Supplementary Table 1. 363 genes with altered expression in an *ace2* delete relative to wildtype grown as yeast cells. (FDR of 0.23%).

				Log2 Ratios (7 experiments)							Average Fold Change
OligoID	**ORF19**[a]	**CGD Gene Name**[a]	**Description (from CandidaDB)**[b]	**Y1**	**Y2**	**Y3**	**Y4**	**Y5**	**Y6**	**Y7**	
2053.1	orf19.5267	orf19.5267	CA4983 IPF2053 unknown function (YJR151C)	-5.6743	-1.7939	-3.6428	-2.3863	-3.1960	-4.6065	-4.2919	-12.61
15862.2	orf19.3893	SCW11	CA1053 SCW11.3eoc glucanase gene family member, 3-prime end (by homology)	-2.5081	-3.5913	-4.2627	-2.3438	-3.4264	-3.8079	-3.9154	-10.61
11998.2	orf19.2758	orf19.2758	CA1898 IPF11998 unknown function (putative GPI-anchored, PGA38)	-1.6258	-2.0039	-5.0951	-3.1896	-3.7743	-4.0424	-3.7335	-10.21
564.2	orf19.7104	orf19.7104	CA5596 IPF564 unknown function (N/A)	-4.3825	-0.8817	-2.8059	-1.1461	-1.3058	-2.3336	-2.4466	-4.55
19968.1	orf19.220	PIR1	CA3030 IPF19968 putative cell wall protein of the PIR family	-1.7947	-1.7249	-2.6484	-2.1117	-2.1235	-2.1374	-2.0700	-4.25
2535.1			CA0355 IPF2535 unknown function	-3.1078	-1.8890	-2.9434	-1.3808	-1.0559	-0.9132	-2.8890	-4.07
696.1	orf19.7586	CHT3	CA5987 CHT3 chitinase 3 precursor	-0.2350	0.0498	-2.8475	-1.8911	-2.6904	-2.1489	-2.7371	-3.45
763.2	orf19.5343	ASH1	CA5502 IPF763 putative transcription factor with a Cys4- zinc finger (ASH1)	-3.0566	-1.5544	-2.6543	-0.4252	-1.1711	-1.0239	-2.0334	-3.26
6235.2	orf19.5372	orf19.5372	CA2216 IPF6235 Candida albicans Tca2 retrotransposon	-1.9658	-1.2416	-0.4129	-1.6029	-2.2518	-2.2239	-2.0125	-3.19
8321.2	orf19.3325	orf19.3325	CA2938 IPF8321 similar to Saccharomyces cerevisiae Glg2p self-glucosylating initiato	-1.3865	-0.6467	-0.7350	-1.5976	-2.3417	-2.2413	-2.6905	-3.17
6238.2	orf19.2374	orf19.2374	CA2752 IPF6238 GAG protein of retrotransposon pCal	-1.7299	-0.5946	-0.7952	-1.9462	-2.0035	-2.4014	-2.1497	-3.16
753.1	orf19.5348	TPS3	CA5505 TPS3.3 alpha,alpha-trehalose-phosphate synthase, regulatory subunit, 3-prim	-1.2723	-0.0058	0.0440	-2.1016	-2.4422	-2.6712	-2.6529	-3.00
9751.2	orf19.3066	ENG1	CA5091 ACF3 endo-1,3-beta-glucanase	-1.3832	-0.4970	-2.5736	-1.1255	-1.5699	-1.5718	-1.6934	-2.80
4065.1	orf19.1862	orf19.1862	CA0386 IPF4065 unknown function (YHR087w)	-1.2836	-0.2456	-0.0148	-1.7253	-1.8334	-2.4448	-2.8450	-2.80
11927.1	orf19.111	CAN2	CA1191 CAN2 amino acid permease (by homology)	-0.5146	-0.6016	-0.2260	-2.1392	-2.3808	-1.6484	-2.2863	-2.64
12467.2	orf19.1206	FET35	CA1431 FET34.3eoc iron transport multicopper oxidase, 3-prime end (by homology)	-1.9254	-1.3849	-0.3082	-1.6889	-1.0517	-1.2266	-2.1647	-2.63
17039.1	orf19.4215	FET34	CA2920 FET5 multicopy oxidase (by homology)	-1.6181	-0.4903	-0.8092	-1.4044	-1.1156	-1.3500	-2.3852	-2.48
4104.2	orf19.2020	HGT6	CA1070 HXT61 sugar transporter	-0.8009	-0.0469	-0.5543	-1.6804	-2.0710	-1.9771	-1.8314	-2.43
10363.2	orf19.3803	MNN22	CA0752 MNN22 Golgi alpha-1,2-mannosyltransferase (by homology)	-0.8520	-1.5064	-0.7809	-0.8520	-1.5995	-1.8997	-1.4620	-2.43
2357.1	orf19.7021	GPH1	CA5206 GPH1 Glycogen phosphorylase (by homology)	-1.0158	-0.0963	-0.5501	-1.7010	-2.0683	-2.0902	-1.4017	-2.42
10835.2	orf19.3629	orf19.3629	CA1278 IPF10835 unknown function (DSE1)	-1.2787	-0.7360	-1.9926	-0.9486	-0.7651	-0.9268	-2.0766	-2.37
14618.1	orf19.6079	orf19.6079	CA0286 IPF14618 unknown function (N/A)	0.0000	-0.4901	-0.0065	-0.8704	-2.7393	-2.0146	-2.5732	-2.37
10349.2	orf19.5079	CDR4	CA3895 CDR4 Multidrug resistance protein	-0.3838	-0.5386	-0.5651	-1.7881	-2.0178	-1.8263	-1.5676	-2.36
4732.2	orf19.3746	IFC1	CA3257 IFC1 Unknown Function (YPR194c, OPT2, peptide transporter)	-2.0218	-0.4070	-1.0589	-1.3111	-0.7312	-1.5494	-1.5358	-2.35
4286.2	orf19.542	HXK2	CA0127 HXK2.3f hexokinase II, 3-prime end (by homology)	-0.1763	-0.2934	-0.4403	-1.8160	-1.9214	-1.7131	-2.2243	-2.34
12812.2	orf19.3749	IFC3	CA2349 IFC3 Unknown function (YPR194c, peptide transporter)	-0.6967	0.0229	-0.9546	-1.8783	-1.0801	-1.7760	-1.9051	-2.27
5940.2	orf19.434	PRD1	CA4059 PRD1 Proteinase (by homology)	-0.4954	-0.5284	-0.1253	-1.6568	-1.5703	-2.0619	-1.8189	-2.27
3121.1	orf19.4438	RME1	CA4651 IPF3121 unknown function (YGR044c, RME1)	-1.0350	-0.3292	-0.1424	-1.1488	-2.5907	-1.6529	-1.3292	-2.26
9108.2	orf19.6124	ACE2	CA2996 IPF9108 similar to Saccharomyces cerevisiae Ace2p transcription factor (by homology)		-1.9159	-1.6082	-0.6620	-0.8678	-0.4266	-1.3401	-2.20
14295.1	orf19.6321	PGA48	CA3287 IPF14295 putative Sed1p-like cell surface protein (by homology)	0.0000	-0.6003	-1.4600	-0.8162	-1.4456	-1.5180	-1.9431	-2.16
872.1	orf19.7218	RBE1	CA5344 PRY2 putative pathogen related proteins (by homology)	-1.8136	-0.5554	-1.7040	-0.6094	-0.7894	-0.8366	-1.4562	-2.16
3735.1	orf19.5288	IFE2	CA2075 IFE2 Unknown function (YAL060W, BDH1, (2R,3R)-2,3-butanediol dehydroge	-0.7774	-0.2881	-0.2961	-1.3994	-1.6759	-1.6649	-1.6275	-2.15
17289.2	orf19.6134	orf19.6134	CA3422 IPF17289 unknown function (YLR440C)	-1.2345	-0.9214	-1.0499	-1.0893	-1.2413	-0.9602	-1.0710	-2.12
17763.2	orf19.6139	FRE7	CA3416 FRE30.3 Strong similarity to ferric reductase Fre2p, 3-prime end (by homolog	-0.3527	-0.3339	-1.5440	-0.6756	-1.8798	-1.3548	-1.3698	-2.10
5750.2	orf19.6540	PFK2	CA3112 PFK2 6-phosphofructokinase, beta subunit	-0.6461	-0.2845	-0.1001	-1.3437	-2.1392	-1.4150	-1.5522	-2.10
12521.2	orf19.6232	NPR1	CA0576 NPR1 nitrogen permease reactivator protein (by homology)	-0.3677	-0.7108	-0.2142	-1.7322	-1.5649	-1.5995	-1.2793	-2.09
17153.2	orf19.1314	orf19.1314	CA2822 IPF14550 unknown function (YMR031C? Zn finger)	-1.6171	-0.3292	-0.0740	-1.3959	-1.1109	-1.3959	-1.4982	-2.09
8762.2	orf19.822	orf19.822	CA4220 IPF8762 unknown function (N/A)	-1.9037	-0.7277	-1.0405	-0.9762	-0.7637	-0.8235	-1.1626	-2.08
14360.2	orf19.2706	CRH11	CA0375 CRH11 Probable membrane protein (by homology) glycosidase	0.0000	-0.9131	-2.1694	-0.6908	-1.7776	-1.1243	-0.5745	-2.05
9116.2	orf19.6119	orf19.6119	CA2994 IPF9116 unknown function (N/A)	-1.2984	-0.5023	-1.2916	-0.6066	-1.5163	-0.9270	-1.0130	-2.03
16625.2	orf19.3591	APE3	CA0871 APE3 aminopeptidase (by homology)	-1.5546	-0.5001	-0.9357	-0.5193	-0.8100	-1.3926	-1.3329	-2.01
4358.1	orf19.5911	CMK1	CA6135 CMK1 Ca2-dependent ser/thr protein kinase (by homology)	-0.5332	-0.2076	-0.5374	-1.1329	-1.6666	-1.6304	-1.3147	-2.00
8505.2	orf19.2613	ECM4	CA2386 ECM41.3 involved in cell wall biogenesis and architecture, 3-prime end (by ho	-0.9602	-0.2210	-0.1376	-1.2142	-1.6171	-1.4941	-1.3111	-1.99
11096.2	orf19.4618	FBA1	CA5180 FBA1 fructose-bisphosphate aldolase (by homology)	-0.7859	-0.0755	-0.1811	-1.2447	-1.5735	-1.6038	-1.4580	-1.98
16784.2	orf19.5113	ADH2	CA3923 ADH2 alcohol dehydrogenase I (by homology)	-0.9078	0.1777	-0.9302	-0.9931	-1.5847	-1.2227	-1.4375	-1.98
4991.2	orf19.2531	CSP37	CA1075 IPF4991 putative membrane protein (YDL058w, USO1, integrin)	-1.5692	-0.4383	0.0186	-1.2863		-1.4739	-1.1078	-1.97
7796.2	orf19.2619	PHO113	CA0616 PHO11 Secreted acid phosphatase		-1.2210	-1.5735	-0.6371	-0.7661	-0.3940	-1.2210	-1.96
10586.2	orf19.2655	BUB3	CA0526 BUB3 cell cycle arrest protein (by homology)	-1.2614	-0.7274	-0.4488	-0.6831	-1.3098	-1.2384	-1.1070	-1.96
15672.1	orf19.2607	orf19.2607	CA2392 IPF15672 unknown function (YKL128c? phosphomutase homologue)	-1.6905	-1.0711	-0.8516	-0.9107	0.0000	-0.9715	-1.2220	-1.94
10991.2	orf19.5801	RNR21	CA4155 RNR21 ribonucleoside-diphosphate reductase (by homology)	-1.1749	-0.4296	-0.4081	-1.0636	-1.5359	-1.2970	-0.7937	-1.94

12215.2	orf19.5058	SMI1	CA1740 SMI1 beta-1,3-glucan synthesis protein (by homology)	-0.6973	-0.9294	-0.3716	-1.2403	-0.9462	-1.1666	-1.2299	-1.92
9411.2	orf19.6147	orf19.6147	CA3410 IPF9411 unknown function (YER030w)	-1.0233	-1.0923	-0.9324	-1.3659	-0.6827	-0.4540	-0.9406	-1.90
4369.1	orf19.5917	STP3	CA6131 IPF4369 similar to Saccharomyces cerevisiae Stp2p involved in pre-tRNA spli	-0.1615	-0.8662	-0.9065	-0.9845	-0.7563	-1.4818	-1.3006	-1.90
7044.2	orf19.125	EBP1	CA1216 EBP1 NADPH dehydrogenase	-0.8237	-0.0321	-0.6082	-1.1424	-1.6574	-1.2828	-0.8916	-1.89
1203.2	orf19.2073	orf19.2073	CA4823 ERC3 ethionine resistance protein (by homology)		-0.8211	-0.6484	-1.1329	-0.9296	-0.8059	-1.1520	-1.89
7968.2	orf19.2693	orf19.2693	CA3260 IPF7968 unknown function (possible URE2, prion)	-0.4623	-0.7965	-0.4916	-1.2708	-0.7528	-1.4252	-1.1845	-1.88
20142.1	orf19.730	RGD3	CA3679 IPF20142 unknown function (YFL047w, RGD2, RhoGAP)	-0.8749	-1.2625	-0.1636	-0.5995	-1.4820	-1.0376	-0.9044	-1.87
8884.2	orf19.3422	FMP27	CA3756 IPF8884 unknown function (YLR454w, mitochondrial)	-1.1180	-0.0254	-1.0497	-0.6430	-1.0131	-1.1550	-1.2655	-1.86
19952.1	orf19.5636	RBT5	CA2558 RBT5 repressed by TUP1 protein 5	-0.6897	-0.3808	-0.6758	-0.7735	-1.4540	-1.0589	-1.2076	-1.86
10469.2	orf19.1789.1	LYS1	CA0343 LYS1.5eoc saccharopine dehydrogenase, 5-prime end (by homology)	-0.5700	-0.5765	-0.9140	-0.9508	-0.6758	-0.9603	-1.5779	-1.85
1147.2	orf19.2098	ARO8	CA4804 ARO8 aromatic amino acid aminotransferase I (by homology)	-0.6850	-0.1361	-0.6461	-1.0087	-1.0145	-0.8651	-1.8417	-1.85
12403.2	orf19.2484	orf19.2484	CA3805 IPF12403 unknown function (YDR415c)	-0.8417	-0.2793	-0.1392	-0.7084	-1.4501	-1.3474	-1.3622	-1.83
8248.2	orf19.1517	ARO3	CA1751 ARO3.exon2 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase, exon 2	-1.1475	-1.0544	-0.1999	-0.8549	-0.7298	-1.1442	-0.9644	-1.83
9939.2	orf19.4752	MSN4	CA2214 IPF9939 similar to Saccharomyces cerevisiae Msn4p transcriptional activator	-0.9164	-0.4503	-0.1844	-1.0273	-0.9994	-1.4416	-1.0703	-1.83
5949.2	orf19.6800	POS5	CA5906 IPF5949 unknown function (YPL188w, POS5, oxidative stress)	-0.4461	-0.8186	-0.1266	-0.7588	-1.2515	-1.0499	-1.6171	-1.82
7403.2	orf19.4664	orf19.4664	CA2710 IPF7403 unknown function (YMR069w, NAT4)	-1.8890	-0.6804	-0.3067	-0.6178	-0.7574	-0.7700	-1.0436	-1.82
7759.1	orf19.3888	PGI1	CA3559 PGI1 Glucose-6-phosphate isomerase	-1.1420	-0.1953	-0.4274	-1.0051	-1.3589	-1.1222	-0.7677	-1.81
17060.2	orf19.3997	ADH1	CA4765 ADH1 alcohol dehydrogenase (by homology)	-0.7408	-0.3215	-0.3743	-0.7999	-1.5330	-1.1256	-1.1177	-1.81
3598.2	orf19.3047	orf19.3047	CA5072 IPF3598 similar to Saccharomyces cerevisiae Sip3p protein which interacts wi	-0.4742	-0.2052	-0.5192	-1.1879	-1.1673	-1.0695	-1.2661	-1.79
19710.1	orf19.2970	LYS2	CA0916 LYS2 L-aminoadipate-semialdehyde dehydrogenase, large subunit	-0.5740	-0.7415	-0.3884	-0.9078	-1.2057	-0.9246	-1.1443	-1.79
4392.1	orf19.1474	SLA1	CA4531 SLA1 cytoskeleton assembly control protein	-1.0058	-0.9241	-0.3808	-0.8160	-0.6943	-0.7984	-1.2584	-1.79
525.1	orf19.7085	orf19.7085	CA5613 IPF525 unknown function (N/A)	-1.3310	-0.8640	-1.2167	-0.4686	-0.6007	-0.6993	-0.6800	-1.79
2795.1	orf19.6763	SLK19	CA5936 IPF2795 unknown function (YOR195w?)	-0.7616	-0.1149	-0.9051	-0.5600	-1.1641	-1.2027	-1.1188	-1.78
14337.2	orf19.1814	orf19.1814	CA0324 STT4 Phosphatidylinositol-4-kinase (by homology)		-0.1488	-0.6920	-0.7710	-1.2793	-0.8757	-1.2109	-1.78
2936.1	orf19.4304	GAP1	CA2638 GAP3 General amino acid permease (by homology)	-0.0908	-0.4673	-0.4103	-1.3394	-1.3026	-0.9702	-1.2004	-1.77
8985.2	orf19.1368	orf19.1368	CA0045 IPF8985.5eoc unknown function, 5-prime end (N/A)	-1.2758	-0.1234	-1.1329	-0.8997	-0.5842	-0.6304	-0.9324	-1.74
11299.2	orf19.5671	orf19.5671	CA4378 IPF11299 unknown function (YCR030C, SYP1)	-1.1392	-1.4659	-0.7131	-0.4982	-0.5973	-0.3147	-0.8314	-1.73
18418.1	orf19.5620	orf19.5620	CA2756 IPF18418 unknown function (YHR029C)	-0.5374	-0.2328	-0.5628	-0.9942	-1.0589	-1.1584	-0.9406	-1.72
4222.2	orf19.7323	CBP1	CA5559 CBP1 Corticosteroid binding protein	-0.2515	-0.1313	-0.7661	-1.1844	-0.9686	-1.0350	-1.1140	-1.72
857.1	orf19.7227	orf19.7227	CA5351 IPF857 unknown function (YFR003c, PP1 inhibitor)	-1.5877	-0.7026	-0.5626	-0.3731	-0.5393	-0.6419	-1.0310	-1.71
13176.2	orf19.5610	ARG3	CA2964 IPF13176.3 ornithine carbamoyltransferase, 3-prime end (by homology)		-0.8890	-0.6529	-0.7108	-1.4779	-0.2345	-0.6804	-1.71
15021.2	orf19.5615	AYR2	CA0163 AYR2 1-acyl dihydroxyacetone phosphate reductase (by homology)	-0.5995	-0.1266	-0.3058	-0.8391	-1.3437	-0.9214	-1.2009	-1.70
2997.1	orf19.6983	orf19.6983	CA5029 IPF2997 unknown function (YDR028c, REG1, Glc7p regulatory subunit)	-0.5994	-0.4172	-0.1165	-1.1437	-0.8521	-0.9610	-1.1775	-1.68
9057.2	orf19.1189	orf19.1189	CA2649 IPF9057 unknown function (YGR140W, CBF2)	-0.9132	-0.9686	-0.5064	-0.2533	-1.4580	-0.6990	-0.4364	-1.68
11858.2	orf19.1277	orf19.1277	CA1411 IPF11858 unknown function (N/A)	-0.8331	-0.2787	-0.6237	-1.0871	-0.5676	-0.8088	-0.9888	-1.67
13378.1	orf19.2351	NIT3	CA2338 NIT3 nitrilase (by homology)	-0.9024	-0.3468	-0.4541	-0.9248	-0.9123	-0.5076	-1.1367	-1.67
10304.1	orf19.2277	TPK2	CA1874 TPK2 cAMP-dependent protein kinase 2 (by homology)	0.0000	-0.2364	-0.3511	-0.7685	-1.3102	-1.4159	-1.0329	-1.66
19782.1	orf19.6135	orf19.6135	CA3421 IPF19782 unknown function (YDR356w?)	-0.8882	-0.0587	-0.7923	-0.5611	-0.6695	-1.2093	-0.9112	-1.66
9407.2	orf19.6151	orf19.6151	CA3408 IPF9407 similar to Saccharomyces cerevisiae Arc15p subunit of the ARP2/3 c	-0.5390	-0.4811	-0.7637	-0.6961	-0.6602	-0.8022	-1.0956	-1.65
9088.2	orf19.3802	PMT6	CA0503 PMT6 protein mannosyltransferase	-0.4600	-0.0203	-0.4112	-1.1424	-0.9743	-1.0000	-1.0203	-1.65
3488.1	orf19.6755	orf19.6755	CA5942 DLD2 D-lactate ferrycytochrome C oxidoreductase (by homology)	-1.0937	0.0025	-0.6202	-0.5596	-0.8014	-0.6873	-1.2654	-1.64
9113.2	orf19.6121	MNL1	CA2995 IPF9113 unknown function (C-TERMINAL REGION HAS HOMOLOGY WITH T	-0.3937	-0.9542	-0.8336	-0.4980	-0.5842	-1.0289	-0.7156	-1.64
2527.2	orf19.6635	orf19.6635	CA4079 IPF2527 unknown function (N/A)		-0.9406	-0.1504	-1.3585	-0.4189	-0.6804	-0.7013	-1.63
7980.2	orf19.2686	orf19.2686	CA2770 CPS1 Carboxypeptidase YSCS precursor, second fragment (by homology)	-0.9898	-0.5126	-0.8255	-0.6491	-0.5229	-0.8376	-0.6183	-1.63
3510.1	orf19.6739	orf19.6739	CA5955 IPF3510 unknown function (YMR278w, similar to phosphomannomutases)	-0.7710	-0.3659	-0.1993	-0.7084	-1.4074	-0.6597	-0.7859	-1.62
868.1	orf19.7219	FTR1	CA5345 FTR1 high affinity iron permease	-1.0831	-0.2109	-0.9602	-0.3902	-0.7322	-1.0029	-0.5146	-1.62
4535.2	orf19.903	GPM1	CA4671 GPM1 phosphoglycerate mutase (by homology)	-0.5661	-0.2396	-0.4316	-0.7902	-0.8213	-0.9737	-1.0323	-1.62
5185.2	orf19.3618	YWP1	CA1678 IPF5185 putative cell wall protein (by homology) (YAR050W, FLO1)	-0.7202	-0.2303	-0.9041	-0.5321	-0.7723	-0.9916	-0.6270	-1.60
1837.2	orf19.5877	orf19.5877	CA6159 IPF1837 unknown function (YOR377W, alcohol acetyltransferase)	-1.1517	-0.4186	-0.7599	-0.6412	-0.4705	-0.6612	-0.5859	-1.59
8847.2	orf19.6127	LPD1	CA2998 LPD1 dihydrolipoamide dehydrogenase (by homology)	-0.5269	-0.6629	-0.3653	-0.5432	-1.1092	-0.7884	-0.6909	-1.59
8025.2	orf19.1333	SNG3	CA2117 SNG3 Drug transporter (by homology)	-0.7909	-0.2294	-0.6529	-0.3346	-0.4921	-0.9828	-1.1910	-1.59
13885.1	orf19.5503	orf19.5503	CA2445 IPF13885 unknown function (N/A)	-0.7270	-0.3206	-0.8717	-0.7551	-0.6466	-0.5584	-0.7909	-1.59
3311.2	orf19.7396	orf19.7396	CA5694 IPF3311 unknown function (N/A)	-0.6897	-0.8116	-0.4165	-0.3320	-0.7391	-0.7315	-0.9246	-1.58
14171.2	orf19.3149	LSP1	CA0622 IPF14171 unknown function (YGR086c, PIL1, Phosphorylation Inhibited by Lo	-1.1750	-1.0605	-0.6553	-0.3293	-0.6563	-0.5585	-0.1756	-1.58
13684.2	orf19.2546	TRP2	CA1059 TRP2 anthranilate synthase component I (by homology)		-0.5500	-0.8365	-0.3328	-0.7060	-0.6850	-0.8314	-1.58

13316.2	orf19.2269	orf19.2269	CA1880 IPF13316 unknown function (YNL010w)	-0.4620	-0.5649	-0.5606	-0.7984	-0.7661	-0.7346	-0.7037	-1.58
10071.2	orf19.2283	orf19.2283	CA0996 IPF10071 catabolic 3-dehydroquinase (by homology)	-0.8236	-0.2450	-0.1166	-0.6171	-0.7899	-0.8213	-1.0955	-1.56
2373.2	orf19.7027	orf19.7027	CA5210 IPF2373 unknown function (weak similarity to mucins)	-0.4941	-0.3474	-0.4659	-0.8365	-0.6126	-0.7013	-1.0000	-1.55
3414.2	orf19.846	orf19.846	CA2017 IPF3414 putative serine/threonine protein kinase	-0.3696	-0.7686	-0.0499	-0.7226	-0.7735	-0.7934	-0.9771	-1.55
4696.2	orf19.5282	orf19.5282	CA4970 IPF4696 unknown Function (YNL144c?)	-0.3752	-0.6986	-0.6193	-0.5310	-0.8852	-0.7428	-0.5883	-1.55
3919.2	orf19.6510	GRX1	CA4963 IPF3919 unknown function (YCL035c?)	-0.9135	-0.3820	-0.4690	-0.6228	-0.5698	-0.5492	-0.8456	-1.54
4068.2	orf19.2164	ORF298	CA0414 IPF4068 reverse transcriptase	-0.6462	-0.5564	-0.0809	-0.7703	-0.6450	-0.7041	-0.9078	-1.53
14202.2	orf19.1078	orf19.1078	CA0934 IPF14203.3f similarity to several transaminases, 3-prime end (by homology)	-1.0985	-0.3959	-0.4840	-0.6529	-0.9051	-0.6304	-0.1140	-1.53
9943.2	orf19.4753	PFK26	CA2215 PFK26 6-phosphofructose-2-kinase (by homology)	-1.0954	-0.4461	-0.4403	-0.4150	-0.7834	-0.5084	-0.5228	-1.52
4071.2	orf19.1861	orf19.1861	CA0385 IPF4071 unknown function (YNL250W, RAD50)	-0.5872	-0.9757	-0.4862	-0.2668	-0.7394	-0.4456	-0.6828	-1.51
13148.2	orf19.54	RHD1	CA2597 IFQ3 unknown function (N/A)	-0.1154	-0.3086	-0.5433	-0.9043	-0.6197	-0.8127	-0.8616	-1.51
7812.2	orf19.3133	GUT2	CA3566 GUT2 Glycerol-3-phosphate dehydrogenase, mitochondrial (by homology)	-0.7909	-0.8468	-0.1313	-0.4305	-1.0649	-0.5249	-0.3677	-1.51
4820.2	orf19.3353	orf19.3353	CA1022 IPF4820 putativecomplex I intermediate associated protein CIA30 (by homolog	-0.8059	-0.4364	-0.6897	-0.9324	-0.4305	-0.3884	-0.4600	-1.51
1387.2	orf19.6448	orf19.6448	CA5094 IPF1387 unknown function (N/A)		-0.7686	-0.5929	-0.3183	-0.3058	-0.5437	-0.9856	-1.50
15555.2	orf19.3150	GRE2	CA0671 GRP4 putative reductase (by homology). NADPH-dependent methylglyoxal re	-0.8468	-0.7060	-0.3237	-0.2758	-0.9658	-0.6943	-0.2863	-1.50
1754.2	orf19.3099	TRP4	CA4410 TRP4 Anthranilate phosphoribosyltransferase	-0.5533	-0.6230	-0.7251	-0.4495	-0.7699	-0.3122	-0.5863	-1.49
4649.1	orf19.6102	orf19.6102	CA3854 IPF4649 unknown Function (CST6, bZIP)	-0.3696	-0.8970	-0.2987	-0.2042	-0.6349	-0.9105	-0.6873	-1.49
3634.1	orf19.6720	orf19.6720	CA4346 IPF3634 unknown function (YDR090c)	-0.5973	0.0086	-0.3640	-0.6552	-0.7710	-0.8262	-0.7418	-1.48
9803.2	orf19.6160	orf19.6160	CA3147 IPF9803 unknown function (YMR031c)	0.0000	-0.9144	-0.2830	-0.3888	-0.7699	-0.9268	-0.6592	-1.48
8340.1	orf19.4099	ECM17	CA4320 ECM17 Putative sulfite reductase (by homology)	-0.3401	-0.1172	-0.8651	-0.5907	-0.8810	-0.7370	-0.4093	-1.48
2303.2	orf19.6671	LAP4	CA4274 LAP42 Aminopeptidase yscI precursor, vacuolar (by homology)	-0.7984	-0.4580	-0.5437	-0.8783	-0.2109	-0.2260	-0.7346	-1.46
9988.2	orf19.2289	ARP3	CA1117 ARP3 actin related protein (by homology)	-0.3548	-0.5864	-0.1844	-0.4325	-0.9630	-0.5187	-0.7539	-1.46
10662.2	orf19.5760	IHD1	CA3827 IPF10662 unknown function (similarity to gucan 1,4-alpha-glucosidase STA1P		-0.6666	-0.5756	-0.1730	-0.5208	-0.7661	-0.5105	-1.45
7136.1	orf19.1559	HOM2	CA3984 HOM2 Aspartate-semialdehyde dehydrogenase (by homology)	-0.3557	-0.3391	-0.4509	-0.6603	-0.5136	-0.5984	-0.8240	-1.45
12039.2	orf19.3664	HSP31	CA4034 HSP31 heat shock protein (by homology)	-0.7637	-0.3752	-0.7226	-0.6237	-0.2793	-0.5929	-0.3383	-1.44
3870.2	orf19.20	RTS1	CA1247 IPF3870 similar to Saccharomyces cerevisiae Rts1p potential regulatory subu	-0.3595	-0.4559	-0.2633	-0.3448	-0.6407	-0.7514	-0.8356	-1.44
5366.2	orf19.3010.1	ECM33	CA3115 ECM33.3 cell wall biogenesis, 3-prime end (by homology)	-0.3157	-0.3548	-0.9743	-0.4662	-0.5833	-0.5523	-0.3847	-1.43
18130.1	orf19.4610.1	orf19.4610.1	CA5173 CPS2.3f Carboxypeptidase YSCS precursor, 3-prime end (by homology)	-0.2758	-0.2226	-0.4800	-0.5670	-0.4325	-0.8262	-0.7934	-1.43
13751.2	orf19.1038	orf19.1038	CA1035 IFI2.3f unknown function, 3-prime end		-0.1633	-0.6850	-0.6215	-0.5585	-0.6215	-0.4093	-1.42
2115.1	orf19.4109	PMT4	CA4314 PMT4 Mannosyltransferase (by homology)	-0.2474	-0.3025	-0.4838	-0.6678	-0.6625	-0.5750	-0.5876	-1.42
7535.2	orf19.4534	orf19.4534	CA4193 IPF7535 unknown function (YBR273c)	-0.5692	-0.3004	-0.7346	-0.6394	-0.3940	-0.2740	-0.6126	-1.42
8796.1	orf19.4035	GAS1	CA4800 IPF8796 putative GPI-anchhored protein related to Phr1, Phr2 and Phr3 (by h	-0.3819	-0.4091	-0.3846	-0.3455	-0.6875	-0.4808	-0.6531	-1.39
1849.1	orf19.5886	CUP5	CA6153 CUP5 Vacuolar H+ATPase (by homology)	-0.2396	-0.3733	-0.3237	-0.4521	-0.6873	-0.6326	-0.5105	-1.38
3885.2	orf19.769	IFE1	CA1958 IFE1 Unknown function (YAL061W, putative polyol dehydrogenase)	-0.5353	-0.3346	-0.6148	-0.5332	-0.0954	-0.5929	-0.4580	-1.37
7309.1	orf19.2864	orf19.2864	CA1663 IPF7309 unknown function (YGL101w)	-0.5146	-0.5125	-0.3474	-0.5585	-0.1062	-0.5670	-0.5105	-1.36
19593.1	orf19.4353	orf19.4353	CA0120 IPF19593 similar to Saccharomyces cerevisiae Ulp1p Smt3-processing enzym	-0.5395	-0.2758	-0.3328	-0.4403		-0.5105	-0.4600	-1.34
6613.2	orf19.6481	orf19.6481	CA1994 IPF6613 unknown function (YDR349c, YPS3, GPI-anchored aspartic protease	-0.3147	-0.4560	-0.3940	-0.2277	-0.4600	-0.3129	-0.4074	-1.29
5882.2	orf19.4120	orf19.4120	CA1610 LAS1 cell morphogenesis, cytoskeletal regulation and bud formation (by homology)		0.2940	0.3033	0.1827	0.4125	0.3288	0.3300	1.24
1499.1	orf19.350	orf19.350	CA4643 PRE9 20S proteasome subunit Y13 (alpha3) (by homology)	0.4636	0.4168	0.2437	0.3471	0.4372	0.3150	0.3357	1.29
3764.2	orf19.1598	ERG24	CA0300 ERG24 C-14 sterol reductase (by homology)	0.3618	0.6880	0.2558	0.3022	0.6126	0.4060	0.3940	1.35
7298.2	orf19.2418	orf19.2418	CA3044 IPF7298 unknown function (N/A)	0.3752	0.6323	0.0990	0.3437	0.7181	0.5489	0.4803	1.37
3873.2			CA1245 IMH3.exon2 IMP dehydrogenase, exon 2 (doesn't exist in CDB)	0.8961	0.4158	0.3718	0.2534	0.5955	0.3907	0.3785	1.39
12897.2	orf19.2244	orf19.2244	CA0271 IPF12897 putative oxidoreductase (by homology)	0.6164	0.3561	0.6050	0.2546	0.4351	0.5018	0.5499	1.39
19574.1	orf19.4468	orf19.4468	CA2423 SDH41 succinate dehydrogenase membrane anchor subunit for sdh2p (by ho	0.6267	0.2461	0.2786	0.2702	0.6853	0.4998	0.7416	1.39
6054.1	orf19.6736	orf19.6736	CA4359 IPF6054 unnown function (localised to mitochondrion)	0.5850	0.1966	0.5646	0.2714	0.4626	0.6031	0.7075	1.40
20033.1	orf19.7592	FAA4	CA5992 FAA4 long-chain fatty acid--CoA ligase and synthetase 4 (by homology)	0.7154	0.1815	0.2107	0.5484	0.6293	0.6652	0.4442	1.40
6754.1	orf19.319	orf19.319	CA3389 IPF6754 unknown function (YDR286C)	0.4854	0.5410	0.4865	0.8616	0.5675	0.0524	0.4190	1.40
4405.1	orf19.1482	orf19.1482	CA0905 IPF4405 unknown function (N/A)	0.6781	0.3323	0.2951	0.3288	0.6031	0.9100	0.2762	1.40
8176.1	orf19.526	NHP2	CA4240 NHP2 nucleolar rRNA processing protein (by homology)	0.4276	0.6853	0.2473	0.3818	0.5291	0.7084	0.4489	1.40
3082.1	orf19.7043.1	ACB1	CA5225 ACB1.exon2 acyl-coenzyme-A-binding protein, exon 2 (by homology)	0.5677	0.3435	0.5064	0.2273	0.6160	0.5870	0.6415	1.41
6872.1	orf19.4252	orf19.4252	CA2183 IPF6872 serine/threonine protein kinase (by homology) (YGR262c, bud site se	0.4854	0.5099	-0.0395	0.6672	0.5509	0.7908	0.5917	1.42
19294.1	orf19.6469	orf19.6469	CA0070 IPF19295.3f unknown function, 3-prime end (YJL207c)	0.6581	0.0621	0.5936	0.3918	0.6351	0.4351	0.8156	1.43
18938.1	orf19.1804	orf19.1804	CA0572 IPF14864 unknown function (YAL046C)	0.5675	0.3929	0.4027	0.4772	0.3150	0.7502	0.7225	1.43
13045.2	orf19.2407	DPS1-1	CA3052 DPS1 aspartyl-tRNA synthetase (by homology)	0.4895	0.1648	0.1557	0.8828	0.6871	0.6060	0.6727	1.44
1211.1			CA4830 ATP8.exon2 F1F0-ATPase complex, Atp8 subunit, exon 2 (by homology)	0.7355	0.0398	0.5028	0.4977	0.5170	0.6933	0.6826	1.44

5986.1	orf19.7307	orf19.7307	CA5545 IPF5986 similar to cytochrome-b5- and nitrate reductases (ER)		0.4510	0.0731	0.4626	0.5361	0.7407	0.9575	1.45
1514.2	orf19.344	orf19.344	CA4637 IPF1514 unknown function (N/A)	0.0000	0.5183	0.4367	0.3225	0.8056	0.7928	0.9046	1.45
13622.2	orf19.3974	PUT2	CA3399 PUT2 1-pyrroline-5-carboxylate dehydrogenase (by homology) (YHR037W, mi	0.3196	0.8213	0.1674	0.4542	0.4049	0.8608	0.7664	1.46
1846.1	orf19.5884	orf19.5884	CA6155 IPF1846 unknown function (YJR041C, nucleolar ribosome biogenesis)	0.6544	0.5965	0.4265	0.3874	0.5251	0.5888	0.6304	1.46
4924.1	orf19.7657	orf19.7657	CA6042 IPF4924 unknown function (RNase P and RNase MRP subunit)		0.2129	0.8891	0.5519	0.5028	0.5636	0.6022	1.47
19861.1			CA0405 IPF19862.3f unknown function, 3-prime end (doesn't exist in CDB)	1.1460	0.2546	0.3550	0.5261	0.4751	0.6285	0.6313	1.49
5890.2	orf19.6938	orf19.6938	CA4708 MEU1 regulator of ADH2 expression (by homology)	0.9351	0.2702	0.1440	0.6267	0.6808	0.6987	0.6672	1.49
1567.1	orf19.961.2	orf19.961.2	CA5413 IPF1567 mitochondrial ribosomal protein L34 (by homology)		0.1440	0.9935	0.6406	0.5763	0.6229	0.4751	1.49
17135.12	orf19.6283	orf19.6283	CA3222 IPF15883 unknown function (YKL040c, mitochondrial matrix)	0.5926	-0.0321	0.7647	0.4457	0.7604	0.6332	0.8766	1.49
3445.1	orf19.6183	orf19.6183	CA3203 IPF3445 Unknown function (YJR135W-A, mitochondrial inner membrane)	0.5211	0.4005	0.8600	0.1609	0.8608	1.0983	0.2774	1.51
7325.1	orf19.2978	orf19.2978	CA3445 IPF7325 unknown function (N/A)	1.1170	0.4340	0.8797	0.2066	0.6498	0.5965	0.3369	1.52
8113.2	orf19.2938	orf19.2938	CA2199 IPF8113 unknown function (localised to mitochondrion)	0.8115	0.0482	0.4071	0.6526	0.4201	0.8899	1.0065	1.52
80.2	orf19.5949	FAS2	CA6107 FAS2.3f fatty-acyl-CoA synthase, alpha chain, 3-prime end	0.5553	0.4203	0.3370	0.8071	0.5963	0.6076	0.9147	1.52
1439.1	orf19.6047	TUF1	CA4909 TUF1 Translation elongation factor TU (by homology)	0.7233	0.6304	1.0881	0.6126	0.4255	0.3606	0.4201	1.52
3222.1	orf19.3577	COQ5	CA3482 COQ5 C-methyltransferase (by homology) mitochondrial	0.3984	0.5190	0.7966	0.9575	0.1017	0.7689	0.7338	1.53
4616.2	orf19.6090	orf19.6090	CA3862 NSR1 nuclear localization sequence binding protein (by homology)	0.9046	0.2327	0.4136	0.7040	0.9701	0.6645	0.4233	1.53
9827.2	orf19.6860	orf19.6860	CA4463 PIS1 CDP diacylglycerol--inositol 3-phosphatidyltransferase (by homology) (Y	0.7066	0.2461	0.2881	0.4854	0.6295	0.6572	1.3132	1.53
13552.2	orf19.1300	orf19.1300	CA0453 IPF13552 putative methyltransferase (by homology) (YDR316W, mitochondrio	0.0688	0.3824	0.7911	0.4991	0.7715	0.9643	0.8613	1.54
16428.2	orf19.1250	orf19.1250	CA1479 IPF16428 unknown function (YIL019w)	0.8286	0.4071	0.1763	0.7286	0.4136	0.8424	0.9553	1.54
3959.2	orf19.875	orf19.875	CA4690 IPF3959 unknown function (N/A)	0.3369	0.0510	1.0208	1.0642	0.6378	0.6599	0.5974	1.54
7706.2	orf19.680	orf19.680	CA4115 IPF7706 putative plasma membrane phosphatase (by homology)	0.6031	-0.0247	0.5271	0.6332	0.9268	0.8237	0.9100	1.55
4189.1	orf19.5444	orf19.5444	CA5795 TIM44 mitochondrial inner membrane import receptor	0.5850	0.8262	0.7286	0.2497	0.6835	0.7832	0.5917	1.55
3365.1	orf19.4022	SDH4	CA4788 SDH42 succinate dehydrogenase membrane anchor subunit for sdh2p (by ho	0.6894	0.1718	0.7544	0.4444	0.8830	0.7847	0.7634	1.56
4785.2	orf19.4499	orf19.4499	CA2330 RIM2 mitochondrial carrier protein (by homology)	0.1827	0.0676	0.8999	0.6295	0.7058	1.0058	1.0144	1.56
12382.2	orf19.1388	orf19.1388	CA0886 IPF12382 unknown function (		0.3311	0.0272	0.8270	0.8065	0.9978	0.8781	1.56
2480.2	orf19.7485	orf19.7485	CA5830 MRPL9 Mitochondrial ribosomal protein of the large subunit (by homology)	0.9702	0.7436	0.9599	0.2634	0.5544	0.6862	0.3715	1.57
19785.1	orf19.4929	orf19.4929	CA3599 IPF19785 unknown function (Specific translational activator for COX1, mitoch	-0.0101	0.5150	1.1150	0.7807	0.4521	0.6517	1.0718	1.57
18468.1	orf19.4467	orf19.4467	CA2424 IPF18468 unknown function (N/A)	0.2141	0.5400	1.0956	0.8504	0.4114	0.6173	0.8984	1.58
8953.2	orf19.4895	orf19.4895	CA2358 IPF8953 unknown function (N/A)	0.8671	0.3940	0.4720	0.3929	0.8440	0.9015	0.7698	1.58
2093.2	orf19.4093	orf19.4093	CA4326 IPF2093 nuclear protein of unknown function (by homology)	0.2821	0.4844	0.3840	1.0370	0.8631	0.8663	0.7260	1.58
4283.2	orf19.543	orf19.543	CA4255 FUM11 fumarate hydratase (mitochondrial matrix)	0.9709	0.2558	0.5675	1.0136	0.4854	0.4244	0.9627	1.59
429.1	orf19.7489.3	orf19.7489.3	CA5835 IPF429 unknown function (YGL220w)		1.2425	0.3651	0.3918	0.6304	0.5965	0.7883	1.59
9638.2	orf19.1578	orf19.1578	CA3165 FMI1 processing of pre-ribosomal RNA	0.7450	0.4038	0.2762	0.9767	0.6050	1.1629	0.5370	1.59
1677.1	orf19.6558	orf19.6558	CA4872 SEC231 Component of COPII coat (by homology)	0.9351	0.2388	-0.0306	0.6415	0.8440	0.9701	1.1124	1.59
5361.2	orf19.3008	COQ4	CA3118 COQ4 ubiquinone biosynthesis (mitochondrion)	1.3144	0.8828	0.6517	-0.0454	0.6378	0.6332	0.6452	1.60
4444.2	orf19.4705	orf19.4705	CA1841 CCA1 tRNA nucleotidyltransferase (by homology) (cytoplasm and mitochondri	0.5850	0.2869	0.7681	0.5370	0.2690	1.1362	1.1545	1.60
14165.2	orf19.4642	orf19.4642	CA1062 IPF14165 unknown function (N/A)	0.5622	0.7840	0.7376	0.7294	0.7785	0.2203	0.9629	1.60
13913.2	orf19.5759	SNQ2	CA3828 SNQ2 multidrug resistance protein (by homology)	0.5868	0.3158	0.4984	0.4239	0.7393	0.7968	1.4272	1.61
1212.1	orf19.2066	orf19.2066	CA4831 IPF1212 unknown function (YJR129C)		0.7493	0.8496	0.5150	0.5763	0.7924	0.6471	1.61
20104.1	orf19.5517	orf19.5517	CA2520 IPF20104 alcohol dehydrogenase (by homology)	0.8938	0.3426	0.6276	0.9819	0.1852	0.8032	0.9891	1.61
10510.2	orf19.240	orf19.240	CA1265 IPF10510 unknown function (YKR065c, localised to mitochondrion)	1.2789	0.3718	0.5727	0.3267	0.7606	0.9174	0.6157	1.62
20121.1	orf19.5599	MDL2	CA2972 MDL2.3f ATP-binding transporter, 3-prime end (by homology) (mitochondrial in	0.9759	0.2700	0.3381	0.6515	0.8435	0.7845	1.0127	1.62
1231.2	orf19.2057	orf19.2057	CA4838 YTA12 Protease of the SEC18/CDC48/PAS1 family of ATPases (AAA) (by hon	1.3408	0.0384	1.0172	0.7883	0.3651	0.5430	0.8213	1.63
13421.2	orf19.182	orf19.182	CA0029 PET56 ribosomal RNA methylase (by homology) (for mitochondrial 21S rRNA)	1.2016	0.4147	0.4136	0.6154	0.4060	0.6563	1.2066	1.63
14810.2	orf19.2016	orf19.2016	CA0913 IPF14810 unknown function (YER044C, ERG28, ER protein)	-0.0203	0.7459	0.9709	0.3057	0.6257	1.0370	1.2636	1.63
8996.2	orf19.4634	orf19.4634	CA0734 IPF8996 unknown function (YGL211W, mitochondrion)		-0.0262	0.6041	1.0229	0.7424	0.7190	1.1699	1.63
14981.2	orf19.3483	orf19.3483	CA2896 IPF14981 unknown function (ER)	0.7829	0.1919	0.4894	0.7035	0.5583	1.0146	1.2263	1.64
14849.2	orf19.2452	orf19.2452	CA0046 IPF14850 Hypothetical protein (N/A)		-0.0877	0.4500	0.8074	1.0250	0.9568	1.1290	1.64
16036.1	orf19.150	orf19.150	CA0010 IPF16036 similar to Saccharomyces cerevisiae Tim17p mitochondrial inner me	1.4828	0.3460	0.8528	0.4287	0.6736	0.7031	0.5079	1.64
2166.1	orf19.7182	orf19.7182	CA5311 IPF2166 unknown function (YGL232w)	0.5926	1.4330	0.2004	0.5685	0.6012	0.9290	0.6817	1.64
863.1	orf19.7223	orf19.7223	CA5348 IPF863 involved in inositol biosynthesis (by homology)	0.9650	0.2738	0.4457	0.7858	0.6951	0.7233	1.1434	1.65
16996.2	orf19.3547	orf19.3547	CA2667 IPF16996 unknown function (YDR496C)	1.1562	0.2797	0.2452	0.9502	0.3996	0.8570	1.1555	1.65
12845.2	orf19.2363	orf19.2363	CA2251 IPF12845 unknown function (localised to mitochondrion)	0.7091	0.1466	0.5587	0.7778	0.8546	0.9812	1.0451	1.65
16549.2	orf19.4273	orf19.4273	CA1819 IPF16549 Unknown function (YLR139C, SLS1, mitochondrial integral membra	0.1583	0.4071	0.7689	0.7527	0.3685	1.1401	1.4823	1.65
10113.1	orf19.2249	orf19.2249	CA3589 IPF10113 unknown function (YNR020C)	0.9398	0.5591	0.6486	0.6224	0.6934	0.7958	0.8519	1.66

8974.2	orf19.498	orf19.498	CA4508 NAM9 mitochondrial ribosomal protein	0.8375	-0.1520	0.6351	0.7579	0.8734	0.9731	1.1878	1.66
8173.2	orf19.522	orf19.522	CA4238 PIM1 mitochondrial ATP-dependent protease (by homology)	1.1204	0.5008	0.8860	0.6295	0.9957	0.5018	0.5018	1.66
13283.2	orf19.1233	ADE4	CA2979 ADE4 amidophosphoribosyltransferase (by homology) (YMR300C)	1.3269	-0.0843	0.6377	0.8907	0.8001	0.7222	0.8922	1.67
15038.2	orf19.500	orf19.500	CA4506 GCD10 translation initiation factor eIF3 RNA-binding subunit (by homology)	0.5955	0.3254	0.8074	1.3465	0.8213	0.8148	0.4865	1.67
10187.1	orf19.3934	CAR1	CA1024 CAR1 arginase by homology	0.4630	1.0454	0.3051	0.6568	1.1986	0.6758	0.8694	1.68
4977.2	orf19.2524	MGE1	CA1738 MGE1 heat shock protein (by homology)(	0.3696	0.0949	1.0391	1.1801	0.7604	0.7485	1.0391	1.68
1399.2	orf19.6068	SVF1	CA4928 IPF1399 unknown function (YDR346C, diauxic shift)	1.1577	0.4433	0.2798	0.7271	0.6678	0.9318	1.0482	1.68
16924.2	orf19.2829	orf19.2829	CA2544 IPF16924 unknown function (YNL149C, ER)	0.6498	-0.0043	0.4751	0.6745	0.9598	1.3033	1.2382	1.69
6223.1	orf19.3297	orf19.3297	CA4607 IPF6223 unknown function (mitochondrial ribosome small subunit component)	0.8679	-0.1140	1.0909	1.1263	0.5792	0.8189	1.0050	1.70
1732.1	orf19.3089	orf19.3089	CA2009 IPF1732 intramitochondrial protein sorting (by homology)	0.0000	0.2245	0.9115	1.0809	0.8476	1.2118	1.1410	1.71
7154.2	orf19.1195	orf19.1195	CA1374 MIP1 Mitochondrial intermediate peptidase (by homology)	1.2630	1.0759	1.0144	0.4947	0.1467	0.7312	0.6924	1.71
3709.1	orf19.3015	orf19.3015	CA5051 IPF3709 unknown function (YDR101C)	1.0462	0.5017	-0.0247	1.1506	0.6933	0.9359	1.1253	1.71
5464.1	orf19.5684	orf19.5684	CA2607 MRPL38 ribosomal protein of the large subunit(L14), mitochondrial, by homolo	1.0524	0.6452	1.2928	0.7949	0.8319	0.6498	0.1827	1.72
14455.1	orf19.1589	orf19.1589	CA3156 IPF14455 similar to Saccharomyces cerevisiae Rrn7p polymerase I specific tr	1.3785	0.9877	0.4222	0.2522	0.9928	0.6871	0.7390	1.72
864.1	orf19.7222	orf19.7222	CA5347 IPF864 unknown function (mitochondrion)	1.2320	0.3774	0.8383	0.1137	0.4319	1.3448	1.1382	1.72
13331.2	orf19.1591	ERG10	CA0290 POT14 acetyl-CoA acetyltransferase (by homology) (YPL028W, ERG10)	1.2960	0.9410	0.2777	0.6378	0.9103	0.9162	0.4993	1.72
1308.1	orf19.6406	orf19.6406	CA5122 IPF1308 Similarity to ribosomal protein S13 (by homology)	0.9833	0.3561	1.3202	0.5039	0.9268	0.7303	0.6727	1.72
12778.1	orf19.6136	orf19.6136	CA3419 IPF12778 ribosomal protein, mitochondrial (by homology)	0.7891	0.2786		1.2690	0.4071	0.8914	1.0807	1.72
19594.1	orf19.169	CHO2	CA1414 CHO2 phosphatidylethanolamine N-methyltransferase (by homology) mitocho	1.1336	0.0172	0.5878	0.6924	0.8899	1.2296	0.9672	1.73
14920.2	orf19.1528	orf19.1528	CA0745 MTF1 RNA polymerase specific factor, mitochondrial (by homology)	0.5850	-0.0072	0.5965	0.7476	1.0628	1.0600	1.4880	1.73
443.1	orf19.7049	CYB5	CA5645 CYB5 Cytochrome b5 (by homology) (mitochondrion)	1.5361	0.5301	0.7732	0.6498	0.7416	0.4233	0.8844	1.73
8302.1	orf19.6007	orf19.6007	CA6061 IPF8302 unknown function (YJL196c?)		0.1725	0.5059	0.9313	0.5231	1.1998	1.4217	1.73
16189.2	orf19.5577	orf19.5577	CA0660 IPF16189.5f panthotenate kinase, 5-prime end (by homology) (YDR531W, Co	1.1757	0.2510	0.2904	0.8115	1.1063	0.8375	1.0786	1.73
11240.1	orf19.1416	COX11	CA3958 COX11 cytochrome-c oxidase assembly protein by homology to S. cerevisiae	1.2558	0.8383	1.1840	0.9891	0.4168	0.2642	0.6201	1.74
20153.1	orf19.1549	orf19.1549	CA3977 IPF20153 unknown function (N/A)	1.2147	-0.1795	0.4988	0.8883	0.9061	1.0433	1.2160	1.74
12306.1	orf19.5039	orf19.5039	CA1695 RRP42 rRNA processing protein (by homology) (YDL111C)	0.1941	0.4005	0.2881	1.0014	0.8504	1.4022	1.4563	1.74
9631.1	orf19.1575	PRS1	CA3168 PRS3 ribose-phosphate pyrophosphokinase (YHL011C)	0.7442	-0.0604	0.4720	1.0902	1.2079	0.7579	1.3818	1.74
1611.2	orf19.979	FAS1	CA5426 FAS1 Fatty-acyl-CoA synthase, beta chain.	1.1170	0.0580	0.1043	1.2750	0.7562	1.1577	1.1447	1.74
7901.2	orf19.6026	ERG2	CA2154 ERG2 C-8 sterol isomerase	0.5420	0.4957	0.1699	0.9030		1.1190	1.6754	1.76
10381.2	orf19.3682	CWH8	CA1146 CWH8 putative required protein for full levels of dolichol-linked oligosaccharide	0.5668	0.5728	0.5738	1.0097	0.6312	0.9143	1.4671	1.76
15527.2	orf19.4519	SUV3	CA2908 SUV3 ATP-dependent RNA helicase, mitochondrial (by homology)	0.8106	-0.0755	1.1434	0.7999	0.5390	1.0363	1.5286	1.77
11393.2	orf19.2852	orf19.2852	CA1669 IPF11393 unknown function (mitochondrial ribosome small subunit component	0.4423	0.4837	1.5242	0.8054	0.7706	0.9501	0.8536	1.78
13798.1	orf19.3946	orf19.3946	CA1090 COX18 protein required for activity of mitochondrial cytochrome oxidase (by h	1.2816	1.1011	0.1863	1.0534	0.5806	1.0147	0.6424	1.79
15660.2	orf19.4159	orf19.4159	CA1226 IPF15660 putative mitochondrial carrier (by homology)	0.8213	0.2522	0.8969	0.5430		1.3231	1.1890	1.79
11364.1	orf19.1716	URA3	CA2801 URA3 orotidine-5 -monophosphate decarboxylase [Candida albicans]	1.3033	0.3907	1.1090	0.5301	0.9389	0.5489	1.0963	1.80
1134.1	orf19.5433	orf19.5433	CA5786 IPF1134 unknown function (YDR493w, mitochondrial)	0.5850	0.8496	1.2079	0.8359	0.4372	0.9508	1.0628	1.80
1848.1	orf19.5885	orf19.5885	CA6154 IPF1848 similar to Saccharomyces cerevisiae Snu13p U4/U6.U5 snRNP asso	0.8123	-0.1811	0.4049	1.1532	1.3369	0.9523	1.5069	1.81
8020.2	orf19.1335	orf19.1335	CA2119 MTR4 RNA Helicase (by homology) (YJL050W)	0.8639	0.1557	0.2104	1.0786	0.7093	1.3663	1.6050	1.81
19955.1	orf19.5705	NAM2	CA2656 NAM2 mitochondrial leucine--tRNA ligase (by homology)	1.1410	0.0956	1.1340	0.7717	0.6685	1.0001	1.1826	1.81
8130.2	orf19.5143	orf19.5143	CA3631 TIM54 Translocase for the insertion of proteins into the mitochondrial inner me	1.2720	0.2714	0.9523	1.0454	0.8270	0.7137	0.9411	1.82
15801.2	orf19.1650	orf19.1650	CA1043 TOM6 mitochondrial outer membrane import receptor subunit (by homology)	0.3684	0.3207	1.5446	0.9221	1.1525	0.9218	0.8226	1.82
1116.1	orf19.5420	orf19.5420	CA5776 RML2 Ribosomal L2 protein, mitochondrial (by homology)	1.6203	1.0049	1.1534	0.5447	0.7446	0.5205	0.4731	1.82
6869.2	orf19.4255	ECM331	CA2181 ECM331 Involved in cell wall biogenesis and architecture (by homology)		0.4844	0.6369	0.7013	0.6933	1.0649	1.6951	1.84
4568.1	orf19.6524	orf19.6524	CA4954 TOM40 mitochondrial import receptor chain TOM40 (by homology)	0.8537	0.1465	0.8884	1.0686	1.0748	1.0155	1.1171	1.84
16061.2	orf19.1753	PUS7	CA0294 IPF16061 unknown function (pseudouridine synthase, nucleus)		-0.0087	1.1210	0.7303	1.1283	1.3317	0.9913	1.84
1023.2	orf19.4578	CYT2	CA5141 CYT2 holocytochrome-c1 synthase (by homology) (mitochondrion)	1.4854	0.9441	0.7485	0.5028	0.7765	0.8930	0.8343	1.84
16143.2	orf19.2259	orf19.2259	CA3581 IPF16143 unknown function (ribosomal protein, similar to chloroplast)	0.4846	0.2195	1.3224	1.1456	0.9504	1.1962	1.0347	1.88
18593.1	orf19.2201	orf19.2201	CA1889 CBP6 Apo-cytochrome B pre-mRNA processing protein (by homology) (mitoch	1.4388	-0.0112	1.8889	0.5445	0.8941	0.7159	0.8858	1.88
7704.2	orf19.679	FGR39	CA4114 IPF7704 unknown function (N/A)	0.7224	0.1722	1.1955	0.3757	1.3882	1.1086	1.4654	1.89
1537.1	orf19.336	YAH1	CA4630 IPF1537 putative adrenodoxin and ferrodoxin (by homolgy) (YPL252C, mitoch	1.2271	-0.4055	1.1871	0.7433	1.4942	1.0193	1.1808	1.89
2516.1	orf19.7466	ACC1	CA5816 ACC1 acetyl-coenzyme-A carboxylase (by homology)	1.3497	0.2214	0.4701	1.3396	1.0320	0.9282	1.1110	1.89
9204.1	orf19.3676	ABP140	CA4045 ABP140 putative methyltransferase (by homology) (YOR239W)	1.6781	0.2388	0.1903	1.1084	0.9531	1.0552	1.2636	1.90
8826.2	orf19.397	orf19.397	CA3872 MRPL28 mitochondrial ribosomal protein of the large subunit (by homology)	0.6768	-0.1332	1.2426	0.8428	1.1715	1.4683	1.2264	1.90
5581.2	orf19.5167	orf19.5167	CA4428 IFM1 translation initiation factor 2 by homology (mitochondrion)	2.1227	0.6915	1.3288	0.5291	0.6871	0.4147	0.7233	1.90
7575.2	orf19.4365	orf19.4365	CA1097 IPF7575 putative endo-exonuclease (by homology) (YKR056W, tRNA methyltr	1.1795	0.0580	0.7891	0.8074	1.1648	1.1382	1.4098	1.91

10140.2	orf19.408	orf19.408	CA1355 IPF10138.3f unknown function, 3-prime end (N/A)	0.3334	0.0482	0.4005	1.5175	1.2975	1.3640	1.5917	1.91
1024.1	orf19.4577.3	orf19.4577.3	CA5140 TIM10 Subunit of the Tim22-complex (by homology) (mitochondrion)	1.2901	0.1068	1.2914	0.5957	0.6314	1.4756	1.1660	1.91
5933.2	orf19.439	orf19.439	CA4062 IPF5933 similar to Saccharomyces cerevisiae Mhr1p involved in mitochondrial	1.5532	-0.0442	1.1222	1.0244	1.0356	1.0241	0.8880	1.92
9841.1	orf19.3204	orf19.3204	CA2482 IPF9841 unknown function (YLR318W, telomerase reverse transcriptase)	0.7655	0.3173	0.1941	0.9069	1.0193	1.2916	2.1154	1.92
16471.1	orf19.2795	orf19.2795	CA2003 IPF16471 unknown function (YDL051W)	0.4678	0.1448	0.7496	1.2222	1.0745	1.3660	1.6218	1.93
18440.1	orf19.4760	orf19.4760	CA2629 IPF10911 unknown function (YIL110W)	0.8480	0.2618	0.1596	1.1609	1.0820	1.4394	1.7137	1.93
5151.1	orf19.6531.1	TOM71	CA4946 TOM71 Translocase of the outer mitochondrial membrane (by homology)	0.3987	0.4228	1.1753	1.1809	1.4763	1.0901	0.9455	1.94
3903.2	orf19.760	orf19.760	CA1932 IPF3903 unknown function (mitochondrial large ribosomal subunit)	0.0000	0.3573	2.0542	1.0711	0.7286	1.4394	1.0766	1.95
15194.2	orf19.4261	TIF5	CA0667 TIF5 Translation initiation factor eIF5 (by homology)	0.7343	-0.2915	0.6465	1.4929	1.3458	1.3151	1.4877	1.95
12009.2	orf19.3171	ACH1	CA0345 ACH1 acetyl-coenzyme-A hydrolase (by homology) (mitochondrion)	1.1017	0.4434	0.1637	1.2972	0.4630	1.4353	1.9129	1.96
19484.1			CA0003 IPF19484 putative zinc amino peptidase (by homology) (doesn't exist in CBD)	1.3115	0.1388	0.5450	1.2277	0.8057	1.2400	1.5893	1.97
14216.2	orf19.2927	MNN11	CA0563 MNN11 Mannosyltransferase complex component (by homology) (YJL183W)	0.9283	-0.0770	0.3896	1.3780	1.3068	1.3138	1.6645	1.98
10823.1	orf19.3938	orf19.3938	CA1632 IPF10181 similar to Saccharomyces cerevisiae Rsm26p protein of the small subunit of the		0.2216	1.5969	0.8742	0.4875	1.2351	1.5700	2.00
7324.2	orf19.2977	orf19.2977	CA3446 IPF7324 unknown function (YKL195w, localised to mitochondrion)	1.7649	0.7787	1.2260	0.4398	1.1592	0.8325	0.7952	2.00
17424.2	orf19.1770	CYC1	CA0038 CYC1 cytochrome-c isoform 1 (mitochondrion)	1.3801	0.4570	0.9866	0.7642	0.8595	1.2416	1.3291	2.00
2203.1	orf19.6916	orf19.6916	CA4597 ATP11 F1F0-ATPase complex assembly protein (by homology) (mitochondrion	2.3389	-0.1408	1.0697	1.0531	1.0552	0.8520	0.8189	2.01
4973.1	orf19.2520	orf19.2520	CA0462 MRPS28 ribosomal protein (by homology)	0.0000	0.2804	1.6290	1.1389	0.9578	1.6323	1.4541	2.02
3492.1	orf19.6752	orf19.6752	CA5945 IPF3492 unknown function (mitochondrial ribosome small subunit component)	0.8258	0.0165	1.0917	1.0375	1.6312	1.2995	1.2675	2.03
14109.2	orf19.2451	PGA45	CA0380 IPF14109 unknown function (N/A)	0.9935	1.3939	0.9645	0.9067	0.8657	0.5441	1.5173	2.04
12940.2	orf19.4932	orf19.4932	CA3603 MEF1 mitochondrial translation elongation factor G (by homology)	0.1375	0.5489	1.2546	1.0772	0.8286	1.6429	1.7198	2.04
17430.1	orf19.73	orf19.73	CA0011 IPF17430 possible zinc protease (by homology) (YIL137C)	1.6323	0.0759	0.7562	1.2203	1.0881	1.2160	1.2277	2.04
16082.2	orf19.4160	orf19.4160	CA1227 IPF16082 unknown function (	0.0000	0.7362	0.9330	1.2690	0.9580	1.6966	1.6275	2.04
15664.2	orf19.5296	orf19.5296	CA2160 IPF15664 unknown function (YIL157c, localised to mitochondrion)	0.6220	0.4093	1.8699	0.6951		1.2271	1.3780	2.05
17996.2			CA2240 CRD2 Cu-binding metallothionein (doesn't exist in CBD)	1.1424	0.3962	0.4439	0.9677	1.4015	1.4954	1.4426	2.06
9361.2	orf19.2382	orf19.2382	CA2103 ISM1 isoleucyl-tRNA synthetase (by homology) (mitochondrion)	1.5642	0.5007	1.5422	0.8448	0.7833	0.9266	1.1720	2.07
6298.2	orf19.1964	orf19.1964	CA2947 IPF6298 unknown function (N/A)	0.8271	0.2760	0.3340	1.2996	1.2366	1.5273	1.9176	2.08
7091.1	orf19.484	orf19.484	CA4521 MRPL40 Putative mitochondrial ribosomal protein (by homology)	0.9775	0.1903	1.4834	1.0264	0.8797	1.3340	1.5787	2.10
6338.1	orf19.1109	orf19.1109	CA1461 IPF6338 unknown function (N/A)	0.4281	0.1506	1.3966	1.3599	0.8957	1.6087	1.6415	2.10
9936.2	orf19.989	orf19.989	CA3526 MRPS5 Probable ribosomal protein S5, mitochondrial (by homology)	0.2414	0.5013	1.4530	1.2965	1.3253	1.3156	1.4033	2.11
6507.2	orf19.1546	orf19.1546	CA3974 IPF6507 unknown function (localised to mitochondrion)		0.5281	1.3080	0.6164	1.1789	1.4335	1.4600	2.12
1453.2	orf19.6041	RPO41	CA4904 RPO41 Mitochondrial DNA-directed RNA polymerase (by homology)	1.8663	0.2055	0.5385	1.2815	1.0104	1.3377	1.4719	2.15
878.1	orf19.7215.3	orf19.7215.3	CA5341 HSP10.3 10 kDa mitochondrial heat shock chaperonin, 3-prime end (by homol	0.9031	0.2791	1.8890	0.8616	1.3182	1.1680	1.3349	2.16
6505.2	orf19.1545	orf19.1545	CA3973 IPF6505 unknown function (Mitochondrial ribosomal protein of the small subur	1.3948	0.4467	1.3587	1.1355	0.8682	1.3019	1.2743	2.16
6970.1	orf19.2639	orf19.2639	CA2072 IPF6970 unknown function (Mitochondrial ribosomal protein of the large subur	0.0000	0.4147	1.7656	1.4494	1.7500	0.4285	1.9793	2.16
11656.2	orf19.6363	orf19.6363	CA3515 MRPL15 mitochondrial ribosomal protein of the large subunit (by homology)	1.0873	0.1487	1.0250	1.2235	1.2869	1.5518	1.5112	2.17
15646.2	orf19.3481	orf19.3481	CA2898 IPF15646 putative ATP-dependent RNA helicase (by homology) (mitochondria	0.6917	0.7031	0.7162	1.6543	0.6708	1.3680	2.0704	2.18
19552.1	orf19.5064	MRPL3	CA0089 MRPL3 ribosomal protein of the large subunit, mitochondrial (by homology)	0.4550	0.4354	1.7767	0.8517	0.9578	1.4115	1.9991	2.18
1663.1	orf19.6565	orf19.6565	CA4878 OXA1 Cytochrome oxidase biogenesis protein (by homology) (mitochondrion)	1.9255	0.2091	1.2909	1.1524	0.6825	1.2261	1.4634	2.20
14569.2	orf19.6231	MRPL19	CA3009 MRPL19 Ribosomal protein (by homology) (mitochondrion)	1.5734	0.6781	1.2628	1.0512	1.3367	1.3650	0.6912	2.20
10301.1	orf19.2275	orf19.2275	CA1876 IPF10301 putative 60S ribosomal protein L7/L12 homolog, mitochondrial precu	1.0326	-0.1917	1.4149	1.2525	1.3906	1.5371	1.5437	2.20
14687.1	orf19.2006.1	orf19.2006.1	CA3936 COX17 cysteine-rich cytoplasmic protein(by homology) (mitochondrion)	1.5201	0.0149	1.9463	0.9228	0.9152	1.2818	1.6165	2.26
11177.2	orf19.51	orf19.51	CA2600 IPF11177 similar to Saccharomyces cerevisiae Clu1p translation initiation facto	2.1816	-0.2043	0.9451	1.1816	0.9884	1.3067	1.8252	2.26
16564.1	orf19.2438	orf19.2438	CA1914 IPF16564 putative mitochondrial ribosomal protein S12	0.7253	0.5885	0.4232	1.3123	1.6735	1.7683	1.7516	2.26
10429.2	orf19.2887	MET13	CA0721 IPF10429 unknown function (YMR295c, cell periphery and bud)	1.3110	0.1990	0.9129	1.2481	1.6256	1.2961	1.7209	2.28
4102.2	orf19.2019	orf19.2019	CA0910 MRPL16 ribosomal protein (mitochondrion)	1.4592	0.4124	1.6761	1.2636	1.2829	1.2092	1.0142	2.28
14193.2	orf19.3357	orf19.3357	CA0790 IPF14193 unknown function (mitochondrion, YHR059w, FYV4)	0.4820	0.1941	1.8686	1.3150	1.1828	1.3869	1.9205	2.29
5446.1	orf19.5698	orf19.5698	CA2613 IPF5446 putative ribosomal protein (by homology) (Mitochondrial ribosomal pr	1.0575	0.2246	1.6657	1.4126	1.3574	1.3225	1.3139	2.29
9838.2	orf19.3205	orf19.3205	CA2481 MRPL36 ribosomal protein YmL36 precursor, mitochondrial (by homology)	1.8505	0.6681	1.3490	0.6901	1.0230	1.7686	1.0329	2.29
7840.1	orf19.4204	orf19.4204	CA2930 IPF7840 similar to Saccharomyces cerevisiae Pet123p ribosomal protein, mitc	1.4957	0.3389	1.5461	1.0875	1.2066	1.3435	1.4007	2.30
8454.2	orf19.6853	orf19.6853	CA4455 IPF8454 unknown function (N/A)	0.0000	0.3184	1.8442	1.6860	1.2495	1.6708	1.6865	2.31
3698.1	orf19.3022	orf19.3022	CA5056 IPF3698 similar to Saccharomyces cerevisiae Rsm24p mitochondrial ribosoma	0.7332	-0.0069	1.3604	1.7622	1.4648	1.6717	1.5385	2.33
917.1	orf19.7577	MSS51	CA5981 MSS51 involved in maturation of COX1 and COB mRNA (by homology)	1.8268	0.1406	1.3367	1.5175	0.9033	1.4489	1.3967	2.34
2873.1	orf19.7443	orf19.7443	CA5733 IPF2873 unknown function (N/A)	0.2630	1.1010	2.1763	1.0793	1.0108	1.2253	1.8532	2.37
12526.2	orf19.1662	orf19.1662	CA3466 MRP1.5f mitochondrial ribosomal protein of the small subunit, 5-prime end (by	1.2206	-0.1846	1.5886	1.2487	1.5572	1.5354	1.7601	2.37
6016.2	orf19.1485	orf19.1485	CA0908 MRPL31 Mitochondrial ribosomal protein	1.2003	0.4593	1.8696	0.9222	0.8951	1.5027	1.9251	2.38

13404.1	orf19.755	MRPL37	CA1928 MRPL37 Mitochondrial ribosomal protein YmL37 (by homology)	1.2677	0.2378	1.8530	1.0564	1.0255	1.5033	1.8634	2.39
3928.1	orf19.6503	orf19.6503	CA4968 IPF3928 unknown function (mitochondrial ribosomal protein)	0.4188	0.0681	1.8441	1.3207	1.5385	1.9406	1.7033	2.40
7585.2	orf19.5201	orf19.5201	CA1768 IPF7585 unknown function (mitochondrial ribosome small subunit component)	0.7948	-0.0636	1.3943	1.3953	1.7118	1.9209	1.6809	2.40
14757.2	orf19.1956	orf19.1956	CA2256 IPF14757 unknown function (localises to mitochondria)	1.5603	0.2478	1.6104	1.1305	1.1301	1.4207	1.8091	2.42
7602.2	orf19.5193	orf19.5193	CA1761 IPF7602 oxidoreductase (by homology) (YIR035C)	1.0437	0.2553	0.5773	1.5041	1.5608	2.1985	1.8122	2.43
15216.2	orf19.3777	orf19.3777	CA0329 IMG2 Required for Integrity of Mitochondrial Genome (by homology)	1.1133	-0.0759	1.7482	1.0089	1.5845	1.6499	1.9529	2.43
18330.1			CA3465 MRP1.3f Mitochondrial ribosomal protein of the small subunit, 3-prime end (by	1.4662	-0.1408	1.2708	1.3334	2.2141	1.7634	1.2660	2.48
2354.1	orf19.7019	YML6	CA5204 YML6 Ribosomal protein, mitochondrial (by homology)	1.0663	-0.0650	2.0623	1.5878	1.0007	1.7565	1.8365	2.50
8066.1	orf19.3696	TOM22	CA1401 TOM22 mitochondrial outer membrane import receptor complex subunit (by ho	0.8188	-0.2328	1.9870	1.6066	1.5696	1.6060	1.9005	2.50
20133.1	orf19.585	orf19.585	CA3432 MRPL17 ribosomal protein of the large subunit (YmL30), mitochondrial (by hor	1.0256	0.1642	2.1703	1.3242	1.2214	1.6909	1.8428	2.55
17681.2	orf19.3480	orf19.3480	CA2899 IPF17681 similar to Saccharomyces cerevisiae Rsm23p involved in mitochond	0.6138	0.6185	1.7257	1.3163	1.2400	1.8927	2.0470	2.55
1621.1	orf19.6585	orf19.6585	CA4893 IPF1621 unknown function	0.9775	0.0963	1.0489	3.4195	1.4552	1.2702	1.2222	2.56
4703.2	orf19.5279	orf19.5279	CA4973 IPF4703 unknown Function (Mitochondrial ribosomal protein of the large subu	1.6978	0.0754	1.9578	1.3970	1.2487	1.6637	1.4691	2.56
16126.1	orf19.172	orf19.172	CA1417 IPF16126 similar to Saccharomyces cerevisiae Rpc19p DNA-directed RNA po	1.0772	0.1170	0.8723	1.5377	1.7505	1.9900	2.2507	2.59
6175.1	orf19.4176	orf19.4176	CA3726 IPF6175 unknown function (Mitochondrial ribosomal protein of the small subur	0.5707	0.7263	1.9156	1.6601	1.3334	1.8198	1.5974	2.59
14895.1	orf19.93	orf19.93	CA1987 IPF14895 unknown function (YMR002W)	1.0533	0.5384	1.7795	1.6294	1.7839	1.7187	1.5922	2.72
15124.2	orf19.5747	orf19.5747	CA1428 MRP4 Ribosomal protein of the small subunit mitochondrial (by homology)	1.7950	0.5060	1.7277	1.5143	0.8403	1.7116	2.0555	2.73
8752.2	orf19.828	orf19.828	CA4226 IPF8752 similar to Saccharomyces cerevisiae Mrpl24p ribosomal protein of the	1.6255	0.3003	2.0224	1.2608	1.5829	1.6289	1.8859	2.77
2599.1	orf19.6696	orf19.6696	CA4298 TIM9 Mitochondrial inner membrane translocase (by homology)	0.0688	0.3503	2.6686	1.3772	1.5872	1.7934	2.6161	2.82
3331.1	orf19.7386	orf19.7386	CA5684 IPF3331 unknown function (assembly of mitochondrial respiratory complexes)	1.0784	0.7198	1.7216	1.3653	1.6652	1.7013	2.4348	2.88
13417.2	orf19.185	orf19.185	CA1445 MRP51 Mitochondrial ribosomal protein of the small subunit (by homology)	1.6781	0.3357	1.5529	2.9718	1.2744	1.5811	1.5984	2.97
16405.2	orf19.4751	orf19.4751	CA2213 IPF16405 similar to saccharomyces cerevisiae Rsm25p protein of the small su	1.6093	0.1077	1.8519	1.7148	1.6466	1.7721	2.3514	2.99
15259.2	orf19.2214	orf19.2214	CA2377 MRPL7 Ribosomal protein of the large subunit, mitochondrial (by homology)	1.4711	-0.0455	2.0080	1.9835	1.7044	2.0489	1.9040	2.99
2343.1	orf19.7012	orf19.7012	CA5198 LPA4 Similar to ribosomal protein S16, mitochondrial (by homology)	1.9992	0.7633	2.1240	0.8942	1.6433	1.9575	1.8294	3.03
7643.1	orf19.863	orf19.863	CA1863 MRPL35 Ribosomal protein of the large subunit, mitochondrial (by homology)	1.8252	0.4959	2.1270	1.4711	1.8078	1.6669	1.8410	3.04
3182.1	orf19.3559	orf19.3559	CA0580 IPF3184.exon2 unknown function, exon 2 (doesn't exist in CDB)	1.6599	0.3356	2.2349	1.7351	1.4201	1.9159	2.1194	3.10
10399.1	orf19.3367	orf19.3367	CA1198 IPF10399 unknown function (Mitochondrial ribosomal protein of the large subu	1.4463	0.1687	2.1989	1.9854	1.8036	1.6982	2.1852	3.12
5569.2	orf19.5161	orf19.5161	CA4434 MRPL49 ribosomal protein mitochondrial	0.0000	0.6846	2.0450	2.7113	2.0709	1.9607	2.0213	3.12
407.1	orf19.7504	orf19.7504	CA5848 IPF407 unknown function (YGR161C)	2.9236	0.4892	0.3723	1.4047	1.7685	1.8236	2.8559	3.17
6295.1	orf19.1967	orf19.1967	CA2945 IMG1 Ribosomal protein, mitochondrial (by homology)	1.1671	0.7191	2.5360	1.7065	1.6890	2.2775	1.9417	3.29
16978.2	orf19.685	YHM1	CA1980 YHM1 member of the mitochondrial carrier family (MCF) (by homology)	1.7403	0.6160	1.8605	1.7313	1.6407	2.0973	2.3911	3.31
14249.2	orf19.3797	orf19.3797	CA1421 MRPL11 Mitochondrial ribosomal protein (by komology)	1.4880	0.2879	2.6690	1.7364	1.8364	1.9877	2.1412	3.33
3361.2	orf19.4018	orf19.4018	CA4785 IPF3361 putative mitochondrial ribosomal protein S7 (by homology)	1.7456	0.4452	2.4432	1.7275	2.0647	2.0676	2.0038	3.45
2131.2	orf19.7203	orf19.7203	CA5329 MRP7 Mitochondrial ribosomal protein YmL2 precursor (by homology)	1.2007	0.2828	2.3593	2.2069	2.0983	2.2802	2.7022	3.67
13943.2	orf19.5235	orf19.5235	CA5012 IPF13943 Unknown function (N/A)	1.1218	0.7219	2.9593	1.4318	2.3931	2.0819	2.7848	3.80
2157.1	orf19.7187	MAM33	CA5316 MAM33 Mitochondrial acidic matrix protein (by homology)	2.0237	0.9114	2.1786	2.2142	1.8740	2.0859	2.6871	3.99
3184.1	orf19.3559	orf19.3559	CA0579 IPF3184.exon1 unknown function, exon 1 (Mitochondrial ribosomal protein of t	0.8671	0.6388	2.5160	4.9941	2.3141	1.8957	1.7225	4.39
2075.1	orf19.4082	DDR48	CA4336 DDR48 stress protein (by homology) (YMR173W)	2.9727	2.1264	0.2084	2.8759	2.6820	2.8988	2.9035	5.21

[a] from http://www.candidagenome.org

[b] from http://genolist.pasteur.fr/CandidaDB/

Supplementary Table 2. 645 genes with altered expression in an *ace2* delete relative to wildtype grown as yeast cells. (FDR of 0.9%).

				Log2Ratios (7 experiments)							
OligoID	ORF19[a]	CGD Gene Name[a]	Description (from CandidaDB)[b]	Y1	Y2	Y3	Y4	Y5	Y6	Y7	Average Fold Change
2053.1	orf19.5267	orf19.5267	CA4983 IPF2053 unknown function (YJR151C)	-5.6743	-1.7939	-3.6428	-2.3863	-3.1960	-4.6065	-4.2919	-12.61
15862.2	orf19.3893	SCW11	CA1053 SCW11.3eoc glucanase gene family member, 3-prime end (by homology)	-2.5081	-3.5913	-4.2627	-2.3438	-3.4264	-3.8079	-3.9154	-10.61
11998.2	orf19.2758	orf19.2758	CA1898 IPF11998 unknown function (putative GPI-anchored, PGA38)	-1.6258	-2.0039	-5.0951	-3.1896	-3.7743	-4.0424	-3.7335	-10.21
9616.1	orf19.4910	FGR41	CA2024 IPF9616 unknown function	-6.6439	-1.6529	-2.8424	-0.9507	-1.2489	-1.3288	-1.8442	-5.13
294.1	orf19.3278	GSY1	CA5467 GSY1 UDP glucose--starch glucosyltransferase, glycogen synthase (by homology)	-0.7131	0.0663	-0.1376	-2.7274	-6.6439	-2.7959	-2.8468	-4.78
564.2	orf19.7104	orf19.7104	CA5596 IPF564 unknown function (N/A)	-4.3825	-0.8817	-2.8059	-1.1461	-1.3058	-2.3336	-2.4466	-4.55
19968.1	orf19.220	PIR1	CA3030 IPF19968 putative cell wall protein of the PIR family	-1.7947	-1.7249	-2.6484	-2.1117	-2.1235	-2.1374	-2.0700	-4.25
2535.1			CA0355 IPF2535 unknown function	-3.1078	-1.8890	-2.9434	-1.3808	-1.0559	-0.9132	-2.8890	-4.07
696.1	orf19.7586	CHT3	CA5987 CHT3 chitinase 3 precursor	-0.2350	0.0498	-2.8475	-1.8911	-2.6904	-2.1489	-2.7371	-3.45
763.2	orf19.5343	ASH1	CA5502 IPF763 putative transcription factor with a Cys4- zinc finger (ASH1)	-3.0566	-1.5544	-2.6543	-0.4252	-1.1711	-1.0239	-2.0334	-3.26
6235.2	orf19.5372	orf19.5372	CA2216 IPF6235 Candida albicans Tca2 retrotransposon	-1.9658	-1.2416	-0.4129	-1.6029	-2.2518	-2.2239	-2.0125	-3.19
8321.2	orf19.3325	orf19.3325	CA2938 IPF8321 similar to Saccharomyces cerevisiae Glg2p self-glucosylating initiator of glycoge	-1.3865	-0.6467	-0.7350	-1.5976	-2.3417	-2.2413	-2.6905	-3.17
6238.2	orf19.2374	orf19.2374	CA2752 IPF6238 GAG protein of retrotransposon pCal	-1.7299	-0.5946	-0.7952	-1.9462	-2.0035	-2.4014	-2.1497	-3.16
4053.1	orf19.1868	RNR22	CA4492 RNR22 ribonucleoside-diphosphate reductase (by homology)	-0.8525	0.1287	-0.6075	-3.1344	-0.9312	-2.9547	-3.1198	-3.11
753.1	orf19.5348	TPS3	CA5505 TPS3.3 alpha,alpha-trehalose-phosphate synthase, regulatory subunit, 3-prime end (by h	-1.1463	0.0135	-0.0082	-2.0337	-2.2939	-2.8241	-2.5094	-2.91
7796.2	orf19.2619	PHO113	CA0616 PHO11 Secreted acid phosphatase	-1.4131	-1.4718	-1.6576	-0.3309	-0.9155	-3.5189	-1.2210	-2.84
9751.2	orf19.3066	ENG1	CA5091 ACF3 endo-1,3-beta-glucanase	-1.3832	-0.4970	-2.5736	-1.1255	-1.5699	-1.5718	-1.6934	-2.80
4065.1	orf19.1862	orf19.1862	CA0386 IPF4065 unknown function (YHR087w)	-1.2836	-0.2456	-0.0148	-1.7253	-1.8334	-2.4448	-2.8450	-2.80
3160.2	orf19.3160	HSP12	CA0627 HSP12 Heat shock protein (by homology)	-2.7039	0.2782	-0.2741	-1.2647	-1.7165	-2.1677	-2.4122	-2.76
4959.1	orf19.7676	orf19.7676	CA6057 IPF4959 D-xylulose reductase (by homology)	-0.9458	0.1974	0.0395	-1.8950	-2.3933	-2.4422	-2.6536	-2.72
11927.1	orf19.111	CAN2	CA1191 CAN2 amino acid permease (by homology)	-0.5146	-0.6016	-0.2260	-2.1392	-2.3808	-1.6484	-2.2863	-2.64
12467.2	orf19.1206	FET35	CA1431 FET34.3eoc iron transport multicopper oxidase, 3-prime end (by homology)	-1.9254	-1.3849	-0.3082	-1.6889	-1.0517	-1.2266	-2.1647	-2.63
17039.1	orf19.4215	FET34	CA2920 FET5 multicopy oxidase (by homology)	-1.6181	-0.4903	-0.8092	-1.4044	-1.1156	-1.3500	-2.3852	-2.48
10363.2	orf19.3803	MNN22	CA0752 MNN22 Golgi alpha-1,2-mannosyltransferase (by homology)	-0.8520	-1.5064	-0.7809	-0.8520	-1.5995	-1.8997	-1.4620	-2.43
2357.1	orf19.7021	GPH1	CA5206 GPH1 Glycogen phosphorylase (by homology)	-1.0158	-0.0963	-0.5501	-1.7010	-2.0683	-2.0902	-1.4017	-2.42
12926.2	orf19.2623	ZCF12	CA0471 ECM22 putative protein involved in cell wall biogenesis (by homology)	-1.8314	-0.5951	-1.2210	-0.3401	-3.5513	-1.1779	-0.0862	-2.39
6455.2	orf19.1893	orf19.1893	CA4475 IPF6455 unknown function	-1.8943	-1.7084	-2.1649	-1.1297	0.5888	-0.8943	-1.5907	-2.39
3588.2	orf19.3038	TPS2	CA5066 TPS2 Trealose-6-phosphate phosphatase (by homology)	-0.5055	-0.1203	-0.3499	-1.4090	-2.2897	-2.2644	-1.8160	-2.38
10835.2	orf19.3629	orf19.3629	CA1278 IPF10835 unknown function (DSE1)	-1.2787	-0.7360	-1.9926	-0.9486	-0.7651	-0.9268	-2.0766	-2.37
14618.1	orf19.6079	orf19.6079	CA0286 IPF14618 unknown function (N/A)	0.0000	-0.4901	-0.0065	-0.8704	-2.7393	-2.0146	-2.5732	-2.37
10349.2	orf19.5079	CDR4	CA3895 CDR4 Multidrug resistance protein	-0.3838	-0.5386	-0.5651	-1.7881	-2.0178	-1.8263	-1.5676	-2.36
4104.2	orf19.2020	HGT6	CA1070 HXT61 sugar transporter	-0.6434	0.0978	-0.4761	-1.6712	-2.0956	-2.0487	-1.7938	-2.35
4732.2	orf19.3746	IFC1	CA3257 IFC1 Unknown Function (YPR194c, OPT2, peptide transporter)	-2.0218	-0.4070	-1.0589	-1.3111	-0.7312	-1.5494	-1.5358	-2.35
1674.1	orf19.6559	orf19.6559	CA4874 IPF1674 putative transcription initiation factor (by homology)	-1.7087	0.0160	0.3618	-1.5715	-1.7327	-1.5872	-2.3625	-2.34
11819.2	orf19.4980	HSP70	CA1230 SSA4 cahsp70 mRNA for heat shock	-0.3954	0.4683	-0.5530	-1.5098	-1.6252	-2.0177	-2.7760	-2.30
4286.2	orf19.542	HXK2	CA0127 HXK2.3f hexokinase II, 3-prime end (by homology)	-0.1625	-0.1679	-0.4012	-1.7277	-1.9132	-1.7957	-2.2044	-2.29
12812.2	orf19.3749	IFC3	CA2349 IFC3 Unknown function (YPR194c, peptide transporter)	-0.6967	0.0229	-0.9546	-1.8783	-1.0801	-1.7760	-1.9051	-2.27
5940.2	orf19.434	PRD1	CA4059 PRD1 Proteinase (by homology)	-0.4954	-0.5284	-0.1253	-1.6568	-1.5703	-2.0619	-1.8189	-2.27
3121.1	orf19.4438	RME1	CA4651 IPF3121 unknown function (YGR044c, RME1)	-1.0350	-0.3292	-0.1424	-1.1488	-2.5907	-1.6529	-1.3292	-2.26
19048.1			CA0311 DAK2.3eoc dihydroxyacetone kinase, 3-prime end (by homology)	-0.6325	-0.0182	0.0218	-1.7631	-1.8484	-1.9914	-1.9800	-2.25
7141.1	orf19.1562	orf19.1562	CA3986 IPF7141 unknown function	-2.0139	0.1717	-2.3848	-0.6379	-0.4970	-1.0275	-1.4246	-2.17
14295.1	orf19.6321	PGA48	CA3287 IPF14295 putative Sed1p-like cell surface protein (by homology)	0.0000	-0.6003	-1.4600	-0.8162	-1.4456	-1.5180	-1.9431	-2.16
872.1	orf19.7218	RBE1	CA5344 PRY2 putative pathogen related proteins (by homology)	-1.8136	-0.5554	-1.7040	-0.6094	-0.7894	-0.8366	-1.4562	-2.16
3735.1	orf19.5288	IFE2	CA2075 IFE2 Unknown function (YAL060W, BDH1, (2R,3R)-2,3-butanediol dehydrogenase)	-0.7774	-0.2881	-0.2961	-1.3994	-1.6759	-1.6649	-1.6275	-2.15
3043.1	orf19.5019	orf19.5019	CA5244 IPF3043 unknown function	0.2091	-1.4461	-2.8262	-0.5125	-0.9241	-0.9714	-1.1681	-2.13
14282.2	orf19.2296	orf19.2296	CA0446 IPF14282 Similar to mucin proteins (by homology)		0.2798	0.0342	-1.5778	-1.6082	-1.6897	-1.9771	-2.13
17763.2	orf19.6139	FRE7	CA3416 FRE30.3 Strong similarity to ferric reductase Fre2p, 3-prime end (by homology)	-0.3527	-0.3339	-1.5440	-0.6756	-1.8798	-1.3548	-1.3698	-2.10
17153.2	orf19.1314	orf19.1314	CA2822 IPF14550 unknown function (YMR031C? Zn finger)	-1.6171	-0.3292	-0.0740	-1.3959	-1.1109	-1.3959	-1.4982	-2.09
5750.2	orf19.6540	PFK2	CA3112 PFK2 6-phosphofructokinase, beta subunit	-0.6820	-0.2561	-0.0515	-1.2479	-2.1392	-1.5454	-1.4759	-2.08
8762.2	orf19.822	orf19.822	CA4220 IPF8762 unknown function (N/A)	-1.9037	-0.7277	-1.0405	-0.9762	-0.7637	-0.8235	-1.1626	-2.08

9108.2	orf19.6124	ACE2	CA2996 IPF9108 similar to Saccharomyces cerevisiae Ace2p transcription factor (by homology)	-1.0728	-1.5684	-1.7486	-0.9516	-0.8036	0.0939	-1.3203	-2.07
14360.2	orf19.2706	CRH11	CA0375 CRH11 Probable membrane protein (by homology) glycosidase	0.0000	-0.9131	-2.1694	-0.6908	-1.7776	-1.1243	-0.5745	-2.05
9116.2	orf19.6119	orf19.6119	CA2994 IPF9116 unknown function (N/A)	-1.2984	-0.5023	-1.2916	-0.6066	-1.5163	-0.9270	-1.0130	-2.03
18773.1	orf19.2021	HGT8	CA1069 HXT5.3f sugar transporter, 3-prime end	-0.5756	-0.0410	-0.3865	-1.3548	-2.0529	-1.5064	-1.2076	-2.02
12521.2	orf19.6232	NPR1	CA0576 NPR1 nitrogen permease reactivator protein (by homology)	-0.2843	-0.4968	-0.1688	-1.6172	-1.5713	-1.4996	-1.4285	-2.01
16625.2	orf19.3591	APE3	CA0871 APE3 aminopeptidase (by homology)	-1.5546	-0.5001	-0.9357	-0.5193	-0.8100	-1.3926	-1.3329	-2.01
11982.1	orf19.691	GPD2	CA0824 GPD2 Glycerol 3-phosphate dehydrogenase (by homology)	-0.4580	0.0936	-0.0923	-1.2793	-2.2109	-1.6666	-1.4305	-2.01
8505.2	orf19.2613	ECM4	CA2386 ECM41.3 involved in cell wall biogenesis and architecture, 3-prime end (by homology)	-1.0690	-0.1857	-0.1569	-0.9003	-1.4447	-1.7528	-1.4170	-1.99
4358.1	orf19.5911	CMK1	CA6135 CMK1 Ca2-dependent ser/thr protein kinase (by homology)	-0.4693	-0.0832	-0.5739	-1.0056	-1.6222	-1.5602	-1.6019	-1.98
5981.1	orf19.7310	orf19.7310	CA5547 IPF5981 similar to Saccharomyces cerevisiae Gin3p (by homology)	-2.2109	-0.0544	-0.4739	-0.7037	-0.8651	-1.2619	-1.3364	-1.98
16784.2	orf19.5113	ADH2	CA3923 ADH2 alcohol dehydrogenase I (by homology)	-0.9078	0.1777	-0.9302	-0.9931	-1.5847	-1.2227	-1.4375	-1.98
5160.1			CA4941 CRN1.53f actin-binding protein, 5-prime end (by homology)	-2.5228	-0.4055	-0.1877	-1.0801	-1.0380	-0.6529	-1.0087	-1.98
8388.2	orf19.1408	orf19.1408	CA0263 GLK1 aldohexose specific glucokinase (by homology)		0.5479	-0.9187	-1.3659	-0.9942	-1.3696	-1.7909	-1.98
4991.2	orf19.2531	CSP37	CA1075 IPF4991 putative membrane protein (YDL058w, USO1, integrin)	-1.5692	-0.4383	0.0186	-1.2863		-1.4739	-1.1078	-1.97
11096.2	orf19.4618	FBA1	CA5180 FBA1 fructose-bisphosphate aldolase (by homology)	-0.6482	-0.1243	-0.1586	-1.2533	-1.5975	-1.6149	-1.4346	-1.97
9998.2	orf19.2284	orf19.2284	CA0997 IPF9998 unknown function	-2.5064	-0.3111	0.0786	-1.1266	-0.8863	-0.8783	-1.1520	-1.96
2523.2	orf19.6637	orf19.6637	CA4081 IPF2523 unknown function	-0.3346	-0.2706	-0.7834	-1.5105	-0.5228	-1.1976	-2.1584	-1.96
10586.2	orf19.2655	BUB3	CA0526 BUB3 cell cycle arrest protein (by homology)	-1.2614	-0.7274	-0.4488	-0.6831	-1.3098	-1.2384	-1.1070	-1.96
2857.1	orf19.7284	ASR2	CA5526 IPF2857 unknown function	-1.8478	0.6162	-0.8353	-0.8115	-0.9138	-1.0726	-1.8732	-1.95
15672.1	orf19.2607	orf19.2607	CA2392 IPF15672 unknown function (YKL128c? phosphomutase homologue)	-1.6905	-1.0711	-0.8516	-0.9107	0.0000	-0.9715	-1.2220	-1.94
10991.2	orf19.5801	RNR21	CA4155 RNR21 ribonucleoside-diphosphate reductase (by homology)	-1.1749	-0.4296	-0.4081	-1.0636	-1.5359	-1.2970	-0.7937	-1.94
12215.2	orf19.5058	SMI1	CA1740 SMI1 beta-1,3-glucan synthesis protein (by homology)	-0.6973	-0.9294	-0.3716	-1.2403	-0.9462	-1.1666	-1.2299	-1.92
7527.2	orf19.4530.1	orf19.4530.1	CA4189 IPF7527 unknown function	-1.0410	0.0243	-0.2845	-1.0321	-0.9051	-1.1779	-2.0893	-1.90
4328.2	orf19.5525	orf19.5525	CA0210 IPF4328 unknown function	-0.7446	-0.4921	0.3583	-0.8567	-1.4977	-1.6551	-1.5951	-1.90
4369.1	orf19.5917	STP3	CA6131 IPF4369 similar to Saccharomyces cerevisiae Stp2p involved in pre-tRNA splicing (by hor	-0.1615	-0.8662	-0.9065	-0.9845	-0.7563	-1.4818	-1.3006	-1.90
16795.1	orf19.2989	orf19.2989	CA0821 IPF16795 glycerate/formate-dehydrogenase (by homology)	-1.5512	-0.1212	-0.6518	-1.1323	0.0688	-1.1509	-1.9164	-1.89
12896.2	orf19.2242	PRB1	CA0270 PRB2 Protease B, vacuolar (by homology)	-0.3787	-0.1727	-0.2637	-1.3184	-1.2897	-1.4280	-1.6019	-1.89
7044.2	orf19.125	EBP1	CA1216 EBP1 NADPH dehydrogenase	-0.8237	-0.0321	-0.6082	-1.1424	-1.6574	-1.2828	-0.8916	-1.89
17009.2	orf19.3651	PGK1	CA1691 PGK1 Phosphoglycerate kinase	-0.4478	0.2722	-0.3606	-1.4193	-1.3184	-1.4239	-1.7325	-1.89
17289.2	orf19.6134	orf19.6134	CA3422 IPF17289 unknown function (YLR440C)	-0.4586	-0.9228	-1.0604	-0.8565	-1.1903	-0.9644	-0.9537	-1.89
1203.2	orf19.2073	orf19.2073	CA4823 ERC3 ethionine resistance protein (by homology)		-0.8211	-0.6484	-1.1329	-0.9296	-0.8059	-1.1520	-1.89
7968.2	orf19.2693	orf19.2693	CA3260 IPF7968 unknown function (possible URE2, prion)	-0.4623	-0.7965	-0.4916	-1.2708	-0.7528	-1.4252	-1.1845	-1.88
20142.1	orf19.730	RGD3	CA3679 IPF20142 unknown function (YFL047w, RGD2, RhoGAP)	-0.8749	-1.2625	-0.1636	-0.5995	-1.4820	-1.0376	-0.9044	-1.87
5949.2	orf19.6800	POS5	CA5906 IPF5949 unknown function (YPL188w, POS5, oxidative stress)	-0.2428	-1.1383	-0.0771	-0.9700	-1.2940	-1.2422	-1.3350	-1.87
8884.2	orf19.3422	FMP27	CA3756 IPF8884 unknown function (YLR454w, mitochondrial)	-1.1180	-0.0254	-1.0497	-0.6430	-1.0131	-1.1550	-1.2655	-1.86
10469.2	orf19.1789.1	LYS1	CA0343 LYS1.5eoc saccharopine dehydrogenase, 5-prime end (by homology)	-0.5700	-0.5765	-0.9140	-0.9508	-0.6758	-0.9603	-1.5779	-1.85
14545.2	orf19.1381	orf19.1381	CA2314 IPF14545 unknown function	-0.3053	-0.5176	0.1855	-0.7838	-1.3040	-1.4798	-1.9686	-1.84
12403.2	orf19.2484	orf19.2484	CA3805 IPF12403 unknown function (YDR415c)	-0.8417	-0.2793	-0.1392	-0.7084	-1.4501	-1.3474	-1.3622	-1.83
7283.2	orf19.388	CAF16	CA3880 CAF16 ABC ATPase (by homology)	0.0597	-0.4200	0.0045	-1.1364	-1.3673	-1.5475	-1.7188	-1.83
8248.2	orf19.1517	ARO3	CA1751 ARO3.exon2 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase, exon 2 (by homolo	-1.1475	-1.0544	-0.1999	-0.8549	-0.7298	-1.1442	-0.9644	-1.83
9939.2	orf19.4752	MSN4	CA2214 IPF9939 similar to Saccharomyces cerevisiae Msn4p transcriptional activator (by homolog	-0.9164	-0.4503	-0.1844	-1.0273	-0.9994	-1.4416	-1.0703	-1.83
7403.2	orf19.4664	orf19.4664	CA2710 IPF7403 unknown function (YMR069w, NAT4)	-1.8890	-0.6804	-0.3067	-0.6178	-0.7574	-0.7700	-1.0436	-1.82
6464.2	orf19.1887	orf19.1887	CA4480 IPF6464 putative triacylglycerol lipase (by homology)	-0.8763	-0.4056	-0.6296	-0.5877	-1.1852	-1.2096	-1.1422	-1.82
7759.1	orf19.3888	PGI1	CA3559 PGI1 Glucose-6-phosphate isomerase	-1.1420	-0.1953	-0.4274	-1.0051	-1.3589	-1.1222	-0.7677	-1.81
17060.2	orf19.3997	ADH1	CA4765 ADH1 alcohol dehydrogenase (by homology)	-0.7408	-0.3215	-0.3743	-0.7999	-1.5330	-1.1256	-1.1177	-1.81
11299.2	orf19.5671	orf19.5671	CA4378 IPF11299 unknown function (YCR030C, SYP1)	-1.1376	-1.8187	-0.7108	-0.2953	-0.5158	-0.5979	-0.9273	-1.81
14429.2	orf19.395	ENO1	CA3874 ENO1 Enolase I (2-phosphoglycerate dehydratase)	-0.8836	0.2606	0.0115	-1.2311	-1.3076	-1.5692	-1.2550	-1.81
1147.2	orf19.2098	ARO8	CA4804 ARO8 aromatic amino acid aminotransferase I (by homology)	-0.7195	0.0105	-0.5691	-0.9788	-0.9916	-0.8678	-1.8213	-1.80
5522.1	orf19.2179	SIT1	CA3740 SIT1 Ferrioxamine B permease by homology		-2.1140	-0.6712	-0.3040	-0.8783	-1.0469	-0.0634	-1.80
16449.2	orf19.5622	GLC3	CA2758 GLC3 1,4-glucan branching enzyme (by homology)	-0.3771	-0.5929	-0.0291	-1.1681	-1.7710	-1.1877	-0.7760	-1.79
3092.1	orf19.4445	orf19.4445	CA4658 IPF3092 unknown function	-1.3808	-0.3219	-0.9942	0.0772	-1.8783	-1.1329	-0.2706	-1.79
3598.2	orf19.3047	orf19.3047	CA5072 IPF3598 similar to Saccharomyces cerevisiae Sip3p protein which interacts with Snf1p pr	-0.4742	-0.2052	-0.5192	-1.1879	-1.1673	-1.0695	-1.2661	-1.79
3533.2	orf19.6842	orf19.6842	CA4444 IPF3533 putative GDP/GTP exchange factor (by homology)	-0.5633	-0.1314	-0.5802	-0.6919	-2.1194	-0.9386	-0.8647	-1.79
19710.1	orf19.2970	LYS2	CA0916 LYS2 L-aminoadipate-semialdehyde dehydrogenase, large subunit	-0.5740	-0.7415	-0.3884	-0.9078	-1.2057	-0.9246	-1.1443	-1.79
4664.2	orf19.1845	orf19.1845	CA3366 FRE43 ferric reductase-like (by homology)	-0.6484	0.2004	-0.4422	-1.6574	-0.8314	-1.0559	-1.4501	-1.79
525.1	orf19.7085	orf19.7085	CA5613 IPF525 unknown function (N/A)	-1.3310	-0.8640	-1.2167	-0.4686	-0.6007	-0.6993	-0.6800	-1.79
2795.1	orf19.6763	SLK19	CA5936 IPF2795 unknown function (YOR195w?)	-0.7616	-0.1149	-0.9051	-0.5600	-1.1641	-1.2027	-1.1188	-1.78

14337.2	orf19.1814	orf19.1814	CA0324 STT4 Phosphatidylinositol-4-kinase (by homology)		-0.1488	-0.6920	-0.7710	-1.2793	-0.8757	-1.2109	-1.78
2936.1	orf19.4304	GAP1	CA2638 GAP3 General amino acid permease (by homology)	-0.0908	-0.4673	-0.4103	-1.3394	-1.3026	-0.9702	-1.2004	-1.77
8369.2	orf19.6077	orf19.6077	CA4936 IPF8369 unknown function	-1.7280	0.0834	-0.4521	-0.9162	-0.6830	-0.8583	-1.2058	-1.77
11493.2	orf19.2393	orf19.2393	CA2094 IPF11493 unknown function	-1.9210	-0.3756	-0.2094	-0.6956	-0.7540	-0.9042	-0.8159	-1.75
1531.2	orf19.338	orf19.338	CA4632 IPF1531 unknown function	-0.7091	0.0503	-0.4044	-0.5871	-1.0692	-1.1722	-1.7588	-1.75
8985.2	orf19.1368	orf19.1368	CA0045 IPF8985.5eoc unknown function, 5-prime end (N/A)	-1.4921	-0.0734	-1.0989	-0.9644	-0.3802	-0.7386	-0.7972	-1.73
9877.2	orf19.1375	LEU42	CA2310 LEU42 2-isopropylmalalate synthase (by homology)	-0.9914	0.0101	0.1230	-1.3696	-1.1456	-1.4941	-0.6735	-1.73
9411.2	orf19.6147	orf19.6147	CA3410 IPF9411 unknown function (YER030w)	-1.0655	-0.9243	-0.9852	-0.9697	-0.2852	-0.4317	-0.8388	-1.72
10148.2	orf19.2172	ARA1	CA3746 ARA1 D-arabinose dehydrogenase (by homology)	-1.1127	0.1329	0.1114	-0.8703	-1.3844	-1.2093	-1.1498	-1.72
857.1	orf19.7227	orf19.7227	CA5351 IPF857 unknown function (YFR003c, PP1 inhibitor)	-1.5877	-0.7026	-0.5626	-0.3731	-0.5393	-0.6419	-1.0310	-1.71
13176.2	orf19.5610	ARG3	CA2964 IPF13176.3 ornithine carbamoyltransferase, 3-prime end (by homology)		-0.8890	-0.6529	-0.7108	-1.4779	-0.2345	-0.6804	-1.71
6156.1	orf19.1034	orf19.1034	CA1625 IPF6156 similar to C.elegans LIM homeobox protein	-0.3940	-0.4880	0.3994	-1.2042	-1.2009	-1.3364	-1.1844	-1.71
7400.2	orf19.1802	orf19.1802	CA0984 IPF7400 unknown function	-1.1617	-0.1345	0.0663	-0.9658	-1.1016	-1.0000	-1.1047	-1.71
19952.1	orf19.5636	RBT5	CA2558 RBT5 repressed by TUP1 protein 5	-0.6273	-0.2506	-0.5292	-0.6128	-1.3459	-0.9362	-1.0563	-1.70
15021.2	orf19.5615	AYR2	CA0163 AYR2 1-acyl dihydroxyacetone phosphate reductase (by homology)	-0.5995	-0.1266	-0.3058	-0.8391	-1.3437	-0.9214	-1.2009	-1.70
2397.2	orf19.6814	TDH3	CA5892 GAP1 Glyceraldehyde-3-phosphate dehydrogenase	-0.9856	0.4005	-0.3273	-0.8625	-0.9434	-1.3659	-1.1910	-1.69
11965.2	orf19.5782	orf19.5782	CA2807 IPF11965 unknown function	-0.5401	0.1037	-0.1587	-1.2006	-1.1932	-1.1030	-1.1830	-1.69
2997.1	orf19.6983	orf19.6983	CA5029 IPF2997 unknown function (YDR028c, REG1, Glc7p regulatory subunit)	-0.5994	-0.4172	-0.1165	-1.1437	-0.8521	-0.9610	-1.1775	-1.68
6173.2	orf19.4177	HIS5	CA3727 HIS5.3f Histidinol-phosphate aminotransferase, 3-prime end (by homology)	-0.9132	-0.3058	-0.6171	-1.9714	-0.3401	-0.3827	-0.7274	-1.68
5353.2	orf19.3003	orf19.3003	CA3124 IPF5353.3 unknown function, 3-prime end	-1.5564	-0.2775	-0.0321	-0.7834	-0.8863	-1.0529	-0.6689	-1.68
3499.1	orf19.6745	TPI1	CA5950 TPI1 Triose phosphate isomerase	-0.5502	0.2455	-0.3828	-0.8568	-1.2280	-1.1145	-1.3533	-1.68
8888.2	orf19.3419	MAE1	CA3757 MAE1 mitochondrial malic enzyme (by homology)	-0.2402	0.0242	-0.8316	-0.7959	-1.5583	-1.0530	-0.7830	-1.68
4222.2	orf19.7323	CBP1	CA5559 CBP1 Corticosteroid binding protein	-0.4432	0.1918	-0.7432	-1.0879	-1.0716	-1.0395	-1.0371	-1.68
13128.2	orf19.1585	ZRT2	CA3160 ZRT2 zinc transport protein (by homology)	-0.8160	0.0841	-0.3733	-0.4679	-1.7084	-0.9828	-0.9658	-1.68
18418.1	orf19.5620	orf19.5620	CA2756 IPF18418 unknown function (YHR029C)	-0.4888	-0.1310	-0.5154	-0.8293	-1.2013	-1.1880	-0.8745	-1.68
11858.2	orf19.1277	orf19.1277	CA1411 IPF11858 unknown function (N/A)	-0.8331	-0.2787	-0.6237	-1.0871	-0.5676	-0.8088	-0.9888	-1.67
13378.1	orf19.2351	NIT3	CA2338 NIT3 nitrilase (by homology)	-0.9024	-0.3468	-0.4541	-0.9248	-0.9123	-0.5076	-1.1367	-1.67
13867.2	orf19.5158	orf19.5158	CA4437 IPF13867 unknown function	-1.3183	0.0356	-0.1392	-0.4422	-1.2243	-1.3364	-0.7563	-1.67
10304.1	orf19.2277	TPK2	CA1874 TPK2 cAMP-dependent protein kinase 2 (by homology)	0.0000	-0.2364	-0.3511	-0.7685	-1.3102	-1.4159	-1.0329	-1.66
7360.1	orf19.575	HYR3	CA2714 IFF2 unknown function		-0.2740	-0.7131	-0.4422	-1.3076	-1.4189	-0.2260	-1.66
19782.1	orf19.6135	orf19.6135	CA3421 IPF19782 unknown function (YDR356w?)	-0.8882	-0.0587	-0.7923	-0.5611	-0.6695	-1.2093	-0.9112	-1.66
10688.2	orf19.5855	orf19.5855	CA2953 MBP1 transcription factor (by homologgy)	-1.3808	-0.5416	-0.3328	-0.3789	-1.3959	-0.4344	-0.6126	-1.65
8527.1	orf19.5305	RHD3	CA5476 IPF8527 unknown function	-1.8314	-0.8943	-0.5564	-0.5105	-0.4679	-0.3273	-0.4820	-1.65
4824.1	orf19.3355	ISN1	CA1020 IPF4824 unknown function	0.0482	-0.0664	-0.4860	-1.1297	-0.9132	-0.9971	-1.5228	-1.65
5002.2			CA0691 Cirt4a Transposase (by homology)	-0.4035	0.0868	-0.3129	-1.3183	-0.6038	-1.0499	-1.4422	-1.65
9407.2	orf19.6151	orf19.6151	CA3408 IPF9407 similar to Saccharomyces cerevisiae Arc15p subunit of the ARP2/3 complex (by	-0.5390	-0.4811	-0.7637	-0.6961	-0.6602	-0.8022	-1.0956	-1.65
9206.2	orf19.3678	orf19.3678	CA4047 IPF9206 unknown function	-1.0770	-0.1047	-1.5649	-0.4800	-0.1313	-1.0469	-0.6304	-1.65
9088.2	orf19.3802	PMT6	CA0503 PMT6 protein mannosyltransferase	-0.4600	-0.0203	-0.4112	-1.1424	-0.9743	-1.0000	-1.0203	-1.65
3488.1	orf19.6755	orf19.6755	CA5942 DLD2 D-lactate ferrycytochrome C oxidoreductase (by homology)	-1.0937	0.0025	-0.6202	-0.5596	-0.8014	-0.6873	-1.2654	-1.64
9113.2	orf19.6121	MNL1	CA2995 IPF9113 unknown function (C-TERMINAL REGION HAS HOMOLOGY WITH THE (PUTA	-0.3937	-0.9542	-0.8336	-0.4980	-0.5842	-1.0289	-0.7156	-1.64
15149.2	orf19.646	GLN1	CA1855 GLN1 glutamate-ammonia ligase (by homology)	0.1191	-0.3595	-0.4970	-0.9282	-0.9409	-1.0674	-1.3241	-1.64
868.1	orf19.7219	FTR1	CA5345 FTR1 high affinity iron permease	-1.3772	-0.3072	-0.9140	-0.4776	-0.4518	-0.9095	-0.5376	-1.64
			COX3a mito	-1.0203	0.1375	0.0524	-0.9296	-1.3622	-0.8573	-0.9856	-1.64
2527.2	orf19.6635	orf19.6635	CA4079 IPF2527 unknown function (N/A)		-0.9406	-0.1504	-1.3585	-0.4189	-0.6804	-0.7013	-1.63
7980.2	orf19.2686	orf19.2686	CA2770 CPS1 Carboxypeptidase YSCS precursor, second fragment (by homology)	-0.9898	-0.5126	-0.8255	-0.6491	-0.5229	-0.8376	-0.6183	-1.63
19766.1			CA2746 IPF19766 unknown function	-0.4334	-0.0262	-0.2232	-0.6877	-1.3391	-0.9504	-1.2620	-1.63
9057.2	orf19.1189	orf19.1189	CA2649 IPF9057 unknown function (YGR140W, CBF2)	-0.9936	-0.8873	-0.5661	-0.1332	-1.2923	-0.5726	-0.4612	-1.63
7205.2	orf19.2474	orf19.2474	CA0035 PRC3 Carboxypeptidase Y precursor (by homology)	-0.5564	-0.4840	-0.4860	-0.5886	-0.6689	-1.7515	-0.3677	-1.62
16916.2	orf19.3175	orf19.3175	CA0510 ETF1 ETF-UBIQUINONE OXIDOREDUCTASE (by homology)	-1.2653	-0.5458	0.3231	-0.7084	-0.9187	-0.9462	-0.8237	-1.62
19548.1	orf19.3433	OYE23	CA4030 EBP4 NADPH dehydrogenase (by homology)	-0.2009	0.2141	-0.6016	-1.0058	-1.1361	-0.9630	-1.1877	-1.62
5619.1	orf19.7499	orf19.7499	CA5843 IPF416 unknown function	-0.4961	-0.3978	-0.1472	-0.7322	-1.5864	-0.9434	-0.5564	-1.62
7646.2	orf19.861	orf19.861	CA1865 IPF7646 putative transcription factor (by homology)	-1.1910	-0.6712	0.0257	-0.8084	-0.2916	-1.2723	-0.6461	-1.62
4535.2	orf19.903	GPM1	CA4671 GPM1 phosphoglycerate mutase (by homology)	-0.5661	-0.2396	-0.4316	-0.7902	-0.8213	-0.9737	-1.0323	-1.62
3510.1	orf19.6739	orf19.6739	CA5955 IPF3510 unknown function (YMR278w, similar to phosphomannomutases)	-0.7649	-0.3053	-0.0434	-0.6649	-1.3041	-0.8328	-0.9075	-1.61
9255.2	orf19.5136	orf19.5136	CA3637 IPF9255 unknown function	-0.7408	-0.5327	0.2765	-0.9242	-0.9311	-0.8874	-1.0736	-1.61
5185.2	orf19.3618	YWP1	CA1678 IPF5185 putative cell wall protein (by homology) (YAR050W, FLO1)	-0.7202	-0.2303	-0.9041	-0.5321	-0.7723	-0.9916	-0.6270	-1.60
9145.2	orf19.6245	orf19.6245	CA0962 IPF9145 unknown function	-1.2898	-0.1408	-0.1926	-0.3771	-1.0619	-0.9024	-0.7418	-1.59

1837.2	orf19.5877	orf19.5877	CA6159 IPF1837 unknown function (YOR377W, alcohol acetyltransferase)	-1.1517	-0.4186	-0.7599	-0.6412	-0.4705	-0.6612	-0.5859	-1.59
8847.2	orf19.6127	LPD1	CA2998 LPD1 dihydrolipoamide dehydrogenase (by homology)	-0.5269	-0.6629	-0.3653	-0.5432	-1.1092	-0.7884	-0.6909	-1.59
8025.2	orf19.1333	SNG3	CA2117 SNG3 Drug transporter (by homology)	-0.7909	-0.2294	-0.6529	-0.3346	-0.4921	-0.9828	-1.1910	-1.59
13885.1	orf19.5503	orf19.5503	CA2445 IPF13885 unknown function (N/A)	-0.7270	-0.3206	-0.8717	-0.7551	-0.6466	-0.5584	-0.7909	-1.59
2490.1	orf19.7479	NTH1	CA5824 NTH1 Neutral trehalase	-0.2863	0.0635	-0.5416	-0.9379	-0.5951	-1.2550	-1.1140	-1.59
3311.2	orf19.7396	orf19.7396	CA5694 IPF3311 unknown function (N/A)	-0.6897	-0.8116	-0.4165	-0.3320	-0.7391	-0.7315	-0.9246	-1.58
14171.2	orf19.3149	LSP1	CA0622 IPF14171 unknown function (YGR086c, PIL1, Phosphorylation Inhibited by Long chain ba	-1.1750	-1.0605	-0.6553	-0.3293	-0.6563	-0.5585	-0.1756	-1.58
4392.1	orf19.1474	SLA1	CA4531 SLA1 cytoskeleton assembly control protein	-0.5029	-0.5269	-0.3257	-0.7012	-0.7667	-0.7417	-1.0398	-1.58
9860.2	orf19.4436	orf19.4436	CA4649 GPX4 glutathione peroxidase (by homology)	-0.5821	-0.5543	-0.0291	-0.8546	-0.3733	-1.2277	-0.9828	-1.58
829.1	orf19.7242	orf19.7242	CA5363 NCR1 Polytopic membrane protein involved in sterol homeostasis and trafficking (by hom	-0.0233	-0.1172	-0.4719	-0.8757	-0.7588	-1.1109	-1.2447	-1.58
1427.1	orf19.6055	orf19.6055	CA4915 IPF1427 Similar to ubiquitination protein Bul1p (by homology)	-0.3698	-0.0802	-0.1427	-0.8770	-0.9661	-1.1993	-0.9523	-1.57
19814.1	orf19.7106	orf19.7106	CA5594 IPF19814 folate hydrolase (by homology)		-0.0770	0.0215	-0.5374	-0.8783	-1.4699	-0.9518	-1.57
12125.2	orf19.5645	MET15	CA2565 MET15 O-acetylhomoserine O-acetylserine sulphydrylase	-1.0058	-0.2226	-1.3219	-0.0954	-0.4521	-0.7834	-0.6597	-1.57
3351.1	orf19.4012	PCL5	CA4779 IPF3351 unknown function		-1.0619	-0.0816	-0.4383	-1.0619	-0.6038	-0.6193	-1.56
10071.2	orf19.2283	orf19.2283	CA0996 IPF10071 catabolic 3-dehydroquinase (by homology)	-0.8236	-0.2450	-0.1166	-0.6171	-0.7899	-0.8213	-1.0955	-1.56
2373.2	orf19.7027	orf19.7027	CA5210 IPF2373 unknown function (weak similarity to mucins)	-0.4941	-0.3474	-0.4659	-0.8365	-0.6126	-0.7013	-1.0000	-1.55
17272.2	orf19.3522	orf19.3522	CA0860 IPF17272 unknown function		-0.3419	0.2881	-0.7108	-0.8546	-1.0740	-1.1172	-1.55
4696.2	orf19.5282	orf19.5282	CA4970 IPF4696 unknown Function (YNL144c?)	-0.3752	-0.6986	-0.6193	-0.5310	-0.8852	-0.7428	-0.5883	-1.55
15753.2	orf19.3363	VTC4	CA0697 VTC4 putative polyphosphate synthetase (by homology)	-0.3952	-0.2587	0.0407	-0.9108	-1.3665	-0.7826	-0.7673	-1.55
6573.1	orf19.6875	VPS35	CA4565 VPS35 Protein-sorting protein, vacuolar (by homology)	-0.2602	-0.6104	-0.4305	-0.2810	-1.0770	-1.2009	-0.5416	-1.55
2645.2	orf19.7405	orf19.7405	CA5705 IPF2645 unknown function	-0.3677	-0.2863	-0.1440	-0.5002	-1.3808	-1.0469	-0.6712	-1.55
6517.2	orf19.1690	TOS1	CA2303 TOS1 putative Anchor subunit of a-agglutinin (by homology)	-1.1172	-0.4719	-1.4820	-0.1600	-0.2515	-0.4921	-0.3997	-1.54
6988.2	orf19.5768	SNF4	CA0122 SNF4 Nuclear regulatory protein (by homology).	-1.2863	-0.3022	-0.1844	-0.6371	-0.4093	-0.7490	-0.7984	-1.54
11759.2			11759.2 IPF11759 unknown function	-0.2362	0.0129	-0.3419	-0.7637	-0.8237	-1.0893	-1.1109	-1.54
3919.2	orf19.6510	GRX1	CA4963 IPF3919 unknown function (YCL035c?)	-0.9135	-0.3820	-0.4690	-0.6228	-0.5698	-0.5492	-0.8456	-1.54
10404.2	orf19.3369	orf19.3369	CA1199 IPF10404 unknown function		-0.3437	-0.0321	-0.9187	-0.5291	-0.8468	-1.0291	-1.53
4068.2	orf19.2164	ORF298	CA0414 IPF4068 reverse transcriptase	-0.6462	-0.5564	-0.0809	-0.7703	-0.6450	-0.7041	-0.9078	-1.53
11492.2	orf19.2392	orf19.2392	CA2095 IPF11492 unknown function	-1.4820	-0.5187	-0.4521	-0.1779	-0.5105	-0.7490	-0.3827	-1.53
3414.2	orf19.846	orf19.846	CA2017 IPF3414 putative serine/threonine protein kinase	-0.2705	-0.5889	-0.0796	-0.7370	-0.6681	-0.8060	-1.0973	-1.52
9887.2	orf19.1240	orf19.1240	CA1261 IPF9887.3eoc unknown function, 3-prime end	-1.0589	0.1725	-0.2987	-0.5821	-0.9714	-0.8237	-0.6620	-1.52
8055.2	orf19.4539	orf19.4539	CA4198 IPF8055 unknown function		-0.0425	-0.3846	-0.5374	-0.7588	-0.7060	-1.1910	-1.52
10526.2	orf19.4059	orf19.4059	CA1483 YHC3 involved in cellular pH homeostasis (by homology)		-0.2758	-0.4150	-0.0816	-0.8160	-1.1234	-0.9024	-1.52
7928.2	orf19.1339	CPY1	CA0430 PRC1 Carboxypeptidase Y precursor	-0.2193	0.2054	-1.0145	-0.9351	-0.9214	-0.5249	-0.7934	-1.52
4071.2	orf19.1861	orf19.1861	CA0385 IPF4071 unknown function (YNL250W, RAD50)	-0.5872	-0.9757	-0.4862	-0.2668	-0.7394	-0.4456	-0.6828	-1.51
16147.2	orf19.5480	ILV1	CA2318 ILV1 Threonine dehydratase (by homology)	-1.0145	-0.6990	-0.0634	-0.4600	-0.9051	-0.6850	-0.3529	-1.51
13148.2	orf19.54	RHD1	CA2597 IFQ3 unknown function (N/A)	-0.1154	-0.3086	-0.5433	-0.9043	-0.6197	-0.8127	-0.8616	-1.51
885.1	orf19.7214	orf19.7214	CA5339 IPF885 glucan 1,3-beta-glucosidase (by homology)	-1.1976	-0.0801	-0.5585	-0.4719	-0.5023	-0.8135	-0.5249	-1.51
4820.2	orf19.3353	orf19.3353	CA1022 IPF4820 putativecomplex I intermediate associated protein CIA30 (by homology)	-0.8059	-0.4364	-0.6897	-0.9324	-0.4305	-0.3884	-0.4600	-1.51
6281.1	orf19.1974	TFS1	CA0748 TFS1 cdc25-dependent nutrient- and ammonia-response cell-cycle regulator (by homolog	-0.7724	-0.2568	0.1114	-0.5956	-1.0574	-0.7922	-0.7787	-1.51
9943.2	orf19.4753	PFK26	CA2215 PFK26 6-phosphofructose-2-kinase (by homology)	-0.5271	-0.4610	-0.3966	-0.4986	-0.9302	-0.7717	-0.5514	-1.51
17283.2	orf19.4907	orf19.4907	CA2021 IPF17283 unknown function	-1.4779	-0.5522	-0.4035	-0.5146	-0.5228	-0.4779	-0.1697	-1.50
15555.2	orf19.3150	GRE2	CA0671 GRP4 putative reductase (by homology). NADPH-dependent methylglyoxal reductase, str	-0.8468	-0.7060	-0.3237	-0.2758	-0.9658	-0.6943	-0.2863	-1.50
13316.2	orf19.2269	orf19.2269	CA1880 IPF13316 unknown function (YNL010w)	-0.4462	-0.2882	-0.4965	-0.7701	-0.8562	-0.6825	-0.5311	-1.50
16104.2	orf19.5651	orf19.5651	CA4361 IPF16104 unknown function	-0.0801	-0.4208	-0.2969	-0.8704	-0.5778	-0.9434	-0.8783	-1.50
1754.2	orf19.3099	TRP4	CA4410 TRP4 Anthranilate phosphoribosyltransferase	-0.5533	-0.6230	-0.7251	-0.4495	-0.7699	-0.3122	-0.5863	-1.49
			Int 3 IR control		-0.4035	0.3528	-0.8059	-0.9159	-0.6371	-1.0350	-1.49
6629.2	orf19.2762	AHP1	CA4127 IPF6629 unknown function	-0.7539	0.0854	-0.6897	-0.6439	-0.8546	-0.7108	-0.4422	-1.49
4649.1	orf19.6102	orf19.6102	CA3854 IPF4649 unknown Function (CST6, bZIP)	-0.3696	-0.8970	-0.2987	-0.2042	-0.6349	-0.9105	-0.6873	-1.49
7812.2	orf19.3133	GUT2	CA3566 GUT2 Glycerol-3-phosphate dehydrogenase, mitochondrial (by homology)	-0.8163	-0.8077	-0.1305	-0.3575	-1.0456	-0.4875	-0.3297	-1.48
9803.2	orf19.6160	orf19.6160	CA3147 IPF9803 unknown function (YMR031c)	0.0000	-0.9144	-0.2830	-0.3888	-0.7699	-0.9268	-0.6592	-1.48
4606.1	orf19.6082	orf19.6082	CA3866 IPF4606 unknown Function	-0.1779	-0.0469	-0.3219	-0.8520	-0.7710	-0.8084	-0.9574	-1.48
4674.2	orf19.1852	orf19.1852	CA3370 IPF4674 unknown Function	-0.8110	-0.8332	-0.4612	-0.0929	-0.3609	-0.5108	-0.8627	-1.48
20161.1	orf19.2765	PGA62	CA4125 IPF20161 unknown function	-0.9574	-0.3255	-1.1233	-0.3619	-0.2786	-0.4009	-0.4672	-1.47
10590.2	orf19.1285	orf19.1285	CA2363 IPF10590 unknown function	-0.9546	-0.9686	-0.1266	-0.3076	-0.6873	-0.1746	-0.6712	-1.47
2283.1	orf19.6660	orf19.6660	CA4266 IPF2283 unknown function	-1.1867	-0.3401	-0.6456	-0.2498	-0.4690	-0.2816	-0.6941	-1.47
14202.2	orf19.1078	orf19.1078	CA0934 IPF14203.3f similarity to several transaminases, 3-prime end (by homology)	-0.8656	-0.2668	-0.5868	-0.6973	-0.7916	-0.5275	-0.1203	-1.46
2303.2	orf19.6671	LAP4	CA4274 LAP42 Aminopeptidase yscI precursor, vacuolar (by homology)	-0.7984	-0.4580	-0.5437	-0.8783	-0.2109	-0.2260	-0.7346	-1.46

14036.2	orf19.2396	IFR2	CA1964 IFR2 unknown function	-0.1313	-0.0291	-0.3865	-1.2042	-0.7013	-0.7490	-0.6259	-1.46
6181.2	orf19.4174	orf19.4174	CA3724 IPF6181 similar to Saccharomyces cerevisiae Fun 26p nucleoside transporter (by homolo	0.0000	-0.4639	-0.3752	-0.3677	-0.7131	-0.8160	-1.0740	-1.46
3372.2	orf19.4026	HIS1	CA4792 HIS1 ATP phosphoribosyltransferase	-0.9187	-0.4112	-0.5395	-0.2584	-0.2294	-0.8890	-0.5043	-1.45
3634.1	orf19.6720	orf19.6720	CA4346 IPF3634 unknown function (YDR090c)	-0.6206	-0.0139	-0.3018	-0.5087	-0.7086	-0.6903	-0.9064	-1.45
10662.2	orf19.5760	IHD1	CA3827 IPF10662 unknown function (similarity to glucan1,4-alpha-glucosidase STA1P)		-0.6666	-0.5756	-0.1730	-0.5208	-0.7661	-0.5105	-1.45
11756.2	orf19.7006	orf19.7006	CA5194 IPF11756 unknown function		-0.1488	-0.2059	-0.5084	-1.0000	-0.8059	-0.5395	-1.45
7136.1	orf19.1559	HOM2	CA3984 HOM2 Aspartate-semialdehyde dehydrogenase (by homology)	-0.3557	-0.3391	-0.4509	-0.6603	-0.5136	-0.5984	-0.8240	-1.45
14899.2	orf19.92	orf19.92	CA1986 IPF14899 unknown function	-0.6920	-0.6439	-0.2226	-0.1440	-0.7686	-0.4305	-0.8237	-1.45
11480.2	orf19.4824	orf19.4824	CA4755 IPF11480 unknown function	-0.6069	-0.4356	-0.0707	-0.2510	-0.8883	-0.9950	-0.4681	-1.44
19652.1	orf19.803	orf19.803	CA1180 UGA12.3f 4-aminobutyrate aminotransferase (GABA transaminase), 3-prime end (by hon	-0.3808	0.0566	-0.4699	-0.9324	-0.2758	-0.6529	-1.0589	-1.44
12039.2	orf19.3664	HSP31	CA4034 HSP31 heat shock protein (by homology)	-0.7637	-0.3752	-0.7226	-0.6237	-0.2793	-0.5929	-0.3383	-1.44
11307.2	orf19.5667	MNR2	CA4376 IPF11307 unknown function		-0.7490	-0.8339	-0.0277	-0.5270	-0.3808	-0.6416	-1.44
8694.2	orf19.1979	GIT1	CA1137 IFN1 glycerophosphoinositol transporter (by homology)	-0.6758	-0.5479	0.0524	-0.5043	-0.6529	-0.8314	-0.5043	-1.44
3870.2	orf19.20	RTS1	CA1247 IPF3870 similar to Saccharomyces cerevisiae Rts1p potential regulatory subunit of protei	-0.3595	-0.4559	-0.2633	-0.3448	-0.6407	-0.7514	-0.8356	-1.44
1798.2	orf19.4998	orf19.4998	CA5264 IPF1798 unknown function	-1.1811	-0.7060	-0.3978	-0.0454	-0.4035	-0.3921	-0.5208	-1.43
12460.2	orf19.2187	ALG7	CA1772 ALG7 UDP-N-acetylglucosamine-1-phosphate transferase (by homology)	-0.4055	0.0841	-0.6259	-0.7959	-0.9105	-0.6060	-0.3771	-1.43
5366.2	orf19.3010.1	ECM33	CA3115 ECM33.3 cell wall biogenesis, 3-prime end (by homology)	-0.3157	-0.3548	-0.9743	-0.4662	-0.5833	-0.5523	-0.3847	-1.43
16613.2	orf19.6951	orf19.6951	CA4715 DPL1 dihydrosphingosine phosphate lyase (by homology)	-0.5692	-0.1681	-0.3808	-0.1795	-1.0000	-0.5166	-0.8160	-1.43
9988.2	orf19.2289	ARP3	CA1117 ARP3 actin related protein (by homology)	-0.2770	-0.3854	-0.2120	-0.3982	-0.9815	-0.6712	-0.6955	-1.43
12359.2	orf19.5639	HIS4	CA2559 HIS4 Histidine biosynthesis trifunctional protein (phosphoribosyl-AMP cyclohydrolase/pho	-0.3255	-0.5628	-0.2653	-0.4501	-0.3183	-0.6735	-1.0203	-1.43
18130.1	orf19.4610.1	orf19.4610.1	CA5173 CPS2.3f Carboxypeptidase YSCS precursor, 3-prime end (by homology)	-0.2758	-0.2226	-0.4800	-0.5670	-0.4325	-0.8262	-0.7934	-1.43
6301.2	orf19.1963	orf19.1963	CA2948 GDS1 nam9-1 suppressor (by homology)	-0.8110	-0.3733	-0.0985	-0.6990		-0.5973	-0.5043	-1.43
15411.2	orf19.1738	UGP1	CA0435 UGP1 UTP--glucose-1-phosphate uridylyltransferase (by homology)	-0.3022	-0.0619	-0.7202	-0.4403	-0.3940	-0.5437	-1.1140	-1.42
7204.2	orf19.2475	PGA26	CA2885 IPF7204 unknown function		0.1309	-0.8625	-0.3733	-0.8211	-0.5395	-0.5973	-1.42
13751.2	orf19.1038	orf19.1038	CA1035 IFI2.3f unknown function, 3-prime end		-0.1633	-0.6850	-0.6215	-0.5585	-0.6215	-0.4093	-1.42
8340.1	orf19.4099	ECM17	CA4320 ECM17 Putative sulfite reductase (by homology)	-0.5160	-0.0165	-0.8010	-0.4691	-0.7853	-0.5731	-0.3960	-1.42
20057.1	orf19.2659	orf19.2659	CA0495 IPF20056 unknown function	-0.1343	-0.3450	-0.3981	-0.6050	-1.1172	-0.7778	-0.1771	-1.42
9167.2	orf19.2737	orf19.2737	CA2697 IPF9167 unknown function	-0.6943	-0.3237	0.1440	-0.5628	-0.6758	-0.6920	-0.7466	-1.42
1853.1	orf19.5890	orf19.5890	CA6151 IPF1853 unknown function	-0.8262	0.0058	-0.1536	-0.5125	-0.6148	-0.6967	-0.7442	-1.42
4544.1	orf19.906	orf19.906	CA4668 ROM2 GDP/GTP exchange factor for Rho1p (by homology)	-0.6171	-0.0649	-0.3273	-0.8678		-0.8186	-0.3364	-1.42
12463.2	orf19.1203	SRO77	CA1434 SNI2 Sec9 interacting protein (by homology)		-0.1472	0.1177	-0.6552	-0.8009	-0.7013	-0.8391	-1.42
2115.1	orf19.4109	PMT4	CA4314 PMT4 Mannosyltransferase (by homology)	-0.2474	-0.3025	-0.4838	-0.6678	-0.6625	-0.5750	-0.5876	-1.42
7535.2	orf19.4534	orf19.4534	CA4193 IPF7535 unknown function (YBR273c)	-0.5692	-0.3004	-0.7346	-0.6394	-0.3940	-0.2740	-0.6126	-1.42
18465.1			CA2460 LYS1.3eoc Saccharopine dehydrogenase, 3-prime end	-0.6574	-0.1993	-1.0589	-0.6850	-0.0454	-0.5628	-0.3004	-1.42
4859.2	orf19.6276	orf19.6276	CA3700 IPF4859 unknown function	-0.7909	-0.9024	-0.2845	-0.3733	-0.1472	-0.8237	-0.1520	-1.41
12162.1	orf19.2670	orf19.2670	CA3329 IPF12162 Unknown function	-0.8520	-0.3752	-0.1392	-0.4442	-0.7612	-0.5713	-0.3004	-1.41
2542.2	orf19.6629	ISC1	CA4076 IPF2542 putative neutral sphingomyelinase (by homology)		-0.5395	-0.7661	-0.4131	0.0356	-0.7418	-0.5228	-1.41
855.1	orf19.7229	orf19.7229	CA5353 IML2 unknown function	-0.1329	-0.0649	-0.4131	-0.7155	-0.8863	-0.6171	-0.5735	-1.40
1387.2	orf19.6448	orf19.6448	CA5094 IPF1387 unknown function (N/A)	0.0000	-0.8025	-0.4095	-0.4677	-0.3424	-0.3874	-0.9757	-1.40
1323.2	orf19.6414	orf19.6414	CA5117 IPF1323 unknown function	0.0000	-0.1945	-1.0030	-0.2654	-0.2544	-0.8966	-0.7501	-1.40
9934.1	orf19.988	orf19.988	CA3527 IPF9934 unknown function	-0.2193	-0.2515	-0.3959	-0.5692	-0.1844	-0.7298	-1.0029	-1.39
18853.1	orf19.1054	orf19.1054	CA0843 IPF18853 unknown function	-0.5713	-0.1552	-0.2210	-0.7466	-0.9324	-0.6282	-0.0970	-1.39
8796.1	orf19.4035	GAS1	CA4800 IPF8796 putative GPI-anchhored protein related to Phr1, Phr2 and Phr3 (by homology)	-0.3819	-0.4091	-0.3846	-0.3455	-0.6875	-0.4808	-0.6531	-1.39
17216.2			CA1194 MET222 protein ser/thr phosphatase (by homology)		-0.5778	-0.2828	-0.6735	-0.1504	-1.0469	-0.1329	-1.39
846.1	orf19.7235	orf19.7235	CA5358 IPF846 WD-repeat protein, beta-transducin (by homology)	-0.3511	-0.2987	-0.2688	-0.3346	-0.6597	-0.8863	-0.5395	-1.39
15204.2	orf19.3767	orf19.3767	CA2171 PEP1.3 Vacuolar protein sorting/targeting protein, 3-prime end (by homology)	-0.8651	-0.2688	-0.4639	-0.0801	-0.7108	-0.5628	-0.3640	-1.39
2384.1	orf19.6809	orf19.6809	CA5897 IPF2384 unknown function	-0.8651	-0.2810	0.0731	-0.4228	-0.6126	-0.6439	-0.5564	-1.39
13684.2	orf19.2546	TRP2	CA1059 TRP2 anthranilate synthase component I (by homology)	0.0000	-0.3697	-0.7424	-0.1642	-0.6921	-0.5745	-0.7444	-1.38
257.1	orf19.3261	orf19.3261	CA5454 IPF257.3 member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pa	-0.6329	-0.6401	-0.4016	-0.5086	-0.4384	-0.0788	-0.5406	-1.38
3409.2	orf19.843	orf19.843	CA2019 IPF3409 unknown function		-0.2706	-0.1031	-0.6060	-0.5084	-0.4659	-0.8186	-1.38
7842.1	orf19.4201	orf19.4201	CA2932 NHX1 NA+-H+ antiporter	-0.6367	0.0060	-0.2553	-0.5482	-0.5347	-0.5734	-0.6816	-1.38
11646.2	orf19.1353	orf19.1353	CA0368 IPF11646 unknown function	-0.5023	-0.2260	-0.4403	-0.6990	-0.7710	-0.4880	-0.0877	-1.37
6315.2	orf19.1665	MNT1	CA3469 MNT1 Mannosyltransferase involved in n-linked and o-linked glycosylation	-0.8494	-0.6758	-0.7274	-0.2311	-0.3022	-0.0604	-0.3456	-1.37
18635.1	orf19.2862	RIB1	CA1665 RIB1 GTP cyclohydrolase II by homology to S.cerevisiae		-0.4383	-0.1894	0.0000	-0.5735	-0.6943	-0.8365	-1.37
9282.2	orf19.1510	orf19.1510	CA2178 IPF9282 unknown function		-0.4779	-0.2159	-0.1376	-0.4228	-0.7155	-0.7539	-1.37
11873.2	orf19.593	FGR32	CA3425 IPF11873 similar to Saccharomyces cerevisiae Swa2p clathrin-binding protein required fo	-0.2663	-0.3300	-0.2712	-0.4112	-0.4268	-0.5018	-0.9646	-1.37
13046.2	orf19.2406	orf19.2406	CA3053 GTR2 GTP-binding protein (by homology)	-0.7959	-0.4501	-0.2498	0.0215	-0.5023	-0.4364	-0.7490	-1.37

7309.1	orf19.2864	orf19.2864	CA1663 IPF7309 unknown function (YGL101w)	-0.5146	-0.5125	-0.3474	-0.5585	-0.1062	-0.5670	-0.5105	-1.36
3740.1	orf19.1011	orf19.1011	CA0951 MNN6 putative golgi alpha-1,2-mannosyltransferase (by homology)	-0.2652	-0.4611	-0.0562	-0.3881	-0.5385	-0.7342	-0.5996	-1.35
1943.2	orf19.7152	orf19.7152	CA5290 IPF1943 similar to Aspergillus (Emericella) nidulans cysteine synthase (by homology)	-0.4074	-0.9024	-0.2863	-0.2810	-0.2059	-0.3456	-0.5291	-1.34
836.1	orf19.7239	orf19.7239	CA5362 IPF836.3 regulation of G-protein function, 3-prime end (by homology)	-0.4364	-0.1345	-0.6326	-0.2498	-0.3364	-0.5395	-0.6016	-1.34
3885.2	orf19.769	IFE1	CA1958 IFE1 Unknown function (YAL061W, putative polyol dehydrogenase)	-0.4704	-0.3923	-0.4820	-0.4019	-0.1055	-0.5466	-0.4832	-1.33
9880.2	orf19.1246	orf19.1246	CA1263 IPF9880 unknown function	-0.7859	-0.0291	-0.3959	-0.3902	-0.3474	-0.4189	-0.4880	-1.33
1849.1	orf19.5886	CUP5	CA6153 CUP5 Vacuolar H+ATPase (by homology)	-0.1212	-0.4564	-0.2989	-0.3763	-0.5512	-0.5624	-0.4695	-1.32
18902.1			CA0688 IPF10555.3eoc unknown function, 3-prime end	-0.2951	-0.4679	-0.1943	-0.3997	-0.4880	-0.6943	-0.2934	-1.32
4077.2	orf19.3846	LYS4	CA4869 LYS4 homoaconitate hydratase	-0.2810	-0.3111	-0.2653	-0.8810	-0.2159	-0.3111	-0.5332	-1.32
2400.1	orf19.6816	orf19.6816	CA5891 IPF2400 putative aldehyde reductase (by homology)	-0.3058	-0.5374	0.0440	-0.4461	-0.6574	-0.5002	-0.3884	-1.32
9605.2	orf19.3071	orf19.3071	CA0578 IPF9605 similar to Saccharomyces cerevisiae Mih1p M-phase inducing protein tyrosine p	-0.5353	-0.6850	-0.1536	-0.2584	-0.3659	-0.5125	-0.2379	-1.31
4611.1	orf19.6086	LEU4	CA3863 LEU41 2-isopropylmalalate synthase (by homology)	-0.6873	-0.4639	-0.3328	-0.1016	-0.0939	-0.6082	-0.4580	-1.31
19933.1	orf19.2268	RCK2	CA1881 RCK2 Ca/calmodulin-dependent ser/thr protein kinase (by homology)	-0.6506	-0.3165	-0.2345	-0.6259	-0.2311	-0.2584	-0.4189	-1.31
13709.2	orf19.335	orf19.335	CA4629 IPF13709 unknown function	-0.5105	-0.1877	-0.2464	-0.5951	-0.5842	-0.1993	-0.4093	-1.31
2391.2	orf19.6812	PMT2	CA5894 PMT2 O-D-mannosyltransferase (by homology)	-0.6282	-0.3808	-0.3827	-0.5043	-0.4150	-0.2584	-0.1329	-1.31
3076.1	orf19.7038	orf19.7038	CA5221 MVP1.exon1 Required for vacuolar protein sorting, exon 1 (by homology)		-0.2076	-0.2706	-0.3040	-0.2567	-0.3940	-0.8237	-1.30
3392.2	orf19.835	orf19.835	CA2086 IPF3392 unknown function	-0.1520	-0.5458	-0.2951	-0.3789	-0.4620	-0.6620	-0.1156	-1.30
7158.2	orf19.1196	orf19.1196	CA1375 IPF7158 putative serine/threonine kinase	-0.5951	-0.2987	-0.3273	-0.4759	-0.3827	-0.1976	-0.3201	-1.29
18048.1	orf19.5870	CTP1	CA6166 CTP1 Citrate transport protein (by homology)	-0.5479	-0.2951	-0.1730	-0.5228	-0.0847	-0.4719	-0.4961	-1.29
6613.2	orf19.6481	orf19.6481	CA1994 IPF6613 unknown function (YDR349c, YPS3, GPI-anchored aspartic protease)	-0.3147	-0.4560	-0.3940	-0.2277	-0.4600	-0.3129	-0.4074	-1.29
8253.2			CA1749 IPF8257.3f unknown function, 3-prime end	-0.2916	-0.6850	-0.5125	-0.2898	-0.3492	-0.1795	-0.2498	-1.29
19510.1			CA0737 SEC16.53f.eoc Multidomain vesicle coat protein, internal fragment (by homology)	-0.2845	-0.6038	-0.4679	-0.1520	-0.2009	-0.3165	-0.4325	-1.28
946.1	orf19.7561	DEF1	CA5968 IPF946 unknown function	-0.3094	-0.1746	-0.5228	-0.4921	-0.1172	-0.2706	-0.5692	-1.28
2583.2	orf19.5505	HIS7	CA2447 HIS7 Histidine biosynthesis	-0.4364	-0.3147	-0.2396	-0.3364	-0.4941	-0.3808	-0.1568	-1.26
2959.2	orf19.4290	TRR1	CA3059 TRR1 Thioredoxin reductase (by homology)	-0.2758	-0.6082	-0.3022	-0.1844	-0.2653	-0.2260	-0.4961	-1.26
824.1	orf19.7244	orf19.7244	CA5365 IPF824 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (by homology)	-0.4286	-0.3273	-0.1861	-0.1811	-0.2533	-0.4860	-0.4921	-1.26
9154.2	orf19.1883	orf19.1883	CA4482 IPF9154 similar to Saccharomyces cerevisiae Ycs4p subunit of condensin protein comple	-0.3959	-0.1894	-0.4266	-0.4247	-0.4422	-0.1140	-0.3566	-1.26
19593.1	orf19.4353	orf19.4353	CA0120 IPF19593 similar to Saccharomyces cerevisiae Ulp1p Smt3-processing enzyme (by homo	-0.5385	-0.2334	-0.2896	-0.4561	0.0000	-0.3344	-0.3549	-1.24
7940.1	orf19.6608	orf19.6608	CA3848 IPF7940 unknown function	-0.2176	-0.2969	-0.3529	-0.3902	-0.3273	-0.3165	-0.1392	-1.22
5882.2	orf19.4120	orf19.4120	CA1610 LAS1 cell morphogenesis, cytoskeletal regulation and bud formation (by homology)		0.2940	0.3033	0.1827	0.4125	0.3288	0.3300	1.24
6404.2	orf19.2721	orf19.2721	CA0150 CDC123 similar to Saccharomyces cerevisiae Cdc123p cell cycle regulator (by homology	0.1414	0.2738	0.2290	0.5311	0.2437	0.3929	0.5049	1.26
1628.1	orf19.6582	PRE10	CA4890 PRE10 20S proteasome subunit C1 (by homology)	0.2892	0.2546	0.4709	0.6462	0.2497	0.3057	0.1506	1.26
18581.1	orf19.764	orf19.764	CA1954 IPF3897.5f unknown function, 5-prime end		0.2041	0.4936	0.3150	0.4594	0.2079	0.3994	1.27
13160.2	orf19.1140	orf19.1140	CA0955 IPF13160 unknown function	0.2559	0.2414	0.5205	0.1168	0.4155	0.3865	0.6166	1.29
1499.1	orf19.350	orf19.350	CA4643 PRE9 20S proteasome subunit Y13 (alpha3) (by homology)	0.4636	0.4168	0.2437	0.3471	0.4372	0.3150	0.3357	1.29
4992.1	orf19.2532	PRS	CA1074 PRORS.5f prolyl-tRNA synthetase, 5-prime end	0.2630	0.0412	0.6862	0.3127	0.4478	0.6645	0.2963	1.31
12158.1	orf19.2668	RHD2	CA3332 GAG GAG protein of pCal retrotransposon	0.6161	0.2360	0.5848	0.3495	0.2295	0.2570	0.4747	1.31
3764.2	orf19.1598	ERG24	CA0300 ERG24 C-14 sterol reductase (by homology)	0.3925	0.4454	0.2772	0.4216	0.5763	0.3345	0.3243	1.32
5191.2	orf19.3616	ERG9	CA1676 ERG9 farnesyl-diphosphate farnesyltransferase	0.6145	0.4436	0.0356	0.4190	0.2810	0.2762	0.8180	1.33
7536.2	orf19.4885	MIR1	CA1513 MIR1 phosphate transport protein, mitochondrial (MCF) (by homology)	0.8090	0.1336	0.1493	0.1903	0.6295	0.4542	0.5420	1.33
17364.2	orf19.2740	orf19.2740	CA2700 IPF14414.exon1 unknown function, exon 1	0.5753	0.7031	0.3730	0.1375	0.6031	0.3471	0.1750	1.33
14903.1	orf19.4146	SMD3	CA3087 SMD3 core snRNP protein (by homology)	0.6012	0.5656	0.1388	0.7841	0.3685	0.2314	0.2437	1.34
2309.1	orf19.6674	orf19.6674	CA4277 BTS1 Geranylgeranyl diphosphate synthase (by homology)	0.5627	0.3092	0.0621	0.6060	0.1467	0.5926	0.6599	1.34
8293.2	orf19.3715	ASF1	CA3144 ASF1 anti-silencing protein (by homology)		0.0580	0.2016	0.2412	0.5390	0.8262	0.6781	1.34
7489.2	orf19.4680	orf19.4680	CA3243 IPF7489 unknown function	0.3785	0.3539	0.2642	0.7832	0.0201	0.6182	0.5607	1.34
19626.1	orf19.1303	orf19.1303	CA1329 MRF2 peptide chain release factor, mitochondrial (by homology)	0.4854	0.0690	0.2774	0.3022	0.3973	0.6050	0.8616	1.35
12897.2	orf19.2244	orf19.2244	CA0271 IPF12897 putative oxidoreductase (by homology)	0.4294	0.2919	0.6698	0.4183	0.3802	0.3391	0.5068	1.35
17994.1			CA3660 IPF17794 unknown function	0.5850	-0.1440	0.6285	0.3918	0.5675	0.6041	0.4038	1.35
3273.1	orf19.4382	orf19.4382	CA3917 IPF3273 similar to Saccharomyces cerevisiae Ret3p coatomer complex zeta chain (by ho	0.2314	-0.1172	0.4751	0.6498	0.5079	0.6192	0.7824	1.37
9177.2	orf19.3733	IDP2	CA0643 IDP2 isocitrate dehydrogenase, cytosolic (by homology)	0.2786	0.1177	0.7974	0.3057	0.2618	0.5539	0.8383	1.37
13116.1	orf19.3463	orf19.3463	CA2030 IPF13116 unknown function	0.2427	0.1669	0.7875	0.5604	0.1280	0.7538	0.5266	1.37
1945.2	orf19.7153	orf19.7153	CA5291 LOS1 pre-tRNA splicing protein (by homology)		-0.0529	0.6690	0.0990	0.6572	0.6599	0.6915	1.37
10436.2	orf19.2891	orf19.2891	CA3775 AFG1 ATPase family gene (by homology)	0.4854	0.2253	0.0314	0.2916	0.7459	0.5380	0.8671	1.37
2856.1	orf19.7285	orf19.7285	CA5527 IPF2856 unknown function	0.3092	0.2179	0.3818	0.3115	0.6088	0.9575	0.4049	1.37
7298.2	orf19.2418	orf19.2418	CA3044 IPF7298 unknown function (N/A)	0.3752	0.6323	0.0990	0.3437	0.7181	0.5489	0.4803	1.37
3341.2	orf19.4006	orf19.4006	CA4774 IPF3341 Unknown function	0.4136	0.2594	0.6960	0.1309	0.4005	0.3516	0.9709	1.38
5890.2	orf19.6938	orf19.6938	CA4708 MEU1 regulator of ADH2 expression (by homology)	0.5721	0.2600	0.1859	0.5550	0.4163	0.5706	0.6649	1.38

1013.1	orf19.4587	orf19.4587	CA5149 HGH1 Similar to human HMG1 and HMG2 proteins (by homology)	0.5380	-0.1456	0.3357	0.6295	0.7732	0.3606	0.7373	1.38
12994.2	orf19.1042	POR1	CA0919 POR1 mitochondrial outer membrane porin (by homology)	0.2619	0.0856	0.4350	0.6562	0.5007	0.3518	0.9493	1.38
5404.2	orf19.5175	orf19.5175	CA4420 SSM4 involved in mRNA turnover by homology	0.4875	0.0854	0.1164	0.3173	0.6229	0.6508	0.9899	1.38
9484.2	orf19.3396	HCH1	CA2434 IPF9484 unknown function	0.8205	0.4436	0.2810	0.6480	0.6654	0.5261	-0.0939	1.39
19574.1	orf19.4468	orf19.4468	CA2423 SDH41 succinate dehydrogenase membrane anchor subunit for sdh2p (by homology) mit	0.5125	0.3000	0.2351	0.2636	0.6225	0.5762	0.7810	1.39
3873.2			CA1245 IMH3.exon2 IMP dehydrogenase, exon 2 (doesn't exist in CDB)	0.8961	0.4158	0.3718	0.2534	0.5955	0.3907	0.3785	1.39
11274.2	orf19.5230	MRPS9	CA1109 MRPS9 ribosomal protein S9 small subunit precursor		0.5529	1.0391	0.0552	0.5039	0.2642	0.4179	1.39
7430.2	orf19.6220	orf19.6220	CA2577 IPF7430 unknown function	0.1375	0.2041	0.2857	0.5529	0.7049	0.6563	0.7740	1.39
4403.2	orf19.1481	HAP42	CA0904 IPF4403 unknown function	0.4854	0.6608	-0.0679	0.7198	0.4297	0.6388	0.4542	1.39
1957.1	orf19.7160	orf19.7160	CA5297 YAR1 Ankyrin repeat-containing protein (by homology)	0.3651	-0.0091	0.6360	0.3735	0.4630	0.7908	0.7167	1.39
16638.1	orf19.1495	orf19.1495	CA1860 UTR4 unknown function	-0.0831	0.6951	0.8278	0.1789	0.5460	0.4761	0.7084	1.39
15412.2	orf19.1738.1	orf19.1738.1	CA0436 RBL2 Beta-tubulin binding protein (by homology)	0.6754	0.0580	0.4782	0.2594	0.5955	0.9471	0.3369	1.39
13045.2	orf19.2407	DPS1-1	CA3052 DPS1 aspartyl-tRNA synthetase (by homology)	0.3696	0.0766	0.2688	0.7696	0.5753	0.5819	0.7165	1.39
6054.1	orf19.6736	orf19.6736	CA4359 IPF6054 unnown function (localised to mitochondrion)	0.5850	0.1966	0.5646	0.2714	0.4626	0.6031	0.7075	1.40
20033.1	orf19.7592	FAA4	CA5992 FAA4 long-chain fatty acid--CoA ligase and synthetase 4 (by homology)	0.7154	0.1815	0.2107	0.5484	0.6293	0.6652	0.4442	1.40
6754.1	orf19.319	orf19.319	CA3389 IPF6754 unknown function (YDR286C)	0.4854	0.5410	0.4865	0.8616	0.5675	0.0524	0.4190	1.40
4405.1	orf19.1482	orf19.1482	CA0905 IPF4405 unknown function (N/A)	0.6781	0.3323	0.2951	0.3288	0.6031	0.9100	0.2762	1.40
15042.2	orf19.501	orf19.501	CA4505 NOP2 nucleolar protein (by homology)	0.5018	0.0300	0.1243	0.6727	0.4415	0.7949	0.8608	1.40
8176.1	orf19.526	NHP2	CA4240 NHP2 nucleolar rRNA processing protein (by homology)	0.4276	0.6853	0.2473	0.3818	0.5291	0.7084	0.4489	1.40
15.1	orf19.5985	orf19.5985	CA6076 PAC10.3 Non-native Actin Binding Complex Component, 3-prime end (by homology)	0.4100	-0.0204	0.3480	0.6196	0.8136	0.7593	0.5201	1.41
2914.1	orf19.4311	YNK1	CA2645 YNK1 Nucleoside diphosphate kinase (by homology)	0.9935	0.4903	0.8326	0.4672	0.2851	0.1681	0.2202	1.41
11127.1	orf19.639	orf19.639	CA1847 IPF11127 unknown function	0.5695	0.0635	0.7816	0.2314	0.4957	0.8172	0.5281	1.41
3082.1	orf19.7043.1	ACB1	CA5225 ACB1.exon2 acyl-coenzyme-A-binding protein, exon 2 (by homology)	0.5677	0.3435	0.5064	0.2273	0.6160	0.5870	0.6415	1.41
668.2	orf19.7599	orf19.7599	CA5999 IPF668 unknown function		0.3929	-0.1665	0.6471	0.5869	0.8148	0.7562	1.42
6872.1	orf19.4252	orf19.4252	CA2183 IPF6872 serine/threonine protein kinase (by homology) (YGR262c, bud site selection)	0.4854	0.5099	-0.0395	0.6672	0.5509	0.7908	0.5917	1.42
12420.1	orf19.3122.2	orf19.3122.2	CA4390 HOD1 regulator of G2/M progression (by homology)	0.5410	0.2302	0.5529	0.4265	0.9456	0.7312	0.1557	1.43
19294.1	orf19.6469	orf19.6469	CA0070 IPF19295.3f unknown function, 3-prime end (YJL207c)	0.6581	0.0621	0.5936	0.3918	0.6351	0.4351	0.8156	1.43
18938.1	orf19.1804	orf19.1804	CA0572 IPF14864 unknown function (YAL046C)	0.5675	0.3929	0.4027	0.4772	0.3150	0.7502	0.7225	1.43
11879.2	orf19.5293	orf19.5293	CA2163 IPF11879 unknown function	0.6145	-0.0262	0.3357	0.7587	0.1903	0.6608	1.1270	1.44
1211.1			CA4830 ATP8.exon2 F1F0-ATPase complex, Atp8 subunit, exon 2 (by homology)	0.7355	0.0398	0.5028	0.4977	0.5170	0.6933	0.6826	1.44
4131.2	orf19.2039	orf19.2039	CA3648 MSF1 phenylalanine--tRNA ligase	0.8584	0.2029	1.0293	0.1916	0.4308	0.3380	0.6192	1.44
11.1	orf19.5987	orf19.5987	CA6074 IPF11 unknown function	0.8552	0.6360	0.0029	0.3752	0.6736	1.0065	0.1953	1.45
5986.1	orf19.7307	orf19.7307	CA5545 IPF5986 similar to cytochrome-b5- and nitrate reductases (ER)		0.4510	0.0731	0.4626	0.5361	0.7407	0.9575	1.45
12599.2	orf19.3291	orf19.3291	CA0696 HMT1 hnRNP methyltransferase (by homology)	0.2515	0.1546	0.2001	0.7878	0.6106	0.7917	0.9653	1.45
1514.2	orf19.344	orf19.344	CA4637 IPF1514 unknown function (N/A)	0.0000	0.5183	0.4367	0.3225	0.8056	0.7928	0.9046	1.45
14710.1	orf19.4820	orf19.4820	CA1080 IPF14710 unknown function	0.0286	0.1953	0.9123	0.3300	0.6808	0.5792	1.0587	1.45
13622.2	orf19.3974	PUT2	CA3399 PUT2 1-pyrroline-5-carboxylate dehydrogenase (by homology) (YHR037W, mitochondrion	0.3196	0.8213	0.1674	0.4542	0.4049	0.8608	0.7664	1.46
1846.1	orf19.5884	orf19.5884	CA6155 IPF1846 unknown function (YJR041C, nucleolar ribosome biogenesis)	0.6544	0.5965	0.4265	0.3874	0.5251	0.5888	0.6304	1.46
19778.1	orf19.6165	KGD1	CA3149 KGD1 2-oxoglutarate dehydrogenase	1.2934	0.1953	0.2473	0.5907		0.4916	0.4885	1.47
4924.1	orf19.7657	orf19.7657	CA6042 IPF4924 unknown function (RNase P and RNase MRP subunit)		0.2129	0.8891	0.5519	0.5028	0.5636	0.6022	1.47
3267.2	orf19.3138	NOP1	CA3570 NOP1 Fibrillarin	0.5792	-0.1282	0.0552	0.8930	0.7493	0.9664	0.7621	1.47
635.1	orf19.7614	orf19.7614	CA6013 IPF635 unknown function	1.1204	0.3663	0.2606	0.4093	0.0635	0.7958	0.8742	1.47
12652.2	orf19.6385	ACO1	CA3546 ACO1 aconitate hydratase (by homology)	0.9313	-0.0770	0.2618	1.1030	0.6844	0.5430	0.4478	1.47
1095.1	orf19.5407	orf19.5407	CA5765 SOF1 Involved in 18S pre-rRNA production (by homology)	1.1063	0.1243	0.1878	0.3505	0.8229	0.7681	0.5430	1.47
7275.2	orf19.2782	orf19.2782	CA1904 GRX5 Glutaredoxin	0.6589	-0.3190	0.6613	0.7977	0.7040	0.6194	0.7925	1.47
165.2			CA1490 IPF165 unknown function	0.5542	-0.1450	0.5988	0.9359	0.4008	0.7984	0.8431	1.48
1212.1	orf19.2066	orf19.2066	CA4831 IPF1212 unknown function (YJR129C)	0.0000	0.8605	0.6023	0.6187	0.5019	0.7193	0.6891	1.48
19861.1			CA0405 IPF19862.3f unknown function, 3-prime end (doesn't exist in CDB)	1.1460	0.2546	0.3550	0.5261	0.4751	0.6285	0.6313	1.49
1567.1	orf19.961.2	orf19.961.2	CA5413 IPF1567 mitochondrial ribosomal protein L34 (by homology)		0.1440	0.9935	0.6406	0.5763	0.6229	0.4751	1.49
4283.2	orf19.543	orf19.543	CA4255 FUM11 fumarate hydratase (mitochondrial matrix)	0.6949	0.1133	0.5438	0.8866	0.4608	0.4621	0.8667	1.49
15595.2	orf19.4640	PWP1	CA1064 PWP1 beta-transducin superfamily (by homology)	1.3063	0.1190	0.0398	0.5898	0.5529	0.5993	0.8560	1.50
7334.1	orf19.3724	orf19.3724	CA0730 IPF7334 unknown function	0.4657	0.6022	0.0909	1.1499	0.1043	1.0718	0.6145	1.50
19872.1	orf19.5067	orf19.5067	CA0533 IPF19872 unknown function		-0.0116	0.1097	0.9804	0.6229	1.0834	0.7294	1.50
1731.2	orf19.3088	orf19.3088	CA2010 IPF1731 unknown function	0.0000	0.8432	-0.0160	0.7681	0.8961	0.9449	0.6897	1.50
12942.22	orf19.4933	orf19.4933	CA3604 IPF12942 delta-12 fatty acid desaturase (by homology)		0.2881	0.2786	0.6304	0.5430	0.4340	1.3768	1.51
12884.2	orf19.4779	orf19.4779	CA0778 IPF12884 unknown function	0.3340	0.0622	1.0765	0.7000	0.2959	0.4633	1.2160	1.51
4785.2	orf19.4499	orf19.4499	CA2330 RIM2 mitochondrial carrier protein (by homology)	0.2960	0.2335	0.8957	0.3642	0.5315	0.8810	0.9637	1.51

3445.1	orf19.6183	orf19.6183	CA3203 IPF3445 Unknown function (YJR135W-A, mitochondrial inner membrane)	0.5211	0.4005	0.8600	0.1609	0.8608	1.0983	0.2774	1.51
20079.1	orf19.713	orf19.713	CA1235 IPF20079 unknown function	0.6517	-0.4170	0.6942	0.9471	0.8528	0.8496	0.6313	1.52
7325.1	orf19.2978	orf19.2978	CA3445 IPF7325 unknown function (N/A)	1.1170	0.4340	0.8797	0.2066	0.6498	0.5965	0.3369	1.52
8113.2	orf19.2938	orf19.2938	CA2199 IPF8113 unknown function (localised to mitochondrion)	0.8115	0.0482	0.4071	0.6526	0.4201	0.8899	1.0065	1.52
80.2	orf19.5949	FAS2	CA6107 FAS2.3f fatty-acyl-CoA synthase, alpha chain, 3-prime end	0.5553	0.4203	0.3370	0.8071	0.5963	0.6076	0.9147	1.52
7721.2	orf19.431	ZCF2	CA4056 IPF7721 unknown function	0.9941	0.0338	-0.0004	0.8485	0.7787	0.9498	0.6367	1.52
2093.2	orf19.4093	orf19.4093	CA4326 IPF2093 nuclear protein of unknown function (by homology)	0.4081	0.3142	0.2021	0.9830	0.9427	0.7549	0.6506	1.52
1439.1	orf19.6047	TUF1	CA4909 TUF1 Translation elongation factor TU (by homology)	0.7233	0.6304	1.0881	0.6126	0.4255	0.3606	0.4201	1.52
3222.1	orf19.3577	COQ5	CA3482 COQ5 C-methyltransferase (by homology) mitochondrial	0.3984	0.5190	0.7966	0.9575	0.1017	0.7689	0.7338	1.53
9827.2	orf19.6860	orf19.6860	CA4463 PIS1 CDP diacylglycerol--inositol 3-phosphatidyltransferase (by homology) (YPR113W, E	0.6596	0.1938	0.2245	0.7427	0.5768	0.6138	1.2769	1.53
17510.1	orf19.4358	orf19.4358	CA2038 IPF17510 unknown function	1.0741	0.9285	0.9947	0.2151	0.6645	0.4207	-0.0026	1.53
4616.2	orf19.6090	orf19.6090	CA3862 NSR1 nuclear localization sequence binding protein (by homology)	0.9046	0.2327	0.4136	0.7040	0.9701	0.6645	0.4233	1.53
8996.2	orf19.4634	orf19.4634	CA0734 IPF8996 unknown function (YGL211W, mitochondrion)	0.0000	0.1292	0.4589	1.3135	0.6180	0.6403	1.1576	1.53
7706.2	orf19.680	orf19.680	CA4115 IPF7706 putative plasma membrane phosphatase (by homology)	0.6107	-0.0694	0.5632	0.5821	0.8145	0.8446	0.9774	1.53
13552.2	orf19.1300	orf19.1300	CA0453 IPF13552 putative methyltransferase (by homology) (YDR316W, mitochondrion)	0.0688	0.3824	0.7911	0.4991	0.7715	0.9643	0.8613	1.54
16428.2	orf19.1250	orf19.1250	CA1479 IPF16428 unknown function (YIL019w)	0.8286	0.4071	0.1763	0.7286	0.4136	0.8424	0.9553	1.54
10886.2	orf19.5050	orf19.5050	CA1746 IPF10886 unknown function	0.6817	0.1110	0.8408	0.1043	0.3150	1.3835	0.9161	1.54
3959.2	orf19.875	orf19.875	CA4690 IPF3959 unknown function (N/A)	0.3369	0.0510	1.0208	1.0642	0.6378	0.6599	0.5974	1.54
227.1	orf19.3244	orf19.3244	CA5441 IPF227 unknown function	0.3901	-0.1843	1.1485	0.5755	0.7659	0.9178	0.7663	1.54
17135.11	orf19.6283	orf19.6283	CA3222 IPF15883 unknown function (YKL040c, mitochondrial matrix)	1.0187	0.0657	0.7116	0.3530	0.8400	0.5638	0.8343	1.54
8405.1	orf19.1721	NCE103	CA2796 IPF8405 similar to Saccharomyces cerevisiae Nce103p involved in non-classical protein export pathw		0.5341	0.4510	0.5291	1.5276	0.0990	0.6388	1.55
15468.1	orf19.2256	orf19.2256	CA3584 IPF15468 unknown function	0.8015	-0.1054	0.4186	0.6663	1.1009	1.0715	0.4710	1.55
11229.1	orf19.5835	orf19.5835	CA3784 IPF11229 similar to Saccharomyces cerevisiae Rrp7p involved in pre-rRNA processing ar	0.1931	0.1798	0.3879	0.9301	0.7170	1.1800	0.8563	1.55
4189.1	orf19.5444	orf19.5444	CA5795 TIM44 mitochondrial inner membrane import receptor	0.5850	0.8262	0.7286	0.2497	0.6835	0.7832	0.5917	1.55
19722.1	orf19.3950	MSM1	CA1093 MSM1 mitochondrial methionyl-tRNA synthetase	1.4592	0.4291	0.9690	0.2557	0.1946	0.5941	0.5693	1.56
3365.1	orf19.4022	SDH4	CA4788 SDH42 succinate dehydrogenase membrane anchor subunit for sdh2p (by homology) (mi	0.6894	0.1718	0.7544	0.4444	0.8830	0.7847	0.7634	1.56
5361.2	orf19.3008	COQ4	CA3118 COQ4 ubiquinone biosynthesis (mitochondrion)	1.4117	0.8165	0.6077	-0.0278	0.6007	0.5272	0.5669	1.56
7981.1	orf19.706	NMD3	CA1706 NMD3 RNA binding (by homology)	0.2004	-0.0740	0.2066	1.0433	1.0086	1.1583	0.9613	1.56
12382.2	orf19.1388	orf19.1388	CA0886 IPF12382 unknown function (		0.3311	0.0272	0.8270	0.8065	0.9978	0.8781	1.56
8302.1	orf19.6007	orf19.6007	CA6061 IPF8302 unknown function (YJL196c?)	0.0000	0.1589	0.4405	0.6488	0.7658	1.2072	1.3012	1.56
13215.1	orf19.4967	COX19	CA0768 COX19 Protein required for cytochrome c oxidase activity (by homology)	1.1230	-0.0262	1.1712	0.3068	0.0538	1.0007	0.8984	1.57
2480.2	orf19.7485	orf19.7485	CA5830 MRPL9 Mitochondrial ribosomal protein of the large subunit (by homology)	0.9702	0.7436	0.9599	0.2634	0.5544	0.6862	0.3715	1.57
19785.1	orf19.4929	orf19.4929	CA3599 IPF19785 unknown function (Specific translational activator for COX1, mitochondrion)	-0.0101	0.5150	1.1150	0.7807	0.4521	0.6517	1.0718	1.57
9216.2	orf19.3710	YHB5	CA3139 YHB3 flavohemoglobin (by homology)		0.3984	-0.1714	1.0786	0.6915	0.6772	1.2522	1.57
5464.1	orf19.5684	orf19.5684	CA2607 MRPL38 ribosomal protein of the large subunit(L14), mitochondrial, by homology	0.6112	0.4024	1.2437	0.7005	0.8709	0.5552	0.2058	1.58
1231.2	orf19.2057	orf19.2057	CA4838 YTA12 Protease of the SEC18/CDC48/PAS1 family of ATPases (AAA) (by homology) (YM	1.2653	-0.0496	1.0014	0.6764	0.4097	0.4938	0.7955	1.58
8974.2	orf19.498	orf19.498	CA4508 NAM9 mitochondrial ribosomal protein	0.8621	-0.2236	0.5281	0.6494	0.8032	0.8504	1.1311	1.58
17243.2			CA0246 IPF14452.repeat2 F1-ATPase epsilon subunit (by homology)	0.1137	-0.0740	0.4885	1.0186	1.0108	0.9694	1.0902	1.58
19924.1	orf19.4324	orf19.4324	CA1658 IPF19924 unknown function	0.2925	-0.1917	0.6394	0.9117	0.9914	1.1808	0.7959	1.58
18468.1	orf19.4467	orf19.4467	CA2424 IPF18468 unknown function (N/A)	0.2141	0.5400	1.0956	0.8504	0.4114	0.6173	0.8984	1.58
8953.2	orf19.4895	orf19.4895	CA2358 IPF8953 unknown function (N/A)	0.8671	0.3940	0.4720	0.3929	0.8440	0.9015	0.7698	1.58
1677.1	orf19.6558	orf19.6558	CA4872 SEC231 Component of COPII coat (by homology)	0.6210	0.3359	0.0074	0.5671	0.8199	1.0786	1.2166	1.58
6296.2	orf19.1966	orf19.1966	CA2946 IPF6296 putative methyltransferase (by homology)	0.0000	0.1004	0.0248	0.8024	1.0952	1.3894	1.2453	1.59
429.1	orf19.7489.3	orf19.7489.3	CA5835 IPF429 unknown function (YGL220w)		1.2425	0.3651	0.3918	0.6304	0.5965	0.7883	1.59
863.1	orf19.7223	orf19.7223	CA5348 IPF863 involved in inositol biosynthesis (by homology)	0.8849	0.0593	0.3844	0.9672	0.6156	0.8416	0.9334	1.59
1557.1	orf19.954	orf19.954	CA5410 IPF1557 similar to dnaJ proteins	0.8210	-0.1747	1.2902	0.5830	0.9082	0.6893	0.5776	1.59
9638.2	orf19.1578	orf19.1578	CA3165 FMI1 processing of pre-ribosomal RNA	0.7450	0.4038	0.2762	0.9767	0.6050	1.1629	0.5370	1.59
2227.1	orf19.6903	orf19.6903	CA4585 IPF2227 unknown function	0.8262	-0.1172	0.1309	0.8600	1.2265	1.0786	0.7111	1.60
17135.11	orf19.6283	orf19.6283	CA3222 IPF15883 unknown function (YKL040c, mitochondrial matrix)	1.4449	0.1634	0.6585	0.2603	0.9197	0.4943	0.7921	1.60
4444.2	orf19.4705	orf19.4705	CA1841 CCA1 tRNA nucleotidyltransferase (by homology) (cytoplasm and mitochondrial matrix)	0.5850	0.2869	0.7681	0.5370	0.2690	1.1362	1.1545	1.60
14508.2	orf19.1828	orf19.1828	CA1781 IPF14508 unknown function		0.7390	-0.0679	0.4114	0.9038	0.9745	1.1223	1.60
14165.2	orf19.4642	orf19.4642	CA1062 IPF14165 unknown function (N/A)	0.5622	0.7840	0.7376	0.7294	0.7785	0.2203	0.9629	1.60
14810.2	orf19.2016	orf19.2016	CA0913 IPF14810 unknown function (YER044C, ERG28, ER protein)	0.0332	0.4984	1.0571	0.4892	0.5883	0.8683	1.2472	1.61
7901.2	orf19.6026	ERG2	CA2154 ERG2 C-8 sterol isomerase	0.5465	0.4600	0.1195	0.8040	0.0000	1.1663	1.6899	1.61
13913.2	orf19.5759	SNQ2	CA3828 SNQ2 multidrug resistance protein (by homology)	0.5868	0.3158	0.4984	0.4239	0.7393	0.7968	1.4272	1.61
19858.1			CA0319 IPF15244.3f unknown function, 3-prime end		-0.1047	0.0496	0.8860	0.8718	1.1157	1.2892	1.61
8173.2	orf19.522	orf19.522	CA4238 PIM1 mitochondrial ATP-dependent protease (by homology)	1.2788	0.4490	0.7642	0.5418	0.9322	0.2799	0.5708	1.61

20104.1	orf19.5517	orf19.5517	CA2520 IPF20104 alcohol dehydrogenase (by homology)	0.8938	0.3426	0.6276	0.9819	0.1852	0.8032	0.9891	1.61
6223.1	orf19.3297	orf19.3297	CA4607 IPF6223 unknown function (mitochondrial ribosome small subunit component)	0.5691	-0.0820	1.1484	0.8322	0.7438	0.6809	0.9416	1.61
7070.2	orf19.1069	RPN4	CA2854 RPN4 26S proteasome subunit (by homology)	0.9523	-0.2135	0.2053	0.9153	0.7628	1.0353	1.1827	1.61
6450.2	orf19.1896	SSC1	CA4474 SSC1 Mitochondrial heat shock protein 70-related protein (by homology)	0.3426	-0.2448	1.0571	1.1203	0.6043	0.9034	1.0600	1.62
10510.2	orf19.240	orf19.240	CA1265 IPF10510 unknown function (YKR065c, localised to mitochondrion)	1.2789	0.3718	0.5727	0.3267	0.7606	0.9174	0.6157	1.62
16809.2	orf19.920	orf19.920	CA0119 RMT2 N-delta-arginine methyltransferase (by homology)	0.8205	0.3068	-0.0145	0.8106		1.0752	1.1725	1.62
20121.1	orf19.5599	MDL2	CA2972 MDL2.3f ATP-binding transporter, 3-prime end (by homology) (mitochondrial inner membr	0.9759	0.2700	0.3381	0.6515	0.8435	0.7845	1.0127	1.62
1822.1	orf19.5010	DIM1	CA5252 DIM1 rRNA (adenine-N6,N6-)-dimethyltransferase (by homology)	0.9260	-0.0262	-0.0710	0.6517	1.0847	0.9411	1.3818	1.62
4977.2	orf19.2524	MGE1	CA1738 MGE1 heat shock protein (by homology)(	0.1941	0.0489	1.0181	1.1432	0.8006	0.6777	1.0170	1.62
13421.2	orf19.182	orf19.182	CA0029 PET56 ribosomal RNA methylase (by homology) (for mitochondrial 21S rRNA)	1.2016	0.4147	0.4136	0.6154	0.4060	0.6563	1.2066	1.63
13746.2	orf19.3686	orf19.3686	CA2113 ATP12 F1F0-ATPase complex assembly protein (by homology)	0.0704	-0.2328	0.9230	0.7058	1.3219	0.8883	1.2630	1.63
8903.2	orf19.3756	CHR1	CA1002 ROK1.3 RNA helicase, 3-prime end	1.7502	0.6526	-0.0801	1.1104	0.4936	0.4082	0.6201	1.63
4420.1	orf19.2953	orf19.2953	CA4179 TOM20 mitochondrial outer membrane import receptor subunit, 20 kD (by homology)	0.0621	0.0957	0.5838	1.2867	0.8092	0.9189	1.1998	1.63
14981.2	orf19.3483	orf19.3483	CA2896 IPF14981 unknown function (ER)	0.7829	0.1919	0.4894	0.7035	0.5583	1.0146	1.2263	1.64
10785.2	orf19.5732	orf19.5732	CA2847 IPF10785.exon1 unknown function, exon 1 (YNR053c, GTP-binding)	-0.1172	1.0514	0.0059	0.6788	1.1289	1.2291	0.9953	1.64
14849.2	orf19.2452	orf19.2452	CA0046 IPF14850 Hypothetical protein (N/A)		-0.0877	0.4500	0.8074	1.0250	0.9568	1.1290	1.64
16036.1	orf19.150	orf19.150	CA0010 IPF16036 similar to Saccharomyces cerevisiae Tim17p mitochondrial inner membrane im	1.4828	0.3460	0.8528	0.4287	0.6736	0.7031	0.5079	1.64
2166.1	orf19.7182	orf19.7182	CA5311 IPF2166 unknown function (YGL232w)	0.5926	1.4330	0.2004	0.5685	0.6012	0.9290	0.6817	1.64
16996.2	orf19.3547	orf19.3547	CA2667 IPF16996 unknown function (YDR496C)	1.1562	0.2797	0.2452	0.9502	0.3996	0.8570	1.1555	1.65
16189.2	orf19.5577	orf19.5577	CA0660 IPF16189.5f panthotenate kinase, 5-prime end (by homology) (YDR531W, CoA synthesis	1.0122	0.4586	0.1770	0.3573	1.1423	0.7960	1.1048	1.65
9757.1	orf19.3064	orf19.3064	CA5089 MRPL27 ribosomal protein (by homology)	1.6933	1.0949	0.9508	-0.1861	0.6079	0.7233	0.1661	1.65
1308.1	orf19.6406	orf19.6406	CA5122 IPF1308 Similarity to ribosomal protein S13 (by homology)	0.9588	0.2029	1.2360	0.3305	0.9130	0.7971	0.6177	1.65
12845.2	orf19.2363	orf19.2363	CA2251 IPF12845 unknown function (localised to mitochondrion)	0.7091	0.1466	0.5587	0.7778	0.8546	0.9812	1.0451	1.65
16549.2	orf19.4273	orf19.4273	CA1819 IPF16549 Unknown function (YLR139C, SLS1, mitochondrial integral membrane protein)	0.1583	0.4071	0.7689	0.7527	0.3685	1.1401	1.4823	1.65
10113.1	orf19.2249	orf19.2249	CA3589 IPF10113 unknown function (YNR020C)	0.9398	0.5591	0.6486	0.6224	0.6934	0.7958	0.8519	1.66
15660.2	orf19.4159	orf19.4159	CA1226 IPF15660 putative mitochondrial carrier (by homology)	1.0559	0.2742	0.9905	0.3909	0.0000	1.1877	1.2468	1.66
864.1	orf19.7222	orf19.7222	CA5347 IPF864 unknown function (mitochondrion)	1.2403	0.3450	0.7994	0.0334	0.4206	1.2921	1.0482	1.67
13283.2	orf19.1233	ADE4	CA2979 ADE4 amidophosphoribosyltransferase (by homology) (YMR300C)	1.3269	-0.0843	0.6377	0.8907	0.8001	0.7222	0.8922	1.67
15038.2	orf19.500	orf19.500	CA4506 GCD10 translation initiation factor eIF3 RNA-binding subunit (by homology)	0.5955	0.3254	0.8074	1.3465	0.8213	0.8148	0.4865	1.67
10187.1	orf19.3934	CAR1	CA1024 CAR1 arginase by homology	0.4630	1.0454	0.3051	0.6568	1.1986	0.6758	0.8694	1.68
11240.1	orf19.1416	COX11	CA3958 COX11 cytochrome-c oxidase assembly protein by homology to S. cerevisiae	1.2227	0.2582	1.2581	0.7404	0.6455	0.5029	0.5914	1.68
3366.1	orf19.4023	MRP2	CA4789 IPF3366 Mitochondrial ribosomal protein (by homology)		-0.2723	1.3374	1.0165	0.6906	1.0058	0.7155	1.68
3986.2	orf19.665	NEP1	CA4099 IPF3986 unknown function	1.2760	-0.0359	0.1590	0.9624	0.7829	0.8564	1.2546	1.68
1399.2	orf19.6068	SVF1	CA4928 IPF1399 unknown function (YDR346C, diauxic shift)	1.1577	0.4433	0.2798	0.7271	0.6678	0.9318	1.0482	1.68
13757.2	orf19.4479	orf19.4479	CA2414 IPF13756.3f unknown function, 3-prime end	1.3380	0.1030	-0.1408	0.8844	0.6880	1.1570	1.2412	1.69
16924.2	orf19.2829	orf19.2829	CA2544 IPF16924 unknown function (YNL149C, ER)	0.6498	-0.0043	0.4751	0.6745	0.9598	1.3033	1.2382	1.69
8073.2	orf19.3700	orf19.3700	CA1397 TOM72 mitochondrial import receptor (by homology)	0.0635	-0.1125	0.6590	0.7613	1.4854	0.9419	1.5405	1.70
12306.1	orf19.5039	orf19.5039	CA1695 RRP42 rRNA processing protein (by homology) (YDL111C)	0.0970	0.3111	0.1625	0.9339	0.8725	1.4758	1.5001	1.70
18618.1	orf19.2650.1	orf19.2650.1	CA1724 MRP10 Mitochondrial ribosomal protein (by homology)	1.0318	-0.3334	1.4115	0.5912	0.8188	0.8967	0.9403	1.70
8616.1	orf19.3704.1	orf19.3704.1	CA0940 IPF8616 similar to Saccharomyces cerevisiae Rsm19p ribosomal protein (by homology)	1.5351	0.5028	0.8082	0.2004	0.7075	1.6699	-0.0649	1.70
19594.1	orf19.169	CHO2	CA1414 CHO2 phosphatidylethanolamine N-methyltransferase (by homology) mitochondrion	1.0559	-0.1425	0.5489	0.7336	0.8605	1.2134	1.1355	1.71
1732.1	orf19.3089	orf19.3089	CA2009 IPF1732 intramitochondrial protein sorting (by homology)	0.0000	0.2245	0.9115	1.0809	0.8476	1.2118	1.1410	1.71
7154.2	orf19.1195	orf19.1195	CA1374 MIP1 Mitochondrial intermediate peptidase (by homology)	1.2630	1.0759	1.0144	0.4947	0.1467	0.7312	0.6924	1.71
1611.2	orf19.979	FAS1	CA5426 FAS1 Fatty-acyl-CoA synthase, beta chain.	0.9885	0.0055	0.0522	1.3206	0.7797	1.1313	1.1480	1.71
3709.1	orf19.3015	orf19.3015	CA5051 IPF3709 unknown function (YDR101C)	1.0462	0.5017	-0.0247	1.1506	0.6933	0.9359	1.1253	1.71
6869.2	orf19.4255	ECM331	CA2181 ECM331 Involved in cell wall biogenesis and architecture (by homology)	0.0000	0.2276	0.5247	0.8786	0.7286	1.2757	1.7975	1.71
443.1	orf19.7049	CYB5	CA5645 CYB5 Cytochrome b5 (by homology) (mitochondrion)	0.9382	1.2458	0.7184	0.6018	0.7007	0.3432	0.8945	1.71
14455.1	orf19.1589	orf19.1589	CA3156 IPF14455 similar to Saccharomyces cerevisiae Rrn7p polymerase I specific transcription	1.3785	0.9877	0.4222	0.2522	0.9928	0.6871	0.7390	1.72
9993.2	orf19.2287	RPA12	CA1115 RPA12 DNA-directed RNA polymerase I (by homology)		0.1635	-0.0970	1.0847	0.9642	1.3940	1.1744	1.72
13331.2	orf19.1591	ERG10	CA0290 POT14 acetyl-CoA acetyltransferase (by homology) (YPL028W, ERG10)	1.2960	0.9410	0.2777	0.6378	0.9103	0.9162	0.4993	1.72
16507.2	orf19.5576	orf19.5576	CA0659 IPF16189.3f panthotenate kinase, 3-prime end (by homology)		0.2497	0.0635	1.0440	0.7277	1.1349	1.4803	1.72
1023.2	orf19.4578	CYT2	CA5141 CYT2 holocytochrome-c1 synthase (by homology) (mitochondrion)	1.0371	0.3093	0.8369	0.6698	0.6106	1.1054	0.9157	1.72
7270.1	orf19.2785	ATP7	CA1907 ATP7 F1F0-ATPase complex, FO D subunit (by homology)	0.8203	-0.3867	0.4468	1.0796	1.0052	1.2084	1.3141	1.72
14775.2	orf19.3585	orf19.3585	CA0866 IPF14775 unknown function	0.9920	-0.4189	0.6817	0.9015	0.9411	0.9920	1.4038	1.72
12778.1	orf19.6136	orf19.6136	CA3419 IPF12778 ribosomal protein, mitochondrial (by homology)	0.7891	0.2786		1.2690	0.4071	0.8914	1.0807	1.72
14920.2	orf19.1528	orf19.1528	CA0745 MTF1 RNA polymerase specific factor, mitochondrial (by homology)	0.5850	-0.0072	0.5965	0.7476	1.0628	1.0600	1.4880	1.73
20153.1	orf19.1549	orf19.1549	CA3977 IPF20153 unknown function (N/A)	1.2147	-0.1795	0.4988	0.8883	0.9061	1.0433	1.2160	1.74

16483.1	orf19.4727	orf19.4727	CA1607 IPF14916 unknown function	0.7543	-0.5279	1.3267	1.0305	0.9696	1.1449	0.9317	1.75
1848.1	orf19.5885	orf19.5885	CA6154 IPF1848 similar to Saccharomyces cerevisiae Snu13p U4/U6.U5 snRNP associated prote	0.5316	-0.0707	0.2982	1.1453	1.2866	0.9947	1.4548	1.75
8844.2	orf19.6129	orf19.6129	CA2999 MRPL8 mitochondrial 60s ribosomal subunit (by homology)	0.5606	-0.1858	0.3565	1.5342	0.8515	1.1914	1.3440	1.75
11006.2	orf19.4658	orf19.4658	CA2706 IPF11006 unknown function	1.5352	0.0025	0.0061	1.0511	0.9314	0.6129	1.5148	1.75
14487.2	orf19.6346	orf19.6346	CA3500 IPF14487 unknown function	1.0841	-0.3921	0.3807	1.0101	0.9222	1.3646	1.2963	1.75
9631.1	orf19.1575	PRS1	CA3168 PRS3 ribose-phosphate pyrophosphokinase (YHL011C)	0.7884	-0.1175	0.3888	1.0803	1.1312	0.9906	1.4130	1.75
1537.1	orf19.336	YAH1	CA4630 IPF1537 putative adrenodoxin and ferrodoxin (by homolgy) (YPL252C, mitochondrial mat	0.7826	-0.3032	1.1640	0.7666	1.1683	0.9851	1.1670	1.76
10381.2	orf19.3682	CWH8	CA1146 CWH8 putative required protein for full levels of dolichol-linked oligosaccharides in the en	0.5668	0.5728	0.5738	1.0097	0.6312	0.9143	1.4671	1.76
12428.1	orf19.2667	orf19.2667	CA0599 IPF12428 unknown function	0.8932	0.0649	-0.2092	1.3477	1.3169	1.2683	1.0734	1.77
9797.2	orf19.6156	orf19.6156	CA3146 IPF9797 unknown function	1.7515	0.3863	1.3431	0.9138	-0.3058	0.7013	1.0108	1.78
8020.2	orf19.1335	orf19.1335	CA2119 MTR4 RNA Helicase (by homology) (YJL050W)	0.6548	0.1307	0.1876	1.2294	0.6878	1.3513	1.5718	1.78
11393.2	orf19.2852	orf19.2852	CA1669 IPF11393 unknown function (mitochondrial ribosome small subunit component)	0.4423	0.4837	1.5242	0.8054	0.7706	0.9501	0.8536	1.78
14266.2	orf19.5832	HPT1	CA3787 HPT1 hypoxanthine guanine phosphoribosy transferase(by homology)	0.5685	-0.1488	0.1401	1.1270	1.5054	1.2382	1.4174	1.78
13798.1	orf19.3946	orf19.3946	CA1090 COX18 protein required for activity of mitochondrial cytochrome oxidase (by homology)	1.2816	1.1011	0.1863	1.0534	0.5806	1.0147	0.6424	1.79
11364.1	orf19.1716	URA3	CA2801 URA3 orotidine-5 -monophosphate decarboxylase [Candida albicans]	1.3033	0.3907	1.1090	0.5301	0.9389	0.5489	1.0963	1.80
1134.1	orf19.5433	orf19.5433	CA5786 IPF1134 unknown function (YDR493w, mitochondrial)	0.5850	0.8496	1.2079	0.8359	0.4372	0.9508	1.0628	1.80
15527.2	orf19.4519	SUV3	CA2908 SUV3 ATP-dependent RNA helicase, mitochondrial (by homology)	1.0440	-0.3430	1.1249	0.9003	0.6188	1.0544	1.5417	1.80
19955.1	orf19.5705	NAM2	CA2656 NAM2 mitochondrial leucine--tRNA ligase (by homology)	1.1410	0.0956	1.1340	0.7717	0.6685	1.0001	1.1826	1.81
2203.1	orf19.6916	orf19.6916	CA4597 ATP11 F1F0-ATPase complex assembly protein (by homology) (mitochondrion)	1.7077	-0.2278	1.1824	0.9441	0.9201	0.6441	0.8594	1.82
7575.2	orf19.4365	orf19.4365	CA1097 IPF7575 putative endo-exonuclease (by homology) (YKR056W, tRNA methyltransferase)	0.7213	-0.0304	0.7782	0.9239	1.1741	1.0464	1.4171	1.82
15801.2	orf19.1650	orf19.1650	CA1043 TOM6 mitochondrial outer membrane import receptor subunit (by homology)	0.3684	0.3207	1.5446	0.9221	1.1525	0.9218	0.8226	1.82
1116.1	orf19.5420	orf19.5420	CA5776 RML2 Ribosomal L2 protein, mitochondrial (by homology)	1.6203	1.0049	1.1534	0.5447	0.7446	0.5205	0.4731	1.82
15664.2	orf19.5296	orf19.5296	CA2160 IPF15664 unknown function (YIL157c, localised to mitochondrion)	0.5194	0.3451	1.9257	0.7329	0.0000	1.1563	1.4226	1.83
19484.1			CA0003 IPF19484 putative zinc amino peptidase (by homology) (doesn't exist in CBD)	1.0257	0.0563	0.4528	0.9877	0.6773	1.2018	1.7063	1.83
17430.1	orf19.73	orf19.73	CA0011 IPF17430 possible zinc protease (by homology) (YIL137C)	0.8161	-0.0700	0.8550	0.9244	1.1345	1.2632	1.2062	1.83
4568.1	orf19.6524	orf19.6524	CA4954 TOM40 mitochondrial import receptor chain TOM40 (by homology)	0.8537	0.1465	0.8884	1.0686	1.0748	1.0155	1.1171	1.84
16061.2	orf19.1753	PUS7	CA0294 IPF16061 unknown function (pseudouridine synthase, nucleus)		-0.0087	1.1210	0.7303	1.1283	1.3317	0.9913	1.84
8130.2	orf19.5143	orf19.5143	CA3631 TIM54 Translocase for the insertion of proteins into the mitochondrial inner membrane(by	1.5380	-0.1618	0.8909	1.0292	0.8704	0.9661	1.0500	1.84
10140.2	orf19.408	orf19.408	CA1355 IPF10138.3f unknown function, 3-prime end (N/A)	0.1580	0.0059	0.4331	1.4715	1.2334	1.3693	1.6110	1.86
15832.1	orf19.4676	orf19.4676	CA3247 IPF15832 unknown function (YKL053ca)	-0.1730	0.2203	2.1030	1.6498	0.7949	1.0482	0.6844	1.87
16143.2	orf19.2259	orf19.2259	CA3581 IPF16143 unknown function (ribosomal protein, similar to chloroplast)	0.4846	0.2195	1.3224	1.1456	0.9504	1.1962	1.0347	1.88
18593.1	orf19.2201	orf19.2201	CA1889 CBP6 Apo-cytochrome B pre-mRNA processing protein (by homology) (mitochondrion)	1.4388	-0.0112	1.8889	0.5445	0.8941	0.7159	0.8858	1.88
6665.2	orf19.6686	orf19.6686	CA4289 IPF6665 unknown function		-0.2533	-0.0770	1.1903	1.5064	1.4657	1.6192	1.88
7704.2	orf19.679	FGR39	CA4114 IPF7704 unknown function (N/A)	0.7224	0.1722	1.1955	0.3757	1.3882	1.1086	1.4654	1.89
2516.1	orf19.7466	ACC1	CA5816 ACC1 acetyl-coenzyme-A carboxylase (by homology)	1.3497	0.2214	0.4701	1.3396	1.0320	0.9282	1.1110	1.89
9204.1	orf19.3676	ABP140	CA4045 ABP140 putative methyltransferase (by homology) (YOR239W)	1.6781	0.2388	0.1903	1.1084	0.9531	1.0552	1.2636	1.90
12940.2	orf19.4932	orf19.4932	CA3603 MEF1 mitochondrial translation elongation factor G (by homology)	-0.1533	0.4072	1.2822	0.9630	0.7894	1.5940	1.6057	1.90
8826.2	orf19.397	orf19.397	CA3872 MRPL28 mitochondrial ribosomal protein of the large subunit (by homology)	0.6768	-0.1332	1.2426	0.8428	1.1715	1.4683	1.2264	1.90
4276.2	orf19.549	orf19.549	CA4260 IPF4276 similar to Saccharomyces cerevisiae Mrpl32p putative mitochondrial ribosomal p	-0.3474	0.1124	1.4849	1.1296	1.4725	1.6844	1.0186	1.91
1024.1	orf19.4577.3	orf19.4577.3	CA5140 TIM10 Subunit of the Tim22-complex (by homology) (mitochondrion)	1.2901	0.1068	1.2914	0.5957	0.6314	1.4756	1.1660	1.91
18440.1	orf19.4760	orf19.4760	CA2629 IPF10911 unknown function (YIL110W)	0.7630	0.3079	0.0962	1.1194	0.9014	1.5894	1.7842	1.92
14782.2	orf19.1566	orf19.1566	CA3990 IPF14782 beta-transducin (by homology)	2.2373	-0.0529	0.1375	1.0745	0.3323	1.2642	1.5835	1.92
5933.2	orf19.439	orf19.439	CA4062 IPF5933 similar to Saccharomyces cerevisiae Mhr1p involved in mitochondrial homologou	1.5532	-0.0442	1.1222	1.0244	1.0356	1.0241	0.8880	1.92
16471.1	orf19.2795	orf19.2795	CA2003 IPF16471 unknown function (YDL051W)	0.4678	0.1448	0.7496	1.2222	1.0745	1.3660	1.6218	1.93
8699.2	orf19.1981	orf19.1981	CA1135 IMP2 mitochondrial inner membrane protease subunit (by homology)		0.6388	0.0172	0.4988	1.3561	1.9638	1.2576	1.94
5151.1	orf19.6531.1	TOM71	CA4946 TOM71 Translocase of the outer mitochondrial membrane (by homology)	0.3987	0.4228	1.1753	1.1809	1.4763	1.0901	0.9455	1.94
3903.2	orf19.760	orf19.760	CA1932 IPF3903 unknown function (mitochondrial large ribosomal subunit)	0.0000	0.3573	2.0542	1.0711	0.7286	1.4394	1.0766	1.95
15194.2	orf19.4261	TIF5	CA0667 TIF5 Translation initiation factor eIF5 (by homology)	0.7343	-0.2915	0.6465	1.4929	1.3458	1.3151	1.4877	1.95
19866.1	orf19.5753	HGT10	CA0472 STL1 sugar transporter (by homology)		-0.0604	0.2203	0.8383	0.8049	2.1375	1.8476	1.95
9652.2	orf19.3990	orf19.3990	CA4760 IPF9652 unknown function		-0.2328	0.8480	0.8278	1.4346	1.4005	1.5524	1.96
12009.2	orf19.3171	ACH1	CA0345 ACH1 acetyl-coenzyme-A hydrolase (by homology) (mitochondrion)	1.1017	0.4434	0.1637	1.2972	0.4630	1.4353	1.9129	1.96
14216.2	orf19.2927	MNN11	CA0563 MNN11 Mannosyltransferase complex component (by homology) (YJL183W)	0.9283	-0.0770	0.3896	1.3780	1.3068	1.3138	1.6645	1.98
10823.1	orf19.3938	orf19.3938	CA1632 IPF10181 similar to Saccharomyces cerevisiae Rsm26p protein of the small subunit of the mitochond		0.2216	1.5969	0.8742	0.4875	1.2351	1.5700	2.00
7324.2	orf19.2977	orf19.2977	CA3446 IPF7324 unknown function (YKL195w, localised to mitochondrion)	1.7649	0.7787	1.2260	0.4398	1.1592	0.8325	0.7952	2.00
17424.2	orf19.1770	CYC1	CA0038 CYC1 cytochrome-c isoform 1 (mitochondrion)	1.3801	0.4570	0.9866	0.7642	0.8595	1.2416	1.3291	2.00
8275.2	orf19.1569	orf19.1569	CA3993 IPF8275 unknown function	0.8335	0.1776	-0.6552	1.7437	1.4756	1.5661	1.9370	2.02
11742.2	orf19.2309	orf19.2309	CA3308 PET127 component of mitochondrial translation (by homology)	2.1375	0.2141	0.2461	0.5705	1.3488	0.8624	1.7031	2.02

4973.1	orf19.2520	orf19.2520	CA0462 MRPS28 ribosomal protein (by homology)	0.0000	0.2804	1.6290	1.1389	0.9578	1.6323	1.4541	2.02
5581.2	orf19.5167	orf19.5167	CA4428 IFM1 translation initiation factor 2 by homology (mitochondrion)	2.4685	0.7981	1.4914	0.4284	0.6666	0.5544	0.7225	2.03
7091.1	orf19.484	orf19.484	CA4521 MRPL40 Putative mitochondrial ribosomal protein (by homology)	0.2754	0.2392	1.5421	1.0419	1.1219	1.3442	1.5869	2.03
3492.1	orf19.6752	orf19.6752	CA5945 IPF3492 unknown function (mitochondrial ribosome small subunit component)	0.8258	0.0165	1.0917	1.0375	1.6312	1.2995	1.2675	2.03
14109.2	orf19.2451	PGA45	CA0380 IPF14109 unknown function (N/A)	0.9935	1.3939	0.9645	0.9067	0.8657	0.5441	1.5173	2.04
4257.2	orf19.1633	orf19.1633	CA4003 IPF4257 unknown function	1.1237	-0.1297	0.1177	1.8714	1.1388	1.4249	1.6576	2.04
16082.2	orf19.4160	orf19.4160	CA1227 IPF16082 unknown function (	0.0000	0.7362	0.9330	1.2690	0.9580	1.6966	1.6275	2.04
9841.1	orf19.3204	orf19.3204	CA2482 IPF9841 unknown function (YLR318W, telomerase reverse transcriptase)	0.3828	0.4531	-0.0244	1.2396	1.1026	1.9626	2.1189	2.05
17996.2			CA2240 CRD2 Cu-binding metallothionein (doesn't exist in CBD)	1.1424	0.3962	0.4439	0.9677	1.4015	1.4954	1.4426	2.06
9361.2	orf19.2382	orf19.2382	CA2103 ISM1 isoleucyl-tRNA synthetase (by homology) (mitochondrion)	1.5642	0.5007	1.5422	0.8448	0.7833	0.9266	1.1720	2.07
6298.2	orf19.1964	orf19.1964	CA2947 IPF6298 unknown function (N/A)	0.8271	0.2760	0.3340	1.2996	1.2366	1.5273	1.9176	2.08
6338.1	orf19.1109	orf19.1109	CA1461 IPF6338 unknown function (N/A)	0.4281	0.1506	1.3966	1.3599	0.8957	1.6087	1.6415	2.10
14559.1	orf19.5126	orf19.5126	CA1757 IPF14559.5f unknown function, 5-prime end	0.0348	0.1901	0.3872	1.8386	1.4592	1.8102	1.7622	2.10
9936.2	orf19.989	orf19.989	CA3526 MRPS5 Probable ribosomal protein S5, mitochondrial (by homology)	0.2414	0.5013	1.4530	1.2965	1.3253	1.3156	1.4033	2.11
6507.2	orf19.1546	orf19.1546	CA3974 IPF6507 unknown function (localised to mitochondrion)		0.5281	1.3080	0.6164	1.1789	1.4335	1.4600	2.12
1453.2	orf19.6041	RPO41	CA4904 RPO41 Mitochondrial DNA-directed RNA polymerase (by homology)	1.8663	0.2055	0.5385	1.2815	1.0104	1.3377	1.4719	2.15
1544.1	orf19.947	orf19.947	CA5405 MRP17 Mitochondrial ribosomal protein (by homology)	0.6471	-0.5799	1.6434	1.5705	1.2172	1.5739	1.6485	2.15
878.1	orf19.7215.3	orf19.7215.3	CA5341 HSP10.3 10 kDa mitochondrial heat shock chaperonin, 3-prime end (by homology)	0.9031	0.2791	1.8890	0.8616	1.3182	1.1680	1.3349	2.16
6505.2	orf19.1545	orf19.1545	CA3973 IPF6505 unknown function (Mitochondrial ribosomal protein of the small subunit)	1.3948	0.4467	1.3587	1.1355	0.8682	1.3019	1.2743	2.16
6970.1	orf19.2639	orf19.2639	CA2072 IPF6970 unknown function (Mitochondrial ribosomal protein of the large subunit)	0.0000	0.4147	1.7656	1.4494	1.7500	0.4285	1.9793	2.16
20032.1	orf19.6828	orf19.6828	CA5882 RRP1 Involved in processing rRNA precursor species to mature rRNAs (by homology)	1.4743	-0.6486	0.2999	1.4623	1.5289	1.7146	1.9962	2.17
11656.2	orf19.6363	orf19.6363	CA3515 MRPL15 mitochondrial ribosomal protein of the large subunit (by homology)	1.0873	0.1487	1.0250	1.2235	1.2869	1.5518	1.5112	2.17
15646.2	orf19.3481	orf19.3481	CA2898 IPF15646 putative ATP-dependent RNA helicase (by homology) (mitochondrial DEAD box	0.6917	0.7031	0.7162	1.6543	0.6708	1.3680	2.0704	2.18
19552.1	orf19.5064	MRPL3	CA0089 MRPL3 ribosomal protein of the large subunit, mitochondrial (by homology)	0.4550	0.4354	1.7767	0.8517	0.9578	1.4115	1.9991	2.18
1663.1	orf19.6565	orf19.6565	CA4878 OXA1 Cytochrome oxidase biogenesis protein (by homology) (mitochondrion)	1.9255	0.2091	1.2909	1.1524	0.6825	1.2261	1.4634	2.20
14569.2	orf19.6231	MRPL19	CA3009 MRPL19 Ribosomal protein (by homology) (mitochondrion)	1.5734	0.6781	1.2628	1.0512	1.3367	1.3650	0.6912	2.20
2873.1	orf19.7443	orf19.7443	CA5733 IPF2873 unknown function (N/A)	0.2146	0.4135	2.1088	1.0192	1.0312	1.5824	1.6089	2.20
10301.1	orf19.2275	orf19.2275	CA1876 IPF10301 putative 60S ribosomal protein L7/L12 homolog, mitochondrial precursor	1.0326	-0.1917	1.4149	1.2525	1.3906	1.5371	1.5437	2.20
19871.1	orf19.3532	MRPL10	CA0519 MRPL10.3 ribosomal protein, 3-prime end (by homology) (mitochondrion)	-0.1313	-0.1746	2.5306	1.7286	1.2636	1.4947	1.4865	2.25
14687.1	orf19.2006.1	orf19.2006.1	CA3936 COX17 cysteine-rich cytoplasmic protein(by homology) (mitochondrion)	1.5201	0.0149	1.9463	0.9228	0.9152	1.2818	1.6165	2.26
11177.2	orf19.51	orf19.51	CA2600 IPF11177 similar to Saccharomyces cerevisiae Clu1p translation initiation factor eIF3 (p13	2.1816	-0.2043	0.9451	1.1816	0.9884	1.3067	1.8252	2.26
16564.1	orf19.2438	orf19.2438	CA1914 IPF16564 putative mitochondrial ribosomal protein S12	0.7253	0.5885	0.4232	1.3123	1.6735	1.7683	1.7516	2.26
10429.2	orf19.2887	MET13	CA0721 IPF10429 unknown function (YMR295c, cell periphery and bud)	1.3110	0.1990	0.9129	1.2481	1.6256	1.2961	1.7209	2.28
4102.2	orf19.2019	orf19.2019	CA0910 MRPL16 ribosomal protein (mitochondrion)	1.4592	0.4124	1.6761	1.2636	1.2829	1.2092	1.0142	2.28
14193.2	orf19.3357	orf19.3357	CA0790 IPF14193 unknown function (mitochondrion, YHR059w, FYV4)	0.4820	0.1941	1.8686	1.3150	1.1828	1.3869	1.9205	2.29
5446.1	orf19.5698	orf19.5698	CA2613 IPF5446 putative ribosomal protein (by homology) (Mitochondrial ribosomal protein of the	1.0575	0.2246	1.6657	1.4126	1.3574	1.3225	1.3139	2.29
9838.2	orf19.3205	orf19.3205	CA2481 MRPL36 ribosomal protein YmL36 precursor, mitochondrial (by homology)	1.8505	0.6681	1.3490	0.6901	1.0230	1.7686	1.0329	2.29
7840.1	orf19.4204	orf19.4204	CA2930 IPF7840 similar to Saccharomyces cerevisiae Pet123p ribosomal protein, mitochondrial (	1.4957	0.3389	1.5461	1.0875	1.2066	1.3435	1.4007	2.30
8454.2	orf19.6853	orf19.6853	CA4455 IPF8454 unknown function (N/A)	0.0000	0.3184	1.8442	1.6860	1.2495	1.6708	1.6865	2.31
3698.1	orf19.3022	orf19.3022	CA5056 IPF3698 similar to Saccharomyces cerevisiae Rsm24p mitochondrial ribosomal protein (	0.7332	-0.0069	1.3604	1.7622	1.4648	1.6717	1.5385	2.33
917.1	orf19.7577	MSS51	CA5981 MSS51 involved in maturation of COX1 and COB mRNA (by homology)	1.8268	0.1406	1.3367	1.5175	0.9033	1.4489	1.3967	2.34
12526.2	orf19.1662	orf19.1662	CA3466 MRP1.5f mitochondrial ribosomal protein of the small subunit, 5-prime end (by homology)	1.2206	-0.1846	1.5886	1.2487	1.5572	1.5354	1.7601	2.37
6016.2	orf19.1485	orf19.1485	CA0908 MRPL31 Mitochondrial ribosomal protein	1.2003	0.4593	1.8696	0.9222	0.8951	1.5027	1.9251	2.38
13404.1	orf19.755	MRPL37	CA1928 MRPL37 Mitochondrial ribosomal protein YmL37 (by homology)	1.2677	0.2378	1.8530	1.0564	1.0255	1.5033	1.8634	2.39
3928.1	orf19.6503	orf19.6503	CA4968 IPF3928 unknown function (mitochondrial ribosomal protein)	0.4188	0.0681	1.8441	1.3207	1.5385	1.9406	1.7033	2.40
7585.2	orf19.5201	orf19.5201	CA1768 IPF7585 unknown function (mitochondrial ribosome small subunit component)	0.7948	-0.0636	1.3943	1.3953	1.7118	1.9209	1.6809	2.40
14757.2	orf19.1956	orf19.1956	CA2256 IPF14757 unknown function (localises to mitochondria)	1.5603	0.2478	1.6104	1.1305	1.1301	1.4207	1.8091	2.42
7602.2	orf19.5193	orf19.5193	CA1761 IPF7602 oxidoreductase (by homology) (YIR035C)	1.0437	0.2553	0.5773	1.5041	1.5608	2.1985	1.8122	2.43
15216.2	orf19.3777	orf19.3777	CA0329 IMG2 Required for Integrity of Mitochondrial Genome (by homology)	1.1133	-0.0759	1.7482	1.0089	1.5845	1.6499	1.9529	2.43
18330.1			CA3465 MRP1.3f Mitochondrial ribosomal protein of the small subunit, 3-prime end (by homology)	1.4662	-0.1408	1.2708	1.3334	2.2141	1.7634	1.2660	2.48
2354.1	orf19.7019	YML6	CA5204 YML6 Ribosomal protein, mitochondrial (by homology)	1.0663	-0.0650	2.0623	1.5878	1.0007	1.7565	1.8365	2.50
3299.1	orf19.4393	CIT1	CA3909 CIT1.exon2 Citrate synthase, exon 2	0.5685	-0.7226	0.1852	2.3592	2.1033	2.2895	2.4670	2.50
8066.1	orf19.3696	TOM22	CA1401 TOM22 mitochondrial outer membrane import receptor complex subunit (by homology)	0.8188	-0.2328	1.9870	1.6066	1.5696	1.6060	1.9005	2.50
20133.1	orf19.585	orf19.585	CA3432 MRPL17 ribosomal protein of the large subunit (YmL30), mitochondrial (by homology)	1.0256	0.1642	2.1703	1.3242	1.2214	1.6909	1.8428	2.55
17681.2	orf19.3480	orf19.3480	CA2899 IPF17681 similar to Saccharomyces cerevisiae Rsm23p involved in mitochondrial functio	0.6138	0.6185	1.7257	1.3163	1.2400	1.8927	2.0470	2.55
1621.1	orf19.6585	orf19.6585	CA4893 IPF1621 unknown function	0.9775	0.0963	1.0489	3.4195	1.4552	1.2702	1.2222	2.56
4703.2	orf19.5279	orf19.5279	CA4973 IPF4703 unknown Function (Mitochondrial ribosomal protein of the large subunit)	1.6978	0.0754	1.9578	1.3970	1.2487	1.6637	1.4691	2.56

16126.1	orf19.172	orf19.172	CA1417 IPF16126 similar to Saccharomyces cerevisiae Rpc19p DNA-directed RNA polymerase I,	1.0772	0.1170	0.8723	1.5377	1.7505	1.9900	2.2507	2.59
6175.1	orf19.4176	orf19.4176	CA3726 IPF6175 unknown function (Mitochondrial ribosomal protein of the small subunit)	0.5707	0.7263	1.9156	1.6601	1.3334	1.8198	1.5974	2.59
14895.1	orf19.93	orf19.93	CA1987 IPF14895 unknown function (YMR002W)	1.0533	0.5384	1.7795	1.6294	1.7839	1.7187	1.5922	2.72
15124.2	orf19.5747	orf19.5747	CA1428 MRP4 Ribosomal protein of the small subunit mitochondrial (by homology)	1.7950	0.5060	1.7277	1.5143	0.8403	1.7116	2.0555	2.73
8752.2	orf19.828	orf19.828	CA4226 IPF8752 similar to Saccharomyces cerevisiae Mrpl24p ribosomal protein of the large subu	1.6255	0.3003	2.0224	1.2608	1.5829	1.6289	1.8859	2.77
2599.1	orf19.6696	orf19.6696	CA4298 TIM9 Mitochondrial inner membrane translocase (by homology)	0.0688	0.3503	2.6686	1.3772	1.5872	1.7934	2.6161	2.82
3331.1	orf19.7386	orf19.7386	CA5684 IPF3331 unknown function (assembly of mitochondrial respiratory complexes)	1.0784	0.7198	1.7216	1.3653	1.6652	1.7013	2.4348	2.88
13417.2	orf19.185	orf19.185	CA1445 MRP51 Mitochondrial ribosomal protein of the small subunit (by homology)	1.6781	0.3357	1.5529	2.9718	1.2744	1.5811	1.5984	2.97
16405.2	orf19.4751	orf19.4751	CA2213 IPF16405 similar to saccharomyces cerevisiae Rsm25p protein of the small subunit of the	1.6093	0.1077	1.8519	1.7148	1.6466	1.7721	2.3514	2.99
15259.2	orf19.2214	orf19.2214	CA2377 MRPL7 Ribosomal protein of the large subunit, mitochondrial (by homology)	1.4711	-0.0455	2.0080	1.9835	1.7044	2.0489	1.9040	2.99
2343.1	orf19.7012	orf19.7012	CA5198 LPA4 Similar to ribosomal protein S16, mitochondrial (by homology)	1.9992	0.7633	2.1240	0.8942	1.6433	1.9575	1.8294	3.03
7643.1	orf19.863	orf19.863	CA1863 MRPL35 Ribosomal protein of the large subunit, mitochondrial (by homology)	1.8252	0.4959	2.1270	1.4711	1.8078	1.6669	1.8410	3.04
3182.1	orf19.3559	orf19.3559	CA0580 IPF3184.exon2 unknown function, exon 2 (doesn't exist in CDB)	1.6599	0.3356	2.2349	1.7351	1.4201	1.9159	2.1194	3.10
10399.1	orf19.3367	orf19.3367	CA1198 IPF10399 unknown function (Mitochondrial ribosomal protein of the large subunit)	1.4463	0.1687	2.1989	1.9854	1.8036	1.6982	2.1852	3.12
5569.2	orf19.5161	orf19.5161	CA4434 MRPL49 ribosomal protein mitochondrial	0.0000	0.6846	2.0450	2.7113	2.0709	1.9607	2.0213	3.12
407.1	orf19.7504	orf19.7504	CA5848 IPF407 unknown function (YGR161C)	2.9236	0.4892	0.3723	1.4047	1.7685	1.8236	2.8559	3.17
6295.1	orf19.1967	orf19.1967	CA2945 IMG1 Ribosomal protein, mitochondrial (by homology)	1.1671	0.7191	2.5360	1.7065	1.6890	2.2775	1.9417	3.29
16978.2	orf19.685	YHM1	CA1980 YHM1 member of the mitochondrial carrier family (MCF) (by homology)	1.7403	0.6160	1.8605	1.7313	1.6407	2.0973	2.3911	3.31
14249.2	orf19.3797	orf19.3797	CA1421 MRPL11 Mitochondrial ribosomal protein (by komology)	1.4880	0.2879	2.6690	1.7364	1.8364	1.9877	2.1412	3.33
3361.2	orf19.4018	orf19.4018	CA4785 IPF3361 putative mitochondrial ribosomal protein S7 (by homology)	1.7456	0.4452	2.4432	1.7275	2.0647	2.0676	2.0038	3.45
2131.2	orf19.7203	orf19.7203	CA5329 MRP7 Mitochondrial ribosomal protein YmL2 precursor (by homology)	1.2007	0.2828	2.3593	2.2069	2.0983	2.2802	2.7022	3.67
13943.2	orf19.5235	orf19.5235	CA5012 IPF13943 Unknown function (N/A)	1.1218	0.7219	2.9593	1.4318	2.3931	2.0819	2.7848	3.80
2157.1	orf19.7187	MAM33	CA5316 MAM33 Mitochondrial acidic matrix protein (by homology)	2.0237	0.9114	2.1786	2.2142	1.8740	2.0859	2.6871	3.99
3184.1	orf19.3559	orf19.3559	CA0579 IPF3184.exon1 unknown function, exon 1 (Mitochondrial ribosomal protein of the small su	0.8671	0.6388	2.5160	4.9941	2.3141	1.8957	1.7225	4.39
2075.1	orf19.4082	DDR48	CA4336 DDR48 stress protein (by homology) (YMR173W)	2.9727	2.1264	0.2084	2.8759	2.6820	2.8988	2.9035	5.21

[a] from http://www.candidagenome.org/

[b] from http://genolist.pasteur.fr/CandidaDB/

Supplementary Table 3. 347 genes with altered expression in an *ace2* delete relative to wildtype grown as hyphal cells. (FDR of 0.99%).

				Log2 Ratios (5 experiments)					
OligoID	**ORF19**[a]	**CGD Gene Name**[a]	**Description (from CandidaDB)**[b]	**H1**	**H2**	**H3**	**H4**	**H5**	**Average Fold Change**
11998.2	orf19.2758	orf19.2758	CA1898 IPF11998 unknown function (putative GPI-anchored, PGA38)	-1.2154	-1.7698	-3.0233	-3.6630	-4.4227	-7.06
20169.1	orf19.5674	PGA10	CA4381 IPF20169 unknown function	-2.1343	-1.5270	-1.4230	-2.6424	-1.8679	-3.78
3022.1	orf19.5025	MET3	CA5238 MET3 ATP sulfurylase	-1.9033	-0.8549	-2.8599	-1.9873	-1.9080	-3.74
19952.1	orf19.5636	RBT5	CA2558 RBT5 repressed by TUP1 protein 5	-1.8087	-1.0078	-1.4833	-2.5363	-1.9536	-3.38
12125.2	orf19.5645	MET15	CA2565 MET15 O-acetylhomoserine O-acetylserine sulphydrylase	-1.8395	-1.1457	-1.5556	-2.0533	-2.1240	-3.35
2053.1	orf19.5267	orf19.5267	CA4983 IPF2053 unknown function (YJR151C)	-0.6803	-1.4183	-1.6388	-1.8946	-3.0297	-3.32
6238.2	orf19.2374	orf19.2374	CA2752 IPF6238 GAG protein of retrotransposon pCal	-2.0088	-1.1346	-1.9877	-1.9462	-1.3483	-3.22
696.1	orf19.7586	CHT3	CA5987 CHT3 chitinase 3 precursor	-1.1095	-0.8486	-1.7665	-1.9630	-2.6450	-3.17
10110.1	orf19.2248	ARE2	CA3590 ARE2 acyl-CoA sterol acyltransferase-like (by homology)	-1.9578	-0.2243	-2.3565	-1.6462	-1.1993	-2.78
6872.1	orf19.4252	orf19.4252	CA2183 IPF6872 serine/threonine protein kinase (by homology) (YGR262c, bud site select	-0.7959	-3.4375	-1.9828	-0.3959	-0.5479	-2.70
7044.2	orf19.125	EBP1	CA1216 EBP1 NADPH dehydrogenase	-2.0903	0.2847	-1.8445	-2.1781	-1.1781	-2.64
2535.1			CA0355 IPF2535 unknown function	-1.3394	-1.1977	-0.8289	-1.1007	-2.4707	-2.62
6235.2	orf19.5372	orf19.5372	CA2216 IPF6235 Candida albicans Tca2 retrotransposon	-1.5296	-0.4162	-1.6349	-1.6712	-1.3430	-2.49
6518.1	orf19.1691	orf19.1691	CA2302 IPF6518 unknown function	-1.7037	-0.2792	-1.9769	-1.5736	-1.0058	-2.48
564.2	orf19.7104	orf19.7104	CA5596 IPF564 unknown function (N/A)	-1.2964	-0.7468	-0.4134	-1.7037	-2.3101	-2.45
8427.2	orf19.922	ERG11	CA1387 ERG16 cytochrome P450 lanosterol 14a-demethylase	-1.1683	-0.5765	-2.0383	-1.4741	-1.0758	-2.41
7796.2	orf19.2619	PHO113	CA0616 PHO11 Secreted acid phosphatase	-1.0366	-0.3111	-1.8686	-1.2286	-1.8727	-2.40
6237.2	orf19.5373	orf19.5373	CA2217 POL0 pol polyprotein, reverse transcripase	-1.4410	-0.8138	-1.2533	-1.5358	-1.1928	-2.37
15731.2	orf19.1442	PLB4.5	CA0185 PLB4.5f Phospholipase, 5-prime end (by homology)	-0.9492	-1.4902	-1.4547	-1.4201	-0.7616	-2.32
5115.2	orf19.6402	CYS3	CA5127 CYS3 cystathionine gamma-lyase by homology	-1.6284	-0.6139	-0.7033	-1.4250	-1.4983	-2.26
14295.1	orf19.6321	PGA48	CA3287 IPF14295 putative Sed1p-like cell surface protein (by homology)	-0.8919	-0.7296	-1.2793	-1.5021	-1.3019	-2.21
9550.1	orf19.6882	OSM1	CA4570 IPF9550 similar to Saccharomyces cerevisiae Osm1p osmotic growth protein	-0.9857	-1.2954	-0.7625	-1.1538	-1.3804	-2.17
13194.2	orf19.4076	MET10	CA1620 MET10 Sulfite reductase flavin-binding subunit (by homology)	-0.6285	-0.7119	-1.1518	-1.2116	-1.8495	-2.16
14343.2	orf19.5871	orf19.5871	CA6165 SNF5.3f Component of SWI/SNF transcription activator complex, 3-prime end (by	-2.0469	-1.4982	-1.2481	-0.2009	-0.5208	-2.15
8762.2	orf19.822	orf19.822	CA4220 IPF8762 unknown function (N/A)	-0.7748	-0.9356	-1.8453	-0.9334	-0.9434	-2.12
10991.2	orf19.5801	RNR21	CA4155 RNR21 ribonucleoside-diphosphate reductase (by homology)	-0.9771	-0.1617	-2.0363	-1.2271	-0.9886	-2.11
12101.1	orf19.5635	PGA7	CA2557 IPF12101 mycelial surface antigen precursor (by homology to Candida gene CSA	-0.8586	-0.6458	-0.7506	-1.4772	-1.6194	-2.10
7968.2	orf19.2693	orf19.2693	CA3260 IPF7968 unknown function (possible URE2, prion)	-1.0931	-0.0373	-1.5003	-1.4620	-1.1828	-2.08
988.1	orf19.4599	PHO89	CA5160 PHO89 Na+-coupled phosphate transport (by homology)	-0.6506	-0.5353	-1.8573	-0.6897	-1.5228	-2.07
9616.1	orf19.4910	FGR41	CA2024 IPF9616 unknown function	-1.1774	-0.7775	-0.6630	-1.4713	-1.0808	-2.05
19548.1	orf19.3433	OYE23	CA4030 EBP4 NADPH dehydrogenase (by homology)	-1.5795	0.3052	-1.4467	-1.6879	-0.7604	-2.05
14417.2	orf19.2738	SUL2	CA2698 SUL1 High-affinity sulfate transport protein (by homology)	-1.1913	-0.1540	-1.0459	-1.2035	-1.4018	-2.00
9407.2	orf19.6151	orf19.6151	CA3408 IPF9407 similar to Saccharomyces cerevisiae Arc15p subunit of the ARP2/3 comp	-0.8079	-0.6055	-0.9435	-1.2479	-1.3682	-1.99
8773.2	orf19.3105	orf19.3105	CA4405 IPF8773 putative cytochrome P450 (by homology)	-1.2076	-0.1465	-1.1803	-1.3179	-1.1166	-1.99
8340.1	orf19.4099	ECM17	CA4320 ECM17 Putative sulfite reductase (by homology)	-1.0808	-0.6876	-0.9791	-1.1322	-1.0864	-1.99
2062.1	orf19.5271	orf19.5271	CA4979 IPF2062 unknown function	-1.0134	-0.3801	-1.2118	-1.0818	-1.2580	-1.98
15733.2	orf19.1442	PLB4.5	CA0186 PLB4.3f phospholipase, 3-prime end (by homology)	-0.9379	-0.3058	-0.9434	-1.2898	-1.4620	-1.98
19663.1	orf19.4747	HEM14	CA1951 HEM14 Mitochondrial protoporphyrinogen oxidase (by homology)	-1.2143	0.1252	-1.5969	-1.2277	-1.0058	-1.98
6041.2	orf19.4612	orf19.4612	CA5175 IPF6041 Similar to Legionella pneumophila sbpA	-0.9833	-0.2477	-0.8604	-1.2070	-1.6149	-1.98
14850.2	orf19.2452	orf19.2452	CA0046 IPF14850 Hypothetical protein (N/A)	-0.8923	-0.4813	-1.5033	-1.0940	-0.9375	-1.97
4104.2	orf19.2020	HGT6	CA1070 HXT61 sugar transporter	-0.8160	0.0129	-1.8943	-1.0000	-1.1456	-1.96

11819.2	orf19.4980	HSP70	CA1230 SSA4 cahsp70 mRNA for heat shock	-0.7191	-0.9700	-0.4566	-1.3078	-1.2857	-1.93
15957.2	orf19.1105.	PGA56	CA0171 IPF15957 unknown function	-0.9189	-0.4670	-2.0445	-0.6435	-0.6018	-1.91
5688.1	orf19.5818	SUR2	CA2225 SUR2 Hydroxylation of C-4 of the sphingoid moiety of ceramide by homology	-1.1446	-0.1662	-1.4410	-0.8466	-1.0087	-1.89
18418.1	orf19.5620	orf19.5620	CA2756 IPF18418 unknown function (YHR029C)	-0.6001	-0.3214	-1.9200	-1.0962	-0.6563	-1.89
753.1	orf19.5348	TPS3	CA5505 TPS3.3 alpha,alpha-trehalose-phosphate synthase, regulatory subunit, 3-prime en	-0.9507	-0.5115	-0.8655	-1.3523	-0.8997	-1.89
6166.2	orf19.1130	orf19.1130	CA0182 IFI1 unknown function	-1.0469	-0.2210	-1.6897	-0.9490	-0.6620	-1.88
1016.1	orf19.4584	PHO114	CA5147 PHO12 Acid phosphatase, secreted (by homology)	-0.6563	-1.5562	-0.9366	-0.7202	-0.6920	-1.88
10248.2	orf19.2947	SNZ1	CA4184 SNZ1 stationary phase protein by homology	-1.1198	-0.3864	-0.8903	-1.1079	-0.9947	-1.87
19729.1	orf19.406	ERG1	CA1353 ERG1 squalene epoxidase	-1.0239	-0.1004	-1.4291	-1.0948	-0.8404	-1.86
16784.2	orf19.5113	ADH2	CA3923 ADH2 alcohol dehydrogenase I (by homology)	-1.3828	-0.0062	-0.8047	-1.2723	-0.9884	-1.85
7076.2	orf19.2768	AMS1	CA4123 AMS1 alpha-mannosidase (by homology)	-0.3787	-0.8534	-1.0710	-0.9001	-1.1896	-1.84
19550.1	orf19.3641	CAN3	CA0884 CAN5 amino acid permease (by homology)	-0.8214	-0.3594	-1.2633	-0.9491	-0.9882	-1.84
14360.2	orf19.2706	CRH11	CA0375 CRH11 Probable membrane protein (by homology) glycosidase	-0.4782	-0.5929	-0.8612	-0.9720	-1.4668	-1.83
7141.1	orf19.1562	orf19.1562	CA3986 IPF7141 unknown function	-0.4164	-0.7375	-0.3862	-1.1382	-1.6730	-1.83
1543.1	orf19.946	MET14	CA5404 MET14 Adenylylsulfate kinase (by homology)	-1.0206	-0.1557	-1.2175	-0.8358	-1.0647	-1.81
3964.2	orf19.675	orf19.675	CA4111 IPF3964 unknown function	-1.1355	-0.5578	-0.4237	-1.3212	-0.8284	-1.81
2837.2	orf19.7297	orf19.7297	CA5536 IPF2837 putative cystathionine gamma-synthase (by homology)	-1.1297	0.1966	-1.5606	-0.8625	-0.8443	-1.79
20054.1	orf19.1407	orf19.1407	CA0262 IPF20054 unknown function	-1.0924	-0.0264	-0.9071	-1.1721	-0.9930	-1.79
			Int 4 IR control	-0.4523	-0.8181	-1.5733	-0.3352	-0.9990	-1.78
4553.2	orf19.909	STP4	CA2167 IPF4553 unknown function	-0.8730	-0.6620	-0.4208	-0.9159	-1.2969	-1.78
6156.1	orf19.1034	orf19.1034	CA1625 IPF6156 similar to C.elegans LIM homeobox protein	-1.3111	0.1070	-1.3474	-1.0291	-0.5628	-1.78
11104.2	orf19.2261	orf19.2261	CA3579 HSH49 spliceosome-associated essential protein [Candida albicans]	-0.8062	0.1245	-1.2658	-1.1604	-1.0294	-1.77
13723.2	orf19.260	orf19.260	CA0109 IPF13723 unknown function	-0.9856	-0.0395	-1.2311	-0.9602	-0.9187	-1.77
3506.2	orf19.6741	orf19.6741	CA5953 IPF3506 unknown function	-0.2951	-0.5995	-1.0174	-0.6304	-1.5735	-1.77
294.1	orf19.3278	GSY1	CA5467 GSY1 UDP glucose--starch glucosyltransferase, glycogen synthase (by homology	-1.2612	-0.0734	-1.2161	-0.9218	-0.6353	-1.77
10469.2	orf19.1789.	LYS1	CA0343 LYS1.5eoc saccharopine dehydrogenase, 5-prime end (by homology)	-1.0634	-0.0738	-1.0600	-0.9328	-0.9658	-1.76
7227.2	orf19.4048	DES1	CA2493 IPF7227 putative fatty acid desaturase (by homology)	-0.8837	-0.9957	-0.3691	-1.0805	-0.7618	-1.76
4905.2	orf19.411	orf19.411	CA0899 IPF4905 unknown function	-0.6851	-0.3015	-1.0790	-1.0345	-0.9628	-1.76
6629.2	orf19.2762	AHP1	CA4127 IPF6629 unknown function	-0.8160	-0.2142	-1.7563	-0.7859	-0.4779	-1.75
15301.2	orf19.3051	orf19.3051	CA5076 IPF15301 unknown function	-1.2076	0.1097	-1.2934	-0.6643	-0.9546	-1.74
4999.2	orf19.5843	orf19.5843	CA2874 IPF4999 unknown function	-0.3094	-0.5002	-1.0116	-0.5395	-1.6484	-1.74
7100.2	orf19.479	orf19.479	CA4526 MON1.3 unknown function, 3-prime end	-0.9324	-0.4344	-1.4699	-0.8468	-0.3076	-1.74
17289.2	orf19.6134	orf19.6134	CA3422 IPF17289 unknown function (YLR440C)	-0.2243	-0.3771	-1.2277	-0.7612	-1.3959	-1.74
19782.1	orf19.6135	orf19.6135	CA3421 IPF19782 unknown function (YDR356w?)	-0.4699	-0.3548	-0.6827	-1.0529	-1.4112	-1.73
3043.1	orf19.5019	orf19.5019	CA5244 IPF3043 unknown function	-0.3794	-0.6698	-1.0253	-0.8841	-1.0044	-1.73
17216.2			CA1194 MET222 protein ser/thr phosphatase (by homology)	-1.0354	0.0229	-1.0458	-0.9601	-0.9338	-1.73
6298.2	orf19.1964	orf19.1964	CA2947 IPF6298 unknown function (N/A)	-0.5864	-0.9914	-1.2828	-0.3401	-0.7250	-1.72
9116.2	orf19.6119	orf19.6119	CA2994 IPF9116 unknown function (N/A)	-0.8659	-0.8586	-0.4296	-0.8150	-0.9439	-1.72
13205.1	orf19.85	GPX2	CA0558 GPX2 glutathione peroxidase (by homology)	-0.6259	-0.1156	-1.5522	-0.5479	-1.0710	-1.72
5940.2	orf19.434	PRD1	CA4059 PRD1 Proteinase (by homology)	-0.8736	-0.4089	-0.9235	-0.8403	-0.8465	-1.72
5769.1	orf19.3967	PFK1	CA1834 PFK1 6-phosphofructokinase, alpha subunit	-0.9034	-0.3296	-1.0221	-0.8959	-0.7346	-1.71
8993.1	orf19.4631	ERG251	CA0875 ERG251 C-4 sterol methyl oxidase (by homology)	-0.6218	-0.5854	-1.5270	-0.7201	-0.4286	-1.71
14109.2	orf19.2451	PGA45	CA0380 IPF14109 unknown function (N/A)	-0.8211	-0.0514	-1.3959	-0.9630	-0.6394	-1.71
16189.2	orf19.5577	orf19.5577	CA0660 IPF16189.5f panthotenate kinase, 5-prime end (by homology) (YDR531W, CoA sy	-0.8472	-0.1538	-0.9475	-1.0787	-0.8376	-1.71
9474.2	orf19.3392	DOG1	CA0716 DOG2 2-deoxyglucose-6-phosphate phosphatase (by homology)	-0.5908	-0.9177	-0.3287	-0.9442	-1.0674	-1.70
6940.2	orf19.3811	orf19.3811	CA4843 GYP1 GTPase activating protein (by homology)	-0.6735	-0.2481	-1.4074	-0.8160	-0.6943	-1.70
15371.2	orf19.1002	orf19.1002	CA3517 IFA22 Unknown function	-0.6758	-0.7834	-1.3959	-0.5353	-0.4383	-1.70

15555.2	orf19.3150	GRE2	CA0671 GRP4 putative reductase (by homology). NADPH-dependent methylglyoxal reduct	-0.6602	-0.1071	-1.1928	-1.2144	-0.6459	-1.70
2397.2	orf19.6814	TDH3	CA5892 GAP1 Glyceraldehyde-3-phosphate dehydrogenase	-1.0425	-0.2714	-0.7948	-0.9987	-0.6975	-1.69
10499.2	orf19.244	orf19.244	CA0390 DCG1 involved in nitrogen-catabolite metabolism (by homology)	-0.9771	-0.1844	-1.5270	-0.6371	-0.4699	-1.69
15925.2	orf19.2988	orf19.2988	CA3437 IPF15925 unknown function	-1.1109	0.1519	-0.9351	-0.7418	-1.1234	-1.68
12039.2	orf19.3664	HSP31	CA4034 HSP31 heat shock protein (by homology)	-1.0559	-0.3827	-0.3219	-1.0469	-0.9296	-1.68
4065.1	orf19.1862	orf19.1862	CA0386 IPF4065 unknown function (YHR087w)	-1.1187	-0.1469	-1.0120	-0.9176	-0.5393	-1.68
12222.2	orf19.6304	LYS5	CA3270 LYS5 L-aminoadipate-semialdehyde dehydrogenase (by homology)	-0.4247	-0.5395	-1.4035	-0.6943	-0.6529	-1.67
1404.1	orf19.6065	orf19.6065	CA4926 IPF1404 unknown function	-0.5628	-0.0755	-1.4501	-0.7322	-0.8943	-1.67
17009.2	orf19.3651	PGK1	CA1691 PGK1 Phosphoglycerate kinase	-1.0478	-0.1567	-0.6577	-1.0251	-0.8212	-1.67
10916.2	orf19.4763	orf19.4763	CA2627 IPF10916 unknown function	-0.1976	-0.4150	-1.3040	-1.0174	-0.7661	-1.67
18761.1	orf19.4947	orf19.4947	CA1104 IPF18761 unknown function	-0.7298	-0.4055	-1.5228	-0.4364	-0.6038	-1.67
7456.1	orf19.2047	orf19.2047	CA3656 IPF7456 unknown function	-0.6621	-0.5274	-0.9501	-0.7569	-0.8005	-1.67
3919.2	orf19.6510	GRX1	CA4963 IPF3919 unknown function (YCL035c?)	-1.0616	-0.1336	-0.7735	-0.8767	-0.8097	-1.66
5668.1	orf19.4943	orf19.4943	CA3706 PSA2 mannose-1-phosphate guanyltransferase by homology	-0.7836	-0.1834	-0.9490	-1.0676	-0.6554	-1.66
4250.1	orf19.1628	LAP41	CA4007 LAP41 aminopeptidase yscl precursor (by homology)	-0.6809	-0.2448	-1.0813	-0.7430	-0.8841	-1.65
6860.1	orf19.1756	GPD1	CA2263 GPD1 Glycerol-3-phosphate dehydrogenase (by homology)	-0.7221	-0.1487	-1.3216	-0.5736	-0.8636	-1.65
19078.1			CA0252 SBP1.5eoc RNA binding protein-like, 5-prime end (by homology)	-0.8430	-0.4997	-0.9927	-0.9625	-0.3315	-1.65
12102.2	orf19.5634	FRP1	CA2556 FRE5 ferric reductase transmembrane component (by homology)	-1.0225	-0.6440	-0.3908	-0.5647	-0.9686	-1.65
19066.1	orf19.1433	orf19.1433	CA0273 IPF19066 unknown function	-0.7322	-0.0395	-1.2584	-0.7710	-0.7884	-1.64
5819.1	orf19.3822	SCS7	CA4852 SCS7 Required for hydroxylation of ceramide (by homology)	-1.0087	-0.1125	-1.0174	-0.8084	-0.6394	-1.64
4979.2	orf19.2525	orf19.2525	CA1737 LYS12 homo-isocitrate dehydrogenase (by homology)	-0.9259	-0.1286	-0.6309	-1.1445	-0.7410	-1.64
11888.1	orf19.5180	orf19.5180	CA4416 IPF11888 unknown function	-0.7234	-0.8488	-0.3481	-0.8985	-0.7238	-1.63
15425.2	orf19.2107.	STF2	CA2738 STF2 ATP synthase regulatory factor (by homology)	-1.1361	-0.0499	-0.4840	-1.0262	-0.8288	-1.63
813.1	orf19.5320	orf19.5320	CA5486 IPF813 unknown function	-0.8423	-0.3054	-0.6250	-0.8542	-0.8520	-1.62
11759.2			11759.2 IPF11759 unknown function	-0.6978	-0.3117	-1.1219	-0.5033	-0.8359	-1.62
17914.2	orf19.5124	orf19.5124	CA1760 IPF17914.3eoc unknown function	-0.7131	-1.0559	-0.9269	-0.2969	-0.4620	-1.61
4535.2	orf19.903	GPM1	CA4671 GPM1 phosphoglycerate mutase (by homology)	-0.9729	-0.2405	-0.7589	-0.8327	-0.6451	-1.61
17048.2	orf19.983	orf19.983	CA0121 IPF17048 unknown function	-0.6735	-0.5208	-0.7060	-0.3978	-1.1488	-1.61
1222.2	orf19.2060	SOD5	CA4836 IPF1222 Similar to superoxide dismutase (by homology)	-0.4286	-0.5332	-1.1392	-0.4880	-0.8391	-1.61
12359.2	orf19.5639	HIS4	CA2559 HIS4 Histidine biosynthesis trifunctional protein (phosphoribosyl-AMP cyclohydrola	-1.0931	-0.1405	-0.5728	-0.8330	-0.7799	-1.61
16014.2	orf19.2903	orf19.2903	CA3766 IPF18298.3 unknown function, 3-prime end	-0.6416	-0.4699	-1.4035	-0.5995	-0.2934	-1.60
7619.1			CA1571 SPO14.3eoc phospholipase D, 3-prime end	-0.9771	-0.2775	-0.5670	-0.7884	-0.7909	-1.60
2282.1	orf19.6659	GAP6	CA4265 GAP6 General amino acid permease (by homology)	-0.4892	-0.6441	-0.4290	-0.8037	-1.0308	-1.60
5949.2	orf19.6800	POS5	CA5906 IPF5949 unknown function (YPL188w, POS5, oxidative stress)	-0.5543	-0.1234	-0.7084	-0.8417	-1.1617	-1.60
14073.2	orf19.2990	XOG1	CA0822 EXG1 glucan 1,3-beta-glucosidase	-0.4941	-0.7298	-1.0087	-0.5995	-0.5228	-1.59
3082.1	orf19.7043.	ACB1	CA5225 ACB1.exon2 acyl-coenzyme-A-binding protein, exon 2 (by homology)	-0.7370	-0.3076	-1.0291	-0.7226	-0.5543	-1.59
2234.1	orf19.6898	orf19.6898	CA4579 IPF2234 unknown function	-0.2042	-1.0649	-0.6371	-0.6920	-0.7322	-1.59
2471.1	orf19.7437	orf19.7437	CA5728 IPF2471 maltose acetyltransferase	-0.6439	-0.4383	-0.2916	-1.0559	-0.8863	-1.58
77.2			CA6106 FAS2.53f fatty-acyl-CoA synthase, alpha chain, internal fragment	-0.6903	-0.8199	-0.2607	-0.9257	-0.6191	-1.58
15021.2	orf19.5615	AYR2	CA0163 AYR2 1-acyl dihydroxyacetone phosphate reductase (by homology)	-0.6439	-0.2159	-0.9490	-1.0439	-0.4560	-1.58
7759.1	orf19.3888	PGI1	CA3559 PGI1 Glucose-6-phosphate isomerase	-0.8030	-0.2733	-0.9450	-0.9002	-0.3780	-1.58
7144.2	orf19.1563	ECM3	CA3987 ECM3 Involved in cell wall biogenesis and architecture (by homology).	-0.6237	-0.3328	-0.7735	-0.7490	-0.8186	-1.58
14429.2	orf19.395	ENO1	CA3874 ENO1 Enolase I (2-phosphoglycerate dehydratase)	-0.3714	-0.9632	-0.4189	-1.0488	-0.4860	-1.58
7797.2	orf19.2618	MET2	CA0617 MET2 Homoserine O-acetyltransferase	-0.7793	-0.0886	-1.0399	-0.5867	-0.7664	-1.57
4026.2	orf19.2496	orf19.2496	CA3813 FRP1 member of the FRP family of proteins related to Yarrowia lipolytica glyoxylat	-0.5166	-0.2987	-1.1877	-0.7760	-0.4501	-1.56
9113.2	orf19.6121	MNL1	CA2995 IPF9113 unknown function (C-TERMINAL REGION HAS HOMOLOGY WITH THE	-0.4860	-0.3401	-0.7959	-0.7563	-0.8339	-1.56
18864.1	orf19.1950	orf19.1950	CA0820 IPF12138 unknown function	-0.4481	-1.2210	-0.5043	-0.2706	-0.7588	-1.56

11566.1	orf19.11	orf19.11	CA0650 IPF11566 unknown function	-0.6689	-0.3585	-1.0469	-0.5270	-0.5907	-1.56
9860.2	orf19.4436	orf19.4436	CA4649 GPX4 glutathione peroxidase (by homology)	-0.4901	-0.4461	-0.5187	-0.6529	-1.0740	-1.55
993.1	orf19.4595	orf19.4595	CA5157 IPF993 unknown function	-0.4383	-0.4679	-1.1456	-0.3902	-0.7370	-1.55
5228.1	orf19.7265	orf19.7265	CA5379 IPF5228.5 similar to Saccharomyces cerevisiae Sad1p snRNP assembly factor re	-0.6371	-0.4074	-0.5778	-0.7322	-0.8160	-1.55
2755.2	orf19.2601	HEM1	CA2266 HEM1 5-aminolevulinic acid synthase	-0.2845	-0.5458	-0.9546	-0.3696	-0.9971	-1.55
9273.2	orf19.3058	orf19.3058	CA5081 COQ6 monooxygenase (by homology)	-0.7588	-0.5084	-0.5023	-0.6371	-0.7370	-1.55
867.2	orf19.7221	SET3	CA5346 IPF867 unknown function	-0.7155	-0.6552	-0.0336	-0.8651	-0.8494	-1.54
8321.2	orf19.3325	orf19.3325	CA2938 IPF8321 similar to Saccharomyces cerevisiae Glg2p self-glucosylating initiator of	-0.8391	-0.2636	-0.2810	-0.9856	-0.7490	-1.54
1408.1	orf19.6064	orf19.6064	CA4925 IPF1408 unknown function	-0.9132	-0.4779	-0.9914	-0.5332	-0.2009	-1.54
2446.1	orf19.7427	orf19.7427	CA5722 IPF2446 unknown function	-0.4131	-0.8704	-0.5187	-0.2775	-1.0087	-1.53
15167.2	orf19.789	PYC2	CA1464 PYC2.exon2 Pyruvate carboxylase 2 (by homology)	-0.4516	-0.6897	-0.8700	-0.5922	-0.4831	-1.53
12982.2	orf19.5725	orf19.5725	CA2049 IPF12982 unknown function	-0.1156	-0.8943	-0.8704	-0.4699	-0.7298	-1.53
4286.2	orf19.542	HXK2	CA0127 HXK2.3f hexokinase II, 3-prime end (by homology)	-0.9743	-0.1345	-0.5670	-0.6259	-0.7588	-1.53
11503.1	orf19.3902	orf19.3902	CA3025 IPF11503 unknown function	-0.3659	-0.4325	-1.1584	-0.4800	-0.6215	-1.53
4988.1	orf19.2529	orf19.2529	CA1734 IPF4988 unknown function	-0.4981	-0.4845	-0.6030	-0.5147	-0.8802	-1.51
12603.1	orf19.3289	orf19.3289	CA0694 IPF12603 unknown function	-0.4854	-0.5940	-0.7517	-0.3415	-0.7762	-1.51
16625.2	orf19.3591	APE3	CA0871 APE3 aminopeptidase (by homology)	-0.6461	-0.4860	-0.5907	-0.4759	-0.7394	-1.50
407.1	orf19.7504	orf19.7504	CA5848 IPF407 unknown function (YGR161C)	-0.3004	-0.8314	-0.4170	-0.8730	-0.4901	-1.50
5398.1	orf19.5178	ERG5	CA4418 ERG5 C-22 sterol desaturase by homology	-0.5735	-0.0985	-0.6597	-0.7612	-0.8160	-1.50
2611.1	orf19.6690	orf19.6690	CA4293 IFA8 Unknown function	-0.3585	-0.5649	-0.7466	-0.5799	-0.6304	-1.49
4908.2	orf19.410.3	orf19.410.3	CA0054 RIB4.3 6,7-dimethyl-8-ribityllumazine synthase, 3-prime end (by homology)	-0.3834	-0.5343	-0.7572	-0.6145	-0.5802	-1.49
11171.2	orf19.3195	HIP1	CA0160 GAP7.5eoc general amino acid permease, 5-prime end	-0.5064	-0.3201	-0.7984	-0.4739	-0.7686	-1.49
19968.1	orf19.220	PIR1	CA3030 IPF19968 putative cell wall protein of the PIR family	-0.6552	-0.1697	-0.5821	-0.6104	-0.8135	-1.48
11096.2	orf19.4618	FBA1	CA5180 FBA1 fructose-bisphosphate aldolase (by homology)	-0.6724	-0.5328	-0.3072	-0.7889	-0.5209	-1.48
19962.1	orf19.4784	CRP1	CA2832 CRD1 Cu-transporting P1-type ATPase	-0.4952	-0.4393	-0.5503	-0.7541	-0.5699	-1.48
15015.2	orf19.5612	orf19.5612	CA0276 IPF15015 unknown function	-0.3921	-0.3456	-0.4699	-0.8034	-0.7784	-1.47
6247.1	orf19.1453	SPT5	CA4546 SPT5 Transcription elongation protein	-0.4739	-0.5187	-0.6484	-0.6148	-0.5332	-1.47
14432.2			14432.2 SAC6.3f Actin filament bundling protein, fimbrin, 3-prime end (by homology)	-0.4880	-0.3846	-0.9296	-0.4247	-0.5500	-1.47
12764.2	orf19.333	FCY2	CA0357 FCY22 purine-cytosine permease (by homology)	-0.3771	-0.9434	-0.4247	-0.3902	-0.5995	-1.46
7220.2	orf19.4044	orf19.4044	CA2490 MUM2 ubiquitin C-terminal hydrolase (by homology)	-0.5713	-0.4305	-0.9351	-0.4639	-0.3273	-1.46
7279.1	orf19.386	SAM4	CA3882 IPF7279 putative cobalamin-dependent homocysteine S-methyltransferase (by ho	-0.5479	-0.3978	-0.5374	-0.4580	-0.7686	-1.46
15083.2			CA1456 IPF11835.3eoc unknown function	-0.6371	-0.1520	-0.7155	-0.6082	-0.5778	-1.45
6129.2	orf19.5188	CHS1	CA1831 CHS1 Chitin synthase (by homology)	-0.3715	-0.3201	-0.7131	-0.6237	-0.6237	-1.44
982.1	orf19.4600.	orf19.4600.1	CA5162 IPF982 Weakly similar to human dolichol-phosphate-mannose synthase	-0.3401	-0.4901	-0.4921	-0.7466	-0.5735	-1.44
19048.1			CA0311 DAK2.3eoc dihydroxyacetone kinase, 3-prime end (by homology)	-0.5458	-0.3255	-0.5799	-0.7418	-0.4461	-1.44
4701.2	orf19.5280	MUP1	CA4972 MUP1 High affinity methionine permease (by homology)	-0.3129	-0.6689	-0.5735	-0.6689	-0.3383	-1.43
18207.1	orf19.489	DAP1	CA4516 IPF18207 unknown function	-0.5209	-0.5241	-0.5760	-0.4422	-0.4194	-1.41
8884.2	orf19.3422	FMP27	CA3756 IPF8884 unknown function (YLR454w, mitochondrial)	-0.3884	-0.5084	-0.4112	-0.4228	-0.7346	-1.41
14577.2	orf19.3642	SUN41	CA0883 SUN41 Putative cell wall beta-glucosidase (by homology)	-0.5186	-0.2611	-0.5942	-0.4682	-0.5968	-1.40
11221.1	orf19.5841	orf19.5841	CA3779 IPF11221 unknown function	-0.5437	-0.5002	-0.3921	-0.4383	-0.4982	-1.39
11432.2	orf19.6463	orf19.6463	CA3663 IPF11432 unknown function	0.3561	0.5271	0.4573	0.4071	0.4668	1.36
1231.2	orf19.2057	orf19.2057	CA4838 YTA12 Protease of the SEC18/CDC48/PAS1 family of ATPases (AAA) (by homolo	0.4351	0.6211	0.3730	0.4244	0.4854	1.38
13043.2	orf19.2408	orf19.2408	CA3051 IPF13043 unknown function	0.3311	0.5211	0.3618	0.5878	0.5984	1.39
8854.2	orf19.4900	orf19.4900	CA0854 IPF8854 similar to Saccharomyces cerevisiae Mnn1p alpha-1,3-mannosyltransfera	0.6425	0.5801	0.3550	0.3185	0.5079	1.40
6296.2	orf19.1966	orf19.1966	CA2946 IPF6296 putative methyltransferase (by homology)	0.4823	0.2678	0.6645	0.6173	0.4730	1.42
1663.1	orf19.6565	orf19.6565	CA4878 OXA1 Cytochrome oxidase biogenesis protein (by homology) (mitochondrion)	0.5200	0.3150	0.4179	0.7260	0.5341	1.42
13717.1	orf19.2167	orf19.2167	CA0712 IPF13717 unknown function	0.3334	0.7883	0.4709	0.4233	0.5079	1.42

6328.2	orf19.1114	orf19.1114	CA1807 IPF6328 unknown function	0.5607	0.5221	0.7181	0.2534	0.5089	1.43
7060.2	orf19.1065	SSA2	CA2857 SSA1 Heat shock protein of HSP70 family	0.3929	0.4740	0.8098	0.4688	0.4340	1.43
15870.2	orf19.2685	PGA54	CA2769 IPF15870 unknown function	0.4093	0.4060	0.4255	0.6681	0.6897	1.43
10568.1	orf19.1440	orf19.1440	CA0279 IPF10568 unknown function	0.8057	0.5714	0.5008	0.3730	0.3595	1.44
12555.2	orf19.1815	orf19.1815	CA0323 CDC95 translation initiation factor 6 (eIF6) (by homology)	0.6162	0.5324	0.2177	0.6310	0.6186	1.44
19815.1	orf19.7354	orf19.7354	CA5652 IPF19815 longevity-assurance protein (by homology)	0.4103	0.6079	0.6906	0.2774	0.6388	1.44
11315.2	orf19.512	orf19.512	CA4498 IPF11315 unknown function	0.5945	0.2881	0.6772	0.6636	0.4049	1.44
4568.1	orf19.6524	orf19.6524	CA4954 TOM40 mitochondrial import receptor chain TOM40 (by homology)	0.5110	0.6627	0.4620	0.7079	0.3097	1.44
447.1	orf19.7050	NOP15	CA5644 IPF447 unknown function	0.3138	0.4730	0.3896	0.7049	0.7732	1.44
15832.1	orf19.4676	orf19.4676	CA3247 IPF15832 unknown function (YKL053ca)	0.4792	0.7689	0.5509	0.4190	0.4372	1.44
15433.2	orf19.6544	LPI9	CA3110 LPI9 Microtubule-associated protein (by homology)	0.3437	0.5753	0.7874	0.4158	0.5801	1.45
3316.1	orf19.7393	orf19.7393	CA5692 UTR1 Associated with ferric reductase activity (by homology)	0.2630	0.6173	0.8131	0.5734	0.4478	1.46
11587.2	orf19.1403	orf19.1403	CA3175 IPF11587 unknown function	0.4158	0.6248	0.4947	0.6563	0.5271	1.46
7161.1	orf19.1199	NOP5	CA1438 NOP58 nucleolar protein required for pre-18S rRNA processing	0.3984	0.2798	0.7999	0.6627	0.5859	1.46
13458.2	orf19.6369	orf19.6369	CA3535 IPF13458 unknown function	0.6397	0.4552	0.8189	0.4287	0.3863	1.46
5426.1	orf19.6378	TRM9	CA3542 IPF5426 putative methyltransferase (by homology)	0.4125	0.4136	0.9426	0.5695	0.3918	1.46
4131.2	orf19.2039	orf19.2039	CA3648 MSF1 phenylalanine--tRNA ligase	0.5291	0.4926	0.6201	0.4823	0.6727	1.47
8359.2	orf19.326	orf19.326	CA3383 IPF8359 unknown function	0.4168	0.7774	0.4823	0.5695	0.5607	1.48
8826.2	orf19.397	orf19.397	CA3872 MRPL28 mitochondrial ribosomal protein of the large subunit (by homology)	0.3471	0.8172	0.7958	0.5646	0.2904	1.48
967.1	orf19.7551	ALO1	CA5962 ALO1 D-arabinono-1,4-lactone oxidase (by homology)	0.5519	0.6763	0.5351	0.4782	0.5878	1.48
7819.2	orf19.3130	orf19.3130	CA3563 IPF7819 unknown function	0.1903	0.5420	0.8131	0.5869	0.7216	1.49
17362.2	orf19.171	orf19.171	CA1416 DBP2.exon1 ATP-dependent RNA helicase of DEAD box family, exon 1 (by homol	0.4510	0.1699	0.6727	0.7493	0.8172	1.49
19924.1	orf19.4324	orf19.4324	CA1658 IPF19924 unknown function	0.3414	0.8156	0.6889	0.4103	0.6126	1.49
4973.1	orf19.2520	orf19.2520	CA0462 MRPS28 ribosomal protein (by homology)	0.3115	0.4730	0.9169	0.8400	0.3818	1.50
11681.2	orf19.1682	orf19.1682	CA0216 IPF11681 unknown function	0.4170	0.3956	0.8162	0.8207	0.4749	1.50
15042.2	orf19.501	orf19.501	CA4505 NOP2 nucleolar protein (by homology)	0.4158	0.7467	0.7137	0.7450	0.3138	1.50
14191.1	orf19.3358	LSC1	CA0791 LSC1 succinate-CoA ligase / synthetase (by homology)	0.6151	0.6029	0.7385	0.4952	0.4895	1.50
9204.1	orf19.3676	ABP140	CA4045 ABP140 putative methyltransferase (by homology) (YOR239W)	0.5221	0.1979	0.8270	0.9260	0.4844	1.51
5277.1	orf19.5660.	orf19.5660.1	CA4369 TIM11 subunit e of mitochondrial F1F0-ATPase by homology	0.3741	0.4222	0.6627	0.8172	0.6844	1.51
4764.2	orf19.2005	REG1	CA3938 IPF4764 unknown Function	0.6906	0.5120	0.8123	0.4916	0.4584	1.51
2587.2	orf19.5507	ENP1	CA2449 ENP1 Essential nuclear protein (by homology)	0.4271	0.4977	0.6661	0.7228	0.6643	1.51
19294.1	orf19.6469	orf19.6469	CA0070 IPF19295.3f unknown function, 3-prime end (YJL207c)	0.2104	0.6978	0.9723	0.4906	0.6135	1.51
6694.2	orf19.2461	PRN4	CA2895 IFS1 Unknown function	0.5440	0.5558	0.3334	0.7216	0.8408	1.51
17790.2	orf19.48	orf19.48	CA0030 IPF17790 unknown function	0.3531	0.5221	0.9186	0.7168	0.4919	1.52
13045.2	orf19.2407	DPS1-1	CA3052 DPS1 aspartyl-tRNA synthetase (by homology)	0.4626	0.7439	0.3366	0.8197	0.6459	1.52
5933.2	orf19.439	orf19.439	CA4062 IPF5933 similar to Saccharomyces cerevisiae Mhr1p involved in mitochondrial hor	0.4926	0.4730	1.0690	0.6572	0.3403	1.52
3366.1	orf19.4023	MRP2	CA4789 IPF3366 Mitochondrial ribosomal protein (by homology)	0.2314	0.3161	0.8528	0.7638	0.8813	1.53
2798.1	orf19.6766	orf19.6766	CA5935 IPF2798 unknown function	0.5519	0.3696	1.1532	0.3785	0.6201	1.53
1732.1	orf19.3089	orf19.3089	CA2009 IPF1732 intramitochondrial protein sorting (by homology)	0.5945	0.4319	0.7476	0.8098	0.4967	1.53
12457.2	orf19.2185	orf19.2185	CA1770 IPF12457 unknown function	0.3334	0.4906	0.9605	0.6088	0.6969	1.53
1948.1	orf19.7154	orf19.7154	CA5292 IPF1948 unknown function	0.5370	0.3818	0.9184	1.0086	0.2461	1.54
20133.1	orf19.585	orf19.585	CA3432 MRPL17 ribosomal protein of the large subunit (YmL30), mitochondrial (by homolo	0.5301	0.3412	0.7873	0.8450	0.5988	1.54
10399.1	orf19.3367	orf19.3367	CA1198 IPF10399 unknown function (Mitochondrial ribosomal protein of the large subunit)	0.5504	0.8354	0.3848	0.8093	0.5350	1.54
1826.2	orf19.5012	orf19.5012	CA5250 IPF1826 unknown function	0.4916	0.1609	0.8464	0.7816	0.8440	1.54
8966.2	orf19.494	orf19.494	CA4511 IPF8966 unknown function	0.5978	0.3797	0.5104	0.7999	0.8656	1.55
16428.2	orf19.1250	orf19.1250	CA1479 IPF16428 unknown function (YIL019w)	0.3482	0.7553	1.0236	0.5341	0.5008	1.55
10301.1	orf19.2275	orf19.2275	CA1876 IPF10301 putative 60S ribosomal protein L7/L12 homolog, mitochondrial precurso	0.2770	0.5803	0.7868	0.8961	0.6240	1.55

6796.2	orf19.5595	orf19.5595	CA2505 IPF6796 unknown function	0.3674	0.8546	1.0674	0.3863	0.5015	1.55
4283.2	orf19.543	orf19.543	CA4255 FUM11 fumarate hydratase (mitochondrial matrix)	0.6020	0.3067	0.8571	0.7458	0.6788	1.56
165.2			CA1490 IPF165 unknown function	0.3885	1.0496	0.4542	0.6313	0.6736	1.56
2093.2	orf19.4093	orf19.4093	CA4326 IPF2093 nuclear protein of unknown function (by homology)	0.4751	0.8065	0.8953	0.5675	0.4647	1.56
4421.2	orf19.2954	orf19.2954	CA4178 IPF4421 unknown function	0.5643	0.8997	0.6248	0.6702	0.4565	1.56
3618.2	orf19.6710	orf19.6710	CA4339 IPF3618 Unknown function	0.3975	0.7857	0.8017	0.6262	0.6047	1.56
3492.1	orf19.6752	orf19.6752	CA5945 IPF3492 unknown function (mitochondrial ribosome small subunit component)	0.3584	1.0510	0.8440	0.4179	0.5479	1.56
7377.1	orf19.3428	orf19.3428	CA3750 IPF7377 unknown function	0.3101	0.4167	0.7823	0.7341	0.9867	1.56
5196.2	orf19.3611	orf19.3611	CA1672 IPF5196 unknown function	0.5739	0.5329	0.3097	0.9608	0.8587	1.57
6943.1	orf19.3812	orf19.3812	CA4844 PDR13 Drug resistance	0.5974	0.6663	0.9811	0.6088	0.3973	1.57
13757.2	orf19.4479	orf19.4479	CA2414 IPF13756.3f unknown function, 3-prime end	0.6332	0.0342	0.8992	0.9561	0.7527	1.57
4703.2	orf19.5279	orf19.5279	CA4973 IPF4703 unknown Function (Mitochondrial ribosomal protein of the large subunit)	0.4060	0.8671	1.0963	0.5597	0.3829	1.58
10339.2	orf19.5077	orf19.5077	CA3896 IPF10339 unknown function	0.4466	1.0540	0.7177	0.6714	0.4510	1.59
13756.2	orf19.4479	orf19.4479	CA2413 IPF13756.5f unknown function, 5-prime end	0.5281	0.8400	0.1583	1.1712	0.6544	1.59
7091.1	orf19.484	orf19.484	CA4521 MRPL40 Putative mitochondrial ribosomal protein (by homology)	0.6827	0.6185	0.7795	0.7340	0.5871	1.60
2354.1	orf19.7019	YML6	CA5204 YML6 Ribosomal protein, mitochondrial (by homology)	0.5684	0.3151	0.7760	0.9763	0.8069	1.61
16279.2	orf19.5608	orf19.5608	CA2966 RPC34 DNA-directed RNA polymerase III (by homology) (YNR003C)	0.5311	0.8472	0.7502	0.7137	0.6012	1.61
4458.2	orf19.3527	CYT1	CA0864 CYT1 cytochrome-c1 (by homology)	0.6135	1.2666	0.7303	0.6489	0.2302	1.62
12940.2	orf19.4932	orf19.4932	CA3603 MEF1 mitochondrial translation elongation factor G (by homology)	0.7982	0.6519	0.4698	0.9630	0.6194	1.63
14407.1	orf19.3334	RPS21	CA1715 RPS21 ribosomal protein (by homology)	0.4865	1.2135	0.9906	0.3685	0.4699	1.63
8752.2	orf19.828	orf19.828	CA4226 IPF8752 similar to Saccharomyces cerevisiae Mrpl24p ribosomal protein of the lar	0.6100	0.3950	0.9160	0.9516	0.6816	1.64
16405.2	orf19.4751	orf19.4751	CA2213 IPF16405 similar to saccharomyces cerevisiae Rsm25p protein of the small subur	0.5898	0.4554	0.7829	0.9753	0.7647	1.64
16944.2	orf19.3287	orf19.3287	CA5474 IPF16944.3eoc unknown function, 3-prime end	0.2987	0.5361	1.0983	0.9176	0.7277	1.64
2343.1	orf19.7012	orf19.7012	CA5198 LPA4 Similar to ribosomal protein S16, mitochondrial (by homology)	0.6258	0.6743	0.9395	0.8323	0.5133	1.64
574.1	orf19.7654	CPR6	CA6040 CPR6 cyclophylin (by homology)	0.3618	0.8237	1.4109	0.6220	0.3807	1.65
12316.2	orf19.5069	orf19.5069	CA1098 IPF12316 unknown function	0.6617	-0.0087	0.7757	0.8544	1.3334	1.65
1453.2	orf19.6041	RPO41	CA4904 RPO41 Mitochondrial DNA-directed RNA polymerase (by homology)	0.7874	0.3196	0.9920	0.7198	0.8123	1.65
7643.1	orf19.863	orf19.863	CA1863 MRPL35 Ribosomal protein of the large subunit, mitochondrial (by homology)	0.5928	0.5696	0.9575	0.9237	0.5985	1.66
12526.2	orf19.1662	orf19.1662	CA3466 MRP1.5f mitochondrial ribosomal protein of the small subunit, 5-prime end (by hor	0.6883	0.9210	0.4226	0.9840	0.6636	1.67
7585.2	orf19.5201	orf19.5201	CA1768 IPF7585 unknown function (mitochondrial ribosome small subunit component)	0.7955	0.8693	0.7243	0.8366	0.4577	1.67
689.2	orf19.7591	orf19.7591	CA5991 IPF690.3f NADH dehydrogenase (ubiquinone) 78K chain precursor, 3-prime end (	0.8002	0.6364	0.6804	0.9167	0.6557	1.67
16368.2	orf19.255	ZCF1	CA0153 IPF16368.5f Unknown function, 5-prime end	0.8895	0.5818	0.4224	0.9634	0.8329	1.67
8454.2	orf19.6853	orf19.6853	CA4455 IPF8454 unknown function (N/A)	0.5068	0.9092	0.8424	0.7535	0.6893	1.67
12601.1	orf19.3290	orf19.3290	CA0695 IPF12601 unknown function	0.4720	1.2738	0.6690	0.7545	0.5410	1.67
2736.2	orf19.2575	orf19.2575	CA2684 IFU3 Unknown function	0.5993	0.8416	0.6763	0.8821	0.7119	1.67
8527.1	orf19.5305	RHD3	CA5476 IPF8527 unknown function	0.5960	0.2608	1.0317	1.0608	0.7672	1.67
17994.1			CA3660 IPF17794 unknown function	0.1806	0.8173	1.1858	0.6419	0.8933	1.67
1439.1	orf19.6047	TUF1	CA4909 TUF1 Translation elongation factor TU (by homology)	0.5781	1.0071	1.0610	0.6961	0.3791	1.68
5924.2	orf19.445	orf19.445	CA4067 IPF5924 unknown function	0.5656	0.2951	1.1590	0.8090	0.8930	1.68
14119.1	orf19.4688	DAG7	CA0689 IPF14119 unknown function	0.5553	0.7634	0.5068	1.0481	0.8689	1.68
16479.2	orf19.2319	orf19.2319	CA0098 IPF16479 unknown function	0.6535	0.3785	1.3068	0.7233	0.6942	1.68
9631.1	orf19.1575	PRS1	CA3168 PRS3 ribose-phosphate pyrophosphokinase (YHL011C)	0.5018	1.3167	0.6790	0.7040	0.5588	1.68
9177.2	orf19.3733	IDP2	CA0643 IDP2 isocitrate dehydrogenase, cytosolic (by homology)	0.1840	0.5792	1.0793	0.9672	0.9546	1.69
16752.2	orf19.2711	orf19.2711	CA1291 IPF16752 unknown function	0.7010	0.3809	0.9956	0.8885	0.8341	1.69
5965.1	orf19.6794	FESUR1	CA5911 IPF5965 NADH-ubiquinone oxidoreductase (by homology)	0.7577	1.1380	0.1968	1.0271	0.6908	1.70
19594.1	orf19.169	CHO2	CA1414 CHO2 phosphatidylethanolamine N-methyltransferase (by homology) mitochondri	0.6873	0.8882	0.5568	0.9066	0.7771	1.70
17991.2	orf19.6465	orf19.6465	CA3661 IPF17991 unknown function	0.9575	1.2875	0.0201	0.7163	0.8464	1.70

16126.1	orf19.172	orf19.172	CA1417 IPF16126 similar to Saccharomyces cerevisiae Rpc19p DNA-directed RNA polym	0.4926	0.8679	0.3595	1.1097	1.0072	1.70
3331.1	orf19.7386	orf19.7386	CA5684 IPF3331 unknown function (assembly of mitochondrial respiratory complexes)	0.8599	0.6638	0.3174	1.1776	0.8215	1.70
3358.2	orf19.4016	orf19.4016	CA4783 IPF3358 ubiquinol-cytochrome-c reductase (by homology)	0.7177	0.7351	0.8922	0.9343	0.5749	1.71
4276.2	orf19.549	orf19.549	CA4260 IPF4276 similar to Saccharomyces cerevisiae Mrpl32p putative mitochondrial ribo	0.4287	1.5729	0.5351	0.6003	0.7216	1.71
12231.1	orf19.3507	MCR1	CA2457 MCR1 NADH-cytochrome-b5 reductase (by homology)	0.5551	1.3567	0.3352	0.9053	0.7141	1.71
6938.2	orf19.3810	orf19.3810	CA4842 MTD1 methylenetetrahydrofolate dehydrogenase	0.3230	1.1284	1.0024	0.7702	0.6744	1.72
3986.2	orf19.665	NEP1	CA4099 IPF3986 unknown function	0.4610	0.6672	0.5705	1.0813	1.1252	1.72
4045.1	orf19.1872	orf19.1872	CA4490 IPF4045 unknown function	0.5245	1.5075	0.5952	0.7586	0.5226	1.72
7724.2	orf19.429	orf19.429	CA4054 TRF4 Topoisomerase I-related protein	0.6360	0.5089	1.2308	0.5859	0.9568	1.72
4899.1	orf19.414	orf19.414	CA2129 IPF4899 unknown function	0.5821	0.0718	1.4212	0.7111	1.1362	1.72
3267.2	orf19.3138	NOP1	CA3570 NOP1 Fibrillarin	0.9635	0.9953	0.6870	0.8523	0.4254	1.72
1398.2	orf19.6070	ENA2	CA4929 ENA22 P-type ATPase involved in Na+ efflux (by homology)	0.7184	0.7211	0.4854	1.0016	1.0282	1.73
14089.2	orf19.2781	orf19.2781	CA0206 IPF14089 putative serine/threonine protein kinase	0.3663	0.6933	1.4854	0.4584	0.9686	1.73
3225.1	orf19.3579	ATP4	CA3479 ATP4 F1F0-ATPase complex, F0 subunit B (by homology)	0.4662	1.1938	0.5878	0.9996	0.7342	1.74
17763.2	orf19.6139	FRE7	CA3416 FRE30.3 Strong similarity to ferric reductase Fre2p, 3-prime end (by homology)	1.0524	1.0936	0.0566	0.9546	0.8711	1.75
19809.1	orf19.7161	SUI3	CA5298 SUI3 Translation initiation factor eIF2 beta subunit (by homology)	0.3641	0.9927	1.4102	0.7021	0.5671	1.75
7981.1	orf19.706	NMD3	CA1706 NMD3 RNA binding (by homology)	0.9910	1.4112	0.5466	0.6402	0.4779	1.76
3435.1	orf19.6178	FBP1	CA3199 FBP1 Fructose-1,6-bisphosphatase	0.5601	0.9722	0.9613	0.9566	0.6245	1.76
9203.2	orf19.3675	GAL7	CA4044 GAL7 UDP-glucose-hexose-1-phosphate uridylyltransferase (by homology)	1.0439	0.3757	0.6093	1.2396	0.8460	1.77
15781.2	orf19.716	orf19.716	CA1238 IPF15781 unknown function	0.6351	1.0724	0.3173	0.4136	1.6776	1.77
5890.2	orf19.6938	orf19.6938	CA4708 MEU1 regulator of ADH2 expression (by homology)	0.5270	0.6763	0.2912	1.3520	1.2726	1.77
4616.2	orf19.6090	orf19.6090	CA3862 NSR1 nuclear localization sequence binding protein (by homology)	0.6514	1.3805	1.3082	0.4859	0.3252	1.78
3698.1	orf19.3022	orf19.3022	CA5056 IPF3698 similar to Saccharomyces cerevisiae Rsm24p mitochondrial ribosomal pr	0.4833	1.3221	0.9943	0.7003	0.6816	1.79
20149.1	orf19.4396	orf19.4396	CA3906 IPF20149 unknown function	0.6667	1.5809	0.0857	0.9692	0.9389	1.80
6450.2	orf19.1896	SSC1	CA4474 SSC1 Mitochondrial heat shock protein 70-related protein (by homology)	0.9217	0.7005	0.7088	1.1436	0.7765	1.80
7589.1	orf19.5198	NOP4	CA1766 NOP4 Nucleolar protein	0.6461	0.6580	1.3565	0.9822	0.6210	1.81
16978.2	orf19.685	YHM1	CA1980 YHM1 member of the mitochondrial carrier family (MCF) (by homology)	0.6477	1.3096	0.3988	0.9225	0.9970	1.81
3751.2	orf19.558	orf19.558	CA0929 GUT1 Glycerol kinase (by homology)	0.3994	0.6853	1.3351	0.8456	1.0129	1.81
19778.1	orf19.6165	KGD1	CA3149 KGD1 2-oxoglutarate dehydrogenase	0.6215	1.3273	0.5252	1.1140	0.6915	1.81
5411.2	orf19.5170	ENA21	CA4425 ENA21.3 P-type ATPase, 3-prime end (by homology)	0.9359	1.1152	0.3207	1.2488	0.6910	1.82
1114.1	orf19.5419	ATP5	CA5775 ATP5 F1F0-ATPase complex, OSCP subunit (by homology)	0.3811	1.5332	0.5235	1.0046	0.8861	1.82
1413.1	orf19.6062.	orf19.6062.3	CA4923 IPF1413.3 unknown function, 3-prime end	0.0998	1.0834	1.1093	1.1619	0.8774	1.82
4000.2	orf19.661	KRR1	CA4096 KRR1 involved in cell division and spore germination	0.7149	1.2223	0.2360	1.1904	0.9723	1.82
1544.1	orf19.947	orf19.947	CA5405 MRP17 Mitochondrial ribosomal protein (by homology)	0.9023	0.0072	1.4255	0.8098	1.2320	1.83
3709.1	orf19.3015	orf19.3015	CA5051 IPF3709 unknown function (YDR101C)	0.9664	0.8223	0.8054	1.1210	0.6884	1.84
17996.2			CA2240 CRD2 Cu-binding metallothionein (doesn't exist in CBD)	1.7617	0.3951	0.3323	1.0800	0.8440	1.84
3182.1	orf19.3559	orf19.3559	CA0580 IPF3184.exon2 unknown function, exon 2 (doesn't exist in CDB)	0.5069	1.0133	0.9402	1.0621	0.8924	1.84
19747.1	orf19.2270	SMF12	CA1879 SMF12 manganese transporter (by homology)	0.8460	1.5841	0.3646	1.1258	0.5131	1.85
8460.2	orf19.6854	ATP1	CA4457 ATP1.exon3 F1F0-ATPase complex, F1 alpha subunit, exon 3	0.7327	1.4051	0.5972	1.1037	0.6566	1.86
1749.1	orf19.3097	PDA1	CA4412 PDA1 Pyruvate dehydrogenase alpha chain (by homology)	0.6434	1.2516	1.2500	0.8781	0.5005	1.87
7638.2	orf19.1172	PHO84	CA1782 PHO84.3eoc Inorganic phosphate transport protein, 3-prime end (by homology)	0.7707	0.4957	0.9282	1.1150	1.2175	1.87
20032.1	orf19.6828	orf19.6828	CA5882 RRP1 Involved in processing rRNA precursor species to mature rRNAs (by homol	0.9252	0.9283	0.7270	1.1181	0.8780	1.89
3640.2	orf19.6724	orf19.6724	CA4349 FUM12.5f Fumarate hydratase, 5-prime end (by homology)	1.1174	-0.2161	1.1220	1.3287	1.2919	1.90
7487.2	orf19.4679	AGP2	CA3244 AGP2 amino-acid permease (by homology)	0.5943	0.6627	1.2049	0.7395	1.4439	1.90
5438.2	orf19.655	orf19.655	CA0083 PHO84 high-affinity inorganic phosphate/H+ symporter by homology	1.3807	-0.2509	0.9273	1.1483	1.4460	1.91
1859.1	orf19.5893	RIP1	CA6149 RIP1 Ubiquinol cytochrome-c reductase (by homology)	0.6685	1.1354	0.8997	1.1288	0.8225	1.91
2914.1	orf19.4311	YNK1	CA2645 YNK1 Nucleoside diphosphate kinase (by homology)	1.1252	0.9071	0.1902	1.3820	1.0983	1.92

1302.2	orf19.7384	orf19.7384	CA5682 NOG1 Nucleolar G-protein (by homology)	1.0249	0.6438	1.4488	0.9201	0.6795	1.92
11475.1	orf19.4826	IDH1	CA4753 IDH1.3 isocitrate dehydrogenase (NAD+) subunit1, mitochondrial, 3-prime end (by	0.8122	1.3119	1.1491	0.9349	0.5399	1.93
14556.2	orf19.5126	orf19.5126	CA1758 IPF14559.3f unknown function, 3-prime end	0.6904	0.7162	1.4968	0.9634	0.9065	1.94
15259.2	orf19.2214	orf19.2214	CA2377 MRPL7 Ribosomal protein of the large subunit, mitochondrial (by homology)	0.7381	1.3883	0.7470	1.2047	0.7132	1.94
7270.1	orf19.2785	ATP7	CA1907 ATP7 F1F0-ATPase complex, FO D subunit (by homology)	0.7178	1.8489	-0.0904	1.2679	1.0798	1.95
5446.1	orf19.5698	orf19.5698	CA2613 IPF5446 putative ribosomal protein (by homology) (Mitochondrial ribosomal protei	0.7307	0.8725	1.7592	0.8144	0.7055	1.97
9955.1	orf19.3499	orf19.3499	CA2452 IPF9955 unknown function	0.2154	0.3840	1.1878	1.7655	1.3465	1.97
15646.2	orf19.3481	orf19.3481	CA2898 IPF15646 putative ATP-dependent RNA helicase (by homology) (mitochondrial DE	0.6873	1.5675	0.8518	1.0659	0.8578	2.01
3641.2	orf19.6725	FUM12	CA4351 FUM12.3f Fumarate hydratase, 3-prime end (by homology)	1.1419	0.3999	1.4811	0.4445	1.5647	2.01
3184.1	orf19.3559	orf19.3559	CA0579 IPF3184.exon1 unknown function, exon 1 (Mitochondrial ribosomal protein of the s	0.9336	1.4963	0.5702	0.9855	1.0488	2.01
1529.1	orf19.339	NDE1	CA4633 NDH1 Mitochondrial NADH dehydrogenase	1.2607	1.0271	0.8330	1.2224	0.8921	2.07
11150.2	orf19.2896	SOU1	CA3771 SOU1 Sorbitol utilization protein Sou1p [Candida albicans]	0.5695	0.2963	1.4844	0.9753	1.9605	2.08
8621.2	orf19.3707	YHB1	CA0943 YHB1 flavohemoglobin (by homology)	1.1720	1.5084	0.3189	1.5697	0.7653	2.09
6978.2	orf19.2644	QCR2	CA2065 QCR2 Ubiquinol--cytochrome-c reductase 40KD chain II (by homology)	0.5264	1.8713	0.4773	1.4462	1.0359	2.10
1164.2	orf19.2091	orf19.2091	CA4810 IPF1164 Subunit NUHM of NADH:Ubiquinone Oxidoreductase (by homology)	0.8989	1.1216	1.2369	1.1443	1.0133	2.12
14895.1	orf19.93	orf19.93	CA1987 IPF14895 unknown function (YMR002W)	0.9033	1.7774	1.0339	1.2842	0.7373	2.21
6415.2			CA1294 MSH5.3f Meiosis-specific protein, 3-prime end (by homology)	0.5231	2.9633	0.9054	0.2845	1.0731	2.22
15977.2	orf19.4698	orf19.4698	CA0641 IPF15977 unknown function	1.3346	1.6508	0.5537	1.5179	0.7589	2.24
3299.1	orf19.4393	CIT1	CA3909 CIT1.exon2 Citrate synthase, exon 2	1.4150	0.7280	1.2348	1.3561	1.1672	2.27
5264.1	orf19.5653	ATP2	CA4362 ATP2 F1F0-ATPase complex, F1 beta subunit (by homology)	1.2299	1.2050	1.1769	1.4266	0.9350	2.29
6536.2	orf19.930	PET9	CA5388 PET9 ADP/ATP carrier protein (by homology)	1.7097	0.6511	1.1107	1.7615	1.5147	2.55
6833.2	orf19.5791	IDH2	CA4148 IDH2 Isocitrate dehydrogenase (NAD+) subunit 2, mitochondrial (by homology)	1.1071	1.8698	1.0408	1.8261	1.4552	2.75
385.1	orf19.7514	PCK1	CA5857 PCK1 phosphoenolpyruvate carboxykinase	2.1604	2.0354	1.4239	2.2090	1.6828	3.74
12652.2	orf19.6385	ACO1	CA3546 ACO1 aconitate hydratase (by homology)	1.8993	1.7618	2.9509	2.1687	1.7495	4.31

a from http://www.candidagenome.org/

[b] from http://genolist.pasteur.fr/CandidaDB/