

Probe set	Gene	A-WT	B-upf1	C-nmd2	D-upf3
10011_at	YLR296W	1	1.7182466	1.7690812	1.2517805
10013_at	YLR298C	1	0.6949604	0.9564731	0.7767751
10021_at	YLR306W	1	3.4747696	3.3783605	4.020038
10027_at	YLR312C	1	1.0098077	1	1
10030_at	YLR315W	1	2.9598076	2.8740385	2.6971154
10036_at	YLR278C	1	0.8773994	0.9272437	1.0063312
10038_i_at	YLR280C	1	1.3881032	1.4461915	1.5323387
10039_s_at	YLR280C	1	0.9140396	1	1
10040_at	YLR281C	1	1.1142308	1.2751923	1
10042_at	YLR283W	1	1.8955808	1.7746463	1.4101181
10043_at	YLR284C	1	3.0909176	2.9050698	2.9960847
10048_at	YLR288C	1	3.849172	3.525041	4.008644
10056_at	YLR254C	1	1.3945137	1.2078702	1.1874043
10060_at	YLR258W	1	2.0883148	2.477825	2.4437344
10067_at	YLR263W	1	4.1870174	5.1778746	4.475827
10070_at	YLR265C	1	1.9489914	1.8298446	1.9127101
10071_at	YLR266C	1	3.0995054	3.6019828	3.7878141
10076_at	YLR271W	1	3.1016388	1.7461123	2.31985
10078_at	YLR273C	1	3.0899389	3.965501	3.7221522
10080_at	YLR233C	1	14.028461	10.4675	14.037308
10085_at	YLR237W	1	0.96264917	1.1757209	1.5019338
10090_at	YLR242C	1	2.4273841	3.0967903	2.71031
10091_at	YLR243W	1	0.84966105	1.0720032	1.2175684
10093_at	YLR245C	1	2.0233545	2.5824237	2.0893917
10094_at	YLR246W	1	1.1335149	1.5991523	1.4039588
10095_at	YLR247C	1	2.7173178	4.889016	4.652807
10099_at	YLR251W	1	7.8498735	13.699138	11.344681
10100_at	YLR252W	1	3.701492	4.091672	3.6669614
10103_at	YLR211C	1	1.9318938	2.4733331	2.576734
10106_at	YLR214W	1	0.63715297	0.6563263	0.7977251
10107_at	YLR215C	1	0.87665814	1.239793	1.0635945
10108_at	YLR216C	1	0.9634629	0.9145774	0.9445366
10110_at	YLR218C	1	0.66466624	0.47208065	0.50705963
10113_at	YLR221C	1	1.0156727	1.2381266	1.3113165
10116_at	YLR224W	1	2.0390277	2.1823678	1.8821108
10117_at	YLR225C	1	0.8752488	0.91965353	0.81362456
10118_at	YLR226W	1	1.4973574	2.0764828	1.9401938
10119_at	YLR227C	1	10.619907	9.843441	9.907245
10120_at	YLR228C	1	1.8031695	1.4363186	1.6006655
10124_at	YLR189C	1	1.8371093	2.1562085	2.1774428
10136_at	YLR201C	1	1.0250725	1.1007714	1.1204518
10143_at	YLR205C	1	0.8134514	0.45069835	0.38927096
10153_at	YLR173W	1	2.3897288	2.4796154	2.8640385
10154_at	YLR174W	1	5.7432013	9.640562	8.929142
10156_at	YLR176C	1	0.6656885	0.7235067	0.70671475
10157_at	YLR177W	1	1.6670504	1.4888055	1.6676773
10158_at	YLR178C	1	1.2313347	1.1603024	1.2027175
10171_at	YLR141W	1	1.0905626	1.3033128	1.1954892
10172_at	YLR142W	1	1.2978287	1.4060712	1.4508617
10174_at	YLR144C	1	1.8880973	2.079173	2.1305878

10175_at	YLR145W	1	1.2561343	1.1185724	1.3204285
10179_at	YLR149C	1	1.9788811	2.2585433	2.020979
10181_at	YLR151C	1	1.0720345	1.0311892	1.3066337
10182_at	YLR152C	1	2.581882	3.1371717	2.9617252
10186_s_at	YLR156W	1	5.6739197	5.4904056	5.0036097
10189_at	YLR164W	1	5.0978045	6.0567307	6.133846
10190_at	YLR165C	1	7.0916924	6.9702992	6.999025
10191_at	YLR166C	1	1.485278	1.6589313	1.5130819
10195_at	YLR122C	1	8.382884	7.259038	7.223077
10196_g_at	YLR122C	1	5.0781627	3.2532587	3.3234973
10197_at	YLR123C	1	3.4253848	2.9115384	2.6551924
10199_at	YLR125W	1	3.4234617	2.4673076	2.3892307
10202_at	YLR128W	1	3.1011958	1.539501	1.8347704
10204_at	YLR130C	1	2.2652247	2.3815973	2.5353768
10206_at	YLR132C	1	1.2557584	1.2877612	1.7747412
10209_at	YLR135W	1	1.2486795	1.6682284	1.6130555
10210_at	YLR136C	1	1	1	1
10211_at	YLR137W	1	2.045631	1.9264592	1.9857965
10216_at	YLR097C	1	4.0113535	4.6847835	5.0020866
10217_at	YLR098C	1	7.1308084	6.855105	8.473588
10221_at	YLR102C	1	1.5107315	1.207011	1.4482872
10224_at	YLR105C	1	1.8093534	1.6706431	1.9877123
10225_at	YLR106C	1	0.9937446	1.6030476	1.5951147
10226_at	YLR107W	1	1.6134284	1.0362582	0.9125921
10234_at	YLR115W	1	1.4366989	1.7178211	1.7583169
10244_at	YLR080W	1	1.352776	1.1281563	1.4458888
10249_at	YLR085C	1	2.4553661	2.301504	2.6143398
10254_at	YLR090W	1	1.4043478	1.2525108	1.319314
10257_at	YLR093C	1	1.2180737	1.3877664	1.0945399
10258_at	YLR094C	1	0.80632836	0.47219813	0.7791483
10263_at	YLR054C	1	2.3504815	2.622951	3.1807418
10266_at	YLR057W	1	0.9856813	1.1329354	1.1064637
10272_at	YLR063W	1	1.2590017	1.2303538	1.1135509
10277_at	YLR068W	1	0.9442519	1.3210723	1.4313905
10281_at	YLR072W	1	1.0237014	0.891265	0.9993953
10282_at	YLR073C	1	1.0616584	1.1485479	1.1116261
10283_at	YLR031W	1	4.4435315	4.1067224	4.4363456
10284_at	YLR032W	1	1.75443	1.3249671	1.380283
10285_at	YLR033W	1	1.2042072	1.1980402	1.5284401
10287_at	YLR035C	1	2.056465	2.250622	2.4778361
10288_at	YLR036C	1	2.425364	2.580283	2.566417
10289_f_at	YLR037C	1	4.609707	3.6424668	3.33599
10292_at	YLR040C	1	0.77600986	0.91903114	0.84025574
10298_at	YLR046C	1	5.289423	4.8398075	5.0175
10304_at	YLR050C	1	0.8812865	0.9346738	1.0104246
10306_at	YLR010C	1	9.395966	8.941154	9.718846
10307_at	YLR011W	1	2.2670193	2.7325706	3.147575
10310_at	YLR014C	1	1.5502893	1.6978319	2.1794114
10311_at	YLR015W	1	1.1270849	1.2682683	1.3383577
10312_at	YLR016C	1	4.640505	4.1480007	4.9764023
10317_at	YLR021W	1	1.8787189	1.6227767	1.7375375

10322_at	YLR026C	1	0.7641407	0.87630117	0.8661359
10334_at	YLL009C	1	0.56562155	0.50211763	0.45380962
10339_at	YLL004W	1	1.9487766	2.7628193	2.8332503
10340_at	YLL003W	1	2.2611027	2.0618184	2.3381178
10344_at	YLR002C	1	0.7919896	0.6798427	0.8185446
10345_at	YLR003C	1	0.8890306	0.924471	0.96824443
10346_at	YLR004C	1	2.374493	2.6070786	2.5877407
10349_at	YLR007W	1	1.4815425	1.7443238	1.6464221
10351_at	YLL035W	1	1.3660808	0.90929496	0.9688161
10353_at	YLL033W	1	3.0955355	2.937444	2.6000028
10357_at	YLL029W	1	0.87618816	0.9099351	0.92865074
10359_at	YLL027W	1	1.0251971	1.0192083	1.2107204
10360_at	YLL026W	1	0.82669175	0.99283504	0.9328143
10361_f_at	YLL025W	1	6.6541357	3.82741	5.8894534
10368_s_at	YLL020C	1	1.02577	1.1874092	1.1946061
10369_at	YLL019C	1	1.5156544	1.8812201	1.9665211
10372_at	YLL016W	1	3.095	3.6486537	3.4849997
10373_at	YLL057C	1	7.761154	7.956731	8.771731
10374_at	YLL056C	1	6.6338806	7.7562385	7.9377003
10375_at	YLL055W	1	4.5397406	7.237727	6.288057
10377_at	YLL053C	1	3.3332067	3.7974637	4.8542714
10378_at	YLL052C	1	4.102997	6.147501	6.4605417
10379_at	YLL051C	1	2.7533374	3.1880684	3.2026327
10389_at	YLL042C	1	2.5954702	2.5427916	2.557622
10393_at	YLL038C	1	2.0978808	2.9437797	3.06331
10396_at	NKR006C	1	3.5056896	2.8525734	2.711526
10404_at	NKR002C	1	1.7039502	2.9436617	2.422606
10405_at	NKR003W	1	14.736773	16.3676	14.544903
10408_at	SNR38	1	0.6301057	0.71091706	0.71693254
10409_at	SNR69	1	0.8831816	0.36296716	0.33437532
10411_f_at	YLL065W	1	2.9824655	2.2260795	2.2937894
10412_f_at	YLL064C	1	9.917419	10.280634	11.803933
10413_at	YLL063C	1	12.151535	9.033206	10.211161
10416_at	YLL060C	1	5.4971795	5.764335	6.664872
10418_at	YLL058W	1	2.0773523	2.5828269	3.0975754
10421_at	NKR013C	1	0.8594227	0.84986985	0.84283656
10432_at	NKL034C	1	11.742768	11.882126	12.959112
10433_at	NKL033C	1	9.995384	6.4509616	6.5878844
10434_at	NKL031C	1	2.8312244	2.943737	2.835708
10437_at	NKL011C	1	22.258654	26.171997	24.269272
10439_at	NKL008W	1	0.8783643	1.2617292	1.0270908
10443_at	YKL162C-A	1	1	1	1
10445_s_at	YKL201C	1	2.2976985	3.3001244	3.0298195
10446_s_at	YKL199C	1	1.899468	2.0269604	2.0542412
10447_s_at	YKL198C	1	2.9187508	3.3911796	3.3699627
10450_at	NKL038W	1	1.6407031	2.1211793	2.0180414
10451_at	NKL028W	1	5.5768924	5.752281	6.064449
10455_at	NKL044C	1	3.0573077	3.0732694	3.0996156
10461_at	NKL019C	1	1.2206153	1.6435275	1.3423892
10462_at	NKL014W	1	1.2124004	1.626125	1.3873684
10466_at	YKR087C	1	1.8969988	2.197755	2.054356

10470_at	YKR091W	1	2.8437886	2.4308562	2.6470828
10478_at	YKR097W	1	6.0199633	6.1802864	6.4093304
10479_at	YKR098C	1	2.1462357	1.341769	1.4556985
10481_at	YKR100C	1	0.93519855	1.1479267	1.1176131
10483_at	YKR102W	1	5.3765645	5.4846454	6.1158123
10484_at	YKR103W	1	2.4791873	2.0716763	2.3591874
10485_at	YKR104W	1	8.008507	6.9844813	8.013485
10489_at	YKR064W	1	1.7575299	1.4877871	1.3015937
10494_at	YKR069W	1	3.4245448	3.5417268	3.7155044
10500_at	YKR075C	1	1.1339332	1.2589905	1.1646951
10505_at	YKR080W	1	1.2570419	1.3523633	1.5622588
10510_at	YKR038C	1	1.5087904	1.5154846	1.7913302
10517_at	YKR045C	1	0.671561	0.51696837	0.6607435
10521_at	YKR049C	1	0.96371686	0.7617161	0.88623893
10522_at	YKR050W	1	2.2144437	2.722305	2.8057938
10524_at	YKR052C	1	1.7209475	2.520152	2.6276462
10525_at	YKR053C	1	1.4113032	1.390826	1.5172468
10530_at	YKR058W	1	1.5175898	1.9214512	1.8451031
10532_at	YKR061W	1	8.651375	11.869127	11.314667
10536_at	YKR019C	1	2.1622908	2.0506303	2.5874033
10539_at	YKR022C	1	3.0016994	2.04564	1.9044693
10544_at	YKR027W	1	1.9221103	2.3019476	2.3641481
10547_at	YKR030W	1	1.3754189	1.3042061	1.394534
10553_at	YKR036C	1	1.7511573	1.8533006	1.9474355
10559_at	YKL005C	1	2.4172754	2.8696566	2.6365166
10567_at	YKR004C	1	2.9955559	4.3190494	4.466515
10568_at	YKR005C	1	2.0567489	1.8208394	1.9112642
10572_at	YKR009C	1	3.9472585	4.322236	4.5285583
10573_at	YKR010C	1	1.1804153	0.57766104	0.6664994
10575_at	YKR012C	1	5.1017313	3.781923	4.815192
10581_at	YKL026C	1	9.187492	8.318369	10.075066
10584_at	YKL023W	1	1.4045918	2.0246942	1.5659028
10590_at	YKL017C	1	3.3152013	2.236558	2.628481
10595_at	YKL012W	1	1.0307988	0.8232647	0.99698144
10596_at	YKL011C	1	4.046652	2.6731231	2.3287208
10601_at	YKL051W	1	1.0456591	1.3617064	1.44995
10602_at	YKL050C	1	1.8521327	2.3054607	2.3515186
10603_at	YKL049C	1	0.62135667	0.68891287	0.72058797
10605_at	YKL047W	1	1.2705932	1.433023	1.5150833
10607_at	YKL045W	1	1.2468183	1.4731795	1.5027254
10619_at	YKL033W-A	1	2.2621217	2.4443786	2.5516503
10625_at	YKL071W	1	3.268381	2.6561067	1.8339425
10632_at	YKL064W	1	1.5771868	1.6647325	1.7567439
10633_at	YKL063C	1	0.7897857	0.9811836	1.0603037
10634_at	YKL062W	1	1.0631963	1.6115382	1.2474571
10635_at	YKL061W	1	1.500762	2.0279408	1.7701678
10645_at	YKL052C	1	1.1961833	1.7680383	1.6011188
10646_at	YKL093W	1	1.0310571	1.483525	1.2743596
10648_at	YKL091C	1	2.032884	1.7774478	1.8677143
10649_at	YKL090W	1	2.57241	2.1934001	2.2171547
10651_at	YKL088W	1	0.8100161	1.0467491	1.0572034

10661_at	YKL079W	1	0.87938213	0.8272548	1.002483
10674_at	YKL110C	1	1.5599685	1.658719	1.6278956
10675_at	YKL109W	1	1.0845988	0.9049606	0.8453866
10679_at	YKL105C	1	0.7217569	0.8405378	0.9387404
10681_at	YKL103C	1	0.95429397	0.6916791	0.5090698
10685_at	YKL099C	1	0.6104605	0.8178866	0.87462384
10686_at	YKL098W	1	3.5812187	4.634467	4.28591
10695_at	YKL133C	1	1.2401062	1.0546286	1.1261538
10696_at	YKL132C	1	3.556957	3.0625024	3.9787161
10701_at	YKL127W	1	0.95459443	0.94363797	0.976981
10703_at	YKL125W	1	2.9068432	8.6913	9.574659
10706_at	YKL123W	1	0.8733957	0.830596	0.90964687
10708_at	YKL121W	1	0.94405955	0.88646394	0.47226757
10712_at	YKL117W	1	0.81933737	0.77788645	0.8834291
10714_at	YKL159C	1	1.3442291	0.9530165	1.2511106
10722_at	YKL151C	1	0.8439096	0.65517116	0.6604909
10724_at	YKL149C	1	2.4049094	2.762503	2.66615
10730_at	YKL143W	1	0.90658987	1.1756213	1.0483557
10734_at	YKL139W	1	0.8298518	0.9264839	0.833025
10738_i_at	YKL180W	1	2.70638	1.7234359	1.1399621
10743_at	YKL176C	1	1.9851508	2.6833708	2.4507551
10751_at	YKL168C	1	2.570441	2.7324278	2.7258346
10756_at	YKL163W	1	1.5246685	1.4653219	1.2212462
10758_at	YKL161C	1	5.026509	4.209594	4.632245
10760_at	YKL206C	1	0.9227671	0.8333757	0.8600259
10775_at	YKL188C	1	9.568478	8.336744	8.850487
10776_at	YKL187C	1	3.304875	3.2652717	4.089815
10777_at	YKL186C	1	1.128471	1.4415745	1.5929673
10779_at	YKL184W	1	1.6061485	2.125148	2.0872083
10784_at	SNR37	1	0.45651278	0.3166361	0.33979815
10785_at	SNR60	1	0.5886298	0.95528203	0.71342844
10789_f_at	YKL224C	1	2.6626458	3.338731	3.1948621
10790_at	YKL222C	1	5.8928795	6.763242	5.5860047
10792_at	YKL220C	1	12.083847	12.646153	12.602307
10795_at	YKL217W	1	1.9217308	3.392692	1.6667308
10804_at	YKL208W	1	1.4676714	1.2137529	1.2861722
10809_g_at	NJR008W	1	2.2476943	2.9214916	3.1853232
10811_at	NJR015C	1	14.287064	14.715315	15.255878
10812_s_at	NJR023C	1	8.471584	9.449778	8.152688
10813_s_at	NJR024C	1	9.705769	9.086924	8.161923
10814_s_at	NJR027W	1	10.010916	10.157952	10.757947
10817_at	NJL011W	1	1.4885218	1.2599471	1.3001754
10819_at	NJL004C	1	4.5809965	4.257286	4.360548
10821_g_at	NJR003W	1	1.1415696	1.1096153	1.0038462
10823_at	NJR012W	1	1.1889734	1.1236945	1.2404304
10827_s_at	NJR025C	1	8.373428	17.838167	16.597687
10828_at	NJR001W	1	2.1803074	2.1792667	2.432146
10830_at	NJR006C	1	3.466346	3.9401922	4.165192
10831_s_at	NJR021C	1	4.83896	5.282302	4.7338705
10832_s_at	NJR026C	1	4.021612	4.5740337	4.2308836
10842_at	NJR016W	1	1.9712691	1.9914147	2.1777987

10846_at	NJL022W	1	1.7838943	1.9846207	2.090793
10848_at	NJL012W	1	1.0173484	0.78671134	0.79499555
10851_at	YJR149W	1	3.3776646	4.924652	5.5182714
10853_at	YJR151C	1	5.599121	6.8294377	6.6918273
10854_at	YJR152W	1	10.618717	9.730002	10.879717
10855_at	YJR153W	1	2.112184	2.2330368	3.0095124
10857_at	YJR155W	1	6.5376377	7.2443705	7.7176385
10858_s_at	YJR156C	1	4.342391	6.049616	7.1024995
10861_s_at	YJR159W	1	2.908103	3.0259356	2.826231
10862_s_at	YJR160C	1	2.2809615	2.1192307	1.9786539
10863_i_at	YJL136W	1	1.8821135	2.4716494	2.1270823
10865_at	YJR025C	1	4.1145287	5.4419317	6.5133123
10868_at	NJL020C	1	2.5692196	1.3386297	1.782725
10869_at	NJL016C	1	1.8740075	1.9625204	1.8293128
10872_at	NJL013C	1	0.5401195	0.16707675	0.17957053
10875_at	YJR127C	1	1.8328402	2.2311053	2.2154958
10877_at	YJR129C	1	0.9132154	1.150444	1.2415568
10878_at	YJR130C	1	2.1454992	2.0031414	1.7617806
10883_at	YJR135C	1	1.5707586	1.3159616	1.4026922
10884_at	YJR136C	1	1.5903482	1.1487863	1.5017668
10889_at	YJR141W	1	1.7558267	1.6825336	2.112508
10900_at	YJR107W	1	2.0037737	2.3323858	2.4405508
10901_at	YJR108W	1	5.9701924	4.1640387	4.5865383
10904_at	YJR111C	1	0.78327394	0.8049639	0.9610598
10905_at	YJR112W	1	0.6652265	0.50199044	0.5200734
10908_at	YJR115W	1	6.6958475	4.8309264	8.019114
10915_at	YJR122W	1	0.9638567	0.78731024	0.99812454
10917_at	YJR124C	1	1.3829685	1.912682	2.0843048
10921_at	YJR082C	1	1.6003736	1.7653481	1.8463314
10922_at	YJR083C	1	1.0575964	1.7699044	1.8225701
10925_at	YJR086W	1	0.68285733	0.52051383	0.54785824
10931_at	YJR093C	1	0.85653603	0.84055007	0.8815849
10932_at	YJR094C	1	0.8884506	0.831664	0.84588337
10935_at	YJR096W	1	1.6446923	1.6257724	1.7337325
10939_at	YJR100C	1	2.0311916	2.0068023	2.149994
10962_at	YJR078W	1	2.1628132	2.4044232	2.5557692
10963_at	YJR079W	1	1.344271	2.2598543	1.4260184
10965_at	YJR036C	1	3.364038	2.79713	2.8670363
10968_at	YJR039W	1	3.9565911	3.7171779	3.4632246
10975_at	YJR046W	1	1.2871563	1.2525132	1.3217955
10977_at	YJR048W	1	0.6644317	0.6563401	0.6415714
10981_at	YJR052W	1	2.4517195	1.8262335	2.5813673
10985_at	YJR056C	1	0.67862034	0.74852896	0.80645466
10987_at	YJR058C	1	1.602315	1.723763	1.7964156
10989_at	YJR012C	1	1.6266478	1.9376926	2.1179352
10998_at	YJR021C	1	10.14902	10.122851	13.2387495
10999_at	YJR021C	1	2.5940385	3.1961536	3.5540383
11003_at	YJR025C	1	0.9206415	0.96467096	1.1769168
11017_at	YJL004C	1	2.5832436	2.851045	2.7909405
11025_at	YJR003C	1	2.1334121	2.172289	2.8718777
11026_at	YJR004C	1	10.462604	7.0120664	6.8504295

11030_at	YJR008W	1	3.1463008	2.8714027	3.0575051
11037_at	YJL030W	1	1.2434794	1.1074529	1.1812301
11042_at	YJL025W	1	1.322712	0.9634945	1.1919602
11043_at	YJL024C	1	2.6611538	1.9188461	3.0751925
11044_at	YJL023C	1	7.3455772	4.493269	5.103846
11046_at	YJL021C	1	0.71397626	0.7472125	0.9163522
11047_at	YJL020C	1	0.8465832	3.332225	2.5922174
11051_at	YJL017W	1	1.7508875	2.2382693	1.9975
11052_at	YJL016W	1	1.8132671	1.5310587	1.8075652
11064_at	YJL049W	1	1.1080319	1.1148248	1.2050414
11065_at	YJL048C	1	0.9528647	0.95450085	0.85278475
11067_at	YJL046W	1	1.4425056	1.7108933	1.5580195
11069_at	YJL044C	1	1.9526608	3.8744845	3.719266
11075_at	YJL037W	1	1.1310492	0.9067089	1.0519406
11077_at	YJL035C	1	1.3112667	1.8340887	1.8129703
11091_at	YJL066C	1	1.5603395	1.0829327	0.98361653
11092_at	YJL065C	1	2.0064735	1.7304673	1.8910122
11099_at	YJL058C	1	2.7216284	2.9360862	3.1345758
11100_at	YJL057C	1	7.0281267	5.613951	8.543424
11101_at	YJL056C	1	2.6788378	2.9041712	3.1522136
11109_at	YJL093C	1	2.4578135	2.75235	3.1178074
11111_at	YJL091C	1	1.5264225	1.8205769	1.6161214
11113_at	YJL089W	1	1.409192	1.1232312	1.1775597
11114_at	YJL088W	1	1.0875243	2.6384726	2.239675
11117_at	YJL085W	1	0.70114446	2.4485662	1.2785941
11135_at	YJL112W	1	1.6212413	1.6096549	1.6242774
11137_at	YJL110C	1	7.367482	13.364622	12.877399
11141_at	YJL106W	1	9.150133	7.7569237	8.817885
11149_at	YJL144W	1	2.1158838	1.0000001	1.5657694
11151_at	YJL142C	1	0.86601615	1.0741808	1.7312644
11152_g_at	YJL142C	1	1.5161451	1.4506984	4.312846
11153_at	YJL141C	1	1.7779619	1.3573743	6.421432
11155_at	YJL139C	1	1.5066851	1.3370965	1.4464581
11162_at	YJL133W	1	0.9874897	1.0360643	1.0705802
11163_at	YJL132W	1	1.7196882	1.5935013	1.7487631
11169_at	YJL126W	1	2.8600707	2.4943366	2.6969657
11170_at	YJL168C	1	1.8843445	7.128147	5.1622305
11175_at	YJL163C	1	0.92783993	0.9935639	0.96429956
11176_at	YJL162C	1	2.602167	2.2065384	2.2198076
11177_at	YJL161W	1	2.2913442	1.9669063	2.4461784
11183_at	YJL155C	1	0.9270668	0.8484111	0.99158055
11185_at	YJL153C	1	2.041397	1.0206217	1.5058589
11195_at	YJL185C	1	2.7156162	4.0656343	4.836403
11216_at	YJL210W	1	1.2354729	1.0214322	1.1101741
11217_at	YJL209W	1	1.9820416	2.2880769	1.9823077
11225_at	YJL201W	1	0.91663206	1.0657926	1.0433121
11227_at	YJL199C	1	2.0694194	1.7358892	1.6440209
11230_at	YJL196C	1	0.80253416	0.97365147	0.8773818
11232_at	YJL194W	1	1.2729026	2.6015868	2.886896
11242_f_at	NAR009W	1	2.1670578	0.318524	1.8601224
11243_s_at	NAR011W	1	1.8109066	0.18074697	1.7543749

11244_s_at	NAR012W	1	1.9067016	0.22016975	1.9028757
11247_s_at	YJL225C	1	1.6815779	1.9079182	2.3547492
11249_f_at	YJL223C	1	28.756773	39.78817	45.748566
11250_s_at	YJL222W	1	7.533069	5.646652	7.542765
11251_s_at	YJL221C	1	4.6768007	3.5993826	4.826466
11256_at	YJL216C	1	2.981731	2.6334615	2.6871152
11257_at	YJL215C	1	2.4428844	1.4832692	1.1792308
11259_at	YJL213W	1	9.7497	8.891188	12.5057
11262_s_at	YAR071W	1	0.82476276	0.5790975	0.8054956
11263_f_at	YAR073W	1	0.8573699	0.5642137	0.824775
11264_f_at	YAR075W	1	0.8476817	0.78328896	0.82359964
11265_i_at	YAL069W	1	1.0821416	1.1616547	0.67468244
11266_f_at	YAL069W	1	3.6281376	6.2993073	6.061816
11279_s_at	NAL010C	1	7.5833435	7.040817	7.5929155
11283_r_at	NAR002C	1	1.392566	1.0970925	1.314381
11284_f_at	NAR002C	1	1.996647	2.0759196	2.09352
11287_f_at	YAR020C	1	3.6979585	4.15924	4.946378
11288_at	YAR023C	1	4.014694	2.5974948	3.2637067
11289_at	YAR027W	1	1.5134032	1.1000849	1.5052445
11294_g_at	YAR031W	1	1.1619217	1.0528839	1.3242458
11297_at	YAR035W	1	1.167992	1.1322045	0.9746984
11302_at	YAR053W	1	2.5670965	1.9500277	2.2068098
11307_s_at	YAR066W	1	2.338025	1.0423452	2.780007
11314_at	YAL007C	1	0.59346735	0.7483488	0.67648023
11318_at	YAL004W	1	1.005807	1.5380814	1.2228901
11321_at	YAL002W	1	2.3366423	2.3855505	2.8186219
11326_at	YAR003W	1	1.9233713	2.9280448	2.8221393
11330_at	YAR015W	1	0.98755735	0.78145856	1.027808
11336_at	YAL030W	1	0.8665336	0.57418954	0.7364719
11339_at	YAL028W	1	2.9100084	3.2961633	3.5413322
11347_at	YAL020C	1	1.8034024	1.5276905	1.833657
11353_at	YAL014C	1	2.597233	2.7400289	2.8999453
11356_at	YAL054C	1	1.260818	1.6454155	1.7935327
11360_at	YAL048C	1	1.8794298	1.9257692	2.412692
11361_at	YAL047C	1	1.4800818	1.277799	1.2312028
11369_at	YAL040C	1	0.87066066	1.0819646	1.0022385
11372_at	YAL037W	1	9.722686	6.952115	7.703269
11376_at	YAL034W-A	1	0.7590734	1.0079882	1.0105795
11377_at	YAL034C	1	3.3253098	2.1377249	1.8872979
11379_at	YAL067C	1	4.9501925	5.984231	7.667115
11384_at	YAL064W	1	6.0876923	2.7021155	3.6434615
11385_s_at	YAL063C	1	7.5374417	10.612318	9.471906
11386_at	YAL062W	1	2.7295938	1.5912116	2.0208948
11387_at	YAL061W	1	1.3490257	1.5095501	1.3051958
11389_at	YAL059W	1	0.7162369	0.9525058	1.275331
11390_at	YAL058W	1	1.4485463	1.9677072	2.2088916
11394_at	gHR06	1	3.064065	4.722928	5.087165
11395_at	gHR06	1	3.8268328	4.207393	4.668975
11396_g_at	gHR06	1	2.6100874	2.3476923	2.4665384
11397_f_at	gHR06	1	7.865769	6.1809616	4.6386538
11398_s_at	gHR06	1	9.019808	6.847692	7.134616

11399_s_at	gHR06	1	2.516905	2.6609817	2.5309787
11400_s_at	gHR07	1	1.2825307	1.2682977	0.9117544
11402_at	gHR07	1	2.2557693	1.6676924	2.104423
11403_at	gHR07	1	6.2819576	3.3259747	3.631814
11405_at	gHR08	1	1.6631473	0.32386678	2.233708
11407_f_at	gHR08	1	0.75913894	0.5413369	0.6579448
11409_f_at	gHR08	1	1.4364638	2.724735	1.8024962
11412_at	gIL01	1	3.2001922	2.375577	3.8576922
11426_s_at	gIL02	1	1.7429903	2.3427072	2.1820347
11428_at	gIL03	1	1.73211	1.2242086	1.4203808
11436_s_at	gIR04	1	3.0651922	3.0159614	3.365
2104_s_at	gHL01	1	0.93482566	1.023609	0.9677806
2106_at	gHL02	1	0.78910416	0.7737416	0.742399
2136_at	gHR05	1	0.92390203	1.6231041	1.4868131
2156_s_at	gGR11	1	0.7731973	2.2840261	2.1870778
2161_at	gGR12	1	1.8884616	1.1753845	1.2365384
2189_at	gGL04	1	1.0355953	1.0350242	1.0519472
2205_at	gGR07	1	1.36748	1.3044872	1.2123092
2210_s_at	gGR07	1	3.1329842	5.710161	4.053064
2211_s_at	gGR07	1	2.0124002	3.03043	2.6951692
2213_at	gGR08	1	3.8546152	4.5115385	4.879808
2232_at	gFL01	1	4.63148	4.620192	3.3043637
2233_at	gFL01	1	4.6104407	6.465443	4.1017942
2246_s_at	gFR03	1	3.1735115	1.5803806	1.6943197
2251_at	gGL01	1	11.12947	11.218226	11.846666
2252_g_at	gGL01	1	1.8749009	1.9703717	1.9710987
2253_s_at	gGL01	1	6.1783824	10.143	11.037127
2257_at	gGL02	1	0.51870495	0.40896899	0.40134695
2272_at	gEL01	1	1.6230556	1.563747	1.6201379
2274_at	gEL01	1	2.5432692	1.9371153	2.4017308
2275_g_at	gEL01	1	1.7013462	3.5955768	3.6799998
2287_at	gER03	1	0.8614289	1.0657372	1.3393058
2289_at	gER03	1	1	1	1
2306_at	gER06	1	2.7174866	2.1960385	2.3551974
2307_at	gER06	1	2.0323906	2.8296113	1.9469173
2313_at	gDR10	1	0.58058774	0.8366917	0.5496575
2326_s_at	gDR12	1	1.2458515	1.3713586	1.1987479
2329_at	gDR13	1	0.92639524	1.1123825	1.1172436
2336_at	gDR14	1	0.7741386	0.5341839	0.8738189
2342_s_at	gDR14	1	1.364393	3.4447532	2.7147474
2376_s_at	gDR06	1	0.7680657	1.3665028	1.336388
2382_s_at	gDR07	1	1.7061539	3.525577	3.8284616
2395_at	gCR03	1	2.5442584	2.2054963	2.3131995
2403_s_at	gCR03	1	1.0277019	1.3771923	1.2794657
2405_at	gDL01	1	2.1614325	2.1167128	1.9171978
2407_at	gDL01	1	4.4484234	4.5665154	4.3822517
2408_at	gDL01	1	5.3193383	4.0323253	4.260291
2420_s_at	gDL02	1	2.599996	5.7282724	4.2448835
2426_at	gBR10	1	0.5004376	0.46502784	0.724196
2430_at	gBR10	1	0.71887136	1.3889778	0.91911834
2432_at	gCL01	1	0.80510354	0.8769783	1.2142396

2434_at	gCL01	1	0.6778183	0.5245859	0.35171944
2436_g_at	gCL01	1	8.956905	10.624065	12.718858
2437_s_at	gCL01	1	3.6650639	5.5979433	6.7191563
2445_s_at	gCR02	1	2.989035	3.5581822	3.6729789
2449_s_at	gBL03	1	0.8924488	0.46600854	0.6208914
2459_at	gBL05	1	2.6914928	3.024978	2.8326354
2465_s_at	gBL05	1	0.78339887	0.49393827	0.60537
2491_s_at	gPL11	1	1.8792946	2.0303702	2.2644775
2493_at	gPR12	1	1.9558767	3.387155	3.1534157
2506_s_at	gPR13	1	1.5096931	1.9101907	1.9169564
2518_at	gBL01	1	0.49281424	0.8548737	0.73422295
2525_at	gBL02	1	0.4822651	0.53540784	0.3754067
2535_s_at	gPL05	1	1.3344542	2.417284	2.8094556
2536_s_at	gPL05	1	0.87223953	1.7532158	2.1498334
2540_at	gPL06	1	0.5911538	0.58917606	0.71862304
2552_at	gPL07	1	4.4467306	3.0501924	4.0667305
2559_at	gPL08	1	1.3000648	1.1539221	1.4087737
2560_at	gPL09	1	6.751154	5.2357693	11.064038
2561_at	gPL09	1	0.61704195	0.32162285	0.42141286
2572_s_at	gPL10	1	2.1505673	2.222652	2.35568
2615_s_at	gPL04	1	2.2642345	1.8765169	2.757422
2624_s_at	gOL02	1	1.4573443	1.6753492	1.3271687
2631_s_at	gOR03	1	2.6792078	2.4521852	3.9592798
2637_g_at	gOR04	1	1.089193	2.426336	2.0915504
2638_s_at	gOR04	1	1.5202974	3.202513	2.9684412
2679_at	gNR09	1	0.9318316	0.42799056	0.46984875
2682_s_at	gNR09	1	1.5109617	1.2271154	1.0421153
2684_at	gNR10	1	1.37	1	1
2686_at	gNR10	1	2.7211778	1.4239752	1.7323697
2691_s_at	gNR10	1	1.2764964	1	1
2692_at	gOL01	1	6.022625	3.653338	4.134801
2693_at	gOL01	1	13.562884	10.5988455	11.2325
2698_s_at	gOL01	1	11.0937195	8.838143	7.4827466
2714_s_at	gNL01	1	2.709763	2.8742642	2.6400824
2729_at	gNL04	1	3.291686	2.519182	2.5839891
2749_s_at	gMR06	1	1.4511745	1.4499938	1.9184864
2767_at	gMR09	1	0.7135155	1.2536619	0.9047037
2772_at	gMR09	1	2.8879857	2.3310664	2.1735232
2774_at	gMR10	1	1.2414706	1.0824136	1.081293
2776_at	gMR10	1	2.399598	4.202959	4.9323006
2794_s_at	gLR14	1	0.8897991	0.8996868	0.6965978
2800_at	gML01	1	1.0645524	0.49379066	0.64387
2807_at	gML02	1	1.717576	2.7643151	1.7912683
2819_s_at	gMR05	1	1.2137363	0.8476031	0.98542273
2822_at	gMR05	1	8.2588	9.225912	9.641272
2839_s_at	gLR09	1	1.1478884	1.7294042	1.0429405
2858_at	gLR12	1	3.1703033	2.3022487	2.7820344
2884_g_at	gLR05	1	0.9129653	0.44871005	0.6355508
2904_s_at	gLR06	1	1.0629548	1.8477612	2.3867419
2918_s_at	gKR07	1	2.9816792	2.6276731	2.9281883
2920_at	gKR08	1	2.867317	2.673193	2.5365505

2921_at	gKR08	1	3.315666	2.019703	2.1502132
2922_at	gKR08	1	6.8526216	6.315951	6.641877
2923_at	gKR08	1	10.795754	8.670063	10.194228
2924_g_at	gKR08	1	4.8609614	4.569231	5.641346
2927_s_at	gKR08	1	2.3718915	2.3084846	2.9624248
2929_at	gKR09	1	4.545491	5.871346	6.106731
2949_at	gLR03	1	1.145577	1	1
2954_at	gLR03	1	1.6830769	1.2038462	1.6513461
2958_at	gLR04	1	3.6651583	6.1590486	6.138831
2975_at	gKL04	1	0.7417762	0.58352005	0.62112457
2987_at	gKR05	1	0.80729747	0.37260112	0.31315947
2998_at	gKR07	1	1.9723595	1.2241145	1.5099572
2999_at	gKR07	1	4.125769	3.0938463	3.3146152
3000_at	gKR07	1	3.8542309	4.1684613	3.4415383
3001_at	gKR07	1	2.0966966	1.5165284	1.2515852
3024_g_at	gJR14	1	1.4776961	0.82790005	1.0179458
3025_s_at	gJR14	1	3.4582505	1.8587587	3.0995264
3032_at	gJR15	1	3.8976922	2.7182693	2.3796155
3033_s_at	gJR15	1	2.6945202	2.7335649	2.5555115
3036_at	gKL01	1	1.5714307	2.2038238	2.3837962
3037_at	gKL01	1	2.301237	1.1725	1.5807693
3038_at	gKL01	1	2.470997	1.9722267	2.500007
3064_at	gJL07	1	0.9154065	0.9680741	1.1778839
3079_s_at	gJR10	1	1.8179653	3.6452825	4.049814
3098_at	gAR04	1	5.563322	4.1436734	5.397214
3099_at	gAR04	1	6.768382	3.521864	5.503539
3101_at	gAR04	1	4.221973	1.7653122	2.364808
3105_g_at	gAR04	1	7.007916	6.446495	7.2122183
3110_s_at	gJL01	1	2.366923	2.1532693	1.5598078
3113_s_at	gJL01	1	2.830021	3.3896356	2.4021175
3114_s_at	gJL01	1	1.9820753	2.4031942	2.105883
3133_f_at	YILCDELTA1	1	0.882916	0.74051774	0.67599666
3136_s_at	YIL082W-A	1	9.815074	3.5844545	3.399692
3137_s_at	YILWTY3-1	1	6.4563346	3.514423	3.4400249
3139_f_at	YILCDELTA2	1	1.0992014	2.1428957	1.7327323
3142_f_at	YILCDELTA3	1	0.6353793	0.4971055	0.43718433
3144_f_at	YILWDELTA4	1	0.98150325	0.7056995	0.7489982
3145_at	YILCDELTA5	1	1.2263461	1	1.1609616
3148_s_at	YCR096C	1	5.5544114	5.781563	5.0227013
3149_at	gAL01	1	3.1475558	2.6625078	2.2155738
3150_at	gAL01	1	5.7573338	3.90789	3.8534412
3153_at	gAL01	1	3.6162496	2.3667016	2.665666
3154_at	gAL01	1	2.583032	1.2239559	1.4623678
3162_at	YHRWTAU3	1	3.1918056	2.6807692	3.4098077
3175_i_at	YHRWDELTA13	1	1.4516617	1.6244233	1.3665384
3176_f_at	YHRWDELTA13	1	0.87997997	0.6053403	0.64282966
3181_f_at	YHRCDELTA16	1	0.92478335	0.6723255	0.7514792
3183_f_at	YIL177C	1	2.146916	2.440817	2.38601
3187_s_at	YHL050C	1	2.8829894	5.1949105	3.2277126
3196_f_at	YHLWTAU1	1	5.860038	4.155909	4.185339
3204_at	YHRCDELTA4	1	3.2743213	3.9812381	4.0020742

3209_f_at	YHRWDELTA7	1	0.7598531	0.68658125	0.6757043
3212_f_at	YGRWDELTA22	1	0.9810945	0.7730074	0.8127676
3214_at	YGRWDELTA23	1	15.993909	13.936923	12.566539
3226_f_at	YGRCDDELTA30	1	0.77086246	0.6205226	0.6003172
3230_f_at	YGRWDELTA31	1	0.8479521	0.65126777	0.6426923
3232_f_at	YGRCTAU3	1	5.0720615	4.1135826	4.0613294
3233_f_at	YGRWDELTA32	1	0.84545994	0.74598867	0.72448874
3235_f_at	YGRCDDELTA15	1	0.7662376	0.7150096	0.6581825
3239_f_at	YGRCDDELTA16	1	0.76165223	0.631328	0.57049245
3245_f_at	YGRWDELTA19	1	0.8295405	0.6710104	0.6328987
3255_at	YGRCDDELTA20	1	3.6732829	3.33884	4.072415
3258_f_at	YGLWDELTA4	1	4.396253	4.677372	4.5214067
3259_at	YGLCDELTA5	1	1.4897393	1.6326536	1.290433
3264_f_at	YGLWDELTA6	1	4.5906434	4.5500264	4.2677073
3269_f_at	YGLWDELTA8	1	0.6281293	0.6043216	0.45065352
3286_f_at	YFLWDELTA5	1	0.7179683	0.5736	0.560248
3290_f_at	YFRWDELTA7	1	0.824394	0.49243706	0.5628226
3291_f_at	YFRCDELTA8	1	0.57426935	0.63293844	0.58764255
3296_at	YFRWDELTA10	1	1.0617307	1.2155769	1
3301_f_at	YGLWTAU1	1	7.389177	4.505167	4.520541
3302_f_at	YGLCDELTA1	1	0.8631526	0.7151075	0.66637534
3303_f_at	YGLWDELTA2	1	0.73744184	0.592181	0.5008294
3306_i_at	YGLWDELTA4	1	5.462158	7.3004885	7.469792
3307_s_at	YERWDELTA18	1	0.9427915	1.58453	1.4715724
3308_s_at	YERWDELTA18	1	0.9373362	0.780605	0.69285643
3309_s_at	YERWDELTA18	1	0.84444785	0.7988486	0.6689725
3310_s_at	YERWDELTA18	1	2.2487707	3.9665463	2.3546724
3315_f_at	YERCSIGMA4	1	0.99267465	1.0330095	0.97953916
3319_f_at	YERCDELTA24	1	0.8498029	0.78452593	0.7641412
3324_at	YERWOMEGA2	1	4.228316	5.4421344	5.536056
3325_f_at	YDR543C	1	2.7140636	3.0009317	2.6099634
3326_at	YFL063W	1	4.002308	3.6182692	4.6251926
3328_at	YFLWDELTA1	1	2.169231	1.6175001	1.3280768
3329_f_at	YFLWDELTA2	1	0.83049965	0.71757054	0.703416
3333_f_at	YERWDELTA11	1	0.763987	0.75980943	0.69080806
3335_at	YERWDELTA13	1	1.3867308	1.3680769	1.3475001
3336_f_at	YERCTAU2	1	6.057438	4.4583097	4.497665
3343_i_at	YERCDELTA15	1	4.419159	4.9986887	5.515558
3344_f_at	YERCDELTA15	1	4.2255187	4.311954	4.298586
3346_at	YERCTAU3	1	6.811952	8.100676	7.486696
3356_f_at	YDR543C	1	1.988957	2.2412543	1.9694896
3359_f_at	YELWDELTA2	1	0.84182614	0.7786084	0.66099894
3367_f_at	YELWDELTA6	1	0.80970997	0.7799869	0.633969
3368_f_at	TR(UCU)E	1	0.5585924	0.64361376	0.7330597
3372_f_at	TH(GUG)E1	1	1.1209943	0.47211093	0.5658818
3374_at	YERWDELTA9	1	4.9627438	2.8637433	2.7616065
3386_f_at	YDRWDELTA23	1	0.8176731	0.6446647	0.60611683
3388_f_at	YDRWDELTA24	1	0.8489754	0.70450646	0.67393506
3389_f_at	YDRWDELTA25	1	0.76657116	0.63701594	0.53456
3391_f_at	YDRWDELTA26	1	0.8382498	0.6932782	0.66972184
3392_f_at	YDRWDELTA27	1	0.8097845	0.6565815	0.66249245

3396_f_at	YDRWDELTA28	1	0.7070029	0.59571826	0.5798482
3402_at	YDRWDELTA31	1	2.4111037	3.1151874	2.7020807
3403_f_at	YDR542W	1	14.0126095	24.173628	26.074242
3406_f_at	YDRWDELTA11	1	0.7007442	0.67010504	0.68609536
3407_at	YDR170W-A	1	2.0632885	1.5393668	1.7496026
3418_f_at	TS(AGA)D2	1	0.8874563	0.49294806	0.59181535
3427_at	YDRCDELTA2	1	2.0468597	1.9848778	2.0773473
3435_f_at	YDRWDELTA7	1	0.7252232	0.6896924	0.5043656
3437_f_at	TR(UCU)D	1	0.68178964	0.5303745	0.5287307
3440_f_at	YDRCDELTA7	1	0.75296146	0.7585757	0.6896658
3444_f_at	YDRCDELTA8	1	0.8116222	0.6203954	0.5512394
3445_f_at	YDRCSIGMA1	1	4.0669193	3.9106736	3.835246
3448_s_at	YDRCSIGMA2	1	2.8541205	2.768804	2.7328115
3452_f_at	YCRCDELTA6	1	0.6347985	0.6370111	0.61370283
3453_at	YCR007C	1	2.3719668	2.7890384	2.5390387
3457_f_at	YCRCDELTA7	1	0.8333419	0.7410134	0.7006098
3458_f_at	YCRWDELTA8	1	0.88123095	0.69772124	0.5840554
3467_f_at	YCRWDELTA13	1	0.7037364	0.9311073	1.1625066
3471_f_at	YDL248W	1	2.191312	3.298924	2.6988404
3474_f_at	YDLCDELTA1	1	0.55378854	0.57964253	0.6753188
3475_f_at	YDLWTAU1	1	6.9903274	5.062113	5.091422
3479_f_at	TR(UCU)B	1	0.62842405	0.562674	0.64406455
3506_s_at	YBLWTAU1	1	2.4600577	2.394386	2.1613793
3510_s_at	YBLWDELTA8	1	2.8614626	3.1306589	2.8381588
3511_f_at	YBLWDELTA9	1	0.74058235	0.68881285	0.6228779
3512_f_at	YBLWTY1-1	1	1.0424999	1.1159507	1.1567158
3513_f_at	YBLWDELTA10	1	0.6901639	0.6733595	0.64173895
3516_f_at	YBRWDELTA12	1	0.78738916	0.6771573	0.63966084
3518_f_at	YBRWDELTA13	1	0.852691	0.67936057	0.64999264
3524_f_at	YPRCTY1-2	1	1.0074792	1.1852517	1.0629197
3527_f_at	YPRCDELTA19	1	0.6606455	0.65238047	0.582405
3530_f_at	YPRWDELTA21	1	0.83061075	0.6813994	0.6661924
3532_f_at	YPRCDELTA23	1	0.8273809	0.65004814	0.6544068
3533_f_at	YPRCTY1-4	1	1.2205737	1.2606474	1.3377049
3534_f_at	YPRCDELTA24	1	0.87422764	0.7225258	0.6625229
3537_f_at	TA(AGC)P	1	0.5736447	0.46121204	0.35140413
3541_at	YPRWTAU4	1	10.887806	10.314396	10.917548
3543_s_at	YBL112C	1	1.8462746	2.362743	2.062162
3551_f_at	YPLCDELTA10	1	0.6036757	0.47566184	0.5613897
3553_f_at	YPLCTAU1	1	7.3795724	3.5300267	3.397156
3554_f_at	YPLCTY4-1	1	5.6489067	3.2194502	3.4525309
3555_s_at	YHL009W-B	1	9.664545	4.191346	4.919039
3556_s_at	YHL009W-B	1	12.726406	5.6494393	6.1752567
3558_f_at	YPLCTAU2	1	5.448983	2.952451	3.338879
3559_f_at	YPRWDELTA12	1	0.814335	0.6306476	0.7299001
3562_f_at	TS(UGA)P	1	0.9143336	2.059657	1.318485
3570_f_at	YPRWDELTA17	1	0.7129718	0.36065483	0.3846042
3571_f_at	YPRCDELTA18	1	0.6510307	0.72802466	0.5898668
3572_f_at	YORCDELTA21	1	0.74605703	0.72304213	0.74353737
3573_f_at	YORWTAU3	1	2.9891515	2.8324842	2.494711
3582_f_at	YORCDELTA25	1	0.6970173	0.6685417	0.6201309

3583_i_at	YPLCDELTA1	1	3.3024738	2.7666972	3.3823528
3584_f_at	YPLCDELTA1	1	3.7853847	4.641731	6.089039
3589_f_at	YPLWTY1-1	1	0.84569204	0.8109755	0.74522114
3590_f_at	YPLWDELTA4	1	0.7605174	0.6817233	0.6215341
3593_f_at	YPLWDELTA6	1	0.7750691	0.53996575	0.48651376
3598_f_at	TR(ACG)O	1	0.7571543	0.32102963	0.24468467
3606_f_at	YORWDELTA13	1	0.76150614	0.6264375	0.5920411
3608_f_at	YORWDELTA14	1	0.8493388	0.70013744	0.66908866
3617_f_at	YORWTAU2	1	5.303036	4.102225	4.037815
3623_f_at	YNRCDELTA8	1	0.91594297	0.72893393	0.7303258
3624_at	YNRCDELTA9	1	4.579358	4.968302	4.4869776
3626_i_at	YNR075W	1	5.643365	7.6063433	6.612838
3627_r_at	YNR075W	1	3.169078	4.540677	4.3395324
3629_f_at	YNR077C	1	3.107945	3.9728062	3.9725041
3631_s_at	YOLWTAU1	1	6.5566983	7.1221657	7.154405
3639_f_at	YOLWDELTA5	1	0.82513857	0.691677	0.6728647
3647_f_at	YNL337W	1	2.2080505	2.4469516	2.3851638
3650_f_at	YNLWTAU1	1	10.87031	8.693214	9.338965
3652_f_at	YNLCTY1-1	1	1.0922794	0.875294	1.0495515
3653_f_at	YNLCDELTA2	1	0.8181746	0.72545284	0.67687804
3660_f_at	YNLWDELTA4	1	0.69172037	0.6776538	0.6240211
3661_at	YNLWSIGMA2	1	3.7142885	2.861061	2.797062
3663_f_at	YNLWTAU2	1	6.5346913	4.898074	4.83058
3664_f_at	YNLCDELTA5	1	0.84594864	0.8907177	0.81230533
3669_f_at	YNRCDELTA7	1	0.71604216	0.58077896	0.5524716
3670_f_at	YNRCTAU3	1	5.383869	5.032483	4.9518776
3683_f_at	YMRWDELTA16	1	5.1726923	5.3411536	3.9996152
3684_f_at	YMRWTAU2	1	5.7373953	4.044425	3.9802132
3685_f_at	YMRWDELTA17	1	0.7617258	0.5823736	0.54548836
3686_f_at	YMRCDELTA18	1	6.0711536	5.3442307	5.4028845
3687_f_at	TR(UCU)M1	1	0.50770193	0.40174833	0.37420744
3691_f_at	YMRCTAU3	1	4.479216	3.6624534	3.0689895
3693_f_at	YMRWDELTA21	1	4.236555	4.4235687	3.8120296
3695_f_at	TR(UCU)M2	1	0.54423153	0.48535955	0.5710485
3697_f_at	YMLCDELTA2	1	0.845849	0.7951384	0.71653384
3699_f_at	YMLWDELTA3	1	0.87878275	0.64492035	0.6864191
3701_f_at	YMLWDELTA4	1	0.8802098	0.65476775	0.6985017
3706_f_at	YMLWDELTA6	1	0.80365944	0.7225689	0.7385839
3711_f_at	YMRCDELTA7	1	0.837302	0.67386794	0.6297673
3718_s_at	YLR410W-B	1	1.9307722	2.9414878	1.9005609
3719_s_at	YLR410W-B	1	2.303659	4.258949	2.6365757
3721_s_at	YLRWTY2-1	1	1.483793	1.0833145	0.99724495
3730_at	YLRCDELTA27	1	4.4711657	6.5521626	5.938957
3735_f_at	YLR466W	1	1.9828756	2.4974031	2.2892141
3737_s_at	YLR467W	1	1.7919662	2.161923	1.5709616
3742_f_at	YLRWDELTA14	1	0.6902581	0.6974003	0.61289966
3743_f_at	TA(AGC)L	1	0.40221894	0.27578464	0.21190402
3746_at	YLRWDELTA15	1	1.9018393	2.2506824	2.066551
3751_f_at	YLRCDELTA18	1	0.8422815	0.70767415	0.6832395
3752_f_at	YLRCDELTA19	1	0.818228	0.2436341	0.5861143
3757_f_at	YLRWDELTA20	1	0.90669066	0.8862054	0.8512944

3759_f_at	YLRCDELTA21	1	0.89880514	0.7783402	0.74115926
3762_s_at	YLR410W-A	1	1.7967098	2.806926	2.0270987
3771_f_at	YLRCDELTA7	1	0.82381165	0.7579466	0.64508903
3775_f_at	YLRCDELTA8	1	0.7777742	0.8866638	0.8374726
3777_f_at	YLRCDELTA9	1	0.6072877	0.46951815	0.6336628
3778_f_at	YLRWDELTA10	1	0.7280005	0.64909166	0.6558392
3782_f_at	YLRWDELTA11	1	0.7240427	0.65307534	0.6471119
3789_s_at	YLL067C	1	6.143397	18.973482	12.488731
3790_s_at	YLL067C	1	3.1712308	4.425666	3.9773288
3791_s_at	YLL067C	1	3.1916962	4.978077	3.0236537
3793_f_at	YLLCDELTA1	1	0.65385103	0.52850735	0.4267212
3799_f_at	YLRCDELTA3	1	0.8501049	0.7748363	0.7573589
3806_s_at	RDN37-1	1	0.48425967	0.79334474	0.51315415
3809_s_at	RDN37-1	1	0.6217721	0.80301905	0.45580667
3814_f_at	TR(UCU)K	1	0.65834814	0.6105147	0.5836653
3820_f_at	YKLCDELTA5	1	0.8235837	0.6939025	0.62370676
3824_f_at	YKRCDELTA8	1	0.7943909	0.6562349	0.6222141
3827_f_at	TR(ACG)K	1	0.49336946	0.29024035	0.2991795
3828_f_at	YKRCDELTA11	1	4.478554	3.1823268	2.9030013
3829_f_at	YKRCDELTA12	1	0.8252086	0.75721097	0.71118736
3832_s_at	YKR106W	1	2.2001925	1.8959615	1.6476922
3834_s_at	YLL067C	1	6.7931366	12.216923	7.59077
3836_f_at	YJRWTY1-2	1	1.1478797	1.1363366	1.2923689
3837_f_at	YJRWDELTA13	1	0.80777335	0.6180632	0.60255396
3843_at	YJLWDELTA16	1	2.3491662	2.481047	2.4107277
3844_f_at	YJRWDELTA17	1	0.9969842	0.991015	0.86879367
3851_s_at	YJR161C	1	2.2256188	2.7548316	2.4485393
3852_f_at	YJR161C	1	1.7690734	2.2374852	2.0549324
3853_f_at	YJR162C	1	3.9557536	3.5607548	3.5648575
3858_s_at	TN(GUU)K	1	0.9521605	1	1
3860_f_at	YJLCDELTA4	1	0.85186505	0.79330516	0.73378956
3862_f_at	TR(UCU)J1	1	0.47784996	0.45631284	0.4548394
3863_f_at	TR(UCU)J2	1	0.43851092	0.33820468	0.30530578
3867_s_at	TV(AAC)J	1	0.6544242	0.54021025	0.54381156
3876_at	YJLWTAU4	1	8.739573	9.3902235	8.925409
3879_f_at	YJRWDELTA11	1	0.7195019	0.7127258	0.63228726
3881_f_at	YJRWTY1-1	1	1.010529	1.3248425	1.3168595
3882_f_at	YJRWTY1-1	1	0.8036007	0.66985524	0.49888802
3883_f_at	YJRWDELTA12	1	0.73653847	0.67777556	0.5613924
3887_f_at	YJLWTAU1	1	5.5299664	4.1664133	4.0521364
3895_s_at	YJL113W	1	9.916618	5.141765	4.68264
3899_s_at	YJLWTY4-1	1	8.502501	3.9984615	4.401346
3900_f_at	YJLWTY4-1	1	4.44829	3.4920583	3.2285278
3901_f_at	YJLWTAU2	1	5.449157	3.9249432	3.8167505
3902_f_at	YJLCDELTA3	1	0.901072	0.8453253	0.77393013
3904_f_at	YJLWDELTA2	1	4.533967	4.964704	5.1451864
3907_f_at	YAL068C	1	5.0117345	6.5134473	6.838214
3912_f_at	YARCDDELTA4	1	0.7972771	0.6325207	0.63505554
3913_s_at	YARCTY1-1	1	0.7233973	2.0734446	1.4308381
3914_s_at	YARCTY1-1	1	0.84698725	0.7459203	0.7838511
3918_f_at	YARCTY1-1	1	0.96187645	0.9699134	0.9288365

3922_f_at	YARCDDELTA5	1	0.78895724	0.6701621	0.6749467
3926_f_at	YARWDELTA6	1	0.69876134	0.6150135	0.58918613
3939_at	YBR006W	1	2.2376785	2.677446	2.5088167
3948_s_at	YKL198C	1	2.593913	1.9798526	1.9573175
3951_at	2mic_FLP1	1	0.70813054	0.93850166	0.49894753
3952_at	2mic_REP1	1	1.2215406	1.3305352	0.4010437
3953_at	2mic_D_protein	1	5.1290455	8.082602	2.333776
3954_at	2mic_REP2	1	0.9622934	1.271763	0.41211608
3955_at	2mic_FLP1	1	1.1012938	1.2779208	0.6501647
3958_r_at	Q0225	1	1.9150742	6.45115	6.384775
3994_at	Q0155	1	1.103871	3.5546715	2.3855073
3997_at	Q0180	1	1.4114664	2.6401708	2.0074148
4009_at	NIL022W	1	3.1826007	3.429389	3.026235
4015_at	NIL007W	1	4.91727	3.9577057	4.2513103
4016_at	NIL006W	1	1.9910046	1.5640473	1.5902293
4018_at	NIR003C	1	3.6591296	4.021581	5.1554365
4019_at	NIR004C	1	6.544588	9.3165865	9.161802
4020_at	NIR005C	1	4.350809	4.3989906	4.5136313
4024_at	NIL021C	1	2.3203845	2.2653847	2.0526924
4025_i_at	NIL020C	1	1.279747	2.6736782	1.4885986
4030_at	NIR002W	1	2.1477933	2.4321275	2.316307
4032_f_at	YIR043C	1	3.6012585	4.389635	3.939491
4037_at	YIL071C	1	3.5722203	4.010577	3.236923
4045_s_at	YIL066C	1	4.8526926	4.827692	5.761154
4056_at	YIR020C	1	10.370388	11.9951935	10.163373
4061_at	YIR025W	1	1.5158504	1.4252023	1.4383769
4064_at	YIR028W	1	1.4434603	2.1925857	1.2824273
4065_at	YIR029W	1	9.157692	7.4338465	7.8198075
4066_at	YIR030C	1	0.93254954	1.1677924	1.2315141
4067_at	YIR031C	1	11.504376	12.028196	13.271347
4068_at	YIR032C	1	4.1130433	5.3830113	5.5826044
4073_at	YIR037W	1	0.7729887	0.744651	0.779909
4075_at	YIR039C	1	6.6628323	8.137316	7.782175
4076_f_at	YIR041W	1	6.5390844	3.8362577	3.6996446
4077_at	YIR042C	1	7.406142	10.13434	10.3633585
4078_i_at	YIR043C	1	12.5131645	17.557158	16.360596
4079_at	YIL003W	1	2.0834303	2.445065	2.134304
4082_at	YIR001C	1	1.6535517	2.0933807	1.8925737
4088_at	YIR007W	1	2.371712	2.3896718	2.1960669
4090_at	YIR009W	1	2.7625408	2.6753767	2.803874
4092_at	YIR011C	1	0.90386087	0.94709057	1.0509739
4095_at	YIR014W	1	1.1624095	1.9929075	1.5142466
4097_at	YIR016W	1	1.0654998	1.2915204	1.0937839
4098_at	YIR017C	1	1.1111343	1.5518131	1.2994056
4099_at	YIR018W	1	1.7299092	1.9516945	1.7653356
4100_at	YIR019C	1	2.6801789	5.276972	4.493788
4101_at	YIL024C	1	1.7610188	2.5999296	2.401434
4102_at	YIL023C	1	1.8535185	1.8044832	1.604757
4106_at	YIL019W	1	0.9579215	0.9014278	0.878447
4107_at	YIL017C	1	1.6426685	1.6855009	1.6291307
4109_at	YIL015W	1	0.48738393	0.62711346	0.6973973

4110_at	YIL015C-A	1	1.0341135	1.053077	1.1361538
4112_at	YIL013C	1	2.1091151	2.5627794	2.1152897
4116_at	YIL009C-A	1	3.079657	3.090053	3.2475896
4117_at	YIL009C-A	1	3.8728948	3.567474	3.693345
4126_at	YIL045W	1	1.3486323	1.5976633	1.4500085
4143_at	YIL028W	1	4.8690386	3.630577	3.3588462
4148_at	YIL071C	1	2.3870776	1.7821153	1.8653847
4149_at	YIL070C	1	0.71189815	0.76734257	0.6732042
4158_at	YIL059C	1	3.8299234	3.6686587	3.7736816
4161_at	YIL056W	1	1.4200116	1.3661927	1.3897513
4162_at	YIL055C	1	1.9837248	2.5223536	1.7860587
4163_at	YIL054W	1	1.2069992	1.4821944	1.2802356
4168_at	YIL049W	1	1.4453993	1.8476565	1.6801747
4174_at	YIL092W	1	2.2393801	1.811734	1.9304652
4177_at	YIL089W	1	3.4178393	4.046897	5.1501036
4179_at	YIL087C	1	1.3249115	1.2808192	1.2935393
4182_at	YIL084C	1	2.1746557	1.1484616	1.7276922
4184_s_at	YIL080W	1	7.3483324	5.0120635	4.078386
4185_at	YIL079C	1	1.3029087	1.5424235	1.5392935
4187_at	YIL077C	1	1.6838119	1.9230343	1.6156335
4191_at	YIL073C	1	2.0773695	1.5611539	1.5753846
4192_at	YIL119C	1	0.3569158	0.5708786	0.45372748
4194_at	YIL117C	1	0.7154728	0.9585795	0.9861243
4195_at	YIL116W	1	2.2418864	2.5728025	2.4609075
4198_at	YIL113W	1	1.2228802	1	1
4200_at	YIL111W	1	0.6418375	0.6580149	0.65184045
4204_at	YIL107C	1	2.8028994	3.1078699	2.651586
4209_at	YIL101C	1	1	1.0011538	1
4211_at	YIL099W	1	1.9666461	2.5017486	1.8169369
4212_g_at	YIL099W	1	1	1.2036538	1
4214_at	YIL097W	1	2.4973867	3.0187404	2.2100532
4220_at	YIL136W	1	1.7468463	1.8544687	1.7624599
4224_at	YIL132C	1	2.1425748	1.8094364	1.8677084
4234_at	YIL122W	1	1.038552	0.6853961	0.7554407
4236_at	YIL120W	1	4.0840387	3.6119232	4.7469234
4237_at	YIL165C	1	9.589611	9.030119	8.949254
4238_at	YIL164C	1	16.338425	20.712864	21.455036
4241_at	YIL160C	1	1	1	1.1763461
4249_at	YIL152W	1	1.4866095	1.7705281	1.5735855
4252_at	YIL149C	1	0.7779952	0.99268204	0.9298814
4255_at	YIL146C	1	2.5857172	3.9893978	3.53239
4256_at	YIL145C	1	1.0154853	1.074201	1.1103904
4257_at	YIL144W	1	1.0417308	1.0184616	1
4263_at	NHR013C	1	4.0073075	3.7984614	3.5725
4269_f_at	NHR030W	1	3.4331362	3.5976605	3.5220425
4270_f_at	NHR031C	1	4.6121154	3.6630769	3.4330769
4275_at	NHR008W	1	2.028764	2.271941	1.9309744
4280_f_at	YIL176C	1	18.899937	35.29737	35.728756
4284_at	YIL167W	1	6.743846	5.359231	5.234231
4285_at	YIL166C	1	2.9824622	4.2990074	3.1630423
4286_s_at	YHR077C	1	1.471777	18.923447	1.7310764

4287_s_at	YHR209W	1	1.8466501	2.0289676	1.7858939
4288_at	NHL005C	1	1.9542346	1.897835	1.5056717
4290_at	NHR027C	1	2.328092	2.8428845	2.7830768
4304_f_at	NHR029W	1	1.6417308	1.5898077	1.583077
4305_at	NHL007C	1	22.187057	38.080612	39.05976
4307_f_at	NHL006C	1	2.3376923	2.1621153	2.2175
4308_at	NHR009C	1	4.1609616	3.7015386	4.292885
4313_at	YHR199C	1	3.016147	3.1847148	3.1344676
4317_at	YHR204W	1	2.8308477	3.1482253	3.1715493
4322_at	YHR210C	1	3.6043816	3.22455	2.93493
4323_f_at	YHR216W	1	0.87404656	0.82539916	0.77250695
4324_s_at	YHR218W	1	2.3726516	6.219946	3.9544125
4336_at	YHR176W	1	1.6023376	1.7651196	1.6383623
4338_at	YHR178W	1	1.5935216	2.2263558	2.2219524
4340_at	YHR180W	1	3.000669	3.3088033	3.5358756
4358_at	YHR153C	1	2.5329728	2.511346	2.0796154
4361_at	YHR156C	1	2.8514905	3.320769	3.1192307
4362_at	YHR157W	1	5.895705	6.1984615	6.367116
4371_at	YHR166C	1	1.6111639	1.7913826	1.6924725
4374_at	YHR169W	1	0.7301978	0.94667006	0.9454749
4377_at	YHR172W	1	0.82667494	1.0839195	0.99395835
4378_at	YHR129C	1	2.2496073	2.0342116	2.204417
4383_at	YHR134W	1	2.1497772	3.4670787	3.7043447
4385_at	YHR136C	1	0.5023953	0.49033576	0.5015418
4386_at	YHR137W	1	1.1386807	1.7509319	1.4242069
4387_at	YHR138C	1	1.1503395	0.8847214	0.8945807
4391_at	YHR142W	1	0.7309815	0.9254982	0.7735222
4400_at	YHR150W	1	6.174873	5.2896156	9.294423
4413_at	YHR120W	1	1.718722	1.9498361	2.1021895
4416_at	YHR123W	1	1.5093979	2.5327902	2.1933224
4417_at	YHR123W	1	1.5634829	2.1491401	1.9235705
4418_at	YHR124W	1	1.1787843	1.3600839	1.1453966
4423_at	YHR087W	1	1.1639163	1.3845658	1.15391
4424_at	YHR088W	1	0.75043416	0.66678965	0.6633872
4426_at	YHR090C	1	1.5706867	1.8383104	1.8434477
4430_at	YHR094C	1	1.0745779	1.6619339	1.8449044
4431_at	YHR095W	1	1.8611538	2.4548078	2.7271152
4432_at	YHR096C	1	1.3241174	1.1313779	1.2880026
4439_at	YHR101C	1	2.3396034	1.4769933	1.3906765
4442_at	YHR104W	1	1.0286353	1.0317404	0.9128762
4448_at	YHR067W	1	2.6820765	3.1847935	2.941303
4452_at	YHR071W	1	1.731472	2.1748157	2.0178995
4456_at	YHR075C	1	2.056877	1.9829851	2.0034668
4458_at	YHR078W	1	1.566397	4.214808	1.4121633
4467_at	YHR085W	1	0.8353642	0.8584005	0.88861287
4469_at	YHR040W	1	1.0362078	1.3549814	1.4579239
4477_at	YHR048W	1	2.0986066	2.4292247	2.317801
4490_at	YHR062C	1	0.85868514	0.9246138	0.9881417
4496_at	YHR022C	1	1.6655513	2.2723076	2.0851922
4503_at	YHR029C	1	1.3163276	1.0485263	1.3603401
4505_at	YHR031C	1	1.6035066	2.049557	1.9412166

4507_at	YHR033W	1	1.3320756	1.5396718	1.3414931
4510_at	YHR036W	1	0.9482378	0.87080276	0.85115373
4521_at	YHR004C	1	1.8339387	2.5604732	2.7352376
4524_at	YHR006W	1	1.0774876	1.113257	1.0462275
4534_at	YHR015W	1	3.5266562	4.1266704	3.996957
4539_at	YHL023C	1	1.3447504	1.722702	1.5443248
4541_at	YHL021C	1	0.72680753	0.85750586	1.0541613
4543_at	YHL019C	1	1.7729402	1.4374539	1.5287745
4545_at	YHL017W	1	1.6805878	3.3294215	3.0805628
4546_at	YHL016C	1	7.0235486	9.473461	7.913269
4556_at	YHL006C	1	2.1419232	1.8034616	2.1828847
4562_at	YHL047C	1	10.608754	9.949444	9.677552
4563_f_at	YHL046C	1	5.116142	6.1545424	5.74064
4564_at	YHL044W	1	1.508816	1.9326923	2.0051923
4566_at	YHL042W	1	6.2696157	5.257885	5.465
4568_at	YHL040C	1	10.319216	8.737311	7.004096
4571_at	YHL037C	1	6.25	6.238846	5.4171157
4573_at	YHL035C	1	5.621089	5.698182	5.290563
4576_at	YHL032C	1	1.7661605	2.0080526	1.915592
4580_at	YHL028W	1	0.36024734	0.46417466	0.46082753
4582_at	YHL026C	1	3.1215396	3.7690601	3.7046957
4583_at	YHL025W	1	1.401557	1.3834307	1.426702
4584_at	YHL024W	1	1.4084616	1.4884615	1.2763461
4587_at	NGR069W	1	2.1287782	2.165	2.133846
4591_at	NGR073W	1	1.4050596	1.4530345	1.3671374
4595_at	NGR114C	1	2.5380094	1.9505076	1.6442608
4605_s_at	SNR39b	1	0.6317495	0.4393793	0.4082365
4609_at	NGR104C	1	5.4524717	4.2657156	4.5312223
4613_at	NGL042W	1	5.1606436	5.426886	5.057127
4617_at	NGL030C	1	1.7589693	1.7486535	1.7019525
4622_at	NGL018W	1	3.6185784	3.9897652	3.9973307
4626_at	NGR042W	1	3.3199778	2.9805236	3.4729176
4627_at	NGR043C	1	3.8617947	4.2601676	4.5201254
4630_at	NGR060W	1	1.5035145	1.2407701	1.2761999
4631_at	NGL040C	1	1.731923	1.4234616	1.3901923
4633_at	NGL039C	1	2.4258819	2.9145424	2.862821
4647_at	NGR050W	1	1.0607692	1	1.0565385
4649_r_at	NGR051C	1	2.5179	1.9219866	2.2222917
4651_at	NGR052C	1	9.953325	13.108622	12.473058
4652_at	NGR053C	1	9.20454	16.358618	14.592527
4653_at	NGR056C	1	5.7107553	5.255192	4.4328847
4656_f_at	NGR078W	1	0.9317591	0.9240216	0.8813708
4668_at	NGR113W	1	3.9790273	4.024249	4.088363
4675_at	NGL008W	1	4.1543717	3.4583397	3.1230159
4683_at	NGR097C	1	1.7727113	2.3267174	2.2165391
4686_s_at	NGR106C	1	0.6665154	0.51217246	0.4160185
4690_at	NGL011W	1	4.084909	4.314052	2.639977
4692_f_at	NGR003C	1	1.843919	2.6741192	1.8399051
4697_at	NGL012W	1	2.0601363	2.0630238	2.0692348
4698_at	NGL010C	1	0.8355232	0.4348253	0.43013754
4708_at	YGR278W	1	0.9637934	1.0072063	1.020775

4714_at	YGR284C	1	0.9406922	1.2942243	1.1120422
4717_at	YGR287C	1	2.4365926	2.1167302	1.9664832
4718_at	YGR288W	1	2.1188712	2.0383835	2.2032518
4719_at	YGR289C	1	25.138824	27.464378	26.352795
4723_f_at	YGR294W	1	26.307243	34.988075	41.66346
4732_at	YGR256W	1	4.330703	5.1748753	5.216776
4735_at	YGR259C	1	2.1178749	2.4083798	2.0459507
4746_at	YGR270W	1	1.8227838	2.1355824	1.9558324
4758_at	YGR238C	1	1.7021093	1.5985916	1.5760784
4759_at	YGR239C	1	1.1930324	1.4381329	1.393341
4763_at	YGR243W	1	1.1615385	1	1.235
4764_at	YGR244C	1	0.73064023	0.6467128	0.59689295
4768_at	YGR248W	1	1.5921801	1.4481516	1.4236919
4769_at	YGR249W	1	1.2486731	1.19065	1.2782872
4778_at	YGR213C	1	4.2043605	4.95607	4.2284746
4782_at	YGR216C	1	2.4187145	2.6816626	3.2141507
4788_at	YGR222W	1	2.0927436	1.6586014	1.9104022
4790_at	YGR224W	1	1.0406606	1.5553846	1.3019232
4797_at	YGR187C	1	0.5978621	0.7471394	0.8223607
4804_at	YGR194C	1	1.0942303	1.2463632	1.0954522
4812_at	YGR202C	1	1.4838238	1.5314404	2.2912467
4821_at	YGR166W	1	0.8531898	0.8967983	0.8691019
4823_at	YGR168C	1	6.6197805	6.6095963	6.104817
4842_at	YGR142W	1	1.3789046	1.1594671	1.0909538
4844_at	YGR144W	1	2.1895556	2.661062	2.699772
4849_at	YGR149W	1	1.5432823	1.5046967	1.4242811
4854_at	YGR153W	1	1.3340107	1.281935	1.1092427
4855_at	YGR154C	1	10.359924	9.342609	8.605234
4857_at	YGR156W	1	1.3633131	0.7930064	0.8212578
4862_at	YGR161C	1	2.2381086	2.068764	2.0750904
4864_at	YGR163W	1	0.6809771	0.726232	0.73339754
4868_at	YGR123C	1	0.8404172	1.244239	1.3437668
4872_at	YGR127W	1	3.1356018	2.9729831	3.391159
4876_at	YGR131W	1	2.052646	1.9149292	2.244238
4878_at	YGR133W	1	3.0990384	4.0886536	5.101346
4882_g_at	YGR136W	1	1.1132524	1.10208	1.0268831
4884_i_at	YGR138C	1	0.7173109	0.63897204	0.44256866
4892_at	YGR102C	1	1.2616303	1.5394821	1.4183476
4894_at	YGR104C	1	1.5979755	1.7254902	1.7041574
4898_at	YGR108W	1	0.6825686	0.93471605	0.7808659
4899_at	YGR109C	1	0.8592115	0.9470798	0.7629322
4900_at	YGR110W	1	0.6011289	0.806158	0.6865277
4903_at	YGR113W	1	1.2813712	1.190886	1.3086334
4908_at	YGR117C	1	1.9589806	2.2999485	2.3897977
4920_at	YGR084C	1	0.6857021	0.5933495	0.51981086
4924_at	YGR088W	1	1.8797345	2.21042	2.244513
4928_at	YGR092W	1	0.84560907	0.7474064	0.8041881
4929_at	YGR093W	1	1.0700895	1.419043	1.4150293
4938_at	YGR057C	1	5.2061253	6.0268407	6.4919686
4945_at	YGR064W	1	2.4078407	2.5313299	2.2852583
4947_at	YGR066C	1	3.4455771	2.7373078	3.0703845

4949_at	YGR068C	1	1.0471886	0.9397489	1.0672867
4951_at	YGR070W	1	2.5203195	2.6815286	2.047959
4952_at	YGR071C	1	1.0809087	1.2246544	3.0420597
4953_at	YGR072W	1	0.8162448	1.2303352	0.9237968
4954_at	YGR073C	1	1.6045763	2.1764975	2.5383859
4955_at	YGR074W	1	1.797876	2.2097278	1.9077233
4957_at	YGR030C	1	0.83737713	0.99184906	0.8298341
4959_at	YGR032W	1	2.4307249	2.2038834	2.2684958
4965_at	YGR039W	1	2.33514	2.8842008	2.83539
4966_at	YGR040W	1	3.7094767	4.019848	3.7120714
4968_at	YGR042W	1	3.2925265	3.6753075	3.722121
4969_at	YGR043C	1	3.3402305	3.5176177	3.5863538
4980_at	YGR008C	1	0.78430873	0.70945776	0.67003024
4988_at	YGR015C	1	5.516731	5.0561543	4.8684616
4989_at	YGR016W	1	2.3150861	1.781923	1.5578847
4992_at	YGR019W	1	1.6135569	1.1618954	1.1625835
4997_at	YGR024C	1	2.1373324	2.3900762	2.3261387
5007_at	YGL010W	1	1.3482716	1.60947	1.0553796
5013_at	YGL004C	1	1.7543241	3.236135	3.2132177
5020_at	YGR003W	1	2.0305276	2.3760595	2.3893783
5025_at	YGL037C	1	0.8991708	0.84154195	0.7810487
5033_at	YGL029W	1	0.63258237	0.65762055	0.657075
5044_at	YGL018C	1	1.1143326	1.0232286	1.1218207
5050_at	YGL057C	1	0.6782263	1.1374698	0.8678737
5051_at	YGL056C	1	1.1968249	1.6482573	1.4802439
5054_at	YGL053W	1	1.4478121	1.6791482	1.4775573
5056_at	YGL051W	1	3.1085281	2.8864126	2.6980162
5086_at	YGL066W	1	1.2034141	1.460717	1.0455967
5089_at	YGL063W	1	10.343847	10.206731	9.435769
5099_at	YGL098W	1	1.4473865	1.9484916	1.834502
5101_at	YGL096W	1	1.9416152	3.129759	2.9229813
5102_at	YGL095C	1	0.76580834	0.7304355	0.82914513
5109_at	YGL088W	1	0.6752806	0.577646	0.5613915
5117_at	YGL125W	1	1.4484868	1.4596164	1.2855191
5121_at	YGL121C	1	1.4459383	1.7089441	1.384391
5126_at	YGL116W	1	0.97833204	1.1863387	1.1457785
5142_i_at	YGL147C	1	0.7454198	0.78114665	0.6373941
5160_at	YGL128C	1	3.5375607	2.9270718	2.989632
5162_at	YGL173C	1	0.7531815	0.81793654	0.85279655
5166_at	YGL169W	1	1.0152016	1.202126	1.2500844
5169_at	YGL166W	1	1.276062	1.2516165	1.1864835
5171_at	YGL164C	1	0.9968438	1.2159934	1.0410974
5179_at	YGL156W	1	3.0408683	2.3954003	2.2604847
5181_at	YGL154C	1	2.162304	2.6532567	2.5282829
5185_at	YGL194C	1	0.978334	1.5985247	1.2190064
5186_at	YGL193C	1	10.169846	10.075173	8.473883
5195_at	YGL185C	1	1.4862598	1.3198354	1.3636315
5214_at	YGL211W	1	1.6346753	2.2268765	2.1390276
5231_at	YGL237C	1	0.80383706	0.47077042	0.38463694
5246_at	YGL224C	1	1.47088	1.6924357	1.5412596
5247_at	YGL223C	1	4.7457285	5.5927057	5.167682

5251_f_at	YGL261C	1	4.6686225	5.677373	4.9785395
5253_g_at	YGL259W	1	3.3040385	4.208846	3.0753846
5256_at	YGL257C	1	1.5428141	2.6345778	2.2201679
5257_at	YGL256W	1	3.0793324	3.9002984	2.9852593
5259_at	YGL254W	1	2.2396119	2.298487	1.9067926
5262_at	YGL251C	1	5.6807694	4.4525	5.5584617
5265_at	YGL248W	1	1.5703297	1.6136854	1.6115848
5266_at	YGL247W	1	2.3326604	2.8685994	2.939497
5270_at	YGL243W	1	2.9228454	3.4919524	3.7426758
5281_f_at	NFL013C	1	4.209808	3.058269	4.2767305
5284_at	NFL008W	1	2.5756836	2.9117634	2.7940502
5291_at	NFR001W	1	2.554751	2.073438	2.4898648
5292_at	NFR003C	1	1.1961236	1.1455047	1.1328968
5299_at	YFR045W	1	0.99264795	0.94108903	0.8856441
5300_at	YFR046C	1	1.995722	2.0358222	1.9917798
5310_at	YFR055W	1	1.7444415	1.756489	1.9319136
5312_s_at	YFL043C	1	1.3542283	1.2004614	1.0037495
5314_at	YFL021W	1	1.0838461	1.1642308	1
5317_s_at	YFL042C	1	1.4271195	1.4967308	1.5074999
5319_at	NFL007C	1	1.2240819	2.423801	1.4414877
5323_at	YFR026C	1	14.164055	11.3782835	10.483751
5324_at	YFR027W	1	0.8918406	0.821429	0.9638312
5326_at	YFR029W	1	1.1722658	1.0835485	1.0834556
5343_at	YFR044C	1	0.87432164	0.89592385	0.86780334
5347_at	YFR005C	1	2.243123	3.0393074	3.020146
5356_at	YFR014C	1	2.2680962	1.8656242	2.1625504
5357_at	YFR015C	1	0.80112946	0.85589683	1.0315781
5359_at	YFR017C	1	1.8542176	1.5717713	1.4536544
5362_at	YFR020W	1	4.542617	3.7699795	3.8017993
5364_at	YFR022W	1	5.608073	5.1926594	5.4748974
5367_at	YFL018C	1	0.76207924	0.6854187	0.68703854
5372_at	YFL014W	1	0.41175106	0.90056753	0.5560905
5373_at	YFL013C	1	1.141426	1.6507666	1.7871175
5400_at	YFL030W	1	1.4513012	1.8940114	1.5651041
5401_at	YFL029C	1	1.6269879	1.4434421	1.3341539
5402_at	YFL028C	1	1.375427	1.3515707	1.3443317
5403_at	YFL027C	1	2.8966887	2.355764	2.960732
5406_at	YFL024C	1	0.9616878	1.0924171	1.0489434
5410_f_at	YFL020C	1	4.9829555	4.1596575	3.9356675
5423_s_at	YFL057C	1	6.33111	7.6845	7.625944
5425_at	YFL055W	1	2.4506788	2.7563462	2.8180768
5426_at	YFL054C	1	3.222733	2.754686	2.8999493
5430_at	YFL050C	1	9.932307	10.830769	9.215962
5431_at	YFL049W	1	1.2899772	1.6748322	1.6527262
5440_at	NER031W	1	2.0404744	2.1666226	2.0463595
5444_at	NER038W	1	0.6982628	0.5258924	0.6651387
5453_at	NER022W	1	4.0184617	3.5298076	2.5390382
5454_at	NER024W	1	10.496731	9.433462	8.571731
5455_at	NER027C	1	1.6597847	0.49078652	0.88515466
5460_at	NER042C	1	0.90026796	0.9051662	1.012044
5468_at	NEL017W	1	2.3753963	2.5780435	2.6490917

5471_at	NEL006W	1	0.9311667	1.9399945	1.3501817
5474_at	NER029C	1	2.6845942	1.75407	1.8249772
5476_at	NER034C	1	0.8070941	0.8514417	0.9338323
5478_i_at	NER049C	1	3.3370137	5.342732	4.7178626
5479_r_at	NER049C	1	3.4481244	6.1270437	5.8587675
5489_at	NEL010C	1	0.64687	0.7692013	0.71753496
5500_at	YER067W	1	1.4050951	1.3121407	1.0808389
5509_at	NER004C	1	12.167509	15.808185	14.640814
5512_at	NER048C	1	10.527622	20.28206	18.92244
5514_at	NEL024C	1	3.716085	4.9049683	4.057367
5515_at	NEL020C	1	5.704548	6.4124475	6.356096
5518_at	NER017W	1	4.850132	5.1763334	4.627124
5521_at	YER173W	1	2.1852627	3.4718156	3.3984585
5523_at	YER175C	1	1.8680433	1.7701558	1.5324955
5529_at	YER180C	1	7.5829153	8.595085	8.962152
5533_at	YER184C	1	2.5695255	2.994355	2.8633938
5534_at	YER185W	1	6.0427833	6.4421153	6.0430765
5535_at	YER186C	1	2.9442635	2.8867922	2.8006935
5536_at	YER187W-A	1	5.606255	4.696154	6.0798078
5537_at	YER188W	1	6.5055532	7.0833344	7.69491
5539_at	YER039C-A	1	1.9258891	1.7228847	1.798846
5544_at	YER150W	1	2.6213713	1.9999318	2.3370354
5552_at	YER158C	1	1.0599515	1.3022072	1.123954
5553_at	YER159C	1	1.0064075	1.2134267	1.3754246
5555_at	YER162C	1	1.7018572	2.2718148	2.4014716
5556_at	YER163C	1	1.5977265	1.8899367	2.0401678
5564_at	YER171W	1	1.4069378	1.7822826	1.8953328
5567_at	YER127W	1	0.66106224	0.8524101	0.9402175
5570_at	YER130C	1	1.3564576	1.3905538	1.4062668
5578_at	YER137C	1	0.63524896	0.6420431	0.74594986
5579_at	YER139C	1	2.030198	2.3823855	2.2595127
5586_at	YER146W	1	0.7164055	0.67087615	0.70239645
5587_at	YER147C	1	1.1625029	1.1736712	1.0911577
5588_at	YER103W	1	3.4225924	3.338494	3.1040938
5589_at	YER104W	1	2.8211727	3.3215384	3.4571154
5593_at	YER108C	1	2.551652	2.4017308	2.5326924
5600_at	YER115C	1	4.757613	4.2098985	4.074821
5601_at	YER116C	1	2.823381	2.1978836	2.4804676
5606_at	YER121W	1	1.0499737	0.88014126	1.2275848
5608_at	YER123W	1	0.86488676	1.3807231	1.356409
5609_at	YER124C	1	0.7133576	0.92095864	0.88905686
5610_at	YER082C	1	0.80768925	0.86420834	0.8119902
5617_at	YER088C	1	0.97346795	1.3261681	1.2604558
5621_at	YER092W	1	1.8667983	1.7252429	1.8207135
5627_at	YER096W	1	1.5938174	1.4407692	1.3698077
5629_at	YER098W	1	1.891808	2.2175262	1.7522627
5632_at	YER101C	1	2.6338365	2.8565183	2.6873453
5634_at	YER063W	1	0.862188	0.886819	0.94087356
5636_at	YER065C	1	3.9162922	4.8792496	4.622053
5637_at	YER066W	1	23.78812	23.230963	22.85
5638_g_at	YER066W	1	3.0171084	3.4554782	3.1317863

5640_at	YER067W	1	1.8843068	1.1933353	1.3503879
5642_at	YER069W	1	1.5566006	1.8117783	1.7258065
5643_at	YER070W	1	0.7702892	0.89743525	0.8245832
5646_at	YER073W	1	0.94530344	1.062999	0.9820257
5649_at	YER076C	1	5.5696373	5.4828596	5.252862
5650_at	YER077C	1	0.7672869	0.8652477	0.8380237
5653_at	YER080W	1	0.6337655	0.609697	0.59355766
5654_at	YER081W	1	2.4018774	2.8761249	2.753871
5656_at	YER045C	1	1.7054831	1.6885269	1.6036694
5657_at	YER046W	1	2.2090685	2.1335022	1.6772872
5665_at	YER053C	1	1.2918501	1.3442671	1.2438992
5672_at	YER057C	1	0.90264237	0.7787274	0.86366844
5673_at	YER058W	1	0.7012199	0.6170962	0.62759954
5676_at	YER060w-A	1	1.916446	1.7408861	1.7407544
5677_at	YER061C	1	1.0559595	0.86454403	0.82038087
5678_at	YER023W	1	0.83960307	0.84200335	0.8441411
5679_at	YER024W	1	5.57406	6.166491	6.2999296
5683_at	YER028C	1	5.8013463	6.4298077	7.7249994
5685_at	YER030W	1	0.86998856	0.8542911	0.82608837
5689_at	YER034W	1	1.034166	1.0365129	1.099277
5690_at	YER035W	1	0.8852641	0.7614771	0.7686894
5696_at	YER041W	1	4.5113487	3.7244918	3.8722913
5697_at	YER042W	1	0.74943316	0.9555306	0.8955164
5699_at	YER044C	1	0.90244526	0.88608885	0.8610398
5706_at	YER007W	1	1.9235063	1.9268459	2.2356079
5715_at	YER015W	1	3.103958	2.9163709	2.1278434
5716_at	YER016W	1	1.1822673	1.2444305	1.2559533
5718_at	YER018C	1	1.3702241	0.87098324	0.90519255
5725_at	YEL020C	1	1.3504927	1.6662037	1.8985717
5731_at	YEL016C	1	2.685846	3.073944	2.6803415
5732_at	YEL015W	1	0.8400508	0.848024	0.8718829
5735_at	YEL011W	1	1.3561957	1.31665	1.2350847
5740_at	YEL006W	1	2.6864147	2.7271733	2.7528417
5741_at	YEL005C	1	2.2667198	2.3694232	2.268077
5742_at	YEL004W	1	1.8328032	2.2192626	2.4443579
5745_at	YEL001C	1	0.6812317	0.7641308	0.7919789
5749_at	YEL041W	1	2.5476923	2.9903846	2.4386537
5751_at	YEL039C	1	0.6876601	0.55357623	0.5447334
5760_at	YEL030W	1	4.762628	7.983677	7.86444
5762_at	YEL028W	1	8.454699	8.751492	9.23258
5765_at	YEL025C	1	1.9283104	2.5558863	2.2775617
5767_at	YEL023C	1	2.5178847	2.9578843	2.5873077
5769_at	YEL065W	1	1.8916794	2.7749114	2.2441602
5771_at	YEL063C	1	9.673417	12.08626	11.038882
5772_at	YEL062W	1	2.286091	2.2370207	2.0372865
5775_at	YEL059C-A	1	1.0230995	0.858718	0.18352933
5778_at	YEL057C	1	1.8809124	2.3527179	1.4567792
5786_f_at	YEL049W	1	8.239486	6.3981156	5.303102
5787_at	YEL048C	1	7.7622232	7.2853847	5.799038
5793_at	NDR076W	1	2.2441456	2.2068055	1.9235506
5798_at	NDR104W	1	1.8890575	1.3819062	1.2141418

5799_at	NDR129W	1	1.776082	2.6112463	1.8861002
5802_at	NDR163W	1	4.070577	4.1748075	3.4840384
5804_at	SNR63	1	0.6930479	0.5565743	0.5045489
5807_at	SNR13	1	0.6389349	0.49876353	0.47194296
5809_i_at	YEL074W	1	13.265511	13.369102	13.241328
5810_s_at	YEL074W	1	4.6036186	4.6198416	4.199269
5811_at	YEL073C	1	7.1813464	5.151154	5.732308
5812_at	YEL072W	1	3.3276925	3.361731	3.6248076
5820_at	NDR166C	1	0.6019999	0.39985374	0.43788612
5831_at	NDR001C	1	2.543458	2.1581924	2.7396398
5838_at	NDR042C	1	1.1032267	1.3697289	1.1412808
5850_at	NDL014W	1	1.0788304	1.1451924	1.1038462
5853_at	NDL006C	1	2.9745276	2.711833	2.027771
5854_at	NDR002C	1	8.415779	3.439035	3.1373992
5855_at	NDR012W	1	1	1	1
5862_at	NDR077C	1	2.4654884	2.814787	2.5359716
5863_at	NDR136C	1	1.8268437	1.891504	1.6058016
5864_at	NDR078W	1	1.8422914	1.4356153	1.4241712
5867_at	NDR105C	1	1.6083713	1.1074669	0.7387825
5872_at	NDR155W	1	1.8567035	1.8748732	1.7075552
5873_at	NDR159C	1	1.3045696	1.5965753	1.3662744
5874_at	NDR164W	1	0.5489832	0.4930914	0.48397127
5877_i_at	NDL041C	1	1.7142445	1.6265512	1.5192235
5878_r_at	NDL041C	1	1.8960904	1.7196326	1.6631255
5880_at	NDL023C	1	0.83438635	0.7729852	0.7694384
5892_at	NDR005C	1	2.3508232	2.2496154	2.9253845
5897_at	NDL036C	1	2.4991696	2.3160253	2.8174353
5898_at	NDL035C	1	14.761943	17.035866	16.10297
5913_at	YDR534C	1	3.485867	4.4509516	2.8547673
5920_at	YDR541C	1	2.2972932	2.8347452	2.9768324
5922_s_at	YDL185W	1	0.9691739	1.4242008	1.1135209
5923_at	YDL085C-A	1	0.839748	0.7028228	0.7138401
5929_at	NDL015C	1	4.845197	5.297357	4.974863
5933_at	NDR045W	1	1.0355349	1.3417886	1.1500185
5936_at	YDR512C	1	0.35924366	0.48921248	0.5983472
5937_at	YDR513W	1	0.66781473	0.6399843	0.6412305
5938_at	YDR514C	1	0.7890961	2.288838	1.893324
5940_at	YDR516C	1	0.8795173	0.66248643	0.603046
5948_at	YDR524C	1	1.2433913	1.1786219	1.1754211
5954_at	YDR530C	1	4.4980206	4.2028093	4.472361
5958_at	YDR489W	1	1.1396449	1.0128905	1.0370313
5959_at	YDR490C	1	1.8217118	1.3225458	1.2883044
5968_at	YDR499W	1	2.061362	1.9486974	1.9269743
5981_at	YDR467C	1	1.8869605	2.0314057	1.272861
5987_at	YDR473C	1	2.0149999	2.3530557	2.084918
5993_at	YDR479C	1	2.2241914	2.5211504	2.263419
5994_at	YDR480W	1	1.6760733	1.4444683	1.7344656
6005_at	YDR444W	1	1.734795	2.153492	2.1254416
6012_at	YDR453C	1	2.1994424	2.364914	2.205527
6018_at	YDR459C	1	1.9631082	2.5690699	2.4905133
6021_f_at	YDR461W	1	0.46134663	0.3258681	0.340352

6026_at	YDR420W	1	0.7374734	0.8362487	0.7776052
6027_at	YDR421W	1	3.0884845	2.436204	2.5172472
6045_at	YDR438W	1	2.028228	2.2852883	2.1975832
6046_at	YDR439W	1	2.055347	1.6923238	1.4566331
6047_at	YDR440W	1	0.53763556	0.3914199	0.53935045
6054_at	YDR403W	1	2.301154	1.6138461	1.9059615
6056_at	YDR405W	1	0.83097684	0.49126732	0.61012304
6057_at	YDR406W	1	2.930269	3.2509463	3.299134
6079_at	YDR381W	1	0.7928579	0.87994593	0.8952039
6082_at	YDR384C	1	1.0629514	0.96427554	0.9476051
6084_at	YDR387C	1	4.4444766	4.97417	4.2908316
6088_at	YDR391C	1	2.7315254	3.3127007	3.391874
6089_at	YDR392W	1	1.2790973	0.87406415	0.95833564
6099_at	YDR358W	1	1.1357927	1.0358086	1.0481899
6100_at	YDR359C	1	1.0429212	0.8271955	0.8563193
6104_at	YDR363W	1	1.5247371	1.4344511	1.5959111
6106_at	YDR364C	1	3.8099632	4.522606	4.792199
6110_at	YDR368W	1	0.74726516	0.7733151	0.9291462
6112_at	YDR370C	1	1.8354263	2.1728003	2.3720841
6118_at	YDR332W	1	8.702137	8.219065	9.752615
6120_at	YDR334W	1	0.8548668	0.732742	0.8208918
6122_at	YDR336W	1	3.1382806	2.949615	3.306422
6135_at	YDR349C	1	1.8218424	2.2699628	2.337227
6136_at	YDR350C	1	1.3494954	1.290659	1.1816953
6149_at	YDR318W	1	3.2659755	2.7498775	2.7346425
6155_at	YDR323C	1	1.0136011	1.0228846	1.3303846
6165_at	YDR291W	1	2.126666	2.2444327	2.243722
6190_at	YDR270W	1	0.71802264	0.66324234	0.6140893
6193_at	YDR273W	1	2.7898076	1.8848077	2.625
6195_at	YDR275W	1	2.7720451	4.0553336	4.2610846
6197_at	YDR277C	1	1.5523485	2.2549622	2.4708443
6201_at	YDR281C	1	0.2554179	0.44769505	0.37667182
6202_at	YDR282C	1	2.001636	1.8411206	1.9923544
6205_at	YDR285W	1	7.2176495	8.848959	8.1534195
6208_at	YDR288W	1	1.5818502	1.6011153	1.4280317
6214_at	YDR249C	1	1.6841662	2.1738276	1.9726388
6215_at	YDR250C	1	1.6064596	1.6137568	1.6387928
6217_at	YDR252W	1	2.611197	2.876275	2.72428
6221_at	YDR256C	1	1.4307692	1.1703846	1.0748076
6222_at	YDR257C	1	1.8997667	2.256842	1.9252094
6223_at	YDR258C	1	1.0836072	1.2292969	1.0368361
6225_at	YDR260C	1	1.6065707	1.9337611	1.9141101
6227_at	YDR262W	1	1.0992008	1.318192	1.3536205
6228_at	YDR263C	1	2.090805	2.8647447	2.9449737
6230_at	YDR265W	1	4.0773554	2.971158	2.9621522
6247_at	YDR236C	1	2.5139763	2.685865	2.493465
6253_at	YDR242W	1	12.709528	10.718977	13.442421
6262_at	YDR205W	1	1.4483832	2.2237568	2.2149246
6263_at	YDR206W	1	4.532161	4.004888	4.5468283
6270_at	YDR213W	1	0.9264913	1.0271212	0.93160206
6272_at	YDR215C	1	1.4276924	1.2090385	1

6273_at	YDR216W	1	1.0821154	1.2940385	1.3857692
6277_at	YDR220C	1	0.47635612	0.6395852	0.54684395
6281_at	YDR179W-A	1	1.2638305	1.5373551	1.4679348
6282_at	YDR180W	1	0.7173511	0.8500011	0.71652085
6293_at	YDR191W	1	1.0432334	0.8549481	0.6512682
6297_at	YDR195W	1	1.2233529	1.0203471	1.0787718
6306_at	YDR160W	1	3.1583571	3.1430302	2.7874491
6308_at	YDR162C	1	1.1314045	1.2240511	1.3023747
6309_at	YDR163W	1	1.0624796	1.1318076	1.001005
6317_at	YDR171W	1	0.9120318	0.7011226	0.7871735
6319_at	YDR173C	1	1.4566941	1.8879582	1.910893
6337_at	YDR146C	1	1.0201575	1.5437497	1.4145852
6338_at	YDR147W	1	5.3994427	5.841892	6.8308477
6342_at	YDR151C	1	1.0733161	0.9672688	1.0143614
6346_at	YDR111C	1	1.0639665	1.4684217	1.234535
6348_at	YDR113C	1	0.61177325	0.5813304	0.75525695
6353_at	YDR118W	1	1.7061224	1.824812	2.214515
6356_at	YDR121W	1	0.62809765	0.79619956	0.9631772
6358_at	YDR123C	1	2.3486247	2.7628846	2.1523077
6359_at	YDR124W	1	2.0165386	1.1942308	1.3465384
6361_at	YDR126W	1	3.7193737	4.2126927	3.9248075
6365_at	YDR130C	1	1.4144396	1.7628247	1.6027042
6366_at	YDR131C	1	3.4170294	4.565008	4.2492375
6368_at	YDR089W	1	1.1381528	1.6847197	1.5018525
6375_at	YDR095C	1	0.69643533	0.8836075	0.6153015
6388_at	YDR108W	1	1.629286	1.7973719	2.004941
6389_at	YDR109C	1	1.9109082	2.7099004	2.5141187
6394_at	YDR070C	1	2.2466187	1.9047165	1.8990974
6397_at	YDR073W	1	3.2696695	3.1843886	4.0297093
6398_at	YDR074W	1	0.8631517	0.80797374	0.8570011
6399_at	YDR075W	1	0.7250477	1.0236886	0.9873531
6402_at	YDR078C	1	7.203393	8.7665615	10.103939
6406_at	YDR082W	1	12.134759	13.949566	14.360947
6409_at	YDR085C	1	1.4695498	1.8388484	1.8115457
6412_at	YDR088C	1	0.84587795	1.8327878	0.9348115
6416_at	YDR047W	1	1.9910185	2.3257	2.0999963
6423_at	YDR054C	1	1.0909634	1.6736538	1.9875662
6427_at	YDR058C	1	0.8716354	1.0014352	0.96816593
6428_at	YDR059C	1	0.80840546	0.8269878	0.7761746
6434_at	YDR065W	1	2.0864103	2.7835994	2.102022
6436_at	YDR021W	1	1.128032	1.0412929	1.219279
6437_at	YDR022C	1	3.6470551	3.042923	4.1810327
6440_at	YDR026C	1	1.6503097	1.6747304	1.6509027
6444_at	YDR030C	1	1.246595	1.4794031	1.2971039
6446_at	YDR032C	1	0.9060798	0.8193481	0.77207065
6448_at	YDR034C	1	1.8225931	1.7744014	1.5098834
6449_at	YDR034W-B	1	1.3696054	1.2474729	1.2926704
6451_at	YDR036C	1	1.1427829	1.1186174	1.3602585
6458_at	YDR043C	1	0.943618	0.7375095	0.8620044
6459_at	YDL003W	1	0.5303952	0.6399635	0.6283797
6461_at	YDL001W	1	0.9551756	1.0503263	0.9611216

6462_at	YDR001C	1	1.3277457	0.9830712	1.0219878
6464_at	YDR003W	1	2.2726946	2.3137124	2.3466277
6465_at	YDR004W	1	3.150174	2.717254	2.7293558
6466_at	YDR005C	1	2.5820327	2.603238	2.413052
6468_at	YDR007W	1	17.978832	14.521455	14.294668
6469_at	YDR008C	1	2.7476535	2.2616458	2.8269784
6474_at	YDR013W	1	1.7178817	1.5899997	1.5814563
6477_at	YDR016C	1	1.0895649	1.0600548	1.3012844
6478_at	YDR017C	1	0.96230036	1.7153063	1.758075
6479_at	YDR018C	1	1.1501924	1.0173076	1.0642308
6480_at	YDR019C	1	2.9557135	3.6074495	3.9537122
6481_at	YDR020C	1	1.7716424	1.6828846	1.5219231
6482_at	YDL025C	1	1.9385273	3.08175	2.9575138
6483_at	YDL024C	1	1.5844101	3.0223012	2.9797502
6485_at	YDL022W	1	0.7797397	0.80756074	0.6590504
6487_at	YDL020C	1	1.5023844	1.5758541	1.6175942
6502_at	YDL005C	1	0.8751468	1.1782067	0.84234715
6504_at	YDL047W	1	1.0812018	1.9563658	2.0703104
6508_at	YDL044C	1	1.3235836	1.5202335	1.561347
6513_at	YDL039C	1	0.43375123	0.20130222	0.21481685
6514_at	YDL038C	1	0.40935504	0.1936186	0.18442012
6519_at	YDL033C	1	2.2613447	2.1694086	2.068801
6529_at	YDL069C	1	1.5099312	1.2860951	1.2882767
6540_at	YDL058W	1	0.77484316	1.0526527	1.1585094
6549_at	YDL049C	1	1.1740384	1.2023077	1
6562_at	YDL080C	1	1.9845979	1.8434781	2.0632834
6565_at	YDL078C	1	0.75579065	0.6992729	0.7035649
6573_at	YDL113C	1	1.1217799	1.5955429	1.317542
6577_at	YDL109C	1	2.775011	3.3625228	3.10714
6579_at	YDL107W	1	1.9347931	1.1175001	1.2690384
6595_at	YDL133W	1	1.2581575	1.5515563	1.4713745
6608_at	YDL123W	1	2.7118337	2.38451	2.5931513
6616_at	YDL115C	1	7.227475	10.0079155	11.108437
6621_at	YDL154W	1	4.172008	4.1819234	4.7784615
6629_at	YDL146W	1	1.8086231	2.2845533	1.8455317
6636_at	YDL139C	1	1.7223564	1.5107903	1.0343931
6643_at	YDL177C	1	1.5811535	1.4038438	1.6364621
6644_at	YDL176W	1	1.2625543	1.3119231	1
6645_at	YDL175C	1	1.5393939	1.2612433	1.4076374
6650_at	YDL170W	1	2.58835	2.5808814	2.352283
6651_at	YDL169C	1	0.8335386	0.5627412	0.62276244
6660_at	YDL160C	1	1.0560783	1.1941164	1.0966805
6663_at	YDL200C	1	1.2596624	1.0607958	1.2002963
6666_at	YDL197C	1	3.334115	3.708619	3.465517
6677_at	YDL187C	1	2.596923	2.1103847	1.9338461
6693_at	YDL215C	1	5.831198	7.9577503	7.416788
6701_at	YDL207W	1	1.1694494	1.1664308	1.0974414
6702_at	YDL206W	1	1.8600909	2.742189	2.5626829
6703_at	YDL205C	1	1.1634592	1.6236459	1.746615
6704_at	YDL204W	1	3.8091786	4.536795	4.2226634
6710_at	YDL243C	1	9.983261	9.989287	9.969587

6712_at	YDL241W	1	2.931137	2.4617405	2.56757
6713_at	YDL240W	1	0.73086184	0.77882165	0.7370795
6714_at	YDL239C	1	3.7780507	4.43017	4.1206326
6715_at	YDL238C	1	2.0139425	1.6925058	1.5872254
6719_at	YDL234C	1	2.0653014	1.8407111	1.7825389
6720_at	YDL233W	1	0.9298905	0.76832443	0.70616376
6722_at	YDL231C	1	4.37687	5.1795716	5.128331
6725_at	YDL227C	1	0.6315346	0.52933496	0.4967758
6729_at	YDL223C	1	4.032688	4.259628	5.167637
6730_at	YDL222C	1	1	1	1
6735_i_at	NCR021W	1	0.6946408	0.87578356	0.58331186
6738_at	NCL011C	1	8.530315	9.261553	9.595841
6744_at	NCR002W	1	13.594795	11.7305765	15.755961
6745_at	NCR011C	1	3.5238376	3.4698899	4.2316465
6746_at	NCR024W	1	3.962493	3.6155624	4.861392
6756_at	YCR020W-B	1	5.3087306	4.0799937	4.0741205
6761_at	YCR068W	1	2.2471154	2.6684616	2.268269
6763_at	YCL008C	1	1.2498256	1.2404013	1.3061292
6764_g_at	YCL008C	1	1.7469752	1.1883049	1.4488757
6765_at	NCL004W	1	1	1	1
6766_at	NCR007W	1	5.2046156	3.3298078	3.4326925
6782_at	YCR087C-A	1	1.195977	1.0394224	0.90382516
6783_at	YCR088W	1	0.8490352	0.7800015	0.7338203
6784_at	YCR089W	1	8.979529	5.181018	5.667983
6788_at	YCR093W	1	0.8522675	0.7933385	0.7341788
6793_at	YCR098C	1	3.2813942	4.4193954	4.1012506
6794_at	YCR099C	1	3.6857696	3.6946154	3.4936538
6795_at	YCR100C	1	4.837156	6.094335	4.2187743
6797_at	YCR102C	1	5.5192904	6.830362	7.7193427
6798_f_at	YCR104W	1	2.7552369	2.5295343	2.6779761
6800_at	YCR106W	1	2.7927055	2.2213032	2.3136463
6805_at	YCR063W	1	4.895672	7.499768	7.6762834
6807_at	YCR066W	1	1.1423072	0.9702464	1.0478516
6817_at	YCR076C	1	1.8243577	1.1736057	1.3645358
6827_at	YCR037C	1	3.4469469	3.3589563	3.828043
6845_at	YCR060W	1	1.0041819	0.78063023	0.8467393
6850_at	YCR018C	1	1.6229585	1.6318913	1.6781986
6852_at	YCR020C	1	25.129007	25.143269	27.720768
6854_at	YCR021C	1	0.6412184	0.6937355	0.7566583
6862_at	YCR028C	1	1.9824789	2.4256926	2.2637234
6870_at	YCL010C	1	4.5523806	5.1835694	5.4224453
6875_at	YCL004W	1	2.2698078	2.709423	2.3001924
6876_at	YCL002C	1	1.6635978	1.8333399	1.6022142
6882_at	YCR004C	1	0.8136711	0.64449507	0.6935178
6889_at	YCR013C	1	0.7738032	0.7537763	0.86972815
6893_at	YCL039W	1	3.949128	3.0442443	3.4653525
6894_at	YCL038C	1	1.0721464	0.985312	1.073022
6909_at	YCL018W	1	2.1726809	3.4716928	3.60255
6911_at	YCL016C	1	2.2662873	2.1632926	2.21774
6921_at	YCL056C	1	2.806755	2.4954023	2.7652872
6927_at	YCL049C	1	1.2082897	1.3317412	1.2380157

6936_g_at	YCL042W	1	1.1071389	1.2531891	0.8891283
6939_g_at	SCIIYLEFT	1	4.8022547	4.295976	3.2335055
6941_s_at	SCIIYLEFT	1	1.3620517	2.199108	1.6145862
6945_g_at	SCIIYLEFT	1	5.506346	6.4890385	4.784038
6946_at	SCIIYLEFT	1	8.271935	9.479027	7.406133
6947_g_at	SCIIYLEFT	1	5.409086	5.3907027	5.1447372
6949_f_at	SCIIYLEFT	1	5.878419	4.5205	4.253987
6950_at	SNR56	1	0.58532155	0.28586552	0.281213
6958_s_at	YCL067C	1	5.497714	5.738574	7.137618
6962_at	NBR033C	1	2.4496155	1.4430768	1.7253846
6963_at	NBR034W	1	5.4860497	5.471631	5.601221
6964_s_at	NBR035W	1	7.5932903	7.5125585	7.360305
6965_i_at	NBR036W	1	3.4138465	2.9844232	2.9428847
6967_at	NBR045C	1	1.185435	0.8280175	0.94081765
6978_at	NBR007C	1	1.0304449	1.0939803	1.1341068
6980_at	NBR016C	1	3.4540386	3.6525002	4.576154
6989_at	NBR042C	1	6.01371	4.52	5.665192
6991_i_at	NBR054C	1	0.87349236	0.90798366	0.6078898
6993_f_at	NBR054C	1	0.8076697	0.9698213	0.8695256
6996_at	NBL013C	1	6.208768	6.4744644	6.865961
7008_at	NBR032C	1	2.7456658	2.3019397	2.2576983
7009_g_at	NBR032C	1	3.525872	2.978017	3.2431273
7016_at	NBL005W	1	2.717697	2.761136	3.228074
7017_at	NBR001C	1	0.9320785	1.4216083	1.5760454
7037_s_at	YBR006W	1	2.0911992	1.7723575	1.7804627
7042_at	NBL024W	1	2.375635	1.7664368	1.9950647
7047_at	NBR047W	1	0.6219964	0.454062	0.5378041
7054_i_at	NBR041W	1	2.1113462	1.0096154	1.005577
7057_at	YBR284W	1	4.0434294	3.649394	3.8873682
7064_at	YBR291C	1	2.1274736	2.0160139	2.182841
7066_at	YBR293W	1	5.7244334	6.149831	5.939245
7067_at	YBR294W	1	1.4623448	1.3558154	1.4119637
7068_at	YBR295W	1	3.944727	4.933128	4.7069416
7070_at	YBR297W	1	2.936931	3.3728786	3.550073
7071_s_at	YBR298C	1	22.111153	16.908846	15.86731
7072_s_at	YBR299W	1	2.2175	1.6855769	1.8542306
7074_f_at	YBR301W	1	4.257138	4.609255	4.8272066
7076_at	YBR056W-A	1	2.5446014	2.4907484	2.5495732
7078_at	YBR085C-A	1	2.8050828	2.8642368	3.0719595
7079_at	YBR259W	1	1.9923985	1.961852	1.7240384
7083_at	YBR263W	1	0.9277849	0.95887375	0.9311747
7087_at	YBR269C	1	0.8058258	0.69084895	0.5720998
7088_at	YBR270C	1	12.037254	15.829479	16.270233
7089_at	YBR271W	1	0.937255	0.98700285	1.2567967
7092_at	YBR274W	1	1.8596463	1.8009307	1.9614868
7093_at	YBR275C	1	0.9342223	1.7121847	2.1876981
7096_at	YBR278W	1	3.0270627	1.8418844	1.929995
7102_at	YBR237W	1	2.5199065	1.9618607	1.9355197
7103_at	YBR238C	1	0.8701659	0.8657265	0.80307466
7104_at	YBR239C	1	1.0690905	0.8869693	0.88646877
7109_at	YBR244W	1	3.1449509	2.6249237	2.82674

7115_at	YBR250W	1	2.426923	1.7994231	2.873846
7118_at	YBR253W	1	2.4376469	2.4916565	2.959351
7119_at	YBR254C	1	0.95563483	0.9164603	1.068727
7122_at	YBR257W	1	1.210395	1.3039664	1.2613038
7124_at	YBR214W	1	1.3760228	1.2601726	1.1155052
7126_at	YBR216C	1	2.0332422	2.3380141	2.9736218
7127_at	YBR217W	1	5.129515	6.9934273	7.5916996
7129_at	YBR220C	1	1.1024743	1.1833599	1.1998494
7133_at	YBR223C	1	2.56753	1.8337435	1.9789464
7138_at	YBR228W	1	3.537891	3.276483	3.6062708
7142_at	YBR232C	1	0.6716163	0.6271995	0.4949823
7149_at	YBR193C	1	2.3393395	3.3525934	3.9867425
7150_at	YBR194W	1	1.0241358	1.2046534	1.1726234
7153_at	YBR197C	1	3.0348334	3.39362	3.0093632
7161_g_at	YBR205W	1	0.86520356	0.68231004	0.7547896
7164_at	YBR208C	1	2.76925	2.9383523	3.4847481
7170_at	YBR168W	1	3.0850768	3.0909615	2.911923
7171_at	YBR169C	1	0.96580297	1.0747291	1.0941358
7177_at	YBR175W	1	1.7881641	1.7883269	1.9081165
7183_at	YBR182C	1	3.7968185	5.534012	7.122263
7185_at	YBR184W	1	6.1580853	3.9254987	4.558878
7193_at	YBR147W	1	1.3144338	1.3961236	1.0889878
7194_at	YBR148W	1	2.136923	1.5701922	2.3163462
7196_at	YBR150C	1	0.7767965	0.91204625	1.0276712
7199_at	YBR153W	1	0.97911435	0.952981	1.0260532
7202_at	YBR156C	1	1.8601794	1.3275466	1.5610731
7210_at	YBR163W	1	3.2054098	3.7761548	4.00098
7212_at	YBR165W	1	0.7746596	0.8443175	0.8581633
7214_at	YBR167C	1	1.6077007	1.630171	1.5757818
7222_at	YBR131W	1	0.9968993	1.1192285	1.2517575
7232_at	YBR141C	1	0.8396247	0.86927915	0.9968903
7236_at	YBR145W	1	2.3356209	1.7733933	1.7085226
7241_at	YBR105C	1	0.6769045	0.6846289	0.8142619
7243_at	YBR107C	1	2.2444181	2.4353118	2.8711534
7247_at	YBR111C	1	0.99038124	0.7509022	0.798167
7252_at	YBR116C	1	1.9471631	2.6465492	2.482348
7253_g_at	YBR116C	1	1.5094782	2.0826397	1.8747038
7254_at	YBR117C	1	1.3894231	1.4557692	1.1634616
7263_at	YBR085W	1	2.048441	1.7456224	2.1657975
7266_at	YBR088C	1	0.6350111	0.6525646	0.6985788
7275_at	YBR094W	1	1.5172591	1.4431167	1.7280713
7276_at	YBR095C	1	0.7964716	0.8375356	0.8164383
7280_at	YBR099C	1	1.805798	1.7384471	1.6908092
7281_at	YBR100W	1	1.6718299	1.5496862	1.6101854
7286_at	YBR063C	1	2.1756718	2.4117813	2.4028203
7289_at	YBR066C	1	1.1212472	1.009872	1.040359
7294_at	YBR071W	1	0.63194585	0.70794684	0.56689847
7295_at	YBR072W	1	0.8695965	0.8441684	0.9384556
7297_at	YBR074W	1	1.6254506	2.3611038	1.6107821
7299_at	YBR076W	1	1.3999126	1.2369231	1.1117308
7300_at	YBR077C	1	2.002689	1.6938413	2.0173988

7311_at	YBR043C	1	6.387043	6.6291265	7.15702
7314_at	YBR046C	1	0.92338914	0.9509778	1.0073411
7315_at	YBR047W	1	2.266594	1.9889334	2.4217808
7318_at	YBR050C	1	5.0941305	3.110971	2.9696598
7320_at	YBR052C	1	0.7752398	0.6495936	0.70213807
7321_at	YBR053C	1	0.87269366	0.75335556	0.7619535
7322_at	YBR054W	1	2.0242639	3.9430585	2.5465248
7323_at	YBR055C	1	2.1742475	1.6168696	2.2995224
7325_at	YBR057C	1	0.7380189	0.71104664	0.75300986
7329_at	YBR016W	1	0.6866393	0.46821278	0.55238277
7331_at	YBR018C	1	2.6339736	1.9248562	2.5223176
7333_at	YBR020W	1	2.3581145	2.8076923	3.039423
7339_at	YBR026C	1	0.6857791	0.63277316	0.5677122
7343_at	YBR030W	1	3.0641465	2.3765092	2.8774447
7347_at	YBR033W	1	1.2213461	1.1438462	1.0307692
7364_at	YBR004C	1	1.349233	1.3494246	1.261785
7367_at	YBR008C	1	8.546457	9.991407	10.916827
7374_at	YBL031W	1	1.1256663	1.23238	1.3815194
7376_at	YBL029W	1	0.8985869	0.7286366	0.76820254
7380_f_at	YBL026W	1	1.0899789	0.5665685	0.50728106
7382_at	YBL025W	1	6.7715883	5.0118246	6.4007215
7386_at	YBL021C	1	1.2768878	1.4945121	1.4564471
7388_at	YBL019W	1	4.8794603	4.381354	5.0042934
7397_at	YBL010C	1	1.322746	1.3953149	1.9857585
7398_at	YBL054W	1	0.74242926	0.8219062	0.89978325
7399_at	YBL053W	1	1.1941555	2.0519373	1.567989
7403_at	YBL049W	1	1.5505426	1.7259272	1.4317608
7404_at	YBL048W	1	1.5817378	1.0649688	1.2328867
7409_at	YBL043W	1	0.8063677	0.9386245	0.9386245
7410_at	YBL042C	1	0.9126631	0.940719	1.099825
7422_at	YBL075C	1	6.4385905	4.7435513	5.8292627
7431_at	YBL065W	1	1.2421348	0.8636417	0.80934715
7434_at	YBL062W	1	0.8098905	1.0767326	1.0405322
7436_at	YBL060W	1	4.9527955	5.575783	5.930338
7453_at	YBL088C	1	3.0008695	2.6038861	2.7214837
7464_at	YBL078C	1	1.2220459	0.97392625	1.0957462
7465_at	YBL077W	1	0.9258511	1.1377816	1.1343958
7469_at	NPR012W	1	2.1888523	1.7876925	1.6375002
7475_at	SNR70	1	0.9561087	1.0043566	0.85241425
7478_s_at	YBL109W	1	10.769218	10.313801	7.554401
7480_at	YBL106C	1	1.4810598	1.599318	1.6700473
7483_at	YBL103C	1	0.92220616	0.963361	1.1015717
7490_at	NPR090C	1	1.6646365	1.6500494	1.6510451
7494_at	NPL016W	1	5.7281847	4.0064645	4.578119
7499_at	NPR009C	1	0.8793951	0.52318525	0.41759235
7505_at	NPR089C	1	17.808462	14.665577	13.135769
7506_at	NPL013C	1	1.3499671	2.1109686	1.8807777
7509_at	NPL009C	1	2.5524962	2.0777807	2.449711
7510_at	NPL005W	1	2.1649451	2.6880035	2.6651204
7511_at	NPL001W	1	1.395712	2.2952604	1.6554115
7513_f_at	NPR041W	1	1.97932	2.597726	2.047492

7518_at	NPL007W	1	2.8514993	2.6519275	2.7331514
7524_at	NPR015C	1	0.93505096	1.103833	0.74196565
7526_i_at	NPR023C	1	1.1133089	1.0861061	1.0227845
7530_s_at	NPR082W	1	0.45578134	0.6423346	0.8401473
7538_at	YPR186C	1	1.0054595	1.4605997	1.8670332
7544_at	YPR192W	1	1.9802909	2.1392717	1.1861978
7545_at	YPR193C	1	6.070577	4.1342306	4.5898075
7546_at	YPR194C	1	7.0640507	11.321786	11.532639
7548_at	YPR196W	1	6.2659616	3.8332694	4.4663463
7549_g_at	YPR196W	1	3.660909	3.3956678	3.904416
7552_at	YPR199C	1	2.7478883	2.628349	2.6191702
7553_at	YPR200C	1	1.5140917	2.2342033	2.4486237
7555_s_at	YPL075W	1	1.7250354	2.0955675	2.1763778
7556_at	NPL022C	1	0.74657655	0.910355	0.6767974
7566_at	YPR168W	1	3.8349967	3.0917656	3.394084
7567_at	YPR169W	1	2.1055176	1.9688985	2.0955203
7570_at	YPR172W	1	0.6286299	0.73986244	0.6860237
7576_at	YPR178W	1	1.6394596	1.6100668	1.8969814
7582_at	YPR184W	1	1.5888282	1.6812317	1.6225218
7587_at	YPR144C	1	1.4039657	1.3762786	1.5203853
7595_at	YPR152C	1	1.262008	1.1499667	1.0398307
7596_at	YPR153W	1	2.877308	2.8392308	2.5882692
7604_at	YPR160W	1	0.7529975	0.8285159	0.6786095
7607_at	YPR121W	1	6.189401	7.3080244	7.16201
7610_at	YPR124W	1	0.6785976	0.378619	0.54757154
7612_at	YPR126C	1	0.8602985	0.8049266	0.7292905
7631_at	YPR101W	1	1.9299188	1.1525	1.0792308
7637_at	YPR106W	1	1.2198615	1.2478967	1.3547829
7638_at	YPR107C	1	1.0829754	0.98052055	1.225859
7643_at	YPR111W	1	0.95038396	0.9711888	1.4368917
7644_at	YPR112C	1	0.61712265	0.7927472	0.8312812
7657_at	YPR081C	1	2.005243	2.2837248	2.2303467
7658_at	YPR082C	1	1.9343191	2.0781884	1.9992627
7660_at	YPR084W	1	0.9895211	0.9255557	0.9177834
7661_at	YPR085C	1	6.329947	6.391609	6.8425336
7669_at	YPR093C	1	1.0939832	0.9237974	0.96520925
7677_at	YPR057W	1	2.5984936	2.5048997	2.3349469
7686_at	YPR066W	1	2.4419231	2.4426923	3.1257694
7688_at	YPR068C	1	3.189423	2.5651922	2.4969232
7690_at	YPR070W	1	5.024893	3.942079	5.256199
7691_at	YPR071W	1	2.7283316	2.7097158	2.6768506
7695_at	YPR075C	1	0.91234404	0.8815327	0.98425555
7697_i_at	YPR077C	1	1.0940385	1	1
7711_at	YPR046W	1	2.0431755	1.759265	1.7374887
7712_at	YPR047W	1	0.70181227	0.7682495	0.7249433
7717_at	YPR052C	1	0.7231811	0.7505106	0.80573577
7724_at	YPR017C	1	1.5922785	1.9185756	2.2129219
7728_at	YPR021C	1	2.1173139	2.4087555	2.0095742
7733_at	YPR026W	1	2.4611495	2.1467304	1.9220802
7745_at	YPL008W	1	2.0194192	2.7836607	2.7861135
7749_at	YPL004C	1	0.8747654	0.805135	0.7956163

7750_at	YPL003W	1	2.2766685	2.6463957	2.209303
7751_at	YPL002C	1	2.1402328	1.4531171	1.4579753
7754_at	YPR002W	1	1.8404359	1.4598078	1.6626923
7757_at	YPR005C	1	4.7736726	3.9394765	3.973565
7764_at	YPR012W	1	4.8598666	5.258335	4.3634024
7765_at	YPR013C	1	2.8794231	1.4725	1.4748077
7774_at	YPL024W	1	1.7930967	1.6448475	1.7072209
7776_at	YPL022W	1	4.40329	3.9611502	3.6061049
7780_at	YPL018W	1	2.1123	2.2376924	1.7069231
7786_at	YPL012W	1	0.75628316	0.9268922	1.018199
7787_at	YPL011C	1	0.80413216	0.7928885	0.75503534
7796_at	YPL047W	1	3.5393696	4.006095	4.0952373
7804_at	YPL039W	1	1.208752	1.0717484	0.98752487
7809_at	YPL034W	1	6.730958	7.3294	7.2796187
7817_at	YPL072W	1	2.587896	2.4934902	1.8805108
7818_at	YPL071C	1	6.2825994	4.018401	4.528231
7819_at	YPL070W	1	1.1447778	1.9706517	1.8563411
7823_at	YPL066W	1	2.6579397	2.1173027	1.9634387
7825_at	YPL064C	1	3.304411	3.4907956	3.8877277
7828_at	YPL061W	1	0.99003816	0.8236989	0.95669705
7831_at	YPL058C	1	1.9034038	2.4583683	2.7292204
7833_at	YPL056C	1	1.3420925	1.1987208	1.2242563
7840_at	YPL095C	1	3.9405856	3.409285	4.2162833
7843_at	YPL092W	1	1.5554887	1.7249446	1.7575808
7846_at	YPL089C	1	1.0152124	1.0594845	1.0405993
7847_at	YPL088W	1	4.0228634	3.7660294	3.7842314
7853_at	YPL082C	1	0.7461413	0.7732505	0.7490533
7857_at	YPL123C	1	0.9496931	0.9987719	1.4751524
7868_at	YPL112C	1	0.633149	0.6817506	0.8137499
7869_at	YPL111W	1	1.4518576	1.1966348	1.187572
7876_at	YPL104W	1	0.8859655	0.88983786	0.86120725
7881_at	YPL144W	1	2.0205054	1.9038137	1.8675253
7885_at	YPL140C	1	1.4767025	1.2913203	1.3310071
7887_at	YPL138C	1	1.8514335	1.8646088	2.1657162
7892_at	YPL133C	1	2.5273852	2.0029497	1.8842896
7898_at	YPL127C	1	0.58631355	0.53591996	0.6539258
7901_at	YPL124W	1	0.7711383	0.63611007	0.67242146
7903_at	YPL167C	1	2.397725	2.5013702	2.443926
7906_at	YPL164C	1	6.0467496	5.030769	5.8617306
7908_at	YPL162C	1	1.8341024	2.519312	1.9888117
7914_at	YPL156C	1	2.415059	2.4058068	2.4998498
7915_at	YPL155C	1	1.1738627	1.239285	1.2426488
7918_at	YPL152W	1	1.6327336	1.9331648	1.8967782
7919_at	YPL151C	1	2.405879	2.121559	2.2681909
7921_at	YPL149W	1	2.9706655	3.3448007	3.416123
7922_at	YPL148C	1	5.4092426	5.7851615	6.305384
7923_at	YPL147W	1	3.178937	3.3900795	3.233669
7925_at	YPL189W	1	1.5184919	1.4789788	1.4679177
7928_at	YPL186C	1	1.9311742	1.883842	1.6514788
7940_at	YPL175W	1	1.884635	1.6733629	1.5954752
7942_at	YPL173W	1	0.6342019	0.5600816	0.5101425

7944_at	YPL171C	1	1.4271324	1.0791014	1.2056375
7956_at	YPL202C	1	1.422333	1.4488379	1.4159522
7963_at	YPL197C	1	1.3015437	1.8202502	1.6000894
7964_at	YPL196W	1	1.0931996	1.1335831	1.2238395
7971_at	YPL233W	1	2.328702	2.5773618	2.002582
7975_at	YPL229W	1	1.0395302	1.1103058	1.0794774
7981_at	YPL223C	1	1.6337687	1.2662575	1.231222
7982_at	YPL222W	1	2.0257914	0.95016944	1.3118343
7988_at	YPL216W	1	2.0980794	1.7128808	1.9653009
7990_at	YPL214C	1	3.2687309	2.6849153	3.1337953
7991_at	YPL213W	1	1.4146475	1.1846824	0.75825334
7992_at	YPL212C	1	0.8160833	0.7564857	0.780674
7997_at	YPL252C	1	0.7048325	0.6718602	0.7189995
7999_at	YPL250C	1	1.1874231	1.2542756	1.1313472
8003_at	YPL247C	1	0.9164609	0.92566	0.9669829
8005_at	YPL245W	1	1.4797641	1.4808321	1.4270613
8008_at	YPL242C	1	1.43481	1.5552404	1.4676273
8010_i_at	YPL240C	1	1.0749233	1.1325167	0.9972559
8014_at	YPL236C	1	3.5229855	4.4500117	3.902183
8019_s_at	YPL277C	1	3.4257693	2.8311539	2.6482692
8023_at	YPL272C	1	5.7200227	7.145611	5.805823
8031_at	YPL264C	1	3.2175648	2.7220798	2.329689
8037_at	YPL258C	1	13.349421	12.400873	13.900747
8038_at	YPL257W	1	3.4007692	3.1651921	3.6598077
8042_at	NOR038W	1	4.460636	4.5654087	4.8617916
8044_at	NOR052W	1	7.055195	6.471539	6.9929304
8045_at	NOR056W	1	1.084465	1.7114204	1.609345
8048_at	NOR077W	1	1.6120573	1.6891534	1.7311039
8049_at	NOR080W	1	1.7844231	1.4698076	1.9157692
8056_at	SNR9	1	0.7512007	0.6232982	0.6393034
8059_at	SNR36	1	0.6995129	0.45789796	0.40596345
8062_at	SNR8	1	0.628435	0.30147937	0.2964023
8064_at	NOR060C	1	3.4615383	2.8619232	3.4934614
8066_at	NOR069C	1	5.4343386	4.8574376	5.0789046
8074_s_at	NOR086C	1	1.5677955	2.5066192	1.7713108
8076_at	NOL055C	1	2.8788462	2.748077	2.3428845
8078_at	NOL053C	1	2.3003845	2.2038462	2.3303847
8091_at	NOR068C	1	0.8044763	1.2658968	1.1288728
8092_i_at	NOR079W	1	1.3316879	1.664939	1.3354949
8093_r_at	NOR079W	1	1.215994	1.7686192	1.1971526
8096_at	NOR003W	1	0.8523352	0.75441587	0.68863946
8099_at	NOL052C	1	2.5315385	2.4048076	1.9661539
8102_at	NOL020W	1	2.1166377	2.1706278	2.5736513
8106_at	NOR005W	1	4.8194947	2.7594075	3.3988142
8107_at	NOR007W	1	0.5990336	0.42334148	0.4736501
8112_at	NOL056C	1	6.2238507	7.4240975	7.6682267
8115_f_at	NOR009W	1	0.547904	0.48377457	0.47181183
8120_at	NOL039W	1	3.7290034	3.5087857	2.9659698
8131_at	NOR006W	1	16.03611	14.777402	15.082811
8143_at	YOR389W	1	4.3857327	4.1242733	4.711966
8144_g_at	YOR389W	1	5.315943	7.846659	8.630915

8145_s_at	YOR390W	1	1.408252	3.2329676	2.5146675
8147_s_at	YOR394W	1	1.6526923	1.4982693	1.3165386
8149_at	YOL038C	1	1.3130683	2.0140538	2.0487254
8153_at	NOL046W	1	5.198908	4.300844	4.4688044
8157_at	NOR011W	1	1.7298077	1.3763461	1.5009617
8159_at	NOR012W	1	1.8515384	1.1811538	1.1465385
8162_at	YOR363C	1	2.966145	2.9228787	2.7737894
8165_at	YOR366W	1	2.4105768	2.0901923	1.9646153
8173_at	YOR374W	1	0.8979516	0.8611495	0.9146058
8176_at	YOR377W	1	3.9997969	3.8144474	3.9327722
8179_at	YOR380W	1	3.338848	3.634267	3.9168332
8180_at	YOR381W	1	14.417	11.862109	15.092659
8187_at	YOR343C	1	1	1.4534615	1
8191_at	YOR347C	1	1.2742485	1.0469697	1.1346161
8193_at	YOR349W	1	1.8665652	1.6885003	1.5375123
8194_at	YOR350C	1	1.5643786	1.4655539	1.7246367
8202_at	YOR358W	1	2.6546984	2.7014189	2.6056352
8208_at	YOR318C	1	3.6794484	2.7988286	2.9644132
8209_at	YOR319W	1	3.7869542	3.7559297	5.2238417
8218_at	YOR328W	1	3.2816103	3.534288	3.6701083
8223_at	YOR333C	1	1.9280646	1.4154004	1.3364459
8227_at	YOR337W	1	1.5781803	2.0529869	1.6824002
8229_at	YOR297C	1	1.5872818	1.6557728	1.830961
8234_at	YOR300W	1	2.0233004	2.2698755	1.7118124
8236_at	YOR302W	1	4.985522	6.8127284	5.725745
8237_at	YOR303W	1	3.8326766	5.540056	5.562236
8239_at	YOR304C-A	1	2.6170945	2.888876	2.7654798
8240_at	YOR305W	1	2.2984543	2.7376132	2.9234228
8241_at	YOR306C	1	1.1015744	1.1404642	1.099695
8243_at	YOR308C	1	0.942468	1.4501545	1.5669374
8249_at	YOR313C	1	3.2108078	2.779423	2.645
8254_at	YOR278W	1	2.2663255	2.0462987	2.1313784
8260_at	YOR284W	1	4.0286417	2.654461	2.6735148
8263_at	YOR287C	1	0.8340318	1.021794	1.15789
8265_at	YOR289W	1	0.81508815	0.7102306	0.768898
8268_at	YOR292C	1	1.9333813	1.5953096	1.9830785
8290_at	YOR269W	1	0.98149925	1.067782	1.053753
8293_at	YOR272W	1	0.73203146	0.78828806	0.86606836
8294_at	YOR273C	1	0.8621745	1.3062947	1.4100195
8302_at	YOR236W	1	0.7047358	0.6765471	0.7183478
8304_at	YOR238W	1	2.1724494	2.4355168	2.6559327
8308_at	YOR242C	1	1.7966385	2.803057	2.5248735
8311_at	YOR245C	1	1.3278615	1.4133061	1.3737392
8319_at	YOR252W	1	0.9396867	1.1272783	1.0540318
8324_at	YOR213C	1	1.8936682	1.9049166	1.9091709
8331_at	YOR220W	1	1.2486525	1.0078708	1.059115
8332_at	YOR221C	1	1.2100437	0.923442	1.418608
8334_at	YOR222W	1	2.9333868	2.521855	3.1956537
8348_i_at	YOR192C	1	4.3883395	3.8722892	4.162165
8349_f_at	YOR192C	1	3.47767	3.6788445	3.685388
8350_at	YOR193W	1	1.8665928	1.6209111	1.6776737

8359_at	YOR202W	1	22.914553	24.083324	25.497198
8360_at	YOR203W	1	25.26879	31.256939	31.106045
8362_at	YOR205C	1	1.9146249	1.9545939	1.8844424
8364_at	YOR207C	1	1.0665693	1.2057031	1.2703404
8375_at	YOR173W	1	1.587426	1.5877686	1.6087995
8380_at	YOR178C	1	0.90514076	0.8474163	0.77405906
8381_at	YOR179C	1	2.4198556	3.724027	3.329472
8382_at	YOR180C	1	3.0973077	2.8376925	2.0690384
8392_at	YOR145C	1	0.7372459	0.7416034	0.75818676
8395_at	YOR148C	1	3.4370704	4.8358755	4.4197254
8396_at	YOR149C	1	2.0521662	2.566104	2.088711
8399_at	YOR152C	1	3.5594635	5.28286	4.4670177
8402_at	YOR155C	1	1.0501313	0.98286986	1.0268933
8409_at	YOR162C	1	3.4801874	2.7603402	3.5976892
8412_at	YOR120W	1	3.9287965	6.2671347	5.530083
8420_at	YOR128C	1	42.16234	41.655167	53.707813
8422_at	YOR130C	1	2.2833838	1.3931819	2.1705215
8430_at	YOR138C	1	1.0445586	1.1205342	1.1333799
8434_at	YOR097C	1	1.0098634	0.8261988	1.0152382
8437_at	YOR100C	1	4.568077	3.261923	3.7367306
8448_at	YOR111W	1	2.0388615	2.1697907	2.3231053
8451_at	YOR114W	1	0.9958697	1.2387009	1.0552638
8456_at	YOR119C	1	1.4971532	2.5197914	2.2242117
8461_at	YOR080W	1	1.9153376	2.270365	1.7363614
8466_at	YOR085W	1	0.85355	1.0469258	0.94709086
8480_at	YOR052C	1	1.1926033	0.9372693	0.94960415
8484_at	YOR056C	1	1.1765302	1.317353	1.330655
8485_at	YOR057W	1	1.6052086	1.547946	1.702352
8487_at	YOR059C	1	5.226944	3.6711826	4.575668
8488_at	YOR060C	1	2.8197513	1.8665385	2.2248077
8490_at	YOR062C	1	2.4759803	1.8520886	1.8401743
8492_at	YOR064C	1	2.222514	1.9214678	2.0690875
8498_at	YOR071C	1	1.868363	2.9732823	2.7705827
8499_at	YOR072W	1	6.342885	5.292885	4.9259615
8500_at	YOR073W	1	1.1898637	1.251575	1.332066
8501_at	YOR075W	1	1.4102544	2.2884197	1.9539685
8504_at	YOR031W	1	1.2884294	1.2109437	1.2946177
8505_at	YOR032C	1	0.5831923	0.6876456	0.603086
8507_at	YOR034C	1	1.3617808	1.5303183	1.4191774
8508_at	YOR035C	1	1.6674622	2.7788088	2.853525
8509_at	YOR036W	1	0.9804491	0.8610881	0.8502637
8510_at	YOR037W	1	1.7747986	2.189397	2.2775207
8516_at	YOR043W	1	0.8222537	1.0187831	1.0646065
8517_at	YOR044W	1	0.92266816	0.88154775	1.011817
8526_at	YOR009W	1	12.919624	16.90369	14.772586
8528_at	YOR011W	1	2.58804	3.200601	3.504107
8529_at	YOR012W	1	2.1072438	2.7955768	2.4607534
8530_g_at	YOR012W	1	3.047942	3.5321798	4.4360247
8537_at	YOR019W	1	8.153306	10.33577	10.726924
8541_at	YOR023C	1	0.98670405	0.9645493	0.9920698
8544_at	YOR026W	1	2.3066459	2.258585	2.5003262

8545_at	YOR027W	1	0.9446529	0.92014015	0.9417962
8546_at	YOR028C	1	1.6686398	2.101704	2.1613421
8547_at	YOL015W	1	10.970196	7.419423	8.601346
8548_at	YOL014W	1	2.8891692	2.341104	2.884457
8551_at	YOL011W	1	2.2147858	2.642687	2.343918
8552_at	YOL010W	1	0.87587714	0.72844124	0.87460005
8553_at	YOL009C	1	2.995304	3.35297	3.6764462
8559_at	YOL003C	1	1.613009	1.6201543	1.9222791
8561_at	YOL001W	1	2.2809827	1.7607348	2.0899029
8564_at	YOR003W	1	2.0660112	2.4853904	2.3544593
8566_at	YOR005C	1	5.92319	5.673422	7.086504
8575_at	YOL032W	1	1.1081369	0.7882719	0.7222237
8576_at	YOL031C	1	1.2555183	2.2512827	1.8172591
8578_at	YOL029C	1	1.5567423	1.780464	1.8046649
8579_at	YOL028C	1	1.7826409	2.9997652	2.7684228
8591_at	YOL016C	1	0.66199255	0.55206037	0.561235
8596_at	YOL055C	1	7.9669037	7.8053517	7.911649
8599_at	YOL052C-A	1	0.68696356	1.0303622	0.7415463
8603_at	YOL049W	1	0.7400365	0.8272217	0.8032385
8604_at	YOL048C	1	1.0361059	1.0293779	0.91597575
8607_at	YOL045W	1	1.003426	1.1758544	1.2311146
8609_at	YOL043C	1	3.830919	3.5726926	3.6987453
8622_at	YOL076W	1	0.9853115	1.0888681	1.0492145
8625_at	YOL072W	1	1.3049718	0.9642058	1.1924622
8629_at	YOL068C	1	2.2549324	2.667121	2.9669142
8635_at	YOL062C	1	1.6131892	1.8262562	1.4702808
8639_at	YOL104C	1	3.4052942	1.6086538	2.8017309
8641_at	YOL102C	1	1.7971975	1.5991343	1.9942684
8642_at	YOL101C	1	1.2675543	0.6492923	1.0195154
8643_at	YOL100W	1	0.95816916	0.82299125	0.9384606
8650_at	YOL093W	1	0.9091806	0.83912873	0.7867249
8652_at	YOL091W	1	1.4975	2.3998077	1.5265385
8659_at	YOL084W	1	1.2666783	1.3008275	0.861102
8661_at	YOL128C	1	1.2686865	1.2947075	1.2324879
8663_at	YOL126C	1	1.4087197	1.4814193	1.4263777
8664_at	YOL125W	1	1.5579623	1.8746293	1.6302686
8669_at	YOL119C	1	1.594067	2.2434697	2.1550066
8671_at	YOL117W	1	1.6326208	1.5608126	1.8946533
8675_at	YOL113W	1	1.5379645	1.5586597	1.5332623
8676_at	YOL112W	1	3.3243961	3.9227896	3.8217678
8680_at	YOL108C	1	3.1404068	2.607234	2.7258892
8681_at	YOL107W	1	4.7900214	5.428106	6.1313944
8682_at	YOL106W	1	3.4404545	3.3162773	3.9985764
8683_at	YOL151W	1	1.0335119	0.7964053	1.009712
8685_at	YOL149W	1	0.6759218	0.7701651	0.8018578
8690_at	YOL144W	1	0.973735	1.0051081	0.77625513
8692_at	YOL142W	1	1.1122603	0.93852806	1.1770537
8694_at	YOL140W	1	2.3932595	2.3382459	2.9045913
8696_at	YOL138C	1	1.5208671	1.4483147	1.7477404
8697_at	YOL137W	1	1.3944414	1.3342465	1.5229931
8701_at	YOL133W	1	2.2316597	2.032077	2.2370808

8704_at	YOL130W	1	2.1499374	2.5110855	2.4852977
8708_at	NNL034W	1	1.8679965	1.5334734	1.6040784
8710_at	NNL001W	1	3.5315385	1.9321154	1.9042308
8716_s_at	YOL165C	1	6.0442905	7.1473227	7.651192
8717_at	YOL164W	1	9.267432	12.862173	11.538901
8718_at	YOL163W	1	11.671347	8.912885	9.518077
8719_at	YOL162W	1	24.476345	21.26923	20.25
8720_f_at	YOL161C	1	12.747885	13.84673	14.315962
8722_at	YOL159C	1	1.9834667	2.3256547	1.8047087
8723_at	YOL158C	1	6.462041	9.003889	8.312632
8724_at	YOL155C	1	1.345213	3.118769	1.774004
8725_g_at	YOL155C	1	2.0644612	5.744607	3.2446969
8726_at	YOL154W	1	3.2344203	3.4800525	3.1126976
8727_at	YOL153C	1	3.8890386	4.1825	3.0165386
8728_at	YOL152W	1	0.6845937	0.43947414	0.628053
8730_g_at	NNL072W	1	0.6450398	0.61593586	0.59930605
8733_at	NNL045W	1	3.6131697	3.6179972	4.399638
8736_at	NNL040W	1	3.8411539	3.0940385	2.6882691
8739_at	NNL012W	1	1.8253846	2.1509616	1.7088461
8742_at	NNL004W	1	1.4964565	2.0140307	1.4109799
8752_f_at	NNL025C	1	1.9390962	2.8771768	2.0523825
8759_at	NNL042C	1	3.4902885	3.4439414	3.583245
8769_g_at	NNL053C	1	1.0529912	1.1034778	0.94656694
8774_at	NNL005C	1	1.8617765	2.367173	2.2461472
8775_at	NNL073W	1	0.4899508	0.30228978	0.25332323
8777_at	YNR065C	1	1.9101832	2.4868412	2.4334197
8779_at	YNR067C	1	0.9278702	1.1782764	1.0913458
8780_at	YNR068C	1	17.815321	16.20636	17.307434
8784_s_at	YNR073C	1	1.0459615	1	1
8786_f_at	YNR076W	1	7.0291686	8.21046	8.482658
8788_at	YNR034W-A	1	1.3745095	1.3873553	1.2475055
8793_at	NNL057C	1	1.7175016	1.9717739	1.9511483
8794_i_at	NNL036W	1	5.848846	4.418269	5.121923
8795_r_at	NNL036W	1	2.7616515	2.5138006	2.5876434
8796_at	NNR010W	1	2.6681468	2.6906095	2.4736652
8797_f_at	NNL062W	1	1.882839	3.43313	2.1258662
8807_at	YNR049C	1	1.1906229	0.99605167	0.9697499
8812_at	YNR053C	1	0.663563	0.8922072	0.79321396
8816_at	YNR057C	1	2.2559955	3.2313483	2.534099
8817_at	YNR058W	1	3.8192463	5.3337817	4.557823
8818_at	YNR059W	1	10.847197	10.9425	10.020962
8827_at	YNR024W	1	0.711595	1.0187691	1.0744699
8832_at	YNR029C	1	1.9283501	1.5437729	1.7822256
8835_at	YNR032W	1	1.0323511	1.1128609	1.1264685
8837_at	YNR034W	1	1.022454	1.5956392	1.6236533
8846_at	YNL003C	1	2.5063968	2.7943478	2.8305473
8850_at	YNR002C	1	1.3386815	1.0723622	1.433232
8851_at	YNR003C	1	0.8887888	0.8338909	0.873175
8854_at	YNR006W	1	1.1872025	1.1693559	1.4425881
8855_at	YNR007C	1	0.9780078	0.93430734	0.7782271
8858_at	YNR010W	1	0.9712408	0.9890932	0.94198173

8860_at	YNR012W	1	1.028834	0.9714866	0.97808874
8868_at	YNL027W	1	1.0023757	0.98928314	1.0487199
8870_at	YNL025C	1	2.5246377	1.5910337	1.7746085
8871_at	YNL024C	1	1.2143184	1.1216136	0.9569799
8881_at	YNL014W	1	6.103269	4.845577	4.7759614
8883_at	YNL012W	1	1.6962186	1.3713461	1.5578846
8884_at	YNL011C	1	2.6544406	3.700666	3.6122658
8886_at	YNL009W	1	2.187097	3.2244608	3.104579
8887_at	YNL008C	1	2.3454678	2.3763137	2.4391518
8888_at	YNL007C	1	0.8104795	0.87703234	0.82937473
8889_at	YNL006W	1	1.8768111	1.9880664	2.1131222
8892_at	YNL050C	1	1.2503716	1.6296202	1.4990664
8896_at	YNL046W	1	4.190559	5.1923823	4.745574
8899_at	YNL042W	1	1.6201488	2.0802057	1.9388201
8903_at	YNL038W	1	1.7832147	2.0179198	2.1771574
8904_at	YNL037C	1	1.3578231	1.005932	1.0181062
8905_at	YNL036W	1	1.5517614	1.3374141	1.4031081
8906_at	YNL035C	1	2.4724033	3.8306603	3.928764
8907_s_at	YNL034W	1	3.1503847	2.6317499	2.3944585
8909_at	YNL032W	1	2.2330625	1.9203088	2.2882857
8925_at	YNL063W	1	2.2807922	2.0923579	2.1949627
8930_at	YNL057W	1	2.7563062	4.170044	3.0954072
8934_at	YNL053W	1	0.8296231	0.8151096	0.8525455
8938_at	YNL094W	1	2.2634606	3.1658664	2.816896
8940_at	YNL092W	1	1.6607692	1.0063462	1.0221153
8953_at	YNL079C	1	0.7071006	0.8174625	0.8258969
8960_at	YNL116W	1	1.0708169	1.0458784	1.12064
8962_at	YNL114C	1	1.6726373	3.7238116	3.657065
8964_at	YNL112W	1	0.877547	1.2529376	1.2463875
8980_at	YNL097C	1	0.88431084	0.9558209	0.90125227
8993_at	YNL129W	1	1.0630136	1.0280865	1.042804
8994_at	YNL128W	1	4.1403847	2.2792308	2.488269
8997_at	YNL125C	1	1.8789158	2.3849814	2.191246
8998_at	YNL124W	1	1.0822698	1.1835399	1.2475387
9000_at	YNL122C	1	0.70844734	0.46142256	0.4643157
9004_at	YNL118C	1	0.69657665	0.79252625	0.70602924
9009_at	YNL159C	1	1.6392398	2.025779	1.8198122
9010_at	YNL158W	1	5.68091	7.4558754	6.8230352
9025_at	YNL143C	1	4.1742415	4.430339	4.0525074
9026_at	YNL142W	1	2.4651785	3.2994416	3.468004
9034_at	YNL179C	1	2.8415163	2.796423	2.3794131
9040_at	YNL173C	1	0.8336813	0.7727868	0.5851753
9049_at	YNL164C	1	0.649796	0.6143219	0.7254904
9050_at	YNL208W	1	0.8158316	0.77010775	0.7701712
9052_at	YNL206C	1	1.6527185	1.8475269	2.5817795
9057_at	YNL202W	1	1.9266789	1.4071685	1.4232688
9060_at	YNL199C	1	0.9651404	1.1504303	1.1502814
9066_at	YNL193W	1	1.7256426	1.5712199	1.4382195
9072_at	YNL187W	1	3.3069866	3.9854012	3.8890433
9073_at	YNL230C	1	3.429315	3.7473974	3.3082607
9075_at	YNL227C	1	0.8395349	1.0038974	1.0640235

9082_at	YNL221C	1	1.2203	1.2284654	1.2449855
9090_at	YNL213C	1	0.9300261	1.4076564	1.2670796
9092_at	YNL211C	1	1.6162231	1.6421705	1.4513665
9095_at	YNL254C	1	2.4198914	2.1607692	2.2048078
9098_at	YNL251C	1	1.2122782	1.0924456	1.0206611
9100_at	YNL249C	1	4.8818073	5.290351	5.4327683
9104_at	YNL245C	1	2.0262272	3.540577	2.2788463
9107_at	YNL242W	1	1.931752	1.8904378	2.3746428
9109_at	YNL240C	1	1.3094349	1.3258418	1.3626931
9111_at	YNL237W	1	1.817889	2.1249893	1.3305217
9116_at	YNL232W	1	0.92276907	0.8329303	1.0163008
9118_at	YNL276C	1	1.4336538	2.3534615	1.6507692
9120_at	YNL274C	1	1.0899737	1.0541459	1.1218188
9124_at	YNL270C	1	3.007283	2.3459952	2.7567072
9133_at	YNL261W	1	1.8568192	1.9912586	1.7173141
9134_at	YNL260C	1	2.3105702	1.9912872	2.3100138
9137_at	YNL257C	1	2.5676405	2.376746	2.334078
9145_at	YNL294C	1	2.8195348	3.612428	3.6026635
9150_at	YNL289W	1	0.67798734	0.77447015	0.708126
9157_at	YNL282W	1	3.3126106	3.997358	3.744257
9160_at	YNL279W	1	3.1553755	2.923873	2.9728413
9162_at	YNL277W	1	0.9007335	1.5789497	1.4792318
9170_at	YNL314W	1	2.464493	2.2424989	2.356773
9175_at	YNL309W	1	0.7847292	0.6654837	0.7391645
9179_at	YNL305C	1	0.95154464	1.1406345	1.0365152
9189_at	SNR77	1	0.73420024	0.56526005	0.60110694
9190_at	SNR76	1	0.4944639	0.6045757	0.49024686
9192_at	SNR74	1	0.900245	0.91044426	0.7822963
9193_at	SNR73	1	0.6553698	0.6951363	0.6294745
9194_at	SNR72	1	1.4848052	1.1621544	1.1326473
9196_s_at	YNL335W	1	5.8801928	5.7330766	6.4063463
9197_s_at	YNL334C	1	2.9633086	2.843451	3.3223567
9198_s_at	YNL333W	1	2.287293	2.2171297	2.353638
9199_at	YNL331C	1	5.164171	5.3190804	5.800802
9201_at	YNL329C	1	4.2414346	4.7521772	4.2286344
9204_at	YNL326C	1	1.5313619	2.252397	2.0085394
9215_at	NMR001W	1	2.5945814	2.9422135	2.6273985
9218_at	NMR016W	1	4.4149504	0.964288	1.0470308
9219_i_at	NMR030W	1	1.0740438	1.146035	1.0854993
9220_r_at	NMR030W	1	0.76115805	1.5478505	1.1854041
9224_at	NMR047C	1	1.7664125	2.082278	1.755885
9226_at	NMR053W	1	2.0986254	3.0039377	2.578251
9231_s_at	NMR057W	1	0.91507566	1.3896567	1.1398011
9235_at	NMR019W	1	2.0554147	1.5419503	1.4084756
9236_at	NMR020W	1	4.494971	4.4549127	4.567548
9237_at	NMR022W	1	3.0654278	3.9611588	3.116366
9238_at	NMR023C	1	3.2915986	3.548314	3.0838253
9241_at	NMR026W	1	0.6942004	0.65108824	0.73969877
9252_at	NMR061C	1	1.0071442	1.2451301	1.2325038
9253_at	NMR063C	1	1.0379405	1.3170714	1.2259121
9254_at	NMR069W	1	3.765603	3.8287144	3.9909515

9260_at	NMR007C	1	2.8734615	3.06	2.270577
9261_at	NMR008W	1	2.47822	2.0149999	1.4286538
9263_at	NMR032C	1	1.2950436	1.1968621	1.3680393
9271_at	NMR015C	1	4.2994704	1.0890378	1.2522644
9275_g_at	NML016C	1	1.7373078	1.2484615	1.2559614
9280_at	NMR017C	1	3.5075	2.7782693	2.7061539
9281_at	YMR316C-B	1	7.1126795	8.421955	8.669001
9284_at	YMR319C	1	1.2008036	1.2297065	1.5252827
9285_at	YMR320W	1	1.7152516	1.7411379	1.6999888
9287_s_at	YMR322C	1	1.7325886	1.9770298	1.5602901
9288_s_at	YMR323W	1	1.186146	1.1726923	1.2959615
9290_f_at	YMR325W	1	3.0373	3.187184	3.3760335
9299_at	NML006C	1	5.9451923	8.426154	6.3409615
9305_at	YMR299C	1	1.2736708	0.99390805	1.1004934
9306_at	YMR300C	1	0.99003464	1.8198419	1.633346
9309_at	YMR303C	1	0.8979345	0.8466336	0.77068806
9313_at	YMR306W	1	3.1916778	2.3790898	1.7612648
9318_at	YMR310C	1	0.8579693	0.77397823	0.8409268
9324_at	YMR316W	1	1.6232853	1.9276378	2.3443897
9327_at	YMR278W	1	1.0528039	1.1771452	0.94055134
9332_at	YMR283C	1	2.709888	2.9531586	3.3922336
9333_at	YMR284W	1	2.3823662	3.179153	2.729443
9334_at	YMR285C	1	1.7928573	2.2540977	2.5419178
9340_at	YMR290W-A	1	1.8074255	1.4072579	2.1389613
9341_at	YMR291W	1	1.3531468	1.1473409	1.1934264
9343_at	YMR293C	1	1.8129777	1.8292793	2.2645018
9344_at	YMR294W	1	2.627982	3.4584427	3.377668
9349_at	YMR255W	1	1.3556619	1.9439623	2.2413
9356_at	YMR262W	1	2.2171626	2.0884924	2.5705113
9359_at	YMR265C	1	1.5279089	1.5600983	1.7840593
9360_at	YMR266W	1	0.69729614	0.73983765	0.85507816
9365_at	YMR271C	1	4.982482	3.7710378	3.4067025
9371_at	YMR232W	1	3.3559027	2.9955769	2.9071155
9373_at	YMR234W	1	2.5900595	2.5376983	2.5177774
9379_at	YMR240C	1	2.9470713	5.5673394	6.1678996
9388_at	YMR250W	1	1.9980841	1.8616085	1.7602609
9391_at	YMR252C	1	1.6970624	2.2211082	2.25229
9397_at	YMR215W	1	0.72927064	0.87234515	0.7854632
9401_at	YMR219W	1	1.7547839	2.0424385	2.0583668
9413_f_at	YMR230W	1	0.54499876	0.581286	0.48970062
9423_at	YMR196W	1	2.2412887	2.2568135	2.3675847
9424_at	YMR197C	1	0.922166	1.1002756	1.1172519
9438_at	YMR211W	1	2.1888962	2.4877353	2.5530205
9439_at	YMR171C	1	1.0810896	0.86919737	0.71355855
9442_s_at	YMR173W	1	0.5816494	0.6500287	0.58707964
9444_at	YMR174C	1	1.140953	1.0593159	0.9446495
9446_at	YMR176W	1	2.6879292	2.4385118	2.1486926
9450_at	YMR180C	1	4.582076	4.7716393	4.5594883
9451_at	YMR181C	1	2.8890972	3.3575246	2.6715374
9452_at	YMR182C	1	4.4223423	5.5095725	4.3634453
9454_at	YMR184W	1	1.50566	1.61399	1.5734849

9455_at	YMR185W	1	1.4377322	1.6979117	1.752629
9458_at	YMR187C	1	1.1500939	2.6930451	2.6704648
9466_at	YMR155W	1	1.7591405	2.12608	1.6316456
9467_at	YMR156C	1	2.1864345	1.9916091	1.8152552
9480_at	YMR168C	1	4.1271286	3.4446154	3.5226922
9481_at	YMR169C	1	10.076185	10.232116	10.458654
9482_g_at	YMR169C	1	3.3071964	2.6469955	2.5570605
9483_at	YMR170C	1	1.6245694	1.6000297	1.4430621
9485_at	YMR132C	1	1.2039537	1.2372644	1.335411
9488_at	YMR135C	1	2.6683154	3.349561	3.3114192
9490_at	YMR136W	1	0.9349565	0.7111966	0.7145586
9491_at	YMR137C	1	0.9848266	1.2462068	1.6708816
9494_at	YMR140W	1	1.9086353	1.783793	1.6055225
9510_at	YMR114C	1	4.0204287	4.664231	3.8986537
9515_at	YMR118C	1	1.3673078	1.1296153	1.1532692
9519_at	YMR120C	1	1.741373	1.5751373	1.6702061
9526_at	YMR127C	1	3.001842	3.999981	4.358052
9532_at	YMR090W	1	2.6733794	3.0364904	2.76899
9537_at	YMR095C	1	1.222774	1.3107035	1.2407557
9538_at	YMR096W	1	2.0912027	2.1690264	2.1497147
9542_at	YMR100W	1	1.0362806	1.2701037	1.2784517
9545_at	YMR103C	1	2.1673782	2.1143997	1.9366739
9546_at	YMR104C	1	1.9411174	2.709423	2.4107695
9547_at	YMR105C	1	1.632123	1.9004004	2.0360708
9549_at	YMR107W	1	1	1	1
9553_at	YMR068W	1	3.225278	3.90822	4.162257
9554_at	YMR069W	1	1.310673	1.2430769	1.3521154
9566_at	YMR080C	1	0.14827165	1.7403616	1.7399194
9567_at	YMR081C	1	0.8983304	1.1004053	1.0180401
9573_at	YMR086C-A	1	2.100594	2.2123382	1.8924644
9574_at	YMR087W	1	2.6232343	2.3690524	2.6679313
9575_at	YMR042W	1	1.287189	1.4056027	1.5786813
9581_at	YMR052W	1	1.5926641	1.4701923	1.719423
9582_at	YMR052C-A	1	2.4705074	2.1422086	1.96342
9585_at	YMR055C	1	0.7415409	0.84479403	0.80170035
9588_at	YMR058W	1	0.34329924	0.4132989	0.29456255
9589_at	YMR059W	1	0.8478075	0.8714961	0.9551213
9594_at	YMR064W	1	2.3495426	3.019059	2.9963992
9595_at	YMR065W	1	8.933065	8.056365	8.561047
9600_at	YMR023C	1	3.3651109	3.4992628	3.9918878
9605_at	YMR028W	1	1.7093791	2.0462646	2.0416782
9616_at	YMR038C	1	0.908144	0.81313705	0.9511024
9618_at	YMR040W	1	2.9827602	3.5607028	2.9314487
9619_at	YMR041C	1	1.9815701	2.8148603	2.6739883
9621_at	YML002W	1	7.4250517	6.72062	6.8214655
9622_at	YML001W	1	0.73689616	0.75805336	0.7521701
9628_at	YMR006C	1	1.3244399	1.2611387	1.2995204
9635_at	YMR013C	1	1.0034952	1.2749542	1.2682626
9636_at	YMR014W	1	0.72919536	1.0405918	1.2269869
9638_at	YMR016C	1	0.94549495	0.7086836	0.8010984
9642_at	YMR020W	1	3.44039	3.1032677	4.1474237

9645_at	YML019W	1	1.4458058	1.9528198	1.9961274
9649_at	YML015C	1	0.9317417	0.8644095	0.94304323
9650_at	YML014W	1	1.2755582	1.1908969	1.3518087
9654_at	YML011C	1	1.3196535	1.5513833	1.7518783
9664_at	YML005W	1	7.0329437	7.0040183	7.675402
9668_at	YML042W	1	4.3684635	5.2257934	4.695011
9675_at	YML034W	1	1.4758456	3.7885714	3.020771
9687_at	YML023C	1	3.9368048	3.8570168	4.4130955
9690_at	YML064C	1	0.933418	0.9696205	0.93033
9694_at	YML060W	1	0.7858419	1.2563881	1.2132566
9698_at	YML057W	1	0.92829585	0.95702785	1.0480124
9701_at	YML055W	1	1.9156604	2.7571597	2.6253963
9702_at	YML054C	1	1.5538969	1.8698962	1.985389
9703_at	YML053C	1	0.68250483	0.83347183	0.84568334
9706_at	YML050W	1	2.4080694	2.913669	3.6162753
9717_at	YML082W	1	0.99581754	1.0192993	1.0976577
9727_at	YML072C	1	0.7878831	0.9681063	0.96016467
9731_at	YML068W	1	2.2091913	1.7521464	1.9578661
9735_at	YML107C	1	3.5030122	3.377056	3.9468265
9740_at	YML102W	1	1.1007589	1.0537412	1.0885067
9743_at	YML100W	1	1.0010773	1.6758748	1.9084401
9745_at	YML099C	1	3.0454354	3.1586602	3.6333761
9746_at	YML098W	1	2.1645124	2.5975032	2.8643894
9757_at	YML128C	1	2.1549926	2.770064	2.5612848
9766_at	YML119W	1	1.0773653	1.2082505	1.0750362
9768_at	YML117W	1	1.4521847	1.234714	1.8121254
9769_g_at	YML117W	1	1.0936007	0.69111	0.7621031
9770_at	YML117W-A	1	0.9289941	0.79879564	0.9319668
9771_at	YML116W	1	2.8246546	3.0570726	3.2657273
9773_at	YML114C	1	1.1683198	1.0731612	1.1115876
9774_at	YML113W	1	0.9267664	1.1581651	1.1135387
9775_at	YML112W	1	1.0270356	1.1704233	1.2358263
9776_at	YML111W	1	1.1134521	1.3137757	1.431129
9778_at	YML109W	1	1.1655967	1.1394343	1.0899001
9785_at	NLR134W	1	2.6172056	2.6056309	2.7561343
9786_at	NLR135W	1	2.9072025	3.4655128	3.7454011
9788_at	NLR139W	1	2.154611	3.445308	2.9915996
9799_at	SNR34	1	0.8923764	0.75879145	0.4871049
9800_s_at	YML133C	1	3.3434224	5.3242126	3.6157882
9801_at	YML131W	1	0.90829647	0.7625912	0.76374453
9804_at	NLR029W	1	0.9858958	1.1678646	1.172912
9807_at	NLR114C	1	4.773013	3.8510213	3.7359846
9812_at	NLL005C	1	3.8446438	4.42939	4.577182
9813_at	NLR016C	1	4.8879304	5.262194	4.9872656
9818_at	NLR116W	1	2.57	2.2246153	1.9090385
9834_at	NLL003W	1	0.77436113	0.65549785	0.5255051
9837_s_at	NLR033W	1	0.36429226	0.41118854	0.45027444
9847_at	NLR024W	1	1.3974392	1.2022262	1.2567443
9849_at	NLR027W	1	5.9902873	7.3306265	6.980979
9855_at	YLR451W	1	2.8744946	2.5832431	2.8563313
9860_at	YLR456W	1	1.7141383	1.5080123	2.0160985

9861_at	YLR457C	1	2.702037	2.7183647	2.7923536
9864_at	YLR460C	1	3.018927	3.41505	3.9328346
9865_f_at	YLR461W	1	4.564944	4.3122034	4.837469
9868_at	YLL018C-A	1	4.2245407	4.431868	4.6572256
9871_at	NLR018W	1	2.293712	3.454001	3.9072793
9873_at	YLR426W	1	1.8841932	1.1792107	1.4494597
9902_at	YLR411W	1	2.2197785	1.7555177	2.0872855
9908_at	YLR417W	1	2.6202765	3.9570189	4.6385736
9914_at	YLR423C	1	2.0223215	3.4791284	2.643836
9918_at	YLR383W	1	1.4766976	1.6891104	1.6500187
9929_at	YLR394W	1	3.0705369	3.7970967	3.8863502
9939_at	YLR404W	1	1.519706	1.9353893	2.298569
9941_at	YLR362W	1	1.8733832	1.7144293	1.7889712
9942_at	YLR363C	1	5.96131	8.162706	8.574476
9956_at	YLR375W	1	1.3892837	1.6812499	1.6355914
9957_at	YLR376C	1	1.7301034	1.8449883	1.5299761
9962_at	YLR381W	1	2.23239	1.86292	1.8292696
9967_at	YLR343W	1	1.7909782	2.5760937	2.5336776
9969_at	YLR345W	1	0.96593475	1.0047895	0.94149435
9976_at	YLR352W	1	2.040889	2.5582287	2.2530637
9986_at	YLR317W	1	3.147894	4.3632975	3.5206566
9987_at	YLR318W	1	2.7323077	2.7176924	2.1667309
9988_at	YLR319C	1	0.81232405	0.8948423	1.548186
9989_at	YLR320W	1	1.5754987	2.4474845	2.2906163
9992_at	YLR323C	1	1.6703731	1.7544166	1.8394542
9993_at	YLR324W	1	1.3360822	1.1897247	1.1370701
9996_at	YLR327C	1	2.2584202	1.7811403	1.621654
9997_at	YLR328W	1	1.0328302	1.0204408	1.051919

Max 53.707813

Min 0.02956932

E-dcp1	F-xrn1	
2.2330642	2.818216	YLR296W hypothetical protein
3.237075	4.80272	YLR298C U1 snRNP protein required for pre-mRNA splicing
7.3009224	6.635961	YLR306W Ubiquitin-conjugating enzyme
3.4221542	2.279231	YLR312C hypothetical protein
2.850154	2.468077	YLR315W weak similarity to rat apolipoprotein A-IV
2.9735048	3.034257	YLR278C weak similarity to regulatory proteins
8.186274	7.664154	YLR280C questionable ORF
4.2745857	5.106651	YLR280C questionable ORF
4.4729233	4.670577	YLR281C similarity to polypeptide chain release factors
2.5921469	1.644972	YLR283W weak similarity to Smc2p
3.6902905	1.072157	YLR284C Peroxisomal enoyl-CoA hydratase
3.970327	3.412484	YLR288C involved in checkpoint control and DNA repair
2.434239	3.807773	YLR254C hypothetical protein
4.9751005	1.939091	YLR258W Glycogen synthase (UDP-glucose--starch glucosyltransferase)
3.2397294	3.113205	YLR263W Meiosis-specific protein involved in homologous chromosome syn
2.1780002	2.135958	YLR265C hypothetical protein
3.6818895	3.07779	YLR266C weak similarity to transcription factors
4.8406653	3.948021	YLR271W hypothetical protein
3.5330234	1.914872	YLR273C Protein similar to Gac1p, a putative type 1 protein phosphatase ta
9.946461	8.836538	YLR233C Telomere elongation protein (ever shorter telomeres)
3.4102862	2.9883	YLR237W thiamine transporter
3.7834938	3.849702	YLR242C weak similarity to C.elegans R05H5.5 protein and Nup120p
2.0263658	2.974083	YLR243W strong similarity to YOR262w
1.3700798	1.703781	YLR245C strong similarity to B.subtilis cytidine deaminase
3.8859847	2.415476	YLR246W similarity to human DHHC-domain-containing cysteine-rich proteir
3.52637	2.213974	YLR247C similarity to S.pombe rad8 protein and Rdh54p
23.07237	3.087443	YLR251W similarity to peroxisomal rat membrane protein PMP22
8.451952	2.036564	YLR252W questionable ORF
2.4844282	1.651497	YLR211C hypothetical protein
0.34986338	0.396874	YLR214W Ferric (and cupric) reductase
1.0864202	2.097646	YLR215C strong similarity to rat cell cycle progression related D123 protein
1.4123117	0.41724	YLR216C a cyclophilin related to the mammalian CyP-40\; physically interac
0.780051	0.20823	YLR218C hypothetical protein
1.6118	2.17263	YLR221C hypothetical protein
2.7506406	3.247949	YLR224W hypothetical protein
2.431789	2.375916	YLR225C strong similarity to YDR222w
1.9954811	3.042365	YLR226W hypothetical protein
6.2606344	5.732073	YLR227C hypothetical protein
2.9248064	2.531717	YLR228C strong similarity to YDR213w, weak similarity to Lys14p
1.8299195	1.571522	YLR189C similarity to P.aeruginosa rhamnosyltransferase 1 chain B
2.2942555	1.133463	YLR201C similarity to hypothetical S. pombe protein
1.322938	2.076647	YLR205C hypothetical protein
4.5698204	2.919475	YLR173W hypothetical protein
13.121628	7.789681	YLR174W Cytosolic form of NADP-dependent isocitrate dehydrogenase
2.5438504	2.330049	YLR176C DNA binding protein, homologous to a family of mammalian RFX1
2.2688925	1.159987	YLR177W similarity to suppressor protein Psp5p
4.04776	0.902683	YLR178C suppressor of cdc25
2.5637116	3.188843	YLR141W transcription factor, member of UAF (upstream activation factor) a
5.7475367	7.450529	YLR142W proline oxidase
2.458216	2.43012	YLR144C Identified as an activity necessary for actin polymerization in perm

2.0056329	2.94213	YLR145W hypothetical protein
4.87986	1.051008	YLR149C hypothetical protein
4.129645	2.810029	YLR151C weak similarity to <i>A.thaliana</i> hypothetical protein ATU78721
5.1987967	3.045669	YLR152C similarity to YOR3165w and YNL095c
4.6391892	3.992459	YLR156W identical to hypothetical proteins YLR161w and YLR159w
5.2784495	5.815146	YLR164W strong similarity to Sdh4p
8.514367	6.506879	YLR165C weak similarity to <i>H.influenzae</i> hypothetical protein HI0176
5.332175	3.94709	YLR166C 100 kD component of the Exocyst complex; required for exocytosis
9.902461	7.565769	YLR122C hypothetical protein
8.662087	5.17328	YLR122C hypothetical protein
5.4627695	2.846731	YLR123C questionable ORF
2.6135385	2.043462	YLR125W hypothetical protein
8.402896	3.93287	YLR128W similarity to <i>S.pombe</i> hypothetical protein SPBC24E9
2.3585465	3.47353	YLR130C Low-affinity zinc transport protein
3.7937942	1.469264	YLR132C hypothetical protein
1.3423642	2.393137	YLR135W hypothetical protein
1.1306154	3.124615	YLR136C zinc finger containing homolog of mammalian TIS11, glucose repressor
2.7402678	2.282392	YLR137W hypothetical protein
6.8180184	3.953201	YLR097C hypothetical protein
9.26823	10.4915	YLR098C DNA-binding transcriptional activator or CHA1
2.9423628	2.550388	YLR102C subunit of the anaphase promoting complex (APC)
2.4205906	2.349072	YLR105C tRNA splicing endonuclease subunit
1.2675753	2.881844	YLR106C similarity to Kaposi's sarcoma-associated herpes-like virus ORF73
1.8372331	1.934203	YLR107W similarity to Pan troglodytes prot GOR
2.099853	1.531151	YLR115W Component of cleavage factor II (CF II); 105-kDa protein associated with pre-mRNA splicing
2.7953186	0.660674	YLR080W strong similarity to Emp47p
2.5328898	2.149634	YLR085C Actin-related protein
1.5270741	2.637766	YLR090W Homolog of <i>E. coli</i> DnaJ, closely related to Ydj1p
2.5325181	1.836103	YLR093C vacuolar v-SNARE
1.6089942	2.824136	YLR094C hypothetical protein
3.6982393	3.419364	YLR054C hypothetical protein
1.4005809	2.025196	YLR057W weak similarity to mouse alpha-mannosidase
2.121317	2.677457	YLR063W ser/thr protein kinase
1.5745524	3.126883	YLR068W hypothetical protein
1.7068471	2.154369	YLR072W similarity to YFL042c, YFL043c, YDR326c and YHR080c
1.1285803	2.775825	YLR073C hypothetical protein
11.184481	4.471616	YLR031W similarity to hypothetical protein YMR124w
2.1215167	2.292499	YLR032W putative ATPase/DNA helicase
1.4512632	2.282663	YLR033W hypothetical protein
1.9659957	2.10177	YLR035C similarity to human mutL protein homolog
2.4160452	3.216005	YLR036C similarity to YIL089w
6.8027306	5.134561	YLR037C strong similarity to members of the Srp1p/Tip1p family
0.38456604	0.485356	YLR040C weak similarity to hypothetical protein YIL011w
8.092308	5.28577	YLR046C strong similarity to Rta1p and Rtm1p protein
0.77839404	0.459298	YLR050C weak similarity to human MAC30 C-terminus
20.602633	14.16432	YLR010C weak similarity to <i>Aquifex aeolicus</i> adenylosuccinate synthetase
6.169986	4.096161	YLR011W weak similarity to <i>E.coli</i> hypothetical 20.4 kDa protein
3.2913213	4.789343	YLR014C zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster
2.3370075	2.168767	YLR015W weak similarity to <i>S.pombe</i> hypothetical protein SPBC13G1
5.8462577	5.231122	YLR016C hypothetical protein
2.2185059	1.896797	YLR021W hypothetical protein

1.6548309	2.463682	YLR026C Sed5p is a t-SNARE (soluble NSF attachment protein receptor) re
1.0090499	0.358793	YLL009C cysteine-rich cytoplasmic protein
1.5753487	1.904429	YLL004W Third subunit of the origin recognition complex
5.5537753	4.909391	YLL003W protein of unknown function
0.8987471	2.03771	YLR002C similarity to hypothetical <i>C. elegans</i> protein
1.2005525	2.28575	YLR003C hypothetical protein
2.334085	1.940117	YLR004C similarity to allantoin transport protein
2.2041996	2.131744	YLR007W hypothetical protein
2.2813609	3.104232	YLL035W hypothetical protein
3.4202733	2.978806	YLL033W hypothetical protein
1.892531	2.126021	YLL029W similarity to <i>M.jannaschii</i> X-Pro dipeptidase and <i>S.pombe</i> hypothe
1.9811038	3.073027	YLL027W similarity to <i>H.influenzae</i> and <i>E.coli</i> hypothetical proteins
2.73657	1.005927	YLL026W heat shock protein 104
10.075625	8.757042	YLL025W strong similarity to members of the Srp1p/Tip1p family
2.3214695	2.893731	YLL020C questionable ORF
4.4838276	7.224322	YLL019C protein kinase homolog
4.3656926	1.603462	YLL016W homologous to <i>cdc25</i>
11.318308	10.48	YLL057C similarity to <i>E.coli</i> dioxygenase
5.6432047	6.572411	YLL056C weak similarity to <i>Y.pseudotuberculosis</i> CDP-3,6-dideoxy-D-glycer
4.4949665	5.436607	YLL055W similarity to Dal5p
3.060429	2.358234	YLL053C similarity to water channel proteins
3.4068902	2.468478	YLL052C member of mip family transmembrane channels
4.7140427	4.655041	YLL051C similar to FRE2
1.6848029	1.279729	YLL042C hypothetical protein
2.0407012	8.024986	YLL038C weak similarity to YJR125c and YDL161w
2.8952088	1.580434	non-annotated SAGE orf Found reverse in NC_001143 between 468759 and
2.7630045	2.542624	non-annotated SAGE orf Found reverse in NC_001143 between 447932 and
9.002449	7.415031	non-annotated SAGE orf Found forward in NC_001143 between 456740 and
0.6284797	0.400912	SNR38 snRNA
0.6114778	0.711889	SNR69 snRNA
3.3855882	2.599335	YLL065W Growth INhibitory protein
11.573948	11.54242	YLL064C strong similarity to members of the Srp1/Tip1p family
11.673861	16.11351	YLL063C transacetylase
4.42837	4.420648	YLL060C Glutathione transferase
2.5637472	2.734086	YLL058W similarity to <i>N.crassa</i> O-succinylhomoserine (thiol)-lyase
2.0915785	3.025148	non-annotated SAGE orf Found reverse in NC_001143 between 638531 and
9.109126	11.72374	non-annotated SAGE orf Found reverse in NC_001143 between 136056 and
6.787077	7.700769	non-annotated SAGE orf Found reverse in NC_001143 between 136275 and
16.948795	10.84919	non-annotated SAGE orf Found reverse in NC_001143 between 142825 and
18.922129	17.37112	non-annotated SAGE orf Found reverse in NC_001143 between 264148 and
2.3030317	5.565861	non-annotated SAGE orf Found forward in NC_001143 between 308848 and
2.8419998	2.861538	YKL162C-A hypothetical protein identified by SAGE
4.800329	2.709042	YKL201C regulates the mannosylphosphorylation
2.0709782	4.182603	YKL199C Protein of unknown function
3.0895061	6.361028	YKL198C probable serine/threonine-specific protein kinase (EC 2.7.1.-)
6.958008	3.983282	non-annotated SAGE orf Found forward in NC_001143 between 94073 and
12.683457	10.95557	non-annotated SAGE orf Found forward in NC_001143 between 146588 and
3.2713845	3.976731	non-annotated SAGE orf Found reverse in NC_001143 between 16801 and
1.5600061	3.836526	non-annotated SAGE orf Found reverse in NC_001143 between 195028 and
26.380772	24.53328	non-annotated SAGE orf Found forward in NC_001143 between 233585 and
2.0649498	2.384826	YKR087C similarity to hypothetical <i>Myxococcus xanthus</i> protein

5.3844185	3.682914	YKR091W Suppressor of rad53 lethality
11.740578	11.81799	YKR097W phosphoenolpyruvate carboxylkinase
3.753949	2.73814	YKR098C Ubiquitin-specific protease
1.5676752	2.46895	YKR100C cause growth inhibition when overexpressed
5.709078	6.103475	YKR102W Protein with similarity to flocculation protein Flo1p
1.4410131	1.886342	YKR103W similarity to multidrug resistance proteins
6.1934986	6.24677	YKR104W similarity to multidrug resistance proteins
2.8943307	3.071572	YKR064W weak similarity to transcription factors
3.146024	2.962946	YKR069W siroheme synthase
1.2963846	2.224759	YKR075C weak similarity to negative regulator Reg1p
3.058343	4.872184	YKR080W NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase
2.1431339	2.754919	YKR038C probable calcium-binding protein
3.2782342	2.060167	YKR045C hypothetical protein
2.9756238	1.074047	YKR049C hypothetical protein
2.7806387	1.698569	YKR050W membrane protein\; low affinity potassium transport
2.5594137	1.723443	YKR052C mitochondrial carrier protein, highly homologous to Mrs3p
2.651611	1.675413	YKR053C DHS-1-P phosphatase
2.9875793	1.350604	YKR058W self-glucosylating initiator of glycogen synthesis\; similar to mamn
27.017977	34.11739	YKR061W putative mannosyltransferase\; type 2 membrane protein
2.1245875	1.927881	YKR019C Increased rDNA silencing
3.7812269	1.94563	YKR022C hypothetical protein
1.9903184	1.453708	YKR027W strong similarity to Chs6p
1.7336159	2.02183	YKR030W weak similarity to NADH dehydrogenases
2.6222084	3.45866	YKR036C CCR4 associated factor
3.0677812	2.335933	YKL005C weak similarity to YKR029c and D.melanogaster transcription elon
1.8212426	2.898285	YKR004C ExtraCellular Mutant
2.153476	2.355572	YKR005C hypothetical protein
4.836776	4.051015	YKR009C peroxisomal multifunctional beta-oxidation protein
1.6827431	5.231788	YKR010C topoisomerase I interacting factor 2
2.2073846	1.425962	YKR012C questionable ORF
15.945814	5.327549	YKL026C strong similarity to glutathione peroxidase
2.4235585	2.25383	YKL023W weak similarity to human cylicin II
6.5752463	3.838135	YKL017C DNA helicase A
3.426752	1.886583	YKL012W Splicing component that associates with the yeast U1 small nucle
1.9250101	1.757616	YKL011C cruciform cutting endonuclease
3.300849	2.232915	YKL051W hypothetical protein
2.242185	2.919553	YKL050C similarity to YMR031c
1.9744068	2.870683	YKL049C high similarity to histone H3 and to human centromere protein CEI
2.625499	2.782591	YKL047W hypothetical protein
2.7910256	2.174397	YKL045W p58 polypeptide of DNA primase
2.5172412	2.961546	YKL033W-A hypothetical protein
5.9596195	3.474521	YKL071W weak similarity to A.parasiticus nor-1 protein
2.2885215	2.155803	YKL064W overexpression overcomes manganese toxicity
1.5764489	2.03482	YKL063C weak similarity to mammalian microtubule-associated protein MAF
2.1429927	2.462691	YKL062W zinc finger protein
1.9306065	1.245011	YKL061W hypothetical protein
2.541752	2.87675	YKL052C hypothetical protein
2.8847735	1.140223	YKL093W MBR1 protein precursor
5.646503	1.540005	YKL091C strong similarity to Sec14p
3.0502553	3.226538	YKL090W hypothetical protein
1.6769817	3.313003	YKL088W similarity to C.tropicalis hal3 protein, to C-term. of Sis2p and to hy

2.5885873	1.662244	YKL079W kinesin heavy chain homolog, but is not believed to act as a kinesin
1.3823521	2.07486	YKL110C Protein involved in resistance to <i>K. lactis</i> killer toxin
3.1880836	3.77053	YKL109W transcriptional activator protein of CYC1 (component of HAP2VHA)
1.4849288	0.479861	YKL105C similarity to YMR086w
0.6514388	0.342658	YKL103C vacuolar aminopeptidase ysc1
1.1262317	2.109375	YKL099C similarity to <i>C.elegans</i> hypothetical proteins C18G6.06 and C16C1
4.6022806	2.724832	YKL098W hypothetical protein
2.9747353	2.194113	YKL133C probable purine nucleotide-binding protein
2.2126377	3.279292	YKL132C probable foyl-polyglutamate synthetase
0.48205504	0.430231	YKL127W phosphoglucomutase, minor isoform
1.5769949	3.103324	YKL125W DNA-independent RNA Polymerase I transcription factor
2.3873048	2.572983	YKL123W questionable ORF
2.6111116	1.353558	YKL121W strong similarity to YMR102c
0.804112	0.4218	YKL117W Hsp90 (Ninety) Associated Co-chaperone
3.1941364	2.075317	YKL159C hypothetical protein
3.4973679	0.78714	YKL151C similarity to <i>C.elegans</i> hypothetical protein R107.2
2.3736653	2.43813	YKL149C debranching enzyme
1.3660469	2.397051	YKL143W low temperature viability protein
1.5908073	2.265604	YKL139W alpha subunit of the kinase which phosphorylates the RNA polymerase
3.1461747	5.596396	YKL180W Ribosomal protein L17A (L20A) (YL17)
2.053391	3.428881	YKL176C hypothetical protein
2.509329	1.832972	YKL168C probable serine/threonine-specific protein kinase (EC 2.7.1.-)
20.871428	7.486888	YKL163W Protein containing tandem internal repeats
8.037034	5.457695	YKL161C probable serine/threonine-specific protein kinase (EC 2.7.1.-)
2.343604	2.08555	YKL206C hypothetical protein
11.176441	6.480815	YKL188C peroxisomal ABC transporter 2
4.294073	1.470252	YKL187C strong similarity to hypothetical protein YLR413w
1.785615	2.761715	YKL186C mRNA transport regulator
1.8375208	2.855945	YKL184W Ornithine decarboxylase
0.42750466	0.354481	SNR37 small nuclear RNA37
0.4919157	0.379306	SNR60 snRNA
5.0858335	3.466622	YKL224C strong similarity to members of the Srp1p/Tip1p family
7.2873473	6.010462	YKL222C weak similarity to transcription factors, similarity to finger proteins
10.046923	7.485384	YKL220C Ferric reductase, similar to Fre1p
16.849846	2.754038	YKL217W carboxylic acid transporter protein homolog
2.582083	2.197608	YKL208W Subunit of complex involved in processing of the 3' end of cytochrome c
1.7053862	1.728259	non-annotated SAGE orf Found forward in NC_001142 between 471954 and 471954
16.186247	11.65481	non-annotated SAGE orf Found reverse in NC_001142 between 626834 and 626834
14.807015	7.335619	non-annotated SAGE orf Found reverse in NC_001142 between 731905 and 731905
18.478308	10.28731	non-annotated SAGE orf Found reverse in NC_001142 between 734995 and 734995
6.6145153	6.004283	non-annotated SAGE orf Found forward in NC_001142 between 741740 and 741740
1.7471437	2.290818	non-annotated SAGE orf Found forward in NC_001142 between 283262 and 283262
8.137398	9.021522	non-annotated SAGE orf Found reverse in NC_001142 between 396887 and 396887
1.3668065	3.127636	non-annotated SAGE orf Found forward in NC_001142 between 447886 and 447886
1.5327713	2.384448	non-annotated SAGE orf Found forward in NC_001142 between 549543 and 549543
7.5299106	5.979425	non-annotated SAGE orf Found reverse in NC_001142 between 737313 and 737313
1.7000412	1.595573	non-annotated SAGE orf Found forward in NC_001142 between 444820 and 444820
1.0415385	1.012885	non-annotated SAGE orf Found reverse in NC_001142 between 451797 and 451797
3.4777899	2.374194	non-annotated SAGE orf Found reverse in NC_001142 between 731735 and 731735
3.6256049	1.976917	non-annotated SAGE orf Found reverse in NC_001142 between 740830 and 740830
3.1759691	2.352138	non-annotated SAGE orf Found forward in NC_001142 between 637618 and 637618

2.709903	5.278282	non-annotated SAGE orf Found forward in NC_001142 between 142442 and
2.1740336	1.1385	non-annotated SAGE orf Found forward in NC_001142 between 236437 and
1.8644394	1.552618	YJR149W similarity to 2-nitropropane dioxygenase
10.815127	3.985079	YJR151C similarity to mucin proteins, YKL224c, Sta1p
8.733864	8.564526	YJR152W allantoate permease
6.8154707	1.712319	YJR153W Endo-polygalacturonase
10.283144	6.181097	YJR155W Hypothetical aryl-alcohol dehydrogenase (AAD)
17.749315	11.42485	YJR156C Thiamine biosynthetic enzyme
2.773809	1.591879	YJR159W sorbitol-induced sorbitol dehydrogenase
2.9878464	1.164808	YJR160C strong similarity to Mal31p
2.365881	3.608738	YJL136W identified by SAGE
8.550157	3.857267	YJR025C C-terminal part of YJR030c
14.999862	7.033706	non-annotated SAGE orf Found reverse in NC_001142 between 159321 and
3.036119	2.192782	non-annotated SAGE orf Found reverse in NC_001142 between 181250 and
0.504987	0.244455	non-annotated SAGE orf Found reverse in NC_001142 between 227590 and
5.7503605	2.413284	YJR127C similarity to regulatory protein Ard1p
1.3796993	2.443729	YJR129C weak similarity to hypothetical protein YNL024c
3.2600877	2.678645	YJR130C similarity to O-succinylhomoserine (thiol)-lyase
3.255955	2.833972	YJR135C Required for maintenance of chromosomes and minichromosomes
2.9721127	3.523484	YJR136C weak similarity to human 3',5'-cyclic-GMP phosphodiesterase
2.106982	2.97754	YJR141W hypothetical protein
1.982779	1.176044	YJR107W weak similarity to acylglycerol lipase
4.5160003	3.829231	YJR108W similarity to hypothetical protein YIL014c-a
1.4838864	3.052613	YJR111C weak similarity to E.coli colanic acid biosynthesis positive regulator
1.4308497	2.44209	YJR112W involved in nuclear function
17.18277	12.37154	YJR115W similarity to hypothetical protein YBL043w
1.2778758	0.520806	YJR122W CCR4 associated factor
1.3256308	2.518488	YJR124C weak similarity to Staphylococcus multidrug resistance protein
2.48696	2.188867	YJR082C hypothetical protein
1.589974	2.774715	YJR083C hypothetical protein
2.719418	3.080203	YJR086W gamma subunit of G protein coupled to mating factor receptors
1.8328207	2.659632	YJR093C Component of a pre-mRNA polyadenylation factor that interacts with
2.9090261	1.258068	YJR094C meiotic gene expression; meiosis inducing protein
3.0944571	1.491557	YJR096W similarity to Corynebacterium 2,5-diketo-D-gluconic acid reductase
2.9263105	1.856063	YJR100C weak similarity to Bud3p
1.5497319	4.00435	YJR078W similarity to mammalian indoleamine 2,3-dioxygenase
1.7248988	2.82287	YJR079W questionable ORF
3.9763908	2.148891	YJR036C similarity to human E6-associated protein
4.375073	2.84091	YJR039W hypothetical protein
2.914553	2.776752	YJR046W weak similarity to Xenopus vimentin 4
0.3598411	0.634116	YJR048W iso-1-cytochrome c
2.5397868	2.483401	YJR052W Nucleotide excision repair protein involved in G(sub)2 repair of inc
3.629273	5.987048	YJR056C hypothetical protein
2.663665	1.440237	YJR058C Clathrin-associated protein, small subunit
4.5982666	3.087675	YJR012C hypothetical protein
19.822056	12.41344	YJR021C meiotic recombination protein
1.7635386	1.265385	YJR021C meiotic recombination protein
0.34791133	0.545588	YJR025C 3-hydroxyanthranilic acid dioxygenase
2.5824883	2.436133	YJL004C Multicopy suppressor of ypt6 null mutation
1.6916469	3.596788	YJR003C hypothetical protein
16.080969	9.478829	YJR004C alpha-agglutinin

7.062619	2.418118	YJR008W similarity to <i>S.pombe</i> hypothetical protein
1.6183571	2.116557	YJL030W spindle-assembly checkpoint protein
2.6211717	2.205954	YJL025W member of yeast Pol I core factor (CF) also composed of Rrn11p,
4.127692	3.389808	YJL024C similar to Aps1p and mammalian small subunit (sigma-2 adaptin) c
7.673538	9.594808	YJL023C Nuclear gene encoding mitochondrial protein
1.2306583	0.40613	YJL021C weak similarity to <i>S.pombe</i> hypothetical protein SPAC23A1.16
0.90436864	0.472757	YJL020C similarity to <i>P.falciparum</i> glutamic acid-rich protein
3.9517515	2.806302	YJL017W hypothetical protein
3.2352257	2.530293	YJL016W weak similarity to hypothetical protein YNL278w and YLR187w
2.4416506	2.945119	YJL049W hypothetical protein
2.3098948	1.650231	YJL048C similarity to hypothetical protein YBR273c
3.298694	1.64943	YJL046W similarity to <i>E.coli</i> lipoate-protein ligase A
2.3287446	1.93268	YJL044C GTPase-activating protein for Ypt6
8.515537	5.147348	YJL037W strong similarity to hypothetical protein YJL038c
3.2073221	3.358271	YJL035C weak similarity to <i>P.gingivalis</i> PgaA and <i>B.japonicum</i> nitrogen fixat
3.906727	1.755067	YJL066C hypothetical protein
2.956359	3.161165	YJL065C weak similarity to DNA-directed DNA polymerase II chain C
2.7830985	4.260071	YJL058C strong similarity to hypothetical protein YBR270c
9.075382	5.840653	YJL057C probable serine/threonine kinase
1.5468509	2.028177	YJL056C Metalloregulatory protein involved in zinc-responsive transcriptiona
3.5286305	2.684102	YJL093C outward-rectifier potassium channel
2.4448092	1.773201	YJL091C weak similarity to human G protein-coupled receptor
2.2865295	3.019071	YJL089W shows homology to DNA binding domain of Gal4p, has a leucine z
1.0361718	2.348963	YJL088W Ornithine carbamoyltransferase
2.734483	4.667357	YJL085W 70 kD component of the Exocyst complex\; required for exocytosis
2.0397396	2.077732	YJL112W similarity to Met30p and <i>N.crassa</i> sulfur controller-2
7.87915	7.525997	YJL110C GATA zinc finger protein 3 homologous to Dal80 in structure and fi
10.339474	4.242461	YJL106W Serine/Threonine protein kinase, positively regulated by IME1
18.319197	2.042357	YJL144W hypothetical protein
3.317978	1.353962	YJL142C questionable ORF
5.0319786	1.984959	YJL142C questionable ORF
7.026828	3.01812	YJL141C Serine-threonine protein kinase
2.9987702	1.6287	YJL139C Probable glycosyltransferase of KRE2VKTR1/YUR1 family\; locate
1.0118763	2.4703	YJL133W mitochondrial carrier protein
2.5677252	1.687358	YJL132W weak similarity to human phospholipase D
3.0652335	3.025895	YJL126W Nit2 nitrilase
2.5364993	2.943083	YJL168C transcription factor containing a SET domain
4.0279613	0.814149	YJL163C hypothetical protein
3.0553296	2.600293	YJL162C weak similarity to dnaJ proteins
11.760443	3.453283	YJL161W hypothetical protein
3.5373487	2.158007	YJL155C Fructose-2,6-bisphosphatase
10.377422	2.48921	YJL153C L-myo-inositol-1-phosphate synthase
2.648101	2.56727	YJL185C hypothetical protein
2.687696	1.536754	YJL210W CH3HC4 zinc-binding integral peroxisomal membrane protein
2.9999394	2.737619	YJL209W Protein required for COB mRNA stability or 5' processing
1.2020028	2.717603	YJL201W ExtraCellular Mutant
3.248578	1.130545	YJL199C hypothetical protein
0.63591355	0.447952	YJL196C Elongation enzyme 1, required for the elongation of the saturated f
0.6595643	1.287974	YJL194W Protein involved in initiation of DNA replication
2.3549526	1.7577	non-annotated SAGE orf Found forward in NC_001133 between 223093 anc
2.0697114	2.102175	non-annotated SAGE orf Found forward in NC_001133 between 223253 anc

2.6016262	2.18162	non-annotated SAGE orf Found forward in NC_001133 between 223333 and
1.8012931	1.993824	YJL225C strong similarity to members of the Sir1p/Tip1p family
21.94359	22.35827	YJL223C strong similarity to members of the Srp1p/Tip1p family
5.7245846	5.466388	YJL222W strong similarity to Pep1p
7.9984517	6.137192	YJL221C homology to maltase(alpha-D-glucosidase)
2.6156924	2.397308	YJL216C strong similarity to Mal62p
2.404923	1.749231	YJL215C hypothetical protein
6.9424896	22.90447	YJL213W similarity to Methanobacterium aryldialkylphosphatase related prot
0.42323467	0.816614	YAR071W Acid phosphatase, secreted
0.2258202	0.189804	YAR073W strong similarity to IMP dehydrogenases
0.4112201	0.439734	YAR075W strong similarity to IMP dehydrogenases
0.7099098	0.350462	YAL069W hypothetical protein
2.3858104	2.178006	YAL069W hypothetical protein
6.9401736	7.232199	non-annotated SAGE orf Found reverse in NC_001133 between 22397 and
4.362493	1.950323	non-annotated SAGE orf Found reverse in NC_001133 between 182850 and
1.7975614	1.578248	non-annotated SAGE orf Found reverse in NC_001133 between 182850 and
4.6593013	3.457667	YAR020C strong similarity to members of the srp1p/Tip1p family
4.6907015	5.02786	YAR023C membrane protein
3.8103976	1.932405	YAR027W membrane protein
2.701237	1.354115	YAR031W membrane protein
3.5149693	2.068636	YAR035W Outer carnitine acetyltransferase, mitochondrial
1.8572884	4.123525	YAR053W predicted membrane protein
0.9527115	0.802537	YAR066W identical to YHR214w hypothetical protein, similarity to Sta1p
0.6645254	0.482884	YAL007C p24 protein involved in membrane trafficking
0.8911005	0.408897	YAL004W strong similarity to A.klebsiana glutamate dehydrogenase
2.8170831	2.62023	YAL002W Vps8p is a membrane-associated hydrophilic protein which contain
1.2738191	1.881278	YAR003W beta transducin domain
1.9198204	2.671636	YAR015W phosphoribosyl amino imidazolesuccinocarboxamide synthetase
0.86122894	0.334238	YAL030W homolog of Snc2p, vesicle-associated membrane protein (synaptic)
6.427738	3.244146	YAL028W similarity to hypothetical protein YOR324c
4.0931954	3.151584	YAL020C Protein with similarity to human RCC1 protein
5.2459707	4.831353	YAL014C protein of unknown function
3.380589	2.120396	YAL054C inducible acetyl-coenzyme A synthetase
2.9914875	2.640024	YAL048C weak similarity to GTP-binding proteins
3.1394212	2.097889	YAL047C Spc72p interacts with Stu2p in the two-hybrid assay; Spc72p local
2.9549067	2.722491	YAL040C G(sub)1 cyclin
1.7102932	5.723539	YAL037W strong similarity to GTP-binding proteins
2.0584998	3.362115	YAL034W-A hypothetical protein
6.0628057	4.165167	YAL034C Function unknown now
1	7.724423	YAL067C Suppressor of Sulfoxide Ethionine resistance
7.3796916	6.021154	YAL064W hypothetical protein
5.7447343	4.182597	YAL063C putative Flo1p homolog
11.2853565	3.910315	YAL062W NADP-linked glutamate dehydrogenase
8.622544	2.183031	YAL061W similarity to alcohol/sorbitol dehydrogenase
0.8517529	2.31688	YAL059W ExtraCellular Mutant
2.5519667	2.069641	YAL058W Calnexin and calreticulin homolog
2.9640183	3.458009	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequen
3.1433067	4.906743	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequen
3.8100803	2.919628	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequen
5.715846	5.408654	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequen
8.518616	6.186154	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequen

2.8620489	2.132998	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequer
2.5777652	1.185549	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequer
4.625846	2.018269	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequer
13.768977	11.17024	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequer
2.7524884	0.509768	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequer
0.4318231	0.363824	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequer
2.6167998	1.987246	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequer
10.363693	1.607885	Saccharomyces cerevisiae chromosome IX, complete chromosome sequenc
1.2916563	1.126127	Saccharomyces cerevisiae chromosome IX, complete chromosome sequenc
2.3882704	1.939642	Saccharomyces cerevisiae chromosome IX, complete chromosome sequenc
4.3946157	1.799615	Saccharomyces cerevisiae chromosome IX, complete chromosome sequenc
0.54299194	0.524532	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequer
0.92668533	0.455656	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequer
0.41268495	0.329447	Saccharomyces cerevisiae chromosome VIII, complete chromosome sequer
0.49388877	0.753625	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
4.224923	3.295192	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
0.8137452	5.138502	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
2.3562362	1.784039	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
5.686601	4.418173	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
3.6958194	2.451689	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
7.8376923	5.868462	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
2.0894687	1.588909	Saccharomyces cerevisiae chromosome VI, complete chromosome sequenc
1.8925407	1.276548	Saccharomyces cerevisiae chromosome VI, complete chromosome sequenc
3.5009446	2.386439	Saccharomyces cerevisiae chromosome VI, complete chromosome sequenc
3.925379	4.885668	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
1.1413357	1.046016	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
3.7962668	4.024811	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
0.6490726	0.55162	Saccharomyces cerevisiae chromosome VII, complete chromosome sequen
1.3910517	3.803094	Saccharomyces cerevisiae chromosome V, complete chromosome sequenci
3.2992308	5.482884	Saccharomyces cerevisiae chromosome V, complete chromosome sequenci
3.1393843	9.076923	Saccharomyces cerevisiae chromosome V, complete chromosome sequenci
5.9446874	1.257749	Saccharomyces cerevisiae chromosome V, complete chromosome sequenci
11.726	5.318654	Saccharomyces cerevisiae chromosome V, complete chromosome sequenci
2.9915693	1.926922	Saccharomyces cerevisiae chromosome V, complete chromosome sequenci
1.3673965	1.281649	Saccharomyces cerevisiae chromosome V, complete chromosome sequenci
0.54717416	0.389113	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
0.5803539	0.468364	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
2.4158006	4.240995	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
2.3379982	1.199962	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
1.8338916	2.024336	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
1.5777332	2.275287	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
2.4267688	6.862692	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
2.416361	1.608015	Saccharomyces cerevisiae chromosome III, complete chromosome sequenc
0.4823828	0.491108	Saccharomyces cerevisiae chromosome III, complete chromosome sequenc
3.3186138	1.152876	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
2.9435945	4.903773	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
5.42074	8.364495	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
2.540717	3.877659	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
0.21059689	0.332676	Saccharomyces cerevisiae chromosome II, complete chromosome sequenc
0.5201798	0.49385	Saccharomyces cerevisiae chromosome II, complete chromosome sequenc
0.42601195	0.37546	Saccharomyces cerevisiae chromosome III, complete chromosome sequenc

1.51575	0.579164	Saccharomyces cerevisiae chromosome III, complete chromosome sequenc
3.6125317	4.908071	Saccharomyces cerevisiae chromosome III, complete chromosome sequenc
2.479614	2.6	Saccharomyces cerevisiae chromosome III, complete chromosome sequenc
3.000809	2.604624	Saccharomyces cerevisiae chromosome III, complete chromosome sequenc
0.96513164	1.001986	Saccharomyces cerevisiae chromosome II, complete chromosome sequenc
2.461713	1.996982	Saccharomyces cerevisiae chromosome II, complete chromosome sequenc
0.45339894	0.54769	Saccharomyces cerevisiae chromosome II, complete chromosome sequenc
1.250783	0.962889	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
2.8532538	2.236188	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
1.1203326	2.301734	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
0.22498941	0.303328	Saccharomyces cerevisiae chromosome II, complete chromosome sequenc
0.7980348	0.60675	Saccharomyces cerevisiae chromosome II, complete chromosome sequenc
0.9508106	0.540111	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
0.4435864	0.520049	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
0.40274096	0.594039	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
8.661539	7.051923	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
2.3295956	1.867694	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
5.262615	13.07308	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
0.42598388	0.765392	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
2.0930357	2.099837	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
2.308208	2.274363	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
2.4785857	1.907751	Saccharomyces cerevisiae chromosome XV, complete chromosome sequen
3.8921676	2.95061	Saccharomyces cerevisiae chromosome XV, complete chromosome sequen
1.1473714	0.901128	Saccharomyces cerevisiae chromosome XV, complete chromosome sequen
1.3173409	0.738742	Saccharomyces cerevisiae chromosome XV, complete chromosome sequen
1.278158	0.711909	Saccharomyces cerevisiae chromosome XIV, complete chromosome sequer
3.773077	5.867116	Saccharomyces cerevisiae chromosome XIV, complete chromosome sequer
5.1756926	1.019615	Saccharomyces cerevisiae chromosome XIV, complete chromosome sequer
2.1814039	2.138333	Saccharomyces cerevisiae chromosome XIV, complete chromosome sequer
1.2455634	9.017385	Saccharomyces cerevisiae chromosome XIV, complete chromosome sequer
3.2630558	2.570437	Saccharomyces cerevisiae chromosome XV, complete chromosome sequen
9.695847	9.835961	Saccharomyces cerevisiae chromosome XV, complete chromosome sequen
6.3951	6.614173	Saccharomyces cerevisiae chromosome XV, complete chromosome sequen
1.9904348	1.495861	Saccharomyces cerevisiae chromosome XIV, complete chromosome sequer
2.8585882	2.254332	Saccharomyces cerevisiae chromosome XIV, complete chromosome sequer
3.2548714	3.249052	Saccharomyces cerevisiae chromosome XIII, complete chromosome sequer
0.42071223	0.544701	Saccharomyces cerevisiae chromosome XIII, complete chromosome sequer
1.8803686	3.978105	Saccharomyces cerevisiae chromosome XIII, complete chromosome sequer
3.2064853	1.783197	Saccharomyces cerevisiae chromosome XIII, complete chromosome sequer
5.8689227	2.724039	Saccharomyces cerevisiae chromosome XIII, complete chromosome sequer
0.6406076	0.42945	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
0.6500517	0.896267	Saccharomyces cerevisiae chromosome XIII, complete chromosome sequer
0.6118081	0.814292	Saccharomyces cerevisiae chromosome XIII, complete chromosome sequer
0.43961012	0.377911	Saccharomyces cerevisiae chromosome XIII, complete chromosome sequer
10.015769	7.202817	Saccharomyces cerevisiae chromosome XIII, complete chromosome sequer
0.42733827	0.776693	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
8.201371	2.413995	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
0.6741288	0.574801	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
2.8098485	3.00348	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
0.7941205	0.972923	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
1.9789131	2.245741	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc

3.589893	2.026431	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
7.503283	5.280939	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
9.8210535	7.778197	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
4.407077	1.941923	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
1.9340512	1.916376	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
1.0400352	1.674424	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
4.6487694	2.180769	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
7.612615	3.445	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
1.4429754	1.442253	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
0.5445158	0.360896	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
0.63122094	1.153743	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
3.686163	2.708273	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
4.486308	3.9375	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
3.6316924	3.552116	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
3.0857189	2.288079	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
1.8943121	2.134758	Saccharomyces cerevisiae chromosome X, complete chromosome sequenci
6.1691074	6.464114	Saccharomyces cerevisiae chromosome X, complete chromosome sequenci
1.6725385	1.503285	Saccharomyces cerevisiae chromosome X, complete chromosome sequenci
1.5538516	1.428968	Saccharomyces cerevisiae chromosome X, complete chromosome sequenci
1.4800925	1.154775	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
3.0576575	2.63164	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
2.2162447	2.243747	Saccharomyces cerevisiae chromosome XI, complete chromosome sequenc
0.67141914	0.268464	Saccharomyces cerevisiae chromosome X, complete chromosome sequenci
2.4788933	2.844629	Saccharomyces cerevisiae chromosome X, complete chromosome sequenci
4.548678	5.440152	Saccharomyces cerevisiae chromosome I, complete chromosome sequence
5.61925	7.984255	Saccharomyces cerevisiae chromosome I, complete chromosome sequence
6.518763	1.199912	Saccharomyces cerevisiae chromosome I, complete chromosome sequence
7.8223042	7.018013	Saccharomyces cerevisiae chromosome I, complete chromosome sequence
5.3006153	1.325192	Saccharomyces cerevisiae chromosome X, complete chromosome sequenci
2.7305062	3.197081	Saccharomyces cerevisiae chromosome X, complete chromosome sequenci
1.6769785	2.412958	Saccharomyces cerevisiae chromosome X, complete chromosome sequenci
0.5624939	0.496356	YILCDELTA1 Ty1 LTR
10.3904295	3.641156	Saccharomyces cerevisiae chromosome IX, complete chromosome sequenc
8.552955	4.044172	YILWTY3-1 Full length Ty3
0.96788275	2.277893	YILCDELTA2 Ty2 LTR
0.5883133	0.40727	YILCDELTA3 Ty1 LTR
0.6942986	0.491055	YILWDELTA4 Ty1 LTR
1.781846	2.314231	YILCDELTA5 Ty1 LTR
6.6836777	5.544399	YCR096C mating hormone a2
2.5745234	3.052846	Saccharomyces cerevisiae chromosome I, complete chromosome sequence
4.464791	4.953583	Saccharomyces cerevisiae chromosome I, complete chromosome sequence
1.820661	3.574657	Saccharomyces cerevisiae chromosome I, complete chromosome sequence
1.5418037	2.288405	Saccharomyces cerevisiae chromosome I, complete chromosome sequence
5.637244	4.185008	YHRWTAU3 Ty4 LTR
2.3821151	2.143778	YHRWDELTA13 Ty1 LTR
0.73900545	0.427121	YHRWDELTA13 Ty1 LTR
0.6432989	0.516411	YHRCDELTA16 Ty1 LTR
2.163112	2.308065	YIL177C strong similarity to subtelomeric encoded proteins
1.1320772	1.349014	YHL050C strong similarity to subtelomeric encoded proteins
6.722048	4.985475	YHLWTAU1 Ty4 LTR
5.3828874	3.542879	YHRCDELTA4 Ty1 LTR

0.56659824	0.387143	YHRWDELTA7 Ty1 LTR
0.62188506	0.406014	YGRWDELTA22 Ty1 LTR
14.033707	12.41995	YGRWDELTA23 Ty1 LTR
0.5030056	0.395853	YGRWDELTA30 Ty1 LTR
0.6206435	0.480699	YGRWDELTA31 Ty1 LTR
7.0595307	4.487815	YGRCTAU3 Ty4 LTR
0.56188184	0.408857	YGRWDELTA32 Ty1 LTR
0.472597	0.343765	YGRWDELTA15 Ty1 LTR
0.5433678	0.425244	YGRWDELTA16 Ty1 LTR
0.7366313	0.513325	YGRWDELTA19 Ty1 LTR
1.7267573	1.818054	YGRWDELTA20 Ty1 LTR
5.226704	3.694514	YGLWDELTA4 Ty1 LTR
3.6077225	1.638214	YGLCDELTA5 Ty1 LTR
3.3879306	5.263413	YGLWDELTA6 Ty1 LTR
0.47355175	0.364214	YGLWDELTA8 Ty1 LTR
0.5029893	0.401728	YFLWDELTA5 Ty1 LTR
0.7946104	0.436142	YFRWDELTA7 Ty1 LTR
0.47255844	0.324274	YFRCDELTA8 Ty1 LTR
2.7072306	1.809038	YFRWDELTA10 Ty1 LTR
9.775132	6.124085	YGLWTAU1 Ty4 LTR
0.5834787	0.485267	YGLCDELTA1 Ty1 LTR
0.44383505	0.378429	YGLWDELTA2 Ty1 LTR
6.015316	4.139709	YGLWDELTA4 Ty1 LTR
0.4125726	0.403423	YERWDELTA18 Ty1 LTR
0.28981376	0.283676	YERWDELTA18 Ty1 LTR
0.3677537	0.409069	YERWDELTA18 Ty1 LTR
1.3096395	1.895167	YERWDELTA18 Ty1 LTR
0.51624995	0.371275	YERCSIGMA4 Ty3 LTR
0.6611408	0.447934	YERCDELTA24 Ty1 LTR
0.7060804	0.754929	YERWOMEGA2 Ty5 LTR
2.111683	2.254156	YDR543C
4.826462	4.054231	YFL063W strong similarity to subtelomeric encoded proteins
10.926308	3.221731	YFLWDELTA1 Ty1 LTR
0.6632629	0.503224	YFLWDELTA2 Ty1 LTR
0.6403326	0.455653	YERWDELTA11 Ty1 LTR
2.6452308	3.902885	YERWDELTA13 Ty1 LTR
7.5397573	5.610926	YERCTAU2 Ty4 LTR
6.4779496	3.213475	YERCDELTA15 Ty1 LTR
5.0254	3.763403	YERCDELTA15 Ty1 LTR
10.254414	11.80928	YERCTAU3 Ty4 LTR
2.5488036	2.203666	YDR543C strong similarity to subtelomeric encoded proteins
0.6316812	0.468293	YELWDELTA2 Ty1 LTR
0.6316086	0.442054	YELWDELTA6 Ty1 LTR
0.77587783	3.283318	TR(UCU)E tRNA-Arg
1.0046753	1.764616	TH(GUG)E1 tRNA-His
4.188752	3.168184	YERWDELTA9 Ty1 LTR
0.5678404	0.457167	YDRWDELTA23 Ty1 LTR
0.56750387	0.470402	YDRWDELTA24 Ty1 LTR
0.51397717	0.36226	YDRWDELTA25 Ty1 LTR
0.58288735	0.439495	YDRWDELTA26 Ty1 LTR
0.53040546	0.388012	YDRWDELTA27 Ty1 LTR

0.46552807	0.427561	YDRWDELTA28 Ty1 LTR
3.1823163	1.652047	YDRWDELTA31 Ty1 LTR
7.9572086	10.77763	YDR542W strong similarity to subtelomeric encoded proteins
0.58949566	0.381498	YDRWDELTA11 Ty1 LTR
5.470287	2.620083	Saccharomyces cerevisiae chromosome IV, complete chromosome sequenc
0.7169337	1.041582	TS(AGA)D2 tRNA-Ser
1.7953769	2.253798	YDRCDELTA2 Ty1 LTR
0.6792884	0.570859	YDRWDELTA7 Ty1 LTR
0.9481006	4.96269	TR(UCU)D tRNA-Arg
0.5797108	0.394798	YDRCDELTA7 Ty1 LTR
0.5539034	0.448447	YDRCDELTA8 Ty1 LTR
3.7745001	2.863296	YDRCSIGMA1 Ty3 LTR
3.0469902	2.683732	YDRCSIGMA2 Ty3 LTR
0.5124903	0.417332	YCRCDELTA6 Ty1 LTR
4.792035	4.180862	YCR007C strong similarity to subtelomeric encoded proteins
0.5763985	0.449461	YCRCDELTA7 Ty1 LTR
0.5910254	0.432531	YCRWDELTA8 Ty1 LTR
0.74309903	0.31019	YCRWDELTA13 Ty1 LTR
1.8925306	1.316275	YDL248W Protein with strong similarity to other subtelomerically-encoded pr
0.5458526	0.494832	YDLCDELTA1 Ty1 LTR
15.240115	9.508738	YDLWTAU1 Ty4 LTR
0.5688709	3.073225	TR(UCU)B tRNA-Arg
2.706294	2.812101	YBLWTAU1 Ty4 LTR
2.915925	2.242544	YBLWDELTA8 Ty1 LTR
0.5472712	0.417142	YBLWDELTA9 Ty1 LTR
0.66434777	0.461654	YBLWTY1-1 Full length Ty1
0.5203185	0.38448	YBLWDELTA10 Ty1 LTR
0.5632254	0.417837	YBRWDELTA12 Ty1 LTR
0.56250197	0.420301	YBRWDELTA13 Ty1 LTR
0.64008504	0.433561	YPRCTY1-2 Full length Ty1
0.4691646	0.332969	YPRCDELTA19 Ty1 LTR
0.5966103	0.470484	YPRWDELTA21 Ty1 LTR
0.5697415	0.451969	YPRCDELTA23 Ty1 LTR
0.4862215	0.372962	YPRCTY1-4 Full length Ty1
0.5805325	0.481061	YPRCDELTA24 Ty1 LTR
0.43167117	0.708292	TA(AGC)P tRNA-Ala
8.906956	11.97761	YPRWTAU4 Ty4 LTR
1.7203076	2.675798	YBL112C strong similarity to subtelomeric encoded proteins
0.3694171	0.253558	YPLCDELTA10 Ty1 LTR
10.757779	6.156194	YPLCTAU1 Ty4 LTR
8.27774	5.357959	YPLCTY4-1 Full length Ty4
8.713441	5.665837	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
13.7254505	7.079035	Saccharomyces cerevisiae chromosome XVI, complete chromosome sequer
7.6950254	5.066189	YPLCTAU2 Ty4 LTR
0.57130426	0.504902	YPRWDELTA12 Ty1 LTR
0.49325377	0.432279	TS(UGA)P tRNA-Ser
0.49339712	0.459979	YPRWDELTA17 Ty1 LTR
0.5132518	0.410328	YPRCDELTA18 Ty1 LTR
0.70145804	0.536014	YORCDELTA21 Ty2 LTR
4.883466	3.263842	YORWTAU3 Ty4 LTR
0.5365455	0.453144	YORCDELTA25 Ty1 LTR

6.600995	2.765106	YPLCDELTA1 Ty1 LTR
10.683078	3.698654	YPLCDELTA1 Ty1 LTR
0.56488097	0.418651	YPLWTY1-1 Full length Ty1
0.5407608	0.397919	YPLWDELTA4 Ty1 LTR
0.59226066	0.427309	YPLWDELTA6 Ty1 LTR
0.7555919	2.035944	TR(ACG)O tRNA-Arg
0.53266495	0.437303	YORWDELTA13 Ty1 LTR
0.51889473	0.432775	YORWDELTA14 Ty1 LTR
7.8797097	5.786185	YORWTAU2 Ty4 LTR
0.68079865	0.488956	YNRCDELTA8 Ty1 LTR
3.4810994	3.116407	YNRCDELTA9 Ty1 LTR
2.2335758	5.368122	YNR075W Protein with strong similarity to subtelomerically-encoded proteins
0.9688962	2.248114	YNR075W Protein with strong similarity to subtelomerically-encoded proteins
2.1913197	2.637236	YNR077C strong similarity to subtelomeric encoded proteins
6.6625857	5.415583	YOLWTAU1 Ty4 LTR
0.5795309	0.476789	YOLWDELTA5 Ty1 LTR
2.930228	2.709965	YNL337W strong similarity to subtelomeric encoded proteins
20.190702	12.92826	YNLWTAU1 Ty4 LTR
0.6987602	0.470505	YNLCTY1-1 Full length Ty1
0.55894697	0.453803	YNLCDELTA2 Ty1 LTR
0.558784	0.427584	YNLWDELTA4 Ty1 LTR
5.214765	4.231332	YNLWSIGMA2 Ty3 LTR
8.788436	4.339016	YNLWTAU2 Ty4 LTR
0.61087066	0.421406	YNLCDELTA5 Ty2 LTR
0.52287155	0.390138	YNRCDELTA7 Ty1 LTR
13.0707855	7.736905	YNRCTAU3 Ty4 LTR
3.7873847	4.5325	YMRWDELTA16 Ty1 LTR
7.27229	4.711665	YMRWTAU2 Ty4 LTR
0.5519476	0.475869	YMRWDELTA17 Ty1 LTR
3.958154	2.776923	YMRDELTA18 Ty1 LTR
0.56956565	2.705585	TR(UCU)M1 tRNA-Arg
8.150818	4.793672	YMRCTAU3 Ty4 LTR
1.3814317	1.883021	YMRWDELTA21 Ty1 LTR
0.48637652	2.461863	TR(UCU)M2 tRNA-Arg
0.6339485	0.600139	YMLCDELTA2 Ty2 LTR
0.61221826	0.471287	YMLWDELTA3 Ty1 LTR
0.6036751	0.473963	YMLWDELTA4 Ty1 LTR
0.6156217	0.514954	YMLWDELTA6 Ty1 LTR
0.57602805	0.48161	YMRDELTA7 Ty1 LTR
1.0794241	0.496429	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
1.3280994	0.610485	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
3.51388	0.812219	YLRWTY2-1 Full length Ty2
10.030577	5.70803	YLRCDELTA27 Ty1 LTR
1.7048717	1.925242	YLR466W strong similarity to subtelomeric encoded proteins
1.010442	1.386598	YLR467W strong similarity to subtelomeric encoded proteins
0.5732668	0.4562	YLRWDELTA14 Ty1 LTR
0.6483073	0.877751	TA(AGC)L tRNA-Ala
6.623038	3.807591	YLRWDELTA15 Ty1 LTR
0.57311237	0.47137	YLRCDELTA18 Ty2 LTR
0.60475415	0.436896	YLRCDELTA19 Ty1 LTR
0.6708703	0.528251	YLRWDELTA20 Ty1 LTR

0.75375026	0.508278	YLRCDELTA21 Ty1 LTR
2.8356717	0.869316	Saccharomyces cerevisiae chromosome XII, complete chromosome sequen
0.5849743	0.447024	YLRCDELTA7 Ty1 LTR
0.5426216	0.479254	YLRCDELTA8 Ty1 LTR
0.45399585	0.358739	YLRCDELTA9 Ty1 LTR
0.565782	0.449517	YLRWDELTA10 Ty1 LTR
0.52461964	0.432733	YLRWDELTA11 Ty1 LTR
4.4790797	7.441015	YLL067C strong similarity to subtelomeric encoded proteins
1.9528157	2.454084	YLL067C strong similarity to subtelomeric encoded proteins
3.5364492	3.182281	YLL067C strong similarity to subtelomeric encoded proteins
0.53356194	0.428952	YLLCDELTA1 Ty1 LTR
0.6195047	0.508894	YLRCDELTA3 Ty1 LTR
0.30438417	0.382989	RDN37-1 35S ribosomal RNA
1.0677888	0.569514	RDN37-1 35S ribosomal RNA
0.60260904	4.03469	TR(UCU)K tRNA-Arg
0.55500114	0.37571	YKLCDELTA5 Ty1 LTR
0.51586854	0.404911	YKRCDELTA8 Ty1 LTR
0.31310612	1.090489	TR(ACG)K tRNA-Arg
4.241777	3.500146	YKRCDELTA11 Ty1 LTR
0.49780998	0.419793	YKRCDELTA12 Ty1 LTR
1.0036923	2.202308	YKR106W strong similarity to subtelomeric encoded proteins
1.2227589	2.444373	YLL067C strong similarity to subtelomeric encoded proteins
0.6974565	0.362185	YJRWTY1-2 Full length Ty1
0.56152797	0.45428	YJRWDELTA13 Ty1 LTR
2.6917946	2.921253	YJLWDELTA16 Ty1 LTR
0.6475107	0.464154	YJRWDELTA17 Ty1 LTR
2.8855577	1.571481	YJR161C Protein with similarity to members of the Ybr302p/Ycr007p/Cos8
2.628405	1.51861	YJR161C Protein with similarity to members of the Ybr302p/Ycr007p/Cos8
4.7605767	4.454826	YJR162C strong similarity to subtelomeric encoded proteins
1.7762884	2.342372	TN(GUU)K tRNA-Asn
0.6755284	0.527849	YJLCDELTA4 Ty1 LTR
0.53006554	3.001632	TR(UCU)J1 tRNA-Arg
0.43308914	2.739825	TR(UCU)J2 tRNA-Arg
0.69418585	2.7815	TV(AAC)J tRNA-Val
18.206009	9.512918	YJLWTAU4 Ty4 LTR
0.57594115	0.433235	YJRWDELTA11 Ty1 LTR
0.6586264	0.516437	YJRWTY1-1 Full length Ty1
0.56751543	0.426239	YJRWTY1-1 Full length Ty1
0.49786997	0.402823	YJRWDELTA12 Ty1 LTR
7.7656994	5.209791	YJLWTAU1 Ty4 LTR
9.198928	6.114702	Saccharomyces cerevisiae chromosome X, complete chromosome sequenc
8.691231	4.281154	YJLWTY4-1 Full length Ty4
5.923724	3.780441	YJLWTY4-1 Full length Ty4
6.9590144	4.524733	YJLWTAU2 Ty4 LTR
0.653043	0.459159	YJLCDELTA3 Ty1 LTR
4.035179	2.835412	YJLWDELTA2 Ty1 LTR
3.2412784	3.618555	YAL068C strong similarity to subtelomeric encoded proteins
0.5147835	0.440702	YARCDELTA4 Ty1 LTR
0.39378178	0.252525	YARCTY1-1 Full length Ty1
0.8955224	0.375236	YARCTY1-1 Full length Ty1
0.6321854	0.425855	YARCTY1-1 Full length Ty1

0.58183265	0.500273	YARCDELTA5 Ty1 LTR
0.5434924	0.479479	YARWDELTA6 Ty1 LTR
3.7537105	1.943966	YBR006W Probable aldehyde dehydrogenase (EC 1.2.1.-)
2.0111165	3.617889	YKL198C probable serine/threonine-specific protein kinase (EC 2.7.1.-)
0.030697174	0.519863	2mic_FLP1 2 micron plasmid recombinase
0.03665547	1.884553	2mic_REP1 2 micron plasmid rep1 protein
0.032669548	4.278574	2mic_D_protein 2 micron plasmid D protein
0.02956932	1.272834	2mic_REP2 2 micron plasmid rep2 protein
0.27526972	0.895814	2mic_FLP1 2 micron plasmid recombinase
0.5782255	0.347971	similarity to mouse Gcap1 Found forward in NC_001224 between 28122 and 28122
1.8672978	0.814334	similarity to Sauroleishmania NADH dehydrogenase (ubiquinone) chain 5 Found forward in NC_001224 between 13748 and 14122
0.6099828	0.885318	questionable ORF Found reverse in NC_001224 between 13748 and 14122
2.8533602	2.092857	non-annotated SAGE orf Found forward in NC_001141 between 26990 and 26990
7.433759	5.531116	non-annotated SAGE orf Found forward in NC_001141 between 258363 and 258363
4.785148	3.489065	non-annotated SAGE orf Found forward in NC_001141 between 258506 and 258506
4.100038	2.582869	non-annotated SAGE orf Found reverse in NC_001141 between 385561 and 385561
9.491376	5.373789	non-annotated SAGE orf Found reverse in NC_001141 between 385816 and 385816
7.4467907	3.228165	non-annotated SAGE orf Found reverse in NC_001141 between 386017 and 386017
1.8661538	2.118077	non-annotated SAGE orf Found reverse in NC_001141 between 30695 and 30695
2.987131	1.750682	non-annotated SAGE orf Found reverse in NC_001141 between 51611 and 51611
2.4492223	3.831934	non-annotated SAGE orf Found forward in NC_001141 between 385618 and 385618
3.051447	2.922995	YIR043C putative pseudogene
6.040264	1.400254	YIL071C
7.018923	3.581539	YIL066C Ribonucleotide reductase (ribonucleoside-diphosphate reductase) I
6.23294	4.866496	YIR020C hypothetical protein
3.0025823	2.542476	YIR025W hypothetical protein
6.423059	3.940984	YIR028W allantoin permease
6.4123077	5.974808	YIR029W allantoicase
0.30715317	0.611821	YIR030C involved in nitrogen-catabolite metabolism
6.058459	4.798966	YIR031C Malate synthase 2
5.011902	4.071314	YIR032C ureidoglycolate hydrolase
0.6516555	0.417159	YIR037W putative glutathione-peroxidase
12.398659	6.184079	YIR039C GPI-anchored aspartic protease
9.292211	8.534006	YIR041W similarity to members of the Srp1p/Tip1p family
3.437946	5.733944	YIR042C weak similarity to B.licheniformi hypothetical protein P20
3.9853535	6.781941	YIR043C putative pseudogene
1.805123	2.324531	YIL003W strong similarity to Nbp35p and human nucleotide-binding protein
1.8861557	3.211734	YIR001C similarity to D.melanogaster RNA binding protein
3.1890607	1.663755	YIR007W hypothetical protein
2.9646857	3.610873	YIR009W encodes YU2B, a component of yeast U2 snRNP
2.3221107	3.570019	YIR011C restores protein transport when overexpressed and rRNA stability
3.211156	2.732542	YIR014W hypothetical protein
4.020585	1.849647	YIR016W weak similarity to YOL036w
3.067314	1.681361	YIR017C Transcriptional activator of sulfur amino acid metabolism
2.4746659	2.64628	YIR018W bZIP protein; transcription factor
3.0642397	1.333757	YIR019C cell surface flocculin with structure similar to serine/threonine-rich
2.93535	2.534684	YIL024C hypothetical protein
4.0329413	3.775827	YIL023C similarity to mouse MHC H-2K/t-w5-linked ORF precursor
1.4393429	2.925321	YIL019W weak similarity to S.pombe hypothetical protein SPAC3F10
2.3149107	1.425934	YIL017C hypothetical protein
0.38223746	0.336862	YIL015W encodes a-cell barrier activity on alpha factor

2.7629912	2.921508	YIL015C-A strong similarity to hypothetical protein YIL102c
2.157298	1.861855	YIL013C Putative member of the ABC family of membrane transporters
2.1169012	1.979542	YIL009C-A 181aa protein - 20.5 kD
2.6160793	2.275097	YIL009C-A 181aa protein - 20.5 kD
3.2379959	1.847018	YIL045W Protein with 30%% identity to protein corresponding to YER054
4.736615	3.373077	YIL028W putative pseudogene
2.3622046	1.359056	YIL071C hypothetical protein
0.59307677	0.340343	YIL070C mitochondrial acidic matrix protein
6.484586	7.850891	YIL059C hypothetical protein
1.9506843	2.94884	YIL056W similarity to YER064c
6.594036	2.130365	YIL055C hypothetical protein
4.9358435	0.911938	YIL054W weak similarity to fruit fly NADH dehydrogenase
2.1591113	1.54612	YIL049W Protein required for filamentous growth, cell polarity, and cellular e
2.1642745	2.822153	YIL092W hypothetical protein
1.6582017	1.70463	YIL089W similarity to hypothetical protein YLR036c
3.1020348	1.029553	YIL087C hypothetical protein
1.409499	4.181991	YIL084C Functions are similar to those of SIN3 and RPD3
5.2525797	2.654709	YIL080W Ty3-2 orf C fragment
2.1538253	5.421049	YIL079C strong similarity to hypothetical protein YDL175c
2.5376377	2.607547	YIL077C hypothetical protein
3.1866016	1.926552	YIL073C weak similarity to mouse polycystic kidney disease-related protein
0.8527584	0.968202	YIL119C inhibitor of ras
2.6592069	1.8099	YIL117C hydrophobic transmembrane domain
1.6444415	1.818684	YIL116W histidinol-phosphate aminotransferase
3.905057	0.885079	YIL113W strong similarity to dual-specificity phosphatase Msg5p
1.3233026	0.387573	YIL111W Cytochrome-c oxidase chain Vb
2.5066733	2.069382	YIL107C 6-Phosphofructose-2-kinase
6.7264614	2.846154	YIL101C DNA-binding transcriptional repressor
11.685817	2.703312	YIL099W intracellular glucoamylase
13.3047695	1.370962	YIL099W intracellular glucoamylase
3.9014468	3.209717	YIL097W hypothetical protein
6.272121	1.824638	YIL136W 45-kDa mitochondrial outer membrane protein
1.8543943	1.944263	YIL132C hypothetical protein
1.9265449	3.052686	YIL122W hypothetical protein
8.152	6.852307	YIL120W similarity to antibiotic resistance proteins
11.430848	10.41615	YIL165C putative pseudogene
16.232939	14.88644	YIL164C Nit1 nitrilase
4.4286056	0.939173	YIL160C peroxisomal 3-oxoacyl CoA thiolase
4.0396123	3.254627	YIL152W hypothetical protein
0.5228813	0.475302	YIL149C similarity to Mlp1p and myosin heavy chains
1.8499553	3.740064	YIL146C ExtraCellular Mutant
1.1769589	2.350498	YIL145C similarity to E.coli pantothenate synthetase
1.1146154	2.570192	YIL144W Dmc1p interacting protein
2.7503076	1.438077	non-annotated SAGE orf Found reverse in NC_001140 between 204089 anc
2.3836591	2.600959	non-annotated SAGE orf Found forward in NC_001140 between 530130 anc
5.0227695	4.522692	non-annotated SAGE orf Found reverse in NC_001140 between 530754 anc
1.5672864	1.943321	non-annotated SAGE orf Found forward in NC_001140 between 198428 anc
24.268887	19.19105	YIL176C strong similarity to members of the Srp1p/Tip1p family
4.086	3.331154	YIL167W serine dehydratase
2.051919	1.813703	YIL166C similarity to allantoate permease Dal5p
2.0833478	2.311617	YHR077C Highly acidic C-terminus

5.765942	3.238712	YHR209W similarity to hypothetical protein YER175c
4.5960245	8.133341	non-annotated SAGE orf Found reverse in NC_001140 between 34593 and
4.2315154	2.129188	non-annotated SAGE orf Found reverse in NC_001140 between 519037 and
1.3244615	3.818462	non-annotated SAGE orf Found forward in NC_001140 between 528967 and
6.8064685	5.878846	non-annotated SAGE orf Found reverse in NC_001140 between 5662 and 5
1.9913846	2.120962	non-annotated SAGE orf Found reverse in NC_001140 between 5778 and 5
5.8215384	2.449615	non-annotated SAGE orf Found reverse in NC_001140 between 202505 and
2.0859122	1.982841	YHR199C strong similarity to hypothetical protein YHR198c
2.802904	2.901404	YHR204W similarity to alpha-mannosidases
2.8373241	3.350664	YHR210C UDP-glucose-4-epimerase (GAL10, galE)
0.41237706	0.473946	YHR216W IMP dehydrogenase\; probable PUR5 gene
1.1429875	2.18786	YHR218W gene in Y' repeat region
2.421864	1.692181	YHR176W Dimethylaniline monooxygenase
1.146818	1.230222	YHR178W Zinc finger (6-Cys)
5.0346456	4.309563	YHR180W hypothetical protein
2.1749485	2.344193	YHR153C sporulation protein
2.660067	2.467055	YHR156C weak similarity to mouse kinesin KIF3B
4.2277236	4.360002	YHR157W mRNA is induced early in meiosis
2.5165553	3.394558	YHR166C Cell division cycle protein
0.8143331	1.906662	YHR169W DEAD-box protein
0.42116612	0.837189	YHR172W spindle pole body component, associates in a complex with Spc9
2.8211517	2.902783	YHR129C Centractin
1.7125759	1.255604	YHR134W hypothetical protein
0.5821461	1.738808	YHR136C 17 kDa protein
2.4157116	1.268527	YHR137W aromatic amino acid aminotransferase II
2.4591715	1.197792	YHR138C hypothetical protein
2.3874753	1.885706	YHR142W weak similarity to cytochrome-c oxidases
3.8989663	4.606042	YHR150W weak similarity to YDR479c
1.248774	1.631066	YHR120W mutS homolog involved in mitochondrial DNA repair
0.9463959	0.891049	YHR123W sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferas
1.0800201	1.059759	YHR123W sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferas
2.9447508	2.033323	YHR124W meiosis-specific gene, mRNA is sporulation-specific
8.363665	1.166511	YHR087W hypothetical protein
0.9126612	2.452523	YHR088W similarity to hypothetical protein YNL075w
2.4861417	3.192591	YHR090C NuBbiN
0.2533249	0.79847	YHR094C High-affinity hexose (glucose) transporter
2.5706155	2.347885	YHR095W hypothetical protein
7.976164	2.602003	YHR096C hexose transporter
4.8364763	3.047043	YHR101C Bad in glucose or big cells
3.72106	0.907333	YHR104W Aldo-keto reductase
2.6922894	1.938294	YHR067W hypothetical protein
1.4479616	2.227981	YHR071W G1VS cyclin (weak)
3.938743	2.911024	YHR075C ribosomal protein of the small subunit, mitochondrial
2.021678	1.9429	YHR078W hypothetical protein
0.82135797	3.254854	YHR085W weak similarity to fruit fly brahma transcriptional activator
2.8306904	4.615946	YHR040W weak similarity to Hit1p
3.6296504	5.516453	YHR048W similarity to multidrug resistance proteins
1.0952863	2.113359	YHR062C Protein subunit of nuclear ribonuclease P (RNase P)
3.6546242	3.360233	YHR022C RAS-related protein
0.29811537	0.41448	YHR029C Thymidylate synthase (putative\; weak)
1.8481206	2.515791	YHR031C Pif1p, mitochondrial DNA repair and recombination protein

3.821323	5.126415	YHR033W Pro1p (Gamma-glutamyl kinase)
1.178255	2.425029	YHR036W similarity to hypothetical protein YGL247w
1.3602849	1.702226	YHR004C similarity to YLL010c, YLR019w
2.1666307	2.292894	YHR006W Zinc finger (Cys(2)-His(2))
1.2774439	3.671459	YHR015W PolyA-binding protein
2.6031806	2.981352	YHL023C hypothetical protein
3.3309972	1.123515	YHL021C weak similarity to Pseudomonas gamma-butyrobetaine hydroxylas
2.782694	1.456402	YHL019C Similiar to clathrin coat proteins
1.5890598	2.335455	YHL017W Probable transmembrane protein PTM1
13.006453	13.97948	YHL016C Urea transporter
3.9727693	1.786923	YHL006C hypothetical protein
9.789781	10.36215	YHL047C similarity to C.carbonum toxin pump
3.831239	4.296795	YHL046C strong similarity to members of the Srp1p/Tip1p family
3.6504867	1.36988	YHL044W similarity to subtelomeric encoded proteins
7.204308	2.620962	YHL042W similarity to subtelomeric encoded proteins
7.8630004	8.701411	YHL040C similarity to C.carbonum toxin pump
3.9992304	4.905192	YHL037C hypothetical protein
8.992395	5.209849	YHL035C ABC transporter
2.5658076	1.76894	YHL032C glycerol kinase (converts glycerol to glycerol-3-phosphate
0.4589082	0.737909	YHL028W Putative integral membrane protein containing novel cysteine mot
2.4430196	3.772745	YHL026C hypothetical protein
2.6695092	3.353545	YHL025W transcriptional regulator
7.2775383	3.252308	YHL024W RNA binding domain (N-term) with asparagine rich region?
1.554388	2.80436	non-annotated SAGE orf Found forward in NC_001139 between 788087 anc
3.2888722	1.812529	non-annotated SAGE orf Found forward in NC_001139 between 810507 anc
3.3485558	2.389282	non-annotated SAGE orf Found reverse in NC_001139 between 974572 anc
0.74583447	0.912724	SNR39b snRNA
12.790299	6.24818	non-annotated SAGE orf Found reverse in NC_001139 between 919562 anc
3.4269435	6.066078	non-annotated SAGE orf Found forward in NC_001139 between 23385 and
2.6095161	1.888108	non-annotated SAGE orf Found reverse in NC_001139 between 139723 anc
3.650324	2.985524	non-annotated SAGE orf Found forward in NC_001139 between 318551 anc
2.2663848	4.253876	non-annotated SAGE orf Found forward in NC_001139 between 576609 anc
4.0037456	4.356731	non-annotated SAGE orf Found reverse in NC_001139 between 604571 anc
2.605457	1.628635	non-annotated SAGE orf Found forward in NC_001139 between 733406 anc
3.6101537	1.637885	non-annotated SAGE orf Found reverse in NC_001139 between 74536 and
1.8353864	1.042558	non-annotated SAGE orf Found reverse in NC_001139 between 74628 and
5.4324613	2.257115	non-annotated SAGE orf Found forward in NC_001139 between 700362 anc
3.3121996	3.22709	non-annotated SAGE orf Found reverse in NC_001139 between 701262 anc
11.787511	10.71391	non-annotated SAGE orf Found reverse in NC_001139 between 707583 anc
9.906643	10.63428	non-annotated SAGE orf Found reverse in NC_001139 between 707915 anc
6.11735	6.079618	non-annotated SAGE orf Found reverse in NC_001139 between 708217 anc
0.45296663	0.504353	non-annotated SAGE orf Found forward in NC_001139 between 818376 anc
6.251177	4.889854	non-annotated SAGE orf Found forward in NC_001139 between 974544 anc
3.8198135	7.995995	non-annotated SAGE orf Found forward in NC_001139 between 384772 anc
2.2694545	2.331494	non-annotated SAGE orf Found reverse in NC_001139 between 836381 anc
0.7361768	0.40659	non-annotated SAGE orf Found reverse in NC_001139 between 939417 anc
0.697627	2.580582	non-annotated SAGE orf Found forward in NC_001139 between 363944 anc
1.1399593	1.587124	non-annotated SAGE orf Found reverse in NC_001139 between 536199 anc
2.2178833	2.844483	non-annotated SAGE orf Found forward in NC_001139 between 326361 anc
0.9694438	0.911137	non-annotated SAGE orf Found reverse in NC_001139 between 366397 anc
1.9814479	2.384559	YGR278W similarity to C.elegans LET-858

1.0002434	0.437033	YGR284C similarity to mouse Surf-4 protein
1.9910616	1.824648	YGR287C strong similarity to maltase
1.9665343	2.392169	YGR288W maltose pathway regulatory protein
18.096144	16.01455	YGR289C alpha-glucoside transporter
30.820192	24.36164	YGR294W strong similarity to members of the Srp1p/Tip1p family
7.4068136	4.979653	YGR256W 6-phosphogluconate dehydrogenase
19.593224	8.512869	YGR259C questionable ORF
1.6950366	1.475123	YGR270W Member of CDC48VPAS1VSEC18 family of ATPases
3.139367	1.996864	YGR238C protein containing kelch repeats, similar to YHR158c and YPL263
4.937249	4.456744	YGR239C weak similarity to hypothetical protein YHR160c
6.5752306	2.040962	YGR243W strong similarity to hypothetical protein YHR162w
1.0691541	0.420103	YGR244C Succinate-CoA Ligase (ADP-Forming)
8.64257	1.276894	YGR248W similar to SOL3
0.96614856	2.345413	YGR249W Mga1p shows similarity to heat shock transcription factor
8.48021	2.768801	YGR213C involved in 7-aminocholesterol resistance
2.528804	4.564234	YGR216C Participates in synthesis of N-acetylglucoaminyolphosphatidylinosit
3.1468759	3.151414	YGR222W translational activator of cytochrome c oxidase subunit III
4.983404	1.808545	YGR224W strong similarity to drug resistance protein SGE1
0.39702347	0.808232	YGR187C HMG1V2 homolog
2.370666	0.884801	YGR194C xylulokinase
2.572644	2.208881	YGR202C phosphorylcholine transferase\; or cholinephosphate cytidylitrans
3.4170787	2.912603	YGR166W Involved in biosynthetic pathway for cell wall beta-glucans
8.382611	7.449399	YGR168C hypothetical protein
2.7797418	0.850787	YGR142W similarity to hypothetical protein YPR158w
1.9502978	1.161096	YGR144W component of the biosynthetic pathway producing the thiazole pr
2.696455	1.572747	YGR149W hypothetical protein
3.6527987	1.512258	YGR153W hypothetical protein
11.974799	5.786902	YGR154C strong similarity to hypothetical proteins YKR076w and YMR251w
2.1833506	5.780375	YGR156W hypothetical protein
11.215821	19.85214	YGR161C hypothetical protein
2.0841804	1.870056	YGR163W GTP-binding protein
0.42376968	2.036921	YGR123C serine\threonine phosphatase
4.128821	3.227025	YGR127W weak similarity to mouse T10 protein
2.3933141	2.437709	YGR131W strong similarity to Nce2p
7.1376925	2.035385	YGR133W Member of ubiquitin-conjugating protein family
2.3130574	1.627466	YGR136W weak similarity to chicken growth factor receptor-binding protein (
2.6775851	4.082262	YGR138C similarity to multidrug resistance proteins
2.614137	1.713202	YGR102C hypothetical protein
2.409223	2.903412	YGR104C subunit of RNA polymerase II holoenzyme\mediator complex
0.88807803	2.943938	YGR108W G(sub)2-specific B-type cyclin
0.6698965	2.123707	YGR109C B-type cyclin
2.8660903	1.533915	YGR110W weak similarity to YLR099c and YDR125c
2.8467317	5.052498	YGR113W Duo1 And Mps1 interacting
1.3800124	1.422732	YGR117C hypothetical protein
0.8138967	0.773312	YGR084C 35 kDa mitochondrial ribosomal small subunit protein
9.715519	1.619791	YGR088W cytoplasmic catalase T
2.0188403	2.289543	YGR092W Serine\threonine protein kinase
2.2183762	2.547473	YGR093W similarity to hypothetical S.pombe protein
4.205248	4.531721	YGR057C Required for amino acid permease transport from the Golgi to the
2.013056	2.462515	YGR064W questionable ORF
5.5595384	1.447692	YGR066C similarity to hypothetical protein YBR105c

2.0462186	2.568899	YGR068C weak similarity to Rod1p
10.106112	3.36726	YGR070W GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-bir
1.2399824	2.242758	YGR071C similarity to hypothetical protein YLR373c
1.7450479	3.30202	YGR072W factor stimulating decay of mRNAs containing premature stop cod
1.5633435	1.79785	YGR073C questionable ORF
1.17013	1.407522	YGR074W Homolog of human core snRNP protein D1, involved in snRNA m
1.401472	2.225284	YGR030C integral subunit of RNase P and apparent subunit of RNase MRP
4.611864	3.7003	YGR032W catalytic component of 1,3-beta-D-glucan synthase
4.364935	2.708917	YGR039W questionable ORF
2.7722635	4.745617	YGR040W MAP protein kinase homolog involved in pheromone signal trans
3.6212232	3.631987	YGR042W hypothetical protein
10.514241	2.789611	YGR043C strong similarity to transaldolase
3.3811312	1.167478	YGR008C ATPase stabilizing factor
3.8276908	4.21719	YGR015C similarity to hypothetical protein YGR031w
2.7293317	1.79417	YGR016W weak similarity to M.jannaschii hypothetical protein MJ1317
2.6037385	0.922889	YGR019W gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate a
2.639178	2.244701	YGR024C weak similarity to Methanobacterium thermoautotrophicum hypot
5.083195	3.015313	YGL010W similarity to hypothetical S. pombe protein
2.0559356	1.516496	YGL004C weak similarity to Tup1p
2.3054514	3.036968	YGR003W similarity to D.melanogaster lin19 protein
1.5529902	0.435156	YGL037C similarity to E.coli hypothetical 23K protein
1.2630177	2.36775	YGL029W weak similarity to human chromatin assembly factor I p150 chain
3.006188	1.975593	YGL018C Homolog of E. coli Hsc20 co-chaperone protein
1.1962872	2.226898	YGL057C hypothetical protein
2.1724539	7.087451	YGL056C homologue of pombe SDS23\; localizes to spindle pole body
2.407745	1.373577	YGL053W strong similarity to hypothetical proteins YAR031w, YGL051w, YA
3.5476286	2.197125	YGL051W strong similarity to YAR033w protein
3.6152587	4.565852	YGL066W hypothetical protein
8.887692	17.76154	YGL063W pseudouridine synthase 2
1.6129707	1.133061	YGL098W hypothetical protein
4.8975024	6.846851	YGL096W similarity to copper homeostasis protein Cup9p
2.4104908	1.783256	YGL095C cytosolic and peripheral membrane protein
0.5164513	0.43771	YGL088W questionable ORF
1.4462713	2.458418	YGL125W putative methylenetetrahydrofolate reductase (mthfr)
6.851556	1.943005	YGL121C hypothetical protein
1.2940645	2.156179	YGL116W beta-transducin homolog
0.46653932	0.554534	YGL147C Ribosomal protein L9A (L8A) (rp24) (YL11)
5.3010836	3.290408	YGL128C weak similarity to rat cysteine string protein
1.0329113	0.049276	YGL173C DNA strand-transfer protein exoribonuclease I\; catalyzes the form
1.2510058	2.297333	YGL169W Protein involved in translation initiation
1.881468	2.758446	YGL166W Activator of transcription
1.5888078	2.21951	YGL164C similarity to S.pombe hypothetical protein SPAC31A2.10
3.4006429	1.901502	YGL156W vacuolar alpha mannosidase
2.4670043	4.516477	YGL154C aminoadipate-semialdehyde dehydrogenase small subunit (alpha-
2.9256556	11.44	YGL194C Protein with similarity to Hda1p, Rpd3p, Hos1p, and Hos3p
9.821358	8.459684	YGL193C questionable ORF
2.6067855	1.318589	YGL185C weak similarity to dehydrogenases
1.4503298	2.460916	YGL211W similarity to M.jannaschii hypothetical proteins MJ1157 and MJ14
1.0822432	1.535218	YGL237C transcriptional activator protein of CYC1
1.8444129	2.546709	YGL224C strong similarity to hypothetical protein YER037w
7.817692	7.04153	YGL223C weak similarity to Clostridium regulatory protein

4.9081917	4.835092	YGL261C strong similarity to members of the Srp1/Tip1 family
4.4245877	2.23757	YGL259W GPI-anchored aspartic protease
1.1050768	1.208459	YGL257C similarity to Mnn1p
2.5105164	3.651055	YGL256W alcohol dehydrogenase isoenzyme IV
1.6381317	2.80942	YGL254W putative transcription factor, has five zinc fingers
4.3086157	4.953077	YGL251C C4 zinc finger DNA-binding protein of low sequence specificity in \
3.7032325	2.0653	YGL248W 3',5'-Cyclic-nucleotide phosphodiesterase, low affinity
3.166833	2.227058	YGL247W similarity to hypothetical protein YHR036w
4.0138044	3.540203	YGL243W tRNA-specific adenosine deaminase 1 (TAD1)\; Tad1pVscADAT1
3.8949232	2.56	non-annotated SAGE orf Found reverse in NC_001138 between 5806 and 6
3.5710602	2.962798	non-annotated SAGE orf Found forward in NC_001138 between 48735 and
4.823163	3.322774	non-annotated SAGE orf Found forward in NC_001138 between 161226 anc
3.185209	1.47649	non-annotated SAGE orf Found reverse in NC_001138 between 181991 anc
2.1100245	1.255825	YFR045W similarity to mitochondrial citrate transport proteins
2.175046	1.9092	YFR046C hypothetical protein
1.1396672	2.201915	YFR055W strong similarity to beta-cystathionases
4.2036667	3.027482	YFL043C hypothetical protein
4.568308	1.2	YFL021W
2.6563976	1.620812	YFL042C similarity to hypothetical protein YLR072w
0.50556916	0.776331	non-annotated SAGE orf Found reverse in NC_001138 between 76336 and
15.389248	10.17535	YFR026C hypothetical protein
1.9186888	2.404637	YFR027W hypothetical protein
1.774735	2.369845	YFR029W Regulator of expression of the PTR2, GAP1, and BAP2 genes\; ir
0.553403	0.48891	YFR044C similarity to hypothetical protein YBR281c
3.0705252	3.774728	YFR005C similarity to hypothetical A. thaliana proteins
3.2208204	2.049144	YFR014C Calmodulin-dependent protein kinase
3.091639	0.819118	YFR015C Glycogen synthase (UDP-glucose--starch glucosyltransferase)
10.530605	3.303461	YFR017C hypothetical protein
3.7528827	3.862329	YFR020W hypothetical protein
5.4409714	7.533177	YFR022W similarity to Rod1p
0.70978475	0.437505	YFL018C dihydrolipoamide dehydrogenase precursor (mature protein is the
7.3373866	4.68485	YFL014W 12 kDa heat shock protein
1.8819612	3.160402	YFL013C weak similarity to Dictyostelium protein kinase
4.7925415	3.251842	YFL030W similarity to several transaminases
2.322815	1.751051	YFL029C Cyclin-dependent kinase-activating kinase
1.683989	1.896993	YFL028C ABC ATPase
2.6453226	2.547126	YFL027C weak similarity to P.falciparum Pfmdr2 protein
1.9203799	2.135982	YFL024C Probable chromatin protein because of homology to Drosophila Er
4.8129835	4.425976	YFL020C member of the seripauperin proteinVgene family (see Gene_class
4.372024	4.57619	YFL057C strong similarity to aryl-alcohol dehydrogenases
2.375818	2.723688	YFL055W Amino acid permease
6.093276	2.50137	YFL054C similarity to channel proteins
10.075693	11.115	YFL050C ALuminium Resistance 2
3.3522696	2.28123	YFL049W weak similarity to Npl6p
2.3295228	2.57829	non-annotated SAGE orf Found forward in NC_001137 between 367587 anc
0.5359453	0.409199	non-annotated SAGE orf Found forward in NC_001137 between 422560 anc
23.005384	16.6125	non-annotated SAGE orf Found forward in NC_001137 between 284585 anc
9.252062	5.376268	non-annotated SAGE orf Found forward in NC_001137 between 289637 anc
4.6733503	4.737443	non-annotated SAGE orf Found reverse in NC_001137 between 311731 anc
1.018383	0.174521	non-annotated SAGE orf Found reverse in NC_001137 between 467935 anc
4.0334773	2.271979	non-annotated SAGE orf Found forward in NC_001137 between 77473 and

0.5023171	0.747264	non-annotated SAGE orf Found forward in NC_001137 between 122467 and
3.8240178	4.921652	non-annotated SAGE orf Found reverse in NC_001137 between 314164 and
1.374436	2.718517	non-annotated SAGE orf Found reverse in NC_001137 between 407032 and
3.8310547	3.274778	non-annotated SAGE orf Found reverse in NC_001137 between 561482 and
1.9939965	2.3054	non-annotated SAGE orf Found reverse in NC_001137 between 561482 and
0.6361926	0.516632	non-annotated SAGE orf Found reverse in NC_001137 between 117183 and
4.3870387	1.178697	YER067W
11.916063	10.08614	non-annotated SAGE orf Found reverse in NC_001137 between 187315 and
3.2527764	4.318355	non-annotated SAGE orf Found reverse in NC_001137 between 550562 and
2.439355	2.910858	non-annotated SAGE orf Found reverse in NC_001137 between 31419 and
3.043057	7.614534	non-annotated SAGE orf Found reverse in NC_001137 between 64206 and
6.7103157	9.41594	non-annotated SAGE orf Found forward in NC_001137 between 251443 and
2.5973055	2.844899	YER173W checkpoint protein
2.5176406	2.877688	YER175C similarity to hypothetical protein YHR209w
2.4735222	4.435764	YER180C Meiosis-specific protein required for spore formation
1.9867448	2.059196	YER184C similarity to multidrug resistance proteins Pdr3p and Pdr1p
5.2075033	6.436783	YER185W strong similarity to Rtm1p
2.3116226	2.699711	YER186C weak similarity to hypothetical protein YMR316w
0.96623194	1.698537	YER187W-A similarity to killer toxin KHS precursor
1.4381518	1.498569	YER188W hypothetical protein
2.6077006	2.396602	YER039C-A hypothetical protein
9.667869	3.924351	YER150W strong similarity to putative cell surface glycoprotein Sed1p
2.440289	1.511549	YER158C weak similarity to Afr1p
2.2593207	1.595681	YER159C Transcriptional regulator which functions in modulating the activity
1.6942909	1.765124	YER162C Nucleotide excision repair protein
3.109437	1.690687	YER163C weak similarity to E.coli cation transport protein
1.8386098	2.331448	YER171W DNA repair helicase component of transcription factor b
0.9876147	2.443572	YER127W Lethal with conditional pap1 allele
1.9062384	3.172681	YER130C similarity to Msn2p and weak similarity to Msn4p
2.62166	4.182577	YER137C weak similarity to Mycoplasma hominis P120 protein
2.2081008	2.045667	YER139C similarity to hypothetical protein YDR066c
0.44655734	0.731667	YER146W Sm-like protein
1.8682915	4.088638	YER147C weak similarity to mouse NAD(P)H dehydrogenase (quinone)
5.909526	1.80507	YER103W member of 70 kDa heat shock protein family
3.2692597	3.672844	YER104W hypothetical protein
3.61937	3.644314	YER108C putative transcriptional activator of FLO1
3.292219	3.714333	YER115C sporulation-specific protein
2.1642964	2.765072	YER116C zinc-finger protein
7.5665784	3.559441	YER121W hypothetical protein
1.2893037	3.320414	YER123W plasma membrane-bound casein kinase I homolog
1.3969121	2.8378	YER124C weak similarity to Dictyostelium WD40 repeat protein 2
1.2541933	2.190626	YER082C similarity to M.sexata steroid regulated MNG10 protein
2.6351578	3.758394	YER088C Derepression Of Telomeric silencing
2.6743946	2.136105	YER092W hypothetical protein
3.3373044	2.925916	YER096W sporulation-specific homolog of csd4
4.1785946	3.179948	YER098W ubiquitin carboxyl-terminal hydrolase
4.039465	2.42812	YER101C Protein involved in targeting of plasma membrane [H ⁺]ATPase
1.2144823	0.472597	YER063W Suppressor of the Transcriptional (T) defect of Hpr1 (H) by Overe
1.9801546	1.433915	YER065C isocitrate lyase
20.017464	16.37159	YER066W strong similarity to cell division control protein Cdc4p
2.5202765	2.631226	YER066W strong similarity to cell division control protein Cdc4p

15.829584	2.671983	YER067W strong similarity to hypothetical protein YIL057c
1.4975873	2.112524	YER069W N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutam
0.4427612	1.058009	YER070W ribonucleotide reductase
1.1117885	2.682947	YER073W aldehyde dehydrogenase (NAD+)
4.2040386	3.553204	YER076C similarity to killer toxin Khr1p
2.5921528	5.169726	YER077C hypothetical protein
0.5793231	0.391563	YER080W hypothetical protein
3.6328015	7.082542	YER081W strong similarity to phosphoglycerate dehydrogenases
4.506206	4.82265	YER045C weak similarity to transcription factor Sko1p
3.924111	2.860116	YER046W hypothetical protein
3.309008	1.857258	YER053C strong similarity to mitochondrial phosphate carrier protein
0.7022717	0.481611	YER057C Inhibitor of cell Growth\; heat shock inducible
0.65958154	0.379912	YER058W cytochrome c oxidase assembly factor
3.0916696	0.453234	YER060w-A purine-cytosine permease
1.635446	2.398097	YER061C Protein homologous to beta-keto-acyl synthase
0.4228059	0.525517	YER023W delta 1-pyrroline-5-carboxylate reductase
4.599371	5.476924	YER024W similarity to carnitine O-acetyltransferase Yat1p
3.1529229	3.690769	YER028C similarity to Mig1p
0.71833366	0.444643	YER030W similarity to mouse nucleolin
1.4742566	2.15409	YER034W hypothetical protein
3.0407407	2.92444	YER035W hypothetical protein
3.439588	2.981083	YER041W weak similarity to DNA repair protein Rad2p and Dsh1p
0.77644926	0.501283	YER042W responsible for the reduction of methionine sulfoxide
0.5120418	0.488326	YER044C hypothetical protein
2.1371195	2.161371	YER007W Required for viability in the absence of the kinesin-related mitotic
2.4103556	1.629031	YER015W Acyl-CoA synthetase (fatty acid activator 2)
2.0965502	2.533978	YER016W Binding to Microtubules
3.2096152	4.227756	YER018C component of spindle pole
1.7407875	1.91857	YEL020C similarity to O.formigenes oxalyl-CoA decarboxylase
2.3849654	3.08514	YEL016C similarity to human nucleotide pyrophosphatase
1.4374563	1.945437	YEL015W weak similarity to Spa2p
5.0022507	1.5977	YEL011W 1,4-glucan-6-(1,4-glucano)-transferase
2.559959	2.624937	YEL006W similarity to peroxisomal membrane and mitochondrial carrier prot
3.4532669	2.29701	YEL005C hypothetical protein
2.1747682	3.304519	YEL004W Shows sequence similarity to GOG5, a gene involved in vanadate
0.6078026	0.476787	YEL001C hypothetical protein
5.916308	2.455769	YEL041W strong similarity to Utr1p
2.9559152	0.472961	YEL039C iso-2-cytochrome c
3.5815365	2.884325	YEL030W ExtraCellular Mutant
6.3617043	6.863698	YEL028W hypothetical protein
1.6709356	1.735109	YEL025C hypothetical protein
2.3443077	1.660577	YEL023C hypothetical protein
4.1257157	2.791692	YEL065W probably multidrug resistance protein
4.9012427	6.467564	YEL063C arginine permease
2.0539708	2.221421	YEL062W Non-membrane-embedded, PEST sequence-containing protein
1.5176243	1.511141	YEL059C-A high copy suppressor of imp1 mutation, may be required for the
4.5975184	3.076243	YEL057C hypothetical protein
10.352689	9.315075	YEL049W member of the seripauperin proteinVgene family (see Gene_class
2.0840933	9.034153	YEL048C hypothetical protein
1.0062568	3.209531	non-annotated SAGE orf Found forward in NC_001136 between 909701 and
2.6936045	3.096058	non-annotated SAGE orf Found forward in NC_001136 between 1013978 and

2.3827624	1.681405	non-annotated SAGE orf Found forward in NC_001136 between 1108476 ar
6.0233846	1.636538	non-annotated SAGE orf Found forward in NC_001136 between 1362215 ar
0.45714498	0.498223	SNR63 snRNA
0.35568246	0.353281	SNR13 snRNA
6.7471156	6.802053	YEL074W similarity to subtelomeric encoded proteins
3.0956368	2.542935	YEL074W similarity to subtelomeric encoded proteins
3.6027691	2.390961	YEL073C similarity to YJR108w
4.322769	6.100577	YEL072W hypothetical protein
1.1785799	0.286055	non-annotated SAGE orf Found reverse in NC_001136 between 1385513 ar
4.3392324	3.886009	non-annotated SAGE orf Found reverse in NC_001136 between 463178 anc
1.488121	2.063244	non-annotated SAGE orf Found reverse in NC_001136 between 678003 anc
1.3013678	3.024301	non-annotated SAGE orf Found forward in NC_001136 between 362352 anc
1.9900242	3.702922	non-annotated SAGE orf Found reverse in NC_001136 between 386539 anc
10.265998	10.89439	non-annotated SAGE orf Found reverse in NC_001136 between 471227 anc
4.914	3.731923	non-annotated SAGE orf Found forward in NC_001136 between 542286 anc
1.0196031	1.872617	non-annotated SAGE orf Found reverse in NC_001136 between 909885 anc
3.1699018	1.519803	non-annotated SAGE orf Found reverse in NC_001136 between 1182750 ar
4.1462965	3.429345	non-annotated SAGE orf Found forward in NC_001136 between 930871 anc
2.3696115	2.967579	non-annotated SAGE orf Found reverse in NC_001136 between 1014227 ar
2.9920366	2.060519	non-annotated SAGE orf Found forward in NC_001136 between 1224746 ar
1.8059734	2.284763	non-annotated SAGE orf Found reverse in NC_001136 between 1276382 ar
0.54364604	0.46975	non-annotated SAGE orf Found forward in NC_001136 between 1385570 ar
2.613123	1.913792	non-annotated SAGE orf Found reverse in NC_001136 between 34050 and
2.9238539	2.200839	non-annotated SAGE orf Found reverse in NC_001136 between 34050 and
0.40880883	0.536768	non-annotated SAGE orf Found reverse in NC_001136 between 217125 anc
2.1047926	2.265219	non-annotated SAGE orf Found reverse in NC_001136 between 512499 anc
1.147715	1.681508	non-annotated SAGE orf Found reverse in NC_001136 between 76964 and
26.048319	11.99496	non-annotated SAGE orf Found reverse in NC_001136 between 104660 anc
2.765747	2.501924	YDR534C similarity to YOR383c,Sta1p and pig mucin
0.8138757	1.609462	YDR541C similarity to dihydroflavonol-4-reductases
0.62555283	0.481518	YDL185W
0.48976657	0.493862	YDL085C-A
4.6653085	4.995963	non-annotated SAGE orf Found reverse in NC_001136 between 340810 anc
8.210716	4.809547	non-annotated SAGE orf Found forward in NC_001136 between 691007 anc
0.6950716	0.404339	YDR512C questionable ORF
1.2683177	0.442258	YDR513W Glutaredoxin (thioltransferase) (glutathione reductase)
3.0146976	8.953484	YDR514C strong similarity to hypothetical protein YCL036w
1.1234634	0.361619	YDR516C strong similarity to glucokinase
1.0898566	2.602994	YDR524C similarity to hypothetical human protein and YIL044c
6.0147753	3.747784	YDR530C 5',5'''-P-1,P-4-tetraphosphate phosphorylase II
1.5586013	2.695826	YDR489W hypothetical protein
2.636424	1.226168	YDR490C SerVThr protein kinase
1.9200996	2.099504	YDR499W weak similarity to hypothetical C.elegans protein, M.genitalium pe
1.3348178	1.338325	YDR467C questionable ORF
2.4532504	3.395247	YDR473C essential splicing factor
3.9737113	2.058631	YDR479C weak similarity to YHR150w
4.4549346	2.0778	YDR480W MAP kinase-associated protein
1.6745105	2.549659	YDR444W similarity to hypothetical protein YGL144c and YDL109c
3.2469952	1.935937	YDR453C strong similarity to thiol-specific antioxidant proteins
3.0448623	3.825389	YDR459C weak similarity to YNL326c
0.84080786	0.50023	YDR461W a-factor mating pheromone precursor

0.54664433	0.694443	YDR420W Type 1 membrane protein with EF hand motif
4.965825	3.261888	YDR421W hypothetical protein
2.8986309	3.642076	YDR438W strong similarity to hypothetical protein YML018c
1.77057	2.299251	YDR439W Loss of rDNA silencing
0.70635	1.298263	YDR440W Pachytene CHeckpoint
4.997846	3.29	YDR403W first enzyme in dityrosine synthesis in the outer layer of the spore
3.5570574	4.823958	YDR405W 263-amino acid mitochondrial ribosomal large subunit protein\; sir
6.108062	2.589048	YDR406W probable multidrug resistance transporter
1.4454565	2.085245	YDR381W Nuclear RNA-binding RNA annealing protein
2.3947346	2.397975	YDR384C strong similarity to Y.lipolytica GPR1 gene
2.7336345	3.117034	YDR387C similarity to Itr1p and Itr2p and E.coli araE
7.10234	2.830481	YDR391C strong similarity to hypothetical protein YOR013w
3.3255162	2.775012	YDR392W transcription factor, member of the histone acetyltransferase SAC
2.5679023	1.699765	YDR358W strong similarity to hypothetical protein YHR108w and weak simil
1.5267633	2.376953	YDR359C hypothetical protein
2.5703459	1.619322	YDR363W Establishes Silent omatin
3.222753	4.234169	YDR364C Member of the beta transducin family
0.6878384	0.337823	YDR368W homologous to the aldo-keto reductase protein family
2.2282002	3.374299	YDR370C hypothetical protein
11.849021	9.549371	YDR332W similarity to E.coli hypothetical protein and weak similarity to RNA
0.60264343	0.35702	YDR334W similarity to nuclear Sth1p, Snf2p and related proteins
3.2614667	3.589525	YDR336W weak similarity to B.subtilis hypothetical protein X
2.5061765	2.221319	YDR349C GPI-anchored aspartic protease
2.5137563	2.85202	YDR350C protein of unknown function
2.059853	2.628807	YDR318W Involved in minichromosome maintenance
1.6471264	2.326004	YDR323C cytosolic and peripheral membrane protein with three zinc fingers'
1.8699403	1.729051	YDR291W similarity to B.subtilis helicases
0.48998162	0.326333	YDR270W Copper-transporting P-type ATPase with similarity to human Men
4.0016923	4.293269	YDR273W weak similarity to YOR042w
4.4118886	8.098664	YDR275W weak similarity to YOR042w
3.0225706	3.704993	YDR277C Protein is 61% identical to Msn3p
0.13388327	0.197926	YDR281C hypothetical protein
3.3446462	2.480501	YDR282C similarity to hypothetical protein YDL001w, YFR048w and S.pomt
4.169618	4.06405	YDR285W Synaptonemal complex protein, component of the central elemen
2.099247	2.682717	YDR288W hypothetical protein
2.155562	2.610616	YDR249C weak similarity to cytochrome b
3.0649147	1.553783	YDR250C hypothetical protein
2.1638064	2.091029	YDR252W Negative effect on expression of several genes transcribed by RN
3.9684618	2.025769	YDR256C catalase A
1.7521803	2.362726	YDR257C Transcription regulator
2.6754339	0.586477	YDR258C Mitochondrial heat shock protein 78 kDa
2.8006961	2.9329	YDR260C hypothetical protein
2.6861496	2.906412	YDR262W hypothetical protein
2.4617164	2.677687	YDR263C DNA-damage inducible gene
4.4576526	3.867218	YDR265W C3HC4 zinc-binding integral peroxisomal membrane protein
1.8144618	1.570805	YDR236C similarity to hypothetical A. thaliana protein
10.171522	9.449511	YDR242W putative amidase
1.2538881	1.377907	YDR205W similarity to A.eutrophus cation efflux system membrane protein c
4.25984	5.622417	YDR206W EST1-like bcy1 Suppressor
1.7720219	4.872204	YDR213W regulatory protein involved in control of sterol uptake
3.5687692	1	YDR215C hypothetical protein

8.373327	3.818862	YDR216W positive transcriptional regulator of ADH2 and peroxisomal protein
0.49122167	0.525894	YDR220C questionable ORF
1.3773022	2.376848	YDR179W-A hypothetical protein
0.35655132	0.642057	YDR180W Sister chromatid cohesion protein
1.9152108	4.013345	YDR191W Homolog of SIR2
1.5493989	2.003417	YDR195W RNA-binding protein involved in cleavage step of mRNA 3'-end fc
2.9171765	2.563161	YDR160W Ssy1p controls expression of several transporter genes, including
2.0713644	2.15363	YDR162C Nap1p-binding protein
1.7625786	3.122932	YDR163W weak similarity to <i>S.pombe</i> hypothetical protein
4.236308	0.589372	YDR171W Similar to HSP26\; expression is regulated by stress conditions
3.0409062	2.408789	YDR173C Regulator of arginine-responsive genes with ARG80 and ARG81
0.87406784	2.052593	YDR146C transcriptional activator
4.934052	6.299292	YDR147W Ethanolamine Kinase
2.9413776	3.628609	YDR151C member of the CCCH zinc finger protein family that has two or mc
3.196741	2.413986	YDR111C strong similarity to alanine transaminase
1.5319225	2.755337	YDR113C 42-kDa nuclear protein
2.0656176	3.043357	YDR118W subunit of the anaphase promoting complex (APC)
1.4614735	2.060652	YDR121W weak similarity to YNC2beta protein
3.3854	6.288373	YDR123C helix-loop-helix protein
2.8350768	2.447308	YDR124W hypothetical protein
8.7014885	9.17741	YDR126W similarity to hypothetical protein YLR246w and YOL003c
1.6404876	2.018804	YDR130C weak similarity to sea urchin myosin heavy chain
3.2360444	3.161174	YDR131C similarity to hypothetical protein YJL149w
1.7343827	3.117019	YDR089W weak similarity to <i>Streptococcus</i> transposase
0.44000846	0.626264	YDR095C hypothetical protein
1.5749072	2.0569	YDR108W Probably has role late in meiosis following DNA replication
2.129544	2.260718	YDR109C similarity to Mpa43p
9.085837	2.129838	YDR070C hypothetical protein
2.4867976	3.106129	YDR073W component of SWI/SNF global transcription activator complex
2.7891357	1.174143	YDR074W Trehalose-6-phosphate phosphatase
1.1562718	2.227465	YDR075W protein phosphatase type 2A
6.250545	4.522001	YDR078C Preferential Use of Neither donor locus during mating type switchi
11.140754	12.75534	YDR082W Involved in telemere length regulation, may be functional in telem
3.7050686	1.865291	YDR085C coordinates regulation of alpha-factor receptor signalling and indu
3.0286431	3.702311	YDR088C involved in 3' splice site choices and 2nd step of splicing
1.7080014	1.607984	YDR047W uroporphyrinogen decarboxylase
1.9495344	2.620752	YDR054C ubiquitin-conjugating enzyme, E2
3.7471972	3.523434	YDR058C TriGlyceride Lipase
2.3568332	0.999191	YDR059C ubiquitin-conjugating enzyme
2.2586617	1.92887	YDR065W hypothetical protein
1.5174181	3.964434	YDR021W DEAD-box protein, putative RNA helicase
2.7312963	1.748242	YDR022C cik1 suppressor
2.5417678	2.077249	YDR026C strong similarity to DNA-binding protein Reb1p
3.0956838	3.652726	YDR030C Protein involved in the same pathway as Rad26p, has beta-transc
0.82928336	0.443166	YDR032C strong similarity to <i>S.pombe</i> obr1
2.2392416	2.781206	YDR034C Transcriptional activator of lysine pathway genes with 2-aminoadij
5.3019757	2.724516	YDR034W-B identified by SAGE expression analysis
0.69437087	0.423005	YDR036C similarity to enoyl CoA hydratase
3.7148874	8.84185	YDR043C Suppressor of SNF
0.38548523	0.817476	YDL003W Mitotic oosome Determinant\; similar to <i>S. pombe</i> RAD21\; may
1.8906975	2.816689	YDL001W similarity to hypothetical protein YFR048w, YDR282c and <i>S.pomt</i>

2.8673615	1.213983	YDR001C neutral trehalase (alpha,alpha-trehalase)
2.662929	1.637162	YDR003W strong similarity to hypothetical protein YBR005w
1.9816737	3.070239	YDR004W RecA homolog (similar to DMC1, RAD51, and RAD55), interacts
2.4394016	2.394125	YDR005C required for sorting of Mod5p
21.145227	12.93033	YDR007W n-(5'-phosphoribosyl)-anthranilate isomerase
1.5126429	1.502533	YDR008C questionable ORF
2.0998573	2.506607	YDR013W similarity to human hypothetical KIAA0186 protein
2.4383113	1.476525	YDR016C hypothetical protein
1.6619642	2.249288	YDR017C Shows homology to basic leucine zipper family of transcription fac
4.586461	1.499423	YDR018C strong similarity to hypothetical protein YBR042c
4.8501697	4.375784	YDR019C glycine cleavage T protein (T subunit of glycine decarboxylase co
1.037659	3.887672	YDR020C weak similarity to uridine kinases and phosphoribulokinases
3.8200455	2.467108	YDL025C ser/thr protein kinase of the DEAD/DEAH box family
2.1294472	1.511285	YDL024C strong similarity to acid phosphatase
1.4488516	0.344159	YDL022W glycerol-3-phosphate dehydrogenase
2.2477398	1.892694	YDL020C involved in ubiquitin degradation pathway
2.2301154	2.115647	YDL005C Stoichiometric member of mediator complex
2.0676558	2.304153	YDL047W SIT4 suppress mutations in DBF2
2.0556495	2.198239	YDL044C Necessary for the stability andVor processing of some large mitocl
0.3044923	0.301219	YDL039C questionable ORF
0.3692787	0.460031	YDL038C similarity to mucin proteins
1.8470668	2.925645	YDL033C similarity to H.influenzae hypothetical protein HI0174
2.53911	2.299101	YDL069C translational activator of cytochrome b
0.516747	0.473459	YDL058W Integrin analogue gene
2.8643079	4.158077	YDL049C KRE9 homolog
1.9185277	2.219445	YDL080C positive regulatory factor with thiamin pyrophosphate-binding moti
0.7757724	0.418898	YDL078C malate dehydrogenase
3.0318568	1.947921	YDL113C similarity to hypothetical protein YDR425w
2.2422466	2.739331	YDL109C strong similarity to thiamine-repressed protein Thi4p
2.718557	1.612595	YDL107W cox1 pre-mRNA splicing factor
2.7155824	2.390681	YDL133W hypothetical protein
1.4779055	2.299763	YDL123W similarity to hypothetical protein YJL151c
4.6538596	3.475939	YDL115C hypothetical protein
2.8032417	1.744014	YDL154W MutS homolog involved in chromosome exchange
1.7617723	3.188572	YDL146W weak similarity to Orc3p
2.7419882	3.553266	YDL139C hypothetical protein
2.4873676	2.804713	YDL177C similarity to hypothetical protein YCR059c
1.7952403	2.538908	YDL176W hypothetical protein
3.337833	5.646313	YDL175C strong similarity to hypothetical protein YIL079c and weak similarit
2.8888404	7.145894	YDL170W zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluste
2.1827366	0.718983	YDL169C protein of unknown function
3.3178456	5.124702	YDL160C Putative RNA helicase of DEAD box family, required for Rap1p loc
2.776662	1.505582	YDL200C 6-O-methylguanine-DNA methylase
4.943641	2.922973	YDL197C Anti-silencing protein that causes depression of silent loci when ov
8.112154	1.925577	YDL187C questionable ORF
5.458182	4.786143	YDL215C NAD-dependent glutamate dehydrogenase
1.5174905	2.200052	YDL207W Nuclear-export-signal (NES)-containing protein
2.1039658	1.741312	YDL206W weak similarity to transporter proteins
1.083377	2.526547	YDL205C phorphobilinogen deaminase (uroporphyrinogen synthase), the thi
8.042301	2.978653	YDL204W similarity to hypothetical protein YDR233c
6.5654993	4.781428	YDL243C Hypothetical aryl-alcohol dehydrogenase

2.4271224	2.475552	YDL241W hypothetical protein
0.45724115	0.544009	YDL240W Protein similar to LIM-domain proteins and to rho/vrac GTPase-ac
2.8489728	4.703759	YDL239C hypothetical protein
7.4691076	2.087507	YDL238C similarity to E.coli hypothetical protein and to chlorohydrolases
3.5668154	2.300443	YDL234C protein of unknown function
2.1149185	1.701483	YDL233W hypothetical protein
5.1036367	6.389927	YDL231C hypothetical protein
0.2812038	0.36997	YDL227C Homothallic switching endonuclease
5.9389157	4.538848	YDL223C weak similarity to mucin
15.027077	1.162692	YDL222C strong similarity to hypothetical protein YNL194c and similarity to `
0.56948185	0.671791	non-annotated SAGE orf Found forward in NC_001135 between 258696 anc
3.3860075	8.513166	non-annotated SAGE orf Found reverse in NC_001135 between 9263 and 9
26.974945	20.62033	non-annotated SAGE orf Found forward in NC_001135 between 125368 anc
2.3521101	4.331898	non-annotated SAGE orf Found reverse in NC_001135 between 168999 anc
2.4755754	2.246076	non-annotated SAGE orf Found forward in NC_001135 between 288361 anc
3.2002943	3.619104	YCR020W-B high-temperature lethal
1.8186154	1.074808	YCR068W similarity to starvation induced pSI-7 protein of C. fluvum
2.1474726	2.124416	YCL008C homologous to mouse and human Tsg101 tumor susceptibility ger
2.9546735	2.871117	YCL008C homologous to mouse and human Tsg101 tumor susceptibility ger
14.481077	2.358077	non-annotated SAGE orf Found forward in NC_001135 between 41465 and
6.3106155	6.714616	non-annotated SAGE orf Found forward in NC_001135 between 157511 anc
1.3968042	3.375859	YCR087C-A nucleic acid-binding protein
0.68586826	0.444976	YCR088W Actin binding protein
7.8986006	6.592244	YCR089W predicted GPI-anchored cell wall protein
0.47670987	0.420685	YCR093W nuclear protein that negatively regulates basal transcription
4.3751483	11.04476	YCR098C permease involved in the uptake of glycerophosphoinositol (GroP
8.101385	5.338846	YCR099C strong similarity to Pep1p
6.5429683	5.452395	YCR100C strong similarity to Pep1p
1.60558	2.045039	YCR102C Alcohol dehydrogenase
2.6416094	2.189189	YCR104W member of the seripauperin protein/vgene family (see Gene_class
1.3206642	1.890166	YCR106W Transcription regulator
11.638845	23.36247	YCR063W G10-like protein
1.84807	2.619123	YCR066W Zn finger protein, putative ATPase
3.4158044	2.10015	YCR076C hypothetical protein
2.8158236	3.920036	YCR037C May collaborate with Pho86p and Pho84p in inorganic phosphate
2.4069052	1.623349	YCR060W regulatory protein
3.4498327	2.532766	YCR018C Transcription regulator
12.159032	18.32335	YCR020C Transcription regulator
5.0365324	3.157742	YCR021C Protein induced by heat shock, ethanol treatment, and entry into s
1.520706	2.584296	YCR028C Amino acid permease
3.3375945	2.70432	YCL010C strong similarity to Saccharomyces pastorianus hypothetical prote
1.1221539	1.153462	YCL004W 17-kDa phosphatidylserine synthase
1.1692353	2.052255	YCL002C strong similarity to Saccharomyces pastorianus hypothetical prote
0.7207952	0.402592	YCR004C FMN-binding protein
0.5315386	0.430378	YCR013C weak similarity to M.leprae B1496_F1_41 protein
3.578849	6.397823	YCL039W regulatory protein
1.6308491	2.219194	YCL038C Membrane transporter
1.5954517	1.657079	YCL018W beta-IPM (isopropylmalate) dehydrogenase
1.9453903	2.745148	YCL016C hypothetical protein
2.5506759	2.420742	YCL056C hypothetical protein
3.557176	1.983064	YCL049C hypothetical protein

2.0149946	0.460252	YCL042W questionable ORF
2.7075613	4.250638	Saccharomyces cerevisiae chromosome II, complete chromosome sequence
0.88621974	1.64158	Saccharomyces cerevisiae chromosome II, complete chromosome sequence
6.4498463	2.126154	Saccharomyces cerevisiae chromosome II, complete chromosome sequence
7.350802	5.678614	Saccharomyces cerevisiae chromosome II, complete chromosome sequence
3.1049876	2.206029	Saccharomyces cerevisiae chromosome II, complete chromosome sequence
6.6824975	5.665947	Saccharomyces cerevisiae chromosome II, complete chromosome sequence
0.2757999	0.456629	SNR56 snRNA
5.569695	5.940645	YCL067C Mating type protein alpha-2
3.100923	2.730385	non-annotated SAGE orf Found reverse in NC_001134 between 554921 and
4.8754435	3.717169	non-annotated SAGE orf Found forward in NC_001134 between 555545 and
7.428832	5.158777	non-annotated SAGE orf Found forward in NC_001134 between 555685 and
3.9043076	3.491154	non-annotated SAGE orf Found forward in NC_001134 between 555695 and
3.7574508	3.137227	non-annotated SAGE orf Found reverse in NC_001134 between 624453 and
0.48883408	1.162293	non-annotated SAGE orf Found reverse in NC_001134 between 308633 and
9.834924	7.877692	non-annotated SAGE orf Found reverse in NC_001134 between 376102 and
4.850913	4.129108	non-annotated SAGE orf Found reverse in NC_001134 between 593218 and
0.37075013	1.059695	non-annotated SAGE orf Found reverse in NC_001134 between 694564 and
0.44750953	0.905468	non-annotated SAGE orf Found reverse in NC_001134 between 694564 and
1.387049	2.919832	non-annotated SAGE orf Found reverse in NC_001134 between 159883 and
2.5149276	2.418432	non-annotated SAGE orf Found reverse in NC_001134 between 554862 and
3.138763	3.213268	non-annotated SAGE orf Found reverse in NC_001134 between 554862 and
2.3708947	3.678715	non-annotated SAGE orf Found forward in NC_001134 between 172044 and
2.5364099	5.048699	non-annotated SAGE orf Found reverse in NC_001134 between 241413 and
2.7305768	1.459278	YBR006W Probable aldehyde dehydrogenase (EC 1.2.1.-)
2.5206401	2.11322	non-annotated SAGE orf Found forward in NC_001134 between 46929 and
1.6373158	0.670322	non-annotated SAGE orf Found forward in NC_001134 between 680321 and
10.894	5.938269	non-annotated SAGE orf Found forward in NC_001134 between 592971 and
4.5889616	4.005936	YBR284W similarity to AMP deaminase
3.6281426	2.574918	YBR291C citrate transporter in mitochondrial inner membrane
5.537536	5.852726	YBR293W Probable multidrug resistance protein
4.9494843	2.061197	YBR294W Probable sulfate transport protein
3.606977	8.378908	YBR295W Putative P-type Cu(2+)-transporting ATPase
5.162681	4.649104	YBR297W Maltose fermentation regulatory protein
20.006	15.46058	YBR298C maltose permease
4.6583076	1.866346	YBR299W Maltase (EC 3.2.1.20)
3.8215945	3.681504	YBR301W YKL224 c homolog
4.006903	4.868504	YBR056W-A identified by SAGE
5.090387	2.223888	YBR085C-A hypothetical protein
2.0355964	2.749985	YBR259W hypothetical protein
0.40944886	0.897333	YBR263W Serine hydroxymethyltransferase, mitochondrial
2.3222673	1.391054	YBR269C hypothetical protein
10.2571335	16.39732	YBR270C Probable ATPVGTP-binding protein
1.2892251	2.329204	YBR271W weak similarity to S.pombe uvi22 protein and hypothetical protein
1.7285131	2.442357	YBR274W Probable protein kinase (growth factor & cytokine receptor family)
0.8625161	3.087254	YBR275C RAP1-interacting factor, involved in establishment of repressed ch
3.047645	3.524675	YBR278W C and C' subunits of DNA polymerase II
2.941307	2.510976	YBR237W RNA helicase homolog
0.44081	1.079991	YBR238C strong similarity to general chromatin factor Spt16p
1.9604352	2.866413	YBR239C Probable Zn-finger protein
2.4281666	1.975635	YBR244W Probable glutathione peroxidase (EC 1.11.1.9)

1.2558463	2.678654	YBR250W hypothetical protein
2.8621066	3.408372	YBR253W transcription factor, part of SrbV/Mediator complex
1.470909	2.714319	YBR254C probable membrane protein
1.6467413	2.861876	YBR257W Required for normal 5.8S rRNA processing and for tRNA process
4.1208124	1.454362	YBR214W strong similarity to hypothetical protein YGL056c
2.1822183	2.670337	YBR216C strong similarity to hypothetical protein YGL060w
6.4438534	5.551749	YBR217W autophagy
0.45362797	1.001683	YBR220C similarity to human acetyl-coenzyme A transporter
2.324142	2.274164	YBR223C hypothetical protein
5.3627844	4.995536	YBR228W similarity to hypothetical A.thaliana protein
0.58353347	0.465602	YBR232C questionable ORF
4.7334485	3.037831	YBR193C Stoichiometric member of mediator complex
3.1207817	2.309547	YBR194W hypothetical protein
2.1126564	3.870164	YBR197C weak similarity to hypothetical protein YPL077c
0.57924384	0.491168	YBR205W Putative alpha-1,2-mannosyltransferase
1.5277117	1.845045	YBR208C Urea amidolyase (contains urea carboxylase and allophanate hyd
2.815236	3.491788	YBR168W weak similarity to hypothetical protein YLR324w
4.2075405	1.099059	YBR169C HSP70 family member, highly homologous to Sse1p
1.8395619	2.711062	YBR175W Probable GTP-binding protein
2.063175	2.101985	YBR182C Probable DNA-binding transcription factor, Homolog to SRFVSL-2
7.3126154	4.634423	YBR184W alpha-galactosidase
4.830035	2.614171	YBR147W strong similarity to hypothetical protein YOL092w
1.119077	1	YBR148W Spore-specific protein
0.49329174	0.413326	YBR150C Probable Zn-finger protein
1.590707	2.446308	YBR153W Riboflavin biosynthesis protein
2.723776	2.459515	YBR156C weak similarity to myosins
2.572457	3.459316	YBR163W hypothetical protein
1.2019122	2.125911	YBR165W General positive regulator of CDC34\; Suppress some cdc34 mut
2.8178535	2.787299	YBR167C Pop7 protein, an integral subunit of RNase P and apparent subun
1.223941	2.770774	YBR131W Calcium Caffeine Zinc sensitivity
1.0408281	2.133231	YBR141C hypothetical protein
1.220971	1.329327	YBR145W alcohol dehydrogenase isoenzyme V
3.1873634	2.461453	YBR105C involved in fructose-1,6-bisphosphatase degradation
2.8076224	2.101487	YBR107C weak similarity to N.crassa chitin synthase
0.8071109	0.49668	YBR111C Homolog to serendipity protein (D. melanogaster)
9.317997	1.17106	YBR116C questionable ORF
6.024871	0.905125	YBR116C questionable ORF
4.9772305	1	YBR117C transketolase, homologous to tk11
0.83583593	0.652275	YBR085W mitochondrial ADPVATP translocator
0.440388	0.650669	YBR088C proliferating cell nuclear antigen (PCNA)\; accessory factor for DN
1.7654483	3.663428	YBR094W weak similarity to pig tubulin-tyrosine ligase
1.1903418	2.088386	YBR095C hypothetical protein
2.345482	3.120925	YBR099C weak similarity to T.brucei mitochondrion hypothetical protein 6
2.4284568	2.038781	YBR100W questionable ORF
3.3608077	2.620936	YBR063C Probable phosphopanthethein-binding protein
1.4991384	2.072979	YBR066C Probable Zn-finger protein
1.2422577	1.976764	YBR071W hypothetical protein
7.99277	1.307936	YBR072W heat shock protein 26
0.8125402	0.968556	YBR074W Homolog to aminopeptidase Y (S. cerevisiae)
2.8341448	1.666361	YBR076W ExtraCellular Mutant
2.1394033	2.008244	YBR077C hypothetical protein

8.12528	7.160223	YBR043C similarity to benomyl/methotrexate resistance protein
1.303758	0.415263	YBR046C Homolog to quinone oxidoreductase (E. coli)
2.1644645	1.502842	YBR047W hypothetical protein
3.1848772	2.325733	YBR050C Possible regulatory subunit for the PP1 family protein phosphatas
1.1523453	0.373236	YBR052C Homolog to YCR004, obr1 (S. pombe), trp repressor binding prote
1.2654116	0.271102	YBR053C similarity to rat regucalcin
5.0592856	7.958444	YBR054W Homolog to HSP30 heat shock protein YRO1 (S. cerevisiae) 7
1.945656	2.655882	YBR055C RNA splicing factor
1.7917938	2.709537	YBR057C Muddled Meiosis
1.1202192	1.224907	YBR016W strong similarity to hypothetical proteins YDL012c and YDR210w
2.0313847	1.141539	YBR018C galactose-1-phosphate uridyl transferase
3.4065144	3.221394	YBR020W galactokinase
1.397512	0.467052	YBR026C Nuclear protein that binds to T-rich strand of core consensus sequ
2.3426495	3.652371	YBR030W involved in inositol biosynthesis
4.0058465	1.278462	YBR033W Probable regulatory Zn-finger protein,V homolog to YKL251V
1.7626435	2.963831	YBR004C similarity to S.pombe hypothetical protein SPAC18B11.05
5.6389093	6.858415	YBR008C Major Facilitator Transporter
0.8586517	2.456232	YBL031W hypothetical protein
1.3544726	3.193498	YBL029W hypothetical protein
1.0420046	0.731499	YBL026W snRNA-associated protein of the Sm class
5.216557	7.644054	YBL025W Upstream activation factor subunit
3.065755	3.849513	YBL021C transcriptional activator protein of CYC1
3.6326325	3.844784	YBL019W AP endonuclease
1.841328	2.464974	YBL010C hypothetical protein
0.89115417	2.560667	YBL054W Homolog to myb transforming proteins
0.4676744	0.733966	YBL053W questionable ORF
5.304364	1.68509	YBL049W hypothetical protein
13.993418	6.312479	YBL048W hypothetical protein
3.595565	4.048208	YBL043W ExtraCellular Mutant
1.4615021	2.448796	YBL042C uridine permease
14.017745	4.706948	YBL075C heat-inducible cytosolic member of the 70 kDa heat shock protein
4.284154	1.204038	YBL065W questionable ORF
1.0118394	2.245326	YBL062W questionable ORF
5.9662194	7.048895	YBL060W hypothetical protein
2.1333094	1.93218	YBL088C putative phosphatidylinositol kinase
2.9681122	1.067285	YBL078C Form a protein complex with Aut2p, to mediate attachment of auto
0.4171648	0.689715	YBL077W questionable ORF
1.4752649	1.444804	non-annotated SAGE orf Found forward in NC_001148 between 703978 anc
1.0163481	2.434195	SNR70 snRNA
10.839063	9.23925	YBL109W similarity to subtelomeric encoded proteins
2.8532035	2.241915	YBL106C yeast homolog of the Drosophila tumor suppressor, lethal giant larv
1.6348629	2.412377	YBL103C Probable cytochrome c subunit, copper binding
3.476448	2.922576	non-annotated SAGE orf Found reverse in NC_001148 between 927488 anc
3.7571669	5.056478	non-annotated SAGE orf Found forward in NC_001148 between 297125 anc
3.5017443	0.74235	non-annotated SAGE orf Found reverse in NC_001148 between 678411 anc
11.593077	11.14269	non-annotated SAGE orf Found reverse in NC_001148 between 921211 anc
2.0780203	1.667323	non-annotated SAGE orf Found reverse in NC_001148 between 324023 anc
3.156691	3.20201	non-annotated SAGE orf Found reverse in NC_001148 between 409022 anc
7.6346006	4.875561	non-annotated SAGE orf Found forward in NC_001148 between 427735 anc
0.33204123	0.337737	non-annotated SAGE orf Found forward in NC_001148 between 497768 anc
1.1790857	1.551326	non-annotated SAGE orf Found forward in NC_001148 between 809943 anc

3.8488286	4.161227	non-annotated SAGE orf Found forward in NC_001148 between 411416 and
1.224854	3.183125	non-annotated SAGE orf Found reverse in NC_001148 between 718768 and
0.43849874	1.491298	non-annotated SAGE orf Found reverse in NC_001148 between 773596 and
0.5526947	0.589729	non-annotated SAGE orf Found forward in NC_001148 between 880290 and
1.0817187	2.879574	YPR186C Transcription factor IIIA (TFIIIA) with putative Zn-fingers
1.0039392	1.003791	YPR192W similarity to plasma membrane and water channel proteins
3.5493846	3.177885	YPR193C Histone and other Protein Acetyltransferase; Has sequence homology
2.017018	4.506743	YPR194C similarity to S.pombe isp4 protein
2.939846	5.03827	YPR196W strong similarity to regulatory protein Mal63p
3.4344277	3.436004	YPR196W strong similarity to regulatory protein Mal63p
2.5027118	2.221736	YPR199C Similar to transcriptional regulatory elements YAP1 and cad1
0.8669083	1.98086	YPR200C Required for arsenate but not for arsenite resistance
1.7578132	1.349605	YPL075W trans-acting positive regulator of the enolase and glyceraldehyde-
2.9447753	3.539328	non-annotated SAGE orf Found reverse in NC_001148 between 188306 and
1.7920977	2.598655	YPR168W negative regulator of URS2 of the HO promoter
1.6443164	2.420672	YPR169W hypothetical protein
0.361139	0.626207	YPR172W strong similarity to YLR456w
2.0054088	2.080041	YPR178W associated with the U4/U6 snRNP
2.3541267	1.083675	YPR184W similarity to human 4-alpha-glucanotransferase (EC 2.4.1.25)/amylase
1.9623291	3.673436	YPR144C similarity to YDR060w and C.elegans hypothetical protein
1.9028566	2.112083	YPR152C hypothetical protein
2.163513	2.624468	YPR153W hypothetical protein
4.4288044	0.714402	YPR160W Glycogen phosphorylase
3.1448286	3.717771	YPR121W similarity to B.subtilis transcriptional activator tenA, strong similarity
0.2639401	0.298529	YPR124W High affinity copper transporter into the cell, probable integral membrane
0.38896662	0.598588	YPR126C questionable ORF
5.516797	6.380508	YPR101W splicing factor
1.3385706	1.853383	YPR106W protein kinase
2.1007996	1.879902	YPR107C Yeast 30kDa Homologue
2.120025	2.752288	YPR111W kinase required for late nuclear division
0.9604986	1.993086	YPR112C similarity to RNA-binding proteins
2.8632746	2.829194	YPR081C strong similarity to glycyl-tRNA synthetases
2.6335125	2.486423	YPR082C S. pombe dim1+ in budding yeast
2.4678144	3.172478	YPR084W hypothetical protein
7.2129593	7.560902	YPR085C hypothetical protein
2.8956976	2.531045	YPR093C weak similarity to zinc-finger proteins
2.7216487	3.124383	YPR057W Protein involved in snRNP biogenesis
2.1280763	1.594828	YPR066W ubiquitin-like protein activating enzyme
1.5493846	2.596923	YPR068C Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos3p
3.347285	4.377671	YPR070W hypothetical protein
2.2982814	2.723577	YPR071W strong similarity to YIL029c
1.0908949	2.799356	YPR075C imparts Far- phenotype
3.3387694	1.878462	YPR077C questionable ORF
2.1950877	2.940918	YPR046W Required for chromosome segregation
1.0303109	0.437321	YPR047W alpha subunit of yeast mitochondrial phenylalanyl-tRNA synthetase
0.5392898	0.476698	YPR052C 11-kDa nonhistone chromosomal protein
2.3137126	2.448654	YPR017C GDP dissociation factor for Sec4p
1.7042367	2.378781	YPR021C similarity to human citrate transporter protein
2.9670224	1.273787	YPR026W null mutant is viable; increased tolerance to dehydration, freezing
1.9893997	2.045304	YPL008W kinetochore protein in the DEAH box family
0.84522605	0.408856	YPL004C strong similarity to YGR086c

2.786092	1.419695	YPL003W Required for activation of RUB1 (ubiquitin-like protein) together wi
2.3827114	1.99858	YPL002C appears to be functionally related to SNF7
7.114291	1.345618	YPR002W similarity to B.subtilis mmgE protein
5.8817077	3.171811	YPR005C polar 32k Da cytoplasmic protein
6.830139	6.350424	YPR012W hypothetical protein
3.4476924	4.092115	YPR013C similarity to transcription factors
2.8314822	2.602099	YPL024W (N)egative regulator of (C)ts1 (E)xpression
6.151707	6.025796	YPL022W UV endonuclease
1.1940767	2.07317	YPL018W Important for chromosome segregation
0.4810721	1.152857	YPL012W hypothetical protein
1.4633806	2.196138	YPL011C Component of the TAF(II) complex (TBP-associated protein compl
3.12103	3.342451	YPL047W hypothetical protein
2.263557	3.028063	YPL039W hypothetical protein
6.6175356	4.996389	YPL034W questionable ORF
1.6763426	1.017768	YPL072W encodes putative deubiquitinating enzyme
7.387588	5.612612	YPL071C hypothetical protein
3.657518	2.629622	YPL070W weak similarity to Vps9p
4.99769	2.425625	YPL066W hypothetical protein
3.8463542	3.68534	YPL064C weak similarity to S.pombe peptidyl-prolyl cis-trans isomerase
0.32714036	0.632094	YPL061W cytosolic aldehyde dehydrogenase
1.3895191	1.589407	YPL058C multidrug resistance transporter
1.8397969	2.742099	YPL056C hypothetical protein
3.5175083	4.196412	YPL095C strong similarity to YBR177c
4.370916	4.367053	YPL092W sensitive to sulfite
3.1514688	2.08202	YPL089C serum response factor-like protein
3.6473327	4.081888	YPL088W similarity to aryl-alcohol dehydrogenases
0.3482442	0.500119	YPL082C putative helicase
2.5171673	0.82482	YPL123C similarity to ribonucleases
4.8417673	5.257594	YPL112C weak similarity to YOR193w
2.470811	2.006108	YPL111W arginase
0.95089304	0.491326	YPL104W Aspartyl-tRNA synthetase, mitochondrial
2.4636402	3.093371	YPL144W encodes snRNA U3, SNR17A also encodes snRNA U3
2.3981848	3.137111	YPL140C protein kinase
2.4142873	2.983232	YPL138C weak similarity to fruit fly polycombl like nuclear protein
3.1624043	3.242412	YPL133C weak similarity to transcription factors
0.6981857	0.464742	YPL127C histone H1
1.0232415	2.373706	YPL124W Nuclear import protein
3.03822	2.356206	YPL167C DNA polymerase
4.4400396	6.095633	YPL164C similarity to mismatch repair protein Mlh1p
2.4193974	2.382406	YPL162C hypothetical protein
1.4773853	2.307505	YPL156C weak similarity to YDL010w
1.6941761	2.89496	YPL155C kinesin-related protein
2.408895	2.195391	YPL152W Resistant to Rapamycin Deletion 2
3.6421494	3.560799	YPL151C strong similarity to A.thaliana PRL1 and PRL2 proteins
2.6895208	3.83871	YPL149W involved in autophagy
9.210376	6.477233	YPL148C Phosphopantetheine
2.1599581	2.767713	YPL147W Pxa1p and Pxa2p appear to be subunits of a peroxisomal ATP-bir
3.1409633	2.225002	YPL189W strong similarity to YGL084c
7.5760713	2.296098	YPL186C weak similarity to Xenopus protein xlgv7
2.446912	3.633258	YPL175W N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein
0.7837449	0.626648	YPL173W Mitochondrial ribosomal protein MRPL40 (YmL40)

5.165661	1.487978	YPL171C NAD(P)H dehydrogenase
2.773406	2.604457	YPL202C similarity to cell size regulation protein Rcs1p
0.47905663	1.022118	YPL197C questionable ORF
2.6931257	1.288897	YPL196W weak similarity to <i>S.pombe</i> hypothetical protein SPAC8C9
1.4058961	1.333955	YPL233W hypothetical protein
2.0118487	3.277452	YPL229W weak similarity to YMR181c
6.3904133	1.391947	YPL223C Induced by osmotic stress
6.6259403	1.892923	YPL222W similarity to <i>C.perfringens</i> hypothetical protein
2.3214672	2.589117	YPL216W similarity to YGL133w
3.9667659	2.735716	YPL214C TMP pyrophosphorylase, hydroxyethylthiazole kinase
2.215337	3.373394	YPL213W similarity to <i>A.thaliana</i> U2 snRNP protein A'
0.84220195	2.458839	YPL212C intranuclear protein which exhibits a nucleotide-specific intron-dep
0.43800116	0.737478	YPL252C iron-sulfur protein homologous to human adrenodoxin
2.8198664	5.260048	YPL250C weak similarity to YMR195w
2.34558	1.132904	YPL247C similarity to human HAN11 protein and <i>petunia</i> an11 protein
1.2319422	2.306359	YPL245W weak similarity to human mutL protein homolog
1.6099392	2.206488	YPL242C Homolog of the mammalian IQGAP1 and 2 genes\; probable regul
1.2657267	0.259159	YPL240C heat shock protein
3.5121624	4.82608	YPL236C similarity to Prk1p, and serine/threonine protein kinase homolog fi
4.655077	3.675385	YPL277C strong similarity to hypothetical protein YOR389w/putative pseudo
4.043677	6.486886	YPL272C hypothetical protein
4.3895526	5.152544	YPL264C strong similarity to YMR253c
13.83374	10.16135	YPL258C similarity to <i>B.subtilis</i> transcriptional activator tenA, and strong sim
5.2773843	3.333077	YPL257W weak similarity to YIL029c
1.9786639	2.495974	non-annotated SAGE orf Found forward in NC_001147 between 690271 anc
7.602576	8.68334	non-annotated SAGE orf Found forward in NC_001147 between 758077 anc
1.502688	2.767366	non-annotated SAGE orf Found forward in NC_001147 between 778364 anc
2.8826098	4.016814	non-annotated SAGE orf Found forward in NC_001147 between 1004147 ar
2.1263077	3.543269	non-annotated SAGE orf Found forward in NC_001147 between 1070794 ar
0.38099864	0.565124	SNR9 snRNA
1.2231385	0.651168	SNR36 snRNA
0.20211725	0.293634	SNR8 snRNA
39.05708	9.509808	non-annotated SAGE orf Found reverse in NC_001147 between 836569 anc
4.9640956	5.648506	non-annotated SAGE orf Found reverse in NC_001147 between 969027 anc
1.0123382	1.723126	non-annotated SAGE orf Found reverse in NC_001147 between 1089906 ar
3.2280002	2.465	non-annotated SAGE orf Found reverse in NC_001147 between 16559 and
2.6021538	1.925	non-annotated SAGE orf Found reverse in NC_001147 between 16760 and
2.9773564	4.123872	non-annotated SAGE orf Found reverse in NC_001147 between 922939 anc
1.7794688	2.980112	non-annotated SAGE orf Found forward in NC_001147 between 1004376 ar
2.0416653	3.114352	non-annotated SAGE orf Found forward in NC_001147 between 1004376 ar
3.2572122	2.756476	non-annotated SAGE orf Found forward in NC_001147 between 413491 anc
6.16	4.703846	non-annotated SAGE orf Found reverse in NC_001147 between 17812 and
4.4770083	4.475143	non-annotated SAGE orf Found forward in NC_001147 between 136219 anc
6.501471	2.896351	non-annotated SAGE orf Found forward in NC_001147 between 418190 anc
0.37066033	0.791325	non-annotated SAGE orf Found forward in NC_001147 between 438710 anc
6.841349	5.678363	non-annotated SAGE orf Found reverse in NC_001147 between 14772 and
0.43519476	0.828981	non-annotated SAGE orf Found forward in NC_001147 between 464469 anc
4.457011	5.87784	non-annotated SAGE orf Found forward in NC_001147 between 60049 and
11.2122965	11.81966	non-annotated SAGE orf Found forward in NC_001147 between 423955 anc
5.1450615	4.685993	YOR389W strong similarity to putative pseudogenes YPL277c and YPL278c
7.882268	6.43612	YOR389W strong similarity to putative pseudogenes YPL277c and YPL278c

0.9821982	2.87477	YOR390W nearly identical to YPL279c
1.638	2.899808	YOR394W strong similarity to members of the Srp1p/Tip1p family
1.7009712	2.750057	YOL038C identified by SAGE
6.125447	3.7191	non-annotated SAGE orf Found forward in NC_001147 between 33183 and
4.914769	2.627692	non-annotated SAGE orf Found forward in NC_001147 between 571039 and
3.36753	1.951216	non-annotated SAGE orf Found forward in NC_001147 between 571131 and
4.0073266	2.530249	YOR363C Activator of peroxisome proliferation
2.4555387	1.935192	YOR366W questionable ORF
2.359718	0.644952	YOR374W aldehyde dehydrogenase (E.C. 1.2.1.5) (sold by SIGMA under th
5.2111363	3.462956	YOR377W Alcohol acetyltransferase
4.1398773	3.083026	YOR380W weak similarity to Pdr3p
8.871742	12.97042	YOR381W similar to FRE2
9.039846	6.584615	YOR343C hypothetical protein
2.7679276	1.111866	YOR347C Pyruvate kinase, glucose-repressed isoform
6.252	2.430192	YOR349W Protein involved in chromosome segregation, required for microtu
2.4792373	2.281694	YOR350C weak similarity to Esp1p and mitochondrial L.illustris cytochrome c
2.7860065	1.690729	YOR358W Component, along with Hap2p and Hap3p, of CCAAT-binding tra
3.8510454	4.767148	YOR318C hypothetical protein
2.3331892	3.001901	YOR319W homolog of mammalian splicing factorU2 snRNP protein
3.950158	2.524105	YOR328W Putative ABC transporter highly similar to Pdr5p
1.9693723	2.066127	YOR333C questionable ORF
1.7449579	2.773514	YOR337W Mutants are defective in Ty1 Enhancer-mediated Activation
1.7734492	2.263387	YOR297C similarity to Sdh4p
2.3817868	2.475223	YOR300W questionable ORF
3.38911	4.004336	YOR302W CPA1 leader peptide
3.297956	4.067751	YOR303W Carbamoyl phosphate synthetase, arginine specific
2.5177066	1.730829	YOR304C-A AIP3 binding protein
2.079723	2.344531	YOR305W hypothetical protein
0.8985494	2.124511	YOR306C similarity to human X-linked PEST-containing transporter
1.8385625	3.977657	YOR308C weak similarity to YIL149c
2.6628487	2.182367	YOR313C sporulation-specific protein
1.7678163	1.689337	YOR278W uroporphyrinogen III synthase
2.3523068	2.47468	YOR284W weak similarity to M.jannaschii hypothetical protein MJ0694
0.8578545	2.639378	YOR287C weak similarity to PITSLRE protein kinase isoforms
3.5078042	0.810721	YOR289W similarity to C.elegans hypothetical protein
3.0326817	2.410037	YOR292C similarity to human and mouse glomerulosclerosis protein Mpv17
1.1939948	3.540684	YOR269W Required for viability in the absence of the kinesin-related Cin8p
0.92263263	1.804125	YOR272W microtubule-associated protein
3.1885464	2.582337	YOR273C similarity to resistance proteins
0.39925206	0.715209	YOR236W dihydrofolate reductase
3.2534873	2.881605	YOR238W similarity to hypothetical S. pombe protein
2.8335736	3.616814	YOR242C Sporulation Specific
2.1245122	1.98166	YOR245C similarity to hypothetical C. elegans proteins
1.3732266	2.952258	YOR252W hypothetical protein
2.324992	4.433728	YOR213C Involved in silencing at telomeres, HML and HMR
2.9986887	1.678564	YOR220W hypothetical protein
2.6072576	2.360997	YOR221C malonyl-CoA:ACP transferase
2.1464248	2.470648	YOR222W similarity to ADP/ATP carrier proteins
6.1483274	4.376086	YOR192C strong similarity to Thi10p
2.346509	2.382935	YOR192C strong similarity to Thi10p
2.3036168	2.555032	YOR193W weak similarity to YPL112c

20.263763	14.73097	YOR202W imidazoleglycerol-phosphate dehydratase
15.391571	13.10379	YOR203W questionable ORF
2.9112203	3.039734	YOR205C hypothetical protein
1.5737879	1.923006	YOR207C second-largest subunit of RNA polymerase III
8.029453	1.35403	YOR173W strong similarity to YLR270w
17.089552	8.42951	YOR178C Regulatory subunit for Glc7p
2.2765603	1.747102	YOR179C similarity to BRR5 protein
2.1010768	4.41423	YOR180C Peroxisomal enoyl-CoA hydratase
0.91176176	1.927369	YOR145C strong similarity to hypothetical S. pombe protein and to hypothetic
3.8732188	3.930563	YOR148C required for final stages of spliceosome maturation\; promotes step
2.3843846	1.989821	YOR149C Involved in plasmid maintenance
3.9119475	1.867986	YOR152C hypothetical protein
2.6221426	1.837967	YOR155C similarity to 5'-flanking region of the Pichia MOX gene
3.6581855	2.642262	YOR162C transcription factor
16.645132	7.791431	YOR120W Similar to mammalian aldo\keto reductases
14.983185	35.1147	YOR128C phosphoribosylamino-imidazole-carboxylase
1.8561873	3.292037	YOR130C mitochondrial integral membrane protein
2.12789	1.89948	YOR138C hypothetical protein
2.1072512	1.40376	YOR097C hypothetical protein
28.109077	8.306346	YOR100C similarity to mitochondrial carrier proteins
2.3756447	1.830931	YOR111W weak similarity to B.subtilis maf protein
2.3315394	1.943448	YOR114W hypothetical protein
1.6161714	2.618351	YOR119C similarity to a C.elegans ZK632.3 protein
1.4077874	2.054323	YOR080W hypothetical protein
0.41841465	0.69979	YOR085W 34-kDa, gamma subunit of oligosaccharyl transferase glycoprotei
3.142187	2.730184	YOR052C hypothetical protein
0.8616338	2.420409	YOR056C weak similarity to human phosphorylation regulatory protein HP-1
2.3885808	2.584867	YOR057W G2 allele of skp1 suppressor
5.607622	4.399383	YOR059C weak similarity to YGL144c
3.009904	3.538888	YOR060C hypothetical protein
7.3388834	10.31881	YOR062C strong similarity to YKR075c
2.9831455	3.498818	YOR064C weak similarity to human retinoblastoma binding protein 2
0.67371696	0.575463	YOR071C strong similarity to Thi10p
3.6844616	5.913847	YOR072W hypothetical protein
1.904755	2.812926	YOR073W hypothetical protein
2.2940462	3.590474	YOR075W endoplasmic reticulum t-SNARE, coprecipitates with Sec20p, Tip
3.7270806	2.031958	YOR031W Metallothionein-like protein
0.671291	0.374734	YOR032C myc-family transcription factor homolog
1.679694	2.672427	YOR034C Protein involved in constitutive endocytosis of Ste3p
2.7492003	1.932449	YOR035C Required for mother cell-specific HO expression
2.8474224	1.416373	YOR036W integral membrane protein\; c-terminal TMD\; located in endosom
3.5591092	2.987867	YOR037W cytochrome c mitochondrial import factor
1.8069631	2.215519	YOR043W Protein involved in growth regulation
3.9290438	3.404998	YOR044W weak similarity to YDR275w
11.212216	9.801388	YOR009W similarity to Tir1p and Tir2p
3.7940974	3.27169	YOR011W strong similarity to ATP-dependent permeases
0.81996703	1.388449	YOR012W similarity to YDR391c
1.3325931	1.615259	YOR012W similarity to YDR391c
7.4590707	8.915412	YOR019W similarity to YDR474c
2.458612	1.806534	YOR023C hypothetical protein
2.2209678	3.41627	YOR026W Protein required for cell cycle arrest in response to loss of microt

1.0727476	0.44586	YOR027W Heat shock protein also induced by canavanine and entry into sta
5.3435354	4.604738	YOR028C bZIP protein, can activate transcription from a promoter containing
3.8348477	3.530546	YOL015W weak similarity to YKR015c
1.0221925	2.268935	YOL014W hypothetical protein
2.8994641	5.475368	YOL011W strong similarity to phospholipases
1.1648482	2.350467	YOL010W putative RNA 3'-terminal phosphate cyclase
3.8941317	3.618684	YOL009C Mdm12p is a mitochondrial outer membrane protein. An Mdm12p
1.5492536	1.287211	YOL003C similarity to C.elegans hypothetical protein, YDR126w, YNL326c a
2.2206283	3.172025	YOL001W negative transcriptional regulator
3.2133322	2.169115	YOR003W subtilisin-like protease III
10.137445	7.45978	YOR005C ATP dependent DNA ligase
3.5088677	1.803617	YOL032W hypothetical protein
1.3474966	1.001598	YOL031C weak similarity to Y.lipolytica SIs1 protein precursor
1.3658158	2.300826	YOL029C hypothetical protein
0.9627396	1.748583	YOL028C bZIP protein
2.2513874	1.852666	YOL016C Calmodulin-dependent protein kinase
8.5775385	6.990782	YOL055C similarity to B. subtilis transcriptional activator tenA
8.852579	1.630588	YOL052C-A DNA Damage Responsive
0.7403803	0.468812	YOL049W Glutathione Synthetase
2.3728774	1.569681	YOL048C similarity to YAL018c and YOL047c
2.5200844	3.152801	YOL045W similarity to ser/thr protein kinase
5.7190876	3.750911	YOL043C Endonuclease III-like glycosylase 2
0.44815192	1.242677	YOL076W Dislikes Extra CIN8, (MDM) Mitochondrial distribution and morphc
2.2357612	3.63124	YOL072W hypothetical protein
1.8348607	2.674355	YOL068C Homolog of SIR2
2.1578536	2.019779	YOL062C Clathrin associated protein, medium subunit
8.741125	1.915807	YOL104C Involved in meiotic chromosome segregation\; may stabilize homo
1.2263279	1.450849	YOL102C tRNA 2'-phosphotransferase
1.3934772	5.094873	YOL101C similarity to YOL002c and YDR492w
2.693938	1.910364	YOL100W SerV/Thr protein kinase
1.3055966	2.476189	YOL093W similarity to C.elegans hypothetical protein F25H8.1
6.0658464	3.029423	YOL091W hypothetical protein
3.3846297	0.939699	YOL084W similarity to A.thaliana hyp1 protein
1.4389209	2.730012	YOL128C strong similarity to protein kinase Mck1p
2.6451795	1.781117	YOL126C cytosolic malate dehydrogenase
1.1310223	2.458791	YOL125W hypothetical protein
2.6981113	2.65053	YOL119C similarity to monocarboxylate transporter proteins
2.835636	2.712854	YOL117W weak similarity to human sodium channel alpha chain HBA
1.7849545	2.114708	YOL113W Serine/threonine protein kinase with similarity to Ste20p and Cla
3.5110965	3.306826	YOL112W Multicopy Suppressor of Bud Emergence
3.5075784	2.694679	YOL108C Transcription factor involved in activation of phospholipid synthetic
5.93901	2.816395	YOL107W weak similarity to human PL6 protein
4.8431644	3.05159	YOL106W questionable ORF
0.7618878	0.255822	YOL151W induced by osmotic stress\; similar to dihydroflavonol 4-reductase
0.19950227	1.484077	YOL149W Decapping protein involved in mRNA degradation
0.90894437	3.375673	YOL144W hypothetical protein
1.0024219	2.008699	YOL142W strong similarity to hypothetical S. pombe protein
2.5093784	3.401367	YOL140W Acetylornithine aminotransferase
2.158534	1.784557	YOL138C hypothetical protein
2.1457	3.068358	YOL137W weak similarity to tetracycline resistance proteins
1.844529	1.298588	YOL133W High level expression Reduces Ty3 Transposition

1.4303962	2.53637	YOL130W ALuminium Resistance 1
3.1800592	1.121333	non-annotated SAGE orf Found forward in NC_001146 between 452136 and
1.2446153	2.163077	non-annotated SAGE orf Found forward in NC_001146 between 623131 and
4.851751	4.772074	YOL165C Hypothetical aryl-alcohol dehydrogenase (AAD)
6.7630873	6.460462	YOL164W similarity to Pseudomonas alkyl sulfatase
5.6492305	3.681538	YOL163W similarity to P.putida phthalate transporter
14.498154	12.85615	YOL162W strong similarity to hypothetical protein YIL166c
7.3267694	13.99192	YOL161C strong similarity to members of the Srp1p/Tip1p family
4.7555757	3.080421	YOL159C hypothetical protein
5.1949224	6.663858	YOL158C similarity to subtelomeric encoded proteins
4.8560066	1.56293	YOL155C similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
13.536346	3.637293	YOL155C similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w
3.5425997	2.302138	YOL154W similarity to S.fumigata Asp FII
4.801077	1.202115	YOL153C strong similarity to Cps1p
0.504987	0.47258	YOL152W similar to FRE2
0.48498535	0.359207	non-annotated SAGE orf Found forward in NC_001146 between 89212 and
5.3374934	7.588982	non-annotated SAGE orf Found forward in NC_001146 between 330326 and
3.5356922	2.558077	non-annotated SAGE orf Found forward in NC_001146 between 366082 and
1.8247693	2.458077	non-annotated SAGE orf Found forward in NC_001146 between 553015 and
2.933548	2.141545	non-annotated SAGE orf Found forward in NC_001146 between 591162 and
1.1404505	1.660156	non-annotated SAGE orf Found reverse in NC_001146 between 519600 and
3.4169252	3.195349	non-annotated SAGE orf Found reverse in NC_001146 between 351383 and
2.8215892	1.766369	non-annotated SAGE orf Found reverse in NC_001146 between 254027 and
1.1926706	1.689834	non-annotated SAGE orf Found reverse in NC_001146 between 586598 and
0.4291373	0.380322	non-annotated SAGE orf Found forward in NC_001146 between 89019 and
2.7781434	3.932923	YNR065C strong similarity to YJL222w, YIL173w and Pep1p
0.4158231	0.741914	YNR067C similarity to beta-glucan-elicitor receptor - Glycine max
8.441403	5.783829	YNR068C similarity to Bul1p
11.662922	1.437885	YNR073C strong similarity to E.coli D-mannonate oxidoreductase, identical t
7.6759663	8.387306	YNR076W member of the seripauperin protein\gene family
12.347981	3.873765	YNR034W-A hypothetical protein
6.099597	4.106213	non-annotated SAGE orf Found reverse in NC_001146 between 118895 and
13.379076	9.126347	non-annotated SAGE orf Found forward in NC_001146 between 440983 and
4.4841733	3.735894	non-annotated SAGE orf Found forward in NC_001146 between 440983 and
3.4349942	3.144161	non-annotated SAGE orf Found forward in NC_001146 between 728144 and
1.3054776	1.689546	non-annotated SAGE orf Found forward in NC_001146 between 101909 and
2.4012861	2.877188	YNR049C small hydrophilic protein, enriched in microsomal membrane fracti
0.8120899	2.824415	YNR053C strong similarity to human breast tumor associated autoantigen
6.5538917	7.032556	YNR057C dethiobiotin synthetase
5.932468	6.319387	YNR058W 7,8-diamino-pelargonic acid aminotransferase (DAPA) aminotran:
5.048545	6.349181	YNR059W similarity to alpha-1,3-mannosyltransferase
0.8628589	2.111157	YNR024W weak similarity to Rpc31p
2.0164797	2.283056	YNR029C similarity to P.denitrificans cobW protein
1.498512	2.438222	YNR032W Serine\threonine protein phosphatase involved in glycogen accu
2.52892	1.965561	YNR034W shows similarity to glucose-6-phosphate dehydrogenase non-cat
2.2236109	1.644755	YNL003C Member of family of mitochondrial carrier proteins
8.063479	2.31763	YNR002C Putative transmembrane protein
1.6063179	2.257	YNR003C 34-kDa subunit of RNA polymerase III (C)
2.634437	2.526563	YNR006W hydrophilic protein\; has cysteine rich putative zinc finger esential
2.1819322	1.983933	YNR007C Protein involved in autophagocytosis during starvation
2.5688589	2.855592	YNR010W Protein required for accurate mitotic chromosome segregation

1.6247288	2.831956	YNR012W Uridine kinase
1.3467244	2.355999	YNL027W putative transcription factor
4.137599	2.46666	YNL025C C-type cyclin associated with the Ssn3p cyclin-dependent kinase
1.7953641	2.377558	YNL024C weak similarity to YBR271w and YJR129c
6.007077	5.373846	YNL014W translation elongation factor eEF3 homolog
2.4205458	1.232361	YNL012W encodes a protein with high similarity to phospholipase B
4.180303	3.062856	YNL011C similarity to hypothetical A. thaliana protein T14G11.21
2.782658	2.297332	YNL009W peroxisomal NADP-dependent isocitrate dehydrogenase
2.3020155	2.648562	YNL008C similarity to YMR119w
0.94184667	0.294426	YNL007C sit4 suppressor, dnaJ homolog
2.8879251	1.498481	YNL006W Required for amino acid permease transport from the Golgi to the
1.6162733	3.169554	YNL050C hypothetical protein
5.927929	3.635531	YNL046W hypothetical protein
2.488506	2.793637	YNL042W Bypass of PAM1
2.1604168	2.924742	YNL038W hypothetical protein
2.5149584	1.378929	YNL037C alpha-4-beta-4 subunit of mitochondrial isocitrate dehydrogenase
3.3664818	2.262084	YNL036W involved in secretion of proteins that lack classical secretory signal
0.83755684	3.854976	YNL035C hypothetical protein
1.6578226	1.079771	YNL034W nearly identical to YNL018c
2.6843085	2.580647	YNL032W Tyrosine phosphatase
3.740431	2.532644	YNL063W weak similarity to Mycoplasma protoporphyrinogen oxidase
1.7461216	2.116121	YNL057W questionable ORF
1.8557271	2.784745	YNL053W Tyrosine protein phosphatase involved in adaptation response to
3.3796823	2.283971	YNL094W similarity to S.pombe hypothetical protein
4.1956925	1.031154	YNL092W similarity to hypothetical C. elegans proteins Y48E1C.2 and Y48E
0.6013724	0.365654	YNL079C tropomyosin I
1.7844102	3.101668	YNL116W weak similarity to RING zinc finger protein from Gallus gallus
0.9089883	0.859658	YNL114C questionable ORF
0.8695965	2.295656	YNL112W ATP-dependent RNA helicase of DEAD box family
1.9354502	2.614636	YNL097C involved in transcriptional regulation of PHO5
1.9755024	2.559627	YNL129W weak similarity to M.pneumoniae uridine kinase udk
3.1315386	3.825192	YNL128W Similar to human tumor suppressor gene known as TEP1, MMAC
4.1354995	3.218977	YNL125C Protein with similarity to mammalian monocarboxylate transporters
1.9969399	2.510208	YNL124W similarity to hypothetical S. pombe protein
1.3206178	0.969132	YNL122C hypothetical protein
1.4915116	2.530064	YNL118C essential suppressor of the respiratory deficiency of a pet mutant
2.6166563	1.488928	YNL159C hypothetical protein
3.811084	4.713428	YNL158W hypothetical protein
4.5529985	4.937151	YNL143C hypothetical protein
1.008265	1.776877	YNL142W Ammonia transport protein
3.2006872	2.713717	YNL179C hypothetical protein
0.9023346	0.351774	YNL173C multicopy suppressor of bem1 mutation, may be involved in G-pro
1.8251313	2.912488	YNL164C hypothetical protein
0.7878628	0.434173	YNL208W weak similarity to Colletotrichum gloeosporioides nitrogen starvati
1.8216354	2.655853	YNL206C similarity to structure-specific recognition proteins
3.6716902	1.166656	YNL202W peroxisomal 2,4-dienoyl-CoA reductase
1.4480354	2.330145	YNL199C Activates transcription of glycolytic genes; homologous to GCR1;
3.1572387	1.656546	YNL193W hypothetical protein
3.3260145	2.392263	YNL187W hypothetical protein
3.9209795	4.837889	YNL230C weak similarity to mammalian transcription elongation factor elong
1.4333634	2.695408	YNL227C similarity to dnaJ-like proteins

1.3673903	2.221706	YNL221C Component of nuclear RNase P and RNase MRP
2.527397	2.05602	YNL213C hypothetical protein
2.9812152	3.286725	YNL211C hypothetical protein
1.5568218	2.348676	YNL254C hypothetical protein
2.0268404	6.230053	YNL251C RNA recognition motif-containing protein that participates in seque
3.3000345	2.065542	YNL249C similarity to YDR109c
1.6620104	2.056961	YNL245C hypothetical protein
1.3760145	1.730638	YNL242W similarity to human hypothetical protein KIAA0404
2.2005463	4.226297	YNL240C strong similarity to K.marxianus LET1 protein
2.3867888	1.042181	YNL237W Yeast putative Transmembrane Protein
1.382409	2.283616	YNL232W hypothetical protein
1.6043077	3.232115	YNL276C questionable ORF
4.750184	0.857648	YNL274C similarity to glycerate- and formate-dehydrogenases
5.8503656	4.063188	YNL270C Protein highly homologous to permeases Can1p and Lyp1p for ba
1.6963571	1.880982	YNL261W Fifth largest subunit of origin recognition complex\; contains possi
3.603111	2.988891	YNL260C hypothetical protein
2.554423	1.864121	YNL257C Interacts with SNF1 protein kinase
4.4083257	3.688833	YNL294C hypothetical protein
1.4176162	2.07987	YNL289W G(sub)1 cyclin that associates with PHO85
2.7244487	3.52753	YNL282W involved in processing of tRNAs and rRNAs
3.852125	2.085604	YNL279W hypothetical protein
0.4841456	0.279276	YNL277W homoserine O-trans-acetylase
4.689402	3.94234	YNL314W positive regulator of allophanate inducible genes
2.5120804	4.147804	YNL309W Binds Sin3p in two-hybrid assay and is present in a large protein
2.3529181	1.430825	YNL305C similarity to C-term. of A.nidulans regulatory protein (qutR)
0.42011738	0.670232	SNR77 snRNA
1.241806	3.082458	SNR76 snRNA
1.0763099	3.899244	SNR74 snRNA
1.1516228	8.207232	SNR73 snRNA
1.6208868	3.883535	SNR72 snRNA
16.970306	5.517693	YNL335W similarity to M.verrucaria cyanamide hydratase, identical to hypot
2.7227798	2.540869	YNL334C SNZ2 proximal ORF, stationary phase induced gene
1.5721964	1.371102	YNL333W Snooze: stationary phase-induced gene family
6.5789437	4.868168	YNL331C Hypothetical aryl-alcohol dehydrogenase
3.4685729	3.061953	YNL329C Member of the AAA-protein family that includes NSFp and PEX1p
1.6816543	1.953179	YNL326C similarity to YOL003c, YLR246w and C.elegans hypothetical prote
4.703013	3.25022	non-annotated SAGE orf Found forward in NC_001145 between 271996 anc
1.7748982	1.894448	non-annotated SAGE orf Found forward in NC_001145 between 426559 anc
19.673834	1.571578	non-annotated SAGE orf Found forward in NC_001145 between 483361 anc
16.859354	1.689225	non-annotated SAGE orf Found forward in NC_001145 between 483361 anc
4.1870127	1.426324	non-annotated SAGE orf Found reverse in NC_001145 between 623382 anc
2.1519485	1.898355	non-annotated SAGE orf Found forward in NC_001145 between 667253 anc
1.5748265	3.342104	non-annotated SAGE orf Found forward in NC_001145 between 733267 anc
3.7225785	1.513565	non-annotated SAGE orf Found forward in NC_001145 between 433828 anc
11.312702	9.274984	non-annotated SAGE orf Found forward in NC_001145 between 434355 anc
6.369651	4.65324	non-annotated SAGE orf Found forward in NC_001145 between 465271 anc
2.7608972	2.929864	non-annotated SAGE orf Found reverse in NC_001145 between 465281 anc
4.052353	1.742162	non-annotated SAGE orf Found forward in NC_001145 between 480923 anc
2.1433382	2.442376	non-annotated SAGE orf Found reverse in NC_001145 between 762446 anc
2.1188388	2.845702	non-annotated SAGE orf Found reverse in NC_001145 between 762597 anc
3.023999	3.317708	non-annotated SAGE orf Found forward in NC_001145 between 837034 anc

1.244923	1.807115	non-annotated SAGE orf Found reverse in NC_001145 between 347179 and
7.755474	3.799664	non-annotated SAGE orf Found forward in NC_001145 between 363103 and
2.2939656	1.946753	non-annotated SAGE orf Found reverse in NC_001145 between 492187 and
1.5408428	1.869209	non-annotated SAGE orf Found reverse in NC_001145 between 426343 and
4.4523077	1.9125	non-annotated SAGE orf Found reverse in NC_001145 between 29913 and
3.6455383	3.180385	non-annotated SAGE orf Found reverse in NC_001145 between 433097 and
5.5647326	5.623438	YMR316C-B questionable ORF
1.9116052	2.388578	YMR319C Low-affinity Fe(II) transport protein
2.7124834	2.556127	YMR320W hypothetical protein
6.6237392	2.282284	YMR322C strong similarity to YPL280w, YOR391c and YDR533c
3.692993	1.996133	YMR323W strong similarity to phosphopyruvate hydratases
4.3701887	2.98093	YMR325W strong similarity to members of the Srp1p/Tip1p family
4.4786153	3.823654	non-annotated SAGE orf Found reverse in NC_001145 between 122312 and
2.9662373	2.978156	YMR299C weak similarity to hypothetical protein YJL062w
1.5634925	3.798852	YMR300C phosphoribosylpyrophosphate amidotransferase
9.236018	0.784374	YMR303C alcohol dehydrogenase II
4.910307	3.528512	YMR306W Protein with similarity to Gls1p and Gls2p (GB:Z49212)
1.1435329	2.324767	YMR310C similarity to YGR283c
3.2081363	4.717115	YMR316W similarity to YOR385w and YNL165w
5.3952613	1.327353	YMR278W similarity to phosphomannomutases
3.1507387	3.908115	YMR283C Initiator methionine tRNA 2'-O-ribosyl phosphate transferase
3.1138191	1.503055	YMR284W DNA binding protein
2.22694	2.882843	YMR285C similarity to Ccr4p
5.2753496	1.4463	YMR290W-A questionable ORF
3.9328656	5.352812	YMR291W similarity to ser/thr protein kinase
3.168885	2.223614	YMR293C similarity to amidases
3.7475886	4.112256	YMR294W Coiled-coil domain protein required for proper nuclear migration c
2.268138	2.710243	YMR255W hypothetical protein
5.814451	2.600756	YMR262W similarity to S.pombe scn1 protein
2.0101657	2.273302	YMR265C hypothetical protein
0.35703844	0.758029	YMR266W similarity to A.thaliana hyp1 protein
4.9170213	4.37591	YMR271C Orotate phosphoribosyltransferase 2
3.0412724	2.883301	YMR232W involved in cell fusion during mating, also required for the alignm
1.7502893	2.086775	YMR234W ribonuclease H
3.3503776	3.066874	YMR240C U2 snRNP protein
4.335614	1.492783	YMR250W similarity to glutamate decarboxylases
2.7453814	1.958376	YMR252C hypothetical protein
0.35881925	0.658926	YMR215W similarity to GAS1 protein
3.1350298	1.711637	YMR219W Establishes Silent omatin
0.46737477	0.61249	YMR230W Ribosomal protein S10B
3.152429	1.946001	YMR196W hypothetical protein
2.5729623	1.750405	YMR197C Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and
2.2911377	2.953205	YMR211W weak similarity to beta tubulins
1.9513397	2.884228	YMR171C similarity to YKL124w
0.7394572	0.292566	YMR173W flocculent specific protein\; contains >35 repeats of the amino aci
2.0457828	1.200456	YMR174C Cytoplasmic inhibitor of proteinase Pep4p
3.2883072	2.256927	YMR176W ExtraCellular Mutant
10.112067	6.538277	YMR180C similarity to YPL228w
5.9739585	1.75331	YMR181C similarity to YPL229w
2.8480327	1.66365	YMR182C Putative transcriptional repressor with proline-rich zinc fingers
2.6553855	1.464596	YMR184W hypothetical protein

1.7820334	2.886366	YMR185W hypothetical protein
1.5898999	1.858377	YMR187C hypothetical protein
1.6641675	1.597384	YMR155W weak similarity to E.coli hypothetical protein f402
3.729326	3.425654	YMR156C weak similarity to S.pombe hypothetical protein SPAC23C11
4.2299266	4.088533	YMR168C contains an N-terminal Zn2Cys6 type zinc finger domain, a C-tern
39.358078	7.89159	YMR169C Aldehyde Dehydrogenase (NAD(P)+)
6.760231	2.233275	YMR169C Aldehyde Dehydrogenase (NAD(P)+)
2.6500273	1.165511	YMR170C aldehyde dehydrogenase, (NAD(P)+), likely cytosolic
1.810232	3.85666	YMR132C similarity to hypothetical S. pombe protein
3.3407164	5.249297	YMR135C hypothetical protein
1.510956	2.926564	YMR136W weak similarity to YIR013c and YLR013w
5.5387692	3.663846	YMR137C interstrand crosslink repair protein
3.482285	3.752001	YMR140W hypothetical protein
4.7594705	3.335278	YMR114C similarity to B. subtilis conserved hypothetical proteins yoqW and
6.9513845	2.338846	YMR118C strong similarity to succinate dehydrogenase
1.8174411	9.275506	YMR120C 5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transfor
2.0388796	4.392604	YMR127C Protein involved in silencing HMR, homologous to acetyltransfera
3.2829564	2.276611	YMR090W strong similarity to B. subtilis conserved hypothetical protein yhfK
3.8524942	5.013628	YMR095C SNZ1 proximal ORF, stationary phase induced gene
6.4244833	8.254239	YMR096W encodes highly conserved 35 kDa protein that shows increased ϵ
2.5871813	7.079647	YMR100W Homolog of samB gene of Aspergillus nidulans (deletion of samB
9.069906	8.398247	YMR103C hypothetical protein
6.179483	5.218527	YMR104C protein kinase
6.288428	1.381484	YMR105C Phosphoglucomutase
12.757847	1.004423	YMR107W hypothetical protein
3.0233781	3.313841	YMR068W weak similarity to mouse transcription factor NF-kappaB
3.1234515	3.105879	YMR069W hypothetical protein
1.5311763	1.785326	YMR080C putative helicase
3.5787253	1.50917	YMR081C May regulate NAM7 function, possibly at level of mRNA turnover
1.5708524	0.966282	YMR086C-A questionable ORF
3.920436	3.422939	YMR087W hypothetical protein
0.9326848	3.428556	YMR042W Regulator of arginine-responsive genes with ARG81 and ARG82
4.9275575	5.142426	YMR052W Required for arrest in G1 in response to pheromone
3.679933	4.048835	YMR052C-A questionable ORF
2.2859201	1.562459	YMR055C Protein required for cell cycle arrest in response to loss of microtu
0.2685412	0.921725	YMR058W multicopper oxidase
1.573114	2.455179	YMR059W 15kDa subunit of the tetrameric tRNA splicing endonuclease
2.639315	2.139411	YMR064W basic, hydrophilic protein of 59 kDa
6.686087	7.192002	YMR065W appears to be required for the completion of nuclear membrane f
3.4912853	2.190912	YMR023C putative mitochondrial GTPase
1.5190644	2.690473	YMR028W 42 kDa protein that pysicaly associates with the PP2A and SIT4
0.52128625	0.407575	YMR038C Homocitrate
4.9716487	2.832352	YMR040W strong similarity to Yet1p
7.2776966	4.961716	YMR041C weak similarity to Pseudomonas L-fucose dehydrogenase
5.41992	4.957627	YML002W hypothetical protein
0.52813	0.459661	YML001W GTP-binding protein of the rab family\; required for homotypic fus
0.4878875	0.723444	YMR006C strong similarity to Plb1p
1.4367287	2.324495	YMR013C membrane protein required for core glycosylation
0.9453995	2.049394	YMR014W weak similarity to S.pombe hypothetical protein SPAC4F10
3.2877753	3.059753	YMR016C displays homologies to several transcription factors
3.2747197	2.676193	YMR020W Multicopy suppressor of fenpropimorph resistance (fen2 mutant),

0.83628094	1.237426	YML019W Putative new 37kDa subunit of N-oligosaccharyltransferase comp
1.4015996	2.139459	YML015C TFIID subunit
2.1255944	3.080108	YML014W similarity to C.elegans hypothetical protein C14B1.5
2.4024644	1.731822	YML011C hypothetical protein
11.20476	10.16881	YML005W similarity to hypothetical S.pombe protein
6.24024	4.013537	YML042W Carnitine O-acetyltransferase, peroxisomal and mitochondrial
1.5492475	2.235734	YML034W similarity to YDR458c
3.5326576	5.064174	YML023C weak similarity to Nmd2p
2.132171	3.311661	YML064C GTP-binding protein of the ras superfamily involved in termination
1.3132653	2.570397	YML060W 43-kDa 8-oxo-guanine DNA glycosylase
2.224907	1.584278	YML057W Catalytic A subunit of calcineurin, type 2B protein serine/threonin
1.5573142	1.521089	YML055W subunit of signal peptidase complex, homologous to mammalian
6.809884	2.679084	YML054C Cytochrome b2 [L--lactate cytochrome-c oxidoreductase]
3.9177651	5.814325	YML053C hypothetical protein
4.4689174	2.728543	YML050W weak similarity to potato sucrose cleavage protein
1.0180181	2.140269	YML082W similarity to N.crassa O-succinylhomoserine (thiol)-lyase
0.7522572	0.44792	YML072C similarity to YOR3141c and YNL087w
2.8877342	2.046043	YML068W similarity to C.elegans hypothetical protein
3.2616582	2.981283	YML107C hypothetical protein
1.3650663	2.282571	YML102W p60 subunit of the yeast omatin Assembly Factor-I (CAF-I)
3.573092	0.707728	YML100W 123 kD regulatory subunit of trehalose-6-phosphate synthase
4.080328	3.490723	YML099C zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluste
3.1334305	2.722871	YML098W TFIID subunit
5.841547	1.29071	YML128C C-terminal part starting with aa 262 cause growth inhibition when
2.9089637	4.36776	YML119W hypothetical protein
5.673948	3.248692	YML117W similarity to YPL184c
3.2061245	1.964238	YML117W similarity to YPL184c
3.174307	2.056124	YML117W-A questionable ORF
1.917383	3.53183	YML116W predicted protein is very hydrophobic, has many membrane-span
1.9004121	2.757455	YML114C hypothetical protein
1.3661407	2.375327	YML113W datin, an oligo(dA).oligo(dT)-binding protein
1.7621206	2.445388	YML112W CTD kinase-I gamma subunit
1.7090638	2.276643	YML111W strong similarity to ubiquitination protein Bul1p
1.9186971	2.28133	YML109W multicopy suppressor of a sin4 defect
2.853074	3.287077	non-annotated SAGE orf Found forward in NC_001144 between 949308 and
3.0843837	3.967464	non-annotated SAGE orf Found forward in NC_001144 between 949499 and
2.7886388	3.774142	non-annotated SAGE orf Found forward in NC_001144 between 988140 and
0.86020726	0.545593	SNR34 snRNA
3.1442394	2.610725	YML133C hypothetical protein Y'.2
1.0266054	0.259213	YML131W similarity to human leukotriene b4 12-hydroxydehydrogenase
1.6387421	3.833797	non-annotated SAGE orf Found forward in NC_001144 between 441497 and
4.5668426	6.090913	non-annotated SAGE orf Found reverse in NC_001144 between 669739 and
3.4339635	3.585247	non-annotated SAGE orf Found reverse in NC_001144 between 13652 and
9.464674	4.09915	non-annotated SAGE orf Found reverse in NC_001144 between 223615 and
1.0332308	1.469808	non-annotated SAGE orf Found forward in NC_001144 between 677930 and
0.41829905	0.448919	non-annotated SAGE orf Found forward in NC_001144 between 92566 and
0.94834745	0.874836	non-annotated SAGE orf Found forward in NC_001144 between 451607 and
2.0650804	1.917815	non-annotated SAGE orf Found forward in NC_001144 between 371240 and
5.197941	5.743779	non-annotated SAGE orf Found forward in NC_001144 between 390278 and
7.681461	16.73178	YLR451W zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluste
2.4588094	3.81847	YLR456W strong similarity to YPR172w

2.2592652	2.640489	YLR457C Nap1p-binding protein
1.4053026	0.860777	YLR460C similarity to <i>C.carbonum</i> toxD protein
6.4130583	5.345315	YLR461W member of the seripauperin proteinVgene family (see Gene_class
3.7898672	5.390568	YLL018C-A hypothetical protein identified by SAGE
3.8542948	2.717821	non-annotated SAGE orf Found forward in NC_001144 between 230974 and
3.0109444	3.058536	YLR426W weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from <i>E</i>
2.0609655	1.454831	YLR411W Copper Transporter
5.4667	2.846622	YLR417W defective in vacuolar protein sorting
5.2462354	2.699553	YLR423C hypothetical protein
2.3437557	1.744967	YLR383W Protein involved in recombination repair, homologous to <i>S. pombe</i>
4.273025	4.244697	YLR394W weak similarity to chicken RING zinc finger protein
1.6383505	1.641078	YLR404W hypothetical protein
1.6683176	2.318032	YLR362W Ser/Thr protein kinase; MEKK homolog
3.6834018	3.664706	YLR363C putative Upf1p-interacting protein
2.4650924	2.941331	YLR375W Involved in pre-tRNA splicing and in uptake of branched-chain amino
4.7647123	3.569878	YLR376C hypothetical protein
2.2074091	2.012482	YLR381W hypothetical protein
2.0505335	1.493879	YLR343W strong similarity to Gas1p and <i>C.albicans</i> pH responsive protein
3.01181	1.03827	YLR345W similarity to Pfk26p and other 6-phosphofructo-2-kinases
1.4247651	1.056708	YLR352W hypothetical protein
3.3301036	3.252019	YLR317W questionable ORF
2.3884616	3.046154	YLR318W 103 kD basic protein, catalytic subunit of telomerase
1.7129145	2.135467	YLR319C Actin Interacting Protein
1.3738798	1.706043	YLR320W hypothetical protein
2.4541917	2.522872	YLR323C weak similarity to <i>N.crassa</i> uvs2 protein
2.5400121	1.385087	YLR324W strong similarity to YGR004w
29.593319	3.956477	YLR327C strong similarity to Stf2p
1.1494925	2.359123	YLR328W strong similarity to YGR010w

apsis and chiasmata formation\; localizes to chromosome cores independently of Mei4p and Spo11p\; i

rgeting subunit

1

ts with RPD3 gene product

-4 proteins which have a novel highly conserved DNA binding domain

along with Rrn9p and Rrn10p

stabilized cells

is. The Exocyst complex contains the gene products encoded by SEC3, SEC5, SEC6, SEC8, SEC10, 9

essible gene

homolog gene

ted with polyadenylation factor 1 (PF I)

r domain type

quired in ER to Golgi transport.

tical protein

o-L-glycero-4-hexulose-5-epimerase

1 468899 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1 448156 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1 456883 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

1 638722 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1 136247 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1 136457 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1 142992 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1 264333 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1 309084 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

94228 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
1 146755 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
17055 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
1 195171 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1 233836 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

nalian glycogenin

igation factor DmS-II

ar ribonucleoprotein particle

NP-A

› 1B

pothetical protein YOR054c

in, colocalizes with Myo2p

\P3 heteromer)

10.2

erase largest subunit CTD (carboxyl-terminal domain)

YOR162c, YOR172w and YLR266c

ome b pre-mRNA

1 472142 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 627004 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 732069 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 735165 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 741883 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 283426 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 397036 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 448050 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 549719 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 737453 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 444969 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 451979 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 731896 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 741003 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 637857 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

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236625 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

159545 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
181408 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
227742 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

s

r RcsB

ith poly(A) polymerase

e and aldehyde reductases

active genes

Rrn6p and TATA-binding protein
of plasma membrane-associated clathrin assembly complex (AP-2)

ion protein

al regulation

zipper motif and acidic region\; lexA-Sip4p activates transcription

s

unction

ed in the Golgi

fatty acid tetradecanoic acid (14:0) to that of hexadecanoic acid (16:0)

d 223230 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 223423 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

1223476 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t

tein

22687 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
1183005 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1183005 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

ins a C-terminal cysteine-rich region that conforms to the H2 variant of the RING finger Zn²⁺ binding mo

obrevin) homolog, forms a complex with Snc2p and Sec9p

ilizes to the spindle pole bodies. Molecular weight is 72 kD

1ice. Found forward in NC_001140 between 523872 and 524871 with 100% identity.
1ice. Found forward in NC_001140 between 524872 and 525871 with 100% identity.
1ice. Found forward in NC_001140 between 524872 and 525871 with 100% identity.
1ice. Found forward in NC_001140 between 525872 and 526871 with 100% identity.
1ice. Found forward in NC_001140 between 526872 and 527871 with 100% identity.

1ce. Found forward in NC_001140 between 527872 and 528114 with 100% identity.
1ce. Found forward in NC_001140 between 532177 and 533176 with 100% identity.
1ce. Found forward in NC_001140 between 534177 and 535176 with 100% identity.
1ce. Found forward in NC_001140 between 535177 and 536176 with 100% identity.
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1ce. Found forward in NC_001140 between 546488 and 547487 with 100% identity.
1ce. Found forward in NC_001140 between 548488 and 549487 with 100% identity.
æ. Found forward in NC_001141 between 10696 and 11695 with 100% identity.
æ. Found forward in NC_001141 between 115607 and 116404 with 100% identity.
æ. Found forward in NC_001141 between 205053 and 206052 with 100% identity.
æ. Found forward in NC_001141 between 371963 and 372495 with 100% identity.
1ce. Found forward in NC_001140 between 43533 and 44532 with 100% identity.
1ce. Found forward in NC_001140 between 84563 and 85562 with 100% identity.
1ce. Found forward in NC_001140 between 436206 and 437169 with 100% identity.
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æ. Found forward in NC_001136 between 800686 and 801685 with 100% identity.
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.e. Found forward in NC_001134 between 76564 and 77563 with 100% identity.
.e. Found forward in NC_001134 between 220363 and 221362 with 100% identity.
.e. Found forward in NC_001134 between 230363 and 231362 with 100% identity.
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.ce. Found forward in NC_001148 between 390268 and 391267 with 100% identity.
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.ce. Found forward in NC_001148 between 541315 and 541465 with 100% identity.
.ce. Found forward in NC_001148 between 146119 and 146628 with 100% identity.
.ce. Found forward in NC_001147 between 178973 and 179808 with 100% identity.
.ce. Found forward in NC_001147 between 352694 and 353362 with 100% identity.
.ce. Found forward in NC_001147 between 544261 and 545260 with 100% identity.
.ce. Found forward in NC_001147 between 545261 and 545831 with 100% identity.
.ce. Found forward in NC_001146 between 684191 and 685190 with 100% identity.
.ce. Found forward in NC_001146 between 686191 and 686613 with 100% identity.
.ce. Found forward in NC_001146 between 762618 and 763617 with 100% identity.
.ce. Found forward in NC_001146 between 764618 and 765617 with 100% identity.
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.ce. Found forward in NC_001147 between 2078 and 3077 with 100% identity.
.ce. Found forward in NC_001147 between 3078 and 4077 with 100% identity.
.ce. Found forward in NC_001147 between 7078 and 7615 with 100% identity.
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.ce. Found forward in NC_001146 between 161130 and 162129 with 100% identity.
.ce. Found forward in NC_001145 between 379593 and 379699 with 100% identity.
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.ce. Found forward in NC_001145 between 361810 and 362701 with 100% identity.
.ce. Found forward in NC_001144 between 812817 and 813816 with 100% identity.
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.e. Found forward in NC_001143 between 647133 and 648132 with 100% identity.
.e. Found forward in NC_001143 between 649494 and 650493 with 100% identity.

⌘. Found forward in NC_001143 between 650494 and 651493 with 100% identity.
⌘. Found forward in NC_001143 between 651494 and 652493 with 100% identity.
⌘. Found forward in NC_001143 between 652494 and 653493 with 100% identity.
⌘. Found forward in NC_001143 between 652494 and 653493 with 100% identity.
⌘. Found forward in NC_001143 between 655494 and 655865 with 100% identity.
⌘. Found forward in NC_001143 between 663918 and 664917 with 100% identity.
ce. Found forward in NC_001144 between 188164 and 189163 with 100% identity.
ce. Found forward in NC_001144 between 193164 and 194163 with 100% identity.
ce. Found forward in NC_001144 between 308356 and 309355 with 100% identity.
⌘. Found forward in NC_001143 between 415757 and 416756 with 100% identity.
⌘. Found forward in NC_001143 between 545784 and 546783 with 100% identity.
⌘. Found forward in NC_001143 between 642133 and 643132 with 100% identity.
⌘. Found forward in NC_001143 between 643133 and 644132 with 100% identity.
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⌘. Found forward in NC_001143 between 645133 and 646132 with 100% identity.
e. Found forward in NC_001142 between 694939 and 695938 with 100% identity.
e. Found forward in NC_001142 between 695939 and 696138 with 100% identity.
e. Found forward in NC_001142 between 718444 and 719443 with 100% identity.
e. Found forward in NC_001142 between 719444 and 720443 with 100% identity.
⌘. Found forward in NC_001143 between 11592 and 12591 with 100% identity.
⌘. Found forward in NC_001143 between 12592 and 13591 with 100% identity.
⌘. Found forward in NC_001143 between 13592 and 14591 with 100% identity.
e. Found forward in NC_001142 between 373944 and 374811 with 100% identity.
e. Found forward in NC_001142 between 514427 and 515426 with 100% identity.
⌘. Found forward in NC_001133 between 208649 and 209648 with 100% identity.
⌘. Found forward in NC_001133 between 209649 and 210648 with 100% identity.
⌘. Found forward in NC_001133 between 211649 and 212648 with 100% identity.
⌘. Found forward in NC_001133 between 214649 and 215648 with 100% identity.
e. Found forward in NC_001142 between 11138 and 12137 with 100% identity.
e. Found forward in NC_001142 between 14138 and 15137 with 100% identity.
e. Found forward in NC_001142 between 15138 and 15624 with 100% identity.

⌘. Found forward in NC_001141 between 206488 and 210129 with 100% identity.

⌘. Found forward in NC_001133 between 13744 and 14743 with 100% identity.
⌘. Found forward in NC_001133 between 14744 and 15743 with 100% identity.
⌘. Found forward in NC_001133 between 16744 and 17743 with 100% identity.
⌘. Found forward in NC_001133 between 17744 and 18743 with 100% identity.

æ. Found forward in NC_001136 between 804494 and 805681 with 100% identity.

oteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

γce. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.

γce. Found reverse in NC_001148 between 437328 and 439490 with 100% identity.

¸ such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
¸ such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

ce. Found forward in NC_001144 between 942777 and 946791 with 100% identity.
ce. Found forward in NC_001144 between 942777 and 946791 with 100% identity.

ce. Found forward in NC_001144 between 941478 and 942778 with 100% identity.

ɔ\Cos9p family, coded from subtelomeric region
ɔ\Cos9p family, coded from subtelomeric region

e. Found forward in NC_001142 between 198701 and 203026 with 100% identity.

128444 with 88.588589% identity.

found forward in NC_001224 between 3940 and 4167 with 99.122807% identity.

with 100% identity.

27169 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar

1258509 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

1258640 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

1385698 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

1385959 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

1386157 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

30898 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar

51751 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar

1385767 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

large subunit

to a sec23 mutation

GPI-anchored cell wall proteins

longation

d 204277 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 530267 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 530897 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 198592 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

34790 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
d 519228 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 529113 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
796 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transc
924 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transc
d 202657 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

18p and Tub4p perhaps as part of the microtubule attachment site of the SBP

3e
3e

iiif. Similarity to SLG1 (WSC1), WSC2 and WSC3

1788224 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
1810659 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
1974772 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t

1919735 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
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1326609 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
1366531 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t

lc

itol, the first intermediate in synthesis of glycosylphosphatidylinositol (GPI) anchors

sferase

ecursor of thiamine

/

GRB2 homolog

cell surface

ding Protein

dons\; acts with Nmd2p and Nam7p

aturation

duction

minotransferase)
etrical protein MTH972

\R028w, YAR033w and YCR007c

ation of hybrid DNA in vitro\; has 5'-to-3' exonuclease activity on DNA and RNA\; binds to G4 tetraplex

-aminoadipate reductase)

vitro); Probable 119 kD DNA/RNA helicase family member

033 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transc
48926 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
d 161405 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 182221 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

76470 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar

involved in the the control of peptide transport

E3 component of alpha-ketoacid dehydrogenase complexes)

inhibitor of Polycomb
(PAU)

d 367721 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 422781 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 284719 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 289906 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 311907 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 468081 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
77622 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar

122670 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
314310 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
407214 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
561634 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
561634 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
117380 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t

187524 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
550699 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
31562 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
64373 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
251697 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t

of the general transcription machinery in vivo

expression (O)

late kinase

motor Cin8p); required for normal microtubule stability

bins

: resistance

function of the Imp1 peptidase and/or the protein sorting machinery

: PAU)

d 909844 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 1014130 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas

rd 1108613 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
rd 1362352 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas

rd 1385758 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
rd 463426 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 678185 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 362528 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 386772 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 471388 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 542432 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 910028 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 1182914 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
rd 931032 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 1014367 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
rd 1225015 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
rd 1276564 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
rd 1385815 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
34184 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
34184 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
rd 217325 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 512651 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
77110 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
rd 104806 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

rd 340977 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
rd 691207 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

ptide chain release factor 1 and YJL149w

· wall pathway converting L-tyrosine to N-formyl-L-tyrosine, expressed late (10-16 hr) in sporulation
milar to L23 family of ribosomal proteins

3A complex
arity to signal transducing adaptor from mouse and man

\ helicase MSS116 / YDR194c

\; cysteine rich regions of amino acids are essential for function

ikes and Wilsons genes

je hypothetical protein SPAC12G12.14
it

VA polymerase II\; BTF3 homolog

:zcd, rat zinc transport protein ZnT-1 and Cot1p

n genes

ormation, prior to polyadenylation
j BAP2, TAT1, PTR2 and YDR046c

ore repeats of a novel zinc finger motif consisting of Cys and His residues in the form Cx8Cx5Cx3H [wh

ing.
ere metabolism during late S phase
iction of morphogenesis during conjugation

lucin (WD-40) repeats

pate semialdehyde as co-inducer\; saccharopine reductase synthesis

function in chromosome morphogenesis from S phase through mitosis
e hypothetical protein SPAC12G12.14

with Rad 55p by two-hybrid analysis

ctors

mplex

ondrial transcripts

f for thiamin metabolism

y to cellular nucleic acid binding proteins
r domain type

alization to telomeres

verexpressed

ird step in heme biosynthesis

ivating family of proteins

YML052w

1258884 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1469 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transc
1125520 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1169175 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1288519 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

nes

nes

41704 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
1157669 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

Ins)

s PAU)

uptake); protein contains 12 predicted transmembrane domains

stationary phase); located in plasma membrane

in LgYCL010c

in LgYCL002c

- ⊖. Found forward in NC_001134 between 1 and 1000 with 100% identity.
- ⊖. Found forward in NC_001134 between 2001 and 3000 with 100% identity.
- ⊖. Found forward in NC_001134 between 4001 and 5000 with 100% identity.
- ⊖. Found forward in NC_001134 between 5001 and 6000 with 100% identity.
- ⊖. Found forward in NC_001134 between 5001 and 6000 with 100% identity.
- ⊖. Found forward in NC_001134 between 6001 and 6215 with 100% identity.

⌋ 555088 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 555691 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 555879 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 555919 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 624656 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 308923 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 376293 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 593355 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 694710 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 694710 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 160056 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 555011 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 555011 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 172202 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 241568 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

47189 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
⌋ 680521 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
⌋ 593117 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

YNL024c
)
romatin

ing); associated with RNase MRP and RNase P

rolase)

:

ations when over-expressed
it of RNase MRP

IA polymerase delta, mRNA increases in G1, peaks in S in mitosis, and increases prior to DNA synthesis

e Glc7p
in (E. coli)

ence of autonomously replicating sequence

family

phagosomes to microtubules. Aut7p shows homologies to LC3, a microtubule-associated protein from i

d 704121 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

ae

d 927640 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

d 297292 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

d 678614 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

d 921453 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

d 324286 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

d 409276 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

d 427896 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

d 497959 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

d 810116 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

d 411688 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
d 718944 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
d 773742 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
d 880439 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

ology to known HATs and NATs

3-phosphate dehydrogenase gene families

d 188512 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

glyco-1,6-glucosidase (EC 3.2.1.33)

identity to hypothetical proteins YPL258c and YOL055c
membrane protein

see

g, and toxic levels of ethanol

with UBA3. Related to AOS1 and to N-terminus of UBA1. Collaborates with UBC12 in conjugation of RUB

lex)

binding cassette transporter necessary for transport of long-chain fatty acids into peroxisomes

endent tRNA pseudouridine synthase activity

lator of cellular morphogenesis, inducing actin-ring formation in association with cytokinesis

rom *A. thaliana*
gene

ilarity to hypothetical proteins YOL055c and YPR121w

l 690495 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
l 758286 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
l 778516 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
rd 1004431 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
rd 1071003 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas

l 836709 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
l 969179 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
rd 1090073 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
16696 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
16939 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
l 923082 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
rd 1004510 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
rd 1004510 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeas
l 413682 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
17970 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
l 136404 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
l 418375 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
l 438853 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
15044 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
l 464630 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
60273 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
l 424104 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

;

;

33335 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
d 571224 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
d 571283 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

e catalogue number A5550, according to A. Blomberg)

.bule stability
oxidase I
nscription factor

mitotic motor.

al C. elegans protein
1 of splicing

in complex

0

1p. and Sec22p

ie

.bule function

stationary phase
containing a Yap recognition site

homolog exists in *S. Pombe* which confers a dominant negative phenotype when expressed in *S. cerev*
and YLR246w

biology

telomere DNA interactions at telomeres and is required for a telomere activity in distributive segregation; i

4p

3 genes

from plants

1452276 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1623265 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr

89394 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
1330544 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1366222 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1553233 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1591341 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1519773 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1351577 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1254161 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1586816 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
89186 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar

o YEL070w

1119086 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1441117 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1441117 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1728293 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
1102082 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast tr
ion, interacts with Sec1p

sferase

mulation
alytic domains\; homologous to Sol2p and Sol3p

for function

cell surface

1
al sequences

pheromone

:1C.c

:1 and PTEN1. Contains sequence motifs characteristic of protein tyrosine phosphatases.
s MCT1 and MCT2

tein mediated signal transduction

ion-induced glutamine rich protein

; may function in complex with Gcr2p

in A

ance-specific regulation of nuclear pre-mRNA abundance

ic amino acids
ble ATP-binding site

complex with Sin3p and Stb2p

netical protein YFL061w

in ZK757.1

1 272136 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 426696 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 483495 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 483495 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 623516 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 667450 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 733455 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 434049 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 434564 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 465411 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 465418 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 481186 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 762586 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 762764 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 837171 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

1 347406 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 363273 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 492357 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
1 426489 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
30104 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
1 433231 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

1 122605 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

during mitosis (but not during conjugation)

ent of parental nuclei before nuclear fusion

I Pep12p

id sequence NNDSYGS

ninal acidic domain and a putative coiled coil dimerization domain

yoaM

mylase/IMP cyclohydrolase

ses

:

expression after entry into stationary phase

} results in mislocalization of septa

ibule function

usion and may play a role in the organization of the membrane fusion complex

protein phosphatase catalytic subunits

ion event in vacuole inheritance, for endosome-endosome fusion, and for fusion of endosomes to vacu

shows similarity to *Candida albicans* corticosteroid-binding protein CBP1

plex

of M-phase

ie phosphatase\; redundant with Cna1\; cytoplasmic
protein SPC25

osphatase complex\; homologous to TPS3 gene product
r domain type

overexpressed

ning regions, several potential glycosylation sites, potential ATP-binding site

l 949442 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
l 949633 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
l 988277 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti

l 441667 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
l 669894 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
l 13819 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
l 223821 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
l 678073 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
l 92730 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast trar
l 451783 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
l 371515 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
l 390421 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast ti
r domain type

PAU)

231108 with 100% identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast t
E. coli

rad18

ino acids

mRNA is induced in meiosis

SEC15 and EXO70.

ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251

ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251
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otif.

ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251

iscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251
:riptome. Cell 8:243-251
:riptome. Cell 8:243-251
ranscriptome. Cell 8:243-251

DNA and cuts in a single-stranded region 5' to the G4 structure\; protein increases several-fold in meiot

ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251
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ranscriptome. Cell 8:243-251

ranscriptome. Cell 8:243-251
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ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251

ere x is a variable amino acid (aa)]

ranscriptome. Cell 8:243-251
:riptome. Cell 8:243-251
ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251

iscriptome. Cell 8:243-251
ranscriptome. Cell 8:243-251

ranscriptome. Cell 8:243-251
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