GOID	GO_term	Frequency	Genome Frequency	Probability	Gene(s)	Directly Annotated GOID List
6350	transcription	11 out of 13 genes, 84.6%	493 out of 7292 annotated genes, 6.7%	9.25E-12	ABF1 RCS1 SKN7 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1 SWI4	45944:30466:122:6350:6357:6355:7329:7068:6363
6355	regulation of transcription, DNA-dependent	9 out of 13 genes, 69.2%	311 out of 7292 annotated genes, 4.2%	2.85E-10	ABF1 RCS1 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1	45944:30466:122:6357:6355:7329:7068
45449	regulation of transcription	9 out of 13 genes, 69.2%	331 out of 7292 annotated genes, 4.5%	4.95E-10	ABF1 RCS1 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1	45944:30466:122:6357:6355:7329:7068
19219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	9 out of 13 genes, 69.2%	362 out of 7292 annotated genes, 4.9%	1.09E-09	ABF1 RCS1 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1	45944:30466:122:6357:6355:7329:7068
6139	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	13 out of 13 genes, 100%	1526 out of 7292 annotated genes, 20.9%	1.47E-09	ABF1 RCS1 CBF1 MBP1 SKN7 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1 SWI4	45944:30466:715:6260:6338:122:6333:6350:6357:6355:7329:7068:7131:6363
31323	regulation of cellular metabolism	9 out of 13 genes, 69.2%	419 out of 7292 annotated genes, 5.7%	3.94E-09	ABF1 RCS1 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1	45944:30466:122:6357:6355:7329:7068
51244	regulation of cellular physiological process	10 out of 13 genes, 76.9%	613 out of 7292 annotated genes, 8.4%	3.97E-09	ABF1 RCS1 MBP1 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1	45944:30466:122:74:6357:6355:7329:7068
50794	regulation of cellular process	10 out of 13 genes, 76.9%	614 out of 7292 annotated genes, 8.4%	4.03E-09	ABF1 RCS1 MBP1 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1	45944:30466:122:74:6357:6355:7329:7068
50791	regulation of physiological process	10 out of 13 genes, 76.9%	631 out of 7292 annotated genes, 8.6%	5.26E-09	ABF1 RCS1 MBP1 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1	45944:30466:122:74:6357:6355:7329:7068
50789	regulation of biological	10 out of 13 genes, 76.9%	641 out of 7292 annotated genes,	6.13E-09	ABF1 RCS1 MBP1 NRG1 MSN4 STE12	45944:30466:122:74:6357:6355:7329:7068

	process		8.7%		YAP6 UME6 CIN5 REB1	
19222	regulation of metabolism	9 out of 13 genes, 69.2%	445 out of 7292 annotated genes, 6.1%	6.69E-09	ABF1 RCS1 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1	45944:30466:122:6357:6355:7329:7068
6351	transcription, DNA-dependent	9 out of 13 genes, 69.2%	450 out of 7292 annotated genes, 6.1%	7.38E-09	ABF1 RCS1 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1	45944:30466:122:6357:6355:7329:7068:6363
6357	regulation of transcription from RNA polymerase II promoter	7 out of 13 genes, 53.8%	187 out of 7292 annotated genes, 2.5%	1.09E-08	ABF1 RCS1 NRG1 STE12 YAP6 CIN5 REB1	45944:122:6357:7329
6366	transcription from RNA polymerase II promoter	7 out of 13 genes, 53.8%	285 out of 7292 annotated genes, 3.9%	1.94E-07	ABF1 RCS1 NRG1 STE12 YAP6 CIN5 REB1	45944:122:6357:7329
45944	positive regulation of transcription from RNA polymerase II promoter	4 out of 13 genes, 30.7%	53 out of 7292 annotated genes, 0.7%	1.89E-06	ABF1 RCS1 STE12 YAP6	45944:7329
45893	positive regulation of transcription, DNA-dependent	4 out of 13 genes, 30.7%	64 out of 7292 annotated genes, 0.8%	3.98E-06	ABF1 RCS1 STE12 YAP6	45944:7329
45941	positive regulation of transcription	4 out of 13 genes, 30.7%	69 out of 7292 annotated genes, 0.9%	5.35E-06	ABF1 RCS1 STE12 YAP6	45944:7329
45935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	4 out of 13 genes, 30.7%	70 out of 7292 annotated genes, 0.9%	5.66E-06	ABF1 RCS1 STE12 YAP6	45944:7329
9893	positive regulation of	4 out of 13 genes, 30.7%	72 out of 7292 annotated genes,	6.32E-06	ABF1 RCS1 STE12 YAP6	45944:7329

	metabolism		0.9%			
31325	positive regulation of cellular metabolism	4 out of 13 genes, 30.7%	72 out of 7292 annotated genes, 0.9%	6.32E-06	ABF1 RCS1 STE12 YAP6	45944:7329
43119	positive regulation of physiological process	4 out of 13 genes, 30.7%	76 out of 7292 annotated genes, 1.0%	7.82E-06	ABF1 RCS1 STE12 YAP6	45944:7329
48522	positive regulation of cellular process	4 out of 13 genes, 30.7%	76 out of 7292 annotated genes, 1.0%	7.82E-06	ABF1 RCS1 STE12 YAP6	45944:7329
51242	positive regulation of cellular physiological process	4 out of 13 genes, 30.7%	76 out of 7292 annotated genes, 1.0%	7.82E-06	ABF1 RCS1 STE12 YAP6	45944:7329
48518	positive regulation of biological process	4 out of 13 genes, 30.7%	84 out of 7292 annotated genes, 1.1%	1.15E-05	ABF1 RCS1 STE12 YAP6	45944:7329
44238	primary metabolism	13 out of 13 genes, 100%	3206 out of 7292 annotated genes, 43.9%	2.29E-05	ABF1 RCS1 CBF1 MBP1 SKN7 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1 SWI4	45944:30466:715:6260:6338:122:9086:6333:6350:6357:6006:6355:7329:7068:7131:6363
44237	cellular metabolism	13 out of 13 genes, 100%	3400 out of 7292 annotated genes, 46.6%	4.92E-05	ABF1 RCS1 CBF1 MBP1 SKN7 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1 SWI4	45944:30466:715:6260:6338:122:9086:6333:6350:6979:6357:6006:1324:6355:7329:7068:7131:6363
8152	metabolism	13 out of 13 genes, 100%	3490 out of 7292 annotated genes, 47.8%	6.91E-05	ABF1 RCS1 CBF1 MBP1 SKN7 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1 SWI4	45944:30466:715:6260:6338:122:9086:6333:6350:6979:6357:6006:1324:6355:7329:7068:7131:6363
9628	response to	5 out of 13	314 out of 7292	0.00014	SKN7 NRG1 MSN4	6979:6970:9268

	abiotic stimulus	genes, 38.4%	annotated genes, 4.3%		STE12 CIN5	:1324:7329:9651:42493
50896	response to stimulus	6 out of 13 genes, 46.1%	588 out of 7292 annotated genes, 8.0%	0.00028	ABF1 SKN7 NRG1 MSN4 STE12 CIN5	715:6979:6970:9268:1324:6950:7329:9651:42493
42221	response to chemical stimulus	4 out of 13 genes, 30.7%	233 out of 7292 annotated genes, 3.1%	0.00059	SKN7 MSN4 STE12 CIN5	6979:1324:7329:42493
1403	invasive growth (sensu Saccharomyces)	2 out of 13 genes, 15.3%	34 out of 7292 annotated genes, 0.4%	0.00163	NRG1 STE12	1403
50875	cellular physiological process	13 out of 13 genes, 100%	4722 out of 7292 annotated genes, 64.7%	0.00352	ABF1 RCS1 CBF1 MBP1 SKN7 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1 SWI4	45944:30466:715:6260:6338:122:6827:9086:6333:7059:74:6350:6979:6357:6006:1302:1324:6355:7329:747:30437:7001:45836:7068:7131:6363:7049:82
9987	cellular process	13 out of 13 genes, 100%	4761 out of 7292 annotated genes, 65.2%	0.00391	ABF1 RCS1 CBF1 MBP1 SKN7 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1 SWI4	45944:30466:715:6260:6338:122:6827:9086:6333:7059:74:6350:6979:6357:6006:1302:1324:6355:7329:747:30437:7001:45836:7068:7131:6363:7049:82
6979	response to oxidative stress	2 out of 13 genes, 15.3%	54 out of 7292 annotated genes, 0.7%	0.00405	SKN7 MSN4	6979:1324
7582	physiological process	13 out of 13 genes, 100%	4790 out of 7292 annotated genes, 65.6%	0.00423	ABF1 RCS1 CBF1 MBP1 SKN7 NRG1 MSN4 STE12 YAP6 UME6 CIN5 REB1 SWI4	45944:30466:715:6260:6338:122:6827:9086:6333:7059:74:6350:6979:6357:6006:1302:1324:6355:7329:747:30437:7001:45836:7068:7131:6363:7049:82

6800	oxygen and reactive oxygen species metabolism	2 out of 13 genes, 15.3%	56 out of 7292 annotated genes, 0.7%	0.00434	SKN7 MSN4	6979:1324
6970	response to osmotic stress	2 out of 13 genes, 15.3%	61 out of 7292 annotated genes, 0.8%	0.00513	SKN7 CIN5	6970:9651
6950	response to stress	4 out of 13 genes, 30.7%	426 out of 7292 annotated genes, 5.8%	0.00543	ABF1 SKN7 MSN4 CIN5	715:6979:6970:1324:6950:9651
30447	filamentous growth	2 out of 13 genes, 15.3%	91 out of 7292 annotated genes, 1.2%	0.01108	NRG1 STE12	1403:7124
6333	chromatin assembly or disassembly	2 out of 13 genes, 15.3%	100 out of 7292 annotated genes, 1.3%	0.01326	ABF1 CBF1	30466:6333
6259	DNA metabolism	4 out of 13 genes, 30.7%	564 out of 7292 annotated genes, 7.7%	0.01449	ABF1 CBF1 MBP1 UME6	30466:715:6260:6338:6333:7131
6260	DNA replication	2 out of 13 genes, 15.3%	105 out of 7292 annotated genes, 1.4%	0.01455	ABF1 MBP1	6260
45892	negative regulation of transcription, DNA-dependent	2 out of 13 genes, 15.3%	125 out of 7292 annotated genes, 1.7%	0.02021	ABF1 UME6	30466:122:7068
40007	growth	2 out of 13 genes, 15.3%	125 out of 7292 annotated genes, 1.7%	0.02021	NRG1 STE12	1403:7124
16481	negative regulation of transcription	2 out of 13 genes, 15.3%	129 out of 7292 annotated genes, 1.7%	0.02144	ABF1 UME6	30466:122:7068
45934	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid	2 out of 13 genes, 15.3%	139 out of 7292 annotated genes, 1.9%	0.02465	ABF1 UME6	30466:122:7068

	metabolism					
7001	chromosome organization and biogenesis (sensu Eukaryota)	3 out of 13 genes, 23.0%	374 out of 7292 annotated genes, 5.1%	0.02619	ABF1 CBF1 UME6	30466:6338:6333:7001
51276	chromosome organization and biogenesis	3 out of 13 genes, 23.0%	385 out of 7292 annotated genes, 5.2%	0.02824	ABF1 CBF1 UME6	30466:6338:6333:7001
31324	negative regulation of cellular metabolism	2 out of 13 genes, 15.3%	151 out of 7292 annotated genes, 2.0%	0.02874	ABF1 UME6	30466:122:7068
9892	negative regulation of metabolism	2 out of 13 genes, 15.3%	158 out of 7292 annotated genes, 2.1%	0.03125	ABF1 UME6	30466:122:7068
7049	cell cycle	3 out of 13 genes, 23.0%	406 out of 7292 annotated genes, 5.5%	0.03241	MBP1 UME6 SWI4	74:45836:7068 :7131:7049:82
51243	negative regulation of cellular physiological process	2 out of 13 genes, 15.3%	171 out of 7292 annotated genes, 2.3%	0.03613	ABF1 UME6	30466:122:7068
48523	negative regulation of cellular process	2 out of 13 genes, 15.3%	171 out of 7292 annotated genes, 2.3%	0.03613	ABF1 UME6	30466:122:7068
43118	negative regulation of physiological process	2 out of 13 genes, 15.3%	173 out of 7292 annotated genes, 2.3%	0.0369	ABF1 UME6	30466:122:7068
48519	negative regulation of biological process	2 out of 13 genes, 15.3%	179 out of 7292 annotated genes, 2.4%	0.03927	ABF1 UME6	30466:122:7068
50876	reproductive physiological process	2 out of 13 genes, 15.3%	197 out of 7292 annotated genes, 2.7%	0.04672	STE12 UME6	747:30437

48610	reproductive cellular physiological process	2 out of 13 genes, 15.3%	197 out of 7292 annotated genes, 2.7%	0.04672	STE12 UME6	747:30437
6325	establishment and/or maintenance of chromatin architecture	2 out of 13 genes, 15.3%	211 out of 7292 annotated genes, 2.8%	0.05285	ABF1 CBF1	30466:6338:6333
6323	DNA packaging	2 out of 13 genes, 15.3%	211 out of 7292 annotated genes, 2.8%	0.05285	ABF1 CBF1	30466:6338:6333
278	mitotic cell cycle	2 out of 13 genes, 15.3%	235 out of 7292 annotated genes, 3.2%	0.064	UME6 SWI4	7068:82
3	reproduction	2 out of 13 genes, 15.3%	263 out of 7292 annotated genes, 3.6%	0.07796	STE12 UME6	747:30437