

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	-1.83	0.002	0.221	0.191	206	tags=38%, list=15%, signal=43%
2	SWR1P COMPLEX	<a href="#">Details ...</a>	8	-0.70	-1.65	0.014	0.584	0.674	353	tags=88%, list=26%, signal=117%
3	MICROTUBULE ORGANIZING CENTER	<a href="#">Details ...</a>	24	-0.49	-1.64	0.012	0.429	0.713	186	tags=38%, list=14%, signal=43%
4	COMPASS COMPLEX	<a href="#">Details ...</a>	5	-0.78	-1.63	0.014	0.352	0.740	270	tags=80%, list=20%, signal=99%
5	RIBOSOMAL SMALL SUBUNIT BIOGENESIS	<a href="#">Details ...</a>	26	-0.47	-1.59	0.020	0.380	0.839	334	tags=42%, list=24%, signal=55%
6	SET3P COMPLEX	<a href="#">Details ...</a>	7	-0.67	-1.57	0.041	0.373	0.883	356	tags=71%, list=26%, signal=96%
7	RNA SPLICING	<a href="#">Details ...</a>	28	-0.43	-1.49	0.034	0.522	0.961	206	tags=39%, list=15%, signal=45%
8	REGULATION OF PROTEIN MODIFICATION PROCESS	<a href="#">Details ...</a>	55	-0.36	-1.48	0.034	0.507	0.982	239	tags=36%, list=17%, signal=42%
9	SIGNAL TRANSDUCER ACTIVITY	<a href="#">Details ...</a>	14	-0.51	-1.45	0.053	0.521	0.991	88	tags=43%, list=6%, signal=45%
10	RESPONSE TO OSMOTIC STRESS	<a href="#">Details ...</a>	42	-0.37	-1.42	0.057	0.564	0.995	135	tags=29%, list=10%, signal=31%
11	RPD3L COMPLEX	<a href="#">Details ...</a>	12	-0.50	-1.41	0.069	0.546	0.998	596	tags=83%, list=43%, signal=146%
12	METHYLTRANSFERASE ACTIVITY	<a href="#">Details ...</a>	24	-0.42	-1.41	0.077	0.504	0.998	335	tags=54%, list=24%, signal=70%
13	SAC AND APC	<a href="#">Details ...</a>	19	-0.45	-1.40	0.076	0.486	0.999	392	tags=42%, list=29%, signal=58%
14	TRANSPOSITION	<a href="#">Details ...</a>	8	-0.57	-1.39	0.097	0.480	0.999	218	tags=38%, list=16%, signal=44%
15	CYTOSKELETON ORGANIZATION	<a href="#">Details ...</a>	91	-0.30	-1.38	0.036	0.493	1.000	199	tags=25%, list=14%, signal=28%
16	PROTEIN ALKYLATION	<a href="#">Details ...</a>	20	-0.40	-1.25	0.188	0.892	1.000	287	tags=45%, list=21%, signal=56%
17	CHROMOSOME SEGREGATION	<a href="#">Details ...</a>	82	-0.29	-1.25	0.099	0.851	1.000	328	tags=33%, list=24%, signal=41%

18	GOLGI VESICLE TRANSPORT	<a href="#">Details ...</a>	70	-0.29	-1.25	0.116	0.808	1.000	177	tags=24%, list=13%, signal=26%
19	INVASIVE GROWTH IN RESPONSE TO GLUCOSE LIMITATION	<a href="#">Details ...</a>	26	-0.37	-1.24	0.166	0.806	1.000	112	tags=19%, list=8%, signal=21%
20	ANAPHASE-PROMOTING COMPLEX	<a href="#">Details ...</a>	14	-0.43	-1.23	0.209	0.797	1.000	561	tags=64%, list=41%, signal=107%
21	ENZYME REGULATOR ACTIVITY	<a href="#">Details ...</a>	97	-0.27	-1.22	0.132	0.803	1.000	247	tags=28%, list=18%, signal=32%
22	MITOTIC START CONTROL	<a href="#">Details ...</a>	43	-0.31	-1.21	0.190	0.789	1.000	394	tags=37%, list=29%, signal=51%
23	ISOMERASE ACTIVITY	<a href="#">Details ...</a>	14	-0.43	-1.20	0.225	0.777	1.000	188	tags=43%, list=14%, signal=49%
24	GOLGI APPARATUS	<a href="#">Details ...</a>	66	-0.28	-1.20	0.170	0.758	1.000	138	tags=21%, list=10%, signal=22%
25	CYTOPLASMIC RIBOSOMAL SMALL SUBUNIT	<a href="#">Details ...</a>	19	-0.38	-1.20	0.212	0.738	1.000	334	tags=47%, list=24%, signal=62%
26	MRNA BINDING	<a href="#">Details ...</a>	48	-0.30	-1.19	0.196	0.722	1.000	161	tags=23%, list=12%, signal=25%
27	NUCLEASE ACTIVITY	<a href="#">Details ...</a>	28	-0.33	-1.16	0.253	0.785	1.000	242	tags=25%, list=18%, signal=30%
28	HISTONE MODIFICATION	<a href="#">Details ...</a>	79	-0.26	-1.14	0.222	0.841	1.000	239	tags=25%, list=17%, signal=29%
29	CCR4-NOT CORE COMPLEX	<a href="#">Details ...</a>	9	-0.45	-1.13	0.316	0.853	1.000	516	tags=78%, list=38%, signal=124%
30	DNA REPLICATION	<a href="#">Details ...</a>	63	-0.28	-1.13	0.259	0.827	1.000	223	tags=24%, list=16%, signal=27%
31	PEPTIDYL-AMINO ACID MODIFICATION	<a href="#">Details ...</a>	75	-0.26	-1.11	0.244	0.860	1.000	312	tags=29%, list=23%, signal=36%
32	LYASE ACTIVITY	<a href="#">Details ...</a>	10	-0.42	-1.10	0.340	0.849	1.000	171	tags=30%, list=12%, signal=34%
33	COMA COMPLEX	<a href="#">Details ...</a>	5	-0.53	-1.09	0.372	0.886	1.000	653	tags=100%, list=47%, signal=190%
34	NUCLEUS ORGANIZATION	<a href="#">Details ...</a>	27	-0.30	-1.03	0.391	1.000	1.000	158	tags=19%, list=11%, signal=21%
35	RRNA PROCESSING	<a href="#">Details ...</a>	42	-0.27	-1.02	0.404	1.000	1.000	334	tags=29%, list=24%, signal=37%
36	HISTONE BINDING	<a href="#">Details ...</a>	34	-0.28	-1.02	0.430	1.000	1.000	385	tags=35%, list=28%, signal=48%

37	RNA BINDING	<a href="#">Details ...</a>	90	-0.23	-1.02	0.434	1.000	1.000	198	tags=20%, list=14%, signal=22%
38	ORGANELLE FUSION	<a href="#">Details ...</a>	27	-0.30	-1.01	0.454	1.000	1.000	293	tags=37%, list=21%, signal=46%
39	TELOMERE ORGANIZATION	<a href="#">Details ...</a>	32	-0.27	-1.00	0.465	1.000	1.000	349	tags=34%, list=25%, signal=45%
40	NUCLEAR PORE COMPLEX	<a href="#">Details ...</a>	12	-0.35	-0.98	0.468	1.000	1.000	140	tags=25%, list=10%, signal=28%
41	STRUCTURAL CONSTITUENT OF RIBOSOME	<a href="#">Details ...</a>	44	-0.25	-0.96	0.503	1.000	1.000	447	tags=41%, list=33%, signal=59%
42	CYTOSKELETON	<a href="#">Details ...</a>	73	-0.22	-0.96	0.531	1.000	1.000	186	tags=21%, list=14%, signal=23%
43	NUA4 HISTONE ACETYLTRANSFERASE COMPLEX	<a href="#">Details ...</a>	9	-0.38	-0.96	0.509	1.000	1.000	39	tags=22%, list=3%, signal=23%
44	RIBOSOME ASSEMBLY	<a href="#">Details ...</a>	10	-0.36	-0.95	0.502	1.000	1.000	134	tags=20%, list=10%, signal=22%
45	DNA RECOMBINATION	<a href="#">Details ...</a>	70	-0.22	-0.94	0.538	1.000	1.000	361	tags=37%, list=26%, signal=48%
46	ENZYME BINDING	<a href="#">Details ...</a>	29	-0.27	-0.94	0.540	1.000	1.000	224	tags=28%, list=16%, signal=32%
47	SECRETORY STRESS	<a href="#">Details ...</a>	12	-0.35	-0.94	0.524	1.000	1.000	239	tags=33%, list=17%, signal=40%
48	REGULATION OF TRANSPORT	<a href="#">Details ...</a>	33	-0.25	-0.93	0.554	1.000	1.000	279	tags=30%, list=20%, signal=37%
49	RIBOSOME	<a href="#">Details ...</a>	73	-0.21	-0.91	0.631	1.000	1.000	142	tags=14%, list=10%, signal=14%
50	TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER	<a href="#">Details ...</a>	26	-0.26	-0.91	0.607	1.000	1.000	327	tags=31%, list=24%, signal=40%
51	NUCLEOTIDYLTRANSFERASE ACTIVITY		28	-0.26	-0.91	0.621	1.000	1.000	299	tags=29%, list=22%, signal=36%
52	PROTEIN DEPHOSPHORYLATION		25	-0.27	-0.90	0.613	1.000	1.000	390	tags=40%, list=28%, signal=55%
53	TRANSLATIONAL ELONGATION		10	-0.34	-0.90	0.595	1.000	1.000	909	tags=100%, list=66%, signal=293%
54	CYTOPLASMIC TRANSLATION		43	-0.23	-0.90	0.610	1.000	1.000	134	tags=14%, list=10%, signal=15%
55	RESPONSE TO HEAT		35	-0.25	-0.90	0.636	0.992	1.000	102	tags=14%, list=7%, signal=15%

56	PROTEIN PHOSPHORYLATION		89	-0.20	-0.89	0.680	0.995	1.000	319	tags=30%, list=23%, signal=37%
57	PROTEIN MATURATION		16	-0.29	-0.88	0.613	0.991	1.000	120	tags=19%, list=9%, signal=20%
58	ENDOSOMAL TRANSPORT		45	-0.23	-0.88	0.665	0.980	1.000	336	tags=33%, list=24%, signal=43%
59	PROTEIN GLYCOSYLATION		27	-0.25	-0.88	0.648	0.969	1.000	105	tags=15%, list=8%, signal=16%
60	NUCLEOSOMAL PROTEIN COMPLEX		5	-0.43	-0.88	0.605	0.955	1.000	788	tags=100%, list=57%, signal=233%
61	CONJUGATION		48	-0.22	-0.87	0.700	0.952	1.000	255	tags=27%, list=19%, signal=32%
62	CYTOPLASMIC RIBOSOMAL LARGE SUBUNIT		22	-0.27	-0.87	0.647	0.940	1.000	59	tags=9%, list=4%, signal=9%
63	MEMBRANE FUSION		20	-0.27	-0.87	0.665	0.935	1.000	293	tags=40%, list=21%, signal=50%
64	NUCLEAR TRANSPORT		59	-0.21	-0.86	0.704	0.940	1.000	140	tags=15%, list=10%, signal=16%
65	CARBOHYDRATE TRANSPORT		10	-0.33	-0.86	0.619	0.927	1.000	432	tags=60%, list=31%, signal=87%
66	NUCLEIC ACID BINDING TRANSCRIPTION FACTOR ACTIVITY		62	-0.21	-0.85	0.750	0.922	1.000	265	tags=24%, list=19%, signal=29%
67	REGULATION OF TRANSLATION		30	-0.24	-0.85	0.670	0.911	1.000	498	tags=47%, list=36%, signal=72%
68	ORGANELLE INHERITANCE		23	-0.26	-0.85	0.700	0.899	1.000	313	tags=30%, list=23%, signal=39%
69	REGULATION OF DNA METABOLIC PROCESS		58	-0.21	-0.85	0.742	0.887	1.000	212	tags=19%, list=15%, signal=21%
70	LIPID TRANSPORT		15	-0.29	-0.85	0.712	0.875	1.000	363	tags=47%, list=26%, signal=63%
71	RNA CATABOLIC PROCESS		54	-0.21	-0.85	0.705	0.863	1.000	230	tags=22%, list=17%, signal=26%
72	GUANYL-NUCLEOTIDE EXCHANGE FACTOR ACTIVITY		14	-0.28	-0.80	0.747	0.943	1.000	275	tags=36%, list=20%, signal=44%
73	CELL WALL		10	-0.31	-0.80	0.715	0.931	1.000	266	tags=30%, list=19%, signal=37%
74	CELLULAR AMINO ACID METABOLIC PROCESS		26	-0.22	-0.77	0.829	0.977	1.000	113	tags=15%, list=8%, signal=16%

75	G1 TO S TRANSITION OF MITOTIC CELL CYCLE		17	-0.24	-0.74	0.808	1.000	1.000	508	tags=53%, list=37%, signal=83%
76	RIBOSOMAL SUBUNIT EXPORT FROM NUCLEUS		5	-0.35	-0.73	0.784	0.999	1.000	75	tags=20%, list=5%, signal=21%
77	HYDROLASE ACTIVITY, ACTING ON GLYCOSYL BONDS		7	-0.33	-0.73	0.799	0.989	1.000	94	tags=14%, list=7%, signal=15%
78	CARBOHYDRATE METABOLIC PROCESS		53	-0.18	-0.71	0.928	0.998	1.000	151	tags=11%, list=11%, signal=12%
79	TRANSFERASE ACTIVITY, TRANSFERRING GLYCOSYL GROUPS		27	-0.21	-0.71	0.878	0.991	1.000	409	tags=37%, list=30%, signal=52%
80	TRAVERSING START CONTROL POINT OF MITOTIC CELL CYCLE		7	-0.30	-0.70	0.831	0.983	1.000	225	tags=29%, list=16%, signal=34%
81	NUCLEOLUS		52	-0.17	-0.70	0.947	0.975	1.000	269	tags=21%, list=20%, signal=25%
82	OLIGOSACCHARIDE METABOLIC PROCESS		8	-0.28	-0.69	0.861	0.974	1.000	987	tags=100%, list=72%, signal=352%
83	TRANSCRIPTION FROM RNA POLYMERASE III PROMOTER		10	-0.27	-0.69	0.876	0.965	1.000	226	tags=30%, list=16%, signal=36%
84	UBIQUITIN-LIKE PROTEIN BINDING		27	-0.20	-0.69	0.912	0.956	1.000	434	tags=37%, list=32%, signal=53%
85	PROTEIN LIPIDATION		8	-0.28	-0.68	0.857	0.950	1.000	381	tags=50%, list=28%, signal=69%
86	NUCLEOBASE-CONTAINING COMPOUND TRANSPORT		44	-0.17	-0.66	0.952	0.957	1.000	321	tags=25%, list=23%, signal=32%
87	VACUOLE ORGANIZATION		31	-0.19	-0.66	0.936	0.946	1.000	311	tags=26%, list=23%, signal=33%
88	MITOCHONDRION ORGANIZATION		59	-0.15	-0.62	0.983	0.958	1.000	194	tags=12%, list=14%, signal=13%