

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	ANAPHASE-PROMOTING COMPLEX	Details ...	14	0.72	2.39	0.000	0.003	0.003	95	tags=43%, list=7%, signal=46%
2	SAC AND APC	Details ...	19	0.65	2.30	0.000	0.003	0.006	95	tags=32%, list=7%, signal=33%
3	NUCLEAR PORE COMPLEX	Details ...	12	0.67	2.11	0.000	0.008	0.020	431	tags=75%, list=31%, signal=108%
4	MITOTIC START CONTROL	Details ...	43	0.39	1.75	0.000	0.091	0.263	154	tags=30%, list=11%, signal=33%
5	COMA COMPLEX	Details ...	5	0.78	1.72	0.018	0.096	0.329	303	tags=100%, list=22%, signal=128%
6	SIGNAL TRANSDUCER ACTIVITY	Details ...	14	0.53	1.71	0.024	0.089	0.357	251	tags=57%, list=18%, signal=69%
7	REGULATION OF PROTEIN MODIFICATION PROCESS	Details ...	55	0.36	1.69	0.000	0.082	0.380	130	tags=29%, list=9%, signal=31%
8	SET3P COMPLEX	Details ...	7	0.64	1.62	0.050	0.117	0.546	215	tags=71%, list=16%, signal=84%
9	PROTEIN PHOSPHORYLATION	Details ...	89	0.29	1.54	0.000	0.161	0.698	205	tags=29%, list=15%, signal=32%
10	ENZYME REGULATOR ACTIVITY	Details ...	97	0.26	1.43	0.012	0.269	0.891	191	tags=26%, list=14%, signal=28%
11	CHROMOSOME SEGREGATION	Details ...	82	0.27	1.41	0.024	0.273	0.916	257	tags=29%, list=19%, signal=34%
12	RNA CATABOLIC PROCESS	Details ...	54	0.29	1.41	0.026	0.259	0.920	229	tags=31%, list=17%, signal=36%
13	SECRETORY STRESS	Details ...	12	0.45	1.39	0.098	0.255	0.935	215	tags=50%, list=16%, signal=59%
14	NUCLEOTIDYLTRANSFERASE ACTIVITY	Details ...	28	0.33	1.39	0.080	0.246	0.941	162	tags=32%, list=12%, signal=36%
15	PROTEIN DEPHOSPHORYLATION	Details ...	25	0.34	1.32	0.079	0.313	0.981	323	tags=36%, list=23%, signal=46%
16	NUCLEAR TRANSPORT	Details ...	59	0.27	1.31	0.056	0.304	0.984	232	tags=27%, list=17%, signal=31%
17	CYTOPLASMIC RIBOSOMAL LARGE SUBUNIT	Details ...	22	0.34	1.28	0.123	0.340	0.992	324	tags=50%, list=24%, signal=64%

18	CONJUGATION	Details ...	48	0.27	1.24	0.150	0.389	0.997	109	tags=19%, list=8%, signal=20%
19	CCR4-NOT CORE COMPLEX	Details ...	9	0.43	1.22	0.216	0.391	0.997	26	tags=22%, list=2%, signal=23%
20	NUCLEASE ACTIVITY	Details ...	28	0.29	1.21	0.183	0.406	0.999	91	tags=21%, list=7%, signal=22%
21	CYTOPLASMIC TRANSLATION	Details ...	43	0.27	1.18	0.188	0.431	0.999	293	tags=37%, list=21%, signal=46%
22	TRANSCRIPTION FROM RNA POLYMERASE III PROMOTER	Details ...	10	0.41	1.17	0.224	0.423	0.999	45	tags=20%, list=3%, signal=21%
23	REGULATION OF TRANSLATION	Details ...	30	0.25	1.04	0.365	0.691	1.000	231	tags=30%, list=17%, signal=35%
24	G1 TO S TRANSITION OF MITOTIC CELL CYCLE	Details ...	17	0.30	1.01	0.420	0.737	1.000	275	tags=47%, list=20%, signal=58%
25	DNA REPLICATION	Details ...	63	0.20	0.99	0.493	0.781	1.000	253	tags=29%, list=18%, signal=33%
26	NUCLEOBASE-CONTAINING COMPOUND TRANSPORT	Details ...	44	0.22	0.98	0.457	0.758	1.000	112	tags=16%, list=8%, signal=17%
27	DNA-DIRECTED RNA POLYMERASE II COMPLEX	Details ...	7	0.38	0.97	0.425	0.760	1.000	207	tags=57%, list=15%, signal=67%
28	DNA RECOMBINATION	Details ...	70	0.19	0.97	0.554	0.744	1.000	303	tags=30%, list=22%, signal=37%
29	VACUOLE ORGANIZATION	Details ...	31	0.23	0.96	0.537	0.743	1.000	115	tags=16%, list=8%, signal=17%
30	RESPONSE TO OSMOTIC STRESS	Details ...	42	0.22	0.95	0.551	0.729	1.000	53	tags=12%, list=4%, signal=12%
31	ORGANELLE FUSION	Details ...	27	0.24	0.95	0.539	0.706	1.000	115	tags=22%, list=8%, signal=24%
32	MRNA BINDING	Details ...	48	0.19	0.91	0.638	0.783	1.000	184	tags=21%, list=13%, signal=23%
33	STRUCTURAL CONSTITUENT OF RIBOSOME	Details ...	44	0.20	0.88	0.733	0.823	1.000	293	tags=32%, list=21%, signal=39%
34	TRANSLATIONAL ELONGATION	Details ...	10	0.29	0.86	0.630	0.839	1.000	202	tags=30%, list=15%, signal=35%
35	GUANYL-NUCLEOTIDE EXCHANGE FACTOR ACTIVITY	Details ...	14	0.26	0.86	0.659	0.819	1.000	166	tags=21%, list=12%, signal=24%
36	MRNA PROCESSING	Details ...	37	0.19	0.79	0.823	0.927	1.000	204	tags=24%, list=15%, signal=28%

37	NUA4 HISTONE ACETYLTRANSFERASE COMPLEX	Details ...	9	0.28	0.79	0.764	0.907	1.000	332	tags=56%, list=24%, signal=73%
38	PHOSPHATASE ACTIVITY	Details ...	36	0.18	0.77	0.902	0.915	1.000	305	tags=31%, list=22%, signal=38%
39	CYTOPLASMIC RIBOSOMAL SMALL SUBUNIT	Details ...	19	0.21	0.74	0.852	0.930	1.000	1090	tags=100%, list=79%, signal=476%
40	RIBOSOMAL SUBUNIT EXPORT FROM NUCLEUS	Details ...	5	0.31	0.70	0.857	0.948	1.000	423	tags=80%, list=31%, signal=115%
41	LIGASE ACTIVITY	Details ...	6	0.25	0.58	0.952	1.000	1.000	69	tags=17%, list=5%, signal=17%
42	LIPID TRANSPORT	Details ...	15	0.16	0.56	0.985	0.985	1.000	283	tags=27%, list=21%, signal=33%