

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	<a href="#">Details ...</a>	32	-0.57	-1.90	0.000	0.024	0.027	222	tags=41%, list=16%, signal=47%
2	TRANSMEMBRANE TRANSPORT	<a href="#">Details ...</a>	43	-0.53	-1.84	0.000	0.027	0.059	306	tags=49%, list=22%, signal=61%
3	PEROXISOME	<a href="#">Details ...</a>	23	-0.59	-1.84	0.000	0.018	0.061	314	tags=65%, list=23%, signal=83%
4	PEROXISOME ORGANIZATION	<a href="#">Details ...</a>	23	-0.58	-1.80	0.001	0.022	0.098	314	tags=61%, list=23%, signal=78%
5	SAGA COMPLEX	<a href="#">Details ...</a>	16	-0.63	-1.79	0.004	0.019	0.107	312	tags=75%, list=23%, signal=96%
6	TRNA PROCESSING	<a href="#">Details ...</a>	33	-0.52	-1.75	0.001	0.027	0.178	222	tags=36%, list=16%, signal=42%
7	HISTONE MODIFICATION	<a href="#">Details ...</a>	79	-0.42	-1.62	0.002	0.102	0.565	344	tags=46%, list=25%, signal=57%
8	RIBOSOMAL LARGE SUBUNIT BIOGENESIS	<a href="#">Details ...</a>	19	-0.54	-1.59	0.013	0.121	0.672	283	tags=53%, list=21%, signal=65%
9	PROTEIN ACYLATION	<a href="#">Details ...</a>	40	-0.46	-1.58	0.005	0.122	0.719	344	tags=50%, list=25%, signal=65%
10	PLASMA MEMBRANE	<a href="#">Details ...</a>	91	-0.39	-1.56	0.003	0.144	0.805	449	tags=51%, list=33%, signal=70%
11	TRANSCRIPTION FACTOR ACTIVITY, PROTEIN BINDING	<a href="#">Details ...</a>	57	-0.41	-1.54	0.020	0.148	0.845	335	tags=39%, list=24%, signal=49%
12	CELL CORTEX	<a href="#">Details ...</a>	60	-0.40	-1.51	0.022	0.187	0.923	349	tags=40%, list=25%, signal=51%
13	RRNA PROCESSING	<a href="#">Details ...</a>	42	-0.43	-1.50	0.022	0.183	0.931	376	tags=43%, list=27%, signal=57%
14	PROTEIN ALKYLATION	<a href="#">Details ...</a>	20	-0.49	-1.47	0.052	0.226	0.971	302	tags=40%, list=22%, signal=51%
15	LIPID METABOLIC PROCESS	<a href="#">Details ...</a>	87	-0.37	-1.46	0.018	0.224	0.977	527	tags=53%, list=38%, signal=80%
16	ENDOPLASMIC RETICULUM	<a href="#">Details ...</a>	184	-0.34	-1.45	0.003	0.226	0.981	499	tags=44%, list=36%, signal=60%
17	CHROMATIN BINDING	<a href="#">Details ...</a>	46	-0.40	-1.43	0.042	0.245	0.990	353	tags=46%, list=26%, signal=59%

18	HYDROLASE ACTIVITY	<a href="#">Details ...</a>	232	-0.32	-1.39	0.003	0.312	0.998	414	tags=39%, list=30%, signal=46%
19	MITOCHONDRION	<a href="#">Details ...</a>	181	-0.32	-1.37	0.016	0.354	1.000	379	tags=34%, list=28%, signal=40%
20	MICROTUBULE ORGANIZING CENTER	<a href="#">Details ...</a>	24	-0.45	-1.37	0.088	0.345	1.000	75	tags=25%, list=5%, signal=26%
21	MITOCHONDRION ORGANIZATION	<a href="#">Details ...</a>	59	-0.36	-1.36	0.078	0.341	1.000	544	tags=49%, list=40%, signal=78%
22	CYTOSKELETON ORGANIZATION	<a href="#">Details ...</a>	91	-0.34	-1.35	0.040	0.351	1.000	330	tags=34%, list=24%, signal=42%
23	MITOCHONDRIAL ENVELOPE	<a href="#">Details ...</a>	47	-0.37	-1.32	0.094	0.400	1.000	454	tags=40%, list=33%, signal=58%
24	CELL BUDDING	<a href="#">Details ...</a>	22	-0.44	-1.32	0.123	0.389	1.000	292	tags=41%, list=21%, signal=51%
25	KORNBERG'S MEDIATOR (SRB) COMPLEX	<a href="#">Details ...</a>	19	-0.44	-1.31	0.126	0.392	1.000	194	tags=37%, list=14%, signal=42%
26	PEPTIDYL-AMINO ACID MODIFICATION	<a href="#">Details ...</a>	75	-0.34	-1.31	0.086	0.381	1.000	361	tags=37%, list=26%, signal=48%
27	TRANSMEMBRANE TRANSPORTER ACTIVITY	<a href="#">Details ...</a>	35	-0.38	-1.30	0.120	0.387	1.000	296	tags=34%, list=22%, signal=43%
28	TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER	<a href="#">Details ...</a>	233	-0.29	-1.27	0.048	0.459	1.000	344	tags=32%, list=25%, signal=35%
29	HISTONE BINDING	<a href="#">Details ...</a>	34	-0.38	-1.27	0.139	0.450	1.000	252	tags=35%, list=18%, signal=42%
30	INVASIVE GROWTH IN RESPONSE TO GLUCOSE LIMITATION	<a href="#">Details ...</a>	26	-0.40	-1.27	0.165	0.442	1.000	548	tags=69%, list=40%, signal=113%
31	CELL WALL ORGANIZATION OR BIOGENESIS	<a href="#">Details ...</a>	63	-0.33	-1.24	0.149	0.497	1.000	370	tags=37%, list=27%, signal=48%
32	PROTEIN MATURATION	<a href="#">Details ...</a>	16	-0.44	-1.24	0.193	0.487	1.000	374	tags=44%, list=27%, signal=59%
33	ENDOCYTOSIS	<a href="#">Details ...</a>	33	-0.37	-1.23	0.195	0.508	1.000	475	tags=48%, list=35%, signal=72%
34	CELLULAR ION HOMEOSTASIS	<a href="#">Details ...</a>	29	-0.38	-1.23	0.184	0.498	1.000	298	tags=31%, list=22%, signal=39%
35	LIPID BINDING	<a href="#">Details ...</a>	40	-0.35	-1.22	0.178	0.505	1.000	427	tags=40%, list=31%, signal=56%
36	NUCLEOLUS	<a href="#">Details ...</a>	52	-0.33	-1.22	0.180	0.493	1.000	283	tags=33%, list=21%, signal=40%

37	ION TRANSPORT	<a href="#">Details ...</a>	52	-0.33	-1.21	0.182	0.491	1.000	471	tags=42%, list=34%, signal=62%
38	RESPONSE TO STARVATION	<a href="#">Details ...</a>	16	-0.42	-1.21	0.223	0.498	1.000	427	tags=56%, list=31%, signal=81%
39	PROTEIN BINDING, BRIDGING	<a href="#">Details ...</a>	30	-0.37	-1.21	0.216	0.488	1.000	439	tags=47%, list=32%, signal=67%
40	GENERATION OF PRECURSOR METABOLITES AND ENERGY	<a href="#">Details ...</a>	25	-0.38	-1.20	0.208	0.482	1.000	529	tags=52%, list=38%, signal=83%
41	CYTOSKELETAL PROTEIN BINDING	<a href="#">Details ...</a>	29	-0.37	-1.20	0.242	0.481	1.000	253	tags=31%, list=18%, signal=37%
42	PROTEIN TARGETING	<a href="#">Details ...</a>	106	-0.29	-1.18	0.201	0.517	1.000	399	tags=33%, list=29%, signal=43%
43	CYTOSKELETON	<a href="#">Details ...</a>	73	-0.31	-1.17	0.215	0.534	1.000	330	tags=33%, list=24%, signal=41%
44	CHROMATIN ORGANIZATION	<a href="#">Details ...</a>	193	-0.27	-1.17	0.184	0.528	1.000	352	tags=31%, list=26%, signal=36%
45	HELICASE ACTIVITY	<a href="#">Details ...</a>	16	-0.41	-1.16	0.282	0.542	1.000	411	tags=56%, list=30%, signal=79%
46	CARBOHYDRATE METABOLIC PROCESS	<a href="#">Details ...</a>	53	-0.32	-1.15	0.272	0.545	1.000	493	tags=43%, list=36%, signal=65%
47	ENDOMEMBRANE SYSTEM	<a href="#">Details ...</a>	315	-0.26	-1.13	0.173	0.589	1.000	474	tags=37%, list=34%, signal=43%
48	ORGANELLE INHERITANCE	<a href="#">Details ...</a>	23	-0.36	-1.12	0.312	0.608	1.000	177	tags=17%, list=13%, signal=20%
49	PSEUDOHYPHAL GROWTH	<a href="#">Details ...</a>	38	-0.31	-1.05	0.391	0.793	1.000	404	tags=42%, list=29%, signal=58%
50	PEPTIDASE ACTIVITY	<a href="#">Details ...</a>	30	-0.32	-1.04	0.405	0.796	1.000	299	tags=27%, list=22%, signal=33%
51	DNA-TEMPLATED TRANSCRIPTION, ELONGATION		55	-0.28	-1.04	0.391	0.789	1.000	369	tags=35%, list=27%, signal=45%
52	NUCLEUS ORGANIZATION		27	-0.32	-1.04	0.410	0.786	1.000	52	tags=15%, list=4%, signal=15%
53	TRANSFERASE ACTIVITY		276	-0.24	-1.03	0.436	0.780	1.000	439	tags=35%, list=32%, signal=41%
54	RESPONSE TO OXIDATIVE STRESS		22	-0.34	-1.03	0.430	0.770	1.000	588	tags=64%, list=43%, signal=109%
55	RESPONSE TO HEAT		35	-0.30	-1.03	0.411	0.765	1.000	218	tags=23%, list=16%, signal=26%

56	RIBOSOMAL SMALL SUBUNIT BIOGENESIS		26	-0.32	-1.02	0.445	0.780	1.000	414	tags=38%, list=30%, signal=54%
57	TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER		26	-0.32	-1.01	0.434	0.787	1.000	293	tags=35%, list=21%, signal=43%
58	TELOMERE ORGANIZATION		32	-0.31	-1.01	0.460	0.783	1.000	463	tags=38%, list=34%, signal=55%
59	MITOTIC CELL CYCLE		151	-0.24	-1.00	0.480	0.779	1.000	338	tags=27%, list=25%, signal=32%
60	GTPASE ACTIVITY		18	-0.34	-0.99	0.490	0.793	1.000	471	tags=50%, list=34%, signal=75%
61	CELLULAR AMINO ACID METABOLIC PROCESS		26	-0.31	-0.99	0.483	0.789	1.000	300	tags=27%, list=22%, signal=34%
62	REGULATION OF DNA METABOLIC PROCESS		58	-0.26	-0.98	0.505	0.814	1.000	234	tags=21%, list=17%, signal=24%
63	CYTOPLASMIC VESICLE		79	-0.25	-0.97	0.528	0.805	1.000	471	tags=38%, list=34%, signal=54%
64	NUCLEIC ACID BINDING TRANSCRIPTION FACTOR ACTIVITY		62	-0.26	-0.96	0.543	0.820	1.000	343	tags=31%, list=25%, signal=39%
65	VESICLE ORGANIZATION		24	-0.31	-0.96	0.524	0.818	1.000	426	tags=38%, list=31%, signal=53%
66	PROTEIN FOLDING		33	-0.29	-0.96	0.559	0.812	1.000	635	tags=55%, list=46%, signal=99%
67	METHYLTRANSFERASE ACTIVITY		24	-0.31	-0.96	0.518	0.803	1.000	302	tags=29%, list=22%, signal=37%
68	KINASE ACTIVITY		69	-0.25	-0.96	0.545	0.792	1.000	307	tags=29%, list=22%, signal=35%
69	OXIDOREDUCTASE ACTIVITY		32	-0.28	-0.95	0.538	0.796	1.000	208	tags=22%, list=15%, signal=25%
70	CYTOKINESIS		27	-0.30	-0.95	0.551	0.785	1.000	351	tags=37%, list=26%, signal=49%
71	DNA-TEMPLATED TRANSCRIPTION, TERMINATION		16	-0.33	-0.95	0.541	0.776	1.000	251	tags=31%, list=18%, signal=38%
72	RNA BINDING		90	-0.24	-0.94	0.580	0.772	1.000	287	tags=27%, list=21%, signal=31%
73	ENDOSOMAL TRANSPORT		45	-0.26	-0.94	0.531	0.766	1.000	550	tags=47%, list=40%, signal=75%
74	VACUOLE		82	-0.24	-0.93	0.594	0.774	1.000	401	tags=28%, list=29%, signal=37%

75	SPORULATION		40	-0.27	-0.93	0.588	0.769	1.000	394	tags=35%, list=29%, signal=48%
76	COFACTOR METABOLIC PROCESS		21	-0.31	-0.92	0.590	0.776	1.000	392	tags=33%, list=29%, signal=46%
77	DNA BINDING		149	-0.22	-0.92	0.660	0.775	1.000	358	tags=28%, list=26%, signal=34%
78	UNFOLDED PROTEIN BINDING		17	-0.32	-0.92	0.583	0.771	1.000	477	tags=47%, list=35%, signal=71%
79	PROTEIN GLYCOSYLATION		27	-0.28	-0.90	0.606	0.783	1.000	508	tags=44%, list=37%, signal=69%
80	MONOCARBOXYLIC ACID METABOLIC PROCESS		27	-0.27	-0.88	0.654	0.817	1.000	527	tags=41%, list=38%, signal=65%
81	DNA-TEMPLATED TRANSCRIPTION, INITIATION		32	-0.26	-0.88	0.658	0.815	1.000	259	tags=28%, list=19%, signal=34%
82	TRANSFERASE ACTIVITY, TRANSFERRING GLYCOSYL GROUPS		27	-0.27	-0.88	0.651	0.806	1.000	382	tags=26%, list=28%, signal=35%
83	CELLULAR BUD		78	-0.22	-0.87	0.700	0.802	1.000	351	tags=28%, list=26%, signal=36%
84	ORGANELLE ASSEMBLY		44	-0.24	-0.86	0.689	0.815	1.000	434	tags=34%, list=32%, signal=48%
85	REGULATION OF TRANSPORT		33	-0.25	-0.84	0.703	0.838	1.000	202	tags=21%, list=15%, signal=24%
86	SITE OF POLARIZED GROWTH		85	-0.21	-0.83	0.771	0.846	1.000	291	tags=24%, list=21%, signal=28%
87	GOLGI VESICLE TRANSPORT		70	-0.21	-0.82	0.769	0.863	1.000	426	tags=33%, list=31%, signal=45%
88	ENZYME BINDING		29	-0.24	-0.80	0.754	0.886	1.000	327	tags=28%, list=24%, signal=35%
89	NUCLEOBASE-CONTAINING SMALL MOLECULE METABOLIC PROCESS		24	-0.25	-0.80	0.762	0.876	1.000	529	tags=46%, list=38%, signal=73%
90	MEIOTIC CELL CYCLE		109	-0.19	-0.78	0.857	0.892	1.000	524	tags=39%, list=38%, signal=57%
91	RIBOSOME		73	-0.20	-0.77	0.845	0.890	1.000	303	tags=23%, list=22%, signal=28%
92	PROTEOLYSIS INVOLVED IN CELLULAR PROTEIN CATABOLIC PROCESS		104	-0.18	-0.75	0.895	0.905	1.000	409	tags=27%, list=30%, signal=35%
93	GOLGI APPARATUS		66	-0.19	-0.73	0.886	0.920	1.000	550	tags=44%, list=40%, signal=70%

94	TRANSCRIPTION FACTOR BINDING		34	-0.21	-0.71	0.864	0.930	1.000	541	tags=47%, list=39%, signal=76%
95	UBIQUITIN-LIKE PROTEIN BINDING		27	-0.21	-0.69	0.881	0.938	1.000	365	tags=26%, list=27%, signal=35%
96	MEMBRANE FUSION		20	-0.23	-0.66	0.916	0.954	1.000	476	tags=40%, list=35%, signal=60%
97	RNA SPLICING		28	-0.19	-0.63	0.943	0.968	1.000	450	tags=36%, list=33%, signal=52%
98	PROTEIN TRANSPORTER ACTIVITY		15	-0.22	-0.61	0.936	0.965	1.000	187	tags=20%, list=14%, signal=23%