

Probe set	Gene	B-upf1	C-nmd2	D-upf3
6201_at	YDR281C	0.2554179	0.44769505	0.37667182
5936_at	YDR512C	0.35924366	0.48921248	0.5983472
4580_at	YHL028W	0.36024734	0.46417466	0.46082753
9588_at	YMR058W	0.34329924	0.4132989	0.29456255
9566_at	YMR080C	0.14827165	1.7403616	1.7399194
6513_at	YDL039C	0.43375123	0.20130222	0.21481685
4192_at	YIL119C	0.3569158	0.5708786	0.45372748
7530_s_at	NPR082W	0.45578134	0.6423346	0.8401473
6514_at	YDL038C	0.40935504	0.1936186	0.18442012
2525_at	gBL02	0.4822651	0.53540784	0.3754067
9837_s_at	NLR033W	0.36429226	0.41118854	0.45027444
2518_at	gBL01	0.49281424	0.8548737	0.73422295
3743_f_at	TA(AGC)L	0.40221894	0.27578464	0.21190402
3863_f_at	TR(UCU)J2	0.43851092	0.33820468	0.30530578
3827_f_at	TR(ACG)K	0.49336946	0.29024035	0.2991795
5874_at	NDR164W	0.5489832	0.4930914	0.48397127
5372_at	YFL014W	0.41175106	0.90056753	0.5560905
3687_f_at	TR(UCU)M1	0.50770193	0.40174833	0.37420744
6693_at	YDL215C	5.831198	7.9577503	7.416788
6666_at	YDL197C	3.334115	3.708619	3.465517
6650_at	YDL170W	2.58835	2.5808814	2.352283
6722_at	YDL231C	4.37687	5.1795716	5.128331
6710_at	YDL243C	9.983261	9.989287	9.969587
6608_at	YDL123W	2.7118337	2.38451	2.5931513
6577_at	YDL109C	2.775011	3.3625228	3.10714
6704_at	YDL204W	3.8091786	4.536795	4.2226634
6621_at	YDL154W	4.172008	4.1819234	4.7784615
6616_at	YDL115C	7.227475	10.0079155	11.108437
6793_at	YCR098C	3.2813942	4.4193954	4.1012506
6784_at	YCR089W	8.979529	5.181018	5.667983
6766_at	NCR007W	5.2046156	3.3298078	3.4326925
6797_at	YCR102C	5.5192904	6.830362	7.7193427
6795_at	YCR100C	4.837156	6.094335	4.2187743
6744_at	NCR002W	13.594795	11.7305765	15.755961
6738_at	NCL011C	8.530315	9.261553	9.595841
6729_at	YDL223C	4.032688	4.259628	5.167637
6794_at	YCR099C	3.6857696	3.6946154	3.4936538
6756_at	YCR020W-B	5.3087306	4.0799937	4.0741205
6745_at	NCR011C	3.5238376	3.4698899	4.2316465
6205_at	YDR285W	7.2176495	8.848959	8.1534195
6149_at	YDR318W	3.2659755	2.7498775	2.7346425
6118_at	YDR332W	8.702137	8.219065	9.752615
6253_at	YDR242W	12.709528	10.718977	13.442421
6247_at	YDR236C	2.5139763	2.685865	2.493465
6057_at	YDR406W	2.930269	3.2509463	3.299134
6027_at	YDR421W	3.0884845	2.436204	2.5172472
5954_at	YDR530C	4.4980206	4.2028093	4.472361
6230_at	YDR265W	4.0773554	2.971158	2.9621522
6106_at	YDR364C	3.8099632	4.522606	4.792199
6084_at	YDR387C	4.4444766	4.97417	4.2908316
6437_at	YDR022C	3.6470551	3.042923	4.1810327
6406_at	YDR082W	12.134759	13.949566	14.360947
6402_at	YDR078C	7.203393	8.7665615	10.103939

6480_at	YDR019C	2.9557135	3.6074495	3.9537122
6468_at	YDR007W	17.978832	14.521455	14.294668
6361_at	YDR126W	3.7193737	4.2126927	3.9248075
6338_at	YDR147W	5.3994427	5.841892	6.8308477
6306_at	YDR160W	3.1583571	3.1430302	2.7874491
6465_at	YDR004W	3.150174	2.717254	2.7293558
6397_at	YDR073W	3.2696695	3.1843886	4.0297093
6366_at	YDR131C	3.4170294	4.565008	4.2492375
7153_at	YBR197C	3.0348334	3.39362	3.0093632
7138_at	YBR228W	3.537891	3.276483	3.6062708
7133_at	YBR223C	2.56753	1.8337435	1.9789464
7210_at	YBR163W	3.2054098	3.7761548	4.00098
7185_at	YBR184W	6.1580853	3.9254987	4.558878
7109_at	YBR244W	3.1449509	2.6249237	2.82674
7088_at	YBR270C	12.037254	15.829479	16.270233
7078_at	YBR085C-A	2.8050828	2.8642368	3.0719595
7164_at	YBR208C	2.76925	2.9383523	3.4847481
7127_at	YBR217W	5.129515	6.9934273	7.5916996
7118_at	YBR253W	2.4376469	2.4916565	2.959351
7422_at	YBL075C	6.4385905	4.7435513	5.8292627
7388_at	YBL019W	4.8794603	4.381354	5.0042934
7382_at	YBL025W	6.7715883	5.0118246	6.4007215
7494_at	NPL016W	5.7281847	4.0064645	4.578119
7478_s_at	YBL109W	10.769218	10.313801	7.554401
7331_at	YBR018C	2.6339736	1.9248562	2.5223176
7318_at	YBR050C	5.0941305	3.110971	2.9696598
7311_at	YBR043C	6.387043	6.6291265	7.15702
7436_at	YBL060W	4.9527955	5.575783	5.930338
7367_at	YBR008C	8.546457	9.991407	10.916827
7343_at	YBR030W	3.0641465	2.3765092	2.8774447
6947_g_at	SCIIYLEFT	5.409086	5.3907027	5.1447372
6946_at	SCIIYLEFT	8.271935	9.479027	7.406133
6945_g_at	SCIIYLEFT	5.506346	6.4890385	4.784038
6963_at	NBR034W	5.4860497	5.471631	5.601221
6958_s_at	YCL067C	5.497714	5.738574	7.137618
6870_at	YCL010C	4.5523806	5.1835694	5.4224453
6852_at	YCR020C	25.129007	25.143269	27.720768
6827_at	YCR037C	3.4469469	3.3589563	3.828043
6949_f_at	SCIIYLEFT	5.878419	4.5205	4.253987
6911_at	YCL016C	2.2662873	2.1632926	2.21774
6893_at	YCL039W	3.949128	3.0442443	3.4653525
7068_at	YBR295W	3.944727	4.933128	4.7069416
7066_at	YBR293W	5.7244334	6.149831	5.939245
7016_at	NBL005W	2.717697	2.761136	3.228074
7074_f_at	YBR301W	4.257138	4.609255	4.8272066
7071_s_at	YBR298C	22.111153	16.908846	15.86731
6996_at	NBL013C	6.208768	6.4744644	6.865961
6989_at	NBR042C	6.01371	4.52	5.665192
6964_s_at	NBR035W	7.5932903	7.5125585	7.360305
7070_at	YBR297W	2.936931	3.3728786	3.550073
7009_g_at	NBR032C	3.525872	2.978017	3.2431273
7008_at	NBR032C	2.7456658	2.3019397	2.2576983
5257_at	YGL256W	3.0793324	3.9002984	2.9852593
5253_g_at	YGL259W	3.3040385	4.208846	3.0753846

5251_f_at	YGL261C	4.6686225	5.677373	4.9785395
5270_at	YGL243W	2.9228454	3.4919524	3.7426758
5262_at	YGL251C	5.6807694	4.4525	5.5584617
5179_at	YGL156W	3.0408683	2.3954003	2.2604847
5160_at	YGL128C	3.5375607	2.9270718	2.989632
5089_at	YGL063W	10.343847	10.206731	9.435769
5259_at	YGL254W	2.2396119	2.298487	1.9067926
5247_at	YGL223C	4.7457285	5.5927057	5.167682
5186_at	YGL193C	10.169846	10.075173	8.473883
5425_at	YFL055W	2.4506788	2.7563462	2.8180768
5423_s_at	YFL057C	6.33111	7.6845	7.625944
5410_f_at	YFL020C	4.9829555	4.1596575	3.9356675
5453_at	NER022W	4.0184617	3.5298076	2.5390382
5430_at	YFL050C	9.932307	10.830769	9.215962
5362_at	YFR020W	4.542617	3.7699795	3.8017993
5323_at	YFR026C	14.164055	11.3782835	10.483751
5281_f_at	NFL013C	4.209808	3.058269	4.2767305
5426_at	YFL054C	3.222733	2.754686	2.8999493
5403_at	YFL027C	2.8966887	2.355764	2.960732
5364_at	YFR022W	5.608073	5.1926594	5.4748974
4723_f_at	YGR294W	26.307243	34.988075	41.66346
4719_at	YGR289C	25.138824	27.464378	26.352795
4690_at	NGL011W	4.084909	4.314052	2.639977
4823_at	YGR168C	6.6197805	6.6095963	6.104817
4778_at	YGR213C	4.2043605	4.95607	4.2284746
4653_at	NGR056C	5.7107553	5.255192	4.4328847
4652_at	NGR053C	9.20454	16.358618	14.592527
4651_at	NGR052C	9.953325	13.108622	12.473058
4732_at	YGR256W	4.330703	5.1748753	5.216776
4675_at	NGL008W	4.1543717	3.4583397	3.1230159
4668_at	NGR113W	3.9790273	4.024249	4.088363
4968_at	YGR042W	3.2925265	3.6753075	3.722121
4966_at	YGR040W	3.7094767	4.019848	3.7120714
4965_at	YGR039W	2.33514	2.8842008	2.83539
5056_at	YGL051W	3.1085281	2.8864126	2.6980162
4988_at	YGR015C	5.516731	5.0561543	4.8684616
4878_at	YGR133W	3.0990384	4.0886536	5.101346
4872_at	YGR127W	3.1356018	2.9729831	3.391159
4855_at	YGR154C	10.359924	9.342609	8.605234
4969_at	YGR043C	3.3402305	3.5176177	3.5863538
4947_at	YGR066C	3.4455771	2.7373078	3.0703845
4938_at	YGR057C	5.2061253	6.0268407	6.4919686
5762_at	YEL028W	8.454699	8.751492	9.23258
5760_at	YEL030W	4.762628	7.983677	7.86444
5740_at	YEL006W	2.6864147	2.7271733	2.7528417
5787_at	YEL048C	7.7622232	7.2853847	5.799038
5786_f_at	YEL049W	8.239486	6.3981156	5.303102
5696_at	YER041W	4.5113487	3.7244918	3.8722913
5679_at	YER024W	5.57406	6.166491	6.2999296
5654_at	YER081W	2.4018774	2.8761249	2.753871
5771_at	YEL063C	9.673417	12.08626	11.038882
5731_at	YEL016C	2.685846	3.073944	2.6803415
5715_at	YER015W	3.103958	2.9163709	2.1278434
5854_at	NDR002C	8.415779	3.439035	3.1373992

5853_at	NDL006C	2.9745276	2.711833	2.027771
5831_at	NDR001C	2.543458	2.1581924	2.7396398
5929_at	NDL015C	4.845197	5.297357	4.974863
5913_at	YDR534C	3.485867	4.4509516	2.8547673
5810_s_at	YEL074W	4.6036186	4.6198416	4.199269
5809_i_at	YEL074W	13.265511	13.369102	13.241328
5802_at	NDR163W	4.070577	4.1748075	3.4840384
5898_at	NDL035C	14.761943	17.035866	16.10297
5812_at	YEL072W	3.3276925	3.361731	3.6248076
5811_at	YEL073C	7.1813464	5.151154	5.732308
5533_at	YER184C	2.5695255	2.994355	2.8633938
5529_at	YER180C	7.5829153	8.595085	8.962152
5518_at	NER017W	4.850132	5.1763334	4.627124
5536_at	YER187W-A	5.606255	4.696154	6.0798078
5535_at	YER186C	2.9442635	2.8867922	2.8006935
5512_at	NER048C	10.527622	20.28206	18.92244
5509_at	NER004C	12.167509	15.808185	14.640814
5454_at	NER024W	10.496731	9.433462	8.571731
5534_at	YER185W	6.0427833	6.4421153	6.0430765
5515_at	NEL020C	5.704548	6.4124475	6.356096
5514_at	NEL024C	3.716085	4.9049683	4.057367
5636_at	YER065C	3.9162922	4.8792496	4.622053
5632_at	YER101C	2.6338365	2.8565183	2.6873453
5600_at	YER115C	4.757613	4.2098985	4.074821
5649_at	YER076C	5.5696373	5.4828596	5.252862
5638_g_at	YER066W	3.0171084	3.4554782	3.1317863
5588_at	YER103W	3.4225924	3.338494	3.1040938
5544_at	YER150W	2.6213713	1.9999318	2.3370354
5537_at	YER188W	6.5055532	7.0833344	7.69491
5637_at	YER066W	23.78812	23.230963	22.85
5593_at	YER108C	2.551652	2.4017308	2.5326924
9034_at	YNL179C	2.8415163	2.796423	2.3794131
9026_at	YNL142W	2.4651785	3.2994416	3.468004
9025_at	YNL143C	4.1742415	4.430339	4.0525074
9124_at	YNL270C	3.007283	2.3459952	2.7567072
9100_at	YNL249C	4.8818073	5.290351	5.4327683
8925_at	YNL063W	2.2807922	2.0923579	2.1949627
8896_at	YNL046W	4.190559	5.1923823	4.745574
8887_at	YNL008C	2.3454678	2.3763137	2.4391518
9072_at	YNL187W	3.3069866	3.9854012	3.8890433
9010_at	YNL158W	5.68091	7.4558754	6.8230352
8994_at	YNL128W	4.1403847	2.2792308	2.488269
9218_at	NMR016W	4.4149504	0.964288	1.0470308
9201_at	YNL329C	4.2414346	4.7521772	4.2286344
9199_at	YNL331C	5.164171	5.3190804	5.800802
9238_at	NMR023C	3.2915986	3.548314	3.0838253
9237_at	NMR022W	3.0654278	3.9611588	3.116366
9170_at	YNL314W	2.464493	2.2424989	2.356773
9160_at	YNL279W	3.1553755	2.923873	2.9728413
9157_at	YNL282W	3.3126106	3.997358	3.744257
9236_at	NMR020W	4.494971	4.4549127	4.567548
9197_s_at	YNL334C	2.9633086	2.843451	3.3223567
9196_s_at	YNL335W	5.8801928	5.7330766	6.4063463
8723_at	YOL158C	6.462041	9.003889	8.312632

8720_f_at	YOL161C	12.747885	13.84673	14.315962
8719_at	YOL162W	24.476345	21.26923	20.25
8733_at	NNL045W	3.6131697	3.6179972	4.399638
8727_at	YOL153C	3.8890386	4.1825	3.0165386
8716_s_at	YOL165C	6.0442905	7.1473227	7.651192
8710_at	NNL001W	3.5315385	1.9321154	1.9042308
8682_at	YOL106W	3.4404545	3.3162773	3.9985764
8726_at	YOL154W	3.2344203	3.4800525	3.1126976
8718_at	YOL163W	11.671347	8.912885	9.518077
8717_at	YOL164W	9.267432	12.862173	11.538901
8818_at	YNR059W	10.847197	10.9425	10.020962
8817_at	YNR058W	3.8192463	5.3337817	4.557823
8796_at	NNR010W	2.6681468	2.6906095	2.4736652
8884_at	YNL011C	2.6544406	3.700666	3.6122658
8881_at	YNL014W	6.103269	4.845577	4.7759614
8780_at	YNR068C	17.815321	16.20636	17.307434
8759_at	NNL042C	3.4902885	3.4439414	3.583245
8736_at	NNL040W	3.8411539	3.0940385	2.6882691
8846_at	YNL003C	2.5063968	2.7943478	2.8305473
8794_i_at	NNL036W	5.848846	4.418269	5.121923
8786_f_at	YNR076W	7.0291686	8.21046	8.482658
9785_at	NLR134W	2.6172056	2.6056309	2.7561343
9771_at	YML116W	2.8246546	3.0570726	3.2657273
9745_at	YML099C	3.0454354	3.1586602	3.6333761
9807_at	NLR114C	4.773013	3.8510213	3.7359846
9800_s_at	YML133C	3.3434224	5.3242126	3.6157882
9687_at	YML023C	3.9368048	3.8570168	4.4130955
9668_at	YML042W	4.3684635	5.2257934	4.695011
9664_at	YML005W	7.0329437	7.0040183	7.675402
9786_at	NLR135W	2.9072025	3.4655128	3.7454011
9735_at	YML107C	3.5030122	3.377056	3.9468265
9731_at	YML068W	2.2091913	1.7521464	1.9578661
9902_at	YLR411W	2.2197785	1.7555177	2.0872855
9868_at	YLL018C-A	4.2245407	4.431868	4.6572256
9865_f_at	YLR461W	4.564944	4.3122034	4.837469
9987_at	YLR318W	2.7323077	2.7176924	2.1667309
9986_at	YLR317W	3.147894	4.3632975	3.5206566
9849_at	NLR027W	5.9902873	7.3306265	6.980979
9813_at	NLR016C	4.8879304	5.262194	4.9872656
9812_at	NLL005C	3.8446438	4.42939	4.577182
9942_at	YLR363C	5.96131	8.162706	8.574476
9864_at	YLR460C	3.018927	3.41505	3.9328346
9855_at	YLR451W	2.8744946	2.5832431	2.8563313
9371_at	YMR232W	3.3559027	2.9955769	2.9071155
9365_at	YMR271C	4.982482	3.7710378	3.4067025
9333_at	YMR284W	2.3823662	3.179153	2.729443
9452_at	YMR182C	4.4223423	5.5095725	4.3634453
9450_at	YMR180C	4.582076	4.7716393	4.5594883
9281_at	YMR316C-B	7.1126795	8.421955	8.669001
9280_at	NMR017C	3.5075	2.7782693	2.7061539
9271_at	NMR015C	4.2994704	1.0890378	1.2522644
9379_at	YMR240C	2.9470713	5.5673394	6.1678996
9299_at	NML006C	5.9451923	8.426154	6.3409615
9290_f_at	YMR325W	3.0373	3.187184	3.3760335

9600_at	YMR023C	3.3651109	3.4992628	3.9918878
9595_at	YMR065W	8.933065	8.056365	8.561047
9553_at	YMR068W	3.225278	3.90822	4.162257
9642_at	YMR020W	3.44039	3.1032677	4.1474237
9621_at	YML002W	7.4250517	6.72062	6.8214655
9482_g_at	YMR169C	3.3071964	2.6469955	2.5570605
9481_at	YMR169C	10.076185	10.232116	10.458654
9480_at	YMR168C	4.1271286	3.4446154	3.5226922
9618_at	YMR040W	2.9827602	3.5607028	2.9314487
9532_at	YMR090W	2.6733794	3.0364904	2.76899
9510_at	YMR114C	4.0204287	4.664231	3.8986537
7923_at	YPL147W	3.178937	3.3900795	3.233669
7922_at	YPL148C	5.4092426	5.7851615	6.305384
7921_at	YPL149W	2.9706655	3.3448007	3.416123
8019_s_at	YPL277C	3.4257693	2.8311539	2.6482692
8014_at	YPL236C	3.5229855	4.4500117	3.902183
7840_at	YPL095C	3.9405856	3.409285	4.2162833
7825_at	YPL064C	3.304411	3.4907956	3.8877277
7823_at	YPL066W	2.6579397	2.1173027	1.9634387
7990_at	YPL214C	3.2687309	2.6849153	3.1337953
7906_at	YPL164C	6.0467496	5.030769	5.8617306
7847_at	YPL088W	4.0228634	3.7660294	3.7842314
8076_at	NOL055C	2.8788462	2.748077	2.3428845
8066_at	NOR069C	5.4343386	4.8574376	5.0789046
8044_at	NOR052W	7.055195	6.471539	6.9929304
8106_at	NOR005W	4.8194947	2.7594075	3.3988142
8099_at	NOL052C	2.5315385	2.4048076	1.9661539
8037_at	YPL258C	13.349421	12.400873	13.900747
8031_at	YPL264C	3.2175648	2.7220798	2.329689
8023_at	YPL272C	5.7200227	7.145611	5.805823
8078_at	NOL053C	2.3003845	2.2038462	2.3303847
8042_at	NOR038W	4.460636	4.5654087	4.8617916
8038_at	YPL257W	3.4007692	3.1651921	3.6598077
7549_g_at	YPR196W	3.660909	3.3956678	3.904416
7548_at	YPR196W	6.2659616	3.8332694	4.4663463
7546_at	YPR194C	7.0640507	11.321786	11.532639
7607_at	YPR121W	6.189401	7.3080244	7.16201
7566_at	YPR168W	3.8349967	3.0917656	3.394084
7509_at	NPL009C	2.5524962	2.0777807	2.449711
7505_at	NPR089C	17.808462	14.665577	13.135769
5589_at	YER104W	2.8211727	3.3215384	3.4571154
7552_at	YPR199C	2.7478883	2.628349	2.6191702
7545_at	YPR193C	6.070577	4.1342306	4.5898075
7518_at	NPL007W	2.8514993	2.6519275	2.7331514
7776_at	YPL022W	4.40329	3.9611502	3.6061049
7764_at	YPR012W	4.8598666	5.258335	4.3634024
7757_at	YPR005C	4.7736726	3.9394765	3.973565
7818_at	YPL071C	6.2825994	4.018401	4.528231
7809_at	YPL034W	6.730958	7.3294	7.2796187
7688_at	YPR068C	3.189423	2.5651922	2.4969232
7677_at	YPR057W	2.5984936	2.5048997	2.3349469
7661_at	YPR085C	6.329947	6.391609	6.8425336
7796_at	YPL047W	3.5393696	4.006095	4.0952373
7750_at	YPL003W	2.2766685	2.6463957	2.209303

7690_at	YPR070W	5.024893	3.942079	5.256199
8437_at	YOR100C	4.568077	3.261923	3.7367306
8420_at	YOR128C	42.16234	41.655167	53.707813
8412_at	YOR120W	3.9287965	6.2671347	5.530083
8499_at	YOR072W	6.342885	5.292885	4.9259615
8490_at	YOR062C	2.4759803	1.8520886	1.8401743
8395_at	YOR148C	3.4370704	4.8358755	4.4197254
8382_at	YOR180C	3.0973077	2.8376925	2.0690384
8360_at	YOR203W	25.26879	31.256939	31.106045
8487_at	YOR059C	5.226944	3.6711826	4.575668
8409_at	YOR162C	3.4801874	2.7603402	3.5976892
8399_at	YOR152C	3.5594635	5.28286	4.4670177
8566_at	YOR005C	5.92319	5.673422	7.086504
8561_at	YOL001W	2.2809827	1.7607348	2.0899029
8553_at	YOL009C	2.995304	3.35297	3.6764462
8676_at	YOL112W	3.3243961	3.9227896	3.8217678
8609_at	YOL043C	3.830919	3.5726926	3.6987453
8537_at	YOR019W	8.153306	10.33577	10.726924
8530_g_at	YOR012W	3.047942	3.5321798	4.4360247
8526_at	YOR009W	12.919624	16.90369	14.772586
8596_at	YOL055C	7.9669037	7.8053517	7.911649
8548_at	YOL014W	2.8891692	2.341104	2.884457
8547_at	YOL015W	10.970196	7.419423	8.601346
8176_at	YOR377W	3.9997969	3.8144474	3.9327722
8162_at	YOR363C	2.966145	2.9228787	2.7737894
8153_at	NOL046W	5.198908	4.300844	4.4688044
8202_at	YOR358W	2.6546984	2.7014189	2.6056352
8180_at	YOR381W	14.417	11.862109	15.092659
8131_at	NOR006W	16.03611	14.777402	15.082811
8120_at	NOL039W	3.7290034	3.5087857	2.9659698
8112_at	NOL056C	6.2238507	7.4240975	7.6682267
8179_at	YOR380W	3.338848	3.634267	3.9168332
8144_g_at	YOR389W	5.315943	7.846659	8.630915
8143_at	YOR389W	4.3857327	4.1242733	4.711966
8334_at	YOR222W	2.9333868	2.521855	3.1956537
8260_at	YOR284W	4.0286417	2.654461	2.6735148
8254_at	YOR278W	2.2663255	2.0462987	2.1313784
8359_at	YOR202W	22.914553	24.083324	25.497198
8349_f_at	YOR192C	3.47767	3.6788445	3.685388
8236_at	YOR302W	4.985522	6.8127284	5.725745
8218_at	YOR328W	3.2816103	3.534288	3.6701083
8209_at	YOR319W	3.7869542	3.7559297	5.2238417
8348_i_at	YOR192C	4.3883395	3.8722892	4.162165
8239_at	YOR304C-A	2.6170945	2.888876	2.7654798
3150_at	gAL01	5.7573338	3.90789	3.8534412
10494_at	YKR069W	3.4245448	3.5417268	3.7155044
10485_at	YKR104W	8.008507	6.9844813	8.013485
3153_at	gAL01	3.6162496	2.3667016	2.665666
10532_at	YKR061W	8.651375	11.869127	11.314667
10559_at	YKL005C	2.4172754	2.8696566	2.6365166
3148_s_at	YCR096C	5.5544114	5.781563	5.0227013
3137_s_at	YILWTY3-1	6.4563346	3.514423	3.4400249
3136_s_at	YIL082W-A	9.815074	3.5844545	3.399692
10470_at	YKR091W	2.8437886	2.4308562	2.6470828

10478_at	YKR097W	6.0199633	6.1802864	6.4093304
3258_f_at	YGLWDELTA4	4.396253	4.677372	4.5214067
10455_at	NKL044C	3.0573077	3.0732694	3.0996156
3196_f_at	YHLWTAU1	5.860038	4.155909	4.185339
10483_at	YKR102W	5.3765645	5.4846454	6.1158123
3232_f_at	YGRCTAU3	5.0720615	4.1135826	4.0613294
3214_at	YGRWDELTA23	15.993909	13.936923	12.566539
3162_at	YHRWTAU3	3.1918056	2.6807692	3.4098077
10590_at	YKL017C	3.3152013	2.236558	2.628481
10596_at	YKL011C	4.046652	2.6731231	2.3287208
10581_at	YKL026C	9.187492	8.318369	10.075066
2999_at	gKR07	4.125769	3.0938463	3.3146152
10686_at	YKL098W	3.5812187	4.634467	4.28591
10696_at	YKL132C	3.556957	3.0625024	3.9787161
2929_at	gKR09	4.545491	5.871346	6.106731
10649_at	YKL090W	2.57241	2.1934001	2.2171547
2924_g_at	gKR08	4.8609614	4.569231	5.641346
3099_at	gAR04	6.768382	3.521864	5.503539
3098_at	gAR04	5.563322	4.1436734	5.397214
3105_g_at	gAR04	7.007916	6.446495	7.2122183
3101_at	gAR04	4.221973	1.7653122	2.364808
3033_s_at	gJR15	2.6945202	2.7335649	2.5555115
3025_s_at	gJR14	3.4582505	1.8587587	3.0995264
10572_at	YKR009C	3.9472585	4.322236	4.5285583
3038_at	gKL01	2.470997	1.9722267	2.500007
3000_at	gKR07	3.8542309	4.1684613	3.4415383
3553_f_at	YPLCTAU1	7.3795724	3.5300267	3.397156
10412_f_at	YLL064C	9.917419	10.280634	11.803933
3555_s_at	YHL009W-B	9.664545	4.191346	4.919039
3554_f_at	YPLCTY4-1	5.6489067	3.2194502	3.4525309
10416_at	YLL060C	5.4971795	5.764335	6.664872
3475_f_at	YDLWTAU1	6.9903274	5.062113	5.091422
3541_at	YPRWTAU4	10.887806	10.314396	10.917548
10413_at	YLL063C	12.151535	9.033206	10.211161
10432_at	NKL034C	11.742768	11.882126	12.959112
3617_f_at	YORWTAU2	5.303036	4.102225	4.037815
3584_f_at	YPLCDELTA1	3.7853847	4.641731	6.089039
3626_i_at	YNR075W	5.643365	7.6063433	6.612838
3624_at	YNRCDELTA9	4.579358	4.968302	4.4869776
3573_f_at	YORWTAU3	2.9891515	2.8324842	2.494711
3558_f_at	YPLCTAU2	5.448983	2.952451	3.338879
10405_at	NKR003W	14.736773	16.3676	14.544903
10411_f_at	YLL065W	2.9824655	2.2260795	2.2937894
3556_s_at	YHL009W-B	12.726406	5.6494393	6.1752567
3325_f_at	YDR543C	2.7140636	3.0009317	2.6099634
3324_at	YERWOMEGA2	4.228316	5.4421344	5.536056
3336_f_at	YERCTAU2	6.057438	4.4583097	4.497665
3326_at	YFL063W	4.002308	3.6182692	4.6251926
3301_f_at	YGLWTAU1	7.389177	4.505167	4.520541
3264_f_at	YGLWDELTA6	4.5906434	4.5500264	4.2677073
10445_s_at	YKL201C	2.2976985	3.3001244	3.0298195
3306_i_at	YGLWDELTA4	5.462158	7.3004885	7.469792
10451_at	NKL028W	5.5768924	5.752281	6.064449
10437_at	NKL011C	22.258654	26.171997	24.269272

3445_f_at	YDRCSIGMA1	4.0669193	3.9106736	3.835246
10433_at	NKL033C	9.995384	6.4509616	6.5878844
10434_at	NKL031C	2.8312244	2.943737	2.835708
3346_at	YERCTAU3	6.811952	8.100676	7.486696
3344_f_at	YERCDELTA15	4.2255187	4.311954	4.298586
3403_f_at	YDR542W	14.0126095	24.173628	26.074242
3374_at	YERWDELTA9	4.9627438	2.8637433	2.7616065
3343_i_at	YERCDELTA15	4.419159	4.9986887	5.515558
11384_at	YAL064W	6.0876923	2.7021155	3.6434615
11379_at	YAL067C	4.9501925	5.984231	7.667115
11386_at	YAL062W	2.7295938	1.5912116	2.0208948
11385_s_at	YAL063C	7.5374417	10.612318	9.471906
10901_at	YJR108W	5.9701924	4.1640387	4.5865383
10965_at	YJR036C	3.364038	2.79713	2.8670363
11372_at	YAL037W	9.722686	6.952115	7.703269
11353_at	YAL014C	2.597233	2.7400289	2.8999453
10968_at	YJR039W	3.9565911	3.7171779	3.4632246
10857_at	YJR155W	6.5376377	7.2443705	7.7176385
11398_s_at	gHR06	9.019808	6.847692	7.134616
11412_at	gIL01	3.2001922	2.375577	3.8576922
11403_at	gHR07	6.2819576	3.3259747	3.631814
11395_at	gHR06	3.8268328	4.207393	4.668975
10865_at	YJR025C	4.1145287	5.4419317	6.5133123
10861_s_at	YJR159W	2.908103	3.0259356	2.826231
11397_f_at	gHR06	7.865769	6.1809616	4.6386538
11394_at	gHR06	3.064065	4.722928	5.087165
11195_at	YJL185C	2.7156162	4.0656343	4.836403
11176_at	YJL162C	2.602167	2.2065384	2.2198076
11026_at	YJR004C	10.462604	7.0120664	6.8504295
11030_at	YJR008W	3.1463008	2.8714027	3.0575051
11137_at	YJL110C	7.367482	13.364622	12.877399
11044_at	YJL023C	7.3455772	4.493269	5.103846
11169_at	YJL126W	2.8600707	2.4943366	2.6969657
11141_at	YJL106W	9.150133	7.7569237	8.817885
11100_at	YJL057C	7.0281267	5.613951	8.543424
11279_s_at	NAL010C	7.5833435	7.040817	7.5929155
11259_at	YJL213W	9.7497	8.891188	12.5057
11288_at	YAR023C	4.014694	2.5974948	3.2637067
11287_f_at	YAR020C	3.6979585	4.15924	4.946378
11251_s_at	YJL221C	4.6768007	3.5993826	4.826466
11250_s_at	YJL222W	7.533069	5.646652	7.542765
11017_at	YJL004C	2.5832436	2.851045	2.7909405
11256_at	YJL216C	2.981731	2.6334615	2.6871152
11249_f_at	YJL223C	28.756773	39.78817	45.748566
2714_s_at	gNL01	2.709763	2.8742642	2.6400824
2698_s_at	gOL01	11.0937195	8.838143	7.4827466
10811_at	NJR015C	14.287064	14.715315	15.255878
2729_at	gNL04	3.291686	2.519182	2.5839891
10812_s_at	NJR023C	8.471584	9.449778	8.152688
2552_at	gPL07	4.4467306	3.0501924	4.0667305
2693_at	gOL01	13.562884	10.5988455	11.2325
2692_at	gOL01	6.022625	3.653338	4.134801
10813_s_at	NJR024C	9.705769	9.086924	8.161923
10775_at	YKL188C	9.568478	8.336744	8.850487

2922_at	gKR08	6.8526216	6.315951	6.641877
10758_at	YKL161C	5.026509	4.209594	4.632245
2923_at	gKR08	10.795754	8.670063	10.194228
2822_at	gMR05	8.2588	9.225912	9.641272
10790_at	YKL222C	5.8928795	6.763242	5.5860047
2921_at	gKR08	3.315666	2.019703	2.1502132
2920_at	gKR08	2.867317	2.673193	2.5365505
10792_at	YKL220C	12.083847	12.646153	12.602307
10854_at	YJR152W	10.618717	9.730002	10.879717
2251_at	gGL01	11.12947	11.218226	11.846666
10851_at	YJR149W	3.3776646	4.924652	5.5182714
10853_at	YJR151C	5.599121	6.8294377	6.6918273
2213_at	gGR08	3.8546152	4.5115385	4.879808
2210_s_at	gGR07	3.1329842	5.710161	4.053064
2233_at	gFL01	4.6104407	6.465443	4.1017942
2232_at	gFL01	4.63148	4.620192	3.3043637
11436_s_at	gIR04	3.0651922	3.0159614	3.365
2436_g_at	gCL01	8.956905	10.624065	12.718858
2408_at	gDL01	5.3193383	4.0323253	4.260291
10814_s_at	NJR027W	10.010916	10.157952	10.757947
10819_at	NJL004C	4.5809965	4.257286	4.360548
10830_at	NJR006C	3.466346	3.9401922	4.165192
10831_s_at	NJR021C	4.83896	5.282302	4.7338705
2407_at	gDL01	4.4484234	4.5665154	4.3822517
10827_s_at	NJR025C	8.373428	17.838167	16.597687
4204_at	YIL107C	2.8028994	3.1078699	2.651586
10197_at	YLR123C	3.4253848	2.9115384	2.6551924
4237_at	YIL165C	9.589611	9.030119	8.949254
4236_at	YIL120W	4.0840387	3.6119232	4.7469234
10202_at	YLR128W	3.1011958	1.539501	1.8347704
10216_at	YLR097C	4.0113535	4.6847835	5.0020866
10199_at	YLR125W	3.4234617	2.4673076	2.3892307
4184_s_at	YIL080W	7.3483324	5.0120635	4.078386
10217_at	YLR098C	7.1308084	6.855105	8.473588
10186_s_at	YLR156W	5.6739197	5.4904056	5.0036097
4270_f_at	NHR031C	4.6121154	3.6630769	3.4330769
4280_f_at	YIL176C	18.899937	35.29737	35.728756
10182_at	YLR152C	2.581882	3.1371717	2.9617252
10190_at	YLR165C	7.0916924	6.9702992	6.999025
10195_at	YLR122C	8.382884	7.259038	7.223077
10189_at	YLR164W	5.0978045	6.0567307	6.133846
4269_f_at	NHR030W	3.4331362	3.5976605	3.5220425
4238_at	YIL164C	16.338425	20.712864	21.455036
4068_at	YIR032C	4.1130433	5.3830113	5.5826044
4067_at	YIR031C	11.504376	12.028196	13.271347
4076_f_at	YIR041W	6.5390844	3.8362577	3.6996446
4075_at	YIR039C	6.6628323	8.137316	7.782175
10288_at	YLR036C	2.425364	2.580283	2.566417
4032_f_at	YIR043C	3.6012585	4.389635	3.939491
4065_at	YIR029W	9.157692	7.4338465	7.8198075
4056_at	YIR020C	10.370388	11.9951935	10.163373
10289_f_at	YLR037C	4.609707	3.6424668	3.33599
4143_at	YIL028W	4.8690386	3.630577	3.3588462
4117_at	YIL009C-A	3.8728948	3.567474	3.693345

10249_at	YLR085C	2.4553661	2.301504	2.6143398
4158_at	YIL059C	3.8299234	3.6686587	3.7736816
4088_at	YIR007W	2.371712	2.3896718	2.1960669
4078_i_at	YIR043C	12.5131645	17.557158	16.360596
4116_at	YIL009C-A	3.079657	3.090053	3.2475896
10283_at	YLR031W	4.4435315	4.1067224	4.4363456
4568_at	YHL040C	10.319216	8.737311	7.004096
4566_at	YHL042W	6.2696157	5.257885	5.465
10067_at	YLR263W	4.1870174	5.1778746	4.475827
4571_at	YHL037C	6.25	6.238846	5.4171157
4546_at	YHL016C	7.0235486	9.473461	7.913269
10080_at	YLR233C	14.028461	10.4675	14.037308
4563_f_at	YHL046C	5.116142	6.1545424	5.74064
4562_at	YHL047C	10.608754	9.949444	9.677552
4534_at	YHR015W	3.5266562	4.1266704	3.996957
4627_at	NGR043C	3.8617947	4.2601676	4.5201254
4626_at	NGR042W	3.3199778	2.9805236	3.4729176
8237_at	YOR303W	3.8326766	5.540056	5.562236
10030_at	YLR315W	2.9598076	2.8740385	2.6971154
4609_at	NGR104C	5.4524717	4.2657156	4.5312223
10048_at	YLR288C	3.849172	3.525041	4.008644
4622_at	NGL018W	3.6185784	3.9897652	3.9973307
4613_at	NGL042W	5.1606436	5.426886	5.057127
4573_at	YHL035C	5.621089	5.698182	5.290563
4313_at	YHR199C	3.016147	3.1847148	3.1344676
4308_at	NHR009C	4.1609616	3.7015386	4.292885
4322_at	YHR210C	3.6043816	3.22455	2.93493
4317_at	YHR204W	2.8308477	3.1482253	3.1715493
10154_at	YLR174W	5.7432013	9.640562	8.929142
4284_at	YIL167W	6.743846	5.359231	5.234231
4307_f_at	NHL006C	2.3376923	2.1621153	2.2175
4305_at	NHL007C	22.187057	38.080612	39.05976
4077_at	YIR042C	7.406142	10.13434	10.3633585
4362_at	YHR157W	5.895705	6.1984615	6.367116
10099_at	YLR251W	7.8498735	13.699138	11.344681
4400_at	YHR150W	6.174873	5.2896156	9.294423
4378_at	YHR129C	2.2496073	2.0342116	2.204417
4340_at	YHR180W	3.000669	3.3088033	3.5358756
4324_s_at	YHR218W	2.3726516	6.219946	3.9544125
10100_at	YLR252W	3.701492	4.091672	3.6669614
4361_at	YHR156C	2.8514905	3.320769	3.1192307
10119_at	YLR227C	10.619907	9.843441	9.907245
10361_f_at	YLL025W	6.6541357	3.82741	5.8894534
3789_s_at	YLL067C	6.143397	18.973482	12.488731
3790_s_at	YLL067C	3.1712308	4.425666	3.9773288
3791_s_at	YLL067C	3.1916962	4.978077	3.0236537
3693_f_at	YMRWDELTA21	4.236555	4.4235687	3.8120296
3719_s_at	YLR410W-B	2.303659	4.258949	2.6365757
3730_at	YLRDELTA27	4.4711657	6.5521626	5.938957
10372_at	YLL016W	3.095	3.6486537	3.4849997
3887_f_at	YJLWTAU1	5.5299664	4.1664133	4.0521364
3895_s_at	YJL113W	9.916618	5.141765	4.68264
3899_s_at	YJLWTY4-1	8.502501	3.9984615	4.401346
3900_f_at	YJLWTY4-1	4.44829	3.4920583	3.2285278

3828_f_at	YKRCDELTA11	4.478554	3.1823268	2.9030013
10353_at	YLL033W	3.0955355	2.937444	2.6000028
3851_s_at	YJR161C	2.2256188	2.7548316	2.4485393
3876_at	YJLWTAU4	8.739573	9.3902235	8.925409
3631_s_at	YOLWTAU1	6.5566983	7.1221657	7.154405
3650_f_at	YNLWTAU1	10.87031	8.693214	9.338965
3661_at	YNLWSIGMA2	3.7142885	2.861061	2.797062
3663_f_at	YNLWTAU2	6.5346913	4.898074	4.83058
10832_s_at	NJR026C	4.021612	4.5740337	4.2308836
10379_at	YLL051C	2.7533374	3.1880684	3.2026327
3629_f_at	YNR077C	3.107945	3.9728062	3.9725041
10378_at	YLL052C	4.102997	6.147501	6.4605417
3684_f_at	YMRWTAU2	5.7373953	4.044425	3.9802132
3686_f_at	YMRCDDELTA18	6.0711536	5.3442307	5.4028845
3691_f_at	YMRCTAU3	4.479216	3.6624534	3.0689895
10373_at	YLL057C	7.761154	7.956731	8.771731
3670_f_at	YNRCTAU3	5.383869	5.032483	4.9518776
10375_at	YLL055W	4.5397406	7.237727	6.288057
3683_f_at	YMRWDELTA16	5.1726923	5.3411536	3.9996152
10374_at	YLL056C	6.6338806	7.7562385	7.9377003
3953_at	2mic_D_protein	5.1290455	8.082602	2.333776
4020_at	NIR005C	4.350809	4.3989906	4.5136313
10298_at	YLR046C	5.289423	4.8398075	5.0175
10312_at	YLR016C	4.640505	4.1480007	4.9764023
10306_at	YLR010C	9.395966	8.941154	9.718846
4019_at	NIR004C	6.544588	9.3165865	9.161802
4015_at	NIL007W	4.91727	3.9577057	4.2513103
3901_f_at	YJLWTAU2	5.449157	3.9249432	3.8167505
10567_at	YKR004C	2.9955559	4.3190494	4.466515
10090_at	YLR242C	2.4273841	3.0967903	2.71031
9545_at	YMR103C	2.1673782	2.1143997	1.9366739
10868_at	NJL020C	2.5692196	1.3386297	1.782725
10071_at	YLR266C	3.0995054	3.6019828	3.7878141
8870_at	YNL025C	2.5246377	1.5910337	1.7746085
8422_at	YOR130C	2.2833838	1.3931819	2.1705215
10862_s_at	YJR160C	2.2809615	2.1192307	1.9786539
10619_at	YKL033W-A	2.2621217	2.4443786	2.5516503
10522_at	YKR050W	2.2144437	2.722305	2.8057938
9861_at	YLR457C	2.702037	2.7183647	2.7923536
9574_at	YMR087W	2.6232343	2.3690524	2.6679313
9332_at	YMR283C	2.709888	2.9531586	3.3922336
9198_s_at	YNL333W	2.287293	2.2171297	2.353638
8304_at	YOR238W	2.1724494	2.4355168	2.6559327
11043_at	YJL024C	2.6611538	1.9188461	3.0751925
10389_at	YLL042C	2.5954702	2.5427916	2.557622
9962_at	YLR381W	2.23239	1.86292	1.8292696
10043_at	YLR284C	3.0909176	2.9050698	2.9960847
8832_at	YNR029C	1.9283501	1.5437729	1.7822256
8249_at	YOR313C	3.2108078	2.779423	2.645
8240_at	YOR305W	2.2984543	2.7376132	2.9234228
10396_at	NKR006C	3.5056896	2.8525734	2.711526
9260_at	NMR007C	2.8734615	3.06	2.270577
9254_at	NMR069W	3.765603	3.8287144	3.9909515
10998_at	YJR021C	10.14902	10.122851	13.2387495

9873_at	YLR426W	1.8841932	1.1792107	1.4494597
9215_at	NMR001W	2.5945814	2.9422135	2.6273985
8795_r_at	NNL036W	2.7616515	2.5138006	2.5876434
10377_at	YLL053C	3.3332067	3.7974637	4.8542714
9929_at	YLR394W	3.0705369	3.7970967	3.8863502
9538_at	YMR096W	2.0912027	2.1690264	2.1497147
10568_at	YKR005C	2.0567489	1.8208394	1.9112642
10575_at	YKR012C	5.1017313	3.781923	4.815192
9526_at	YMR127C	3.001842	3.999981	4.358052
8629_at	YOL068C	2.2549324	2.667121	2.9669142
10346_at	YLR004C	2.374493	2.6070786	2.5877407
9446_at	YMR176W	2.6879292	2.4385118	2.1486926
10196_g_at	YLR122C	5.0781627	3.2532587	3.3234973
8639_at	YOL104C	3.4052942	1.6086538	2.8017309
8909_at	YNL032W	2.2330625	1.9203088	2.2882857
9073_at	YNL230C	3.429315	3.7473974	3.3082607
9095_at	YNL254C	2.4198914	2.1607692	2.2048078
10340_at	YLL003W	2.2611027	2.0618184	2.3381178
9438_at	YMR211W	2.1888962	2.4877353	2.5530205
10211_at	YLR137W	2.045631	1.9264592	1.9857965
10263_at	YLR054C	2.3504815	2.622951	3.1807418
10484_at	YKR103W	2.4791873	2.0716763	2.3591874
10789_f_at	YKL224C	2.6626458	3.338731	3.1948621
8681_at	YOL107W	4.7900214	5.428106	6.1313944
8680_at	YOL108C	3.1404068	2.607234	2.7258892
9423_at	YMR196W	2.2412887	2.2568135	2.3675847
8704_at	YOL130W	2.1499374	2.5110855	2.4852977
10776_at	YKL187C	3.304875	3.2652717	4.089815
9344_at	YMR294W	2.627982	3.4584427	3.377668
10625_at	YKL071W	3.268381	2.6561067	1.8339425
8492_at	YOR064C	2.222514	1.9214678	2.0690875
10855_at	YJR153W	2.112184	2.2330368	3.0095124
9137_at	YNL257C	2.5676405	2.376746	2.334078
9818_at	NLR116W	2.57	2.2246153	1.9090385
10858_s_at	YJR156C	4.342391	6.049616	7.1024995
9908_at	YLR417W	2.6202765	3.9570189	4.6385736
9356_at	YMR262W	2.2171626	2.0884924	2.5705113
9488_at	YMR135C	2.6683154	3.349561	3.3114192
8544_at	YOR026W	2.3066459	2.258585	2.5003262
9594_at	YMR064W	2.3495426	3.019059	2.9963992
9451_at	YMR181C	2.8890972	3.3575246	2.6715374
10447_s_at	YKL198C	2.9187508	3.3911796	3.3699627
10153_at	YLR173W	2.3897288	2.4796154	2.8640385
9373_at	YMR234W	2.5900595	2.5376983	2.5177774
10724_at	YKL149C	2.4049094	2.762503	2.66615
6012_at	YDR453C	2.1994424	2.364914	2.205527
6018_at	YDR459C	1.9631082	2.5690699	2.4905133
5892_at	NDR005C	2.3508232	2.2496154	2.9253845
6122_at	YDR336W	3.1382806	2.949615	3.306422
6193_at	YDR273W	2.7898076	1.8848077	2.625
6217_at	YDR252W	2.611197	2.876275	2.72428
5968_at	YDR499W	2.061362	1.9486974	1.9269743
6054_at	YDR403W	2.301154	1.6138461	1.9059615
5767_at	YEL023C	2.5178847	2.9578843	2.5873077

3904_f_at	YJLWDELTA2	4.533967	4.964704	5.1451864
5772_at	YEL062W	2.286091	2.2370207	2.0372865
4009_at	NIL022W	3.1826007	3.429389	3.026235
3834_s_at	YLL067C	6.7931366	12.216923	7.59077
5862_at	NDR077C	2.4654884	2.814787	2.5359716
6088_at	YDR391C	2.7315254	3.3127007	3.391874
3907_f_at	YAL068C	5.0117345	6.5134473	6.838214
3853_f_at	YJR162C	3.9557536	3.5607548	3.5648575
6677_at	YDL187C	2.596923	2.1103847	1.9338461
3506_s_at	YBLWTAU1	2.4600577	2.394386	2.1613793
3453_at	YCR007C	2.3719668	2.7890384	2.5390387
6469_at	YDR008C	2.7476535	2.2616458	2.8269784
3448_s_at	YDRCSIGMA2	2.8541205	2.768804	2.7328115
6746_at	NCR024W	3.962493	3.6155624	4.861392
3310_s_at	YERWDELTA18	2.2487707	3.9665463	2.3546724
3510_s_at	YBLWDELTA8	2.8614626	3.1306589	2.8381588
6712_at	YDL241W	2.931137	2.4617405	2.56757
3627_r_at	YNR075W	3.169078	4.540677	4.3395324
6389_at	YDR109C	1.9109082	2.7099004	2.5141187
6394_at	YDR070C	2.2466187	1.9047165	1.8990974
3843_at	YJLWDELTA16	2.3491662	2.481047	2.4107277
6263_at	YDR206W	4.532161	4.004888	4.5468283
3583_i_at	YPLCDELTA1	3.3024738	2.7666972	3.3823528
6466_at	YDR005C	2.5820327	2.603238	2.413052
6714_at	YDL239C	3.7780507	4.43017	4.1206326
6434_at	YDR065W	2.0864103	2.7835994	2.102022
4997_at	YGR024C	2.1373324	2.3900762	2.3261387
4358_at	YHR153C	2.5329728	2.511346	2.0796154
5181_at	YGL154C	2.162304	2.6532567	2.5282829
4959_at	YGR032W	2.4307249	2.2038834	2.2684958
4448_at	YHR067W	2.6820765	3.1847935	2.941303
5284_at	NFL008W	2.5756836	2.9117634	2.7940502
5291_at	NFR001W	2.554751	2.073438	2.4898648
5347_at	YFR005C	2.243123	3.0393074	3.020146
4989_at	YGR016W	2.3150861	1.781923	1.5578847
4290_at	NHR027C	2.328092	2.8428845	2.7830768
4595_at	NGR114C	2.5380094	1.9505076	1.6442608
4582_at	YHL026C	3.1215396	3.7690601	3.7046957
4649_r_at	NGR051C	2.5179	1.9219866	2.2222917
4717_at	YGR287C	2.4365926	2.1167302	1.9664832
4945_at	YGR064W	2.4078407	2.5313299	2.2852583
4951_at	YGR070W	2.5203195	2.6815286	2.047959
5266_at	YGL247W	2.3326604	2.8685994	2.939497
4718_at	YGR288W	2.1188712	2.0383835	2.2032518
4782_at	YGR216C	2.4187145	2.6816626	3.2141507
4090_at	YIR009W	2.7625408	2.6753767	2.803874
5601_at	YER116C	2.823381	2.1978836	2.4804676
4162_at	YIL055C	1.9837248	2.5223536	1.7860587
4148_at	YIL071C	2.3870776	1.7821153	1.8653847
5683_at	YER028C	5.8013463	6.4298077	7.7249994
6464_at	YDR003W	2.2726946	2.3137124	2.3466277
4112_at	YIL013C	2.1091151	2.5627794	2.1152897
4037_at	YIL071C	3.5722203	4.010577	3.236923
5440_at	NER031W	2.0404744	2.1666226	2.0463595

4195_at	YIL116W	2.2418864	2.5728025	2.4609075
4788_at	YGR222W	2.0927436	1.6586014	1.9104022
4263_at	NHR013C	4.0073075	3.7984614	3.5725
4177_at	YIL089W	3.4178393	4.046897	5.1501036
4024_at	NIL021C	2.3203845	2.2653847	2.0526924
4255_at	YIL146C	2.5857172	3.9893978	3.53239
5468_at	NEL017W	2.3753963	2.5780435	2.6490917
5474_at	NER029C	2.6845942	1.75407	1.8249772
7711_at	YPR046W	2.0431755	1.759265	1.7374887
7733_at	YPR026W	2.4611495	2.1467304	1.9220802
2306_at	gER06	2.7174866	2.1960385	2.3551974
2395_at	gCR03	2.5442584	2.2054963	2.3131995
2307_at	gER06	2.0323906	2.8296113	1.9469173
7765_at	YPR013C	2.8794231	1.4725	1.4748077
11399_s_at	gHR06	2.516905	2.6609817	2.5309787
7892_at	YPL133C	2.5273852	2.0029497	1.8842896
7691_at	YPR071W	2.7283316	2.7097158	2.6768506
7751_at	YPL002C	2.1402328	1.4531171	1.4579753
2615_s_at	gPL04	2.2642345	1.8765169	2.757422
2445_s_at	gCR02	2.989035	3.5581822	3.6729789
7469_at	NPR012W	2.1888523	1.7876925	1.6375002
7596_at	YPR153W	2.877308	2.8392308	2.5882692
7686_at	YPR066W	2.4419231	2.4426923	3.1257694
2253_s_at	gGL01	6.1783824	10.143	11.037127
2631_s_at	gOR03	2.6792078	2.4521852	3.9592798
2437_s_at	gCL01	3.6650639	5.5979433	6.7191563
8165_at	YOR366W	2.4105768	2.0901923	1.9646153
11242_f_at	NAR009W	2.1670578	0.318524	1.8601224
11321_at	YAL002W	2.3366423	2.3855505	2.8186219
11302_at	YAR053W	2.5670965	1.9500277	2.2068098
11109_at	YJL093C	2.4578135	2.75235	3.1178074
11099_at	YJL058C	2.7216284	2.9360862	3.1345758
8528_at	YOR011W	2.58804	3.200601	3.504107
11266_f_at	YAL069W	3.6281376	6.2993073	6.061816
7919_at	YPL151C	2.405879	2.121559	2.2681909
7928_at	YPL186C	1.9311742	1.883842	1.6514788
7567_at	YPR169W	2.1055176	1.9688985	2.0955203
7903_at	YPL167C	2.397725	2.5013702	2.443926
11339_at	YAL028W	2.9100084	3.2961633	3.5413322
8064_at	NOR060C	3.4615383	2.8619232	3.4934614
8208_at	YOR318C	3.6794484	2.7988286	2.9644132
7914_at	YPL156C	2.415059	2.4058068	2.4998498
7971_at	YPL233W	2.328702	2.5773618	2.002582
3149_at	gAL01	3.1475558	2.6625078	2.2155738
7042_at	NBL024W	2.375635	1.7664368	1.9950647
3154_at	gAL01	2.583032	1.2239559	1.4623678
6965_i_at	NBR036W	3.4138465	2.9844232	2.9428847
7076_at	YBR056W-A	2.5446014	2.4907484	2.5495732
7079_at	YBR259W	1.9923985	1.961852	1.7240384
6980_at	NBR016C	3.4540386	3.6525002	4.576154
7057_at	YBR284W	4.0434294	3.649394	3.8873682
6875_at	YCL004W	2.2698078	2.709423	2.3001924
6921_at	YCL056C	2.806755	2.4954023	2.7652872
6798_f_at	YCR104W	2.7552369	2.5295343	2.6779761

6800_at	YCR106W	2.7927055	2.2213032	2.3136463
3187_s_at	YHL050C	2.8829894	5.1949105	3.2277126
6962_at	NBR033C	2.4496155	1.4430768	1.7253846
6939_g_at	SCIIYLEFT	4.8022547	4.295976	3.2335055
7315_at	YBR047W	2.266594	1.9889334	2.4217808
7323_at	YBR055C	2.1742475	1.6168696	2.2995224
7236_at	YBR145W	2.3356209	1.7733933	1.7085226
7243_at	YBR107C	2.2444181	2.4353118	2.8711534
2772_at	gMR09	2.8879857	2.3310664	2.1735232
7453_at	YBL088C	3.0008695	2.6038861	2.7214837
11377_at	YAL034C	3.3253098	2.1377249	1.8872979
7286_at	YBR063C	2.1756718	2.4117813	2.4028203
2858_at	gLR12	3.1703033	2.3022487	2.7820344
3204_at	YHRCDELTA4	3.2743213	3.9812381	4.0020742
7096_at	YBR278W	3.0270627	1.8418844	1.929995
7194_at	YBR148W	2.136923	1.5701922	2.3163462
2927_s_at	gKR08	2.3718915	2.3084846	2.9624248
7102_at	YBR237W	2.5199065	1.9618607	1.9355197
7170_at	YBR168W	3.0850768	3.0909615	2.911923
7183_at	YBR182C	3.7968185	5.534012	7.122263
10784_at	SNR37	0.45651278	0.3166361	0.33979815
5897_at	NDL036C	2.4991696	2.3160253	2.8174353
5676_at	YER060w-A	1.916446	1.7408861	1.7407544
4224_at	YIL132C	2.1425748	1.8094364	1.8677084
5478_i_at	NER049C	3.3370137	5.342732	4.7178626
7544_at	YPR192W	1.9802909	2.1392717	1.1861978
3255_at	YGRCDDELTA20	3.6732829	3.33884	4.072415
3113_s_at	gJL01	2.830021	3.3896356	2.4021175
2987_at	gKR05	0.80729747	0.37260112	0.31315947
6021_f_at	YDR461W	0.46134663	0.3258681	0.340352
7610_at	YPR124W	0.6785976	0.378619	0.54757154
6950_at	SNR56	0.58532155	0.28586552	0.281213
3752_f_at	YLRCDELTA19	0.818228	0.2436341	0.5861143
5820_at	NDR166C	0.6019999	0.39985374	0.43788612
3570_f_at	YPRWDELTA17	0.7129718	0.36065483	0.3846042
10872_at	NJL013C	0.5401195	0.16707675	0.17957053
11243_s_at	NAR011W	1.8109066	0.18074697	1.7543749
11244_s_at	NAR012W	1.9067016	0.22016975	1.9028757
8775_at	NNL073W	0.4899508	0.30228978	0.25332323
8062_at	SNR8	0.628435	0.30147937	0.2964023
8059_at	SNR36	0.6995129	0.45789796	0.40596345
4385_at	YHR136C	0.5023953	0.49033576	0.5015418
4698_at	NGL010C	0.8355232	0.4348253	0.43013754
4605_s_at	SNR39b	0.6317495	0.4393793	0.4082365
9000_at	YNL122C	0.70844734	0.46142256	0.4643157
6056_at	YDR405W	0.83097684	0.49126732	0.61012304
6047_at	YDR440W	0.53763556	0.3914199	0.53935045
7047_at	NBR047W	0.6219964	0.454062	0.5378041
8115_f_at	NOR009W	0.547904	0.48377457	0.47181183
5444_at	NER038W	0.6982628	0.5258924	0.6651387
8728_at	YOL152W	0.6845937	0.43947414	0.628053
7329_at	YBR016W	0.6866393	0.46821278	0.55238277
3862_f_at	TR(UCU)J1	0.47784996	0.45631284	0.4548394
2336_at	gDR14	0.7741386	0.5341839	0.8738189

2449_s_at	gBL03	0.8924488	0.46600854	0.6208914
2465_s_at	gBL05	0.78339887	0.49393827	0.60537
2561_at	gPL09	0.61704195	0.32162285	0.42141286
10409_at	SNR69	0.8831816	0.36296716	0.33437532
10110_at	YLR218C	0.66466624	0.47208065	0.50705963
10905_at	YJR112W	0.6652265	0.50199044	0.5200734
11405_at	gHR08	1.6631473	0.32386678	2.233708
3598_f_at	TR(ACG)O	0.7571543	0.32102963	0.24468467
2800_at	gML01	1.0645524	0.49379066	0.64387
2884_g_at	gLR05	0.9129653	0.44871005	0.6355508
3372_f_at	TH(GUG)E1	1.1209943	0.47211093	0.5658818
3418_f_at	TS(AGA)D2	0.8874563	0.49294806	0.59181535
5101_at	YGL096W	1.9416152	3.129759	2.9229813
4844_at	YGR144W	2.1895556	2.661062	2.699772
5013_at	YGL004C	1.7543241	3.236135	3.2132177
8529_at	YOR012W	2.1072438	2.7955768	2.4607534
5749_at	YEL041W	2.5476923	2.9903846	2.4386537
4275_at	NHR008W	2.028764	2.271941	1.9309744
4211_at	YIL099W	1.9666461	2.5017486	1.8169369
4214_at	YIL097W	2.4973867	3.0187404	2.2100532
4286_s_at	YHR077C	1.471777	18.923447	1.7310764
4082_at	YIR001C	1.6535517	2.0933807	1.8925737
4079_at	YIL003W	2.0834303	2.445065	2.134304
4101_at	YIL024C	1.7610188	2.5999296	2.401434
4100_at	YIR019C	2.6801789	5.276972	4.493788
4633_at	NGL039C	2.4258819	2.9145424	2.862821
8724_at	YOL155C	1.345213	3.118769	1.774004
8725_g_at	YOL155C	2.0644612	5.744607	3.2446969
4692_f_at	NGR003C	1.843919	2.6741192	1.8399051
8752_f_at	NNL025C	1.9390962	2.8771768	2.0523825
4458_at	YHR078W	1.566397	4.214808	1.4121633
4383_at	YHR134W	2.1497772	3.4670787	3.7043447
4683_at	NGR097C	1.7727113	2.3267174	2.2165391
7149_at	YBR193C	2.3393395	3.3525934	3.9867425
6909_at	YCL018W	2.1726809	3.4716928	3.60255
6805_at	YCR063W	4.895672	7.499768	7.6762834
7513_f_at	NPR041W	1.97932	2.597726	2.047492
5993_at	YDR479C	2.2241914	2.5211504	2.263419
6222_at	YDR257C	1.8997667	2.256842	1.9252094
8448_at	YOR111W	2.0388615	2.1697907	2.3231053
6195_at	YDR275W	2.7720451	4.0553336	4.2610846
5769_at	YEL065W	1.8916794	2.7749114	2.2441602
11170_at	YJL168C	1.8843445	7.128147	5.1622305
10999_at	YJR021C	2.5940385	3.1961536	3.5540383
2211_s_at	gGR07	2.0124002	3.03043	2.6951692
2420_s_at	gDL02	2.599996	5.7282724	4.2448835
10751_at	YKL168C	2.570441	2.7324278	2.7258346
10908_at	YJR115W	6.6958475	4.8309264	8.019114
10809_g_at	NJR008W	2.2476943	2.9214916	3.1853232
10795_at	YKL217W	1.9217308	3.392692	1.6667308
8930_at	YNL057W	2.7563062	4.170044	3.0954072
3735_f_at	YLR466W	1.9828756	2.4974031	2.2892141
8997_at	YNL125C	1.8789158	2.3849814	2.191246
9976_at	YLR352W	2.040889	2.5582287	2.2530637

3997_at	Q0180	1.4114664	2.6401708	2.0074148
4018_at	NIR003C	3.6591296	4.021581	5.1554365
4045_s_at	YIL066C	4.8526926	4.827692	5.761154
10021_at	YLR306W	3.4747696	3.3783605	4.020038
4030_at	NIR002W	2.1477933	2.4321275	2.316307
8797_f_at	NNL062W	1.882839	3.43313	2.1258662
2958_at	gLR04	3.6651583	6.1590486	6.138831
9145_at	YNL294C	2.8195348	3.612428	3.6026635
9104_at	YNL245C	2.0262272	3.540577	2.2788463
9871_at	NLR018W	2.293712	3.454001	3.9072793
2776_at	gMR10	2.399598	4.202959	4.9323006
2918_s_at	gKR07	2.9816792	2.6276731	2.9281883
9914_at	YLR423C	2.0223215	3.4791284	2.643836
2459_at	gBL05	2.6914928	3.024978	2.8326354
9226_at	NMR053W	2.0986254	3.0039377	2.578251
9967_at	YLR343W	1.7909782	2.5760937	2.5336776
2535_s_at	gPL05	1.3344542	2.417284	2.8094556
9989_at	YLR320W	1.5754987	2.4474845	2.2906163
9788_at	NLR139W	2.154611	3.445308	2.9915996
9757_at	YML128C	2.1549926	2.770064	2.5612848
8074_s_at	NOR086C	1.5677955	2.5066192	1.7713108
9204_at	YNL326C	1.5313619	2.252397	2.0085394
9224_at	NMR047C	1.7664125	2.082278	1.755885
8551_at	YOL011W	2.2147858	2.642687	2.343918
8576_at	YOL031C	1.2555183	2.2512827	1.8172591
8579_at	YOL028C	1.7826409	2.9997652	2.7684228
8564_at	YOR003W	2.0660112	2.4853904	2.3544593
9133_at	YNL261W	1.8568192	1.9912586	1.7173141
8510_at	YOR037W	1.7747986	2.189397	2.2775207
8501_at	YOR075W	1.4102544	2.2884197	1.9539685
9313_at	YMR306W	3.1916778	2.3790898	1.7612648
8907_s_at	YNL034W	3.1503847	2.6317499	2.3944585
8774_at	NNL005C	1.8617765	2.367173	2.2461472
8777_at	YNR065C	1.9101832	2.4868412	2.4334197
8886_at	YNL009W	2.187097	3.2244608	3.104579
8906_at	YNL035C	2.4724033	3.8306603	3.928764
9111_at	YNL237W	1.817889	2.1249893	1.3305217
8669_at	YOL119C	1.594067	2.2434697	2.1550066
8962_at	YNL114C	1.6726373	3.7238116	3.657065
8722_at	YOL159C	1.9834667	2.3256547	1.8047087
9573_at	YMR086C-A	2.100594	2.2123382	1.8924644
8308_at	YOR242C	1.7966385	2.803057	2.5248735
9706_at	YML050W	2.4080694	2.913669	3.6162753
9701_at	YML055W	1.9156604	2.7571597	2.6253963
8102_at	NOL020W	2.1166377	2.1706278	2.5736513
9746_at	YML098W	2.1645124	2.5975032	2.8643894
9582_at	YMR052C-A	2.4705074	2.1422086	1.96342
8396_at	YOR149C	2.0521662	2.566104	2.088711
9401_at	YMR219W	1.7547839	2.0424385	2.0583668
8498_at	YOR071C	1.868363	2.9732823	2.7705827
9334_at	YMR285C	1.7928573	2.2540977	2.5419178
8456_at	YOR119C	1.4971532	2.5197914	2.2242117
8461_at	YOR080W	1.9153376	2.270365	1.7363614
8938_at	YNL094W	2.2634606	3.1658664	2.816896

9466_at	YMR155W	1.7591405	2.12608	1.6316456
8381_at	YOR179C	2.4198556	3.724027	3.329472
2807_at	gML02	1.717576	2.7643151	1.7912683
2572_s_at	gPL10	2.1505673	2.222652	2.35568
11217_at	YJL209W	1.9820416	2.2880769	1.9823077
11390_at	YAL058W	1.4485463	1.9677072	2.2088916
11409_f_at	gHR08	1.4364638	2.724735	1.8024962
3762_s_at	YLR410W-A	1.7967098	2.806926	2.0270987
3737_s_at	YLR467W	1.7919662	2.161923	1.5709616
3746_at	YLRWDELTA15	1.9018393	2.2506824	2.066551
3958_r_at	Q0225	1.9150742	6.45115	6.384775
3994_at	Q0155	1.103871	3.5546715	2.3855073
3852_f_at	YJR161C	1.7690734	2.2374852	2.0549324
3939_at	YBR006W	2.2376785	2.677446	2.5088167
3036_at	gKL01	1.5714307	2.2038238	2.3837962
3079_s_at	gJR10	1.8179653	3.6452825	4.049814
3032_at	gJR15	3.8976922	2.7182693	2.3796155
3471_f_at	YDL248W	2.191312	3.298924	2.6988404
3543_s_at	YBL112C	1.8462746	2.362743	2.062162
3183_f_at	YIL177C	2.146916	2.440817	2.38601
10339_at	YLL004W	1.9487766	2.7628193	2.8332503
10393_at	YLL038C	2.0978808	2.9437797	3.06331
10287_at	YLR035C	2.056465	2.250622	2.4778361
10307_at	YLR011W	2.2670193	2.7325706	3.147575
10466_at	YKR087C	1.8969988	2.197755	2.054356
10404_at	NKR002C	1.7039502	2.9436617	2.422606
10446_s_at	YKL199C	1.899468	2.0269604	2.0542412
10093_at	YLR245C	2.0233545	2.5824237	2.0893917
10095_at	YLR247C	2.7173178	4.889016	4.652807
10103_at	YLR211C	1.9318938	2.4733331	2.576734
10116_at	YLR224W	2.0390277	2.1823678	1.8821108
10060_at	YLR258W	2.0883148	2.477825	2.4437344
10078_at	YLR273C	3.0899389	3.965501	3.7221522
10204_at	YLR130C	2.2652247	2.3815973	2.5353768
10174_at	YLR144C	1.8880973	2.079173	2.1305878
10179_at	YLR149C	1.9788811	2.2585433	2.020979
10962_at	YJR078W	2.1628132	2.4044232	2.5557692
11025_at	YJR003C	2.1334121	2.172289	2.8718777
10875_at	YJR127C	1.8328402	2.2311053	2.2154958
10900_at	YJR107W	2.0037737	2.3323858	2.4405508
10939_at	YJR100C	2.0311916	2.0068023	2.149994
3402_at	YDRWDELTA31	2.4111037	3.1151874	2.7020807
11051_at	YJL017W	1.7508875	2.2382693	1.9975
11069_at	YJL044C	1.9526608	3.8744845	3.719266
10602_at	YKL050C	1.8521327	2.3054607	2.3515186
10539_at	YKR022C	3.0016994	2.04564	1.9044693
10544_at	YKR027W	1.9221103	2.3019476	2.3641481
10828_at	NJR001W	2.1803074	2.1792667	2.432146
10842_at	NJR016W	1.9712691	1.9914147	2.1777987
10635_at	YKL061W	1.500762	2.0279408	1.7701678
6702_at	YDL206W	1.8600909	2.742189	2.5626829
6483_at	YDL024C	1.5844101	3.0223012	2.9797502
6629_at	YDL146W	1.8086231	2.2845533	1.8455317
6941_s_at	SCIIYLEFT	1.3620517	2.199108	1.6145862

6761_at	YCR068W	2.2471154	2.6684616	2.268269
6862_at	YCR028C	1.9824789	2.4256926	2.2637234
6262_at	YDR205W	1.4483832	2.2237568	2.2149246
6135_at	YDR349C	1.8218424	2.2699628	2.337227
6165_at	YDR291W	2.126666	2.2444327	2.243722
6228_at	YDR263C	2.090805	2.8647447	2.9449737
6358_at	YDR123C	2.3486247	2.7628846	2.1523077
6416_at	YDR047W	1.9910185	2.3257	2.0999963
7657_at	YPR081C	2.005243	2.2837248	2.2303467
7506_at	NPL013C	1.3499671	2.1109686	1.8807777
7510_at	NPL005W	2.1649451	2.6880035	2.6651204
7728_at	YPR021C	2.1173139	2.4087555	2.0095742
7745_at	YPL008W	2.0194192	2.7836607	2.7861135
7780_at	YPL018W	2.1123	2.2376924	1.7069231
7817_at	YPL072W	2.587896	2.4934902	1.8805108
7064_at	YBR291C	2.1274736	2.0160139	2.182841
7297_at	YBR074W	1.6254506	2.3611038	1.6107821
7322_at	YBR054W	2.0242639	3.9430585	2.5465248
7333_at	YBR020W	2.3581145	2.8076923	3.039423
7252_at	YBR116C	1.9471631	2.6465492	2.482348
4862_at	YGR161C	2.2381086	2.068764	2.0750904
4908_at	YGR117C	1.9589806	2.2999485	2.3897977
4735_at	YGR259C	2.1178749	2.4083798	2.0459507
4746_at	YGR270W	1.8227838	2.1355824	1.9558324
5020_at	YGR003W	2.0305276	2.3760595	2.3893783
5099_at	YGL098W	1.4473865	1.9484916	1.834502
4954_at	YGR073C	1.6045763	2.1764975	2.5383859
4955_at	YGR074W	1.797876	2.2097278	1.9077233
4285_at	YIL166C	2.9824622	4.2990074	3.1630423
4338_at	YHR178W	1.5935216	2.2263558	2.2219524
10743_at	YKL176C	1.9851508	2.6833708	2.4507551
4064_at	YIR028W	1.4434603	2.1925857	1.2824273
4095_at	YIR014W	1.1624095	1.9929075	1.5142466
4477_at	YHR048W	2.0986066	2.4292247	2.317801
4545_at	YHL017W	1.6805878	3.3294215	3.0805628
4576_at	YHL032C	1.7661605	2.0080526	1.915592
4587_at	NGR069W	2.1287782	2.165	2.133846
4417_at	YHR123W	1.5634829	2.1491401	1.9235705
4431_at	YHR095W	1.8611538	2.4548078	2.7271152
4452_at	YHR071W	1.731472	2.1748157	2.0178995
5920_at	YDR541C	2.2972932	2.8347452	2.9768324
5981_at	YDR467C	1.8869605	2.0314057	1.272861
5793_at	NDR076W	2.2441456	2.2068055	1.9235506
5799_at	NDR129W	1.776082	2.6112463	1.8861002
6112_at	YDR370C	1.8354263	2.1728003	2.3720841
6005_at	YDR444W	1.734795	2.153492	2.1254416
6045_at	YDR438W	2.028228	2.2852883	2.1975832
5471_at	NEL006W	0.9311667	1.9399945	1.3501817
5479_r_at	NER049C	3.4481244	6.1270437	5.8587675
5214_at	YGL211W	1.6346753	2.2268765	2.1390276
5256_at	YGL257C	1.5428141	2.6345778	2.2201679
5319_at	NFL007C	1.2240819	2.423801	1.4414877
5741_at	YEL005C	2.2667198	2.3694232	2.268077
5765_at	YEL025C	1.9283104	2.5558863	2.2775617

5778_at	YEL057C	1.8809124	2.3527179	1.4567792
5521_at	YER173W	2.1852627	3.4718156	3.3984585
3952_at	2mic_REP1	1.2215406	1.3305352	0.4010437
5231_at	YGL237C	0.80383706	0.47077042	0.38463694
2257_at	gGL02	0.51870495	0.40896899	0.40134695
7142_at	YBR232C	0.6716163	0.6271995	0.4949823
10334_at	YLL009C	0.56562155	0.50211763	0.45380962
7499_at	NPR009C	0.8793951	0.52318525	0.41759235
3806_s_at	RDN37-1	0.48425967	0.79334474	0.51315415
3435_f_at	YDRWDELTA7	0.7252232	0.6896924	0.5043656
4952_at	YGR071C	1.0809087	1.2246544	3.0420597
9343_at	YMR293C	1.8129777	1.8292793	2.2645018
7831_at	YPL058C	1.9034038	2.4583683	2.7292204
2275_g_at	gEL01	1.7013462	3.5955768	3.6799998
2274_at	gEL01	2.5432692	1.9371153	2.4017308
10418_at	YLL058W	2.0773523	2.5828269	3.0975754
11152_g_at	YJL142C	1.5161451	1.4506984	4.312846
11153_at	YJL141C	1.7779619	1.3573743	6.421432
10124_at	YLR189C	1.8371093	2.1562085	2.1774428
9134_at	YNL260C	2.3105702	1.9912872	2.3100138
9546_at	YMR104C	1.9411174	2.709423	2.4107695
8701_at	YOL133W	2.2316597	2.032077	2.2370808
8889_at	YNL006W	1.8768111	1.9880664	2.1131222
8816_at	YNR057C	2.2559955	3.2313483	2.534099
5742_at	YEL004W	1.8328032	2.2192626	2.4443579
4876_at	YGR131W	2.052646	1.9149292	2.244238
4924_at	YGR088W	1.8797345	2.21042	2.244513
4556_at	YHL006C	2.1419232	1.8034616	2.1828847
4413_at	YHR120W	1.718722	1.9498361	2.1021895
11307_s_at	YAR066W	2.338025	1.0423452	2.780007
7887_at	YPL138C	1.8514335	1.8646088	2.1657162
7988_at	YPL216W	2.0980794	1.7128808	1.9653009
11402_at	gHR07	2.2557693	1.6676924	2.104423
7724_at	YPR017C	1.5922785	1.9185756	2.2129219
11247_s_at	YJL225C	1.6815779	1.9079182	2.3547492
11177_at	YJL161W	2.2913442	1.9669063	2.4461784
3114_s_at	gJL01	1.9820753	2.4031942	2.105883
7115_at	YBR250W	2.426923	1.7994231	2.873846
2491_s_at	gPL11	1.8792946	2.0303702	2.2644775
2382_s_at	gDR07	1.7061539	3.525577	3.8284616
4884_i_at	YGR138C	0.7173109	0.63897204	0.44256866
4686_s_at	NGR106C	0.6665154	0.51217246	0.4160185
5775_at	YEL059C-A	1.0230995	0.858718	0.18352933
4920_at	YGR084C	0.6857021	0.5933495	0.51981086
2434_at	gCL01	0.6778183	0.5245859	0.35171944
5807_at	SNR13	0.6389349	0.49876353	0.47194296
9799_at	SNR34	0.8923764	0.75879145	0.4871049
7942_at	YPL173W	0.6342019	0.5600816	0.5101425
7380_f_at	YBL026W	1.0899789	0.5665685	0.50728106
3793_f_at	YLLCDELTA1	0.65385103	0.52850735	0.4267212
3142_f_at	YILCDELTA3	0.6353793	0.4971055	0.43718433
3551_f_at	YPLCDELTA10	0.6036757	0.47566184	0.5613897
3954_at	2mic_REP2	0.9622934	1.271763	0.41211608
3809_s_at	RDN37-1	0.6217721	0.80301905	0.45580667

3537_f_at	TA(AGC)P	0.5736447	0.46121204	0.35140413
2679_at	gNR09	0.9318316	0.42799056	0.46984875
8694_at	YOL140W	2.3932595	2.3382459	2.9045913
2560_at	gPL09	6.751154	5.2357693	11.064038
10981_at	YJR052W	2.4517195	1.8262335	2.5813673
8641_at	YOL102C	1.7971975	1.5991343	1.9942684
10889_at	YJR141W	1.7558267	1.6825336	2.112508
9939_at	YLR404W	1.519706	1.9353893	2.298569
8559_at	YOL003C	1.613009	1.6201543	1.9222791
8546_at	YOR028C	1.6686398	2.101704	2.1613421
8508_at	YOR035C	1.6674622	2.7788088	2.853525
9107_at	YNL242W	1.931752	1.8904378	2.3746428
10310_at	YLR014C	1.5502893	1.6978319	2.1794114
9458_at	YMR187C	1.1500939	2.6930451	2.6704648
9052_at	YNL206C	1.6527185	1.8475269	2.5817795
9324_at	YMR316W	1.6232853	1.9276378	2.3443897
9391_at	YMR252C	1.6970624	2.2211082	2.25229
9675_at	YML034W	1.4758456	3.7885714	3.020771
9645_at	YML019W	1.4458058	1.9528198	1.9961274
9702_at	YML054C	1.5538969	1.8698962	1.985389
10524_at	YKR052C	1.7209475	2.520152	2.6276462
10779_at	YKL184W	1.6061485	2.125148	2.0872083
10536_at	YKR019C	2.1622908	2.0506303	2.5874033
9619_at	YMR041C	1.9815701	2.8148603	2.6739883
5987_at	YDR473C	2.0149999	2.3530557	2.084918
5706_at	YER007W	1.9235063	1.9268459	2.2356079
5725_at	YEL020C	1.3504927	1.6662037	1.8985717
3647_f_at	YNL337W	2.2080505	2.4469516	2.3851638
6482_at	YDL025C	1.9385273	3.08175	2.9575138
6388_at	YDR108W	1.629286	1.7973719	2.004941
6562_at	YDL080C	1.9845979	1.8434781	2.0632834
4812_at	YGR202C	1.4838238	1.5314404	2.2912467
4521_at	YHR004C	1.8339387	2.5604732	2.7352376
4416_at	YHR123W	1.5093979	2.5327902	2.1933224
5555_at	YER162C	1.7018572	2.2718148	2.4014716
11326_at	YAR003W	1.9233713	2.9280448	2.8221393
11284_f_at	NAR002C	1.996647	2.0759196	2.09352
7553_at	YPR200C	1.5140917	2.2342033	2.4486237
7555_s_at	YPL075W	1.7250354	2.0955675	2.1763778
10917_at	YJR124C	1.3829685	1.912682	2.0843048
11232_at	YJL194W	1.2729026	2.6015868	2.886896
8145_s_at	YOR390W	1.408252	3.2329676	2.5146675
11047_at	YJL020C	0.8465832	3.332225	2.5922174
2638_s_at	gOR04	1.5202974	3.202513	2.9684412
2637_g_at	gOR04	1.089193	2.426336	2.0915504
7263_at	YBR085W	2.048441	1.7456224	2.1657975
2252_g_at	gGL01	1.8749009	1.9703717	1.9710987
11426_s_at	gIL02	1.7429903	2.3427072	2.1820347
7126_at	YBR216C	2.0332422	2.3380141	2.9736218
7092_at	YBR274W	1.8596463	1.8009307	1.9614868
2342_s_at	gDR14	1.364393	3.4447532	2.7147474

YDR281C hypothetical protein
YDR512C questionable ORF
YHL028W Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC
YMR058W multicopper oxidase
YMR080C putative helicase
YDL039C questionable ORF
YIL119C inhibitor of ras
non-annotated SAGE orf Found forward in NC_001148 between 880290 and 880439 with 100% identit
YDL038C similarity to mucin proteins
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_00
non-annotated SAGE orf Found forward in NC_001144 between 451607 and 451783 with 100% identit
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_00
TA(AGC)L tRNA-Ala
TR(UCU)J2 tRNA-Arg
TR(ACG)K tRNA-Arg
non-annotated SAGE orf Found forward in NC_001136 between 1385570 and 1385815 with 100% ider
YFL014W 12 kDa heat shock protein
TR(UCU)M1 tRNA-Arg
YDL215C NAD-dependent glutamate dehydrogenase
YDL197C Anti-silencing protein that causes depression of silent loci when overexpressed
YDL170W zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
YDL231C hypothetical protein
YDL243C Hypothetical aryl-alcohol dehydrogenase
YDL123W similarity to hypothetical protein YJL151c
YDL109C strong similarity to thiamine-repressed protein Thi4p
YDL204W similarity to hypothetical protein YDR233c
YDL154W MutS homolog involved in chromosome exchange
YDL115C hypothetical protein
YCR098C permease involved in the uptake of glycerophosphoinositol (GroPIs)
YCR089W predicted GPI-anchored cell wall protein
non-annotated SAGE orf Found forward in NC_001135 between 157511 and 157669 with 100% identit
YCR102C Alcohol dehydrogenase
YCR100C strong similarity to Pep1p
non-annotated SAGE orf Found forward in NC_001135 between 125368 and 125520 with 100% identit
non-annotated SAGE orf Found reverse in NC_001135 between 9263 and 9469 with 100% identity. Se
YDL223C weak similarity to mucin
YCR099C strong similarity to Pep1p
YCR020W-B high-temperature lethal
non-annotated SAGE orf Found reverse in NC_001135 between 168999 and 169175 with 100% identit
YDR285W Synaptonemal complex protein, component of the central element
YDR318W Involved in minichromosome maintenance
YDR332W similarity to E.coli hypothetical protein and weak similarity to RNA helicase MSS116 / YDR11
YDR242W putative amidase
YDR236C similarity to hypothetical A. thaliana protein
YDR406W probable multidrug resistance transporter
YDR421W hypothetical protein
YDR530C 5',5'''-P-1,P-4-tetraphosphate phosphorylase II
YDR265W C3HC4 zinc-binding integral peroxisomal membrane protein
YDR364C Member of the beta transducin family
YDR387C similarity to Itr1p and Itr2p and E.coli araE
YDR022C cik1 suppressor
YDR082W Involved in telomere length regulation, may be functional in telomere metabolism during late
YDR078C Preferential Use of Neither donor locus during mating type switching.

YDR019C glycine cleavage T protein (T subunit of glycine decarboxylase complex
YDR007W n-(5'-phosphoribosyl)-anthranilate isomerase
YDR126W similarity to hypothetical protein YLR246w and YOL003c
YDR147W Ethanolamine Kinase
YDR160W Ssy1p controls expression of several transporter genes, including BAP2, TAT1, PTR2 and Y
YDR004W RecA homolog (similar to DMC1, RAD51, and RAD55), interacts with Rad 55p by two-hybrid
YDR073W component of SWI/SNF global transcription activator complex
YDR131C similarity to hypothetical protein YJL149w
YBR197C weak similarity to hypothetical protein YPL077c
YBR228W similarity to hypothetical A.thaliana protein
YBR223C hypothetical protein
YBR163W hypothetical protein
YBR184W alpha-galactosidase
YBR244W Probable glutathione peroxidase (EC 1.11.1.9)
YBR270C Probable ATP/GTP-binding protein
YBR085C-A hypothetical protein
YBR208C Urea amidolyase (contains urea carboxylase and allophanate hydrolase)
YBR217W autophagy
YBR253W transcription factor, part of SrbV/Mediator complex
YBL075C heat-inducible cytosolic member of the 70 kDa heat shock protein family
YBL019W AP endonuclease
YBL025W Upstream activation factor subunit
non-annotated SAGE orf Found forward in NC_001148 between 297125 and 297292 with 100% identity
YBL109W similarity to subtelomeric encoded proteins
YBR018C galactose-1-phosphate uridyl transferase
YBR050C Possible regulatory subunit for the PP1 family protein phosphatase Glc7p
YBR043C similarity to benomyl/methotrexate resistance protein
YBL060W hypothetical protein
YBR008C Major Facilitator Transporter
YBR030W involved in inositol biosynthesis
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_00
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_00
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_00
non-annotated SAGE orf Found forward in NC_001134 between 555545 and 555691 with 100% identity
YCL067C Mating type protein alpha-2
YCL010C strong similarity to Saccharomyces pastorianus hypothetical protein LgYCL010c
YCR020C Transcription regulator
YCR037C May collaborate with Pho86p and Pho84p in inorganic phosphate uptake; protein contains 1
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_00
YCL016C hypothetical protein
YCL039W regulatory protein
YBR295W Putative P-type Cu(2+)-transporting ATPase
YBR293W Probable multidrug resistance protein
non-annotated SAGE orf Found forward in NC_001134 between 172044 and 172202 with 100% identity
YBR301W YKL224 c homolog
YBR298C maltose permease
non-annotated SAGE orf Found reverse in NC_001134 between 159883 and 160056 with 100% identity
non-annotated SAGE orf Found reverse in NC_001134 between 593218 and 593355 with 100% identity
non-annotated SAGE orf Found forward in NC_001134 between 555685 and 555879 with 100% identity
YBR297W Maltose fermentation regulatory protein
non-annotated SAGE orf Found reverse in NC_001134 between 554862 and 555011 with 100% identity
non-annotated SAGE orf Found reverse in NC_001134 between 554862 and 555011 with 100% identity
YGL256W alcohol dehydrogenase isoenzyme IV
YGL259W GPI-anchored aspartic protease

YGL261C strong similarity to members of the Srp1/Tip1 family
YGL243W tRNA-specific adenosine deaminase 1 (TAD1); Tad1p/VscADAT1
YGL251C C4 zinc finger DNA-binding protein of low sequence specificity in vitro; Probable 119 kD DN
YGL156W vacuolar alpha mannosidase
YGL128C weak similarity to rat cysteine string protein
YGL063W pseudouridine synthase 2
YGL254W putative transcription factor, has five zinc fingers
YGL223C weak similarity to Clostridium regulatory protein
YGL193C questionable ORF
YFL055W Amino acid permease
YFL057C strong similarity to aryl-alcohol dehydrogenases
YFL020C member of the seripauperin protein/gene family (see Gene_class PAU)
non-annotated SAGE orf Found forward in NC_001137 between 284585 and 284719 with 100% identit
YFL050C ALuminium Resistance 2
YFR020W hypothetical protein
YFR026C hypothetical protein
non-annotated SAGE orf Found reverse in NC_001138 between 5806 and 6033 with 100% identity. Se
YFL054C similarity to channel proteins
YFL027C weak similarity to P.falciparum Pfmdr2 protein
YFR022W similarity to Rod1p
YGR294W strong similarity to members of the Srp1p/Tip1p family
YGR289C alpha-glucoside transporter
non-annotated SAGE orf Found forward in NC_001139 between 363944 and 364078 with 100% identit
YGR168C hypothetical protein
YGR213C involved in 7-amincholesterol resistance
non-annotated SAGE orf Found reverse in NC_001139 between 708217 and 708372 with 100% identit
non-annotated SAGE orf Found reverse in NC_001139 between 707915 and 708058 with 100% identit
non-annotated SAGE orf Found reverse in NC_001139 between 707583 and 707720 with 100% identit
YGR256W 6-phosphogluconate dehydrogenase
non-annotated SAGE orf Found forward in NC_001139 between 384772 and 384945 with 100% identit
non-annotated SAGE orf Found forward in NC_001139 between 974544 and 974699 with 100% identit
YGR042W hypothetical protein
YGR040W MAP protein kinase homolog involved in pheromone signal transduction
YGR039W questionable ORF
YGL051W strong similarity to YAR033w protein
YGR015C similarity to hypothetical protein YGR031w
YGR133W Member of ubiquitin-conjugating protein family
YGR127W weak similarity to mouse T10 protein
YGR154C strong similarity to hypothetical proteins YKR076w and YMR251w
YGR043C strong similarity to transaldolase
YGR066C similarity to hypothetical protein YBR105c
YGR057C Required for amino acid permease transport from the Golgi to the cell surface
YEL028W hypothetical protein
YEL030W ExtraCellular Mutant
YEL006W similarity to peroxisomal membrane and mitochondrial carrier proteins
YEL048C hypothetical protein
YEL049W member of the seripauperin protein/gene family (see Gene_class PAU)
YER041W weak similarity to DNA repair protein Rad2p and Dsh1p
YER024W similarity to carnitine O-acetyltransferase Yat1p
YER081W strong similarity to phosphoglycerate dehydrogenases
YEL063C arginine permease
YEL016C similarity to human nucleotide pyrophosphatase
YER015W Acyl-CoA synthetase (fatty acid activator 2)
non-annotated SAGE orf Found reverse in NC_001136 between 471227 and 471388 with 100% identit

non-annotated SAGE orf Found reverse in NC_001136 between 386539 and 386772 with 100% identity
non-annotated SAGE orf Found reverse in NC_001136 between 463178 and 463426 with 100% identity
non-annotated SAGE orf Found reverse in NC_001136 between 340810 and 340977 with 100% identity
YDR534C similarity to YOR383c, Sta1p and pig mucin
YEL074W similarity to subtelomeric encoded proteins
YEL074W similarity to subtelomeric encoded proteins
non-annotated SAGE orf Found forward in NC_001136 between 1362215 and 1362352 with 100% identity
non-annotated SAGE orf Found reverse in NC_001136 between 104660 and 104806 with 100% identity
YEL072W hypothetical protein
YEL073C similarity to YJR108w
YER184C similarity to multidrug resistance proteins Pdr3p and Pdr1p
YER180C Meiosis-specific protein required for spore formation
non-annotated SAGE orf Found forward in NC_001137 between 251443 and 251697 with 100% identity
YER187W-A similarity to killer toxin KHS precursor
YER186C weak similarity to hypothetical protein YMR316w
non-annotated SAGE orf Found reverse in NC_001137 between 550562 and 550699 with 100% identity
non-annotated SAGE orf Found reverse in NC_001137 between 187315 and 187524 with 100% identity
non-annotated SAGE orf Found forward in NC_001137 between 289637 and 289906 with 100% identity
YER185W strong similarity to Rtm1p
non-annotated SAGE orf Found reverse in NC_001137 between 64206 and 64373 with 100% identity.
non-annotated SAGE orf Found reverse in NC_001137 between 31419 and 31562 with 100% identity.
YER065C isocitrate lyase
YER101C Protein involved in targeting of plasma membrane [H⁺]ATPase
YER115C sporulation-specific protein
YER076C similarity to killer toxin Khr1p
YER066W strong similarity to cell division control protein Cdc4p
YER103W member of 70 kDa heat shock protein family
YER150W strong similarity to putative cell surface glycoprotein Sed1p
YER188W hypothetical protein
YER066W strong similarity to cell division control protein Cdc4p
YER108C putative transcriptional activator of FLO1
YNL179C hypothetical protein
YNL142W Ammonia transport protein
YNL143C hypothetical protein
YNL270C Protein highly homologous to permeases Can1p and Lyp1p for basic amino acids
YNL249C similarity to YDR109c
YNL063W weak similarity to Mycoplasma protoporphyrinogen oxidase
YNL046W hypothetical protein
YNL008C similarity to YMR119w
YNL187W hypothetical protein
YNL158W hypothetical protein
YNL128W Similar to human tumor suppressor gene known as TEP1, MMAC1 and PTEN1. Contains se
non-annotated SAGE orf Found forward in NC_001145 between 426559 and 426696 with 100% identity
YNL329C Member of the AAA-protein family that includes NSFp and PEX1p
YNL331C Hypothetical aryl-alcohol dehydrogenase
non-annotated SAGE orf Found reverse in NC_001145 between 465281 and 465418 with 100% identity
non-annotated SAGE orf Found forward in NC_001145 between 465271 and 465411 with 100% identity
YNL314W positive regulator of allophanate inducible genes
YNL279W hypothetical protein
YNL282W involved in processing of tRNAs and rRNAs
non-annotated SAGE orf Found forward in NC_001145 between 434355 and 434564 with 100% identity
YNL334C SNZ2 proximal ORF, stationary phase induced gene
YNL335W similarity to M. verrucaria cyanamide hydratase, identical to hypothetical protein YFL061w
YOL158C similarity to subtelomeric encoded proteins

YOL161C strong similarity to members of the Srp1p/Tip1p family
YOL162W strong similarity to hypothetical protein YIL166c
non-annotated SAGE orf Found forward in NC_001146 between 330326 and 330544 with 100% identity
YOL153C strong similarity to Cps1p
YOL165C Hypothetical aryl-alcohol dehydrogenase (AAD)
non-annotated SAGE orf Found forward in NC_001146 between 623131 and 623265 with 100% identity
YOL106W questionable ORF
YOL154W similarity to *S.fumigata* Asp FII
YOL163W similarity to *P.putida* phthalate transporter
YOL164W similarity to *Pseudomonas* alkyl sulfatase
YNR059W similarity to alpha-1,3-mannosyltransferase
YNR058W 7,8-diamino-pelargonic acid aminotransferase (DAPA) aminotransferase
non-annotated SAGE orf Found forward in NC_001146 between 728144 and 728293 with 100% identity
YNL011C similarity to hypothetical *A. thaliana* protein T14G11.21
YNL014W translation elongation factor eEF3 homolog
YNR068C similarity to Bul1p
non-annotated SAGE orf Found reverse in NC_001146 between 351383 and 351577 with 100% identity
non-annotated SAGE orf Found forward in NC_001146 between 366082 and 366222 with 100% identity
YNL003C Member of family of mitochondrial carrier proteins
non-annotated SAGE orf Found forward in NC_001146 between 440983 and 441117 with 100% identity
YNR076W member of the seripauperin proteinVgene family
non-annotated SAGE orf Found forward in NC_001144 between 949308 and 949442 with 100% identity
YML116W predicted protein is very hydrophobic, has many membrane-spanning regions, several potential
YML099C zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
non-annotated SAGE orf Found reverse in NC_001144 between 669739 and 669894 with 100% identity
YML133C hypothetical protein Y'.2
YML023C weak similarity to Nmd2p
YML042W Carnitine O-acetyltransferase, peroxisomal and mitochondrial
YML005W similarity to hypothetical *S.pombe* protein
non-annotated SAGE orf Found forward in NC_001144 between 949499 and 949633 with 100% identity
YML107C hypothetical protein
YML068W similarity to *C.elegans* hypothetical protein
YLR411W Copper Transporter
YLL018C-A hypothetical protein identified by SAGE
YLR461W member of the seripauperin proteinVgene family (see Gene_class PAU)
YLR318W 103 kD basic protein, catalytic subunit of telomerase
YLR317W questionable ORF
non-annotated SAGE orf Found forward in NC_001144 between 390278 and 390421 with 100% identity
non-annotated SAGE orf Found reverse in NC_001144 between 223615 and 223821 with 100% identity
non-annotated SAGE orf Found reverse in NC_001144 between 13652 and 13819 with 100% identity.
YLR363C putative Upf1p-interacting protein
YLR460C similarity to *C.carbonum* toxD protein
YLR451W zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
YMR232W involved in cell fusion during mating, also required for the alignment of parental nuclei before
YMR271C Orotate phosphoribosyltransferase 2
YMR284W DNA binding protein
YMR182C Putative transcriptional repressor with proline-rich zinc fingers
YMR180C similarity to YPL228w
YMR316C-B questionable ORF
non-annotated SAGE orf Found reverse in NC_001145 between 433097 and 433231 with 100% identity
non-annotated SAGE orf Found reverse in NC_001145 between 426343 and 426489 with 100% identity
YMR240C U2 snRNP protein
non-annotated SAGE orf Found reverse in NC_001145 between 122312 and 122605 with 100% identity
YMR325W strong similarity to members of the Srp1p/Tip1p family

YMR023C putative mitochondrial GTPase
YMR065W appears to be required for the completion of nuclear membrane fusion and may play a role i
YMR068W weak similarity to mouse transcription factor NF-kappaB
YMR020W Multicopy suppressor of fenpropimorph resistance (fen2 mutant), shows similarity to Candid
YML002W hypothetical protein
YMR169C Aldehyde Dehydrogenase (NAD(P)+)
YMR169C Aldehyde Dehydrogenase (NAD(P)+)
YMR168C contains an N-terminal Zn2Cys6 type zinc finger domain, a C-terminal acidic domain and a p
YMR040W strong similarity to Yet1p
YMR090W strong similarity to B. subtilis conserved hypothetical protein yhfK
YMR114C similarity to B. subtilis conserved hypothetical proteins yoqW and yoam
YPL147W Pxa1p and Pxa2p appear to be subunits of a peroxisomal ATP-binding cassette transporter i
YPL148C Phosphopantetheine
YPL149W involved in autophagy
YPL277C strong similarity to hypothetical protein YOR389w/putative pseudogene
YPL236C similarity to Prk1p, and serine/threonine protein kinase homolog from A. thaliana
YPL095C strong similarity to YBR177c
YPL064C weak similarity to S.pombe peptidyl-prolyl cis-trans isomerase
YPL066W hypothetical protein
YPL214C TMP pyrophosphorylase, hydroxyethylthiazole kinase
YPL164C similarity to mismatch repair protein Mlh1p
YPL088W similarity to aryl-alcohol dehydrogenases
non-annotated SAGE orf Found reverse in NC_001147 between 16559 and 16696 with 100% identity.
non-annotated SAGE orf Found reverse in NC_001147 between 969027 and 969179 with 100% identit
non-annotated SAGE orf Found forward in NC_001147 between 758077 and 758286 with 100% identit
non-annotated SAGE orf Found forward in NC_001147 between 418190 and 418375 with 100% identit
non-annotated SAGE orf Found reverse in NC_001147 between 17812 and 17970 with 100% identity.
YPL258C similarity to B.subtilis transcriptional activator tenA, and strong similarity to hypothetical protei
YPL264C strong similarity to YMR253c
YPL272C hypothetical protein
non-annotated SAGE orf Found reverse in NC_001147 between 16760 and 16939 with 100% identity.
non-annotated SAGE orf Found forward in NC_001147 between 690271 and 690495 with 100% identit
YPL257W weak similarity to YIL029c
YPR196W strong similarity to regulatory protein Mal63p
YPR196W strong similarity to regulatory protein Mal63p
YPR194C similarity to S.pombe isp4 protein
YPR121W similarity to B.subtilis transcriptional activator tenA, strong similarity to hypothetical proteins `
YPR168W negative regulator of URS2 of the HO promoter
non-annotated SAGE orf Found reverse in NC_001148 between 409022 and 409276 with 100% identit
non-annotated SAGE orf Found reverse in NC_001148 between 921211 and 921453 with 100% identit
YER104W hypothetical protein
YPR199C Similar to transcriptional regulatory elements YAP1 and cad1
YPR193C Histone and other Protein Acetyltransferase\; Has sequence homology to known HATs and H
non-annotated SAGE orf Found forward in NC_001148 between 411416 and 411688 with 100% identit
YPL022W UV endonuclease
YPR012W hypothetical protein
YPR005C polar 32k Da cytoplasmic protein
YPL071C hypothetical protein
YPL034W questionable ORF
YPR068C Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos3p
YPR057W Protein involved in snRNP biogenesis
YPR085C hypothetical protein
YPL047W hypothetical protein
YPL003W Required for activation of RUB1 (ubiquitin-like protein) together with UBA3. Related to AOS1

YPR070W hypothetical protein
YOR100C similarity to mitochondrial carrier proteins
YOR128C phosphoribosylamino-imidazole-carboxylase
YOR120W Similar to mammalian aldo/keto reductases
YOR072W hypothetical protein
YOR062C strong similarity to YKR075c
YOR148C required for final stages of spliceosome maturation; promotes step 1 of splicing
YOR180C Peroxisomal enoyl-CoA hydratase
YOR203W questionable ORF
YOR059C weak similarity to YGL144c
YOR162C transcription factor
YOR152C hypothetical protein
YOR005C ATP dependent DNA ligase
YOL001W negative transcriptional regulator
YOL009C Mdm12p is a mitochondrial outer membrane protein. An Mdm12p homolog exists in *S. Pombe*
YOL112W Multicopy Suppressor of Bud Emergence
YOL043C Endonuclease III-like glycosylase 2
YOR019W similarity to YDR474c
YOR012W similarity to YDR391c
YOR009W similarity to Tir1p and Tir2p
YOL055C similarity to *B. subtilis* transcriptional activator tenA
YOL014W hypothetical protein
YOL015W weak similarity to YKR015c
YOR377W Alcohol acetyltransferase
YOR363C Activator of peroxisome proliferation
non-annotated SAGE orf Found forward in NC_001147 between 33183 and 33335 with 100% identity.
YOR358W Component, along with Hap2p and Hap3p, of CCAAT-binding transcription factor
YOR381W similar to FRE2
non-annotated SAGE orf Found forward in NC_001147 between 423955 and 424104 with 100% identity
non-annotated SAGE orf Found forward in NC_001147 between 60049 and 60273 with 100% identity.
non-annotated SAGE orf Found reverse in NC_001147 between 14772 and 15044 with 100% identity.
YOR380W weak similarity to Pdr3p
YOR389W strong similarity to putative pseudogenes YPL277c and YPL278c
YOR389W strong similarity to putative pseudogenes YPL277c and YPL278c
YOR222W similarity to ADP/ATP carrier proteins
YOR284W weak similarity to *M.jannaschii* hypothetical protein MJ0694
YOR278W uroporphyrinogen III synthase
YOR202W imidazoleglycerol-phosphate dehydratase
YOR192C strong similarity to Thi10p
YOR302W CPA1 leader peptide
YOR328W Putative ABC transporter highly similar to Pdr5p
YOR319W homolog of mammalian splicing factor VU2 snRNP protein
YOR192C strong similarity to Thi10p
YOR304C-A AIP3 binding protein
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001
YKR069W siroheme synthase
YKR104W similarity to multidrug resistance proteins
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001
YKR061W putative mannosyltransferase; type 2 membrane protein
YKL005C weak similarity to YKR029c and *D.melanogaster* transcription elongation factor DmS-II
YCR096C mating hormone a2
YILWY3-1 Full length Ty3
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001
YKR091W Suppressor of rad53 lethality

YKR097W phosphoenolpyruvate carboxylkinase
YGLWDELTA4 Ty1 LTR
non-annotated SAGE orf Found reverse in NC_001143 between 16801 and 17055 with 100% identity.
YHLWTAU1 Ty4 LTR
YKR102W Protein with similarity to flocculation protein Flo1p
YGRCTAU3 Ty4 LTR
YGRWDELTA23 Ty1 LTR
YHRWTAU3 Ty4 LTR
YKL017C DNA helicase A
YKL011C cruciform cutting endonuclease
YKL026C strong similarity to glutathione peroxidase
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143
YKL098W hypothetical protein
YKL132C probable folyl-polyglutamate synthetase
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143
YKL090W hypothetical protein
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001143
YKR009C peroxisomal multifunctional beta-oxidation protein
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001143
YPLCTAU1 Ty4 LTR
YLL064C strong similarity to members of the Srp1/Tip1p family
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001143
YPLCTY4-1 Full length Ty4
YLL060C Glutathione transferase
YDLWTAU1 Ty4 LTR
YPRWTAU4 Ty4 LTR
YLL063C transacetylase
non-annotated SAGE orf Found reverse in NC_001143 between 136056 and 136247 with 100% identity.
YORWTAU2 Ty4 LTR
YPLCDELTA1 Ty1 LTR
YNR075W Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p,
YNRCDELTA9 Ty1 LTR
YORWTAU3 Ty4 LTR
YPLCTAU2 Ty4 LTR
non-annotated SAGE orf Found forward in NC_001143 between 456740 and 456883 with 100% identity.
YLL065W Growth INhibitory protein
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found reverse in NC_001143
YDR543C
YERWOMEGA2 Ty5 LTR
YERCTAU2 Ty4 LTR
YFL063W strong similarity to subtelomeric encoded proteins
YGLWTAU1 Ty4 LTR
YGLWDELTA6 Ty1 LTR
YKL201C regulates the mannosylphosphorylation
YGLWDELTA4 Ty1 LTR
non-annotated SAGE orf Found forward in NC_001143 between 146588 and 146755 with 100% identity.
non-annotated SAGE orf Found reverse in NC_001143 between 264148 and 264333 with 100% identity.

YDRCSIGMA1 Ty3 LTR
non-annotated SAGE orf Found reverse in NC_001143 between 136275 and 136457 with 100% identity
non-annotated SAGE orf Found reverse in NC_001143 between 142825 and 142992 with 100% identity
YERCTAU3 Ty4 LTR
YERCDELTA15 Ty1 LTR
YDR542W strong similarity to subtelomeric encoded proteins
YERWDELTA9 Ty1 LTR
YERCDELTA15 Ty1 LTR
YAL064W hypothetical protein
YAL067C Suppressor of Sulfoxide Ethionine resistance
YAL062W NADP-linked glutamate dehydrogenase
YAL063C putative Flo1p homolog
YJR108W similarity to hypothetical protein YIL014c-a
YJR036C similarity to human E6-associated protein
YAL037W strong similarity to GTP-binding proteins
YAL014C protein of unknown function
YJR039W hypothetical protein
YJR155W Hypothetical aryl-alcohol dehydrogenase (AAD)
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001143
YJR025C C-terminal part of YJR030c
YJR159W sorbitol-induced sorbitol dehydrogenase
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001143
YJL185C hypothetical protein
YJL162C weak similarity to dnaJ proteins
YJR004C alpha-agglutinin
YJR008W similarity to S.pombe hypothetical protein
YJL110C GATA zinc finger protein 3 homologous to Dal80 in structure and function
YJL023C Nuclear gene encoding mitochondrial protein
YJL126W Nit2 nitrilase
YJL106W Serine/Threonine protein kinase, positively regulated by IME1
YJL057C probable serine/threonine kinase
non-annotated SAGE orf Found reverse in NC_001133 between 22397 and 22687 with 100% identity.
YJL213W similarity to Methanobacterium arylalkylphosphatase related protein
YAR023C membrane protein
YAR020C strong similarity to members of the srp1p/Tip1p family
YJL221C homology to maltase(alpha-D-glucosidase)
YJL222W strong similarity to Pep1p
YJL004C Multicopy suppressor of ypt6 null mutation
YJL216C strong similarity to Mal62p
YJL223C strong similarity to members of the Srp1p/Tip1p family
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001143
non-annotated SAGE orf Found reverse in NC_001142 between 626834 and 627004 with 100% identity
Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001143
non-annotated SAGE orf Found reverse in NC_001142 between 731905 and 732069 with 100% identity
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001143
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001143
non-annotated SAGE orf Found reverse in NC_001142 between 734995 and 735165 with 100% identity
YKL188C peroxisomal ABC transporter 2

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001024.1:YKL161C probable serine/threonine-specific protein kinase (EC 2.7.1.-)

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001024.1:YKL161C

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001024.1:YKL222C weak similarity to transcription factors, similarity to finger proteins YOR162c, YOR172w and YOR172w

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001024.1:YKL220C

Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001024.1:YKL220C Ferric reductase, similar to Fre1p

YJR152W allantoin permease

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001024.1:YJR149W similarity to 2-nitropropane dioxygenase

YJR151C similarity to mucin proteins, YKL224c, Sta1p

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001024.1:YJR151C

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001024.1:YJR151C

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001024.1:YJR151C

Saccharomyces cerevisiae chromosome VI, complete chromosome sequence. Found forward in NC_001024.1:YJR151C

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001024.1:YJR151C

Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001024.1:YJR151C

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001024.1:YJR151C

non-annotated SAGE orf Found forward in NC_001142 between 741740 and 741883 with 100% identity

non-annotated SAGE orf Found reverse in NC_001142 between 396887 and 397036 with 100% identity

non-annotated SAGE orf Found reverse in NC_001142 between 451797 and 451979 with 100% identity

non-annotated SAGE orf Found reverse in NC_001142 between 731735 and 731896 with 100% identity

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001024.1:YIL107C

YIL107C 6-Phosphofructose-2-kinase

YLR123C questionable ORF

YIL165C putative pseudogene

YIL120W similarity to antibiotic resistance proteins

YLR128W similarity to S.pombe hypothetical protein SPBC24E9

YLR097C hypothetical protein

YLR125W hypothetical protein

YIL080W Ty3-2 orf C fragment

YLR098C DNA-binding transcriptional activator or CHA1

YLR156W identical to hypothetical proteins YLR161w and YLR159w

non-annotated SAGE orf Found reverse in NC_001140 between 530754 and 530897 with 100% identity

YIL176C strong similarity to members of the Srp1p/Tip1p family

YLR152C similarity to YOR3165w and YNL095c

YLR165C weak similarity to H.influenzae hypothetical protein HI0176

YLR122C hypothetical protein

YLR164W strong similarity to Sdh4p

non-annotated SAGE orf Found forward in NC_001140 between 530130 and 530267 with 100% identity

YIL164C Nit1 nitrilase

YIR032C ureidoglycolate hydrolase

YIR031C Malate synthase 2

YIR041W similarity to members of the Srp1p/Tip1p family

YIR039C GPI-anchored aspartic protease

YLR036C similarity to YIL089w

YIR043C putative pseudogene

YIR029W allantoinase

YIR020C hypothetical protein

YLR037C strong similarity to members of the Srp1p/Tip1p family

YIL028W putative pseudogene

YIL009C-A 181aa protein - 20.5 kD

YLR085C Actin-related protein
YIL059C hypothetical protein
YIR007W hypothetical protein
YIR043C putative pseudogene
YIL009C-A 181aa protein - 20.5 kD
YLR031W similarity to hypothetical protein YMR124w
YHL040C similarity to C.carbonum toxin pump
YHL042W similarity to subtelomeric encoded proteins
YLR263W Meiosis-specific protein involved in homologous chromosome synapsis and chiasmata formation
YHL037C hypothetical protein
YHL016C Urea transporter
YLR233C Telomere elongation protein (ever shorter telomeres)
YHL046C strong similarity to members of the Srp1p/Tip1p family
YHL047C similarity to C.carbonum toxin pump
YHR015W PolyA-binding protein
non-annotated SAGE orf Found reverse in NC_001139 between 604571 and 604726 with 100% identity
non-annotated SAGE orf Found forward in NC_001139 between 576609 and 576782 with 100% identity
YOR303W Carbamoyl phosphate synthetase, arginine specific
YLR315W weak similarity to rat apolipoprotein A-IV
non-annotated SAGE orf Found reverse in NC_001139 between 919562 and 919735 with 100% identity
YLR288C involved in checkpoint control and DNA repair
non-annotated SAGE orf Found forward in NC_001139 between 318551 and 318691 with 100% identity
non-annotated SAGE orf Found forward in NC_001139 between 23385 and 23675 with 100% identity.
YHL035C ABC transporter
YHR199C strong similarity to hypothetical protein YHR198c
non-annotated SAGE orf Found reverse in NC_001140 between 202505 and 202657 with 100% identity
YHR210C UDP-glucose-4-epimerase (GAL10, galE)
YHR204W similarity to alpha-mannosidases
YLR174W Cytosolic form of NADP-dependent isocitrate dehydrogenase
YIL167W serine dehydratase
non-annotated SAGE orf Found reverse in NC_001140 between 5778 and 5924 with 100% identity. See
non-annotated SAGE orf Found reverse in NC_001140 between 5662 and 5796 with 100% identity. See
YIR042C weak similarity to B.licheniformi hypothetical protein P20
YHR157W mRNA is induced early in meiosis
YLR251W similarity to peroxisomal rat membrane protein PMP22
YHR150W weak similarity to YDR479c
YHR129C Centractin
YHR180W hypothetical protein
YHR218W gene in Y' repeat region
YLR252W questionable ORF
YHR156C weak similarity to mouse kinesin KIF3B
YLR227C hypothetical protein
YLL025W strong similarity to members of the Srp1p/Tip1p family
YLL067C strong similarity to subtelomeric encoded proteins
YLL067C strong similarity to subtelomeric encoded proteins
YLL067C strong similarity to subtelomeric encoded proteins
YMRWDELTA21 Ty1 LTR
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001140
YLRDELTA27 Ty1 LTR
YLL016W homologous to cdc25
YJLWTAU1 Ty4 LTR
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001140
YJLWTY4-1 Full length Ty4
YJLWTY4-1 Full length Ty4

YKRCDELTA11 Ty1 LTR
YLL033W hypothetical protein
YJR161C Protein with similarity to members of the Ybr302p/Ycr007p/VCos8p/VCos9p family, coded from YJLWTAU4 Ty4 LTR
YOLWTAU1 Ty4 LTR
YNLWTAU1 Ty4 LTR
YNLWSIGMA2 Ty3 LTR
YNLWTAU2 Ty4 LTR
non-annotated SAGE orf Found reverse in NC_001142 between 740830 and 741003 with 100% identity
YLL051C similar to FRE2
YNR077C strong similarity to subtelomeric encoded proteins
YLL052C member of mip family transmembrane channels
YMRWTAU2 Ty4 LTR
YMRDELTA18 Ty1 LTR
YMRCTAU3 Ty4 LTR
YLL057C similarity to E.coli dioxygenase
YNRCTAU3 Ty4 LTR
YLL055W similarity to Dal5p
YMRWDELTA16 Ty1 LTR
YLL056C weak similarity to Y.pseudotuberculosis CDP-3,6-dideoxy-D-glycero-L-glycero-4-hexulose-5-ε 2mic_D_protein 2 micron plasmid D protein
non-annotated SAGE orf Found reverse in NC_001141 between 386017 and 386157 with 100% identity
YLR046C strong similarity to Rta1p and Rtm1p protein
YLR016C hypothetical protein
YLR010C weak similarity to Aquifex aeolicus adenylosuccinate synthetase
non-annotated SAGE orf Found reverse in NC_001141 between 385816 and 385959 with 100% identity
non-annotated SAGE orf Found forward in NC_001141 between 258363 and 258509 with 100% identity
YJLWTAU2 Ty4 LTR
YKR004C ExtraCellular Mutant
YLR242C weak similarity to C.elegans R05H5.5 protein and Nup120p
YMR103C hypothetical protein
non-annotated SAGE orf Found reverse in NC_001142 between 159321 and 159545 with 100% identity
YLR266C weak similarity to transcription factors
YNL025C C-type cyclin associated with the Ssn3p cyclin-dependent kinase
YOR130C mitochondrial integral membrane protein
YJR160C strong similarity to Mal31p
YKL033W-A hypothetical protein
YKR050W membrane protein; low affinity potassium transport
YLR457C Nap1p-binding protein
YMR087W hypothetical protein
YMR283C Initiator methionine tRNA 2'-O-ribosyl phosphate transferase
YNL333W Snooze: stationary phase-induced gene family
YOR238W similarity to hypothetical S. pombe protein
YJL024C similar to Aps1p and mammalian small subunit (sigma-2 adaptin) of plasma membrane-associated
YLL042C hypothetical protein
YLR381W hypothetical protein
YLR284C Peroxisomal enoyl-CoA hydratase
YNR029C similarity to P.denitrificans cobW protein
YOR313C sporulation-specific protein
YOR305W hypothetical protein
non-annotated SAGE orf Found reverse in NC_001143 between 468759 and 468899 with 100% identity
non-annotated SAGE orf Found reverse in NC_001145 between 347179 and 347406 with 100% identity
non-annotated SAGE orf Found forward in NC_001145 between 837034 and 837171 with 100% identity
YJR021C meiotic recombination protein

YLR426W weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase from E. coli
non-annotated SAGE orf Found forward in NC_001145 between 271996 and 272136 with 100% identity
non-annotated SAGE orf Found forward in NC_001146 between 440983 and 441117 with 100% identity
YLL053C similarity to water channel proteins
YLR394W weak similarity to chicken RING zinc finger protein
YMR096W encodes highly conserved 35 kDa protein that shows increased expression after entry into S phase
YKR005C hypothetical protein
YKR012C questionable ORF
YMR127C Protein involved in silencing HMR, homologous to acetyltransferases
YOL068C Homolog of SIR2
YLR004C similarity to allantoin transport protein
YMR176W ExtraCellular Mutant
YLR122C hypothetical protein
YOL104C Involved in meiotic chromosome segregation; may stabilize homologous DNA interactions at 1
YNL032W Tyrosine phosphatase
YNL230C weak similarity to mammalian transcription elongation factor elongin A
YNL254C hypothetical protein
YLL003W protein of unknown function
YMR211W weak similarity to beta tubulins
YLR137W hypothetical protein
YLR054C hypothetical protein
YKR103W similarity to multidrug resistance proteins
YKL224C strong similarity to members of the Srp1p/Tip1p family
YOL107W weak similarity to human PL6 protein
YOL108C Transcription factor involved in activation of phospholipid synthetic genes
YMR196W hypothetical protein
YOL130W ALuminium Resistance 1
YKL187C strong similarity to hypothetical protein YLR413w
YMR294W Coiled-coil domain protein required for proper nuclear migration during mitosis (but not during meiosis)
YKL071W weak similarity to A.parasiticus nor-1 protein
YOR064C weak similarity to human retinoblastoma binding protein 2
YJR153W Endo-polygalacturonase
YNL257C Interacts with SNF1 protein kinase
non-annotated SAGE orf Found forward in NC_001144 between 677930 and 678073 with 100% identity
YJR156C Thiamine biosynthetic enzyme
YLR417W defective in vacuolar protein sorting
YMR262W similarity to S.pombe scn1 protein
YMR135C hypothetical protein
YOR026W Protein required for cell cycle arrest in response to loss of microtubule function
YMR064W basic, hydrophilic protein of 59 kDa
YMR181C similarity to YPL229w
YKL198C probable serine/threonine-specific protein kinase (EC 2.7.1.-)
YLR173W hypothetical protein
YMR234W ribonuclease H
YKL149C debranching enzyme
YDR453C strong similarity to thiol-specific antioxidant proteins
YDR459C weak similarity to YNL326c
non-annotated SAGE orf Found reverse in NC_001136 between 512499 and 512651 with 100% identity
YDR336W weak similarity to B.subtilis hypothetical protein X
YDR273W weak similarity to YOR042w
YDR252W Negative effect on expression of several genes transcribed by RNA polymerase III; BTF3 homolog
YDR499W weak similarity to hypothetical C.elegans protein, M.genitalium peptide chain release factor
YDR403W first enzyme in dityrosine synthesis in the outer layer of the spore wall pathway converting L-tyrosine to dityrosine
YEL023C hypothetical protein

YJLWDELTA2 Ty1 LTR
YEL062W Non-membrane-embedded, PEST sequence-containing protein
non-annotated SAGE orf Found forward in NC_001141 between 26990 and 27169 with 100% identity.
YLL067C strong similarity to subtelomeric encoded proteins
non-annotated SAGE orf Found reverse in NC_001136 between 909885 and 910028 with 100% identity.
YDR391C strong similarity to hypothetical protein YOR013w
YAL068C strong similarity to subtelomeric encoded proteins
YJR162C strong similarity to subtelomeric encoded proteins
YDL187C questionable ORF
YBLWTAU1 Ty4 LTR
YCR007C strong similarity to subtelomeric encoded proteins
YDR008C questionable ORF
YDRCSIGMA2 Ty3 LTR
non-annotated SAGE orf Found forward in NC_001135 between 288361 and 288519 with 100% identity.
YERWDELTA18 Ty1 LTR
YBLWDELTA8 Ty1 LTR
YDL241W hypothetical protein
YNR075W Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Ybr302p,
YDR109C similarity to Mpa43p
YDR070C hypothetical protein
YJLWDELTA16 Ty1 LTR
YDR206W EST1-like bcy1 Suppressor
YPLCDELTA1 Ty1 LTR
YDR005C required for sorting of Mod5p
YDL239C hypothetical protein
YDR065W hypothetical protein
YGR024C weak similarity to Methanobacterium thermoautotrophicum hypothetical protein MTH972
YHR153C sporulation protein
YGL154C aminoadipate-semialdehyde dehydrogenase small subunit (alpha-aminoadipate reductase)
YGR032W catalytic component of 1,3-beta-D-glucan synthase
YHR067W hypothetical protein
non-annotated SAGE orf Found forward in NC_001138 between 48735 and 48926 with 100% identity.
non-annotated SAGE orf Found forward in NC_001138 between 161226 and 161405 with 100% identity.
YFR005C similarity to hypothetical A. thaliana proteins
YGR016W weak similarity to M.jannaschii hypothetical protein MJ1317
non-annotated SAGE orf Found reverse in NC_001140 between 519037 and 519228 with 100% identity.
non-annotated SAGE orf Found reverse in NC_001139 between 974572 and 974772 with 100% identity.
YHL026C hypothetical protein
non-annotated SAGE orf Found reverse in NC_001139 between 701262 and 701477 with 100% identity.
YGR287C strong similarity to maltase
YGR064W questionable ORF
YGR070W GDP-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein
YGL247W similarity to hypothetical protein YHR036w
YGR288W maltose pathway regulatory protein
YGR216C Participates in synthesis of N-acetylglucoaminyolphosphatidylinositol, the first intermediate in
YIR009W encodes YU2B, a component of yeast U2 snRNP
YER116C zinc-finger protein
YIL055C hypothetical protein
YIL071C hypothetical protein
YER028C similarity to Mig1p
YDR003W strong similarity to hypothetical protein YBR005w
YIL013C Putative member of the ABC family of membrane transporters
YIL071C
non-annotated SAGE orf Found forward in NC_001137 between 367587 and 367721 with 100% identity.

YIL116W histidinol-phosphate aminotransferase
YGR222W translational activator of cytochrome c oxidase subunit III
non-annotated SAGE orf Found reverse in NC_001140 between 204089 and 204277 with 100% identity
YIL089W similarity to hypothetical protein YLR036c
non-annotated SAGE orf Found reverse in NC_001141 between 30695 and 30898 with 100% identity.
YIL146C ExtraCellular Mutant
non-annotated SAGE orf Found forward in NC_001137 between 77473 and 77622 with 100% identity.
non-annotated SAGE orf Found reverse in NC_001137 between 314164 and 314310 with 100% identity
YPR046W Required for chromosome segregation
YPR026W null mutant is viable; increased tolerance to dehydration, freezing, and toxic levels of ethanol
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001137
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_001137
YPR013C similarity to transcription factors
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001137
YPL133C weak similarity to transcription factors
YPR071W strong similarity to YIL029c
YPL002C appears to be functionally related to SNF7
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001137
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001137
non-annotated SAGE orf Found forward in NC_001148 between 703978 and 704121 with 100% identity
YPR153W hypothetical protein
YPR066W ubiquitin-like protein activating enzyme
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001137
Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001137
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_001137
YOR366W questionable ORF
non-annotated SAGE orf Found forward in NC_001133 between 223093 and 223230 with 100% identity
YAL002W Vps8p is a membrane-associated hydrophilic protein which contains a C-terminal cysteine-rich domain
YAR053W predicted membrane protein
YJL093C outward-rectifier potassium channel
YJL058C strong similarity to hypothetical protein YBR270c
YOR011W strong similarity to ATP-dependent permeases
YAL069W hypothetical protein
YPL151C strong similarity to A.thaliana PRL1 and PRL2 proteins
YPL186C weak similarity to Xenopus protein xlgv7
YPR169W hypothetical protein
YPL167C DNA polymerase
YAL028W similarity to hypothetical protein YOR324c
non-annotated SAGE orf Found reverse in NC_001147 between 836569 and 836709 with 100% identity
YOR318C hypothetical protein
YPL156C weak similarity to YDL010w
YPL233W hypothetical protein
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001134
non-annotated SAGE orf Found forward in NC_001134 between 46929 and 47189 with 100% identity.
Saccharomyces cerevisiae chromosome I, complete chromosome sequence. Found forward in NC_001134
non-annotated SAGE orf Found forward in NC_001134 between 555695 and 555919 with 100% identity
YBR056W-A identified by SAGE
YBR259W hypothetical protein
non-annotated SAGE orf Found reverse in NC_001134 between 376102 and 376293 with 100% identity
YBR284W similarity to AMP deaminase
YCL004W 17-kDa phosphatidylserine synthase
YCL056C hypothetical protein
YCR104W member of the seripauperin protein/vgene family (see Gene_class PAU)

YCR106W Transcription regulator
YHL050C strong similarity to subtelomeric encoded proteins
non-annotated SAGE orf Found reverse in NC_001134 between 554921 and 555088 with 100% identity
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001134
YBR047W hypothetical protein
YBR055C RNA splicing factor
YBR145W alcohol dehydrogenase isoenzyme V
YBR107C weak similarity to N.crassa chitin synthase
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001134
YBL088C putative phosphatidylinositol kinase
YAL034C Function unknown now
YBR063C Probable phosphopantethein-binding protein
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001134
YHRCDELTA4 Ty1 LTR
YBR278W C and C' subunits of DNA polymerase II
YBR148W Spore-specific protein
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001134
YBR237W RNA helicase homolog
YBR168W weak similarity to hypothetical protein YLR324w
YBR182C Probable DNA-binding transcription factor, Homolog to SRFVSL-2
SNR37 small nuclear RNA37
non-annotated SAGE orf Found reverse in NC_001136 between 76964 and 77110 with 100% identity.
YER060w-A purine-cytosine permease
YIL132C hypothetical protein
non-annotated SAGE orf Found reverse in NC_001137 between 561482 and 561634 with 100% identity
YPR192W similarity to plasma membrane and water channel proteins
YGRCDELTA20 Ty1 LTR
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_001134
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001134
YDR461W a-factor mating pheromone precursor
YPR124W High affinity copper transporter into the cell, probable integral membrane protein
SNR56 snRNA
YLRCDELTA19 Ty1 LTR
non-annotated SAGE orf Found reverse in NC_001136 between 1385513 and 1385758 with 100% identity
YPRWDELTA17 Ty1 LTR
non-annotated SAGE orf Found reverse in NC_001142 between 227590 and 227742 with 100% identity
non-annotated SAGE orf Found forward in NC_001133 between 223253 and 223423 with 100% identity
non-annotated SAGE orf Found forward in NC_001133 between 223333 and 223476 with 100% identity
non-annotated SAGE orf Found forward in NC_001146 between 89019 and 89186 with 100% identity.
SNR8 snRNA
SNR36 snRNA
YHR136C 17 kDa protein
non-annotated SAGE orf Found reverse in NC_001139 between 366397 and 366531 with 100% identity
SNR39b snRNA
YNL122C hypothetical protein
YDR405W 263-amino acid mitochondrial ribosomal large subunit protein\; similar to L23 family of ribosomal proteins
YDR440W Pachytene Checkpoint
non-annotated SAGE orf Found forward in NC_001134 between 680321 and 680521 with 100% identity
non-annotated SAGE orf Found forward in NC_001147 between 464469 and 464630 with 100% identity
non-annotated SAGE orf Found forward in NC_001137 between 422560 and 422781 with 100% identity
YOL152W similar to FRE2
YBR016W strong similarity to hypothetical proteins YDL012c and YDR210w
TR(UCU)J1 tRNA-Arg
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001134

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001111

Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001111

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001111

SNR69 snRNA

YLR218C hypothetical protein

YJR112W involved in nuclear function

Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_001111

TR(ACG)O tRNA-Arg

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001111

Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001111

TH(GUG)E1 tRNA-His

TS(AGA)D2 tRNA-Ser

YGL096W similarity to copper homeostasis protein Cup9p

YGR144W component of the biosynthetic pathway producing the thiazole precursor of thiamine

YGL004C weak similarity to Tup1p

YOR012W similarity to YDR391c

YEL041W strong similarity to Utr1p

non-annotated SAGE orf Found forward in NC_001140 between 198428 and 198592 with 100% identity

YIL099W intracellular glucoamylase

YIL097W hypothetical protein

YHR077C Highly acidic C-terminus

YIR001C similarity to D.melanogaster RNA binding protein

YIL003W strong similarity to Nbp35p and human nucleotide-binding protein

YIL024C hypothetical protein

YIR019C cell surface flocculin with structure similar to serine/threonine-rich GPI-anchored cell wall protein

non-annotated SAGE orf Found reverse in NC_001139 between 74628 and 74810 with 100% identity.

YOL155C similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w

YOL155C similarity to glucan 1,4-alpha-glucosidase Sta1p and YAR066w

non-annotated SAGE orf Found reverse in NC_001139 between 536199 and 536372 with 100% identity

non-annotated SAGE orf Found reverse in NC_001146 between 519600 and 519773 with 100% identity

YHR078W hypothetical protein

YHR134W hypothetical protein

non-annotated SAGE orf Found reverse in NC_001139 between 836381 and 836659 with 100% identity

YBR193C Stoichiometric member of mediator complex

YCL018W beta-IPM (isopropylmalate) dehydrogenase

YCR063W G10-like protein

non-annotated SAGE orf Found forward in NC_001148 between 809943 and 810116 with 100% identity

YDR479C weak similarity to YHR150w

YDR257C Transcription regulator

YOR111W weak similarity to B.subtilis maf protein

YDR275W weak similarity to YOR042w

YEL065W probably multidrug resistance protein

YJL168C transcription factor containing a SET domain

YJR021C meiotic recombination protein

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001111

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001111

YKL168C probable serine/threonine-specific protein kinase (EC 2.7.1.-)

YJR115W similarity to hypothetical protein YBL043w

non-annotated SAGE orf Found forward in NC_001142 between 471954 and 472142 with 100% identity

YKL217W carboxylic acid transporter protein homolog

YNL057W questionable ORF

YLR466W strong similarity to subtelomeric encoded proteins

YNL125C Protein with similarity to mammalian monocarboxylate transporters MCT1 and MCT2

YLR352W hypothetical protein

questionable ORF Found reverse in NC_001224 between 13748 and 14122 with 100% identity.
non-annotated SAGE orf Found reverse in NC_001141 between 385561 and 385698 with 100% identity
YIL066C Ribonucleotide reductase (ribonucleoside-diphosphate reductase) large subunit
YLR306W Ubiquitin-conjugating enzyme
non-annotated SAGE orf Found forward in NC_001141 between 385618 and 385767 with 100% identity
non-annotated SAGE orf Found forward in NC_001146 between 101909 and 102082 with 100% identity
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_001146
YNL294C hypothetical protein
YNL245C hypothetical protein
non-annotated SAGE orf Found forward in NC_001144 between 230974 and 231108 with 100% identity
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_001144
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_001144
YLR423C hypothetical protein
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_001144
non-annotated SAGE orf Found forward in NC_001145 between 667253 and 667450 with 100% identity
YLR343W strong similarity to Gas1p and C.albicans pH responsive protein
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001145
YLR320W hypothetical protein
non-annotated SAGE orf Found forward in NC_001144 between 988140 and 988277 with 100% identity
YML128C C-terminal part starting with aa 262 cause growth inhibition when overexpressed
non-annotated SAGE orf Found reverse in NC_001147 between 1089906 and 1090073 with 100% identity
YNL326C similarity to YOL003c, YLR246w and C.elegans hypothetical protein ZK757.1
non-annotated SAGE orf Found reverse in NC_001145 between 623382 and 623516 with 100% identity
YOL011W strong similarity to phospholipases
YOL031C weak similarity to Y.lipolytica SIs1 protein precursor
YOL028C bZIP protein
YOR003W subtilisin-like protease III
YNL261W Fifth largest subunit of origin recognition complex\; contains possible ATP-binding site
YOR037W cytochrome c mitochondrial import factor
YOR075W endoplasmic reticulum t-SNARE, coprecipitates with Sec20p, Tip1p. and Sec22p
YMR306W Protein with similarity to Gls1p and Gls2p (GB:Z49212)
YNL034W nearly identical to YNL018c
non-annotated SAGE orf Found reverse in NC_001146 between 586598 and 586816 with 100% identity
YNR065C strong similarity to YJL222w, YIL173w and Pep1p
YNL009W peroxisomal NADP-dependent isocitrate dehydrogenase
YNL035C hypothetical protein
YNL237W Yeast putative Transmembrane Protein
YOL119C similarity to monocarboxylate transporter proteins
YNL114C questionable ORF
YOL159C hypothetical protein
YMR086C-A questionable ORF
YOR242C Sporulation Specific
YML050W weak similarity to potato sucrose cleavage protein
YML055W subunit of signal peptidase complex, homologous to mammalian protein SPC25
non-annotated SAGE orf Found forward in NC_001147 between 136219 and 136404 with 100% identity
YML098W TFIID subunit
YMR052C-A questionable ORF
YOR149C Involved in plasmid maintenance
YMR219W Establishes Silent omatin
YOR071C strong similarity to Thi10p
YMR285C similarity to Ccr4p
YOR119C similarity to a C.elegans ZK632.3 protein
YOR080W hypothetical protein
YNL094W similarity to S.pombe hypothetical protein

YMR155W weak similarity to E.coli hypothetical protein f402
YOR179C similarity to BRR5 protein
Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence. Found forward in NC_(
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_(
YJL209W Protein required for COB mRNA stability or 5' processing
YAL058W Calnexin and calreticulin homolog
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_(
Saccharomyces cerevisiae chromosome XII, complete chromosome sequence. Found forward in NC_0
YLR467W strong similarity to subtelomeric encoded proteins
YLRWDELTA15 Ty1 LTR
similarity to mouse Gcap1 Found forward in NC_001224 between 28122 and 28444 with 88.588589% i
similarity to Sauroleishmania NADH dehydrogenase (ubiquinone) chain 5 Found forward in NC_001224
YJR161C Protein with similarity to members of the Ybr302pVYcr007pVCos8pVCos9p family, coded from
YBR006W Probable aldehyde dehydrogenase (EC 1.2.1.-)
Saccharomyces cerevisiae chromosome XI, complete chromosome sequence. Found forward in NC_0(
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_00
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_00
YDL248W Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr:
YBL112C strong similarity to subtelomeric encoded proteins
YIL177C strong similarity to subtelomeric encoded proteins
YLL004W Third subunit of the origin recognition complex
YLL038C weak similarity to YJR125c and YDL161w
YLR035C similarity to human mutL protein homolog
YLR011W weak similarity to E.coli hypothetical 20.4 kDa protein
YKR087C similarity to hypothetical Myxococcus xanthus protein
non-annotated SAGE orf Found reverse in NC_001143 between 447932 and 448156 with 100% identit
YKL199C Protein of unknown function
YLR245C strong similarity to B.subtilis cytidine deaminase
YLR247C similarity to S.pombe rad8 protein and Rdh54p
YLR211C hypothetical protein
YLR224W hypothetical protein
YLR258W Glycogen synthase (UDP-glucose--starch glucosyltransferase)
YLR273C Protein similar to Gac1p, a putative type 1 protein phosphatase targeting subunit
YLR130C Low-affinity zinc transport protein
YLR144C Identified as an activity necessary for actin polymerization in permeabilized cells
YLR149C hypothetical protein
YJR078W similarity to mammalian indoleamine 2,3-dioxygenase
YJR003C hypothetical protein
YJR127C similarity to regulatory protein Ard1p
YJR107W weak similarity to acylglycerol lipase
YJR100C weak similarity to Bud3p
YDRWDELTA31 Ty1 LTR
YJL017W hypothetical protein
YJL044C GTPase-activating protein for Ypt6
YKL050C similarity to YMR031c
YKR022C hypothetical protein
YKR027W strong similarity to Chs6p
non-annotated SAGE orf Found forward in NC_001142 between 444820 and 444969 with 100% identit
non-annotated SAGE orf Found forward in NC_001142 between 637618 and 637857 with 100% identit
YKL061W hypothetical protein
YDL206W weak similarity to transporter proteins
YDL024C strong similarity to acid phosphatase
YDL146W weak similarity to Orc3p
Saccharomyces cerevisiae chromosome II, complete chromosome sequence. Found forward in NC_00

YCR068W similarity to starvation induced pSI-7 protein of *C. fluvum*
YCR028C Amino acid permease
YDR205W similarity to *A. eutrophus* cation efflux system membrane protein *czcD*, rat zinc transport prot
YDR349C GPI-anchored aspartic protease
YDR291W similarity to *B. subtilis* helicases
YDR263C DNA-damage inducible gene
YDR123C helix-loop-helix protein
YDR047W uroporphyrinogen decarboxylase
YPR081C strong similarity to glycyl-tRNA synthetases
non-annotated SAGE orf Found reverse in NC_001148 between 324023 and 324286 with 100% identit
non-annotated SAGE orf Found forward in NC_001148 between 427735 and 427896 with 100% identit
YPR021C similarity to human citrate transporter protein
YPL008W kinetochore protein in the DEAH box family
YPL018W Important for chromosome segregation
YPL072W encodes putative deubiquitinating enzyme
YBR291C citrate tranporter in mitochondrial inner membrane
YBR074W Homolog to aminopeptidase Y (*S. cerevisiae*)
YBR054W Homolog to HSP30 heat shock protein YRO1 (*S. cerevisiae*) 7
YBR020W galactokinase
YBR116C questionable ORF
YGR161C hypothetical protein
YGR117C hypothetical protein
YGR259C questionable ORF
YGR270W Member of CDC48VPAS1VSEC18 family of ATPases
YGR003W similarity to *D. melanogaster* *lin19* protein
YGL098W hypothetical protein
YGR073C questionable ORF
YGR074W Homolog of human core snRNP protein D1, involved in snRNA maturation
YIL166C similarity to allantate permease *Dal5p*
YHR178W Zinc finger (6-Cys)
YKL176C hypothetical protein
YIR028W allantoin permease
YIR014W hypothetical protein
YHR048W similarity to multidrug resistance proteins
YHL017W Probable transmembrane protein *PTM1*
YHL032C glycerol kinase (converts glycerol to glycerol-3-phosphate
non-annotated SAGE orf Found forward in NC_001139 between 788087 and 788224 with 100% identit
YHR123W sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase
YHR095W hypothetical protein
YHR071W G1VS cyclin (weak)
YDR541C similarity to dihydroflavonol-4-reductases
YDR467C questionable ORF
non-annotated SAGE orf Found forward in NC_001136 between 909701 and 909844 with 100% identit
non-annotated SAGE orf Found forward in NC_001136 between 1108476 and 1108613 with 100% ider
YDR370C hypothetical protein
YDR444W similarity to hypothetical protein *YGL144c* and *YDL109c*
YDR438W strong similarity to hypothetical protein *YML018c*
non-annotated SAGE orf Found forward in NC_001137 between 122467 and 122670 with 100% identit
non-annotated SAGE orf Found reverse in NC_001137 between 561482 and 561634 with 100% identit
YGL211W similarity to *M. jannaschii* hypothetical proteins *MJ1157* and *MJ1478*
YGL257C similarity to *Mnn1p*
non-annotated SAGE orf Found reverse in NC_001138 between 76336 and 76470 with 100% identity.
YEL005C hypothetical protein
YEL025C hypothetical protein

YEL057C hypothetical protein
YER173W checkpoint protein
2mic_REP1 2 micron plasmid rep1 protein
YGL237C transcriptional activator protein of CYC1
Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_0
YBR232C questionable ORF
YLL009C cysteine-rich cytoplasmic protein
non-annotated SAGE orf Found reverse in NC_001148 between 678411 and 678614 with 100% identit
RDN37-1 35S ribosomal RNA
YDRWDELTA7 Ty1 LTR
YGR071C similarity to hypothetical protein YLR373c
YMR293C similarity to amidases
YPL058C multidrug resistance transporter
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_00
Saccharomyces cerevisiae chromosome V, complete chromosome sequence. Found forward in NC_00
YLL058W similarity to N.crassa O-succinylhomoserine (thiol)-lyase
YJL142C questionable ORF
YJL141C Serine-threonine protein kinase
YLR189C similarity to P.aeruginosa rhamnosyltransferase 1 chain B
YNL260C hypothetical protein
YMR104C protein kinase
YOL133W High level expression Reduces Ty3 Transposition
YNL006W Required for amino acid permease transport from the Golgi to the cell surface
YNR057C dethiobiotin synthetase
YEL004W Shows sequence similarity to GOG5, a gene involved in vanadate resistance
YGR131W strong similarity to Nce2p
YGR088W cytoplasmic catalase T
YHL006C hypothetical protein
YHR120W mutS homolog involved in mitochondrial DNA repair
YAR066W identical to YHR214w hypothetical protein, similarity to Sta1p
YPL138C weak similarity to fruit fly polycomblike nuclear protein
YPL216W similarity to YGL133w
Saccharomyces cerevisiae chromosome VIII, complete chromosome sequence. Found forward in NC_(
YPR017C GDP dissociation factor for Sec4p
YJL225C strong similarity to members of the Sir1p/Tip1p family
YJL161W hypothetical protein
Saccharomyces cerevisiae chromosome X, complete chromosome sequence. Found forward in NC_00
YBR250W hypothetical protein
Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_(
Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_00
YGR138C similarity to multidrug resistance proteins
non-annotated SAGE orf Found reverse in NC_001139 between 939417 and 939581 with 100% identit
YEL059C-A high copy suppressor of imp1 mutation, may be required for the function of the Imp1 peptid
YGR084C 35 kDa mitochondrial ribosomal small subunit protein
Saccharomyces cerevisiae chromosome III, complete chromosome sequence. Found forward in NC_00
SNR13 snRNA
SNR34 snRNA
YPL173W Mitochondrial ribosomal protein MRPL40 (YmL40)
YBL026W snRNA-associated protein of the Sm class
YLLCDELTA1 Ty1 LTR
YILCDELTA3 Ty1 LTR
YPLCDELTA10 Ty1 LTR
2mic_REP2 2 micron plasmid rep2 protein
RDN37-1 35S ribosomal RNA

TA(AGC)P tRNA-Ala

Saccharomyces cerevisiae chromosome XIV, complete chromosome sequence. Found forward in NC_001022.1
YOL140W Acetylornithine aminotransferase

Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence. Found forward in NC_001022.1
YJR052W Nucleotide excision repair protein involved in G(sub)2 repair of inactive genes

YOL102C tRNA 2'-phosphotransferase

YJR141W hypothetical protein

YLR404W hypothetical protein

YOL003C similarity to C.elegans hypothetical protein, YDR126w, YNL326c and YLR246w

YOR028C bZIP protein, can activate transcription from a promoter containing a Yap recognition site

YOR035C Required for mother cell-specific HO expression

YNL242W similarity to human hypothetical protein KIAA0404

YLR014C zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type

YMR187C hypothetical protein

YNL206C similarity to structure-specific recognition proteins

YMR316W similarity to YOR385w and YNL165w

YMR252C hypothetical protein

YML034W similarity to YDR458c

YML019W Putative new 37kDa subunit of N-oligosaccharyltransferase complex

YML054C Cytochrome b2 [L-lactate cytochrome-c oxidoreductase]

YKR052C mitochondrial carrier protein, highly homologous to Mrs3p

YKL184W Ornithine decarboxylase

YKR019C Increased rDNA silencing

YMR041C weak similarity to Pseudomonas L-fucose dehydrogenase

YDR473C essential splicing factor

YER007W Required for viability in the absence of the kinesin-related mitotic motor Cin8p; required for

YEL020C similarity to O.formigenes oxalyl-CoA decarboxylase

YNL337W strong similarity to subtelomeric encoded proteins

YDL025C ser/thr protein kinase of the DEAD/DEAH box family

YDR108W Probably has role late in meiosis following DNA replication

YDL080C positive regulatory factor with thiamin pyrophosphate-binding motif for thiamin metabolism

YGR202C phosphorylcholine transferase; or cholinephosphate cytidyltransferase

YHR004C similarity to YLL010c, YLR019w

YHR123W sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase

YER162C Nucleotide excision repair protein

YAR003W beta transducin domain

non-annotated SAGE orf Found reverse in NC_001133 between 182850 and 183005 with 100% identity

YPR200C Required for arsenate but not for arsenite resistance

YPL075W trans-acting positive regulator of the enolase and glyceraldehyde-3-phosphate dehydrogenase

YJR124C weak similarity to Staphylococcus multidrug resistance protein

YJL194W Protein involved in initiation of DNA replication

YOR390W nearly identical to YPL279c

YJL020C similarity to P.falciparum glutamic acid-rich protein

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001022.1

Saccharomyces cerevisiae chromosome XV, complete chromosome sequence. Found forward in NC_001022.1

YBR085W mitochondrial ADP/VATP translocator

Saccharomyces cerevisiae chromosome VII, complete chromosome sequence. Found forward in NC_001022.1

Saccharomyces cerevisiae chromosome IX, complete chromosome sequence. Found forward in NC_001022.1

YBR216C strong similarity to hypothetical protein YGL060w

YBR274W Probable protein kinase (growth factor & cytokine receptor family)

Saccharomyces cerevisiae chromosome IV, complete chromosome sequence. Found forward in NC_001022.1

1), WSC2 and WSC3

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
1134 between 54513 and 55512 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
1134 between 27441 and 28440 with 100% identity.

ity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

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y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

94c

S phase

DR046c
I analysis

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

1134 between 5001 and 6000 with 100% identity.

1134 between 5001 and 6000 with 100% identity.

1134 between 4001 and 5000 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

2 predicted transmembrane domains

1134 between 6001 and 6215 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

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y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

AVRNA helicase family member

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

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See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

quence motifs characteristic of protein tyrosine phosphatases.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

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y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
potential glycosylation sites, potential ATP-binding site

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

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e nuclear fusion

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

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y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

n the organization of the membrane fusion complex

a albicans corticosteroid-binding protein CBP1

mutative coiled coil dimerization domain

necessary for transport of long-chain fatty acids into peroxisomes

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
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See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
ins YOL055c and YPR121w

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

YPL258c and YOL055c

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

YATs

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

and to N-terminus of UBA1. Collaborates with UBC12 in conjugation of RUB1 to other proteins. Require

e which confers a dominant negative phenotype when expressed in *S. cerevisiae*

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

I133 between 14744 and 15743 with 100% identity.

I133 between 16744 and 17743 with 100% identity.

J1141 between 206488 and 210129 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

J1143 between 643133 and 644132 with 100% identity.

J1143 between 663918 and 664917 with 100% identity.

J1143 between 652494 and 653493 with 100% identity.

I133 between 209649 and 210648 with 100% identity.

I133 between 208649 and 209648 with 100% identity.

I133 between 214649 and 215648 with 100% identity.

I133 between 211649 and 212648 with 100% identity.

H142 between 719444 and 720443 with 100% identity.

H142 between 695939 and 696138 with 100% identity.

J1143 between 13592 and 14591 with 100% identity.

J1143 between 644133 and 645132 with 100% identity.

001148 between 437328 and 439490 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

001148 between 437328 and 439490 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

J01140 between 526872 and 527871 with 100% identity.
J1141 between 10696 and 11695 with 100% identity.
J01140 between 535177 and 536176 with 100% identity.
J01140 between 524872 and 525871 with 100% identity.

J01140 between 525872 and 526871 with 100% identity.
J01140 between 523872 and 524871 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

J01146 between 5871 and 6080 with 100% identity.
J01147 between 7078 and 7615 with 100% identity.
y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
J01146 between 161130 and 162129 with 100% identity.
y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
J01148 between 442759 and 443758 with 100% identity.
J01147 between 3078 and 4077 with 100% identity.
J01147 between 2078 and 3077 with 100% identity.
y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

J1143 between 651494 and 652493 with 100% identity.

J1143 between 652494 and 653493 with 100% identity.

J01145 between 361810 and 362701 with 100% identity.

rLR266c

J1143 between 650494 and 651493 with 100% identity.

J1143 between 649494 and 650493 with 100% identity.

01139 between 20307 and 21306 with 100% identity.

01139 between 660764 and 661763 with 100% identity.

01139 between 551463 and 552462 with 100% identity.

J1138 between 73614 and 74613 with 100% identity.

J1138 between 72614 and 73613 with 100% identity.

J1141 between 371963 and 372495 with 100% identity.

J1135 between 90220 and 91219 with 100% identity.

J1136 between 82795 and 83794 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

J1136 between 81795 and 82794 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

ation\; localizes to chromosome cores independently of Mei4p and Spo11p\; mRNA is induced in meiosi

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

1144 between 942777 and 946791 with 100% identity.

1142 between 198701 and 203026 with 100% identity.

n subtelomeric region

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

primase

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

iated clathrin assembly complex (AP-2)

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

stationary phase

telomeres and is required for a telomere activity in distributive segregation\; is associated with telomere:

ing conjugation)

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

omolog

1 and YJL149w

-tyrosine to N-formyl-L-tyrosine, expressed late (10-16 hr) in sporulation

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

synthesis of glycosylphosphatidylinositol (GPI) anchors

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

yl

l1137 between 497954 and 498953 with 100% identity.

l1135 between 275986 and 276985 with 100% identity.

l1137 between 498954 and 499172 with 100% identity.

l01140 between 527872 and 528114 with 100% identity.

l001148 between 146119 and 146628 with 100% identity.

l1135 between 183526 and 184252 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

l01139 between 21307 and 21608 with 100% identity.

l01147 between 352694 and 353362 with 100% identity.

l1135 between 91220 and 91533 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
ch region that conforms to the H2 variant of the RING finger Zn²⁺ binding motif.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

l1133 between 13744 and 14743 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

l1133 between 17744 and 18743 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
1134 between 1 and 1000 with 100% identity.

01145 between 731433 and 731964 with 100% identity.

01144 between 981430 and 982429 with 100% identity.

01143 between 655494 and 655865 with 100% identity.

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

1142 between 14138 and 15137 with 100% identity.
01143 between 545784 and 546783 with 100% identity.

identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

small proteins

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

01136 between 1346165 and 1347164 with 100% identity.

1134 between 76564 and 77563 with 100% identity.
1134 between 230363 and 231362 with 100% identity.
001148 between 520230 and 521229 with 100% identity.

001140 between 543488 and 544487 with 100% identity.

001145 between 64082 and 65081 with 100% identity.
01144 between 332178 and 333177 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

teins

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

01139 between 552463 and 553445 with 100% identity.

01136 between 156704 and 157405 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25
01144 between 308356 and 309355 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

001145 between 830528 and 831527 with 100% identity.
01143 between 647133 and 648132 with 100% identity.

1134 between 220363 and 221362 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

001148 between 389268 and 390267 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

identity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

01145 between 153719 and 154718 with 100% identity.
001148 between 541315 and 541465 with 100% identity.

01140 between 548488 and 549487 with 100% identity.
01144 between 941478 and 942778 with 100% identity.

identity.

l between 3940 and 4167 with 99.122807% identity.
n subtelomeric region

01143 between 11592 and 12591 with 100% identity.
01142 between 514427 and 515426 with 100% identity.
01142 between 718444 and 719443 with 100% identity.
302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. *Cell* 8:243-25

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. *Cell* 8:243-25
y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. *Cell* 8:243-25

1134 between 2001 and 3000 with 100% identity.

ein ZnT-1 and Cot1p

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
ity. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251
y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-251

01139 between 106045 and 107044 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

01137 between 13553 and 13915 with 100% identity.

01137 between 13553 and 13915 with 100% identity.

001140 between 534177 and 535176 with 100% identity.

01142 between 15138 and 15624 with 100% identity.

001148 between 546577 and 547576 with 100% identity.

01136 between 634598 and 635597 with 100% identity.

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25
lase and/or the protein sorting machinery

01135 between 84220 and 85219 with 100% identity.

001146 between 684191 and 685190 with 100% identity.

001148 between 519230 and 520229 with 100% identity.

normal microtubule stability

y. See citation Velculescu, V.E., et al. (1997) Characterization of the yeast transcriptome. Cell 8:243-25

se gene families

01147 between 545261 and 545831 with 100% identity.

01147 between 544261 and 545260 with 100% identity.

01139 between 20307 and 21306 with 100% identity.

01141 between 115607 and 116404 with 100% identity.

01136 between 1351165 and 1351842 with 100% identity.

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ed for modification of CDC53Vcullin with RUB1

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