

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	EXOCYTOSIS	Details ...	11	0.70	1.87	0.002	0.114	0.119	205	tags=73%, list=15%, signal=85%
2	ELONGATOR COMPLEX	Details ...	5	0.82	1.71	0.004	0.283	0.450	247	tags=100%, list=18%, signal=121%
3	TRANSMEMBRANE TRANSPORT	Details ...	43	0.42	1.67	0.010	0.249	0.541	268	tags=35%, list=19%, signal=42%
4	VITAMIN METABOLIC PROCESS	Details ...	5	0.77	1.67	0.019	0.193	0.553	179	tags=60%, list=13%, signal=69%
5	RIBOSOMAL LARGE SUBUNIT BIOGENESIS	Details ...	19	0.48	1.53	0.039	0.450	0.919	337	tags=37%, list=25%, signal=48%
6	TRANSMEMBRANE TRANSPORTER ACTIVITY	Details ...	35	0.39	1.47	0.030	0.546	0.979	263	tags=31%, list=19%, signal=38%
7	PEROXISOME ORGANIZATION	Details ...	23	0.42	1.42	0.073	0.627	0.993	357	tags=48%, list=26%, signal=64%
8	PEPTIDASE ACTIVITY	Details ...	30	0.38	1.38	0.067	0.693	0.998	176	tags=30%, list=13%, signal=34%
9	PLASMA MEMBRANE	Details ...	91	0.30	1.36	0.042	0.693	0.998	240	tags=25%, list=17%, signal=29%
10	SAGA COMPLEX	Details ...	16	0.44	1.35	0.130	0.687	0.998	106	tags=31%, list=8%, signal=33%
11	UNFOLDED PROTEIN BINDING	Details ...	17	0.43	1.33	0.125	0.678	1.000	169	tags=35%, list=12%, signal=40%
12	TRNA PROCESSING	Details ...	33	0.36	1.32	0.120	0.656	1.000	308	tags=45%, list=22%, signal=57%
13	RNA MODIFICATION	Details ...	32	0.36	1.31	0.102	0.624	1.000	308	tags=44%, list=22%, signal=55%
14	AMINO ACID TRANSPORT	Details ...	6	0.56	1.23	0.219	0.881	1.000	52	tags=17%, list=4%, signal=17%
15	PROTEIN ACYLATION	Details ...	40	0.31	1.22	0.173	0.846	1.000	211	tags=30%, list=15%, signal=34%
16	SITE OF POLARIZED GROWTH	Details ...	85	0.27	1.22	0.147	0.814	1.000	325	tags=35%, list=24%, signal=43%
17	ENDOCYTOSIS	Details ...	33	0.30	1.14	0.263	1.000	1.000	275	tags=30%, list=20%, signal=37%

18	RESPONSE TO STARVATION	Details ...	16	0.37	1.13	0.296	1.000	1.000	16	tags=13%, list=1%, signal=13%
19	ION TRANSPORT	Details ...	52	0.27	1.13	0.276	1.000	1.000	252	tags=25%, list=18%, signal=29%
20	TRANSCRIPTION FACTOR ACTIVITY, PROTEIN BINDING	Details ...	57	0.27	1.12	0.239	0.977	1.000	232	tags=26%, list=17%, signal=30%
21	PROTEIN FOLDING	Details ...	33	0.30	1.11	0.318	0.951	1.000	438	tags=55%, list=32%, signal=78%
22	SLIK (SAGA-LIKE) COMPLEX	Details ...	14	0.38	1.09	0.340	0.988	1.000	106	tags=21%, list=8%, signal=23%
23	CYTOKINESIS	Details ...	27	0.30	1.09	0.303	0.955	1.000	392	tags=48%, list=29%, signal=66%
24	DNA-TEMPLATED TRANSCRIPTION, INITIATION	Details ...	32	0.30	1.09	0.340	0.918	1.000	431	tags=44%, list=31%, signal=62%
25	CELL CORTEX	Details ...	60	0.25	1.07	0.342	0.951	1.000	392	tags=38%, list=29%, signal=51%
26	CELLULAR BUD	Details ...	78	0.24	1.07	0.337	0.924	1.000	217	tags=23%, list=16%, signal=26%
27	MONOCARBOXYLIC ACID METABOLIC PROCESS	Details ...	27	0.30	1.06	0.360	0.925	1.000	332	tags=30%, list=24%, signal=38%
28	DNA-TEMPLATED TRANSCRIPTION, ELONGATION	Details ...	55	0.23	0.99	0.511	1.000	1.000	453	tags=45%, list=33%, signal=65%
29	CYTOPLASMIC VESICLE	Details ...	79	0.21	0.96	0.516	1.000	1.000	386	tags=35%, list=28%, signal=46%
30	VESICLE ORGANIZATION	Details ...	24	0.28	0.96	0.497	1.000	1.000	365	tags=38%, list=27%, signal=50%
31	PEROXISOME	Details ...	23	0.28	0.95	0.516	1.000	1.000	268	tags=30%, list=19%, signal=37%
32	LIPID BINDING	Details ...	40	0.24	0.95	0.539	1.000	1.000	236	tags=28%, list=17%, signal=32%
33	TRANSCRIPTION FACTOR TFIID COMPLEX	Details ...	9	0.37	0.95	0.519	1.000	1.000	431	tags=56%, list=31%, signal=80%
34	RESPONSE TO OXIDATIVE STRESS	Details ...	22	0.28	0.93	0.544	1.000	1.000	128	tags=23%, list=9%, signal=25%
35	KINASE ACTIVITY	Details ...	69	0.21	0.91	0.609	1.000	1.000	280	tags=26%, list=20%, signal=31%
36	CELL BUDDING	Details ...	22	0.27	0.90	0.620	1.000	1.000	395	tags=45%, list=29%, signal=63%

37	PHOSPHATASE ACTIVITY	Details ...	36	0.23	0.89	0.634	1.000	1.000	227	tags=22%, list=17%, signal=26%
38	LIGASE ACTIVITY	Details ...	6	0.40	0.87	0.624	1.000	1.000	177	tags=33%, list=13%, signal=38%
39	HELICASE ACTIVITY	Details ...	16	0.28	0.87	0.623	1.000	1.000	362	tags=44%, list=26%, signal=59%
40	CYTOSKELETAL PROTEIN BINDING	Details ...	29	0.24	0.86	0.673	1.000	1.000	281	tags=28%, list=20%, signal=34%
41	PROTEIN TRANSPORTER ACTIVITY	Details ...	15	0.28	0.86	0.662	1.000	1.000	260	tags=33%, list=19%, signal=41%
42	COFACTOR METABOLIC PROCESS	Details ...	21	0.26	0.85	0.698	1.000	1.000	491	tags=52%, list=36%, signal=80%
43	CHROMATIN BINDING	Details ...	46	0.21	0.84	0.762	1.000	1.000	305	tags=33%, list=22%, signal=41%
44	PSEUDOHYPHAL GROWTH	Details ...	38	0.21	0.83	0.768	1.000	1.000	425	tags=39%, list=31%, signal=56%
45	GTPASE ACTIVITY	Details ...	18	0.27	0.82	0.727	1.000	1.000	406	tags=50%, list=30%, signal=70%
46	VACUOLE	Details ...	82	0.18	0.80	0.880	1.000	1.000	387	tags=29%, list=28%, signal=38%
47	CELL WALL ORGANIZATION OR BIOGENESIS	Details ...	63	0.18	0.78	0.870	1.000	1.000	387	tags=29%, list=28%, signal=38%
48	DNA-DIRECTED RNA POLYMERASE II COMPLEX	Details ...	7	0.33	0.77	0.751	1.000	1.000	356	tags=43%, list=26%, signal=58%
49	NUCLEOBASE-CONTAINING SMALL MOLECULE METABOLIC PROCESS	Details ...	24	0.23	0.77	0.813	1.000	1.000	355	tags=38%, list=26%, signal=50%
50	TRANSLATIONAL INITIATION	Details ...	14	0.26	0.75	0.796	1.000	1.000	511	tags=64%, list=37%, signal=101%
51	CELL MORPHOGENESIS		12	0.27	0.75	0.791	1.000	1.000	352	tags=33%, list=26%, signal=44%
52	SWI/SNF COMPLEX		8	0.30	0.74	0.798	1.000	1.000	487	tags=63%, list=35%, signal=96%
53	CELLULAR RESPIRATION		10	0.27	0.73	0.823	1.000	1.000	472	tags=50%, list=34%, signal=76%
54	RSC COMPLEX		7	0.31	0.73	0.807	1.000	1.000	446	tags=57%, list=32%, signal=84%
55	GENERATION OF PRECURSOR METABOLITES AND ENERGY		25	0.21	0.72	0.888	1.000	1.000	472	tags=40%, list=34%, signal=60%

56	OXIDOREDUCTASE ACTIVITY		32	0.19	0.72	0.883	1.000	1.000	147	tags=16%, list=11%, signal=17%
57	PROTEIN BINDING, BRIDGING		30	0.20	0.70	0.908	1.000	1.000	268	tags=27%, list=19%, signal=32%
58	ORGANELLE ASSEMBLY		44	0.18	0.70	0.946	1.000	1.000	365	tags=32%, list=27%, signal=42%
59	MITOCHONDRIAL TRANSLATION		7	0.30	0.70	0.869	1.000	1.000	81	tags=14%, list=6%, signal=15%
60	TRANSCRIPTION FACTOR BINDING		34	0.19	0.70	0.928	1.000	1.000	410	tags=38%, list=30%, signal=53%
61	DNA-TEMPLATED TRANSCRIPTION, TERMINATION		16	0.23	0.70	0.896	1.000	1.000	393	tags=44%, list=29%, signal=61%
62	SPORULATION		40	0.18	0.69	0.956	1.000	1.000	368	tags=30%, list=27%, signal=40%
63	SNORNA PROCESSING		6	0.30	0.68	0.853	0.996	1.000	430	tags=50%, list=31%, signal=72%
64	LIPID METABOLIC PROCESS		87	0.15	0.67	0.994	0.988	1.000	334	tags=22%, list=24%, signal=27%
65	TRANSLATION FACTOR ACTIVITY, RNA BINDING		6	0.29	0.64	0.909	0.990	1.000	467	tags=67%, list=34%, signal=101%
66	MITOCHONDRIAL ENVELOPE		47	0.16	0.64	0.972	0.978	1.000	414	tags=34%, list=30%, signal=47%
67	CELLULAR ION HOMEOSTASIS		29	0.17	0.62	0.968	0.976	1.000	408	tags=34%, list=30%, signal=48%
68	KORNBERG'S MEDIATOR (SRB) COMPLEX		19	0.16	0.51	0.996	0.994	1.000	1157	tags=100%, list=84%, signal=622%