Table S11. All significant condition categories from CRACR analysis for each TF examined in this study.

Specific conditions in which a TF is predicted to be active by CRACR are searched for enrichment of general condition categories (“attributes”).

For each TF, the attributes represent a search for condition category enrichment among all significant conditions, ordered by their area statistic.

N, M, and X are defined as follows— N out of the top M expression conditions (ordered by CRACR area statistic) belong to the condition category shown, out of X total conditions that belong to this category in the entire 1,327 condition dataset.

LOD = log10 odds ratio for overrepresentation of this condition category in the set of significant conditions for this TF.

P = single hypothesis one-sided P-value of condition category enrichment within query condition set (by Fisher’s Exact Test)

P-adj = significance of condition category enrichment adjusted for multiple hypothesis testing by 1000 null-hypothesis simulations.

Aft1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	12	21	66	1.577	1.50E-12	<0.001	Mitochondrion
2	8	21	74	1.167	1.50E-06	<0.001	Aerobic respiration
3	4	12	36	1.414	8.60E-05	0.028	Protein sorting
4	2	3	13	2.372	0.00017	0.048	Vacuole organization and biogenesis
Aro80 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	19	227	20	1.944	4.50E-16	<0.001	Stationary_phase
2	60	139	362	0.479	4.80E-09	<0.001	Response to stress
3	18	140	56	0.758	2.60E-07	<0.001	Cellular response to glucose starvation
4	89	611	160	0.36	5.60E-07	0.003	General regulation of transcription
5	29	596	40	0.668	2.90E-06	0.01	Histone modification
6	11	524	11	1.698	3.40E-06	0.011	SAGA complex
7	121	671	221	0.279	6.40E-06	0.015	Severe stress
8	4	6	46	1.828	7.90E-06	0.018	Response to drug
9	4	24	11	1.672	1.10E-05	0.019	Diamide
10	17	213	44	0.656	1.30E-05	0.022	Heat shock

11	19	596	24	0.804	2.10E-05	0.03	HDAC
12	18	156	68	0.578	3.00E-05	0.042	Transport
Bas1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	15	99	25	1.427	3.70E-13	<0.001	AA_starvation
2	23	115	77	0.835	3.70E-10	<0.001	Amino acid metabolism
3	10	72	27	1.172	6.70E-08	<0.001	Purine base metabolism
4	5	27	21	1.373	1.40E-05	0.009	Ergosterol biosynthesis
Cbf1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	9	32	25	1.59	2.10E-10	<0.001	AA_starvation
2	9	32	27	1.54	4.60E-10	<0.001	Purine base metabolism
3	14	51	77	0.967	2.50E-08	<0.001	Amino acid metabolism
4	35	161	160	0.48	1.20E-06	0.001	General regulation of transcription
5	10	39	74	0.928	4.30E-06	0.003	Nitrogen utilization
6	3	7	14	2.04	1.70E-05	0.016	Nitrogen_depletion
Cep3 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	15	153	20	1.479	1.90E-12	<0.001	Stationary_phase
2	46	201	160	0.538	2.20E-09	<0.001	General regulation of transcription
Cha4 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	155	458	362	0.38	3.20E-12	<0.001	Response to stress
2	7	7	46	2.781	8.70E-12	<0.001	Response to drug
3	19	387	20	1.644	1.40E-11	<0.001	Stationary_phase
4	7	7	68	2.583	1.60E-10	<0.001	Transport
5	60	468	110	0.516	2.90E-09	<0.001	Short stress (<40)
6	98	458	221	0.369	1.50E-08	<0.001	Severe stress
7	14	88	44	0.987	1.80E-08	<0.001	Heat shock
8	111	800	160	0.411	2.80E-08	<0.001	General regulation of transcription

9	42	693	56	0.622	4.60E-07	<0.001	Cellular response to glucose starvation
10	5	34	11	1.661	1.20E-06	0.003	Diamide
11	38	152	197	0.447	2.40E-06	0.008	Carbohydrate metabolism
12	35	718	45	0.653	2.80E-06	0.01	Galactose metabolism
13	11	578	11	1.633	1.00E-05	0.021	SAGA complex
14	16	393	25	0.755	2.10E-05	0.044	H2O2
Cup9 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	11	14	56	2.057	9.20E-15	<0.001	Sporulation
2	11	14	60	2.019	2.10E-14	<0.001	Meiosis
3	3	8	3	3.317	7.70E-08	<0.001	Late sporulation
4	3	10	6	2.336	3.30E-06	<0.001	W303 meiosis
5	3	11	7	2.172	7.80E-06	0.002	SK1 meiosis
6	2	11	2	2.933	4.10E-05	0.01	Meiosis 2
7	2	14	2	2.813	6.80E-05	0.016	Mid-late sporulaiton
Pbf2 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	146	273	362	0.785	9.20E-37	<0.001	Response to stress
2	46	92	110	1.361	2.10E-33	<0.001	Short stress (<40)
3	102	273	221	0.794	1.90E-29	<0.001	Severe stress
4	8	12	23	2.293	1.90E-13	<0.001	Rapamycin treatment
5	22	147	44	1.068	7.90E-13	<0.001	Heat shock
6	8	12	29	2.149	1.60E-12	<0.001	Rapamycin related
7	33	219	73	0.786	8.20E-12	<0.001	Response to oxidative stress
8	41	403	65	0.753	2.10E-11	<0.001	Medium stress (40-60)
9	8	12	56	1.788	5.00E-10	<0.001	Cellular response to glucose starvation
10	8	12	74	1.646	5.10E-09	<0.001	Nitrogen utilization
11	17	394	20	1.216	1.30E-08	<0.001	Stationary_phase
12	8	12	84	1.583	1.40E-08	<0.001	Protein biosynthesis
13	8	12	125	1.385	3.60E-07	<0.001	Ribosome
14	14	218	25	0.939	4.30E-07	<0.001	H2O2
15	6	59	11	1.541	6.80E-07	0.002	Diamide

16	4	92	4	2.196	9.40E-06	0.009	H2O2 in mutants
17	8	12	197	1.156	1.20E-05	0.011	Carbohydrate metabolism
18	18	271	40	0.64	1.80E-05	0.014	Response to heat shock
19	36	369	85	0.431	2.20E-05	0.021	Response to DNA damage
20	10	196	20	0.885	3.00E-05	0.033	DTT
21	13	252	26	0.758	3.20E-05	0.033	Mild stress
Ecm22 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	19	212	20	1.981	1.20E-16	<0.001	Stationary_phase
2	104	242	362	0.521	1.60E-15	<0.001	Response to stress
3	173	893	221	0.539	3.50E-15	<0.001	Severe stress
4	46	283	110	0.593	2.70E-10	<0.001	Short stress (<40)
5	22	150	56	0.868	4.80E-10	<0.001	Cellular response to glucose starvation
6	38	748	44	0.867	1.70E-08	<0.001	Heat shock
7	44	166	197	0.494	4.50E-08	<0.001	Carbohydrate metabolism
8	32	684	40	0.744	6.80E-07	0.001	Response to heat shock
9	11	79	42	0.911	2.10E-06	0.006	Alternative_carbon
10	69	447	160	0.344	4.00E-06	0.008	General regulation of transcription
11	32	651	45	0.578	1.60E-05	0.032	Galactose metabolism
12	9	39	68	0.906	1.70E-05	0.035	Transport
13	4	7	46	1.682	1.80E-05	0.036	Response to drug
14	46	888	57	0.55	2.10E-05	0.041	Long stress (>60)
15	7	167	11	1.183	2.40E-05	0.047	Diamide
Fhl1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	18	58	27	1.878	1.70E-21	<0.001	Short pheromone signal
2	18	51	32	1.777	9.90E-21	<0.001	Alpha factor stimulus
3	16	58	23	1.911	1.40E-19	<0.001	Saturating pheromone
4	26	51	110	1.267	1.10E-18	<0.001	Ste7 targets
5	26	51	118	1.225	7.50E-18	<0.001	Ste12 targets
6	26	51	131	1.164	1.30E-16	<0.001	MAPK signaling
7	12	28	26	1.921	3.50E-16	<0.001	Cell cycle G1 arrest

8	27	51	150	1.124	3.50E-16	<0.001	Mating (sensu Saccharomyces)
9	14	102	48	0.853	4.50E-07	<0.001	G1
10	39	125	243	0.466	9.80E-07	<0.001	Cell cycle
11	25	113	140	0.546	3.20E-06	0.004	No stress
12	8	58	33	1.011	1.10E-05	0.012	a factor stimulus
13	12	339	17	0.953	1.20E-05	0.013	Shmoo formation
14	9	180	17	0.975	2.20E-05	0.029	Gamma irradiation
15	8	43	52	0.921	3.70E-05	0.048	Pheromone signaling partial mutants
Fkh1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	18	51	32	1.777	9.90E-21	<0.001	Alpha factor stimulus
2	15	46	26	1.83	2.80E-18	<0.001	Cell cycle G1 arrest
3	21	51	110	1.072	7.80E-13	<0.001	Ste7 targets
4	21	51	118	1.032	3.40E-12	<0.001	Ste12 targets
5	23	51	150	0.975	5.70E-12	<0.001	Mating (sensu Saccharomyces)
6	11	46	27	1.49	2.30E-11	<0.001	Short pheromone signal
7	21	51	131	0.974	2.90E-11	<0.001	MAPK signaling
8	10	46	23	1.527	9.70E-11	<0.001	Saturating pheromone
9	22	65	140	0.803	3.40E-09	<0.001	No stress
10	31	80	243	0.605	6.10E-08	<0.001	Cell cycle
11	6	41	12	1.651	1.40E-07	<0.001	G2
12	6	34	17	1.499	5.30E-07	0.001	Shmoo formation
13	3	10	4	2.704	6.60E-07	0.001	Non-saturating pheromone
14	5	10	52	1.522	6.00E-06	0.006	Pheromone signaling partial mutants
15	8	90	24	0.981	2.20E-05	0.012	M_G1
16	3	34	4	2.074	3.20E-05	0.019	Long pheromone signal
17	6	34	37	1.056	7.40E-05	0.039	Cell wall integrity pathway
Fkh2 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	20	102	32	1.481	1.50E-17	<0.001	Alpha factor stimulus
2	16	102	26	1.443	5.10E-14	<0.001	Cell cycle G1 arrest
3	26	102	110	0.775	3.70E-10	<0.001	Ste7 targets

4	26	102	118	0.733	2.00E-09	<0.001	Ste12 targets
5	26	87	140	0.733	2.30E-09	<0.001	No stress
6	31	112	150	0.658	2.70E-09	<0.001	Mating (sensu Saccharomyces)
7	26	102	131	0.672	2.20E-08	<0.001	MAPK signaling
8	32	87	243	0.569	1.60E-07	<0.001	Cell cycle
9	11	102	27	1.063	1.80E-07	<0.001	Short pheromone signal
10	10	102	23	1.107	3.30E-07	<0.001	Saturating pheromone
11	14	95	56	0.798	1.50E-06	0.001	Sporulation
12	3	27	3	2.663	4.00E-06	0.006	Late sporulation
13	6	81	12	1.313	8.90E-06	0.007	G2
14	8	87	24	0.998	1.70E-05	0.01	M_G1
15	3	29	4	2.151	2.00E-05	0.012	Non-saturating pheromone
16	4	7	52	1.623	3.00E-05	0.019	Pheromone signaling partial mutants
17	6	76	17	1.094	6.80E-05	0.043	Shmoo formation
Gal4 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	16	272	20	1.289	5.90E-10	<0.001	Stationary_phase
2	60	303	160	0.485	1.70E-09	<0.001	General regulation of transcription
3	113	331	362	0.343	9.40E-09	<0.001	Response to stress
4	33	551	45	0.745	4.00E-08	<0.001	Galactose metabolism
5	34	614	44	0.759	6.00E-08	<0.001	Heat shock
6	113	584	221	0.322	3.00E-07	0.003	Severe stress
7	33	735	40	0.755	8.70E-07	0.004	Response to heat shock
8	22	200	65	0.606	2.80E-06	0.008	Medium stress (40-60)
9	6	87	10	1.438	3.40E-06	0.008	SWI/SNF complex
10	4	7	46	1.682	1.80E-05	0.028	Response to drug
11	10	310	14	1.012	2.50E-05	0.042	Nitrogen_depletion
Gat1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	37	25	2.204	1.40E-24	<0.001	AA_starvation
2	19	24	74	1.998	8.90E-23	<0.001	Nitrogen utilization
3	13	18	27	2.434	1.80E-21	<0.001	Purine base metabolism

4	10	18	14	2.647	1.20E-18	<0.001	Nitrogen_depletion
5	13	18	77	1.772	1.40E-14	<0.001	Amino acid metabolism
6	13	45	29	1.599	4.00E-14	<0.001	Rapamycin related
7	12	45	23	1.71	4.30E-14	<0.001	Rapamycin treatment
8	28	37	362	1.055	3.20E-12	<0.001	Response to stress
9	10	20	57	1.519	1.60E-10	<0.001	Long stress (>60)
10	15	20	221	1.285	4.90E-10	<0.001	Severe stress
11	12	45	84	0.894	1.10E-06	<0.001	Protein biosynthesis
12	6	47	24	1.124	3.70E-05	0.015	Diauxic_shift
13	12	45	125	0.687	7.60E-05	0.026	Ribosome
14	8	47	56	0.835	0.00013	0.045	Cellular response to glucose starvation
Gat3 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	2	5	3	2.89	2.20E-05	0.007	Late sporulation
2	3	12	10	1.9	3.50E-05	0.013	SWI/SNF complex
3	3	12	11	1.846	4.80E-05	0.016	SAGA complex
4	4	20	20	1.423	6.90E-05	0.022	Stationary_phase
Gat4 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	2	6	3	2.781	3.40E-05	0.009	Late sporulation
Gcn4 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	107	25	1.54	1.40E-15	<0.001	AA_starvation
2	23	73	77	1.111	9.60E-15	<0.001	Amino acid metabolism
3	13	107	27	1.174	1.80E-09	<0.001	Purine base metabolism
4	33	262	84	0.575	1.00E-07	<0.001	Protein biosynthesis
5	10	117	22	1.071	7.40E-07	0.001	Cell aging
6	12	60	74	0.796	7.30E-06	0.005	Nitrogen utilization
7	9	236	13	1.113	9.90E-06	0.008	Vacuole organization and biogenesis
8	29	258	85	0.479	1.40E-05	0.014	Response to DNA damage
9	6	276	6	1.816	2.20E-05	0.019	W303 meiosis

10	8	119	21	0.929	5.60E-05	0.045	Ergosterol biosynthesis
11	2	8	3	2.621	6.30E-05	0.047	Histidine metabolism
Gln3 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	15	25	25	2.353	8.70E-24	<0.001	AA_starvation
2	15	25	27	2.276	4.50E-23	<0.001	Purine base metabolism
3	17	23	74	1.863	1.70E-19	<0.001	Nitrogen utilization
4	10	18	14	2.647	1.20E-18	<0.001	Nitrogen_depletion
5	15	25	77	1.564	6.90E-15	<0.001	Amino acid metabolism
6	23	27	362	1.291	3.50E-12	<0.001	Response to stress
7	9	19	57	1.467	2.80E-09	<0.001	Long stress (>60)
8	14	19	221	1.254	2.90E-09	<0.001	Severe stress
9	9	37	29	1.41	4.00E-09	<0.001	Rapamycin related
10	8	37	23	1.469	1.20E-08	<0.001	Rapamycin treatment
11	9	37	84	0.828	6.10E-05	0.017	Protein biosynthesis
Gsm1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	113	20	1.897	5.40E-18	<0.001	Stationary_phase
2	122	291	362	0.522	1.90E-17	<0.001	Response to stress
3	144	652	221	0.523	2.50E-16	<0.001	Severe stress
4	19	106	56	0.948	3.10E-10	<0.001	Cellular response to glucose starvation
5	57	412	110	0.55	4.40E-10	<0.001	Short stress (<40)
6	7	15	46	1.549	4.70E-08	<0.001	Response to drug
7	13	97	42	0.913	3.10E-07	0.001	Alternative_carbon
8	31	106	197	0.534	6.10E-07	0.003	Carbohydrate metabolism
9	7	15	68	1.35	7.70E-07	0.004	Transport
10	39	626	57	0.558	2.60E-06	0.008	Long stress (>60)
11	21	295	44	0.643	4.40E-06	0.011	Heat shock
12	13	230	25	0.841	6.60E-06	0.014	H2O2
13	24	230	73	0.513	2.20E-05	0.031	Response to oxidative stress
14	15	617	17	1.02	2.30E-05	0.031	Gamma irradiation
15	4	32	11	1.527	3.60E-05	0.049	Glycolysis

Gzf3 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	36	25	2.226	7.60E-25	<0.001	AA_starvation
2	22	32	74	1.802	4.40E-24	<0.001	Nitrogen utilization
3	13	18	27	2.434	1.80E-21	<0.001	Purine base metabolism
4	10	16	14	2.764	2.10E-19	<0.001	Nitrogen_depletion
5	12	32	29	1.743	1.30E-14	<0.001	Rapamycin related
6	13	18	77	1.772	1.40E-14	<0.001	Amino acid metabolism
7	11	32	23	1.834	2.80E-14	<0.001	Rapamycin treatment
8	26	33	362	1.124	4.00E-12	<0.001	Response to stress
9	9	16	57	1.614	3.70E-10	<0.001	Long stress (>60)
10	14	18	221	1.341	8.50E-10	<0.001	Severe stress
11	11	32	84	1.047	1.80E-07	0.001	Protein biosynthesis
12	11	32	125	0.843	1.10E-05	0.008	Ribosome
13	7	31	56	0.984	5.20E-05	0.026	Cellular response to glucose starvation
Hal9 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	124	308	362	0.49	5.30E-16	<0.001	Response to stress
2	162	795	221	0.529	9.20E-16	<0.001	Severe stress
3	19	287	20	1.815	4.40E-14	<0.001	Stationary_phase
4	63	503	110	0.519	2.00E-09	<0.001	Short stress (<40)
5	7	12	46	1.739	6.20E-09	<0.001	Response to drug
6	34	617	44	0.755	6.90E-08	<0.001	Heat shock
7	7	12	68	1.54	1.10E-07	<0.001	Transport
8	16	307	25	0.896	6.50E-07	0.002	H2O2
9	61	362	160	0.382	9.20E-07	0.002	General regulation of transcription
10	33	639	45	0.639	2.40E-06	0.005	Galactose metabolism
11	102	608	197	0.297	5.70E-06	0.01	Carbohydrate metabolism
12	44	663	65	0.503	5.70E-06	0.01	Medium stress (40-60)
13	29	617	40	0.643	6.50E-06	0.013	Response to heat shock
14	38	639	56	0.531	8.50E-06	0.021	Cellular response to glucose starvation
15	20	698	23	0.908	1.30E-05	0.024	Rapamycin treatment

16	19	594	24	0.806	1.90E-05	0.033	Diauxic_shift
17	9	183	17	0.967	2.50E-05	0.045	Gamma irradiation
Leu3 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	16	96	20	1.845	2.20E-17	<0.001	Stationary_phase
2	121	346	362	0.37	3.20E-10	<0.001	Response to stress
3	7	18	46	1.417	2.20E-07	<0.001	Response to drug
4	16	111	56	0.802	2.90E-07	<0.001	Cellular response to glucose starvation
5	109	568	221	0.307	1.00E-06	0.002	Severe stress
6	34	126	197	0.488	1.30E-06	0.002	Carbohydrate metabolism
7	60	543	110	0.413	1.40E-06	0.002	Short stress (<40)
8	7	18	68	1.218	3.50E-06	0.004	Transport
9	7	35	42	1.065	1.70E-05	0.024	Alternative_carbon
10	22	357	44	0.574	2.70E-05	0.04	Heat shock
Lys14 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	125	359	362	0.37	1.90E-10	<0.001	Response to stress
2	8	15	46	1.669	1.20E-09	<0.001	Response to drug
3	14	236	20	1.146	2.00E-08	<0.001	Stationary_phase
4	8	15	68	1.466	3.00E-08	<0.001	Transport
5	8	143	10	1.573	1.10E-07	<0.001	SWI/SNF complex
6	17	103	65	0.792	1.60E-07	<0.001	Medium stress (40-60)
7	13	416	14	1.435	1.70E-07	<0.001	Nitrogen_depletion
8	79	357	221	0.358	2.10E-07	<0.001	Severe stress
9	13	334	17	1.084	9.30E-07	0.001	Gamma irradiation
10	15	99	60	0.78	1.00E-06	0.001	Response to ionizing radiation
11	15	99	62	0.76	1.60E-06	0.001	Double strand break repair
12	19	118	85	0.632	3.70E-06	0.004	Response to DNA damage
13	8	210	11	1.233	7.60E-06	0.011	SAGA complex
14	65	425	160	0.328	1.40E-05	0.02	General regulation of transcription
15	15	351	25	0.748	2.80E-05	0.036	AA_starvation

Matalpha2 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	2	2	2	4.214	7.50E-07	0.002	Rox1 overexpression
2	3	20	4	2.334	6.20E-06	0.002	FK506 related
3	3	20	6	1.965	3.10E-05	0.009	Calcium ion homeostasis
4	3	20	7	1.856	5.30E-05	0.014	Calcineurin signaling
Mbp1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	65	138	243	0.819	1.10E-21	<0.001	Cell cycle
2	16	34	32	1.934	9.50E-21	<0.001	Alpha factor stimulus
3	16	42	27	1.933	1.60E-20	<0.001	Short pheromone signal
4	18	83	23	1.901	2.00E-20	<0.001	Saturating pheromone
5	14	33	26	1.977	6.40E-19	<0.001	Cell cycle G1 arrest
6	31	68	140	1.049	5.00E-17	<0.001	No stress
7	26	59	110	1.146	1.10E-16	<0.001	Ste7 targets
8	26	59	118	1.104	7.50E-16	<0.001	Ste12 targets
9	26	59	131	1.043	1.20E-14	<0.001	MAPK signaling
10	20	34	150	1.203	2.40E-13	<0.001	Mating (sensu Saccharomyces)
11	16	178	26	1.147	4.10E-10	<0.001	fkh1 fkh2 double KO
12	15	78	48	1.046	1.20E-09	<0.001	G1
13	21	146	68	0.717	1.10E-07	0.001	Mitosis
14	17	146	53	0.731	1.10E-06	0.004	M
15	10	115	24	1.015	1.70E-06	0.005	M_G1
16	5	33	17	1.391	1.30E-05	0.014	Shmoo formation
Mcm1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	57	170	243	0.542	5.70E-11	<0.001	Cell cycle
2	74	271	227	0.475	7.10E-11	<0.001	Lethal
3	18	163	53	0.712	1.10E-06	<0.001	M
4	33	170	140	0.489	1.60E-06	0.002	No stress
5	20	163	68	0.623	3.50E-06	0.004	Mitosis

Met32 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	8	17	25	1.914	1.90E-11	<0.001	AA_starvation
2	7	17	27	1.746	2.50E-09	<0.001	Purine base metabolism
3	9	17	77	1.404	1.30E-08	<0.001	Amino acid metabolism
4	8	158	11	1.377	8.20E-07	0.001	Diamide
5	4	17	14	1.709	7.50E-06	0.008	Nitrogen_depletion
6	6	242	6	1.885	9.90E-06	0.01	W303 meiosis
7	12	235	22	0.87	1.00E-05	0.011	Cell aging
8	10	17	221	0.97	1.40E-05	0.014	Severe stress
9	4	4	110	2.111	1.90E-05	0.023	Short stress (<40)
10	13	243	27	0.746	3.60E-05	0.034	Protein degradation
Mga1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	4	16	10	1.952	1.20E-06	0.002	SWI/SNF complex
Mig1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	88	150	362	0.797	1.10E-24	<0.001	Response to stress
2	17	81	20	2.081	1.20E-20	<0.001	Stationary_phase
3	48	211	110	0.811	6.00E-17	<0.001	Short stress (<40)
4	112	432	221	0.546	6.20E-17	<0.001	Severe stress
5	16	72	44	1.197	5.70E-12	<0.001	Heat shock
6	25	193	56	0.832	3.00E-10	<0.001	Cellular response to glucose starvation
7	34	606	42	0.861	4.60E-09	<0.001	Alternative_carbon
8	31	99	197	0.579	1.10E-07	0.002	Carbohydrate metabolism
9	5	125	5	2.14	2.40E-06	0.004	Flocculation
10	18	499	23	0.899	2.70E-06	0.006	Rapamycin treatment
11	31	704	40	0.658	7.50E-06	0.011	Response to heat shock
12	7	33	45	1.061	1.80E-05	0.033	Galactose metabolism
13	3	9	11	2.011	1.90E-05	0.034	Glycolysis
14	5	61	11	1.371	2.40E-05	0.042	Diamide
15	14	305	25	0.757	2.80E-05	0.049	H2O2

Mig2 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	18	88	20	2.211	4.20E-22	<0.001	Stationary_phase
2	171	438	362	0.528	6.70E-22	<0.001	Response to stress
3	67	391	110	0.76	7.50E-18	<0.001	Short stress (<40)
4	110	437	221	0.518	2.00E-15	<0.001	Severe stress
5	13	52	44	1.227	1.80E-10	<0.001	Heat shock
6	21	131	56	0.907	2.40E-10	<0.001	Cellular response to glucose starvation
7	17	149	42	0.88	2.90E-08	<0.001	Alternative_carbon
8	34	119	197	0.524	3.00E-07	0.001	Carbohydrate metabolism
9	44	733	57	0.63	4.10E-07	0.001	Long stress (>60)
10	5	108	5	2.211	1.10E-06	0.001	Flocculation
11	17	438	23	0.882	2.70E-06	0.002	Rapamycin treatment
12	21	512	29	0.76	5.20E-06	0.006	Rapamycin related
13	13	119	45	0.763	8.20E-06	0.012	Galactose metabolism
14	18	264	40	0.654	1.20E-05	0.022	Response to heat shock
15	29	764	36	0.666	2.70E-05	0.044	Protein sorting
Mig3 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	159	383	362	0.565	1.90E-23	<0.001	Response to stress
2	18	88	20	2.211	4.20E-22	<0.001	Stationary_phase
3	63	337	110	0.786	1.50E-18	<0.001	Short stress (<40)
4	103	380	221	0.555	9.50E-17	<0.001	Severe stress
5	23	128	56	0.992	1.90E-12	<0.001	Cellular response to glucose starvation
6	16	92	44	1.06	3.10E-10	<0.001	Heat shock
7	17	137	42	0.924	7.70E-09	<0.001	Alternative_carbon
8	38	128	197	0.557	1.60E-08	<0.001	Carbohydrate metabolism
9	5	120	5	2.16	2.00E-06	0.006	Flocculation
10	17	465	23	0.845	6.80E-06	0.012	Rapamycin treatment
11	22	380	40	0.624	1.10E-05	0.023	Response to heat shock
12	13	124	45	0.742	1.30E-05	0.03	Galactose metabolism
13	26	612	36	0.64	1.90E-05	0.035	Protein sorting

14	5	60	11	1.379	2.20E-05	0.038	Diamide
Ndt80 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	11	11	56	2.903	2.70E-17	<0.001	Sporulation
2	11	11	60	2.865	6.30E-17	<0.001	Meiosis
3	3	5	3	3.66	1.40E-08	<0.001	Late sporulation
4	8	37	26	1.392	3.60E-08	<0.001	Cell cycle G1 arrest
5	13	125	32	0.963	1.60E-07	<0.001	Alpha factor stimulus
6	10	99	27	1.009	1.50E-06	0.002	Short pheromone signal
7	3	11	6	2.281	4.50E-06	0.003	W303 meiosis
8	3	10	7	2.226	5.70E-06	0.004	SK1 meiosis
9	20	102	118	0.559	1.70E-05	0.011	Ste12 targets
10	19	102	110	0.567	2.20E-05	0.015	Ste7 targets
11	2	9	2	3.036	2.70E-05	0.017	Mid-late sporulaiton
12	2	10	2	2.981	3.40E-05	0.023	Meiosis 2
13	3	41	4	1.985	5.70E-05	0.042	Middle sporulation
Nhp6a Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	10	21	56	1.489	2.50E-10	<0.001	Sporulation
2	10	21	60	1.452	5.30E-10	<0.001	Meiosis
3	3	10	3	3.182	1.60E-07	<0.001	Late sporulation
4	3	17	6	2.047	1.80E-05	0.007	W303 meiosis
5	5	38	20	1.225	6.20E-05	0.021	Stationary_phase
6	3	28	7	1.69	0.00015	0.049	SK1 meiosis
Nhp6b Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	10	24	56	1.388	1.30E-09	<0.001	Sporulation
2	10	24	60	1.351	2.70E-09	<0.001	Meiosis
3	3	11	3	3.127	2.30E-07	<0.001	Late sporulation
4	3	24	6	1.875	5.40E-05	0.015	W303 meiosis

Nrg1 Significant Attributes

Rank	N	M	X	LOD	P	P-adj	Attribute
1	108	190	362	0.79	4.40E-29	<0.001	Response to stress
2	85	245	221	0.691	4.80E-21	<0.001	Severe stress
3	34	97	110	1.017	5.00E-18	<0.001	Short stress (<40)
4	16	123	20	1.712	1.50E-15	<0.001	Stationary_phase
5	22	116	44	1.201	4.20E-15	<0.001	Heat shock
6	112	548	227	0.337	7.10E-08	<0.001	Lethal
7	14	110	40	0.93	9.00E-08	<0.001	Response to heat shock
8	14	214	25	0.949	3.40E-07	<0.001	H2O2
9	22	223	56	0.65	1.00E-06	0.002	Cellular response to glucose starvation
10	42	715	57	0.568	2.90E-06	0.006	Long stress (>60)
11	33	407	65	0.518	3.90E-06	0.006	Medium stress (40-60)

Oaf1 Significant Attributes

Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	146	20	1.759	5.30E-16	<0.001	Stationary_phase
2	11	20	46	1.732	3.40E-13	<0.001	Response to drug
3	11	20	68	1.517	3.50E-11	<0.001	Transport
4	115	328	362	0.366	9.40E-10	<0.001	Response to stress
5	17	91	56	0.953	1.80E-09	<0.001	Cellular response to glucose starvation
6	69	395	160	0.428	1.80E-08	<0.001	General regulation of transcription
7	11	54	42	1.115	3.50E-08	<0.001	Alternative_carbon
8	7	20	41	1.407	2.20E-07	0.001	Membrane organization and biogenesis
9	21	54	197	0.709	2.50E-07	0.001	Carbohydrate metabolism
10	73	334	221	0.34	1.40E-06	0.002	Severe stress
11	6	20	37	1.354	2.70E-06	0.003	Cell wall integrity pathway
12	8	36	45	1.095	2.90E-06	0.003	Galactose metabolism

Pdr1 Significant Attributes

Rank	N	M	X	LOD	P	P-adj	Attribute
1	94	315	221	0.602	3.60E-18	<0.001	Severe stress
2	130	315	362	0.518	4.80E-18	<0.001	Response to stress
3	27	187	65	0.798	1.90E-10	<0.001	Medium stress (40-60)

4	48	311	110	0.571	6.00E-10	<0.001	Short stress (<40)
5	20	147	60	0.76	6.20E-08	<0.001	Response to ionizing radiation
6	14	143	32	0.951	9.70E-08	0.001	MMS (radiomimetic)
7	24	147	85	0.664	1.00E-07	0.001	Response to DNA damage
8	20	147	62	0.739	1.20E-07	0.001	Double strand break repair
9	8	146	10	1.563	1.30E-07	0.001	SWI/SNF complex
10	7	94	12	1.38	1.00E-06	0.003	Sfp1 related
11	8	189	11	1.286	3.30E-06	0.004	SAGA complex
12	21	311	44	0.613	1.10E-05	0.014	Heat shock
13	41	222	160	0.395	1.20E-05	0.015	General regulation of transcription
14	14	16	570	1.046	1.90E-05	0.023	Regulation of transcription
Phd1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	38	109	160	0.791	6.50E-14	<0.001	General regulation of transcription
2	4	9	10	2.31	8.70E-08	<0.001	SWI/SNF complex
3	2	3	5	2.89	2.20E-05	0.013	Flocculation
4	19	99	114	0.564	2.40E-05	0.014	Chromatin modification
5	7	108	18	0.989	7.80E-05	0.05	mec1 mutant
Pho2 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	3	12	3	3.078	3.00E-07	<0.001	Late sporulation
2	5	12	56	1.351	2.60E-05	0.008	Sporulation
3	5	12	60	1.317	3.60E-05	0.012	Meiosis
Pho4 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	58	293	160	0.479	3.70E-09	<0.001	General regulation of transcription
Put3 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	122	20	1.855	2.20E-17	<0.001	Stationary_phase
2	216	687	362	0.402	1.10E-14	<0.001	Response to stress

3	147	730	221	0.452	1.50E-12	<0.001	Severe stress
4	79	711	110	0.553	4.30E-10	<0.001	Short stress (<40)
5	33	412	56	0.655	4.80E-08	<0.001	Cellular response to glucose starvation
6	26	88	197	0.533	4.50E-06	0.01	Carbohydrate metabolism
7	12	104	44	0.795	8.80E-06	0.023	Heat shock
8	5	51	11	1.459	9.70E-06	0.024	Diamide
9	4	7	46	1.682	1.80E-05	0.039	Response to drug
10	4	30	11	1.559	2.80E-05	0.049	Glycolysis
Rap1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	106	227	362	0.596	3.30E-19	<0.001	Response to stress
2	69	220	221	0.581	5.20E-14	<0.001	Severe stress
3	28	261	44	1.003	4.90E-13	<0.001	Heat shock
4	15	227	20	1.27	7.20E-10	<0.001	Stationary_phase
5	42	252	110	0.589	1.10E-09	<0.001	Short stress (<40)
6	20	220	40	0.843	1.90E-08	<0.001	Response to heat shock
7	26	267	56	0.683	7.10E-08	<0.001	Cellular response to glucose starvation
8	23	287	45	0.72	1.80E-07	<0.001	Galactose metabolism
9	24	216	65	0.627	6.40E-07	<0.001	Medium stress (40-60)
10	11	140	23	1.023	6.80E-07	<0.001	Rapamycin treatment
11	6	117	7	1.771	7.80E-07	<0.001	Heat shock in mutants
12	19	118	84	0.639	3.10E-06	0.001	Protein biosynthesis
13	5	37	12	1.556	3.20E-06	0.002	Sfp1 related
14	60	295	197	0.353	3.70E-06	0.002	Carbohydrate metabolism
15	10	113	29	0.894	1.10E-05	0.012	Rapamycin related
16	10	140	25	0.886	1.60E-05	0.018	AA_starvation
Rdr1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	7	7	46	2.781	8.70E-12	<0.001	Response to drug
2	7	7	68	2.583	1.60E-10	<0.001	Transport
3	19	582	20	1.386	3.20E-08	<0.001	Stationary_phase
4	40	662	56	0.578	1.80E-06	0.006	Cellular response to glucose starvation

5	130	433	362	0.255	4.10E-06	0.01	Response to stress
6	4	7	41	1.737	1.10E-05	0.024	Membrane organization and biogenesis
7	6	105	11	1.259	2.10E-05	0.048	Diamide
8	77	433	197	0.291	2.40E-05	0.049	Carbohydrate metabolism
Rds1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	116	281	362	0.501	7.70E-16	<0.001	Response to stress
2	17	209	20	1.569	2.80E-13	<0.001	Stationary_phase
3	47	278	110	0.622	3.30E-11	<0.001	Short stress (<40)
4	6	7	46	2.231	2.40E-09	<0.001	Response to drug
5	13	65	44	1.1	3.60E-09	<0.001	Heat shock
6	95	439	221	0.371	1.50E-08	<0.001	Severe stress
7	6	7	68	2.036	2.80E-08	<0.001	Transport
8	19	140	56	0.796	4.30E-08	<0.001	Cellular response to glucose starvation
9	6	49	11	1.634	2.20E-07	<0.001	Diamide
10	40	163	197	0.438	2.00E-06	0.003	Carbohydrate metabolism
11	13	134	42	0.745	1.40E-05	0.027	Alternative_carbon
12	25	422	45	0.573	1.60E-05	0.03	Galactose metabolism
13	29	643	40	0.613	1.70E-05	0.032	Response to heat shock
14	10	160	23	0.879	2.30E-05	0.042	Rapamycin treatment
Rds2 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	205	20	1.579	2.00E-13	<0.001	Stationary_phase
2	141	421	362	0.355	1.80E-10	<0.001	Response to stress
3	123	649	221	0.326	1.70E-07	<0.001	Severe stress
4	30	363	56	0.634	1.70E-07	<0.001	Cellular response to glucose starvation
5	50	428	110	0.404	4.60E-06	0.008	Short stress (<40)
6	2	2	5	3.368	7.50E-06	0.01	Flocculation
7	35	402	73	0.478	7.60E-06	0.011	Response to oxidative stress
8	11	55	68	0.836	7.90E-06	0.012	Transport
9	4	6	46	1.828	7.90E-06	0.012	Response to drug
10	11	95	42	0.815	1.30E-05	0.026	Alternative_carbon

11	28	543	44	0.558	2.70E-05	0.039	Heat shock
12	2	2	10	2.981	3.40E-05	0.05	SWI/SNF complex
Rgt1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	8	14	46	1.731	5.50E-10	<0.001	Response to drug
2	18	469	20	1.281	1.40E-08	<0.001	Stationary_phase
3	8	14	68	1.529	1.40E-08	<0.001	Transport
4	4	51	6	1.778	1.20E-05	0.02	Mediator complex
5	19	258	45	0.619	1.50E-05	0.028	Galactose metabolism
6	68	457	160	0.316	2.10E-05	0.036	General regulation of transcription
Rph1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	85	146	362	0.784	1.80E-23	<0.001	Response to stress
2	18	132	20	1.988	1.10E-18	<0.001	Stationary_phase
3	35	101	110	1.014	2.20E-18	<0.001	Short stress (<40)
4	96	353	221	0.539	1.90E-15	<0.001	Severe stress
5	18	71	44	1.303	1.40E-14	<0.001	Heat shock
6	14	118	40	0.893	2.20E-07	0.001	Response to heat shock
7	29	377	56	0.579	1.70E-06	0.005	Cellular response to glucose starvation
8	24	429	42	0.59	1.70E-05	0.035	Alternative_carbon
9	5	187	5	1.942	1.90E-05	0.038	Flocculation
Rpn4 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	146	327	362	0.611	3.70E-25	<0.001	Response to stress
2	98	327	221	0.616	2.80E-19	<0.001	Severe stress
3	17	215	20	1.553	4.60E-13	<0.001	Stationary_phase
4	36	310	65	0.767	2.10E-11	<0.001	Medium stress (40-60)
5	7	45	12	1.75	5.30E-09	<0.001	Sfp1 related
6	24	287	44	0.781	1.80E-08	<0.001	Heat shock
7	47	333	110	0.511	2.50E-08	<0.001	Short stress (<40)
8	52	220	197	0.435	1.40E-07	<0.001	Carbohydrate metabolism

9	13	177	25	0.978	2.90E-07	<0.001	AA_starvation
10	21	287	40	0.741	3.60E-07	0.001	Response to heat shock
11	7	170	8	1.652	8.50E-07	0.002	TFIID complex
12	8	117	14	1.257	1.10E-06	0.002	Nitrogen_depletion
13	12	192	23	0.936	2.10E-06	0.002	Rapamycin treatment
14	11	109	32	0.913	2.70E-06	0.002	MMS (radiomimetic)
15	25	192	84	0.55	3.70E-06	0.002	Protein biosynthesis
16	13	192	29	0.814	6.60E-06	0.003	Rapamycin related
17	21	175	74	0.564	1.20E-05	0.009	Nitrogen utilization
18	14	109	60	0.685	1.90E-05	0.017	Response to ionizing radiation
19	7	166	11	1.186	2.30E-05	0.02	SAGA complex
20	22	262	57	0.548	2.30E-05	0.02	Long stress (>60)
21	14	109	62	0.666	2.90E-05	0.026	Double strand break repair
Rsc3 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	18	39	32	1.973	2.40E-23	<0.001	Alpha factor stimulus
2	17	66	23	1.93	1.90E-20	<0.001	Saturating pheromone
3	15	34	27	2.005	2.40E-20	<0.001	Short pheromone signal
4	24	39	110	1.442	6.50E-20	<0.001	Ste7 targets
5	24	39	118	1.401	3.90E-19	<0.001	Ste12 targets
6	24	39	131	1.341	5.60E-18	<0.001	MAPK signaling
7	13	29	26	1.985	6.70E-18	<0.001	Cell cycle G1 arrest
8	24	39	150	1.265	1.60E-16	<0.001	Mating (sensu Saccharomyces)
9	38	98	243	0.616	1.50E-09	<0.001	Cell cycle
10	25	81	140	0.751	2.30E-09	<0.001	No stress
11	15	98	48	0.922	3.40E-08	<0.001	G1
12	8	39	52	0.974	1.70E-05	0.028	Pheromone signaling partial mutants
13	5	38	17	1.319	2.60E-05	0.041	Shmoo formation
14	8	66	33	0.945	2.80E-05	0.044	a factor stimulus
15	15	337	26	0.732	3.20E-05	0.046	fkh1 fkh2 double KO
Rsc30 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute

1	14	52	32	1.504	5.20E-14	<0.001	Alpha factor stimulus
2	8	16	27	1.915	2.10E-11	<0.001	Short pheromone signal
3	14	100	26	1.311	2.20E-11	<0.001	Cell cycle G1 arrest
4	17	219	23	1.274	3.90E-11	<0.001	Saturating pheromone
5	11	16	110	1.505	2.50E-10	<0.001	Ste7 targets
6	11	16	118	1.469	5.60E-10	<0.001	Ste12 targets
7	11	16	131	1.416	1.80E-09	<0.001	MAPK signaling
8	11	16	150	1.347	7.90E-09	<0.001	Mating (sensu Saccharomyces)
9	20	778	20	1.667	3.00E-07	0.001	Stationary_phase
10	7	30	48	1.081	1.50E-05	0.025	G1
Rtg3 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	79	150	362	0.674	5.00E-18	<0.001	Response to stress
2	58	165	221	0.639	3.70E-14	<0.001	Severe stress
3	26	165	65	0.838	6.20E-11	<0.001	Medium stress (40-60)
4	7	26	12	2.051	8.00E-11	<0.001	Sfp1 related
5	24	102	110	0.718	1.20E-08	<0.001	Short stress (<40)
6	7	26	45	1.196	3.30E-06	0.004	Galactose metabolism
7	6	140	8	1.461	8.60E-06	0.007	TFIID complex
8	19	128	85	0.587	1.30E-05	0.007	Response to DNA damage
9	11	128	32	0.831	1.40E-05	0.007	MMS (radiomimetic)
10	22	167	84	0.542	1.40E-05	0.007	Protein biosynthesis
11	10	163	23	0.87	2.70E-05	0.023	Rapamycin treatment
12	13	144	44	0.678	5.20E-05	0.041	Heat shock
13	37	166	197	0.374	5.80E-05	0.048	Carbohydrate metabolism
Sfl1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	18	91	114	0.578	2.60E-05	0.03	Chromatin modification
Sfp1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	213	500	362	0.691	1.30E-37	<0.001	Response to stress

2	152	500	221	0.828	7.80E-37	<0.001	Severe stress
3	78	448	110	0.878	6.20E-23	<0.001	Short stress (<40)
4	29	147	65	0.997	5.10E-15	<0.001	Medium stress (40-60)
5	14	97	20	1.613	7.50E-14	<0.001	Stationary_phase
6	49	498	73	0.7	4.00E-11	<0.001	Response to oxidative stress
7	23	203	44	0.932	8.40E-11	<0.001	Heat shock
8	7	41	12	1.799	2.60E-09	<0.001	Sfp1 related
9	13	143	25	1.089	2.10E-08	<0.001	AA_starvation
10	20	499	23	1.142	2.40E-08	<0.001	Rapamycin treatment
11	19	203	40	0.842	3.30E-08	<0.001	Response to heat shock
12	17	236	32	0.853	2.20E-07	<0.001	MMS (radiomimetic)
13	9	143	14	1.282	3.20E-07	<0.001	Nitrogen_depletion
14	35	505	56	0.591	6.60E-07	<0.001	Cellular response to glucose starvation
15	21	194	60	0.644	1.50E-06	0.001	Response to ionizing radiation
16	19	484	25	0.869	1.80E-06	0.001	H2O2
17	35	319	85	0.496	1.80E-06	0.002	Response to DNA damage
18	11	54	62	0.896	2.50E-06	0.002	Double strand break repair
19	21	499	29	0.776	3.30E-06	0.002	Rapamycin related
20	28	359	57	0.561	3.60E-06	0.003	Long stress (>60)
21	11	143	27	0.891	6.00E-06	0.006	Purine base metabolism
22	6	248	6	1.872	1.10E-05	0.012	Response to alkali
23	15	462	20	0.868	1.70E-05	0.019	DTT
24	7	278	8	1.398	2.60E-05	0.033	TFIID complex
Sip4 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	18	136	20	1.971	2.00E-18	<0.001	Stationary_phase
2	69	139	362	0.607	5.60E-14	<0.001	Response to stress
3	37	212	110	0.595	4.50E-09	<0.001	Short stress (<40)
4	69	335	197	0.377	2.50E-07	0.001	Carbohydrate metabolism
5	21	199	56	0.678	6.20E-07	0.001	Cellular response to glucose starvation
6	18	203	44	0.724	1.30E-06	0.002	Heat shock
7	82	402	221	0.306	5.10E-06	0.006	Severe stress
8	16	187	42	0.714	5.10E-06	0.006	Alternative_carbon

9	71	471	160	0.332	6.80E-06	0.008	General regulation of transcription
10	3	7	11	2.172	7.80E-06	0.012	Glycolysis
11	20	280	45	0.614	1.30E-05	0.021	Galactose metabolism
Skn7 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	16	30	221	0.89	1.90E-07	<0.001	Severe stress
2	17	27	362	0.786	4.80E-06	0.001	Response to stress
3	10	30	110	0.886	1.20E-05	0.004	Short stress (<40)
4	6	21	60	1.08	6.70E-05	0.018	Response to ionizing radiation
5	6	21	62	1.064	8.00E-05	0.025	Double strand break repair
Smp1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	6	7	56	2.132	8.40E-09	<0.001	Sporulation
2	6	7	60	2.098	1.30E-08	<0.001	Meiosis
3	3	19	3	2.837	1.30E-06	<0.001	Late sporulation
4	2	20	2	2.641	0.00014	0.044	Mid-late sporulaiton
Spt15 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	78	195	362	0.435	1.20E-09	<0.001	Response to stress
2	55	194	221	0.485	3.60E-09	<0.001	Severe stress
3	35	193	110	0.609	4.80E-09	<0.001	Short stress (<40)
4	12	141	20	1.228	7.40E-09	<0.001	Stationary_phase
5	16	125	44	0.895	3.50E-08	<0.001	Heat shock
Srd1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	4	7	17	2.188	2.70E-07	<0.001	Histones
2	5	34	10	1.734	6.70E-07	<0.001	SWI/SNF complex
3	9	129	20	1.011	7.10E-06	0.006	Stationary_phase
4	2	2	5	3.368	7.50E-06	0.006	Flocculation
5	4	7	40	1.749	1.00E-05	0.008	Histone modification

6	2	2	11	2.933	4.10E-05	0.039	SAGA complex
7	8	142	18	0.951	5.50E-05	0.048	mec1 mutant
8	12	35	160	0.717	5.70E-05	0.049	General regulation of transcription
Stb3 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	135	202	362	1.028	1.40E-49	<0.001	Response to stress
2	135	374	221	0.887	1.30E-40	<0.001	Severe stress
3	75	342	110	1.001	7.70E-29	<0.001	Short stress (<40)
4	15	87	20	1.779	2.80E-16	<0.001	Stationary_phase
5	25	159	44	1.152	2.30E-15	<0.001	Heat shock
6	53	589	65	0.917	1.90E-14	<0.001	Medium stress (40-60)
7	22	453	23	1.614	6.20E-12	<0.001	Rapamycin treatment
8	18	143	40	0.984	6.70E-10	<0.001	Response to heat shock
9	23	453	29	0.996	7.90E-09	<0.001	Rapamycin related
10	35	328	73	0.601	3.70E-08	<0.001	Response to oxidative stress
11	18	242	32	0.895	4.30E-08	<0.001	MMS (radiomimetic)
12	11	125	25	1.016	5.90E-07	0.003	AA_starvation
13	7	99	12	1.354	1.50E-06	0.003	Sfp1 related
14	43	461	84	0.454	3.90E-06	0.004	Protein biosynthesis
15	20	608	24	0.9	4.00E-06	0.004	Diauxic_shift
16	10	51	56	0.923	4.20E-06	0.005	Cellular response to glucose starvation
17	18	125	74	0.647	4.40E-06	0.005	Nitrogen utilization
18	9	194	14	1.127	4.60E-06	0.005	Nitrogen_depletion
19	16	357	25	0.811	5.60E-06	0.005	H2O2
20	20	197	60	0.601	8.40E-06	0.008	Response to ionizing radiation
21	19	192	57	0.614	9.70E-06	0.01	Long stress (>60)
22	20	197	62	0.58	1.50E-05	0.014	Double strand break repair
23	6	261	6	1.845	1.60E-05	0.017	Response to alkali
24	12	194	27	0.8	1.90E-05	0.022	Purine base metabolism
25	5	204	5	1.898	2.90E-05	0.029	De-heat
26	6	215	7	1.468	3.00E-05	0.032	Heat shock in mutants
27	8	253	11	1.136	3.20E-05	0.032	Diamide

Stp2 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	14	154	20	1.37	5.70E-11	<0.001	Stationary_phase
2	92	417	227	0.357	5.40E-08	<0.001	Lethal
3	28	567	36	0.82	1.10E-07	<0.001	Protein sorting
4	19	198	56	0.609	1.20E-05	0.018	Cellular response to glucose starvation
5	7	96	17	1.087	2.30E-05	0.037	Histones
6	25	444	44	0.564	2.50E-05	0.04	Endoplasmic reticulum
Stp4 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	16	162	20	1.566	1.40E-13	<0.001	Stationary_phase
2	53	115	362	0.526	2.60E-09	<0.001	Response to stress
3	22	192	56	0.732	6.30E-08	<0.001	Cellular response to glucose starvation
4	15	122	44	0.861	1.90E-07	<0.001	Heat shock
5	12	20	197	1.055	3.50E-07	<0.001	Carbohydrate metabolism
6	16	181	42	0.731	3.30E-06	0.01	Alternative_carbon
7	14	134	45	0.75	5.70E-06	0.014	Galactose metabolism
8	41	328	110	0.411	1.00E-05	0.016	Short stress (<40)
9	3	10	11	1.949	2.60E-05	0.03	Glycolysis
Sum1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	147	307	362	0.677	1.20E-29	<0.001	Response to stress
2	106	307	221	0.745	2.60E-27	<0.001	Severe stress
3	18	147	20	1.93	8.70E-18	<0.001	Stationary_phase
4	51	307	110	0.633	5.40E-12	<0.001	Short stress (<40)
5	20	108	65	0.878	1.10E-09	<0.001	Medium stress (40-60)
6	21	195	44	0.872	2.40E-09	<0.001	Heat shock
7	7	46	12	1.739	6.20E-09	<0.001	Sfp1 related
8	13	133	25	1.126	8.50E-09	<0.001	AA_starvation
9	16	281	23	1.049	3.00E-08	<0.001	Rapamycin treatment
10	12	73	40	1.04	5.10E-08	<0.001	Response to heat shock
11	9	125	14	1.349	9.70E-08	<0.001	Nitrogen_depletion

12	18	263	32	0.849	1.70E-07	<0.001	MMS (radiomimetic)
13	27	305	57	0.625	4.30E-07	<0.001	Long stress (>60)
14	17	281	29	0.852	4.50E-07	<0.001	Rapamycin related
15	34	302	84	0.515	1.10E-06	0.001	Protein biosynthesis
16	11	125	27	0.959	1.50E-06	0.001	Purine base metabolism
17	4	39	7	1.762	9.20E-06	0.006	Heat shock in mutants
18	29	307	73	0.486	1.60E-05	0.012	Response to oxidative stress
19	23	263	60	0.542	1.80E-05	0.017	Response to ionizing radiation
20	6	284	6	1.801	2.60E-05	0.026	Response to alkali
21	23	263	62	0.519	3.40E-05	0.042	Double strand break repair
Sut2 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	19	156	20	2.146	2.60E-19	<0.001	Stationary_phase
2	13	98	42	0.908	3.50E-07	0.002	Alternative_carbon
3	45	242	160	0.407	3.00E-06	0.007	General regulation of transcription
4	99	310	362	0.279	5.10E-06	0.01	Response to stress
5	8	242	10	1.305	7.10E-06	0.012	SWI/SNF complex
6	7	24	68	1.034	3.10E-05	0.04	Transport
7	6	24	46	1.135	3.20E-05	0.043	Response to drug
Tbf1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	219	20	1.543	6.30E-13	<0.001	Stationary_phase
2	100	257	362	0.434	1.70E-11	<0.001	Response to stress
3	16	126	44	0.891	3.90E-08	<0.001	Heat shock
4	40	263	110	0.525	5.80E-08	<0.001	Short stress (<40)
5	62	242	227	0.411	7.50E-08	<0.001	Lethal
6	62	257	221	0.389	2.90E-07	<0.001	Severe stress
7	15	212	40	0.635	6.10E-05	0.043	Response to heat shock
Tbs1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	8	8	46	2.847	2.10E-13	<0.001	Response to drug

2	8	8	68	2.644	5.90E-12	<0.001	Transport
3	19	508	20	1.477	2.50E-09	<0.001	Stationary_phase
4	206	723	362	0.286	2.40E-08	<0.001	Response to stress
5	109	616	197	0.357	5.60E-08	<0.001	Carbohydrate metabolism
6	25	383	45	0.632	2.40E-06	0.004	Galactose metabolism
7	10	398	11	1.349	5.70E-06	0.009	SAGA complex
8	136	780	221	0.282	5.90E-06	0.009	Severe stress
9	33	500	56	0.531	7.10E-06	0.009	Cellular response to glucose starvation
10	7	146	11	1.25	9.50E-06	0.013	Diamide
11	20	713	23	0.891	1.90E-05	0.038	Rapamycin treatment
12	47	558	84	0.412	2.00E-05	0.038	Protein biosynthesis
13	4	8	41	1.628	2.20E-05	0.041	Membrane organization and biogenesis
Tea1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	18	305	20	1.535	6.30E-12	<0.001	Stationary_phase
2	7	7	46	2.781	8.70E-12	<0.001	Response to drug
3	7	7	68	2.583	1.60E-10	<0.001	Transport
4	6	23	37	1.271	6.70E-06	0.011	Cell wall integrity pathway
5	7	175	10	1.269	1.30E-05	0.021	SWI/SNF complex
6	7	36	40	1.076	1.50E-05	0.024	Histone modification
7	7	92	17	1.108	1.70E-05	0.027	Histones
8	56	354	160	0.33	2.80E-05	0.035	General regulation of transcription
9	21	360	41	0.589	3.00E-05	0.038	Membrane organization and biogenesis
Tec1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	19	25	52	2.151	1.40E-25	<0.001	Pheromone signaling partial mutants
2	26	34	131	1.646	2.80E-23	<0.001	MAPK signaling
3	23	28	118	1.831	4.60E-23	<0.001	Ste12 targets
4	22	28	110	1.775	5.30E-22	<0.001	Ste7 targets
5	23	28	150	1.696	1.80E-20	<0.001	Mating (sensu Saccharomyces)
6	14	25	33	2.013	3.00E-19	<0.001	a factor stimulus
7	10	61	32	1.149	8.30E-08	<0.001	Alpha factor stimulus

8	9	81	36	0.863	3.60E-05	0.029	Psueodohyphal or invasive growth
Tye7 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	9	27	25	1.696	3.60E-11	<0.001	AA_starvation
2	8	27	27	1.551	3.20E-09	<0.001	Purine base metabolism
3	9	27	77	1.063	1.70E-06	<0.001	Amino acid metabolism
4	3	8	14	1.952	2.70E-05	0.017	Nitrogen_depletion
5	5	11	74	1.278	6.20E-05	0.038	Nitrogen utilization
Ume6 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	16	232	20	1.375	4.80E-11	<0.001	Stationary_phase
2	5	31	5	2.824	1.70E-09	<0.001	Early sporulation
3	8	114	11	1.54	6.00E-08	<0.001	Diamide
4	93	446	227	0.318	9.30E-07	0.002	Lethal
5	16	199	44	0.648	2.40E-05	0.028	Heat shock
Usv1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	85	116	362	1.085	1.30E-34	<0.001	Response to stress
2	36	71	110	1.314	6.10E-26	<0.001	Short stress (<40)
3	57	116	221	0.902	2.40E-22	<0.001	Severe stress
4	20	71	44	1.399	2.70E-17	<0.001	Heat shock
5	18	224	20	1.704	2.30E-14	<0.001	Stationary_phase
6	13	71	40	1.111	3.00E-09	<0.001	Response to heat shock
7	116	563	227	0.352	1.70E-08	<0.001	Lethal
8	14	181	25	1.037	3.80E-08	<0.001	H2O2
9	23	181	73	0.616	1.10E-06	0.001	Response to oxidative stress
10	44	771	57	0.587	2.30E-06	0.005	Long stress (>60)
11	27	338	56	0.58	2.50E-06	0.005	Cellular response to glucose starvation
12	30	357	65	0.514	7.20E-06	0.014	Medium stress (40-60)
13	6	99	11	1.287	1.50E-05	0.026	Diamide
14	15	698	16	1.152	2.50E-05	0.05	Regulation of pH

Xbp1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	4	9	14	2.101	4.10E-07	<0.001	Nitrogen_depletion
2	4	9	25	1.787	5.10E-06	0.001	AA_starvation
3	4	9	27	1.747	7.00E-06	0.001	Purine base metabolism
4	5	10	77	1.332	4.20E-05	0.014	Amino acid metabolism
5	5	38	20	1.225	6.20E-05	0.026	Stationary_phase
6	4	9	57	1.382	0.00015	0.05	Long stress (>60)
Yap1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	24	38	73	1.724	4.00E-25	<0.001	Response to oxidative stress
2	13	43	25	1.748	1.70E-15	<0.001	H2O2
3	24	38	221	1.079	7.30E-13	<0.001	Severe stress
4	27	38	362	0.955	9.50E-11	<0.001	Response to stress
5	9	11	110	1.757	1.00E-09	<0.001	Short stress (<40)
6	6	49	11	1.634	2.20E-07	<0.001	Diamide
7	5	26	13	1.684	8.00E-07	<0.001	Menadione
8	2	5	4	2.668	4.50E-05	0.028	H2O2 in mutants
Yap6 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	23	94	160	0.527	1.40E-05	0.017	General regulation of transcription
Pbf1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	139	257	362	0.785	2.10E-35	<0.001	Response to stress
2	44	87	110	1.359	4.30E-32	<0.001	Short stress (<40)
3	100	272	221	0.776	4.90E-28	<0.001	Severe stress
4	8	12	23	2.293	1.90E-13	<0.001	Rapamycin treatment
5	22	151	44	1.053	1.40E-12	<0.001	Heat shock
6	8	12	29	2.149	1.60E-12	<0.001	Rapamycin related
7	33	227	73	0.766	2.40E-11	<0.001	Response to oxidative stress

8	43	446	65	0.748	2.60E-11	<0.001	Medium stress (40-60)
9	8	12	56	1.788	5.00E-10	<0.001	Cellular response to glucose starvation
10	8	12	74	1.646	5.10E-09	<0.001	Nitrogen utilization
11	8	12	84	1.583	1.40E-08	<0.001	Protein biosynthesis
12	17	426	20	1.169	4.60E-08	<0.001	Stationary_phase
13	8	12	125	1.385	3.60E-07	<0.001	Ribosome
14	14	227	25	0.917	7.20E-07	<0.001	H2O2
15	6	67	11	1.478	1.50E-06	0.001	Diamide
16	35	331	85	0.474	4.60E-06	0.004	Response to DNA damage
17	18	261	40	0.66	1.00E-05	0.01	Response to heat shock
18	8	12	197	1.156	1.20E-05	0.012	Carbohydrate metabolism
19	4	101	4	2.152	1.40E-05	0.017	H2O2 in mutants
20	13	253	26	0.756	3.40E-05	0.047	Mild stress
Ybr239c Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	8	10	46	2.147	9.00E-12	<0.001	Response to drug
2	8	10	68	1.945	2.50E-10	<0.001	Transport
3	71	450	160	0.364	1.00E-06	<0.001	General regulation of transcription
4	11	11	570	1.642	8.60E-06	0.015	Regulation of transcription
5	8	252	10	1.284	9.70E-06	0.015	SWI/SNF complex
6	15	457	20	0.874	1.50E-05	0.017	Stationary_phase
7	4	8	41	1.628	2.20E-05	0.025	Membrane organization and biogenesis
8	9	343	11	1.167	2.60E-05	0.032	SAGA complex
Ydr520c Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	45	178	160	0.599	9.50E-11	<0.001	General regulation of transcription
2	7	9	46	2.082	3.00E-10	<0.001	Response to drug
3	7	9	68	1.883	5.30E-09	<0.001	Transport
4	8	64	17	1.394	6.50E-08	<0.001	Gamma irradiation
5	7	64	18	1.249	2.30E-06	0.002	mec1 mutant
6	7	142	11	1.264	7.90E-06	0.006	SAGA complex
7	12	103	45	0.787	1.00E-05	0.006	Galactose metabolism

8	5	65	10	1.413	1.80E-05	0.012	SWI/SNF complex
9	6	24	42	1.181	1.90E-05	0.013	Alternative_carbon
10	85	174	570	0.285	3.90E-05	0.03	Regulation of transcription
Yer130c Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	122	218	362	0.794	2.10E-32	<0.001	Response to stress
2	36	79	110	1.223	7.50E-24	<0.001	Short stress (<40)
3	100	322	221	0.647	3.90E-21	<0.001	Severe stress
4	14	22	44	1.948	3.00E-18	<0.001	Heat shock
5	18	208	20	1.744	5.80E-15	<0.001	Stationary_phase
6	14	86	40	1.061	3.20E-09	<0.001	Response to heat shock
7	134	689	227	0.345	2.30E-08	<0.001	Lethal
8	39	595	57	0.594	5.60E-07	0.001	Long stress (>60)
9	29	324	65	0.543	3.00E-06	0.008	Medium stress (40-60)
10	9	92	25	1.023	3.70E-06	0.009	Hyperosmolarity
11	31	322	73	0.51	4.20E-06	0.01	Response to oxidative stress
12	13	225	25	0.852	5.10E-06	0.011	H2O2
13	9	92	31	0.887	2.70E-05	0.034	Hyperosmotic response
14	12	403	16	0.941	2.90E-05	0.034	Regulation of pH
15	22	461	36	0.613	3.00E-05	0.037	Protein sorting
Ygr067c Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	121	246	362	0.664	6.40E-25	<0.001	Response to stress
2	55	235	110	0.873	1.50E-20	<0.001	Short stress (<40)
3	17	53	44	1.434	1.10E-15	<0.001	Heat shock
4	75	237	221	0.6	1.40E-15	<0.001	Severe stress
5	19	271	20	1.847	1.40E-14	<0.001	Stationary_phase
6	24	187	56	0.816	1.00E-09	<0.001	Cellular response to glucose starvation
7	22	301	40	0.759	1.50E-07	0.001	Response to heat shock
8	17	190	42	0.75	1.20E-06	0.005	Alternative_carbon
9	5	42	11	1.555	3.60E-06	0.009	Diamide
10	44	194	197	0.395	5.80E-06	0.014	Carbohydrate metabolism

11	15	337	25	0.771	1.60E-05	0.023	H2O2
Yil130w Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	18	148	20	1.926	9.90E-18	<0.001	Stationary_phase
2	193	566	362	0.441	6.30E-17	<0.001	Response to stress
3	129	566	221	0.496	5.70E-15	<0.001	Severe stress
4	17	88	56	0.971	1.00E-09	<0.001	Cellular response to glucose starvation
5	40	132	197	0.574	3.10E-09	<0.001	Carbohydrate metabolism
6	55	413	110	0.514	5.80E-09	<0.001	Short stress (<40)
7	32	574	44	0.702	2.80E-07	<0.001	Heat shock
8	6	12	46	1.593	2.90E-07	<0.001	Response to drug
9	9	29	68	1.082	1.10E-06	0.001	Transport
10	14	129	45	0.77	3.60E-06	0.009	Galactose metabolism
11	28	574	40	0.642	5.60E-06	0.012	Response to heat shock
12	48	819	62	0.543	6.20E-06	0.013	Double strand break repair
13	46	819	60	0.523	1.60E-05	0.035	Response to ionizing radiation
14	44	690	65	0.472	2.00E-05	0.044	Medium stress (40-60)
15	23	404	42	0.584	2.20E-05	0.047	Alternative_carbon
16	6	107	11	1.249	2.40E-05	0.049	Diamide
Ykl222c Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	144	20	1.767	4.20E-16	<0.001	Stationary_phase
2	162	468	362	0.409	5.20E-14	<0.001	Response to stress
3	11	18	46	1.835	6.70E-14	<0.001	Response to drug
4	11	18	68	1.62	7.10E-12	<0.001	Transport
5	126	606	221	0.412	6.40E-11	<0.001	Severe stress
6	70	613	110	0.499	7.40E-09	<0.001	Short stress (<40)
7	14	73	56	0.941	4.60E-08	<0.001	Cellular response to glucose starvation
8	7	18	41	1.477	9.50E-08	<0.001	Membrane organization and biogenesis
9	5	23	11	1.867	1.50E-07	<0.001	Diamide
10	28	458	45	0.643	1.20E-06	0.001	Galactose metabolism
11	6	18	37	1.419	1.30E-06	0.001	Cell wall integrity pathway

12	78	413	197	0.335	1.50E-06	0.001	Carbohydrate metabolism
13	10	73	42	0.892	7.80E-06	0.017	Alternative_carbon
14	88	647	160	0.302	2.20E-05	0.038	General regulation of transcription
15	4	86	5	1.751	3.40E-05	0.049	Flocculation
Yll054c Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	19	237	20	1.92	1.00E-15	<0.001	Stationary_phase
2	105	251	362	0.5	1.10E-14	<0.001	Response to stress
3	150	777	221	0.423	4.00E-11	<0.001	Severe stress
4	47	170	197	0.527	2.90E-09	<0.001	Carbohydrate metabolism
5	75	690	110	0.499	1.10E-08	<0.001	Short stress (<40)
6	22	178	56	0.774	1.50E-08	<0.001	Cellular response to glucose starvation
7	5	9	46	1.67	1.60E-06	0.002	Response to drug
8	36	754	45	0.67	2.40E-06	0.002	Galactose metabolism
9	13	236	23	0.903	2.50E-06	0.002	Rapamycin treatment
10	19	238	44	0.68	2.90E-06	0.002	Heat shock
11	5	42	11	1.555	3.60E-06	0.004	Diamide
12	97	721	160	0.322	6.80E-06	0.009	General regulation of transcription
13	37	1006	40	0.842	7.90E-06	0.012	Response to heat shock
14	11	93	42	0.826	1.10E-05	0.019	Alternative_carbon
15	5	9	68	1.479	1.20E-05	0.02	Transport
16	13	263	24	0.805	1.70E-05	0.026	Diauxic_shift
17	11	638	11	1.564	3.00E-05	0.044	SAGA complex
18	49	1004	57	0.581	3.30E-05	0.047	Long stress (>60)
Yml081w Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	136	302	362	0.604	1.50E-23	<0.001	Response to stress
2	66	337	110	0.84	5.50E-21	<0.001	Short stress (<40)
3	18	147	20	1.93	8.70E-18	<0.001	Stationary_phase
4	85	297	221	0.55	7.50E-15	<0.001	Severe stress
5	13	32	44	1.539	1.40E-13	<0.001	Heat shock
6	20	123	56	0.904	5.90E-10	<0.001	Cellular response to glucose starvation

7	17	160	42	0.842	8.80E-08	0.001	Alternative_carbon
8	19	251	40	0.726	1.10E-06	0.001	Response to heat shock
9	18	502	23	0.895	3.00E-06	0.004	Rapamycin treatment
10	5	45	11	1.52	5.10E-06	0.007	Diamide
11	32	123	197	0.462	6.90E-06	0.008	Carbohydrate metabolism
12	5	160	5	2.019	8.40E-06	0.009	Flocculation
13	20	502	29	0.702	2.10E-05	0.03	Rapamycin related
14	16	405	25	0.737	3.20E-05	0.043	H2O2
Ynr063w Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	18	187	20	1.801	8.00E-16	<0.001	Stationary_phase
2	7	8	46	2.304	6.80E-11	<0.001	Response to drug
3	7	8	68	2.106	1.20E-09	<0.001	Transport
4	16	110	56	0.807	2.60E-07	0.002	Cellular response to glucose starvation
5	11	11	570	1.642	8.60E-06	0.009	Regulation of transcription
6	3	11	10	1.949	2.60E-05	0.028	SWI/SNF complex
7	58	164	362	0.324	2.90E-05	0.031	Response to stress
8	3	11	11	1.894	3.60E-05	0.036	SAGA complex
9	7	40	41	1.006	3.70E-05	0.037	Membrane organization and biogenesis
10	4	88	5	1.74	3.80E-05	0.039	Flocculation
Yox1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	9	20	150	0.936	2.50E-05	0.007	Mating (sensu Saccharomyces)
2	10	36	110	0.772	7.20E-05	0.034	Ste7 targets
Ypr013c Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	66	108	362	0.814	1.10E-19	<0.001	Response to stress
2	16	108	20	1.782	1.70E-16	<0.001	Stationary_phase
3	29	106	110	0.831	3.80E-12	<0.001	Short stress (<40)
4	39	106	221	0.636	2.70E-10	<0.001	Severe stress
5	16	94	44	1.048	4.40E-10	<0.001	Heat shock

6	17	144	56	0.704	2.20E-06	<0.001	Cellular response to glucose starvation
7	9	89	31	0.903	2.10E-05	0.014	Hyperosmotic response
8	8	89	25	0.96	2.80E-05	0.022	Hyperosmolarity
9	10	94	40	0.79	4.90E-05	0.033	Response to heat shock
Ypr015c Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	291	20	1.389	8.10E-11	<0.001	Stationary_phase
2	31	112	160	0.62	1.50E-08	<0.001	General regulation of transcription
3	39	265	110	0.502	2.40E-07	0.001	Short stress (<40)
4	101	302	362	0.316	2.90E-07	0.001	Response to stress
5	8	222	10	1.35	3.60E-06	0.011	SWI/SNF complex
6	23	78	197	0.527	1.80E-05	0.028	Carbohydrate metabolism
7	61	282	221	0.316	2.20E-05	0.031	Severe stress
Ypr196w Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	24	109	85	0.835	1.60E-10	<0.001	Response to DNA damage
2	33	301	65	0.7	1.40E-09	<0.001	Medium stress (40-60)
3	10	185	11	1.763	2.70E-09	<0.001	SAGA complex
4	18	109	60	0.85	1.50E-08	<0.001	Response to ionizing radiation
5	18	109	62	0.829	2.70E-08	<0.001	Double strand break repair
6	73	308	221	0.395	3.40E-08	<0.001	Severe stress
7	16	195	32	0.9	9.70E-08	<0.001	MMS (radiomimetic)
8	104	311	362	0.318	1.80E-07	<0.001	Response to stress
9	39	185	160	0.471	6.00E-07	<0.001	General regulation of transcription
10	7	182	8	1.617	1.40E-06	<0.001	TFIID complex
11	7	100	12	1.349	1.60E-06	<0.001	Sfp1 related
12	7	171	10	1.28	1.10E-05	0.01	SWI/SNF complex
13	6	299	6	1.773	3.60E-05	0.03	SAGA unique
14	4	70	6	1.627	4.30E-05	0.037	Mediator complex
Yrm1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute

1	64	206	221	0.564	1.00E-12	<0.001	Severe stress
2	89	217	362	0.466	1.00E-11	<0.001	Response to stress
3	26	206	65	0.714	1.10E-08	<0.001	Medium stress (40-60)
4	23	149	85	0.627	5.80E-07	0.002	Response to DNA damage
5	15	206	32	0.816	1.50E-06	0.002	MMS (radiomimetic)
6	7	104	12	1.33	2.10E-06	0.002	Sfp1 related
7	17	149	60	0.642	1.00E-05	0.009	Response to ionizing radiation
8	17	149	62	0.622	1.70E-05	0.015	Double strand break repair
9	23	217	73	0.516	2.70E-05	0.02	Response to oxidative stress
10	7	128	14	1.092	3.30E-05	0.022	Nitrogen_depletion
11	25	166	110	0.466	4.60E-05	0.035	Short stress (<40)
12	5	169	6	1.515	6.10E-05	0.05	SAGA unique
Yrr1 Significant Attributes							
Rank	N	M	X	LOD	P	P-adj	Attribute
1	17	111	20	1.906	3.90E-18	<0.001	Stationary_phase
2	10	11	46	2.484	1.20E-15	<0.001	Response to drug
3	10	11	68	2.273	8.40E-14	<0.001	Transport
4	62	130	362	0.564	1.30E-11	<0.001	Response to stress
5	10	42	42	1.192	3.30E-08	<0.001	Alternative_carbon
6	6	11	37	1.777	3.70E-08	<0.001	Cell wall integrity pathway
7	13	61	56	0.992	4.00E-08	<0.001	Cellular response to glucose starvation
8	6	11	41	1.724	7.10E-08	<0.001	Membrane organization and biogenesis
9	7	23	45	1.27	1.30E-06	0.003	Galactose metabolism
10	12	12	570	1.679	2.90E-06	0.007	Regulation of transcription
11	5	44	11	1.532	4.60E-06	0.008	Diamide
12	5	54	10	1.504	7.20E-06	0.011	SWI/SNF complex
13	3	26	5	1.982	3.50E-05	0.035	Flocculation