

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	MRNA PROCESSING	<a href="#">Details ...</a>	37	-0.49	-1.82	0.006	0.148	0.132	206	tags=38%, list=15%, signal=43%
2	RIBOSOMAL SMALL SUBUNIT BIOGENESIS	<a href="#">Details ...</a>	26	-0.47	-1.62	0.014	0.441	0.590	334	tags=42%, list=24%, signal=55%
3	MICROTUBULE ORGANIZING CENTER	<a href="#">Details ...</a>	24	-0.49	-1.61	0.021	0.295	0.592	186	tags=38%, list=14%, signal=43%
4	RNA SPLICING	<a href="#">Details ...</a>	28	-0.43	-1.50	0.037	0.509	0.866	206	tags=39%, list=15%, signal=45%
5	REGULATION OF PROTEIN MODIFICATION PROCESS	<a href="#">Details ...</a>	55	-0.36	-1.47	0.021	0.495	0.911	239	tags=36%, list=17%, signal=42%
6	METHYLTRANSFERASE ACTIVITY	<a href="#">Details ...</a>	24	-0.42	-1.45	0.066	0.502	0.945	335	tags=54%, list=24%, signal=70%
7	SAC AND APC	<a href="#">Details ...</a>	19	-0.45	-1.42	0.060	0.532	0.977	392	tags=42%, list=29%, signal=58%
8	ORGANELLE FISSION	<a href="#">Details ...</a>	141	-0.29	-1.41	0.017	0.478	0.980	399	tags=40%, list=29%, signal=50%
9	RESPONSE TO OSMOTIC STRESS	<a href="#">Details ...</a>	42	-0.37	-1.38	0.066	0.522	0.989	135	tags=29%, list=10%, signal=31%
10	CYTOSKELETON ORGANIZATION	<a href="#">Details ...</a>	91	-0.30	-1.37	0.031	0.501	0.991	199	tags=25%, list=14%, signal=28%
11	DNA REPAIR	<a href="#">Details ...</a>	119	-0.29	-1.35	0.029	0.498	0.994	325	tags=32%, list=24%, signal=38%
12	CHROMOSOME	<a href="#">Details ...</a>	160	-0.27	-1.34	0.036	0.511	0.998	257	tags=28%, list=19%, signal=30%
13	CHROMATIN ORGANIZATION	<a href="#">Details ...</a>	193	-0.26	-1.30	0.029	0.602	1.000	223	tags=24%, list=16%, signal=24%
14	PROTEIN ALKYLATION	<a href="#">Details ...</a>	20	-0.40	-1.27	0.158	0.660	1.000	287	tags=45%, list=21%, signal=56%
15	CHROMOSOME SEGREGATION	<a href="#">Details ...</a>	82	-0.29	-1.26	0.085	0.652	1.000	328	tags=33%, list=24%, signal=41%
16	INVASIVE GROWTH IN RESPONSE TO GLUCOSE LIMITATION	<a href="#">Details ...</a>	26	-0.37	-1.25	0.155	0.620	1.000	112	tags=19%, list=8%, signal=21%
17	CELLULAR RESPONSE TO DNA DAMAGE STIMULUS	<a href="#">Details ...</a>	139	-0.26	-1.24	0.090	0.629	1.000	325	tags=29%, list=24%, signal=35%

18	GOLGI VESICLE TRANSPORT	<a href="#">Details ...</a>	70	-0.29	-1.23	0.127	0.611	1.000	177	tags=24%, list=13%, signal=26%
19	ENZYME REGULATOR ACTIVITY	<a href="#">Details ...</a>	97	-0.27	-1.22	0.135	0.612	1.000	247	tags=28%, list=18%, signal=32%
20	MITOTIC START CONTROL	<a href="#">Details ...</a>	43	-0.31	-1.22	0.189	0.605	1.000	394	tags=37%, list=29%, signal=51%
21	GOLGI APPARATUS	<a href="#">Details ...</a>	66	-0.28	-1.21	0.174	0.602	1.000	138	tags=21%, list=10%, signal=22%
22	MRNA BINDING	<a href="#">Details ...</a>	48	-0.30	-1.19	0.193	0.636	1.000	161	tags=23%, list=12%, signal=25%
23	CYTOPLASMIC RIBOSOMAL SMALL SUBUNIT	<a href="#">Details ...</a>	19	-0.38	-1.19	0.244	0.619	1.000	334	tags=47%, list=24%, signal=62%
24	MITOTIC CELL CYCLE	<a href="#">Details ...</a>	151	-0.24	-1.16	0.168	0.667	1.000	228	tags=22%, list=17%, signal=23%
25	DNA REPLICATION	<a href="#">Details ...</a>	63	-0.28	-1.14	0.217	0.703	1.000	223	tags=24%, list=16%, signal=27%
26	NUCLEASE ACTIVITY	<a href="#">Details ...</a>	28	-0.33	-1.14	0.263	0.689	1.000	242	tags=25%, list=18%, signal=30%
27	REGULATION OF ORGANELLE ORGANIZATION	<a href="#">Details ...</a>	105	-0.25	-1.14	0.199	0.665	1.000	313	tags=30%, list=23%, signal=35%
28	HISTONE MODIFICATION	<a href="#">Details ...</a>	79	-0.26	-1.14	0.224	0.647	1.000	239	tags=25%, list=17%, signal=29%
29	PEPTIDYL-AMINO ACID MODIFICATION	<a href="#">Details ...</a>	75	-0.26	-1.13	0.230	0.654	1.000	312	tags=29%, list=23%, signal=36%
30	NUCLEUS ORGANIZATION	<a href="#">Details ...</a>	27	-0.30	-1.04	0.369	0.936	1.000	158	tags=19%, list=11%, signal=21%
31	ORGANELLE FUSION	<a href="#">Details ...</a>	27	-0.30	-1.02	0.458	0.972	1.000	293	tags=37%, list=21%, signal=46%
32	REGULATION OF CELL CYCLE	<a href="#">Details ...</a>	123	-0.22	-1.02	0.423	0.963	1.000	247	tags=24%, list=18%, signal=26%
33	RRNA PROCESSING	<a href="#">Details ...</a>	42	-0.27	-1.01	0.439	0.952	1.000	334	tags=29%, list=24%, signal=37%
34	HISTONE BINDING	<a href="#">Details ...</a>	34	-0.28	-1.01	0.475	0.950	1.000	385	tags=35%, list=28%, signal=48%
35	RNA BINDING	<a href="#">Details ...</a>	90	-0.23	-1.00	0.460	0.931	1.000	198	tags=20%, list=14%, signal=22%
36	TELOMERE ORGANIZATION	<a href="#">Details ...</a>	32	-0.27	-0.96	0.504	1.000	1.000	349	tags=34%, list=25%, signal=45%

37	MEIOTIC CELL CYCLE	<a href="#">Details ...</a>	109	-0.21	-0.95	0.562	1.000	1.000	397	tags=35%, list=29%, signal=45%
38	CYTOSKELETON	<a href="#">Details ...</a>	73	-0.22	-0.94	0.572	1.000	1.000	186	tags=21%, list=14%, signal=23%
39	ENZYME BINDING	<a href="#">Details ...</a>	29	-0.27	-0.94	0.558	1.000	1.000	224	tags=28%, list=16%, signal=32%
40	STRUCTURAL CONSTITUENT OF RIBOSOME	<a href="#">Details ...</a>	44	-0.25	-0.94	0.559	1.000	1.000	447	tags=41%, list=33%, signal=59%
41	DNA RECOMBINATION	<a href="#">Details ...</a>	70	-0.22	-0.94	0.584	1.000	1.000	361	tags=37%, list=26%, signal=48%
42	REGULATION OF TRANSPORT	<a href="#">Details ...</a>	33	-0.25	-0.92	0.577	1.000	1.000	279	tags=30%, list=20%, signal=37%
43	DNA BINDING	<a href="#">Details ...</a>	149	-0.19	-0.91	0.679	1.000	1.000	349	tags=28%, list=25%, signal=33%
44	PROTEIN PHOSPHORYLATION	<a href="#">Details ...</a>	89	-0.20	-0.91	0.615	1.000	1.000	319	tags=30%, list=23%, signal=37%
45	NUCLEOTIDYLTRANSFERASE ACTIVITY	<a href="#">Details ...</a>	28	-0.26	-0.91	0.606	1.000	1.000	299	tags=29%, list=22%, signal=36%
46	RIBOSOME	<a href="#">Details ...</a>	73	-0.21	-0.90	0.670	1.000	1.000	142	tags=14%, list=10%, signal=14%
47	RESPONSE TO HEAT	<a href="#">Details ...</a>	35	-0.25	-0.89	0.656	1.000	1.000	102	tags=14%, list=7%, signal=15%
48	ENDOSOMAL TRANSPORT	<a href="#">Details ...</a>	45	-0.23	-0.89	0.650	1.000	1.000	336	tags=33%, list=24%, signal=43%
49	PROTEIN DEPHOSPHORYLATION	<a href="#">Details ...</a>	25	-0.27	-0.89	0.626	0.989	1.000	390	tags=40%, list=28%, signal=55%
50	CYTOPLASMIC TRANSLATION	<a href="#">Details ...</a>	43	-0.23	-0.89	0.631	0.970	1.000	134	tags=14%, list=10%, signal=15%
51	CYTOPLASMIC RIBOSOMAL LARGE SUBUNIT		22	-0.27	-0.88	0.660	0.958	1.000	59	tags=9%, list=4%, signal=9%
52	TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER		26	-0.26	-0.88	0.651	0.948	1.000	327	tags=31%, list=24%, signal=40%
53	CONJUGATION		48	-0.22	-0.88	0.704	0.943	1.000	255	tags=27%, list=19%, signal=32%
54	NUCLEAR TRANSPORT		59	-0.21	-0.87	0.696	0.932	1.000	140	tags=15%, list=10%, signal=16%
55	PROTEIN GLYCOSYLATION		27	-0.25	-0.87	0.651	0.931	1.000	105	tags=15%, list=8%, signal=16%

56	REGULATION OF DNA METABOLIC PROCESS		58	-0.21	-0.86	0.721	0.919	1.000	212	tags=19%, list=15%, signal=21%
57	PROTEIN MATURATION		16	-0.29	-0.86	0.683	0.911	1.000	120	tags=19%, list=9%, signal=20%
58	MEMBRANE FUSION		20	-0.27	-0.86	0.690	0.898	1.000	293	tags=40%, list=21%, signal=50%
59	NUCLEIC ACID BINDING TRANSCRIPTION FACTOR ACTIVITY		62	-0.21	-0.86	0.717	0.884	1.000	265	tags=24%, list=19%, signal=29%
60	RNA CATABOLIC PROCESS		54	-0.21	-0.86	0.739	0.877	1.000	230	tags=22%, list=17%, signal=26%
61	REGULATION OF TRANSLATION		30	-0.24	-0.86	0.689	0.865	1.000	498	tags=47%, list=36%, signal=72%
62	LIPID TRANSPORT		15	-0.29	-0.85	0.661	0.868	1.000	363	tags=47%, list=26%, signal=63%
63	ORGANELLE INHERITANCE		23	-0.26	-0.85	0.685	0.855	1.000	313	tags=30%, list=23%, signal=39%
64	MITOCHONDRION		181	-0.16	-0.81	0.922	0.909	1.000	338	tags=24%, list=25%, signal=28%
65	CELLULAR AMINO ACID METABOLIC PROCESS		26	-0.22	-0.78	0.785	0.944	1.000	113	tags=15%, list=8%, signal=16%
66	G1 TO S TRANSITION OF MITOTIC CELL CYCLE		17	-0.24	-0.72	0.844	1.000	1.000	508	tags=53%, list=37%, signal=83%
67	TRANSFERASE ACTIVITY, TRANSFERRING GLYCOSYL GROUPS		27	-0.21	-0.71	0.887	1.000	1.000	409	tags=37%, list=30%, signal=52%
68	CARBOHYDRATE METABOLIC PROCESS		53	-0.18	-0.70	0.938	0.995	1.000	151	tags=11%, list=11%, signal=12%
69	UBIQUITIN-LIKE PROTEIN BINDING		27	-0.20	-0.69	0.908	0.988	1.000	434	tags=37%, list=32%, signal=53%
70	NUCLEOLUS		52	-0.17	-0.68	0.949	0.982	1.000	269	tags=21%, list=20%, signal=25%
71	VACUOLE ORGANIZATION		31	-0.19	-0.68	0.914	0.972	1.000	311	tags=26%, list=23%, signal=33%
72	NUCLEOBASE-CONTAINING COMPOUND TRANSPORT		44	-0.17	-0.66	0.960	0.971	1.000	321	tags=25%, list=23%, signal=32%
73	MITOCHONDRION ORGANIZATION		59	-0.15	-0.62	0.987	0.976	1.000	194	tags=12%, list=14%, signal=13%