

Table: Gene sets enriched in phenotype na [\[plain text format\]](#)

	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
1	RNA MODIFICATION	Details ...	32	-0.57	-1.90	0.001	0.036	0.038	222	tags=41%, list=16%, signal=47%
2	TRANSMEMBRANE TRANSPORT	Details ...	43	-0.53	-1.82	0.000	0.057	0.116	306	tags=49%, list=22%, signal=61%
3	PEROXISOME	Details ...	23	-0.59	-1.81	0.003	0.046	0.140	314	tags=65%, list=23%, signal=83%
4	PEROXISOME ORGANIZATION	Details ...	23	-0.58	-1.79	0.003	0.040	0.161	314	tags=61%, list=23%, signal=78%
5	OLIGOSACCHARIDE METABOLIC PROCESS	Details ...	8	-0.75	-1.78	0.001	0.036	0.179	108	tags=50%, list=8%, signal=54%
6	SAGA COMPLEX	Details ...	16	-0.63	-1.76	0.005	0.043	0.249	312	tags=75%, list=23%, signal=96%
7	TRNA PROCESSING	Details ...	33	-0.52	-1.74	0.002	0.048	0.310	222	tags=36%, list=16%, signal=42%
8	ELONGATOR COMPLEX	Details ...	5	-0.84	-1.69	0.003	0.078	0.488	222	tags=100%, list=16%, signal=119%
9	SLIK (SAGA-LIKE) COMPLEX	Details ...	14	-0.59	-1.63	0.011	0.132	0.710	312	tags=71%, list=23%, signal=91%
10	RIBOSOMAL LARGE SUBUNIT BIOGENESIS	Details ...	19	-0.54	-1.61	0.013	0.136	0.757	283	tags=53%, list=21%, signal=65%
11	HISTONE MODIFICATION	Details ...	79	-0.42	-1.60	0.007	0.134	0.784	344	tags=46%, list=25%, signal=57%
12	SWI/SNF COMPLEX	Details ...	8	-0.68	-1.59	0.036	0.145	0.837	108	tags=50%, list=8%, signal=54%
13	PROTEIN ACYLATION	Details ...	40	-0.46	-1.58	0.017	0.142	0.851	344	tags=50%, list=25%, signal=65%
14	PLASMA MEMBRANE	Details ...	91	-0.39	-1.58	0.003	0.137	0.859	449	tags=51%, list=33%, signal=70%
15	TRANSCRIPTION FACTOR ACTIVITY, PROTEIN BINDING	Details ...	57	-0.41	-1.53	0.015	0.185	0.947	335	tags=39%, list=24%, signal=49%
16	CELL CORTEX	Details ...	60	-0.40	-1.53	0.023	0.179	0.954	349	tags=40%, list=25%, signal=51%
17	RRNA PROCESSING	Details ...	42	-0.43	-1.52	0.018	0.182	0.963	376	tags=43%, list=27%, signal=57%

18	PROTEIN ALKYLATION	Details ...	20	-0.49	-1.47	0.052	0.260	0.995	302	tags=40%, list=22%, signal=51%
19	LIPID METABOLIC PROCESS	Details ...	87	-0.37	-1.46	0.017	0.274	0.997	527	tags=53%, list=38%, signal=80%
20	CHROMATIN BINDING	Details ...	46	-0.40	-1.45	0.042	0.271	0.997	353	tags=46%, list=26%, signal=59%
21	HYDROLASE ACTIVITY, ACTING ON GLYCOSYL BONDS	Details ...	7	-0.65	-1.45	0.059	0.264	0.997	360	tags=71%, list=26%, signal=96%
22	MICROTUBULE ORGANIZING CENTER	Details ...	24	-0.45	-1.43	0.077	0.284	0.998	75	tags=25%, list=5%, signal=26%
23	SNORNA PROCESSING	Details ...	6	-0.64	-1.38	0.088	0.380	1.000	109	tags=33%, list=8%, signal=36%
24	MITOCHONDRION ORGANIZATION	Details ...	59	-0.36	-1.36	0.070	0.412	1.000	544	tags=49%, list=40%, signal=78%
25	CYTOSKELETON ORGANIZATION	Details ...	91	-0.34	-1.36	0.043	0.416	1.000	330	tags=34%, list=24%, signal=42%
26	CELL BUDDING	Details ...	22	-0.44	-1.36	0.124	0.401	1.000	292	tags=41%, list=21%, signal=51%
27	AMINO ACID TRANSPORT	Details ...	6	-0.62	-1.35	0.100	0.393	1.000	378	tags=83%, list=27%, signal=114%
28	COMPASS COMPLEX	Details ...	5	-0.68	-1.35	0.107	0.395	1.000	294	tags=60%, list=21%, signal=76%
29	KORNBERG'S MEDIATOR (SRB) COMPLEX	Details ...	19	-0.44	-1.34	0.117	0.404	1.000	194	tags=37%, list=14%, signal=42%
30	NUCLEOSOMAL PROTEIN COMPLEX	Details ...	5	-0.66	-1.33	0.120	0.403	1.000	47	tags=40%, list=3%, signal=41%
31	PEPTIDYL-AMINO ACID MODIFICATION	Details ...	75	-0.34	-1.32	0.076	0.429	1.000	361	tags=37%, list=26%, signal=48%
32	MITOCHONDRIAL ENVELOPE	Details ...	47	-0.37	-1.31	0.116	0.428	1.000	454	tags=40%, list=33%, signal=58%
33	TRANSMEMBRANE TRANSPORTER ACTIVITY	Details ...	35	-0.38	-1.30	0.130	0.431	1.000	296	tags=34%, list=22%, signal=43%
34	VITAMIN METABOLIC PROCESS	Details ...	5	-0.63	-1.30	0.130	0.440	1.000	507	tags=100%, list=37%, signal=158%
35	TRANSLATIONAL INITIATION	Details ...	14	-0.46	-1.28	0.155	0.467	1.000	341	tags=50%, list=25%, signal=66%
36	RSC COMPLEX	Details ...	7	-0.57	-1.28	0.181	0.462	1.000	369	tags=43%, list=27%, signal=58%

37	HISTONE BINDING	Details ...	34	-0.38	-1.27	0.167	0.468	1.000	252	tags=35%, list=18%, signal=42%
38	PROTEIN MATURATION	Details ...	16	-0.44	-1.26	0.175	0.476	1.000	374	tags=44%, list=27%, signal=59%
39	PROTEIN LIPIDATION	Details ...	8	-0.53	-1.26	0.178	0.466	1.000	400	tags=50%, list=29%, signal=70%
40	INVASIVE GROWTH IN RESPONSE TO GLUCOSE LIMITATION	Details ...	26	-0.40	-1.26	0.163	0.465	1.000	548	tags=69%, list=40%, signal=113%
41	CELL WALL ORGANIZATION OR BIOGENESIS	Details ...	63	-0.33	-1.25	0.129	0.457	1.000	370	tags=37%, list=27%, signal=48%
42	ION TRANSPORT	Details ...	52	-0.33	-1.24	0.143	0.483	1.000	471	tags=42%, list=34%, signal=62%
43	ENDOCYTOSIS	Details ...	33	-0.37	-1.23	0.181	0.486	1.000	475	tags=48%, list=35%, signal=72%
44	CELLULAR ION HOMEOSTASIS	Details ...	29	-0.38	-1.23	0.186	0.479	1.000	298	tags=31%, list=22%, signal=39%
45	PROTEIN BINDING, BRIDGING	Details ...	30	-0.37	-1.22	0.204	0.497	1.000	439	tags=47%, list=32%, signal=67%
46	CYTOSKELETAL PROTEIN BINDING	Details ...	29	-0.37	-1.21	0.203	0.499	1.000	253	tags=31%, list=18%, signal=37%
47	LIPID BINDING	Details ...	40	-0.35	-1.21	0.188	0.488	1.000	427	tags=40%, list=31%, signal=56%
48	NUCLEOLUS	Details ...	52	-0.33	-1.21	0.181	0.480	1.000	283	tags=33%, list=21%, signal=40%
49	RESPONSE TO STARVATION	Details ...	16	-0.42	-1.19	0.261	0.516	1.000	427	tags=56%, list=31%, signal=81%
50	GENERATION OF PRECURSOR METABOLITES AND ENERGY	Details ...	25	-0.38	-1.19	0.236	0.513	1.000	529	tags=52%, list=38%, signal=83%
51	EXOCYTOSIS		11	-0.46	-1.19	0.245	0.507	1.000	617	tags=82%, list=45%, signal=147%
52	CYTOSKELETON		73	-0.31	-1.17	0.227	0.534	1.000	330	tags=33%, list=24%, signal=41%
53	CARBOHYDRATE METABOLIC PROCESS		53	-0.32	-1.16	0.239	0.557	1.000	493	tags=43%, list=36%, signal=65%
54	MITOCHONDRIAL TRANSLATION		7	-0.51	-1.15	0.301	0.585	1.000	618	tags=86%, list=45%, signal=155%
55	TRANSLATION FACTOR ACTIVITY, RNA BINDING		6	-0.53	-1.14	0.300	0.594	1.000	458	tags=67%, list=33%, signal=100%

56	HELICASE ACTIVITY		16	-0.41	-1.14	0.312	0.588	1.000	411	tags=56%, list=30%, signal=79%
57	ORGANELLE INHERITANCE		23	-0.36	-1.13	0.310	0.591	1.000	177	tags=17%, list=13%, signal=20%
58	RIBOSOME ASSEMBLY		10	-0.44	-1.09	0.377	0.695	1.000	414	tags=50%, list=30%, signal=71%
59	TRANSPOSITION		8	-0.46	-1.07	0.399	0.724	1.000	4	tags=13%, list=0%, signal=12%
60	PSEUDOHYPHAL GROWTH		38	-0.31	-1.06	0.374	0.731	1.000	404	tags=42%, list=29%, signal=58%
61	PEPTIDASE ACTIVITY		30	-0.32	-1.06	0.391	0.736	1.000	299	tags=27%, list=22%, signal=33%
62	DNA-TEMPLATED TRANSCRIPTION, ELONGATION		55	-0.28	-1.05	0.392	0.745	1.000	369	tags=35%, list=27%, signal=45%
63	NUCLEUS ORGANIZATION		27	-0.32	-1.04	0.417	0.748	1.000	52	tags=15%, list=4%, signal=15%
64	RESPONSE TO OXIDATIVE STRESS		22	-0.34	-1.04	0.413	0.753	1.000	588	tags=64%, list=43%, signal=109%
65	RESPONSE TO HEAT		35	-0.30	-1.03	0.438	0.750	1.000	218	tags=23%, list=16%, signal=26%
66	TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER		26	-0.32	-1.02	0.426	0.766	1.000	293	tags=35%, list=21%, signal=43%
67	RIBOSOMAL SMALL SUBUNIT BIOGENESIS		26	-0.32	-1.02	0.442	0.764	1.000	414	tags=38%, list=30%, signal=54%
68	TELOMERE ORGANIZATION		32	-0.31	-1.02	0.446	0.756	1.000	463	tags=38%, list=34%, signal=55%
69	CELLULAR RESPIRATION		10	-0.40	-1.01	0.446	0.756	1.000	690	tags=80%, list=50%, signal=159%
70	CYTOPLASMIC VESICLE		79	-0.25	-0.99	0.490	0.788	1.000	471	tags=38%, list=34%, signal=54%
71	GTPASE ACTIVITY		18	-0.34	-0.99	0.524	0.796	1.000	471	tags=50%, list=34%, signal=75%
72	CELLULAR AMINO ACID METABOLIC PROCESS		26	-0.31	-0.99	0.497	0.785	1.000	300	tags=27%, list=22%, signal=34%
73	REGULATION OF DNA METABOLIC PROCESS		58	-0.26	-0.98	0.522	0.784	1.000	234	tags=21%, list=17%, signal=24%
74	VESICLE ORGANIZATION		24	-0.31	-0.97	0.509	0.789	1.000	426	tags=38%, list=31%, signal=53%

75	METHYLTRANSFERASE ACTIVITY		24	-0.31	-0.97	0.516	0.799	1.000	302	tags=29%, list=22%, signal=37%
76	KINASE ACTIVITY		69	-0.25	-0.97	0.538	0.788	1.000	307	tags=29%, list=22%, signal=35%
77	CYTOKINESIS		27	-0.30	-0.96	0.526	0.799	1.000	351	tags=37%, list=26%, signal=49%
78	NUCLEIC ACID BINDING TRANSCRIPTION FACTOR ACTIVITY		62	-0.26	-0.95	0.561	0.796	1.000	343	tags=31%, list=25%, signal=39%
79	ENDOSOMAL TRANSPORT		45	-0.26	-0.95	0.540	0.791	1.000	550	tags=47%, list=40%, signal=75%
80	PROTEIN FOLDING		33	-0.29	-0.95	0.543	0.783	1.000	635	tags=55%, list=46%, signal=99%
81	COFACTOR METABOLIC PROCESS		21	-0.31	-0.95	0.558	0.777	1.000	392	tags=33%, list=29%, signal=46%
82	DNA-TEMPLATED TRANSCRIPTION, TERMINATION		16	-0.33	-0.94	0.557	0.773	1.000	251	tags=31%, list=18%, signal=38%
83	RNA BINDING		90	-0.24	-0.93	0.610	0.782	1.000	287	tags=27%, list=21%, signal=31%
84	LYASE ACTIVITY		10	-0.37	-0.93	0.549	0.777	1.000	411	tags=40%, list=30%, signal=57%
85	OXIDOREDUCTASE ACTIVITY		32	-0.28	-0.93	0.585	0.769	1.000	208	tags=22%, list=15%, signal=25%
86	SPORULATION		40	-0.27	-0.93	0.585	0.768	1.000	394	tags=35%, list=29%, signal=48%
87	VACUOLE		82	-0.24	-0.92	0.609	0.766	1.000	401	tags=28%, list=29%, signal=37%
88	UNFOLDED PROTEIN BINDING		17	-0.32	-0.92	0.573	0.761	1.000	477	tags=47%, list=35%, signal=71%
89	PROTEIN GLYCOSYLATION		27	-0.28	-0.89	0.614	0.818	1.000	508	tags=44%, list=37%, signal=69%
90	CELLULAR BUD		78	-0.22	-0.89	0.684	0.813	1.000	351	tags=28%, list=26%, signal=36%
91	DNA-TEMPLATED TRANSCRIPTION, INITIATION		32	-0.26	-0.88	0.626	0.817	1.000	259	tags=28%, list=19%, signal=34%
92	MONOCARBOXYLIC ACID METABOLIC PROCESS		27	-0.27	-0.88	0.635	0.816	1.000	527	tags=41%, list=38%, signal=65%
93	TRANSFERASE ACTIVITY, TRANSFERRING GLYCOSYL GROUPS		27	-0.27	-0.87	0.664	0.817	1.000	382	tags=26%, list=28%, signal=35%

94	ORGANELLE ASSEMBLY		44	-0.24	-0.87	0.685	0.815	1.000	434	tags=34%, list=32%, signal=48%
95	CARBOHYDRATE TRANSPORT		10	-0.34	-0.85	0.669	0.831	1.000	572	tags=60%, list=42%, signal=102%
96	REGULATION OF TRANSPORT		33	-0.25	-0.85	0.705	0.827	1.000	202	tags=21%, list=15%, signal=24%
97	SITE OF POLARIZED GROWTH		85	-0.21	-0.84	0.738	0.830	1.000	291	tags=24%, list=21%, signal=28%
98	GOLGI VESICLE TRANSPORT		70	-0.21	-0.82	0.776	0.867	1.000	426	tags=33%, list=31%, signal=45%
99	TRAVERSING START CONTROL POINT OF MITOTIC CELL CYCLE		7	-0.35	-0.79	0.745	0.894	1.000	132	tags=29%, list=10%, signal=31%
100	NUCLEOBASE-CONTAINING SMALL MOLECULE METABOLIC PROCESS		24	-0.25	-0.79	0.750	0.887	1.000	529	tags=46%, list=38%, signal=73%
101	ENZYME BINDING		29	-0.24	-0.79	0.779	0.886	1.000	327	tags=28%, list=24%, signal=35%
102	RIBOSOME		73	-0.20	-0.78	0.839	0.884	1.000	303	tags=23%, list=22%, signal=28%
103	RPD3L COMPLEX		12	-0.30	-0.78	0.757	0.878	1.000	548	tags=67%, list=40%, signal=110%
104	GOLGI APPARATUS		66	-0.19	-0.74	0.852	0.918	1.000	550	tags=44%, list=40%, signal=70%
105	TRANSCRIPTION FACTOR BINDING		34	-0.21	-0.71	0.869	0.948	1.000	541	tags=47%, list=39%, signal=76%
106	UBIQUITIN-LIKE PROTEIN BINDING		27	-0.21	-0.70	0.869	0.951	1.000	365	tags=26%, list=27%, signal=35%
107	MEMBRANE FUSION		20	-0.23	-0.68	0.878	0.962	1.000	476	tags=40%, list=35%, signal=60%
108	SWR1P COMPLEX		8	-0.28	-0.66	0.918	0.975	1.000	666	tags=75%, list=48%, signal=145%
109	CELL WALL		10	-0.26	-0.65	0.902	0.976	1.000	625	tags=50%, list=45%, signal=91%
110	RNA SPLICING		28	-0.19	-0.63	0.935	0.976	1.000	450	tags=36%, list=33%, signal=52%
111	PROTEIN TRANSPORTER ACTIVITY		15	-0.22	-0.62	0.924	0.972	1.000	187	tags=20%, list=14%, signal=23%
112	TRANSCRIPTION FACTOR TFIID COMPLEX		9	-0.26	-0.62	0.933	0.969	1.000	311	tags=33%, list=23%, signal=43%

113	CELL MORPHOGENESIS		12	-0.23	-0.60	0.950	0.967	1.000	387	tags=33%, list=28%, signal=46%
114	ISOMERASE ACTIVITY		14	-0.20	-0.55	0.981	0.980	1.000	320	tags=14%, list=23%, signal=18%