

	Spot	Fold Change
Contig4-2977_0018/orf6.7609/orf6.7609//		2.57
Contig4-2666_0003/orf6.8623/orf6.8623;orf6.8622//		2.58
Contig4-2865_0010/orf6.5479/orf6.5479;orf6.4801;orf6.5480;orf6.4802//		2.56
LRG1/LRG1/orf6.8741/rho-like GTPase/		2.52
Contig4-2576_0004/orf6.2077/orf6.2077///molecular_function unknown;biological_process unknown		2.22
Contig4-3093_0006/orf6.8531/orf6.8531/Transcription regulator/Transcription regulator/molecular_function unknown		2.36
Contig4-2841_0016/orf6.4006/orf6.4006/dicarboxylic amino acid permease/dicarboxylic amino acid permease		2.29
Contig4-2096_0006///		2.56
Contig4-2968_0008/CGT1/orf6.5728;orf6.5729;CGT1;CFL1/mRNA capping enzyme alpha subunit/mRNA capping enzyme		2.07
Contig4-3106_0006/YDR514/orf6.8450;YDR514/-//molecular_function unknown;biological_process unknown		2.06
Contig4-3066_0016/orf6.7572/orf6.7572/translation initiation factor eIF3 subunit/translation initiation factor eIF3		2.09
Contig4-2718_0008/orf6.4351/orf6.4351//		2.67
Contig4-2768_0013/HWP2/orf6.2933//		2.09
Contig4-2955_0014/orf6.4229/orf6.4229//		2.20
Contig4-2844_0012/orf6.850/orf6.850;orf6.1436/required for killer toxin sensitivity/required for killer toxin sensitivity		2.17
Contig4-2827_0002/orf6.6131/orf6.6131/ATPase family gene/ATPase family gene/cellular_component unknown		2.11
Contig4-3069_0019/AFG3/orf6.5744;orf6.7498;AFG3/respiration/ATP-dependent metalloprotease/mitochondrial metalloprotease		2.17
Contig4-3104_0014/orf6.7872/orf6.7872;orf6.2403///molecular_function unknown;biological_process unknown		2.07
Contig4-3047_0003/RTS1/orf6.2653;RTS1/suppressor of chaperonin mutation/B-type regulatory subunit of chaperonin		2.22
Contig4-1997_0001/SAP3/orf6.9036;orf6.5306;orf6.4644;orf6.4645;SAP3;SAP2;SAP1/secreted aspartyl protease		2.10
Contig4-2822_0002/WHI3/orf6.3359;orf6.3360;WHI3/cell size/Putative RNA binding protein/molecular_function unknown		2.03
Contig4-2587_0002/orf6.267/orf6.267;orf6.1369/Putative methyltransferase/Putative methyltransferase/nucleic acid methyltransferase		2.13
Contig4-3084_0010/SNF5/orf6.9166;orf6.774;SNF5/transcription factor/subunit of the chromatin remodeling complex		2.10
Contig4-2686_0002/HPC2/orf6.7974;HPC2/histone promoter regulation/highly charged, basic protein/transcription factor		2.09
Contig4-2184_0004/XOG1/orf6.1982;XOG1;YPT7;YOR359;YKL195;YHR194;CDC73;CAX12;CAX11;CAX1		2.13
Contig4-3098_0006/orf6.7795/orf6.7795/COQ6 monooxygenase/COQ6 monooxygenase/ubiquinone metabolism		2.09
Contig4-2878_0008/orf6.6063/orf6.6063;orf6.123//		2.07
Contig4-2383_0003///		2.10
Contig4-2904_0004/orf6.7075/orf6.7075;orf6.7076/mutS homolog involved in mitochondrial DNA repair/mutS		2.13
Contig4-2504_0009/orf6.4780/orf6.4780//		2.24
Contig4-3106_0015/YLR1/orf6.8457;YLR1/-//molecular_function unknown;biological_process unknown		2.02
Contig4-3085_0029/YJL83/orf6.7339;YJL83/IRS4-like protein//molecular_function unknown;biological_process unknown		2.64
Contig4-2953_0005/orf6.5671/orf6.5671//		2.19
Contig4-2875_0009/orf6.4223/orf6.4223/component of peripheral vacuolar membrane protein complex/component of peripheral vacuolar membrane protein complex		2.24
Contig4-3060_0005/orf6.7530/orf6.7530;orf6.7529/transcription factor tau (TFIIIC) subunit 138/transcription factor		2.21
Contig4-3092_0032/orf6.6969/orf6.6969/mitochondrial initiation factor 2/mitochondrial initiation factor 2/mitochondrial initiation factor 2		2.20
Contig4-3048_0005/orf6.8789/orf6.8789/contains formin homology domains\; homologous to BNR1 (BNI1) protein		2.07
Contig4-2301_0003///		2.14
MMM1/MMM1/orf6.3644/mitochondrial shape/		2.04
Contig4-3102_0052/TRE1/orf6.8329;TRE1/tre-related protein//molecular_function unknown;biological_process unknown		2.15
Contig4-3079_0006/YLR51/orf6.5396;orf6.5395;YLR51;SEC61/-//molecular_function unknown;biological_process unknown		2.14
Contig4-3078_0022/MLS1/orf6.7377;MLS1/catabolite-sensitive malate synthase/		2.29
Contig4-3098_0033/orf6.7784/orf6.7784/Putative transcriptional activator/Putative transcriptional activator/		2.14
Contig4-3076_0009/YJR96/orf6.8815;YJR96/reductase//molecular_function unknown;biological_process unknown		2.09
Contig4-3103_0035/orf6.8204/orf6.8204//		2.21
Contig4-3086_0006/AST2/orf6.7133;AST2/protein sorting/involved in targeting of plasma membrane [H+]ATPase		2.24
Contig4-3020_0001/ORC1/orf6.4864;orf6.4866;ORC1/origin recognition complex subunit/120-kDa (largest)		2.10
Contig4-2090_0003/orf6.4492/orf6.4492/31-kDa subunit of RNA polymerase III (C)\; HMG1 like protein/31-kDa		2.05
Contig4-3084_0047/orf6.9143/orf6.9143///molecular_function unknown;biological_process unknown		2.13
Contig4-3096_0014/orf6.5282/orf6.5282///molecular_function unknown;biological_process unknown		2.04
Contig4-2482_0003/orf6.4896/orf6.4896//		2.05

Contig4-2155_0005/SDS23/orf6.6345;SDS23;PLB97;OLE1;LTP1;CAX14;CAX13/spindle pole body protein/	2.60
Contig4-3001_0023/YER113/orf6.3027;YER113/EMP70-like protein//molecular_function unknown;biologica	2.04
Contig4-2618_0004/orf6.3432/orf6.3432;orf6.1511///molecular_function unknown;biological_process unknow	2.09
Contig4-3031_0004/orf6.6264/orf6.6264//	2.10
Contig4-3085_0025/orf6.7338/orf6.7338;orf6.231/Ploidy-related/Ploidy-related/molecular_function unknown	2.04
Contig4-2814_0005/YJR75/orf6.6460;YJR75/mannosyltransferase/putative mannosyltransferase/mannosyl	2.24
Contig4-2920_0005/orf6.7352/orf6.7352/component of vacuolar membrane protein complex/component of v	2.29
Contig4-2563_0010/orf6.6389/orf6.6389//	2.13
Contig4-2374_0004/orf6.6005/orf6.6005//	2.02
Contig4-2953_0002/orf6.7928/orf6.7928;orf6.2052/Rsp5p ubiquitin ligase binding protein/Rsp5p ubiquitin lig	2.19
Contig4-2844_0002/orf6.7010/orf6.7010/subunit of the anaphase promoting complex/subunit of the anapha	2.19
Contig4-3060_0003/TFC3/orf6.7528;orf6.7527;TFC3;YGR280/transcription factor IIIC subunit/transcription f	2.12
ANX1/ANX1//glycoamidase/	3.36
Contig4-2753_0016/orf6.3433/orf6.3433//	2.09
Contig4-2437_0007////	2.22
RPO21/RPO21//RNA polymerase II subunit/	2.59
Contig4-2900_0029/orf6.3478/orf6.3478///biological_process unknown	2.27
Contig4-3068_0004/orf6.4357/orf6.4357;orf6.959;orf6.6812//	2.28
Contig4-1935_0004/YJR15/orf6.4581;YJR15/SNG1-like protein/involved in nitrosoguanidine resistance/mol	2.09
Contig4-3021_0032/orf6.184/orf6.184;orf6.5612;orf6.185;orf6.5613/Similar to ferric reductases Fre1p and F	2.22
Contig4-2691_0009/YFR16/orf6.3704;YFR16/-//molecular_function unknown;biological_process unknown	2.26
Contig4-2646_0014/orf6.7728/orf6.7728///molecular_function unknown;biological_process unknown	2.04
Contig4-2815_0013////	2.07
Contig4-2992_0008/PDK2/orf6.8362;PDK2/pyruvate dehydrogenase kinase//molecular_function unknown;bi	4.15
Contig4-3108_0115/BPL1/orf6.8993;BPL1;YHR34/biotin apo-protein ligase/Biotin:apoprotein ligase/intracell	2.10
Contig4-3058_0002/orf6.3574/orf6.3574//	2.08
Contig4-2758_0008/orf6.1424/orf6.1424/Transcription factor/Transcription factor/transcription factor	2.06
Contig4-3097_0048/orf6.8097/orf6.8097///molecular_function unknown;biological_process unknown	2.07
Contig4-3072_0008/YKL40/orf6.7488;YKL40/nifU-like protein/Nifu-like protein/mitochondrial matrix;molecul	2.07
Contig4-3106_0069/orf6.8488/orf6.8488///molecular_function unknown;biological_process unknown	2.09
Contig4-2245_0002/orf6.8382/orf6.8382;orf6.1910//	2.02
Contig4-3005_0018/HOL98/orf6.5337;HOL98/HOL1-like protein/Putative ion transporter similar to the major	2.13
Contig4-2985_0006/orf6.5601/orf6.5601;orf6.5602//	2.17
Contig4-2966_0007/FAL1/orf6.6169;FAL1/rRNA processing/DEAD-box protein, putative RNA helicase/nucl	2.06
Contig4-3085_0023/orf6.7337/orf6.7337/dihydrosphingosine phosphate lyase (also known as sphingosine p	2.12
Contig4-2781_0021/orf6.923/orf6.923/Protein with homology to mammalian Nup107p/Protein with homolog	2.05
Contig4-2478_0002/YPL246/orf6.7634;YPL246/-//molecular_function unknown;biological_process unknown	2.02
Contig4-2565_0003/orf6.4706/orf6.4706/peptide transporter/peptide transporter/cellular_component unknow	2.10
Contig4-3071_0019/YJR33/orf6.8631;orf6.8630;YJR33/-/Regulator of (H+)-ATPase in vacuolar membrane/i	2.19
Contig4-3105_0053/UBC4/orf6.8919;UBC4/ubiquitin-conjugating enzyme/ubiquitin-conjugating enzyme/cell	2.13
Contig4-2753_0014/orf6.3434/orf6.3434//	2.13
Contig4-3065_0030/orf6.5983/orf6.5983//	2.14
Contig4-2823_0007/orf6.4443/orf6.4443//	2.23
Contig4-3089_0004/TRL1/orf6.7649;TRL1/tRNA ligase/tRNA ligase/nuclear inner membrane;nucleoplasm;f	2.34
DUR1/DUR1//urea amidolyase/	2.27
Contig4-3100_0014/orf6.6371/orf6.6371;orf6.8710;orf6.6377;orf6.8711///molecular_function unknown;biolog	2.45
Contig4-3072_0031/orf6.7477/orf6.7477/medium subunit of the clathrin-associated protein complex/mediu	2.08
Contig4-2628_0003/orf6.6787/orf6.6787///molecular_function unknown;biological_process unknown	2.01
Contig4-2824_0021/orf6.355/orf6.355;orf6.6413/Leucine permease transcriptional regulator/Leucine perme	2.11
Contig4-2933_0003/orf6.364/orf6.364;orf6.2385;orf6.365;orf6.2383///molecular_function unknown;biologica	2.50
Contig4-2717_0017/YOR338/orf6.5295;YOR338;YAL34/-//molecular_function unknown;biological_process	2.13
Contig4-2669_0002////	2.18

Contig4-1978_0003/orf6.3917/orf6.3917//	4.72
BUF2/BUF2//DNA replication/	4.18
Contig4-2959_0003/YOR166/orf6.8494;YOR166/-//molecular_function unknown;biological_process unknow	2.60
Contig4-3032_0004/YOR243/orf6.2883;orf6.7930;orf6.7161;YOR243;SPT23;CAX4;CAX3;CAX2;CAX1;YBL	3.79
Contig4-2298_0005////	6.56
Contig4-3081_0047/orf6.5649/orf6.5649///molecular_function unknown;biological_process unknown	3.21
Contig4-2889_0017/orf6.7960/orf6.7960//	2.68
Contig4-2876_0017/RBT4/orf6.537;orf6.5422;orf6.5423;orf6.538;RBT4;YJL79/Similar to plant PR-1 class of	3.52
Contig4-2077_0005/YBR22/orf6.1976;orf6.918;YBR22/-//molecular_function unknown;biological_process ui	3.78
Contig4-2998_0014/orf6.6255/orf6.6255/alpha-isopropylmalate synthase (2-Isopropylmalate Synthase)/alpf	2.61
Contig4-2387_0006/orf6.1556/orf6.1556;orf6.3141;orf6.1555;orf6.1557;orf6.1893/putative transcription fact	2.60
Contig4-2476_0010/orf6.1581/orf6.1581;orf6.1580/anchorage subunit of a-agglutinin/anchorage subunit of :	2.52
Contig4-3064_0019////	6.25
Contig4-2677_0006/VMA8/VMA8;SOU2;SOU1/vacuolar H+-ATPase subunit 8/	2.40
Contig4-2811_0017////	2.46
Contig4-3005_0008/ZRT2/orf6.5335;ZRT2/zinc transport protein/Low-affinity zinc transport protein/low-affin	4.90
Contig4-2947_0008/orf6.4661/orf6.4661//	4.27
Contig4-3058_0032/orf6.4344/orf6.4344/Dimethylaniline monooxygenase/Dimethylaniline monooxygenase/mc	2.18
Contig4-2786_0008/orf6.3584/orf6.3584/positive transcriptional regulator of ADH2 and peroxisomal protein	4.03
YKL175/YKL175//-/	7.97
Contig4-1746_0004////	2.78
Contig4-2995_0008/orf6.8434/orf6.8434;orf6.8433/DNA repair helicase component of transcription factor b/	3.85
Contig4-2661_0010/orf6.4395/orf6.4395//	2.11
Contig4-3032_0004/YOR243/orf6.2883;orf6.7930;orf6.7161;YOR243;SPT23;CAX4;CAX3;CAX2;CAX1;YBL	3.45
Contig4-2375_0009/YBR22/orf6.918;orf6.1976;YBR22/-//molecular_function unknown;biological_process ui	4.17
Contig4-2797_0003/orf6.5637/orf6.5637/very low affinity methionine permease/very low affinity methionine	2.11
Contig4-3084_0038/orf6.9148/orf6.9148;orf6.9146//	12.05
Contig4-3036_0007/orf6.8552/orf6.8552/ATP-dependent RNA helicase of DEAD box family/ATP-dependen	2.01
Contig4-2263_0006/YDR470/orf6.5148;orf6.2339;YDR470/mitochondrial carrier protein//mitochondrial oute	3.65
Contig4-2520_0001/orf6.6098/orf6.6098//	2.62
Contig4-2986_0007/LSM5/orf6.8157;orf6.8156;LSM5/Sm-like protein/MutL Homolog/	2.95
Contig4-3050_0029/YNL157/orf6.4814;YNL157/-//molecular_function unknown;biological_process unknowr	3.04
Contig4-2965_0012/YOR243/orf6.7161;orf6.2883;orf6.7930;YOR243;SPT23;CAX4;CAX3;CAX2;CAX1;YBL	2.10
Contig4-2472_0001/CHS2/orf6.8379;CHS2/chitin synthase 2/chitin synthase 1/chitin synthase;cytokinesis	2.11
Contig4-2437_0009/orf6.5260/orf6.5260///molecular_function unknown;biological_process unknown	2.13
Contig4-2757_0014/orf6.5565/orf6.5565//	2.10
Contig4-2947_0010/orf6.4661/orf6.4661///biological_process unknown	4.25
Contig4-2878_0006/orf6.6064/orf6.6064;orf6.1945;orf6.765;orf6.362;orf6.2030;orf6.2029;orf6.1946;orf6.194	2.10
Contig4-2362_0001/orf6.1489/orf6.1489//	3.25
Contig4-3050_0016/YHR134/orf6.4302;YHR134/-/Weak suppressor of smt3 mutant/molecular_function unk	4.18
Contig4-2379_0005/orf6.8423/orf6.8423//	2.31
Contig4-2096_0002/orf6.3879/orf6.3879/bovine prefoldin subunit 1 homolog (putative)/bovine prefoldin subi	2.72
Contig4-2979_0019/orf6.7504/orf6.7504;orf6.1870/transcription factor/transcription factor/transcription facto	2.71
Contig4-2244_0002/STE14/orf6.1442;STE14/farnesyl cysteine carboxyl-methyltransferase/farnesyl cysteine	2.15
Contig4-1838_0002/orf6.863/orf6.863;orf6.3677///molecular_function unknown;biological_process unknown	5.39
Contig4-3102_0051/YPL249/orf6.8329;YPL249;YMR192;TRE1;RPS7/-//molecular_function unknown;biolog	2.15
Contig4-2591_0004/YOR243/orf6.2021;orf6.1825;orf6.2022;YOR243;SPT23;CAX4;CAX3;CAX2;CAX1/-/	3.13
Contig4-3056_0035/orf6.5500/orf6.5500//	4.97
Contig4-3089_0050/orf6.7635/orf6.7635//	2.87
YCL48/YCL48//-/	4.22
Contig4-1616_0007////	5.49
Contig4-3056_0012/orf6.5507/orf6.5507/16-kDa RNA polymerase subunit (common to polymerases I, II anc	2.31

Contig4-2012_0004////	2.23
Contig4-2746_0012/LIP1/orf6.2398;orf6.7355;LIP1;MTX7/extracellular lipase/	3.23
Contig4-2397_0004/orf6.3214/orf6.3214;orf6.3215//	2.27
ROX1/ROX1//DNA-binding protein/	6.68
Contig4-3000_0025/orf6.980/orf6.980///molecular_function unknown;biological_process unknown	2.37
Contig4-2971_0003/orf6.7473/orf6.7473/GPI-anchored aspartic protease/GPI-anchored aspartic protease/p	2.74
Contig4-2819_0013/orf6.4071/orf6.4071;orf6.4716//	2.93
Contig4-2797_0022/orf6.5643/orf6.5643/Integrin analogue gene/Integrin analogue gene/	2.99
Contig4-2724_0006////	3.09
Contig4-2827_0010/orf6.6134/orf6.6134//	3.51
Contig4-3037_0007/DUR96/orf6.9122;DUR96/DUR3-like protein/Urea transporter/transport	2.29
Contig4-3063_0011/YNL129/orf6.7059;YNL129/-//molecular_function unknown;biological_process unknown	3.02
Contig4-2479_0008/orf6.5735/orf6.5735//	13.86
Contig4-2629_0008/NGR1/orf6.8841;NGR1/growth regulation/negative growth regulatory protein/biological_	3.26
Contig4-2539_0007/orf6.5533/orf6.5533//	3.59
Contig4-2705_0009/NPR2/orf6.5630;NPR2/nitrogen permease regulator/Non-membrane-embedded, PEST	2.87
Contig4-2660_0010/ABZ1/orf6.910;orf6.1154;orf6.1155;ABZ1/para-aminobenzoate synthase/para-aminobe	2.77

Spot	Fold Change
Contig4-2573_0009/YPT7/orf6.5705;YPT7;YOR359;YKL195;YHR194;CDC73;CAX12;CAX11;CAX10	-2.83
Contig4-2647_0005/orf6.2129/orf6.2129///cellular_component unknown;molecular_function unknown;	-2.18
Contig4-2852_0012/YPL275/orf6.3525;orf6.3469;orf6.485;orf6.2662;orf6.3470;orf6.486;orf6.2663;YPI	-2.95
Contig4-2511_0008/orf6.8402/orf6.8402///molecular_function unknown;biological_process unknown	-2.53
Contig4-2394_0006/orf6.3443/orf6.3443;orf6.3444/USO1 homolog (S. cerevisiae), cytoskeletal-relate	-2.52
Contig4-2640_0015/BAT99/orf6.7740;BAT99/branched-chain amino acid transaminase/Branched-Ch	-2.80
Contig4-2933_0007/CSP37/CSP37/membrane protein/Integrin analogue gene/	-3.47
Contig4-2980_0004/YNL206/orf6.1744;orf6.817;orf6.1745;YNL206/-/Regulator of Ty1 Transposition -	-2.23
Contig4-2984_0022/orf6.1728/orf6.1728/spindle pole body component, associates in a complex with 9	-2.67
YGL224/YGL224//-	-2.13
Contig4-1996_0006/KIN28/orf6.5117;orf6.903;KIN28/threonine protein kinase/serine-threonine kinase	-2.25
Contig4-2684_0006/YOR273/orf6.2283;YOR273/-/vacuolar membrane;molecular_function unknown;:	-2.37
Contig4-3043_0004/FTR1/orf6.8119;orf6.8131;FTR1;YER145/iron permease/Iron permease/transport	-3.23
Contig4-2520_0008/HYP2/orf6.6099;HYP2/translation initiation factor eIF-5A/anaerobically expressec	-3.80
Contig4-2817_0007/YJR100/orf6.1917;orf6.4047;YJR100/-/molecular_function unknown;biological_p	-2.53
Contig4-2993_0015/RIM2/orf6.4191;RIM2/respiration/Probable carrier protein, mitochondrial/transpor	-2.42
Contig4-2410_0006/PRS1/orf6.5345;orf6.1887;PRS1/phosphoribosyl pyrophosphate synthetase/ribose	-3.25
Contig4-2727_0001/CYS4/orf6.6682;CYS4/cystathionine beta-synthase/Cystathionine beta-synthase/	-3.90
Contig4-3001_0010/YCR17/orf6.3024;YCR17/-/molecular_function unknown;biological_process unkr	-3.14
Contig4-3056_0018/RPS3/orf6.5505;RPS3/ribosomal protein S3/Ribosomal protein S3 (rp13) (YS3)/c	-3.04
Contig4-2110_0005/orf6.6423/orf6.6423///molecular_function unknown;biological_process unknown	-2.42
YML117/YML117//-	-2.30
Contig4-2603_0002/HXT7/orf6.2376;orf6.1210;orf6.2379;orf6.187;orf6.2377;orf6.2378;HXT7;HXT98;t	-3.53
Contig4-2976_0016/GLG2/orf6.5029;GLG2/glycogenin/glycogen synthesis initiator/glycogen metaboli	-2.36
Contig4-2604_0006/YSH1/orf6.4180;YSH1/polyadenylation factor 1 subunit/subunit of Polyadenylatio	-2.83
YER157/YER157//-	-2.45
Contig4-2305_0001/HXT4/orf6.2379;orf6.187;orf6.2376;orf6.1210;orf6.2377;orf6.2378;HXT4;HXT98;t	-5.11
Contig4-2163_0004/YJR125/orf6.6411;orf6.6412;YJR125/-/Ent3p/actin cortical patch (sensu Sacchar	-2.60
Contig4-2711_0009/orf6.6157/orf6.6157;orf6.6156///molecular_function unknown;biological_process t	-2.13
Contig4-2639_0004/orf6.2965/orf6.2965//	-2.23
Contig4-3102_0006/orf6.8359/orf6.8359;orf6.2476///molecular_function unknown;biological_process t	-2.29
PET100/PET100//cytochrome c oxidase assembly/	-2.55
YNL45/YNL45//protease/	-2.15
YLR386/YLR386//-	-2.86
YBR103/YBR103//telomeric silencing/	-3.03
Contig4-2116_0004/MSS4/orf6.1660;MSS4/supressor of stt4 mutation/Phosphatidylinositol 4-phosph	-2.19
Contig4-2552_0003/orf6.2155/orf6.2155;orf6.5304;orf6.5303/involved in targeting of plasma membrar	-2.46
Contig4-2823_0011////	-2.56
Contig4-2770_0009/AOS99/orf6.4496;AOS99/AOS1-like protein/Similar to ubiquitin activating protein:	-2.94
Contig4-2896_0005/orf6.8672/orf6.8672;orf6.8670///molecular_function unknown;biological_process t	-2.55
Contig4-3107_0010/orf6.8741/orf6.8741/Protein similar to LIM-domain proteins and to rhoVrac GTPas	-2.76
Contig4-2790_0009/orf6.6219/orf6.6219//	-2.82
Contig4-3097_0033/orf6.8085/orf6.8085/subunit of a cytoplasmic histone acetyltransferase/subunit of	-2.32
YNL246/YNL246//-	-2.37
YLR20/YLR20//lipase/	-2.19
Contig4-2558_0011/MET25/orf6.4513;MET25/O-acetylhomoserine sulfhydrylase//molecular_function	-2.54
Contig4-2815_0003////	-2.14
Contig4-2976_0009/RNC1/orf6.5027;orf6.5028;RNC1;SPX49/nuclease/Endo-exonuclease/tRNA metl	-3.92
Contig4-2658_0006/orf6.3675/orf6.3675//	-2.86
Contig4-3054_0013///subunit e of mitochondrial F1F0-ATPase/subunit e of mitochondrial F1F0-ATPas	-2.55

Contig4-2163_0001/orf6.6409/orf6.6409;orf6.6410//	-2.10
Contig4-3010_0022/orf6.7042/orf6.7042/Stoichiometric member of mediator complex/Stoichiometric n	-3.20
Contig4-2967_0007/orf6.5158/orf6.5158///molecular_function unknown;biological_process unknown	-2.55
Contig4-2127_0004/RBL2/RBL2/beta-tubulin binding protein/beta-tubulin binding protein/cytoplasm;cc	-2.49
Contig4-2775_0009/YNL200/orf6.6490;YNL200/TGR-CL10C like protein//molecular_function unknowi	-2.36
Contig4-2813_0010/YCR47/orf6.5038;YCR47/SAM-binding protein/Protein carboxyl methylase/molec	-3.69
Contig4-2993_0011/MED8/orf6.4189;orf6.30;MED8/mediator complex subunit/Stoichiometric member	-2.07
Contig4-2567_0004/YIR426/orf6.6076;YIR426/-//molecular_function unknown;biological_process unk	-2.65
YJL73/YJL73//dnaJ-like protein/	-2.38
Contig4-2301_0005/HMG1/orf6.3220;HMG1/3-hydroxy-3-methyl-glutaryl coenzyme A reductase/3-hy	-3.19
Contig4-3009_0023/TOP2/orf6.4380;orf6.6509;TOP2;SDH99/DNA topoisomerase II/Flavoprotein subu	-3.30
Contig4-2940_0008/MET16/orf6.6939;MET16/3'phosphoadenylylsulfate reductase/3'phosphoadenyly	-2.28
Contig4-3025_0013/SEC18/orf6.8016;SEC18/ER-golgi transport/cytoplasmic protein involved in prote	-2.15
Contig4-2974_0006/orf6.4139/orf6.4139;orf6.1588/(putative) histone deacetylase/(putative) histone d	-3.33
Contig4-1925_0002/YDR104/orf6.5363;YDR104/-//molecular_function unknown	-2.27
Contig4-2666_0002/YAR3/orf6.8624;YAR3/-/beta transducin domain/molecular_function unknown;bio	-2.71
Contig4-2997_0011/STE50/orf6.6436;STE50/signal transduction/STE50/	-2.51
Contig4-2972_0017/orf6.7582/orf6.7582/zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear c	-2.19
Contig4-3003_0022/orf6.9010/orf6.9010/regulator of Ty1 Transposition/regulator of Ty1 Transposition	-2.38
Contig4-2708_0001/orf6.4857/orf6.4857//	-2.20
Contig4-2604_0010/YLR281/orf6.4182;YLR281/-//molecular_function unknown;biological_process un	-2.54
Contig4-2540_0001/orf6.4368/orf6.4368///molecular_function unknown;biological_process unknown	-2.58
Contig4-2917_0009/orf6.6564/orf6.6564///molecular_function unknown;biological_process unknown	-3.17
Contig4-3029_0002/ERV25/orf6.8566;ERV25/protein secretion/	-2.16
Contig4-2513_0002/orf6.6585/orf6.6585;orf6.6587;orf6.6588//	-2.84
Contig4-2828_0010/ARH1/orf6.2820;orf6.2034;ARH1/adrenodoxin oxidoreductase-like protein/adrenc	-2.60
Contig4-2918_0009/YGR215/orf6.7192;YGR215/-/protein of the small subunit of the mitochondrial rib	-3.10
Contig4-3095_0030/YGR103/orf6.6843;YGR103/-//nucleolus;nucleus;molecular_function unknown;bi	-2.31
Contig4-2862_0007/orf6.6355/orf6.6355/regulator of phosphatase Glc7p, involved in glucose repressi	-2.24
Contig4-2290_0009/ARE2/orf6.5898;ARE2/sterol esterification/Acyl-CoA cholesterol acyltransferase (-2.11
Contig4-1818_0003/PLB99/orf6.3690;orf6.1985;PLB99/phospholipase B/phospholipase B/lysosphosp	-2.99
Contig4-2626_0004/orf6.1217/orf6.1217//	-2.60
Contig4-2739_0005/orf6.6931/orf6.6931///molecular_function unknown;biological_process unknown	-2.15
Contig4-2332_0005/orf6.2043/orf6.2043;orf6.274///molecular_function unknown;biological_process ur	-2.09
Contig4-3082_0015/NUT2/orf6.7674;NUT2/transcription factor/21 kD mediator subunit of RNA polym	-2.17
Contig4-3103_0019/YLR412/orf6.8219;YLR412/-//molecular_function unknown;biological_process un	-2.33
Contig4-2558_0008/orf6.4511/orf6.4511///molecular_function unknown;biological_process unknown	-2.42
Contig4-2997_0005/orf6.625/orf6.625;orf6.6434/cytoplasmic GTPase-activating protein/cytoplasmic G	-2.39
Contig4-2832_0006/YKL27/orf6.4746;orf6.117;orf6.4745;YKL27;YHR3/molybdopterin biosynthesis-lik	-3.27
Contig4-2986_0032/orf6.749/orf6.749;orf6.748//	-2.37
Contig4-2941_0003/orf6.7546/orf6.7546/cytoplasmic GTPase-activating protein/cytoplasmic GTPase-	-2.05
Contig4-2658_0008/YNL227/orf6.3674;orf6.229;YNL227/dnaJ-like protein//molecular_function unknow	-2.81
Contig4-2553_0006/LIP5/orf6.6578;orf6.6579;LIP5/lipoic acid synthase/lipoic acid synthase/fatty acid	-3.02
Contig4-2918_0008/YGR215/orf6.7191;YGR215/-/	-2.45
Contig4-2928_0005/orf6.3977/orf6.3977;orf6.6598//	-2.05
Contig4-2746_0017/orf6.2399/orf6.2399///molecular_function unknown;biological_process unknown	-2.37
Contig4-2916_0011/orf6.5100/orf6.5100//	-2.43
Contig4-2332_0007/YNL274/orf6.2042;orf6.275;orf6.6087;YNL274/alpha-ketoisocaproate reductase//	-2.34
Contig4-2972_0022/orf6.7584/orf6.7584/involved in glucose derepression/involved in glucose derepre	-3.22
Contig4-3099_0035/ELO1/orf6.3946;orf6.7270;orf6.5772;ELO1;FEN1/fatty acid elongation/Probable s	-2.52
Contig4-2715_0008/orf6.4414/orf6.4414;orf6.4415//	-2.38

Contig4-2816_0007/YPT7/orf6.5716;YPT7;YOR359;YKL195;YHR194;CDC73;CAX12;CAX11;CAX10	-3.00
Contig4-2976_0002/CRL1/orf6.5024;CRL1/GTP-binding protein/ras homolog--GTP binding protein/int	-2.58
Contig4-2610_0003/YLR326/orf6.4755;YLR326/-//molecular_function unknown;biological_process un	-2.20
Contig4-2527_0007/orf6.1999/orf6.1999//	-2.53
Contig4-2692_0012/orf6.2863/orf6.2863//	-3.32
Contig4-2934_0009/ECM21/orf6.3053;orf6.3331;ECM21/-/involved in cell wall biogenesis/molecular_f	-2.32
Contig4-2307_0005/YEL15/orf6.7007;YEL15/-//molecular_function unknown;biological_process unkn	-3.45
Contig4-2948_0015/DPH2/orf6.6067;orf6.6918;orf6.814;DPH2/diphthamide biosynthesis/diphthamide s	-2.61
Contig4-2945_0021/orf6.7923/orf6.7923/High level expression reduced Ty3 Transposition/High level e	-2.38
Contig4-2291_0005/orf6.5870/orf6.5870/glycerol-3-phosphate dehydrogenase, mitochondrial/glycerol	-3.93
Contig4-2185_0005/orf6.3400/orf6.3400/regulatory protein/regulatory protein/molecular_function unkr	-3.53
Contig4-2690_0011/YLL27/orf6.4463;YLL27/-/Iron Sulfur Assembly -- IscAVNifA homolog/mitochondri	-2.37
Contig4-2882_0016/RPS18/orf6.3417;RPS18/ribosomal protein S18/protein of the small subunit of the	-2.73
Contig4-2949_0007/orf6.5457/orf6.5457/Amino acid permease/Amino acid permease/endoplasmic re	-2.79
Contig4-2696_0016/MAS20/orf6.6663;MAS20/mitochondrial assembly/20 kDa mitochondrial outer me	-3.37
Contig4-2582_0009/orf6.3872/orf6.3872//	-2.84
Contig4-3090_0040/PRE9/orf6.7234;PRE9/proteasome subunit Y13/proteasome component Y13/20S	-2.15
YMR230/YMR230//ribosomal protein/	-3.25
Contig4-2537_0005/SEC17/orf6.1399;SEC17/ER-golgi vesicle transport/peripheral membrane protein	-2.47
Contig4-2662_0008/YCF1/orf6.4035;YCF1/metal resistance protein/ABC-type transmembrane transp	-2.46
SOK1/SOK1/orf6.3088/suppressor of cyclic AMP-dependent protein kinase mutant/	-2.27
YJR130/YJR130//-	-2.17
Contig4-2680_0006/SPX9/orf6.1271;SPX9/-//biological_process unknown	-2.12
Contig4-2676_0017/orf6.3850/orf6.3850;orf6.3849;orf6.1125///molecular_function unknown;biological	-2.73
Contig4-2583_0014/orf6.5605/orf6.5605///molecular_function unknown;biological_process unknown	-2.43
Contig4-2249_0005/YOL107/orf6.3784;orf6.1564;YOL107/-//molecular_function unknown;biological_p	-2.25
Contig4-2711_0006/SGT2/orf6.6155;SGT2/-/small glutamine-rich tetratricopeptide repeat containing p	-3.32
Contig4-2975_0008/YPL133/orf6.4951;YPL133/transcription factor//molecular_function unknown;biolc	-2.32
Contig4-2734_0006/HSP12/orf6.2761;orf6.1771;orf6.1668;HSP12/12kd heat-shock protein/12 kDa he	-3.00
Contig4-2678_0010/orf6.5789/orf6.5789///molecular_function unknown;biological_process unknown	-3.57
Contig4-2870_0002/orf6.1317/orf6.1317;orf6.8183//	-3.78
Contig4-2944_0011/orf6.2296/orf6.2296;orf6.2236///molecular_function unknown;biological_process u	-2.22
Contig4-3028_0013/APS1/orf6.2168;APS1/clathrin associated protein/clathrin-associated protein com	-2.18
Contig4-3098_0053/orf6.7771/orf6.7771;orf6.7769/putative member of nontransporter group of ATP-b	-2.36
Contig4-2978_0004/orf6.7203/orf6.7203/Zinc finger (6-Cys)/Zinc finger (6-Cys)/molecular_function un	-2.11
Contig4-2862_0005/YPL162/orf6.6354;YPL162/-//molecular_function unknown;biological_process unl	-2.24
YNR65/YNR65//vacuolar protein sorting/	-3.43
Contig4-2258_0001/YBL64/orf6.6956;YBL64;MTX4;CAX6;CAX5/rehydrin/similar to thiol-specific antic	-2.15
Contig4-2826_0003/TOP2/orf6.4382;TOP2/DNA topoisomerase II/topoisomerase II, Top2p localizes t	-2.38
Contig4-2612_0011////	-2.04
Contig4-3065_0027/YOR311/orf6.5984;YOR311/-//endoplasmic reticulum membrane, integral protein	-2.48
SOP2/SOP2//phosphatidylinositol phosphate phosphatase/	-3.53
YFR7/YFR7//-	-2.41
SSK1/SSK1/orf6.3767/two-component response regulator/	-2.81
Contig4-3030_0008/orf6.8861/orf6.8861/Ent4p/Ent4p/actin cortical patch (sensu Saccharomyces);cyt	-2.20
Contig4-2314_0004/YCL47/orf6.1486;orf6.44;YCL47/-//molecular_function unknown;biological_proce	-3.18
Contig4-2969_0002/orf6.2831/orf6.2831///molecular_function unknown;biological_process unknown	-2.46
YOR80/YOR80//-	-2.57
Contig4-2107_0004/YJL171/orf6.799;orf6.1967;orf6.800;YJL171/-//molecular_function unknown;biolo	-2.70
Contig4-2856_0010/orf6.6535/orf6.6535/Type 2C protein phosphatase/Type 2C protein phosphatase/	-2.39
Contig4-2997_0025/DYS1/orf6.6446;DYS1/deoxyhypusine synthase/Deoxyhypusine synthase/deoxy	-2.43

Contig4-2646_0008/orf6.7725/orf6.7725///molecular_function unknown	-2.21
SPX42/SPX42//-/	-2.32
Contig4-2320_0004/APE3/orf6.2049;orf6.806;APE3/aminopeptidase/Aminopeptidase yscIII/vacuole;a	-2.16
Contig4-2740_0017/orf6.7407/orf6.7407/34-kDa, gamma subunit of oligosaccharyl transferase glycop	-2.81
Contig4-2690_0008/orf6.4465/orf6.4465;orf6.873//	-2.51
Contig4-2937_0012/orf6.7305/orf6.7305//	-2.87
Contig4-2933_0014/orf6.3369/orf6.3369/90 kd subunit of TFIIIB, also called TFIIIB90 or B" or B"90 cc	-2.82
Contig4-2886_0006/orf6.609/orf6.609;orf6.4079/negative transcriptional regulator/negative transcripti	-2.33
Contig4-3052_0015/orf6.3905/orf6.3905/involved in vacuolar protein targeting/involved in vacuolar pr	-2.41
Contig4-3107_0051/orf6.8758/orf6.8758;orf6.2173;orf6.8759/ISWI One Complex/ISWI One Complex/	-3.29
Contig4-2918_0012/orf6.7193/orf6.7193/putative calcium channel/putative calcium channel/transport	-2.79
Contig4-2671_0010/FET96/orf6.5010;orf6.2939;orf6.790;orf6.5009;orf6.5008;FET96;FET3/FET3-like	-2.83
Contig4-3100_0008/YDL201/orf6.2916;YDL201/-//molecular_function unknown;biological_process un	-2.68
PYC2/PYC2//pyruvate carboxylase 2/	-2.35
YLR151/YLR151//-/	-2.33
Contig4-1995_0008/orf6.3473/orf6.3473;orf6.1196//	-2.66
Contig4-2347_0004/orf6.6429/orf6.6429;orf6.2338///molecular_function unknown;biological_process t	-3.49
Contig4-2821_0006/RPA43/orf6.4104;orf6.4103;RPA43/RNA polymerase I subunit A43/DNA-dependi	-4.22
Contig4-2973_0009/RPS0A/orf6.7721;orf6.7720;YST99/Ribosomal protein S0A/Ribosomal protein SC	-2.46
Contig4-2513_0002/orf6.6585/orf6.6585;orf6.6587;orf6.6588//	-2.07
SSK2/SSK2/orf6.2292/protein kinase/	-2.07
Contig4-2693_0008/HCP1/orf6.3728;HCP1/cysteine protease/(putative) transamidase involved in GP	-2.98
Contig4-2732_0015/YGL30/orf6.152;orf6.2559;YGL30/ribosomal protein/	-2.15
Contig4-2681_0014/YBL64/orf6.1877;orf6.3125;orf6.3502;orf6.566;orf6.6016;orf6.5083;orf6.7931;orf6	-2.53
Contig4-2991_0005/orf6.3856/orf6.3856//	-2.43
YNL155/YNL155//-/	-2.66
Contig4-2091_0003/ERV1/ERV1/mitochondrial biogenesis/involved in mitochondrial biogenesis/molec	-2.33
Contig4-2599_0006/orf6.4067/orf6.4067/aspartate aminotransferase, cytosolic/aspartate aminotransfe	-2.54
Contig4-2864_0003/orf6.8659/orf6.8659/181aa protein - 20.5 kD/181aa protein - 20.5 kD/molecular_fi	-2.02
Contig4-2953_0015/ARC15/orf6.5663;ARC15/ARP complex subunit/ARP2/3 complex component/Arp	-2.25
Contig4-3103_0007/FAS1/orf6.8228;FAS1/fatty acid synthase beta subunit/pentafunctional enzyme c	-3.30
YJL200/YJL200//aconitase/	-2.17
Contig4-1856_0005/PEC1/orf6.4754;PEC1/phosphoethanolamine cytidyltransferase/choline phosph	-7.07
Contig4-2069_0002/YMR74/orf6.407;orf6.2634;YMR74/-//molecular_function unknown;biological_pro	-2.95
Contig4-1801_0005/YLR215/orf6.2698;orf6.676;YLR215/D123-like protein//molecular_function unkno	-4.30
Contig4-2917_0017/orf6.6568/orf6.6568;orf6.132;orf6.131//	-2.49
Contig4-2944_0008/RPB2/orf6.2239;RPB2/RNA polymerase II subunit/second largest subunit of RNA	-2.08
Contig4-3108_0010/orf6.8939/orf6.8939;orf6.8938//	-2.90
Contig4-2697_0005/HAT1/orf6.4117;orf6.894;HAT1/histone acetyltransferase/histone acetyltransfera	-3.32
YLR152/YLR152//-/	-2.24
Contig4-2124_0003/orf6.5182/orf6.5182///molecular_function unknown;biological_process unknown	-3.00
Contig4-2539_0011/YDR365/orf6.504;orf6.5589;orf6.5590;orf6.505;YDR365/-//cellular_component ur	-2.56
Contig4-2599_0003/orf6.4066/orf6.4066;orf6.4065/Protein containing zinc fingers very similar to zinc f	-3.72
Contig4-3074_0028/orf6.7817/orf6.7817/Cell division cycle protein/Cell division cycle protein/anaphas	-3.11
YFR47/YFR47//quinolinate phosphoribosyl transferase/	-2.18
Contig4-2584_0003/YBL64/orf6.8027;orf6.5530;orf6.1954;orf6.1367;orf6.5412;orf6.4578;orf6.8703;YE	-2.25
Contig4-3031_0024/STO1/orf6.6277;STO1/glycolytic enzyme transcription/transcriptional activator of	-3.15
Contig4-2999_0011/orf6.5904/orf6.5904//	-2.34
Contig4-2972_0011/orf6.7581/orf6.7581//	-2.38
Contig4-2782_0005/TYS1/orf6.5482;TYS1/tyrosyl-tRNA synthetase/tyrosyl-tRNA synthetase, cytoplasmic	-2.43
Contig4-2971_0010/NYV1/orf6.7466;NYV1/synaptobrevin/vacuolar v-SNARE/vacuolar membrane;v-S	-2.51

Contig4-3038_0009/orf6.6769/orf6.6769/Highly acidic C-terminus/Highly acidic C-terminus/molecular_	-2.75
Contig4-2070_0004/CDC10/orf6.6760;CDC10/cell cycle/conserved potential GTP-ginding protein/sep	-4.36
Contig4-2886_0003/orf6.4077/orf6.4077///molecular_function unknown;biological_process unknown	-2.29
Contig4-2941_0014/orf6.7554/orf6.7554//	-2.34
Contig4-3010_0009/orf6.7049/orf6.7049/DEAH-box protein, putative RNA helicase/DEAH-box protein	-2.90
Contig4-2990_0021/RHO3/orf6.607;orf6.4279;RHO3;YDR512/ras-like protein//molecular_function unk	-3.47
Contig4-2716_0006/RSC1/orf6.6652;RSC1/chromatin structure/Member of RSC complex/nucleosome	-3.54
Contig4-2668_0002/YFL47/orf6.6013;orf6.2648;orf6.5661;YFL47/-/molecular_function unknown;biolc	-2.80
Contig4-2559_0010/YKR3/orf6.1881;YKR3;YCR97;PIK99/oxysterol-binding protein/60kD chaperonin	-3.52
Contig4-1977_0002/YOR251/orf6.331;orf6.1001;YOR251/-/thiosulfate sulfurtransferase	-2.36
Contig4-3031_0023/CAF16/orf6.6276;CAF16/CCR4 associated factor/ABC ATPase/transport	-2.38
Contig4-2999_0005/orf6.5908/orf6.5908/GDPVGTP exchange factor for Sec4p/GDPVGTP exchange f	-3.40
RPB4/RPB4/orf6.1177/RNA polymerase II subunit/	-2.93
Contig4-2488_0001/RVS167/orf6.3078;RVS167/starvation viability/(putative) cytoskeletal protein/actir	-3.40
Contig4-3023_0023/RPC40/orf6.5765;RPC40/RNA polymerase subunit/RNA polymerase III (C) subu	-3.24
NUP188/NUP188/orf6.5214/nucleoporin/	-2.21
Contig4-3086_0015/RPS8/orf6.7137;RPS8/ribosomal protein S8/Ribosomal protein S8B (S14B) (rp1	-4.80
Contig4-3000_0020/TEF2/orf6.339;orf6.6331;orf6.1202;orf6.6330;orf6.1201;orf6.340;TEF2;TEF1/tran	-6.66
Contig4-3003_0028/orf6.9005/orf6.9005/RNase P and RNase MRP subunit/RNase P and RNase MR	-3.08
Contig4-2981_0018/orf6.4840/orf6.4840///cellular_component unknown;helicase;biological_process u	-6.11
Contig4-2292_0006/SRP101/orf6.2275;orf6.2419;orf6.2420;orf6.928;orf6.2276;SRP101/signal recogn	-3.31
Contig4-2867_0012/RPS15/orf6.9110;RPS15/ribosomal protein/	-8.19
Contig4-2912_0002/orf6.3819/orf6.3819/40 kDa ubiquinol cytochrome-c reductase core protein 2/40 k	-2.92
Contig4-2882_0004/orf6.3411/orf6.3411/uridine-monophosphate kinase (uridylyate kinase)/uridine-mor	-5.92
Contig4-2877_0005/PDA1/orf6.6948;PDA1/pyruvate dehydrogenase subunit E1 alpha/alpha subunit c	-7.57
Contig4-2905_0019/ANC1/orf6.1138;ANC1/TFIIF subunit/transcription initiation factor TFIIF small sub	-2.78
Contig4-3006_0013/TPI1/orf6.8886;TPI1/triose phosphate isomerase/triosephosphate isomerase/cytc	-13.10
Contig4-2941_0012/OXA1/orf6.7553;orf6.7552;OXA1/cytochrome oxidase processing/involved in cytc	-4.46
Contig4-3049_0031/YGL68/orf6.3566;YGL68/ribosomal protein//molecular_function unknown;biologic	-5.43
Contig4-3046_0019/RPL7/orf6.5257;RPL7;RPL7/ribosomal protein/Protein with similarity to ribosoma	-3.70
Contig4-3013_0031/YBL98/orf6.8679;YBL98/oxidoreductase/similar to kynurenine 3-monoxygenase/r	-2.67
Contig4-2957_0004/YDR430/orf6.8570;YDR430/-/molecular_function unknown;biological_process ur	-2.63
TOM7/TOM7//mitochondrial protein import/	-2.46
Contig4-3067_0031/orf6.7706/orf6.7706/cis-prenyltransferase homologue/cis-prenyltransferase homo	-2.52
GSY1/GSY1/orf6.8278/glycogen synthase/	-4.75
Contig4-2993_0004/ERG20/orf6.2952;ERG20/farnesyl-diphosphate synthetase/Farnesyl diphosphate	-5.57
Contig4-2878_0009/orf6.6062/orf6.6062;orf6.124/Pop7 protein, an integral subunit of RNase P and a	-4.61
YLR243/YLR243//	-4.08
Contig4-2262_0004/GLY1/orf6.1595;orf6.5812;orf6.1596;orf6.5811;GLY1/glycine metabolism/Threoni	-3.71
Contig4-2607_0006/orf6.3693/orf6.3693;orf6.686///molecular_function unknown;biological_process ur	-3.85
Contig4-2708_0006/YOR133/orf6.4860;orf6.6622;orf6.4859;orf6.4858;YOR133/translation elongation	-6.32
Contig4-2886_0002/orf6.4076/orf6.4076/mitochondrial C1-tetrahydroflate synthase/mitochondrial C1-t	-4.70
Contig4-3038_0027/MDJ1/orf6.6781;MDJ1/heat-shock protein/DnaJ homolog involved in mitochondri	-2.39
Contig4-3060_0012/EFB1/orf6.7533;EFB1/elongation factor 1B/Translation elongation factor EF-1bet	-3.54
Contig4-3096_0045/YDR175/orf6.7759;YDR175/-/protein of the small subunit of the mitochondrial rib	-4.57
Contig4-3076_0010/TDH3/orf6.8817;TDH3/glyceraldehyde-3-phosphate dehydrogenase/Glyceraldeh	-12.08
YDR492/YDR492//	-3.65
SPO14/SPO14//phospholipase D/	-9.86
YJL12/YJL12//	-2.42
Contig4-2928_0003/orf6.6599/orf6.6599;orf6.3978///molecular_function unknown;biological_process u	-3.86
Contig4-1834_0003/orf6.7081/orf6.7081///molecular_function unknown;biological_process unknown	-3.74

Contig4-2045_0001/MAS2/orf6.5445;MAS2/mitochondrial protease/53 kDa subunit of the mitochondri	-7.25
Contig4-1775_0006/orf6.2115/orf6.2115/49-kDa alpha subunit of RNA polymerase A/49-kDa alpha su	-3.81
Contig4-1720_0004/YNL22/orf6.3595;orf6.3596;YNL22/-//nucleus;molecular_function unknown;biolog	-2.10
Contig4-2511_0007/orf6.8402/orf6.8402//	-3.22
Contig4-2386_0003/orf6.2577/orf6.2577;orf6.1787/Integral membrane component of the endoplasmic	-3.22
Contig4-2304_0003/HDA1/orf6.3593;HDA1/histone deacetylase subunit/histone deacetylase, shares :	-2.16
Contig4-2621_0003/orf6.8846/orf6.8846/40S ribosomal protein S12/40S ribosomal protein S12/cytosc	-10.42
Contig4-2520_0017/orf6.6102/orf6.6102;orf6.6101/Translation initiation factor eIF-4B/Translation initi	-5.99
Contig4-2581_0004/YNL260/orf6.4073;orf6.4765;YNL260/-//molecular_function unknown;biological_p	-2.89
Contig4-2901_0007/orf6.6867/orf6.6867//	-4.59
Contig4-2867_0011/RPS15/orf6.9110;RPS15/ribosomal protein/40S ribosomal protein S15 (S21) (rp5	-9.19
Contig4-2803_0010/SPX5/orf6.7653;SPX5/curved-DNA binding protein/methionine aminopeptidase 2	-7.14
Contig4-2793_0010/YKL56/orf6.8268;YKL56/tumor protein homolog//molecular_function unknown;bic	-6.43
Contig4-2931_0012/ERG8/orf6.7905;orf6.199;ERG8/phosphomevalonate kinase/48 kDa Phosphome	-4.29
Contig4-2913_0009/YMR193/orf6.6719;YMR193/mitochonrial ribosomal protein L24/Mitochondrial rib	-3.20
Contig4-2905_0017/BAT2/orf6.1137;orf6.2998;orf6.2997;BAT2/branch-chain amino acid transaminas	-2.96
Contig4-3006_0011/orf6.8883/orf6.8883//	-10.05
Contig4-2985_0003/SNF1/orf6.5603;orf6.832;SNF1/protein kinase/protein serine\threonine kinase/cy	-4.86
Contig4-3003_0004/orf6.9023/orf6.9023;orf6.9022/Mitochondrial ribosomal protein MRPL25 (YmL25),	-3.17
Contig4-3029_0004/YIL167/orf6.8564;YIL167;SDL1/serine dehydratase/catabolic serine (threonine) d	-5.24
Contig4-3013_0030/YBL98/orf6.8680;YBL98;MPI1/oxidoreductase/48.8 kDa protein involved in mitoc	-3.12
Contig4-2991_0018/MOT2/orf6.1380;orf6.3869;orf6.3868;orf6.1379;MOT2/zinc finger protein/putative	-3.18
Contig4-3005_0028/RRP5/orf6.5342;RRP5/ribosomal RNA processing/Protein required for processin	-3.79
Contig4-2779_0001/MEX67/orf6.7083;MEX67/mRNA export from nucleus/a poly(A)+RNA binding pro	-2.57
Contig4-2649_0008/orf6.1931/orf6.1931/Membrane transporter/Membrane transporter/cellular_compc	-2.48
Contig4-3020_0001/ORC1/orf6.4864;orf6.4866;ORC1/origin recognition complex subunit/120-kDa (la	-3.42
Contig4-3002_0007/orf6.3247/orf6.3247;orf6.376;orf6.3248/ribonuclease H/ribonuclease H/cell;ribonu	-8.72
Contig4-2981_0015/YJL55/orf6.4837;YJL55/-//molecular_function unknown;biological_process unkno	-4.54
Contig4-2985_0001/HST3*/orf6.5604;orf6.830;HST3/silencing/involved in telomeric silencing/molecul	-3.08
Contig4-3058_0034/orf6.4345/orf6.4345;orf6.4346///molecular_function unknown;biological_process t	-3.13
Contig4-3019_0023/HIR2/orf6.5191;HIR2/histone gene regulation/putative repressor protein\; contain	-4.10
Contig4-2639_0001/orf6.2964/orf6.2964/PAKVSte20 kinase family/PAKVSte20 kinase family/	-2.35
Contig4-2499_0005/orf6.3177/orf6.3177/Acyl-CoA synthetase (fatty acid activator 2)/Acyl-CoA synthe	-3.15
Contig4-2232_0005/orf6.5777/orf6.5777//	-4.01
YKL88/YKL88//salt tolerance/	-2.71
YDR93/YDR93//ATPase/	-2.53
Contig4-2717_0005/orf6.5293/orf6.5293/23 kDa mitochondrial inner membrane protein/23 kDa mitoch	-2.55
Contig4-2886_0001/MIS1/orf6.4076;MIS1/C-1-tetrahydrofolate synthase/mitochondrial C1-tetrahydrof	-2.44
Contig4-2974_0009/ERG4/orf6.4141;ERG4/C24 sterol reductase/Sterol C-24 reductase/endoplasmic	-5.23
Contig4-1392_0002/CYP1/orf6.2216;orf6.2215;orf6.6410;orf6.6408;CYP1/peptidyl proline isomerase/	-5.57
Contig4-2393_0003/RPC82/orf6.4941;RPC82/RNA polymerase subunit/82-kDa subunit of RNA polym	-2.69
Contig4-3106_0036/orf6.8468/orf6.8468//	-3.23
Contig4-2927_0010/THS1/orf6.4563;THS1/threonyl-tRNA synthetase/Threonyl-tRNA synthetase, cytc	-9.88
ACH1/ACH1/orf6.1164/acetyl-CoA hydrolase/	-3.12
Contig4-3103_0012/YDL74/orf6.8225;YDL74/-//cellular_component unknown;molecular_function unki	-4.12
RPS30/RPS30//ribosomal protein 30/	-6.16
Contig4-2688_0009/SSA2/orf6.4924;orf6.2627;SSA2;HSP70/cell wall protein/member of 70 kDa heat	-8.53
Contig4-2739_0010/RPS9/orf6.1126;RPS9/ribosomal protein/Ribosomal protein S9B (S13) (rp21) (Y	-5.68
Contig4-2869_0013/YOR91/orf6.3038;orf6.3037;orf6.3036;YOR91/-//cytoplasm;molecular_function ur	-3.16
Contig4-2688_0009/SSA2/orf6.4924;orf6.2627;SSA2;HSP70/cell wall protein/member of 70 kDa heat	-3.33
Contig4-3055_0012/NOP58*/orf6.2946;orf6.2852;NOP58/nucleolar protein/57 kDa nucleolar protein/b	-10.28

Contig4-2109_0001/orf6.1611/orf6.1611//	-3.35
Contig4-2594_0009/CDC99/orf6.3735;CDC99/CDC1-like protein/100 kD component of the Exocyst cc	-3.69
Contig4-2534_0003/ADH1/orf6.106;orf6.7410;orf6.6337;ADH1;SDS23;PLB97;OLE1;LTP1;CAX14;CA	-6.48
Contig4-2701_0011/YIL74/orf6.7679;YIL74/2-hydroxyacid dehydrogenase/3-phosphoglycerate dehyd	-3.35
Contig4-2655_0004/LPD1/orf6.5108;orf6.5109;LPD1/lipoamide dehydrogenase/dihydrolipoamide deh	-5.62
Contig4-2619_0005/orf6.3830/orf6.3830/involved in protein disulfide bond formation in the ER/involve	-4.22
Contig4-2779_0009/YPL173/orf6.7087;YPL173/mitochondrial ribosomal protein/Mitochondrial riboson	-3.68
Contig4-2945_0004/FBA1/orf6.7917;orf6.7918;FBA1/fructose-bisphosphate aldolase/aldolase/cytosol	-8.88
Contig4-2997_0015/orf6.6438/orf6.6438/Acyl-CoA-binding protein (ACBP)VDiazepam binding inhibito	-3.30
Contig4-2995_0028/RPE1/orf6.8446;RPE1/ribulose-5-phosphate-epimerase//molecular_function unkr	-6.02
Contig4-2956_0006/orf6.8796/orf6.8796;orf6.434;orf6.6229;orf6.321;orf6.1631;orf6.4420;orf6.1466;or	-5.41
Contig4-2927_0012/orf6.4566/orf6.4566///molecular_function unknown;biological_process unknown	-2.40
Contig4-3094_0036/COR1/orf6.7429;COR1/coenzyme QH2 cytochrome c reductase subunit/44 kDa c	-6.44
Contig4-3093_0012/SNP99/orf6.8535;SNP99/small nuclear ribonucleoprotein/encodes YU2B, a comp	-3.56
Contig4-2956_0001/NHA1/orf6.2060;orf6.2061;NHA1/H+ antiporter/Putative Na+VH+ antiporter/	-3.33
SYG1/SYG1/orf6.698/membrane protein/	-2.68
NAM9/NAM9/orf6.7073/mitochondrial ribosomal protein S4/	-5.12
Contig4-2073_0006/GDH2/orf6.3428;GDH2/NAD-dependent glutamate dehydrogenase/NAD-depend	-3.59
Contig4-1837_0007/YER67/orf6.1464;orf6.1218;YER67/-//molecular_function unknown;biological_prc	-6.61
Contig4-2050_0001/YDR412/orf6.1521;YDR412/-//cytoplasm;molecular_function unknown;biological_	-2.91
Contig4-1775_0004/RPA49/orf6.2115;orf6.2382;RPA49/RNA polymerase I A49 subunit/49-kDa alpha	-5.44
Contig4-2322_0007/YLR183/orf6.6561;YLR183;YDR501/-/PLasmid Maintenance/molecular_function	-6.73
Contig4-2189_0002/PEP1/orf6.7029;orf6.7028;APR1;PEP1/-/vacuolar proteinase A/vacuole;endopep	-2.71
Contig4-2573_0010/YPT7/orf6.5706;YPT7;YOR359;YKL195;YHR194;CDC73;CAX12;CAX11;CAX10	-5.92
Contig4-2622_0005/DBP3/orf6.2585;orf6.3829;DBP3/RNA helicase/ATP-dependent RNA helicase C/	-6.71
Contig4-2527_0012/TFP1/orf6.2002;TFP1/vacuolar H+ ATPase catalytic subunit/vacuolar ATPase V1	-3.71
Contig4-2740_0008/orf6.7403/orf6.7403///molecular_function unknown;biological_process unknown	-2.99
Contig4-2675_0008/orf6.6523/orf6.6523//	-3.39
Contig4-2646_0009/orf6.7725/orf6.7725///molecular_function unknown	-4.09
Contig4-2581_0003/orf6.4766/orf6.4766///molecular_function unknown;biological_process unknown	-3.36
Contig4-2867_0010/YOL39/orf6.9109;YOL39/ribosomal protein A2/Ribosomal protein P2B (YP2beta)	-5.72
Contig4-2803_0009/YMR75/orf6.7654;orf6.7655;orf6.7656;YMR75;SPX25/-//molecular_function unkn	-3.83
Contig4-2838_0014/RPL116/orf6.1888;RPL116;RPL11/ribosomal protein L16/Ribosomal protein L11/	-13.49
Contig4-2961_0028/orf6.3937/orf6.3937;orf6.3936/Component of transcription initiation factor IIb, 75 I	-3.73
Contig4-2933_0005/YER87/orf6.2386;YER87/prolyl-tRNA synthetase//cellular_component unknown;c	-3.09
Contig4-2913_0005/GCD7/orf6.6716;orf6.6715;GCD7/translation factor eIF2b/translation initiation fac	-2.70
Contig4-2882_0001/orf6.3409/orf6.3409;orf6.6986///molecular_function unknown;biological_process u	-3.47
Contig4-2878_0020/YJR14/orf6.6058;orf6.6059;YJR14/-//molecular_function unknown;biological_pro	-7.99
Contig4-2905_0016/YKL189/orf6.1136;orf6.2996;YKL189/membrane protein/The homologue in Aspe	-8.96
Contig4-3010_0024/orf6.7040/orf6.7040;orf6.7041/ferrochelata (protoheme ferrolyase)/ferrochelata	-4.36
Contig4-2988_0018/YML9/orf6.8737;YML9/mitochondrial ribosomal protein L9/Mitochondrial ribosom	-13.86
Contig4-3006_0010/KRS1/orf6.8882;orf6.8881;KRS1;YBR61/lysyl-tRNA synthetase/lysyl-tRNA synth	-9.31
Contig4-3003_0003/orf6.9022/orf6.9022;orf6.9023;orf6.9024//	-4.52
Contig4-2983_0023/RNX1/orf6.8395;RNX1/cysteine dioxygenase/	-4.31
Contig4-2968_0010/CFL99/orf6.5731;orf6.5730;CFL99;CFL1/CFL1-like protein/Similar to ferric reduct	-2.66
Contig4-3029_0003/orf6.8565/orf6.8565//	-4.79
Contig4-2064_0001/NPI46/orf6.3221;NPI46/rapamycin-binding protein/60 kDa nuclear FK506 binding	-4.92
Contig4-3107_0030/orf6.8753/orf6.8753/nucleosome assembly protein I/nucleosome assembly protei	-2.87
Contig4-3006_0018/FCP1/orf6.8889;FCP1/CTD phosphatase component/TFIIF interacting componer	-3.41
Contig4-2966_0010/YDR20/orf6.6166;YDR20/-/Nucleoporin highly similar to Nup157p and to mamma	-3.73
Contig4-3084_0044/RIP1/orf6.9144;RIP1/Rieske iron-sulfur protein/Rieske iron-sulfur protein of the m	-7.08

Contig4-3067_0032/orf6.7707/orf6.7707/component of the spindle pole body that interacts with Spc42	-5.34
Contig4-3003_0028/orf6.9005/orf6.9005/RNase P and RNase MRP subunit/RNase P and RNase MR	-4.31
Contig4-2982_0013/orf6.8556/orf6.8556//	-4.01
Contig4-2674_0010/YTM1/orf6.5221;YTM1/microtubule function/microtubule-associated protein/nucle	-3.95
Contig4-2642_0009/YKR71/orf6.1898;orf6.1251;YKR71-//molecular_function unknown;biological_prc	-2.36
Contig4-2987_0013/orf6.8260/orf6.8260//molecular_function unknown;biological_process unknown	-2.92
Contig4-3054_0004/orf6.6907/orf6.6907;orf6.6908//molecular_function unknown	-2.25
Contig4-2238_0008/ARC18/orf6.406;ARC18/3 complex subunit/Arp2V3 Complex Subunit/Arp2/3 prote	-3.08
Contig4-1999_0005/orf6.8842/orf6.8842/spindle pole body protein/spindle pole body protein/spindle p	-2.32
VMA5/VMA5/orf6.1314/vacuolar ATPase subunt/	-3.54
HST7/HST7//threonine protein kinase/	-6.40
Contig4-3013_0007/orf6.8703/orf6.8703;orf6.8027;orf6.6230;orf6.6229;orf6.1799;orf6.1798;orf6.9028	-8.51
YKL133/YKL133//-	-2.23
Contig4-1942_0004/RPB3/orf6.3011;RPB3/RNA polymerase II subunit/45 kDa subunit of RNA polym	-3.32
Contig4-1611_0001/YKX1/orf6.4401;YKX1;YCR40;YCL67;PIK1/YKR3-like protein//molecular_functio	-2.22
Contig4-2334_0001/orf6.5113/orf6.5113//	-3.77
Contig4-2125_0001/SUI2/orf6.4525;SUI2/translation initiation factor eIF-2 alpha subunit/Translation ir	-9.34
Contig4-2607_0004/RPL25/RPL25/ribosomal protein L25/Ribosomal protein L25 (rpl6L) (YL25)/cytos	-8.53
Contig4-2540_0002/MCR1/orf6.4367;MCR1/NADH-cytochrome b5 reductase/NADH-cytochrome b5 r	-3.69
Contig4-2494_0009/orf6.2630/orf6.2630;orf6.8026//	-5.39
Contig4-2375_0005/orf6.1975/orf6.1975/putative GTP-binding protein\; similar to mammalian Mx prote	-3.22
Contig4-2670_0009/YPL146/orf6.7151;YPL146/-/	-5.57
Contig4-2704_0009/YER139/orf6.3302;YER139-//molecular_function unknown;biological_process ur	-3.49
Contig4-2817_0006/ATX2/orf6.1916;ATX2-/ubiquitin hydrolase/cytoplasm;ubiquitin-specific protease;	-5.00
Contig4-2775_0010/orf6.6489/orf6.6489//	-2.44
Contig4-2813_0011/orf6.5037/orf6.5037/mitochondrial ribosomal protein/mitochondrial ribosomal prot	-10.56
Contig4-2947_0019/orf6.4665/orf6.4665/U1 snRNP protein/U1 snRNP protein/mRNA splicing	-2.56
Contig4-2917_0002/SMT3/orf6.6563;SMT3/kinetochore component/ubiquitin-like protein/	-4.81
Contig4-2854_0009/PET123/orf6.5017;PET123/mitochondrial ribosomal protein/Mitochondrial ribosor	-10.47
Contig4-2998_0001/TRP1/orf6.6245;orf6.6244;TRP1/phosphoribosyl anthranilate isomerase/n-(5'-phc	-2.31
Contig4-2977_0010/////molecular_function unknown;biological_process unknown	-4.14
Contig4-3040_0028/IPP2/orf6.5213;IPP2/mitochondrial inorganic pyrophosphatase/mitochondrial inor	-2.29
Contig4-2916_0013/YER130/orf6.5102;orf6.5101;orf6.5103;YER130/zinc finger protein//molecular_fu	-3.69
Contig4-2861_0010/orf6.4146/orf6.4146/Transcriptional Activator of OCH1/Transcriptional Activator o	-2.30
Contig4-2620_0015/orf6.5261/orf6.5261//	-4.86
Contig4-3060_0002/YGR280/orf6.7526;orf6.7525;YGR280-//molecular_function unknown;biological_	-3.36
Contig4-2718_0002/HIS7/orf6.4353;HIS7/glutamine amidotransferase:cyclase/glutamine amidotransf	-3.38
MCI3/MCI3//14kd subunit of mitochondrial complex I/	-2.62
YKL35/YKL35//UDP-glucose pyrophosphorylase/	-3.02
STB2/STB2/orf6.4418/sin3 binding protein/	-2.68
NPL3/NPL3/orf6.8138/mRNA export from nucleus/	-4.53
Contig4-2578_0004/IRO1/orf6.4845;IRO1/-/	-2.50
Contig4-2739_0007/orf6.3851/orf6.3851;orf6.1127/Ribosomal protein L21B/Ribosomal protein L21B/c	-7.59
Contig4-2903_0008/YKL29/orf6.6106;YKL29/malolactic enzyme/mitochondrial malic enzyme/mitocho	-3.49
Contig4-2992_0017/RPN7/orf6.8367;RPN7/proteasome subunit/Subunit of the regulatory particle of tr	-3.45
Contig4-2662_0011/YCF1/orf6.4035;YCF1/metal resistance protein/ABC-type transmembrane transp	-3.86
Contig4-3001_0011/YCR17/orf6.3024;YCR17-//molecular_function unknown;biological_process unkr	-2.66
Contig4-2964_0004/orf6.4026/orf6.4026;orf6.4773;orf6.4769//	-13.23
RPL33/RPL33//ribosomal protein/	-23.75
Contig4-1950_0005/ASN2/orf6.5930;orf6.209;orf6.5929;orf6.208;ASN2/asparagine synthetase/aspar	-6.37
Contig4-2342_0002/MVD1/orf6.6236;orf6.6237;MVD1;TUP1/mevalonate pyrophosphate decarboxyla	-3.41

Contig4-2673_0001/HCA4/orf6.2728;HCA4/helicase/putative RNA helicase/nucleolus;ATP dependent	-6.40
Contig4-3000_0008/SDS23/orf6.6333;orf6.6335;orf6.6334;SDS23;PLB97;OLE1;LTP1;CAX14;CAX13	-4.52
Contig4-2997_0012/YEL54/orf6.6437;YEL54;RPL12/ribosomal protein/Ribosomal protein L12A (L15A	-5.41
Contig4-2956_0004/orf6.2055/orf6.2055;orf6.323/vacuolar ATPase V0 domain subunit d (36 kDa)/vac	-7.09
Contig4-3065_0023/orf6.5987/orf6.5987//	-2.58
Contig4-2539_0012/orf6.503/orf6.503///molecular_function unknown;biological_process unknown	-3.24
Contig4-2558_0008/orf6.4511/orf6.4511///molecular_function unknown;biological_process unknown	-3.60
Contig4-3006_0012/YDR51/orf6.8884;orf6.8885;YDR51;TPI1/-//molecular_function unknown;biologic	-3.61
YER183/YER183//10-methenyltetrahydrofolate synthetase/	-3.05
TAF145/TAF145/orf6.996/TAFII subunit/	-3.87
OST4/OST4//oligosaccharide transport/	-2.80
SPX60/SPX60//-	-4.42
Contig4-2201_0005/orf6.5679/orf6.5679///molecular_function unknown	-5.10
Contig4-2306_0003/YMR2/orf6.159;orf6.3705;YMR2/-//molecular_function unknown;biological_proce	-3.57
Contig4-2190_0003/GLC8/orf6.2726;GLC8/protein phosphatase regulator/Regulates activity of protei	-3.06
Contig4-2294_0001/SMD3/orf6.235;orf6.5233;SMD3/snRNP biogenesis/encodes a core snRNP prote	-2.44
Contig4-2640_0005/PRE3/orf6.7737;PRE3/proteasome subunit/Subunit of 20S proteasome/20S core	-13.48
Contig4-2405_0005/NUP57/orf6.1528;NUP57/nucleoporin subunit/Contains GLFG repeats in N-termi	-5.98
Contig4-2684_0004/TBP1/orf6.4249;orf6.4248;TBP1/TATA-binding protein/TATA-binding protein (tflc	-5.67
Contig4-2988_0016/ADE1/orf6.8736;ADE1/CAIR:aspartate ligase/phosphoribosyl amino imidazolesu	-9.76
Contig4-2941_0006/ODP2/orf6.7549;orf6.7548;ODP2/dihydrolipoamide S-acetyltransferase/Dihydrolip	-6.30
Contig4-3029_0001/ERV25/orf6.8569;orf6.8568;ERV25/protein secretion/vesicle coat component/	-10.04
Contig4-3008_0029/orf6.7249/orf6.7249/ATPase component of a four subunit chromatin remodeling c	-2.84
Contig4-2712_0006/FUN12/orf6.6295;FUN12/-/97 kDa protein/molecular_function unknown;biologica	-7.92
Contig4-2954_0018/CPY96/orf6.230;orf6.4961;CPY96/carboxypeptidase/carboxypeptidase Y (protein	-2.70
Contig4-2988_0007/NTC1/orf6.8731;NTC1/neutral trehalase/neutral trehalase/cellular_component un	-4.28
Contig4-2964_0003/orf6.4027/orf6.4027;orf6.6008;orf6.4770/The TyB Gag-Pol protein. Gag processir	-2.33
Contig4-3016_0024/orf6.3807/orf6.3807//	-3.22
YNL47/YNL47//transcription factor/	-2.47
Contig4-2117_0001/orf6.5784/orf6.5784/RiboSome Assembly 2/RiboSome Assembly 2/molecular_fur	-3.51
Contig4-2607_0002/YNL306/orf6.3691;YNL306/mitochondrial ribosomal protein//mitochondrial small r	-11.66
Contig4-2375_0001/VPS1/orf6.919;orf6.1975;VPS1/vacuolar protein sorting/putative GTP-binding prc	-2.51
Contig4-2670_0008/YPL146/orf6.7150;YPL146/-//nucleolus;nucleus;molecular_function unknown;biol	-10.53
Contig4-2552_0002/YHB1/orf6.2156;orf6.5305;YHB1/flavohemoprotein/Flavohemoglobin/cellular_cor	-12.26
Contig4-2887_0015/orf6.7557/orf6.7557//	-2.90
Contig4-2850_0007/RPS11/orf6.5230;RPS11/ribosomal protein/	-11.81
Contig4-2788_0008/KRR1/orf6.6554;orf6.254;KRR1/cell division and spore germination/involved in ce	-11.65
Contig4-2947_0017/orf6.4664/orf6.4664/GTP-binding protein/GTP-binding protein/	-7.19
Contig4-2921_0004/SER2/orf6.6140;SER2/phosphoserine phosphatase/phosphoserine phosphatase,	-8.27
Contig4-2898_0014/YNR67/orf6.4770;orf6.4027;orf6.6008;orf6.8178;YNR67/-/Reverse transcriptase/I	-4.81
Contig4-2864_0013/ESA1/orf6.8652;orf6.8650;orf6.8651;ESA1/SAS family acetyltransferase/Acetyltra	-2.55
Contig4-2977_0005/YPL98/orf6.7606;YPL98/-//molecular_function unknown;biological_process unkn	-4.23
Contig4-2995_0005/orf6.8430/orf6.8430//	-2.96
Contig4-2954_0003/orf6.4972/orf6.4972//	-2.85
Contig4-3094_0053/CCT3/orf6.7417;CCT3/chaperonin/Cytoplasmic chaperonin subunit gamma/cytop	-4.35
Contig4-2862_0011/HNM1/orf6.6357;HNM1/choline transport/Transporter (permease) for choline and	-3.51
Contig4-2672_0008/SLY1/orf6.5865;SLY1/ER-golgi vesicle traffic/SNARE docking complex subunit/	-2.92
Contig4-2624_0009/orf6.2529/orf6.2529;orf6.530;orf6.4158;orf6.1146//	-7.74
Contig4-3060_0001/PHR1/orf6.7524;PHR1/pH response/cell surface glycoprotein 115-120 kDa/biolog	-2.65
Contig4-2899_0005/YJL178/orf6.8311;YJL178/-//molecular_function unknown;biological_process unk	-5.85
Contig4-2414_0007/YHR111/orf6.5584;YHR111/molybdopterin biosynthesis/moeB, thiF, UBA1/molec	-5.85

SPT8/SPT8/orf6.3164/transcription factor/	-3.97
Contig4-2626_0005/YER67/orf6.1218;orf6.1464;YER67/-//molecular_function unknown;biological_prc	-5.05
Contig4-2869_0009/YNL96/orf6.3041;YNL96/RPS7-like protein/Ribosomal protein S7A (rp30)/cytosol	-10.78
Contig4-2936_0007/GCD11/orf6.2768;orf6.6621;GCD11/eIF-2 gamma/gamma subunit of translationa	-2.29
Contig4-2911_0005/YLR253/orf6.5235;orf6.719;YLR253/ABC1-like protein//molecular_function unknc	-3.59
Contig4-2907_0015/PHO13/orf6.7257;PHO13/p-nitrophenyl phosphatase/p-nitrophenyl phosphatase/	-7.86
Contig4-1879_0002/orf6.6859/orf6.6859///molecular_function unknown;biological_process unknown	-5.14
Contig4-2096_0004/orf6.3877/orf6.3877///molecular_function unknown;biological_process unknown	-2.64
Contig4-2239_0002/AAT1/orf6.4647;orf6.1447;AAT1/aspartate aminotransferase/aspartate aminotran	-3.50
Contig4-2612_0009/DIP1/orf6.5425;DIP1/DOM34-interacting protein/DNA helicase A/alpha DNA poly	-3.88
Contig4-2594_0005/RPS31/orf6.3734;orf6.8860;RPS31;UBI1;UBI4/ribosomal protein/Ribosomal prot	-2.44
Contig4-2619_0001/DBP3/orf6.2585;orf6.3829;DBP3/RNA helicase/ATP-dependent RNA helicase C/	-8.77
Contig4-2830_0003/PEP3/orf6.2203;orf6.3801;orf6.4426;orf6.621;orf6.513;orf6.514;PEP3/vacuolar m	-3.03
Contig4-2946_0020/YGL1/orf6.6113;YGL1/cholesterol dehydrogenase/C-3 sterol dehydrogenase/cell	-4.66
Contig4-2865_0003/orf6.4798/orf6.4798;orf6.4799/Net1-Associated Nucleolar protein 1/Net1-Associa	-3.46
Contig4-2896_0013/orf6.8666/orf6.8666//	-3.35
Contig4-2863_0020/orf6.5978/orf6.5978/alpha subunit of yeast mitochondrial phenylalanyl-tRNA syntl	-5.64
Contig4-2892_0003/MSS116/orf6.3651;MSS116/RNA helicase/Mitochondrial DEAD box RNA helicase	-5.47
Contig4-3019_0025/MSW1/orf6.4604;orf6.4605;MSW1/mitochondrial trp-tRNA synthetase/mitochond	-2.80
Contig4-2880_0001/orf6.1940/orf6.1940;orf6.1939/presumed vesicle coat protein/presumed vesicle c	-3.81
Contig4-3058_0025/PHO86/orf6.4342;PHO86/phosphate transport/Putative inorganic phosphate tran	-2.67
Contig4-3054_0012/YHR76/orf6.6901;YHR76/-//mitochondrion;molecular_function unknown;biologica	-6.08
Contig4-3102_0037/orf6.8337/orf6.8337;orf6.8338/115 kD regulatory subunit of trehalose-6-phosphat	-4.48
Contig4-2888_0006/orf6.1908/orf6.1908/Membrane transporter/Membrane transporter/biological_proc	-3.64
Contig4-2621_0003/orf6.8846/orf6.8846/40S ribosomal protein S12/40S ribosomal protein S12/cytosc	-6.74
SEC2/SEC2/orf6.5908/vesicle transport/	-2.90
SPX63/SPX63//cyclin C/	-2.65
Contig4-2278_0006/orf6.4576/orf6.4576;orf6.4577///molecular_function unknown;biological_process u	-7.98
Contig4-2201_0003/YLR439/orf6.5678;YLR439/mitochondrial ribosomal protein L4/Mitochondrial 60S	-13.67
Contig4-2295_0006/orf6.1782/orf6.1782;orf6.7187/Transcription regulator/Transcription regulator/mol	-3.02
Contig4-2684_0002/orf6.4247/orf6.4247/RNA polymerase I subunit 190 (alpha)/RNA polymerase I su	-4.80
Contig4-2901_0002/YDR90/orf6.6869;YDR90/YRO2-like protein//molecular_function unknown;biologi	-4.14
Contig4-2958_0013/orf6.5852/orf6.5852;orf6.5851//	-4.01
Contig4-2931_0007/YAL49/orf6.7908;orf6.7911;YAL49/-//molecular_function unknown;biological_pro	-8.35
Contig4-2883_0011/orf6.3775/orf6.3775//	-2.37
Contig4-2910_0009/CDC5/orf6.5090;CDC5/protein kinase/protein kinase which functions at the G(sul	-3.14
Contig4-2905_0010/orf6.2993/orf6.2993/Cyclin-dependent kinase-activating kinase/Cyclin-dependent	-3.26
Contig4-2988_0015/CRM1/orf6.8735;CRM1/-/omosome region maintenance protein/	-4.93
Contig4-3006_0008/YDR41/orf6.8879;YDR41/mitochondrial ribosomal protein S10/protein of the sma	-11.91
Contig4-2983_0016/HCS1/orf6.8393;HCS1/HMG-CoA synthase/3-hydroxy-3-methylglutaryl coenzym	-12.65
Contig4-2968_0003/ATX5/orf6.5727;ATX5;CGT1/U2 small nuclear ribonucleoprotein A/similar to hur	-4.78
Contig4-2941_0005/YNL108/orf6.7547;YNL108/-//molecular_function unknown;biological_process un	-6.87
Contig4-2938_0019/orf6.6587/orf6.6587;orf6.6588;orf6.6585//	-2.94
Contig4-3030_0015/orf6.8869/orf6.8869;orf6.8866;orf6.8867;orf6.8870/Integrin analogue gene/Integri	-3.65
Contig4-3026_0015/SNF4/orf6.583;orf6.6190;orf6.6189;SNF4/glucose repression/associates with Snf	-4.25
Contig4-2991_0014/orf6.3865/orf6.3865/Exhibits DNA binding activity on its own, associates with Hdf	-4.12
Contig4-2304_0006/orf6.3594/orf6.3594/Predicted SerVthr kinase/Predicted SerVthr kinase/actin corti	-2.13
Contig4-3009_0023/TOP2/orf6.4380;orf6.6509;TOP2;SDH99/DNA topoisomerase II/flavoprotein sub	-8.86
Contig4-2855_0006/orf6.7972/orf6.7972//	-2.98
Contig4-2704_0006/orf6.3305/orf6.3305/cytochrome oxidase assembly factor/cytochrome oxidase as	-5.00
Contig4-2984_0023/PUP2/orf6.1729;PUP2/proteosome subunit/Proteasome subunit/20S core protea	-4.82

Contig4-2790_0012/orf6.6220/orf6.6220//	-2.56
Contig4-3104_0059/CLC1/orf6.7893;CLC1/clathrin light chain/Clathrin light chain/	-4.09
Contig4-2008_0002/ERG9/orf6.3286;ERG9/squalene synthetase/squalene synthetase/endoplasmic r	-10.82
Contig4-3019_0033/orf6.4609/orf6.4609;orf6.4607/general amino acid permease/general amino acid	-3.03
YLR410/YLR410//-	-2.75
Contig4-2089_0009/CDC3/orf6.4934;orf6.2011;CDC3/cell cycle/Septin\; component of 10 nm filament	-4.27
Contig4-1872_0004/YCR16/orf6.6879;orf6.6877;YCR16//molecular_function unknown;biological_prc	-7.81
Contig4-1322_0001/RPL29/RPL29/ribosomal protein L29/Ribosomal protein L28 (L29) (rp44) (YL24)/	-9.90
Contig4-2127_0003/orf6.1349/orf6.1349/Uridinephosphoglucose pyrophosphorylase/Uridinephosphoc	-15.44
Contig4-2598_0004/SOH1/orf6.6398;SOH1/recombination/SOH1 encodes a novel 14-kD protein with	-2.34
Contig4-2376_0009/orf6.4536/orf6.4536/Transaldolase, enzyme in the pentose phosphate pathway/T	-9.53
Contig4-2365_0004/YOR250/orf6.7317;orf6.7318;YOR250/polyadenylation factor subunit/cleavageVp	-2.88
Contig4-2671_0010/FET96/orf6.5010;orf6.2939;orf6.790;orf6.5009;orf6.5008;FET96;FET3/FET3-like	-2.90
Contig4-2553_0008/IDI1/orf6.6577;orf6.3090;IDI1/isopentenyl diphosphate isomerase/Isopentenyl dip	-3.86
Contig4-2887_0014/NUP99/orf6.7558;NUP99/nucleoside permease/	-2.41
Contig4-2898_0012/orf6.434/orf6.434;orf6.1798;orf6.1367;orf6.322;orf6.433;orf6.1799;orf6.321;orf6.8	-4.33
Contig4-2993_0009/NDH51/orf6.4187;orf6.2956;NDH51/NADH dehydrogenase 51kd subunit/	-4.67
Contig4-2928_0007/YLR118/orf6.6597;orf6.3976;orf6.6596;orf6.3975;YLR118/lysophospholipase//mc	-3.54
Contig4-2084_0003/orf6.4390/orf6.4390;orf6.296/involved in mannose metabolism/involved in manno	-4.54
Contig4-2672_0010/YDR190/orf6.5866;YDR190/TATA-binding interacting protein/RUVB-like protein/r	-7.04
Contig4-2633_0002/FUN9/orf6.5694;FUN9/-ER-Golgi transport vesicle protein/molecular_function un	-3.14
Contig4-3056_0040/YEL46/orf6.5498;YEL46/threonine aldolase/Threonine Aldolase/threonine aldolase	-2.90
Contig4-3098_0048/TPS2/orf6.7775;TPS2/trehalose-6-phosphate phosphatase/Trehalose-6-phospha	-6.64
Contig4-2858_0010/SHM2/orf6.2091;SHM2/serine hydroxymethyl transferase/serine hydroxymethyltr	-14.27
Contig4-2320_0001/IPP1/orf6.807;orf6.2048;IPP1/inorganic pyrophosphatase/Inorganic pyrophospha	-2.57
ARP8/ARP8//actin-related protein/	-3.69
YJL82/YJL82//-	-2.54
Contig4-2154_0002/ADK1/orf6.3696;orf6.1810;ADK1/adenylate kinase/adenylate kinase/adenylate ki	-9.96
Contig4-2080_0001///Ribosomal protein S17B (rp51B)/Ribosomal protein S17B (rp51B)/cytosolic sma	-9.16
Contig4-1851_0008/orf6.5129/orf6.5129;orf6.5130//	-3.18
Contig4-2509_0013/orf6.122/orf6.122;orf6.7152//	-2.30
Contig4-2570_0009/VPS4/orf6.2796;orf6.1673;VPS4/vacuolar protein sorting/AAA-type ATPase/	-3.03
Contig4-2745_0001/YLR419/orf6.8813;YLR419/RNA helicase//cellular_component unknown;helicase	-3.66
Contig4-2728_0003/YPL276/orf6.2663;orf6.3525;orf6.3469;orf6.485;YPL276/formate dehydrogenase,	-2.38
Contig4-2904_0011/ADE16/orf6.7079;ADE16/IMP synthase/5-aminoimidazole-4-carboxamide ribonuc	-6.34
Contig4-3011_0017/YHR113/orf6.5573;YHR113/aminopeptidase/Vacuolar aminopeptidase/molecular	-3.21
Contig4-3014_0009/TIF35/orf6.8136;TIF35/translation initiation factor 3 subunit/translation initiation fa	-7.95
Contig4-2911_0019/orf6.2616/orf6.2616///molecular_function unknown;biological_process unknown	-3.09
Contig4-2665_0002/orf6.5889/orf6.5889///molecular_function unknown;biological_process unknown	-5.19
Contig4-3056_0004/orf6.5510/orf6.5510/5'-phosphoribosylformyl glycinamidase/5'-phospho	-18.50
Contig4-3033_0021/PRE8/orf6.8416;PRE8/proteasome Y7 subunit/proteasome component Y7/20S c	-10.35
Contig4-2790_0004/orf6.6216/orf6.6216//	-2.70
Contig4-2142_0001/orf6.4493/orf6.4493///molecular_function unknown;biological_process unknown	-3.35
Contig4-2972_0019/SED5*/orf6.7583;SED5/ER-golgi transport/Sed5p is a t-SNARE (soluble NSF att	-4.96
RPL39/RPL39//ribosomal protein L39/	-13.64
RDN1/RDN1//ribosomal RNA/	-5.92
Contig4-2471_0002/RPL6/orf6.4956;RPL6/ribosomal protein/Ribosomal protein L7A (L6A) (rp11) (YL	-9.34
Contig4-2373_0006///Ribosomal protein S13 (S27a) (YS15)/Ribosomal protein S13 (S27a) (YS15)/cy	-3.60
Contig4-2701_0006/SEN3/orf6.7682;SEN3/tRNA processing/RPN2p is a component of the 26S prote	-3.59
Contig4-2826_0007/orf6.4386/orf6.4386/pyruvate decarboxylase/pyruvate decarboxylase/alpha-1,3-r	-5.13
Contig4-2972_0005/TUB2/orf6.7578;TUB2/beta tubulin/beta-tubulin/cytoplasmic microtubule;kinetoch	-6.03

Contig4-3023_0003/CDC19/orf6.5754;orf6.5753;CDC19;PYK2/pyruvate kinase/Pyruvate kinase/cytosol	-12.48
Contig4-3039_0017///G-beta like protein/G-beta like protein/	-3.67
Contig4-3019_0024/CKB2/orf6.4602;orf6.5189;orf6.4603;CKB2/casein kinase II beta subunit/Casein kinase II beta subunit	-3.28
Contig4-3016_0002/YLR63/orf6.4674;orf6.4673;YLR63;YGL157;YFL10;MSH4;FRS1/protein kinase/F	-7.28
Contig4-2982_0013/orf6.8556/orf6.8556//	-2.47
Contig4-2882_0008/YHR47/orf6.3413;YHR47/metalloproteinase/arginine\alanine aminopeptidase/ce	-4.63
Contig4-3058_0021/CBP6/orf6.4340;orf6.3582;CBP6/cytochrome b expression/Translational activator	-2.35
Contig4-2919_0011/RPL4/orf6.5539;orf6.9035;RPL4/ribosomal protein L4/Ribosomal protein L8B (L4	-9.10
Contig4-2561_0002/orf6.1035/orf6.1035;orf6.2390;orf6.1036/vacuolar protease B/vacuolar protease E	-2.86
Contig4-2844_0005/orf6.7012/orf6.7012/vacuolar ATPase V0 domain subunit a (100 kDa)/vacuolar A	-3.09
Contig4-2374_0007/YHR122/orf6.6004;YHR122/-//molecular_function unknown;biological_process un	-2.35
Contig4-2941_0005/YNL108/orf6.7547;YNL108/-//molecular_function unknown;biological_process un	-4.45
Contig4-3052_0007/IDP1/orf6.3902;IDP1/mitochondrial NADP-linked isocitrate dehydrogenase/Mitoch	-3.09
Contig4-2279_0002/SAM1/orf6.2190;SAM1;SAM2/S-adenosylmethionine synthetase/S-adenosylmet	-8.64
Contig4-1838_0003/orf6.864/orf6.864//	-2.75
Contig4-2396_0006/CDC36/orf6.7619;orf6.7620;CDC36/start B/nuclear protein that negatively regula	-3.52
Contig4-2322_0001/SMT3/orf6.6563;SMT3/kinetochore component/ubiquitin-like protein/	-6.21
Contig4-2201_0002/orf6.5677/orf6.5677//	-3.07
Contig4-2295_0005/orf6.1781/orf6.1781;orf6.7186/nuclear protein arginine methyltransferase (mono-	-4.34
Contig4-2168_0002/EGD2/orf6.5050;EGD2/GAL4 enhancer protein/GAL4 enhancer protein, homolog	-6.58
Contig4-2623_0008/SSM1/orf6.3768;SSM1/ribosomal protein/Ribosomal protein L1A, forms part of th	-3.43
Contig4-2913_0001/SDS22/orf6.6711;orf6.6712;SDS22/GLC7-interacting protein/Glc7p regulatory su	-4.40
Contig4-2965_0008/YBL64/orf6.2884;orf6.6183;orf6.6016;orf6.7931;orf6.3125;orf6.5083;orf6.566;orf6	-3.19
Contig4-2938_0018/orf6.6587/orf6.6587;orf6.6588;orf6.6585//	-3.15
Contig4-3030_0014/YNL175/orf6.8865;YNL175/RNA-binding protein/nucleolar protein/molecular_func	-3.66
Contig4-3026_0010/orf6.6187/orf6.6187/Homolog to human hnRNP complex K protein/Homolog to hu	-2.58
Contig4-2991_0013/YMR97/orf6.3864;YMR97/-//molecular_function unknown;biological_process unk	-2.18
Contig4-2682_0003/orf6.6669/orf6.6669/encodes highly conserved 35 kDa protein that shows increas	-7.81
Contig4-3011_0012/CDC48/orf6.5568;CDC48/cell cycle/microsomal ATPase/microsome;nucleus;ade	-5.73
Contig4-3084_0029/YEL26/orf6.9152;YEL26/-U4/U6.U5 snRNP component/	-3.68
Contig4-3003_0022/orf6.9010/orf6.9010/regulator of Ty1 Transposition/regulator of Ty1 Transposition	-3.20
Contig4-2984_0015/NMD3/orf6.1726;orf6.3330;NMD3/UPF1-interacting protein/cytoplasmic factor rec	-4.37
Contig4-2966_0006/orf6.6170/orf6.6170/Karyopherin beta 4/Karyopherin beta 4/	-4.20
Contig4-2811_0001/orf6.6202/orf6.6202/vacuolar H+-ATPase assembly protein/vacuolar H+-ATPase	-2.37
Contig4-3075_0013/DOR14*/orf6.7985;DOR14/6-phosphogluconate dehydrogenase/Phosphogluconate	-5.77
Contig4-2357_0008/YBR146/orf6.2438;YBR146/mitochondrial ribosomal protein/Probable mitochondri	-4.24
Contig4-2598_0002/orf6.6397/orf6.6397//	-2.66
Contig4-2828_0009/orf6.2820/orf6.2820/adrenodoxin oxidoreductase homolog/adrenodoxin oxidoreduct	-4.34
Contig4-2864_0007/YIL39/orf6.8654;YIL39/-//molecular_function unknown;biological_process unknow	-2.50
Contig4-2977_0003/orf6.7604/orf6.7604/Member of ATP-binding cassette (ABC) family of proteins/M	-4.73
Contig4-2975_0016/TFB2/orf6.4948;TFB2/repair factor TFIIH subunit/TFIIH subunit Tfb2\; has homol	-3.36
Contig4-2955_0023/YJL145/orf6.4233;YJL145/-//molecular_function unknown;biological_process unk	-3.81
Contig4-3020_0012/YDX5/orf6.4873;orf6.4872;YDX5;YPT7;YOR359;YKL195;YHR194;CDC73;CAX1	-5.48
Contig4-1646_0003/ARO4/orf6.3017;ARO4/3-deoxy-D-arabinoheptulosonate-7-P synthase/3-deoxy-I	-3.58
Contig4-2865_0004/MGM1/orf6.4800;MGM1/mitochondrial DNA maintenance/encodes protein with G	-4.35
Contig4-2640_0002/orf6.7735/orf6.7735;orf6.7734/Multiple RNA Binding Domain/Multiple RNA Bindin	-2.99
Contig4-3061_0012/ACT1/orf6.8002;orf6.8001;ACT1/actin/Actin/actin cable (sensu Saccharomyces);;	-2.59
Contig4-2416_0004/orf6.4786/orf6.4786///molecular_function unknown;biological_process unknown	-3.18
Contig4-3065_0009/RCA1/orf6.7498;orf6.5744;RCA1/respiratory chain assembly/mitochondrial mem	-8.14
Contig4-1399_0002/orf6.3409/orf6.3409;orf6.6986///molecular_function unknown;biological_process u	-10.92
COX9/COX9//cytochrome oxidase subunit VIIa/	-9.05

CCT6/CCT6/orf6.6919/chaperonin/	-4.84
Contig4-2320_0007/SUG1/orf6.700;orf6.2051;SUG1/-/ATPase/19S proteasome regulatory particle;ad	-5.61
Contig4-2198_0009/YDR427/orf6.6366;YDR427/-/Subunit of the regulatory particle of the proteasome	-4.01
Contig4-2644_0011/SCJ1/orf6.6467;SCJ1/dnaJ-like protein/dnaJ homolog/molecular_function unknow	-5.39
Contig4-2579_0009/YML13/orf6.5872;YML13/-/molecular_function unknown;biological_process unkn	-3.14
Contig4-2627_0007/orf6.4556/orf6.4556/F-box protein/F-box protein/molecular_function unknown	-6.29
Contig4-2904_0008/orf6.7078/orf6.7078;orf6.269/Ribosomal protein L15B (YL10) (L13B) (rp15R)/Ribi	-7.18
Contig4-2960_0011/RRT4/orf6.1756;RRT4/reverse transcriptase//molecular_function unknown;biolog	-2.33
Contig4-2990_0007/SUP45/orf6.4287;SUP45/peptide release factor subunit/Homolog of eRF1 (eukar	-5.51
Contig4-3031_0010/ENO1/orf6.6269;ENO1/enolase/enolase I/enolase;phosphopyruvate hydratase;gl	-6.74
Contig4-3014_0006/YKL121/orf6.8135;YKL121/-/molecular_function unknown;biological_process unl	-2.26
Contig4-2992_0012/PEX13/orf6.8363;PEX13/peroxisomal protein import/Peroxisomal membrane prot	-2.70
Contig4-2735_0003/orf6.2458/orf6.2458;orf6.654/Component of the exosome 3->5 exoribonuclease c	-3.03
Contig4-2806_0005/orf6.5554/orf6.5554///molecular_function unknown;biological_process unknown	-2.93
Contig4-2977_0003/orf6.7604/orf6.7604/Member of ATP-binding cassette (ABC) family of proteins/Mc	-3.23
Contig4-3015_0015/RPS26/orf6.7103;RPS26/ribosomal protein S26/Ribosomal protein S26A/cytosoli	-14.05
Contig4-2997_0019/ERG6/orf6.6441;ERG6/sterol transmethylase/S-adenosylmethionine: delta 24-me	-3.49
Contig4-2695_0002/RNR3/orf6.4851;RNR3;RNR99/ribonucleotide reductase subunit/ribonucleotide r	-4.92
Contig4-2975_0014/orf6.4949/orf6.4949/second-largest subunit of RNA polymerase III/second-larges	-4.62
Contig4-2791_0001/orf6.8272/orf6.8272;orf6.324;orf6.8271/Heat shock protein also induced by cana	-2.28
Contig4-2581_0002////	-3.14
Contig4-3103_0044/orf6.8198/orf6.8198///cellular_component unknown;molecular_function unknown;	-4.98
Contig4-3061_0003/PCM1/orf6.7997;PCM1/phosphoacetylglucosamine mutase/	-2.43
RPL42/RPL42//ribosomal protein/	-9.01
Contig4-2613_0008/SPX8/orf6.5995;orf6.2212;SPX8/-/	-4.07
Contig4-2558_0006/CAR2/orf6.4510;CAR2/ornithine aminotransferase/ornithine aminotransferase/orr	-3.09
Contig4-2890_0016/orf6.319/orf6.319;orf6.3636///molecular_function unknown;biological_process unl	-3.79
Contig4-2826_0006/PDC3/orf6.4386;PDC3/pyruvate decarboxylase/pyruvate decarboxylase/alpha-1,	-3.01
Contig4-2995_0022/YIL65/orf6.8442;YIL65/-/mitochondrial fission/mitochondrial outer membrane;mol	-2.51
Contig4-3039_0016/ASC1/orf6.7170;ASC1/G-beta-like protein/G-beta like protein/	-10.06
Contig4-2982_0009/orf6.8584/orf6.8584;orf6.8558///nucleus;molecular_function unknown;biological_p	-7.26
Contig4-1860_0002/GCN4/orf6.5290;GCN4/amino acid starvation response/transcriptional activator o	-2.64
Contig4-3053_0037/orf6.7585/orf6.7585/mitochondrial RNA polymerase/mitochondrial RNA polymera	-9.04
Contig4-2055_0004/ADE13/orf6.551;orf6.5841;ADE13/adenylosuccinate lyase/Adenylosuccinate Lya	-6.17
Contig4-2416_0004/orf6.4786/orf6.4786///molecular_function unknown;biological_process unknown	-4.08
Contig4-2742_0007/TRP2/orf6.2355;orf6.1008;TRP2/anthranilate synthase Component I/anthranilate	-8.06
Contig4-2931_0004/orf6.7910/orf6.7910/ribose-phosphate pyrophosphokinase 3/ribose-phosphate py	-6.03
Contig4-2883_0005/orf6.2425/orf6.2425/may be involved in high osmolarity signaling pathway/may be	-5.66
Contig4-2983_0007/TUB1/orf6.8389;TUB1/alpha tubulin/alpha-tubulin/cytoplasmic microtubule;kineto	-2.81
Contig4-3033_0014/QRI8/orf6.8410;QRI8/ubiquitin-conjugating enzyme/ubiquitin conjugating enzyme	-2.97
Contig4-3030_0012/YHL29/orf6.8862;orf6.8864;YHL29/-/molecular_function unknown;biological_pro	-2.29
Contig4-3026_0009/orf6.6186/orf6.6186/Actin Overexpression Resistant/Actin Overexpression Resist	-4.81
Contig4-3013_0017/orf6.8691/orf6.8691/Homolog of S. pombe nrf1 (78% identical in predicted aminc	-2.76
Contig4-2991_0011/YKL99/orf6.3862;YKL99/-/molecular_function unknown;biological_process unkn	-11.40
Contig4-2016_0002/RBT7/orf6.4792;orf6.742;RBT7;TOA1/TUP1-regulated gene/Transcription factor	-4.64
Contig4-2653_0010/orf6.1671/orf6.1671///molecular_function unknown;biological_process unknown	-3.25
Contig4-2347_0006/YFR1/orf6.6430;YFR1/-/Double-stranded RNA-binding protein/	-6.03
Contig4-3003_0019/YCR86/orf6.9012;YCR86/-/molecular_function unknown;biological_process unkn	-7.49
Contig4-2990_0009/orf6.4286/orf6.4286/Probable pre-mRNA splicing RNA-helicase/Probable pre-mR	-3.59
Contig4-2968_0009/CFL1/orf6.5730;orf6.5731;CFL1;CGT1/ferric reductase-like protein/Ferric reducta	-2.45
Contig4-3058_0005/orf6.3575/orf6.3575///molecular_function unknown;biological_process unknown	-3.41

Contig4-3055_0020/YKL134/orf6.2848;YKL134/mitochondrial intermediate peptidase/mitochondrial in	-3.66
Contig4-2776_0008/orf6.6573/orf6.6573;orf6.1796///biological_process unknown	-6.14
Contig4-2811_0003/orf6.6203/orf6.6203/coenzyme A diphosphatase/coenzyme A diphosphatase/biol	-4.83
Contig4-2521_0007/YOR241/orf6.4994;YOR241/folylpolylglutamate synthetase/Contains a purine-bin	-12.44
Contig4-3104_0027/orf6.7879/orf6.7879///molecular_function unknown;biological_process unknown	-3.68
Contig4-3079_0026/orf6.5412/orf6.5412;orf6.4578;orf6.6230;orf6.6229;orf6.1799;orf6.1798;orf6.1367	-8.18
TOR2/TOR2/orf6.2450/rapamycin target/	-2.41
YKL207/YKL207//-/	-2.77
YOR19/YOR19//-/	-4.59
Contig4-2089_0002///	-2.66
Contig4-1966_0003/ADK1/orf6.1810;orf6.3696;ADK1/adenylate kinase/adenylate kinase/adenylate ki	-6.12
Contig4-2699_0008/orf6.2949/orf6.2949/transcription factor/transcription factor/nucleosome remodeli	-2.20
Contig4-2771_0008/RPS19/RPS19/ribosomal protein/40S ribosomal protein S19A (S16aA) (rp55A) (-3.41
Contig4-2864_0006/ATP5/orf6.8655;ATP5/ATP synthase subunit/ATP synthase subunit 5; oligomyci	-11.93
Contig4-2977_0001/orf6.7603/orf6.7603/Glutaredoxin (thioltransferase) (glutathione reductase)/Gluta	-5.71
Contig4-2993_0006/YKL172/orf6.2953;YKL172/nucleolar protein/Nucleolar protein/nucleolus;molecul	-5.00
Contig4-2971_0021/orf6.7461/orf6.7461/karyopherin-beta family protein/karyopherin-beta family prote	-2.44
Contig4-2955_0022/RPA34/orf6.4232;RPA34/RNA polymerase I subunit/unshared RNA polymerase I	-3.53
Contig4-2952_0008/MNS1/orf6.2321;MNS1/alpha-mannosidase/specific alpha-mannosidase/mannos	-2.63
Contig4-3020_0010/YPT7/orf6.4871;YPT7;YOR359;YKL195;YHR194;YDL82;CDC73;CAX12;CAX11;	-6.12
Contig4-2569_0002/YDL202/orf6.2915;orf6.3070;YDL202/-/Mitochondrial ribosomal protein MRPL11	-10.66
Contig4-1822_0003/YNL308/orf6.1340;orf6.1935;YNL308/-/Binding Protein of Krr1p/nucleolus;molec	-2.75
Contig4-2509_0007/RFC1/orf6.7155;RFC1/replication factor C subunit/Subunit 1 of Replication Facto	-3.46
Contig4-2729_0006/orf6.3750/orf6.3750/SerVThr protein kinase\; MEKK homolog/SerVThr protein kin	-3.04
Contig4-2678_0018/MRP99/orf6.5792;orf6.2261;MRP99/mitochondrial ribosomal protein L15/Mitoch	-2.54
Contig4-2649_0006/CEX3/orf6.1932;CEX3/-/	-7.92
Contig4-2962_0002/HIP99/orf6.6050;HIP99/HIP1-like permease/histidine permease/transport	-2.39
Contig4-2933_0022/MGE1/orf6.3373;MGE1/mitochondrial matrix protein/GrpE homolog, mitochondri	-4.12
Contig4-2907_0005/orf6.7253/orf6.7253/Sec34p is a 92.5 kD protein that is primarily cytosolic but a s	-2.80
Contig4-2990_0004/YNL323/orf6.4288;YNL323/-/integral membrane protein;molecular_function unkr	-2.96
Contig4-2986_0005/orf6.8154/orf6.8154;orf6.8153///molecular_function unknown;biological_process u	-2.17
Contig4-2745_0004/APC2/orf6.8810;APC2/anaphase promoting complex subunit/subunit of the anap	-6.43
Contig4-2978_0018/YOL27/orf6.7216;orf6.5033;YOL27;YPR125/-/molecular_function unknown;biolo	-9.98
Contig4-3085_0005/MEU1/orf6.7324;MEU1/ADH2 regulation/regulator of ADH2 expression/	-5.12
Contig4-3035_0013/BRF1/orf6.6546;BRF1/transcription factor IIIB/RNA polymerase III transcription fe	-3.96
Contig4-3063_0020/orf6.6729/orf6.6729/transcriptional activator protein of CYC1/transcriptional activa	-2.69
POL3/POL3//DNA polymerase III/	-3.10
YJL136/YJL136//ribosomal protein/	-16.74
YNR47/YNR47//protein kinase/	-2.93
RPL43/RPL43//ribosomal protein L34/	-16.24
Contig4-2124_0007/orf6.40/orf6.40;orf6.5179///membrane fraction;mitochondrion;molecular_function	-3.78
Contig4-2613_0007/YJR72/orf6.5996;orf6.2211;orf6.5997;YJR72/-/molecular_function unknown;biol	-6.01
Contig4-2492_0006/YHR78/orf6.6507;YHR78/-/molecular_function unknown;biological_process unkr	-2.54
Contig4-2715_0007/HTS1/orf6.4417;orf6.4416;orf6.4418;HTS1/histidine-tRNA synthetase/cytoplasmic	-6.02
Contig4-2792_0005/orf6.7801/orf6.7801/Mitochondrial ribosomal protein MRPL27 (YmL27)/Mitochon	-9.98
Contig4-2826_0005/CBF1/orf6.4385;CBF1/centromere binding factor/basic helix-loop-helix protein/mi	-7.61
Contig4-2816_0005/YPT7/orf6.5715;YPT7;YOR359;YKL195;YHR194;CDC73;CAX12;CAX11;CAX10	-4.44
Contig4-2896_0007/orf6.8669/orf6.8669///molecular_function unknown;biological_process unknown	-3.09
Contig4-2893_0015/HEM13/orf6.1494;HEM13/coproporphyrinogen III oxidase/Coproporphyrinogen II	-12.68
Contig4-2979_0018/MTD1/orf6.7505;MTD1/methylenetetrahydrofolate dehydrogenase/NAD-depende	-4.00
Contig4-2998_0022/PHR2/orf6.6260;orf6.1067;PHR2/pH response/cell surface glycoprotein 115-120	-2.66

Contig4-3021_0017/HHT2/orf6.5620;orf6.4928;orf6.8840;HHT2;HHT1/histone H3/Histone H3 (HHT1 :	-12.59
Contig4-2333_0003/YGR162/orf6.315;orf6.2228;YGR162;YGL49/mRNA cap-binding protein/mRNA c	-9.33
Contig4-2660_0014/orf6.913/orf6.913;orf6.911/Integrin analogue gene/Integrin analogue gene/	-8.79
Contig4-2611_0007/RPL14/RPL14/ribosomal protein/Ribosomal protein L14A/cytosolic large ribosom	-6.88
Contig4-2548_0002/PRE6/PRE6/proteasome alpha subunit/alpha-type of subunit of 20S proteasome/	-4.75
Contig4-2447_0008/YGR17/orf6.5962;YGR17/-//molecular_function unknown;biological_process unkn	-3.52
Contig4-2376_0009/orf6.4536/orf6.4536/Transaldolase, enzyme in the pentose phosphate pathway/T	-7.94
Contig4-2850_0015/TEF3/orf6.5226;orf6.552;TEF3/translation elongation factor 3//molecular_functio	-4.46
Contig4-2627_0002/orf6.4554/orf6.4554/(putative) mitochondrial metal transporter/(putative) mitochor	-2.29
Contig4-3055_0022/orf6.2846/orf6.2846;orf6.4630;orf6.2847/high-affinity glutamine permease/high-af	-3.71
Contig4-2550_0010/YDL103/orf6.3492;YDL103/UDP-N-AcGln pyrophosphorylase/UDP-N-acetylglu	-2.76
SRP68/SRP68/orf6.8827/signal recognition particle protein/	-7.17
Contig4-2283_0006/EMP24/orf6.5860;orf6.5443;EMP24/membrane protein/type I transmembrane p	-4.49
Contig4-2324_0003/YBR293/orf6.2772;orf6.3105;YBR293/MDR-like protein/Probable multidrug resist	-3.20
Contig4-2308_0006/orf6.6097/orf6.6097///molecular_function unknown;biological_process unknown	-6.40
Contig4-2641_0013/orf6.6281/orf6.6281/OSbp Homologue (OSBP stands for Oxysterol binding protei	-2.78
Contig4-2623_0005/SAR1/orf6.3765;SAR1/protein transport/GTP-binding protein of the ARF family/C	-5.65
Contig4-2528_0007/YJR142/orf6.6824;orf6.6823;YJR142/thiamine pyrophosphokinase//molecular_fu	-3.76
Contig4-2692_0010/THR1/orf6.2865;orf6.99;THR1/homoserine kinase/homoserine kinase/homoserin	-3.85
Contig4-2732_0018/RPL30/orf6.3062;orf6.2560;orf6.3063;RPL30/ribosomal protein L30/Ribosomal p	-5.75
Contig4-2902_0014/YNK1/orf6.4616;orf6.3163;YNK1/nucleoside diphosphate kinase/Nucleoside diph	-6.27
Contig4-2883_0004/YJL209/orf6.3773;orf6.2424;YJL209/mitochondrial mRNA processing/Endo-exon	-2.29
Contig4-2910_0001/////molecular_function unknown;biological_process unknown	-2.93
Contig4-2988_0006/COQ1/orf6.8730;COQ1/hexaprenyl pyrophosphate synthetase/hexaprenyl pyropl	-6.76
Contig4-2986_0029/orf6.8170/orf6.8170//	-5.17
Contig4-3004_0010/SSH1/orf6.2095;SSH1/SEC61-like protein/Probable SEC61 protein homolog/tran	-2.38
Contig4-2991_0009/orf6.3861/orf6.3861///molecular_function unknown;biological_process unknown	-4.29
Contig4-1856_0002/orf6.4753/orf6.4753;orf6.4752//	-3.44
Contig4-3078_0020/URA1/orf6.7375;URA1/dihydroorotate dehydrogenase/	-4.61
Contig4-2070_0001/YCR3/orf6.6761;YCR3;PDX3/mitochondrial ribosomal protein L32/Mitochondrial r	-5.34
Contig4-3081_0007/orf6.1551/orf6.1551;orf6.1552/Putative RNA-dependent helicase/Putative RNA-d	-3.38
Contig4-2649_0004/PDX3/orf6.6762;PDX3/pyridoxiamine phosphate oxidase/pyridoxine (pyridoxiami	-7.90
Contig4-3055_0008/YHR11/orf6.2944;YHR11/seryl-tRNA synthetase/Seryl-tRNA synthetase/cellular_	-8.29
Contig4-2779_0007/CDC31/orf6.7086;CDC31/spindle pole body duplication/Required for spindle pole	-3.39
Contig4-2815_0019/HAM1/orf6.2984;HAM1/6-hydroxyl-aminopurine sensitivity//molecular_function ur	-4.37
Contig4-3105_0026/orf6.8909/orf6.8909;orf6.8910//	-2.24
Contig4-3095_0028/SRB5/orf6.6845;SRB5/RNA polymerase complex subunit/subunit of RNA polyme	-3.99
Contig4-2359_0006/YDR237/orf6.4259;YDR237/mitochondrial ribosomal protein/Mitochondrial riboso	-4.25
Contig4-2592_0004/YER51/orf6.8281;YER51/-//molecular_function unknown;biological_process unkn	-2.69
Contig4-2664_0006/orf6.2124/orf6.2124/Outer mitochondrial membrane porin (voltage-dependent ani	-3.83
Contig4-2658_0002/////molecular_function unknown;biological_process unknown	-3.35
Contig4-2922_0012/orf6.5837/orf6.5837/Aconitase, mitochondrial/Aconitase, mitochondrial/cytosol;mi	-10.11
Contig4-2945_0020/HRT2/orf6.7923;HRT2/transposition/High level expression reduced Ty3 Transpos	-6.32
Contig4-2918_0005/YOR298/orf6.7189;YOR298/multiprotein bridging factor/multiprotein bridging fact	-3.97
Contig4-2864_0005/RML2/orf6.8656;orf6.8657;RML2/mitochondrial ribosomal protein L2/mitochondri	-13.48
Contig4-2993_0003/QCR8/QCR8/ubiquinol-cytochrome c oxidoreductase subunit/Ubiquinol cytochr	-6.09
Contig4-2929_0019/YPR43/YPR43/ribosomal protein/Ribosomal protein L43A/cytosolic large ribosom	-11.82
Contig4-3020_0009/YPT7/YPT7;YOR359;YKL195;YHR194;CDC73;CAX12;CAX11;CAX10;CAX9;CA	-5.58
Contig4-2950_0017/MET99/orf6.6837;MET99/NADPH-sulfite reductase hemoprotein/Putative sulfite r	-5.93
Contig4-2863_0001/RFC5/orf6.5968;orf6.593;RFC5/replication factor C subunit/Subunit 5 of Replicati	-3.06
Contig4-2796_0009/orf6.8833/orf6.8833/Transcription regulatory protein/Transcription regulatory prot	-4.79

SKY1/SKY1//protein kinase/	-2.58
COX17/COX17//cytochrome oxidase assembly/	-4.56
MSI3/MSI3//HSP70-like protein/	-2.22
YJL103/YJL103//-/	-2.47
Contig4-1852_0002/orf6.5932/orf6.5932/(putative) involved in transcription/(putative) involved in trans	-3.67
Contig4-2036_0005/SRA1/orf6.574;orf6.2117;SRA1/cAMP-dependent protein kinase regulatory subun	-4.94
Contig4-2518_0002/orf6.1360/orf6.1360/Spliced mRNA and Cell cycle regulated gene/Spliced mRNA	-3.80
Contig4-2331_0002/YOR155/orf6.2293;orf6.1924;YOR155/-//molecular_function unknown;biological_	-4.91
Contig4-2302_0005/orf6.1304/orf6.1304///molecular_function unknown;biological_process unknown	-3.18
Contig4-2185_0004/PDI1/orf6.3401;PDI1/protein disulfide isomerase/protein disulfide isomerase/prote	-9.08
Contig4-2638_0008/orf6.2256/orf6.2256//	-3.56
Contig4-2426_0005/YHM2/orf6.2738;orf6.2737;YHM2/mtDNA stability/DNA-binding protein, mtDNA s	-4.77
Contig4-2690_0009/orf6.4464/orf6.4464//	-3.57
Contig4-2730_0015/orf6.4060/orf6.4060//	-2.68
Contig4-2802_0011/YER6/orf6.3461;orf6.3460;YER6/GTP binding protein//nucleolus;nucleus;molecu	-4.63
Contig4-2963_0017/CFL95/orf6.6384;CFL95/CFL1-like protein/Similar to ferric reductases Fre1p and	-2.31
Contig4-2933_0021/LYS12/orf6.3372;orf6.3371;LYS12/homoisocitrate dehydrogenase/Homo-isocitra	-6.46
Contig4-2916_0003/GLK1/orf6.1017;orf6.6009;orf6.1703;orf6.5097;GLK1/glucokinase/Glucokinase/cy	-3.65
Contig4-2886_0007/orf6.610/orf6.610/carbamoyl-phosphate synthetase, aspartate transcarbamylase, c	-4.87
Contig4-2990_0002/orf6.4289/orf6.4289//	-5.57
Contig4-2986_0003/orf6.8154/orf6.8154;orf6.8153//	-5.91
Contig4-2967_0010/VPS28/orf6.5161;VPS28/endosome transport/involved in vacuolar protein targetin	-4.10
Contig4-2940_0002/RPO31/orf6.6942;RPO31/RNA polymerase III largest subunit/RNA polymerase II	-7.80
Contig4-3048_0003/orf6.8786/orf6.8786;orf6.8785/encodes the cytoplasmic trifunctional enzyme C1-t	-3.89
Contig4-3079_0022/PSA1/orf6.5410;PSA1/mannose-1-phosphate guanyltransferase//molecular_func	-4.10
Contig4-2333_0001/SUG1/orf6.2051;orf6.700;SUG1/-/ATPase/19S proteasome regulatory particle;ad	-6.19
Contig4-1990_0003/YMR166/orf6.2623;orf6.2622;YMR166;YMX7/mitochondrial carrier protein//molec	-2.55
Contig4-2841_0011/YFL46/orf6.4003;YFL46/-//molecular_function unknown;biological_process unknc	-3.11
Contig4-3086_0042/OSM1/orf6.7146;OSM1;CEX11/osmotic sensitivity/osmotic growth protein/cytopl	-3.25
Contig4-3083_0027/RHD2/orf6.5566//	-3.24
Contig4-2851_0006/orf6.4094/orf6.4094/transcription factor containing a SET domain/transcription fac	-3.58
Contig4-3016_0021/CDC60/orf6.3809;CDC60/leucyl-tRNA synthetase/cytosolic leucyl tRNA syntheta	-9.16
Contig4-3009_0007/YPL105/orf6.1852;YPL105/-/Kinesin-related protein suppressing myosin defects	-4.21
Contig4-3034_0021/orf6.6886/orf6.6886//	-5.99
POR1/POR1/orf6.2124/outer mitochondrial membrane porin/	-4.95
Contig4-2987_0017/SEC11*/orf6.8259;SEC11;SLN1/signal peptidase subunit/signal peptidase subun	-2.70
YKL69/YKL69//-/	-7.91
YMR259/YMR259//-/	-3.23
YOR294/YOR294//-/	-4.97
Contig4-2097_0002/MXR1/orf6.592;orf6.473;MXR1/peptide methionine sulfoxide reductase/peptide r	-2.40
Contig4-1933_0004/STI1/orf6.1022;orf6.4488;orf6.905;STI1/heat-shock protein/Heat shock protein al	-4.85
Contig4-2613_0002/YDR231/orf6.5998;YDR231/AMP binding protein/protein required for maturation ;	-3.14
Contig4-2492_0003/GRS1/orf6.6506;orf6.6505;GRS1;YPR81/glycyl-tRNA synthetase/Glycyl-tRNA sy	-7.46
Contig4-2674_0006/GUA1/orf6.5219;GUA1/GMP synthase/GMP synthase/GMP synthase (glutamine	-5.47
Contig4-2715_0005/orf6.4420/orf6.4420;orf6.8796;orf6.1631;orf6.434;orf6.6229;orf6.321;orf6.1466;or	-6.71
Contig4-2890_0012/orf6.3637/orf6.3637///late endosome;vacuolar transport;vacuolar transport	-2.38
Contig4-2831_0005/YGR86/orf6.1659;orf6.893;orf6.892;YGR86;YPL4/-//molecular_function unknown	-6.86
Contig4-2785_0006/SOD2/orf6.4732;SOD2;YDR341/manganese superoxide dismutase//cytoplasm;a	-7.41
Contig4-2821_0009/YLR63/orf6.4100;YLR63;YGL157;YFL10;MSH4;VMA4/protein kinase/vacuolar A	-13.66
Contig4-2950_0011/RPN10/orf6.6834;orf6.6833;RPN10/proteasome subunit/homolog of the mammal	-3.11
Contig4-2920_0005/orf6.7352/orf6.7352/component of vacuolar membrane protein complex/compone	-2.57

Contig4-2998_0019/GSF2/orf6.6259;GSF2/glucose signalling/involved in glucose repression/molecul	-4.45
Contig4-2957_0008/YKL120/orf6.8571;YKL120/mitochondrial carrier protein/mitochondrial oxaloaceta	-2.44
Contig4-2982_0006/YDR155/orf6.8581;YDR155/peptidyl-prolyl cis-trans isomerase/Cyclophilin D, Pej	-5.42
Contig4-2884_0002/orf6.7733/orf6.7733/Dynamin-related protein/Dynamin-related protein/mitochondr	-6.66
Contig4-2661_0011/orf6.4394/orf6.4394/Mitochondrial ribosomal protein MRPL36 (YmL36)/Mitochon	-7.95
Contig4-2557_0006/orf6.4597/orf6.4597//	-5.34
Contig4-3054_0006/SUB1/orf6.6906;SUB1/suppressor of TFIID mutants/transcriptional coactivator/tr	-2.27
Contig4-2959_0005/orf6.8496/orf6.8496///glutamate-tRNA ligase	-4.82
Contig4-2922_0012/orf6.5837/orf6.5837/Aconitase, mitochondrial/Aconitase, mitochondrial/cytosol;mi	-10.16
Contig4-3105_0047/orf6.8917/orf6.8917/homology to microtubule binding proteins and to X90565_5.c	-3.34
Contig4-3055_0024/HPX1/orf6.4628;HPX1/-involved in HMG-CoA reductase degradation/	-3.53
Contig4-2569_0002/YDL202/orf6.2915;orf6.3070;YDL202/-/Mitochondrial ribosomal protein MRPL11	-6.73
SEC14/SEC14/orf6.8190/phoshatidylcholine transfer protein/	-4.09
LYS1/LYS1/orf6.1158/saccharopine dehydrogenase/	-10.44
YIL112/YIL112//-	-3.90
PAN2/PAN2/orf6.4591/polyA ribonuclease subunit/	-3.75
Contig4-1809_0003/orf6.1992/orf6.1992/putative 1-acyl-sn-gylcerol-3-phosphate acyl transferase/put	-4.24
Contig4-2406_0002/YBL64/orf6.3496;YBL64;MTX4;CAX6;CAX5;RCC1;CHS1/rehydrin/pheromone re	-5.15
Contig4-2692_0009/ERG11/orf6.2866;orf6.98;ERG11;THR1/lanosterol 14-alpha demethylase/cytochr	-4.94
Contig4-2732_0016/YGL30/YGL30/ribosomal protein/Large ribosomal subunit protein L30 (L32) (rp73	-4.69
Contig4-2727_0010/CCL1/orf6.6688;CCL1/cyclin/novel cyclin gene\; encodes subunits of TFIIK, a suk	-3.35
Contig4-2647_0017/HTA2/orf6.2007;orf6.7310;HTA2;HTA1/histone 2A/Histone H2A (HTA1 and HTA2	-8.87
Contig4-2840_0016/YKR70/orf6.1739;orf6.237;YKR70/phosphatidyl synthase//molecular_function unl	-3.09
Contig4-2934_0003/MIR1/orf6.3051;MIR1/mitochondrial phosphate transport//mitochondrial membrar	-5.57
Contig4-2880_0015/RPL23/orf6.4364;RPL23/ribosomal protein L23/Ribosomal protein L23B (L17aB)	-9.69
Contig4-2874_0011/RPL19/orf6.9133;RPL19/ribosomal protein/Ribosomal protein L19A (L23A) (rpl5L	-5.79
Contig4-2989_0015/orf6.7516/orf6.7516//	-6.37
Contig4-2986_0024/YDR71/orf6.8169;orf6.8168;YDR71/-//molecular_function unknown;biological_prc	-5.31
Contig4-3004_0007/orf6.2096/orf6.2096//	-2.20
Contig4-2991_0006/orf6.3857/orf6.3857///molecular_function unknown;biological_process unknown	-4.68
Contig4-3097_0023/PRE5/orf6.8078;PRE5/alpha-type proteasome subunit/alpha-type of subunit of 20	-4.79
Contig4-2705_0016////	-7.02
Contig4-2070_0006/PDX3/orf6.6762;PDX3/pyridoxiamine phosphate oxidase/pyridoxine (pyridoxiami	-3.17
Contig4-1966_0001/YNL281/orf6.1809;YNL281;YLR144;YJL149;YHL8;YDR485;RPL32;CAX18;CAX1	-3.66
Contig4-2985_0003/SNF1/orf6.5603;orf6.832;SNF1/protein kinase/protein serine/threonine kinase/cy	-8.23
Contig4-2728_0007/orf6.2665/orf6.2665/putative deubiquitinating enzyme/putative deubiquitinating er	-5.35
Contig4-2895_0002/ATP11/orf6.7179;ATP11/F1-ATPase assembly/localizes to discrete sites in rad5C	-2.46
Contig4-3068_0024/orf6.3888/orf6.3888;orf6.223/RNA helicase/RNA helicase/nucleolus;ATP depend	-15.83
Contig4-2779_0003/orf6.7084/orf6.7084;orf6.7085/N-acetylglucosaminyl-phosphatidylinositol biosynt	-3.91
Contig4-2263_0007/orf6.2340/orf6.2340///molecular_function unknown;biological_process unknown	-2.14
Contig4-2045_0002/orf6.5444/orf6.5444/Contains a purine-binding domain, two heptad repeats and a	-5.09
Contig4-3091_0046/orf6.7937/orf6.7937///molecular_function unknown;biological_process unknown	-7.40
YML14/YML14//-	-2.68
Contig4-1945_0002/orf6.8795/orf6.8795;orf6.1798;orf6.6230;orf6.9027;orf6.4419;orf6.1632;orf6.322;c	-2.70
Contig4-1616_0003/RPB5/orf6.5769;RPB5/RNA polymerase subunit/25-kDa RNA polymerase subun	-2.41
Contig4-2234_0001/ATP4/orf6.5750;ATP4/ATP synthase subunit 4/F(1)F(0)-ATPase complex delta s	-18.55
Contig4-2548_0004/RPR2/orf6.6755;orf6.596;orf6.6873;RPR2/RNase P component/mitochondrial an	-6.81
Contig4-2618_0004/orf6.3432/orf6.3432;orf6.1511///molecular_function unknown;biological_process u	-2.78
Contig4-2828_0004/orf6.2512/orf6.2512/nucleolar protein that is immunologically and structurally rela	-3.87
Contig4-2781_0003/RRP4/orf6.2776;RRP4/ribosomal RNA processing/3->5 exoribonuclease\; Comp	-2.46
Contig4-2945_0015/NHP6/NHP6;YBX1/non-histone (HMG)-like protein/11-kDa nonhistone chromoso	-3.73

Contig4-2894_0002/orf6.4998/orf6.4998;orf6.280;orf6.4997;orf6.279//	-2.78
Contig4-2978_0018/YOL27/orf6.7216;orf6.5033;YOL27;YPR125/-//molecular_function unknown;biolo	-7.99
Contig4-2975_0006/orf6.4952/orf6.4952///nucleus;molecular_function unknown;biological_process un	-7.31
Contig4-2971_0016/NDH24/orf6.7464;NDH24/NADH dehydrogenase 24 kDa subunit/	-7.48
Contig4-3095_0023/SGT1/orf6.6847;SGT1/suppressor of SKP1/skp1 suppressor of skp1/molecular_f	-3.98
Contig4-2866_0002/END1/orf6.2825;orf6.656;orf6.2901;END1/vacuole biogenesis/peripheral vacuol	-4.19
Contig4-2526_0003/ARO4/orf6.3017;ARO4/3-deoxy-D-arabinoheptulosonate-7-P synthase/3-deoxy-L	-3.47
Contig4-3054_0025/ATP2/orf6.6893;ATP2/F1 ATPase beta subunit/F(1)F(0)-ATPase complex beta su	-4.77
Contig4-2994_0001/TYE7/orf6.6049;TYE7/glycolytic gene expression/TYE7, a 33 kDa serine-rich pro	-3.56
SLA1/SLA1/orf6.7099/cytoskeleton/	-2.84
YGL141/YGL141//-/	-2.75
Contig4-2509_0001/YOR216/orf6.630;orf6.7157;orf6.7158;orf6.7156;orf6.631;YOR216/-/involved in s	-14.46
Contig4-2638_0003/orf6.2109/orf6.2109/15.5 kDa mitochondrial ribosomal protein YmL31/15.5 kDa r	-5.34
Contig4-2628_0002/HSX2/orf6.6788;HSX2/alpha-adducin/	-2.74
Contig4-2414_0007/YHR111/orf6.5584;YHR111/molybdopterin biosynthesis/moeB, thiF, UBA1/molec	-2.24
Contig4-2678_0008/MMS2/orf6.5788;MMS2/postreplication repair/involved in mitochondrial inner pep	-4.65
Contig4-2649_0003/YCR3/orf6.6761;YCR3;PDX3/mitochondrial ribosomal protein L32/Mitochondrial i	-8.41
Contig4-2904_0003/orf6.7074/orf6.7074/Guanine nucleotide exchange protein for ARF/Guanine nucl	-6.41
Contig4-2871_0008/CYB5/orf6.8504;CYB5/cytochrome b5/cytochrome b5/cytochrome b5;lipid metab	-2.69
Contig4-2802_0005/YCX1/orf6.167;orf6.3458;YCX1/-//molecular_function unknown;biological_proces	-3.26
Contig4-2836_0010/orf6.4041/orf6.4041/Syngomycin response protein 2/Syngomycin response prc	-8.60
Contig4-2963_0013/CFL95/orf6.6383;CFL95/CFL1-like protein//molecular_function unknown;biologic	-4.02
Contig4-2912_0008/orf6.3823/orf6.3823/UPRTase/UPRTase/cytoplasm;uracil phosphoribosyltransfer	-2.81
Contig4-2882_0010/APE2/orf6.3413;APE2/leucine aminopeptidase/aminopeptidase yscII/cytoplasm;p	-13.91
Contig4-2990_0001/orf6.4290/orf6.4290///molecular_function unknown;biological_process unknown	-2.75
Contig4-2986_0002/orf6.8151/orf6.8151/Putative integral membrane protein containing novel cysteine	-2.65
Contig4-2970_0009/PTR2/orf6.4683;PTR2;YLR63;YGL157;YFL10;MSH4/peptide transport//molecula	-5.04
Contig4-2944_0009/MRP20/orf6.2238;MRP20/mitochonrial ribosomal protein L41/263-amino acid mit	-4.29
Contig4-2967_0009/NIN1/orf6.5160;NIN1/nuclear integrity/cytoplasmic 32 - 34 kDa protein/19S prote	-7.12
Contig4-3048_0002/YMR90/orf6.8783;orf6.8784;YMR90/-//molecular_function unknown;biological_pr	-9.65
Contig4-1909_0001/SAC6/orf6.1299;orf6.2202;orf6.1298;SAC6/fimbrin/fibrin homolog (actin-filament	-2.50
Contig4-3108_0111/COQ2/orf6.8991;COQ2/p-hydroxybenzoate:polyprenyl transferase/para hydroxyk	-2.60
Contig4-2978_0009/YBR254/orf6.7207;orf6.7208;YBR254/-//molecular_function unknown;biological_p	-5.02
Contig4-2699_0008/orf6.2949/orf6.2949/transcription factor/transcription factor/nucleosome remodelir	-3.68
Contig4-3089_0048/orf6.7636/orf6.7636/Mitochondrial outer membrane protein\; forms the outer merr	-4.45
Contig4-3086_0038/YTH1/orf6.7145;YTH1/polyadenylation/Polyadenylation factor subunit/mRNA pro	-5.83
Contig4-2740_0015/orf6.7406/orf6.7406;orf6.7407//	-2.68
Contig4-2980_0027/CPH2/orf6.4624;CPH2/myc-family transcription factor homolog/myc-family transc	-5.35
Contig4-3034_0016/orf6.6885/orf6.6885///molecular_function unknown;biological_process unknown	-3.18
Contig4-2796_0002/orf6.8836/orf6.8836//	-2.85
Contig4-2360_0004/orf6.4134/orf6.4134/An armadillo repeat-containing protein localized on the vacu	-4.35
YKL174/YKL174//-/	-2.76
YNR70/YNR70//CDR1-like protein/	-3.30
SHE3/SHE3//mother cell specific expression/	-2.78
CPS1/CPS1//carboxypeptidase S/	-3.33
YOR304/YOR304//transcription/	-3.47
Contig4-2099_0006/YBL64/orf6.7931;orf6.3125;orf6.3502;orf6.1877;orf6.7160;orf6.566;orf6.2884;orf6	-3.24
Contig4-1712_0002/orf6.6307/orf6.6307//	-2.54
Contig4-1957_0002/ZUO1/orf6.2725;ZUO1/zuotin/Zuotin, putative Z-DNA binding protein/cytosol;ribo	-8.95
Contig4-1497_0003/YOR252/orf6.1469;orf6.1470;YOR252/-//molecular_function unknown;biological_	-2.59
Contig4-2474_0008/orf6.1509/orf6.1509;orf6.722/cell cycle checkpoint protein/cell cycle checkpoint pi	-3.83

Contig4-2276_0004/CSE4/orf6.5324;CSE4/histone H3 like protein/high similarity to histone H3 and to	-3.02
Contig4-2596_0004/orf6.2366/orf6.2366//	-10.21
Contig4-2492_0002/orf6.6503/orf6.6503/Saccharolysin (oligopeptidase yscD)/Saccharolysin (oligopep	-11.64
Contig4-2716_0008/orf6.6651/orf6.6651///molecular_function unknown;biological_process unknown	-7.20
Contig4-2707_0002/VMA13/VMA13/vacuolar H+ ATPase subunit/vacuolar ATPase V1 domain subun	-3.86
Contig4-2890_0011/orf6.3638/orf6.3638/non-clathrin coat protein involved in transport between ER ar	-7.01
Contig4-2831_0003/GRE2/orf6.1740;GRE2/osmotic stress response/putative reductase/molecular_fu	-10.10
Contig4-2785_0004/SOD2/orf6.4731;SOD2;MAS6/manganese superoxide dismutase/Manganese-coi	-4.26
Contig4-2816_0002/YPT7/orf6.5712;orf6.5713;YPT7;YOR359;YKL195;YHR194;CDC73;CAX12;CAX	-8.50
Contig4-2921_0012/YER73/orf6.6640;orf6.6641;YER73/aldehyde dehydrogenase/mitochondrial Aldel	-5.28
Contig4-2979_0013/PDR13/orf6.7507;PDR13/drug resistance/Hsp70 Protein/	-3.12
Contig4-2977_0025/YDR346/orf6.7612;orf6.7611;YDR346/-//molecular_function unknown;biological_	-3.46
Contig4-2931_0017/MDH1/orf6.7901;MDH1/malate dehydrogenase/mitochondrial malate dehydroger	-8.29
Contig4-2927_0002/orf6.4559/orf6.4559//	-4.18
Contig4-3041_0019/orf6.664/orf6.664;orf6.3312///molecular_function unknown;biological_process unl	-2.59
Contig4-3039_0009/YLR270/orf6.7165;YLR270/-//molecular_function unknown;biological_process un	-2.44
Contig4-3017_0017/APL1/orf6.8112;APL1;YDR291/beta-adaptin/beta-adaptin, large subunit of the cla	-2.27
Contig4-2910_0009/CDC5/orf6.5090;CDC5/protein kinase/protein kinase which functions at the G(sul	-3.02
Contig4-2886_0007/orf6.610/orf6.610/carbamoyl-phosphate synthetase, aspartate transcarbamylase, :	-4.40
Contig4-2890_0003/orf6.3665/orf6.3665/similar to bovine rhodopsin kinase\; suppressor of GTPase r	-2.54
Contig4-1791_0006/HHF1/orf6.4930;orf6.5621;HHF1;HHF2/histone H4/Histone H4 (HHF1 and HHF2	-7.77
Contig4-2000_0003/orf6.3633/orf6.3633/probable purine nucleotide-binding protein/probable purine n	-3.27
Contig4-1727_0004/orf6.4479/orf6.4479;orf6.4478/Contains seven cysteine rich zinc finger motifs of t	-4.03
Contig4-2204_0001/YDR496/orf6.4654;YDR496/-//molecular_function unknown;biological_process ur	-10.49
Contig4-2310_0003/orf6.5321/orf6.5321;orf6.5319;orf6.5320;orf6.5322;orf6.5318///molecular_functio	-3.92
Contig4-2192_0002/////molecular_function unknown;biological_process unknown	-2.86
Contig4-2297_0004/SDS23/orf6.4036;SDS23;PLB97;OLE1;LTP1;CAX14;CAX13;CCR4/spindle pole	-3.98
Contig4-2634_0003/orf6.2588/orf6.2588;orf6.72;orf6.2587//	-5.64
Contig4-2418_0003/orf6.1984/orf6.1984/glycerol-3-phosphate dehydrogenase/glycerol-3-phosphate c	-8.57
Contig4-2521_0005/orf6.4993/orf6.4993//	-5.26
Contig4-2647_0010/YPL88/orf6.2130;orf6.2004;orf6.4310;orf6.4311;orf6.425;YPL88/-//molecular_fun	-3.66
Contig4-2584_0004/orf6.1798/orf6.1798;orf6.1632;orf6.8795;orf6.6230;orf6.322;orf6.4419;orf6.434;or	-4.72
Contig4-2902_0012/GRE99/orf6.4614;orf6.3162;GRE99/GRE2-like protein/putative reductase/molecul	-6.69
Contig4-2868_0015/orf6.2686/orf6.2686///molecular_function unknown;biological_process unknown	-3.43
Contig4-2794_0005/URA4/orf6.1407;URA4/dihydroorotase/dihydroorotase/dihydroorotase	-4.71
Contig4-2961_0009/RHD3/orf6.8294//	-3.85
Contig4-2936_0020/PRE4/orf6.6615;orf6.967;PRE4/proteosome subunit/proteasome subunit necessa	-5.24
Contig4-2906_0010/YNL181/orf6.5123;orf6.1585;YNL181/-//molecular_function unknown;biological_p	-4.54
Contig4-3010_0010/orf6.7048/orf6.7048;orf6.283//	-5.60
Contig4-2989_0014/SCS7/orf6.7517;SCS7/fatty acid hydroxylation/desaturase\hydroxylase enzyme/	-4.30
Contig4-2986_0022/orf6.8167/orf6.8167///cellular_component unknown;molecular_function unknown;	-2.62
Contig4-2969_0012/orf6.2719/orf6.2719//	-5.20
Contig4-2942_0011/YDR322/orf6.3551;YDR322/mitochondrial ribosomal protein/Mitochondrial riboso	-3.17
Contig4-3033_0006/SCO1/orf6.8406;SCO1/mitochondrial membrane protein/inner mitochondrial mem	-4.40
Contig4-3030_0005/UBI4/orf6.8860;orf6.3734;UBI4;UBI1;RPS31/polyubiquitin/ubiquitin/cytoplasm;prc	-6.71
Contig4-3013_0010/orf6.8699/orf6.8699;orf6.8700/88 kD component of the Exocyst complex, which c	-2.64
Contig4-2020_0009/ERG1/orf6.2816;ERG1/squalene epoxidase/Squalene monooxygenase/endoplas	-5.35
Contig4-3014_0004/orf6.8134/orf6.8134/chromatin remodeling complex subunit/chromatin remodeling	-4.97
Contig4-2384_0003/orf6.3607/orf6.3607//	-2.06
Contig4-3026_0018/orf6.6193/orf6.6193;orf6.586/82-kDa protein, with putative coiled-coil domain, ha	-3.07
Contig4-2986_0014/GDI1/orf6.8161;orf6.8162;GDI1/GDP disassociation inhibitor/GDP dissociation in	-3.89

Contig4-2678_0010/orf6.5789/orf6.5789///molecular_function unknown;biological_process unknown	-3.09
Contig4-3059_0011/SHA3/orf6.6480;SHA3/protein kinase/serine/threonine protein kinase homolog	-3.55
Contig4-3024_0028/NDH1/orf6.7629;NDH1/NADH dehydrogenase 49kd subunit/	-5.91
Contig4-2826_0004/orf6.4384/orf6.4384/sit4 suppressor, dnaJ homolog/sit4 suppressor, dnaJ homolog	-3.03
Contig4-3096_0049/orf6.7764/orf6.7764/actin related protein, subunit of the chromatin remodeling Sn	-7.00
Contig4-2929_0012/CUP1/orf6.3226;orf6.2302;CUP1;YJR88/copper resistance-associated metallothi	-5.73
YKR96/YKR96//dehydrogenase/	-3.21
RPA135/RPA135//RNA polymerase I A135 subunit/	-3.11
YPR1/YPR1//keto reductase/	-3.87
YOR81/YOR81//-/	-2.29
Contig4-1973_0007/DIS3/orf6.2439;DIS3/Ran-binding protein/3'-5' exonuclease complex subunit/	-3.13
Contig4-1684_0005/orf6.686/orf6.686;orf6.3693///molecular_function unknown;biological_process un	-2.78
Contig4-2479_0009/DBP5/orf6.5736;DBP5/RNA helicase/RNA helicase/RNA helicase	-6.33
Contig4-2267_0001/TEF2/orf6.1202;orf6.339;orf6.6331;orf6.1201;orf6.340;orf6.6330;TEF2;TEF1/tran	-5.78
Contig4-2610_0009/YGL20/orf6.4760;YGL20//molecular_function unknown;biological_process unkn	-3.07
Contig4-2497_0006/PDB1/orf6.3940;PDB1/pyruvate dehydrogenase E1-beta subunit/beta subunit of	-7.12
Contig4-2720_0005/RNA12/orf6.2807;orf6.4544;orf6.575;orf6.6327;orf6.2808;orf6.4545;orf6.352;RNA	-4.95
Contig4-2672_0009/orf6.5865/orf6.5865/SNARE docking complex subunit/SNARE docking complex s	-4.28
Contig4-2659_0010/orf6.7002/orf6.7002//	-9.52
Contig4-2888_0009/DAK2/orf6.1906;orf6.1104;DAK2/dihydroxyacetone kinase/dihydroxyacetone kin	-7.01
Contig4-2828_0002/TFC2/orf6.2514;orf6.2513;TFC2/transcription factor IIIA/Transcription factor IIIA (-3.06
Contig4-2777_0002/PET9/orf6.8179;PET9/ATP translocator/mitochondrial ADP/ATP translocator/mit	-12.22
Contig4-2945_0012///	-5.16
Contig4-2861_0006/orf6.6704/orf6.6704//	-2.83
Contig4-2929_0016/CUP1/orf6.3228;CUP1/copper resistance-associated metallothionein/CTP syntha	-3.47
Contig4-1657_0002/orf6.1684/orf6.1684///molecular_function unknown;biological_process unknown	-4.70
Contig4-2929_0016/CUP1/orf6.3228;CUP1/copper resistance-associated metallothionein/CTP syntha	-5.99
Contig4-2481_0004/orf6.5372/orf6.5372/cytoplasmic isoleucyl-tRNA synthetase/cytoplasmic isoleucyl	-6.42
Contig4-2820_0003/orf6.6496/orf6.6496/RAP1-interacting factor, involved in establishment of repress	-2.97
Contig4-2753_0010/orf6.1466/orf6.1466;orf6.8796;orf6.434;orf6.6229;orf6.1631;orf6.321;orf6.4420;or	-12.37
Contig4-2519_0003/RPL2/orf6.8117;RPL2/ribosomal protein L2/Ribosomal protein L4B (L2B) (rp2) (Y	-5.57
Contig4-2320_0001/IPP1/orf6.807;orf6.2048;IPP1/inorganic pyrophosphatase/Inorganic pyrophospha	-7.80
Contig4-2199_0001/YOR243/orf6.2015;orf6.4925;YOR243;SPT23;CAX4;CAX3;CAX2;CAX1/-/inducib	-2.75
Contig4-2303_0006/YPR4/orf6.5384;YPR4/flavoprotein//molecular_function unknown;biological_proci	-4.12
Contig4-2526_0006/SPX22/orf6.3019;SPX22/small subunit of U2AF splicing factor/	-3.05
Contig4-2696_0009/orf6.6665/orf6.6665/Homoserine dehydrogenase (L-homoserine:NADP oxidoredu	-5.01
Contig4-2871_0006/orf6.8503/orf6.8503///nucleus;molecular_function unknown;biological_process un	-3.65
Contig4-2813_0019/CVB1/orf6.5034;CVB1/vacuole biogenesis/	-4.64
Contig4-2963_0011/YFH1/orf6.6382;YFH1;CFL95/frataxin-like protein/mitochondrial protein that regu	-4.37
Contig4-2960_0004/orf6.1753/orf6.1753;orf6.3521///lipid particle;molecular_function unknown;lipid me	-2.46
Contig4-2933_0011/TFC5/orf6.3369;TFC5/transcription factor IIIB subunit/90 kd subunit of TFIIIB, also	-2.47
Contig4-2882_0008/YHR47/orf6.3413;YHR47/metalloproteinase/arginine/alanine aminopeptidase/ce	-5.42
Contig4-2986_0001/orf6.8150/orf6.8150///cellular_component unknown;molecular_function unknown;	-3.56
Contig4-2985_0015/orf6.5598/orf6.5598/53-kDa coiled-coil protein/53-kDa coiled-coil protein/spindle p	-3.29
Contig4-2970_0008/YLR63/orf6.4683;YLR63;YGL157;YFL10;MSH4;PTR2/protein kinase//molecular_	-2.59
Contig4-2967_0007/orf6.5158/orf6.5158///molecular_function unknown;biological_process unknown	-3.11
Contig4-2941_0016/RHC18/orf6.7556;RHC18/DNA repair/involved in recombination repair/molecular_	-3.03
Contig4-3031_0002/CCT1/orf6.6263;CCT1/chaperonin/chaperonin subunit alpha/cytoplasm;cytoskele	-5.63
Contig4-3078_0035/IDH1/orf6.7385;IDH1;YOR243;SPT23;CAX4;CAX3;CAX2;YBL64;MTX4;CAX6;C/	-7.62
Contig4-3098_0049/PAB1/orf6.7774;PAB1/polyA-binding protein/Poly(A) binding protein, cytoplasmic	-4.26
Contig4-1997_0002/RPL4/orf6.9035;orf6.5539;RPL4/ribosomal protein L4/Ribosomal protein L8B (L4	-9.51

Contig4-2742_0003/YBL58/orf6.1714;orf6.1005;orf6.1006;YBL58/-/putative regulatory subunit for Glc	-12.72
Contig4-2869_0008/orf6.3042/orf6.3042/Ribose-5-phosphate ketol-isomerase/Ribose-5-phosphate ke	-4.03
YDR465/YDR465//-	-2.17
Contig4-2100_0001/RAM2/orf6.5223;RAM2/CAAX farnesyl-protein transferase/CAAX farnesyltransfe	-3.66
Contig4-2484_0002/orf6.1365/orf6.1365;orf6.2911/vacuole import and degradation/vacuole import an	-2.60
Contig4-2474_0006/RMS1/orf6.721;orf6.3349;RMS1/regulation of transcription/(putative) transcrip	-6.18
Contig4-2348_0004/YBL64/orf6.6958;YBL64;MTX4;CAX6;CAX5;ERG5;CYP61/rehydrin/cytochrome I	-2.25
Contig4-2144_0005/NAB2/orf6.3340;NAB2/RNA binding protein/nuclear polyadenylated RNA binding	-5.60
Contig4-2244_0003/FAD1/orf6.1443;orf6.5913;FAD1/delta-12 oleate desaturase/	-2.65
Contig4-2615_0003/SDS23/orf6.6343;orf6.142;orf6.6342;SDS23;PLB97;OLE1;LTP1;CAX14;CAX13;C	-5.03
Contig4-2551_0002/SPX62/orf6.5203;SPX62/-/	-5.33
Contig4-2606_0006/YBL64/orf6.3502;orf6.1877;orf6.3125;orf6.6016;orf6.566;orf6.7931;orf6.6183;orf6	-3.69
Contig4-2596_0003/NMT1/orf6.2367;NMT1/myristoyl-CoA:protein N-myristoyltransferase/N-myristoyl	-4.78
Contig4-2502_0004/orf6.1262/orf6.1262///molecular_function unknown;biological_process unknown	-5.21
Contig4-2492_0001/YCL57/orf6.6503;orf6.6504;YCL57/saccharolysin/Saccharolysin (oligopeptidase)	-7.44
Contig4-2374_0007/YHR122/orf6.6004;YHR122/-/molecular_function unknown;biological_process ur	-3.29
Contig4-2674_0003/YOR271/orf6.5217;orf6.5216;YOR271/tricarboxylate carrier protein//molecular_fu	-6.72
Contig4-2668_0003/orf6.6012/orf6.6012///molecular_function unknown;biological_process unknown	-5.01
Contig4-2708_0009/IDH2/orf6.6625;orf6.6624;IDH2/isocitrate dehydrogenase/NAD+-dependent isocit	-8.79
Contig4-2663_0005/ARP5/orf6.7067;ARP5/actin-related protein/Actin-related protein/cell;molecular_fu	-4.29
Contig4-2896_0003/RHR2/orf6.8673;RHR2/glycerol-3-phosphatase/DL-glycerol-3-phosphatase/glyce	-6.73
Contig4-2954_0011/orf6.4964/orf6.4964;orf6.4965/bovine prefoldin subunit 5 homolog (putative)/bovii	-4.76
Contig4-3019_0016/PEP12/orf6.5194;PEP12/membrane protein - proteinase deficient/integral membi	-2.28
Contig4-2523_0004/orf6.7615/orf6.7615/involved in mitochondrial inheritance and actin assembly/invc	-3.11
Contig4-2432_0004/orf6.1867/orf6.1867;orf6.263///molecular_function unknown;biological_process ur	-2.29
SPC98/SPC98/orf6.4098/microtubule organization/	-2.31
Contig4-2516_0008/YNL281/orf6.1808;YNL281;YLR144;YJL149;YHL8;YDR485;RPL32;CAX18;CAX	-2.85
Contig4-2298_0010/GLN1/orf6.3536;orf6.313;orf6.2713;orf6.3535;GLN1/glutamine synthetase/glutarr	-5.41
Contig4-2641_0003/orf6.6283/orf6.6283/homolog of Snf5p, member of the chromatin remodeling com	-7.43
Contig4-2576_0010/orf6.2075/orf6.2075;orf6.2241//	-3.59
Contig4-2635_0010/YPR131/orf6.2198;YPR131/-/N-terminal acetyltransferase/	-3.38
Contig4-2743_0006/YOL10/orf6.190;orf6.7034;YOL10/RNA 3'-terminal phosphate cyclase/protein sirr	-3.42
Contig4-2738_0007/orf6.1624/orf6.1624;orf6.3841/Small subunit of TFIIE transcription factor/Small su	-6.13
Contig4-2868_0008/RPL9/orf6.955;orf6.954;RPL9/ribosomal protein/Ribosomal protein L9B (L8B) (rp	-9.56
Contig4-2911_0014/YDR527/orf6.2614;YDR527/-/molecular_function unknown;biological_process ur	-2.65
Contig4-2906_0007/YNL182/orf6.5122;orf6.1584;YNL182/-/molecular_function unknown;biological_p	-11.07
Contig4-3010_0006/RNR2/orf6.7052;orf6.6635;RNR2/ribonucleoside diphosphate reductase small su	-7.30
Contig4-2984_0026/LSC2/orf6.1730;LSC2/succinyl-CoA synthetase beta-subunit/Succinate-CoA Lige	-2.87
Contig4-2969_0008/SKP1/orf6.2718;orf6.2827;SKP1/kinetochore subunit/Skp1p encodes Cbf3d, a 2C	-6.64
Contig4-2966_0014/YDR415/orf6.6165;YDR415/leucine aminopeptidase//molecular_function unknow	-6.21
Contig4-2939_0004/YOR261/orf6.1236;orf6.2670;YOR261/proteasome regulatory component/Subuni	-6.30
Contig4-1973_0005/RIB3/orf6.3689;orf6.2440;RIB3/4-dihydroxy-2-butanone 4-phosphate synthase/3,	-3.60
Contig4-3015_0018/orf6.7105/orf6.7105/Protein phosphatase 2A regulatory subunit B/Protein phosph	-5.45
Contig4-2989_0013/ZDS1/orf6.7518;ZDS1/cell polarity/peripheral plasma membrane protein/bud tip;e	-6.75
Contig4-3082_0036/YPR100/orf6.7663;YPR100/-/molecular_function unknown;biological_process ur	-3.19
Contig4-2988_0011/MDH2/orf6.8733;orf6.8312;MDH2;MDH3/malate dehydrogenase/mitochondrial m	-5.80
Contig4-2655_0003/orf6.5110/orf6.5110;orf6.5111/Mitochondrial ribosomal protein MRPL8 (YmL8) (E	-7.72
Contig4-3071_0006/orf6.8642/orf6.8642//	-2.66
Contig4-3096_0003/YML63/orf6.5287;orf6.4862;YML63/ribosomal protein 10/Ribosomal protein S1B	-15.00
YNL161/YNL161//threonine protein kinase/	-6.24
Contig4-2134_0003/orf6.1060/orf6.1060//	-3.42

Contig4-2610_0007/CKB1/orf6.4759;orf6.4758;CKB1/protein kinase/beta (38kDa) subunit of casein ki	-6.44
Contig4-2549_0012/ARO2/orf6.1285;orf6.1876;ARO2/chorismate synthase/Chorismate synthase/cho	-2.64
Contig4-2497_0004/orf6.3941/orf6.3941;orf6.35//	-4.20
Contig4-2712_0006/FUN12/orf6.6295;FUN12/-/97 kDa protein/molecular_function unknown;biologica	-3.70
Contig4-2659_0004/ATP1/orf6.7003;ATP1/F1 ATPase alpha subunit/mitochondrial F1F0-ATPase alpl	-12.64
Contig4-2829_0014/orf6.1414/orf6.1414/zinc finger transcription factor of the Zn(2)-Cys(6) binuclear c	-2.68
Contig4-2819_0011/orf6.4715/orf6.4715;orf6.4072///molecular_function unknown;biological_process u	-4.33
Contig4-2923_0025/YNL281/orf6.4325;YNL281;YLR144;YJL149;YHL8;YDR485;RPL32;CAX18;CAX'	-2.55
Contig4-2919_0011/RPL4/orf6.5539;orf6.9035;RPL4/ribosomal protein L4/Ribosomal protein L8B (L4	-6.07
Contig4-2899_0010/orf6.8309/orf6.8309/involved in cell separation/involved in cell separation/	-2.77
Contig4-2864_0002/YKR79/orf6.8661;YKR79/-//molecular_function unknown;biological_process unkn	-3.12
Contig4-2955_0011/orf6.4229/orf6.4229//	-4.70
Contig4-2929_0008/orf6.3224/orf6.3224;orf6.2300///molecular_function unknown;biological_process u	-2.38
Contig4-3022_0004/STM1/STM1/POP2 suppressor/gene product has affinity for quadruplex nucleic a	-14.55
Contig4-2980_0004/YNL206/orf6.1744;orf6.817;orf6.1745;YNL206/-/Regulator of Ty1 Transposition -	-3.55
Contig4-2941_0016/RHC18/orf6.7556;RHC18/DNA repair/involved in recombination repair/molecular_	-3.38
Contig4-1856_0004/YLR237/YLR237/-//molecular_function unknown;biological_process unknown	-4.42
Contig4-2511_0010/YPL225/orf6.8403;YPL225;CBP1/-//molecular_function unknown;biological_proce	-11.11
Contig4-2427_0006////	-5.16
Contig4-2912_0005/orf6.3820/orf6.3820/subunit common to RNA polymerases I, II, and III/subunit coi	-3.07
Contig4-2944_0005/RPB2/orf6.2239;orf6.4740;RPB2/RNA polymerase II subunit/second largest subu	-4.39
Contig4-2993_0022/orf6.4195/orf6.4195//	-10.19
Contig4-2922_0008/orf6.7865/orf6.7865;orf6.5839/104 kDa heat shock protein/104 kDa heat shock pr	-3.14
Contig4-3064_0025/orf6.8608/orf6.8608/Saccharopine dehydrogenase (NADP+, L-glutamate forming	-3.79
Contig4-2871_0005/YOR111*/orf6.8502;YOR111/-//cellular_component unknown;molecular_function	-2.34
Contig4-2629_0010/HHT1/orf6.8840;orf6.4928;orf6.5620;HHT1;HHT2/histone H3/Histone H3 (HHT1 :	-11.22
Contig4-3091_0041/RPL10/orf6.7941;orf6.7940;RPL10/ribosomal protein L10e/60S ribosomal protein	-12.84
KAR2/KAR2/orf6.572/ER membrane protein translocation/	-6.49
Contig4-2674_0002/ERG12/orf6.5215;ERG12/mevalonate kinase/mevalonate kinase/cytosol;mevalor	-3.76
Contig4-2897_0018/orf6.5326/orf6.5326/alpha-ketoglutarate dehydrogenase/alpha-ketoglutarate dehy	-5.96
Contig4-2995_0012/LEO1/orf6.8437;orf6.8436;LEO1/-//molecular_function unknown;biological_proce	-2.56
Contig4-2958_0024/PGI1/orf6.5859;PGI1/phosphoglucosomerase/Glucose-6-phosphate isomerase/c	-10.81
Contig4-2982_0001/TSA1/orf6.8577;orf6.8578;TSA1/thiol-specific antioxidant/thioredoxin-peroxidase	-7.74
Contig4-1791_0001/HHT2/orf6.4928;orf6.5620;orf6.8840;HHT2;HHT1/histone H3/Histone H3 (HHT1 :	-8.89
Contig4-2327_0004/TOP1/orf6.3708;TOP1/DNA topoisomerase I/topoisomerase I/nucleus;DNA topoi	-4.60
Contig4-2687_0001/YLF2/orf6.5362;YLF2/-/GTP-binding protein and glycogen phosphorylase (weak),	-3.84
Contig4-2732_0011/YKR38/orf6.2558;orf6.2557;YKR38/glycoprotease/probable calcium-binding prote	-2.46
Contig4-2647_0006/YMR49/orf6.2129;orf6.2128;YMR49/beta-transducin-like protein//cellular_comp	-3.51
Contig4-2936_0017/YOR164/orf6.6617;YOR164/-//molecular_function unknown;biological_process u	-2.72
Contig4-2959_0005/orf6.8496/orf6.8496///glutamate-tRNA ligase	-2.92
Contig4-2875_0013/CMD1/orf6.2969;orf6.4226;CMD1/calmodulin/Calmodulin/bud neck;bud tip;centra	-3.96
Contig4-3013_0008/YEL74/orf6.8702;YEL74/ribosomal protein S24E/40S ribosomal protein S24B/cyt	-15.56
Contig4-2075_0005/orf6.3428/orf6.3428/NAD-dependent glutamate dehydrogenase/NAD-dependent	-3.45
Contig4-3088_0039/DED81/orf6.6811;DED81;YSP3/asparaginyl-tRNA synthetase/Asparaginyl-tRNA	-3.55
Contig4-2716_0008/orf6.6651/orf6.6651///molecular_function unknown;biological_process unknown	-3.99
Contig4-3024_0006/YPL235/orf6.5275;YPL235/TATA-binding protein interactor/RUVB-like protein/mc	-2.78
HIG1/HIG1//heat-shock protein/	-4.92
YNL162/YNL162//ribosomal protein/	-4.89
Contig4-2610_0005/orf6.4757/orf6.4757/member of the 20-kDa J-protein family of co-chaperones\; hc	-2.77
Contig4-2602_0009/orf6.3441/orf6.3441//	-3.09
Contig4-2497_0003/orf6.3941/orf6.3941//	-2.38

Contig4-2722_0006/YFR27/orf6.3383;YFR27/-/involved in establishment of cohesion between sister c	-2.64
Contig4-2673_0012/YLR215/orf6.2698;orf6.676;YLR215/D123-like protein//molecular_function unkno	-3.18
Contig4-2712_0003/YAL36/orf6.6293;orf6.6292;YAL36/GTP-binding protein/similar to Xenopus GTP-	-3.64
Contig4-2665_0004/YCR51/orf6.5890;YCR51/ankrin-like protein//molecular_function unknown;biologi	-5.57
Contig4-2619_0014/TTP99/orf6.3833;orf6.112;TTP99/-/putative Golgi alpha-1,2-mannosyltransferase	-6.38
Contig4-2852_0014///Mitochondrial ribosomal protein MRPL44 (YmL44)/Mitochondrial ribosomal prote	-3.41
Contig4-2819_0005/PRP21/orf6.4710;PRP21/mRNA splicing/RNA splicing factor/mRNA splicing	-2.82
Contig4-2945_0009/orf6.7921/orf6.7921/vacuole import and degradation/vacuole import and degrada	-4.12
Contig4-2919_0008/YIL18/YIL18;RPL5/ribosomal protein/Ribosomal protein L2B (L5B) (rp8) (YL6)/cy	-9.80
Contig4-2899_0009/MET12/orf6.8310;MET12/methylenetetrahydrofolate reductase/putative methylen	-2.70
Contig4-2856_0005/VMA2/orf6.6531;VMA2/vacuolar ATPase subunit b/vacuolar ATPase V1 domain :	-9.92
Contig4-2955_0006/TPK1/orf6.4228;orf6.3336;orf6.3564;TPK1;TPK2/cAMP-dependent protein kinase	-2.88
Contig4-2953_0011/orf6.5667/orf6.5667///molecular_function unknown;biological_process unknown	-5.64
Contig4-3040_0010/ENX3/orf6.3058;ENX3;CEF1/pH signalling/Component of a protein complex assc	-4.13
Contig4-3003_0030/orf6.9003/orf6.9003;orf6.9004/RNA polymerase II large subunit/RNA polymerase	-3.01
Contig4-2650_0018/orf6.1307/orf6.1307/omosome STability/omosome STability/cellular_component t	-2.33
Contig4-2471_0002/RPL6/orf6.4956;RPL6/ribosomal protein/Ribosomal protein L7A (L6A) (rp11) (YL	-22.65