

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	SAC AND APC	Details ...	19	0.65	2.29	0.000	0.003	0.002	95	tags=32%, list=7%, signal=33%
2	MITOTIC START CONTROL	Details ...	43	0.39	1.83	0.006	0.065	0.080	154	tags=30%, list=11%, signal=33%
3	REGULATION OF PROTEIN MODIFICATION PROCESS	Details ...	55	0.36	1.74	0.000	0.077	0.139	130	tags=29%, list=9%, signal=31%
4	PROTEIN PHOSPHORYLATION	Details ...	89	0.29	1.53	0.000	0.232	0.438	205	tags=29%, list=15%, signal=32%
5	ENZYME REGULATOR ACTIVITY	Details ...	97	0.26	1.41	0.000	0.377	0.682	191	tags=26%, list=14%, signal=28%
6	CHROMOSOME SEGREGATION	Details ...	82	0.27	1.41	0.018	0.315	0.682	257	tags=29%, list=19%, signal=34%
7	RNA CATABOLIC PROCESS	Details ...	54	0.29	1.40	0.027	0.280	0.697	229	tags=31%, list=17%, signal=36%
8	PROTEIN DEPHOSPHORYLATION	Details ...	25	0.34	1.34	0.071	0.348	0.836	323	tags=36%, list=23%, signal=46%
9	NUCLEAR TRANSPORT	Details ...	59	0.27	1.32	0.066	0.345	0.874	232	tags=27%, list=17%, signal=31%
10	NUCLEOTIDYLTRANSFERASE ACTIVITY	Details ...	28	0.33	1.31	0.101	0.322	0.882	162	tags=32%, list=12%, signal=36%
11	CYTOPLASMIC RIBOSOMAL LARGE SUBUNIT	Details ...	22	0.34	1.30	0.112	0.324	0.902	324	tags=50%, list=24%, signal=64%
12	REGULATION OF CELL CYCLE	Details ...	123	0.23	1.25	0.031	0.373	0.949	258	tags=28%, list=19%, signal=32%
13	CYTOPLASMIC TRANSLATION	Details ...	43	0.27	1.22	0.128	0.420	0.977	293	tags=37%, list=21%, signal=46%
14	CONJUGATION	Details ...	48	0.27	1.20	0.136	0.418	0.984	109	tags=19%, list=8%, signal=20%
15	NUCLEASE ACTIVITY	Details ...	28	0.29	1.20	0.179	0.402	0.985	91	tags=21%, list=7%, signal=22%
16	ORGANELLE FISSION	Details ...	141	0.20	1.17	0.114	0.433	0.992	215	tags=23%, list=16%, signal=24%
17	PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	Details ...	115	0.20	1.05	0.343	0.746	1.000	248	tags=27%, list=18%, signal=30%

18	REGULATION OF TRANSLATION	Details ...	30	0.25	1.03	0.387	0.770	1.000	231	tags=30%, list=17%, signal=35%
19	RESPONSE TO OSMOTIC STRESS	Details ...	42	0.22	1.01	0.438	0.803	1.000	53	tags=12%, list=4%, signal=12%
20	G1 TO S TRANSITION OF MITOTIC CELL CYCLE	Details ...	17	0.30	1.01	0.442	0.767	1.000	275	tags=47%, list=20%, signal=58%
21	NUCLEOBASE-CONTAINING COMPOUND TRANSPORT	Details ...	44	0.22	1.00	0.400	0.739	1.000	112	tags=16%, list=8%, signal=17%
22	DNA REPLICATION	Details ...	63	0.20	1.00	0.433	0.717	1.000	253	tags=29%, list=18%, signal=33%
23	VACUOLE ORGANIZATION	Details ...	31	0.23	0.97	0.505	0.782	1.000	115	tags=16%, list=8%, signal=17%
24	ORGANELLE FUSION	Details ...	27	0.24	0.96	0.478	0.760	1.000	115	tags=22%, list=8%, signal=24%
25	DNA RECOMBINATION	Details ...	70	0.19	0.96	0.564	0.746	1.000	303	tags=30%, list=22%, signal=37%
26	REGULATION OF ORGANELLE ORGANIZATION	Details ...	105	0.17	0.92	0.703	0.818	1.000	314	tags=31%, list=23%, signal=38%
27	MRNA BINDING	Details ...	48	0.19	0.90	0.673	0.850	1.000	184	tags=21%, list=13%, signal=23%
28	STRUCTURAL CONSTITUENT OF RIBOSOME	Details ...	44	0.20	0.89	0.697	0.837	1.000	293	tags=32%, list=21%, signal=39%
29	CHROMOSOME	Details ...	160	0.15	0.88	0.875	0.826	1.000	130	tags=13%, list=9%, signal=13%
30	DNA REPAIR	Details ...	119	0.15	0.85	0.843	0.869	1.000	213	tags=19%, list=15%, signal=21%
31	CELLULAR RESPONSE TO DNA DAMAGE STIMULUS	Details ...	139	0.15	0.84	0.886	0.848	1.000	213	tags=19%, list=15%, signal=21%
32	MRNA PROCESSING	Details ...	37	0.19	0.80	0.846	0.895	1.000	204	tags=24%, list=15%, signal=28%
33	PHOSPHATASE ACTIVITY	Details ...	36	0.18	0.76	0.913	0.932	1.000	305	tags=31%, list=22%, signal=38%
34	CYTOPLASMIC RIBOSOMAL SMALL SUBUNIT	Details ...	19	0.21	0.73	0.850	0.927	1.000	1090	tags=100%, list=79%, signal=476%
35	LIPID TRANSPORT	Details ...	15	0.16	0.55	0.992	0.993	1.000	283	tags=27%, list=21%, signal=33%