

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	TRANSMEMBRANE TRANSPORT	Details ...	43	0.42	1.67	0.006	0.450	0.386	268	tags=35%, list=19%, signal=42%
2	RIBOSOMAL LARGE SUBUNIT BIOGENESIS	Details ...	19	0.48	1.56	0.045	0.550	0.681	337	tags=37%, list=25%, signal=48%
3	TRANSMEMBRANE TRANSPORTER ACTIVITY	Details ...	35	0.39	1.48	0.026	0.642	0.871	263	tags=31%, list=19%, signal=38%
4	PEROXISOME ORGANIZATION	Details ...	23	0.42	1.42	0.054	0.732	0.963	357	tags=48%, list=26%, signal=64%
5	PEPTIDASE ACTIVITY	Details ...	30	0.38	1.36	0.067	0.874	0.989	176	tags=30%, list=13%, signal=34%
6	UNFOLDED PROTEIN BINDING	Details ...	17	0.43	1.35	0.120	0.781	0.996	169	tags=35%, list=12%, signal=40%
7	TRNA PROCESSING	Details ...	33	0.36	1.35	0.085	0.674	0.996	308	tags=45%, list=22%, signal=57%
8	PLASMA MEMBRANE	Details ...	91	0.30	1.34	0.053	0.617	0.996	240	tags=25%, list=17%, signal=29%
9	SAGA COMPLEX	Details ...	16	0.44	1.33	0.138	0.571	0.996	106	tags=31%, list=8%, signal=33%
10	RNA MODIFICATION	Details ...	32	0.36	1.30	0.116	0.606	1.000	308	tags=44%, list=22%, signal=55%
11	PROTEIN ACYLATION	Details ...	40	0.31	1.23	0.156	0.852	1.000	211	tags=30%, list=15%, signal=34%
12	SITE OF POLARIZED GROWTH	Details ...	85	0.27	1.19	0.183	0.951	1.000	325	tags=35%, list=24%, signal=43%
13	RESPONSE TO STARVATION	Details ...	16	0.37	1.14	0.279	1.000	1.000	16	tags=13%, list=1%, signal=13%
14	ION TRANSPORT	Details ...	52	0.27	1.13	0.235	1.000	1.000	252	tags=25%, list=18%, signal=29%
15	TRANSCRIPTION FACTOR ACTIVITY, PROTEIN BINDING	Details ...	57	0.27	1.12	0.279	1.000	1.000	232	tags=26%, list=17%, signal=30%
16	PROTEIN FOLDING	Details ...	33	0.30	1.11	0.293	1.000	1.000	438	tags=55%, list=32%, signal=78%
17	ENDOCYTOSIS	Details ...	33	0.30	1.11	0.295	1.000	1.000	275	tags=30%, list=20%, signal=37%

18	DNA-TEMPLATED TRANSCRIPTION, INITIATION	Details ...	32	0.30	1.10	0.308	0.993	1.000	431	tags=44%, list=31%, signal=62%
19	ENDOPLASMIC RETICULUM	Details ...	184	0.21	1.09	0.232	0.957	1.000	357	tags=29%, list=26%, signal=34%
20	CELL CORTEX	Details ...	60	0.25	1.09	0.279	0.922	1.000	392	tags=38%, list=29%, signal=51%
21	TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER	Details ...	233	0.20	1.09	0.239	0.893	1.000	258	tags=22%, list=19%, signal=22%
22	CELLULAR BUD	Details ...	78	0.24	1.09	0.310	0.853	1.000	217	tags=23%, list=16%, signal=26%
23	CYTOKINESIS	Details ...	27	0.30	1.07	0.328	0.869	1.000	392	tags=48%, list=29%, signal=66%
24	MONOCARBOXYLIC ACID METABOLIC PROCESS	Details ...	27	0.30	1.05	0.371	0.908	1.000	332	tags=30%, list=24%, signal=38%
25	ENDOMEMBRANE SYSTEM	Details ...	315	0.19	1.04	0.366	0.935	1.000	357	tags=30%, list=26%, signal=31%
26	PROTEIN TARGETING	Details ...	106	0.22	1.03	0.378	0.906	1.000	396	tags=39%, list=29%, signal=50%
27	DNA-TEMPLATED TRANSCRIPTION, ELONGATION	Details ...	55	0.23	0.97	0.500	1.000	1.000	453	tags=45%, list=33%, signal=65%
28	HYDROLASE ACTIVITY	Details ...	232	0.18	0.96	0.576	1.000	1.000	250	tags=21%, list=18%, signal=21%
29	CYTOPLASMIC VESICLE	Details ...	79	0.21	0.96	0.541	1.000	1.000	386	tags=35%, list=28%, signal=46%
30	PROTEOLYSIS INVOLVED IN CELLULAR PROTEIN CATABOLIC PROCESS	Details ...	104	0.20	0.95	0.577	1.000	1.000	127	tags=13%, list=9%, signal=13%
31	LIPID BINDING	Details ...	40	0.24	0.94	0.560	1.000	1.000	236	tags=28%, list=17%, signal=32%
32	RESPONSE TO OXIDATIVE STRESS	Details ...	22	0.28	0.94	0.553	1.000	1.000	128	tags=23%, list=9%, signal=25%
33	VESICLE ORGANIZATION	Details ...	24	0.28	0.93	0.559	1.000	1.000	365	tags=38%, list=27%, signal=50%
34	PEROXISOME	Details ...	23	0.28	0.92	0.576	1.000	1.000	268	tags=30%, list=19%, signal=37%
35	KINASE ACTIVITY	Details ...	69	0.21	0.90	0.655	1.000	1.000	280	tags=26%, list=20%, signal=31%
36	PHOSPHATASE ACTIVITY	Details ...	36	0.23	0.90	0.642	1.000	1.000	227	tags=22%, list=17%, signal=26%

37	CELL BUDDING	Details ...	22	0.27	0.90	0.595	1.000	1.000	395	tags=45%, list=29%, signal=63%
38	CYTOSKELETAL PROTEIN BINDING	Details ...	29	0.24	0.87	0.675	1.000	1.000	281	tags=28%, list=20%, signal=34%
39	COFACTOR METABOLIC PROCESS	Details ...	21	0.26	0.87	0.653	1.000	1.000	491	tags=52%, list=36%, signal=80%
40	HELICASE ACTIVITY	Details ...	16	0.28	0.86	0.663	1.000	1.000	362	tags=44%, list=26%, signal=59%
41	PROTEIN TRANSPORTER ACTIVITY	Details ...	15	0.28	0.86	0.654	1.000	1.000	260	tags=33%, list=19%, signal=41%
42	TRANSFERASE ACTIVITY	Details ...	276	0.16	0.85	0.903	1.000	1.000	301	tags=24%, list=22%, signal=24%
43	GTPASE ACTIVITY	Details ...	18	0.27	0.84	0.703	1.000	1.000	406	tags=50%, list=30%, signal=70%
44	PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	Details ...	115	0.17	0.83	0.858	1.000	1.000	213	tags=17%, list=15%, signal=18%
45	CHROMATIN BINDING	Details ...	46	0.21	0.82	0.772	1.000	1.000	305	tags=33%, list=22%, signal=41%
46	PSEUDOHYPHAL GROWTH	Details ...	38	0.21	0.82	0.763	1.000	1.000	425	tags=39%, list=31%, signal=56%
47	VACUOLE	Details ...	82	0.18	0.80	0.874	1.000	1.000	387	tags=29%, list=28%, signal=38%
48	NUCLEOBASE-CONTAINING SMALL MOLECULE METABOLIC PROCESS	Details ...	24	0.23	0.79	0.769	1.000	1.000	355	tags=38%, list=26%, signal=50%
49	CELL WALL ORGANIZATION OR BIOGENESIS	Details ...	63	0.18	0.79	0.862	1.000	1.000	387	tags=29%, list=28%, signal=38%
50	GENERATION OF PRECURSOR METABOLITES AND ENERGY	Details ...	25	0.21	0.72	0.844	1.000	1.000	472	tags=40%, list=34%, signal=60%
51	OXIDOREDUCTASE ACTIVITY		32	0.19	0.71	0.911	1.000	1.000	147	tags=16%, list=11%, signal=17%
52	TRANSCRIPTION FACTOR BINDING		34	0.19	0.71	0.932	1.000	1.000	410	tags=38%, list=30%, signal=53%
53	ORGANELLE ASSEMBLY		44	0.18	0.70	0.921	1.000	1.000	365	tags=32%, list=27%, signal=42%
54	SPORULATION		40	0.18	0.69	0.935	1.000	1.000	368	tags=30%, list=27%, signal=40%
55	PROTEIN BINDING, BRIDGING		30	0.20	0.69	0.915	1.000	1.000	268	tags=27%, list=19%, signal=32%

56	LIPID METABOLIC PROCESS		87	0.15	0.69	0.984	1.000	1.000	334	tags=22%, list=24%, signal=27%
57	DNA-TEMPLATED TRANSCRIPTION, TERMINATION		16	0.23	0.68	0.916	0.995	1.000	393	tags=44%, list=29%, signal=61%
58	MITOCHONDRIAL ENVELOPE		47	0.16	0.63	0.981	1.000	1.000	414	tags=34%, list=30%, signal=47%
59	CELLULAR ION HOMEOSTASIS		29	0.17	0.62	0.974	0.992	1.000	408	tags=34%, list=30%, signal=48%
60	KORNBERG'S MEDIATOR (SRB) COMPLEX		19	0.16	0.52	0.994	0.996	1.000	1157	tags=100%, list=84%, signal=622%