0	YKR066C	*CCP1*	1.0	1.3	1.5	1.2	Cytochrome-c peroxidase precursor (by homology)
CA3435	orf19.583	*IPF6391*	1.0	-1.1	-1.1	-1.0	YJR078W		1.0	-1.1	-1.1	1.1	similarity to mammalian indoleamine 2,3-dioxygenase (by homology)
CA3436	orf19.581	*NRD1*	-1.0	1.0	1.0	1.0	YNL251C	*NRD1*	1.0	-1.3	-1.1	-1.2	Involved in regulation of nuclear pre-mRNA abundance
CA3438	orf19.2987	*IPF11330*	-1.2	-1.1	-1.2	-1.1	YHR194W		1.0	1.2	1.3	1.3	unknown function
CA3441	orf19.2984	*MST1*	-1.1	-1.0	-1.1	-1.0	YKL194C	*MST1*	1.0	-1.1	-1.2	-1.4	mitochondrial threonyl tRNA synthetase [Candida albicans]
CA3442	orf19.2983	*IPF11326*	-1.1	-1.1	-1.1	-1.0	YLR418C	*CDC73*	1.0	-1.6	-1.7	-1.7	similar to Saccharomyces cerevisiae (by homology)
CA3443	orf19.2982	*IPF11324*	1.0	1.1	1.0	1.0	YLR423C	*APG17*	1.0	-1.1	-1.2	-1.5	unknown function
CA3444	orf19.2980	*IPF11323*	-1.1	-1.1	-1.1	-1.0	YLR424W		1.0	-1.1	1.3	1.4	unknown function
CA3446	orf19.2977	*IPF7324*	-1.1	-1.1	-1.2	-1.1	YKL195W		1.0	-1.2	-1.2	-1.1	unknown function
CA3448	orf19.2974	*YKT6*	-1.1	-1.1	-1.1	-1.1	YKL196C	*YKT6*	1.0	-1.1	-1.3	-1.4	Endoplasmic Reticulum-Golgi transport (by homology)
CA3449	orf19.2973	*IPF7320*	1.0	-1.1	-1.0	1.0	YOR359W		1.0	-1.6	-1.6	-1.6	unknown function
CA3450	orf19.2972	*PDE2*	-1.0	1.1	-1.0	1.0	YOR360C	*PDE2*	1.0	1.1	-1.1	1.3	Nucleotide phosphodiesterase
CA3452	orf19.1253	*IPF10541*	-1.1	-1.1	-1.1	-1.1	YFR034C	*PHO4*	1.0	1.1	1.3	1.4	unknown function
CA3453	orf19.1254	*SEC23*	-1.1	1.2	1.0	1.0	YPR181C	*SEC23*	1.0	-1.8	-1.2	1.2	Component of COPII coat (by homology)
CA3456	orf19.1259	*IPF19986*	-1.0	1.0	-1.3	-1.1	YGL131C		1.0	-1.2	-1.3	-1.3	unknown function
CA3457	orf19.1260	*IPF8521*	1.0	-1.0	1.1	-1.0	YPL213W	*LEA1*	1.0	-1.1	-1.2	-1.2	unknown function
CA3459	orf19.1261	*CGT1.3F*	1.0	-1.1	-1.0	1.0	YGL130W	*CEG1*	1.0	-1.4	-1.4	-1.2	mRNA capping enzyme alpha subunit, 3-prime end
CA3462	orf19.1265	*IPF14959*	-1.2	-1.1	-1.3	-1.1	YMR218C	*TRS130*	1.0	-1.3	-1.1	1.2	similar to Saccharomyces cerevisiae Trs130p TRAPP subunit of 130 kDa
CA3463	orf19.1659	*ALG8*	1.2	1.2	1.5	1.2	YOR067C	*ALG8*	1.0	-1.3	-1.1	-1.1	glucosyltransferase (by homology)
CA3464	orf19.1661	*DBP5*	-1.2	-1.2	-1.2	-1.1	YOR046C	*DBP5*	1.0	-1.2	-1.0	1.1	RNA helicase (by homology)
CA3465		*MRP1.3F*	-1.0	-1.1	-1.1	1.0	YDR347W	*MRP1*	1.0	-1.5	-1.5	-1.2	Mitochondrial ribosomal protein of the small subunit, 3-prime end (by hon
CA3467	orf19.1663	*MNT2*	1.0	-1.0	1.1	1.1	YDR483W	*KRE2*	1.0	-1.7	-1.4	-1.4	Alpha-1,2-mannosyltransferase (by homology)
CA3469	orf19.1665	*MNT1*	-1.2	1.1	1.2	1.1	YOR099W	*KTR1*	1.0	-1.2	-1.1	1.1	Mannosyltransferase involved in n-linked and o-linked glycosylation
CA3472		*IPF6305.EXON*	1.1	1.1	-1.0	1.0	YLR218C		1.0	-1.1	1.1	1.1	unknown function, exon 2
CA3473	orf19.1668	*F6305.EXON*	1.0	-1.1	-1.0	-1.1	YDL139C	*SCM3*	1.0	-1.1	-1.4	-1.4	unknown function, exon 1
CA3474	orf19.1669	*AFG3*	-1.3	-1.5	-1.8	-1.5	YER017C	*AFG3*	1.0	1.1	1.2	1.2	Member of the Sec18p, Pas1p, Cdc48p, TBP-1 family of ATPases (by ho
CA3475	orf19.1670	*BRO1*	1.0	1.0	-1.0	1.0	YPL084W	*BRO1*	1.0	1.1	1.1	1.3	required for normal response to nutrient limitation (by homology)
CA3476	orf19.3583	*NUP2.3EOC*	-1.0	-1.1	-1.1	-1.0	YIL063C	*YRB2*	1.0	-1.0	-1.1	1.0	nucleoporine involved in nuclear protein export, 3-prime end (by homolog
CA3477	orf19.3582	*IPF3229*	1.0	-1.0	-1.1	-1.1	YIL064W		1.0	-1.4	-1.7	-1.5	unknown function
CA3478	orf19.3581	*IPF3227*	1.0	-1.0	-1.1	1.0	YBR195C	*MSI1*	1.0	-1.1	-1.1	1.6	similar to Saccharomyces cerevisiae chromatin assembly complex, subu
CA3479	orf19.3579	*ATP4*	-1.2	-1.4	-1.6	-1.4	YPL078C	*ATP4*	1.0	-1.0	-1.1	-1.9	F1F0-ATPase complex, F0 subunit B (by homology)

CA3482	orf19.3577	*COQ5*	1.1	1.0	-1.0	1.0	YML110C	*COQ5*	1.0	-1.1	1.1	-1.2	C-methyltransferase (by homology)
CA3483	orf19.3575	*CDC19*	-1.1	3.2	2.1	4.2	YAL038W	*CDC19*	1.0	2.3	3.6	5.4	pyruvate kinase (by homology)
CA3484	orf19.3574	*IPF3214*	1.0	1.1	-1.0	-1.0	YNL328C	*MDJ2*	1.0	-1.1	-1.0	-1.0	HSP-mitochondrial chaperone (by homology)
CA3485	orf19.3573	*IPF3213*	-1.7	-3.2	-4.4	-3.0	YNL329C	*PEX6*	1.0	-1.1	-1.1	-1.2	similar to Saccharomyces cerevisiae Pex6p peroxisomal assembly protei
CA3487	orf19.3569	*IPF3203*	-1.2	-1.4	-1.5	-1.2	YLR407W		1.0	-1.9	-2.1	-2.1	unknown function
CA3488	orf19.3568	*IPF3198*	-1.1	-1.0	-1.0	-1.0	YDL076C		1.0	1.0	-1.0	-1.2	unknown function
CA3491	orf19.3564	*RPC40*	1.1	1.0	1.0	1.0	YPR110C	*RPC40*	1.0	1.5	2.0	2.6	RNA polymerase (by homology)
CA3493	orf19.3561	*CDC7*	-1.1	1.1	1.0	1.0	YDL017W	*CDC7*	1.0	-1.0	1.1	1.0	serine/threonine protein kinase (by homology)
CA3494	orf19.6340	*RPB5*	1.1	1.0	1.1	-1.0	YBR154C	*RPB5*	1.0	-1.2	-1.3	1.0	DNA-directed RNA polymerase I, II, III (by homology)
CA3495	orf19.6341	*RIB7*	-1.4	-1.1	-1.3	-1.1	YBR153W	*RIB7*	1.0	-1.7	-1.4	-1.3	HTP reductase (By homology)
CA3497	orf19.6343	*FEN11*	1.5	1.6	2.1	1.8	YCR034W	*FEN1*	1.0	1.5	1.9	2.4	Fatty acid elongase required for sphingolipid formation (by homology)
CA3498	orf19.6344	*RBK1*	-1.1	-1.3	-1.4	-1.3	YCR036W	*RBK1*	1.0	-1.1	-1.4	-1.3	Ribokinase (by homology)
CA3499	orf19.6345	*RPG1*	-1.5	-1.3	-1.9	-1.5	YBR079C	*RPG1*	1.0	-1.2	1.6	1.7	Translation initiation factor eIF3 (by homology)
CA3500	orf19.6346	*IPF14487*	-1.1	1.0	1.0	-1.0	YDR361C	*BCP1*	1.0	1.1	1.5	1.5	unknown function
CA3501	orf19.6347	*CDC40*	-1.0	1.1	-1.0	1.0	YDR364C	*CDC40*	1.0	-1.4	-1.2	-1.1	cell division control protein (by homology)
CA3508	orf19.6355	*RSA2*	-1.1	-1.1	-1.2	-1.1	YMR131C	*RRB1*	1.0	1.1	1.5	2.0	Involved in ribosome biogenesis (by homology)
CA3509	orf19.6356	*PRP6*	-1.1	-1.1	-1.1	-1.1	YBR055C	*PRP6*	1.0	-1.1	-1.1	-1.0	snRNP(U4/U6)-associated splicing factor (by homology)
CA3510	orf19.6357	*MAD1*	-1.0	1.0	-1.0	1.0	YGL086W	*MAD1*	1.0	-1.4	-1.2	-1.1	coiled-coil protein involved in the spindle-assembly checkpoint (by homol
CA3511	orf19.6358	*MMS2*	1.0	1.0	1.2	1.0	YGL087C	*MMS2*	1.0	1.2	1.4	1.1	ubiquitin-conjugating enzyme (by homology)
CA3514	orf19.6362	*IPF11245*	-1.3	-1.4	-2.1	-1.5	YLL021W	*SPA2*	1.0	-1.3	-1.1	-1.0	similar to Saccharomyces cerevisiae Spa2p involved in cell polarity (by h
CA3524	orf19.992	*LKH1.3*	-1.3	-1.0	-1.1	-1.2	YNL045W		1.0	-1.1	-1.1	-1.4	PROBABLE LEUKOTRIENE A-4 HYDROLASE (LTA-4 HYDROLASE) (L
CA3525	orf19.8606	*DJP1*	1.0	-1.1	-1.2	-1.1	YIR004W	*DJP1*	1.0	-1.2	-1.2	-1.3	DnaJ-like protein involved in peroxisome biogenesis (by homology)
CA3526	orf19.8604	*MRPS5*	-1.0	-1.3	-1.3	-1.2	YBR251W	*MRPS5*	1.0	1.1	1.1	-1.0	Probable ribosomal protein S5, mitochondrial (by homology)
CA3527	orf19.8603	*IPF9934*	1.2	1.6	2.4	1.5	YGR149W		1.0	1.6	2.0	2.2	unknown function
CA3529	orf19.8600	*IPF9929*	-1.0	-1.1	-1.2	-1.0	YEL043W		1.0	-1.3	1.2	1.6	unknown function
CA3532	orf19.6365	*IPF13448*	1.0	-1.0	1.0	1.0	YDL230W	*PTP1*	1.0	1.1	-1.0	-1.3	similar to Saccharomyces Ptp1p protein tyrosine phosphatase (by homol
CA3534	orf19.6367	*SSB1*	-1.1	1.0	-1.1	-1.2	YNL209W	*SSB2*	1.0	1.3	1.5	2.3	heat shock protein 70
CA3535	orf19.6369	*IPF13458*	-1.1	-1.1	-1.1	-1.1	YNL207W		1.0	1.1	1.1	1.1	unknown function
CA3537	orf19.6373	*PSU1*	-1.1	-1.1	-1.3	-1.1	YNL118C	*DCP2*	1.0	-1.0	1.3	1.5	suppressor of petit mutations by homology
CA3538	orf19.6374	*ATP10*	-1.1	-1.1	-1.2	-1.0	YLR393W	*ATP10*	1.0	1.1	1.0	1.0	F1F0 ATPase complex assembly protein (by homology)
CA3539	orf19.6375	*RPS22*	-1.2	-1.3	-1.2	-1.2	YHL015W	*RPS20*	1.0	1.1	2.1	1.6	ribosomal protein by homology
CA3540	orf19.6376	*PTC5*	-1.2	-1.0	-1.0	1.0	YOR090C	*PTC5*	1.0	-1.1	1.1	1.1	Type 2C Protein Phosphatase by homology
CA3541	orf19.6377	*IPF5425*	1.1	1.0	-1.1	-1.0	YDR435C	*PPM1*	1.0	-1.6	-1.4	-1.5	similar to Saccharomyces cerevisiae Ppm1p carboxy methyltransferase (
CA3542	orf19.6378	*IPF5426*	1.0	-1.0	-1.0	1.0	YML014W		1.0	-1.4	-1.6	-1.0	putative methyltransferase (by homology)
CA3546	orf19.6385	*ACO1*	1.2	1.1	-1.1	-1.4	YLR304C	*ACO1*	1.0	-2.8	-3.8	-8.9	aconitate hydratase (by homology)
CA3547	orf19.3870	*ADE13*	1.1	-1.2	-1.1	-1.1	YLR359W	*ADE13*	1.0	-1.1	1.1	1.7	adenylosuccinate lyase (by homology)
CA3548	orf19.3872	*IPF12179*	1.0	-1.1	-1.0	-1.0	YGR026W		1.0	-1.1	1.1	-1.1	unknown function
CA3549	orf19.3873	*ARC40*	1.1	-1.1	1.1	1.1	YBR234C	*ARC40*	1.0	-1.4	-1.6	-1.6	subunit of the Arp2/3 complex involved in the control of actin polymerizati
CA3551	orf19.3876	*IPF13229*	1.1	1.0	1.1	-1.0	YDR520C		1.0	-2.3	-1.9	-1.8	unknown function
CA3554	orf19.3881	*IPF7770*	1.1	1.1	-1.0	1.0	YOL053W		1.0	1.0	1.0	-1.3	unknown function
CA3559	orf19.3888	*PGI1*	1.0	1.7	1.8	1.7	YBR196C	*PGI1*	1.0	-1.4	1.1	1.7	Glucose-6-phosphate isomerase
CA3561	orf19.3128	*SLY1*	-1.1	1.0	-1.1	-1.0	YDR189W	*SLY1*	1.0	-1.1	-1.1	-1.1	hydrophilic suppressor of YPT1 and member of the Sec1p family (by hom
CA3562	orf19.3129	*IPF7823*	-1.2	-1.2	-1.3	-1.1	YDR190C	*RVB1*	1.0	1.3	1.8	1.8	similar to Saccharomyces cerevisiae Rvb1p RuvB-like protein (by homol
CA3563	orf19.3130	*IPF7819*	-1.0	1.0	1.0	-1.0	YLR243W		1.0	-1.7	-1.1	1.2	unknown function
CA3565	orf19.3132	*MSC2*	1.2	1.2	1.3	1.2	YDR205W	*MSC2*	1.0	-2.4	-1.7	-1.2	Probable membrane protein
CA3566	orf19.3133	*GUT2*	1.1	-1.6	-1.6	-1.8	YIL155C	*GUT2*	1.0	-1.8	-2.8	-5.1	Glycerol-3-phosphate dehydrogenase, mitochondrial (by homology)
CA3568	orf19.3135	*IPF7804.3F*	-1.1	-1.1	-1.2	-1.0	YML013W		1.0	-1.6	-2.0	-1.8	unknown function, 3-prime end
CA3570	orf19.3138	*NOP1*	1.1	1.2	1.1	1.1	YDL014W	*NOP1*	1.0	1.7	1.8	4.4	Fibrillarin
CA3573	orf19.2267	*RFA2*	-1.1	-1.0	-1.1	-1.0	YNL312W	*RFA2*	1.0	-1.0	-1.1	-1.1	DNA replication factor by homology to S. cerevisiae
CA3574	orf19.2266	*IPF19584*	1.1	-1.0	-1.1	-1.1	YFR013W	*IOC3*	1.0	-1.3	-1.5	-1.5	unknown function
CA3575	orf19.2265	*IPF11108*	-1.0	1.0	-1.1	-1.0	YCR052W	*RSC6*	1.0	-1.4	1.0	1.1	unknown function
CA3578	orf19.2262	*IPF11105*	1.1	1.1	1.1	1.0	YBR046C	*ZTA1*	1.0	1.0	-1.1	1.0	probable quinone oxidoreductase
CA3579	orf19.2261	*HSH49*	1.0	1.2	1.2	1.3	YOR319W	*HSH49*	1.0	-1.2	-1.2	-1.2	spliceosome-associated essential protein [Candida albicans]
CA3580	orf19.2260	*IPF16141*	1.0	-1.0	-1.0	-1.2	YHR040W		1.0	1.2	1.2	1.2	unknown function
CA3583	orf19.2257	*IPF20137*	-1.0	-1.2	-1.2	-1.2	YNR021W		1.0	-1.1	1.1	1.1	unknown function
CA3584	orf19.2256	*IPF15468*	1.0	-1.0	-1.1	-1.1	YCR051W		1.0	-1.4	-1.0	1.2	unknown function
CA3587	orf19.2251	*AAH1*	1.1	1.3	1.2	1.2	YNL141W	*AAH1*	1.0	-1.0	1.4	2.0	adenosine deaminase (by homology)
CA3588	orf19.2250	*SPE3*	1.2	1.1	1.1	1.0	YPR069C	*SPE3*	1.0	-2.4	-2.2	-1.8	putrescine aminopropyltransferase by homology
CA3589	orf19.2249	*IPF10113*	1.1	1.0	-1.1	1.0	YNR020C		1.0	-1.0	-1.1	-1.1	unknown function
CA3590	orf19.2248	*ARE2*	1.2	2.2	3.6	3.0	YNR019W	*ARE2*	1.0	-1.5	-1.2	-1.0	acyl-CoA sterol acyltransferase-like (by homology)
CA3592	orf19.2246	*IPF12900*	1.0	1.0	1.0	1.0	YPL199C		1.0	1.3	1.4	1.4	unknown function

CA3593	orf19.2245	*YPT71*	1.2	1.1	1.0	1.1	YML001W	*YPT7*	1.0	-1.1	1.1	1.2	GTP-binding protein of the RAB family (by homology)
CA3594	orf19.4922	*IPF6076.3*	1.0	1.0	1.1	1.1	YGL161C		1.0	-1.2	-1.1	-1.3	unknown function, 3-prime end
CA3597	orf19.4927	*BNI1*	-1.1	-1.0	-1.2	-1.0	YNL271C	*BNI1*	1.0	-2.7	-2.5	-2.2	regulator of budding (by homology)
CA3598	orf19.12394	*SEC2*	-1.2	-1.1	-1.1	-1.1	YNL272C	*SEC2*	1.0	-1.0	-1.1	-1.1	GDP/GTP exchange factor (by homology)
CA3599	orf19.4929	*IPF19785*	-1.1	-1.0	-1.1	-1.0	YLR067C	*PET309*	1.0	1.1	1.7	2.2	unknown function
CA3600	orf19.4930	*SPC3*	1.1	1.1	1.2	1.1	YLR066W	*SPC3*	1.0	1.3	1.1	-1.1	signal peptidase subunit (by homology)
CA3601	orf19.4931	*IPF15618*	-1.3	-1.3	-1.7	-1.4	YNL247W		1.0	-1.2	-1.1	-1.1	cysteinyl-tRNA synthetase (by homology)
CA3602		*RPL14B.3*	1.0	-1.0	-1.1	1.0	YKL006W	*RPL14A*	1.0	1.8	1.7	2.5	ribosomal protein L14B, 3-prime end (by homology)
CA3603	orf19.4932	*MEF1*	-1.3	-1.8	-2.0	-2.0	YLR069C	*MEF1*	1.0	-2.3	-5.7	-2.6	mitochondrial translation elongation factor G (by homology)
CA3607	orf19.24	*RTA2*	1.0	1.4	2.0	1.5	YOR049C		1.0	-1.9	-1.4	-1.3	Unknown function
CA3608	orf19.25	*IPF3857*	-1.1	-1.2	-1.2	-1.2	YOL093W		1.0	1.1	1.2	1.4	unknown function
CA3609	orf19.26	*IPF3856*	-1.1	-1.0	-1.1	-1.0	YPL096W	*PNG1*	1.0	-1.2	-1.1	-1.0	similar to Saccharomyces cerevisiae Png1P peptide:N-glycanase (by hor
CA3611	orf19.28	*IPF3853*	-1.1	-1.1	-1.1	-1.0	YGR096W		1.0	1.0	-1.0	-1.1	unknown function
CA3612	orf19.29	*IPF3852*	1.1	1.0	-1.0	1.0	YJR046W	*TAH11*	1.0	-1.5	-1.3	1.1	unknown function
CA3613	orf19.30	*SPF1*	1.0	1.1	1.2	1.2	YEL031W	*SPF1*	1.0	-1.2	-1.3	-1.3	P-type ATPase
CA3615	orf19.34	*GIT1*	-1.0	1.0	-1.0	-1.0	YCR098C	*GIT1*	1.0	-1.4	-1.7	-1.4	glycerophosphoinositol transporter (by homology)
CA3616		*ASN1*	-1.1	1.0	1.1	1.0	YPR145W	*ASN1*	1.0	1.0	2.3	3.5	asparagine synthetase (by homology)
CA3618	orf19.200	*THO1*	-1.1	-1.0	-1.1	-1.1	YER063W	*THO1*	1.0	-1.4	-1.1	-1.2	suppressor of the hpr1 ts phenotype (by homology)
CA3619	orf19.202	*CDC47.5*	-1.3	-1.2	-1.2	-1.2	YBR202W	*CDC47*	1.0	1.1	1.1	1.2	cell division control protein, , 5-prime end (by homology)
CA3620	orf19.203	*IPF9063*	1.1	1.1	1.2	1.0	YDR169C	*STB3*	1.0	1.3	1.2	1.3	similar to Saccharomyces cerevisiae Stb3p protein binding Sin3p (by hor
CA3625	orf19.12617	*CYR1.3F*	1.0	1.1	1.1	1.0	YJL005W	*CYR1*	1.0	1.1	-1.1	-1.1	adenylate cyclase, 3-prime end
CA3627	orf19.12613	*IPF18318*	-1.2	-1.0	-1.1	1.0	YLL007C		1.0	-1.1	-1.2	-1.1	unknown function
CA3631	orf19.12608	*TIM54*	-1.1	-1.4	-1.4	-1.4	YJL054W	*TIM54*	1.0	-1.4	-1.3	-1.0	Translocase for the insertion of proteins into the mitochondrial inner mem
CA3632	orf19.5142	*DFR1*	1.0	1.0	1.0	-1.1	YOR236W	*DFR1*	1.0	-1.1	-1.2	1.0	dihydrofolate reductase
CA3637	orf19.5136	*IPF9255*	-1.1	2.5	3.1	2.1	YGR017W		1.0	-1.7	-1.4	-1.5	unknown function
CA3639	orf19.5133	*IPF9251*	1.0	1.9	1.9	1.8	YOR363C	*PIP2*	1.0	-1.3	-1.1	-1.1	unknown function
CA3640	orf19.2031	*VPS24*	-1.0	1.0	1.0	1.1	YKL041W	*VPS24*	1.0	-1.1	-1.2	-1.2	endosomal Vps protein complex subunit
CA3648	orf19.2039	*MSF1*	-1.1	-1.1	-1.1	-1.1	YPR047W	*MSF1*	1.0	-1.4	-1.4	-1.6	phenylalanine--tRNA ligase
CA3649	orf19.2040	*IPF4132*	-1.0	-1.0	-1.0	1.0	YPR048W	*TAH18*	1.0	-1.0	1.5	1.7	unknown function
CA3650	orf19.2041	*IPF4134*	-1.3	1.0	-1.3	-1.1	YKR008W	*RSC4*	1.0	-1.1	-1.2	-1.1	unknown function
CA3651	orf19.2042	*MSS1*	-1.1	-1.1	-1.0	1.1	YMR023C	*MSS1*	1.0	1.1	1.5	1.2	Mitochondrial GTPase involved in expression of COX1 (by homology).
CA3654	orf19.2045	*IPF7452*	1.2	-1.0	1.2	-1.0	YOR311C	*HSD1*	1.0	1.2	1.2	1.6	unknown function
CA3656	orf19.2047	*IPF7456*	1.0	1.1	1.2	1.1	YOR289W		1.0	-1.1	-1.1	-1.1	unknown function
CA3658	orf19.2050	*TGL1*	-1.1	1.3	1.5	1.2	YKL140W	*TGL1*	1.0	-1.5	-1.9	-2.4	Triacylglycerol lipase (by homology)
CA3663	orf19.6463	*IPF11432*	-1.0	-1.1	-1.1	-1.1	YJR072C		1.0	1.2	1.4	1.4	unknown function
CA3664	orf19.6462	*IPF11433.3F*	1.1	-1.0	1.0	1.0	YKL207W		1.0	-1.7	-1.0	-1.0	unknown function, 3-prime end
CA3666	orf19.6461	*IPF11435*	1.0	-1.1	1.1	-1.0	YDR231C	*COX20*	1.0	1.1	-1.1	-1.1	unknown function
CA3667	orf19.6460	*IPF16323*	-1.4	-1.8	-2.1	-1.4	YKL197C	*PEX1*	1.0	-1.3	-1.2	-1.3	similar to Saccharomyces cerevisiae Pex1p peroxisomal assembly protei
CA3668	orf19.6459	*DPP3*	1.1	1.0	1.1	1.0	YDR284C	*DPP1*	1.0	1.0	-1.1	-1.3	Diacylglycerol Pyrophosphate Phosphatase by homology
CA3671	orf19.6457	*IPF13933*	1.0	-1.0	-1.0	1.0	YBL086C		1.0	1.0	1.0	1.0	unknown function
CA3673	orf19.6455	*IPF13667*	1.2	1.2	1.4	1.2	YHR122W		1.0	-1.7	-1.5	-1.3	unknown function
CA3676	orf19.6452	*RBP1*	1.4	1.1	1.4	1.3	YNL135C	*FPR1*	1.0	1.5	1.5	1.3	rapamycin-binding protein
CA3678	orf19.731	*IPF8392*	-1.1	-1.2	-1.4	-1.1	YLR080W		1.0	1.0	-1.0	-1.0	unknown function
CA3679	orf19.730	*IPF20142*	-1.0	1.0	-1.0	-1.1	YFL047W	*RGD2*	1.0	1.0	1.3	1.2	unknown function
CA3681	orf19.728	*IPF19787*	-1.1	1.0	-1.0	-1.1	YER093C		1.0	-1.4	-1.8	-1.8	unknown function
CA3683	orf19.726	*PPZ1*	1.1	1.2	1.3	1.1	YML016C	*PPZ1*	1.0	-2.0	-1.9	-2.0	ser/thr phosphatase required for normal osmoregulation (by homology)
CA3685	orf19.723	*IPF19540*	1.2	-1.0	1.2	1.1	YPL230W	*USV1*	1.0	1.6	1.5	-1.1	unknown function
CA3686	orf19.13642	*IPF4890*	1.4	1.4	2.2	1.5	YOL119C		1.0	-1.8	-1.2	1.1	unknown function
CA3688		*YIP3.3*	1.3	1.2	1.6	1.3	YNL044W	*YIP3*	1.0	1.0	-1.1	1.0	protein of unknown function, 3-prime end (by homology)
CA3689	orf19.6265	*RPS22A*	1.9	1.2	1.2	1.4	YJL190C	*RPS22A*	1.0	1.1	1.2	1.4	ribosomal protein S15a.e.c10 (by homology)
CA3690		*RPS14B*	1.1	1.0	-1.1	1.1	YJL191W	*RPS14B*	1.0	1.2	1.4	1.7	ribosomal protein (by homology)
CA3693	orf19.6268	*IPF4874*	-1.1	-1.1	-1.1	-1.0	YBR007C		1.0	-1.8	-1.2	1.1	unknown function
CA3696	orf19.13650	*IPF4868*	-1.1	-1.1	-1.0	1.1	YPR045C		1.0	-1.5	-1.4	-1.5	unknown function
CA3697	orf19.13651	*IPF4866*	1.0	1.1	1.1	-1.0	YJR099W	*YUH1*	1.0	-2.2	-1.5	-1.4	similar to Saccharomyces cerevisiae Yuh1p ubiquitin-specific protease
CA3699	orf19.6275	*IPF4860*	1.1	1.0	-1.0	-1.0	YBR028C		1.0	-1.2	-1.4	-1.4	similarity to ribosomal protein kinases (by homology)
CA3705	orf19.4945	*MSH6*	-1.1	1.0	1.0	-1.0	YDR097C	*MSH6*	1.0	-1.3	-1.1	1.1	DNA mismatch repair protein by homology
CA3707	orf19.4941	*TYE7*	-1.1	16.4	15.0	11.4	YOR344C	*TYE7*	1.0	1.4	2.2	3.2	Basic helix-loop-helix transcription factor by homology
CA3709	orf19.4939	*IPF7880*	-1.4	1.1	-1.1	1.1	YNL297C	*MON2*	1.0	-1.1	-1.1	-1.0	unknown function
CA3711	orf19.4937	*CHS3.3F*	1.0	1.1	1.2	1.0	YBR023C	*CHS3*	1.0	-1.4	-1.7	-1.5	chitin-UDP acetyl-glucosaminyl transferase 3, 5-prime end
CA3714	orf19.11639	*IPF16223*	-1.3	-1.3	-1.6	-1.2	YGR198W		1.0	-1.8	-1.3	-1.5	unknown function
CA3715	orf19.4164	*IPF6205*	1.1	-1.0	-1.1	-1.0	YJR014W		1.0	-1.2	-1.1	-1.1	unknown function

CA3717	orf19.11643	*IPF6192*	1.1	-1.1	-1.0	-1.0	YPL108W		1.0	1.1	1.0	1.1	unknown function
CA3718	orf19.11644	*POP7*	-1.1	-1.1	1.0	-1.1	YBR167C	*POP7*	1.0	1.3	1.4	1.9	Nuclear RNase P subunit (by homology)
CA3723	orf19.4173	*DPH2*	1.0	-1.0	-1.0	-1.0	YKL191W	*DPH2*	1.0	-1.2	-1.2	-1.1	Diphtheria toxin resistance protein (by homology)
CA3724	orf19.4174	*IPF6181*	1.0	1.1	1.6	1.1	YAL022C	*FUN26*	1.0	-1.6	-1.4	-1.3	similar to Saccharomyces cerevisiae Fun 26p nucleoside transporter (by
CA3725	orf19.4175	*TOK1.3*	-1.1	-1.0	1.1	-1.0	YJL093C	*TOK1*	1.0	-1.5	-1.7	-1.8	Outward-rectifier potassium channel, 3-prime end (by homology)
CA3726	orf19.4176	*IPF6175*	-1.1	-1.1	1.1	1.0	YMR188C		1.0	-1.1	-1.4	-1.7	unknown function
CA3727	orf19.4177	*HIS5.3F*	-1.1	-1.1	-1.0	-1.0	YIL116W	*HIS5*	1.0	1.1	1.2	2.0	Histidinol-phosphate aminotransferase, 3-prime end (by homology)
CA3730	orf19.4180	*IPF11900*	1.1	1.1	1.1	1.1	YLR292C	*SEC72*	1.0	-1.5	-1.8	-1.7	unknown function
CA3731	orf19.4181	*SPC2*	1.1	1.1	1.1	-1.0	YML055W	*SPC2*	1.0	-1.3	-1.2	-1.4	signal peptidase 18 kDa subunit (by homology)
CA3736	orf19.2183	*IPF5533*	1.3	1.5	1.2	1.1	YER036C	*KRE30*	1.0	1.1	1.4	2.8	ABC transporter (by homology)
CA3737	orf19.2182	*BLM3*	-1.2	1.4	1.1	1.2	YFL007W	*BLM3*	1.0	-1.5	-1.4	-1.2	bleomycin resistance (by homology)
CA3738	orf19.2180	*IPF5526*	1.1	-1.0	-1.0	-1.0	YGR058W		1.0	1.2	1.3	1.3	unknown function
CA3739		*RPS10.3*	1.4	-1.1	-1.1	1.0	YOR293W	*RPS10A*	1.0	1.6	2.2	2.6	ribosomal protein, 3-prime end (by homology)
CA3740	orf19.2179	*SIT1*	1.1	1.2	1.6	1.1	YHL040C	*ARN1*	1.0	-1.2	-1.3	-1.2	Ferrioxamine B permease by homology
CA3741	orf19.2178	*MRS4*	1.1	1.2	1.3	1.3	YKR052C	*MRS4*	1.0	-1.4	-1.3	-1.3	RNA splicing protein and member of the mitochondrial carrier family (MC
CA3743	orf19.2175	*IPF19998*	1.0	1.1	1.2	1.1	YNR074C		1.0	1.1	1.0	-1.1	unknown function
CA3744	orf19.2174	*RAD57*	-1.0	-1.0	-1.0	-1.0	YDR004W	*RAD57*	1.0	1.1	1.2	1.0	DNA-repair like protein
CA3745	orf19.2173	*MAF1*	-1.0	-1.1	1.1	1.0	YDR005C	*MAF1*	1.0	1.1	1.2	1.2	nuclear protein by homology
CA3746	orf19.2172	*ARA1*	1.1	1.2	1.2	1.1	YBR149W	*ARA1*	1.0	-1.2	-1.4	-1.7	D-arabinose dehydrogenase (by homology)
CA3747	orf19.2170	*IPF10153*	1.5	1.3	1.2	1.1	YOL084W	*PHM7*	1.0	-1.1	1.1	-1.1	membrane transporter by homology
CA3752	orf19.3426	*TIF51.3*	1.2	-1.2	-1.2	-1.0	YEL034W	*HYP2*	1.0	1.5	1.8	1.7	translation initiation factor eIF-5A, 3-prime end
CA3754	orf19.3423	*TIF3*	-1.2	-1.1	-1.5	-1.3	YPR163C	*TIF3*	1.0	1.6	2.9	3.5	translation initiation factor eIF4B (by homology)
CA3755		*IPF17743*	-1.0	-1.0	-1.2	-1.0	YBL093C	*ROX3*	1.0	-1.4	-1.3	-1.3	Unknown function
CA3756	orf19.3422	*IPF8884*	-1.1	-1.0	-1.3	-1.1	YLR454W		1.0	1.1	-1.8	-2.7	unknown function
CA3757	orf19.3419	*MAE1*	-1.2	1.0	1.2	-1.2	YKL029C	*MAE1*	1.0	1.2	1.8	4.4	mitochondrial malic enzyme (by homology)
CA3760	orf19.2909	*ERG26*	1.0	-1.0	-1.1	1.0	YGL001C	*ERG26*	1.0	1.2	1.9	2.1	C-3 sterol dehydrogenase (C-4 decarboxylase) (by homology)
CA3767	orf19.2901	*NUP60*	-1.1	1.1	-1.0	1.0	YAR002W	*NUP60*	1.0	-1.5	-1.2	1.1	Putative nuclear pore protein (by homology)
CA3769	orf19.2898	*IPF13465*	1.1	-1.1	-1.0	1.0	YNL275W		1.0	1.1	1.0	1.3	Putative anion transport protein (by homology)
CA3772	orf19.2895	*VMA8*	-1.0	-1.1	-1.0	1.0	YEL051W	*VMA8*	1.0	-1.2	1.6	1.3	CANAL VACUOLAR ATP SYNTHASE SUBUNIT D
CA3773	orf19.2893	*IPF11153*	-1.0	-1.1	1.0	1.1	YDR416W	*SYF1*	1.0	-1.2	-1.2	1.1	unknown function
CA3774	orf19.2892	*IPF10437*	1.0	-1.0	1.0	1.0	YHR103W	*SBE22*	1.0	-1.5	-1.4	-1.2	budding protein-like (by homology)
CA3775	orf19.2891	*AFG1*	-1.0	-1.5	-1.4	-1.2	YEL052W	*AFG1*	1.0	1.2	1.2	-1.1	ATPase family gene (by homology)
CA3777	orf19.2889	*IPF10432*	1.0	1.1	1.0	1.1	YEL044W	*IES6*	1.0	-2.4	-2.1	-1.7	unknown function
CA3781	orf19.5839	*IPF11224*	-1.0	1.0	-1.0	1.0	YNL231C	*PDR16*	1.0	-1.0	-1.1	-1.1	similar to Saccharomyces cerevisiae Pdr16p protein involved in lipid bios
CA3782	orf19.5838	*SER2*	1.0	-1.1	-1.1	-1.0	YGR208W	*SER2*	1.0	1.3	1.1	1.7	phosphoserine phosphatase by homology to S. cerevisiae
CA3783	orf19.5837	*IPF11226*	1.0	1.0	1.0	1.1	YMR289W		1.0	-1.3	1.2	1.1	unknown function
CA3784	orf19.5835	*IPF11229*	1.0	-1.1	-1.1	1.1	YCL031C	*RRP7*	1.0	-1.3	-1.0	1.2	similar to Saccharomyces cerevisiae Rrp7p involved in pre-rRNA process
CA3785	orf19.5834	*IPF19788*	-1.0	1.0	-1.1	-1.0	YDR395W	*SXM1*	1.0	-1.3	1.0	-1.1	similar to Saccharomyces cerevisiae Sxm1p putative beta-karyopherin (b
CA3786	orf19.5833	*UFD1*	-1.1	1.2	1.1	1.1	YGR048W	*UFD1*	1.0	-1.1	-1.0	1.1	Ubiquitin fusion degradation protein (by homology)
CA3787	orf19.5832	*HPT1*	-1.2	-1.1	1.1	-1.0	YDR399W	*HPT1*	1.0	-1.1	-1.3	1.4	hypoxanthine guanine phosphoribosy transferase(by homology)
CA3789	orf19.13252	*IPF11217*	-1.4	-1.3	-1.6	-1.2	YKL073W	*LHS1*	1.0	-1.4	-1.5	-1.5	similar to Saccharomyces cerevisiae Lhs1p chaperone of the ER lumen (
CA3790	orf19.13250	*IPF11215*	-1.1	-1.0	-1.1	-1.1	YKL074C	*MUD2*	1.0	-1.2	-1.1	1.1	unknown function
CA3791	orf19.5827	*IPF11212*	1.0	1.0	1.0	1.0	YMR055C	*BUB2*	1.0	-1.2	1.3	1.4	similar to Saccharomyces cerevisiae Bub2 cell cycle arrest protein (by ho
CA3793		*IPF5701*	1.1	1.0	1.1	1.1	YER074W	*RPS24A*	1.0	2.2	2.2	2.5	unknown function
CA3794	orf19.5825	*NCB2*	-1.0	1.2	1.1	1.0	YDR397C	*NCB2*	1.0	-1.3	-1.4	-1.2	Transcriptional repressor by homology
CA3796	orf19.5823	*SGT2*	-1.2	-1.1	-1.3	-1.2	YOR007C	*SGT2*	1.0	-1.0	1.2	1.5	small glutamine-rich tetratricopeptide repeat containing protein by homol
CA3797	orf19.5821	*IPF5623*	-1.2	-1.1	-1.0	-1.1	YML002W		1.0	-1.9	-1.5	-1.7	unknown function
CA3800		*RPL7A.3*	1.0	-1.1	-1.2	-1.1	YPL198W	*RPL7B*	1.0	1.4	2.5	2.9	60S Ribosomal Protein L7-A, 3-prime end
CA3802		*AUT7.EXON2*	1.1	1.0	1.2	-1.0	YBL078C	*AUT7*	1.0	1.1	-1.2	-1.4	microtubule-associated protein essential for autophagy, exon 2 (by homo
CA3805	orf19.2484	*IPF12403*	1.0	1.1	1.2	1.1	YDR415C		1.0	-1.4	-1.2	-1.2	unknown function
CA3806	orf19.2485	*IPF9224*	-1.1	1.0	-1.0	1.0	YBL079W	*NUP170*	1.0	-1.4	-1.3	-1.4	similar to Saccharomyces cerevisiae Nup170p nuclear pore protein (by h
CA3807	orf19.2487	*IPF9225*	-1.1	1.0	1.0	-1.1	YDR020C		1.0	-1.4	-1.3	-1.1	unknown function
CA3808	orf19.2488	*FAL1*	-1.0	-1.1	-1.3	-1.3	YDR021W	*FAL1*	1.0	-1.4	-1.2	-1.3	ATP-dependent RNA helicase
CA3809	orf19.2489	*KAP123*	1.3	1.3	1.2	1.1	YER110C	*KAP123*	1.0	-1.0	1.6	2.8	karyopherin-beta protein (by homology)
CA3810	orf19.2492	*IPF9230*	-1.0	1.0	-1.1	-1.0	YKL178C	*STE3*	1.0	-1.8	-1.4	-1.5	similar to Saccharomyces cerevisiae Ste3p pheromone a-factor receptor
CA3811	orf19.2494	*PET112*	-1.0	-1.0	-1.1	1.0	YBL080C	*PET112*	1.0	-1.2	-1.2	-1.0	glutamyl-tRNA (GLN) amidotransferase subunit B (by homology)
CA3814	orf19.2498	*IPF4023*	1.0	1.1	1.2	1.1	YDR143C	*SAN1*	1.0	1.2	1.3	1.7	unknown function
CA3815	orf19.2499	*CYP7*	1.0	-1.0	1.0	-1.0	YJR032W	*CPR7*	1.0	-1.2	-1.3	-1.3	peptidyl-prolyl cis-trans isomerase cyp7 (ppiase)
CA3818	orf19.5773	*IPF6695*	-1.5	-2.2	-2.5	-1.9	YOL057W		1.0	-1.2	-1.1	-1.1	unknown function
CA3819	orf19.5772	*IPF6993*	-1.0	-1.1	-1.1	-1.1	YBR231C	*AOR1*	1.0	1.0	1.1	1.2	unknown function
CA3820	orf19.5771	*PBP2*	-1.1	-1.1	-1.1	-1.1	YBR233W	*PBP2*	1.0	-1.3	-1.3	-1.3	PAB1 binding protein (by homology)

CA3821	orf19.5770	*IPF6990*	-1.0	-1.0	1.1	-1.0	YGL114W		1.0	-1.1	1.1	1.2	unknown function
CA3822	orf19.5767	*CUS2*	-1.0	-1.0	-1.1	-1.1	YNL286W	*CUS2*	1.0	-1.1	-1.1	-1.0	cold sensitive U2 snRNA Suppressor(by homology)
CA3823	orf19.5765	*IPF10651*	-1.1	-1.0	-1.1	-1.1	YJL061W	*NUP82*	1.0	-1.2	-1.2	1.1	unknown function
CA3824	orf19.5764	*SKI8*	-1.1	-1.1	-1.0	-1.0	YGL213C	*SKI8*	1.0	-1.1	1.1	1.4	antiviral protein-like (by homology)
CA3828	orf19.5759	*SNQ2*	-1.0	1.8	2.0	1.4	YDR011W	*SNQ2*	1.0	-1.1	-1.3	1.0	multidrug resistance protein (by homology)
CA3830	orf19.6589	*SSF1*	1.1	1.0	-1.0	1.0	YDR312W	*SSF2*	1.0	1.2	1.2	1.6	mating protein (by homology)
CA3831	orf19.6590	*VMA22*	1.1	1.0	-1.0	-1.0	YHR060W	*VMA22*	1.0	-1.2	1.1	1.4	vacuolar ATPase assembly protein (by homology)
CA3832	orf19.6591	*IPF8193*	-1.1	-1.1	-1.1	-1.1	YLR151C	*PCD1*	1.0	-1.9	-1.3	1.0	unknown function
CA3834	orf19.6594	*PLB3*	-1.1	1.3	1.3	1.2	YMR008C	*PLB1*	1.0	-1.8	-1.7	-1.3	phospholipase B (by homology)
CA3836	orf19.6596	*IPF8179*	1.2	1.3	1.4	1.3	YJL068C		1.0	-1.2	-1.1	-1.5	putative esterase (by homology)
CA3838	orf19.6598	*LAS17*	1.1	1.1	1.1	-1.1	YOR181W	*LAS17*	1.0	-1.0	1.1	1.1	actin assembly factor (by homology)
CA3840	orf19.6600	*IPF12745*	1.0	1.2	1.2	1.1	YLR193C		1.0	1.0	1.0	1.1	unknown function
CA3842		*YKE2.3*	1.1	-1.1	1.1	1.1	YLR200W	*YKE2*	1.0	-1.7	-1.5	-1.3	Gim complex component, 3-prime end (by homology)
CA3843	orf19.6602	*IPF7947*	-1.1	-1.0	1.1	-1.0	YLR201C		1.0	-2.8	-2.6	-2.9	unknown function
CA3845	orf19.6605	*IPF7944*	-1.1	1.0	1.1	1.1	YOR292C		1.0	-1.3	-1.1	-1.0	unknown function
CA3849	orf19.6610	*IPF7938*	-1.0	1.1	1.1	-1.0	YLR045C	*STU2*	1.0	-2.3	-2.2	-1.9	similar to Saccharomyces cerevisiae Stu2p suppressor of cold-sensitive
CA3850	orf19.6612	*IPF7932*	1.1	-1.2	-1.1	-1.0	YGR207C		1.0	-1.0	1.1	-1.1	similar to Saccharomyces cerevisiae Etf-beta electron-transferring flavop
CA3852	orf19.6109	*TUP1*	1.0	1.0	1.1	-1.0	YCR084C	*TUP1*	1.0	-1.0	1.3	-1.2	general transcription repressor
CA3853	orf19.6105	*MVD1.3*	1.1	1.1	1.2	1.1	YNR043W	*MVD1*	1.0	1.2	1.8	2.0	mevalonate pyrophosphate decarboxylase, 3-prime end
CA3854	orf19.6102	*IPF4649*	1.0	1.1	1.2	-1.0	YIL036W	*CST6*	1.0	-1.1	1.1	1.2	unknown Function
CA3855	orf19.6103	*IPF4645*	1.0	1.0	-1.0	-1.0	YER046W	*SPO73*	1.0	1.0	1.0	1.3	unknown Function
CA3856	orf19.6100	*IPF4641*	1.1	1.1	1.1	1.0	YDL142C	*CRD1*	1.0	-1.3	-1.1	-1.1	similar to Saccharomyces cerevisiae Crd1p cardiolipin synthase (by hom
CA3857	orf19.6099	*CCT8*	1.0	-1.1	-1.1	-1.1	YJL008C	*CCT8*	1.0	-1.2	1.2	1.2	component of chaperonin-containing T-complex
CA3858	orf19.6096	*TRP1*	-1.1	1.0	1.1	-1.0	YDR007W	*TRP1*	1.0	1.1	1.0	-1.1	phosphoribosylanthranilate isomerase
CA3859	orf19.6094	*IPF4632*	-1.0	1.1	1.1	1.0	YJL029C	*VPS53*	1.0	1.2	1.1	1.3	similar to Saccharomyces cerevisiae Vps53p subunit of VP52-54 comple
CA3860	orf19.6092	*KEL1*	-1.0	-1.2	-1.4	-1.2	YGR238C	*KEL2*	1.0	-1.3	-1.3	-1.5	involved in cell fusion and morphology (by homology)
CA3861	orf19.6091	*RIM8*	1.0	-1.0	-1.0	1.0	YGL046W		1.0	1.0	1.1	-1.1	regulator of PH response
CA3862	orf19.6090	*NSR1*	1.2	1.1	1.1	1.1	YGR159C	*NSR1*	1.0	1.2	1.5	2.9	nuclear localization sequence binding protein (by homology)
CA3863	orf19.6086	*LEU41*	1.1	-1.0	-1.0	-1.0	YNL104C	*LEU4*	1.0	-1.4	-1.2	1.1	2-isopropylmalalate synthase (by homology)
CA3864	orf19.6085	*RPL16A*	-1.0	-1.2	-1.4	-1.2	YNL069C	*RPL16B*	1.0	1.6	2.9	3.9	ribosomal protein (by homology)
CA3866	orf19.6082	*IPF4606*	-1.3	-1.3	-1.2	-1.1	YML048W	*GSF2*	1.0	1.2	1.5	1.3	unknown Function
CA3867	orf19.13500	*PHR2*	1.1	1.1	1.4	1.2	YMR307W	*GAS1*	1.0	1.1	2.3	2.4	pH-regulated protein 2
CA3868	orf19.401	*CCT1*	-1.2	-1.0	-1.1	-1.2	YDR212W	*TCP1*	1.0	1.2	1.4	1.5	component of chaperonin-containing T-complex (by homology)
CA3870	orf19.399	*YPK1*	-1.1	1.3	1.5	1.3	YMR104C	*YPK2*	1.0	1.0	1.3	-1.1	ser/thr-specific protein kinase (by homology)
CA3872	orf19.397	*MRPL28*	1.0	-1.0	-1.2	-1.0	YDR462W	*MRPL28*	1.0	-1.4	-1.3	-1.6	mitochondrial ribosomal protein of the large subunit (by homology)
CA3873	orf19.396	*IPF8825*	1.0	1.0	-1.0	1.1	YJR082C		1.0	-1.3	-1.3	-1.4	unknown function
CA3874	orf19.395	*ENO1*	1.6	1.6	1.2	1.5	YGR254W	*ENO1*	1.0	1.8	2.7	4.2	Enolase I (2-phosphoglycerate dehydratase)
CA3875	orf19.8024	*IPF14430*	-1.1	-1.1	-1.0	1.1	YLR231C		1.0	-1.0	1.1	1.1	putative kynureninase (by homology)
CA3876	orf19.8023	*APS3*	1.1	1.2	1.1	1.1	YJL024C	*APS3*	1.0	-1.6	-1.4	-1.4	AP-3 complex subunit, sigma3 subunit (by homology)
CA3877	orf19.392	*CBP4*	-1.0	-1.1	-1.1	-1.0	YGR174C	*CBP4*	1.0	-1.0	-1.3	-1.7	Ubiquinol--cytochrome-c reductase assembly factor (by homology)
CA3878	orf19.391	*IPF7289*	-1.2	1.1	1.2	1.2	YDR213W	*UPC2*	1.0	-1.2	-1.4	-1.3	similar to Saccharomyces cerevisiae Upc2p RNA polymerase II transcrip
CA3879	orf19.390	*CDC42*	1.1	1.3	1.5	1.3	YLR229C	*CDC42*	1.0	1.3	1.5	1.9	Cell Division Control
CA3880	orf19.388	*CAF16*	-1.0	1.2	1.2	1.2	YFL028C	*CAF16*	1.0	-1.3	1.2	1.3	ABC ATPase (by homology)
CA3881	orf19.387	*GCR3*	-1.3	-1.0	-1.2	-1.0	YMR125W	*STO1*	1.0	-1.4	1.0	1.1	Large subunit of the nuclear cap-binding protein complex CBC (by homol
CA3882	orf19.386	*IPF7279*	-1.0	-1.1	-1.2	-1.1	YPL273W	*SAM4*	1.0	1.9	3.5	4.3	putative cobalamin-dependent homocysteine S-methyltransferase (by ho
CA3883	orf19.8015	*GCV2*	-1.2	-3.7	-5.2	-3.7	YMR189W	*GCV2*	1.0	1.0	-1.2	-1.2	Glycine decarboxylase P subunit
CA3884	orf19.8014	*IPF6367*	1.0	1.0	1.0	1.0	YPL247C		1.0	1.2	-1.1	-1.4	unknown function
CA3885	orf19.5095	*IPF19790*	-1.0	1.0	-1.2	-1.2	YDL019C	*OSH2*	1.0	-1.3	-1.2	-1.4	unknown function
CA3887	orf19.5093	*IPF12964*	-1.0	-1.0	-1.1	-1.0	YLR321C	*SFH1*	1.0	1.0	-1.0	1.2	similar to Saccharomyces cerevisiae Sfh1p subunit of the RSC chromati
CA3889	orf19.5090	*TAD3*	1.1	1.0	-1.0	1.1	YLR316C	*TAD3*	1.0	-1.1	-1.1	-1.3	tRNA-specific adenosine-34 deaminase subunit (by homology)
CA3890	orf19.5089	*TERT2*	-1.1	-1.0	-1.1	1.0	YLR318W	*EST2*	1.0	-1.6	-1.3	-1.1	telomerase reverse transcriptase 2
CA3891	orf19.5087	*BUD6*	-1.1	-1.1	-1.1	-1.0	YLR319C	*BUD6*	1.0	1.2	1.2	1.4	bud site selection protein (by homology)
CA3892	orf19.5085	*PSE1*	-1.2	-1.0	-1.2	-1.2	YMR308C	*PSE1*	1.0	-1.1	1.5	1.8	karyopherin-beta protein (by homology)
CA3893	orf19.5083	*FUN11*	-1.3	-1.1	-1.2	-1.1	YAL036C	*FUN11*	1.0	-1.1	1.0	1.5	putative GTP-binding protein (by homology)
CA3894	orf19.5081	*YIF2*	-1.0	1.1	-1.0	-1.1	YAL035W	*FUN12*	1.0	-1.6	-1.4	1.1	general translation factor eIF2 homolog (by homology)
CA3897	orf19.5076	*PFY1*	1.2	-1.0	1.0	1.0	YOR122C	*PFY1*	1.0	1.1	1.2	1.0	BINDS TO ACTIN
CA3898	orf19.5074	*UBA2*	-1.3	-1.0	-1.2	-1.2	YDR390C	*UBA2*	1.0	-1.2	1.1	1.0	ubiquitin-activating -like enzyme by homology
CA3899	orf19.5073	*DPM1*	1.1	1.3	1.5	1.6	YPR183W	*DPM1*	1.0	1.2	1.8	1.8	dolichol-phosphate (beta-D) mannosyltransferase 1 by homology
CA3900	orf19.5071	*IPF10092*	-1.0	1.1	-1.0	-1.0	YDL167C	*NRP1*	1.0	1.2	1.4	2.1	unknown function
CA3902	orf19.4401	*YVH1*	1.1	1.0	1.1	1.1	YIR026C	*YVH1*	1.0	1.1	1.1	1.4	protein tyrosine phosphatase (by homology)
CA3904	orf19.11877	*IPF14888*	-1.1	-1.1	-1.1	-1.1	YNL119W		1.0	1.0	1.4	1.7	unknown function

CA3905	orf19.11876	*IPF19792*	1.1	1.0	1.0	-1.0	YPR147C		1.0	-1.1	-1.4	-1.3	unknown function
CA3906	orf19.11874	*IPF20149*	-1.0	-1.2	-1.2	-1.1	YKR016W		1.0	-1.2	-1.1	-1.7	unknown function
CA3907	orf19.11873	*IPF3304*	-1.1	1.1	1.1	1.1	YMR092C	*AIP1*	1.0	1.0	1.5	1.1	similar to Saccharomyces cerevisiae Aip1p actin cytoskeleton componen
CA3909	orf19.4393	*CIT1.EXON2*	-1.0	-1.0	-1.2	-1.3	YNR001C	*CIT1*	1.0	-2.0	-2.4	-5.8	Citrate synthase, exon 2
CA3910	orf19.4392	*IPF3293*	-1.1	1.0	-1.0	1.1	YBR163W	*DEM1*	1.0	-1.1	-1.1	-1.1	unknown function
CA3913	orf19.4388	*IPF3283*	1.0	-1.0	-1.1	-1.0	YPL011C	*TAF47*	1.0	1.0	1.1	1.3	unknown function
CA3916	orf19.4383	*IPF3274*	1.0	1.0	-1.0	1.0	YOR258W	*HNT3*	1.0	-1.4	-1.1	-1.4	Unknown function
CA3917	orf19.4382	*IPF3273*	1.2	1.2	1.2	1.2	YPL010W	*RET3*	1.0	1.1	1.1	-1.1	similar to Saccharomyces cerevisiae Ret3p coatomer complex zeta chai
CA3918	orf19.4381	*VTC2*	1.0	1.5	1.9	1.8	YFL004W	*VTC2*	1.0	-1.4	-1.1	-1.1	putative polyphosphate synthetase (by homology)
CA3920	orf19.5118	*SDS24*	-1.0	-1.0	-1.1	-1.0	YBR214W	*SDS24*	1.0	1.4	1.1	-1.0	Similar to S. cerevisiae YBR214w which presents strong similarity to hyp
CA3921	orf19.5117	*OLE1*	-1.2	-1.3	-1.1	-1.1	YGL055W	*OLE1*	1.0	-2.0	1.9	2.0	Stearoyl-CoA desaturase (by homology)
CA3922	orf19.5114	*GRD19*	-1.0	1.1	1.1	1.0	YOR357C	*GRD19*	1.0	1.1	-1.1	-1.1	Probable golgi membrane protein-sorting protein (by homology)
CA3923	orf19.5113	*ADH2*	1.2	2.4	2.1	2.0	YOL086C	*ADH1*	1.0	1.6	2.2	2.4	alcohol dehydrogenase I (by homology)
CA3924	orf19.5112	*TKL1*	1.2	-1.2	-1.0	-1.1	YPR074C	*TKL1*	1.0	-1.3	-1.1	-1.2	transketolase 1
CA3926	orf19.5107	*IPF16198*	1.0	-1.0	-1.1	-1.1	YPR072W	*NOT5*	1.0	-1.6	1.4	1.2	possible regulatory protein
CA3927	orf19.5106	*DIP2*	-1.0	-1.1	-1.1	-1.0	YLR129W	*DIP2*	1.0	-1.2	-1.1	1.2	beta transducin
CA3928	orf19.5105	*GAL11*	1.1	1.0	1.1	1.0	YOL051W	*GAL11*	1.0	-1.1	1.3	1.1	DNA-directed RNA polymerase II holoenzyme and Kornberg s mediator
CA3930	orf19.5104	*LPT1.EXON2*	1.1	-1.0	1.0	-1.0	YPR073C	*LTP1*	1.0	1.6	2.4	3.0	protein-tyrosine-phosphatase, exon 2
CA3933	orf19.9560	*IPF18281*	-1.0	-1.2	-1.3	-1.1	YMR026C	*PEX12*	1.0	-1.1	1.0	-1.1	similar to Saccharomyces cerevisiae Pex12p peroxisome assembly (by
CA3934	orf19.2008	*IPF17119*	-1.1	1.0	-1.1	1.0	YPR118W		1.0	1.3	1.2	1.5	unknown function
CA3935	orf19.2007	*IPF14688*	-1.2	-1.0	1.1	-1.0	YDR027C	*LUV1*	1.0	1.1	-1.0	1.0	unknown function
CA3936		*COX17*	1.0	1.1	1.1	1.1	YLL009C	*COX17*	1.0	-1.9	-2.2	-2.2	cysteine-rich cytoplasmic protein(by homology)
CA3937	orf19.9557	*IPF14686*	-1.0	1.1	-1.0	1.0	YPL162C		1.0	-1.1	1.0	1.1	unknown function
CA3938	orf19.9556	*IPF4764*	1.1	1.2	1.1	1.1	YDR028C	*REG1*	1.0	1.0	-1.0	-1.1	unknown Function
CA3940	orf19.9553	*NIC96*	-1.0	-1.0	-1.0	-1.0	YFR002W	*NIC96*	1.0	1.2	1.3	1.2	nuclear pore protein (by homology)
CA3942	orf19.2000	*CHL1*	1.0	1.0	-1.0	-1.0	YPL008W	*CHL1*	1.0	-1.4	-1.2	-1.3	protein of the DEAH box family (by homology)
CA3948	orf19.1993	*RPN9*	-1.2	-1.1	-1.0	-1.0	YDR427W	*RPN9*	1.0	-1.1	1.4	1.5	26S proteasome regulatory particle (by homology)
CA3950	orf19.9542	*PTM1*	1.1	1.1	1.3	1.3	YKL039W	*PTM1*	1.0	-1.1	-1.4	-1.3	Possibly involved in the TCA cycle (by homology)
CA3951	orf19.1409	*VAC7.3*	1.0	-1.1	-1.1	-1.0	YNL054W	*VAC7*	1.0	-2.5	-2.5	-2.0	Vacuolar protein, 3-prime end (by homology)
CA3954	orf19.1413	*YFH1*	1.0	1.0	-1.0	1.0	YDL120W	*YFH1*	1.0	1.0	1.1	1.1	Regulates mitochondrial iron accumulation (by homology)
CA3958	orf19.1416	*COX11*	1.1	1.1	1.3	1.0	YPL132W	*COX11*	1.0	-1.1	-1.0	-1.2	cytochrome-c oxidase assembly protein by homology to S. cerevisiae
CA3960	orf19.1419	*IPF11236.5F*	-1.0	1.0	-1.0	-1.0	YGL233W	*SEC15*	1.0	-1.0	-1.0	1.1	similar to Saccharomyces cerevisiae Sec15p component of the exocyst
CA3961	orf19.1420	*IPF11235*	-1.0	-1.1	1.0	1.0	YFR043C		1.0	-1.1	1.1	1.1	unknown function
CA3962	orf19.1421	*IPF11234*	1.0	1.0	1.0	1.0	YIR032C	*DAL3*	1.0	-1.3	-1.3	-1.1	similar to saccharomyces cerevisiae Dal3p ureidoglycolate hydrolase (by
CA3963	orf19.1422	*IPF11233*	-1.1	1.0	1.1	1.1	YBR179C	*FZO1*	1.0	1.1	-1.1	1.2	similar to Saccharomyces cerevisiae Fzo1p required for biogenesis of mi
CA3964	orf19.1424	*IPF9370*	1.0	-1.1	-1.1	-1.1	YMR155W		1.0	1.2	1.2	1.1	unknown function
CA3966	orf19.1427	*IPF9376*	1.1	1.1	1.4	1.1	YLR004C		1.0	-1.1	-1.0	-1.2	unknown function
CA3968	orf19.1429	*IPF9378*	-1.0	-1.1	-1.1	-1.1	YGL127C	*SOH1*	1.0	-1.1	-1.2	1.0	similar to Saccharomyces cerevisiae Soh1p suppressor of Hpr1p (by ho
CA3970	orf19.1542	*IPF6497*	-1.1	-1.0	-1.1	-1.0	YDL013W	*HEX3*	1.0	1.2	1.1	1.4	unknown function
CA3972	orf19.9118	*IPF6504*	1.1	1.0	-1.0	1.0	YDL099W		1.0	1.0	-1.0	1.2	unknown function
CA3973	orf19.1545	*IPF6505*	1.2	1.1	1.3	1.0	YMR158W		1.0	-1.8	-1.4	-1.4	unknown function
CA3974	orf19.1546	*IPF6507*	1.0	-1.1	-1.1	-1.1	YMR157C		1.0	-1.1	-1.2	-1.4	unknown function
CA3975	orf19.1547	*IPF20152*	1.0	1.0	-1.1	-1.0	YMR156C	*TPP1*	1.0	-1.7	-1.4	-1.6	unknown function
CA3976	orf19.1548	*SNU23*	-1.0	1.1	1.1	-1.0	YDL098C	*SNU23*	1.0	1.1	1.1	1.1	RNA binding zinc finger protein (by homology)
CA3979	orf19.1553	*ENT3.3F*	-1.1	1.1	1.1	1.0	YJR125C	*ENT3*	1.0	1.5	2.5	3.1	putative endocytosis and cytoskeleton protein, 3-prime end (by homolog
CA3982	orf19.9129	*SAC3*	-1.0	-1.1	-1.1	-1.0	YDR159W	*SAC3*	1.0	-1.4	-1.4	-1.1	Leucine permease transcriptional regulator
CA3983	orf19.9130	*IPF7133.3*	-1.0	1.1	1.1	1.0	YLR137W		1.0	1.1	1.2	1.1	unknown function, 3-prime end
CA3984	orf19.9132	*HOM2*	-1.3	1.3	1.3	1.2	YDR158W	*HOM2*	1.0	1.8	2.3	2.8	Aspartate-semialdehyde dehydrogenase (by homology)
CA3985	orf19.1560	*POB3*	-1.3	-1.1	-1.0	-1.0	YML069W	*POB3*	1.0	-1.0	1.1	-1.0	Binds DNA polymerase delta (by homology)
CA3987	orf19.1563	*ECM3*	1.2	1.2	1.6	1.2	YOR092W	*ECM3*	1.0	-1.1	-1.1	1.6	Involved in cell wall biogenesis and architecture (by homology).
CA3988	orf19.1564	*IPF7145*	1.1	1.5	1.8	1.9	YDL072C		1.0	1.1	1.1	1.1	unknown function
CA3989	orf19.1565	*IPF7147*	1.1	-1.0	1.0	1.0	YLR401C		1.0	-1.5	1.0	1.0	unknown function
CA3990	orf19.1566	*IPF14782*	1.1	-1.6	-1.9	-1.6	YLR409C		1.0	-2.2	-2.1	-2.1	beta-transducin (by homology)
CA3992	orf19.1568	*VAM6.3F*	-1.3	-1.1	-1.4	-1.1	YDL077C	*VAM6*	1.0	-1.2	-1.3	-1.3	Vacuolar carboxypeptidase Y, 3-prime end (by homology)
CA3993	orf19.9142	*IPF8275*	-1.3	-1.4	-1.8	-1.7	YGR090W		1.0	-1.3	-1.2	1.2	unknown function
CA3994	orf19.9143	*ERG7*	-1.1	-1.5	-1.6	-1.5	YHR072W	*ERG7*	1.0	1.1	1.5	1.6	lanosterol synthase
CA3996	orf19.1643	*IPF10440*	-1.0	-1.2	1.1	-1.1	YGR101W		1.0	-1.1	-1.0	1.0	unknown function
CA3997	orf19.1642	*LOC1*	-1.0	-1.1	-1.0	-1.1	YFR001W	*LOC1*	1.0	1.0	1.5	1.8	putative double-stranded RNA-binding protein (by homology)
CA4000	orf19.1636	*IPF4262*	-1.0	1.0	1.1	1.0	YCL032W	*STE50*	1.0	-1.9	-1.9	-1.6	similar to Saccharomyces cerevisiae Ste50p pheromone response path
CA4001	orf19.1635	*RPL12*	-1.0	-1.0	-1.0	-1.1	YEL054C	*RPL12A*	1.0	-2.3	1.8	2.6	ribosomal protein
CA4003	orf19.1633	*IPF4257*	-1.1	-1.1	-1.2	-1.1	YDR324C		1.0	1.3	1.4	1.8	unknown function

CA4005	orf19.1631	*ERG6*	1.2	-1.5	-1.4	-1.4	YML008C	*ERG6*	1.0	-1.3	1.0	1.0	sterol transmethylase
CA4006	orf19.1630	*IPF4253*	-1.1	-1.1	-1.1	-1.0	YML017W	*PSP2*					unknown function
CA4007	orf19.1628	*LAP41*	-1.0	-1.1	-1.1	-1.0	YKL103C	*LAP4*	1.0	1.1	-1.1	-1.8	aminopeptidase yscI precursor (by homology)
CA4008	orf19.1626	*DYS1*	-1.1	-1.1	-1.1	-1.1	YHR068W	*DYS1*	1.0	1.1	1.3	1.9	deoxyhypusine synthase
CA4010	orf19.1624	*MAK10.3*	-1.2	-1.2	-1.3	-1.2	YEL053C	*MAK10*	1.0	-1.0	-1.0	1.4	glucose-repressible protein, 3-prime end (by homology)
CA4011	orf19.1622	*IPF4240*	-1.2	-1.2	-1.2	-1.0	YDR325W	*YCG1*	1.0	1.0	1.0	1.0	similar to Saccharomyces cerevisiae Ycg1p condensin G (by homology)
CA4012	orf19.1621	*GPA2*	1.1	1.1	1.2	-1.1	YER020W	*GPA2*	1.0	-1.2	1.1	1.1	nucleotide-binding regulatory protein GPA2
CA4014	orf19.1619	*CTK1*	-1.1	-1.1	-1.1	-1.1	YKL139W	*CTK1*	1.0	-1.3	-1.3	-1.2	probable cell division protein kinase
CA4016	orf19.1618	*GFA1*	-1.2	1.8	1.8	1.8	YKL104C	*GFA1*	1.0	1.0	1.2	1.2	glutamine:fructose-6-phosphate amidotransferase
CA4017	orf19.3447	*PBN1*	1.0	1.0	1.0	-1.0	YCL052C	*PBN1*	1.0	1.4	1.7	1.0	protease by homology
CA4018	orf19.3446	*MOG1*	-1.0	1.0	-1.1	1.1	YJR074W	*MOG1*	1.0	-1.3	-1.6	-1.6	Ran-Binding Protein by homology
CA4019	orf19.3445	*HOC1*	1.0	-1.0	-1.0	1.0	YJR075W	*HOC1*	1.0	-1.0	1.1	1.4	GLYCOSYLTRANSFERASE by homology
CA4025	orf19.3438	*SCJ1*	-1.0	1.0	-1.0	-1.0	YMR214W	*SCJ1*	1.0	-1.4	1.2	1.4	Mitochondrial and ER import protein (by homology)
CA4029	orf19.3434	*IPF7171.5F*	-1.3	-1.5	-1.9	-1.5	YGR067C		1.0	-1.4	-1.2	-1.1	unknown function, 5-prime end
CA4030	orf19.3433	*EBP4*	1.0	4.4	6.0	4.4	YHR179W	*OYE2*	1.0	1.0	1.6	3.1	NADPH dehydrogenase (by homology)
CA4033	orf19.3431	*IPF19795*	1.1	1.1	1.0	-1.0	YOR330C	*MIP1*	1.0	1.1	1.3	1.4	similar to Saccharomyces cerevisiae Mip1p DNA-directed DNA polymera
CA4035	orf19.3665	*IPF12040*	1.0	-1.0	-1.1	-1.0	YPL165C		1.0	1.0	-1.0	-1.2	unknown function
CA4036	orf19.3666	*IPF12042*	-1.1	-1.1	-1.1	1.0	YGR093W		1.0	-1.1	-1.1	-1.1	unknown function
CA4039	orf19.3669	*SKS1*	-1.5	-1.1	-1.5	-1.3	YPL026C	*SKS1*	1.0	1.0	1.3	2.0	serine/threonine kinase by homology
CA4040	orf19.3670	*GAL1*	-1.0	1.1	1.2	1.1	YDR009W	*GAL3*	1.0	-1.4	-1.4	-1.5	galactokinase
CA4041	orf19.3672	*GAL10*	-1.4	1.5	1.2	1.1	YBR019C	*GAL10*	1.0	1.1	1.0	-1.0	UDP-glucose 4-epimerase by homology
CA4042	orf19.3673	*TRS23*	1.1	1.2	1.2	1.1	YDR246W	*TRS23*					targeting and fusion of ER to golgi transport vesicles by homology
CA4044	orf19.3675	*GAL7*	-1.1	2.3	2.4	1.5	YBR018C	*GAL7*	1.0	-1.1	-1.2	-1.3	UDP-glucose-hexose-1-phosphate uridylyltransferase (by homology)
CA4046	orf19.3677	*IPF9205*	-1.0	1.0	-1.0	-1.0	YPL149W	*APG5*	1.0	1.1	1.4	1.4	similar to Saccharomyces cerevisiae Apg5p involved in autophagy and n
CA4048	orf19.11163	*IPF9207*	-1.0	-1.0	1.1	1.0	YNL200C		1.0	-1.0	-1.1	-1.4	unknown function
CA4050	orf19.425	*10482.EXO*	1.1	-1.0	1.0	-1.0	YOL114C		1.0	-1.1	-1.3	-1.4	unknown function, exon 2
CA4052	orf19.427	*10231.EXO*	1.0	-1.1	-1.2	1.0	YBR275C	*RIF1*	1.0	1.2	1.0	1.2	similar to Saccharomyces cerevisiae Rif1p Rap1p-interacting factor 1, ex
CA4053	orf19.428	*IKS1*	-1.0	-1.0	1.1	1.0	YJL057C	*IKS1*	1.0	1.0	-1.1	-1.2	PROBABLE SERINE/THREONINE-PROTEIN KINASE
CA4054	orf19.429	*TRF4*	-1.2	-1.3	-1.4	-1.5	YOL115W	*TRF4*	1.0	-1.1	-1.1	1.1	Topoisomerase I-related protein
CA4055	orf19.430	*YPT522*	1.0	-1.0	1.0	1.0	YBR264C	*YPT10*	1.0	1.1	-1.0	1.1	GTP-binding protein of the rab family(by homology)
CA4057	orf19.432	*IPF7719*	-1.1	-1.1	-1.1	-1.1	YDR306C		1.0	1.0	-1.1	-1.3	unknown function
CA4058	orf19.8063	*IPF7717*	-1.0	-1.0	-1.0	-1.1	YGR166W	*KRE11*	1.0	-3.6	-7.4	-5.1	unknown function
CA4059	orf19.8064	*PRD1*	-1.3	-1.2	-1.2	-1.1	YCL057W	*PRD1*	1.0	1.0	1.0	-1.1	Proteinase (by homology)
CA4060	orf19.437	*GRS1*	-1.8	-1.4	-1.5	-1.3	YBR121C	*GRS1*	1.0	-1.4	-1.3	-1.2	glycine-tRNA ligase (by homology)
CA4061	orf19.438	*IPF5935*	-1.0	1.1	1.2	1.1	YHR078W		1.0	1.0	1.1	1.2	Unknown function
CA4062	orf19.439	*IPF5933*	1.1	-1.1	-1.1	-1.1	YDR296W	*MHR1*	1.0	-1.5	-1.4	-1.6	similar to Saccharomyces cerevisiae Mhr1p involved in mitochondrial hor
CA4063	orf19.440	*SDH11*	-1.1	-1.1	-1.1	-1.1	YKL148C	*SDH1*	1.0	-1.3	-1.5	-2.1	Succinate dehydrogenase (by homology)
CA4064	orf19.441	*RPT1*	-1.1	1.1	1.1	1.1	YKL145W	*RPT1*	1.0	-1.1	1.2	1.2	26S PROTEASE REGULATORY SUBUNIT 7 (by homology)
CA4065	orf19.443	*RPC25*	1.1	-1.1	-1.0	-1.0	YKL144C	*RPC25*	1.0	1.3	1.3	1.2	DNA-direcred RNA polymerase III (by homology)
CA4067	orf19.445	*IPF5924*	-1.1	-1.1	-1.1	-1.1	YNR040W		1.0	-1.0	1.0	1.0	unknown function
CA4070	orf19.6623	*IPF2562*	1.2	1.3	1.4	1.1	YKL160W		1.0	-1.5	-1.7	-2.2	unknown function
CA4071	orf19.6624	*IPF2561*	1.1	1.0	1.1	-1.0	YJL044C	*GYP6*	1.0	1.2	1.2	1.3	unknown function
CA4072	orf19.6625	*IPF2560*	1.0	-1.1	-1.1	-1.1	YNL246W		1.0	-1.1	-1.1	-1.2	unknown function
CA4074	orf19.6627	*IPF2557*	1.2	-1.2	-1.1	-1.0	YDR476C		1.0	1.6	2.2	1.0	unknown function
CA4076	orf19.6629	*IPF2542*	-1.1	-1.3	-1.3	-1.3	YER019W	*ISC1*	1.0	1.0	1.3	1.3	putative neutral sphingomyelinase (by homology)
CA4077	orf19.6632	*ACO2*	-1.2	-1.1	-1.6	-1.6	YJL200C		1.0	-1.0	1.2	1.6	aconitate hydratase (by homology)
CA4078	orf19.6634	*VMA2*	-1.3	-1.2	-1.2	-1.2	YBR127C	*VMA2*	1.0	1.2	1.4	1.5	H+-transporting ATPase (by homology)
CA4080	orf19.6636	*IPF2524*	-1.0	-1.0	1.1	1.0	YPR084W		1.0	1.1	1.3	1.6	unknown function
CA4082	orf19.6638	*PTC4*	-1.0	1.0	1.1	1.1	YBR125C	*PTC4*	1.0	-1.3	-1.4	-1.2	ser/thr protein phosphatase PP2C(by homology)
CA4084	orf19.6640	*TPS1*	-1.0	1.5	2.1	1.5	YBR126C	*TPS1*	1.0	1.6	1.4	-1.1	TREHALOSE-6-PHOSPHATE SYNTHASE
CA4086	orf19.6642	*IPF5014*	-1.0	-1.0	-1.0	1.0	YNL263C	*YIF1*	1.0	1.0	1.4	1.4	unknown function
CA4087	orf19.6643	*IPF5013*	-1.0	-1.1	-1.1	-1.0	YOR221C	*MCT1*	1.0	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Mct1p malonyl-CoA:ACP transferas
CA4088	orf19.6645	*HMO1*	-1.2	1.1	1.2	1.4	YDR174W	*HMO1*	1.0	1.2	1.5	1.2	High-mobility protein 1 by homology
CA4089	orf19.6648	*IPF5009*	-1.1	-1.1	-1.1	-1.1	YGR245C	*SDA1*	1.0	1.3	1.7	1.3	unknown function
CA4090	orf19.6649	*BRF1*	-1.1	-1.1	-1.1	-1.0	YGR246C	*BRF1*	1.0	-1.2	1.2	1.2	TFIIIB subunit
CA4092	orf19.6652	*DBP8*	-1.0	-1.0	-1.0	-1.0	YHR169W	*DBP8*	1.0	-1.2	-1.3	1.3	DEAD box protein ATP-dependent RNA helicase (by homology)
CA4093	orf19.6653	*IPF5002*	-1.0	-1.0	-1.1	-1.0	YHR168W		1.0	-1.3	-1.4	-1.2	GTP binding protein (by homology)
CA4094	orf19.658	*IPF4004*	-1.1	-1.1	-1.3	-1.1	YCL061C	*MRC1*	1.0	1.0	1.1	-1.1	unknown function
CA4096	orf19.661	*KRR1*	1.1	-1.0	1.0	-1.0	YCL059C	*KRR1*	1.0	1.4	1.9	2.1	involved in cell division and spore germination
CA4097	orf19.663	*GIN4*	-1.1	-1.1	-1.0	-1.1	YDR507C	*GIN4*	1.0	-1.4	1.0	-1.3	ser/thr protein kinase (by homology)
CA4099	orf19.665	*IPF3986*	1.1	1.0	1.1	1.1	YLR186W	*EMG1*	1.0	-1.7	-2.0	-1.8	unknown function

CA4100	orf19.666	*IPF3985*	-1.0	1.0	-1.1	1.0	YDR499W	*LCD1*	1.0	-1.1	-1.1	1.0	unknown function
CA4102		*RPL37B*	1.1	1.1	1.1	1.1	YDR500C	*RPL37B*	1.0	1.2	1.3	1.5	Ribosomal protein
CA4103	orf19.668	*IPF3980*	1.1	1.4	1.2	1.2	YLR183C	*TOS4*	1.0	-1.2	-1.1	1.0	unknown function
CA4104	orf19.669	*IPF20157*	-1.0	1.0	1.0	1.1	YNL279W	*PRM1*	1.0	-1.0	1.3	1.3	unknown function
CA4105	orf19.670	*SMT3*	1.3	1.1	1.1	1.2	YDR510W	*SMT3*	1.0	-2.6	-1.6	-1.5	Ubiquitin-like protein (by homology)
CA4107	orf19.671	*IPF3970*	-1.1	-1.1	-1.1	-1.1	YLR177W		1.0	1.1	1.4	-1.1	unknown function
CA4108	orf19.672	*IPF3968*	1.0	-1.0	1.0	-1.0	YDR243C	*PRP28*					similar to Saccharomyces cerevisiae pre-mRNA splicing factor RNA helic
CA4110	orf19.674	*IPF3965*	1.1	1.0	1.0	1.0	YDL209C		1.0	-1.2	-1.2	-1.1	unknown function
CA4112	orf19.676	*BIM1*	-1.0	1.0	-1.0	1.0	YER016W	*BIM1*	1.0	1.5	1.7	2.7	microtubule-binding protein (by homology)
CA4113	orf19.677	*CHO1*	1.4	-1.3	-1.2	-1.3	YER026C	*CHO1*	1.0	-1.1	-1.2	-1.7	Phosphatidylserine synthase
CA4115	orf19.680	*IPF7706*	-1.2	-1.3	-1.3	-1.2	YPL063W		1.0	-1.0	1.1	-1.0	putative plasma membrane phosphatase (by homology)
CA4116	orf19.2775	*IDI1*	1.2	-1.0	1.0	1.0	YPL117C	*IDI1*	1.0	1.2	1.8	1.6	isopentenyl-diphosphate delta-isomerase (by homology)
CA4117	orf19.2774	*LAB5*	-1.0	-1.5	-1.6	-1.3	YOR196C	*LIP5*	1.0	-1.2	-1.2	-1.2	lipoic acid synthase (by homology)
CA4118	orf19.2772	*IPF11952*	-1.3	-1.0	-1.3	1.1	YPL116W	*HOS3*	1.0	-1.0	-1.2	-1.4	similar to Saccharomyces cerevisiae Hos3p putative histone deacetylase
CA4119	orf19.2771	*BEM3*	-1.0	-1.1	-1.0	-1.1	YPL115C	*BEM3*	1.0	-1.1	-1.2	-1.1	GTPase-activating protein for Cdc42p and Rho1p (by homology)
CA4120		*SOD1.3*	1.1	1.1	1.1	1.1	YJR104C	*SOD1*	1.0	1.2	1.3	-1.7	Cu,Zn-superoxide dismutase, 3-prime end
CA4122	orf19.2769	*PBI2*	1.0	1.1	1.0	1.0	YNL015W	*PBI2*	1.0	-1.2	-1.7	-2.3	proteinase B inhibitor 2 (by homology)
CA4123	orf19.2768	*AMS1*	-1.2	-1.1	-1.1	-1.1	YGL156W	*AMS1*	1.0	-1.3	-1.7	-1.8	alpha-mannosidase (by homology)
CA4127	orf19.2762	*IPF6629*	1.7	5.0	7.2	7.7	YLR109W	*AHP1*	1.0	-1.0	-1.1	-1.3	unknown function
CA4129	orf19.11723	*IPF6878*	1.2	-1.0	1.0	1.1	YLR118C		1.0	-2.1	-1.3	-1.1	unknown function
CA4130	orf19.11720	*IPF20009*	1.1	1.1	1.1	1.2	YBR129C	*OPY1*	1.0	1.0	-1.1	-1.1	Unknown function
CA4131	orf19.11718	*IPF6886*	1.0	-1.0	-1.0	-1.1	YKL090W		1.0	-1.7	-1.8	-1.8	unknown function
CA4132	orf19.4242	*STE20*	1.1	1.0	1.1	-1.1	YHL007C	*STE20*	1.0	-1.5	-1.5	-1.1	serine/threonine-specific protein kinase
CA4134	orf19.4240	*COS162*	-1.0	1.0	1.0	-1.0	YCR044C	*PER1*	1.0	1.1	1.0	1.2	involved in manganese homeostasis (by homology)
CA4136	orf19.4236	*RET2*	-1.5	-1.1	-1.2	-1.2	YFR051C	*RET2*	1.0	-1.7	1.1	-1.2	Coatomer complex delta chain (by homology)
CA4137	orf19.4235	*CNA1*	1.1	-1.0	1.0	1.0	YGL248W	*PDE1*	1.0	1.1	1.0	1.3	cyclic nucleotide phosphodiesterase
CA4138	orf19.4234	*IPF11954*	-1.1	-1.1	-1.1	-1.1	YCR054C	*CTR86*	1.0	-1.2	-1.3	-1.2	unknown function
CA4139	orf19.4233	*THR4*	-1.1	-1.1	-1.1	1.0	YCR053W	*THR4*	1.0	-1.4	1.1	1.5	threonine synthase (by homology)
CA4140	orf19.4232	*IPF11959*	-1.1	-1.2	-1.0	-1.1	YGR046W		1.0	1.1	1.1	-1.0	unknown function
CA4142	orf19.11705	*PRE4*	-1.0	1.1	1.1	1.1	YFR050C	*PRE4*	1.0	1.3	1.6	1.5	20S proteasome subunit(beta7) (by homology)
CA4143	orf19.4229	*DDP1*	-1.1	-1.3	-1.3	-1.1	YOR163W	*DDP1*	1.0	-1.3	-1.3	-1.6	diadenosine and diphosphoinositol polyphosphate phosphohydrolase (by
CA4144	orf19.4228	*IPF13340*	-1.1	-1.1	1.0	1.0	YOR164C		1.0	-1.6	-1.1	-1.2	unknown function
CA4146	orf19.11700	*LEU3*	1.0	1.0	-1.1	-1.1	YLR451W	*LEU3*	1.0	-1.5	-1.9	-1.5	Binds to UASs in promoters of LEU1, LEU2, LEU4, ILV2, ILV5, and GDH
CA4147	orf19.13211	*ADE8*	1.1	-1.1	-1.1	-1.1	YDR408C	*ADE8*	1.0	1.1	1.1	1.4	Phosphoribosylglycinamide formyltransferase (GART)
CA4148	orf19.13213	*IDH2*	-1.0	1.4	1.4	1.4	YOR136W	*IDH2*	1.0	-1.6	-1.6	-2.3	Isocitrate dehydrogenase (NAD+) subunit 2, mitochondrial (by homology)
CA4149	orf19.5792	*SMP3*	1.0	1.1	1.1	1.1	YOR149C	*SMP3*	1.0	-1.2	-1.0	1.0	Protein kinase C pathway protein
CA4150	orf19.5793	*RPT3*	-1.3	-1.0	-1.0	-1.1	YDR394W	*RPT3*	1.0	1.1	1.3	1.3	26S proteasome regulatory subunit
CA4151	orf19.5796	*SHE9*	1.0	-1.1	-1.1	1.0	YDR393W	*SHE9*	1.0	1.1	1.1	1.0	causes lethality when overexpressed
CA4153	orf19.5798	*DNLI*	-1.0	-1.0	1.1	1.1	YOR005C	*DNL4*	1.0	-1.2	-1.0	-1.1	CANAL DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [A
CA4155	orf19.5801	*RNR21*	1.2	2.9	2.7	4.0	YJL026W	*RNR2*	1.0	1.3	1.8	2.4	ribonucleoside-diphosphate reductase (by homology)
CA4156	orf19.5802	*IPF10990*	-1.1	-1.1	-1.0	1.0	YOR006C		1.0	-1.4	1.0	-1.1	unknown function
CA4157	orf19.5804	*HYU1*	-1.3	1.2	-1.1	-1.1	YKL215C		1.0	-1.2	-1.1	1.1	hydantoin utilization protein A (hyuA) homolog
CA4159	orf19.13228	*ALD5*	1.5	-3.3	-2.7	-3.7	YER073W	*ALD5*	1.0	1.2	1.2	2.4	aldehyde dehydrogenase (NAD+) (by homology)
CA4160	orf19.5808	*IPF9294*	1.0	1.1	1.0	1.0	YBR271W		1.0	-1.2	-1.2	1.0	unknown function
CA4161	orf19.5809	*IPF20164*	1.0	-1.2	1.1	-1.1	YJL060W		1.0	1.4	1.1	1.4	putative kynurenine aminotransferase (by homology)
CA4162	orf19.5811	*MET1*	1.0	-1.0	1.0	1.1	YKR069W	*MET1*	1.0	-1.6	-1.8	-1.7	siroheme synthase (by homology)
CA4163	orf19.5812	*IPF9301*	1.1	1.2	1.2	1.2	YOR051C		1.0	-1.4	1.1	1.3	unknown function
CA4164	orf19.13235	*IPF9302*	1.4	2.4	3.2	2.3	YOR052C		1.0	1.1	1.1	-1.2	unknown function
CA4166	orf19.2967	*TIF34*	-1.2	-1.2	-1.2	-1.1	YMR146C	*TIF34*	1.0	-1.7	-1.4	-1.2	Translation initiation factor eIF3, p39 subunit
CA4167	orf19.2966	*IPF7778*	-1.2	1.0	-1.0	-1.0	YDL086W		1.0	1.3	1.5	1.4	putative carboxymethylenebutenolidase (dienelactone hydrolase, DLH) (I
CA4168	orf19.2965	*IPF7781*	-1.1	1.0	-1.0	-1.0	YDL100C		1.0	1.2	1.6	1.4	putative pump-driving ATPase
CA4169	orf19.2964	*RSC2*	-1.3	-1.1	-1.4	-1.4	YGR056W	*RSC1*	1.0	1.2	1.5	1.7	Member of RSC complex, which remodels the structure of chromatin
CA4173	orf19.2960	*FRS2*	-1.1	-1.1	-1.0	-1.1	YFL022C	*FRS2*	1.0	-1.3	1.0	1.4	phenylalanine--tRNA ligase beta chain, cytosolic (by homolog
CA4177	orf19.2956	*MGM101*	-1.0	1.0	1.1	1.0	YJR144W	*MGM101*	1.0	-2.4	-2.3	-2.0	mitochondrial genome maintenance protein (by homology)
CA4179	orf19.2953	*TOM20*	1.2	1.1	1.5	1.4	YGR082W	*TOM20*	1.0	1.2	1.1	-1.1	mitochondrial outer membrane import receptor subunit, 20 kD
CA4181	orf19.2951	*HOM6*	1.0	1.0	1.0	-1.0	YJR139C	*HOM6*	1.0	-1.0	1.0	-1.1	homoserine dehydrogenase (by homology)
CA4182	orf19.10466	*IPF19797*	1.1	-1.1	-1.3	-1.0	YJR138W	*IML1*	1.0	-2.1	-2.1	-2.4	similar to Saccharomyces cerevisiae Iml1pinvolved in chromosomal stabi
CA4183	orf19.10465	*SNO1*	-1.0	-2.2	-2.1	-1.8	YMR095C	*SNO1*	1.0	-1.1	1.1	-1.1	hisH-like protein (by homology)
CA4184	orf19.2947	*SNZ1*	-1.2	-3.6	-4.6	-2.8	YMR096W	*SNZ1*	1.0	-1.1	-1.1	1.2	stationary phase protein by homology
CA4187	orf19.12003	*IPF7524*	1.0	1.0	1.0	1.1	YLR065C		1.0	1.3	1.2	1.6	unknown function
CA4190	orf19.12006	*IPF7530*	-1.0	1.2	1.6	1.3	YOL075C		1.0	1.2	1.2	1.2	ATP-binding-cassette protein (by homology to A.gambiae)

CA4191	orf19.12007	*IPF7531*	-1.0	1.3	1.3	1.2	YER156C		1.0	1.5	2.1	2.8	unknown function
CA4192	orf19.4533	*IPF7533*	-1.1	-1.1	-1.0	-1.0	YDR117C		1.0	-1.6	-1.5	-1.5	unknown function
CA4193	orf19.4534	*IPF7535*	-1.1	1.1	1.1	-1.0	YBR273C		1.0	-1.1	-1.2	-1.2	unknown function
CA4194	orf19.4535	*PTR3*	-1.1	-1.0	-1.0	-1.0	YFR029W	*PTR3*	1.0	-1.1	1.0	1.1	transcriptional regulator (by homology)
CA4195	orf19.4536	*CYS4*	-1.2	-1.0	1.1	-1.0	YGR155W	*CYS4*	1.0	1.1	1.5	1.8	cystathionine beta-synthase (by homology)
CA4196	orf19.4537	*DST1*	1.0	-1.0	-1.0	-1.1	YGL043W	*DST1*	1.0	-1.9	-1.6	-1.3	RNA polymerase II elongation factor (by homology)
CA4197	orf19.4538	*IPF8057*	1.0	-1.0	1.0	1.0	YGL044C	*RNA15*	1.0	-1.1	1.1	1.2	similar to Saccharomyces cerevisiae Rna15p component of pre-mRNA 3
CA4199	orf19.4540	*UBC8*	1.3	2.1	3.6	2.5	YEL012W	*UBC8*	1.0	1.1	-1.0	-1.1	ubiquitin-conjugating enzyme (by homology)
CA4200	orf19.4542	*CCL1*	1.1	-1.0	-1.0	1.0	YPR025C	*CCL1*	1.0	-1.1	1.1	1.1	cyclin (by homology)
CA4206	orf19.4550	*IPF9079*	1.1	1.1	1.3	1.2	YCR023C		1.0	1.2	1.3	1.4	Membrane transporter (by homology)
CA4207	orf19.4551	*YAT1*	-1.1	-1.1	-1.0	1.0	YAR035W	*YAT1*	1.0	-1.5	-1.6	-1.4	carnitine acetyltransferase (by homology)
CA4209	orf19.8427	*DEP1.3F*	-1.5	-1.2	-1.8	-1.3	YAL013W	*DEP1*	1.0	-1.1	1.1	1.2	Regulator of phospholipid metabolism, 3-prime end (by homology)
CA4211	orf19.809	*IPF5052*	-1.0	-1.1	-1.1	-1.0	YOL041C	*NOP12*	1.0	-1.3	-1.3	-1.4	RNA-binding protein (by homology)
CA4212	orf19.810	*HFM1*	1.0	1.0	-1.0	-1.0	YGL251C	*HFM1*	1.0	-1.2	-1.2	-1.1	DNA/RNA helicase by homology
CA4213	orf19.811	*IPF5795*	-1.0	-1.1	-1.1	-1.0	YLR283W		1.0	-1.2	-1.3	-1.4	unknown function
CA4215	orf19.8434	*SSY1*	1.0	1.1	1.1	1.0	YDR160W	*SSY1*	1.0	1.2	1.1	1.1	Regulator of transporters (by homology)
CA4216	orf19.8435	*IPF5806*	-1.2	1.2	1.1	1.1	YLR422W		1.0	-1.1	-1.2	-1.3	unknown function
CA4218	orf19.819	*ACP1*	1.2	-1.1	1.3	1.3	YKL192C	*ACP1*	1.0	1.1	-1.1	-1.3	mitochondrial acyl carrier protein (by homology)
CA4219	orf19.820	*SDS22*	1.1	1.1	1.0	1.1	YKL193C	*SDS22*	1.0	1.4	1.1	-1.2	regulatory subunit for the mitotic function of type I protein phosphatase (b
CA4222	orf19.825	*GCD7*	1.1	1.1	1.2	1.1	YLR291C	*GCD7*	1.0	-1.0	1.2	1.3	translation initiation factor eIF2b subunit (by homology)
CA4225		*RPL39.3*	1.4	1.1	1.2	1.1	YMR194W	*RPL36A*					ribosomal protein L39, 3-prime end
CA4226	orf19.828	*IPF8752*	-1.1	-1.2	-1.3	-1.1	YMR193W	*MRPL24*	1.0	1.1	-1.0	-1.3	similar to Saccharomyces cerevisiae Mrpl24p ribosomal protein of the lar
CA4227	orf19.829	*SCH9*	1.2	1.4	1.9	1.4	YHR205W	*SCH9*	1.0	-1.3	-1.0	-1.0	strong similarity to S.pombe sck1 protein kinase (by homology)
CA4228	orf19.831	*IPF16057*	1.1	1.0	1.0	1.0	YHL025W	*SNF6*	1.0	-1.1	1.3	1.1	unknown function
CA4231	orf19.514	*SNP3*	1.1	1.1	1.0	-1.0	YBL026W	*LSM2*	1.0	-1.0	-1.3	1.0	snRNP-related protein (by homology)
CA4232	orf19.515	*IPF12484*	1.0	-1.1	1.0	1.0	YER137C		1.0	-1.5	-1.4	-1.4	unknown function
CA4233	orf19.516	*RFT1*	1.2	-1.1	-1.0	-1.0	YBL020W	*RFT1*	1.0	1.0	1.0	1.2	nuclear division protein (by homology)
CA4234	orf19.517	*HAP3*	1.1	-1.0	1.1	1.0	YBL021C	*HAP3*	1.0	-1.3	-1.4	-1.3	CCAAT-binding factor subunit (by homology)
CA4235	orf19.518	*NCL1*	-1.3	-1.3	-1.5	-1.2	YBL024W	*NCL1*	1.0	1.1	1.1	1.3	Probable proliferating-cell nucleolar antigen (by homology)
CA4236	orf19.519	*IPF8166*	-1.0	1.0	1.0	1.0	YBL025W	*RRN10*	1.0	1.2	1.2	1.1	unknown function
CA4238	orf19.522	*PIM1*	-1.0	-1.0	-1.1	-1.2	YBL022C	*PIM1*	1.0	-1.2	-1.2	-1.2	mitochondrial ATP-dependent protease (by homology)
CA4240	orf19.526	*NHP2*	1.1	1.1	1.1	1.1	YDL208W	*NHP2*	1.0	1.7	1.9	2.6	nucleolar rRNA processing protein (by homology)
CA4242	orf19.528	*SEC26*	-1.3	-1.1	-1.5	-1.2	YDR238C	*SEC26*					beta chain of secretory vesicles coatomer complex (by homology)
CA4247	orf19.536	*TAF90*	1.1	1.1	1.1	-1.1	YBR198C	*TAF90*	1.0	-1.1	1.1	1.1	Probable transcription-associated factor protein
CA4248	orf19.537	*IPF4294*	-1.0	1.0	1.0	-1.0	YBR197C		1.0	-1.9	-2.0	-1.2	unknown function
CA4249	orf19.538	*IPF4293*	1.0	1.1	1.1	1.0	YPL076W	*GPI2*	1.0	-1.2	1.1	1.1	similar to Saccharomyces cerevisiae Gpi2p N-acetylglucosaminyl-phosph
CA4250	orf19.539	*IPF4292*	-1.0	1.0	1.0	1.1	YNL239W	*LAP3*	1.0	1.1	1.1	1.0	bleomycin Hydrolase
CA4255	orf19.543	*FUM11*	-1.2	-2.0	-2.1	-2.0	YPL262W	*FUM1*	1.0	-1.5	-1.6	-2.3	fumarate hydratase
CA4256	orf19.544	*IPF4282*	-1.0	-1.2	-1.2	-1.1	YIR015W	*RPR2*	1.0	-1.5	-1.5	-1.5	unknown function
CA4257		*PRE6*	1.0	1.1	1.1	1.1	YOL038W	*PRE6*	1.0	1.1	1.4	1.4	20S proteasome subunit
CA4258	orf19.547	*IPF4279*	-1.1	1.0	1.1	1.0	YKL113C	*RAD27*	1.0	-1.5	-1.5	-1.6	unknown function
CA4259	orf19.548	*CDC10*	-1.0	-1.0	-1.0	-1.1	YCR002C	*CDC10*	1.0	1.1	1.5	1.3	cell division control protein
CA4260	orf19.549	*IPF4276*	1.1	-1.1	-1.1	-1.0	YCR003W	*MRPL32*	1.0	-1.1	-1.1	-1.2	similar to Saccharomyces cerevisiae Mrpl32p putative mitochondrial ribos
CA4261	orf19.550	*PDX3*	-1.1	1.0	-1.0	1.0	YBR035C	*PDX3*	1.0	1.1	-1.1	-1.1	pyridoxamine-phosphate oxidase (by homology)
CA4266	orf19.6660	*IPF2283*	-1.1	1.3	1.3	1.4	YHR131C		1.0	-1.0	-1.2	1.0	unknown function
CA4268	orf19.6662	*IPF2287*	1.0	1.0	1.1	1.0	YOL008W		1.0	-1.2	-1.1	-1.2	unknown function
CA4269	orf19.6663	*RPS25B*	1.2	1.0	1.0	1.1	YLR333C	*RPS25B*	1.0	1.2	1.4	1.9	Cytosolic ribosomal protein (by homology)
CA4270	orf19.6665	*NUP2*	-1.3	-1.6	-2.0	-1.6	YLR335W	*NUP2*	1.0	-2.3	-2.7	-2.1	Nuclear pore protein (by homology)
CA4271	orf19.6667	*SAP30*	1.0	1.0	-1.0	1.0	YMR263W	*SAP30*	1.0	2.2	1.4	-1.1	Subunit of the histone deacetylase B complex (by homology)
CA4272	orf19.6668	*CUE1*	1.1	1.1	1.1	1.2	YMR264W	*CUE1*	1.0	-1.1	1.0	1.1	Involved in ubiquitination and degradation at the ER surface (by homolog
CA4273	orf19.6670	*CAC2*	-1.0	1.1	-1.0	-1.0	YML102W	*CAC2*	1.0	-1.0	1.0	-1.1	Chromatin assembly complex, subunit p60 (by homology)
CA4275	orf19.6672	*MDJ1*	1.0	1.0	1.0	1.0	YFL016C	*MDJ1*	1.0	1.0	1.1	-1.2	Heat shock protein - chaperone (by homology)
CA4277	orf19.6674	*BTS1*	-1.1	1.0	-1.0	1.1	YPL069C	*BTS1*	1.0	1.0	-1.1	-1.1	Geranylgeranyl diphosphate synthase (by homology)
CA4279	orf19.6676	*DPH51*	1.1	1.1	1.2	-1.0	YLR172C	*DPH5*	1.0	1.1	1.3	1.4	Diphthamide methyltransferase (by homology)
CA4288	orf19.6685	*IPF6662*	1.0	-1.0	1.0	-1.0	YJR050W	*ISY1*	1.0	-1.9	-2.3	-2.2	similar to Saccharomyces cerevisiae Isy1p pre-mRNA splicing factor (by
CA4289	orf19.6686	*IPF6665*	-1.0	-1.3	-1.3	-1.2	YGR145W		1.0	-1.2	-1.3	-1.1	unknown function
CA4294	orf19.6691	*ERC1*	-1.0	-1.4	-1.6	-1.5	YHR032W		1.0	-1.7	-1.3	1.2	ethionine resistance protein (by homology)
CA4296	orf19.6693	*IPF2605*	-1.4	-1.2	-1.4	-1.2	YOL098C		1.0	-2.0	-2.1	-1.8	unknown function
CA4299	orf19.6698	*IPF2598*	1.0	1.0	-1.0	1.0	YCR024C		1.0	1.2	1.0	1.2	unknown function
CA4300	orf19.6699	*HIS2*	-1.0	1.2	1.2	1.1	YFR025C	*HIS2*	1.0	-1.3	1.1	1.1	Histidinol phosphatase (by homology)
CA4301	orf19.6701	*IPF2593*	-1.7	-1.3	-1.5	-1.6	YHR020W		1.0	-1.2	1.4	1.7	amino acid-tRNA ligase homolog (by homology)

CA4302	orf19.6702	*DED81*	-1.2	-1.0	-1.3	-1.2	YHR019C	*DED81*	1.0	1.1	1.5	1.5	Asparaginyl-tRNA synthetase (by homology)
CA4305	orf19.6705	*IPF6654*	1.0	-1.0	1.0	-1.1	YBL060W		1.0	-1.0	-1.1	-1.1	unknown function
CA4306	orf19.6706	*GYP7*	-1.0	1.1	1.0	1.1	YDL234C	*GYP7*	1.0	-1.2	-1.1	-1.5	GTPase activating protein (by homology)
CA4307	orf19.6707	*IPF20013*	1.0	1.0	1.0	-1.0	YNL217W		1.0	1.1	1.0	1.3	Unknown function
CA4312	orf19.4112	*IPF2122*	-1.2	-1.3	-1.3	-1.3	YJR142W		1.0	-2.2	-1.6	-1.6	similar to thiamin pyrophosphokinase
CA4314	orf19.4109	*PMT4*	1.0	1.6	2.1	1.8	YJR143C	*PMT4*	1.0	-1.5	-1.0	1.2	Mannosyltransferase (by homology)
CA4315	orf19.4107	*PPX1*	-1.1	-1.1	-1.1	-1.0	YHR201C	*PPX1*	1.0	-1.8	-1.5	-1.2	Exopolyphosphatase (by homology)
CA4316	orf19.4106	*IPF2111*	-1.0	1.0	1.0	1.0	YJR141W		1.0	-1.8	-1.9	-2.3	unknown function
CA4317	orf19.4105	*IPF2109*	1.0	-1.0	-1.2	-1.0	YMR048W	*CSM3*	1.0	-1.4	-1.5	-1.6	unknown function
CA4319	orf19.4102	*RPN10*	1.0	1.1	1.1	1.1	YHR200W	*RPN10*	1.0	1.1	1.3	1.4	Protein degradation (by homology)
CA4320	orf19.4099	*ECM17*	-1.1	1.2	-1.2	-1.2	YJR137C	*ECM17*	1.0	-1.6	-1.1	-1.1	Putative sulfite reductase (by homology)
CA4321	orf19.4100	*KAR3.53*	-1.0	-1.0	-1.0	1.0	YPR141C	*KAR3*	1.0	-1.0	-1.2	-1.4	Kinesin-related protein, internal fragment
CA4323	orf19.4096	*IPF2096*	-1.1	-1.1	-1.2	-1.1	YPR140W		1.0	-1.2	-1.1	-1.5	putative acyltransferase (by homology)
CA4326	orf19.4093	*IPF2093*	-1.2	-1.3	-1.5	-1.5	YGR103W	*RRP13*	1.0	-1.7	-1.2	-1.0	nuclear protein of unknown function (by homology)
CA4327	orf19.4092	*IPF2091*	1.1	-1.1	-1.0	-1.0	YGR102C		1.0	-3.3	-1.4	-1.2	unknown function
CA4328	orf19.4091	*IPF2090*	1.0	-1.0	-1.0	-1.0	YGR104C	*SRB5*	1.0	-1.5	-2.0	-1.8	similar to Saccharomyces cerevisiae Srb5p DNA-directed RNA polymera
CA4329		*VMA21*	1.1	1.0	-1.0	-1.0	YGR105W	*VMA21*	1.0	1.1	-1.1	-1.1	Vacuolar H+-ATPase assembly (by homology)
CA4331	orf19.4089	*IPF2086*	-1.1	-1.2	-1.5	-1.3	YOR057W	*SGT1*	1.0	-1.3	-1.4	-1.2	unknown function
CA4332	orf19.4088	*GLO2*	-1.1	1.0	1.1	1.0	YDR272W	*GLO2*	1.0	1.0	-1.2	-1.4	Glyoxalase II (hydroxyacylglutathione hydrolase) (by homology)
CA4333	orf19.4086	*IPF2083*	1.1	-1.0	1.0	1.0	YNL056W		1.0	-1.4	-1.1	-1.1	unknown function
CA4335	orf19.4084	*GAL83*	-1.0	1.1	-1.1	-1.1	YER027C	*GAL83*	1.0	1.2	1.1	1.1	Glucose repression protein (by homology)
CA4338	orf19.6709	*IPF3616*	-1.0	1.0	1.0	1.1	YNR064C		1.0	-1.1	1.1	1.0	Unknown function
CA4340	orf19.6712	*IPF3621*	-1.1	-1.1	-1.2	-1.1	YJR134C	*SGM1*	1.0	-2.0	-2.5	-2.1	unknown function
CA4342	orf19.6716	*IPF3629*	1.0	1.0	1.1	-1.1	YBR236C	*ABD1*	1.0	1.1	1.0	1.0	RNA (guanine-N7-) methyltransferase
CA4343	orf19.6717	*IPF3630*	1.0	1.1	1.1	1.0	YHR049W		1.0	-1.9	-1.1	1.2	unknown function
CA4345	orf19.6719	*IPF3633.3*	-1.0	-1.0	-1.1	-1.0	YJR140C	*HIR3*	1.0	-1.2	-1.1	-1.0	similar to Saccharomyces cerevisiae Hir3p involved in cell cycle regulati
CA4346	orf19.6720	*IPF3634*	1.0	-1.0	1.1	1.0	YDR090C		1.0	1.0	-1.0	1.1	unknown function
CA4347	orf19.6722	*IPF3636*	-1.0	-1.1	-1.1	-1.1	YER162C	*RAD4*	1.0	-1.4	-1.3	-1.5	similar to Saccharomyces cerevisiae Rad4p excision repair protein (by h
CA4352	orf19.6726	*IPF3642*	1.0	1.1	-1.0	-1.0	YER161C	*SPT2*	1.0	-2.6	-2.4	-2.7	Unknown function
CA4353	orf19.6727	*IPF3645*	-1.1	-1.1	-1.0	-1.0	YMR283C	*RIT1*	1.0	1.0	-1.2	-1.2	similar to Saccharomyces cerevisiae Rit1p initiator tRNA phosphoribosyl-
CA4355	orf19.6730	*IPF3649*	1.0	1.1	-1.1	-1.0	YCR016W		1.0	-1.1	1.2	1.4	unknown function
CA4357	orf19.6732	*IPF19800*	-1.0	1.0	1.0	1.0	YCR015C		1.0	1.1	1.1	1.1	unknown function
CA4359	orf19.6736	*IPF6054*	-1.0	-1.0	-1.1	-1.0	YOR205C		1.0	-1.4	-1.1	1.0	unnown function
CA4361	orf19.13096	*IPF16104*	-1.1	-1.1	-1.2	-1.3	YJR119C		1.0	1.0	-1.1	-1.1	unknown function
CA4362	orf19.5653	*ATP2*	2.1	1.4	1.2	1.2	YJR121W	*ATP2*	1.0	-1.4	-1.4	-2.7	F1F0-ATPase complex, F1 beta subunit (by homology)
CA4363	orf19.5654	*STE24*	1.1	1.4	1.8	1.6	YJR117W	*STE24*	1.0	-1.1	1.1	1.1	zinc metallo-protease by homology
CA4366	orf19.5657	*SWI1*	1.2	1.3	1.7	1.2	YPL016W	*SWI1*	1.0	-1.3	-1.7	-1.8	Transcription regulation by homology
CA4367	orf19.5658	*MNN10*	1.1	-1.0	1.1	1.0	YDR245W	*MNN10*					galactosyltransferase (by homology)
CA4368	orf19.5660	*PEX10.3*	1.1	-1.0	-1.1	1.0	YDR265W	*PEX10*	1.0	-1.4	-1.5	-1.3	peroxisomal assembly protein, 3-prime end (by homology)
CA4370	orf19.5661	*IPF5279*	-1.2	1.1	-1.1	1.0	YHR076W		1.0	-1.2	-1.2	-1.2	unknown function
CA4371	orf19.5662	*PEP7*	-1.1	-1.0	-1.1	-1.0	YDR323C	*PEP7*	1.0	1.0	-1.0	-1.1	vacuolar segregation protein by homology
CA4372	orf19.5663	*IPF5282*	1.0	1.0	1.0	-1.0	YMR034C		1.0	1.3	1.3	1.1	unknown function
CA4373	orf19.5664	*IPF5287*	-1.1	-1.1	-1.1	-1.1	YMR032W	*HOF1*	1.0	-1.1	1.1	1.2	signal transduction protein (by homology)
CA4374	orf19.5665	*IPF5288*	1.0	1.1	1.2	1.1	YMR041C		1.0	1.1	-1.0	-1.1	Unknown function
CA4375	orf19.5666	*IPF11309*	1.1	-1.1	-1.1	1.0	YMR039C	*SUB1*	1.0	1.1	1.2	1.3	unknown function
CA4376	orf19.5667	*IPF11307*	-1.0	1.0	1.1	1.0	YKL064W	*MNR2*	1.0	1.1	1.2	1.1	unknown function
CA4378	orf19.5671	*IPF11299*	-1.0	1.1	1.1	1.0	YCR030C		1.0	-1.2	-1.0	1.1	unknown function
CA4379	orf19.5672	*MEP2*	1.0	1.0	1.0	-1.0	YNL142W	*MEP2*	1.0	-1.9	-1.4	-1.4	high affinity low capacity ammonia (by homology)
CA4382	orf19.5675	*IPF8576*	-1.1	-1.1	-1.1	-1.1	YOR191W	*RIS1*	1.0	-1.5	1.0	1.2	similar to Saccharomyces cerevisiae Ris1p DNA helicase (by homology)
CA4383	orf19.13121	*IPF8573*	-1.1	1.0	1.1	1.0	YLR427W		1.0	-2.3	-2.6	-2.3	unknown function
CA4385	orf19.3126	*CCT6*	-1.4	-1.2	-1.4	-1.3	YDR188W	*CCT6*	1.0	-1.1	1.1	1.5	component of chaperonin-containing T-complex (zeta subunit)(by homol
CA4387	orf19.3124	*MAP1*	1.1	-1.0	-1.0	-1.1	YLR244C	*MAP1*	1.0	-1.2	1.1	1.3	methionine aminopeptidase, isoform 1 (by homology)
CA4388		*IPF12416.3*	1.0	1.0	1.0	1.0	YLR245C	*CDD1*	1.0	-2.7	-7.4	-3.2	cytidine deaminase, 3-prime end (by homology)
CA4389	orf19.3123	*RPT5*	-1.0	-1.0	-1.1	-1.1	YOR117W	*RPT5*	1.0	1.1	1.5	1.7	26S proteasome regulatory subunit (by homology)
CA4391	orf19.3122	*ARR3*	1.0	1.3	1.5	1.3	YPR201W	*ARR3*	1.0	-1.1	-1.1	-1.1	involved in arsenite transport (by homology)
CA4395	orf19.3116	*EXM2*	-1.1	1.0	1.1	1.0	YDL087C	*LUC7*	1.0	1.1	1.1	1.2	EXit from Mitosis (by homology)
CA4397	orf19.3114	*IPF14369*	-1.0	1.0	1.1	1.0	YLR165C	*PUS5*	1.0	-1.0	-1.1	-1.1	unknown function
CA4399	orf19.3111	*PRA1*	1.0	-1.0	1.1	-1.0	YOL154W		1.0	-1.3	-1.1	-1.2	pH-regulated antigen
CA4402	orf19.3108	*MGT1*	1.0	1.0	1.0	-1.0	YDL200C	*MGT1*	1.0	-1.2	-1.2	-1.3	O6-methylguanine DNA repair methyltransferase (by homology)
CA4404	orf19.3106	*MET16*	1.1	-1.0	-1.1	1.0	YPR167C	*MET16*	1.0	1.1	1.1	1.4	3 -phosphoadenylylsulfate reductase (by homology)
CA4406	orf19.3104	*YDC1*	1.1	1.0	1.3	1.0	YPL087W	*YDC1*	1.0	1.0	1.1	-1.0	alkaline dihydroceramidase (by homology)

CA4407	orf19.3103	*RPO31*	1.1	-1.1	-1.2	-1.0	YOR116C	*RPO31*	1.0	-1.3	-1.1	1.1	DNA-directed RNA polymerase III (by homology)
CA4410	orf19.3099	*TRP4*	-1.0	-1.1	1.0	1.0	YDR354W	*TRP4*	1.0	1.2	1.2	1.5	Anthranilate phosphoribosyltransferase
CA4411	orf19.3098	*BRR2*	-1.1	-1.1	-1.4	-1.2	YER172C	*BRR2*	1.0	-1.2	-1.2	-1.1	RNA helicase-related protein (by homology)
CA4412	orf19.3097	*PDA1*	1.1	-1.0	-1.5	-1.5	YER178W	*PDA1*	1.0	-1.1	1.1	-1.2	Pyruvate dehydrogenase alpha chain (by homology)
CA4413	orf19.3093	*MSH2*	-1.0	1.0	-1.1	-1.1	YOL090W	*MSH2*	1.0	-1.2	-1.2	-1.0	DNA mismatch repair protein (by homology)
CA4416	orf19.5180	*IPF11888*	1.1	1.4	1.8	1.5	YBL064C		1.0	-1.7	-2.0	-1.9	unknown function
CA4418	orf19.5178	*ERG5*	1.1	-1.3	-1.2	-1.1	YMR015C	*ERG5*	1.0	1.5	1.8	1.2	C-22 sterol desaturase by homology
CA4420	orf19.5175	*SSM4*	1.1	1.2	1.3	1.3	YIL030C	*SSM4*	1.0	-1.2	1.0	1.1	involved in mRNA turnover by homology
CA4421	orf19.5174	*TAF19*	-1.0	1.0	1.0	-1.0	YML098W	*TAF19*	1.0	1.0	1.1	1.0	TBP-associated factor by homology
CA4424	orf19.5171	*PMT1*	1.1	1.5	2.0	1.8	YDL095W	*PMT1*	1.0	-1.1	1.5	1.6	mannosyltransferase
CA4427	orf19.5168	*IPF5584*	1.1	1.0	1.0	-1.0	YOL022C		1.0	1.1	1.6	1.6	unknown function
CA4428	orf19.5167	*IFM1*	-1.2	-1.3	-1.6	-1.4	YOL023W	*IFM1*	1.0	-1.1	-1.2	-1.3	translation initiation factor 2 by homology
CA4429	orf19.5166	*DBF4*	1.0	-1.1	-1.1	-1.1	YDR052C	*DBF4*	1.0	-1.1	1.1	1.0	regulatory subunit for Cdc7 by homology
CA4430	orf19.5165	*IPF5577*	-1.0	1.1	1.2	1.1	YNR029C		1.0	-1.7	1.1	1.2	unknown function
CA4431	orf19.5164	*ECM39*	1.2	-1.0	1.1	1.0	YNR030W	*ECM39*	1.0	-1.1	1.0	1.1	cell wall biogenesis by homology
CA4432	orf19.5163	*IPF5574*	-1.1	-1.2	-1.3	-1.1	YLL003W	*SFI1*	1.0	-1.1	-1.1	-1.3	unknown function
CA4433	orf19.5162	*BCK1*	1.0	-1.2	-1.3	-1.2	YJL095W	*BCK1*	1.0	-1.1	-1.5	-1.5	serine/threonine protein kinase of the MEKK family (by homology)
CA4434	orf19.5161	*MRPL49*	1.5	1.1	1.4	1.2	YJL096W	*MRPL49*	1.0	-1.3	-1.4	-1.5	ribosomal protein mitochondrial
CA4435	orf19.5160	*SAP190*	-1.3	-1.0	-1.3	-1.1	YKR028W	*SAP190*	1.0	1.0	1.1	1.2	phosphatase associated protein by homology
CA4436	orf19.5159	*IPF13868*	1.2	1.9	2.5	1.6	YNL191W		1.0	-1.0	1.0	1.2	unknown function
CA4439	orf19.5156	*IPF13865*	1.3	1.1	1.3	1.2	YJL097W		1.0	-1.1	-1.1	-1.0	unknown function
CA4440	orf19.5155	*IPF13864*	-1.0	-1.0	-1.0	-1.0	YJL099W	*CHS6*	1.0	-1.2	-1.1	1.0	similar to Saccharomyces cerevisiae Chs6p chitin biosynthesis protein (b
CA4444	orf19.6842	*IPF3533*	1.0	1.1	1.2	-1.0	YLR425W	*TUS1*	1.0	-1.9	-1.8	-1.9	putative GDP/GTP exchange factor (by homology)
CA4446	orf19.6844	*ICL1*	-1.0	-1.9	-2.0	-1.6	YER065C	*ICL1*	1.0	-4.4	-5.3	-4.8	Isocitrate lyase
CA4448	orf19.6846	*PHO85*	1.1	1.1	1.2	1.1	YPL031C	*PHO85*	1.0	-1.0	1.1	-1.2	Negative regulator of PHO system
CA4449	orf19.6847	*IPF3520*	-1.0	-1.1	-1.1	-1.1	YPL030W		1.0	-1.0	-1.2	1.2	unknown function
CA4450	orf19.6848	*IPF3518*	-1.5	-1.2	-1.5	-1.3	YPL045W	*VPS16*	1.0	-1.2	-1.1	-1.1	similar to Saccharomyces cerevisiae Vps16p vacuolar sorting protein (by
CA4451	orf19.6849	*ELC1*	1.1	-1.0	1.0	1.1	YPL046C	*ELC1*	1.0	-1.1	1.8	1.1	Transcription elongation factor (by homology)
CA4452	orf19.6850	*IPF3514*	1.0	1.1	1.0	-1.1	YDR255C		1.0	1.1	1.2	1.2	unknown function
CA4453	orf19.6851	*CHL4*	1.0	1.1	1.1	1.1	YDR254W	*CHL4*	1.0	-1.6	-1.1	-1.0	chromosome segregation protein (by homology)
CA4454	orf19.6852	*IPF15160*	-1.0	-1.0	1.0	1.0	YEL072W		1.0	1.1	1.8	2.4	unknown function
CA4457	orf19.6854	*ATP1.EXON3*	-1.0	-1.4	-1.4	-1.4	YBL099W	*ATP1*	1.0	-3.3	-4.0	-2.0	F1F0-ATPase complex, F1 alpha subunit, exon 3
CA4459	orf19.6856	*NSP49.3F*	-1.2	-1.2	-1.3	-1.3	YGL092W	*NUP145*	1.0	-1.4	-1.3	-1.9	nucleoporin, 3-prime end (by homology)
CA4461	orf19.6858	*IPF8470*	-1.1	-1.1	-1.3	-1.2	YEL015W		1.0	1.4	1.3	1.7	unknown function
CA4463	orf19.6860	*PIS1*	1.2	-1.1	-1.0	-1.1	YPR113W	*PIS1*	1.0	1.6	1.9	2.4	CDP diacylglycerol--inositol 3-phosphatidyltransferase (by homology)
CA4464	orf19.6861	*IPF9828*	-1.0	1.0	1.0	1.0	YOR249C	*APC5*	1.0	1.0	1.1	-1.2	similar to Saccharomyces cerevisiae Apc5p component of the anaphase-
CA4465	orf19.6862	*IPF9829*	1.1	1.0	1.1	1.0	YHR197W		1.0	-1.1	1.1	1.2	unknown function
CA4466	orf19.6863	*VPH1*	-1.1	-1.0	1.3	1.2	YOR270C	*VPH1*	1.0	-1.1	1.3	1.4	H+-ATPase V0 domain subunit (by homology)
CA4469	orf19.1903	*TOR2.3F*	1.1	1.1	-1.2	-1.1	YKL203C	*TOR2*	1.0	-1.5	-1.4	-1.5	phosphatidylinositol 3-kinase, 3-prime end (by homology)
CA4470	orf19.1902	*IPF9717*	-1.1	-1.1	-1.2	-1.1	YPR144C		1.0	-1.2	1.1	1.1	unknown function
CA4471	orf19.1901	*MCM3*	-1.3	-1.1	-1.3	-1.2	YEL032W	*MCM3*	1.0	-1.4	-1.3	-1.1	replication initiation protein (by homology)
CA4472	orf19.1900	*IPF6444*	1.1	-1.1	-1.1	1.0	YPL157W		1.0	-1.1	1.1	1.1	putative methyltransferase (by homology)
CA4474	orf19.1896	*SSC1*	1.4	-1.1	-1.2	-1.6	YJR045C	*SSC1*	1.0	-1.3	-1.2	-1.5	Mitochondrial heat shock protein 70-related protein (by homology)
CA4476	orf19.1891	*01-Apr*	1.1	1.3	1.6	1.4	YPL154C	*PEP4*	1.0	-1.3	-1.5	-2.1	aspartyl protease
CA4477	orf19.1890	*IPF6459*	-1.1	1.3	1.3	1.2	YMR210W		1.0	-1.4	-1.1	-1.1	unknown function
CA4478	orf19.1889	*IPF6461*	1.1	1.0	-1.0	1.0	YKR043C		1.0	-1.1	1.1	1.7	unknown function
CA4479	orf19.1888	*URH1*	1.1	-1.0	-1.0	-1.0	YDR400W	*URH1*	1.0	1.1	1.2	1.3	Uridine ribohydrolase (by homology)
CA4480	orf19.1887	*IPF6464*	1.0	1.1	1.1	1.0	YLL012W		1.0	-1.7	-1.5	-1.2	putative triacylglycerol lipase (by homology)
CA4481	orf19.9441	*IPF9150*	-1.1	-1.1	-1.2	-1.1	YMR005W	*MPT1*	1.0	1.0	1.1	1.1	similar to Saccharomyces cerevisiae Mpt1p required for protein synthesis
CA4482	orf19.1883	*IPF9154*	-1.0	1.3	1.2	1.1	YLR272C	*YCS4*	1.0	-1.4	1.1	1.3	similar to Saccharomyces cerevisiae Ycs4p subunit of condensin protein
CA4483	orf19.1881	*IPF9156*	-1.1	-1.1	1.0	1.0	YOR175C		1.0	1.0	-1.1	-1.3	unknown function
CA4484	orf19.1880	*HEM15*	-1.1	1.4	1.4	1.4	YOR176W	*HEM15*	1.0	-1.1	-1.1	-1.4	ferrochelatase precursor (by homology)
CA4485	orf19.1878	*IPF9160*	1.0	1.1	1.2	1.1	YOR174W	*MED4*	1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Med4ptranscription regulation medi
CA4486	orf19.1877	*IPF9162*	2.3	-1.1	-1.1	-1.0	YLR271W		1.0	-1.7	-1.6	-1.4	unknown function
CA4487	orf19.1876	*IPF4039*	-1.0	1.0	-1.1	1.0	YHR086W	*NAM8*	1.0	-1.1	-1.3	1.0	similar to Saccharomyces cerevisiae Nam8p recombination protein (by h
CA4488	orf19.1875	*MEK1.3F*	-1.0	1.0	1.0	1.0	YOR351C	*MEK1*	1.0	-1.1	1.2	1.2	serine/threonine protein kinase, 3-prime end
CA4491	orf19.9427	*SWR1*	-1.1	-1.1	-1.6	-1.2	YDR334W	*SWR1*	1.0	-1.5	-1.4	1.0	putative DNA helicase (by homology)
CA4495	orf19.1865	*IPF4059*	-1.4	-1.5	-1.5	-1.4	YHR039C	*MSC7*	1.0	1.0	1.1	1.1	aldehyde dehydrogenase (by homology)
CA4496	orf19.9420	*IPF4062*	-1.4	-1.1	-1.2	-1.1	YDR333C		1.0	1.3	1.2	1.2	unknown function
CA4498	orf19.8143	*IPF11315*	-1.1	-1.1	-1.3	-1.1	YNL132W	*KRE33*	1.0	-1.0	1.7	2.0	unknown function
CA4499	orf19.511	*IPF11316*	-1.1	-1.0	1.1	1.1	YNL129W		1.0	-1.7	-1.2	1.2	unknown function

CA4501	orf19.8138	*QDR1*	1.0	8.1	13.2	7.0	YIL120W	*QDR1*	1.0	-1.1	-1.3	-1.3	putative antibiotic resistance proteins (by homology)
CA4502	orf19.8136	*IPF10391*	-1.0	1.1	-1.0	-1.0	YNL064C	*YDJ1*	1.0	1.1	1.6	2.3	Similar to dnaJ proteins
CA4503	orf19.505	*SRV2*	-1.0	-1.0	1.0	1.0	YNL138W	*SRV2*	1.0	-1.4	-1.4	-1.7	adenylate cyclase-associated protein homolog
CA4504	orf19.504	*ARP5*	-1.3	-1.2	-1.8	-1.5	YNL059C	*ARP5*	1.0	-1.2	1.1	-1.0	actin-related protein (by homology)
CA4505	orf19.501	*NOP2*	-1.3	-1.1	-1.3	-1.4	YNL061W	*NOP2*	1.0	1.3	2.0	2.4	nucleolar protein (by homology)
CA4506	orf19.500	*GCD10*	-1.0	-1.1	-1.2	-1.1	YNL062C	*GCD10*	1.0	1.2	1.8	1.6	translation initiation factor eIF3 RNA-binding subunit (by homology)
CA4507	orf19.499	*IPF20015*	1.1	1.0	-1.0	-1.1	YNL063W		1.0	1.1	1.1	1.1	unknown function
CA4508	orf19.498	*NAM9*	-1.1	-1.1	-1.2	-1.1	YNL137C	*NAM9*	1.0	-1.3	-1.2	-1.4	mitochondrial ribosomal protein
CA4509	orf19.497	*IPF8973*	1.0	-1.1	-1.2	-1.1	YNL136W		1.0	1.1	1.1	1.0	unknown function
CA4510	orf19.496	*IPF8970*	-1.1	-1.1	-1.1	-1.1	YHR120W	*MSH1*	1.0	-1.2	-1.2	-1.1	similar to Saccharomyces cerevisiae Msh1p DNA mismatch repair protei
CA4511	orf19.8124	*IPF8966*	-1.0	1.0	-1.0	-1.0	YNL124W		1.0	-1.2	-1.1	1.0	unknown function
CA4512	orf19.8123	*RPL15B*	1.1	-1.0	-1.1	1.1	YLR029C	*RPL15A*	1.0	1.1	1.2	1.9	ribosomal protein L15.e.c13 (by homology)
CA4513	orf19.492	*ADE17*	-1.3	-1.7	-1.8	-1.6	YMR120C	*ADE17*					5-aminoimidazole-4-carboxamide ribotide transformylase (by homology t
CA4514	orf19.491	*IPF20016*	-1.4	1.1	1.0	1.1	YOR254C	*SEC63*	1.0	-1.5	-1.6	-1.4	similar to Saccharomyces cerevisiae Sec63p ER protein-translocation co
CA4515	orf19.490	*IPF16652*	1.2	1.6	1.6	1.8	YOR253W		1.0	1.1	-1.0	1.0	unknown function
CA4516	orf19.489	*IPF18207*	-1.1	2.1	2.0	2.3	YPL170W		1.0	-1.6	-1.6	-1.5	unknown function
CA4517	orf19.488	*MEX67*	-1.2	-1.1	-1.3	-1.1	YPL169C	*MEX67*	1.0	1.1	1.5	1.9	poly(A)+RNA binding protein involved in nuclear mRNA export (by homol
CA4518	orf19.487	*SPT14*	-1.1	1.0	1.0	1.0	YPL175W	*SPT14*	1.0	-1.5	-1.4	-1.0	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein (by homol
CA4519	orf19.486	*IPF7088*	-1.0	1.1	1.1	1.0	YPL174C	*NIP100*	1.0	-1.2	-1.1	-1.1	similar to Saccharomyces cerevisiae Nip100p myosin-like protein, putativ
CA4520	orf19.485	*CDC31*	-1.0	1.0	1.0	1.0	YOR257W	*CDC31*	1.0	-1.3	-1.4	-1.5	spindle pole body component, centrin (by homology)
CA4521	orf19.484	*MRPL40*	-1.1	-1.3	-1.4	-1.2	YPL173W	*MRPL40*	1.0	1.0	-1.2	-1.3	Putative mitochondrial ribosomal protein (by homology)
CA4522	orf19.482	*RPT4*	-1.0	-1.1	-1.1	1.0	YOR259C	*RPT4*	1.0	-1.0	1.4	1.4	26S proteasome regulatory subunit (by homology)
CA4523	orf19.481	*GCD1*	-1.2	-1.2	-1.3	-1.1	YOR260W	*GCD1*	1.0	-1.2	1.5	1.4	translation initiation factor eIF2bgamma (by homology)
CA4524	orf19.480	*IPF7097*	1.1	-1.1	1.0	-1.1	YJR056C		1.0	-2.1	-1.9	-1.9	unknown function
CA4525		*SEC22*	1.0	1.2	1.3	1.2	YLR268W	*SEC22*	1.0	-1.3	-1.2	-1.3	synaptobrevin-type protein transport protein (by homology)
CA4526	orf19.8109	*MON1.3*	-1.0	1.0	1.0	1.0	YGL124C	*MON1*	1.0	-1.0	1.2	1.0	unknown function, 3-prime end
CA4527	orf19.9054	*IPF4398*	1.2	1.3	1.5	1.2	YGL023C	*PIB2*	1.0	-1.4	1.2	1.4	unknown function
CA4528	orf19.1478	*STT3*	-1.2	1.2	1.4	1.3	YGL022W	*STT3*	1.0	1.0	1.2	1.5	oligosaccharyl transferase (by homology)
CA4529	orf19.1477	*IPF4395*	1.3	-1.2	1.1	-1.1	YGL010W		1.0	1.1	-1.2	-1.1	unknown function
CA4530	orf19.1476	*IME4*	-1.0	1.0	1.0	1.0	YGL192W	*IME4*	1.0	1.1	1.2	-1.0	positive transcription factor for IME2 (by homology)
CA4531	orf19.1474	*SLA1*	1.1	1.2	1.2	-1.0	YBL007C	*SLA1*	1.0	-1.1	-1.2	-1.1	cytoskeleton assembly control protein
CA4533	orf19.1471	*COX4*	1.2	1.1	1.3	1.1	YGL187C	*COX4*	1.0	1.1	-1.0	-1.9	cytochrome-c oxidase (by homology)
CA4534	orf19.1470	*RPS26A*	1.7	1.3	1.3	1.5	YGL189C	*RPS26A*	1.0	1.3	1.8	1.8	ribosomal protein S26.e.A, cytosolic (by homology)
CA4535	orf19.1468	*CDC55*	1.0	1.1	1.1	1.1	YGL190C	*CDC55*	1.0	1.1	-1.2	-1.3	B subunit of protein phosphatase 2A (by homology)
CA4536	orf19.1467	*COX13*	1.2	-1.0	1.1	1.2	YGL191W	*COX13*	1.0	-1.2	-1.5	-2.4	cytochrome-c oxidase chain VIa (by homology)
CA4537	orf19.1466	*YNT2*	1.1	-1.1	1.0	-1.0	YLR059C	*REX2*	1.0	-1.6	-1.9	-1.7	suppressor of rna12/yme2 (by homology)
CA4540	orf19.1462	*SMP2*	-1.1	-1.0	-1.1	1.0	YMR165C	*SMP2*	1.0	1.1	-1.1	-1.2	Involved in plasmid maintenance, respiration and cell proliferation (by ho
CA4542	orf19.1460	*IPF6255*	-1.3	-1.4	-1.5	-1.4	YHR074W	*QNS1*	1.0	1.1	1.5	1.1	unknown function
CA4543	orf19.1459	*PPE1*	-1.0	1.0	1.1	1.0	YHR075C	*PPE1*	1.0	-1.3	-1.2	-1.2	Ribosomal protein of the small subunit, mitochondrial (by homology)
CA4544	orf19.1458	*IPF6252*	-1.0	-1.0	1.1	1.0	YJL035C	*TAD2*	1.0	-2.2	-2.2	-2.6	similar to Saccharomyces cerevisiae Tad2p tRNA-specific adenosine dea
CA4545	orf19.1457	*SSL1*	-1.0	-1.0	1.1	1.1	YLR005W	*SSL1*	1.0	1.1	-1.0	1.4	TFIIH subunit (transcription initiation factor), factor B
CA4546	orf19.1453	*SPT5*	1.1	1.0	-1.0	-1.1	YML010W	*SPT5*	1.0	1.1	1.5	1.6	Transcription elongation protein
CA4547	orf19.1451	*SRB9*	-1.0	1.0	1.0	-1.1	YDR443C	*SSN2*	1.0	1.1	1.2	1.1	DNA-directed RNA polymerase II holoenzyme and Srb10 CDK subcompl
CA4549	orf19.1449	*IPF7863*	1.0	-1.2	-1.2	-1.2	YNL335W		1.0	1.4	1.3	1.1	unknown function
CA4550		*DYN2.3*	1.1	-1.0	1.1	-1.0	YDR424C	*DYN2*	1.0	1.1	1.0	-1.1	Dynein light chain 1, cytosolic, 3-prime end
CA4551	orf19.1448	*APT1*	1.5	1.8	1.8	1.8	YML022W	*APT1*	1.0	1.1	1.6	1.9	adenine phosphoribosyltransferase
CA4553	orf19.1446	*CYB1*	-1.1	1.1	-1.0	1.0	YPR119W	*CLB2*	1.0	-1.1	-1.1	1.2	G2/Mitotic-specific cyclin
CA4554	orf19.1445	*IPF7874*	1.0	1.0	-1.0	-1.2	YHR154W	*ESC4*	1.0	-1.0	1.4	1.0	similar to Saccharomyces cerevisiae Esc4p involved in chromatin silenci
CA4555	orf19.9019	*IPF17555.3*	-1.0	1.1	1.0	1.1	YLR206W	*ENT2*	1.0	-1.4	-1.2	-1.6	unknown function, 3-prime end
CA4556	orf19.6866	*IPF8044*	-1.0	-1.0	-1.1	-1.0	YIL061C	*SNP1*	1.0	-1.3	1.0	1.2	similar to Saccharomyces cerevisiae Snp1p U1 small nuclear ribonucleo
CA4560	orf19.6871	*IPF8038*	-1.1	1.1	-1.0	-1.0	YMR124W		1.0	1.1	1.3	1.2	unknown function
CA4561	orf19.6872	*IPF8031*	1.0	1.5	1.5	1.1	YLR126C		1.0	-1.2	-1.1	-1.1	unknown function
CA4562	orf19.6873	*RPS8A*	1.1	-1.0	-1.1	-1.0	YER102W	*RPS8B*	1.0	2.4	3.4	5.0	ribosomal protein (by homology)
CA4565	orf19.6875	*VPS35*	1.1	1.0	-1.0	1.1	YJL154C	*VPS35*	1.0	-1.1	-1.1	-1.1	Protein-sorting protein, vacuolar (by homology)
CA4567	orf19.6879	*IPF9555*	1.0	1.2	1.1	1.1	YAR008W	*SEN34*	1.0	1.1	1.2	1.2	unknown function
CA4568	orf19.6880	*IPF9554*	-1.1	1.1	-1.1	1.0	YPR105C	*COD1*	1.0	-1.1	-1.1	-1.0	unknown function
CA4569	orf19.6881	*IPF9552*	1.1	3.1	3.4	2.8	YPR107C	*YTH1*	1.0	-1.2	-1.1	-1.2	unknown function
CA4570	orf19.6882	*IPF9550*	-1.1	8.4	7.2	7.3	YJR051W	*OSM1*	1.0	-3.4	-1.7	-1.4	similar to Saccharomyces cerevisiae Osm1p osmotic growth protein
CA4571		*RPL33.3*	1.5	1.2	1.3	1.7	YPL143W	*RPL33A*	1.0	1.0	1.7	2.1	ribosomal protein L35a, 3-prime end
CA4572	orf19.6883	*KES1*	-1.3	-1.2	-1.5	-1.3	YPL145C	*KES1*	1.0	1.2	1.8	1.7	involved in ergosterol biosynthesis (by homology)
CA4573	orf19.6884	*IPF9431*	1.0	1.1	1.2	1.0	YJL091C		1.0	-1.6	-2.0	-1.9	unknown function

CA4574	orf19.6885	*IPF9430*	-1.1	-1.3	-1.2	-1.1	YAL009W	*SPO7*	1.0	-1.5	-1.5	-1.2	similar to Saccharomyces cerevisiae Spo7p meiotic protein (by homology
CA4575	orf19.6886	*IPF9428*	-1.0	-1.2	-1.1	-1.1	YPL146C		1.0	1.0	1.6	1.6	unknown function
CA4577	orf19.6889	*MKK2*	-1.3	1.2	1.3	1.3	YPL140C	*MKK2*	1.0	1.0	-1.0	-1.1	Protein kinase of MEK (by homology)
CA4578	orf19.6891	*RFC1*	-1.0	-1.1	-1.3	-1.2	YOR217W	*RFC1*	1.0	-1.4	-1.1	-1.3	DNA replication factor C (by homology)
CA4582	orf19.6900	*MDM12*	-1.1	-1.0	-1.1	-1.1	YOL009C	*MDM12*	1.0	-1.1	1.0	-1.1	Involved in mitochondrial inheritance (by homology)
CA4583	orf19.6901	*IPF2229*	-1.1	-1.1	-1.0	-1.0	YOR173W		1.0	-1.3	-1.3	1.1	unknown function
CA4584	orf19.6902	*IPF2228*	-1.1	-1.2	-1.2	-1.0	YKR024C	*DBP7*	1.0	-1.9	-1.5	-1.3	similar to Saccharomyces cerevisiae Dbp7p RNA helicase required for 6
CA4585	orf19.6903	*IPF2227*	-1.1	-1.1	-1.1	-1.0	YKR025W	*RPC37*	1.0	-2.2	-1.2	-1.2	unknown function
CA4586	orf19.6904	*GCN3*	1.0	1.0	1.1	1.0	YKR026C	*GCN3*	1.0	-2.1	-1.8	-1.5	Translation initiation factor eIF2B alpha subunit (by homology)
CA4587	orf19.6905	*IPF2223*	-1.3	1.5	1.4	1.4	YNL011C		1.0	-1.4	-1.4	-1.5	unknown function
CA4588	orf19.6906	*BEL1.EXON1*	1.3	1.0	1.1	1.0	YMR116C	*ASC1*					protein of the 40S ribosomal subunit, exon 1 (by homology)
CA4590	orf19.6907	*IPF2218*	1.1	-1.1	1.0	-1.1	YDL156W		1.0	1.1	1.2	1.1	unknown function
CA4591	orf19.6908	*IPF2216*	-1.0	-1.0	-1.0	1.0	YMR113W	*FOL3*	1.0	-1.4	2.2	1.4	putative folylpolyglutamate synthetase (by homology)
CA4592	orf19.6909	*IPF2215*	1.1	1.0	-1.0	1.0	YMR112C	*MED11*	1.0	-1.1	-1.0	1.5	unknown function
CA4593	orf19.6910	*IPF2214*	1.0	-1.0	1.0	-1.0	YDR013W		1.0	-1.0	1.2	1.6	unknown function
CA4595	orf19.6913	*GCN2*	-1.2	-1.1	-1.1	-1.1	YDR283C	*GCN2*	1.0	-1.5	-1.8	-1.5	Ser/thr protein kinase (by homology)
CA4596	orf19.6915	*MRE11*	1.0	-1.0	-1.0	-1.0	YMR224C	*MRE11*	1.0	-1.0	-1.1	-1.1	DNA repair and meiotic recombination protein (by homology)
CA4597	orf19.6916	*ATP11*	1.0	-1.0	-1.0	1.0	YNL315C	*ATP11*	1.0	-1.1	-1.2	-1.4	F1F0-ATPase complex assembly protein (by homology)
CA4598	orf19.6917	*IPF20019*	1.0	1.1	-1.0	1.0	YNL310C		1.0	-1.2	-1.3	-1.3	unknown function
CA4602	orf19.10802	*IPF6231*	1.1	1.1	1.1	1.2	YCL033C		1.0	-1.0	-1.4	-1.4	unknown function
CA4603	orf19.10803	*IPF6230*	1.6	1.1	1.6	1.3	YDL015C	*TSC13*	1.0	1.4	1.7	1.5	unknown function
CA4607	orf19.3297	*IPF6223*	1.1	-1.0	1.1	1.0	YGR215W	*RSM27*	1.0	-1.4	-1.3	-1.2	unknown function
CA4608	orf19.3298	*CCH1*	-1.2	1.1	1.3	1.1	YGR217W	*CCH1*	1.0	-1.5	-1.3	-1.0	Calcium channel protein (by homology)
CA4609	orf19.3300	*ZPR1*	1.0	1.0	-1.1	-1.0	YGR211W	*ZPR1*	1.0	-1.2	1.2	1.4	Zinc finger protein (by homology)
CA4610	orf19.3301	*IPF19802*	1.1	1.3	1.4	1.3	YIL046W	*MET30*	1.0	-1.3	-1.3	-1.2	similar to Saccharomyces cerevisiae Met30p involved in regulation of sul
CA4612	orf19.3303	*PPM2*	-1.1	-1.1	-1.1	1.0	YOL141W	*PPM2*	1.0	-1.5	1.2	1.4	carboxy methyl transferase
CA4613	orf19.3304	*IPF7950*	1.0	-1.1	-1.1	-1.1	YOL142W	*RRP40*	1.0	1.4	1.6	1.9	similar to Saccharomyces cerevisiae Rrp40p involved in ribosomal RNA
CA4615	orf19.3306	*IPF7955*	1.0	1.0	1.0	-1.0	YIL072W	*HOP1*	1.0	-1.1	-1.1	-1.1	DNA binding protein (by homology)
CA4616	orf19.3307	*IPF5761*	1.0	1.1	1.2	1.1	YHR176W		1.0	-1.0	-1.2	-1.1	flavin-containing monooxigenase (by homology)
CA4617	orf19.3308	*STB5*	1.1	1.2	1.5	1.3	YHR178W	*STB5*	1.0	1.2	-1.0	1.0	SIN3 binding protein (by homology)
CA4621	orf19.3312	*IPF5753*	-1.0	1.2	1.5	1.2	YER080W		1.0	-1.3	-1.1	-1.8	unknown function
CA4622	orf19.3314	*IPF5751*	-1.2	1.1	1.0	1.0	YBR254C	*TRS20*	1.0	1.1	1.1	1.1	TRAPP subunit of 20 kDa involved in targeting and fusion of ER to golgi t
CA4624	orf19.3318	*IPF5747*	-1.1	1.0	-1.0	-1.0	YBR255W		1.0	1.1	1.0	1.1	unknown function
CA4626	orf19.10831	*MRS7*	-1.1	-1.1	-1.2	-1.0	YOL027C		1.0	-1.3	-1.3	-1.3	suppressor splicing defects (by homology)
CA4627	orf19.10832	*DUT1*	1.2	1.0	1.0	1.1	YBR252W	*DUT1*	1.0	-1.1	-1.1	-1.0	dUTP pyrophosphatase
CA4630	orf19.336	*IPF1537*	1.0	1.1	1.1	1.1	YPL252C	*YAH1*	1.0	1.0	-1.1	1.1	putative adrenodoxin and ferrodoxin (by homolgy)
CA4631	orf19.337	*VTI1*	-1.0	1.2	1.2	1.1	YMR197C	*VTI1*	1.0	-1.0	1.2	1.2	v-SNARE involved in Golgi retrograde traffic (by homology)
CA4632	orf19.338	*IPF1531*	-1.2	-1.3	-1.8	-1.4	YMR196W		1.0	-1.1	-1.3	-1.3	unknown function
CA4633	orf19.339	*NDH1*	-1.2	3.1	3.7	2.9	YMR145C		1.0	-1.0	1.2	-1.0	Mitochondrial NADH dehydrogenase
CA4634	orf19.340	*IPF1526*	-1.0	1.0	-1.0	1.0	YLR119W	*SRN2*	1.0	-1.2	-1.1	-1.3	unknown function
CA4638	orf19.345	*UGA2*	-1.1	-1.6	-2.7	-1.8	YBR006W	*UGA2*	1.0	1.3	-1.1	1.1	succinate-semialdehyde dehydrogenase (NAD(P)+) (by homology)
CA4639	orf19.346	*IPF1509*	-1.1	-1.7	-1.9	-1.6	YLR089C		1.0	-1.1	1.2	1.3	putative alanine transaminase (by homology)
CA4642	orf19.349	*IPF1500*	-1.1	-1.0	1.0	1.0	YPR155C	*NCA2*	1.0	1.1	1.1	-1.2	similar to Saccharomyces cerevisiae Nca2p regulating expression of mito
CA4643	orf19.350	*PRE9*	-1.0	1.0	1.0	1.1	YGR135W	*PRE9*	1.0	-1.0	-1.1	1.2	20S proteasome subunit Y13 (alpha3) (by homology)
CA4644	orf19.351	*IPF1497*	-1.0	1.0	-1.0	1.0	YPR153W		1.0	-1.3	-1.1	-1.1	unknown function
CA4647	orf19.354	*IPF1493*	-1.0	-1.0	1.0	1.0	YER078C		1.0	1.1	1.1	1.3	similarity to E.coli X-Pro aminopeptidase II (by homology)
CA4648	orf19.11914	*IPF9864*	-1.3	-1.0	-1.1	-1.1	YBL034C	*STU1*	1.0	-1.3	-1.2	1.1	similar to Saccharomyces cerevisiae Stu1p mitotic spindle protein (by ho
CA4650	orf19.11916	*ISW1.3*	-1.3	-1.4	-1.9	-1.4	YBR245C	*ISW1*	1.0	-1.6	-1.4	-1.4	ATPase component of a four subunit chromatin remodeling complex, 3-p
CA4651	orf19.11918	*IPF3121*	-1.0	1.0	1.1	-1.0	YGR044C	*RME1*	1.0	1.2	1.5	2.2	unknown function
CA4653	orf19.4440	*IPF3102*	1.2	1.1	1.1	1.0	YER157W	*SEC34*	1.0	1.1	1.2	1.1	similar to Saccharomyces cerevisiae Sec34p required for vesicle tetherin
CA4654	orf19.4441	*IPF3101*	-1.0	-1.0	-1.0	1.1	YIL150C	*DNA43*	1.0	-1.3	1.3	1.1	unknown function
CA4655	orf19.4442	*IPF3098*	1.1	1.0	1.5	1.1	YNL219C	*ALG9*	1.0	1.1	1.2	1.1	Putative mannosyltransferase (by homology)
CA4656	orf19.4443	*IPF3095*	-1.1	-1.1	-1.0	-1.0	YDL235C	*YPD1*	1.0	-1.1	-1.1	-1.1	unknown function
CA4657	orf19.4444	*IPF3094*	1.1	2.2	2.6	2.1	YDL236W	*PHO13*	1.0	1.2	1.4	1.5	4-nitrophenyl phosphatase (by homology)
CA4660	orf19.4447	*YMC1*	1.0	-1.1	-1.1	-1.0	YPR058W	*YMC1*	1.0	1.0	1.1	1.3	mitochondrial carrier protein (MCF) (by homology)
CA4661	orf19.4448	*IPF6561*	-1.1	-1.1	-1.0	-1.1	YOR353C		1.0	1.1	1.4	1.2	unknown function
CA4662	orf19.4449	*LYS7*	-1.0	-1.0	-1.0	-1.0	YMR038C	*LYS7*	1.0	1.3	1.7	2.0	Copper chaperone for superoxide dismutase Sod1p (by homology)
CA4663	orf19.4450	*IPF6554*	-1.2	-1.9	-2.1	-1.9	YJL103C		1.0	-1.1	-1.0	-1.1	unknown function
CA4665	orf19.4451	*IPF6548*	-1.3	-1.2	-1.6	-1.4	YNL163C	*RIA1*	1.0	1.1	-1.3	1.3	translation elongation factor eEF4 (by homology)
CA4666	orf19.4455	*IPF6542*	-1.1	-1.3	-1.2	-1.2	YNL164C		1.0	-1.3	-1.3	-1.2	unknown function
CA4668	orf19.906	*ROM2*	-1.0	1.0	1.2	-1.0	YLR371W	*ROM2*	1.0	-1.3	-1.2	1.0	GDP/GTP exchange factor for Rho1p (by homology)

CA4669	orf19.905	*IPF4537*	1.2	1.3	1.7	1.3	YIL088C		1.0	-1.2	-1.2	-1.5	putative permease (by homology)
CA4671	orf19.903	*GPM1*	-1.1	2.2	1.9	2.2	YKL152C	*GPM1*	1.0	1.5	1.8	2.1	phosphoglycerate mutase (by homology)
CA4672	orf19.900	*IPF3659*	-1.6	-1.5	-2.1	-2.0	YJL041W	*NSP1*	1.0	-1.1	1.0	1.1	similar to Saccharomyces cerevisiae Nsp1p nuclear pore protein (by hor
CA4674	orf19.898	*HEM2*	1.1	-1.1	1.0	-1.0	YGL040C	*HEM2*	1.0	1.0	1.0	-1.3	Porphobilinogen synthase (by homology)
CA4675	orf19.897	*IPF3664*	1.1	1.0	1.1	1.0	YMR077C	*VPS20*	1.0	-1.0	-1.2	-1.3	unknown function
CA4677	orf19.895	*HOG1*	1.1	1.0	-1.0	-1.1	YLR113W	*HOG1*	1.0	1.3	1.7	1.6	Ser/thr protein kinase of MAPK family
CA4678	orf19.894	*IPF3670*	-1.2	1.0	1.0	1.1	YDR137W	*RGP1*	1.0	-1.2	1.2	1.0	unknown function
CA4680	orf19.891	*AMD1*	-1.3	1.1	-1.1	1.0	YML035C	*AMD1*	1.0	-2.0	-2.1	-2.1	AMP deaminase (by homology)
CA4681	orf19.889	*IPF3679*	-1.1	-1.1	-1.2	-1.0	YOL055C	*THI20*	1.0	-3.0	-2.0	-2.5	similar to Saccharomyces cerevisiae Thi20p hydroxymethylpyrimidine ph
CA4682	orf19.886	*IPF3687*	1.0	1.1	-1.2	-1.0	YIR006C	*PAN1*	1.0	-1.8	-2.0	-2.0	similar to Saccharomyces cerevisiae Pan1p actin-cytoskeleton assembly
CA4685	orf19.881	*IPF9013*	-1.2	1.1	-1.1	-1.0	YOR030W	*DFG16*	1.0	-1.8	-1.7	-1.7	unknown function
CA4686	orf19.880	*IPF9015*	-1.0	1.1	1.1	1.1	YHR098C	*SFB3*	1.0	-1.7	-1.9	-1.7	unknown function
CA4687	orf19.879	*IPF9017*	-1.0	-1.0	1.0	1.0	YOR035C	*SHE4*	1.0	1.1	1.2	1.1	similar to Saccharomyces cerevisiae She4p required for mother cell-spec
CA4688	orf19.878	*NBN1*	1.0	-1.0	1.0	1.0	YHR090C	*YNG2*	1.0	1.5	1.0	1.1	involved in chromatin remodeling and possibly transcription regulation (by
CA4692		*COX6.3*	1.0	-1.0	1.0	-1.0	YHR051W	*COX6*	1.0	1.2	1.1	-1.3	cytochrome-c oxidase subunit VI, 3-prime end (by homology)
CA4695	orf19.6923	*IPF4229*	-1.1	-1.0	1.1	1.0	YML015C	*TAF40*	1.0	-1.5	-2.0	-1.9	unknown function
CA4696	orf19.6924	*HTA1*	1.5	1.7	1.6	1.9	YDR225W	*HTA1*	1.0	1.1	1.3	-1.1	Histone H2A (by homology)
CA4697	orf19.6925	*HTB1*	1.1	1.3	1.5	1.3	YDR224C	*HTB1*	1.0	-1.3	1.3	1.1	Histone H2B (by homology)
CA4698	orf19.6926	*CDC25*	1.1	1.0	1.2	1.1	YLR310C	*CDC25*	1.0	-1.1	1.1	1.1	cell division cycle protein
CA4699	orf19.6927	*IPF4220*	1.1	-1.0	1.0	-1.1	YJL053W	*PEP8*	1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Pep8p involved in vacuolar protein s
CA4700	orf19.6928	*SAP9*	-1.0	1.6	2.2	1.3	YLR120C	*YPS1*	1.0	-3.2	-3.6	-4.6	aspartyl proteinase 9 (by homology)
CA4701	orf19.6929	*IPF4214*	1.0	1.0	1.1	1.0	YER134C		1.0	1.1	1.1	-1.5	unknown function
CA4703	orf19.6931	*CLP1*	-1.1	-1.1	1.0	1.1	YOR250C	*CLP1*	1.0	-1.0	1.1	1.0	probable cleaveage/polyadenylation factor
CA4704	orf19.6933	*RRD2*	-1.0	1.0	1.1	1.0	YPL152W	*RRD2*	1.0	-1.1	-1.1	-1.3	hosphotyrosyl phosphatase activator
CA4706	orf19.6936	*RAD53*	1.0	1.0	1.0	1.1	YPL153C	*RAD53*	1.0	-1.2	-1.4	-1.6	protein kinase
CA4707	orf19.6937	*PTR21*	-1.0	2.6	3.4	3.2	YKR093W	*PTR2*	1.0	-1.9	-2.0	-1.5	peptide transporter
CA4708	orf19.6938	*MEU1*	-1.0	1.1	1.1	-1.0	YLR017W	*MEU1*	1.0	1.1	1.4	1.6	regulator of ADH2 expression (by homology)
CA4709	orf19.6941	*IPF5895*	1.0	1.0	1.0	-1.1	YOR245C	*DGA1*	1.0	-1.4	-1.4	-1.4	unknown function
CA4710	orf19.6942	*ORC3*	-1.1	-1.1	-1.2	-1.1	YLL004W	*ORC3*	1.0	1.0	-1.2	-1.3	Origin recognition complex (by homology)
CA4711	orf19.6944	*PHB1*	-1.0	-1.3	-1.3	-1.3	YGR132C	*PHB1*	1.0	-1.4	-1.1	-1.1	Prohibitin, antiproliferative protein (by homology)
CA4712	orf19.6947	*GTT1.3*	1.0	-1.1	-1.2	-1.2	YIR038C	*GTT1*	1.0	-1.1	-1.2	-1.4	glutathione S-transferase, 3-prime end (by homology)
CA4713	orf19.6948	*CCC1*	1.0	-1.7	-1.4	-1.5	YLR220W	*CCC1*	1.0	-1.3	-1.1	-1.3	Transmembrane Ca2+ transporter (by homology)
CA4714	orf19.6950	*IPF5912*	-1.1	1.0	1.0	-1.0	YDR352W		1.0	-1.1	1.3	1.0	unknown function
CA4715	orf19.6951	*DPL1*	1.1	1.1	1.1	1.1	YDR294C	*DPL1*	1.0	-1.5	-1.3	-1.0	dihydrosphingosine phosphate lyase (by homology)
CA4716	orf19.6952	*IPF8666*	-1.0	1.1	1.1	1.1	YDR295C	*PLO2*	1.0	-1.6	-1.8	-1.4	unknown function
CA4717	orf19.6953	*IPF8663*	-1.1	-1.1	-1.3	-1.1	YJL083W		1.0	-1.1	-1.3	-1.1	Unknown function
CA4718	orf19.6955	*IPF8661*	-1.0	-1.2	-1.3	-1.1	YOR056C		1.0	1.3	1.6	1.7	unknown function
CA4719	orf19.6956	*DAL51*	1.0	1.1	1.2	1.1	YJR152W	*DAL5*	1.0	-1.7	-1.5	-1.7	allantoate permease (by homology)
CA4720	orf19.6958	*ECM18*	1.0	1.2	1.0	1.0	YDR125C	*ECM18*	1.0	-1.8	-1.6	-1.3	Involved in cell wall biogenesis and architecture (by homology)
CA4721	orf19.12330	*CPP1*	-1.1	-1.0	-1.1	-1.1	YNL053W	*MSG5*	1.0	-1.1	-1.1	-1.1	probable protein-tyrosine phosphatase
CA4722	orf19.12329	*SAC1*	1.1	1.1	1.3	1.2	YKL212W	*SAC1*	1.0	-1.1	1.3	1.6	integral membrane protein localizing to the ER and Golgi (by homology)
CA4723	orf19.12328	*IPF18177*	1.1	-1.3	-1.2	-1.2	YKL094W	*YJU3*	1.0	-2.8	-2.0	-1.7	Unknown function
CA4724	orf19.12327	*PDC2*	-1.1	-1.1	-1.1	-1.2	YDR081C	*PDC2*	1.0	1.1	1.1	1.1	pyruvate decarboxylase regulator
CA4725		*PET100*	-1.0	1.0	1.0	-1.0	YDR079W	*PET100*	1.0	-1.7	-1.3	-1.4	cytochrome-c oxidase assembly protein (by homology)
CA4726	orf19.12326	*IPF12255*	1.1	1.2	1.2	1.1	YDR084C		1.0	1.3	1.8	1.6	unknown function
CA4728	orf19.12322	*VPS41.3F*	-1.2	-1.2	-1.3	-1.2	YDR080W	*VPS41*	1.0	-1.2	-1.1	-1.1	required for the vacuolar assembly, 3-prime end (by homology)
CA4732	orf19.4855	*IPF7733*	-1.1	-1.1	-1.0	-1.0	YCR063W	*BUD31*	1.0	1.3	-1.1	1.1	unknown function
CA4733	orf19.4853	*IPF7732*	-1.0	-1.0	-1.0	1.0	YCR065W	*HCM1*	1.0	-1.1	-1.4	-1.1	similar to Saccharomyces cerevisiae Hcm1p transcription factor with fork
CA4734	orf19.4851	*TFA1*	-1.0	-1.0	-1.1	1.1	YKL028W	*TFA1*	1.0	-1.1	-1.1	-1.1	Large subunit of transcription factor tfIIE
CA4735	orf19.4850	*IPF7726*	-1.2	1.1	1.0	-1.1	YPL260W		1.0	1.1	1.6	1.2	unknown function
CA4736	orf19.4849	*IPF4503*	1.0	1.0	-1.1	-1.0	YIR011C	*STS1*	1.0	1.1	1.3	1.3	unknown function
CA4737	orf19.4848	*SKI3*	1.0	1.0	-1.0	-1.0	YPR189W	*SKI3*	1.0	-1.5	-1.6	-1.4	antiviral protein
CA4738	orf19.4846	*IPF4500*	-1.0	-1.0	-1.0	-1.0	YGR210C		1.0	1.0	1.3	1.1	putative GTP-binding protein (by homology)
CA4739	orf19.4845	*IPF4498*	1.4	1.2	2.1	1.5	YMR071C		1.0	-1.7	-1.4	-1.6	unknown function
CA4740	orf19.4844	*IPF4497*	1.0	-1.1	1.0	-1.0	YIL079C		1.0	1.0	-1.1	1.1	unknown function
CA4741	orf19.4843	*IPF4496*	-1.1	-1.0	-1.0	-1.0	YLR047C		1.0	-1.5	-1.7	-1.5	unknown function
CA4742	orf19.4841	*SHY1*	1.1	-1.1	1.1	1.0	YGR112W	*SHY1*	1.0	-1.1	1.1	1.3	SURF homologue protein (by homology)
CA4743	orf19.4839	*IPF4491*	-1.0	-1.0	-1.1	-1.0	YER083C		1.0	-1.4	-1.4	-1.4	unknown function
CA4744	orf19.4837	*IPF4489*	1.0	1.0	1.1	1.0	YGR113W	*DAM1*	1.0	-1.1	1.2	1.4	unknown function
CA4746	orf19.4835	*IPF4485*	-1.0	-1.2	-1.2	-1.1	YER082C	*KRE31*	1.0	-1.8	-1.8	-1.5	unknown function
CA4748	orf19.4833	*MLS1*	-1.6	-4.2	-7.3	-4.8	YNL117W	*MLS1*	1.0	-3.7	-3.8	-3.3	malate synthase

CA4750	orf19.4829	*IPF4477*	-1.0	1.1	1.2	1.1	YKL213C	*DOA1*	1.0	-1.3	-1.1	-1.2	similar to Saccharomyces cerevisiae Doa1p involved in ubiquitin-depend
CA4752	orf19.4827	*ADE12*	-1.5	-1.3	-1.2	-1.2	YNL220W	*ADE12*	1.0	-1.1	1.1	1.5	adenylosuccinate synthetase (by homology)
CA4753	orf19.4826	*IDH1.3*	-1.1	1.0	-1.1	1.1	YNL037C	*IDH1*	1.0	-1.3	-1.7	-2.9	isocitrate dehydrogenase (NAD+) subunit1, mitochondrial, 3-prime end (
CA4754	orf19.4825	*IPF11479*	1.1	1.0	1.1	1.1	YIL098C	*FMC1*	1.0	-1.1	-1.2	-1.4	unknown function
CA4758	orf19.3986	*PPR1*	-1.0	1.0	-1.1	-1.0	YLR014C	*PPR1*	1.0	-1.0	-1.1	1.1	transcription factor regulating pyrimidine pathway (by homology)
CA4760	orf19.3990	*IPF9652*	1.0	1.0	-1.1	-1.0	YJL011C		1.0	-1.2	-1.2	-1.4	unknown function
CA4761	orf19.3991	*IPF9650*	-1.2	-1.0	-1.2	-1.0	YGL144C		1.0	-1.4	-1.4	-1.0	lipase family protein containing serine active site (by homology)
CA4762	orf19.3994	*IPF9647*	1.2	1.4	1.6	1.8	YOR085W	*OST3*	1.0	1.3	1.8	1.5	similar to Saccharomyces cerevisiae Ost3p oligosaccharyltransferase ga
CA4763	orf19.3995	*IPF9645*	-1.1	-1.0	-1.1	1.0	YMR154C	*RIM13*	1.0	1.0	1.1	1.3	similar to Saccharomyces cerevisiae Rim13p calpain-like cysteine protea
CA4764	orf19.3996	*GPI10*	1.2	1.5	1.8	1.6	YGL142C	*GPI10*	1.0	-1.0	-1.2	1.0	required for Glycosyl Phosphatdyl Inositol synthesis (by homo
CA4768	orf19.4000	*IPF9385*	1.0	-1.1	-1.1	-1.0	YDL106C	*PHO2*	1.0	1.1	1.2	1.0	similar to Saccharomyces cerevisiae Pho2p homeobox-domain containin
CA4769	orf19.4001	*IPF9384*	-1.1	-1.1	-1.1	-1.1	YDL107W	*MSS2*	1.0	-1.2	-1.4	-1.5	similar to Saccharomyces cerevisiae Mss2p serine/threonine protein kina
CA4770	orf19.4002	*IPF9382.3*	1.0	1.1	1.0	1.0	YDL101C	*DUN1*	1.0	-1.4	-1.4	-1.7	similar to Saccharomyces cerevisiae Dun1p protein kinase, 3-prime end
CA4771	orf19.4003	*IPF3336*	-1.2	-1.0	-1.2	-1.1	YGL145W	*TIP20*	1.0	-1.6	-1.1	1.1	unknown function
CA4772	orf19.4004	*CCT3*	-1.0	-1.4	-1.5	-1.3	YJL014W	*CCT3*	1.0	1.3	1.8	2.3	Chaperonin (by homology)
CA4773	orf19.4005	*IPF3340*	1.1	1.0	-1.0	-1.0	YDR196C		1.0	-1.1	-1.2	-1.6	unknown function
CA4774	orf19.4006	*IPF3341*	-1.1	-1.0	-1.1	-1.0	YHR063C	*PAN5*	1.0	1.0	1.2	1.2	Unknown function
CA4775	orf19.4007	*IPF3342*	-1.1	-1.0	1.0	-1.1	YDR198C		1.0	-1.4	-1.1	-1.1	Unknown function
CA4776	orf19.4009	*CNB1*	1.1	1.1	1.0	1.1	YKL190W	*CNB1*	1.0	-1.4	-1.3	-1.1	Protein phosphatase, Calcineurin B (by homology)
CA4777	orf19.4010	*PAN3*	2.6	1.0	1.1	1.0	YKL025C	*PAN3*	1.0	-1.1	1.0	1.2	component of the Pab1p-dependent poly(A) ribonuclease (by hom
CA4779	orf19.4012	*IPF3351*	1.0	1.2	1.1	1.0	YHR071W	*PCL5*	1.0	-1.0	1.3	1.8	unknown function
CA4780	orf19.4013	*IPF3352*	1.0	1.1	1.1	1.2	YHR045W		1.0	-1.2	-1.1	1.1	unknown function
CA4783	orf19.4016	*IPF3358*	-1.1	-1.3	-1.6	-1.4	YBL045C	*COR1*	1.0	-1.8	-1.9	-2.4	ubiquinol-cytochrome-c reductase (by homology)
CA4785	orf19.4018	*IPF3361*	1.2	-1.1	-1.1	-1.1	YJR113C	*RSM7*	1.0	1.2	1.1	1.2	putative mitochondrial ribosomal protein S7 (by homology)
CA4786	orf19.4019	*IPF3362*	1.0	-1.0	1.1	1.0	YBL046W		1.0	-1.6	-1.4	1.2	Unknown function
CA4789	orf19.4023	*IPF3366*	1.1	1.0	1.0	1.0	YPR166C	*MRP2*	1.0	-1.1	-1.1	-1.2	Mitochondrial ribosomal protein (by homology)
CA4790	orf19.4024	*IPF3367*	-1.1	-1.1	-1.2	-1.0	YBR256C	*RIB5*	1.0	1.5	1.3	1.6	Riboflavin synthase (by homology)
CA4791	orf19.4025	*IPF3370*	1.4	1.4	1.4	1.4	YER012W	*PRE1*	1.0	-1.1	-1.0	-1.1	similar to Saccharomyces cerevisiae Pre1p 20S proteasome subunit C11
CA4792	orf19.4026	*HIS1*	1.1	1.1	1.1	1.1	YER055C	*HIS1*	1.0	1.6	1.2	3.6	ATP phosphoribosyltransferase
CA4793	orf19.4028	*IPF3375*	-1.0	-1.0	-1.1	-1.1	YBR002C	*RER2*	1.0	1.0	1.1	1.4	similar to Saccharomyces cerevisiae Rer2p cis-prenyltransferase, a key
CA4794	orf19.4029	*SQT1*	1.1	1.1	-1.0	-1.0	YIR012W	*SQT1*	1.0	1.4	1.5	2.4	suppresses dominant-negative mutants of the ribosomal protein Q
CA4795	orf19.4030	*IPF3378*	-1.1	-1.1	-1.0	-1.1	YIR008C	*PRI1*	1.0	-1.1	1.2	1.0	similar to Saccharomyces cerevisiae Pri1p DNA-directed DNA polymeras
CA4796	orf19.4031	*IPF3380*	1.1	-1.1	-1.2	-1.2	YIR007W		1.0	-1.3	-1.1	-1.2	unknown function
CA4797	orf19.4033	*PRP22*	-1.0	-1.0	-1.1	-1.1	YER013W	*PRP22*	1.0	-1.2	-1.3	-1.2	RNA-dependent ATPase (by homology)
CA4798	orf19.4032	*RPN5.3F*	-1.1	1.1	1.0	-1.0	YDL147W	*RPN5*	1.0	1.2	1.7	1.5	subunit of the regulatory particle of the proteasome, 3-prime end (by hom
CA4800	orf19.4035	*IPF8796*	-1.1	1.1	1.1	1.1	YOL030W		1.0	1.6	1.8	1.9	putative GPI-anchhored protein related to Phr1, Phr2 and Phr3 (by homo
CA4801	orf19.4036	*APM1*	-1.0	-1.1	-1.0	-1.0	YPL259C	*APM1*	1.0	1.0	1.4	1.5	AP-1 complex subunit, mu1 subunit (by homology)
CA4802	orf19.4040	*ILV3*	2.8	1.0	1.0	1.0	YJR016C	*ILV3*	1.0	-1.9	-1.3	1.0	dihydroxyacid dehydratase (by homology)
CA4803	orf19.4041	*PEX4*	1.3	-2.5	-3.0	-2.4	YGR133W	*PEX4*	1.0	-1.3	-1.3	-1.1	E2 ubiquitin-conjugating enzyme -peroxin (by homology)
CA4804	orf19.2098	*ARO8*	-1.3	-1.2	-1.3	-1.2	YGL202W	*ARO8*	1.0	1.3	1.5	2.0	aromatic amino acid aminotransferase I (by homology)
CA4805	orf19.2097	*RAD5*	-1.0	1.0	-1.0	-1.0	YLR032W	*RAD5*	1.0	-1.1	1.0	1.0	DNA helicase (by homology)
CA4806	orf19.2095	*IPF1155*	-1.2	-1.0	-1.1	-1.1	YLL029W		1.0	1.1	1.0	-1.1	Putative dipeptidase (by homology)
CA4807	orf19.2094	*PDR6*	-1.2	1.1	1.2	1.2	YGL016W	*KAP122*	1.0	1.2	1.1	1.4	Pleiotropic drug resistance regulatory protein (by homology)
CA4808	orf19.2093	*RFA1*	-1.6	-1.2	-1.4	-1.3	YAR007C	*RFA1*	1.0	1.2	1.4	2.2	DNA replication factor A, 69 KD subunit (by homology)
CA4809	orf19.2092	*IPF1162*	-1.0	1.3	1.3	1.2	YGL184C	*STR3*	1.0	-1.0	-1.2	-1.2	Cystathionine beta-lyase (by homology)
CA4811	orf19.2090	*ECM16*	-1.0	-1.1	-1.1	-1.1	YMR128W	*ECM16*	1.0	-1.1	-1.1	-1.0	RNA helicase (by homology)
CA4812	orf19.2089	*IPF1171*	1.0	-1.1	-1.0	-1.0	YLR093C	*NYV1*	1.0	1.1	1.1	-1.0	Putative synaptobrevin (by homology)
CA4813	orf19.2088	*DPB4*	-1.0	1.1	-1.1	1.0	YDR121W	*DPB4*	1.0	1.1	1.2	1.2	DNA-directed DNA polymerase epsilon, subunit D (by homology)
CA4814	orf19.2087	*SAS2*	1.1	1.1	1.1	1.0	YMR127C	*SAS2*	1.0	1.2	1.1	1.2	Zinc finger protein involved in silencing (by homology)
CA4815	orf19.2084	*CDH1*	-1.0	1.0	-1.0	-1.0	YGL003C	*CDH1*	1.0	2.0	3.2	4.6	Substrate-specific activator of APC-dependent proteolysis (by homology)
CA4817	orf19.2081	*POM152*	-1.1	1.0	-1.3	-1.2	YMR129W	*POM152*	1.0	-1.3	1.0	1.2	Nuclear pore membrane glycoprotein (by homology)
CA4818	orf19.2079	*IPF1193*	1.3	1.2	1.3	1.1	YHL018W		1.0	-1.6	-1.5	-1.2	unknown function
CA4819	orf19.2078	*IPF1194*	-1.1	1.2	-1.0	1.1	YHL019C	*APM2*	1.0	-1.2	-1.3	-1.3	Similar to clathrin coat proteins
CA4821	orf19.2076	*IPF1197*	-1.0	-1.1	1.0	-1.1	YMR130W		1.0	1.2	1.2	1.4	unknown function
CA4822	orf19.2075	*DFG5*	1.1	1.4	1.9	1.5	YMR238W	*DFG5*	1.0	-1.1	1.0	1.2	Required for filamentous growth (by homology)
CA4823	orf19.2073	*ERC3*	1.1	1.6	2.4	1.5	YDR338C		1.0	1.0	1.0	1.1	ethionine resistance protein (by homology)
CA4824	orf19.2072	*HNM2*	-1.0	1.1	-1.0	-1.0	YGL077C	*HNM1*	1.0	-1.3	-1.2	-1.2	Choline permease (by homology)
CA4826	orf19.2070	*IPF1206*	-1.1	-1.1	-1.3	-1.2	YLR033W	*RSC58*	1.0	-1.1	1.0	-1.1	unknown function
CA4827	orf19.2069	*SMF2*	-1.1	2.0	3.3	2.1	YLR034C	*SMF3*	1.0	1.0	1.0	1.2	Manganese transporter (by homology)
CA4829	orf19.2067	*IPF1210*	-1.0	1.1	1.1	1.1	YKL040C	*NFU1*	1.0	1.1	-1.0	-1.0	similar to Saccharomyces cerevisiae Nfu1p involved in homeostasis (by
CA4831	orf19.2066	*IPF1212*	-1.1	-1.2	-1.0	-1.2	YJR129C		1.0	-1.3	-1.3	-1.3	unknown function

CA4832	orf19.2065	*DAL2*	-1.0	-1.0	-1.1	-1.0	YIR029W	*DAL2*	1.0	-1.2	-1.1	-1.2	Allantoinase
CA4838	orf19.2057	*YTA12*	-1.4	-1.3	-1.8	-1.5	YMR089C	*YTA12*	1.0	-1.3	1.2	-1.1	Protease of the SEC18/CDC48/PAS1 family of ATPases (AAA) (by homc
CA4839	orf19.2055	*NPL6*	1.0	-1.1	-1.1	-1.2	YMR091C	*NPL6*	1.0	1.0	1.2	1.2	Nuclear protein localization factor (by homology)
CA4841	orf19.3809	*IPF10355*	1.2	1.0	1.0	-1.1	YKR099W	*BAS1*	1.0	1.1	1.2	1.1	unknown function
CA4842	orf19.3810	*MTD1*	1.1	-1.3	-1.2	-1.1	YKR080W	*MTD1*	1.0	-1.5	-1.7	-1.7	methylenetetrahydrofolate dehydrogenase
CA4843	orf19.3811	*GYP1*	-1.1	1.1	1.2	-1.0	YOR070C	*GYP1*	1.0	-1.4	-1.2	-1.4	GTPase activating protein (by homology)
CA4844	orf19.3812	*PDR13*	-1.3	1.1	-1.0	-1.1	YHR064C	*PDR13*	1.0	1.0	1.6	1.7	Drug resistance
CA4847	orf19.3815	*IPF6951*	1.0	1.2	-1.0	1.0	YKR098C	*UBP11*	1.0	1.1	1.1	1.2	similar to Saccharomyces cerevisiae Ubp11p ubiquitin C-terminal hydrola
CA4848	orf19.3817	*RTS2*	1.1	1.1	1.1	1.0	YOR077W	*RTS2*	1.0	-1.1	-1.1	-1.1	Unknown function
CA4852	orf19.3822	*SCS7*	1.1	1.7	4.1	2.0	YMR272C	*SCS7*	1.0	1.0	1.3	1.7	Required for hydroxylation of ceramide (by homology)
CA4853	orf19.3823	*IPF5823*	1.0	1.0	-1.1	-1.0	YMR273C	*ZDS1*					similar to Saccharomyces cerevisiae Zds1p involved in negative regulatic
CA4854	orf19.3825	*RCE1*	1.2	1.3	1.7	1.4	YMR274C	*RCE1*	1.0	-1.2	1.0	1.1	CAAX PRENYL PROTEASE 2 (by homology)
CA4856	orf19.3827	*IPF15950*	1.1	-1.1	1.0	-1.1	YKR087C		1.0	-1.1	-1.1	-1.3	unknown function
CA4858	orf19.3831	*IPF15927.3F*	-1.0	1.0	1.0	-1.0	YGR280C		1.0	-1.0	1.1	1.0	similar to Saccharomyces cerevisiae Tfc3p transcription initiation factor T
CA4859	orf19.3833	*IPF15927.5F*	-1.1	-1.1	-1.2	-1.0	YAL001C	*TFC3*	1.0	-1.1	-1.2	-1.1	similar to Saccharomyces cerevisiae Tfc3p transcription initiation factor T
CA4861	orf19.3836	*IPF4094*	1.0	1.1	-1.2	-1.0	YGR001C		1.0	-1.9	-1.2	-1.0	unknown function
CA4862	orf19.3838	*EFB1*	1.2	1.4	1.6	1.6	YAL003W	*EFB1*	1.0	1.2	1.1	2.0	translation elongation factor eEF1beta
CA4864	orf19.3840	*IPF4087*	-1.1	-1.4	-1.8	-1.4	YER129W	*PAK1*	1.0	-1.4	-1.9	-1.8	similar to Saccharomyces cerevisiae Pak1p protein kinase suppressing
CA4865	orf19.3841	*IPF4085*	-1.1	-1.0	1.0	-1.0	YGL180W	*APG1*	1.0	1.0	-1.3	-1.2	similar to Saccharomyces cerevisiae Apg1p essential for autophagocytos
CA4866	orf19.3843	*IPF4083*	-1.1	-1.0	-1.2	1.4	YBR171W	*SEC66*	1.0	1.1	1.1	1.2	similar to Saccharomyces cerevisiae Sec66p ER protein-translocation co
CA4867	orf19.3844	*IPF4080*	-1.0	1.0	-1.0	1.1	YKL142W	*MRP8*	1.0	-2.4	-1.8	-2.9	similar to Saccharomyces cerevisiae Mrp8p ribosomal protein, mitochonc
CA4869	orf19.3846	*LYS4*	-1.1	-1.1	-1.3	-1.3	YDR234W	*LYS4*	1.0	1.4	1.9	2.7	homoaconitate hydratase
CA4871	orf19.6557	*IPF1680*	-1.0	1.0	1.0	1.0	YDR242W	*AMD2*					probable amidase
CA4874	orf19.6559	*IPF1674*	1.0	2.5	2.1	2.1	YNL108C		1.0	-1.2	-1.4	-1.1	putative transcription initiation factor (by homology)
CA4875	orf19.6561	*LAT1*	-1.4	-1.4	-1.7	-1.5	YNL071W	*LAT1*	1.0	-1.1	1.2	1.2	Dihydrolipoamide S-acetyltransferase (by homology)
CA4876	orf19.6562	*RNH35*	1.0	-1.0	-1.1	-1.0	YNL072W	*RNH35*	1.0	-1.4	-1.0	1.1	RNase H (by homology)
CA4877	orf19.6563	*IPF1667*	-1.1	-1.1	-1.1	-1.0	YJR054W		1.0	-1.7	-1.9	-2.2	unknown function
CA4878	orf19.6565	*OXA1*	-1.0	-1.2	-1.2	-1.2	YER154W	*OXA1*	1.0	1.5	1.7	-1.1	Cytochrome oxidase biogenesis protein (by homology)
CA4880	orf19.6568	*RHC18*	1.0	-1.1	-1.0	-1.0	YLR383W	*RHC18*	1.0	-1.1	-1.2	-1.2	Recombination repair protein (by homology)
CA4883	orf19.6573	*IPF1649*	-1.6	-1.1	-2.0	-1.5	YER155C	*BEM2*	1.0	-1.1	-1.1	1.0	similar to Saccharomyces cerevisiae Bem2p GTPase-activating protein (
CA4885	orf19.6577	*IPF1636*	1.3	1.4	1.9	1.6	YLL028W	*TPO1*	1.0	-1.3	-1.7	-1.8	similar to Saccharomyces cerevisiae Tpo1p multidrug resistance protein
CA4889	orf19.6581	*IPF1629*	1.0	1.1	1.1	1.0	YOL003C		1.0	-1.0	-1.1	-1.1	unknown function
CA4890	orf19.6582	*PRE10*	1.1	1.1	1.0	1.2	YOR362C	*PRE10*	1.0	-1.8	-2.0	-2.9	20S proteasome subunit C1 (by homology)
CA4892	orf19.6584	*PRT1*	-1.2	-1.3	-1.5	-1.3	YOR361C	*PRT1*	1.0	1.2	1.5	1.8	Translation initiation factor eIF3 (by homology)
CA4893	orf19.6585	*IPF1621*	-1.1	1.1	-1.0	1.0	YAL046C		1.0	1.0	-1.2	-1.2	unknown function
CA4895	orf19.6587	*IPF18161*	-1.1	-1.3	-1.1	-1.1	YDR152W		1.0	-1.1	1.0	1.1	unknown function
CA4896	orf19.6588	*IPF18160*	1.1	1.0	1.0	-1.0	YDR162C	*NBP2*	1.0	-1.3	1.1	1.5	unknown function
CA4897	orf19.6034	*TUB2.3*	1.4	1.3	1.7	1.6	YFL037W	*TUB2*	1.0	-1.1	1.3	1.3	Beta-tubulin, 3-prime end
CA4899	orf19.6036	*IPF1460*	-1.0	-1.0	1.0	-1.1	YLR039C	*RIC1*	1.0	-1.7	-1.1	1.2	unknown function
CA4902	orf19.6039	*SED5*	1.0	-1.0	-1.1	1.1	YLR026C	*SED5*	1.0	-1.4	-1.5	-1.4	Syntaxin (by homology)
CA4903	orf19.6040	*SNF7*	1.0	-1.0	-1.1	-1.1	YLR025W	*SNF7*	1.0	-1.2	-1.1	-1.3	Class E Vps protein (by homology)
CA4904	orf19.6041	*RPO41*	-1.2	-1.3	-1.9	-1.5	YFL036W	*RPO41*	1.0	-1.1	-1.3	-1.3	Mitochondrial DNA-directed RNA polymerase (by homology)
CA4907	orf19.6045	*PSD1*	-1.1	1.1	1.1	1.1	YNL169C	*PSD1*	1.0	-1.2	1.0	1.2	Phosphatidylserine decarboxylase 1 (by homology)
CA4908	orf19.6046	*IPF1445*	-1.1	1.1	-1.2	-1.1	YNL172W	*APC1*	1.0	-2.5	-1.9	-1.5	similar to Saccharomyces cerevisiae Apc1p subunit of anaphase-promoti
CA4909	orf19.6047	*TUF1*	-1.1	-1.3	-1.3	-1.6	YOR187W	*TUF1*	1.0	-1.3	-1.3	-2.0	Translation elongation factor TU (by homology)
CA4911	orf19.6049	*IPF1435*	-1.1	-1.0	1.0	1.0	YBR156C	*SLI15*	1.0	1.2	1.3	1.4	unknown function
CA4912	orf19.6052	*CNS1*	1.0	-1.0	-1.1	1.0	YBR155W	*CNS1*	1.0	1.2	1.1	1.4	Cyclophilin Seven Suppressor (by homology)
CA4913	orf19.6053	*CIS2*	-1.0	1.0	-1.0	-1.0	YLR299W	*ECM38*	1.0	1.0	1.1	1.1	Gamma-glutamyltransferase (by homology)
CA4916	orf19.6056	*IPF1425*	-1.0	1.0	-1.0	-1.0	YOR283W		1.0	-1.3	1.3	1.7	Hypothetical phosphoglycerate mutase (by homology)
CA4917	orf19.6057	*ECM31*	1.0	-1.1	-1.0	-1.0	YBR176W	*ECM31*	1.0	-1.7	-1.5	-1.3	Involved in cell wall biogenesis and architecture (by homology)
CA4918	orf19.6058	*GLO1*	1.0	-1.0	1.0	1.0	YML004C	*GLO1*	1.0	1.1	1.1	-1.2	Glyoxalase I (by homology)
CA4919	orf19.6059	*TTR1*	1.3	1.7	1.6	1.8	YDR513W	*TTR1*	1.0	1.4	1.2	-1.1	Glutaredoxin (by homology)
CA4920	orf19.6060	*GCN20*	-1.2	-1.1	-1.1	-1.1	YFR009W	*GCN20*	1.0	1.1	1.4	1.4	Positive effector of Gcn2p (by homology)
CA4921	orf19.6061	*IPF1416*	1.0	1.5	1.8	1.5	YPL103C		1.0	-1.1	-1.0	-1.1	unknown function
CA4922	orf19.6062	*IPF1415*	1.3	1.1	1.2	1.1	YPL098C		1.0	-1.1	-1.1	-1.2	unknown function
CA4923		*IPF1413.3*	1.2	1.2	1.1	1.2	YFR011C		1.0	-1.2	-1.3	-1.9	unknown function, 3-prime end
CA4924	orf19.6063	*UBP6.3*	-1.1	1.1	-1.0	1.0	YFR010W	*UBP6*	1.0	1.3	1.4	1.1	Ubiquitin-specific protease, 3-prime end (by homology)
CA4925	orf19.6064	*IPF1408*	1.0	-1.1	-1.1	-1.0	YFR021W	*AUT10*	1.0	-1.6	-1.4	-1.0	unknown function
CA4927	orf19.6066	*IPF1401*	1.1	-1.2	-1.2	-1.1	YMR110C		1.0	1.2	1.1	-1.4	similarity to aldehyde dehydrogenase (by homology)
CA4928	orf19.6068	*IPF1399*	-1.2	-1.5	-1.4	-1.4	YDR346C		1.0	-1.1	1.3	1.8	unknown function
CA4929	orf19.6070	*ENA22*	-1.0	1.6	1.5	1.7	YDR038C	*ENA5*	1.0	-1.0	1.1	1.1	P-type ATPase involved in Na+ efflux (by homology)

CA4930	orf19.6071	*IPF8381*	-1.2	1.0	1.1	1.1	YOL076W	*MDM20*	1.0	-1.0	1.1	1.2	similar to Saccharomyces cerevisiae Mdm20p involved in mitochondrial i
CA4932	orf19.6073	*IPF8374*	1.0	1.2	1.2	1.1	YLR205C	*HMX1*	1.0	-1.4	1.1	1.1	unknown function
CA4933	orf19.6074	*IPF8372*	1.1	-1.1	-1.1	1.0	YDL166C		1.0	-1.0	1.0	1.1	unknown function
CA4934	orf19.6075	*CDC36*	1.1	1.1	1.0	1.1	YDL165W	*CDC36*	1.0	-1.2	-1.1	1.0	transcription factor (by homology)
CA4935	orf19.6076	*VPS29*	-1.0	1.1	-1.0	1.1	YHR012W	*VPS29*	1.0	1.0	-1.1	-1.1	vacuolar protein sorting protein (by homology)
CA4936	orf19.13498	*IPF8369*	1.2	1.2	1.8	1.3	YOR161C		1.0	2.0	1.2	-1.2	unknown function
CA4937	orf19.6538	*TFP3*	1.0	1.1	1.4	1.2	YPL234C	*TFP3*	1.0	1.2	1.2	1.1	H+-ATPase by homology
CA4938	orf19.6537	*IPF5166*	-1.0	1.1	1.0	1.1	YPL233W		1.0	1.0	-1.1	-1.0	unknown function
CA4939	orf19.6536	*IQG1*	-1.3	-1.1	-1.4	-1.2	YPL242C	*IQG1*	1.0	1.0	1.1	1.0	RAS GTPase-activating-like protein by homology
CA4941		*CRN1.53F*	1.0	-1.1	-1.2	-1.1	YLR429W	*CRN1*	1.0	-1.5	-1.4	-1.9	actin-binding protein, 5-prime end (by homology)
CA4944	orf19.6533	*MSK1*	-1.1	-1.0	-1.0	-1.1	YNL073W	*MSK1*	1.0	-1.2	1.0	1.2	lysyl-tRNA synthetase by homology
CA4945	orf19.6532	*FLX1*	1.1	1.1	1.1	1.0	YIL134W	*FLX1*	1.0	-1.4	-1.3	-1.3	MITOCHONDRIAL FAD CARRIER by homology
CA4946		*TOM71*	1.1	1.0	1.1	1.0	YNL070W	*TOM7*	1.0	-1.6	-1.1	-1.2	Translocase of the outer mitochondrial membrane (by homology)
CA4949	orf19.6529	*CDC34*	1.2	1.6	2.5	1.7	YDR054C	*CDC34*	1.0	-1.7	-1.4	-1.6	Ubiquitin-conjugating enzyme (by homology)
CA4951	orf19.6527	*IPF13607*	1.1	2.2	3.6	2.4	YJL108C	*PRM10*	1.0	-1.0	1.1	1.2	unknown function
CA4952	orf19.6526	*IPF13609*	1.0	-1.0	1.1	1.1	YPL246C		1.0	-2.1	-1.6	-1.3	unknown function
CA4954	orf19.6524	*TOM40*	-1.3	-1.3	-1.4	-1.5	YMR203W	*TOM40*	1.0	-1.1	-1.0	-1.1	mitochondrial import receptor chain TOM40 (by homology)
CA4956	orf19.6520	*IPF4583*	1.0	1.0	1.1	1.0	YIL166C		1.0	-2.8	-2.8	-3.2	putative allantoate permease (by homology)
CA4958	orf19.6517	*RAD14*	-1.0	1.0	-1.0	1.0	YMR201C	*RAD14*					nucleotide excision repair protein (by homology)
CA4959	orf19.6515	*HSP90*	-1.2	-1.1	-1.5	-1.2	YMR186W	*HSC82*	1.0	-1.3	1.1	1.0	heat shock protein
CA4960	orf19.6514	*IPF3912*	1.3	1.1	1.4	-1.0	YPL177C	*CUP9*	1.0	-1.0	1.1	1.0	unknown function
CA4961	orf19.6512	*IPF3916*	-1.1	-1.1	-1.2	-1.1	YJL085W	*EXO70*	1.0	-1.0	1.0	1.1	similar to Saccharomyces cerevisiae Exo70p 70 kDa exocyst component
CA4962	orf19.6511	*TRL1*	-1.1	-1.1	-1.2	-1.1	YJL087C	*TRL1*	1.0	-1.3	-1.2	-1.1	tRNA ligase
CA4965	orf19.6508	*IPF3921*	1.0	1.0	-1.1	-1.0	YGR057C	*LST7*	1.0	-1.0	-1.0	1.2	unknown function
CA4967	orf19.6506	*IPF3927*	-1.1	-1.1	-1.1	-1.0	YMR075W		1.0	-1.1	-1.0	-1.1	unknown function
CA4969	orf19.6502	*IPF3930*	1.1	-1.0	1.1	1.0	YDL114W		1.0	-1.0	-1.0	-1.1	unknown function
CA4971	orf19.5281	*IPF4697*	-1.0	1.1	-1.6	-1.1	YJL080C	*SCP160*	1.0	-1.4	1.2	1.3	similar to Saccharomyces cerevisiae Scp160p required for maintenance
CA4972	orf19.5280	*MUP1*	1.2	1.1	1.6	1.3	YGR055W	*MUP1*	1.0	-1.2	-1.1	1.2	High affinity methionine permease (by homology)
CA4973	orf19.5279	*IPF4703*	1.1	1.0	1.1	1.0	YPR100W		1.0	-2.3	-1.7	-2.2	unknown Function
CA4974	orf19.5278	*IPF4704*	1.0	-1.1	-1.2	-1.1	YJR111C		1.0	1.1	1.0	1.6	unknown Function
CA4975	orf19.5277	*IPF4706*	1.0	-1.0	-1.1	-1.1	YGR072W	*UPF3*	1.0	-1.5	-1.5	-1.3	unknown Function
CA4976	orf19.5276	*IPF4708*	1.0	-1.0	1.0	-1.0	YOL072W	*THP1*	1.0	-1.0	-1.1	1.2	unknown Function
CA4977	orf19.5275	*IPF4710*	-1.0	-1.1	-1.1	1.0	YLR181C		1.0	-1.3	-1.2	-1.1	unknown Function
CA4978	orf19.5274	*IPF2065*	1.0	1.1	-1.0	-1.0	YLR187W		1.0	-1.2	-1.5	-1.0	unknown function
CA4982	orf19.5268	*NUT2*	1.1	-1.0	1.0	1.0	YPR168W	*NUT2*	1.0	-1.5	-1.1	-1.2	Negative transcription regulator from artifical reporters (by homology)
CA4985	orf19.5265	*IPF2050*	1.1	1.0	1.1	1.1	YBL063W	*KIP1*	1.0	1.2	1.5	1.3	similar to Saccharomyces cerevisiae Kip1p kinesin-related protein (by ho
CA4986	orf19.5263	*SER33*	-1.1	1.6	1.8	1.5	YIL074C	*SER33*	1.0	-1.1	1.6	1.8	Phosphoglycerate dehydrogenase (by homology)
CA4988	orf19.5260	*RPN2*	-1.3	1.1	-1.1	-1.0	YIL075C	*RPN2*	1.0	-1.6	-1.4	-1.3	Proteasome regulatory subunit (by homology)
CA4991	orf19.5257	*LCB4*	-1.0	1.1	1.1	1.1	YOR171C	*LCB4*	1.0	1.1	1.2	1.4	Sphingolipid long chain base kinase (by homology)
CA4993	orf19.5255	*PXA2*	1.0	-1.7	-1.8	-1.5	YKL188C	*PXA2*	1.0	1.0	1.0	1.2	ABC transporter, peroxisomal (by homology)
CA4999	orf19.5248	*IPF2024*	-1.0	-1.1	-1.4	-1.2	YNR049C	*MSO1*	1.0	1.1	1.1	1.1	unknown function
CA5000	orf19.5247	*IPF2023*	-1.0	1.0	-1.1	-1.0	YCR095C		1.0	-1.2	-1.1	-1.2	unknown function
CA5003	orf19.5244	*MCD4*	1.3	1.3	1.6	1.3	YKL165C	*MCD4*	1.0	-1.3	-1.3	-1.1	Sporulation protein (by homology)
CA5004	orf19.5243	*TRP3*	-1.2	-1.2	-1.2	-1.3	YKL211C	*TRP3*	1.0	-1.2	-1.0	1.5	Anthranilate synthase / indole glycerol phosphate synthase (by homology
CA5006	orf19.5241	*IPF12584*	1.1	-1.3	-1.4	-1.3	YCR033W		1.0	-1.1	-1.1	1.1	unknown function
CA5007	orf19.5239	*IPF12579*	-1.0	1.0	1.0	1.1	YNL040W		1.0	-1.0	-1.0	-1.1	putative phospholipase A2 (by homology)
CA5009	orf19.5237	*VPH2*	-1.1	-1.1	-1.0	1.0	YKL119C	*VPH2*	1.0	-1.5	-1.5	-1.5	H+-ATPase assembly protein (by homology)
CA5014	orf19.6966	*IPF11120*	-1.0	-1.1	-1.0	-1.0	YLR133W	*CKI1*	1.0	-1.3	-1.0	-1.2	similar to Saccharomyces cerevisiae Cki1p choline kinase (by homology)
CA5018	orf19.6971	*IPF7558*	-1.0	1.0	1.0	1.1	YGR227W	*DIE2*	1.0	-1.2	-1.3	-1.2	unknown function
CA5021	orf19.6975	*YST1.EXON2*	-1.1	-1.3	-1.3	-1.3	YGR214W	*RPS0A*	1.0	1.5	1.6	2.5	Ribosomal protein, exon 2
CA5023	orf19.6976	*IPF7547*	1.1	-1.4	-1.4	-1.4	YJL163C		1.0	-1.3	-1.4	-1.6	unknown function
CA5024	orf19.6977	*IPF3009*	-1.2	1.0	1.4	1.1	YGR216C	*GPI1*	1.0	-1.9	-1.2	-1.3	similar to Saccharomyces cerevisiae Gpi1p required for N-acetylglucosar
CA5025	orf19.6979	*AMI3*	-1.1	1.2	1.3	1.2	YOL060C	*AMI3*	1.0	1.0	1.1	1.1	protein required for normal mitochondrial structure (by homology)
CA5027	orf19.6981	*IPF2999*	-1.5	-1.3	-1.6	-1.4	YKR051W		1.0	1.0	-1.0	1.1	unknown function
CA5028	orf19.6982	*IPF2998*	1.0	1.0	1.0	1.1	YJL131C		1.0	-1.2	-1.5	-1.8	unknown function
CA5031	orf19.6985	*IPF20023*	1.0	1.0	1.1	1.0	YOR337W	*TEA1*	1.0	1.1	-1.2	1.4	similar to Saccharomyces cerevisiae Tea1p activator of Ty1 enhance(by
CA5033	orf19.6987	*DNM1*	-1.3	-1.2	-1.4	-1.1	YLL001W	*DNM1*	1.0	-1.5	-1.3	-1.1	Dynamin-related protein (by homology)
CA5034	orf19.6988	*OST1*	1.1	1.3	1.4	1.2	YJL002C	*OST1*	1.0	-1.4	-1.3	-1.2	oligosaccharyltransferase
CA5037	orf19.6991	*PRE3*	1.0	1.3	1.5	1.3	YJL001W	*PRE3*	1.0	1.1	1.3	1.3	20S proteasome subunit (beta1)(by homology)
CA5039	orf19.6993	*GAP2*	1.0	-1.0	1.2	1.1	YKR039W	*GAP1*	1.0	1.1	1.1	1.3	general amino acid permease (by homology)
CA5046	orf19.7001	*YCK2*	1.2	1.2	1.5	1.4	YNL154C	*YCK2*	1.0	1.2	1.8	2.0	casein kinase I (by homology)

CA5048	orf19.10530	*IPF20024*	-1.0	-1.1	1.1	-1.0	YDR421W	*ARO80*	1.0	-1.0	1.0	-1.3	unknown function
CA5049	orf19.3013	*IPF3714*	-1.0	1.0	1.3	1.1	YHR107C	*CDC12*	1.0	-1.1	1.1	1.1	similar to Saccharomyces cerevisiae Cdc12p septin (by homology)
CA5050	orf19.3014	*BMH2*	-1.3	-1.1	-1.1	-1.1	YDR099W	*BMH2*	1.0	1.2	1.4	1.2	similar to Saccharomyces cerevisae Bmh2p suppressor of clathrin defice
CA5051	orf19.3015	*IPF3709*	-1.1	-1.0	-1.1	-1.1	YDR101C		1.0	-1.5	-1.5	-1.1	unknown function
CA5053	orf19.3018	*IPF3707*	1.0	-1.0	1.0	-1.2	YPL138C	*SPP1*	1.0	1.2	1.1	-1.1	unknown function
CA5054	orf19.3019	*IPF3704*	-1.0	-1.0	-1.0	-1.0	YNL218W	*MGS1*	1.0	-1.4	-1.7	-1.3	unknown function
CA5055	orf19.3021	*IPF3701*	1.0	1.0	1.0	1.0	YMR114C		1.0	-1.2	1.0	-1.2	unknown function
CA5056	orf19.3022	*IPF3698*	1.1	-1.3	-1.4	-1.2	YDR175C	*RSM24*	1.0	-1.5	-1.5	-1.6	similar to Saccharomyces cerevisiae Rsm24p mitochondrial ribosomal pr
CA5057	orf19.3023	*IPF3695*	-1.0	-1.2	-1.3	-1.1	YDR176W	*NGG1*	1.0	1.7	1.7	2.0	similar to Saccharomyces cerevisiae Ngg1p general transcriptional adapt
CA5060	orf19.3029	*IPF3690*	-1.2	-1.9	-2.1	-1.8	YDR036C		1.0	1.2	1.5	1.9	unknown function
CA5062	orf19.3031	*SEC62*	1.0	1.1	1.3	1.1	YPL094C	*SEC62*	1.0	-2.1	-1.8	-2.1	subunit of ER protein-translocation complex (by homology)
CA5063	orf19.3034	*IPF8493*	1.1	-1.2	-1.1	-1.2	YDR091C	*RLI1*	1.0	-1.7	-1.1	1.0	putative member of nontransporter group of ATP-binding cassette (ABC)
CA5064	orf19.3035	*CHD1*	-1.2	-1.1	-1.3	-1.1	YER164W	*CHD1*	1.0	-1.1	1.3	1.2	transcriptional regulator (by homology)
CA5065	orf19.3037	*IPF3584*	1.0	1.2	1.3	1.2	YER165W	*PAB1*	1.0	1.7	2.9	6.1	similar to Saccharomyces cerevisiae Pab1p mRNA polyadenylate-bindin
CA5066	orf19.3038	*TPS2*	1.2	3.9	4.8	4.9	YDR074W	*TPS2*	1.0	1.1	-1.1	-1.1	Threalose-6-phosphate phosphatase (by homology)
CA5067	orf19.3040	*IPF3589*	1.1	1.6	1.9	1.2	YBR177C	*EHT1*	1.0	-1.3	1.0	1.3	putative alcohol acyl transferase (by homology)
CA5068	orf19.3041	*IPF3592*	-1.0	1.2	1.2	1.1	YGR068C		1.0	-1.7	-1.7	-1.7	unknown function
CA5070	orf19.3043	*IPF3594*	1.1	-1.0	1.0	1.0	YDR058C	*TGL2*	1.0	-1.3	-1.3	-1.2	triglyceride lipase (by homology)
CA5072	orf19.3047	*IPF3598*	-1.2	1.0	1.1	1.0	YNL257C	*SIP3*	1.0	-1.2	-1.2	-1.3	similar to Saccharomyces cerevisiae Sip3p protein which interacts with S
CA5074	orf19.3049	*IPF3607*	1.0	1.1	-1.0	1.1	YDR523C	*SPS1*	1.0	-1.1	-1.1	1.1	putative serine/threonine protein kinase
CA5075	orf19.3050	*IPF3610*	-1.1	-1.1	-1.1	-1.2	YDR524C	*AGE1*	1.0	1.1	1.3	1.4	unknown function
CA5076	orf19.3051	*IPF15301*	1.3	-1.1	1.4	1.2	YJR116W		1.0	-1.1	-1.1	-1.0	unknown function
CA5077	orf19.3052	*YPT1*	1.3	1.2	1.2	1.2	YFL038C	*YPT1*	1.0	-1.5	-1.1	-1.1	GTP-binding protein of the rab family (by homology)
CA5079	orf19.3054	*RPN3*	-1.2	1.1	1.1	1.1	YER021W	*RPN3*	1.0	-1.2	1.2	1.1	26S proteasome regulatory subunit (by homology)
CA5080	orf19.3055	*IPF9268.3*	-1.0	1.1	1.1	1.0	YER022W	*SRB4*	1.0	-1.3	-1.2	-1.2	similar to Saccharomyces cerevisiae Srb4p DNA-directed RNA polymera
CA5081	orf19.3058	*COQ6*	-1.2	-1.0	1.0	1.1	YGR255C	*COQ6*	1.0	1.2	1.1	1.1	monooxygenase (by homology)
CA5082	orf19.3059	*SUA70*	-1.2	1.4	1.6	1.4	YPR086W	*SUA7*	1.0	1.4	1.7	1.9	TFIIB subunit (transcription initiation factor E)(by homology)
CA5083	orf19.3060	*IPF9278*	1.1	1.2	1.6	1.4	YMR149W	*SWP1*	1.0	-1.4	-1.4	-1.7	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltransferase de
CA5084	orf19.3061	*IMP1*	1.1	1.3	1.3	1.2	YMR150C	*IMP1*	1.0	-1.1	-1.1	-1.1	protease, mitochondrial (by homology)
CA5087	orf19.3062	*IPF20025*	-1.1	1.0	-1.0	1.0	YKL033W		1.0	-1.4	-1.2	-1.2	unknown function
CA5088	orf19.3063	*IPF9758*	1.0	-1.0	-1.1	-1.0	YBR278W	*DPB3*	1.0	-1.3	-1.2	-1.0	similar to Saccharomyces cerevisiae Dpb3p DNA-directed DNA polymera
CA5089	orf19.3064	*MRPL27*	1.1	1.0	1.0	1.0	YBR282W	*MRPL27*	1.0	-1.1	-1.2	-1.2	ribosomal protein (by homology)
CA5091	orf19.10584	*ACF3*	1.1	1.3	1.2	1.1	YNR067C		1.0	-1.1	-1.2	1.0	endo-1,3-beta-glucanase
CA5096	orf19.6445	*IPF1384*	1.1	-1.2	-1.3	-1.2	YLR284C	*ECI1*	1.0	-1.5	-1.2	-1.1	similar to Saccharomyces cerevisiae Eci1p delta3-cis-delta2-trans-enoyl-
CA5097	orf19.6444	*IPF1382*	-1.1	-1.4	-1.2	-1.6	YHL023C		1.0	-1.2	-1.1	-1.2	unknown function
CA5099	orf19.6442	*PRP8*	1.1	-1.1	-1.4	-1.3	YHR165C	*PRP8*	1.0	-1.2	-1.1	-1.2	U5 snRNP protein, pre-mRNA splicing factor (by homology)
CA5100	orf19.6440	*IPF1372*	-1.1	-1.0	1.0	1.0	YNL008C	*ASI3*	1.0	-1.3	-1.3	-1.2	unknown function
CA5101	orf19.6438	*LCB1*	-1.0	1.0	1.3	1.0	YMR296C	*LCB1*	1.0	-1.1	1.4	2.0	Serine C-palmitoyltransferase subunit (by homology)
CA5102	orf19.6437	*CDC23*	1.0	-1.0	1.0	-1.0	YHR166C	*CDC23*	1.0	-1.1	1.1	-1.1	Subunit of anaphase-promoting complex (by homology)
CA5104	orf19.6435	*IPF1364*	1.4	-1.2	-1.2	-1.1	YGR243W		1.0	1.7	1.5	-1.7	unknown function
CA5105	orf19.6434	*PEX19*	1.0	-1.4	-1.4	-1.3	YDL065C	*PEX19*	1.0	1.1	1.0	-1.2	Required for biogenesis of peroxisomes (by homology)
CA5106	orf19.6432	*AFG2*	1.0	-1.1	-1.0	-1.0	YLR397C	*AFG2*	1.0	-1.3	-1.4	-1.1	Member of the Sec18p, Pas1p, Cdc48p, TBP-1 family of ATPases (by ho
CA5108	orf19.6425	*SKI2*	-1.1	-1.2	-1.3	-1.3	YLR398C	*SKI2*	1.0	-2.0	-1.9	-2.4	Antiviral protein and putative helicase
CA5109	orf19.6424	*UBC9*	1.0	1.2	1.1	1.0	YDL064W	*UBC9*	1.0	1.3	1.2	-1.1	E2 ubiquitin-conjugating enzyme (by homology)
CA5110	orf19.6423	*FBP26*	-1.0	-1.1	-1.3	-1.2	YJL155C	*FBP26*	1.0	-1.9	-2.1	-2.3	Fructose-2,6-bisphosphatase (by homology)
CA5111	orf19.6422	*SSY5*	-1.1	-1.0	-1.1	-1.1	YJL156C	*SSY5*	1.0	-1.4	-1.6	-1.5	Involved in sulfonylurea herbicide sensitivity (by homology)
CA5113	orf19.6418	*IPF20026*	-1.1	-1.1	-1.2	-1.0	YDL063C		1.0	-1.1	-1.1	1.0	unknown function
CA5114	orf19.6417	*IPF1334*	-1.0	-1.2	-1.4	-1.2	YDL060W	*TSR1*	1.0	1.0	1.4	2.1	Conserved hypothetical protein
CA5115	orf19.6416	*IPF1331*	1.0	1.0	1.0	1.0	YNL080C		1.0	-1.1	1.0	1.1	unknown function
CA5116		*TPM2.3*	1.5	-1.1	-1.0	-1.0	YIL138C	*TPM2*	1.0	1.2	1.3	-1.0	Tropomyosin, 3-prime end
CA5119	orf19.6411	*IPF1320*	-1.4	-1.1	-1.4	-1.3	YLR386W		1.0	-1.7	-1.6	-1.8	unknown function
CA5121	orf19.6407	*IPF1310*	-1.1	-1.1	-1.1	-1.0	YLR387C		1.0	-1.1	-1.1	-1.1	unknown function
CA5122	orf19.6406	*IPF1308*	-1.0	-1.0	-1.1	1.1	YNL081C		1.0	-1.2	-1.1	-1.1	Similarity to ribosomal protein S13 (by homology)
CA5123	orf19.6405	*IPF1306*	-1.0	-1.0	1.0	1.0	YAL018C		1.0	-1.7	-2.1	-1.4	unknown function
CA5124	orf19.6404	*GSH2*	-1.2	-1.2	-1.3	-1.2	YOL049W	*GSH2*	1.0	1.1	1.2	1.4	Glutathione synthetase (by homology)
CA5125		*RPP2*	1.1	1.0	-1.0	-1.0	YOL039W	*RPP2A*	1.0	2.3	2.8	3.3	acidic ribosomal protein by homology
CA5126	orf19.6403	*SLS1*	1.0	1.0	-1.1	-1.1	YOL031C		1.0	1.2	1.4	1.3	Endoplasmic translocation machinery by homology
CA5127	orf19.6402	*CYS3*	-1.1	1.3	1.2	-1.1	YAL012W	*CYS3*	1.0	-1.0	1.7	1.9	cystathionine gamma-lyase by homology
CA5128	orf19.13758	*IPF5118*	-1.0	1.0	-1.0	1.0	YOL032W		1.0	1.2	1.5	1.0	unknown function
CA5129	orf19.13757	*ATS1*	1.1	1.0	1.1	1.0	YAL020C	*ATS1*	1.0	-1.5	-1.4	-1.1	similar to Saccharomyces cerevisiae Ats1p suppressor of alpha-tubulin m
CA5132	orf19.6393	*GTS1*	1.0	1.0	1.0	-1.0	YGL181W	*GTS1*	1.0	-3.4	-2.1	-1.8	Transcription factor by homology

CA5135	orf19.13747	*HSP104*	1.1	-1.0	-1.1	-1.0	YLL026W	*HSP104*	1.0	1.1	1.2	1.3	Heat shock protein (by homology)
CA5137	orf19.4574	*IPF1032*	1.0	1.0	1.1	-1.0	YOR059C		1.0	-1.1	1.3	1.3	similar to probable membrane protein [S. cerevisiae]
CA5138	orf19.4575	*IPF1031*	-1.3	-1.2	-1.4	-1.2	YPL109C		1.0	-1.6	-1.3	-1.2	Similar to aminoglycoside acetyltransferase regulator from P. stuartii
CA5139	orf19.4577	*IPF1027*	-1.0	1.0	1.1	-1.0	YOR371C	*GPE1*	1.0	-1.2	-1.2	1.2	unknown function
CA5141	orf19.4578	*CYT2*	1.0	1.1	1.0	1.0	YKL087C	*CYT2*	1.0	-1.8	-1.6	-1.6	holocytochrome-c1 synthase (by homology)
CA5142	orf19.4579	*IPF1022*	1.4	1.6	2.4	2.1	YGR284C	*ERV29*	1.0	-1.5	-1.4	-1.3	similar to Saccharomyces cerevisiae Erv29p ER-Golgi transport vesicle p
CA5143	orf19.4580	*IPF1020*	1.2	1.4	1.3	1.3	YJR012C		1.0	-1.0	-1.1	-1.1	Weak similarity to N. crassa hypothetical protein
CA5144	orf19.4581	*IPF1019*	1.5	2.2	3.1	2.5	YJR013W		1.0	1.1	-1.0	1.0	unknown function
CA5148	orf19.4585	*TFG1*	-1.1	-1.0	-1.0	-1.1	YGR186W	*TFG1*	1.0	-1.7	-1.1	-1.1	RNA pol.II transcription initiation factor TFIIF (by homology)
CA5149	orf19.4587	*HGH1*	-1.1	-1.1	-1.1	-1.0	YGR187C	*HGH1*	1.0	-1.5	-1.6	-1.4	Similar to human HMG1 and HMG2 proteins (by homology)
CA5150	orf19.4589	*FMS1*	-1.0	1.0	1.1	-1.0	YMR020W	*FMS1*	1.0	1.1	1.2	1.3	Similar to corticosteroid-binding protein CBP1 (by homology)
CA5152	orf19.4591	*CAT2*	1.0	-7.2	-10.2	-10.3	YML042W	*CAT2*	1.0	-1.3	-1.8	-2.1	carnitine O-acetyltransferase (by homology)
CA5154	orf19.4593	*RGA2*	-1.2	-1.2	-1.8	-1.5	YOR127W	*RGA1*	1.0	-1.2	-1.4	-1.3	rho-GTPase activating protein 2 (by homology)
CA5156	orf19.4594	*CLC1*	1.2	-1.1	-1.2	1.0	YGR167W	*CLC1*	1.0	1.0	-1.0	-1.2	clathrin light chain (by homology)
CA5159	orf19.4597	*CAP2*	1.1	1.0	-1.0	-1.0	YIL034C	*CAP2*	1.0	-2.2	-2.2	-2.7	F-actin capping protein, beta subunit (by homology)
CA5160	orf19.4599	*PHO89*	1.1	-1.0	1.1	1.0	YBR296C	*PHO89*	1.0	-1.7	1.0	-1.3	Na+-coupled phosphate transport (by homology)
CA5161	orf19.4600	*IPF983*	-1.0	-1.2	-1.2	-1.1	YPL107W		1.0	-1.4	1.1	1.1	unknown function
CA5163	orf19.4601	*TFC1*	-1.0	1.0	-1.0	1.0	YBR123C	*TFC1*	1.0	1.4	1.4	1.3	Transcription initiation factor TFIIIC 95 kD subunit (by homology)
CA5164	orf19.4602	*MDH1*	1.2	-1.4	-1.4	-1.4	YKL085W	*MDH1*	1.0	-1.3	-1.5	-3.0	Mitochondrial malate dehydrogenase precursor (by homology)
CA5165	orf19.4603	*ARL1*	-1.0	-1.0	-1.0	1.0	YBR164C	*ARL1*	1.0	-1.0	-1.0	-1.1	GTP-binding protein of the ARF family (by homology)
CA5166	orf19.4605	*TYR1*	1.0	1.0	-1.0	1.0	YBR166C	*TYR1*	1.0	-1.1	-1.1	1.1	Prephenate dehydrogenase (NADP+) (by homology)
CA5167	orf19.4606	*ERG8*	-1.1	-1.1	-1.1	-1.0	YMR220W	*ERG8*	1.0	1.1	1.5	1.7	Phosphomevalonate kinase (by homology)
CA5171	orf19.4609	*IPF6037*	1.2	1.5	1.6	1.6	YAL049C		1.0	-1.2	-1.1	-1.5	Similar to Legionella pneumophila sbpA
CA5174	orf19.4611	*PRS4*	1.2	1.1	1.1	-1.1	YER099C	*PRS2*	1.0	-1.3	-1.8	-1.4	Ribose-phosphate pyrophosphokinase 3 (by homology)
CA5176	orf19.4614	*IPF6045*	-1.0	-1.0	-1.0	1.0	YPR049C	*CVT9*	1.0	-1.2	1.0	1.1	unknown function
CA5177	orf19.4615	*IPF11101*	1.0	1.0	1.1	1.0	YBR095C		1.0	-1.1	1.0	-1.1	Weak similarity to C. cerevisiae hypothetical protein (by homology)
CA5178	orf19.4616	*POL30*	-1.0	1.3	1.6	1.4	YBR088C	*POL30*	1.0	-1.0	-1.1	-1.1	Proliferating Cell Nuclear Antigen (by homology)
CA5179	orf19.4617	*MAK3*	1.1	1.1	1.2	1.1	YPR051W	*MAK3*	1.0	-1.1	-1.1	1.2	N-acetyltransferase (by homology)
CA5180	orf19.4618	*FBA1*	-1.2	2.1	1.6	2.1	YKL060C	*FBA1*	1.0	2.0	3.7	4.6	fructose-bisphosphate aldolase (by homology)
CA5181	orf19.4620	*TIM12*	1.0	1.0	1.0	1.0	YBR091C	*MRS5*	1.0	-1.2	-1.2	-1.2	subunit of the TIM22-complex (by homology)
CA5182	orf19.4621	*IPF11093*	-1.0	-1.0	1.1	1.0	YBR094W		1.0	-1.3	-1.2	-1.2	weak similarity to pig tubulin-tyrosine ligase
CA5183	orf19.4622	*11090.EXON*	-1.2	-1.2	-1.9	-1.4	YKL054C	*VID31*	1.0	-1.7	-1.6	-1.4	weak similarity to glutenin, exon 1
CA5186	orf19.4624	*HRT2*	-1.0	1.1	1.2	1.1	YMR027W	*HRT2*	1.0	1.1	1.4	1.1	Similar to ScHRT2 (by homology)
CA5187	orf19.4625	*TOA2*	1.1	1.2	1.2	1.2	YKL058W	*TOA2*	1.0	-2.3	-1.9	-1.5	TFIIA subunit 13.5 kD (by homology)
CA5188	orf19.4626	*TAP42*	-1.0	-1.0	1.1	-1.1	YMR028W	*TAP42*	1.0	-1.7	-1.4	-1.2	Component of the Tor signaling pathway (by homology)
CA5189	orf19.4627	*IPF10158*	-1.3	-1.2	-1.4	-1.2	YKL057C	*NUP120*	1.0	-1.7	-1.7	-1.5	Weak similarity to ScNup12p
CA5190	orf19.4628	*IPF10155*	1.0	-1.1	-1.0	-1.1	YKL059C		1.0	-1.2	1.6	1.5	unknown function
CA5196	orf19.7010	*IPF2338*	-1.0	1.2	1.3	1.1	YIL001W		1.0	-1.1	1.1	-1.2	unknown function
CA5197	orf19.7011	*IPF2342*	-1.2	-1.0	-1.4	-1.1	YPL012W	*RRP12*	1.0	-1.2	1.0	1.4	unknown function
CA5198	orf19.7012	*LPA4*	1.4	1.0	-1.1	1.1	YPL013C		1.0	-1.1	-1.0	1.0	Similar to ribosomal protein S16, mitochondrial (by homology)
CA5200	orf19.7015	*RPL10E*	-1.2	-1.1	-1.1	-1.1	YLR340W	*RPP0*	1.0	1.7	2.6	3.2	Ribosomal protein L10, cytosolic (by homology)
CA5201	orf19.7016	*IPF2349*	-1.0	-1.2	-1.2	-1.0	YDR452W	*PHM5*	1.0	-1.4	-1.3	-1.3	similar to human sphingomyelin
CA5202	orf19.7017	*YOX1*	1.1	-1.1	-1.3	-1.1	YML027W	*YOX1*	1.0	-1.6	-1.7	-1.7	Similar to homoeodomain protein (by homology)
CA5203	orf19.7018	*RPS18*	1.8	1.1	1.1	1.3	YML026C	*RPS18B*					Ribosomal protein S18 (by homology)
CA5204	orf19.7019	*YML6*	-1.0	-1.2	-1.1	-1.1	YML025C						Ribosomal protein, mitochondrial (by homology)
CA5205	orf19.7020	*KEX1*	-1.2	1.1	-1.0	1.1	YGL203C	*KEX1*	1.0	-1.3	-1.2	1.0	Carboxypeptidase-alpha (by homology)
CA5206	orf19.7021	*GPH1*	1.0	-1.0	1.3	1.4	YPR160W	*GPH1*	1.0	1.0	-1.3	-1.3	Glycogen phosphorylase (by homology)
CA5208	orf19.7023	*IPF2361*	-1.1	1.0	1.0	1.0	YLR455W		1.0	-1.5	-2.3	-2.4	unknown function
CA5209	orf19.7025	*MCM1*	1.0	-1.0	1.2	1.0	YMR043W	*MCM1*	1.0	-1.2	1.1	1.2	Transcription factor of the MADS box (by homology)
CA5212	orf19.7029	*IPF3050*	1.1	1.0	1.0	1.0	YDL238C		1.0	-2.1	-1.8	-1.4	unknown function
CA5213	orf19.7030	*SSR1*	1.4	1.2	1.5	1.1	YLR390W	*ECM19*	1.0	1.2	1.4	1.4	Secretory Stress Response protein 1 (by homology)
CA5215	orf19.7033	*PPS1*	1.0	1.1	1.0	1.1	YBR276C	*PPS1*	1.0	1.5	-1.1	1.1	protein tyrosine phosphatase (by homology)
CA5217	orf19.7035	*RFC2*	1.1	1.0	1.0	1.0	YJR068W	*RFC2*	1.0	1.0	1.1	-1.1	Replication factor (by homology)
CA5218	orf19.7036	*WHI2*	-1.1	-1.1	-1.1	-1.1	YOR043W	*WHI2*	1.0	-1.5	-1.2	-1.2	Growth regulation factor (by homology)
CA5219	orf19.7037	*YAE1*	1.0	-1.2	1.1	1.0	YJR067C	*YAE1*	1.0	-1.2	-1.4	-1.5	Essential protein
CA5220	orf19.7038	*VP1.EXON2*	1.1	1.0	-1.0	1.0	YMR004W	*MVP1*	1.0	1.0	1.0	1.0	Required for vacuolar protein sorting, exon 2 (by homology)
CA5222	orf19.7041	*IPF3079*	-1.1	-1.2	-1.2	-1.3	YAL043C	*PTA1*	1.0	-1.2	-1.1	-1.1	similar to Saccharomyces cerevisiae Pta1p pre-tRNA processing protein
CA5224	orf19.7043	*IPF3081*	1.0	1.1	1.0	-1.0	YLR050C		1.0	-1.0	-1.4	-1.3	unknown function
CA5225		*ACB1.EXON2*	1.1	-1.0	1.0	1.0	YGR037C	*ACB1*	1.0	1.2	1.3	1.2	acyl-coenzyme-A-binding protein, exon 2 (by homology)
CA5226	orf19.7044	*RIM15*	1.0	-1.2	-1.1	-1.0	YFL033C	*RIM15*	1.0	-2.3	-2.5	-2.3	Protein kinase involved in the RIM pathway (by homology)
CA5227	orf19.7046	*IPF3087*	1.1	-1.3	-1.2	-1.1	YIR017C	*MET28*	1.0	-1.1	-1.1	-1.0	unknown function

CA5228	orf19.7047	*RTF1.3EOC*	-1.2	-1.3	-1.1	-1.2	YGL244W	*RTF1*	1.0	1.1	1.1	1.2	Regulates DNA binding properties of TBP, 3-prime end (by homology)
CA5229	orf19.5035	*IPF10425*	-1.0	1.0	-1.1	-1.0	YBR215W	*HPC2*	1.0	1.2	1.1	1.2	unknown function
CA5230	orf19.5034	*IPF10424*	1.1	-1.1	-1.0	-1.0	YBR216C		1.0	-1.3	-1.6	-1.3	unknown function
CA5231	orf19.5033	*IPF10422*	1.1	1.1	1.0	1.1	YBR217W	*APG12*	1.0	1.4	1.1	1.1	Similar to APG12, component of the autophagic system
CA5233	orf19.5031	*SSK1*	1.1	1.0	-1.0	-1.0	YLR006C	*SSK1*	1.0	-1.1	1.1	1.3	Putative reponse regulator two-component phosphorelay gene
CA5234	orf19.5030	*IPF3014*	-1.1	-1.3	-1.3	-1.2	YDR068W	*DOS2*	1.0	-1.4	-1.1	-1.1	weak similarity to S. cerevisiae DOS2 involved in genome stability
CA5235	orf19.5029	*IPF3015*	-1.2	-1.3	-1.2	-1.2	YDR061W		1.0	-1.3	-1.2	-1.1	Similar to E.coli modF and photorepair protein phrA
CA5236	orf19.5027	*LCB2*	1.2	1.1	1.4	1.3	YDR062W	*LCB2*	1.0	1.0	1.2	1.7	Palmitoyl transferase (by homology)
CA5237	orf19.5026	*ZMS1*	1.0	-1.2	-1.2	-1.2	YML081W		1.0	1.0	1.3	1.8	Zinc Finger Protein C2H2 (by homology)
CA5238	orf19.5025	*MET3*	-1.0	1.1	1.3	1.1	YJR010W	*MET3*	1.0	-1.3	-1.5	-1.4	ATP sulfurylase
CA5239	orf19.5024	*GND1*	-1.1	-1.2	1.1	-1.1	YHR183W	*GND1*	1.0	1.5	1.1	1.3	6-phosphogluconate dehydrogenase
CA5242	orf19.5021	*PDX1*	-1.3	-1.1	-1.4	-1.3	YGR193C	*PDX1*	1.0	-1.1	1.1	1.1	Pyruvate dehydrogenase complex protein X (by homology)
CA5247	orf19.5015	*MYO2*	-1.5	1.0	-1.1	-1.0	YOR326W	*MYO2*	1.0	-1.5	-1.1	-1.2	Myosin heavy chain (by homology)
CA5248	orf19.5014	*IPF1828*	-1.0	-1.1	-1.1	1.1	YGL085W		1.0	1.0	1.1	-1.1	unknown function
CA5249	orf19.5013	*PCM1*	-1.2	-1.3	-1.3	-1.2	YEL058W	*PCM1*	1.0	1.2	1.5	1.6	phosphoacetylglucosamine mutase (by homology)
CA5251	orf19.5011	*IPF1824*	1.1	1.0	-1.1	1.1	YPL269W	*KAR9*	1.0	-1.1	-1.1	-1.1	unknown function
CA5252	orf19.5010	*DIM1*	1.0	-1.1	-1.0	1.0	YPL266W	*DIM1*	1.0	-1.3	-1.2	-1.3	rRNA (adenine-N6,N6-)-dimethyltransferase (by homology)
CA5253	orf19.5009	*KEL3*	-1.0	-1.0	-1.0	1.0	YPL263C	*KEL3*	1.0	1.1	1.4	1.7	Kelch-repeat protein
CA5254		*IPF1820*	1.0	1.0	1.0	1.0	YDR016C	*DAD1*	1.0	-1.2	-1.4	-1.5	unknown function
CA5255	orf19.5007	*ACT1*	-1.1	-1.0	1.1	1.1	YFL039C	*ACT1*	1.0	1.2	1.6	1.8	actin (by homology)
CA5257		*SNC2.EXON2*	1.2	1.5	1.8	1.5	YOR327C	*SNC2*	1.0	1.2	1.3	1.1	Strong similarity to synaptobrevin, exon 2 (by homology)
CA5258	orf19.5006	*GCV3*	1.0	-1.2	-1.1	-1.0	YAL044C	*GCV3*	1.0	-1.5	-2.0	-2.0	Glycine decarboxylase, subunit H (by homology)
CA5260	orf19.5004	*RAD54*	-1.0	1.1	1.0	1.0	YGL163C	*RAD54*	1.0	-1.5	-1.5	-1.4	DNA-dependent ATPase of the Snf2p family (by homology)
CA5261	orf19.5003	*IPF1805*	-1.3	-1.3	-1.4	-1.2	YGL164C		1.0	1.1	1.3	1.1	unknown function
CA5262	orf19.5001	*IPF1804*	-1.3	-1.4	-1.5	-1.3	YGL166W	*CUP2*	1.0	-1.2	-1.5	-2.1	putative transcription factor (by homology)
CA5263	orf19.5000	*CYB3*	-1.2	-3.2	-2.7	-2.5	YML054C	*CYB2*	1.0	1.1	1.2	-1.7	Lactate dehydrogenase cytochrome b2 (by homology)
CA5266	orf19.4996	*IPF1787.3F*	-1.1	1.0	1.1	-1.1	YBL029W		1.0	-1.3	-1.5	-1.4	unknown function, 3-prime end
CA5268	orf19.4994	*SEC18.3F*	-1.0	-1.1	-1.0	1.1	YBR080C	*SEC18*	1.0	1.0	1.0	-1.0	vesicular fusion protein, 3-prime end (by homology)
CA5271	orf19.4991	*IPF1777*	-1.0	-1.1	-1.0	-1.0	YGL178W	*MPT5*	1.0	-1.3	-1.1	-1.4	similar to Saccharomyces cerevisiae Mpt5p multicopy suppressor of Pop
CA5273	orf19.4987	*NUP49*	-1.1	-1.1	-1.2	-1.1	YGL172W	*NUP49*	1.0	-1.3	-1.1	1.0	nuclear pore protein (by homology)
CA5274	orf19.4985	*IPF1764*	1.2	-1.5	-1.3	-1.3	YGL084C	*GUP1*	1.0	-1.2	-1.0	-1.2	similar to Saccharomyces cerevisiae Gup1p glycerol transporter (by hom
CA5279	orf19.7128	*SYS1*	1.1	1.0	1.1	-1.1	YJL004C	*SYS1*	1.0	-1.1	-1.2	-1.2	Similar to ypt6 suppressor in S. cerevisae (by homology)
CA5280	orf19.7131	*IPF1899*	1.2	-1.0	1.0	-1.0	YHL021C		1.0	1.4	1.6	1.1	unknown function
CA5281	orf19.7136	*SPT6*	1.1	1.1	-1.1	-1.0	YGR116W	*SPT6*	1.0	-1.3	-1.2	-1.2	Transcription elongation protein (by homology)
CA5284	orf19.7141	*UFE1*	-1.0	1.1	-1.1	1.0	YOR075W	*UFE1*	1.0	-1.0	1.1	-1.2	Endoplasmic reticulum t-SNARE (by homology)
CA5285	orf19.7144	*HBS1.3F*	-1.1	1.0	1.2	-1.0	YKR084C	*HBS1*	1.0	-1.8	-1.6	-1.3	Translation elongation factor eEF-1 alpha chain homolog, 3-prime end (b
CA5288	orf19.7149	*IPF1928*	-1.2	-1.4	-1.4	-1.4	YMR258C		1.0	-1.1	-1.2	-1.3	unknown function
CA5289	orf19.7150	*NRG1*	-1.0	1.1	-1.0	1.0	YBR066C	*NRG2*	1.0	-1.1	-1.3	-1.1	similar to transcriptional repressor Nrg1p/Nrg2p
CA5291	orf19.7153	*LOS1*	-1.4	-1.3	-1.3	-1.1	YKL205W	*LOS1*	1.0	1.1	-1.1	-1.3	pre-tRNA splicing protein (by homology)
CA5292	orf19.7154	*IPF1948*	-1.0	-1.4	-1.4	-1.3	YJL069C		1.0	1.1	-1.1	1.3	unknown function
CA5296	orf19.7159	*IPF1956*	1.0	-1.3	-1.7	-1.3	YMR185W		1.0	1.2	1.1	1.1	unknown function
CA5297	orf19.7160	*YAR1*	1.1	1.1	-1.2	1.0	YPL239W	*YAR1*	1.0	1.2	1.7	1.8	Ankyrin repeat-containing protein (by homology)
CA5298	orf19.7161	*SUI3*	-1.0	1.1	-1.0	-1.0	YPL237W	*SUI3*	1.0	1.1	1.1	1.2	Translation initiation factor eIF2 beta subunit (by homology)
CA5299	orf19.7164	*IPF2190*	1.0	1.0	1.0	-1.0	YPL236C		1.0	-1.2	-1.4	-1.5	putative serine/threonine protein kinase (by homology)
CA5305	orf19.7175	*IPF2175*	-1.0	-1.0	-1.2	-1.0	YMR161W	*HLJ1*	1.0	-1.5	-1.7	-1.3	similar to Saccharomyces cerevisiae Hlj1p dnaJ-type protein (by homolog
CA5306	orf19.7176	*NPT1*	-1.0	-1.0	-1.1	1.0	YOR209C	*NPT1*	1.0	1.0	1.3	1.7	Nicotinate phosphoribosyltransferase (by homology)
CA5307	orf19.7177	*IPF2172*	-1.1	1.1	1.6	1.2	YPL125W	*KAP120*	1.0	-1.2	-1.1	-1.2	similar to Saccharomyces cerevisiae Kap120 nuclear transport factor, me
CA5308	orf19.7178	*PRE5*	1.1	1.1	1.0	1.1	YMR314W	*PRE5*	1.0	-1.0	1.2	1.2	20S proteasome subunit alpha6 (by homology)
CA5311	orf19.7182	*IPF2166*	1.1	1.0	1.1	1.0	YGL232W		1.0	1.0	-1.1	-1.0	unknown function
CA5312	orf19.7183	*IPF2165*	1.1	1.0	1.1	1.1	YGL231C		1.0	1.2	1.2	1.2	unknown function
CA5315	orf19.7186	*CYB2*	-1.1	1.0	1.1	-1.0	YLR210W	*CLB4*	1.0	-1.3	-1.3	-1.2	B-type cyclin
CA5316	orf19.7187	*MAM33*	1.3	-1.5	-1.4	-1.4	YIL070C	*MAM33*	1.0	-1.2	-1.2	-1.5	Mitochondrial acidic matrix protein (by homology)
CA5318	orf19.7190	*OGG1*	1.0	-1.0	1.1	-1.1	YML060W	*OGG1*	1.0	-2.1	-2.0	-2.1	8-oxoguanine DNA glycosylase (by homology)
CA5319	orf19.7193	*IPF2150*	-1.2	-1.2	-1.3	-1.1	YKL124W	*SSH4*	1.0	-1.4	-1.2	-1.3	similar to protein involved in ER function
CA5321	orf19.7195	*RAD6.3*	1.1	-1.0	1.1	-1.0	YGL058W	*RAD6*	1.0	1.0	-1.2	-1.0	Ubiquitin protein ligase, 3-prime end
CA5322	orf19.7196	*PRB1*	1.3	1.9	3.2	2.7	YEL060C	*PRB1*	1.0	1.1	1.3	1.1	Protease B, vacuolar (by homology)
CA5323	orf19.7197	*IPF2142*	-1.2	-1.3	-1.2	-1.2	YLR002C	*NOC3*	1.0	-1.1	1.1	1.3	unknown function
CA5324	orf19.7198	*IPF2140*	-1.0	1.0	1.1	1.0	YNL288W	*CAF40*	1.0	-1.0	-1.1	-1.1	unknown function
CA5325	orf19.7199	*IPF2138*	1.0	-1.0	-1.1	-1.1	YBR137W		1.0	1.3	1.1	1.1	unknown function
CA5327	orf19.7201	*SLA2*	-1.3	-1.2	-1.4	-1.2	YNL243W	*SLA2*	1.0	-1.2	-1.1	-1.0	Cytoskeleton assembly control protein
CA5328	orf19.7202	*RER1*	-1.1	-1.0	1.1	-1.0	YCL001W	*RER1*	1.0	1.2	1.2	1.1	Required for correct localization of Sec12p (by homology)

CA5329	orf19.7203	*MRP7*	-1.1	-1.2	-1.1	-1.1	YNL005C	*MRP7*	1.0	1.1	1.0	-1.1	Mitochondrial ribosomal protein YmL2 precursor (by homology)
CA5330	orf19.7204	*IPF2130*	1.1	1.0	-1.0	-1.1	YJR149W		1.0	-1.2	-1.2	-1.2	similar to 2-nitropropane dioxygenases
CA5332	orf19.7206	*IPF900.3*	1.0	-1.0	1.0	-1.0	YDR067C		1.0	1.2	1.3	1.2	unknown function, , 3-prime end
CA5333	orf19.7207	*DOA4*	-1.1	1.4	1.5	1.2	YDR069C	*DOA4*	1.0	-1.1	1.1	1.6	ubiquitin-specific isopeptidase (by homology)
CA5334	orf19.7208	*SMK1*	-1.0	1.1	-1.0	1.0	YPR054W	*SMK1*	1.0	-1.0	-1.1	-1.1	MAP kinase (by homology)
CA5336	orf19.7210	*IPF893*	-1.0	1.1	1.0	-1.0	YJR008W		1.0	1.6	1.3	1.1	unknown function
CA5337	orf19.7212	*APL1*	-1.0	1.0	1.1	1.0	YJR005W	*APL1*	1.0	-2.1	-1.6	-1.4	AP-2 complex subunit, beta2-adaptin (by homology)
CA5338	orf19.7213	*IPF889*	-1.0	1.1	1.0	-1.1	YDR291W		1.0	-1.2	-1.3	-1.3	ATP-dependent RNA helicase (by homology)
CA5339	orf19.7214	*IPF885*	1.1	1.0	1.1	1.0	YBR056W		1.0	-1.2	-1.2	-1.2	glucan 1,3-beta-glucosidase (by homology)
CA5340	orf19.7215	*IPF883*	1.0	-1.1	-1.1	-1.1	YJL109C		1.0	-1.1	-1.0	1.3	unknown function
CA5341		*HSP10.3*	1.1	1.0	1.0	1.1	YOR020C	*HSP10*	1.0	-1.1	-1.2	-1.2	10 kDa mitochondrial heat shock chaperonin, 3-prime end (by homology)
CA5342	orf19.7216	*YPT521*	-1.0	-1.0	1.0	1.0	YKR014C	*YPT52*	1.0	1.1	1.4	1.2	GTP-binding protein of the rab/ypt family (by homology)
CA5343	orf19.7217	*RPL4B*	-1.1	1.1	1.0	-1.0	YDR012W	*RPL4B*	1.0	1.8	2.7	3.0	Ribosomal protein L4B (by homology)
CA5344	orf19.7218	*PRY2*	1.1	1.0	1.2	1.0	YJL079C	*PRY1*	1.0	-1.3	-1.1	-1.1	putative pathogen related proteins (by homology)
CA5345	orf19.7219	*FTR1*	1.1	1.1	1.2	1.0	YER145C	*FTR1*	1.0	1.2	1.1	1.3	high affinity iron permease
CA5346	orf19.7221	*IPF867*	-1.0	-1.5	-1.9	-1.6	YKR029C		1.0	-1.4	-1.4	-1.5	unknown function
CA5347	orf19.7222	*IPF864*	1.1	1.1	1.0	1.1	YJL104W	*MIA1*	1.0	-1.2	-1.3	-1.3	unknown function
CA5348	orf19.7223	*IPF863*	-1.1	-1.1	-1.1	-1.1	YBR030W		1.0	1.2	1.3	1.3	involved in inositol biosynthesis (by homology)
CA5349	orf19.7224	*IPF861*	-1.2	1.1	1.2	1.2	YKR017C		1.0	-1.1	-1.2	-1.1	unknown function
CA5351	orf19.7227	*IPF857*	1.0	-1.0	1.0	-1.0	YFR003C		1.0	-1.1	-1.1	-1.8	unknown function
CA5352	orf19.7228	*IPF856*	1.1	1.3	1.8	1.4	YKR030W		1.0	-1.1	-1.1	1.1	unknown function
CA5353	orf19.7229	*IML2*	-1.1	1.7	1.7	1.4	YKR018C		1.0	-1.2	-1.3	-1.3	unknown function
CA5356	orf19.7233	*IRR1.5F*	-1.1	-1.0	-1.2	-1.1	YIL026C	*IRR1*	1.0	-1.3	-1.3	-1.1	cohesin complex subunit, 5-prime end (by homology)
CA5357	orf19.7234	*RSC8*	-1.0	-1.2	-1.2	-1.1	YFR037C	*RSC8*	1.0	-1.0	1.3	1.4	chromatin remodeling complex subunit (by homology)
CA5358	orf19.7235	*IPF846*	-1.1	1.3	1.1	1.1	YMR102C		1.0	-1.3	-1.2	-1.2	WD-repeat protein, beta-transducin (by homology)
CA5359	orf19.7236	*TIF35*	1.0	-1.1	-1.3	-1.1	YDR429C	*TIF35*	1.0	1.2	1.6	1.9	translation initiation factor eIF3, p33 subunit (by homology)
CA5360	orf19.7237	*IPF839*	1.1	1.1	1.2	1.0	YDR428C		1.0	-1.1	-1.1	1.0	unknown function
CA5361	orf19.7238	*NPL3*	-1.1	1.2	1.2	1.1	YDR432W	*NPL3*	1.0	1.3	2.0	2.6	nucleolar shuttling protein with an RNA recognition motif (by homology)
CA5362	orf19.7239	*IPF836.3*	-1.2	-1.4	-1.5	-1.4	YHR146W	*CRP1*	1.0	1.0	1.2	1.2	regulation of G-protein function, 3-prime end (by homology)
CA5363	orf19.7242	*NCR1*	-1.1	-1.1	-1.1	-1.1	YPL006W	*NCR1*	1.0	-1.3	-1.8	-1.7	Polytopic membrane protein involved in sterol homeostasis and traffickin
CA5364	orf19.7243	*DCD1*	1.1	1.0	1.0	1.1	YHR144C	*DCD1*	1.0	1.0	1.9	1.2	deoxycytidylate deaminase (by homology)
CA5365	orf19.7244	*IPF824*	1.3	-1.3	-1.4	-1.2	YNL168C		1.0	-1.1	1.1	1.1	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (by homology)
CA5366	orf19.7245	*IPF823*	1.1	-1.0	1.0	1.0	YDL033C		1.0	1.2	-1.2	-1.1	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (by homo
CA5367	orf19.7247	*RIM101*	1.1	1.0	1.1	1.0	YHL027W	*RIM101*	1.0	-1.1	1.2	1.1	Zn finger transcription factor homolog
CA5369	orf19.7251	*WSC4*	1.0	1.2	1.2	1.1	YHL028W	*WSC4*	1.0	-1.2	1.0	1.0	Cell wall integrity by homology
CA5370	orf19.7254	*IPF5248*	1.0	1.0	-1.1	-1.0	YPL005W		1.0	-1.4	-1.6	-1.5	unknown function
CA5371	orf19.7255	*RPC10*	-1.0	1.0	-1.0	-1.0	YHR143W		1.0	-1.2	1.1	1.2	DNA-directed RNA polymerases small subunit by homology
CA5372	orf19.7257	*MLH3*	1.0	-1.0	-1.0	-1.1	YPL164C	*MLH3*	1.0	1.1	1.1	-1.0	DNA mismatch repair by homology
CA5373	orf19.7256	*IPF5243*	1.1	1.0	1.1	1.1	YER146W	*LSM5*	1.0	-1.2	-1.0	-1.7	snRNP (by homology)
CA5374	orf19.7258	*DDI1*	1.0	1.1	1.3	1.0	YER143W	*DDI1*	1.0	-1.3	1.1	-1.2	Response to DNA alkylation by homology
CA5376	orf19.7261	*GDI1*	1.1	1.0	1.0	1.0	YER136W	*GDI1*	1.0	-1.1	1.3	1.3	GDP dissociation inhibitor by homology
CA5377	orf19.7263	*IPF5234*	-1.0	-1.0	-1.0	-1.1	YFR006W		1.0	1.2	1.6	1.2	X-Pro dipeptidase (by homology)
CA5378	orf19.7264	*MPR1*	1.1	1.0	1.1	-1.0	YFR004W	*RPN11*	1.0	1.1	1.3	1.0	26S proteasome regulatory subunit by homology
CA5379	orf19.7265	*IPF5228.5*	1.0	1.0	1.1	1.1	YFR005C	*SAD1*	1.0	-1.1	-1.1	-1.1	similar to Saccharomyces cerevisiae Sad1p snRNP assembly factor requ
CA5381	orf19.7269	*IPF5222*	1.3	1.1	1.1	1.1	YDR071C		1.0	1.1	1.5	1.3	arylalkylamine n-acetyltransferase (by homology)
CA5388	orf19.8545	*PET9*	1.1	-1.1	1.0	-1.1	YBL030C	*PET9*	1.0	-2.1	-2.7	-4.4	ADP/ATP carrier protein (by homology)
CA5396	orf19.939	*NAM7*	-1.2	-1.1	-1.1	-1.1	YMR080C	*NAM7*	1.0	-1.4	-1.2	-1.2	nonsense-mediated mRNA decay protein (by homology)
CA5397	orf19.940	*IPF9663*	-1.2	-1.0	-1.2	-1.1	YKL092C	*BUD2*	1.0	-1.4	-1.4	-1.4	similar to Saccharomyces cerevisiae Bud2p GTPase-activating protein fo
CA5398	orf19.941	*SEC14*	-1.0	-1.2	-1.1	-1.0	YMR079W	*SEC14*					phosphatidylinositol(PI)/phosphatidylcholine(PC) transfer
CA5403	orf19.945	*IPF1542*	-1.1	-1.0	-1.1	-1.1	YKL002W	*DID4*	1.0	-1.4	-1.5	-1.7	unknown function
CA5404	orf19.946	*MET14*	1.0	1.1	1.0	1.1	YKL001C	*MET14*	1.0	-1.4	1.0	1.3	Adenylylsulfate kinase (by homology)
CA5405	orf19.947	*MRP17*	1.0	1.0	-1.0	1.1	YKL003C	*MRP17*	1.0	-1.3	-1.4	-1.5	Mitochondrial ribosomal protein (by homology)
CA5409		*COF1*	1.2	1.2	1.3	1.3	YLL050C	*COF1*	1.0	-2.3	-2.5	-2.9	cofilin (by homology)
CA5410	orf19.954	*IPF1557*	-1.1	-1.1	-1.2	-1.0	YLR090W	*XDJ1*	1.0	-1.2	-1.4	-1.3	similar to dnaJ proteins
CA5412	orf19.956	*IPF1566*	-1.1	-1.1	-1.1	-1.1	YLR087C	*CSF1*	1.0	-1.6	-1.3	-1.1	unknown function
CA5413		*IPF1567*	1.2	1.1	1.1	1.2	YDR115W		1.0	-1.6	-1.7	-1.9	mitochondrial ribosomal protein L34 (by homology)
CA5414	orf19.962	*IPF1568*	1.0	-1.0	-1.1	-1.0	YDR156W	*RPA14*	1.0	-1.2	-1.1	-1.4	unknown function
CA5415	orf19.964	*SMC4*	-1.0	-1.1	-1.3	-1.1	YLR086W	*SMC4*	1.0	-1.1	1.3	1.4	Stable Maintenance of Chromosomes (by homology)
CA5416	orf19.966	*IPF1576*	-1.0	-1.0	-1.0	-1.1	YLR405W		1.0	-1.6	-1.9	-1.7	unknown function
CA5417	orf19.967	*NUC1*	1.0	1.0	1.1	-1.0	YJL208C	*NUC1*	1.0	-1.4	-1.1	-1.2	Nuclease, mitochondrial
CA5418	orf19.968	*IPF1580*	1.1	1.5	1.7	1.7	YNL190W		1.0	1.1	1.6	3.4	unknown function

CA5419	orf19.969	*PRS1*	-1.1	-1.1	1.1	1.0	YKL181W	*PRS1*	1.0	1.8	2.3	3.1	Ribose-phosphate pyrophosphokinase
CA5420	orf19.970	*IPF1583*	1.0	-1.0	1.0	-1.1	YLR412W		1.0	-1.0	1.2	1.3	unknown function
CA5421	orf19.971	*SKN7*	1.0	1.0	1.1	1.0	YHR206W	*SKN7*	1.0	-1.1	-1.1	1.2	Transcription factor (by homology)
CA5422	orf19.972	*IPF1588*	1.0	1.0	-1.0	-1.0	YBR228W	*SLX1*	1.0	1.3	1.3	1.3	unknown function
CA5423	orf19.974	*ROT2*	-1.2	-1.2	-1.3	-1.2	YBR229C	*ROT2*	1.0	1.2	1.1	1.1	Glucosidase II, catalytic subunit (by homology)
CA5424	orf19.976	*IPF1598*	-1.3	-1.3	-1.6	-1.3	YDL074C	*BRE1*	1.0	-1.3	-1.3	-1.2	unknown function
CA5425	orf19.978	*BDF1*	-1.2	1.0	-1.1	-1.1	YLR399C	*BDF1*	1.0	-1.3	-1.5	-1.5	sporulation protein (by homology)
CA5426	orf19.979	*FAS1*	-1.2	-1.7	-2.0	-1.9	YKL182W	*FAS1*	1.0	1.1	1.5	1.7	Fatty-acyl-CoA synthase, beta chain.
CA5428	orf19.3230	*BOI2*	-1.1	-1.1	-1.2	-1.0	YER114C	*BOI2*	1.0	-1.2	-1.5	-1.7	budding protein (by homology)
CA5429	orf19.3231	*CDC27*	-1.0	1.1	-1.0	1.1	YBL084C	*CDC27*	1.0	1.3	1.4	1.2	subunit of anaphase-promoting complex (by homology)
CA5431	orf19.3233	*IPF195*	1.1	1.1	1.0	-1.1	YHL002W		1.0	1.2	1.1	1.0	unknown function
CA5432	orf19.3234	*EBP5*	1.0	-1.1	-1.1	-1.0	YPL171C	*OYE3*	1.0	-1.7	-1.9	-1.8	NADPH dehydrogenase (by homology)
CA5434	orf19.3235	*IPF199*	1.1	-1.0	-1.1	1.2	YKL007W	*CAP1*	1.0	-1.5	-1.3	-1.5	F-actin capping protein alpha subunit (by homology)
CA5435	orf19.3237	*UFD4*	-1.1	1.3	1.3	1.4	YKL010C	*UFD4*	1.0	-1.4	-1.4	-1.3	ubiquitin fusion degradation protein (by homology)
CA5436	orf19.3239	*CTF18*	-1.0	-1.0	-1.1	-1.0	YMR078C	*CTF18*	1.0	-1.4	-1.0	-1.1	chromosome transmission in mitosis and maintenance of telomere lengt
CA5437	orf19.3240	*ERG27*	1.1	-1.1	-1.2	-1.1	YLR100W	*ERG27*	1.0	1.1	1.7	1.7	3-keto sterol reductase (by homology)
CA5438	orf19.3241	*IPF223*	1.0	1.0	-1.2	-1.0	YDR128W		1.0	-1.5	-1.2	-1.1	unknown function
CA5439	orf19.3242	*TAF25*	-1.0	-1.0	-1.2	1.0	YDR167W	*TAF25*	1.0	-1.5	-1.1	1.0	transcription initiation factor TFIID subunit (by homology)
CA5440	orf19.3243	*SRP54*	-1.2	-1.1	-1.1	-1.2	YPR088C	*SRP54*	1.0	1.2	1.8	1.9	54 kD signal recognition particle subunit
CA5441	orf19.3244	*IPF227*	1.0	-1.1	-1.2	1.0	YHR116W		1.0	-1.7	-1.0	1.1	unknown function
CA5444	orf19.3247	*IPF230*	-1.3	1.0	1.2	1.2	YJL207C		1.0	-1.8	-1.9	-2.0	unknown function
CA5446	orf19.3249	*LAG1*	1.3	-1.0	1.3	1.0	YHL003C	*LAG1*	1.0	1.1	-1.1	-1.1	longevity-assurance protein (by homology)
CA5447	orf19.3250	*IPF234*	-1.0	-1.0	1.1	-1.0	YKL012W	*PRP40*	1.0	-1.7	-1.1	-1.2	similar to Saccharomyces cerevisiae Prp40p splicing factor (by homology
CA5448	orf19.3251	*RC19.EXON*	1.1	1.1	1.2	1.1	YKL013C	*ARC19*	1.0	-1.4	-1.4	-1.9	subunit of the Arp2/3 complex involved in the control of actin polymerizati
CA5449	orf19.3252	*DAL81*	-1.1	-1.2	-1.2	-1.1	YIR023W	*DAL81*	1.0	-1.3	-1.2	-1.2	Transcriptional activator for allantoin and GABA catabolic genes (by hom
CA5451	orf19.3256	*SLN1*	-1.1	-1.0	-1.0	1.0	YIL147C	*SLN1*	1.0	-1.2	-1.2	-1.1	Two-component signal transducer histidine kinase component
CA5452	orf19.3259	*SEC11*	1.1	1.1	1.0	1.0	YIR022W	*SEC11*	1.0	1.2	1.2	1.1	signal peptidase subunit (by homology)
CA5453	orf19.3260	*IPF256*	1.1	1.1	1.0	-1.0	YKL088W		1.0	-1.2	-1.1	-1.1	control of gene expression (by homology)
CA5457	orf19.3265	*TRM1*	-1.1	-1.0	-1.1	-1.1	YDR120C	*TRM1*	1.0	1.2	1.9	1.9	N2,N2-dimethylguanine tRNA methyltransferase (by homology)
CA5459	orf19.3267	*IPF276*	-1.0	-1.0	-1.0	1.0	YDR126W	*PSL10*	1.0	1.1	1.1	1.2	unknown function
CA5460	orf19.3268	*IPF277*	1.3	1.3	1.3	1.3	YKL056C		1.0	1.4	1.6	2.3	human IgE-dependent histamine-releasing factor homolog (by homology)
CA5464	orf19.3273	*IPF285.5F*	1.0	1.0	1.0	1.0	YCR059C	*YIH1*	1.0	1.4	1.2	1.6	unknown function, 5-prime end
CA5466	orf19.3276	*PWP2*	-1.0	1.1	-1.1	-1.1	YCR057C	*PWP2*	1.0	1.1	-1.0	1.4	periodic tryptophan protein (by homology)
CA5467	orf19.3278	*GSY1*	-1.0	2.3	2.7	3.0	YFR015C	*GSY1*	1.0	1.5	2.3	-1.1	UDP glucose--starch glucosyltransferase, glycogen synthase (by homolo
CA5469	orf19.3281	*IPF298*	1.0	1.0	1.0	-1.0	YER051W		1.0	-1.1	-1.2	-1.1	unknown function
CA5471	orf19.3283	*IPF302*	-1.1	-1.1	-1.1	-1.1	YKL055C	*OAR1*	1.0	-2.6	-2.8	-3.8	short chain dehydrogenase/reductase (by homology)
CA5473	orf19.3286	*IPF16947*	1.0	-1.3	-1.4	-1.1	YDR221W		1.0	-1.1	-1.0	1.1	unknown function
CA5474	orf19.3287	*F16944.3EO*	1.0	-1.4	-1.2	-1.1	YMR014W	*BUD22*	1.0	1.1	1.4	1.4	unknown function, 3-prime end
CA5480	orf19.5312	*IPF8210*	-1.0	1.0	-1.0	1.0	YNL103W	*MET4*	1.0	1.1	1.1	1.2	unknown function
CA5484	orf19.5318	*RAD1.3F*	-1.2	-1.1	1.1	-1.0	YPL022W	*RAD1*	1.0	1.2	-1.1	-1.0	UV endonuclease, component of the nucleotide excision repairosome, 3-
CA5487	orf19.5321	*MET12*	-1.1	1.2	1.1	1.0	YPL023C	*MET12*	1.0	1.3	1.2	1.1	methylenetetrahydrofolate reductase (by homology)
CA5488	orf19.5322	*IPF810*	1.1	1.3	1.5	1.3	YJL178C		1.0	-1.5	-1.4	-1.4	unknown function
CA5489	orf19.5323	*MDH12*	1.2	-1.1	1.2	-1.0	YDL078C	*MDH3*	1.0	-1.0	-1.2	-1.7	mitochondrial malate dehydrogenase (by homology)
CA5490	orf19.5325	*KIN3*	-1.1	-1.2	-1.2	-1.1	YAR018C	*KIN3*	1.0	1.1	1.0	1.0	G2-specific serine/threonine protein kinase (by homology)
CA5491	orf19.5326	*IPF798*	1.1	1.1	1.1	1.1	YGL209W	*MIG2*	1.0	1.0	1.1	1.4	transcriptional regulator (by homology)
CA5493	orf19.5333	*GCN1.5F*	1.1	1.5	1.2	1.1	YGL195W	*GCN1*	1.0	1.1	-1.0	1.3	translational activator, 5-prime end (by homology)
CA5494	orf19.5334	*IPF85*	1.1	3.8	3.4	2.4	YLR136C	*TIS11*	1.0	-1.1	1.0	1.2	similar to Saccharomyces cerevisiae Tis11p tRNA-specific adenosine de
CA5495	orf19.5335	*SGS1*	1.0	1.1	-1.1	-1.0	YMR190C	*SGS1*	1.0	-1.6	-1.5	-1.5	ATP-dependent DNA helicase (by homology)
CA5498	orf19.5340	*IPF772*	-1.2	1.0	1.1	-1.0	YPL249C	*GYP5*	1.0	-1.1	-1.3	-1.4	unknown function
CA5499	orf19.5341	*RPS4A*	1.0	-1.2	-1.3	-1.1	YJR145C	*RPS4A*	1.0	1.3	1.3	2.2	ribosomal protein S4
CA5500	orf19.5342	*IPF768*	-1.1	1.0	-1.1	-1.0	YHR202W		1.0	-1.5	-1.5	-1.3	unknown function
CA5501		*MTR2.3*	1.0	-1.0	-1.1	-1.0	YKL186C	*MTR2*	1.0	-1.1	-1.2	-1.1	mRNA transport protein, 3-prime end (by homology)
CA5502	orf19.5343	*IPF763*	1.1	1.2	1.1	1.0	YKL185W	*ASH1*	1.0	-1.3	-1.2	-1.4	putative transcription factor with a Cys4- zinc finger (by homology)
CA5503	orf19.5345	*DSK2*	1.0	1.3	1.2	1.2	YMR276W	*DSK2*	1.0	1.1	1.2	-1.1	ubiquitin-like protein (by homology)
CA5504	orf19.5346	*TAF65*	1.0	1.0	1.0	1.0	YML114C	*TAF65*	1.0	-1.1	-1.2	-1.2	subunit of transcription factor TFIID (by homology)
CA5505	orf19.5348	*TPS3.3*	-1.1	2.2	1.9	2.2	YMR261C	*TPS3*	1.0	-1.1	-1.3	-1.6	alpha,alpha-trehalose-phosphate synthase, regulatory subunit, 3-prime e
CA5506	orf19.5350	*IPF748*	-1.1	-1.0	1.1	-1.0	YML112W	*CTK3*	1.0	-1.1	-1.1	-1.2	unknown function
CA5507	orf19.5351	*TIF11*	1.3	1.3	1.2	1.3	YMR260C	*TIF11*	1.0	1.2	1.4	1.5	translation initiation factor eIF1a (by homology)
CA5510	orf19.5356	*IPF741*	-1.0	-1.1	-1.2	-1.3	YNL313C		1.0	1.1	1.2	1.2	unknown function
CA5511	orf19.5357	*AKL1*	-1.4	1.0	-1.1	-1.0	YIL095W	*PRK1*	1.0	-1.1	-1.0	1.0	serine/threonine protein kinase (by homology)
CA5512	orf19.5358	*ORC2*	-1.1	-1.0	-1.0	-1.1	YBR060C	*ORC2*	1.0	-1.2	-1.2	-1.2	origin recognition complex subunit 2 (by homology)

CA5513	orf19.5360	*RPC11*	1.1	1.1	1.0	1.0	YDR045C	*RPC11*	1.0	-1.8	-1.3	-1.1	RNA polymerase III C11 subunit (by homology)
CA5515	orf19.5363	*SAT2*	-1.0	1.1	1.1	1.0	YBR070C		1.0	1.1	1.0	1.0	putative glycosyl-transferase involved in osmotolerance (by homology)
CA5516	orf19.5364	*IPF726*	1.1	1.0	-1.1	-1.1	YBR065C	*ECM2*	1.0	1.1	1.3	1.2	rna binding protein (by homology)
CA5518	orf19.5366	*IPF721.5F*	-1.0	-1.0	-1.2	-1.1	YMR259C		1.0	1.1	1.1	1.2	unknown function, 5-prime end
CA5519	orf19.5367	*RDH54*	1.0	1.2	1.3	1.1	YBR073W	*RDH54*	1.0	-1.4	-1.4	-1.2	helicase required for mitotic diploid-specific recombination and repair (by
CA5520	orf19.5368	*IPF714*	-1.0	-1.1	-1.1	1.0	YDR049W		1.0	-1.0	1.2	1.7	unknown function
CA5521	orf19.5369	*HEM12*	-1.1	-1.1	-1.2	-1.1	YDR047W	*HEM12*	1.0	-1.0	1.1	1.1	uroporphyrinogen decarboxylase (by homology)
CA5522	orf19.5370	*IPF708*	-1.1	1.0	1.0	-1.0	YBR075W		1.0	-1.1	1.1	1.2	unknown function
CA5523	orf19.7279	*NIT2*	1.1	-1.0	-1.0	1.0	YJL126W	*NIT2*	1.0	-1.4	-1.2	-1.3	Nitrilase (by homology)
CA5524	orf19.7281	*IPF2861*	-1.1	-1.3	-1.3	-1.3	YIL042C		1.0	1.2	1.0	1.1	putative pyruvate dehydrogenase kinase
CA5525	orf19.7282	*PEX13*	1.0	-1.9	-1.7	-1.4	YLR191W	*PEX13*	1.0	-1.1	-1.3	-1.4	Peroxisome import protein - peroxin (by homology)
CA5527	orf19.7285	*IPF2856*	-1.1	-1.1	-1.1	-1.2	YGR156W	*PTI1*	1.0	-1.2	-1.4	-1.6	unknown function
CA5528	orf19.7286	*RPN7*	-1.0	1.0	-1.1	-1.1	YPR108W	*RPN7*	1.0	1.1	1.5	1.2	Subunit of the regulatory particle of the proteasome (by homology)
CA5530	orf19.7290	*SPB8*	1.1	-1.0	-1.1	-1.0	YJL124C	*LSM1*	1.0	-1.0	1.2	1.1	Suppressor of PAB1 (by homology)
CA5531	orf19.7291	*GCD14*	1.0	-1.0	-1.0	-1.2	YJL125C	*GCD14*	1.0	-1.1	1.1	1.0	Translational repressor of GCN4
CA5532	orf19.7292	*ARP2*	-1.0	1.1	1.2	1.1	YDL029W	*ARP2*	1.0	-1.0	1.2	-1.1	actin-like protein (by homology)
CA5533	orf19.7293	*IPF2846*	1.0	1.0	-1.0	1.0	YDL028C	*MPS1*	1.0	-1.0	-1.1	-1.1	similar to Saccharomyces cerevisiae Mps1p serine/threonine/tyrosine pro
CA5534	orf19.7295	*IPF2843*	1.1	1.0	1.1	-1.0	YOR329C	*SCD5*	1.0	-1.2	1.3	1.5	unknown function
CA5536	orf19.7297	*IPF2837*	1.1	1.1	1.3	1.3	YHR112C		1.0	-1.4	-1.4	-1.4	putative cystathionine gamma-synthase (by homology)
CA5537	orf19.7298	*CHS2*	1.2	1.2	1.6	1.3	YNL192W	*CHS1*	1.0	1.1	1.3	1.5	Chitin synthase
CA5544	orf19.7306	*IPF5987*	1.0	-1.1	-1.1	-1.0	YPR127W		1.0	-1.1	1.1	-1.1	unknown function
CA5545	orf19.7307	*IPF5986*	1.2	-1.1	-1.1	-1.2	YML125C		1.0	-1.3	-1.2	1.3	similar to cytochrome-b5- and nitrate reductases
CA5546	orf19.7308	*TUB1.3*	1.3	1.4	1.9	1.4	YML085C	*TUB1*					Alpha-1 tubulin, 3-prime end
CA5547	orf19.7310	*IPF5981*	-1.1	-1.1	-1.2	-1.0	YML128C	*MSC1*	1.0	1.7	1.0	-2.5	similar to Saccharomyces cerevisiae Gin3p (by homology)
CA5549	orf19.7312	*ERG13*	-1.1	-1.2	-1.2	-1.2	YML126C	*ERG13*	1.0	1.3	1.8	2.1	3-hydroxy-3-methylglutaryl coenzyme A synthase (by homology)
CA5550	orf19.7313	*SSU1*	1.1	1.4	1.8	1.3	YPL092W	*SSU1*	1.0	-1.1	-1.1	1.5	Sulfite sensitivity protein (by homology)
CA5555	orf19.7319	*SUC1*	-1.0	1.0	1.0	1.1	YFL052W		1.0	1.2	1.3	1.2	Putative zinc finger protein Suc1
CA5557	orf19.7321	*IPF1968*	-1.2	-1.1	-1.2	-1.1	YMR029C		1.0	1.1	1.2	-1.1	unknown function
CA5558	orf19.7322	*IPF1969*	1.6	1.6	1.9	1.8	YPL225W		1.0	-1.4	-1.2	-1.3	unknown function
CA5560	orf19.7324	*THI13*	1.0	-1.0	1.0	1.0	YDL244W	*THI13*	1.0	-1.8	-1.4	-1.4	Pyrimidine precursor biosynthesis enzyme (by homology)
CA5561	orf19.7325	*SCO1*	1.0	1.0	1.1	1.1	YBR037C	*SCO1*	1.0	-2.4	-2.1	-1.3	Inner mitochondrial membrane protein (by homology)
CA5563	orf19.7327	*PHO88*	1.2	-1.0	-1.1	1.0	YBR106W	*PHO88*	1.0	-1.5	-1.0	1.1	Involved in phosphate transport (by homology)
CA5565	orf19.7329	*QRI8*	1.1	1.1	1.0	-1.0	YMR022W	*QRI8*	1.0	1.2	1.2	1.0	E2 ubiquitin-conjugation enzyme (by homology)
CA5566	orf19.7330	*PET18*	-1.0	1.0	1.0	-1.0	YCR020C	*PET18*	1.0	1.0	-1.0	1.0	Putative transcriptional regulator (by homology)
CA5568	orf19.7332	*ELF1*	-1.3	-1.2	-1.5	-1.3	YPL226W	*NEW1*	1.0	1.0	1.7	3.1	Elongation-like factor
CA5569	orf19.7335	*PRE8*	1.1	1.0	1.1	1.2	YML092C	*PRE8*	1.0	-1.5	-1.8	-1.5	20S proteasome subunit Y7 (by homology)
CA5576	orf19.7343	*PRP4*	-1.0	1.0	1.0	1.0	YPR178W	*PRP4*	1.0	-1.1	1.2	1.1	pre-mRNA-processing U4/U6 small nuclear ribonucleoprotein (by homolo
CA5577	orf19.7344	*IPF12537*	1.0	-1.0	-1.0	-1.0	YPR179C	*PLO1*	1.0	-1.1	1.1	1.0	unknown function
CA5578	orf19.7345	*IPF12536*	-1.0	-1.0	-1.0	-1.0	YGR205W		1.0	1.0	1.1	1.0	unknown function
CA5580	orf19.7124	*RVS161*	1.1	1.0	1.0	1.1	YCR009C	*RVS161*	1.0	-1.0	-1.3	-1.4	cytoskeletal binding protein (by homology)
CA5581	orf19.7119	*RAD3*	-1.2	1.2	1.2	1.1	YER171W	*RAD3*	1.0	-1.3	-1.4	-1.6	DNA helicase/ATPase by homology
CA5582	orf19.7118	*ADK2*	1.1	-1.6	-1.8	-1.3	YER170W	*ADK2*	1.0	-1.1	-1.2	-1.3	adenylate kinase, mitochondrial (by homology)
CA5583	orf19.7116	*IPF5644*	-1.0	-1.0	-1.2	-1.0	YOR123C	*LEO1*	1.0	-1.0	1.2	1.1	unknown function
CA5584	orf19.7115	*SAC7*	1.2	-1.1	-1.2	-1.1	YDR389W	*SAC7*	1.0	-1.6	-1.7	-2.0	GAP for RHO1 by homology
CA5589	orf19.7111	*IPF5621*	-1.1	-1.1	-1.0	-1.0	YIL065C	*FIS1*	1.0	-1.4	-1.4	-1.5	unknown function
CA5590	orf19.7110	*TAD1*	-1.0	-1.0	1.1	-1.0	YGL243W	*TAD1*	1.0	1.0	-1.0	1.0	Double-stranded rna specific adenosine deaminase by homology
CA5591	orf19.7109	*IPF5618*	-1.1	-1.1	-1.3	-1.0	YGL242C		1.0	1.2	1.2	1.3	unknown function
CA5593	orf19.7107	*IPF5615*	1.0	1.0	1.0	1.0	YJL122W		1.0	-1.4	1.2	1.2	unknown function
CA5594	orf19.7106	*IPF19814*	1.1	-1.0	-1.1	-1.1	YJR126C		1.0	1.1	1.2	1.3	folate hydrolase (by homology)
CA5595	orf19.7105	*IPF568*	1.1	1.0	-1.0	-1.0	YJL157C	*FAR1*	1.0	-1.7	-1.4	-1.2	similar to Saccharomyces cerevisiae Far1p cyclin-dependent kinase inhib
CA5597	orf19.7103	*IPF563*	-1.0	-1.0	-1.0	-1.0	YCL036W		1.0	-1.1	-1.2	-1.2	unknown function
CA5598	orf19.7101	*IPF562*	1.0	1.0	1.1	1.0	YGR099W	*TEL2*	1.0	-1.4	-1.5	-1.6	unknown function
CA5600	orf19.7100	*IPF559*	-1.1	-1.0	1.2	1.0	YJR001W		1.0	-1.2	-1.1	-1.2	unknown function
CA5601	orf19.7098	*IPF556*	1.0	1.1	1.1	1.1	YKL070W		1.0	-2.8	-2.2	-1.8	transcriptional regulator (by homology)
CA5603	orf19.7096	*IPF553*	-1.0	1.1	1.1	1.1	YLR001C		1.0	-1.1	-1.2	-1.1	unknown function
CA5604	orf19.7095	*IPF549*	1.1	1.2	1.7	1.2	YOR390W		1.0	-1.0	1.2	1.4	unknown function
CA5608	orf19.7092	*IPF539*	-1.1	-1.1	-1.2	-1.0	YLR290C		1.0	-1.2	-1.2	-1.4	unknown function
CA5610	orf19.7089	*PMR1*	1.1	1.0	1.1	1.1	YGL167C	*PMR1*	1.0	1.1	-1.0	1.2	calcium/mangenease P-type ATPase
CA5611	orf19.7088	*SUA5*	1.1	-1.2	-1.1	-1.2	YGL169W	*SUA5*	1.0	-1.4	1.0	1.1	translation initiation protein (by homology)
CA5612	orf19.7086	*KAP114*	-1.1	1.2	1.0	1.1	YGL241W	*KAP114*	1.0	1.0	1.2	1.3	putative RAN-binding protein/importin (by homology)
CA5615	orf19.7083	*IPF520*	-1.0	-1.0	1.1	1.0	YCL016C	*DCC1*	1.0	-1.1	-1.3	1.1	unknown function

CA5616	orf19.7082	*PET8*	-1.0	1.1	1.2	-1.0	YNL003C	*PET8*	1.0	-1.1	1.0	1.1	mitochondrial carrier protein (by homology)
CA5617	orf19.7081	*SPL1*	-1.1	-1.0	1.0	-1.1	YCL017C	*NFS1*	1.0	1.1	1.2	1.1	tRNA splicing protein
CA5618	orf19.7080	*LEU2*	-1.2	-1.2	-1.3	-1.1	YCL018W	*LEU2*	1.0	1.4	2.5	2.6	isopropyl malate dehydrogenase
CA5619	orf19.7079	*IPF514*	1.0	-1.0	-1.0	1.0	YCL014W	*BUD3*	1.0	1.0	-1.1	1.1	similar to Saccharomyces cerevisiae Bud3p budding protein (by homolog
CA5621	orf19.7077	*FRE7*	-1.0	-1.5	-1.4	-1.3	YOL152W	*FRE7*	1.0	-1.5	-1.2	-1.2	Ferric reductase transmembrane component (by homology)
CA5622	orf19.7076	*GBP2.3*	1.1	1.0	1.3	1.0	YCL011C	*GBP2*	1.0	-1.1	1.1	1.5	single-strand telomeric DNA-binding protein, 3-prime end (by homology)
CA5623	orf19.7074	*IPF502*	1.0	1.0	-1.0	1.0	YCL010C		1.0	-1.2	-1.0	1.0	unknown function
CA5625	orf19.7072	*PEL1*	-1.0	-1.0	-1.1	-1.0	YCL004W	*PGS1*	1.0	-1.1	-1.1	-1.0	CDP-diacylglycerol-serine-O-phosphatidyltransferase (by homology)
CA5627	orf19.7069	*IPF495*	1.0	1.0	1.0	-1.0	YBR261C		1.0	1.1	1.2	1.7	unknown function
CA5629	orf19.7067	*CTR9*	-1.5	-1.5	-2.9	-2.0	YOL145C	*CTR9*	1.0	1.2	1.3	1.4	required for G1 cyclin expression (by homology)
CA5630	orf19.7065	*IPF486*	1.0	-1.0	-1.0	-1.0	YOL146W		1.0	1.1	-1.0	-1.1	unknown function
CA5631	orf19.7064	*GLN4*	-1.0	-1.0	-1.1	-1.1	YOR168W	*GLN4*	1.0	-1.0	1.6	1.5	glutaminyl-tRNA synthetase (by homology)
CA5632	orf19.7063	*IPF480*	-1.1	-1.1	-1.1	-1.0	YGR024C		1.0	-1.2	1.0	-1.0	unknown function
CA5633	orf19.7062	*RPA135*	-1.0	1.2	-1.1	-1.2	YPR010C	*RPA135*	1.0	1.0	1.7	2.5	DNA-directed RNA polymerase I, 135 KD subunit (by homology)
CA5634	orf19.7061	*IPF477*	1.0	1.0	1.0	1.0	YFR007W		1.0	-1.4	-1.3	-1.4	unknown function
CA5636	orf19.7059	*IPF473*	1.0	-1.0	-1.0	1.0	YOR166C		1.0	-1.3	1.2	1.2	unknown Function
CA5637	orf19.7058	*IPF472*	-1.0	-1.0	1.1	1.0	YFR048W		1.0	-1.6	-1.7	-1.7	unknown Function
CA5638	orf19.7057	*IPF470*	-1.3	-1.2	-1.5	-1.3	YGL245W		1.0	1.2	1.6	1.8	putative glutamine-tRNA ligase (by homology)
CA5641	orf19.7053	*GAC1*	1.2	-1.1	1.0	-1.0	YOR178C	*GAC1*	1.0	1.5	2.5	1.7	ser/thr phosphoprotein phosphatase 1, regulatory chain (by homology)
CA5642	orf19.7052	*INP52*	-1.0	-1.1	-1.1	-1.1	YOR109W	*INP53*	1.0	-1.0	-1.0	1.2	phosphatidylinositol phosphate phosphatase (by homology)
CA5643	orf19.7051	*IPF448*	1.0	-1.0	-1.0	1.0	YOR111W		1.0	1.0	1.1	1.2	unknown function
CA5644	orf19.7050	*IPF447*	-1.0	1.0	1.0	1.1	YNL110C		1.0	1.5	1.7	2.0	unknown function
CA5645	orf19.7049	*CYB5*	1.6	-1.2	1.2	1.0	YNL111C	*CYB5*	1.0	-1.5	-1.0	-1.2	Cytochrome b5 (by homology)
CA5646		*RPS28B.3*	1.6	1.5	1.6	1.6	YLR264W	*RPS28B*	1.0	2.0	1.7	2.5	Ribosomal protein S28B (S33B) (YS27), 3-prime end (by homology)
CA5648	orf19.7347	*UBC6*	-1.0	1.0	1.1	-1.0	YER100W	*UBC6*	1.0	1.0	1.2	1.6	E2 ubiquitin-conjugating enzyme (by homology)
CA5649	orf19.7349	*CHS4*	-1.2	-1.1	-1.2	-1.0	YBL061C	*SKT5*	1.0	-1.1	-1.2	-1.2	Chitin synthase regulatory factor
CA5650	orf19.7350	*IPF7109*	1.1	-1.0	-1.1	-1.1	YNL208W		1.0	-1.2	-1.5	-2.4	unknown function
CA5651	orf19.7353	*KIP3*	-1.1	-1.1	-1.0	-1.0	YGL216W	*KIP3*	1.0	-1.1	-1.1	1.2	Kinesin-related protein required for nuclear migration (by homology)
CA5653	orf19.7355	*SSN8*	1.0	-1.0	1.0	1.0	YNL025C	*SSN8*	1.0	-3.7	-2.7	-2.6	C-type cyclin associated with the Ssn3p cyclin-dependent kinase (by hon
CA5655	orf19.7357	*IPF18080*	-1.5	-2.3	-2.5	-2.2	YIL083C		1.0	1.0	1.1	1.1	unknown function
CA5656	orf19.7358	*IPF14683*	-1.0	-1.1	-1.1	1.1	YNL026W		1.0	-1.3	-1.1	-1.1	unknown function
CA5657	orf19.7359	*IPF14682*	1.2	1.0	1.4	1.1	YNL027W	*CRZ1*	1.0	1.0	1.1	1.1	putative transcription factor (by homology)
CA5658	orf19.7360	*IPF1242*	-1.0	1.0	1.0	-1.0	YPL047W		1.0	-1.6	-1.3	-1.9	unknown function
CA5659	orf19.7361	*SEN54*	1.0	-1.0	-1.1	-1.1	YPL083C	*SEN54*	1.0	-1.4	1.2	1.4	tRNA splicing endonuclease alpha subunit(by homology)
CA5661	orf19.7363	*KRE6*	1.1	1.3	1.8	1.3	YPR159W	*KRE6*	1.0	-1.0	1.2	1.5	Glucan synthase subunit
CA5663	orf19.7365	*IPF1251*	-1.0	-1.0	-1.0	-1.0	YIL097W	*FYV10*	1.0	-1.3	-1.4	-1.5	unknown function
CA5664	orf19.7366	*IPF1252*	-1.0	-1.0	-1.0	-1.1	YIL096C		1.0	-1.0	-1.3	-1.1	Conserved hypothetical protein
CA5665	orf19.7367	*UBP1*	1.0	-1.1	-1.0	-1.0	YDL122W	*UBP1*	1.0	-1.2	-1.1	1.3	Ubiquitin-specific protease (by homology)
CA5666	orf19.7368	*PUB1*	1.3	1.3	1.4	1.3	YNL016W	*PUB1*	1.0	-1.1	-1.1	-1.0	Major polyadenylated RNA-binding protein (by homology)
CA5667	orf19.7369	*IPF1259*	-1.0	1.0	-1.0	-1.0	YML005W		1.0	-1.3	-1.4	-1.3	Conserved hypothetical protein
CA5668	orf19.7370	*IPF1261*	1.2	1.1	-1.0	-1.0	YOL092W		1.0	1.3	1.6	2.1	unknown function
CA5671	orf19.7374	*CTA4*	1.0	1.2	1.2	1.2	YAL051W	*OAF1*	1.0	1.3	1.4	1.2	Probable transcription factor
CA5674	orf19.7377	*IPF1274*	1.0	1.0	1.1	1.0	YOR058C	*ASE1*	1.0	-1.4	-1.4	-1.3	similar to Saccharomyces cerevisiae Ase1p component of the anaphase
CA5675	orf19.7378	*SIS2*	-1.0	1.0	1.2	1.0	YKR072C	*SIS2*	1.0	-1.2	1.1	1.3	Involved in cell cycle-specific gene expression (by homology)
CA5681	orf19.7383	*MNN9*	1.0	1.0	1.0	1.0	YPL050C	*MNN9*	1.0	1.1	1.3	1.3	Required for complex N-glycosylation
CA5682	orf19.7384	*NOG1*	-1.3	-1.2	-1.4	-1.3	YPL093W	*NOG1*	1.0	1.3	1.7	2.7	Nucleolar G-protein (by homology)
CA5683	orf19.7385	*IPF3333*	1.0	-1.0	-1.0	-1.0	YPL054W	*LEE1*	1.0	1.0	-1.2	-1.8	unknown function
CA5684	orf19.7386	*IPF3331*	1.2	1.1	1.1	-1.1	YBR185C	*MBA1*	1.0	-1.4	-1.5	-1.3	unknown function
CA5685	orf19.7387	*HPA1*	-1.0	-1.0	-1.1	-1.1	YPL086C	*ELP3*	1.0	1.3	1.6	1.5	RNA polymerase II-associated Histone acetyltransferase (by homology)
CA5686	orf19.7388	*IPF3329*	-1.1	-1.2	-1.3	-1.3	YJL128C	*PBS2*	1.0	-1.4	-1.1	-1.0	similar to Saccharomyces cerevisiae Pbs2p tyrosine protein kinase of th
CA5687	orf19.7389	*REV3.5F*	-1.0	1.1	-1.0	-1.0	YPL167C	*REV3*	1.0	-1.8	-1.5	-1.3	DNA-directed DNA polymerase zeta subunit, 5-prime end (by homology)
CA5690	orf19.7391	*OCH1*	1.1	1.1	1.1	1.1	YGL038C	*OCH1*	1.0	-1.1	-1.4	1.1	Alpha-1,6-mannosyltransferase (by homology)
CA5691	orf19.7392	*DED1*	1.3	1.6	1.9	1.4	YOR204W	*DED1*	1.0	1.1	2.4	3.3	RNA helicase (by homology)
CA5692	orf19.7393	*UTR1*	-1.1	-1.0	-1.0	-1.1	YJR049C	*UTR1*	1.0	-1.8	-1.4	1.0	Associated with ferric reductase activity (by homology)
CA5693	orf19.7394	*GDA1*	-1.1	-1.0	1.0	-1.0	YEL042W	*GDA1*	1.0	-1.2	1.6	1.6	Golgi guanosine diphosphatase (by homology)
CA5695	orf19.7397	*IPF3310*	-1.1	-1.2	-1.5	-1.3	YPR022C		1.0	1.0	-1.1	1.1	unknown function
CA5701	orf19.7401	*ISW2*	-1.2	-1.4	-1.4	-1.3	YOR304W	*ISW2*	1.0	-1.2	-1.0	1.1	Chromatin remodeling complex (by homology)
CA5702	orf19.7402	*PCH1*	-1.3	1.1	-1.1	-1.0	YDR440W	*DOT1*	1.0	-1.4	-1.2	-1.4	Putative ATPase (by homology)
CA5703	orf19.7403	*IPF2463*	1.0	1.0	-1.1	-1.1	YML020W		1.0	-1.0	-1.1	-1.3	unknown function
CA5704	orf19.7404	*CHA11*	1.0	1.4	1.6	1.4	YCL064C	*CHA1*	1.0	-1.1	-1.3	-1.5	L-serine/L-threonine deaminase (by homology)
CA5707	orf19.7409	*ERV25*	1.1	1.4	1.3	1.3	YML012W	*ERV25*	1.0	-1.3	-1.3	-1.4	Component of COPII-coated vesicles (by homology)

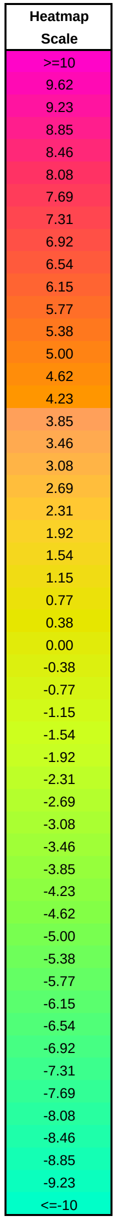
CA5708		*MRPL39*	1.0	-1.0	1.0	-1.0	YML009C	*MRPL39*					Mitochondrial 60S ribosomal protein (by homology)
CA5709	orf19.7410	*IPF2653*	-1.3	-1.0	-1.5	-1.1	YDR430C		1.0	1.4	1.2	1.6	unknown function
CA5710	orf19.7411	*OAC1*	1.0	1.1	1.0	-1.0	YKL120W	*OAC1*	1.0	1.1	1.2	1.4	Mitochondrial oxaloacetate transport protein (by homology)
CA5711	orf19.7412	*MUB1*	1.0	-1.1	-1.1	1.1	YMR100W	*MUB1*	1.0	1.0	1.2	1.6	Regulation of bud site selection (by homology)
CA5712	orf19.7413	*IPF2657*	-1.1	-1.0	1.0	-1.0	YEL019C	*MMS21*	1.0	-1.5	-1.2	-1.1	unknown function
CA5714	orf19.7417	*IPF2431*	1.1	1.1	-1.0	1.2	YML028W	*TSA1*	1.0	-1.3	-1.2	-2.0	similar to Saccharomyces cerevisiae Tsa1p thiol-specific antioxidant-like
CA5715	orf19.7419	*HNT2*	1.1	1.1	1.2	1.1	YDR305C	*HNT2*	1.0	-1.2	-1.4	-1.1	Diadenosine polyphosphate hydrolase
CA5716	orf19.7420	*MED6*	-1.0	1.0	-1.1	-1.0	YHR058C	*MED6*	1.0	-1.3	-1.1	-1.2	RNA polymerase II transcriptional regulation mediator (by homology)
CA5717	orf19.7421	*CYP51*	1.2	1.2	1.1	1.2	YDR304C	*CYP5*	1.0	-1.1	-1.0	-1.3	Cyclophilin - peptidylprolyl cis-trans isomerase or PPIase (by homology)
CA5718	orf19.7422	*LCP5*	-1.1	-1.1	-1.1	-1.1	YER127W	*LCP5*	1.0	-1.2	-1.3	-1.0	Ngg1p interacting protein (by homology)
CA5719	orf19.7424	*IPF2441*	1.0	-1.0	-1.0	-1.0	YER126C	*KRE32*	1.0	-1.3	-1.1	1.3	unknown function
CA5720	orf19.7425	*UNG1*	-1.0	1.0	1.1	1.1	YML021C	*UNG1*	1.0	-1.2	-1.2	-1.0	Uracil-DNA glycosylase (by homology)
CA5721	orf19.7426	*IPF2443*	-1.1	-1.2	-1.1	-1.0	YML019W	*OST6*	1.0	1.0	1.1	-1.1	similar to Saccharomyces cerevisiae Ost6p N-oligosaccharyltransferase
CA5722	orf19.7427	*IPF2446*	1.0	1.0	1.1	1.0	YML018C		1.0	-1.9	-2.4	-2.0	unknown function
CA5723	orf19.7428	*APN1*	-1.1	-1.1	-1.2	-1.1	YKL114C	*APN1*	1.0	-1.1	-1.0	1.2	AP endonuclease, exonuclease III homologue (by homology)
CA5724	orf19.7433	*NUP116*	-1.0	1.0	1.1	-1.0	YMR047C	*NUP116*	1.0	-1.5	-1.6	-1.5	nuclear pore protein (by homology)
CA5727		*ECM15*	1.1	1.1	1.0	-1.0	YBL001C	*ECM15*	1.0	-2.0	-1.4	-1.3	Involved in cell wall biogenesis and architecture (by homology)
CA5728	orf19.7437	*IPF2471*	-1.1	-1.5	-1.5	-1.2	YJL218W		1.0	-1.1	1.1	1.1	maltose acetyltransferase
CA5729	orf19.7438	*UBA1*	-1.2	1.0	-1.2	-1.1	YKL210W	*UBA1*	1.0	-1.4	-1.1	-1.2	Ubiquitin-activating enzyme (by homology)
CA5730	orf19.7440	*HST6*	1.0	-1.0	-1.0	-1.0	YKL209C	*STE6*	1.0	-1.3	1.1	1.3	ATP binding cassette protein
CA5734	orf19.7444	*IPF20029*	1.1	1.0	1.0	1.0	YOR352W		1.0	1.1	1.2	1.1	unknown function
CA5735	orf19.7445	*IPF2878*	1.1	1.7	2.1	1.8	YBR105C	*VID24*	1.0	1.6	2.2	2.3	unknown function
CA5736	orf19.7446	*OPI3*	1.5	-1.0	1.2	1.0	YJR073C	*OPI3*	1.0	-1.9	-1.8	-2.4	Methylene-fatty-acyl-phospholipid synthase (by homology)
CA5737	orf19.7447	*JEN1*	1.0	1.0	-1.0	-1.0	YKL217W	*JEN1*	1.0	-1.6	-1.7	-4.5	Carboxylic acid transporter protein (by homology)
CA5738	orf19.7448	*LYS9*	-1.0	-1.5	-1.3	-1.1	YNR050C	*LYS9*	1.0	-1.1	-1.2	-1.1	Lysine biosynthesis (by homology)
CA5739	orf19.7449	*IPF2884*	-1.0	-1.0	1.0	-1.0	YMR211W		1.0	1.0	1.2	1.4	unknown function
CA5740	orf19.7450	*IPF20030*	1.0	1.0	-1.0	-1.1	YNL166C	*BNI5*	1.0	-1.1	1.2	1.3	unknown function
CA5742	orf19.7451	*FUN31*	1.0	1.1	1.2	1.2	YAL017W	*FUN31*	1.0	1.0	-1.3	-1.3	Serine/threonine kinase (by homology)
CA5743	orf19.7452	*IPF2895*	-1.0	-1.0	-1.0	1.0	YGL113W	*SLD3*	1.0	1.0	1.1	1.3	unknown function
CA5745	orf19.7454	*TAF60*	-1.0	1.0	-1.0	1.0	YGL112C	*TAF60*	1.0	1.1	1.2	1.1	TATA-binding protein-associated-factor (by homology)
CA5749	orf19.7459	*IPF2908*	-1.4	1.3	1.2	1.5	YBR238C		1.0	1.1	1.4	1.6	unknown function
CA5751	orf19.5387	*VPS8*	-1.2	1.0	1.0	-1.0	YAL002W	*VPS8*	1.0	1.1	1.1	1.3	Vacuolar sorting protein (by homology)
CA5752	orf19.5388	*IPF1055*	-1.0	1.1	1.1	-1.0	YAR003W	*SWD1*	1.0	1.1	1.1	1.1	unknown function
CA5753	orf19.5389	*FKH1*	1.1	1.1	1.0	-1.0	YNL068C	*FKH2*	1.0	-1.4	-1.3	-1.1	Fork head protein type transcription factor
CA5755	orf19.5391	*IPF1063*	-1.1	-1.1	-1.1	-1.0	YML049C	*RSE1*	1.0	-2.4	-3.1	-2.7	Spliceosomal protein SAP 130 (by homology)
CA5758	orf19.5395	*IPF1069*	1.0	-1.0	1.1	-1.0	YJR033C	*RAV1*	1.0	-1.2	-1.5	-1.4	similar to Saccharomyces cerevisiae Rav1p involved in regulation of (H+
CA5759		*PET191.3*	1.0	1.0	1.1	1.0	YJR034W	*PET191*	1.0	-1.2	-1.4	-1.4	Assembly of cytochrome oxidase, 3-prime end (by homology)
CA5760	orf19.5397	*IPF1072*	1.0	1.1	1.1	1.0	YGL005C	*COD5*	1.0	-1.3	-1.1	-1.1	unknown function
CA5764	orf19.5406	*IPF20031*	-1.1	1.1	1.1	1.1	YLR019W	*PSR2*	1.0	1.2	1.4	2.0	similar to Saccharomyces cerevisiae Psr2p plasma membrane phosphat
CA5765	orf19.5407	*SOF1*	-1.1	-1.1	-1.1	1.0	YLL011W	*SOF1*	1.0	-1.1	-1.1	1.2	Involved in 18S pre-rRNA production (by homology)
CA5766	orf19.5408	*IPF1097*	-1.3	1.4	1.4	1.4	YOR267C		1.0	-1.4	1.0	1.6	serine/threonine protein kinase (by homology)
CA5767	orf19.5409	*IPF1098*	1.1	1.1	-1.0	1.1	YNL265C	*IST1*	1.0	-1.1	-1.0	-1.1	unknown function
CA5768	orf19.5410	*PAC1*	1.0	1.1	1.0	1.0	YOR269W	*PAC1*	1.0	-1.2	-1.2	-1.2	Similarity to human LIS-1 protein (by homomology)
CA5769	orf19.5411	*UBC12*	-1.0	1.0	-1.1	1.1	YLR306W	*UBC12*	1.0	-1.6	-1.3	-1.5	E2 ubiquitin-conjugating enzyme (by homology)
CA5770	orf19.5412	*IPF1103*	1.0	1.1	1.0	-1.0	YKR004C	*ECM9*	1.0	-1.9	-1.7	-1.7	unknown function
CA5771	orf19.5413	*IPF1104*	-1.0	1.1	1.0	-1.0	YPL151C	*PRP46*	1.0	-1.4	-1.3	-1.2	similar to Saccharomyces cerevisiae Prp28p pre-mRNA splicing factor (b
CA5772	orf19.5416	*ESA1*	-1.0	1.0	1.0	-1.0	YOR244W	*ESA1*	1.0	-1.0	1.1	-1.1	Histone acetyltransferase (by homology)
CA5773	orf19.5417	*DOT5*	1.0	-1.0	-1.0	-1.0	YIL010W	*DOT5*	1.0	-1.1	-1.2	-1.3	Derepression of telomeric silencing (by homology)
CA5774	orf19.5418	*IPF1113*	1.0	1.0	1.1	-1.1	YIL039W		1.0	-1.9	-2.0	-1.9	unknown function
CA5775	orf19.5419	*ATP5*	1.0	-1.2	-1.3	-1.1	YDR298C	*ATP5*	1.0	-1.0	1.0	-1.7	F1F0-ATPase complex, OSCP subunit (by homology)
CA5776	orf19.5420	*RML2*	-1.1	-1.2	-1.3	-1.2	YEL050C	*RML2*	1.0	1.0	-1.3	-1.3	Ribosomal L2 protein, mitochondrial (by homology)
CA5779	orf19.5425	*IPF1121*	-1.1	-1.1	-1.1	-1.1	YKR079C		1.0	-1.3	-1.2	-1.3	unknown function
CA5780	orf19.5426	*IPF1123*	-1.0	-1.0	1.0	-1.0	YKR089C		1.0	1.1	1.2	1.2	unknown function
CA5781	orf19.5428	*IPF1126*	-1.0	1.0	1.1	-1.0	YOR079C	*ATX2*	1.0	-2.1	-2.0	-2.0	unknown function
CA5782	orf19.5429	*IPF1127*	1.0	-1.0	1.0	1.1	YOR080W	*DIA2*	1.0	-1.3	-1.3	-1.4	unknown function
CA5785	orf19.5432	*TPT1*	1.0	1.0	1.1	1.0	YOL102C	*TPT1*	1.0	-1.6	-1.7	-1.8	tRNA 2 -phosphotransferase (by homology)
CA5786	orf19.5433	*IPF1134*	-1.0	-1.0	1.0	-1.0	YDR493W		1.0	-1.4	-1.5	-1.4	unknown function
CA5787	orf19.5436	*IPF1136*	-1.1	-1.2	-1.2	-1.1	YGR128C		1.0	-1.0	-1.1	1.1	unknown function
CA5788	orf19.5437	*RHR2*	1.0	9.7	8.1	9.4	YIL053W	*RHR2*	1.0	3.6	3.5	10.6	DL-glycerol phosphatase
CA5789	orf19.5438	*IPF1143*	-1.1	1.2	1.1	1.2	YER116C	*SLX8*	1.0	-1.0	-1.0	-1.1	Probable zinc-finger protein
CA5791	orf19.5440	*RPT2*	-1.1	-1.2	-1.4	-1.1	YDL007W	*RPT2*	1.0	-1.1	1.5	1.2	26S proteasome regulatory subunit (by homology)

CA5792	orf19.5441	*IPF4195*	-1.0	-1.1	-1.1	-1.0	YIL031W	*ULP2*	1.0	-1.5	-1.3	-1.5	similar to Saccharomyces cerevisiae Ulp2p involved in ubiquitin-mediate
CA5794	orf19.5443	*IPF4191*	-1.0	-1.1	1.2	1.0	YBL098W		1.0	-1.0	1.0	1.0	unknown function
CA5795	orf19.5444	*TIM44*	-1.0	-1.1	-1.3	-1.2	YIL022W	*TIM44*	1.0	-1.3	-1.3	-1.4	mitochondrial inner membrane import receptor
CA5796	orf19.5445	*GLO3*	-1.2	-1.2	-1.4	-1.3	YER122C	*GLO3*	1.0	1.1	1.1	1.2	zinc finger protein
CA5800	orf19.5450	*IPF4175*	1.1	-1.2	-1.1	-1.1	YBR026C	*MRF1'*	1.0	1.0	-1.4	-1.6	mitochondrial respiratory function (by homology)
CA5801	orf19.5454	*DAL1*	1.0	1.1	1.1	-1.1	YIR027C	*DAL1*	1.0	-1.2	-1.3	-1.6	allantoinase
CA5802	orf19.5455	*IPF4164*	1.1	1.5	1.6	1.6	YER072W	*VTC1*	1.0	-1.1	-1.1	1.1	similar to Saccharomyces cerevisiae Vtc1p negative regulator of Cdc42p
CA5803	orf19.5457	*IPF4163*	1.1	-1.0	1.1	1.0	YKL047W		1.0	-2.0	-1.7	-1.5	unknown function
CA5804	orf19.5459	*IPF4160*	1.1	1.2	1.3	1.1	YGR178C	*PBP1*	1.0	1.3	1.4	1.0	unknown function
CA5805	orf19.5463	*IPF4153*	-1.2	1.0	1.2	-1.0	YIL068C	*SEC6*	1.0	1.2	-1.1	-1.1	similar to Saccharomyces cerevisiae Sec6p protein involved in Golgi to p
CA5806	orf19.5465	*IPF4149*	1.0	-1.1	1.0	-1.0	YKL095W	*YJU2*	1.0	-1.0	1.1	1.3	unknown function
CA5807	orf19.5466	*RPS24*	1.3	1.2	-1.1	1.1	YIL069C	*RPS24B*	1.0	1.9	1.9	2.7	ribosomal protein S24.e
CA5813	orf19.7460	*IPF2522*	1.0	-1.0	1.0	-1.0	YOL125W		1.0	-1.1	-1.2	-1.1	unknown function
CA5814	orf19.7463	*IPF2521*	-1.0	1.0	-1.0	-1.0	YCR045C		1.0	1.4	1.4	1.4	putative protease (by homology)
CA5816	orf19.7466	*ACC1*	-1.5	-3.4	-4.4	-3.6	YNR016C	*ACC1*	1.0	-3.0	-1.8	-1.6	acetyl-coenzyme-A carboxylase (by homology)
CA5817	orf19.7468	*IPF2511*	1.0	-1.0	-1.1	-1.1	YER064C		1.0	1.1	1.2	1.5	unknown function
CA5818	orf19.7469	*ARG1*	1.1	1.1	1.2	1.0	YOL058W	*ARG1*	1.0	1.4	1.7	4.4	argininosuccinate synthetase (by homology)
CA5821	orf19.7475	*PHO81*	-1.1	1.0	1.1	1.1	YGR233C	*PHO81*	1.0	-1.1	1.1	-1.1	Cyclin-dependent kinase inhibitor (by homology)
CA5822	orf19.7477	*YRB1*	-1.0	-1.1	-1.1	1.1	YDR002W	*YRB1*	1.0	1.3	1.6	2.0	GTPase-activating protein (by homology)
CA5823	orf19.7478	*COQ1*	-1.2	-1.2	-1.2	-1.1	YBR003W	*COQ1*	1.0	-1.0	-1.1	-1.4	Hexaprenyl pyrophosphate synthetase (by homology)
CA5824	orf19.7479	*NTH1*	-1.1	-1.0	1.4	1.1	YDR001C	*NTH1*	1.0	1.2	1.5	1.2	Neutral trehalase
CA5828	orf19.7483	*CRM1*	-1.7	-1.3	-1.6	-1.3	YGR218W	*CRM1*	1.0	1.0	1.2	1.2	Nuclear export factor
CA5829	orf19.7484	*ADE1*	1.1	1.0	-1.0	1.0	YAR015W	*ADE1*	1.0	1.1	-1.1	1.5	phosphoribosyl-amidoimidazole-succinocarboxamide synthetase
CA5830	orf19.7485	*MRPL9*	1.1	-1.0	-1.2	-1.0	YGR220C	*MRPL9*	1.0	-1.1	-1.3	-1.2	Mitochondrial ribosomal protein of the large subunit (by homology)
CA5831	orf19.7486	*MRPL6*	1.1	-1.0	-1.1	1.0	YHR147C	*MRPL6*	1.0	-1.2	-1.6	-1.7	ribosomal protein L6 precursor, mitochondrial (by homology)
CA5833	orf19.7488	*IMP3*	1.1	1.0	-1.0	1.0	YHR148W	*IMP3*	1.0	-1.2	-1.1	1.1	U3 small nucleolar ribonucleoprotein (by homology)
CA5834	orf19.7489	*LRG1*	-1.1	-1.2	-1.3	-1.2	YDL240W	*LRG1*	1.0	-1.2	-1.1	1.1	GTPase-activating protein of the rho/rac family (by homology)
CA5835		*IPF429*	1.1	1.0	1.1	-1.0	YGL220W		1.0	1.0	1.2	1.1	unknown function
CA5836	orf19.7490	*IPF428*	1.1	1.0	1.2	1.0	YOL137W		1.0	1.0	1.1	1.4	transport protein (by homology)
CA5837	orf19.7491	*IPF426*	1.1	-1.0	1.1	1.1	YLL002W	*REM50*	1.0	-1.4	-1.3	-1.5	unknown function
CA5838	orf19.7492	*IPF424*	-1.1	-1.1	-1.1	-1.1	YGR002C		1.0	-1.9	-2.0	-2.0	unknown function
CA5839	orf19.7494	*IPF423*	1.0	1.0	-1.0	-1.0	YLR320W		1.0	-1.3	1.0	1.1	unknown function
CA5841	orf19.7497	*IPF420*	-1.0	-1.1	-1.1	-1.0	YGR003W		1.0	-1.3	-1.3	-2.1	unknown function
CA5842	orf19.7498	*LEU1*	-1.6	-1.0	-1.2	-1.1	YGL009C	*LEU1*	1.0	1.2	2.4	2.4	3-isopropylmalate dehydratase (by homology)
CA5843	orf19.7499	*IPF416*	-1.1	1.2	1.3	1.1	YLR328W		1.0	-1.1	1.1	1.1	unknown function
CA5844	orf19.7500	*PXA1*	-1.1	-1.4	-1.4	-1.2	YPL147W	*PXA1*	1.0	-1.1	-1.4	-1.7	long chain fatty acid ABC transporter (by homology)
CA5845	orf19.7501	*NAP1*	1.1	1.1	1.0	1.0	YKR048C	*NAP1*	1.0	1.0	1.2	1.5	nucleosome assembly protein (by homology)
CA5847	orf19.7503	*CDA2*	-1.0	1.0	-1.0	1.0	YLR308W	*CDA2*	1.0	-1.4	-1.1	-1.1	chitin deacetylase (by homology)
CA5848	orf19.7504	*IPF407*	-1.1	-3.2	-4.3	-3.0	YGR161C		1.0	-1.5	-1.3	-1.1	unknown function
CA5851	orf19.7510	*KIN2*	1.0	1.1	1.0	1.0	YLR096W	*KIN2*	1.0	-1.2	-1.2	1.0	ser/thr protein kinase (by homology)
CA5852		*ATP17.3*	1.2	1.1	1.1	1.0	YDR377W	*ATP17*	1.0	-1.1	-1.1	-2.1	F1F0-ATPase complex, F1 delta subunit f, 3-prime end (by homology)
CA5853		*LSM6*	1.1	1.1	1.2	1.1	YDR378C	*LSM6*	1.0	-1.1	-1.1	-1.1	U6 snRNA-associated Sm-like protein (by homology)
CA5854	orf19.7511	*IPF393*	1.1	1.2	1.2	1.1	YJL039C	*NUP192*	1.0	-1.1	-1.1	-1.2	similar to Saccharomyces cerevisiae Nup192p nucleoporin (by homology
CA5857	orf19.7514	*PCK1*	1.3	-11.5	-12.0	-19.3	YKR097W	*PCK1*	1.0	-8.0	-4.8	-6.0	phosphoenolpyruvate carboxykinase
CA5862	orf19.7520	*POT11*	-1.2	-8.2	-10.0	-8.1	YIL160C	*POT1*	1.0	1.2	-1.2	-1.5	peroxysomal 3-ketoacyl-CoA thiolase A (by homology)
CA5865	orf19.7523	*MKC1*	-1.1	-1.2	-1.2	-1.1	YHR030C	*SLT2*	1.0	-1.3	1.0	1.2	ser/thr protein kinase of MAP kinase family
CA5867	orf19.7529	*EPL1*	1.0	-1.0	-1.0	-1.0	YFL024C	*EPL1*	1.0	-1.1	-1.4	-1.5	DNA-binding protein (by homology)
CA5868	orf19.7531	*IPF351*	1.1	1.2	1.2	1.1	YMR090W		1.0	-1.6	-1.3	-2.1	unknown function
CA5871	orf19.7538	*PIF2*	1.0	1.1	1.4	1.0	YHR031C	*RRM3*	1.0	-1.2	-1.1	-1.2	DNA helicase (by homology)
CA5876	orf19.6833	*IPF12082.5F*	-1.1	1.1	-1.3	-1.0	YBR235W		1.0	-1.5	-1.4	-1.4	bumetanide-sensitive Na-K-Cl cotransport protein, 5-prime end (by homo
CA5878	orf19.6831	*PRP5*	-1.1	-1.1	-1.2	-1.1	YBR237W	*PRP5*	1.0	-1.2	-1.4	-1.3	pre-mRNA processing RNA-helicase (by homology)
CA5880	orf19.6829	*IPF12074*	-1.0	-1.1	-1.1	-1.0	YMR282C	*AEP2*	1.0	-1.4	-1.4	-1.6	unknown function
CA5881		*SSS1*	1.0	1.0	1.0	-1.0	YDR086C	*SSS1*	1.0	1.0	-1.2	-1.5	ER protein-translocase complex subunit (by homology)
CA5882	orf19.6828	*RRP1*	-1.0	-1.1	-1.1	1.0	YDR087C	*RRP1*	1.0	1.3	1.6	1.8	Involved in processing rRNA precursor species to mature rRNAs (by hom
CA5883	orf19.6827	*IPF2425*	1.0	-1.0	-1.0	-1.0	YDR088C	*SLU7*	1.0	-1.1	-1.1	-1.4	unknown function
CA5884	orf19.6826	*SLF1*	-1.0	-1.0	-1.1	-1.0	YDR515W	*SLF1*	1.0	-1.1	-1.2	1.1	Copper homeostasis protein (by homology)
CA5886	orf19.6822	*IPF2417*	1.1	1.1	1.2	1.1	YLR128W		1.0	1.0	1.1	1.1	unknown function
CA5887	orf19.6821	*IPF2415*	-1.0	1.0	-1.1	-1.1	YLR127C	*APC2*	1.0	-1.3	-1.1	1.1	similar to Saccharomyces cerevisiae Apc2p component of the anaphase
CA5889	orf19.6818	*IPF2409*	-1.1	-1.4	-1.7	-1.4	YLR419W		1.0	-1.4	-1.4	-1.8	RNA-dependent ATPase (by homology)
CA5891	orf19.6816	*IPF2400*	-1.0	1.2	1.2	1.2	YJR096W		1.0	-1.2	-1.5	-1.6	putative aldehyde reductase (by homology)
CA5892	orf19.6814	*GAP1*	1.1	1.9	2.1	2.1	YGR192C	*TDH3*	1.0	-1.1	1.4	1.9	Glyceraldehyde-3-phosphate dehydrogenase

CA5894	orf19.6812	*PMT2*	1.2	1.6	1.7	1.7	YAL023C	*PMT2*	1.0	-1.4	-1.2	1.1	O-D-mannosyltransferase (by homology)
CA5895	orf19.6811	*ISA2*	1.1	1.1	1.1	1.0	YPR067W	*ISA2*	1.0	-1.6	-1.4	-1.4	Mitochondrial protein required for iron metabolism (by homology)
CA5896	orf19.6810	*TPD3*	-1.3	-1.1	-1.2	-1.0	YAL016W	*TPD3*	1.0	-1.3	-1.3	-1.0	Ser/thr protein phosphatase (by homology)
CA5897	orf19.6809	*IPF2384*	1.0	1.3	1.4	1.2	YKL128C	*PMU1*	1.0	-2.2	-2.2	-1.7	unknown function
CA5901	orf19.6805	*IPF2374*	1.0	1.0	-1.0	1.0	YDR089W		1.0	1.1	-1.1	-1.1	unknown function
CA5902	orf19.6804	*SRP68*	-1.4	-1.6	-1.8	-1.3	YPL243W	*SRP68*	1.0	1.0	1.3	1.3	SIGNAL RECOGNITION PARTICLE 68 (by homology)
CA5903	orf19.6803	*IPF5942*	1.1	1.1	1.1	1.0	YPL244C	*HUT1*	1.0	1.1	1.3	1.3	transmembrane sugar transporter (by homology)
CA5904	orf19.6802	*IPF5944*	1.1	1.1	1.5	1.2	YNL326C		1.0	-1.0	1.1	1.1	Unknown function
CA5905	orf19.6801	*RPD32*	-1.3	-1.0	-1.1	-1.0	YNL330C	*RPD3*	1.0	-1.1	-1.1	-1.2	histone deacetylase B (by homology)
CA5906	orf19.6800	*IPF5949*	-1.0	1.0	1.1	1.1	YPL188W	*POS5*	1.0	-1.1	-1.0	1.2	unknown function
CA5907	orf19.6798	*SSN6*	-1.1	1.0	-1.3	-1.1	YBR112C	*CYC8*	1.0	-1.1	-1.1	-1.2	transcriptional repressor (by homology)
CA5909	orf19.6796	*YSA1*	1.1	1.0	1.1	1.0	YBR111C	*YSA1*	1.0	1.2	1.4	-1.0	sugar-nucleotide hydrolase (by homology)
CA5913	orf19.6792	*RRD1*	-1.0	1.0	-1.0	1.0	YIL153W	*RRD1*	1.0	1.1	1.3	1.3	Phosphotyrosyl phosphatase activator involved in cell cycle progression
CA5915	orf19.6790	*IPF10735*	1.1	1.0	1.1	-1.1	YBR212W	*NGR1*	1.0	-1.1	-1.3	-1.3	similar to Saccharomyces cerevisiae Ngr1p negative growth regulatory R
CA5916	orf19.6789	*IPF19818*	-1.0	-1.0	-1.0	-1.0	YOR373W	*NUD1*	1.0	-1.2	-1.4	-1.5	similar to Saccharomyces cerevisiae Nud1p cell cycle regulatory protein
CA5918	orf19.6787	*ERV14*	1.3	1.2	1.5	1.2	YGL054C	*ERV14*	1.0	-1.8	1.2	1.1	membrane protein
CA5920	orf19.6785	*RPS12*	1.4	1.1	1.3	1.4	YOR369C	*RPS12*	1.0	2.5	3.6	3.4	acidic ribosomal protein S12 (by homology)
CA5922	orf19.6783	*MRS6*	-1.2	-1.3	-1.5	-1.1	YOR370C	*MRS6*	1.0	1.1	1.5	1.3	geranylgeranyltransferase regulatory subunit
CA5925	orf19.6780	*MET8*	-1.1	-1.3	-1.2	-1.1	YBR213W	*MET8*	1.0	-1.1	1.0	-1.1	Siroheme synthase (by homology)
CA5926	orf19.6779	*PRO2*	-1.1	-1.1	-1.1	-1.1	YOR323C	*PRO2*	1.0	1.2	1.4	1.7	Proline biosynthetic enzyme (by homology)
CA5927	orf19.6778	*DRS22*	-1.1	1.0	1.1	1.0	YAL026C	*DRS2*	1.0	-1.0	1.1	1.4	Membrane-spanning Ca-ATPase (by homology)
CA5929	orf19.6776	*GCD2*	-1.2	-1.1	-1.3	-1.1	YGR083C	*GCD2*	1.0	1.1	1.2	1.2	Translation initiation factor eIF2B, 71 kDa (delta) subunit (by homology)
CA5930	orf19.6773	*CM29.EXON*	-1.6	1.3	-1.5	-1.2	YHL030W	*ECM29*	1.0	-1.3	-1.4	-1.2	Involved in cell wall biogenesis and architecture, exon 2 (by homology)
CA5932	orf19.6771	*UBI4*	1.0	1.0	-1.0	1.0	YLL039C	*UBI4*	1.0	1.7	1.8	1.5	Polyubiquitin
CA5933	orf19.6770	*IPF2804*	-1.0	1.2	1.4	1.1	YLL038C	*ENT4*	1.0	1.1	1.1	-1.0	unknown function
CA5934	orf19.6769	*IPF2802*	-1.1	-1.2	-1.2	-1.1	YHL029C		1.0	-1.3	-1.2	-1.1	unknown function
CA5935	orf19.6766	*IPF2798*	1.0	-1.1	-1.1	-1.0	YNL175C	*NOP13*	1.0	1.0	1.4	1.6	unknown function
CA5937	orf19.6760	*IPF2784*	-1.2	-1.2	-2.0	-1.4	YER132C	*PMD1*	1.0	-1.3	1.0	1.2	unknown function
CA5940	orf19.6757	*IPF3485*	1.0	-1.2	-1.3	-1.0	YOR120W	*GCY1*	1.0	1.0	-1.1	-1.5	aldo/keto reductase (by homology)
CA5941	orf19.6756	*IPF3486*	1.2	1.3	1.9	1.4	YGL198W		1.0	1.3	1.1	1.4	unknown function
CA5942	orf19.6755	*DLD2*	1.0	1.2	1.3	1.1	YDL174C	*DLD1*	1.0	-2.0	-2.6	-2.0	D-lactate ferrycytochrome C oxidoreductase (by homology)
CA5944	orf19.6753	*IPF3491*	1.1	1.0	1.0	1.0	YBR062C		1.0	-1.1	1.1	1.2	unknown function
CA5945	orf19.6752	*IPF3492*	-1.0	-1.0	-1.1	-1.0	YDR041W	*RSM10*	1.0	-1.5	-1.1	-1.1	unknown function
CA5946	orf19.6751	*IPF3493*	-1.0	-1.0	-1.0	-1.1	YBR061C		1.0	1.1	1.2	1.5	unknown function
CA5947	orf19.6749	*KRS1*	-1.4	-1.2	-1.4	-1.4	YDR037W	*KRS1*	1.0	1.4	1.6	3.8	Lysyl-tRNA synthetase (by homology)
CA5949	orf19.6747	*IPF3498*	1.1	1.1	1.2	1.3	YDR051C		1.0	1.1	1.2	1.6	unknown function
CA5950	orf19.6745	*TPI1*	1.1	2.2	2.3	2.2	YDR050C	*TPI1*	1.0	1.8	2.3	3.7	Triose phosphate isomerase
CA5951	orf19.6744	*IPF3500*	1.1	1.2	1.3	1.2	YMR262W		1.0	-1.3	1.0	1.1	unknown function
CA5952	orf19.6742	*IPF3503*	1.1	-1.0	1.0	-1.0	YMR277W	*FCP1*	1.0	-1.3	1.1	-1.2	similar to Saccharomyces cerevisiae Fcp1p TFIIF interacting component
CA5954	orf19.6740	*IPF3508*	-1.0	1.2	1.2	1.1	YLL036C	*PRP19*	1.0	-1.6	-1.6	-1.2	unknown function
CA5955	orf19.6739	*IPF3510*	-1.2	-1.3	-1.7	-1.5	YMR278W		1.0	-1.1	-1.0	-1.1	unknown function
CA5956	orf19.6738	*VAN1*	-1.2	-1.1	-1.1	-1.1	YML115C	*VAN1*	1.0	1.1	1.4	1.4	Vanadate resistance protein
CA5957	orf19.7546	*RRP3.3EOC*	-1.2	-1.3	-1.3	-1.2	YHR065C	*RRP3*	1.0	-1.2	1.2	1.1	RNA-dependent ATPase, helicase,required for maturation of 35S primary
CA5958	orf19.7547	*PIB1*	-1.1	1.0	-1.0	-1.0	YDR313C	*PIB1*	1.0	1.0	1.1	1.1	phosphatidylinositol(3)-phosphate binding protein (by homology)
CA5959	orf19.7548	*SRB7*	1.1	-1.1	-1.0	-1.1	YDR308C	*SRB7*	1.0	-1.5	-1.8	-1.5	DNA-directed RNA polymerase II holoenzyme and kornberg s mediator
CA5962	orf19.7551	*ALO1*	-1.2	1.1	1.3	1.2	YML086C	*ALO1*					D-arabinono-1,4-lactone oxidase (by homology)
CA5963	orf19.7552	*IPF966*	-1.1	-1.2	-1.3	-1.2	YML093W		1.0	-1.2	-1.1	-1.0	unknown function
CA5967	orf19.7558	*IPF955*	-1.0	-1.0	-1.1	-1.2	YER047C	*SAP1*	1.0	-1.2	-1.2	1.3	member of the AAA ATPase family of proteins (by homology)
CA5969	orf19.7563	*BET2*	1.0	1.0	-1.0	-1.1	YPR176C	*BET2*	1.0	1.3	1.3	1.3	beta subunit of geranylgeranyl transferase type2
CA5970	orf19.7564	*DPB2*	-1.0	-1.0	-1.1	-1.0	YPR175W	*DPB2*	1.0	1.0	1.2	1.2	DNA-directed DNA polymerase epsilon, subunit B (by homology)
CA5973	orf19.7567	*IPF931*	1.1	1.1	1.0	1.0	YDR124W		1.0	-1.0	-1.1	-1.2	unknown function
CA5974	orf19.7568	*IPF930*	-1.0	1.0	1.1	1.1	YOR313C	*SPS4*	1.0	-1.1	-1.1	-1.0	unknown function
CA5975	orf19.7569	*SIK1*	1.1	1.1	1.1	1.0	YLR197W	*SIK1*	1.0	1.7	2.3	2.6	nucleolar protein involved in pre-rRNA processing (by homology)
CA5976	orf19.7570	*IPF928*	-1.0	1.1	1.1	-1.0	YDL170W	*UGA3*	1.0	1.0	1.1	1.3	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster doma
CA5977	orf19.7571	*UBC4.3*	1.3	1.1	1.1	1.1	YBR082C	*UBC4*	1.0	1.1	1.7	1.7	E2 ubiquitin-conjugating enzyme, 3-prime end
CA5978	orf19.7572	*SPT7*	-1.1	-1.1	-1.3	-1.0	YBR081C	*SPT7*	1.0	-1.6	-1.5	-1.2	transcription factor, member of the histone acetyltransferase SAGA comp
CA5981	orf19.7577	*MSS51*	-1.1	-1.1	-1.1	-1.1	YLR203C	*MSS51*	1.0	-1.1	-1.3	-1.5	involved in maturation of COX1 and COB mRNA (by homology)
CA5982	orf19.7578	*IPF915*	1.0	1.1	-1.0	1.1	YDR057W		1.0	-1.3	-1.2	-1.2	unknown function
CA5984	orf19.7581	*CUS1*	-1.1	1.0	1.0	1.1	YMR240C	*CUS1*	1.0	-1.3	-1.3	-1.2	spliceosome associated protein (by homology)
CA5986	orf19.7585	*INO1*	1.0	1.5	2.1	1.3	YJL153C	*INO1*	1.0	-1.6	-1.7	-1.6	myo-inositol-1-phosphate synthase
CA5987	orf19.7586	*CHT3*	1.3	1.2	1.3	1.1	YLR286C	*CTS1*	1.0	1.3	2.3	1.9	chitinase 3 precursor

CA5988	orf19.7588	*IPF693*	1.1	1.1	1.0	-1.0	YOR305W		1.0	1.2	1.2	1.3	unknown function
CA5992	orf19.7592	*FAA4*	-1.1	-2.2	-2.5	-2.3	YMR246W	*FAA4*	1.0	1.1	1.4	2.0	long-chain fatty acid--CoA ligase and synthetase 4 (by homology)
CA5993	orf19.7593	*ASP1*	-1.3	-2.5	-2.7	-2.5	YDR321W	*ASP1*	1.0	-1.4	-1.1	1.2	L-asparaginase (by homology)
CA5998	orf19.7598	*IPF670*	1.1	1.0	1.0	-1.0	YOR023C	*AHC1*	1.0	-1.0	1.0	1.1	unknown function
CA5999	orf19.7599	*IPF668*	1.0	-1.0	1.0	1.0	YDR398W		1.0	-1.9	-1.8	-1.4	unknown function
CA6000	orf19.7600	*FDH11.3*	1.0	1.9	1.8	2.0	YDL168W	*SFA1*	1.0	1.3	1.5	1.5	glutathione-dependent formaldehyde dehydrogenase, 3-prime end (by ho
CA6001	orf19.7601	*IPF662*	1.0	1.0	-1.1	1.0	YGL136C		1.0	1.0	1.1	1.0	unknown function
CA6002	orf19.7602	*IPF661*	1.1	1.3	1.2	1.2	YDR214W		1.0	-1.3	-1.4	-1.5	unknown function
CA6005	orf19.7605	*PUP1*	1.1	1.3	1.4	1.1	YOR157C	*PUP1*	1.0	1.1	1.4	1.3	20S proteasom ebeta2 subunit (by homology)
CA6009	orf19.7610	*IPF643*	-1.1	-1.5	-1.9	-1.5	YER075C	*PTP3*	1.0	1.0	1.0	1.1	similar to Saccharomyces cerevisiae Ptp3p protein tyrosine phosphatase
CA6010	orf19.7611	*TRX1*	1.5	1.5	1.8	1.7	YLR043C	*TRX1*	1.0	1.3	1.1	-1.1	thioredoxin (by homology)
CA6011	orf19.7612	*CTM1*	-1.0	1.4	2.0	1.4	YHR109W	*CTM1*	1.0	-2.3	-1.6	-1.6	cytochrome c methyltransferase (by homology)
CA6012	orf19.7613	*HCR1*	-1.0	1.0	-1.2	-1.0	YLR192C	*HCR1*	1.0	-1.2	-1.0	1.1	putative translation initiation factor 3 subunit (by homology)
CA6014	orf19.7615	*TRS31*	1.0	-1.1	1.0	-1.0	YDR472W	*TRS31*	1.0	-1.4	-1.6	-1.3	targeting complex (TRAPP) component involved in ER to Golgi membran
CA6015	orf19.7617	*ARD1*	1.1	-1.0	-1.0	1.0	YHR013C	*ARD1*	1.0	1.0	-1.0	-1.0	protein N-acetyltransferase subunit (by homology)
CA6016	orf19.7618	*IPF630*	1.1	1.0	-1.1	1.0	YOR145C		1.0	1.1	1.4	1.8	unknown function
CA6018	orf19.7620	*IPF627*	1.1	1.0	-1.0	1.0	YOR148C	*SPP2*	1.0	1.0	1.1	-1.0	unknown function
CA6019	orf19.7621	*IPF625*	1.0	-1.0	-1.0	-1.0	YOR144C	*EFD1*	1.0	-1.1	-1.1	-1.1	unknown function
CA6020	orf19.7622	*SPT3*	-1.0	-1.0	1.0	1.0	YDR392W	*SPT3*	1.0	-1.1	-1.1	1.0	transcription factor
CA6021	orf19.7624	*BFR2*	1.0	-1.1	-1.1	-1.1	YDR299W	*BFR2*	1.0	-1.1	-1.0	1.1	involved in protein transport steps at the Brefeldin A block (by homology)
CA6023	orf19.7626	*CDC33*	1.1	1.0	1.1	1.0	YOL139C	*CDC33*	1.0	1.3	1.6	1.7	translation initiation factor eIF4E, cap binding protein
CA6024	orf19.7627	*IPF615*	-1.2	-1.1	-1.0	-1.0	YNL320W		1.0	-1.0	1.0	1.1	unknown function
CA6025	orf19.7629	*IPF614*	-1.0	-1.1	-1.0	-1.1	YOL138C		1.0	-1.1	-1.0	1.0	unknown function
CA6026	orf19.7631	*IPF610*	-1.0	1.0	-1.0	-1.0	YDR489W		1.0	1.6	2.1	2.7	unknown function
CA6028	orf19.7634	*IPF607*	-1.0	1.0	-1.1	1.0	YDL003W	*MCD1*	1.0	1.0	1.2	1.3	unknown function
CA6029	orf19.7635	*DRS1*	-1.0	-1.4	-1.9	-1.6	YLL008W	*DRS1*	1.0	-1.2	1.1	1.2	ATP dependent RNA helicase (by homology)
CA6031	orf19.7638	*PRO1*	1.0	-1.1	-1.0	-1.0	YDR300C	*PRO1*	1.0	-1.4	1.1	1.3	glutamate 5-kinase (by homology)
CA6032	orf19.7642	*IPF596*	-1.1	1.0	1.0	-1.1	YDR495C	*VPS3*	1.0	-1.3	-1.4	-1.2	similar to Saccharomyces cerevisiae Vps3p vacuolar sorting protein
CA6033	orf19.7643	*COQ2*	1.2	1.2	1.6	1.3	YNR041C	*COQ2*	1.0	1.0	-1.1	-1.1	para-hydroxybenzoate:polyprenyl transferase (by homology)
CA6034	orf19.7644	*APC11*	-1.2	-1.1	1.1	-1.0	YDL008W	*APC11*	1.0	-1.3	-1.2	-1.1	subunit of the anaphase promoting complex (by homology)
CA6035	orf19.7645	*BPL1*	-1.1	1.0	1.0	-1.0	YDL141W	*BPL1*	1.0	-1.5	-1.1	-1.1	biotin holocarboxylase synthetase (by homology)
CA6036	orf19.7646	*IPF585*	1.1	-1.0	1.0	1.1	YHR034C		1.0	-1.8	-1.7	-1.6	unknown function
CA6038	orf19.7650	*LTV1*	1.0	-1.1	-1.1	-1.1	YKL143W	*LTV1*	1.0	1.3	1.7	2.0	low-temperature viability protein (by homology)
CA6039	orf19.7652	*CKA1*	-1.1	1.0	-1.0	1.0	YIL035C	*CKA1*	1.0	-1.1	1.0	1.2	casein kinase II, catalytic alpha chain (by homology)
CA6040	orf19.7654	*CPR6*	-1.2	1.1	-1.3	-1.1	YLR216C	*CPR6*	1.0	-1.2	1.1	-1.1	cyclophylin (by homology)
CA6041	orf19.7655	*RPO21*	1.0	-1.0	-1.0	1.1	YDL140C	*RPO21*	1.0	-1.8	-1.7	-1.4	DNA-directed RNA polymerase II, 215 KD subunit (by homology)
CA6042	orf19.7657	*IPF4924*	1.0	1.0	-1.0	-1.1	YNL282W	*POP3*	1.0	-1.1	1.1	1.2	unknown function
CA6043	orf19.7658	*RFC4*	1.1	1.1	1.0	-1.0	YOL094C	*RFC4*	1.0	1.2	1.2	1.3	DNA replication factor C (by homology)
CA6044	orf19.7660	*IPF4928*	-1.0	-1.1	-1.1	-1.0	YDR484W	*SAC2*	1.0	-1.6	-1.4	-1.4	similar to Saccharomyces cerevisiae Sac2p suppressor of actin mutation
CA6045	orf19.7661	*IPF4929*	-1.1	-1.0	-1.0	-1.1	YOL095C	*HMI1*	1.0	1.0	1.2	1.4	similar to Saccharomyces cerevisiae Hmi1p mitochondrial DNA helicase
CA6046	orf19.7662	*IPF4931*	1.0	1.0	-1.1	-1.2	YDR289C	*RTT103*	1.0	-1.0	1.0	1.0	unknown function
CA6047	orf19.7663	*IPF4933*	1.0	-1.1	-1.0	1.0	YCR086W	*CSM1*	1.0	1.1	-1.1	-1.0	unknown function
CA6049	orf19.7665	*IPF4935*	1.0	1.1	-1.0	-1.0	YJL003W		1.0	1.0	1.1	1.0	unknown function
CA6051	orf19.7667	*IPF4940*	1.0	1.0	-1.0	-1.0	YOR126C	*IAH1*	1.0	-1.4	-1.2	-1.4	unknown function
CA6052	orf19.7668	*IPF4942*	-1.2	-1.5	-1.5	-1.3	YBR299W	*MAL32*	1.0	-1.1	1.1	-1.2	similar to Saccharomyces cerevisiae Mal32p alpha-glucosidase (by homo
CA6053	orf19.7670	*IPF4949*	1.0	-1.0	-1.0	-1.1	YNL321W		1.0	-1.2	-1.3	-1.1	unknown function
CA6054	orf19.7672	*IPF4952*	1.0	-1.0	1.1	-1.0	YDR411C		1.0	-1.3	1.1	-1.2	unknown function
CA6056	orf19.7675	*IPF4955*	1.1	-1.0	1.1	-1.0	YGR076C	*MRPL25*	1.0	-3.0	-5.8	-4.0	similar to Saccharomyces cerevisiae Mrpl25p ribosomal protein YmL25,
CA6057	orf19.7676	*IPF4959*	1.3	2.0	2.8	1.8	YDL246C		1.0	-1.1	-1.1	-1.4	D-xylulose reductase (by homology)
CA6058	orf19.7678	*ATP16*	1.0	-1.0	1.0	-1.0	YDL004W	*ATP16*	1.0	1.2	1.0	-1.5	F1F0-ATPase complex, F1 delta subunit
CA6060	orf19.6008	*IPF8301*	-1.3	-1.3	-1.4	-1.4	YLL032C		1.0	-1.3	-1.4	-1.4	unknown function
CA6063	orf19.6003	*IPF8311*	-1.1	-1.1	-1.1	-1.0	YLR094C	*GIS3*	1.0	-1.5	-1.3	-1.1	unknown function
CA6064	orf19.6002	*RPL81*	1.2	1.0	-1.0	1.0	YLL045C	*RPL8B*	1.0	1.7	2.4	3.1	60S ribosomal protein L7a.e.B (by homology)
CA6066	orf19.6000	*CDR1*	-1.1	2.0	1.6	2.0	YOR153W	*PDR5*	1.0	-1.2	1.6	1.5	multidrug resistance protein (by homology)
CA6067	orf19.5999	*DYN1*	-1.0	1.2	1.2	1.0	YKR054C	*DYN1*	1.0	-1.1	-1.3	-1.3	dynein heavy chain, cytosolic (by homology)
CA6068		*RPS19A.3*	1.4	1.1	-1.0	1.1	YOL121C	*RPS19A*	1.0	1.9	1.9	2.7	ribosomal protein S19.e, 3-prime end (by homology)
CA6069	orf19.5995	*IPF4847*	-1.0	1.1	1.1	-1.0	YOR197W		1.0	1.1	1.3	1.6	unknown function
CA6070	orf19.5994	*IPF4842*	1.1	1.2	1.6	1.2	YCR027C	*RSG1*	1.0	-3.1	-2.5	-1.7	similar to Saccharomyces cerevisiae Rsg1p ras-related GTP-binding prot
CA6072	orf19.5991	*DBP10*	-1.3	-1.5	-2.1	-1.6	YDL031W	*DBP10*	1.0	1.1	1.3	1.8	Putative ATP-dependent RNA helicase (by homology)
CA6073	orf19.5989	*HRP1*	1.1	1.0	1.1	1.0	YOL123W	*HRP1*	1.0	1.2	1.5	1.4	Nuclear polyadenylated RNA-binding protein (by homology)
CA6074	orf19.5987	*IPF11*	1.0	-1.0	-1.0	1.0	YOL124C		1.0	-1.1	-1.1	-1.0	unknown function

CA6075	orf19.5986	*THI4*	-1.0	1.0	1.0	-1.1	YGR144W	*THI4*	1.0	1.1	1.0	1.3	Thiazole biosynthetic enzyme precursor (by homology)
CA6076	orf19.5985	*PAC10.3*	1.1	1.0	-1.1	-1.0	YGR078C	*PAC10*	1.0	-1.9	-1.1	1.1	Non-native Actin Binding Complex Component, 3-prime end (by homolog
CA6077	orf19.5984	*IPF16*	-1.0	-1.1	-1.0	1.0	YOL073C		1.0	1.0	-1.0	1.1	unknown function
CA6079	orf19.5982	*RPL18.EXON2*	-1.0	1.1	1.1	1.1	YOL120C	*RPL18A*	1.0	-1.5	-1.5	-1.2	Ribosomal Protein RPL18B (large subunit), exon 2 (by homology)
CA6082	orf19.5977	*CEM1*	-1.1	-1.1	-1.2	-1.0	YER061C	*CEM1*	1.0	-1.6	1.0	1.4	3-oxoacyl-[acyl-carrier-protein]-synthase (by homology)
CA6083	orf19.5976	*IPF26*	1.0	-1.0	1.0	1.1	YPR152C		1.0	-1.3	-1.1	-1.2	unknown function
CA6085	orf19.5974	*IPF32*	-1.0	1.0	-1.2	-1.1	YDL149W	*APG9*	1.0	-1.6	-1.4	-1.5	similar to Saccharomyces cerevisiae Apg9p integral membrane protein re
CA6086	orf19.5973	*PHB2*	-1.0	-1.2	-1.3	1.0	YGR231C	*PHB2*	1.0	1.2	1.1	-1.0	Mitochondrial protein, prohibitin homolog (by homology)
CA6087	orf19.5971	*YHV1*	-1.0	-1.1	-1.1	-1.0	YHR151C		1.0	-1.0	-1.1	-1.1	unknown function
CA6088	orf19.5970	*HPR5*	-1.2	-1.1	-1.2	-1.1	YJL092W	*HPR5*	1.0	-1.7	-1.7	-1.8	ATP-dependent DNA Helicase (by homology)
CA6089	orf19.5968	*RDI1*	1.2	-1.0	-1.0	1.1	YDL135C	*RDI1*	1.0	-1.7	-1.4	-1.6	Rho GDP dissociation inhibitor (by homology)
CA6090	orf19.5967	*IPF44*	-1.2	-1.2	-1.2	-1.2	YDL189W		1.0	-1.3	-1.1	-1.1	unknown function
CA6091	orf19.5965	*UFD2*	-1.4	1.0	1.0	1.0	YDL190C	*UFD2*	1.0	-1.0	1.0	1.2	Ubiquitin fusion degradation protein 2 (by homology)
CA6092		*RPL35.3*	1.6	1.2	1.7	1.5	YDL191W	*RPL35A*	1.0	2.3	2.6	3.6	Ribosomal protein L35A, 3-prime end (by homology)
CA6093	orf19.5964	*ARF22*	-1.0	1.0	1.0	1.1	YDL137W	*ARF2*	1.0	-1.3	1.2	-1.2	GTP-binding protein of the ARF family (by homology)
CA6094	orf19.5963	*IPF53*	1.0	-1.1	1.0	-1.0	YDL193W		1.0	1.1	1.0	1.1	unknown function
CA6095	orf19.5962	*SNF3*	1.0	-1.7	-2.0	-1.6	YDL194W	*SNF3*	1.0	-1.2	-1.1	-1.2	High affinity glucose transport protein (by homology)
CA6096	orf19.5961	*IPF56*	1.0	1.0	-1.1	1.0	YGR232W	*NAS6*	1.0	1.1	-1.3	-1.2	similar to Saccharomyces cerevisiae Nas6p subunit of 26S proteasome (
CA6097	orf19.5960	*NCE102*	1.3	1.3	1.5	1.3	YPR149W	*NCE102*	1.0	1.3	1.0	-1.6	secretion of proteins that lack classical secretory signal sequence (by ho
CA6098	orf19.5959	*IPF61*	-1.0	-1.2	-1.1	-1.0	YDL148C	*NOP14*	1.0	-1.4	-1.4	1.1	unknown function
CA6100	orf19.5956	*IPF66*	1.1	1.2	-1.0	-1.0	YPR154W	*PIN3*	1.0	-1.3	-1.0	-1.0	unknown function
CA6102	orf19.5954	*SPO70.5F*	-1.0	-1.0	1.1	1.1	YGR225W	*AMA1*	1.0	-2.4	-1.6	-1.1	involved in meiosis and sporulation, 5-prime end
CA6103	orf19.5953	*SFP1*	-1.0	1.3	1.4	1.2	YLR403W	*SFP1*	1.0	1.1	1.3	1.5	zinc finger protein (by homology)
CA6107	orf19.5949	*FAS2.3F*	1.6	-1.2	-1.2	-2.1	YPL231W	*FAS2*	1.0	-2.3	-1.6	-1.3	fatty-acyl-CoA synthase, alpha chain, 3-prime end
CA6108	orf19.5947	*SEC7*	-1.3	1.1	-1.3	-1.1	YDR170C	*SEC7*	1.0	-1.3	-1.6	-1.3	Guanine nucleotide exchange protein for ADP-robosylation factor (by ho
CA6109		*IPF89.3*	1.1	-1.1	-1.3	-1.1	YLR150W	*STM1*	1.0	1.9	2.8	3.2	unknown function, 3-prime end
CA6110	orf19.5943	*IPF91*	1.0	-1.1	-1.2	-1.1	YHR150W		1.0	1.1	1.7	2.4	unknown function
CA6111	orf19.5942	*IPF96*	-1.0	-1.0	-1.0	1.0	YML068W		1.0	1.0	1.1	-1.1	C3HC4 type zinc finger protein (by homology)
CA6112	orf19.5941	*IPF97*	1.0	1.2	1.3	1.1	YML067C	*ERV41*					unknown function
CA6114	orf19.5938	*SEN1*	-1.0	-1.0	-1.2	-1.0	YLR430W	*SEN1*	1.0	-1.3	-1.4	-1.4	positive effector of tRNA-splicing endonuclease (by homology)
CA6116	orf19.5934	*TOP3*	-1.0	-1.0	-1.1	-1.0	YLR234W	*TOP3*	1.0	-1.4	-1.4	-1.4	DNA topoisomerase III (by homology)
CA6118	orf19.5932	*IPF126*	1.1	1.1	1.3	1.1	YLR241W		1.0	-1.0	1.0	1.3	unknown function
CA6119	orf19.5931	*ARV1*	-1.0	1.0	1.0	-1.0	YLR242C	*ARV1*	1.0	1.4	1.3	1.1	involved in sterol uptake and distribution into the plasma membrane
CA6122	orf19.5928	*RPP2B*	1.1	1.1	1.2	1.1	YDR382W	*RPP2B*	1.0	2.5	3.2	3.1	acidic ribosomal protein (by homology)
CA6123	orf19.5927	*RPS15.3*	1.0	-1.2	-1.2	-1.0	YOL040C	*RPS15*	1.0	1.9	2.1	2.8	40S ribosomal protein S15, 3-prime end (by homology)
CA6124	orf19.5926	*ARG11*	1.1	1.0	-1.0	1.1	YOR130C	*ORT1*	1.0	1.1	1.2	1.6	mitochondrial amino acid transporter (by homology)
CA6125	orf19.5925	*IPF138*	-1.2	-1.1	-1.0	-1.1	YDL237W		1.0	-1.2	1.1	1.0	unknown function
CA6128	orf19.5919	*IPF152*	-1.2	-1.3	-1.5	-1.3	YOR129C		1.0	-1.0	-1.0	-1.1	unknown function
CA6129		*YRA1.EXON2*	1.1	1.6	1.7	1.7	YDR381W	*YRA1*	1.0	1.7	2.0	1.8	RNA annealing protein, exon 2 (by homology)
CA6134	orf19.5912	*MAK21*	-1.1	-1.2	-1.2	-1.1	YDR060W		1.0	-1.4	-1.4	-1.4	Ribosome biogenesis protein (by homology)
CA6137	orf19.5910	*IPF4356*	-1.0	1.0	-1.1	-1.1	YPR031W		1.0	-1.1	-1.1	-1.1	unknown function
CA6138	orf19.5908	*IPF4351*	-1.1	-1.0	-1.1	-1.0	YBR083W	*TEC1*	1.0	-1.0	-1.1	-1.2	unknown function
CA6139	orf19.5906	*ADE2*	-1.1	-1.1	-1.3	-1.3	YOR128C	*ADE2*	1.0	-1.1	1.0	1.0	phosphoribosylaminoimidazole carboxylase
CA6140	orf19.5905	*IPF1882*	-1.0	-1.1	-1.0	-1.1	YBL028C		1.0	1.2	1.2	1.2	unknown function
CA6142	orf19.5903	*IPF1879*	1.1	-1.0	1.3	1.1	YOR301W	*RAX1*	1.0	-1.5	-1.2	-1.0	unknown function
CA6144	orf19.5901	*PKC1*	-1.1	-1.1	-1.1	-1.0	YBL105C	*PKC1*	1.0	-1.0	1.2	1.2	Ser/thr protein kinase C
CA6145	orf19.5897	*IPF1869*	-1.2	-1.0	-1.2	-1.0	YBL104C		1.0	-1.1	1.1	1.2	unknown function
CA6146	orf19.5896	*IPF1863*	1.1	-1.0	1.1	1.1	YMR244W		1.0	-1.4	-1.2	-1.3	unknown function
CA6148	orf19.5894	*IPF1862.3F*	1.1	1.0	-1.0	1.0	YEL023C		1.0	-1.1	1.2	2.0	unknown function, 3-prime end
CA6149	orf19.5893	*RIP1*	-1.5	-1.5	-1.7	-1.5	YEL024W	*RIP1*	1.0	1.1	1.2	-1.1	Ubiquinol cytochrome-c reductase (by homology)
CA6150	orf19.5892	*IPF1857*	-1.3	1.4	-1.1	1.1	YJR036C	*HUL4*	1.0	-1.8	-1.9	-2.9	similar to Saccharomyces cerevisiae Hul4p hect domain E3 ubiquitin-pro
CA6152	orf19.5887	*NUP85*	-1.1	1.2	-1.0	1.0	YJR042W	*NUP85*	1.0	-1.9	-2.2	-2.2	Nuclear pore protein (by homology)
CA6154	orf19.5885	*IPF1848*	1.5	1.2	1.7	1.4	YEL026W	*SNU13*	1.0	2.0	2.1	4.8	similar to Saccharomyces cerevisiae Snu13p U4/U6.U5 snRNP associat
CA6155	orf19.5884	*IPF1846*	1.1	1.2	1.4	1.2	YJR041C		1.0	-1.2	-1.2	-1.1	unknown function
CA6157	orf19.5880	*GEF1.5F*	-1.1	1.2	1.1	1.1	YJR040W	*GEF1*	1.0	-1.6	-1.1	-1.3	Voltage-gated chloride channel protein, 5-prime end (by homology)
CA6159	orf19.5877	*IPF1837*	-1.3	-1.3	-1.2	-1.2	YOR377W	*ATF1*	1.0	-1.1	1.2	1.2	unknown function
CA6161	orf19.5875	*IPF1834*	1.0	-1.1	-1.0	1.0	YOR036W	*PEP12*	1.0	1.1	1.3	-1.0	probable syntaxin (by homology)
CA6163	orf19.5873	*POL1*	-1.2	-1.0	-1.3	-1.3	YNL102W	*POL1*	1.0	-1.3	-1.3	-1.3	DNA-directed DNA polymerase alpha (by homology)
CA6165	orf19.5871	*SNF5.3F*	-1.1	1.1	-1.0	-1.1	YBR289W	*SNF5*	1.0	1.1	1.2	-1.0	Component of SWI/SNF transcription activator complex, 3-prime end (by
CA6166	orf19.13291	*CTP1*	-1.0	1.0	1.2	1.1	YBR291C	*CTP1*	1.0	-1.6	-1.5	-1.3	Citrate transport protein (by homology)



Heatmap Scale
>=10
9.62
9.23
8.85
8.46
8.08
7.69
7.31
6.92
6.54
6.15
5.77
5.38
5.00
4.62
4.23
3.85
3.46
3.08
2.69
2.31
1.92
1.54
1.15
0.77
0.38
0.00
-0.38
-0.77
-1.15
-1.54
-1.92
-2.31
-2.69
-3.08
-3.46
-3.85
-4.23
-4.62
-5.00
-5.38
-5.77
-6.15
-6.54
-6.92
-7.31
-7.69
-8.08
-8.46
-8.85
-9.23
<=-10

Comparison of *C. albicans* and *S. cerevisiae* Metabolism & Stress Functions

	Candida dataset			Expression Ratio				***Saccharomyces dataset***		Expression Ratio				
	***C. albicans* gene**			**Glucose Concentration (%)**				***S.cerevisiae* gene homolo**		**Glucose Concentration (%)**				
Function	**Systematic**	**orf19 Number**	**Common**	**0**	**0.01**	**0.1**	**1**	**Systematic**	**Common**	**0**	**0.01**	**0.1**	**1**	**Description**
Glycolysis														
Hxt3	CA1067	orf19.2023	*HXT62*	1.3	45.4	34.6	42.5	YDR345C	*HXT3*	1.0	8.7	11.4	9.1	sugar transporter
Hxt6	CA1070	orf19.2020	*HXT61*	1.2	4.6	8.0	3.9	YDR343C	*HXT6*	1.0	7.1	10.3	3.3	sugar transporter
Glk1	CA0263	orf19.1408	*GLK1*	-1.2	1.0	1.0	1.1	YCL040W	*GLK1*	1.0	1.6	1.0	-1.8	aldohexose specific glucokinase (by homology)
Hxk2	CA0127	orf19.8176	*HXK2*	-1.1	9.5	9.7	7.9	YGL253W	*HXK2*	1.0	-1.1	1.4	1.4	hexokinase II, 3-prime end (by homology)
Pgi1	CA3559	orf19.3888	*PGI1*	1.0	1.7	1.8	1.7	YBR196C	*PGI1*	1.0	-1.4	1.1	1.7	Glucose-6-phosphate isomerase
Pfk1	CA1834	orf19.3967	*PFK1*	-1.2	6.9	6.1	6.6	YGR240C	*PFK1*	1.0	-1.9	-1.1	1.5	6-phosphofructokinase, alpha subunit
Pfk2	CA3112	orf19.6540	*PFK2*	-1.0	9.6	8.3	8.5	YMR205C	*PFK2*	1.0	1.2	2.1	2.7	6-phosphofructokinase, beta subunit
Fba1	CA5180	orf19.4618	*FBA1*	-1.2	2.1	1.6	2.1	YKL060C	*FBA1*	1.0	2.0	3.7	4.6	fructose-bisphosphate aldolase (by homology)
Tpi1	CA5950	orf19.6745	*TPI1*	1.1	2.2	2.3	2.2	YDR050C	*TPI1*	1.0	1.8	2.3	3.7	Triose phosphate isomerase
Tdh3	CA5892	orf19.6814	*GAP1*	1.1	1.9	2.1	2.1	YGR192C	*TDH3*	1.0	-1.1	1.4	1.9	Glyceraldehyde-3-phosphate dehydrogenase
Pgk1	CA1691	orf19.3651	*PGK1*	1.0	2.5	2.4	2.5	YCR012W	*PGK1*	1.0	2.0	2.9	3.5	Phosphoglycerate kinase
Gpm1	CA4671	orf19.903	*GPM1*	-1.1	2.2	1.9	2.2	YKL152C	*GPM1*	1.0	1.5	1.8	2.1	phosphoglycerate mutase (by homology)
Eno1	CA3874	orf19.395	*ENO1*	1.6	1.6	1.2	1.5	YGR254W	*ENO1*	1.0	1.8	2.7	4.2	Enolase I (2-phosphoglycerate dehydratase)
Pyk1	CA3483	orf19.3575	*CDC19*	-1.1	3.2	2.1	4.2	YAL038W	*CDC19*	1.0	2.3	3.6	5.4	pyruvate kinase (by homology)
Mean				***0.0***	***6.7***	***5.9***	***6.4***			***1.0***	***1.7***	***3.2***	***3.1***	
Gluconeogenesis & Glycoxylate Cycle														
Fbp1	CA3199	orf19.6178	*FBP1*	-1.1	-6.2	-7.9	-7.2	YLR377C	*FBP1*	1.0	-3.2	-3.8	-3.3	Fructose-1,6-bisphosphatase
Pck1	CA5857	orf19.7514	*PCK1*	1.3	-11.5	-12.0	-19.3	YKR097W	*PCK1*	1.0	-8.0	-4.8	-6.0	phosphoenolpyruvate carboxykinase
Icl1	CA4446	orf19.6844	*ICL1*	-1.0	-1.9	-2.0	-1.6	YER065C	*ICL1*	1.0	-4.4	-5.3	-4.8	Isocitrate lyase
Mls1	CA4748	orf19.4833	*MLS1*	-1.6	-4.2	-7.3	-4.8	YNL117W	*MLS1*	1.0	-3.7	-3.8	-3.3	malate synthase
Mean				***-0.6***	***-6.0***	***-7.3***	***-8.2***			***1.0***	***-4.8***	***-4.4***	***-4.3***	
TCA Cycle														
Aco1	CA3546	orf19.6385	*ACO1*	1.2	1.1	-1.1	-1.4	YLR304C	*ACO1*	1.0	-2.8	-3.8	-8.9	aconitate hydratase (by homology)
Cit1	CA3909	orf19.4393	*CIT1*	-1.0	-1.0	-1.2	-1.3	YNR001C	*CIT1*	1.0	-2.0	-2.4	-5.8	Citrate synthase, exon 2
Fum1	CA4255	orf19.543	*FUM11*	-1.2	-2.0	-2.1	-2.0	YPL262W	*FUM1*	1.0	-1.5	-1.6	-2.3	fumarate hydratase
Idh1	CA4753	orf19.4826	*IDH1*	-1.1	1.0	-1.1	1.1	YNL037C	*IDH1*	1.0	-1.3	-1.7	-2.9	isocitrate dehydrogenase (NAD+) subunit1, mitochondrial, 3-prime end (by hom
Idh2	CA4148	orf19.13213	*IDH2*	-1.0	1.4	1.4	1.4	YOR136W	*IDH2*	1.0	-1.6	-1.6	-2.3	Isocitrate dehydrogenase (NAD+) subunit 2, mitochondrial (by homology)
Idp2	CA0643	orf19.3733	*IDP2*	-1.1	-3.6	-4.8	-3.1	YLR174W	*IDP2*	1.0	-4.5	-7.5	-7.8	isocitrate dehydrogenase, cytosolic (by homology)
Kgd1	CA3149	orf19.6165	*KGD1*	1.1	-2.0	-2.1	-2.0	YIL125W	*KGD1*	1.0	-2.5	-2.1	-3.6	2-oxoglutarate dehydrogenase
Kgd2	CA2997	orf19.6126	*KGD2*	-1.4	-2.7	-3.2	-2.6	YDR148C	*KGD2*	1.0	-1.9	-1.6	-2.7	2-oxoglutarate dehydrogenase complex E2 component (by homology)
Lpd1	CA2998	orf19.6127	*LPD1*	-1.3	-1.9	-2.6	-2.0	YFL018C	*LPD1*	1.0	-1.9	-2.1	-2.1	dihydrolipoamide dehydrogenase (by homology)
Lsc1	CA0791	orf19.3358	*LSC1*	1.1	-1.9	-1.8	-1.7	YOR142W	*LSC1*	1.0	-1.4	-1.4	-1.6	succinate-CoA ligase / synthetase (by homology)
Lsc2	CA0664	orf19.710	*LSC2*	1.0	-2.7	-2.9	-2.7	YGR244C	*LSC2*	1.0	1.1	-1.3	-2.7	succinate-CoA ligase beta subunit, 3-prime end (by homology)
Mdh1	CA5164	orf19.4602	*MDH1*	1.2	-1.4	-1.4	-1.4	YKL085W	*MDH1*	1.0	-1.3	-1.5	-3.0	Mitochondrial malate dehydrogenase precursor (by homology)
Sdh1	CA4063	orf19.440	*SDH11*	-1.1	-1.1	-1.1	-1.1	YKL148C	*SDH1*	1.0	-1.3	-1.5	-2.1	Succinate dehydrogenase (by homology)
Sdh2	CA1845	orf19.637	*IPF11123*	1.1	-1.1	-1.1	-1.1	YLL041C	*SDH2*	1.0	-1.1	-1.3	-2.7	similar to Saccharomyces cerevisiae Sdh2p succinate dehydrogenase iron-sulfu
Sdh4	CA2423	orf19.11949	*SDH41*	-1.0	-1.5	-1.3	-1.2	YDR178W	*SDH4*	1.0	-1.5	-1.2	-2.2	succinate dehydrogenase membrane anchor subunit for sdh2p (by homology)
Mean				***-0.2***	***-1.3***	***-1.8***	***-1.4***			***1.0***	***-1.7***	***-2.2***	***-3.5***	
Fatty Acid beta-Oxidation														
Erg10	CA0290	orf19.1591	*POT14*	-1.2	-3.4	-2.9	-3.2	YPL028W	*ERG10*	1.0	1.5	2.5	2.0	acetyl-CoA acetyltransferase (by homology)
Faa2	CA1596	orf19.272	*FAA21*	-1.2	-3.0	-3.8	-2.7	YER015W	*FAA2*	1.0	1.1	1.1	1.4	long-chain-fatty-acid-CoA ligase (by homology)
Faa4	CA5992	orf19.7592	*FAA4*	-1.1	-2.2	-2.5	-2.3	YMR246W	*FAA4*	1.0	1.1	1.4	2.0	long-chain fatty acid--CoA ligase and synthetase 4 (by homology)
Pot1	CA5862	orf19.7520	*POT11*	-1.2	-8.2	-10.0	-8.1	YIL160C	*POT1*	1.0	1.2	-1.2	-1.5	peroxysomal 3-ketoacyl-CoA thiolase A (by homology)
Pox1	CA1572	orf19.9221	*POX4*	-1.0	-8.4	-11.0	-8.2	YGL205W	*POX1*	1.0	1.0	1.1	1.1	peroxisomal fatty acyl-CoA oxidase (by homology)
Mean				***-1.1***	***-5.0***	***-6.0***	***-4.9***			***1.0***	***1.2***	***1.0***	***1.0***	
Osmotic Stress														
Ena	CA4929	orf19.6070	*ENA22*	-1.0	1.6	1.5	1.7	YDR038C	*ENA5*	1.0	-1.0	1.1	1.1	P-type ATPase involved in Na+ efflux (by homology)
Gpd2	CA2263	orf19.1756	*GPD1*	-1.0	1.3	1.8	1.8	YOL059W	*GPD2*	1.0	1.7	3.0	6.5	Glycerol-3-phosphate dehydrogenase (by homology)
Hog1	CA4677	orf19.895	*HOG1*	1.1	1.0	-1.0	-1.1	YLR113W	*HOG1*	1.0	1.3	1.7	1.6	Ser/thr protein kinase of MAPK family
Pbs2	CA5686	orf19.7388	*IPF3329*	-1.1	-1.2	-1.3	-1.3	YJL128C	*PBS2*	1.0	-1.4	-1.1	-1.0	similar to Saccharomyces cerevisiae Pbs2p tyrosine protein kinase of the MAP
Rhr2	CA5788	orf19.5437	*RHR2*	1.0	9.7	8.1	9.4	YIL053W	*RHR2*	1.0	3.6	3.5	10.6	DL-glycerol phosphatase
Mean				***-1.1***	***2.5***	***1.8***	***2.1***			***1.0***	***0.8***	***1.6***	***3.7***	
Oxidative Stress														
Yap1	CA0183	orf19.9191	*CAP1*	-1.0	1.8	2.2	1.9	YML007W	*YAP1*	1.0	-2.1	-2.1	-2.6	transcriptional acivator (by homology)
Hyr1	CA0559	orf19.86	*GPX1*	1.0	1.5	1.6	1.3	YIR037W	*HYR1*	1.0	-1.1	-1.2	-1.5	glutathione peroxidase (by homology)
Cta1	CA3011	orf19.6229	*CTA1*	1.0	-9.1	-7.2	-8.5	YDR256C	*CTA1*	1.0	-1.3	-1.1	1.0	catalase A, peroxisomal(by homology)
Grx3	CA1161	orf19.2727	*GRX3*	1.1	1.0	1.2	1.1	YDR098C	*GRX3*	1.0	-1.1	-1.1	-1.0	glutaredoxin-like protein
Grx5	CA1904	orf19.10298	*GRX5*	1.2	-1.0	1.0	1.2	YPL059W	*GRX5*	1.0	-1.4	-1.7	-2.1	Glutaredoxin

Gsh1	CA0583	orf19.12526	*GSH1*	-1.2	-1.1	-1.2	-1.1	YJL101C	*GSH1*	1.0	-1.2	-1.3	-1.2	gamma-glutamylcysteine synthetase, exon 2 (by homology)
Gsh2	CA5124	orf19.6404	*GSH2*	-1.2	-1.2	-1.3	-1.2	YOL049W	*GSH2*	1.0	1.1	1.2	1.4	Glutathione synthetase (by homology)
Gtt1	CA4712	orf19.6947	*GTT1*	1.0	-1.1	-1.2	-1.2	YIR038C	*GTT1*	1.0	-1.1	-1.2	-1.4	glutathione S-transferase, 3-prime end (by homology)
Sod1	CA4120	orf19.2770.1	*SOD1*	1.1	1.1	1.1	1.1	YJR104C	*SOD1*	1.0	1.2	1.3	-1.7	Cu,Zn-superoxide dismutase, 3-prime end
Sod2	CA2719	orf19.3340	*SOD2*	1.2	-1.2	-1.3	-1.2	YHR008C	*SOD2*	1.0	1.1	1.1	-1.3	Manganese-superoxide dismutase
Trr1	CA3059	orf19.11766	*TRR1*	-1.0	1.2	1.1	1.2	YDR353W	*TRR1*	1.0	-1.8	1.2	1.2	Thioredoxin reductase (by homology)
Trx1	CA6010	orf19.7611	*TRX1*	1.5	1.5	1.8	1.7	YLR043C	*TRX1*	1.0	1.3	1.1	-1.1	thioredoxin (by homology)
Mean				***0.4***	***-0.5***	***-0.2***	***-0.3***			***1.0***	***-0.5***	***-0.3***	***-0.9***	
Trehalose metabolism														
	CA4084	orf19.6640	*TPS1*	-1.0	1.5	2.1	1.5	YBR126C	*TPS1*	1.0	1.6	1.4	-1.1	TREHALOSE-6-PHOSPHATE SYNTHASE
	CA5066	orf19.3038	*TPS2*	1.2	3.9	4.8	4.9	YDR074W	*TPS2*	1.0	1.1	-1.1	-1.1	Threalose-6-phosphate phosphatase (by homology)
	CA5505	orf19.5348	*TPS3*	-1.1	2.2	1.9	2.2	YMR261C	*TPS3*	1.0	-1.1	-1.3	-1.6	alpha,alpha-trehalose-phosphate synthase, regulatory subunit, 3-prime end (by
	CA5824	orf19.7479	*NTH1*	-1.1	-1.0	1.4	1.1	YDR001C	*NTH1*	1.0	1.2	1.5	1.2	Neutral trehalase
Mean				***-0.5***	***1.6***	***2.6***	***2.4***			***1.0***	***0.7***	***0.1***	***-0.6***	
Ribosome														
	CA2047	orf19.10452	*RPL10*	1.0	-1.3	-1.4	-1.1	YLR075W	*RPL10*	1.0	2.0	2.6	3.2	Ribosomal protein L10 (by homology)
	CA0763	orf19.2232	*RPL11*	1.4	1.0	-1.1	1.1	YPR102C	*RPL11A*	1.0	1.4	1.7	1.8	60S ribosomal protein (by homology)
	CA4001	orf19.1635	*RPL12*	-1.0	-1.0	-1.0	-1.1	YEL054C	*RPL12A*	1.0	-2.3	1.8	2.6	ribosomal protein
	CA2818	orf19.2994	*RPL13*	1.3	-1.1	-1.2	1.0	YDL082W	*RPL13A*	1.0	1.4	1.6	1.8	Ribosomal protein
	CA3602	orf19.4931.1	*RPL14B*	1.0	-1.0	-1.1	1.0	YKL006W	*RPL14A*	1.0	1.8	1.7	2.5	ribosomal protein L14B, 3-prime end (by homology)
	CA4512	orf19.8123	*RPL15B*	1.1	-1.0	-1.1	1.1	YLR029C	*RPL15A*	1.0	1.1	1.2	1.9	ribosomal protein L15.e.c13 (by homology)
	CA3864	orf19.6085	*RPL16A*	-1.0	-1.2	-1.4	-1.2	YNL069C	*RPL16B*	1.0	1.6	2.9	3.9	ribosomal protein (by homology)
	CA1440	orf19.4490	*RPL17B*	1.0	-1.3	-1.1	1.0	YJL177W	*RPL17B*	1.0	-1.0	1.5	1.6	RPL17B ribosomal protein L17.e
	CA6079	orf19.5982	*RPL18*	-1.0	1.1	1.1	1.1	YOL120C	*RPL18A*	1.0	-1.5	-1.5	-1.2	Ribosomal Protein RPL18B (large subunit), exon 2 (by homology)
	CA2031	orf19.3465	*RPL10A*	1.2	-1.0	1.1	1.2	YPL220W	*RPL1A*	1.0	2.8	4.2	4.3	L10A ribosomal protein
	CA0736	orf19.4632	*RPL20B*	1.3	-1.1	1.2	1.3	YOR312C	*RPL20B*	1.0	1.8	2.1	2.2	ribosomal protein (by homology)
	CA2092	orf19.840	*RPL21A*	1.1	-1.1	-1.1	1.1	YBR191W	*RPL21A*	1.0	1.1	1.2	2.3	Ribosomal protein, 3-prime end (by homology)
	CA2454	orf19.3504	*RPL23B*	1.4	-1.0	1.1	1.4	YER117W	*RPL23B*	1.0	1.9	2.0	2.5	ribosomal protein L23.e, 3-prime end (by homology)
	CA1189	orf19.11269	*RPL24A*	1.1	-1.3	-1.4	-1.1	YGL031C	*RPL24A*	1.0	1.4	1.6	1.7	ribosomal protein L24 (by homology)
	CA1977	orf19.687.1	*RPL25*	1.6	1.2	1.2	1.3	YOL127W	*RPL25*	1.0	1.4	1.5	1.9	ribosomal protein L23a, 3-prime end (by homology)
	CA2108	orf19.3690.2	*RPL26A*	1.1	-1.1	1.2	1.2	YLR344W	*RPL26A*	1.0	1.8	2.1	2.3	ribosomal protein, 3-prime end (by homology)
	CA1972	orf19.5225.2	*RPL27A*	1.6	1.2	1.2	1.2	YHR010W	*RPL27A*	1.0	1.6	1.9	2.1	ribosomal protein L27
	CA1662	orf19.2864.1	*RPL28*	1.3	-1.0	1.1	1.2	YGL103W	*RPL28*	1.0	1.8	1.8	2.2	Ribosomal protein, 3-prime end (by homology)
	CA3307	orf19.2309.2	*RPL2*	1.0	1.0	-1.2	-1.1	YIL018W	*RPL2B*	1.0	-1.6	-1.5	-1.4	ribosomal protein L8, 3-prime end (by homology)
	CA0615	orf19.1601	*RPL3*	-1.2	-1.3	-1.5	-1.4	YOR063W	*RPL3*	1.0	1.8	2.9	3.0	60S large subunit ribosomal protein L3.e (by homology)
	CA1188	orf19.3788.1	*RPL30*	1.9	1.3	1.4	1.4	YGL030W	*RPL30*	1.0	1.4	2.4	2.5	RNA binding, 3-prime end (by homology)
	CA1298	orf19.3415.1	*RPL32*	1.5	1.2	1.2	1.3	YBL092W	*RPL32*	1.0	-1.2	-1.5	1.1	ribosomal protein L32
	CA4571	orf19.6882.1	*RPL33*	1.5	1.2	1.3	1.7	YPL143W	*RPL33A*	1.0	1.0	1.7	2.1	ribosomal protein L35a, 3-prime end
	CA2579	orf19.6220.4	*RPL34B*	1.8	1.3	1.2	1.4	YIL052C	*RPL34B*	1.0	2.0	2.2	2.6	Ribosomal protein L34.e, 3-prime end (by homology)
	CA6092	orf19.5964.2	*RPL35*	1.6	1.2	1.7	1.5	YDL191W	*RPL35A*	1.0	2.3	2.6	3.6	Ribosomal protein L35A, 3-prime end (by homology)
	CA4102	orf19.667.1	*RPL37B*	1.1	1.1	1.1	1.1	YDR500C	*RPL37B*	1.0	1.2	1.3	1.5	Ribosomal protein
	CA2734	orf19.2111.2	*RPL38*	1.5	1.4	1.4	1.3	YLR325C	*RPL38*	1.0	1.1	1.3	1.6	ribosomal protein L38 (by homology)
	CA2023	orf19.4909.1	*RPL42*	1.9	1.1	1.1	1.4	YNL162W	*RPL42A*	1.0	2.5	2.6	3.2	ribosomal protein L36a, 3-prime end (by homology)
	CA1637	orf19.3942.1	*RPL43A*	1.5	1.1	1.4	1.3	YPR043W	*RPL43A*	1.0	2.2	2.4	1.8	ribosomal protein, 3-prime end (by homology)
	CA5343	orf19.7217	*RPL4B*	-1.1	1.1	1.0	-1.0	YDR012W	*RPL4B*	1.0	1.8	2.7	3.0	Ribosomal protein L4B (by homology)
	CA3111	orf19.6541	*RPL5*	-1.1	-1.1	-1.1	-1.1	YPL131W	*RPL5*	1.0	1.5	3.2	4.2	ribosomal protein (by homology)
	CA3123	orf19.3003.1	*RPL6*	1.4	1.1	1.0	1.1	YLR448W	*RPL6B*	1.0	1.6	2.4	2.3	ribosomal protein, 3-prime end
	CA3800	orf19.2478.1	*RPL7A*	1.0	-1.1	-1.2	-1.1	YPL198W	*RPL7B*	1.0	1.4	2.5	2.9	60S Ribosomal Protein L7-A, 3-prime end
	CA6064	orf19.6002	*RPL81*	1.2	1.0	-1.0	1.0	YLL045C	*RPL8B*	1.0	1.7	2.4	3.1	60S ribosomal protein L7a.e.B (by homology)
	CA0239	orf19.236	*RPL9B*	1.4	-1.3	1.1	1.0	YNL067W	*RPL9B*	1.0	1.5	2.4	2.4	RPL9B ribosomal protein L9 by homology
	CA5021	orf19.6975	*YST1*	-1.1	-1.3	-1.3	-1.3	YGR214W	*RPS0A*	1.0	1.5	1.6	2.5	Ribosomal protein, exon 2
	CA3739	orf19.2179.2	*RPS10*	1.4	-1.1	-1.1	1.0	YOR293W	*RPS10A*	1.0	1.6	2.2	2.6	ribosomal protein, 3-prime end (by homology)
	CA5920	orf19.6785	*RPS12*	1.4	1.1	1.3	1.4	YOR369C	*RPS12*	1.0	2.5	3.6	3.4	acidic ribosomal protein S12 (by homology)
	CA1304	orf19.4193.1	*RPS13*	1.5	1.3	1.3	1.4	YDR064W	*RPS13*	1.0	1.3	1.1	1.9	ribosomal protein, 3-prime end (by homology)
	CA3690	orf19.6265.1	*RPS14B*	1.1	1.0	-1.1	1.1	YJL191W	*RPS14B*	1.0	1.2	1.4	1.7	ribosomal protein (by homology)
	CA6123	orf19.5927	*RPS15*	1.0	-1.2	-1.2	-1.0	YOL040C	*RPS15*	1.0	1.9	2.1	2.8	40S ribosomal protein S15, 3-prime end (by homology)
	CA2817	orf19.2994.1	*RPS16*	1.2	1.1	1.1	1.1	YMR143W	*RPS16A*					ribosomal protein, 3-prime end
	CA3341	orf19.2329.1	*RPS17*	1.3	-1.0	1.2	1.2	YDR447C	*RPS17B*	1.0	-1.3	3.1	3.3	Ribosomal protein S17, 3-prime end (by homology)
	CA5203	orf19.7018	*RPS18*	1.8	1.1	1.1	1.3	YML026C	*RPS18B*					Ribosomal protein S18 (by homology)
	CA6068	orf19.5996.1	*RPS19A*	1.4	1.1	-1.0	1.1	YOL121C	*RPS19A*	1.0	1.9	1.9	2.7	ribosomal protein S19.e, 3-prime end (by homology)
	CA2811	orf19.10520	*RPS10*	-1.2	-1.3	-1.4	-1.2	YML063W	*RPS1B*	1.0	1.7	1.8	3.0	Ribosomal protein 10
	CA1715	orf19.3334	*RPS21*	1.0	1.0	-1.1	1.0	YGL123W	*RPS2*	1.0	1.2	1.4	2.2	ribosomal protein (by homology)
	CA3539	orf19.6375	*RPS22*	-1.2	-1.3	-1.2	-1.2	YHL015W	*RPS20*	1.0	1.1	2.1	1.6	ribosomal protein by homology
	CA2937	orf19.3325.3	*RPS21B*	1.9	1.3	1.4	1.4	YJL136C	*RPS21B*	1.0	2.4	2.4	2.5	ribosomal protein S21, 3-prime end
	CA3689	orf19.6265	*RPS22A*	1.9	1.2	1.2	1.4	YJL190C	*RPS22A*	1.0	1.1	1.2	1.4	ribosomal protein S15a.e.c10 (by homology)
	CA0567	orf19.13632	*RPS23*	1.0	-1.1	-1.0	1.1	YPR132W	*RPS23B*	1.0	2.1	2.8	3.5	Ribosomal protein S23 (by homology)

	CA3793	orf19.5825.1	*IPF5701*	1.1	1.0	1.1	1.1	YER074W	*RPS24A*	1.0	2.2	2.2	2.5	unknown function
	CA5807	orf19.5466	*RPS24*	1.3	1.2	-1.1	1.1	YIL069C	*RPS24B*	1.0	1.9	1.9	2.7	ribosomal protein S24.e
	CA4269	orf19.6663	*RPS25B*	1.2	1.0	1.0	1.1	YLR333C	*RPS25B*	1.0	1.2	1.4	1.9	Cytosolic ribosomal protein (by homology)
	CA4534	orf19.1470	*RPS26A*	1.7	1.3	1.3	1.5	YGL189C	*RPS26A*	1.0	1.3	1.8	1.8	ribosomal protein S26.e.A, cytosolic (by homology)
	CA3226	orf19.6286.2	*RPS27*	1.4	-1.0	1.3	1.3	YKL156W	*RPS27A*	1.0	1.4	1.4	1.7	ribosomal protein S27 (by homology)
	CA5646	orf19.7048.1	*RPS28B*	1.6	1.5	1.6	1.6	YLR264W	*RPS28B*	1.0	2.0	1.7	2.5	Ribosomal protein S28B (S33B) (YS27), 3-prime end (by homology)
	CA3278	orf19.6312	*RPS3*	1.1	-1.2	-1.3	-1.0	YNL178W	*RPS3*	1.0	1.8	2.7	3.1	Ribosomal protein S3.e (by homology)
	CA2587	orf19.4375.1	*RPS30*	1.2	1.1	1.1	1.1	YOR182C	*RPS30B*	1.0	1.4	1.8	1.8	40S ribosomal protein S30, 3-prime end (by homology)
	CA2011	orf19.3087	*RPS31*	1.2	1.1	-1.0	1.1	YLR167W	*RPS31*	1.0	2.1	2.4	2.3	Ubiquitin fusion protein
	CA5499	orf19.5341	*RPS4A*	1.0	-1.2	-1.3	-1.1	YJR145C	*RPS4A*	1.0	1.3	1.3	2.2	ribosomal protein S4
	CA0632	orf19.11812	*RPS5*	1.2	-1.2	-1.2	-1.1	YJR123W	*RPS5*	1.0	-1.6	-1.4	-1.1	ribosomal protein S5.e (by homology)
	CA2708	orf19.4660	*RPS6A*	-1.2	-1.5	-1.7	-1.3	YPL090C	*RPS6A*	1.0	1.9	2.3	3.4	ribosomal protein S6 (by homology)
	CA1502	orf19.9267	*RPS7A*	-1.1	-1.1	-1.0	1.1	YOR096W	*RPS7A*	1.0	1.8	2.5	3.2	ribosomal protein (by homology)
	CA4562	orf19.6873	*RPS8A*	1.1	-1.0	-1.1	-1.0	YER102W	*RPS8B*	1.0	2.4	3.4	5.0	ribosomal protein (by homology)
	CA0322	orf19.8459	*RPS9B*	1.4	1.1	1.1	1.2	YPL081W	*RPS9A*	1.0	1.5	1.9	2.1	Ribosomal protein
Mean				***0.9***	***0.0***	***0.1***	***0.6***			***1.0***	***1.3***	***1.9***	***2.3***	

Comparison of *C. albicans* and *S. cerevisiae* Mitochondrial Functions

Candida dataset			Expression Ratio				***Saccharomyces dataset***		Expression Ratio				
***C. albicans* gene**			**Glucose Concentration (%)**				***S.cerevisiae* homologue**		**GlucoseConcentration(%)**				
Systematic	**orf19 Number**	**Common**	**0**	**0.01**	**0.1**	**1**	**Systematic**	**Common**	**0.0**	**0.0**	**0.1**	**1.0**	**Description**
Mitochondrial protein genes													
CA0783	orf19.3931	*ACR1*	1.1	-3.3	-3.5	-2.3	YJR095W	*SFC1*	1.0	-4.3	-4.6	-4.9	Succinate-fumarate transporter (by homology)
CA3474	orf19.1669	*AFG3*	-1.3	-1.5	-1.8	-1.5	YER017C	*AFG3*	1.0	1.1	1.2	1.2	Member of the Sec18p, Pas1p, Cdc48p, TBP-1 family of ATPases (by homology)
CA2406	orf19.300	*AIP2*	-1.2	-1.2	-1.3	-1.3	YDL178W	*AIP2*	1.0	1.2	1.4	1.1	actin interacting protein 2 (by homology)
CA4159	orf19.13228	*ALD5*	1.5	-3.3	-2.7	-3.7	YER073W	*ALD5*	1.0	1.2	1.2	2.4	aldehyde dehydrogenase (NAD+) (by homology)
CA6124	orf19.5926	*ARG11*	1.1	1.0	-1.0	1.1	YOR130C	*ORT1*	1.0	1.1	1.2	1.6	mitochondrial amino acid transporter (by homology)
CA2595	orf19.56	*ARG2*	-1.0	-1.0	-1.0	-1.0	YJL071W	*ARG2*	1.0	-1.2	-1.3	-1.2	acetylglutamate synthase (by homology)
CA4597	orf19.6916	*ATP11*	1.0	-1.0	-1.0	1.0	YNL315C	*ATP11*	1.0	-1.1	-1.2	-1.4	F1F0-ATPase complex assembly protein (by homology)
CA2113	orf19.3686	*ATP12*	-1.1	-1.1	-1.0	-1.0	YJL180C	*ATP12*	1.0	-2.0	-2.5	-2.3	F1F0-ATPase complex assembly protein (by homology)
CA3353	orf19.9500	*AUR1*	1.3	1.2	1.6	1.2	YKL004W	*AUR1*	1.0	1.1	1.0	1.2	aureobasidin-resistance protein
CA1380	orf19.458	*BCS1*	-1.0	-1.1	-1.1	-1.0	YDR375C	*BCS1*	1.0	-1.6	-1.8	-1.7	mitochondrial protein of the CDC48/PAS1/SEC18 (AAA) family of ATPases (by homology)
CA5152	orf19.4591	*CAT2*	1.0	-7.2	-10.2	-10.3	YML042W	*CAT2*	1.0	-1.3	-1.8	-2.1	carnitine O-acetyltransferase (by homology)
CA2518	orf19.5515	*CBP3*	-1.0	1.0	-1.0	-1.0	YPL215W	*CBP3*	1.0	1.1	1.1	-1.0	involved in cytochrome-c reductase assembly (by homology)
CA3877	orf19.392	*CBP4*	-1.0	-1.1	-1.1	-1.0	YGR174C	*CBP4*	1.0	-1.0	-1.3	-1.7	Ubiquinol--cytochrome-c reductase assembly factor (by homology)
CA1889		*CBP6*	1.1	1.1	1.1	1.1	YBR120C	*CBP6*	1.0	-1.2	-1.4	-1.4	Apo-cytochrome B pre-mRNA processing protein (by homology)
CA4698	orf19.6926	*CDC25*	1.1	1.0	1.2	1.1	YLR310C	*CDC25*	1.0	-1.1	1.1	1.1	cell division cycle protein
CA6082	orf19.5977	*CEM1*	-1.1	-1.1	-1.2	-1.0	YER061C	*CEM1*	1.0	-1.6	1.0	1.4	3-oxoacyl-[acyl-carrier-protein]-synthase (by homology)
CA3909	orf19.4393	*CIT1.EXON2*	-1.0	-1.0	-1.2	-1.3	YNR001C	*CIT1*	1.0	-2.0	-2.4	-5.8	Citrate synthase, exon 2
CA3958	orf19.1416	*COX11*	1.1	1.1	1.3	1.0	YPL132W	*COX11*	1.0	-1.1	-1.0	-1.2	cytochrome-c oxidase assembly protein by homology to S. cerevisiae
CA4536	orf19.1467	*COX13*	1.2	-1.0	1.1	1.2	YGL191W	*COX13*	1.0	-1.2	-1.5	-2.4	cytochrome-c oxidase chain VIa (by homology)
CA1688	orf19.3656	*COX15*	-1.1	2.0	2.6	2.5	YER141W	*COX15*	1.0	-1.4	-1.4	-1.6	cytochrome oxidase assembly factor (by homology)
CA1090	orf19.3946	*COX18*	-1.0	1.0	1.3	1.1	YGR062C	*COX18*	1.0	-1.1	-1.2	-1.1	protein required for activity of mitochondrial cytochrome oxidase (by homology)
CA4533	orf19.1471	*COX4*	1.2	1.1	1.3	1.1	YGL187C	*COX4*	1.0	1.1	-1.0	-1.9	cytochrome-c oxidase (by homology)
CA2630	orf19.12223	*COX5A*	1.3	-1.1	1.4	1.1	YNL052W	*COX5A*	1.0	1.3	1.4	-1.4	cytochrome-c oxidase chain V.A precursor (by homology)
CA0031	orf19.227	*COX7*	1.0	-1.0	1.0	1.1	YMR256C	*COX7*					Subunit VII of cytochrome c oxidase (by homology)
CA2134	orf19.5213	*COX8*	1.5	1.3	1.4	1.5	YLR395C	*COX8*	1.0	-1.1	-1.2	-1.5	CYTOCHROME C OXIDASE (by homology)
CA5828	orf19.7483	*CRM1*	-1.7	-1.3	-1.6	-1.3	YGR218W	*CRM1*	1.0	1.0	1.2	1.2	Nuclear export factor
CA6166	orf19.13291	*CTP1*	-1.0	1.0	1.2	1.1	YBR291C	*CTP1*	1.0	-1.6	-1.5	-1.3	Citrate transport protein (by homology)
CA0038	orf19.1770	*CYC1*	1.2	1.2	1.3	1.4	YJR048W	*CYC1*	1.0	-1.5	-1.5	-2.3	cytochrome-c isoform 1
CA5141	orf19.4578	*CYT2*	1.0	1.1	1.0	1.0	YKL087C	*CYT2*	1.0	-1.8	-1.6	-1.6	holocytochrome-c1 synthase (by homology)
CA2763	orf19.5628	*DIC1.3*	1.0	-1.1	-1.1	1.0	YLR348C	*DIC1*	1.0	-1.0	-1.0	-1.2	dicarboxylate carrier protein, 3-prime end (by homology)
CA5942	orf19.6755	*DLD2*	1.0	1.2	1.3	1.1	YDL174C	*DLD1*	1.0	-2.0	-2.6	-2.0	D-lactate ferrycytochrome C oxidoreductase (by homology)
CA5033	orf19.6987	*DNM1*	-1.3	-1.2	-1.4	-1.1	YLL001W	*DNM1*	1.0	-1.5	-1.3	-1.1	Dynamin-related protein (by homology)
CA1732	orf19.6500	*ECM42*	1.0	1.0	1.1	1.0	YMR062C	*ECM40*					Acetylornithine acetyltransferase (by homology)
CA0253	orf19.477	*FIL1*	1.0	1.0	-1.0	-1.0	YHR038W	*FIL1*	1.0	-2.1	-1.5	-1.6	Putative mitochondrial ribosome recycling factor (by homology)
CA4945	orf19.6532	*FLX1*	1.1	1.1	1.1	1.0	YIL134W	*FLX1*	1.0	-1.4	-1.3	-1.3	MITOCHONDRIAL FAD CARRIER by homology
CA2352	orf19.4418	*FMT1*	-1.0	1.0	1.1	1.0	YBL013W	*FMT1*	1.0	1.1	1.0	1.1	Methionyl-tRNA Transformylase (by homology)
CA2948	orf19.1963	*GDS1*	-1.1	-1.1	-1.1	-1.0	YOR355W	*GDS1*	1.0	1.0	1.7	1.3	nam9-1 suppressor (by homology)
CA5206	orf19.7021	*GPH1*	1.0	-1.0	1.3	1.4	YPR160W	*GPH1*	1.0	1.0	-1.3	-1.3	Glycogen phosphorylase (by homology)
CA3566	orf19.3133	*GUT2*	1.1	-1.6	-1.6	-1.8	YIL155C	*GUT2*	1.0	-1.8	-2.8	-5.1	Glycerol-3-phosphate dehydrogenase, mitochondrial (by homology)
CA0749	orf19.1973	*HAP5*	-1.0	-1.0	-1.0	-1.0	YOR358W	*HAP5*	1.0	-1.3	-1.4	-1.4	CCAAT-binding factor subunit (by homology)
CA1271	orf19.2723	*HIT1*	-1.1	-1.1	-1.0	-1.2	YJR055W	*HIT1*	1.0	-1.1	-1.1	-1.1	required for growth at high temperature (by homology)
CA5341		*HSP10.3*	1.1	1.0	1.0	1.1	YOR020C	*HSP10*	1.0	-1.1	-1.2	-1.2	10 kDa mitochondrial heat shock chaperonin, 3-prime end (by homology)
CA1239	orf19.717	*HSP60*	-1.2	-1.3	-1.3	-1.3	YLR259C	*HSP60*	1.0	-1.4	-1.4	-1.9	Heat Shock Protein 60 (HSP60)
CA4753	orf19.4826	*IDH1.3*	-1.1	1.0	-1.1	1.1	YNL037C	*IDH1*	1.0	-1.3	-1.7	-2.9	isocitrate dehydrogenase (NAD+) subunit1, mitochondrial, 3-prime end (by homology)
CA4148	orf19.13213	*IDH2*	-1.0	1.4	1.4	1.4	YOR136W	*IDH2*	1.0	-1.6	-1.6	-2.3	Isocitrate dehydrogenase (NAD+) subunit 2, mitochondrial (by homology)
CA4428	orf19.5167	*IFM1*	-1.2	-1.3	-1.6	-1.4	YOL023W	*IFM1*	1.0	-1.1	-1.2	-1.3	translation initiation factor 2 by homology
CA2945	orf19.1967	*IMG1*	1.1	1.1	1.0	-1.0	YCR046C	*IMG1*	1.0	-1.5	-1.5	-1.3	Ribosomal protein, mitochondrial (by homology)
CA5084	orf19.3061	*IMP1*	1.1	1.3	1.3	1.2	YMR150C	*IMP1*	1.0	-1.1	-1.1	-1.1	protease, mitochondrial (by homology)
CA1135	orf19.1981	*IMP2*	-1.0	1.0	-1.0	1.0	YMR035W	*IMP2*	1.0	-1.1	-1.1	-1.0	mitochondrial inner membrane protease subunit (by homology)
CA1632	orf19.11420	*IPF10181*	1.1	1.0	1.0	1.1	YJR101W	*RSM26*	1.0	1.5	-1.0	1.1	similar to Saccharomyces cerevisiae Rsm26p protein of the small subunit of the mitochondrial r
CA1746	orf19.5050	*IPF10886*	-1.1	-1.1	-1.2	-1.1	YGL236C	*MTO1*	1.0	-1.4	-1.7	-1.7	unknown function
CA1845	orf19.637	*IPF11123*	1.1	-1.1	-1.1	-1.1	YLL041C	*SDH2*	1.0	-1.1	-1.3	-2.7	similar to Saccharomyces cerevisiae Sdh2p succinate dehydrogenase iron-sulfur protein subur
CA1848		*IPF11128*	1.0	1.0	1.0	-1.0	YMR225C	*MRPL44*					unknown function
CA3963	orf19.1422	*IPF11233*	-1.1	1.0	1.1	1.1	YBR179C	*FZO1*	1.0	1.1	-1.1	1.2	similar to Saccharomyces cerevisiae Fzo1p required for biogenesis of mitochondria (by homol
CA1669	orf19.2852	*IPF11393*	1.3	-1.0	-1.2	1.1	YBL090W	*MRP21*	1.0	1.0	-1.1	-1.4	unknown function
CA3666	orf19.6461	*IPF11435*	1.0	-1.1	1.1	-1.0	YDR231C	*COX20*	1.0	1.1	-1.1	-1.1	unknown function
CA3109	orf19.6548	*IPF11829*	1.2	-1.0	-1.1	-1.1	YPL135W	*ISU1*	1.0	1.0	1.1	1.1	unknown function
CA4829	orf19.2067	*IPF1210*	-1.0	1.1	1.1	1.1	YKL040C	*NFU1*	1.0	1.1	-1.0	-1.0	similar to Saccharomyces cerevisiae Nfu1p involved in homeostasis (by homology)
CA3419	orf19.6136	*IPF12778*	1.1	-1.3	-1.3	-1.1	YLR439W	*MRPL4*	1.0	-1.7	-2.1	-2.1	ribosomal protein, mitochondrial (by homology)
CA0370		*IPF13678*	1.1	1.2	1.6	1.3	YDR276C	*PMP3*	1.0	-1.1	-1.1	-1.1	unknown function

CA4642	orf19.349	*IPF1500*	-1.1	-1.0	1.0	1.0	YPR155C	*NCA2*	1.0	1.1	1.1	-1.2	similar to Saccharomyces cerevisiae Nca2p regulating expression of mitochondrial ATP syntha
CA0032	orf19.229	*IPF15248*	-1.0	1.0	1.0	1.0	YOL054W		1.0	-1.1	1.0	-1.1	zinc finger protein (by homology)
CA1015	orf19.11438	*IPF15547*	1.0	1.0	1.1	-1.0	YMR293C		1.0	-1.1	-1.5	-1.4	putative glutamyl-tRNA amidotransferase subunit A (by homology)
CA5413		*IPF1567*	1.2	1.1	1.1	1.2	YDR115W		1.0	-1.6	-1.7	-1.9	mitochondrial ribosomal protein L34 (by homology)
CA0010	orf19.7790	*IPF16036*	1.1	1.2	1.3	1.2	YJL143W	*TIM17*	1.0	-1.3	-1.3	1.0	similar to Saccharomyces cerevisiae Tim17p mitochondrial inner membrane import translocase
CA2213	orf19.4751	*IPF16405*	-1.0	-1.3	-1.1	1.1	YIL093C	*RSM25*	1.0	1.1	-1.1	-1.1	similar to saccharomyces cerevisiae Rsm25p protein of the small subunit of the mitochondrial r
CA0118		*IPF16430.3*	1.1	-1.1	-1.0	1.1	YFR033C	*QCR6*	1.0	1.3	1.1	-1.6	similar to Saccharomyces cerevisiae Qcr6p ubiquinol-cytochrome-c reductase 17K protein, 3-p
CA2899	orf19.3480	*IPF17681*	-1.3	-1.5	-1.7	-1.5	YGL129C	*RSM23*	1.0	-1.1	-1.1	1.2	similar to Saccharomyces cerevisiae Rsm23p involved in mitochondrial function (by homology)
CA0117	orf19.916	*IPF19231*	1.2	1.1	1.4	1.5	YNL305C		1.0	1.2	1.2	-1.3	unknown function
CA4033	orf19.3431	*IPF19795*	1.1	1.1	1.0	-1.0	YOR330C	*MIP1*	1.0	1.1	1.3	1.4	similar to Saccharomyces cerevisiae Mip1p DNA-directed DNA polymerase gamma catalytic su
CA3027	orf19.11381	*IPF20126*	-1.0	-1.0	1.1	-1.0	YDR470C	*UGO1*	1.0	-1.9	-1.8	-1.7	putative chromosome segregation protein (by homology)
CA5441	orf19.3244	*IPF227*	1.0	-1.1	-1.2	1.0	YHR116W		1.0	-1.7	-1.0	1.1	unknown function
CA5208	orf19.7023	*IPF2361*	-1.1	1.0	1.0	1.0	YLR455W		1.0	-1.5	-2.3	-2.4	unknown function
CA4299	orf19.6698	*IPF2598*	1.0	1.0	-1.0	1.0	YCR024C		1.0	1.2	1.0	1.2	unknown function
CA5212	orf19.7029	*IPF3050*	1.1	1.0	1.0	1.0	YDL238C		1.0	-2.1	-1.8	-1.4	unknown function
CA5222	orf19.7041	*IPF3079*	-1.1	-1.2	-1.2	-1.3	YAL043C	*PTA1*	1.0	-1.2	-1.1	-1.1	similar to Saccharomyces cerevisiae Pta1p pre-tRNA processing protein (by homology)
CA5224	orf19.7043	*IPF3081*	1.0	1.1	1.0	-1.0	YLR050C		1.0	-1.0	-1.4	-1.3	unknown function
CA1259	orf19.10676	*IPF3174*	-1.1	-1.0	-1.0	1.0	YPL172C	*COX10*	1.0	-1.1	-1.1	-1.1	Farnesyl transferase (by homology)
CA3484	orf19.3574	*IPF3214*	1.0	1.1	-1.0	-1.0	YNL328C	*MDJ2*	1.0	-1.1	-1.0	-1.0	HSP-mitochondrial chaperone (by homology)
CA5684	orf19.7386	*IPF3331*	1.2	1.1	1.1	-1.1	YBR185C	*MBA1*	1.0	-1.4	-1.5	-1.3	unknown function
CA4783	orf19.4016	*IPF3358*	-1.1	-1.3	-1.6	-1.4	YBL045C	*COR1*	1.0	-1.8	-1.9	-2.4	ubiquinol-cytochrome-c reductase (by homology)
CA4785	orf19.4018	*IPF3361*	1.2	-1.1	-1.1	-1.1	YJR113C	*RSM7*	1.0	1.2	1.1	1.2	putative mitochondrial ribosomal protein S7 (by homology)
CA4789	orf19.4023	*IPF3366*	1.1	1.0	1.0	1.0	YPR166C	*MRP2*	1.0	-1.1	-1.1	-1.2	Mitochondrial ribosomal protein (by homology)
CA5945	orf19.6752	*IPF3492*	-1.0	-1.0	-1.1	-1.0	YDR041W	*RSM10*	1.0	-1.5	-1.1	-1.1	unknown function
CA5056	orf19.3022	*IPF3698*	1.1	-1.3	-1.4	-1.2	YDR175C	*RSM24*	1.0	-1.5	-1.5	-1.6	similar to Saccharomyces cerevisiae Rsm24p mitochondrial ribosomal protein (S24) (by homol
CA4867	orf19.3844	*IPF4080*	-1.0	1.0	-1.0	1.1	YKL142W	*MRP8*	1.0	-2.4	-1.8	-2.9	similar to Saccharomyces cerevisiae Mrp8p ribosomal protein, mitochondrial (by homology)
CA5800	orf19.5450	*IPF4175*	1.1	-1.2	-1.1	-1.1	YBR026C	*MRF1'*	1.0	1.0	-1.4	-1.6	mitochondrial respiratory function (by homology)
CA4260	orf19.549	*IPF4276*	1.1	-1.1	-1.1	-1.0	YCR003W	*MRPL32*	1.0	-1.1	-1.1	-1.2	similar to Saccharomyces cerevisiae Mrpl32p putative mitochondrial ribosomal protein (by hom
CA2524	orf19.5521	*IPF4322*	1.1	-1.2	-1.2	-1.2	YLL027W	*ISA1*	1.0	-1.3	-1.4	-1.6	unknown function
CA3856	orf19.6100	*IPF4641*	1.1	1.1	1.1	1.0	YDL142C	*CRD1*	1.0	-1.3	-1.1	-1.1	similar to Saccharomyces cerevisiae Crd1p cardiolipin synthase (by homology)
CA0986	orf19.3350	*IPF4814*	-1.0	-1.0	-1.1	-1.1	YDR405W	*MRP20*	1.0	-1.1	-1.0	1.1	similar to Saccharomyces cerevisiae Mrp20p ribosomal protein of the large subunit, mitochondr
CA2129	orf19.414	*IPF4899*	-1.0	-1.1	-1.1	1.0	YKL155C	*RSM22*	1.0	-1.2	-1.1	1.0	unknown function
CA6049	orf19.7665	*IPF4935*	1.0	1.1	-1.0	-1.0	YJL003W		1.0	1.0	1.1	1.0	unknown function
CA6056	orf19.7675	*IPF4955*	1.1	-1.0	1.1	-1.0	YGR076C	*MRPL25*	1.0	-3.0	-5.8	-4.0	similar to Saccharomyces cerevisiae Mrpl25p ribosomal protein YmL25, mitochondrial (by hom
CA4087	orf19.6643	*IPF5013*	-1.0	-1.1	-1.1	-1.0	YOR221C	*MCT1*	1.0	-1.0	-1.0	-1.0	similar to Saccharomyces cerevisiae Mct1p malonyl-CoA:ACP transferase (by homology)
CA4370	orf19.5661	*IPF5279*	-1.2	1.1	-1.1	1.0	YHR076W		1.0	-1.2	-1.2	-1.2	unknown function
CA5589	orf19.7111	*IPF5621*	-1.1	-1.1	-1.0	-1.0	YIL065C	*FIS1*	1.0	-1.4	-1.4	-1.5	unknown function
CA4607	orf19.3297	*IPF6223*	1.1	-1.0	1.1	1.0	YGR215W	*RSM27*	1.0	-1.4	-1.3	-1.2	unknown function
CA3446	orf19.2977	*IPF7324*	-1.1	-1.1	-1.2	-1.1	YKL195W		1.0	-1.2	-1.2	-1.1	unknown function
CA1768	orf19.5201	*IPF7585*	1.1	1.0	1.0	1.1	YER050C	*RSM18*	1.0	1.1	1.2	1.0	unknown function
CA2930	orf19.4204	*IPF7840*	1.0	-1.1	-1.1	-1.0	YOR158W	*PET123*	1.0	-1.3	-1.2	-1.3	similar to Saccharomyces cerevisiae Pet123p ribosomal protein, mitochondrial (by homology)
CA0940		*IPF8616*	1.1	1.0	1.0	-1.0	YNR037C	*RSM19*	1.0	-1.1	1.0	1.1	similar to Saccharomyces cerevisiae Rsm19p ribosomal protein (by homology)
CA2465	orf19.1795	*IPF8726*	1.0	-1.1	1.2	1.0	YLL013C	*PUF3*	1.0	-1.1	-1.2	-1.2	unknown function
CA4226	orf19.828	*IPF8752*	-1.1	-1.2	-1.3	-1.1	YMR193W	*MRPL24*	1.0	1.1	-1.0	-1.3	similar to Saccharomyces cerevisiae Mrpl24p ribosomal protein of the large subunit, mitochond
CA1976	orf19.688	*IPF9582*	1.1	-1.1	-1.2	-1.0	YNL306W	*MRPS18*	1.0	-1.3	-1.5	-1.7	similar to Saccharomyces cerevisiae Mrps18p ribosomal protein of the small subunit, mitochon
CA3088	orf19.11621	*IPF9826*	-1.2	-1.1	1.1	1.1	YLR256W	*HAP1*	1.0	-1.4	-1.4	-1.1	unknown function
CA5895	orf19.6811	*ISA2*	1.1	1.1	1.1	1.0	YPR067W	*ISA2*	1.0	-1.6	-1.4	-1.4	Mitochondrial protein required for iron metabolism (by homology)
CA2742	orf19.2104	*JAC1*	-1.0	1.1	1.0	-1.1	YGL018C	*JAC1*	1.0	-1.1	1.2	1.1	molecular chaperone (by homology)
CA5205	orf19.7020	*KEX1*	-1.2	1.1	-1.0	1.1	YGL203C	*KEX1*	1.0	-1.3	-1.2	1.0	Carboxypeptidase-alpha (by homology)
CA3149	orf19.6165	*KGD1*	1.1	-2.0	-2.1	-2.0	YIL125W	*KGD1*	1.0	-2.5	-2.1	-3.6	2-oxoglutarate dehydrogenase
CA2997	orf19.6126	*KGD2*	-1.4	-2.7	-3.2	-2.6	YDR148C	*KGD2*	1.0	-1.9	-1.6	-2.7	2-oxoglutarate dehydrogenase complex E2 component (by homology)
CA2998	orf19.6127	*LPD1*	-1.3	-1.9	-2.6	-2.0	YFL018C	*LPD1*	1.0	-1.9	-2.1	-2.1	dihydrolipoamide dehydrogenase (by homology)
CA0791	orf19.3358	*LSC1*	1.1	-1.9	-1.8	-1.7	YOR142W	*LSC1*	1.0	-1.4	-1.4	-1.6	succinate-CoA ligase / synthetase (by homology)
CA0664	orf19.710	*LSC2.3EOC1*	1.0	-2.7	-2.9	-2.7	YGR244C	*LSC2*	1.0	1.1	-1.3	-2.7	succinate-CoA ligase beta subunit, 3-prime end (by homology)
CA3757	orf19.3419	*MAE1*	-1.2	1.0	1.2	-1.2	YKL029C	*MAE1*	1.0	1.2	1.8	4.4	mitochondrial malic enzyme (by homology)
CA5316	orf19.7187	*MAM33*	1.3	-1.5	-1.4	-1.4	YIL070C	*MAM33*	1.0	-1.2	-1.2	-1.5	Mitochondrial acidic matrix protein (by homology)
CA3234	orf19.6295	*MAS2*	-1.1	-1.0	-1.1	-1.1	YHR024C	*MAS2*	1.0	-1.1	-1.2	-1.1	processing peptidase, catalytic 53kDa (alpha) subunit, mitochondrial (by homology)
CA5209	orf19.7025	*MCM1*	1.0	-1.0	1.2	1.0	YMR043W	*MCM1*	1.0	-1.2	1.1	1.2	Transcription factor of the MADS box (by homology)
CA5164	orf19.4602	*MDH1*	1.2	-1.4	-1.4	-1.4	YKL085W	*MDH1*	1.0	-1.3	-1.5	-3.0	Mitochondrial malate dehydrogenase precursor (by homology)
CA5489	orf19.5323	*MDH12*	1.2	-1.1	1.2	-1.0	YDL078C	*MDH3*	1.0	-1.0	-1.2	-1.7	mitochondrial malate dehydrogenase (by homology)
CA4275	orf19.6672	*MDJ1*	1.0	1.0	1.0	1.0	YFL016C	*MDJ1*	1.0	1.0	1.1	-1.2	Heat shock protein - chaperone (by homology)
CA0236	orf19.7814	*MDM10*	1.0	-1.0	-1.0	-1.0	YAL010C	*MDM10*	1.0	1.0	1.0	1.0	Involved in mitochondrial morphology and inheritance (by homology)
CA4582	orf19.6900	*MDM12*	-1.1	-1.0	-1.1	-1.1	YOL009C	*MDM12*	1.0	-1.1	1.0	-1.1	Involved in mitochondrial inheritance (by homology)
CA3603	orf19.4932	*MEF1*	-1.3	-1.8	-2.0	-2.0	YLR069C	*MEF1*	1.0	-2.3	-5.7	-2.6	mitochondrial translation elongation factor G (by homology)
CA3212	orf19.6208	*MEF2*	-1.1	-1.4	-1.3	-1.4	YJL102W	*MEF2*	1.0	-1.3	-1.4	-1.5	translation elongation factor (by homology)
CA1738	orf19.2524	*MGE1*	1.1	1.0	1.1	-1.0	YOR232W	*MGE1*	1.0	-1.0	-1.3	-1.3	heat shock protein (by homology)
CA2773	orf19.2690	*MGM1*	-1.1	-1.2	-1.1	-1.1	YOR211C	*MGM1*	1.0	-1.2	1.1	1.1	GTPase

CA4177	orf19.2956	*MGM101*	-1.0	1.0	1.1	1.0	YJR144W	*MGM101*	1.0	-2.4	-2.3	-2.0	mitochondrial genome maintenance protein (by homology)
CA1374	orf19.1195	*MIP1*	-1.2	1.0	1.1	-1.1	YKL134C	*01-Oct*	1.0	-1.7	-1.8	-2.2	Mitochondrial intermediate peptidase (by homology)
CA1513	orf19.4885	*MIR1*	-1.0	-1.0	-1.0	-1.1	YJR077C	*MIR1*	1.0	-1.3	-1.2	-1.3	phosphate transport protein, mitochondrial (MCF) (by homology)
CA2250	orf19.2364	*MIS11*	-1.0	-1.3	-1.3	-1.3	YBR084W	*MIS1*	1.0	-1.6	-1.3	1.3	mitochondrial C1-tetrahydrofolate synthase precursor (by homology)
CA1937	orf19.4187	*MMM1*	1.0	-1.0	-1.1	-1.0	YLL006W	*MMM1*	1.0	1.1	-1.0	-1.2	mitochondrial outer membrane protein (by homology)
CA5405	orf19.947	*MRP17*	1.0	1.0	-1.0	1.1	YKL003C	*MRP17*	1.0	-1.3	-1.4	-1.5	Mitochondrial ribosomal protein (by homology)
CA1428	orf19.13170	*MRP4*	-1.3	-1.5	-1.4	-1.3	YHL004W	*MRP4*	1.0	-1.0	-1.2	-1.2	Ribosomal protein of the small subunit mitochondrial (by homology)
CA1445	orf19.185	*MRP51*	1.1	-1.0	-1.0	1.0	YPL118W	*MRP51*	1.0	-1.2	-1.4	-1.5	Mitochondrial ribosomal protein of the small subunit (by homology)
CA5329	orf19.7203	*MRP7*	-1.1	-1.2	-1.1	-1.1	YNL005C	*MRP7*	1.0	1.1	1.0	-1.1	Mitochondrial ribosomal protein YmL2 precursor (by homology)
CA1421	orf19.11278	*MRPL11*	1.1	-1.3	-1.2	-1.1	YDL202W	*MRPL11*	1.0	1.2	1.2	-1.0	Mitochondrial ribosomal protein (by komology)
CA0910	orf19.9569	*MRPL16*	1.3	-1.0	-1.1	1.1	YBL038W	*MRPL16*	1.0	-1.6	-1.7	1.1	ribosomal protein
CA3432	orf19.585	*MRPL17*	1.1	-1.0	1.2	1.1	YNL252C	*MRPL17*	1.0	-1.0	1.1	-1.1	ribosomal protein of the large subunit (YmL30), mitochondrial (by homology)
CA3009	orf19.13611	*MRPL19*	-1.0	-1.0	-1.1	-1.1	YNL185C	*MRPL19*	1.0	-1.2	1.0	-1.1	Ribosomal protein (by homology)
CA2725	orf19.10856	*MRPL23A*	1.0	-1.0	1.0	1.0	YOR150W	*MRPL23*	1.0	-1.4	-1.4	-1.6	mitochondrial ribosomal protein L23 (by homology)
CA5089	orf19.3064	*MRPL27*	1.1	1.0	1.0	1.0	YBR282W	*MRPL27*	1.0	-1.1	-1.2	-1.2	ribosomal protein (by homology)
CA3872	orf19.397	*MRPL28*	1.0	-1.0	-1.2	-1.0	YDR462W	*MRPL28*	1.0	-1.4	-1.3	-1.6	mitochondrial ribosomal protein of the large subunit (by homology)
CA0089	orf19.5064	*MRPL3*	-1.0	-1.2	-1.0	-1.1	YMR024W	*MRPL3*	1.0	1.1	1.1	1.0	ribosomal protein of the large subunit, mitochondrial (by homology)
CA0908	orf19.1485	*MRPL31*	1.3	1.1	1.2	1.1	YKL138C	*MRPL31*	1.0	1.0	-1.1	-1.4	Mitochondrial ribosomal protein
CA2142		*MRPL33*	1.0	1.1	1.0	1.0	YMR286W	*MRPL33*					ribosomal protein of the large subunit, mitochondrial (by homology)
CA1863	orf19.863	*MRPL35*	-1.2	-1.3	-1.4	-1.1	YDR322W	*MRPL35*	1.0	-1.1	-1.1	1.1	Ribosomal protein of the large subunit, mitochondrial (by homology)
CA2481	orf19.3205	*MRPL36*	-1.0	-1.2	-1.2	-1.1	YBR122C	*MRPL36*	1.0	1.1	-1.1	-1.1	ribosomal protein YmL36 precursor, mitochondrial (by homology)
CA1928	orf19.755	*MRPL37*	1.0	1.0	1.0	1.0	YBR268W	*MRPL37*	1.0	-1.0	-1.0	-1.3	Mitochondrial ribosomal protein YmL37 (by homology)
CA4521	orf19.484	*MRPL40*	-1.1	-1.3	-1.4	-1.2	YPL173W	*MRPL40*	1.0	1.0	-1.2	-1.3	Putative mitochondrial ribosomal protein (by homology)
CA4434	orf19.5161	*MRPL49*	1.5	1.1	1.4	1.2	YJL096W	*MRPL49*	1.0	-1.3	-1.4	-1.5	ribosomal protein mitochondrial
CA5831	orf19.7486	*MRPL6*	1.1	-1.0	-1.1	1.0	YHR147C	*MRPL6*	1.0	-1.2	-1.6	-1.7	ribosomal protein L6 precursor, mitochondrial (by homology)
CA2377	orf19.2214	*MRPL7*	1.0	1.0	-1.1	-1.0	YDR237W	*MRPL7*					Ribosomal protein of the large subunit, mitochondrial (by homology)
CA2999	orf19.6129	*MRPL8*	1.0	1.2	1.2	1.1	YJL063C	*MRPL8*	1.0	1.0	1.3	1.2	mitochondrial 60s ribosomal subunit (by homology)
CA5830	orf19.7485	*MRPL9*	1.1	-1.0	-1.2	-1.0	YGR220C	*MRPL9*	1.0	-1.1	-1.3	-1.2	Mitochondrial ribosomal protein of the large subunit (by homology)
CA0462	orf19.2520	*MRPS28*	1.0	-1.1	-1.1	-1.1	YDR337W	*MRPS28*	1.0	-1.0	-1.1	1.1	ribosomal protein (by homology)
CA3526	orf19.8604	*MRPS5*	-1.0	-1.3	-1.3	-1.2	YBR251W	*MRPS5*	1.0	1.1	1.1	-1.0	Probable ribosomal protein S5, mitochondrial (by homology)
CA1109	orf19.5230	*MRPS9*	1.1	-1.0	-1.0	1.0	YBR146W	*MRPS9*	1.0	1.2	1.4	1.2	ribosomal protein S9 small subunit precursor
CA2271	orf19.2597	*MRS2*	-1.0	1.0	-1.0	1.0	YOR334W	*MRS2*	1.0	-1.2	-1.3	-1.1	Mitochondrial RNA splicing protein (by homology)
CA3741	orf19.2178	*MRS4*	1.1	1.2	1.3	1.3	YKR052C	*MRS4*	1.0	-1.4	-1.3	-1.3	RNA splicing protein and member of the mitochondrial carrier family (MCF) by homology
CA3648	orf19.2039	*MSF1*	-1.1	-1.1	-1.1	-1.1	YPR047W	*MSF1*	1.0	-1.4	-1.4	-1.6	phenylalanine--tRNA ligase
CA2036	orf19.4362	*MSP1*	1.0	-1.0	1.0	1.0	YGR028W	*MSP1*	1.0	-1.1	-1.0	-1.0	40 kDa putative membrane-spanning ATPase
CA3651	orf19.2042	*MSS1*	-1.1	-1.1	-1.0	1.1	YMR023C	*MSS1*	1.0	1.1	1.5	1.2	Mitochondrial GTPase involved in expression of COX1 (by homology).
CA1945	orf19.4739	*MSS116*	-1.0	-1.1	-1.0	-1.0	YDR194C	*MSS116*	1.0	-1.7	-1.7	-1.4	RNA helicase of the DEAD box family (by homology)
CA5220	orf19.7038	*MVP1.EXON2*	1.1	1.0	-1.0	1.0	YMR004W	*MVP1*	1.0	1.0	1.0	1.0	Required for vacuolar protein sorting, exon 2 (by homology)
CA4508	orf19.498	*NAM9*	-1.1	-1.1	-1.2	-1.1	YNL137C	*NAM9*	1.0	-1.3	-1.2	-1.4	mitochondrial ribosomal protein
CA4633	orf19.339	*NDH1*	-1.2	3.1	3.7	2.9	YMR145C		1.0	-1.0	1.2	-1.0	Mitochondrial NADH dehydrogenase
CA5417	orf19.967	*NUC1*	1.0	1.0	1.1	-1.0	YJL208C	*NUC1*	1.0	-1.4	-1.1	-1.2	Nuclease, mitochondrial
CA5710	orf19.7411	*OAC1*	1.0	1.1	1.0	-1.0	YKL120W	*OAC1*	1.0	1.1	1.2	1.4	Mitochondrial oxaloacetate transport protein (by homology)
CA4878	orf19.6565	*OXA1*	-1.0	-1.2	-1.2	-1.2	YER154W	*OXA1*	1.0	1.5	1.7	-1.1	Cytochrome oxidase biogenesis protein (by homology)
CA3308	orf19.9845	*PET127*	-1.0	-1.1	-1.0	-1.0	YOR017W	*PET127*	1.0	-1.3	1.1	1.1	component of mitochondrial translation (by homology)
CA5759		*PET191.3*	1.0	1.0	1.1	1.0	YJR034W	*PET191*	1.0	-1.2	-1.4	-1.4	Assembly of cytochrome oxidase, 3-prime end (by homology)
CA0029	orf19.182	*PET56*	-1.0	1.0	-1.1	-1.1	YOR201C	*PET56*	1.0	-1.7	-1.1	1.2	ribosomal RNA methylase (by homology)
CA4711	orf19.6944	*PHB1*	-1.0	-1.3	-1.3	-1.3	YGR132C	*PHB1*	1.0	-1.4	-1.1	-1.1	Prohibitin, antiproliferative protein (by homology)
CA6086	orf19.5973	*PHB2*	-1.0	-1.2	-1.3	1.0	YGR231C	*PHB2*	1.0	1.2	1.1	-1.0	Mitochondrial protein, prohibitin homolog (by homology)
CA3002	orf19.6133	*PIF1*	-1.0	-1.1	-1.1	-1.1	YML061C	*PIF1*	1.0	-1.6	-1.7	-1.6	mitochondrial DNA helicase (by homology)
CA5871	orf19.7538	*PIF2*	1.0	1.1	1.4	1.0	YHR031C	*RRM3*	1.0	-1.2	-1.1	-1.2	DNA helicase (by homology)
CA4238	orf19.522	*PIM1*	-1.0	-1.0	-1.1	-1.2	YBL022C	*PIM1*	1.0	-1.2	-1.2	-1.2	mitochondrial ATP-dependent protease (by homology)
CA0919	orf19.1042	*POR1*	1.6	-1.4	-1.3	-1.3	YNL055C	*POR1*	1.0	-1.1	-1.2	-1.7	mitochondrial outer membrane porin (by homology)
CA3070	orf19.4807	*PPA2*	-1.1	-1.2	-1.2	-1.2	YMR267W	*PPA2*	1.0	1.0	-1.2	-1.3	Mitochondrial inorganic pyrophosphatase
CA5215	orf19.7033	*PPS1*	1.0	1.1	1.0	1.1	YBR276C	*PPS1*	1.0	1.5	-1.1	1.1	protein tyrosine phosphatase (by homology)
CA1349	orf19.4351	*PRP12*	-1.2	1.1	-1.0	-1.2	YMR302C	*PRP12*	1.0	-1.4	-1.2	-1.3	involved in early maturation of pre-rRNA (by homology)
CA1552	orf19.4274	*PUT1*	-1.4	-4.0	-5.4	-3.7	YLR142W	*PUT1*	1.0	-1.5	-1.4	-1.5	proline oxidase (by homology)
CA3399	orf19.3974	*PUT2*	-1.3	-8.3	-9.8	-7.1	YHR037W	*PUT2*	1.0	-1.2	-1.2	1.2	1-pyrroline-5-carboxylate dehydrogenase (by homology)
CA2065	orf19.2644	*QCR2*	1.0	-1.2	-1.2	-1.0	YPR191W	*QCR2*	1.0	-1.2	-1.3	-2.0	Ubiquinol--cytochrome-c reductase 40KD chain II (by homology)
CA1441		*QCR8*	1.5	1.0	1.1	1.1	YJL166W	*QCR8*	1.0	-1.5	-1.4	-2.5	ubiquinol-cytochrome-c reductase chain VIII (by homology)
CA5217	orf19.7035	*RFC2*	1.1	1.0	1.0	1.0	YJR068W	*RFC2*	1.0	1.0	1.1	-1.1	Replication factor (by homology)
CA1111	orf19.12693	*RIB3*	1.1	1.3	1.4	1.1	YDR487C	*RIB3*	1.0	1.3	1.3	1.6	3,4-dihydroxy-2-butanone 4-phosphate synthase (by homology)
CA6149	orf19.5893	*RIP1*	-1.5	-1.5	-1.7	-1.5	YEL024W	*RIP1*	1.0	1.1	1.2	-1.1	Ubiquinol cytochrome-c reductase (by homology)
CA5776	orf19.5420	*RML2*	-1.1	-1.2	-1.3	-1.2	YEL050C	*RML2*	1.0	1.0	-1.3	-1.3	Ribosomal L2 protein, mitochondrial (by homology)
CA4904	orf19.6041	*RPO41*	-1.2	-1.3	-1.9	-1.5	YFL036W	*RPO41*	1.0	-1.1	-1.3	-1.3	Mitochondrial DNA-directed RNA polymerase (by homology)
CA5561	orf19.7325	*SCO1*	1.0	1.0	1.1	1.1	YBR037C	*SCO1*	1.0	-2.4	-2.1	-1.3	Inner mitochondrial membrane protein (by homology)
CA4063	orf19.440	*SDH11*	-1.1	-1.1	-1.1	-1.1	YKL148C	*SDH1*	1.0	-1.3	-1.5	-2.1	Succinate dehydrogenase (by homology)
CA5398	orf19.941	*SEC14*	-1.0	-1.2	-1.1	-1.0	YMR079W	*SEC14*					phosphatidylinositol(PI)/phosphatidylcholine(PC) transfer

CA4742	orf19.4841	*SHY1*	1.1	-1.1	1.1	1.0	YGR112W	*SHY1*	1.0	-1.1	1.1	1.3	SURF homologue protein (by homology)
CA4540	orf19.1462	*SMP2*	-1.1	-1.0	-1.1	1.0	YMR165C	*SMP2*	1.0	1.1	-1.1	-1.2	Involved in plasmid maintenance, respiration and cell proliferation (by homology)
CA4474	orf19.1896	*SSC1*	1.4	-1.1	-1.2	-1.6	YJR045C	*SSC1*	1.0	-1.3	-1.2	-1.5	Mitochondrial heat shock protein 70-related protein (by homology)
CA1911	orf19.2435	*SSE1*	-1.5	-1.5	-1.7	-1.5	YPL106C	*SSE1*	1.0	1.2	2.0	2.8	heat shock protein of HSP70 family (by homology)
CA5213	orf19.7030	*SSR1*	1.4	1.2	1.5	1.1	YLR390W	*ECM19*	1.0	1.2	1.4	1.4	Secretory Stress Response protein 1 (by homology)
CA6075	orf19.5986	*THI4*	-1.0	1.0	1.0	-1.1	YGR144W	*THI4*	1.0	1.1	1.0	1.3	Thiazole biosynthetic enzyme precursor (by homology)
CA5181	orf19.4620	*TIM12*	1.0	1.0	1.0	1.0	YBR091C	*MRS5*	1.0	-1.2	-1.2	-1.2	subunit of the TIM22-complex (by homology)
CA1893	orf19.2754	*TIM13*	1.0	1.1	1.1	1.1	YGR181W	*TIM13*	1.0	-2.1	-1.8	-1.7	subunit of mitochondrial protein import machinery-like by homology
CA0367	orf19.1352	*TIM22*	-1.1	1.5	1.7	1.4	YDL217C	*TIM22*	1.0	1.1	1.1	1.2	Mitochondrial import inner membrane translocase subunit (by homology)
CA5795	orf19.5444	*TIM44*	-1.0	-1.1	-1.3	-1.2	YIL022W	*TIM44*	1.0	-1.3	-1.3	-1.4	mitochondrial inner membrane import receptor
CA4179	orf19.2953	*TOM20*	1.2	1.1	1.5	1.4	YGR082W	*TOM20*	1.0	1.2	1.1	-1.1	mitochondrial outer membrane import receptor subunit, 20 kD (by homology)
CA1401	orf19.3696	*TOM22*	1.0	-1.0	1.0	1.0	YNL131W	*TOM22*	1.0	-1.3	-1.7	-2.2	mitochondrial outer membrane import receptor complex subunit (by homology)
CA4954	orf19.6524	*TOM40*	-1.3	-1.3	-1.4	-1.5	YMR203W	*TOM40*	1.0	-1.1	-1.0	-1.1	mitochondrial import receptor chain TOM40 (by homology)
CA1043	orf19.9219	*TOM6*	1.0	-1.1	1.1	-1.1	YOR045W	*TOM6*	1.0	1.1	-1.1	-1.8	mitochondrial outer membrane import receptor subunit (by homology)
CA5218	orf19.7036	*WHI2*	-1.1	-1.1	-1.1	-1.1	YOR043W	*WHI2*	1.0	-1.5	-1.2	-1.2	Growth regulation factor (by homology)
CA5219	orf19.7037	*YAE1*	1.0	-1.2	1.1	1.0	YJR067C	*YAE1*	1.0	-1.2	-1.4	-1.5	Essential protein
CA1477	orf19.1252	*YME1*	-1.2	-1.3	-1.3	-1.2	YPR024W	*YME1*	1.0	-1.1	1.5	1.2	family of ATPases
CA5204	orf19.7019	*YML6*	-1.0	-1.2	-1.1	-1.1	YML025C						Ribosomal protein, mitochondrial (by homology)
CA4537	orf19.1466	*YNT2*	1.1	-1.1	1.0	-1.0	YLR059C	*REX2*	1.0	-1.6	-1.9	-1.7	suppressor of rna12/yme2 (by homology)
CA2269	orf19.2599	*YOR100*	1.2	-1.8	-2.0	-1.6	YOR100C	*CRC1*	1.0	-1.1	-1.1	-1.1	Putative mitochondrial carrier protein
CA4838	orf19.2057	*YTA12*	-1.4	-1.3	-1.8	-1.5	YMR089C	*YTA12*	1.0	-1.3	1.2	-1.1	Protease of the SEC18/CDC48/PAS1 family of ATPases (AAA) (by homology)
Mean			***0.1***	***-0.4***	***-0.4***	***-0.3***			***1.0***	***-0.7***	***-0.7***	***-0.9***	
***COX* genes**													
CA3958	orf19.1416	*COX11*	1.1	1.1	1.3	1.0	YPL132W	*COX11*	1.0	-1.1	-1.0	-1.2	cytochrome-c oxidase assembly protein by homology to S. cerevisiae
CA4536	orf19.1467	*COX13*	1.2	-1.0	1.1	1.2	YGL191W	*COX13*	1.0	-1.2	-1.5	-2.4	cytochrome-c oxidase chain VIa (by homology)
CA1688	orf19.3656	*COX15*	-1.1	2.0	2.6	2.5	YER141W	*COX15*	1.0	-1.4	-1.4	-1.6	cytochrome oxidase assembly factor (by homology)
CA1090	orf19.3946	*COX18*	-1.0	1.0	1.3	1.1	YGR062C	*COX18*	1.0	-1.1	-1.2	-1.1	protein required for activity of mitochondrial cytochrome oxidase (by homology)
CA4533	orf19.1471	*COX4*	1.2	1.1	1.3	1.1	YGL187C	*COX4*	1.0	1.1	-1.0	-1.9	cytochrome-c oxidase (by homology)
CA2630	orf19.12223	*COX5A*	1.3	-1.1	1.4	1.1	YNL052W	*COX5A*	1.0	1.3	1.4	-1.4	cytochrome-c oxidase chain V.A precursor (by homology)
CA0031	orf19.227	*COX7*	1.0	-1.0	1.0	1.1	YMR256C	*COX7*					Subunit VII of cytochrome c oxidase (by homology)
CA2134	orf19.5213	*COX8*	1.5	1.3	1.4	1.5	YLR395C	*COX8*	1.0	-1.1	-1.2	-1.5	CYTOCHROME C OXIDASE (by homology)
Mean			***0.7***	***0.4***	***1.4***	***1.3***			***1.0***	***-0.5***	***-0.9***	***-1.6***	

PCR primers to generate gene-specific probes

Gene	**Primer**	**Sequence (5'-->3')**
HXT62	HXT62-F	AAGAGTTGGTATCATGACTGC
HXT62	HXT62-R	GCCCAAGCAAAACATAAACCT
PCK1	PCK1-F	ATCTGTGCTAGAGCTTACCATGC
PCK1	PCK1-R	CCAGCATATTCAGTACCCAAGAT
IPF3584	IPF3584-F	AGCCATCGATAACAAAGC
IPF3584	IPF3584-R	GCCTTAACAGCAGATTCAT
QDR1	QDR1-F	AGGGAGTATTATTGTTTTCTGTGC
QDR1	QDR1-R	GCACGATAGTCAATGTTAGTCTAGAT
TEF3	TEF3-F	GGGTAATTGTTAATCTCTGG
TEF3	TEF3-R	ATAAAGCATCAGGAAGCAGCA