GOID	GO_term	Frequency	Genome Frequency	Probability	Gene(s)	Directly Annotated GOID List
722	telomerase-independent telomere maintenance	6 out of 60 genes, 10%	14 out of 7292 annotated genes, 0.1%	2.29E-09	YRF1-1 YRF1-6 YRF1-5 YRF1-2 YRF1-3 YRF1-7	722
6312	mitotic recombination	6 out of 60 genes, 10%	26 out of 7292 annotated genes, 0.3%	8.72E-08	YRF1-1 YRF1-6 YRF1-5 YRF1-2 YRF1-3 YRF1-7	722
723	telomere maintenance	7 out of 60 genes, 11.6%	180 out of 7292 annotated genes, 2.4%	0.00068	YRF1-1 YRF1-6 YRF1-5 YRF1-2 YRF1-3 YRF1-7 MOT3	722:723
6310	DNA recombination	7 out of 60 genes, 11.6%	192 out of 7292 annotated genes, 2.6%	0.00099	YRF1-1 YRF1-6 YRF1-5 YRF1-2 YER138C YRF1-3 YRF1-7	722:6319
7001	chromosome organization and biogenesis (sensu Eukaryota)	8 out of 60 genes, 13.3%	374 out of 7292 annotated genes, 5.1%	0.0113	YRF1-1 YRF1-6 YRF1-5 YRF1-2 UTH1 YRF1-3 YRF1-7 MOT3	722:1308:723
51276	chromosome organization and biogenesis	8 out of 60 genes, 13.3%	385 out of 7292 annotated genes, 5.2%	0.01328	YRF1-1 YRF1-6 YRF1-5 YRF1-2 UTH1 YRF1-3 YRF1-7 MOT3	722:1308:723
45941	positive regulation of transcription	3 out of 60 genes, 5%	69 out of 7292 annotated genes, 0.9%	0.01942	SFG1 UTH1 GAT1	45944:1308:45941
45935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	3 out of 60 genes, 5%	70 out of 7292 annotated genes, 0.9%	0.02016	SFG1 UTH1 GAT1	45944:1308:45941
9893	positive regulation of metabolism	3 out of 60 genes, 5%	72 out of 7292 annotated genes, 0.9%	0.02169	SFG1 UTH1 GAT1	45944:1308:45941
31325	positive regulation of cellular metabolism	3 out of 60 genes, 5%	72 out of 7292 annotated genes, 0.9%	0.02169	SFG1 UTH1 GAT1	45944:1308:45941
15980	energy derivation by oxidation of organic compounds	5 out of 60 genes,	201 out of 7292 annotated genes,	0.02483	QCR6 GID8 TSL1 ZWF1	9060:45721:5992:9051:5977

		8.3%	2.7%		BMH1	
48522	positive regulation of cellular process	3 out of 60 genes, 5%	76 out of 7292 annotated genes, 1.0%	0.02493	SFG1 UTH1 GAT1	45944:1308:45941
51242	positive regulation of cellular physiological process	3 out of 60 genes, 5%	76 out of 7292 annotated genes, 1.0%	0.02493	SFG1 UTH1 GAT1	45944:1308:45941
43119	positive regulation of physiological process	3 out of 60 genes, 5%	76 out of 7292 annotated genes, 1.0%	0.02493	SFG1 UTH1 GAT1	45944:1308:45941
6418	tRNA aminoacylation for protein translation	2 out of 60 genes, 3.3%	30 out of 7292 annotated genes, 0.4%	0.02558	MSR1 FRS2	6420:6432
43038	amino acid activation	2 out of 60 genes, 3.3%	30 out of 7292 annotated genes, 0.4%	0.02558	MSR1 FRS2	6420:6432
43039	tRNA aminoacylation	2 out of 60 genes, 3.3%	30 out of 7292 annotated genes, 0.4%	0.02558	MSR1 FRS2	6420:6432
44262	cellular carbohydrate metabolism	5 out of 60 genes, 8.3%	204 out of 7292 annotated genes, 2.7%	0.02625	GID8 TSL1 ZWF1 EXG1 BMH1	45721:5992:9051:6073:5977
48518	positive regulation of biological process	3 out of 60 genes, 5%	84 out of 7292 annotated genes, 1.1%	0.03216	SFG1 UTH1 GAT1	45944:1308:45941
6139	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	19 out of 60 genes, 31.6%	1526 out of 7292 annotated genes, 20.9%	0.03405	YRF1-1 YRF1-6 YRF1-5 SFG1 YRF1-2 GAT2 UTH1 ZWF1 GAT1 YER138C RPA34 YRF1-3 MSR1 YRF1-7 ROX1 LSM5 HIM1 FRS2 MOT3	722:45944:6350:1308:9051:45941:6367:6319:6360:6420:122:398:6402:6281:6432
45229	external encapsulating structure organization and biogenesis	4 out of 60 genes, 6.6%	150 out of 7292 annotated genes, 2.0%	0.03514	SED1 EXG1 CWP2 UTR2	7047

7047	cell wall organization and biogenesis	4 out of 60 genes, 6.6%	150 out of 7292 annotated genes, 2.0%	0.03514	SED1 EXG1 CWP2 UTR2	7047
6112	energy reserve metabolism	2 out of 60 genes, 3.3%	36 out of 7292 annotated genes, 0.4%	0.03571	TSL1 BMH1	5992:5977
5975	carbohydrate metabolism	5 out of 60 genes, 8.3%	223 out of 7292 annotated genes, 3.0%	0.03645	GID8 TSL1 ZWF1 EXG1 BMH1	45721:5992:9051:6073:5977
6259	DNA metabolism	9 out of 60 genes, 15%	564 out of 7292 annotated genes, 7.7%	0.0403	YRF1-1 YRF1-6 YRF1-5 YRF1-2 UTH1 YER138C YRF1-3 YRF1-7 HIM1	722:1308:6319:6281
6091	generation of precursor metabolites and energy	5 out of 60 genes, 8.3%	233 out of 7292 annotated genes, 3.1%	0.04269	QCR6 GID8 TSL1 ZWF1 BMH1	9060:6122:45721:5992:9051:5977
6066	alcohol metabolism	4 out of 60 genes, 6.6%	161 out of 7292 annotated genes, 2.2%	0.04367	ERG26 GID8 ADH7 ZWF1	6696:45721:6066:9051
6073	glucan metabolism	2 out of 60 genes, 3.3%	41 out of 7292 annotated genes, 0.5%	0.04513	EXG1 BMH1	6073:5977
7124	pseudohyphal growth	2 out of 60 genes, 3.3%	50 out of 7292 annotated genes, 0.6%	0.06408	SFG1 BMH1	7124
5976	polysaccharide metabolism	2 out of 60 genes, 3.3%	56 out of 7292 annotated genes, 0.7%	0.07794	EXG1 BMH1	6073:5977
44264	cellular polysaccharide metabolism	2 out of 60 genes, 3.3%	56 out of 7292 annotated genes, 0.7%	0.07794	EXG1 BMH1	6073:5977
45893	positive regulation of transcription, DNA-dependent	2 out of 60 genes, 3.3%	64 out of 7292 annotated genes, 0.8%	0.09772	SFG1 UTH1	45944:1308