Table: Gene sets enriched in phenotype *Mettl14 (3 samples)* **[plain text format]**

	Shorthand Name for Figure	Gene Set Name(collapsed to mouse orthologs)	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
2	Signature upregulated genes: invasive hepatoblastoma	CAIRO_LIVER_DEVELOPMENT_UP	Details ...	90	0.34	1.61	0	0.902	0.968	1236	tags=23%, list=12%, signal=26%
3	c-Myc targets: hepatocyte proliferation and regeneration	YU_MYC_TARGETS_UP	Details ...	27	0.44	1.66	0.016	0.983	0.931	481	tags=22%, list=5%, signal=23%
20		GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_UP	Details ...	18	0.44	1.46	0.075	0.693	1	1050	tags=28%, list=10%, signal=31%
4	signature upregulated HNF1A targets: hepatocellular carcinoma state	SERVITIA_LIVER_HNF1A_TARGETS_UP	Details ...	89	0.33	1.6	0	0.748	0.978	1062	tags=31%, list=11%, signal=35%
7	Sphingolipid metabolism	REACTOME_SPHINGOLIPID_METABOLISM	Details ...	54	0.34	1.5	0	0.791	0.998	562	tags=17%, list=6%, signal=18%
1	Fatty acid metabolism	WP_FATTY_ACID_BIOSYNTHESIS	Details ...	21	0.49	1.7	0.013	1	0.871	1692	tags=38%, list=17%, signal=46%
9	Mitochondrial fatty acid beta oxidation	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION	Details ...	34	0.39	1.51	0.021	0.835	0.997	1282	tags=26%, list=13%, signal=30%
19	PPAR signaling pathway	WP_PPAR_SIGNALING_PATHWAY	Details ...	58	0.3	1.31	0.061	0.821	1	1507	tags=29%, list=15%, signal=34%
6	signature upregulated HFN4A targets: hepatocellular carcinoma	CHIQUOIR_LIVER_HNF4A_TARGETS_DC	Details ...	27	0.4	1.48	0.066	0.676	0.999	1275	tags=37%, list=13%, signal=42%
40		REACTOME_FATTY_ACID_METABOLISM		119	0.24	1.16	0.085	0.837	1	1302	tags=22%, list=13%, signal=27%
11		WP_SPHINGOLIPID_METABOLISM_OVERVIEW	Details ...	16	0.44	1.38	0.107	0.963	1	486	tags=25%, list=5%, signal=26%
12		WP_SPHINGOLIPID_METABOLISM_INTEGRATED_PATHWAY	Details ...	16	0.44	1.38	0.11	0.887	1	486	tags=25%, list=5%, signal=26%
14		REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	Details ...	15	0.42	1.35	0.113	0.885	1	486	tags=20%, list=5%, signal=21%
28		WENG_POR_TARGETS_LIVER_UP		46	0.28	1.22	0.133	0.897	1	562	tags=17%, list=7%, signal=19%
22	Classic adipogenic targets of PPARG	WANG_CLASSIC_ADIPOGENIC_TARGETS_OF_PPARG		21	0.37	1.29	0.143	0.786	1	1412	tags=38%, list=14%, signal=44%
56	Nucleotide di and triphosphate conversion	REACTOME_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES		19	0.32	1.08	0.352	0.88	1	399	tags=16%, list=4%, signal=16%
79	RNA polymerase III transcription	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION		31	0.26	0.98	0.474	0.924	1	1273	tags=29%, list=13%, signal=33%
90	Metabolism of Nucleotides	REACTOME_METABOLISM_OF_NUCLEOTIDES		72	0.2	0.94	0.611	0.949	1	1618	tags=24%, list=16%, signal=28%
112	Nucleotide salvage	REACTOME_NUCLEOTIDE_SALVAGE		17	0.26	0.85	0.711	0.971	1	1200	tags=24%, list=12%, signal=27%
135	Trans-lesion synthesis by PolH, DNA damage repair	REACTOME_TRANSLESION_SYNTHESIS_BY_POLH		17	0.24	0.74	0.8	0.992	1	991	tags=18%, list=10%, signal=20%
129	rRNA processing in nucleolus and cytosol	REACTOME_MAJOR_PATHWAY_OF_RRNA_PROCESSING_IN_THE_NUCLEOLUS_AND_CYTOSOL		167	0.15	0.78	1	0.975	1	1524	tags=17%, list=15%, signal=20%
20		REACTOME_RECRUITMENT_OF_NUMA_TO_MITOTIC_CENTROSOMES	Details ...	64	0.3	1.31	0.051	0.785	1	628	tags=16%, list=6%, signal=17%
44		REACTOME_REGULATION_OF_PLK1_ACTIVITY_AT_G2_M_TRANSITION		66	0.26	1.15	0.177	0.799	1	991	tags=17%, list=10%, signal=18%
30		REACTOME_MISCELLANEOUS_TRANSPORT_AND_BINDING_EVENTS		16	0.36	1.15	0.249	0.769	1	707	tags=19%, list=7%, signal=20%
29		LAZARO_GENETIC_MOUSE_MODEL_HIGH_GRADE_LARGE_CELL_NEUROENDOCRINE_LUNG_CARCINOMA_DN		222	0.21	1.21	0	0.895	1	1541	tags=24%, list=15%, signal=28%
5		MCCLUNG_COCAINE_REWARD_5D	Details ...	38	0.4	1.59	0.013	0.62	0.981	349	tags=16%, list=3%, signal=16%
35		SOVLAN_MULTIPLE_MYELOMA_PCA3_UP	Details ...	58	0.31	1.35	0.029	0.861	1	1398	tags=31%, list=14%, signal=36%
13		REACTOME_CARDIAC_CONDUCTION	Details ...	29	0.37	1.38	0.051	0.843	1	1604	tags=31%, list=16%, signal=37%
8		CUI_TCF21_TARGETS_DN	Details ...	19	0.45	1.49	0.058	0.742	0.999	1150	tags=37%, list=11%, signal=41%
16		REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	Details ...	15	0.41	1.34	0.097	0.841	1	991	tags=27%, list=10%, signal=30%
24		WENG_POR_TARGETS_GLOBAL_DN		23	0.35	1.28	0.104	0.777	1	1302	tags=39%, list=13%, signal=45%
21		REACTOME_SYNTHESIS_OF_IP3_AND_IP4_IN_THE_CYTOSOL		15	0.4	1.3	0.115	0.8	1	1025	tags=33%, list=10%, signal=37%
17		WENG_POR_DOSAGE	Details ...	22	0.39	1.33	0.122	0.838	1	599	tags=27%, list=6%, signal=29%
27		REACTOME_AURKA_ACTIVATION_BY_TPX2		53	0.29	1.23	0.122	0.877	1	504	tags=13%, list=5%, signal=14%
18		GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_DN	Details ...	21	0.39	1.32	0.128	0.836	1	779	tags=29%, list=8%, signal=31%
47		SANSOM_APC_TARGETS_REQUIRE_MYC		155	0.22	1.15	0.143	0.754	1	1314	tags=21%, list=13%, signal=23%
26		REACTOME_SYNTHESIS_OF_PC		18	0.38	1.27	0.145	0.75	1	179	tags=11%, list=2%, signal=11%
34		MCCLUNG_CREB1_TARGETS_DN		40	0.3	1.19	0.155	0.865	1	95	tags=10%, list=1%, signal=10%
23		ZHENG_IL22_SIGNALING_DN		19	0.37	1.28	0.162	0.8	1	1368	tags=26%, list=14%, signal=30%
33		BURTON_ADIPOGENESIS_PEAK_AT_8HR		31	0.31	1.19	0.172	0.856	1	704	tags=19%, list=7%, signal=21%
39		CHEBOTAEV_GR_TARGETS_DN		58	0.26	1.17	0.177	0.797	1	664	tags=19%, list=7%, signal=20%
25		WP_EICOSANOID_METABOLISM_VIA_LIPOXYGENASES_LOX		17	0.39	1.27	0.18	0.777	1	615	tags=24%, list=6%, signal=25%
32		HEVNER_CORTEX_CAUDAL_SUBVENTRICULAR_ZONE		19	0.35	1.2	0.186	0.866	1	1045	tags=21%, list=10%, signal=23%
36		REACTOME_G_PROTEIN_MEDIATED_EVENTS		22	0.33	1.18	0.186	0.826	1	1025	tags=27%, list=10%, signal=30%
30		WANG_ADIPOGENIC_GENES_REPRESSED_BY_SIRT1		22	0.34	1.2	0.189	0.899	1	610	tags=18%, list=6%, signal=19%
38		REACTOME_GLYCOSPHINGOLIPID_CATABOLISM		25	0.33	1.18	0.197	0.817	1	562	tags=16%, list=6%, signal=17%
41		ZHENG_IL22_SIGNALING_UP		33	0.3	1.16	0.2	0.819	1	292	tags=12%, list=3%, signal=12%
35		WP_CHOLESTEROL_METABOLISM_WITH_BLOCH_AND_KANDUTSCH_RUSSELL_PATHWAYS		47	0.28	1.18	0.203	0.849	1	567	tags=17%, list=6%, signal=18%
31		REACTOME_METABOLISM_OF_COFACTORS		15	0.38	1.2	0.216	0.877	1	382	tags=20%, list=4%, signal=21%
37		TSENG_ADIPOGENIC_POTENTIAL_UP		38	0.35	1.18	0.239	0.817	1	1395	tags=44%, list=14%, signal=51%
43		REACTOME_FORMATION_OF_THE_BETA_CATENIN_TCF_TRANSACTIVATING_COMPLEX		17	0.36	1.16	0.244	0.791	1	909	tags=30%, list=9%, signal=39%
48		ZHANG_GATA6_TARGETS_DN		24	0.32	1.15	0.246	0.743	1	1147	tags=29%, list=11%, signal=33%
52		WP_PRIMARY_FOCAL_SEGMENTAL_GLOMERULOSCLEROSIS_FSGS		45	0.26	1.1	0.254	0.872	1	364	tags=9%, list=4%, signal=9%
57		YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_11		92	0.22	1.07	0.26	0.912	1	1412	tags=18%, list=14%, signal=21%
49		HU_GENOTOXIN_ACTION_DIRECT_VS_INDIRECT_4HR		23	0.33	1.14	0.273	0.754	1	1	tags=4%, list=0%, signal=4%
45		BIOCARTA_CCR5_PATHWAY		15	0.37	1.15	0.294	0.785	1	1287	tags=40%, list=13%, signal=46%
51		MCCLUNG_DELTA_FOSB_TARGETS_2WK		23	0.32	1.11	0.297	0.824	1	1190	tags=30%, list=12%, signal=34%
53		REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS		25	0.3	1.09	0.304	0.892	1	1154	tags=28%, list=11%, signal=32%
42		REACTOME_AZATHIOPRINE_ADME		17	0.37	1.16	0.308	0.805	1	1598	tags=41%, list=16%, signal=49%
54		TERAMOTO_OPN_TARGETS_CLUSTER_6		16	0.34	1.08	0.313	0.899	1	471	tags=25%, list=5%, signal=26%
59		WORSCHECH_TUMOR_REJECTION_UP		24	0.29	1.05	0.313	0.943	1	757	tags=17%, list=7%, signal=18%
50		NADLER_OBESITY_DN		45	0.27	1.12	0.323	0.824	1	848	tags=24%, list=8%, signal=27%
55		REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDUCED_SENESCENCE		16	0.36	1.08	0.326	0.896	1	257	tags=13%, list=3%, signal=13%
58		REACTOME_SIGNAL_AMPLIFICATION		19	0.31	1.05	0.368	0.943	1	1425	tags=47%, list=14%, signal=55%
60		REACTOME_OPIOID_SIGNALLING		37	0.26	1.04	0.368	0.982	1	1025	tags=27%, list=10%, signal=30%
61		HEVNER_INTERMEDIATE_ZONE_AND_UP_POSTMITOTIC_NEURONS		21	0.31	1.03	0.389	1	1	689	tags=14%, list=7%, signal=15%
62		WP_GPCRS_ODORANT		17	0.32	1.02	0.398	1	1	1294	tags=53%, list=24%, signal=69%
65		WP_PURINE_METABOLISM		108	0.2	1.01	0.404	1	1	1618	tags=26%, list=16%, signal=31%
68		GROSS_HYPOXIA_VIA_ELK3_ONLY_DN		31	0.26	1	0.435	0.986	1	1287	tags=26%, list=13%, signal=29%
67		WENG_POR_TARGETS_GLOBAL_UP		22	0.29	1.01	0.436	0.998	1	848	tags=23%, list=8%, signal=25%
70		RAMPON_ENRICHED_LEARNING_ENVIRONMENT_LATE_UP		15	0.32	1	0.44	0.976	1	440	tags=13%, list=4%, signal=14%
85		REACTOME_IKK_COMPLEX_RECRUITMENT_MEDIATED_BY_RIP1		18	0.3	0.96	0.441	0.917	1	991	tags=17%, list=10%, signal=18%
69		NADLER_HYPERGLYCEMIA_AT_OBESITY		38	0.25	1	0.451	0.978	1	1575	tags=32%, list=16%, signal=37%
66		BERENJENO_TRANSFORMED_BY_RHOA_FOREVER_UP		19	0.3	1.01	0.452	1	1	593	tags=21%, list=6%, signal=22%
77		WP_MITOCHONDRIAL_LONG_CHAIN_FATTY_ACID_BETA_OXIDATION		16	0.3	0.99	0.453	0.933	1	610	tags=19%, list=6%, signal=20%
78		SERVITIA_ILET_HNF1A_TARGETS_UP		88	0.21	1	0.459	0.965	1	1233	tags=22%, list=12%, signal=24%
72		REACTOME_GLYCOSPHINGOLIPID_METABOLISM		31	0.27	1	0.46	0.956	1	562	tags=13%, list=6%, signal=14%
73		REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CELL_CYCLE_GENES		23	0.28	0.99	0.462	0.959	1	193	tags=13%, list=2%, signal=13%
74		HOLLERN_SQUAMOUS_BREAST_TUMOR		38	0.25	0.99	0.463	0.956	1	1716	tags=34%, list=17%, signal=41%
75		MARSHALL_VIRAL_INFECTION_RESPONSE_DN		17	0.31	0.99	0.463	0.946	1	1280	tags=29%, list=13%, signal=34%
83		REACTOME_SIGNALING_BY_HIPPO		19	0.29	0.97	0.465	0.915	1	172	tags=11%, list=2%, signal=11%
63		BOYLAN_MULTIPLE_MYELOMA_C_DN		43	0.24	1.02	0.466	0.987	1	1270	tags=28%, list=13%, signal=32%
84		REACTOME_MITOTIC_PROMETAPHASE		129	0.2	1.02	0.468	0.977	1	825	tags=13%, list=8%, signal=14%
80		HEVNER_CORTICAL_PLATE_POSTMITOTIC_PROJECTION_NEURONS		52	0.23	0.98	0.468	0.924	1	101	tags=9%, list=1%, signal=9%
81		BIOCARTA_EDG1_PATHWAY		17	0.3	0.97	0.468	0.93	1	555	tags=18%, list=5%, signal=19%
82		RAO_BOUND_BY_SALL4_ISOFORM_A		101	0.2	0.97	0.475	0.924	1	938	tags=14%, list=9%, signal=15%
84		DARWICHE_PAPILLOMA_PROGRESSION_RISK		37	0.24	0.97	0.494	0.914	1	1092	tags=24%, list=11%, signal=27%
89		REACTOME_SYNTHESIS_OF_VERY_LONG_CHAIN_FATTY_ACYL_COAS		15	0.31	0.94	0.494	0.957	1	993	tags=27%, list=10%, signal=30%
78		REACTOME_RAC3_GTPASE_CYCLE		61	0.22	0.98	0.508	0.93	1	1104	tags=16%, list=11%, signal=18%
76		REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS		23	0.29	0.99	0.522	0.939	1	1115	tags=26%, list=11%, signal=29%
87		REACTOME_CA2_PATHWAY		25	0.26	0.95	0.542	0.936	1	1133	tags=28%, list=11%, signal=31%
86		NABA_ECM_AFFILIATED		52	0.22	0.96	0.571	0.937	1	498	tags=12%, list=5%, signal=12%
91		WP_EICOSANOID_METABOLISM_VIA_CYCLOOXYGENASES_COX		16	0.29	0.91	0.581	1	1	1721	tags=36%, list=17%, signal=43%
88		REACTOME_MUSCLE_CONTRACTION		51	0.22	0.94	0.59	0.957	1	1604	tags=24%, list=16%, signal=28%
101		HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_UP		15	0.28	0.88	0.6	0.996	1	2199	tags=53%, list=22%, signal=68%
97		DAWSON_METHYLATED_IN_LYMPHOMA_TCL1		21	0.26	0.9	0.607	1	1	7464	tags=100%, list=74%, signal=382%
94		GERHOLD_ADIPOGENESIS_UP		42	0.22	0.91	0.608	1	1	1154	tags=24%, list=11%, signal=27%
93		REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS		23	0.26	0.91	0.619	1	1	1114	tags=22%, list=11%, signal=24%
105		BIOCARTA_G1_PATHWAY		17	0.27	0.88	0.62	0.972	1	652	tags=18%, list=6%, signal=19%
104		BIOCARTA_CASPASE_PATHWAY		17	0.27	0.88	0.623	0.976	1	2126	tags=53%, list=21%, signal=67%
96		SCHUNGEMANN_SKIN_CARCINOGENESIS_TPA_DN		17	0.28	0.9	0.624	1	1	607	tags=18%, list=6%, signal=19%
99		WP_GLUTATHIONE_METABOLISM		15	0.28	0.89	0.628	0.997	1	520	tags=13%, list=5%, signal=14%
100		ISHIDA_E2F_TARGETS		31	0.24	0.89	0.629	1	1	346	tags=13%, list=3%, signal=13%
111		MATZUK_SPERMATID_DIFFERENTIATION		19	0.25	0.86	0.636	0.987	1	533	tags=11%, list=5%, signal=11%
95		REACTOME_BASE_EXCISION_REPAIR		25	0.25	0.9	0.644	1	1	516	tags=12%, list=5%, signal=13%
98		REACTOME_PEROXISOMAL_LIPID_METABOLISM		24	0.26	0.89	0.651	0.998	1	1765	tags=42%, list=17%, signal=50%
107		WP_TRACYLGLYCERINE_SYNTHESIS		18	0.26	0.88	0.651	0.964	1	1213	tags=22%, list=12%, signal=25%
103		LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_SMALL_VS_HUGE_UP		32	0.24	0.88	0.658	0.978	1	1520	tags=20%, list=15%, signal=23%
114		REACTOME_RESOLUTION_OF_D_LOOP_STRUCTURES		16	0.28	0.85	0.659	0.957	1	2053	tags=44%, list=20%, signal=55%
119		REACTOME_FANCONI_ANEMIA_PATHWAY		20	0.24	0.83	0.672	0.972	1	1065	tags=20%, list=11%, signal=22%
110		KAMINNGA_E2H2_TARGETS		29	0.23	0.86	0.674	0.968	1	316	tags=10%, list=3%, signal=11%
106		REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYTHESIS		38	0.22	0.88	0.675	0.971	1	874	tags=18%, list=9%, signal=20%
92		WP_CYTOPLASMIC_RIBOSOMAL_PROTEINS		77	0.2	0.91	0.688	1	1	6994	tags=96%, list=69%, signal=[illegible]
124		REACTOME_POLYMERASE_SWITCHING_ON_THE_C_STRAND_OF_THE_TELOMERE		17	0.25	0.81	0.702	0.962	1	1114	tags=24%, list=11%, signal=26%
115		REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM		26	0.23	0.85	0.706	0.954	1	646	tags=12%, list=6%, signal=12%
116		REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM		15	0.26	0.84	0.715	0.977	1	1154	tags=27%, list=11%, signal=30%
113		REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM		29	0.23	0.85	0.718	0.964	1	695	tags=17%, list=7%, signal=18%
121		REACTOME_ION_HOMEOSTASIS		21	0.24	0.83	0.726	0.959	1	1505	tags=29%, list=15%, signal=34%
122		REACTOME_PURINE_CATABOLISM		15	0.26	0.82	0.73	0.964	1	7463	tags=100%, list=74%, signal=382%
118		REACTOME_GLUTATHIONE_CONJUGATION		29	0.23	0.83	0.735	0.969	1	848	tags=17%, list=8%, signal=19%
117		SHETH_LIVER_CANCER_VS_TINIP_LOSS_PAM5		35	0.21	0.83	0.736	0.973	1	1535	tags=29%, list=15%, signal=34%
109		REACTOME_RND1_GTPASE_CYCLE		29	0.22	0.86	0.741	0.976	1	1620	tags=31%, list=16%, signal=37%
108		COATES_MACROPHAGE_M1_VS_M2_UP		64	0.19	0.87	0.755	0.96	1	890	tags=14%, list=9%, signal=15%
123		REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES		25	0.22	0.82	0.759	0.962	1	1505	tags=28%, list=15%, signal=33%
102		BURTON_ADIPOGENESIS_3		59	0.19	0.88	0.794	0.987	1	1443	tags=20%, list=14%, signal=24%
134		BIOCARTA_HDAC_PATHWAY		17	0.23	0.74	0.795	0.997	1	1687	tags=29%, list=17%, signal=35%
126		REACTOME_HDR_THROUGH_HOMOLOGOUS_RECOMBINATION_HRR		33	0.21	0.81	0.799	0.957	1	2053	tags=33%, list=20%, signal=42%
125		WP_FATTY_ACID_BETA_OXIDATION		29	0.21	0.81	0.801	0.956	1	1028	tags=17%, list=10%, signal=19%
128		MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3		24	0.22	0.79	0.802	0.979	1	469	tags=13%, list=5%, signal=13%
131		SCHRAETS_MLL_TARGETS_DN		21	0.22	0.76	0.833	0.993	1	1198	tags=19%, list=12%, signal=22%
133		MESSINA_BRAIN_HCP_WITH_H3K27ME3		56	0.2	0.74	0.834	1	1	1126	tags=17%, list=11%, signal=19%
136		REACTOME_HSF1_DEPENDENT_TRANSACTIVATION		17	0.23	0.74	0.836	0.985	1	1294	tags=24%, list=13%, signal=27%
120		REACTOME_NONSENSE_MEDIATED_DECAY_NMD_INDEPENDENT_OF_THE_EXON_JUNCTION_COMPLEX_EJC		86	0.17	0.83	0.864	0.967	1	8350	tags=100%, list=83%, signal=572%
138		REACTOME_METABOLISM_OF_PORPHYRINS		25	0.2	0.71	0.872	1	1	1674	tags=32%, list=17%, signal=38%
130		CHEBOTAEV_GR_TARGETS_UP		45	0.18	0.77	0.883	0.986	1	984	tags=13%, list=10%, signal=15%
127		LEIN_PONS_MARKERS		41	0.19	0.79	0.887	0.979	1	1056	tags=15%, list=10%, signal=16%
132		REACTOME_PKMTS_METHYLATE_HISTONE_LYSINES		37	0.19	0.76	0.89	0.99	1	1392	tags=24%, list=14%, signal=28%
139		REACTOME_TRANSLESION_SYNTHESIS_BY_POLK		16	0.22	0.7	0.897	1	1	991	tags=19%, list=10%, signal=21%
137		WP_ALZHEIMER_39_S_DISEASE		50	0.17	0.74	0.916	0.979	1	762	tags=10%, list=8%, signal=11%
142		REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES		15	0.2	0.61	0.935	1	1	589	tags=13%, list=6%, signal=14%
140		BRDEAU_IMPRINTED_GENES		27	0.18	0.67	0.949	1	1	945	tags=15%, list=9%, signal=16%
141		WP_STATIN_PATHWAY		18	0.19	0.62	0.962	1	1	1464	tags=22%, list=14%, signal=26%
143		REACTOME_GAP_FILLING_DNA_REPAIR_SYNTHESIS_AND_LIGATION_IN_GG_NER		17	0.18	0.6	0.962	1	1	1114	tags=18%, list=11%, signal=20%
145		REACTOME_CONDENSATION_OF_PROPHASE_CHROMOSOMES		15	0.19	0.57	0.974	1	1	2418	tags=47%, list=24%, signal=61%
144		REACTOME_RUNX1_REGULATES_GENES_INVOLVED_IN_MEGAKARYOCYTE_DIFFERENTIATION_AND_PLATELET_FUNCTION		25	0.16	0.59	0.985	1	1	1747	tags=28%, list=17%, signal=34%
149		REACTOME_ONCOGENE_INDUCED_SENESCENCE		15	0.17	0.53	0.988	1	1	1930	tags=27%, list=19%, signal=33%
147		JIANG_AGING_CEREBRAL_CORTEX_UP		28	0.15	0.54	0.989	1	1	1280	tags=14%, list=13%, signal=16%
150		REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS		52	0.14	0.52	0.994	1	1	1657	tags=22%, list=16%, signal=26%
146		REACTOME_SULFUR_AMINO_ACID_METABOLISM		24	0.16	0.55	0.995	1	1	7432	tags=96%, list=74%, signal=[illegible]
148		WP_TOLL_LIKE_RECEPTOR_SIGNALING		26	0.15	0.54	1	1	1	8586	tags=100%, list=85%, signal=665%
151		REACTOME_RECOGNITION_OF_DNA_DAMAGE_BY_PCNA_CONTAINING_REPLICATION_COMPLEX		23	0.14	0.49	1	1	1	8707	tags=100%, list=86%, signal=727%
152		REACTOME_INTERFERON_ALPHA_BETA_SIGNALING		17	0.14	0.46	1	0.999	1	5719	tags=88%, list=57%, signal=[illegible]

Table: Gene sets enriched in phenotype *WT (3 samples)* *[plain text format]*

	Shorthand name for figure	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
1	Apoptosis downregulated HBF1A targets hepatocellular carcinoma dats	Details	199	-0.53	-1.68	0	0.65	0.629	2864	tags=41%, list=22%,
2	Transcriptional activation, liver regeneration and autophagy	Details	49	-0.72	-1.67	0	0.195	0.725	2710	tags=59%, list=21%,
3	Pattern cell surface receptors: Elevation of transforms patients leading to widespread fibrosis	Details	22	-0.78	-1.78	0	0.166	0.592	1853	tags=64%, list=14%,
4	Assembly of collagen fibrils	Details	19	-0.85	-1.75	0.003	0.221	0.718	1819	tags=68%, list=14%,
5	PRMT4 regulates liver mass response defects	Details	19	-0.81	-1.75	0.003	0.166	0.721	2416	tags=72%, list=18%,
6	IL6 pathway: impaired liver regeneration	Details	18	-0.84	-1.74	0	0.165	0.738	2648	tags=72%, list=20%,
7	MET signaling, Hepatocyte growth factor receptor	Details	18	-0.84	-1.74	0.003	0.172	0.776	2864	tags=72%, list=22%,
8	Metabolism of steroid hormones	Details	19	-0.82	-1.68	0.001	0.171	0.955	1561	tags=63%, list=12%,
119	Lysosome vesicle biogenesis		19	-0.52	-1.47	0.047	0.9	1	1738	tags=47%, list=13%,
119	Activation of insulin-like Growth Factor (IGF) transport and uptake by insulin-like Growth Factor Binding Proteins (IGFBPs)		76	-0.42	-1.46	0.026	0.327	1	2998	tags=49%, list=30%,
120	Fanconi Anemia Pathway FOS Binding Partners: Activation of apoptosis in bone marrow precursors		19	-0.96	-1.34	0.034	0.41	1	2745	tags=84%, list=21%,
121	Genetic downregulated genes: mouse and metastatic hepatoblastoma	Details	190	-0.45	-1.73	0	0.167	0.831	2437	tags=51%, list=19%,
122	Genetic downregulated HPMA targets hepatocellular carcinoma	Details	190	-0.45	-1.73	0	0.147	0.906	2604	tags=51%, list=21%,
123	PTEN regulation		37	-0.65	-1.6	0	0.208	0.999	2710	tags=81%, list=21%,
124	Recycling of bile acids and salts		19	-0.52	-1.23	0.143	0.428	1	1453	tags=47%, list=11%,
166	Transport of bile salts		34	-0.41	-1.25	0.155	0.493	1	2378	tags=38%, list=24%,
140	Synthesis of bile acid salts via 7 alpha hydroxycholesterol		20	-0.43	-1.2	0.22	0.548	1	3437	tags=45%, list=34%,
174	Bile acid and bile salt metabolism		34	-0.37	-1.13	0.1	0.835	1	3437	tags=35%, list=34%,
125	mRNA decay by 5'-to-3'-exoribonuclease		31	-0.63	-1.49	0.014	0.261	0.998	2864	tags=71%, list=22%,
126	Deadenylation dependent mRNA decay		49	-0.48	-1.49	0.008	0.271	1	2806	tags=51%, list=21%,
127	Deadenylation of mRNA		21	-0.55	-1.53	0.031	0.287	1	2693	tags=62%, list=21%,
128	AuU Rich 3D Binding: degradation of mRNAs		20	-0.4	-1.39	0.049	0.493	1	2604	tags=45%, list=21%,
163	Processing of intronless pre-mRNAs		18	-0.49	-1.5	0.065	0.445	1	2639	tags=50%, list=21%,
162	Processing of capped intron-containing pre-mRNA		24	-0.33	-1.23	0.141	0.463	1	3499	tags=42%, list=28%,
399	AU-rich element binding proteins: mRNA destabilization		72	-0.35	-1.24	0.157	0.5	1	3000	tags=40%, list=36%,
114	RNA Polymerase I transcription		41	-0.39	-1.22	0.182	0.53	1	2111	tags=34%, list=17%,
117	mRNA splicing		84	-0.32	-1.2	0.18	0.552	1	3000	tags=29%, list=24%,
118	RNA polymerase II transcription termination		50	-0.35	-1.17	0.234	0.587	1	2222	tags=34%, list=18%,
121	Sumoylation of RNA binding proteins		36	-0.38	-1.16	0.289	0.607	1	1567	tags=39%, list=13%,
151	mRNA processing		102	-0.29	-1.14	0.144	0.616	1	2710	tags=31%, list=21%,
23	Proteasome degradation		47	-0.52	-1.67	0	0.165	0.971	2710	tags=51%, list=21%,
80	Circadian clock peripheral genes		15	-0.57	-1.74	0	0.305	1	2710	tags=60%, list=21%,
101	Autophagy processing: Ubiquitination & Proteasome degradation		23	-0.59	-1.49	0	0.352	1	2791	tags=48%, list=21%,
98	Degradation of extracellular matrix		34	-0.53	-1.49	0.002	0.179	0.977	2221	tags=47%, list=17%,
99	Inflammatory response		20	-0.47	-1.61	0.003	0.206	0.998	1886	tags=40%, list=14%,
69	Gap junction trafficking and regulation: hepatocyte cell cycle regulation		21	-0.55	-1.54	0.031	0.286	1	999	tags=57%, list=8%,
100	Adaptive immune system		455	-0.18	-1.45	0	0.279	1	3499	tags=21%, list=28%,
102	Collagen degradation		22	-0.55	-1.49	0.036	0.28	1	1821	tags=45%, list=15%,
133	Degradation of mitotic proteins in late mitosis / early G1 phase		69	-0.43	-1.44	0.033	0.35	1	2710	tags=42%, list=21%,
132	G1-S phase transition		139	-0.32	-1.28	0.08	0.481	1	2710	tags=36%, list=21%,
169	Regulation of lipid metabolism by PPAR alpha		13	-0.47	-1.19	0.369	0.568	1	756	tags=39%, list=7%, signal=22%
57	L1 activation	Details	17	-0.57	-1.74	0	0.164	0.737	2710	tags=59%, list=21%,
58	Notch signaling: inhibition of hepatic stellate cell activation to myofibroblasts	Details	19	-0.56	-1.68	0.005	0.174	0.945	1561	tags=26%, list=9%, signal=27%
59	EGF pathway: amelioration of liver fibrosis		20	-0.57	-1.65	0.008	0.195	0.998	2648	tags=45%, list=20%,
60	PDGF signaling		20	-0.57	-1.65	0	0.195	1	2648	tags=45%, list=20%,
61	Pluripotency associated mechanisms		203	-0.4	-1.53	0	0.284	1	2111	tags=32%, list=17%,
62	ABC protein family mediated transport: bile salt transport		23	-0.44	-1.43	0.008	0.288	1	3499	tags=52%, list=28%,
193	Cargo targeting to cilia: Hedgehog signaling and liver development		15	-0.59	-1.49	0.039	0.272	1	2416	tags=60%, list=24%,
63	MAPK family signaling cascades		21	-0.54	-1.49	0	0.292	1	2710	tags=33%, list=21%,
64	Dedifferentiation: inhibition of hepatic stellate cell activation to myofibroblasts		18	-0.58	-1.45	0.004	0.372	1	2783	tags=39%, list=22%,
153	Intracellular signaling by second messengers		179	-0.38	-1.41	0.003	0.364	1	2726	tags=35%, list=21%,
154	Hedgehog ligand biogenesis		18	-0.56	-1.45	0.007	0.405	1	2710	tags=52%, list=21%,
155	Hedgehog on state		63	-0.37	-1.37	0.112	0.475	1	2600	tags=48%, list=18%,
156	Vesicle mediated transport: hepatocellular bile secretion		235	-0.31	-1.27	0.033	0.548	1	2600	tags=35%, list=18%,
157	Signaling by hedgehog		84	-0.32	-1.11	0.304	0.66	1	3690	tags=44%, list=26%,
67	Regulation of PTEN stability and activity		51	-0.47	-1.74	0	0.232	1	2710	tags=37%, list=21%,
68	Notch signaling: inhibition of hepatic stellate cell activation to myofibroblasts	Details	19	-0.56	-1.68	0	0.157	0.941	2556	tags=26%, list=19%, signal=27%
70	FOXO family targets up		20	-0.55	-1.56	0	0.407	1	2632	tags=35%, list=20%,
71	MAPK6/MAPK4 signaling		18	-0.55	-1.49	0.003	0.493	1	2600	tags=35%, list=18%,
72	Mitotic G1-G1/S phases		179	-0.33	-1.29	0.061	0.448	1	2644	tags=35%, list=18%,
73	Cell cycle checkpoints	Details	17	-0.68	-1.8	0.001	0.169	0.487	2556	tags=47%, list=19%,
74	CIDS5 HYPOXIA VIA ELK3 AND HIF1A DN		88	-0.45	-1.6	0.001	0.21	0.998	1887	tags=55%, list=14%,
75	REDINESVER RAS SIGNALING NOT VIA ATM DN		19	-0.72	-1.72	0.008	0.201	0.995	2591	tags=21%, list=19%,
76	REACTOME TRANSPORT OF SMALL MOLECULES		379	-0.33	-1.5	0.008	0.445	1	1966	tags=35%, list=14%,
77	REACTOME INFLAMMATORY RESPONSE AND CHOLESTEROL UP		21	-0.48	-1.52	0.01	0.25	1	2636	tags=41%, list=21%,
78	REACTOME REGULATION OF RUNX2 EXPRESSION AND ACTIVITY		18	-0.44	-1.49	0.033	0.26	1	3600	tags=33%, list=26%,
136	REACTOME UBIQUITIN MEDIATED DEGRADATION OF PHOSPHORYLATED CIC[25]		46	-0.45	-1.43	0.039	0.349	1	2710	tags=43%, list=21%,
193	REACTOME ACTIVATION OF ARC C CDC20 ARC C CDC20 MEDIATED DEGRADATION OF NE/MITIC PROTEINS		66	-0.41	-1.38	0.041	0.396	1	2710	tags=41%, list=21%,
171	SHETH LIVER CANCER VS TANP LOSS PAM3		51	-0.45	-1.42	0.044	0.363	1	1817	tags=40%, list=14%,
165	REACTOME TRANSCRIPTIONAL REGULATION BY RUNX2		61	-0.41	-1.36	0.067	0.408	1	2710	tags=41%, list=21%,
172	REACTOME PIWI PRN MEDIATED MITOPHAGY		23	-0.5	-1.38	0.07	0.412	1	2632	tags=43%, list=20%,
166	REACTOME HEDGEHOG OFF STATE		74	-0.35	-1.18	0.253	0.669	1	3600	tags=35%, list=18%,
196	REACTOME GENE SILENCING BY RNA		30	-0.38	-1.11	0.309	0.657	1	3987	tags=33%, list=19%,
224	REACTOME ACTIVATION OF THE MRNA UPON BINDING OF THE CAP BINDING COMPLEX AND EIFS AMP SUBSTITUENT BINDING TO 43S		17	-0.33	-1.08	0.504	0.684	1	4335	tags=47%, list=33%, signal=48%
160	REACTOME TRANSPORT OF MATURE MRNAS DERIVED FROM INTRONLESS TRANSCRIPTS		17	-0.35	-1.07	0.38	0.712	1	2029	tags=27%, list=20%, signal=29%
170	TAUCH HEDGEHOG SIGNALING PARACRINE DN		84	-0.31	-1.04	0.418	0.737	1	3444	tags=31%, list=17%,
219	REACTOME SYNTHESIS OF BILE ACIDS AND BILE SALTS		26	-0.36	-1.04	0.424	0.728	1	1192	tags=46%, list=9%,
164	REACTOME RNA POLYMERASE II PRE TRANSCRIPTION EVENTS		66	-0.28	-0.98	0.481	0.779	1	3807	tags=36%, list=19%,
163	HP DYSREGULATED MRNA TARGETING IN INSULIN PI3K AKT SIGNALING		23	-0.34	-0.97	0.414	0.861	1	1821	tags=39%, list=15%,
162	REACTOME PROCESSING OF CAPPED INTRONLESS PRE MRNA		23	-0.33	-0.97	0.421	0.851	1	2029	tags=39%, list=20%,
161	REACTOME TISTETBAPPOLIN TTP AFF4 BINDS AND DESTABILIZES MRNAS		23	-0.37	-0.97	0.451	0.851	1	2556	tags=39%, list=19%,
167	REACTOME FORMATION OF RNA POL II ELONGATION COMPLEX		66	-0.3	-0.96	0.568	0.893	1	3336	tags=33%, list=17%,
187	REACTOME MRNA CAPPING		23	-0.32	-0.94	0.505	0.893	1	3131	tags=13%, list=8%, signal=13%
164	REACTOME TRANSCRIPTIONAL REGULATION BY SMALL RNAS		55	-0.31	-0.91	0.606	0.837	1	3345	tags=16%, list=18%,
181	REACTOME NUCLEAR TRANSLOCATION OF SHIP1 WHICH INHIBITS NFAT		15	-0.35	-0.91	0.614	0.836	1	1193	tags=16%, list=6%,
182	REACTOME POSITIVE EPIGENETIC REGULATION OF RRNA EXPRESSION		46	-0.31	-0.89	0.604	0.862	1	3987	tags=39%, list=19%,
1024	REACTOME MRNA SPLICING MINOR PATHWAY		21	-0.27	-0.86	0.706	0.872	1	3104	tags=38%, list=17%,
1024	U6 SPLICING VIA NOVA2		21	-0.29	-0.84	0.758	0.856	1	2618	tags=33%, list=14%,
1078	REACTOME RNA POLYMERASE III TRANSCRIPTION INITIATION FROM TYPE 3 PROMOTER		24	-0.29	-0.82	0.728	0.901	1	775	tags=17%, list=6%, signal=18%
1096	REACTOME RNA POLYMERASE III TRANSCRIPTION INITIATION FROM TYPE 1 PROMOTER		25	-0.28	-0.81	0.745	0.907	1	775	tags=16%, list=6%, signal=17%
1097	TAUCH HEDGEHOG SIGNALING PARACRINE UP		82	-0.24	-0.81	0.774	0.909	1	3234	tags=24%, list=17%,
1081	REACTOME RNA POLYMERASE I TRANSCRIBES RRNA GENES		21	-0.24	-0.79	0.804	0.902	1	3104	tags=24%, list=17%,
1125	REACTOME RNA POLYMERASE II PROMOTER ESCAPE		61	-0.25	-0.79	0.804	0.915	1	712	tags=13%, list=2%, signal=13%
1205	REACTOME TRANSPORT OF THE SLIM DERIVEDMAT MATURE MRNA		21	-0.23	-0.69	0.807	0.945	1	3134	tags=14%, list=17%,
1252	HP SPLICING FACTOR NOVA REGULATED SYNAPTIC PROTEINS		26	-0.22	-0.65	0.893	0.972	1	2992	tags=12%, list=16%,
1257	REACTOME FGFR3 ALTERNATIVE SPLICING		15	-0.21	-0.6	0.877	0.987	1	2104	tags=13%, list=11%,
46	CHEN HDAC8 TARGETS DN	Details	109	-0.47	-1.68	0	0.175	0.963	2591	tags=54%, list=21%,
48	CIDS5 HYPOXIA VIA ELK3 DN		119	-0.45	-1.61	0	0.203	0.998	2556	tags=51%, list=19%,
49	REACTOME CLASS I MHC MEDIATED ANTIGEN PROCESSING PRESENTATION		17	-0.7	-1.75	0.001	0.209	1	2591	tags=59%, list=21%,
50	TAKEDA TYRO3 TARGETS 1 UP	Details	17	-0.66	-1.71	0.001	0.15	0.993	2195	tags=59%, list=17%,
205	MARTINEZ RB1 TARGETS UP		19	-0.45	-1.61	0.001	0.468	1	2648	tags=53%, list=20%,
41	REACTOME ANTIGEN PROCESSING CROSS PRESENTATION		68	-0.5	-1.68	0.002	0.168	0.965	2710	tags=50%, list=21%,
42	TAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 5		19	-0.61	-1.67	0.002	0.153	0.981	2591	tags=58%, list=19%,
46	HARKEY RB1 AQUTE LOF DN		109	-0.4	-1.5	0.002	0.21	1	2718	tags=45%, list=21%,
82	REACTOME METABOLISM OF POLYAMINES		64	-0.49	-1.6	0.003	0.21	0.999	2710	tags=51%, list=21%,
132	JAVIN FOXP3 TARGETS CLUSTER 14		24	-0.6	-1.44	0.003	0.292	1	2591	tags=58%, list=19%,
132	REACTOME NEOVOLCIN		179	-0.38	-1.44	0.003	0.361	1	2669	tags=34%, list=19%,
13	CUNI BERRIOS TO HIF TRANSLOCAL UP	Details	17	-0.65	-1.72	0.004	0.168	0.995	672	tags=35%, list=5%, signal=41%
14	HP BONE CHRONIC CARCINOMA	Details	15	-0.66	-1.71	0.004	0.167	0.988	1996	tags=27%, list=14%,
21	REACTOME MULTIPLE MYELOMA PCA1 UP		19	-0.65	-1.71	0.004	0.239	1	2591	tags=58%, list=19%,
22	REACTOME EXTRACELLULAR MATRIX ORGANIZATION		109	-0.43	-1.53	0.004	0.253	1	1993	tags=41%, list=14%,
112	ZHENG FOXP3 TARGETS IN THYMUS UP		68	-0.38	-1.43	0.004	0.362	1	2172	tags=41%, list=15%,
25	DAGOUAUDO LYMPHOMA BY GC STAGE UP		19	-0.55	-1.66	0.005	0.182	0.979	2591	tags=47%, list=19%,
26	GUILLAUMOND KIF10 TARGETS UP		20	-0.55	-1.66	0.005	0.2	0.995	2693	tags=45%, list=20%,
28	REACTOME INTRINSIC PATHWAY	Details	17	-0.57	-1.65	0.005	0.2	0.995	1993	tags=41%, list=14%,
29	REACTOME DOWNSTREAM TCR SIGNALING		21	-0.45	-1.55	0.005	0.365	1	2710	tags=43%, list=21%,
30	TUO TARGETS OF JRK1 AND JRK2		19	-0.41	-1.51	0.006	0.33	1	3437	tags=31%, list=34%,
117	GRKERSMANN RESPONSE TO MC AND SERUM DEPRIVATION UP		119	-0.39	-1.48	0.005	0.33	1	2137	tags=31%, list=16%,
12	REACTOME NOTCH OTHER CWCS	Details	21	-0.62	-1.72	0.006	0.187	0.992	2639	tags=48%, list=21%,
125	REACTOME INTRINSIC PATHWAY UP	Details	19	-0.58	-1.69	0.006	0.173	0.993	2314	tags=47%, list=18%,
126	BROWN MYELOID CELL DEVELOPMENT UP		119	-0.4	-1.45	0.006	0.34	1	2293	tags=41%, list=18%,
127	KOETSCHMAN TRM24 TARGETS UP		21	-0.41	-1.48	0.007	0.249	1	2314	tags=52%, list=18%,
128	TAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 5		21	-0.61	-1.68	0.008	0.19	0.992	2690	tags=48%, list=20%,
33	REACTOME ELASTIC FIBER FORMATION		19	-0.47	-1.58	0.008	0.269	1	2591	tags=47%, list=19%,
34	HP DELTA NOTCH SIGNALING PATHWAY		68	-0.47	-1.58	0.008	0.269	1	1886	tags=47%, list=14%,
35	REACTOME UB SPECIFIC PROCESSING PROTEASES		19	-0.4	-1.48	0.009	0.342	1	2718	tags=45%, list=21%,
36	BAUMANN MLL AF6 FUSION TARGETS C UP		17	-0.43	-1.48	0.009	0.392	1	2718	tags=41%, list=21%,
39	REACTOME ER PHAGOSOME PATHWAY		17	-0.63	-1.67	0.01	0.17	0.971	2520	tags=41%, list=19%,
135	BOGARTA AGR TARGETS		19	-0.61	-1.66	0.01	0.183	0.988	2591	tags=47%, list=19%,
41	HADLER OBSRT3 UP		19	-0.48	-1.53	0.01	0.263	0.998	2718	tags=42%, list=21%,
42	REACTOME TCR SIGNALING		64	-0.44	-1.5	0.01	0.264	1	2172	tags=41%, list=15%,
43	BRUNA IUO RESPONSE MIDDLE		64	-0.44	-1.49	0.01	0.264	1	2171	tags=41%, list=15%,
107	REACTOME PGF CE PATHWAY		17	-0.44	-1.48	0.01	0.363	1	2638	tags=41%, list=21%,
47	ALI TAF2 TARGETS UP		19	-0.44	-1.48	0.011	0.292	0.998	2591	tags=42%, list=19%,
48	REACTOME PLATELET AGGREGATION PLUG FORMATION		68	-0.55	-1.6	0.011	0.215	1	2652	tags=52%, list=20%,
104	CHIBA GRM7 HERVIS HOST DISEASE SRG DN		19	-0.65	-1.7	0.011	0.277	1	1799	tags=47%, list=13%,
122	HP EGFR1 SIGNALING PATHWAY		19	-0.4	-1.45	0.011	0.322	1	2875	tags=41%, list=21%,
123	REACTOME METABOLISM OF AMINO ACIDS AND DERIVATIVES		109	-0.32	-1.32	0.011	0.406	1	2127	tags=31%, list=15%,
124	GRKERSMANN APOPTOSIS BY SERUM DEPRIVATION UP		109	-0.32	-1.32	0.011	0.45	1	2047	tags=31%, list=15%,
58	REACTOME EDN PROTEOGLYCANS		19	-0.6	-1.62	0.012	0.199	0.995	1811	tags=47%, list=13%,
59	WAN AIR SIGNALING DN		19	-0.4	-1.45	0.012	0.269	1	2591	tags=35%, list=19%,
60	REACTOME RHOBTB GTPase CYCLE		32	-0.53	-1.55	0.012	0.269	1	1321	tags=41%, list=9%,
62	CONDOTTA CDR1 TARGETS		19	-0.57	-1.65	0.013	0.266	0.998	2626	tags=47%, list=19%,
63	REACTOME NON INTEGRIN MEMBRANE ECM INTERACTIONS		19	-0.63	-1.65	0.014	0.187	0.987	1846	tags=58%, list=14%,
64	HP TYPE 3 INTERFERON SIGNALING ENG		19	-0.4	-1.45	0.014	0.362	1	2147	tags=41%, list=15%,
145	WANG GATA3 TARGETS UP		109	-0.4	-1.45	0.014	0.366	1	2636	tags=41%, list=21%,
179	REACTOME CELLULAR RESPONSE TO CHEMICAL STRESS		19	-0.38	-1.4	0.014	0.369	1	2710	tags=35%, list=21%,
65	WAYANG PROSTATE CANCER PROGRESSION UP		19	-0.4	-1.45	0.015	0.197	0.996	2591	tags=35%, list=19%,
66	REACTOME G ALPHA Q SIGNALLING EVENTS		68	-0.44	-1.49	0.015	0.392	1	2231	tags=41%, list=17%,
68	REACTOME DEGRADATION OF AXIN		68	-0.44	-1.49	0.015	0.287	1	2710	tags=41%, list=21%,
148	REACTOME FC EPSILON RECEPTOR FCER1 SIGNALING		68	-0.4	-1.45	0.016	0.365	1	2992	tags=41%, list=20%,
149	TAO BOURD BY SALL4		19	-0.37	-1.4	0.016	0.362	1	2591	tags=35%, list=19%,
69	REACTOME SIGNALING BY ERBB2		68	-0.52	-1.58	0.017	0.261	1	2636	tags=51%, list=21%,
70	BOGARTA TPO PATHWAY		21	-0.54	-1.55	0.017	0.286	1	2648	tags=57%, list=20%,
71	TAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 1		19	-0.4	-1.45	0.017	0.289	1	2591	tags=35%, list=19%,
127	REACTOME HDH PROTEINASES		72	-0.43	-1.44	0.017	0.339	1	2690	tags=41%, list=20%,
151	MARTINEZ RB1 AND TP53 TARGETS UP		68	-0.32	-1.45	0.017	0.492	1	3690	tags=35%, list=20%,
152	REACTOME SIGNALING BY FGFR		65	-0.51	-1.56	0.018	0.271	1	2697	tags=51%, list=20%,
153	TODAO SECRETOME OF LUNG CANCER AND ENDOTHELIUM		21	-0.44	-1.49	0.018	0.29	1	2012	tags=41%, list=15%,
92	REACTOME ANTIGEN PRESENTATION FOLDING ASSEMBLY AND PEPTIDE LOADING OF CLASS I MHC		24	-0.55	-1.55	0.019	0.26	1	2314	tags=62%, list=18%,
93	BOGARTA TPT PATHWAY		24	-0.58	-1.53	0.019	0.289	1	1213	tags=67%, list=9%,
195	ZENG GU ICB CONTROL METAGENE 31 PREDICTIVE ICB RESISTANCE		68	-0.46	-1.46	0.019	0.299	1	2657	tags=47%, list=20%,
196	BURDEVKAVUD BRN CARCINOGENESIS DN		19	-0.45	-1.45	0.019	0.277	1	2591	tags=47%, list=19%,
200	MARTINEZ RB1 AND TP53 TARGETS DN		109	-0.32	-1.25	0.019	0.492	1	2044	tags=31%, list=15%,
89	HESS TARGETS OF HOXA9 AND MEIS1 UP		68	-0.47	-1.47	0.02	0.296	1	2591	tags=47%, list=19%,
154	KANDOA HEMATOPOIESIS STEM CELL		109	-0.4	-1.41	0.02	0.363	1	1977	tags=35%, list=14%,
157	CARLSON TGFB1 TARGETS DN		107	-0.34	-1.28	0.02	0.458	1	2591	tags=35%, list=19%,
87	REACTOME RHOJ GTPASE CYCLE		32	-0.52	-1.55	0.021	0.26	1	1321	tags=41%, list=9%,
88	MCDOWELL ACUTE LUNG INJURY UP		24	-0.51	-1.55	0.021	0.291	1	2314	tags=42%, list=18%,
89	BOGARTA IL5 PATHWAY		19	-0.4	-1.45	0.021	0.269	1	2591	tags=35%, list=19%,
90	HP IL 7 SIGNALING PATHWAY		21	-0.49	-1.5	0.022	0.296	1	739	tags=27%, list=5%, signal=29%
108	LEE AGING NEOCORTEX UP		68	-0.44	-1.49	0.022	0.344	1	2710	tags=41%, list=21%,
41	CHEN B CELL LYMPHOMA CLUSTER 2		19	-0.6	-1.55	0.023	0.36	1	1987	tags=47%, list=14%,
111	REACTOME REGULATION OF RAS BY GAPS		21	-0.44	-1.47	0.023	0.317	1	2591	tags=47%, list=19%,
166	HP FOCAL ADHESION		109	-0.38	-1.38	0.023	0.4	1	2745	tags=41%, list=21%,
168	LANDIS ERBB2 BREAST TUMORS 324 UP		19	-0.38	-1.36	0.024	0.386	1	2231	tags=41%, list=17%,
224	BIENG BOUND BY PRKRA		19	-0.38	-1.36	0.024	0.491	1	2591	tags=41%, list=19%,
225	REACTOME MET PROMOTES CELL MOTILITY		65	-0.58	-1.58	0.025	0.262	1	2679	tags=51%, list=20%,
80	REACTOME ENDOGENOUS STEROLS		19	-0.4	-1.45	0.025	0.269	1	1325	tags=35%, list=9%,
80	REACTOME FORMATION OF FIBRIN CLOT CLOTTING CASCADE		24	-0.53	-1.5	0.025	0.292	1	2640	tags=50%, list=20%,
81	REACTOME PEPTIDE LIGAND BINDING RECEPTORS		61	-0.45	-1.48	0.025	0.292	1	2733	tags=41%, list=21%,
112	LEE AGING CEREBELLUM UP		61	-0.44	-1.48	0.025	0.355	1	2319	tags=41%, list=21%,
176	ZENG GU ICB CONTROL METAGENE 42 PREDICTIVE ICB RESISTANCE		19	-0.38	-1.36	0.025	0.455	1	2617	tags=35%, list=20%,
75	WAN AIR SIGNALING UP		19	-0.4	-1.45	0.026	0.304	1	2591	tags=35%, list=19%,
79	REACTOME EPH EPHRIN SIGNALING		68	-0.49	-1.51	0.026	0.361	1	2654	tags=51%, list=20%,
142	REACTOME SIGNALING BY THE B CELL RECEPTOR BCR		68	-0.44	-1.49	0.026	0.365	1	2654	tags=41%, list=20%,
84	ISLANDER RSPH SENSITIVE VIA TBX2		68	-0.52	-1.5	0.027	0.298	1	1886	tags=51%, list=14%,
85	WANG TARGETS OF MLL CBP FUSION UP		19	-0.4	-1.4	0.027	0.395	1	2591	tags=41%, list=19%,
158	REACTOME FCER1 MEDIATED NF KB ACTIVATION		68	-0.41	-1.47	0.027	0.364	1	2710	tags=41%, list=21%,
87	REACTOME DRP32 INTERACTIONS		32	-0.54	-1.5	0.028	0.292	1	2636	tags=51%, list=21%,
91	WEN NEURON MARKERS		19	-0.53	-1.48	0.028	0.292	1	2591	tags=51%, list=19%,
181	REACTOME DEATH RECEPTOR SIGNALING		109	-0.39	-1.38	0.028	0.388	1	2654	tags=41%, list=20%,
130	HP IL 5 SIGNALING PATHWAY		19	-0.4	-1.45	0.029	0.363	1	2591	tags=41%, list=19%,
187	KIM GUSF TARGETS UP		32	-0.43	-1.43	0.029	0.363	1	2636	tags=41%, list=21%,
73	BOGARTA EL5VEC PATHWAY		21	-0.53	-1.45	0.031	0.319	1	2319	tags=43%, list=17%,
109	HUNTLEY RUNX2 TARGETS DN		19	-0.53	-1.45	0.031	0.392	1	2657	tags=35%, list=20%, signal=51%
110	REACTOME SIGNALING BY NTRK1 TRKA		19	-0.38	-1.42	0

135			CHENG FOXP3 TARGETS IN T LYMPHOCYTE DN	61	-0.48	-1.45	0.039	0.35	1	2806		logp=5%, fdr=22%,
156			REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_END_SOSOMES	44	-0.44	-1.41	0.039	0.358	1	2710		logp=45%, fdr=27%, signal=42%
116			REACTOME_EGFR_DOWNREGULATION	18	-0.54	-1.46	0.04	0.35	1	438		logp=15%, fdr=35%, signal=17%
169			LAMMERICH SKIN CANCER PROGRESSION UP	64	-0.42	-1.4	0.04	0.371	1	3148		logp=5%, fdr=23%,
299			REACTOME_SIGNALING_BY_INTERLEUKINS	176	-0.35	-1.3	0.04	0.434	1	2806		logp=3%, fdr=23%,
161			MORIYAN PUBERTAL TGFB1 TARGETS DN	51	-0.46	-1.39	0.043	0.393	1	3344		logp=4%, fdr=23%,
169			ZENG SU IGB CONTROL METAGENE 35 PREDICTIVE IGB RESPONSE	63	-0.39	-1.36	0.044	0.41	1	2878		logp=4%, fdr=24%,
75			REACTOME EPH EPHRIN MEDIATED REPULSION OF CELLS	13	-0.6	-1.52	0.045	0.384	1	928		logp=33%, fdr=3%, signal=37%
188			REACTOME_CELL_CELL_COMMUNICATION	54	-0.43	-1.4	0.045	0.368	1	2707		logp=4%, fdr=21%,
184			REACTOME_DEGRADATION OF BETA CATENIN BY THE DESTRUCTION COMPLEX	72	-0.4	-1.37	0.046	0.388	1	2710		logp=3%, fdr=21%,
247			CHENG GLIOBLASTOMA PLASTICITY UP	129	-0.37	-1.34	0.046	0.414	1	3340		logp=2%, fdr=24%,
268			GOLDRATH ANTIGEN RESPONSE	139	-0.33	-1.28	0.046	0.465	1	2646		logp=1%, fdr=25%,
195			BRUNS IAV RESPONSE VIA TP53 GROUP 0	74	-0.39	-1.3	0.047	0.438	1	3346		logp=2%, fdr=24%,
195			BIOCARTA MAPK PATHWAY	45	-0.42	-1.3	0.049	0.438	1	2498		logp=2%, fdr=24%,
283			ZHENG RESTETIME OF LUNG CANCER AND FIBROBLAST	112	-0.36	-1.31	0.049	0.429	1	3206		logp=1%, fdr=21%,
180			LABRIE BREAST CANCER PROGRESSION UP	62	-0.46	-1.4	0.05	0.368	1	2363		logp=4%, fdr=21%,
187			JACKSON DIMKT1 TARGETS UP	61	-0.41	-1.38	0.05	0.366	1	3160		logp=4%, fdr=21%,
215			REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	65	-0.41	-1.36	0.05	0.408	1	3495		logp=4%, fdr=18%, signal=27%
291			TAO HOXA10 TARGETS VIA PROGESTERONE UP	170	-0.41	-1.35	0.05	0.368	1	1130		logp=2%, fdr=21%,
264			TAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 16	61	-0.44	-1.4	0.051	0.369	1	2907		logp=4%, fdr=22%,
190			SHAOSHI AHC TARGETS	71	-0.38	-1.3	0.052	0.415	1	3097		logp=2%, fdr=24%,
230			REACTOME MHC CLASS II ANTIGEN PRESENTATION	112	-0.36	-1.29	0.052	0.459	1	2661		logp=1%, fdr=22%,
213			REACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	286	-0.32	-1.22	0.052	0.531	1	2935		logp=0%, fdr=12%,
124			RYAN HYPOXIAMPS 22Q11 DELETION DN	18	-0.54	-1.45	0.053	0.398	1	2956		logp=2%, fdr=22%,
182			MARTINEZ TP53 TARGETS DN	180	-0.31	-1.19	0.053	0.568	1	3346		logp=0%, fdr=33%,
138			REACTOME_SIGNALING_BY_EGFR	54	-0.47	-1.42	0.055	0.353	1	3124		logp=4%, fdr=21%,
264			REACTOME_STABILIZATION OF P53	61	-0.41	-1.38	0.055	0.369	1	2710		logp=4%, fdr=21%,
215			TAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 3	61	-0.4	-1.36	0.056	0.407	1	3140		logp=4%, fdr=18%,
175			LEIN MIDBRAIN MARKERS	64	-0.44	-1.38	0.056	0.353	1	2661		logp=4%, fdr=22%,
138			REACTOME SELECTIVE AUTOPHAGY	48	-0.43	-1.38	0.056	0.384	1	2738		logp=4%, fdr=21%,
182			REACTOME DEGRADATION OF DVL	54	-0.42	-1.38	0.056	0.397	1	2710		logp=4%, fdr=21%,
128			REACTOME BINDING AND UPTAKE OF LIGANDS BY SCAVENGER RECEPTORS	28	-0.49	-1.44	0.057	0.355	1	1296		logp=3%, fdr=21%,
227			REACTOME_CELL_JUNCTION_ORGANIZATION	73	-0.44	-1.4	0.057	0.377	1	3306		logp=2%, fdr=21%,
178			REACTOME P75 NTR RECEPTOR MEDIATED SIGNALLING	61	-0.42	-1.38	0.057	0.401	1	2854		logp=4%, fdr=21%,
114			REACTOME_INTEGRIN_SIGNALING	18	-0.51	-1.41	0.058	0.398	1	2707		logp=2%, fdr=22%,
318			PLASARI TGFB1 TARGETS 10HR DN	164	-0.35	-1.28	0.058	0.452	1	3304		logp=0%, fdr=13%,
184			MORIYAN PUBERTAL BREAST 6 7WK DN	180	-0.31	-1.18	0.059	0.387	1	1330		logp=0%, fdr=23%,
182			WP INTERFERON MEDIATED CELL ADHESION	61	-0.41	-1.37	0.059	0.405	1	2817		logp=4%, fdr=21%,
187			WP OXIDATIVE DAMAGE RESPONSE	72	-0.46	-1.4	0.06	0.366	1	976		logp=3%, fdr=10%,
211			REACTOME_TRANSPORT TO THE GOLGI AND SUBSEQUENT MODIFICATION	118	-0.35	-1.29	0.06	0.452	1	3306		logp=1%, fdr=18%,
160			REACTOME_NCAM_SIGNALING FOR NEURITE OUT GROWTH	55	-0.42	-1.39	0.061	0.368	1	3321		logp=4%, fdr=18%,
181			STEARMAN LUNG CANCER EARLY VS LATE DN	61	-0.44	-1.4	0.061	0.409	1	2661		logp=4%, fdr=22%,
229			REACTOME_SIGNALING BY NTRK1 TRKA	80	-0.4	-1.36	0.061	0.459	1	3304		logp=1%, fdr=22%, signal=20%
324			GROSS HYPOXIA VIA ELK3 UP	158	-0.34	-1.28	0.061	0.468	1	2313		logp=0%, fdr=12%,
275			BOHLMAN MULTIPLE MYELOMA C D DN	139	-0.34	-1.28	0.061	0.48	1	3340		logp=1%, fdr=12%,
144			LA MENI TARGETS	13	-0.56	-1.42	0.062	0.368	1	2633		logp=2%, fdr=22%,
180			REREMENO RCK1 SIGNALING NOT VIA RHOA DN	61	-0.41	-1.36	0.062	0.398	1	3321		logp=4%, fdr=21%,
181			ZENG SU IGB CONTROL METAGENE 44 PREDICTIVE IGB RESPONSE	117	-0.35	-1.31	0.062	0.43	1	1806		logp=2%, fdr=21%,
181			REACTOME_SIGNALING BY EGFR	61	-0.39	-1.29	0.062	0.485	1	2710		logp=1%, fdr=18%,
310			REACTOME_RUNX1 RUNX3 BOUND MEF	164	-0.32	-1.25	0.062	0.518	1	3143		logp=0%, fdr=11%,
146			REACTOME_RUNX1_INTERACTS_WITH_CO_FACTORS_WHOSE_PRECISE_EFFECT_ON_RUNX1_TARGETS_IS_NOT_KNOWN	20	-0.49	-1.42	0.063	0.365	1	1530		logp=3%, fdr=15%,
151			KASLER HDAC7 TARGETS 2 DN	61	-0.51	-1.41	0.063	0.366	1	3192		logp=3%,
181			REACTOME DNA REPLICATION PRE INITIATION	61	-0.41	-1.36	0.063	0.407	1	2710		logp=4%, fdr=21%,
166			BIOCARTA RGS7 PATHWAY	28	-0.5	-1.4	0.064	0.368	1	2648		logp=3%, fdr=22%,
268			SEKI INFLAMMATORY RESPONSE LPS UP	139	-0.35	-1.28	0.064	0.412	1	3340		logp=1%, fdr=21%,
148			REACTOME_DOWNREGULATION OF ERBB2 SIGNALING	13	-0.56	-1.44	0.065	0.354	1	148		logp=2%, fdr=1%, signal=20%
193			FREEMAN EGR TARGETS UP	61	-0.41	-1.4	0.065	0.372	1	3304		logp=4%, fdr=21%,
313			REACTOME_DEVELOPMENTAL BIOLOGY	164	-0.34	-1.29	0.065	0.459	1	3113		logp=0%, fdr=12%,
143			GROSS HYPOXIA VIA ELK3 ONLY UP	23	-0.5	-1.42	0.067	0.364	1	3197		logp=2%, fdr=22%,
181			REACTOME GS9 IS PHOSPHORYLATED BY DYRK1B BY THE PROTEASOME	61	-0.41	-1.36	0.068	0.407	1	2800		logp=4%, fdr=21%,
284			FOSTER KDM1A TARGETS UP	64	-0.37	-1.31	0.068	0.427	1	3245		logp=3%, fdr=21%,
181			ZHANG BREAST CANCER PROGENITORS DN	61	-0.38	-1.28	0.069	0.462	1	2338		logp=1%, fdr=21%,
166			BIOCARTA EPO PATHWAY	17	-0.54	-1.41	0.07	0.366	1	2648		logp=3%, fdr=22%,
181			REACTOME_TRANSLOCATION OF THE CDK9 FAMILY	61	-0.41	-1.36	0.07	0.4	1	2710		logp=4%, fdr=21%,
253			REACTOME_THE NRAGE UBIQUITIN LIGASE COMPLEX DIRECTS ALK DEGRADATION	61	-0.4	-1.35	0.07	0.423	1	2710		logp=4%, fdr=21%,
253			ZEMEK IMMUNE CHECKPOINT BLOCKADE OVARIAN CANCER RENCA UP	61	-0.42	-1.35	0.072	0.411	1	2869		logp=4%, fdr=21%,
181			MORIYAN PUBERTAL BREAST 5 6WK DN	61	-0.38	-1.27	0.072	0.472	1	3321		logp=1%, fdr=21%,
213			GAVIN FOXP3 TARGETS CLUSTER P2	61	-0.44	-1.36	0.073	0.41	1	3297		logp=3%, fdr=22%,
246			REACTOME_NUCLEAR_EVENTS_MEDIATED_BY_NFE2L2	61	-0.41	-1.34	0.073	0.415	1	3340		logp=2%, fdr=21%,
265			REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	74	-0.39	-1.33	0.074	0.441	1	2864		logp=1%, fdr=22%,
168			ZHENG IRF1 TARGETS DN	61	-0.37	-1.3	0.074	0.455	1	2707		logp=2%, fdr=22%,
169			REACTOME_G TYPE I TYPE IV PHTN RECEPTORS CLRS	61	-0.37	-1.3	0.074	0.451	1	3347		logp=2%, fdr=22%,
171			STEARMAN TUMOR FIELD EFFECT UP	30	-0.46	-1.4	0.076	0.368	1	2682		logp=4%, fdr=21%,
174			BRACHAT RESPONSE TO CAMPTOTHECIN UP	55	-0.41	-1.38	0.076	0.402	1	3132		logp=3%, fdr=21%,
244			REACTOME_ARYSMERBC_LOCALIZATION_OF_PCP_PROTEINS	55	-0.41	-1.34	0.076	0.416	1	3276		logp=2%, fdr=21%,
246			CASTELLANO NRAS TARGETS UP	61	-0.41	-1.34	0.076	0.414	1	3340		logp=2%, fdr=21%,
268			WP ESC PLURIPOTENCY PATHWAY	61	-0.38	-1.29	0.076	0.454	1	898		logp=1%, fdr=15%,
181			LEE AGING MUSCLE UP	61	-0.46	-1.41	0.077	0.373	1	3310		logp=2%, fdr=21%,
169			BASHI RESPONSE TO IONIZING RADIATION 3	64	-0.37	-1.3	0.078	0.441	1	3356		logp=2%, fdr=21%,
237			ZEMEK IMMUNE CHECKPOINT BLOCKADE OVARIAN CANCER OVBLAP UP	69	-0.42	-1.34	0.079	0.407	1	2869		logp=4%, fdr=21%,
268			MEDA MIR1 TARGETS UP	61	-0.41	-1.34	0.081	0.406	1	3037		logp=4%, fdr=22%,
182			NABA MATRISOME	229	-0.31	-1.18	0.081	0.582	1	3268		logp=0%, fdr=33%,
173			REACTOME_CARGO_CONCENTRATION_IN_THE_ER	61	-0.48	-1.38	0.082	0.378	1	3341		logp=4%, fdr=18%,
166			JOHANSSON BRAIN CANCER EARLY VS LATE DN	61	-0.44	-1.38	0.082	0.397	1	2792		logp=4%, fdr=21%,
181			REACTOME_CARGO_RECOGNITION_FOR_CLATHRIN_MEDIATED_ENDOCYTOSIS	61	-0.38	-1.31	0.082	0.455	1	2710		logp=1%, fdr=21%,
253			MAYLA DIRAS12 TARGETS DN	112	-0.35	-1.29	0.082	0.484	1	3163		logp=1%, fdr=18%,
232			LEE TARGETS OF PTCH1 AND SUFU UP	58	-0.44	-1.35	0.083	0.407	1	3872		logp=3%, fdr=21%,
181			REACTOME APC C MEDIATED DEGRADATION OF CELL CYCLE PROTEINS	61	-0.38	-1.3	0.083	0.493	1	2710		logp=1%, fdr=21%,
181			REACTOME_MACROAUTOPHAGY	55	-0.36	-1.29	0.083	0.469	1	3245		logp=1%, fdr=21%,
243			CHARADONNA NEOPLASTIC TRANSFORMATION XRAS CDC25 DN	61	-0.43	-1.34	0.084	0.416	1	3389		logp=2%, fdr=21%,
187			BURTON ADIPOGENESIS 12	61	-0.41	-1.33	0.084	0.42	1	2806		logp=2%, fdr=22%,
212			LEE AGING MUSCLE DN	61	-0.41	-1.33	0.084	0.411	1	3037		logp=2%, fdr=22%,
206			BIOCARTA KERATINOCYTE PATHWAY	61	-0.44	-1.34	0.085	0.458	1	2710		logp=2%, fdr=21%,
273			REACTOME MAPK6 MAPK4 SIGNALING	63	-0.39	-1.32	0.085	0.425	1	2710		logp=2%, fdr=21%,
181			WANG TUMOR INVASIVENESS DN	136	-0.33	-1.23	0.085	0.52	1	2724		logp=0%, fdr=12%,
293			CHENG GLIOBLASTOMA PLASTICITY DN	58	-0.46	-1.35	0.086	0.404	1	3389		logp=3%, fdr=21%,
246			NICOLAU OCEAN REWIRED 49K	61	-0.41	-1.33	0.086	0.413	1	3303		logp=2%, fdr=21%,
245			REACTOME_CLATHRIN MEDIATED ENDOCYTOSIS	106	-0.36	-1.27	0.086	0.476	1	2890		logp=1%, fdr=22%,
214			REACTOME_CELLULAR RESPONSES TO STRESS1	61	-0.4	-1.31	0.086	0.456	1	3106		logp=2%, fdr=21%,
177			GROSS ELK3 TARGETS UP	61	-0.5	-1.36	0.088	0.403	1	3327		logp=4%, fdr=18%,
256			BIOCARTA NUCLEARRS PATHWAY	28	-0.47	-1.36	0.088	0.402	1	3352		logp=4%, fdr=18%,
180			MARSON FOXP3 TARGETS UP	61	-0.4	-1.31	0.088	0.424	1	3946		logp=2%, fdr=24%,
288			REACTOME_TRANSPORT OF MATURE TRANSCRIPT TO CYTOPLASM	58	-0.39	-1.31	0.088	0.427	1	3222		logp=2%, fdr=22%,
187			WP IL 9 SIGNALING PATHWAY	61	-0.41	-1.32	0.088	0.417	1	3347		logp=2%, fdr=21%,
254			JIANG AGING CEREBRAL CORTEX DN	61	-0.43	-1.35	0.09	0.406	1	3406		logp=1%, fdr=24%,
181			NUS TIF2 TARGETS UP	61	-0.49	-1.39	0.091	0.368	1	3106		logp=4%, fdr=21%,
319			REACTOME EPHB MEDIATED FORWARD SIGNALING	61	-0.48	-1.38	0.091	0.407	1	2661		logp=4%, fdr=21%,
280			MORI PRE B LYMPHOCYTE DN	164	-0.39	-1.31	0.091	0.429	1	3336		logp=2%, fdr=21%,
189			NABA CORE MATRISOME	144	-0.35	-1.28	0.091	0.469	1	2535		logp=1%, fdr=22%,
181			BIOCARTA NGF PATHWAY	18	-0.52	-1.38	0.092	0.398	1	3648		logp=3%, fdr=21%,
199			REACTOME_FCERI_MEDIATED_MAPK_ACTIVATION	61	-0.4	-1.3	0.092	0.398	1	2806		logp=2%, fdr=21%,
260			LEE AGING NEOCORTEX DN	61	-0.45	-1.37	0.092	0.368	1	3260		logp=3%, fdr=22%,
181			WP DNA DAMAGE METABOLISM	61	-0.41	-1.32	0.092	0.456	1	3347		logp=2%, fdr=21%,
286			HOUSTIS ROS	61	-0.41	-1.34	0.092	0.414	1	3892		logp=2%, fdr=21%,
181			CHIBA GRAFT VERSUS HOST DISEASE 930 UP	136	-0.35	-1.24	0.092	0.491	1	2930		logp=0%, fdr=12%,
280			DEMERSMAN APOPTOSIS BY SERUM DEPRIVATION DN	61	-0.34	-1.27	0.092	0.502	1	2830		logp=1%, fdr=21%,
181			LEE AGING CEREBELLUM DN	57	-0.44	-1.34	0.093	0.412	1	3781		logp=2%, fdr=21%,
187			REACTOME CELL DEATH SIGNALLING VIA NRAGE NRIF AND NADE	61	-0.41	-1.32	0.093	0.422	1	3304		logp=2%, fdr=21%,
269			WANG TUMOR INVASIVENESS UP	146	-0.3	-1.16	0.093	0.566	1	3611		logp=0%, fdr=18%,
270			WP ALPHA 6 BETA 4 INTEGRIN SIGNALING PATHWAY	61	-0.42	-1.33	0.094	0.435	1	2710		logp=2%, fdr=21%,
144			REACTOME_ASSEMBLY OF THE PRE REPLICATIVE COMPLEX	61	-0.37	-1.27	0.094	0.478	1	2710		logp=1%, fdr=21%,
189			STEGER ADIPOGENESIS UP	18	-0.52	-1.36	0.095	0.393	1	952		logp=3%, fdr=3%, signal=34%
270			REACTOME_SIGNALING BY ALK	61	-0.47	-1.37	0.095	0.407	1	2697		logp=3%, fdr=21%,
214			REACTOME SCF SKP2 MEDIATED DEGRADATION OF P27 P21	55	-0.39	-1.29	0.095	0.453	1	2710		logp=1%, fdr=21%,
142			BIOGRID_SIH TARGETS UP	61	-0.36	-1.27	0.095	0.472	1	3106		logp=1%, fdr=21%,
179			REACTOME_BIMOLECULAR_OF_INTRACELLULAR_RECEPTORS	18	-0.51	-1.35	0.096	0.369	1	3992		logp=3%, fdr=21%,
211			REACTOME_SIGNAL_TRANSDUCTION BY L1	61	-0.41	-1.31	0.096	0.41	1	3269		logp=2%, fdr=21%,
181			REACTOME CYCLIN A CDK2 ASSOCIATED EVENTS AT S PHASE ENTRY	61	-0.39	-1.3	0.096	0.439	1	2710		logp=2%, fdr=21%,
282			BIOCARTA EGM PATHWAY	18	-0.5	-1.34	0.098	0.411	1	1313		logp=2%, fdr=21%,
211			BLANDES INFLAMMOSIN SENSITIVE VIA TBK1 AND TBK2	61	-0.39	-1.31	0.098	0.427	1	3245		logp=2%, fdr=21%,
265			ZENG SU IGB CONTROL METAGENE 8 PREDICTIVE IGB RESPONSE	57	-0.39	-1.3	0.098	0.446	1	3946		logp=2%, fdr=24%,
266			GAVIN FOXP3 TARGETS CLUSTER P7	61	-0.39	-1.29	0.098	0.446	1	3340		logp=1%, fdr=21%,
197			REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS	7	-0.52	-1.37	0.1	0.402	1	924		logp=24%, fdr=6%, signal=26%
197			REACTOME COMMON PATHWAY OF FIBRIN CLOT FORMATION	11	-0.53	-1.35	0.1	0.403	1	1530		logp=17%, fdr=15%,
284			PID INTEGRIN2 RESPONSE NETWORK	61	-0.42	-1.32	0.101	0.413	1	2710		logp=2%, fdr=21%,
297			CHESLER BRAIN QTL CIS	202	-0.4	-1.3	0.101	0.436	1	3128		logp=0%, fdr=21%,
313			BOCHKIS FOXA2 TARGETS	393	-0.3	-1.16	0.101	0.594	1	3472		logp=0%, fdr=33%,
224			BASHI NPM1 TARGETS	18	-0.53	-1.35	0.102	0.404	1	3321		logp=2%, fdr=21%,
264			SORLAK LIVER CANCER EGF UP	55	-0.43	-1.32	0.102	0.423	1	2231		logp=2%, fdr=22%,
247			GAVIN FOXP3 TARGETS CLUSTER T7	61	-0.38	-1.28	0.102	0.481	1	3235		logp=1%, fdr=21%,
269			REACTOME METABOLISM OF STEROIDS	61	-0.36	-1.25	0.102	0.468	1	3437		logp=1%, fdr=21%,
237			REACTOME INTERLEUKIN 2 FAMILY SIGNALING	61	-0.52	-1.39	0.103	0.406	1	2697		logp=4%, fdr=21%,
260			BIOCARTA P38MAPK PATHWAY	61	-0.47	-1.32	0.104	0.413	1	2710		logp=2%, fdr=21%,
271			MARSON FOXP3 TARGETS DN	38	-0.43	-1.32	0.105	0.426	1	2649		logp=2%, fdr=21%,
224			TOROSIAN TARGETS OF DNSR1 FLI1 FUSION UP	173	-0.33	-1.22	0.105	0.527	1	3372		logp=0%, fdr=12%,
325			CAMORA NOS2 TARGETS DN	71	-0.38	-1.28	0.107	0.468	1	3406		logp=0%, fdr=33%,
330			REACTOME TRANSCRIPTIONAL REGULATION BY RUNX3	61	-0.38	-1.28	0.107	0.468	1	3710		logp=0%, fdr=18%,
187			REACTOME BETA CATENIN INDEPENDENT WNT SIGNALING	64	-0.36	-1.26	0.107	0.485	1	2836		logp=1%, fdr=21%,
281			NABA ECM REGULATORS	61	-0.35	-1.24	0.107	0.487	1	3009		logp=1%, fdr=21%,
270			BURTON ADIPOGENESIS 4	55	-0.43	-1.32	0.108	0.424	1	3346		logp=4%, fdr=21%,
337			REACTOME MEMBRANE TRAFFICKING	205	-0.3	-1.15	0.108	0.607	1	3596		logp=0%, fdr=33%,
283			MCDOWELL ACUTE LUNG INJURY DN	61	-0.41	-1.32	0.109	0.424	1	3106		logp=2%, fdr=21%,
327			DI PLASMACYTOMA DN	55	-0.38	-1.28	0.109	0.468	1	3330		logp=0%, fdr=33%,
312			REACTOME_GAMMA CARBOXYLATION, HYPUSYLATION, HYDROXYLATION, AND ARYLSULFATASE ACTIVATION	64	-0.41	-1.29	0.11	0.451	1	3630		logp=0%, fdr=12%, signal=1%
181			REACTOME_TNFR1 NON CANONICAL NF KB PATHWAY	61	-0.38	-1.27	0.11	0.473	1	3245		logp=1%, fdr=18%,
295			GAZIN EPIGENETIC SILENCING BY KRAS	18	-0.53	-1.35	0.111	0.465	1	1947		logp=3%, fdr=15%,
181			WONKER POSTIRRADIATION TUMOR ESCAPE DN	136	-0.3	-1.13	0.111	0.588	1	3611		logp=0%, fdr=18%,
269			REACTOME_GPCR MEDIATED ACTIVATION CASCADE	61	-0.4	-1.29	0.112	0.466	1	2661		logp=1%, fdr=22%,
269			REACTOME_IRS15 ANTIVIRAL MECHANISM	61	-0.45	-1.31	0.113	0.423	1	3685		logp=2%, fdr=35%,
181			MAKKELEN ES KRT WITH NO UNMETHYLATED	61	-0.39	-1.28	0.113	0.491	1	3321		logp=0%, fdr=35%,
214			REACTOME PARACETAMOL ADME	61	-0.49	-1.35	0.115	0.409	1	3442		logp=3%, fdr=24%,
187			REACTOME SUMOYLATION	61	-0.34	-1.24	0.115	0.501	1	3130		logp=1%, fdr=21%,
270			GROSS HYPOXIA VIA ELK3 AND HIF1A UP	159	-0.35	-1.25	0.116	0.482	1	3938		logp=1%, fdr=29%,
181			REACTOME_CLASS B 2 SECRETIN FAMILY RECEPTORS	61	-0.37	-1.27	0.117	0.412	1	2710		logp=1%, fdr=21%, signal=19%
268			WP WHITE FAT CELL DIFFERENTIATION	61	-0.46	-1.33	0.118	0.424	1	3116		logp=2%, fdr=21%,
282			REACTOME FLT3 SIGNALING	61	-0.46	-1.31	0.119	0.429	1	893		logp=3%, fdr=3%, signal=21%
181			SAVARIMAN MLL AF9 FUSION TARGETS F UP	61	-0.35	-1.24	0.119	0.491	1	3346		logp=1%, fdr=30%,
297			TAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 17	179	-0.32	-1.21	0.119	0.543	1	3388		logp=0%, fdr=33%,
295			GERY CEBP TARGETS	61	-0.45	-1.28	0.12	0.465	1	3346		logp=2%, fdr=27%,
273			HEUNER CORTEX CAUDAL VENTRICULAR ZONE	55	-0.46	-1.32	0.121	0.427	1	1295		logp=3%, fdr=17%,
181			REACTOME DECTIN 1 MEDIATED NONCANONICAL NF KB SIGNALING	61	-0.37	-1.26	0.121	0.46	1	3210		logp=1%, fdr=21%,
315			MONY HIPPOCAMPUS POSTNATAL	61	-0.45	-1.28	0.122	0.461	1	3346		logp=4%, fdr=35%,
268			REACTOME SIGNALING BY SCF KIT	64	-0.47	-1.31	0.123	0.423	1	2697		logp=2%, fdr=35%,
213			REACTOME TRANS GOLGI NETWORK VESICLE BUDDING	61	-0.39	-1.26	0.123	0.491	1	3245		logp=0%, fdr=20%,
272			BURTON ADIPOGENESIS 1	55	-0.46	-1.32	0.124	0.426	1	3389		logp=3%, fdr=21%,
181			MAKKELEN MEF LCP WITH H3K4ME3	71	-0.37	-1.25	0.125	0.485	1	3132		logp=1%, fdr=21%,
265			REACTOME_CD28 CO STIMULATION	55	-0.49	-1.32	0.126	0.425	1	2692		logp=3%, fdr=25%,
246			DAMARIOTIS SKIN CANCER PROGRESSION DN	61	-0.37	-1.25	0.126	0.486	1	3346		logp=1%, fdr=20%,
268			BASHI RESPONSE TO IONIZING RADIATION 3	61	-0.43	-1.29	0.127	0.449	1	3356		logp=3%, fdr=15%,
268			SAFFORD T LYMPHOCYTE ANERGY	61	-0.39	-1.26	0.127	0.48	1	3321		logp=1%, fdr=21%, signal=18%
181			REACTOME GLEC1A BETA 1 SIGNALING	61	-0.36	-1.24	0.128	0.519	1	3884		logp=1%, fdr=21%,
268			WA RAT AGING DN	117	-0.34	-1.23	0.128	0.519	1	3137		logp=0%, fdr=21%,
181			SYSTEMX HEMATOPOIESIS STEM CELL AND BRAIN GTL TRANS	193	-0.34	-1.23	0.129	0.529	1	3111		logp=0%, fdr=21%,
292			BIOCARTA INSULIN PATHWAY	18	-0.49	-1.31

415		BILANDES SERUM SENSITIVE GENES	56	-0.38	-1.22	0.16	0.529	1	2416		sign=0%, list=2%,
236		MULIGAN NTF3 SIGNALING VIA INSR AND IGF1R UP	13	-0.47	-1.22	0.161	0.473	1	2610		sign=0%, list=3%,
483		WP EXERCISE INDUCED CIRCADIAN REGULATION	42	-0.38	-1.22	0.161	0.461	1	2967		sign=0%, list=41%,
264		BURTON ADIPOGENESIS 7	58	-0.4	-1.24	0.161	0.466	1	2196		sign=0%, list=2%,
191		REACTOME INTERFERON-1 FAMILY SIGNALING	67	-0.35	-1.19	0.161	0.49	1	2837		sign=0%, list=3%,
260		BIOCARTA ERK PATHWAY	22	-0.45	-1.26	0.163	0.466	1	2607		sign=41%, list=42%,
287		TSENG ADIPOGENIC POTENTIAL DN	54	-0.4	-1.24	0.163	0.491	1	1381		sign=0%, list=15%,
482		MARTINEZ RB1 TARGETS DN	73	-0.32	-1.19	0.163	0.649	1	2837		sign=0%, list=3%,
456		WP NOTCH SIGNALING PATHWAY	28	-0.44	-1.26	0.164	0.466	1	2342		sign=0%, list=2%,
187		SCHAEFFER PROSTATE DEVELOPMENT 12HR UP	74	-0.4	-1.22	0.164	0.5	1	2318		sign=0%, list=2%,
473		WANG RESPONSE TO BENABTEONE UP	18	-0.47	-1.25	0.166	0.49	1	1921		sign=0%, list=1%,
518		VANDEVELDE MYCGENESIS SNX9 TARGETS	21	-0.41	-1.21	0.167	0.493	1	2604		sign=0%, list=2%,
346		WP ERYTHROID DIFFERENTIATION 12HR	67	-0.37	-1.26	0.168	0.492	1	2314		sign=0%, list=2%,
349		VANASSE BCL2 TARGETS UP	21	-0.46	-1.26	0.168	0.473	1	2196		sign=0%, list=2%,
276		REACTOME LGI4M INTERACTIONS	64	-0.39	-1.25	0.168	0.489	1	2837		sign=0%, list=3%,
268		REACTOME RNA DOUBLE STRAND BREAK RESPONSE	58	-0.41	-1.25	0.169	0.492	1	292		sign=12%, list=3%, signal=12%
269		VAIDI ERBB2 BREAST TUMORS 6D UP	20	-0.47	-1.27	0.172	0.473	1	2168		sign=0%, list=2%,
469		SHIN B CELL LYMPHOMA CLUSTER 8	20	-0.46	-1.25	0.172	0.461	1	1986		sign=0%, list=1%,
257		CHEVILLE BRAIN HEMATE GENETIC VARIANCE	61	-0.42	-1.26	0.173	0.492	1	2837		sign=0%, list=3%,
460		REACTOME RWTORNS OF ORIGINS TO A POST REPLICATIVE STATE	31	-0.5	-1.2	0.174	0.562	1	2710		sign=0%, list=2%,
459		NABA ECM GLYCOPROTEINS	72	-0.35	-1.19	0.177	0.569	1	2745		sign=0%, list=2%,
481		XU MYC TARGETS DN	58	-0.4	-1.24	0.179	0.495	1	2837		sign=0%, list=3%,
418		QUINTENS EMBRYONIC BRAIN RESPONSE TO IR	52	-0.37	-1.22	0.18	0.531	1	2196		sign=0%, list=2%,
488		REACTOME ER TO GOLGI ANTEROGRADE TRANSPORT	18	-0.53	-1.27	0.181	0.577	1	2342		sign=0%, list=2%,
493		REACTOME INITIAL TRIGGERING OF COMPLEMENT	18	-0.48	-1.24	0.183	0.497	1	976		sign=0%, list=1%,
479		FOSTER TOLERANT MACROPHAGE DN	73	-0.39	-1.21	0.184	0.5	1	2610		sign=0%, list=2%,
407		REACTOME GOLGI ASSOCIATED VESICLE BIOGENESIS	20	-0.49	-1.26	0.184	0.528	1	2661		sign=0%, list=2%,
232		IL INDUCED T TO NATURAL KILLER UP	135	-0.31	-1.15	0.184	0.668	1	2274		sign=0%, list=1%,
486		MORIKAWA PURBETAL TGFB1 TARGETS UP	73	-0.32	-1.18	0.185	0.593	1	2837		sign=0%, list=3%,
423		REACTOME SIGNALING BY PTK6	52	-0.41	-1.22	0.186	0.528	1	1195		sign=12%, list=12%,
284		REACTOME INSULIN RECEPTOR SIGNALLING CASCADE	52	-0.42	-1.22	0.187	0.516	1	2196		sign=12%, list=12%,
472		MARKEY RB1 CHRONIC LOF DN	62	-0.34	-1.18	0.187	0.579	1	2196		sign=0%, list=1%,
519		REACTOME PLATELET ACTIVATION SIGNALING AND AGGREGATION	64	-0.34	-1.18	0.187	0.567	1	2710		sign=0%, list=2%,
363		WANG IMMORTALIZED BY HOXA9 AND MEIS1 UP	18	-0.46	-1.25	0.188	0.493	1	2967		sign=0%, list=4%,
487		WP IL 6 SIGNALING PATHWAY	60	-0.34	-1.18	0.188	0.578	1	2416		sign=1%, list=2%,
485		CHARRONDA NEOPLASTIC TRANSFORMATION KRAS DN	118	-0.32	-1.18	0.19	0.579	1	2661		sign=12%, list=10%, signal=10%
238		REACTOME CYTOCHROME P450 ARRANGED BY SUBSTRATE TYPE	38	-0.39	-1.21	0.191	0.547	1	1938		sign=0%, list=1%,
495		REACTOME S PHASE	73	-0.33	-1.17	0.191	0.589	1	2113		sign=0%, list=1%,
484		WP GPCR CLASS A RHODOPSIN LIKE	73	-0.47	-1.25	0.192	0.466	1	558		sign=18%, list=7%, signal=18%
171		REACTOME MTORC1 MEDIATED SIGNALLING	18	-0.45	-1.24	0.192	0.491	1	2604		sign=0%, list=2%,
361		WUYANG PROSTATE CANCER MONSTER	22	-0.45	-1.25	0.193	0.491	1	2607		sign=41%, list=42%,
433		SASAI RESISTANCE TO NEOPLASTIC TRANSFORMATION	20	-0.41	-1.21	0.193	0.535	1	2314		sign=0%, list=2%,
481		PLASARI TGFB1 SIGNALING VIA NFK1 18R DN	71	-0.35	-1.18	0.193	0.561	1	2837		sign=0%, list=3%,
444		REACTOME GPCR LIGAND BINDING	52	-0.36	-1.2	0.195	0.549	1	1337		sign=0%, list=1%,
448		LEE CALORIE RESTRICTION NEOCORTEX UP	54	-0.36	-1.2	0.196	0.553	1	2196		sign=0%, list=2%,
193		PANGAS TUMOR SUPPRESSION BY SMAD1 AND SMAD5 UP	73	-0.34	-1.19	0.196	0.569	1	2603		sign=0%, list=2%,
464		WANDYA HEMATOPOIESIS STEM CELL AND PROGENITOR	73	-0.39	-1.21	0.197	0.518	1	2837		sign=0%, list=3%,
379		REACTOME NEGATIVE REGULATION OF THE PI3K AKT NETWORK	60	-0.37	-1.19	0.198	0.567	1	2604		sign=0%, list=2%,
489		REACTOME TRANSCRIPTIONAL REGULATION BY E2F6	18	-0.47	-1.25	0.199	0.49	1	1267		sign=0%, list=1%,
285		REACTOME NEGATIVE REGULATION OF MRT ACTIVITY	18	-0.47	-1.25	0.199	0.492	1	1267		sign=0%, list=1%,
465		NABA MATRISOME PRIMARY METASTATIC LUNG TUMOR	21	-0.45	-1.24	0.201	0.491	1	2395		sign=0%, list=2%,
469		SHIN B CELL LYMPHOMA CLUSTER 7	18	-0.46	-1.23	0.201	0.517	1	2604		sign=0%, list=2%,
262		WANDYA HEMATOPOIESIS LATE PROGENITOR	58	-0.39	-1.21	0.201	0.557	1	2660		sign=0%, list=2%,
166		WP REGULATION OF ACTIN CYTOSKELETON	67	-0.35	-1.19	0.201	0.593	1	2837		sign=0%, list=3%,
297		WANDYA HEMATOPOIESIS STEM CELL LONG TERM	107	-0.33	-1.18	0.204	0.597	1	2619		sign=0%, list=2%,
432		WP G13 SIGNALING PATHWAY	73	-0.32	-1.18	0.205	0.604	1	2837		sign=0%, list=3%,
484		NIA RAT AGING UP	74	-0.34	-1.18	0.205	0.58	1	2196		sign=0%, list=1%,
148		BIOCARTA VDR PATHWAY	18	-0.46	-1.24	0.206	0.493	1	976		sign=0%, list=1%,
483		REACTOME CLASS A 1 RHODOPSIN LIKE RECEPTORS	61	-0.37	-1.2	0.206	0.55	1	2113		sign=0%, list=1%,
310		REACTOME CELL CELL JUNCTION ORGANIZATION	20	-0.42	-1.21	0.207	0.518	1	2604		sign=0%, list=2%,
464		BOYLAN MULTIPLE MYELOMA C UP	60	-0.37	-1.2	0.207	0.558	1	2196		sign=0%, list=1%,
458		CI HYPOXIA	68	-0.34	-1.17	0.207	0.588	1	2165		sign=0%, list=1%,
495		REACTOME PROTEIN HYDROXYLATION	18	-0.47	-1.22	0.212	0.506	1	1267		sign=0%, list=1%,
412		CHEN FOGE TARGETS	17	-0.47	-1.22	0.213	0.523	1	1938		sign=0%, list=1%,
462		WP TGF BETA SIGNALING PATHWAY	58	-0.38	-1.19	0.213	0.568	1	2837		sign=12%, list=3%, signal=22%
365		ZHONG SECRETOME OF LUNG CANCER AND MACROPHAGE	54	-0.35	-1.18	0.213	0.566	1	2660		sign=12%, list=2%,
230		REACTOME MITOPHAGY	20	-0.42	-1.19	0.214	0.51	1	2604		sign=0%, list=2%,
295		BROEKSEN BCR6 UP WITH HSKIME3	21	-0.4	-1.18	0.214	0.51	1	2172		sign=0%, list=1%,
469		REACTOME G ALPHA S SIGNALLING EVENTS	69	-0.41	-1.19	0.215	0.568	1	1819		sign=0%, list=1%,
441		REACTOME RHOBTB2 GTPASE CYCLE	54	-0.44	-1.2	0.216	0.548	1	2660		sign=0%, list=2%,
478		REACTOME PLASMA LIPOPROTEIN ASSEMBLY REMODELLING AND CLEARANCE	56	-0.36	-1.18	0.216	0.582	1	2196		sign=0%, list=1%,
486		SASA RESPONSE TO IONIZING RADIATION 8	58	-0.35	-1.18	0.216	0.579	1	2346		sign=0%, list=1%,
292		IL INDUCED T TO NATURAL KILLER DN	65	-0.34	-1.17	0.217	0.588	1	2466		sign=0%, list=1%,
479		WANG AGING HYPOTHALAMUS UP	73	-0.37	-1.2	0.217	0.573	1	2837		sign=0%, list=3%,
375		AUD HEK TARGETS UP	60	-0.36	-1.18	0.221	0.579	1	2108		sign=0%, list=1%,
451		REACTOME FOXO MEDIATED TRANSCRIPTION	18	-0.48	-1.23	0.222	0.514	1	2832		sign=0%, list=2%,
417		REACTOME ORC1 REMOVAL FROM CHROMATIN	56	-0.35	-1.18	0.223	0.595	1	2113		sign=0%, list=1%,
439		REACTOME COLLAGEN FORMATION	21	-0.4	-1.21	0.226	0.545	1	2830		sign=0%, list=1%,
291		GU GENOTOXIC DAMAGE 4HR	17	-0.44	-1.22	0.228	0.52	1	2309		sign=0%, list=1%,
229		REACTOME SMAD2 SMAD3 SMAD4 HETEROTRIMER REGULATES TRANSCRIPT	21	-0.43	-1.21	0.228	0.529	1	750		sign=12%, list=1%, signal=12%
193		IN HYPOXIA TARGETS OF HIF1A AND EDAS2	21	-0.43	-1.21	0.228	0.529	1	2165		sign=0%, list=1%,
463		REACTOME DUBOSKATIN MODIFYING ENZYMES	60	-0.37	-1.19	0.229	0.573	1	2165		sign=0%, list=1%,
445		REACTOME REGULATION OF TP53 ACTIVITY THROUGH ACETYLATION	27	-0.41	-1.2	0.23	0.553	1	2634		sign=0%, list=1%,
461		REACTOME IRS MEDIATED SIGNALLING	54	-0.44	-1.2	0.231	0.548	1	2660		sign=0%, list=2%,
483		WP MIR29 AND ARSENITE BETT RIVERONE	27	-0.41	-1.19	0.231	0.567	1	1616		sign=0%, list=1%,
375		REACTOME SMAD2 SMAD3 SMAD4 HETEROTRIMER REGULATES TRANSCRIPT	60	-0.35	-1.18	0.232	0.578	1	750		sign=0%, list=1%,
476		MEISSNER NPC HCP WITH H3K4ME3 AND H3K27ME3	54	-0.35	-1.18	0.234	0.58	1	2871		sign=0%, list=1%,
147		REACTOME LDL CLEARANCE	21	-0.45	-1.19	0.235	0.49	1	2113		sign=0%, list=1%,
454		REACTOME DNA REPLICATION	100	-0.32	-1.18	0.236	0.62	1	1799		sign=0%, list=1%,
456		REACTOME ADHERENS JUNCTIONS INTERACTIONS	27	-0.43	-1.19	0.237	0.566	1	2645		sign=0%, list=1%,
486		REACTOME TOLL LIKE RECEPTOR CASCADES	73	-0.32	-1.18	0.237	0.615	1	2660		sign=0%, list=1%,
216		IOR IL 9 SIGNALING PATHWAY	72	-0.34	-1.18	0.239	0.584	1	2387		sign=0%, list=1%,
227		MARKEY RB1 ACUTE LOF UP	73	-0.3	-1.12	0.241	0.641	1	2306		sign=0%, list=1%,
370		REACTOME HATS ACETYLATE HISTONES	54	-0.39	-1.18	0.243	0.57	1	2167		sign=0%, list=1%,
412		BREDEMEYER RAG SIGNALING NOT VIA ATM UP	60	-0.36	-1.18	0.243	0.58	1	2660		sign=0%, list=1%,
412		REACTOME G1 S DNA DAMAGE CHECKPOINTS	60	-0.36	-1.18	0.243	0.58	1	2710		sign=0%, list=1%,
284		REACTOME E3 UBIQUITIN LIGASES UBIQUITINATE TARGET PROTEINS	58	-0.39	-1.17	0.244	0.588	1	1706		sign=0%, list=1%,
488		WANGSOLAR HNF4 TARGETS DN	58	-0.37	-1.18	0.244	0.596	1	2660		sign=0%, list=1%,
270		REACTOME SIGNALING BY WNT	120	-0.3	-1.12	0.244	0.654	1	2210		sign=0%, list=1%,
486		WOR MATURE B LYMPHOCYTE UP	54	-0.34	-1.17	0.248	0.606	1	2660		sign=0%, list=1%,
287		REACTOME COPI MEDIATED ANTEROGRADE TRANSPORT	23	-0.34	-1.15	0.249	0.615	1	2316		sign=0%, list=1%,
471		WELCH GATA1 TARGETS	27	-0.41	-1.18	0.251	0.57	1	2604		sign=0%, list=1%,
471		REACTOME COLLAGEN BIOSYNTHESIS AND MODIFYING ENZYMES	60	-0.37	-1.18	0.251	0.573	1	2663		sign=0%, list=1%,
414		GROSS ELK3 TARGETS DN	21	-0.44	-1.18	0.251	0.578	1	3116		sign=0%, list=1%,
485		CHARRONDA NEOPLASTIC TRANSFORMATION KRAS CDC25 UP	54	-0.37	-1.18	0.251	0.596	1	2660		sign=0%, list=1%,
479		HOFMANN EPITHELIAL TO MESENCHYMAL TRANSITION DN	100	-0.3	-1.12	0.252	0.643	1	3131		sign=0%, list=1%,
412		REACTOME CONVERSION FROM APC/C COUPLED TO APC/C SUBTR IN CELL ANA	17	-0.46	-1.2	0.253	0.52	1	1938		sign=0%, list=1%,
290		YOSHIA GRAFT VERSUS HOST DISEASE DY DN	41	-0.37	-1.15	0.253	0.668	1	2309		sign=12%, list=3%, signal=24%
464		REACTOME SIGNALING BY FGFR1	60	-0.4	-1.17	0.254	0.545	1	2607		sign=0%, list=1%,
464		WANG TARGETS OF BRL CRP FUSION DN	60	-0.37	-1.17	0.254	0.561	1	2663		sign=0%, list=1%,
248		WP ADIPOGENESIS GENES	64	-0.33	-1.16	0.254	0.614	1	1930		sign=0%, list=1%,
475		KONG BU IOR CONTROL METAZENE 3 PREDICTIVE IOR RESPONSE	58	-0.31	-1.15	0.254	0.614	1	2660		sign=0%, list=1%,
492		REACTOME PREMRNA ADME	15	-0.45	-1.12	0.255	0.565	1	2599		sign=0%, list=1%,
343		VAILOO SPI TARGETS DN	23	-0.34	-1.15	0.256	0.606	1	2647		sign=0%, list=1%,
487		GAUSSMANN MLL AF4 FUSION TARGETS E UP	61	-0.35	-1.16	0.257	0.615	1	2646		sign=0%, list=1%,
466		XU CREBBP TARGETS UP	27	-0.41	-1.16	0.257	0.549	1	2604		sign=0%, list=1%,
264		BOYLAN MULTIPLE MYELOMA C CLUSTER UP	60	-0.37	-1.16	0.258	0.571	1	2663		sign=0%, list=1%,
285		REACTOME TGF DEPENDENT SIGNALING IN RESPONSE TO WNT	122	-0.31	-1.12	0.258	0.649	1	2710		sign=0%, list=1%,
464		BIOCARTA ATR PATHWAY	54	-0.37	-1.16	0.263	0.566	1	2163		sign=0%, list=1%,
238		GOLDRATH IMMUNE MEMORY	52	-0.36	-1.15	0.269	0.567	1	1136		sign=0%, list=1%,
480		BIOCARTA FCER1 PATHWAY	54	-0.34	-1.15	0.269	0.582	1	2660		sign=0%, list=1%,
349		BURTON ADIPOGENESIS 3	68	-0.34	-1.14	0.282	0.614	1	2604		sign=0%, list=1%,
484		WP EPITHELIAL DIFFERENTIATION	73	-0.34	-1.14	0.282	0.61	1	2837		sign=0%, list=1%,
277		REACTOME SIGNALING BY TYPE 1 INSULIN LIKE GROWTH FACTOR 1 RECEPT	24	-0.41	-1.17	1.263	0.588	1	2736		sign=62%, list=27%, signal=62%
229		TERAO AOH1 TARGETS HIS UP	24	-0.41	-1.16	1.263	0.608	1	2732		sign=62%, list=27%,
283		GROSS HYPOXIA VIA HIF1A DN	77	-0.33	-1.13	1.263	0.631	1	1345		sign=37%, list=23%,
277		BIOCARTA CKCM PATHWAY	18	-0.44	-1.18	1.265	0.587	1	1921		sign=22%, list=8%, signal=24%
446		REACTOME IRON UPTAKE AND TRANSPORT	54	-0.36	-1.15	1.265	0.665	1	2645		sign=62%, list=34%,
310		REACTOME INSULIN RECEPTOR RECYCLING	52	-0.42	-1.16	1.265	0.565	1	2104		sign=62%, list=27%,
479		BIOCARTA MTOR PATHWAY	18	-0.44	-1.18	1.267	0.583	1	2387		sign=62%, list=8%,
475		REACTOME AUTOPHAGY ENVELOPE BREAKDOWN	18	-0.47	-1.17	1.267	0.495	1	2167		sign=62%, list=8%,
499		TERAO AOH1 TARGETS 6HR DN	21	-0.45	-1.17	1.268	0.568	1	2311		sign=62%, list=9%,
533		REACTOME NEGATIVE REGULATION OF MAPK PATHWAY	32	-0.39	-1.15	1.268	0.668	1	2651		sign=62%, list=14%,
490		WENG MIR33 TARGETS UP	61	-0.36	-1.15	1.269	0.669	1	2660		sign=62%, list=27%,
490		VILIMAS NOTCH1 TARGETS UP	18	-0.46	-1.18	1.269	0.573	1	2236		sign=62%, list=8%,
415		WP P38 MAPK SIGNALING PATHWAY	73	-0.4	-1.18	1.269	0.566	1	2837		sign=62%, list=27%,
461		MATSUDA NATURAL KILLER DIFFERENTIATION	100	-0.28	-1.08	1.269	0.692	1	2376		sign=62%, list=23%,
411		PASINI SUZ12 TARGETS DN	24	-0.39	-1.1	1.271	0.674	1	2647		sign=62%, list=9%,
481		REACTOME GRB2 SIGNALING	18	-0.44	-1.17	1.271	0.52	1	1815		sign=62%, list=8%,
496		REACTOME SIGNALING BY CSF1 CSF	18	-0.44	-1.17	1.271	0.593	1	2749		sign=62%, list=8%,
487		REACTOME SIGNALING BY TGFB FAMILY MEMBERS	54	-0.33	-1.13	1.272	0.602	1	1836		sign=62%, list=27%,
353		REACTOME IMMUNOREGULATORY INTERACTIONS BETWEEN A LYMPHOID AND A NON LYMPHOID CELL	38	-0.37	-1.14	1.273	0.618	1	2520		sign=47%, list=25%, signal=47%
287		REACTOME MITOTIC METAPHASE AND ANAPHASE	120	-0.3	-1.11	1.273	0.657	1	2710		sign=62%, list=27%,
251		REACTOME REGULATION OF TNFR1 SIGNALING	21	-0.37	-1.09	1.273	0.667	1	2645		sign=62%, list=9%,
292		NABA MATRISOME ASSOCIATED	54	-0.39	-1.09	1.273	0.681	1	2196		sign=62%, list=27%,
545		REACTOME SIGNALING BY VEGF	21	-0.33	-1.09	1.273	0.697	1	2387		sign=27%, list=9%,
545		REACTOME TRANSPORT OF INORGANIC CATIONS ANIONS AND AMINO ACIDS OLIGOPEPTIDES	65	-0.36	-1.14	1.28	0.615	1	2312		sign=31%, list=20%, signal=31%
362		REACTOME SIGNALING BY BMP	60	-0.42	-1.16	1.282	0.604	1	2236		sign=62%, list=27%,
295		REACTOME METABOLISM OF WATER SOLUBLE VITAMINS AND COFACTORS	81	-0.32	-1.11	1.282	0.668	1	2163		sign=62%, list=27%,
483		STARK PREFRONTAL CORTEX 22Q11 DELETION UP	18	-0.5	-1.1	1.282	0.66	1	2730		sign=62%, list=9%,
498		WANG MLL TARGETS	120	-0.3	-1.1	1.282	0.665	1	2398		sign=62%, list=27%,
496		RUAN RESPONSE TO TROGLITAZONE UP	24	-0.43	-1.16	1.283	0.566	1	2311		sign=62%, list=9%, signal=11%
461		WP NEURAL CREST DIFFERENTIATION	61	-0.36	-1.15	1.283	0.608	1	2707		sign=62%, list=27%,
435		FOSTER KDM1A TARGETS DN	18	-0.45	-1.17	1.284	0.466	1	2604		sign=62%, list=8%,
284		WP NUCLEAR RECEPTORS IN LIPID METABOLISM AND TOXICITY	60	-0.4	-1.16	1.286	0.609	1	2662		sign=62%, list=27%,
435		RAY TOMOSIGENESIS BY ERBB2 CDC25A UP	83	-0.32	-1.12	1.286	0.649	1	1921		sign=62%, list=27%,
483		WANDYA HEMATOPOIESIS MATURE CELL	73	-0.32	-1.09	1.287	0.662	1	2837		sign=62%, list=27%,
462		REACTOME NRAGE SIGNALS DEATH THROUGH JNK	52	-0.39	-1.10	1.288	0.667	1	2654		sign=62%, list=33%,
487		REACTOME RHOA GTPASE CYCLE	54	-0.32	-1.09	1.288	0.654	1	2660		sign=62%, list=27%,
469		MILI PSEUDOPOLYA CHEMOTAXIS UP	71	-0.33	-1.10	1.29	0.63	1	2461		sign=62%, list=31%,
317		WANG GU POST IR METAZENE 41	18	-0.43	-1.1	1.29	0.472	1	2387		sign=62%, list=9%,
455		REACTOME METABOLISM	100	-0.3	-1.1	1.291	0.659	1	2710		sign=62%, list=27%,
252		REACTOME ASPRIN ADME	20	-0.42	-1.14	1.291	0.618	1	2442		sign=62%, list=9%,
526		REACTOME ORC1 CDC6 ASSOCIATE WITH THE PRE REPLICATION COMPLEX FOR THE ONset OF ANAPHASE BY MITOTIC SPINDLE CHECKPOINT COMPO	21	-0.44	-1.16	1.292	0.609	1	628		sign=20%, list=16%, signal=20%
572		CALRAO INNUNE RESPONSE TO ENTEROTOXIN	53	-0.34	-1.13	1.292	0.634	1	812		sign=21%, list=9%, signal=23%
569		REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	128	-0.28	-1.07	1.292	0.712	1	2700		sign=62%, list=27%,
550		BIOCARTA INTEGRIN PATHWAY	23	-0.34	-1.14	1.294	0.613	1	2585		sign=62%, list=10%,
540		BERENKO TRANSFORMED BY IBKIA REVERSIBLY DN	21	-0.41	-1.15	1.295	0.605	1	1937		sign=62%, list=13%,
465		NABA MATRISOME METASTATIC LUNG LYMPH NODE METASTASIS	18	-0.43	-1.16	1.295	0.653	1	2379		sign=62%, list=9%,
536		REACTOME METABOLISM OF NITROGEN AMINO ACID AND ANALOGUES	18	-0.45	-1.16	1.296	0.606	1	1208		sign=62%, list=9%,
565		REACTOME REGULATION OF TLR BY ENDOGENOUS LIGAND	15	-0.44	-1.13	1.296	0.63	1	1953		sign=62%, list=9%,
487		HU GENOTOXIC DAMAGE 24HR	25	-0.39	-1.13	1.296	0.629	1	2374		sign=62%, list=9%,
525		WP MAPK SIGNALING PATHWAY	137	-0.3	-1.09	1.299	0.684	1	628		sign=16%, list=9%, signal=15%
581		BIOCARTA IL22R PATHWAY	23	-0.32	-1.12	1.3	0.643	1	2379		sign=62%, list=9%,
541		REACTOME CELL EXTRACELLULAR MATRIX INTERACTIONS	17	-0.44	-1.15	1.304	0.604	1	2127		sign=62%, list=9%,
560		WP COMPREHENSIVE IL 17A SIGNALING	24	-0.33	-1.11	1.304	0.657	1	2607		sign=62%, list=9%,
580		LEE CALORIE RESTRICTION MUSCLE UP	20	-0.4	-1.13	1.305	0.606	1	1356		sign=62%, list=9%,
580		WP FIBRIN COMPLEMENT RECEPTOR 3 SIGNALING PATHWAY	31	-0.38	-1.12	1.305	0.644	1	2102		sign=62%, list=9%,
556		SCHLINGMANN SKIN CARCINOGENESIS TPA UP	28	-0.39	-1.12	1.306	0.621	1	2460		sign=62%, list=9%,
558		MIKKELSEN MCV6 HCP WITH H3K27ME3	43	-0.36	-1.13	1.306	0.625	1	1605		sign=62%, list=9%,
573		BIOCARTA G2A3 PATHWAY	23	-0.42	-1.13	1.31	0.633	1	379		sign=16%, list=6%, signal=17%
589		WP APOPTOSIS	57	-0.34	-1.11	1.31	0.658	1	1370		sign=62%, list=9%,
516		WP ENDOCHONDRAL OSSIFICATION	18	-0.37	-1.1	1.311	0.67	1	2460		sign=62%, list=9%,
540		YAMAZAKI TCBB3 TARGETS DN	106	-0.29	-1.08	1.312	0.691	1	1341		sign=62%, list=9%,
592		WP ESTROGEN SIGNALING	64	-0.33	-1.11	1.314	0.653	1	1337		sign=62%, list=9%,
533		SIETH LIVER CANCER VS TXNIP LOSS PAM1	158	-0.29	-1.08	1.314	0.69	1	2660		sign=62%, list=9%,
598		WP KIT RECEPTOR SIGNALING PATHWAY	43	-0.34	-1.11	1.316	0.656	1	2735		sign=62%, list=9%,
521		REACTOME RAF INDEPENDENT MAPK1 3 ACTIVATION	21	-0.43	-1.12	1.317	0.615	1	581		sign=16%, list=9%,
584		LIAN LIPA TARGETS 6M	47	-0.35	-1.11	1.318	0.658	1	2737		sign=62%, list=9%,
580		REACTOME PLASMA LIPOPROTEIN CLEARANCE	18	-0.37	-1.12	1.319	0.649	1	2130		sign=62%, list=9%,
580		BIOCARTA IGF1 PATHWAY	23	-0.41	-1.11	1.321	0.661	1	2648		sign=62%, list=9%,
565		CHANGOLKAR HNF4 TARGETS UP	43	-0.35	-1.11	1.322	0.66	1	3692		sign=62%, list=9%,
529		CHARRONDA NEOPLASTIC TRANSFORMATION KRAS UP

618			BRACHAT_RESPONSE_TO_METHOTREXATE_UP	42	-0.42	-1.1	0.352	0.671	1	415		logp=18%, lsf=5%, signal=19%
236			DASHI_RESPONSE_TO_IONIZING_RADIATION_4	52	-0.36	-0.89	0.362	0.681	1	1837		logp=26%, lsf=12%,
237			DAVIN_FOXP3_TARGETS_CLUSTER_P4	71	-0.33	-0.89	0.363	0.68	1	2582		logp=26%, lsf=24%,
262			GOLDRATH_HOMEOSTATIC_PROLIFERATION	119	-0.3	-0.89	0.365	0.711	1	2890		logp=26%, lsf=24%,
193			BRADEMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP	54	-0.37	-0.89	0.366	0.733	1	2000		logp=26%, lsf=12%,
263			REACTOME_BIOLOGICAL_OXIDATIONS	114	-0.29	-0.89	0.36	0.721	1	3009		logp=26%, lsf=24%,
236			REACTOME_MTOR_SIGNALLING	56	-0.35	-0.89	0.362	0.686	1	2743		logp=26%, lsf=12%,
489			REACTOME_ERK_MAPK_TARGETS	55	-0.45	-1.1	0.364	0.685	1	2651		logp=26%, lsf=16%,
492			REACTOME_DDX58_IFIH1_MEDIATED_INDUCTION_OF_INTERFERON_ALPHA_BETA	58	-0.37	-0.89	0.364	0.68	1	3101		logp=26%, lsf=21%,
236			NOIR_LARGE_PRE_BI_LYMPHOCYTE_UP	56	-0.33	-0.89	0.364	0.701	1	2981		logp=26%, lsf=12%,
464			REACTOME_MITOCHONDRIAL_BIOGENESIS	55	-0.38	-0.89	0.365	0.681	1	3131		logp=26%, lsf=21%,
167			NOIR_SMALL_PRE_BI_LYMPHOCYTE_DN	113	-0.32	-0.89	0.365	0.714	1	3004		logp=26%, lsf=23%,
262			STEARMAN_LUNG_CANCER_EARLY_VS_LATE_UP	115	-0.31	-0.89	0.366	0.713	1	3007		logp=26%, lsf=23%,
253			REACTOME_MAP3K_AND_MAPK_ACTIVATION	53	-0.36	-0.89	0.367	0.71	1	2836		logp=26%, lsf=12%,
486			GUILLAMOND_ALF10_TARGETS_DN	56	-0.36	-0.89	0.367	0.71	1	2936		logp=26%, lsf=22%,
492			BRUNS_HIF_RESPONSE_EARLY_LATE	229	-0.26	-0.89	0.367	0.722	1	5573		logp=26%, lsf=42%,
210			WOBBER_POSTIRADIATION_TUMOR_ESCAPE_UP	120	-0.27	-0.89	0.367	0.727	1	3000		logp=26%, lsf=24%,
560			NABA_SECRETED_FACTORS	72	-0.32	-0.89	0.368	0.7	1	2921		logp=26%, lsf=24%,
464			LEIN_CHRNB2_PLEXUS_MARKERS	58	-0.37	-0.89	0.368	0.712	1	3000		logp=26%, lsf=21%,
184			REACTOME_G2_M_CHECKPOINTS	108	-0.29	-0.89	0.368	0.718	1	3010		logp=26%, lsf=24%, signal=12%
284			WP_AMINO_ACID_METABOLISM	82	-0.3	-0.89	0.369	0.721	1	3589		logp=26%, lsf=24%,
434			BEVINS_CORTEX_BASAL_INTERMEDIATE_PROGENITOR_CELLS	52	-0.35	-0.89	0.37	0.68	1	2921		logp=26%, lsf=22%,
445			GORESCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_UP	15	-0.42	-0.89	0.37	0.692	1	1498		logp=26%, lsf=11%,
266			GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	57	-0.34	-0.89	0.37	0.713	1	3197		logp=26%, lsf=21%,
374			MCBRYAN_PUBERTAL_BREAST_4_5WK_DN	119	-0.29	-0.89	0.37	0.715	1	3890		logp=26%, lsf=24%,
370			PIGROW_SHH_TARGETS_DN	55	-0.34	-0.89	0.371	0.713	1	3101		logp=26%, lsf=21%,
373			REACTOME_RHOB_GTPASE_CYCLE	60	-0.34	-0.89	0.372	0.713	1	3253		logp=26%, lsf=24%,
463			REACTOME_GLYOXYLATE_METABOLISM_AND_GLYCINE_DEGRADATION	58	-0.36	-0.89	0.373	0.713	1	3381		logp=26%, lsf=23%,
483			NOIR_IMMATURE_B_LYMPHOCYTE_UP	56	-0.35	-0.89	0.374	0.69	1	2936		logp=26%, lsf=22%,
449			MARTIN_NKX8_TARGETS_UP	58	-0.37	-0.89	0.374	0.7	1	3092		logp=26%, lsf=22%,
261			REACTOME_SEALING_OF_THE_NUCLEAR_ENVELOPE_NE_BY_ESCRT_III	63	-0.41	-0.89	0.381	0.712	1	3336		logp=26%, lsf=24%,
473			REACTOME_G_ALPHA_12_13_SIGNALLING_EVENTS	61	-0.34	-0.89	0.381	0.716	1	3864		logp=26%, lsf=24%,
370			REACTOME_RHAB_6_CONJUGATION_OF_CHMP1A_4B	57	-0.31	-0.89	0.382	0.727	1	3747		logp=26%, lsf=21%,
479			DIETH_LIVER_CANCER_VS_TSNF_LOSS_FAMR	118	-0.29	-0.89	0.384	0.711	1	3583		logp=26%, lsf=24%,
492			WP_MAPK_CASCADE	72	-0.38	-0.89	0.386	0.721	1	625		logp=26%, lsf=5%, signal=19%
472			BIOCARTA_PYK2_PATHWAY	64	-0.35	-0.89	0.387	0.715	1	3131		logp=26%, lsf=21%,
266			REACTOME_RHOJ_GTPASE_CYCLE	59	-0.36	-0.89	0.388	0.714	1	3410		logp=26%, lsf=24%,
478			CAI_OVARIAN_CANCER_TUMOR_AND_XENOGRAFTS_XDGS_UP	114	-0.29	-0.89	0.388	0.718	1	3100		logp=26%, lsf=24%,
261			VANASSE_BCL2_TARGETS_DN	61	-0.35	-0.89	0.389	0.713	1	3192		logp=26%, lsf=24%,
464			REACTOME_MYD88_MAL_TIRAP_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	60	-0.31	-0.89	0.391	0.721	1	3792		logp=26%, lsf=21%,
266			WANAGA_CARDIOMYOCYTES_BY_KRAS_PTEN_UP	115	-0.29	-0.89	0.391	0.728	1	3384		logp=26%, lsf=24%,
258			WP_SPINAL_CORD_INJURY	68	-0.32	-0.89	0.391	0.729	1	3251		logp=26%, lsf=24%,
492			REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	63	-0.3	-0.89	0.392	0.727	1	3501		logp=26%, lsf=24%,
292			WP_MICRORNA_IN_CARDIOMYOCYTE_HYPERTROPHY	58	-0.31	-0.89	0.393	0.721	1	3800		logp=26%, lsf=23%,
275			DIETH_LIVER_CANCER_VS_TSNF_LOSS_FAMR	118	-0.29	-0.89	0.396	0.713	1	3854		logp=26%, lsf=24%,
260			MODY_HIPPOCAMPUS_PRENATAL_	61	-0.34	-0.89	0.396	0.727	1	3890		logp=26%, lsf=24%,
191			REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	61	-0.34	-0.89	0.398	0.73	1	3890		logp=26%, lsf=13%,
371			BIOCARTA_HDW_PATHWAY	60	-0.42	-0.89	0.398	0.718	1	4254		logp=26%, lsf=24%, signal=20%
266			KASLER_HDAC7_TARGETS_1_UP	125	-0.29	-0.89	0.399	0.728	1	3739		logp=26%, lsf=24%,
489			LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS	56	-0.41	-0.89	0.401	0.713	1	3192		logp=26%, lsf=23%,
296			GAUSMANN_MLL_AF4_FUSION_TARGETS_G_UP	119	-0.29	-0.89	0.401	0.729	1	3992		logp=27%, lsf=22%,
266			WATZAK_SPERMATOGDA	119	-0.29	-0.89	0.403	0.728	1	3992		logp=27%, lsf=24%,
260			BOYLAN_MULTIPLE_MYELOMA_PCA1_DN	55	-0.33	-0.89	0.404	0.731	1	3374		logp=27%, lsf=24%,
311			REACTOME_COPI_MEDIATED_VESICLE_TRANSPORT	61	-0.31	-0.89	0.404	0.736	1	3891		logp=27%, lsf=21%,
267			REACTOME_XENOBIOTICS_	58	-0.31	-0.89	0.404	0.719	1	3858		logp=27%, lsf=21%,
279			REACTOME_SIALIC_ACID_METABOLISM	58	-0.41	-0.89	0.407	0.718	1	3595		logp=27%, lsf=24%,
427			BIOCARTA_NFKB_PATHWAY	54	-0.34	-0.89	0.408	0.718	1	3180		logp=27%, lsf=21%,
484			REACTOME_DISASSEMBLY_OF_THE_DESTRUCTION_COMPLEX_AND_RECRUITMENT_OF_AXIN_TO_THE_MEMBRANE	22	-0.38	-0.95	0.408	0.729	1	4557		logp=59%, lsf=45%, signal=10%
717			BRACHAT_RESPONSE_TO_CAMPTOTHECIN_DN	52	-0.34	-0.89	0.408	0.725	1	3177		logp=27%, lsf=22%,
489			REACTOME_SIGNALING_BY_FGFR3_	62	-0.37	-0.89	0.409	0.728	1	3397		logp=27%, lsf=21%,
267			RIZ_ERYTHROID_DIFFERENTIATION_CD36_1	61	-0.36	-0.89	0.411	0.728	1	3946		logp=27%, lsf=22%,
267			REACTOME_AUTOPHAGY_	118	-0.31	-0.89	0.411	0.735	1	3739		logp=27%, lsf=24%,
727			REACTOME_RHO_GTPASE_EFFECTORS_	118	-0.28	-0.89	0.411	0.739	1	3995		logp=27%, lsf=24%,
267			HOLLERN_EMT_BREAST_TUMOR_DN	60	-0.31	-0.89	0.412	0.741	1	3336		logp=27%, lsf=21%,
267			REACTOME_RECYCLING_PATHWAY_OF_L1_	118	-0.28	-0.89	0.414	0.722	1	3989		logp=27%, lsf=22%,
226			MCBRYAN_PUBERTAL_BREAST_6_7WK_UP	120	-0.29	-0.89	0.414	0.742	1	4041		logp=27%, lsf=24%,
489			SYSTEMIX_HEMATOPOIESIS_STEM_CELL_OTI_C05	54	-0.3	-0.89	0.416	0.722	1	3106		logp=27%, lsf=24%,
414			BIOCARTA_IGF1MTOR_PATHWAY	118	-0.28	-0.89	0.417	0.741	1	3994		logp=27%, lsf=24%,
711			REACTOME_G1_PHASE_GLYCOSYLATION	118	-0.29	-0.89	0.418	0.735	1	3992		logp=27%, lsf=24%,
216			REGTER_TUMEFACT_MACROPHAGE_UP	119	-0.29	-0.89	0.418	0.736	1	4079		logp=27%, lsf=24%,
281			JEPSEN_SMRT_TARGETS	61	-0.38	-0.89	0.419	0.736	1	3322		logp=27%, lsf=23%,
266			WP_RBM_SUSCEPTIBILITY_PATHWAYS	62	-0.37	-0.89	0.419	0.74	1	3401		logp=27%, lsf=24%,
239			REACTOME_RNTS_METHYLATE_HISTONE_ARGININES	28	-0.35	-0.89	0.42	0.754	1	1284		logp=27%, lsf=12%,
260			LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_UP	57	-0.36	-0.89	0.421	0.728	1	3441		logp=27%, lsf=24%,
267			WP_FOLIC_ACID_NETWORK	117	-0.4	-0.89	0.422	0.728	1	4956		logp=27%, lsf=24%,
267			MOLLING_DRES_TARGETS_UP	61	-0.31	-0.89	0.423	0.741	1	3946		logp=27%, lsf=24%,
229			BEN_OLIGODENDROCYTE_MARKERS	60	-0.33	-0.89	0.424	0.737	1	3583		logp=27%, lsf=24%,
730			GAUSMANN_MLL_AF9_FUSION_TARGETS_A_UP	132	-0.28	-0.89	0.425	0.754	1	3937		logp=27%, lsf=25%,
234			REACTOME_MNT_SIGNALING	118	-0.29	-0.89	0.426	0.746	1	3930		logp=27%, lsf=24%,
267			WP_OVARIAN_INFERTILITY	125	-0.41	-0.89	0.427	0.756	1	4646		logp=27%, lsf=24%,
223			REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A_	61	-0.38	-0.89	0.427	0.74	1	3946		logp=27%, lsf=21%,
266			LEE_CALORIE_RESTRICTION_NEOCORTEX_DN	60	-0.32	-0.89	0.427	0.754	1	3890		logp=27%, lsf=21%,
261			LIANG_NYR_FAMILY_TARGETS	60	-0.36	-0.89	0.428	0.735	1	3914		logp=27%, lsf=24%,
484			REACTOME_SIGNALING_BY_FGFR4_	58	-0.36	-0.89	0.429	0.736	1	3897		logp=27%, lsf=24%,
741			REACTOME_REGULATION_OF_APC_C_ACTIVATORS_BETWEEN_G1_S_AND_EARLY_ANAPHASE_	28	-0.35	-0.93	0.429	0.753	1	1626		logp=25%, lsf=16%, signal=33%
731			REACTOME_RHOV_GTPASE_CYCLE_	57	-0.35	-0.89	0.43	0.743	1	779		logp=28%, lsf=24%, signal=20%
236			REACTOME_EPIGENETIC_REGULATION_OF_GENE_EXPRESSION_	118	-0.29	-0.89	0.431	0.752	1	3810		logp=27%, lsf=24%,
232			REACTOME_RXTBA_NUCLEAR_ESTROGEN_SIGNALING	61	-0.33	-0.89	0.431	0.746	1	3947		logp=27%, lsf=24%,
238			BIOCARTA_CTCF_PATHWAY	57	-0.41	-0.89	0.431	0.741	1	4117		logp=27%, lsf=24%, signal=20%
223			BIOCARTA_MTA3_PATHWAY	61	-0.4	-0.89	0.433	0.742	1	3936		logp=27%, lsf=24%,
231			WANG_VENTROSPIN_ENDOMETRIAL_CANCER_CELLS_UP	61	-0.4	-0.89	0.434	0.747	1	3734		logp=27%, lsf=21%,
222			BROOKLESS_E2_LCP_WITH_H3K4ME3	58	-0.32	-0.89	0.434	0.74	1	3495		logp=27%, lsf=21%,
718			BIOCARTA_NTH_PATHWAY	118	-0.39	-0.89	0.436	0.736	1	3498		logp=27%, lsf=24%,
236			SCHLAGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_DN	56	-0.37	-0.89	0.438	0.737	1	3336		logp=27%, lsf=24%,
267			REACTOME_CHOLESTEROL_BIOSYNTHESIS_	55	-0.35	-0.89	0.438	0.753	1	3583		logp=27%, lsf=23%,
251			MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_UP	61	-0.28	-0.89	0.441	0.76	1	3106		logp=27%, lsf=24%,
258			NOIR_SMALL_PRE_BI_LYMPHOCYTE_UP	58	-0.31	-0.89	0.441	0.753	1	3873		logp=27%, lsf=24%,
744			REACTOME_VASOPRESSIN_REGULATES_RENAL_WATER_HOMEOSTASIS_VIA_AQP_CHANNELS_	18	-0.39	-0.93	0.444	0.755	1	468		logp=13%, lsf=5%, signal=13%
218			REACTOME_DNA_TYPE_I_FUNCTIONALIZATION_OF_COMPOUNDS_	61	-0.3	-0.89	0.444	0.745	1	3739		logp=27%, lsf=21%,
239			BELI_PSEUDOPODIA_	61	-0.34	-0.89	0.444	0.749	1	3458		logp=27%, lsf=24%,
749			REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_TERMINATION_	58	-0.35	-0.89	0.446	0.756	1	3202		logp=27%, lsf=24%,
254			BIOCARTA_ARF6EFF_PATHWAY	58	-0.38	-0.89	0.446	0.764	1	3609		logp=27%, lsf=24%,
267			KENG_SIU_ICB_CONTROL_METAGENE_21_PREDICTIVE_ICB_RESISTANCE	120	-0.29	-0.89	0.447	0.752	1	3892		logp=27%, lsf=24%,
238			WP_FAS_PATHWAY_AND_STRESS_INDUCTION_OF_HSP_REGULATION_	58	-0.35	-0.89	0.447	0.754	1	3458		logp=27%, lsf=24%, signal=15%
750			REACTOME_NEUROTRANSMITTER_RECEPTORS_AND_POSTSYNAPTIC_SIGNAL_TRANSMISSION_	43	-0.32	-0.92	0.447	0.757	1	1261		logp=21%, lsf=15%,
164			WP_GLYCOLYSIS_AND_GLUCONEOGENESIS_	51	-0.35	-0.89	0.447	0.765	1	4130		logp=26%, lsf=21%,
374			MCBRYAN_PUBERTAL_BREAST_5_6WK_UP_	61	-0.29	-0.89	0.448	0.767	1	3992		logp=27%, lsf=21%,
747			REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES_	55	-0.35	-0.89	0.449	0.757	1	4222		logp=26%, lsf=24%,
718			ARBUD_LIF_SIGNALING_1_DN	55	-0.38	-0.89	0.45	0.737	1	3347		logp=26%, lsf=22%,
760			SWEET_LUNG_CANCER_KRAS_DN	274	-0.27	-0.89	0.45	0.765	1	5391		logp=26%, lsf=42%,
742			REACTOME_KINESINS_	55	-0.37	-0.89	0.451	0.753	1	3457		logp=26%, lsf=24%,
755			REACTOME_VEGFR2_MEDIATED_VASCULAR_PERMEABILITY_	53	-0.37	-0.89	0.451	0.764	1	3336		logp=26%, lsf=24%,
753			REACTOME_COPI_INDEPENDENT_GOLGI_TO_ER_RETROGRADE_TRAFFIC_	54	-0.33	-0.89	0.452	0.764	1	3801		logp=26%, lsf=24%,
265			DELASERNA_MYOD_TARGETS_DN_	60	-0.33	-0.89	0.455	0.756	1	3890		logp=26%, lsf=24%,
189			GERHOLD_ADIPOGENESIS_DN_	60	-0.31	-0.89	0.459	0.769	1	3873		logp=26%, lsf=21%,
793			WP_OXIDATIVE_STRESS_RESPONSE_	24	-0.35	-1	0.459	0.775	1	4403		logp=26%, lsf=12%,
270			BERENJENO_TRANSFORMED_BY_RHOA_DN_	230	-0.26	-0.89	0.461	0.77	1	5027		logp=26%, lsf=42%,
781			MCCLUNG_DELTA_FOSB_TARGETS_6WK_	52	-0.34	-0.89	0.462	0.767	1	3289		logp=26%, lsf=21%,
762			REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B_	53	-0.38	-0.89	0.463	0.763	1	3126		logp=26%, lsf=24%,
182			REACTOME_AQUAPORIN_MEDIATED_TRANSPORT_	118	-0.38	-0.89	0.463	0.765	1	810		logp=18%, lsf=5%, signal=17%
771			REACTOME_ION_CHANNEL_TRANSPORT_	61	-0.3	-0.89	0.464	0.769	1	3591		logp=26%, lsf=24%,
186			REACTOME_INOSITOL_PHOSPHATE_METABOLISM_	60	-0.33	-1	0.464	0.778	1	1499		logp=26%, lsf=11%,
735			REACTOME_ACTIVATION_OF_BARK_P_PROTEIN_UPON_ADRENERGIC_RECEPTOR_STIMULATION_	18	-0.4	-0.93	0.465	0.748	1	51		logp=13%, lsf=1%, signal=13%
475			REACTOME_TOLL_LIKE_RECEPTOR_4_TLR4_CASCADE_	68	-0.29	-0.89	0.465	0.77	1	3734		logp=26%, lsf=24%,
799			HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_DN_	54	-0.33	-1	0.467	0.777	1	3429		logp=26%, lsf=24%,
753			PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN_	118	-0.28	-0.89	0.468	0.765	1	3527		logp=26%, lsf=24%,
183			REACTOME_RHOG_GTPASE_CYCLE_	56	-0.31	-0.89	0.468	0.774	1	3995		logp=26%, lsf=21%,
253			MIKKELSEN_IPS_LCP_WITH_H3K4ME3_	64	-0.3	-0.89	0.469	0.766	1	3890		logp=26%, lsf=21%,
172			ISTAM_MAD1_TARGETS_DN_	60	-0.32	-0.89	0.47	0.769	1	3564		logp=26%, lsf=21%,
760			WP_PI3_SIGNALING_	65	-0.32	-0.89	0.471	0.765	1	3944		logp=26%, lsf=24%,
781			WP_WNT_SIGNALING_PATHWAY_WP403_	52	-0.33	-1.01	0.471	0.774	1	3539		logp=26%, lsf=24%, signal=21%
774			BROWN_MYELOID_CELL_DEVELOPMENT_DN_	55	-0.28	-0.89	0.472	0.771	1	1147		logp=26%, lsf=11%,
778			REACTOME_ROS_AND_RNS_PRODUCTION_IN_PHAGOCYTES_	53	-0.37	-0.89	0.472	0.775	1	3523		logp=26%, lsf=24%,
267			BIOCARTA_STRESS_PATHWAY_	61	-0.37	-0.89	0.473	0.768	1	4697		logp=26%, lsf=24%,
267			WP_G1_TO_S_CELL_CYCLE_CONTROL_	61	-0.32	-0.89	0.473	0.776	1	3944		logp=26%, lsf=21%,
789			REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE_	61	-0.34	-1	0.473	0.777	1	3241		logp=26%, lsf=24%,
766			REACTOME_RUNX3_REGULATES_CHEMOKINE_RNA_TRANSCRIPTION_FACTOR_ACTIVITY_	20	-0.38	-0.93	0.476	0.765	1	4697		logp=13%, lsf=5%,
479			KONG_E2F3_TARGETS_	64	-0.32	-0.89	0.476	0.775	1	3539		logp=11%, lsf=6%, signal=12%
782			_SCHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP_	57	-0.31	-0.89	0.479	0.773	1	3120		logp=26%, lsf=21%,
185			BIOCARTA_BCKDPTHES_PATHWAY_	21	-0.41	-0.93	0.48	0.769	1	1585		logp=13%, lsf=5%,
177			HEYNEN_TELENCEPHALON_MICROGLIA_	18	-0.38	-0.93	0.48	0.775	1	328		logp=13%, lsf=3%, signal=17%
780			REACTOME_RHOF_GTPASE_CYCLE_	55	-0.33	-1	0.481	0.776	1	3891		logp=26%, lsf=24%,
780			WP_WNT_SIGNALING_PATHWAY_WP539_	55	-0.3	-0.89	0.481	0.774	1	3556		logp=26%, lsf=21%,
785			LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_DN_	29	-0.34	-1	0.481	0.776	1	573		logp=26%, lsf=12%,
810			HU_GENOTOXIN_ACTION_DIRECT_VS_INDIRECT_24HR_	61	-0.32	-0.89	0.481	0.779	1	3891		logp=26%, lsf=24%,
791			SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_DN_	15	-0.39	-1	0.483	0.775	1	1225		logp=26%, lsf=12%,
798			BIOCARTA_RAS_PATHWAY_	21	-0.37	-1	0.483	0.776	1	471		logp=26%, lsf=5%, signal=12%
815			WP_EPO_RECEPTOR_SIGNALING_	20	-0.36	-0.89	0.483	0.778	1	2597		logp=26%, lsf=24%,
794			LIM_MAMMARY_LUMINAL_MATURE_DN_	61	-0.29	-1	0.484	0.775	1	3992		logp=26%, lsf=24%,
801			REACTOME_TNF_SIGNALING_	60	-0.3	-1	0.485	0.776	1	3583		logp=26%, lsf=24%,
800			REACTOME_CELL_CYCLE_CHECKPOINTS_	197	-0.26	-1	0.486	0.776	1	3710		logp=26%, lsf=42%,
811			BOYLAN_MULTIPLE_MYELOMA_D_UP_	62	-0.3	-0.89	0.486	0.778	1	3717		logp=26%, lsf=21%,
776			CHYLA_CBFA2T3_TARGETS_UP_	214	-0.27	-1.01	0.487	0.775	1	5402		logp=26%, lsf=34%,
756			REACTOME_NEUTROPHIL_DEGRANULATION_	118	-0.28	-1	0.487	0.775	1	3523		logp=26%, lsf=24%,
788			COATES_MACROPHAGE_M1_VS_M2_DN_	61	-0.3	-1	0.488	0.777	1	3892		logp=26%, lsf=21%,
787			KEGG_CENTRAL_GLOCK_	64	-0.32	-0.89	0.488	0.779	1	3891		logp=26%, lsf=23%,
787			ATFAR_YY1_TARGETS_UP_	60	-0.29	-1	0.489	0.777	1	3119		logp=26%, lsf=21%,
816			REACTOME_GLUCONEOGENESIS_	54	-0.35	-0.89	0.489	0.778	1	4696		logp=26%, lsf=21%,
819			WP_TRYPTOPHAN_METABOLISM_	53	-0.33	-0.89	0.49	0.783	1	3501		logp=26%, lsf=24%,
794			PONTEK_PKD1_TARGETS_UP_	54	-0.33	-1	0.491	0.776	1	3515		logp=26%, lsf=23%,
806			DETOR_IPRO1_TARGETS_	57	-0.37	-1	0.494	0.775	1	3214		logp=26%, lsf=24%,
831			REACTOME_RIPK1_MEDIATED_REGULATED_NECROSIS_	20	-0.34	-0.98	0.496	0.79	1	3370		logp=26%, lsf=24%,
807			DAIROHE_PAPILLOMA_RISK_LOW_DN_	61	-0.28	-1	0.497	0.774	1	3864		logp=26%, lsf=24%,
830			LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_SMALL_VS_HUGE_DN_	55	-0.35	-0.98	0.497	0.791	1	3891		logp=26%, lsf=21%,
826			WENG_FOR_TARGETS_LIVER_DN_	22	-0.35	-0.98	0.499	0.795	1	1364		logp=26%, lsf=12%,
829			REACTOME_RAS_PROCESSING_	18	-0.37	-0.98	0.499	0.791	1	328		logp=26%, lsf=12%,
818			REACTOME_RAB_GEF3_EXCHANGE_GTP_FOR_GDP_ON_RABS_	63	-0.29	-0.89	0.5	0.779	1	1324		logp=26%, lsf=12%,
812			WP_G_PROTEIN_SIGNALING_PATHWAYS_	21	-0.41	-0.98	0.501	0.781	1	487		logp=26%, lsf=5%, signal=12%
862			VARELA_ZMPST24_TARGETS_UP_	54	-0.33	-1	0.502	0.777	1	1769		logp=26%, lsf=18%,
864			HOFFMANN_LARGE_TO_SMALL_PRE_BI_LYMPHOCYTE_UP_	54	-0.28	-1	0.502	0.777	1	3119		logp=26%, lsf=21%,
823			DELACROIX_RAR_BOUND_ES_	55	-0.26	-1	0.503	0.777	1	1890		logp=26%, lsf=18%,
825			REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE_	21	-0.36	-0.99	0.505	0.787	1	2389		logp=26%, lsf=12%,
792			HEYNEN_CORTEX_RADIAL_GLIA_PROGENITORS_	28	-0.26	-1	0.506	0.775	1	2510		logp=26%, lsf=12%,
836			MIKKELSEN_MEF_HCP_WITH_H3K27ME3_	54	-0.29	-0.98	0.508	0.79	1	3296		logp=26%, lsf=21%,
837			REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX_	18	-0.37	-0.98	0.509	0.798	1	750		logp=18%, lsf=5%,
839			WP_EUKARYOTIC_TRANSCRIPTION_INITIATION_	20	-0.32	-0.98	0.51	0.785	1	1327		logp=18%, lsf=12%,
839			REACTOME_GOLGI_TO_ER_RETROG

295			REACTOME SYNTHESIS OF PA	38	0.36	0.92	0.55	0.893	1	2421	logn=31%, list=24%,	
897			REACTOME NUCLEOTIDE BINDING DOMAIN LEUCINE RICH REPEAT CONTAINING RECEPTOR NLR SIGNALING PATHWAY	38	0.32	0.95	0.55	0.817	1	2525	logn=30%, list=25%,	
468			GAIL SEN MAYO	58	0.29	0.95	0.522	0.8	1	2621	logn=26%, list=23%,	
973			SCHAEFER PROSTATE DEVELOPMENT 12HR DN	74	0.26	0.94	0.503	0.802	1	2184	logn=22%, list=21%,	
976			FENG GU IDB CONTROL METAGENE 10 PREDICTIVE IQR RESPONSE	84	0.27	0.95	0.493	0.861	1	2160	logn=20%, list=21%,	
480			LION CEREBELLUM MARKER	61	0.3	0.95	0.494	0.813	1	2572	logn=25%, list=23%,	
499			BIOCARTA CREB PATHWAY	41	0.36	0.95	0.556	0.815	1	2179	logn=18%, list=21%,	
235			REACTOME M PHASE	265	0.26	0.95	0.559	0.791	1	2210	logn=9%, list=19%,	
480			DARWICHE SKIN TUMOR PROMOTER UP	56	0.28	0.95	0.493	0.802	1	2130	logn=27%, list=22%,	
492			HP CHOLESTEROL BIOSYNTHESIS	15	0.37	0.94	0.509	0.817	1	1572	logn=33%, list=17%,	
414			ZOTLAN MULTIPLE MYELOMA D CLUSTER DN	23	0.33	0.94	0.52	0.825	1	1148	logn=30%, list=15%,	
865			BIOCARTA GH PATHWAY	22	0.34	0.95	0.56	0.862	1	2369	logn=30%, list=23%,	
515			BIOCARTA TYR PATHWAY	20	0.34	0.95	0.57	0.817	1	2101	logn=31%, list=21%,	
861			FENG FOXP3 TARGETS UP	60	0.34	0.95	0.561	0.813	1	2301	logn=21%, list=23%,	
264			BIOCARTA EPO PATHWAY	21	0.35	0.94	0.562	0.817	1	1845	logn=30%, list=18%,	
481			HOLLEIN EWT BREAST TUMOR UP	78	0.28	0.94	0.493	0.803	1	2656	logn=20%, list=27%,	
261			BREDEMEYER RAS SIGNALING VIA ATM NOT VIA NFKB UP	54	0.31	0.95	0.503	0.815	1	1504	logn=26%, list=15%,	
563			REACTOME TRANSFERRIN ENDOCITOSIS AND RECYCLING	17	0.33	0.94	0.503	0.817	1	1104	logn=29%, list=11%,	
555			RAENE HETOX PATHWAY AND CARCINOGENESIS DN	71	0.35	0.93	0.466	0.845	1	2190	logn=20%, list=21%,	
492			CLASBUR LYMPHATIC VESSELS DURING METASTASIS DN	18	0.35	0.94	0.49	0.816	1	1540	logn=25%, list=12%,	
498			HP TARGETS OF PTCH1 AND SUFU DN	18	0.35	0.95	0.484	0.818	1	1668	logn=25%, list=12%,	
329			REACTOME REGULATION OF INSULIN SECRETION	59	0.32	0.93	0.57	0.825	1	1247	logn=9%, list=16%,	
492			DARWICHE DEGRADATION OF TP53 ACTIVITY THROUGH METHYLATION	18	0.35	0.93	0.47	0.826	1	2034	logn=25%, list=12%,	
412			BILANDES SERUM RESPONSE TRANSLATION	29	0.33	0.94	0.572	0.821	1	1696	logn=22%, list=16%,	
450			TORDAI TARGETS OF ENSEL FUSION DN	23	0.28	0.92	0.57	0.798	1	2419	logn=25%, list=15%,	
877			DURAND STROMA 5 UP	149	0.26	0.95	0.473	0.892	1	2576	logn=20%, list=23%,	
481			REACTOME FORMATION OF WDR5-CONTAINING RESTORE-MODIFYING COMPLEX	21	0.34	0.94	0.49	0.818	1	1121	logn=29%, list=11%,	
307			CLASABE TGFB1 SIGNALING VIA NFIC HIR UP	21	0.34	0.93	0.574	0.826	1	1175	logn=24%, list=11%,	
369			REACTOME SEMAPHORIN INTERACTIONS	39	0.32	0.95	0.576	0.816	1	1370	logn=21%, list=14%,	
492			REACTOME STAT5A1 SENSING CHANNELS	39	0.31	0.94	0.477	0.816	1	2221	logn=25%, list=20%,	
474			DARWICHE SQUAMOUS CELL CARCINOMA UP	129	0.27	0.95	0.478	0.861	1	2648	logn=21%, list=26%,	
480			DARWICHE PAPILOMA RISK HIGH UP	61	0.27	0.95	0.479	0.814	1	2648	logn=20%, list=26%,	
841			HP NUCLEAR RECEPTORS	24	0.32	0.95	0.479	0.833	1	2662	logn=24%, list=22%,	
416			REACTOME TGF BETA RECEPTOR SIGNALING ACTIVATES SMAD8	21	0.34	0.94	0.48	0.817	1	1540	logn=27%, list=12%,	
918			TAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 3	60	0.28	0.95	0.481	0.824	1	2664	logn=20%, list=24%,	
357			BIOCARTA TR1 PATHWAY	17	0.35	0.92	0.561	0.8	1	179	logn=12%, list=3%, signal=12%	
419			REACTOME CHARACTERIZATION OF SMAD2 A SMAD4 TRANSCRIPTORS ACTIVATED BY TGF BETA	18	0.34	0.94	0.483	0.841	1	1836	logn=27%, list=13%,	
295			REACTOME RHOD GTPASE CYCLE	69	0.29	0.93	0.492	0.806	1	2593	logn=21%, list=23%,	
499			REACTOME RHOD GTPASE CYCLE	21	0.28	0.93	0.49	0.825	1	2593	logn=25%, list=23%,	
356			REACTOME RHO GTPASES ACTIVATE IQGAPS	20	0.34	0.93	0.483	0.857	1	1806	logn=25%, list=12%,	
345			LACROIX DUROSTAL BREAST 3 4W DN	19	0.34	0.91	0.484	0.835	1	1540	logn=25%, list=12%,	
493			HP NF93 TARGETS UP	109	0.26	0.95	0.483	0.814	1	2656	logn=20%, list=26%,	
316			MIKKELSEN NPC HCP WITH H3K27ME3	61	0.29	0.94	0.588	0.823	1	1349	logn=19%, list=13%,	
491			SINNAMANN RESPONSE TO MC AND SERUM DEPRIVATION DN	19	0.35	0.93	0.49	0.825	1	1589	logn=25%, list=13%,	
487			HEDA MIR9 TARGETS UP	109	0.27	0.95	0.489	0.813	1	2656	logn=20%, list=26%,	
495			REACTOME INTERLEUKIN 3 INTERLEUKIN 5 AND GM CSF SIGNALING	19	0.37	0.92	0.49	0.827	1	1579	logn=25%, list=13%,	
819			REACTOME SIGNALING BY FGFR2	65	0.29	0.93	0.491	0.845	1	2697	logn=21%, list=24%,	
464			REREDIMO TRANSFORMED BY RVSA FOREVER DN	21	0.33	0.95	0.49	0.845	1	2419	logn=25%, list=15%,	
1106			REACTOME SIGNALLING TO ERKS	20	0.35	0.93	0.493	0.835	1	2406	logn=25%, list=14%,	
359			REACTOME PROTEIN PROTEIN INTERACTIONS AT SYNAPSES	23	0.31	0.91	0.495	0.836	1	1348	logn=22%, list=13%,	
483			BIOCARTA IL1R PATHWAY	20	0.34	0.93	0.495	0.818	1	2243	logn=25%, list=12%,	
442			MILI PSEUDOPODIA HAPTOTAXIS UP	169	0.25	0.95	0.496	0.795	1	2593	logn=20%, list=23%,	
443			CHN B CELL LYMPHOMA CLUSTER 3	19	0.35	0.92	0.49	0.835	1	1618	logn=25%, list=13%,	
371			BIOCARTA PML PATHWAY	15	0.35	0.9	0.497	0.845	1	1496	logn=31%, list=13%,	
492			CHARADONNA NEOPLASTIC TRANSFORMATION CDC25 DN	118	0.26	0.94	0.498	0.822	1	2593	logn=21%, list=23%,	
479			RAY TUMORIGENESIS BY ERBB2 OKCSA DN	109	0.26	0.95	0.491	0.861	1	2638	logn=20%, list=26%,	
264			IGLESIAS E2F TARGETS UP	122	0.26	0.95	0.501	0.815	1	2552	logn=20%, list=25%,	
491			REACTOME VIRUS PHOTOTRANSDUCTION	19	0.35	0.93	0.491	0.844	1	1571	logn=25%, list=13%,	
254			MORI EMU MYC LYMPHOMA BY DNMET TIME UP	72	0.27	0.93	0.492	0.806	1	2736	logn=22%, list=25%,	
487			YANOVA HEMATOPOIESIS EARLY PROGENITOR	22	0.33	0.92	0.49	0.862	1	2243	logn=25%, list=12%,	
359			HORTON SREBF TARGETS	24	0.33	0.92	0.497	0.833	1	1572	logn=25%, list=13%,	
490			REACTOME FLAIL 5 PERIPHERAL MEMBRANE PROTEIN IMPORT	21	0.33	0.91	0.49	0.845	1	1540	logn=25%, list=12%,	
444			REACTOME TP53 METHYLATES HISTONES AND DNA	20	0.33	0.92	0.493	0.834	1	1532	logn=25%, list=12%,	
365			NAKABAYASHI ADIPOGENESIS PPARG BOUND 36HR	22	0.32	0.9	0.503	0.849	1	1824	logn=25%, list=15%,	
492			ZOTLAN MULTIPLE MYELOMA D DN	23	0.28	0.91	0.49	0.825	1	2638	logn=25%, list=21%,	
283			REACTOME TP53 REGULATES METABOLIC GENES	21	0.28	0.92	0.511	0.835	1	2743	logn=25%, list=21%,	
465			ZOTLAN MULTIPLE MYELOMA C CLUSTER DN	19	0.32	0.92	0.49	0.837	1	1736	logn=25%, list=14%,	
493			BURTON ADIPOGENESIS 8	24	0.29	0.93	0.513	0.833	1	2150	logn=21%, list=17%,	
492			SHETH LIVER CANCER VS TXNIP LOSS PAM3	24	0.29	0.94	0.49	0.816	1	2656	logn=21%, list=21%,	
466			REACTOME RESOLUTION OF SISTER CHROMATID COHESION	20	0.26	0.92	0.515	0.833	1	2406	logn=25%, list=19%,	
352			REACTOME CDC42 GTPASE CYCLE	67	0.28	0.92	0.516	0.836	1	2693	logn=21%, list=21%,	
479			HOFMANN PRE BI TO LARGE PRE BII LYMPHOCYTE DN	21	0.28	0.94	0.518	0.846	1	2611	logn=25%, list=19%,	
276			REACTOME RHO GTPASES ACTIVATE PKNS	19	0.35	0.9	0.518	0.845	1	1696	logn=25%, list=13%,	
481			HP GLUTATHIONE AND ONE CARBON METABOLISM	21	0.31	0.9	0.51	0.844	1	1532	logn=25%, list=12%,	
474			REACTOME TELOMERE EXTENSION BY TELOMERASE	15	0.35	0.9	0.519	0.845	1	1513	logn=31%, list=13%,	
460			HALASKA MYOD TARGETS UP	24	0.29	0.91	0.52	0.844	1	2243	logn=25%, list=12%,	
448			HP METAPATHWAY BIOTRANSFORMATION	19	0.27	0.92	0.521	0.832	1	2486	logn=25%, list=15%,	
317			MEISSNER NPC HCP WITH H3 UNMETHYLATED	193	0.25	0.93	0.524	0.824	1	2192	logn=19%, list=17%,	
487			HP IL-2 SIGNALING PATHWAY	24	0.27	0.93	0.525	0.837	1	2397	logn=21%, list=19%,	
290			CLASABE TGFB1 TARGETS 10HR UP	90	0.26	0.93	0.528	0.825	1	1866	logn=21%, list=13%,	
1000			REACTOME RHO GTPASES ACTIVATE WASPS AND WAVES	20	0.3	0.88	0.53	0.865	1	2243	logn=25%, list=12%,	
493			FANG AGING HYPOTHALAMUS DN	28	0.3	0.88	0.53	0.857	1	2416	logn=24%, list=12%,	
357			BYSTRYN HEMATOPOIESIS STEM CELL SCF2 QTL TRANS	20	0.31	0.9	0.53	0.856	1	1540	logn=25%, list=12%,	
487			REACTOME NTRK GIVOR TRAFFIC	20	0.31	0.9	0.53	0.844	1	1537	logn=25%, list=12%,	
487			BIOCARTA CERAMIDE PATHWAY	21	0.33	0.89	0.534	0.852	1	1696	logn=21%, list=13%,	
477			REACTOME CELL CYCLE	579	0.25	0.95	0.536	0.805	1	2710	logn=20%, list=21%,	
481			REACTOME TRANSMISSION ACROSS CHEMICAL SYNAPSES	24	0.27	0.92	0.53	0.835	1	2348	logn=20%, list=21%,	
498			REACTOME MITOTIC SPINDLE CHECKPOINT	21	0.27	0.92	0.537	0.844	1	2406	logn=25%, list=21%,	
493			HOFMANN SMALL PRE BII TO IMMATURE B LYMPHOCYTE DN	21	0.31	0.9	0.534	0.846	1	1824	logn=21%, list=13%,	
497			REACTOME ESTROGEN DEPENDENT GENE EXPRESSION	24	0.29	0.9	0.534	0.846	1	2304	logn=21%, list=13%,	
497			SARTBY NORMAL AT INSULIN RESISTANCE UP	23	0.32	0.88	0.538	0.863	1	835	logn=17%, list=3%, signal=19%	
492			REACTOME ANCHORING OF THE BASAL BODY TO THE PLASMA MEMBRANE	66	0.27	0.9	0.533	0.844	1	2191	logn=21%, list=19%,	
1084			SCHMIDT POR TARGETS IN LMB BUD UP	22	0.31	0.88	0.543	0.866	1	1572	logn=25%, list=12%,	
346			E E2F2 TARGETS DN	17	0.27	0.88	0.544	0.853	1	1243	logn=31%, list=9%,	
1006			HP GLYCEROLIPIDS AND GLYCEROPHOSPHOLIPIDS WP4145	17	0.33	0.88	0.545	0.865	1	870	logn=18%, list=5%, signal=19%	
1012			REACTOME PROTEIN METHYLATION	20	0.28	0.91	0.545	0.844	1	2419	logn=25%, list=12%,	
356			REACTOME PI METABOLISM	60	0.28	0.91	0.547	0.838	1	2536	logn=20%, list=21%,	
356			REACTOME DOWNSTREAM SIGNAL TRANSDUCTION	22	0.31	0.88	0.548	0.861	1	2697	logn=21%, list=24%,	
498			REACTOME ANTIVIRAL MECHANISM BY IFN STIMULATED GENES	21	0.27	0.91	0.49	0.835	1	2604	logn=25%, list=23%,	
270			REACTOME PROGRAMMED CELL DEATH	120	0.25	0.9	0.49	0.843	1	2370	logn=22%, list=21%,	
498			REACTOME METABOLISM OF FAT SOLUBLE VITAMINS	19	0.28	0.89	0.46	0.871	1	2171	logn=25%, list=19%,	
1019			BIOCARTA PTEN PATHWAY	15	0.33	0.87	0.551	0.873	1	1347	logn=31%, list=11%,	
1013			REACTOME SUMOYLATION OF SUMOYLATION PROTEINS	19	0.3	0.87	0.552	0.87	1	1234	logn=25%, list=11%,	
1013			HP GLYCEROLIPIDS AND GLYCEROPHOSPHOLIPIDS WP4236	19	0.33	0.87	0.552	0.87	1	870	logn=18%, list=5%, signal=19%	
375			HP OXIDATIVE STRESS AND REDOX PATHWAY	69	0.26	0.9	0.553	0.844	1	1234	logn=20%, list=11%,	
492			REACTOME NEGATIVE REGULATION OF FGFR3 SIGNALING	19	0.34	0.88	0.553	0.862	1	1234	logn=25%, list=11%,	
1033			REACTOME GLYCOGEN METABOLISM	15	0.34	0.88	0.556	0.873	1	1208	logn=31%, list=12%,	
1039			REACTOME NEGATIVE REGULATION OF FGFR2 SIGNALING	17	0.33	0.88	0.557	0.873	1	1347	logn=25%, list=11%,	
492			MORI EMU MYC LYMPHOMA BY DNMET TIME DN	17	0.33	0.88	0.557	0.873	1	2646	logn=25%, list=23%,	
1006			CLASABE TGFB1 SIGNALING VIA NFIC 0HR DN	17	0.33	0.88	0.557	0.873	1	2243	logn=25%, list=12%,	
466			HM MAMMARY STEM CELL DN	20	0.28	0.91	0.559	0.813	1	2371	logn=25%, list=19%,	
1001			GAVIN FOXP3 TARGETS CLUSTER P5	64	0.28	0.88	0.561	0.866	1	1799	logn=20%, list=16%,	
1002			REACTOME NEGATIVE REGULATION OF FGFR4 SIGNALING	18	0.33	0.88	0.561	0.867	1	1697	logn=25%, list=16%,	
492			REACTOME RHO GTPASES ACTIVATE FORMINS	24	0.26	0.91	0.562	0.837	1	2406	logn=25%, list=21%,	
487			SCHAEFER PROSTATE DEVELOPMENT 6HR UP	21	0.25	0.91	0.562	0.832	1	2180	logn=25%, list=21%,	
1012			HP GPCR5 NON OSDRANT	19	0.28	0.87	0.564	0.871	1	2606	logn=25%, list=23%,	
1006			REACTOME GLUCOSE METABOLISM	20	0.28	0.88	0.564	0.856	1	2371	logn=25%, list=19%,	
493			REACTOME NUCLEOTIDE EXCISION REPAIR	20	0.28	0.9	0.563	0.844	1	1818	logn=25%, list=14%,	
498			REACTOME INTERLEUKIN 17 SIGNALING	49	0.27	0.88	0.563	0.863	1	1697	logn=20%, list=16%,	
1018			REACTOME PKR MEDIATED SIGNALING	24	0.27	0.88	0.57	0.869	1	2131	logn=25%, list=17%,	
1027			HP HEART DEVELOPMENT	24	0.31	0.88	0.57	0.873	1	720	logn=12%, list=7%, signal=12%	
498			RAD BOUND BY SALL4 (SCPDM 3)	19	0.24	0.91	0.571	0.818	1	2243	logn=25%, list=12%,	
345			DI PLAGIARCYTOMA UP	149	0.25	0.92	0.571	0.844	1	2656	logn=25%, list=21%,	
1033			REACTOME PEPTIDE HORMONE METABOLISM	17	0.32	0.87	0.573	0.873	1	1347	logn=25%, list=11%,	
490			REACTOME METABOLISM OF VITAMINS AND COFACTORS	19	0.31	0.87	0.573	0.837	1	2163	logn=25%, list=11%,	
1033			REACTOME SUMOYLATION OF DNA REPLICATION PROTEINS	23	0.29	0.88	0.574	0.874	1	2591	logn=20%, list=21%,	
1015			MIKKELSEN NPC HCP WITH H3K4ME3 AND H3K27ME3	93	0.25	0.91	0.577	0.849	1	2316	logn=19%, list=19%,	
1015			MEISSNER NPC HCP WITH H3K4ME3 AND H3K27ME3	92	0.27	0.92	0.577	0.87	1	2591	logn=20%, list=24%,	
493			SCHAEFER PROSTATE DEVELOPMENT 48HR UP	20	0.24	0.91	0.58	0.838	1	2243	logn=25%, list=12%,	
1006			REACTOME SMOOTH MUSCLE CONTRACTION	20	0.31	0.88	0.58	0.873	1	1460	logn=25%, list=11%,	
492			BAKER FOXP3 TARGETS UP	21	0.27	0.91	0.58	0.874	1	2243	logn=25%, list=12%,	
1000			REACTOME BRANCHED CHAIN AMINO ACID CATABOLISM	17	0.31	0.84	0.583	0.855	1	1664	logn=31%, list=13%,	
321			SHETH LIVER CANCER VS TXNIP LOSS PAM4	195	0.24	0.93	0.586	0.824	1	2389	logn=19%, list=21%,	
484			DARWICHE PAPILOMA RISK HIGH DN	119	0.25	0.9	0.585	0.848	1	2534	logn=20%, list=23%,	
1029			REACTOME CYCLIN D ASSOCIATED EVENTS IN G1	20	0.28	0.88	0.586	0.876	1	2577	logn=25%, list=23%,	
1040			HEUNER TELENCEPHALON MENINGEAL CELLS	20	0.28	0.88	0.59	0.876	1	2545	logn=25%, list=23%,	
366			REACTOME TRANSLOCATION OF RIBOSOME	119	0.25	0.91	0.587	0.837	1	2693	logn=20%, list=21%,	
1006			REACTOME TRANSPORT OF VITAMINS NUCLEOSIDES AND RELATED MOLECULES	19	0.31	0.87	0.59	0.873	1	1347	logn=25%, list=11%,	
1006			MA MYELOID DIFFERENTIATION DN	20	0.29	0.86	0.589	0.874	1	2649	logn=25%, list=21%,	
313			MIKKELSEN ES ICP WITH H3K4ME3	199	0.24	0.94	0.591	0.82	1	2398	logn=19%, list=21%,	
1000			REACTOME RHOD GTPASE CYCLE	24	0.27	0.84	0.593	0.861	1	2593	logn=25%, list=23%,	
295			CHARADONNA NEOPLASTIC TRANSFORMATION CDC25 UP	67	0.25	0.89	0.595	0.859	1	2172	logn=21%, list=23%,	
465			GAVIN FOXP3 TARGETS CLUSTER P3	21	0.28	0.89	0.596	0.854	1	2391	logn=25%, list=21%,	
1045			REACTOME HOMOLOGOUS END JOINING MHEJ	21	0.28	0.85	0.598	0.879	1	1874	logn=25%, list=16%,	
1041			REACTOME TP53 REGULATES TRANSCRIPTION OF DNA REPAIR GENES	19	0.27	0.85	0.599	0.88	1	2398	logn=25%, list=21%,	
489			CANDI FRIBO BREAST TUMORS 3W DN	119	0.24	0.89	0.704	0.858	1	2576	logn=20%, list=23%,	
281			DARWICHE SKIN TUMOR PROMOTER UP	119	0.25	0.89	0.705	0.858	1	2261	logn=20%, list=22%,	
1002			BRUNS UVC RESPONSE VIA TP53 GROUP A	119	0.24	0.89	0.706	0.864	1	2519	logn=20%, list=23%,	
1022			REACTOME CHROMOSOME MAINTENANCE	20	0.26	0.86	0.71	0.875	1	2591	logn=21%, list=21%,	
1063			REACTOME DEADSYNTHYLASE, UP, THE 36 TR_CATENER_TRANSACTIVATING_COMPLEX	20	0.28	0.84	0.711	0.88	1	2243	logn=25%, list=12%,	
1046			HUANG GATA2 TARGETS DN	21	0.27	0.85	0.712	0.883	1	1460	logn=31%, list=11%,	
1015			TAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 2	67	0.27	0.84	0.712	0.88	1	2664	logn=20%, list=24%,	
1039			REACTOME CELLULAR SENESCENCE	69	0.26	0.86	0.713	0.88	1	2666	logn=20%, list=24%,	
1067			STEGER ADIPOGENESIS DN	19	0.32	0.83	0.717	0.886	1	629	logn=13%, list=3%, signal=14%	
1037			REACTOME DRUG ADME	19	0.25	0.86	0.719	0.876	1	2604	logn=25%, list=23%,	
1024			CANDI BREAST CANCER PROGRESSION DN	67	0.26	0.87	0.72	0.873	1	2293	logn=20%, list=22%,	
1048			REACTOME PROCESSING OF DNA DOUBLE STRAND BREAK ENDS	21	0.27	0.85	0.721	0.884	1	1818	logn=25%, list=14%,	
1076			CINGUBAHA TP53 TARGETS	21	0.25	0.85	0.72	0.892	1	1187	logn=25%, list=11%,	
1037			REACTOME DNA DOUBLE STRAND BREAK REPAIR	21	0.24	0.86	0.72	0.876	1	2591	logn=25%, list=21%,	
1066			REACTOME SYNTHESIS OF DNA OMEGA-6 FATTY ACIDS UP TO AT AND AT ANALOGS	20	0.24	0.85	0.722	0.856	1	2243	logn=25%, list=12%,	
1071			REACTOME TAK1 DEPENDENT IKK AND NF KAPPA B ACTIVATION	69	0.25	0.85	0.722	0.9	1	2453	logn=20%, list=22%,	
1047			BIOCARTA BRAKE PATHWAY	24	0.26	0.85	0.723	0.884	1	2243	logn=25%, list=12%,	
1069			REACTOME DNA DAMAGE RECOGNITION IN GG NER	24	0.26	0.85	0.723	0.887	1	2538	logn=25%, list=23%,	
1067			DURAND STROMA NS UP	24	0.26	0.85	0.724	0.88	1	2576	logn=25%, list=23%,	
1064			TAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 10	61	0.25	0.85	0.725	0.88	1	2406	logn=22%, list=21%,	
1068			REACTOME ETHYL ACID FATTY ACIDS TOA CYCLE	24	0.25	0.85	0.725	0.889	1	2419	logn=25%, list=21%,	
1068			DARWICHO MYELOID MN1 NETWORK	21	0.31	0.81	0.725	0.909	1	2132	logn=18%, list=11%,	
942			LAZARO GENETIC MOUSE MODEL HIGH GRADE SMALL CELL NEUROENDOCRINE LUNG CARCINOMA UP	266	0.24	0.92	0.726	0.836	1	2437	logn=24%, list=24%, signal=24%	
1018			DARWICHE SQUAMOUS CELL CARCINOMA DN	139	0.25	0.87	0.729	0.871	1	2622	logn=20%, list=22%,	
1014			REACTOME PROTEIN LOCALIZATION	20	0.27	0.87	0.73	0.87	1	2591	logn=25%, list=21%,	
1051			GUO HEX TARGETS DN	21	0.26	0.84	0.73	0.881	1	429	logn=10%, list=4%, signal=10%	
1102			REACTOME METALLOPROTEASE DUBS	21	0.21	0.85	0.73	0.905	1	1511	logn=31%, list=11%,	
1056			MORI IMMATURE B LYMPHOCYTE DN	24	0.25	0.84	0.731	0.895	1	2799	logn=21%, list=23%,	
1079			REACTOME METABOLISM OF CARBOHYDRATES	19	0.24	0.81	0.731	0.9	1	2171	logn=25%, list=19%,	
1098			REACTOME G PROTEIN BETA GAMMA SIGNALING	19	0.24	0.81	0.732	0.907	1	2347	logn=25%, list=19%,	
1064			BRUNS UVC RESPONSE VIA TP53 GROUP C	62	0.26	0.84	0.733	0.881	1	2324	logn=21%, list=21%,	
1065			REACTOME RAB GERANYLGERANYLATION	24	0.25	0.83	0.737	0.89	1	2419	logn=25%, list=21%,	
1074			REACTOME ACTIVATION OF BIR ONLY PROTEINS	15	0.32	0.82	0.737	0.903	1	1108	logn=31%, list=11%,	
1082			MIKKELSEN MEF LCP WITH H3K27ME3	61	0.24	0.82	0.737	0.902	1	2172	logn=20%, list=21%,	
1069			REACTOME ORGANELLE BIOGENESIS AND MAINTENANCE	149	0.24	0.88	0.738	0.866	1	2419	logn=20%, list=21%,	
1042			REACTOME DNA DOUBLE STRAND BREAK REPAIR	24	0.24	0.84	0.739	0.89	1	2591	logn=25%, list=21%,	
1059			HP CALCIUM REGULATION IN CARDIAC CELLS	20	0.26	0.84	0.739	0.896	1	1679	logn=25%, list=13%,	
1061			BURTON ADIPOGENESIS PEAK AT 24HR	24	0.28	0.83	0.741	0.887	1	2668	logn=21%, list=23%,	
1073			HP OXIDATIVE PHOSPHORYLATION	24	0.24	0.81	0.8	0.9	1	2591	logn=25%, list=21%,	
1077			REACTOME TRANSLESION SYNTHESIS BY Y FAMILY DNA POLYMERASES BYPASS LESIONS ON DNA TEMPLATE	31	0.28	0.82	0.744	0.901	1	1417	logn=19%, list=14%, signal=20%	
1091			HP LUNG FIBROSIS	20	0.28	0.81	0.744	0.908	1	2330	logn=25%, list=23%,	
1080			REACTOME POST TRANSLATIONAL MODIFICATION SYNTHESIS OF GPI ANCHORED PROTEINS	34	0.27	0.82	0.747	0.901	1	1695	logn=14%, list=10%, signal=16%	
1093			REACTOME

1115		JOHNSON GLIOMAGENESIS BY PDGFR UP	66	0.25	0.8	0.786	0.912	1	3326		sig=24%, lid=23%,
1164		SCHAEFFER SOX9 TARGETS IN PROSTATE DEVELOPMENT DN	51	0.26	0.77	0.786	0.951	1	3597		sig=45%, lid=33%,
1097		REACTOME SNRNP ASSEMBLY	64	0.26	0.81	0.786	0.967	1	3383		sig=24%, lid=21%,
1137		BIOCARTA FAS PATHWAY	24	0.28	0.78	0.787	0.918	1	830		sig=13%, lid=5%, qval=1%
1093		FARRELL ATG14L1 TARGETS DN	64	0.24	0.81	0.787	0.967	1	3358		sig=24%, lid=21%,
1104		REACTOME AMPLIFICATION OF SIGNAL FROM THE KINETOCHORES	60	0.24	0.81	0.788	0.954	1	3371		sig=21%, lid=22%,
1155		REACTOME ACTIVATION OF NMDA RECEPTORS AND POSTSYNAPTIC EVENTS	15	0.3	0.76	0.789	0.935	1	51		sig=7%, lid=3%, qval=1%
1133		REACTOME SUMOYLATION OF UBIQUITINATION PROTEINS	54	0.25	0.78	0.79	0.944	1	3462		sig=18%, lid=18%,
1149		BIOCARTA BAD PATHWAY	18	0.29	0.78	0.79	0.927	1	1840		sig=61%, lid=33%,
1123		DATZA SPERMATOCYTE	24	0.27	0.78	0.792	0.914	1	1284		sig=33%, lid=33%,
1151		GAUSMANN MLL AF4 FUSION TARGETS B UP	17	0.29	0.78	0.792	0.932	1	3762		sig=32%, lid=32%,
1107		PATSANOU ELAVL1 TARGETS UP	31	0.27	0.81	0.793	0.955	1	2367		sig=22%, lid=17%,
1072		REACTOME TRANSCRIPTION COUPLED NUCLEOTIDE EXCISION REPAIR TC NER	67	0.23	0.81	0.794	0.954	1	3918		sig=24%, lid=23%,
1136		YANAGA CARCINOGENESIS BY KRAS UP	106	0.23	0.83	0.799	0.899	1	3195		sig=22%, lid=22%,
1136		REACTOME G2 M DNA DAMAGE CHECKPOINT	58	0.24	0.78	0.804	0.916	1	3934		sig=24%, lid=24%,
1152		REACTOME PYRIMIDINE METABOLISM	18	0.26	0.78	0.805	0.955	1	3594		sig=64%, lid=33%,
1141		REACTOME PLATELET HOMEOSTASIS	36	0.25	0.79	0.807	0.92	1	3430		sig=24%, lid=24%,
1175		HP PROSTAGLANDIN SYNTHESIS AND REGULATION	15	0.29	0.74	0.81	0.942	1	2430		sig=27%, lid=21%,
1140		REACTOME GLYCOLYSIS	24	0.24	0.79	0.811	0.919	1	3107		sig=17%, lid=17%,
1153		REACTOME ENERGY DEPENDENT REGULATION OF MTOR BY LKB1 AMPK	30	0.27	0.78	0.812	0.934	1	3743		sig=24%, lid=21%,
1176		SCHRAETS MEL TARGETS UP	18	0.27	0.74	0.814	0.941	1	3934		sig=24%, lid=24%,
1190		MORI LARGE PRE BII LYMPHOCYTE DN	36	0.25	0.78	0.815	0.922	1	3478		sig=24%, lid=24%,
1171		REACTOME RESOLUTION OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PATCH REPLACEMENT PATHWAY	18	0.27	0.74	0.817	0.943	1	3362		sig=32%, lid=32%, qval=17%
1135		HOWLIN CTEN1 TARGETS 1 DN	28	0.27	0.78	0.818	0.915	1	3138		sig=22%, lid=21%,
1129		REACTOME APOPTOSIS	75	0.23	0.81	0.821	0.911	1	3370		sig=21%, lid=21%,
1157		BIOCARTA FMLP PATHWAY	24	0.27	0.75	0.822	0.937	1	717		sig=33%, lid=3%, qval=6%
1163		MIKKELSEN MEF LCP WITH H3K4M3	31	0.26	0.76	0.823	0.92	1	3530		sig=24%, lid=24%,
1172		REACTOME RHO GTPASES ACTIVATE PAKS	31	0.29	0.74	0.823	0.943	1	3927		sig=24%, lid=24%,
1030		CUI TCF21 TARGETS 2 UP	232	0.23	0.88	0.824	0.878	1	1831		sig=17%, lid=15%,
1112		FIEDLER BRD1 TARGETS UP	58	0.24	0.8	0.824	0.91	1	1869		sig=24%, lid=18%,
1183		HP IL 1 SIGNALING PATHWAY	52	0.25	0.74	0.828	0.942	1	3385		sig=28%, lid=33%,
1095		REACTOME PHOSPHOLIPID METABOLISM	74	0.22	0.81	0.829	0.908	1	3945		sig=18%, lid=18%,
1108		REACTOME RAC1 GTPASE CYCLE	116	0.22	0.81	0.829	0.903	1	3856		sig=24%, lid=24%,
1154		MAKELENA IF5 WITH H3K4M3 AND H3K27M3	28	0.28	0.75	0.83	0.914	1	3263		sig=24%, lid=24%,
1154		REACTOME TNFR1 INDUCED NF KAPPA B SIGNALING PATHWAY	28	0.28	0.76	0.83	0.914	1	3263		sig=24%, lid=24%,
1092		IWAKABAYASHI ARPC5SENS PPARG RXRA BOUND WITH IMR90MET MARK	132	0.22	0.81	0.831	0.908	1	3731		sig=25%, lid=24%,
1105		REACTOME INTERFERON SIGNALING	96	0.23	0.81	0.833	0.903	1	3937		sig=25%, lid=24%,
1122		REACTOME NEURONAL SYSTEM	51	0.24	0.79	0.834	0.914	1	3389		sig=22%, lid=21%,
1160		BIOCARTA GPCR PATHWAY	21	0.27	0.75	0.834	0.938	1	635		sig=14%, lid=5%, qval=12%
1116		REACTOME RESPIRATORY ELECTRON TRANSPORT ATP SYNTHESIS BY CHEMIOSMOTIC COUPLING AND HEAT PRODUCTION BY UNCOUPLING PROTEINS	110	0.22	0.79	0.835	0.915	1	4238		sig=30%, lid=46%,
1143		REACTOME HOMOLOGY DIRECTED REPAIR	61	0.23	0.77	0.836	0.92	1	3596		sig=24%, lid=24%,
1165		REACTOME APOPTOTIC CLEAVAGE OF CELLULAR PROTEINS	24	0.26	0.75	0.837	0.942	1	3940		sig=24%, lid=24%,
1187		HARRIS BRAIN CANCER PROGENITORS	30	0.27	0.73	0.838	0.934	1	3864		sig=24%, lid=24%,
1173		GAUSMANN MLL AF4 FUSION TARGETS D DN	18	0.27	0.74	0.837	0.943	1	583		sig=11%, lid=5%, qval=12%
1181		MATRIX MALE REPRODUCTION SERTOLI	18	0.28	0.73	0.839	0.941	1	3946		sig=24%, lid=24%,
1169		REACTOME NUCLEAR PORE COMPLEX NPC DISASSEMBLY	28	0.25	0.74	0.84	0.941	1	1987		sig=21%, lid=13%,
1188		SYSTROM CORRELATED WITH IL3 UP	24	0.26	0.74	0.84	0.945	1	3303		sig=41%, lid=41%,
1101		REACTOME EUKARYOTIC TRANSLATION INITIATION	119	0.23	0.81	0.841	0.906	1	3310		sig=21%, lid=21%,
1113		REACTOME RESPIRATORY ELECTRON TRANSPORT	60	0.22	0.79	0.841	0.915	1	4017		sig=18%, lid=15%,
1139		BURTON ADIPOGENESIS 2	30	0.24	0.78	0.841	0.92	1	3816		sig=18%, lid=15%,
1148		HOFFMANN SMALL PRE BII TO IMMATURE B LYMPHOCYTE UP	24	0.24	0.77	0.841	0.927	1	3378		sig=24%, lid=24%,
1125		YANAGA CARCINOGENESIS BY KRAS DN	79	0.23	0.79	0.843	0.917	1	3931		sig=24%, lid=24%,
1164		SUNWOO MYC TARGETS DN	54	0.25	0.74	0.844	0.943	1	3841		sig=24%, lid=23%,
1128		HARRY IRX1 CHRONIC LOF UP	73	0.23	0.79	0.845	0.912	1	3372		sig=16%, lid=17%,
1180		REACTOME REGULATION OF SIGNALING BY CBL	17	0.28	0.73	0.845	0.942	1	3379		sig=24%, lid=24%,
1183		REACTOME DNA STRAND ELONGATION	24	0.27	0.73	0.848	0.943	1	3940		sig=24%, lid=24%,
1185		WILLERN MICROCACHAR BREAST TUMOR UP	30	0.25	0.73	0.848	0.942	1	3106		sig=24%, lid=11%,
1146		YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 12	79	0.23	0.77	0.85	0.923	1	3596		sig=24%, lid=24%,
1178		PLASARI TIPF1 SIGNALING VIA NFKI IKBB UP	19	0.28	0.73	0.854	0.943	1	3934		sig=24%, lid=24%,
1177		HP TYROBP CAUSAL NETWORK IN MICROGLIA	28	0.24	0.73	0.855	0.941	1	3374		sig=21%, lid=21%,
1052		MIKKELSEN NPC ICP WITH H3K4M3	293	0.22	0.84	0.861	0.861	1	3341		sig=20%, lid=20%,
1189		BIOCARTA VIP PATHWAY	17	0.28	0.71	0.861	0.952	1	3106		sig=21%, lid=21%,
1093		HP MITOCHONDRIAL GENE EXPRESSION	31	0.26	0.76	0.861	0.953	1	3107		sig=21%, lid=17%,
1179		YANGYIN NOS2 TARGETS UP	30	0.25	0.75	0.867	0.942	1	3362		sig=24%, lid=24%,
1168		REACTOME INTEGRATION OF ENERGY METABOLISM	62	0.24	0.74	0.868	0.942	1	1247		sig=18%, lid=18%,
1184		REACTOME RHO GTPASE CYCLE	58	0.24	0.7	0.872	0.942	1	3914		sig=24%, lid=24%,
1191		REACTOME NICOTINATE METABOLISM	21	0.25	0.71	0.876	0.958	1	1117		sig=13%, lid=11%,
1214		SEDA MIR30 TARGETS DN	15	0.27	0.67	0.879	0.972	1	3317		sig=7%, lid=3%, qval=12%
1195		RUAN RESPONSE TO TNF TROGLITAZONE DN	24	0.24	0.7	0.88	0.963	1	1860		sig=17%, lid=17%,
1199		BIOCARTA AKT PATHWAY	24	0.26	0.7	0.884	0.963	1	3311		sig=21%, lid=17%,
1196		REACTOME RUNX INDSIGN IN SIG NER	24	0.23	0.7	0.884	0.963	1	1316		sig=16%, lid=16%,
1113		REACTOME THE CITRIC ACID TCA CYCLE AND RESPIRATORY ELECTRON TRANSPORT	149	0.22	0.8	0.885	0.913	1	4038		sig=40%, lid=46%, qval=21%
1127		LAZARO GENETIC MOUSE MODEL HIGH GRADE LARGE CELL NEUROENDOCRINE LUNG CARCINOMA UP	176	0.21	0.79	0.886	0.912	1	2163		sig=21%, lid=21%, qval=24%
1182		REACTOME BIOSYNTHESIS OF THE N GLYCAN PRECURSOR DOLICHOL LIPID	45	0.23	0.73	0.886	0.942	1	1661		sig=18%, lid=18%,
1166		REACTOME GLYCEROPHOSPHOLIPID BIOSYNTHESIS	88	0.22	0.74	0.888	0.941	1	3379		sig=18%, lid=17%,
1203		REACTOME DNA DAMAGE BYPASS	58	0.22	0.68	0.893	0.963	1	3417		sig=18%, lid=14%,
1124		AFFAR YY1 TARGETS DN	139	0.22	0.75	0.89	0.913	1	1825		sig=18%, lid=18%,
1161		HP ELECTRON TRANSPORT CHAIN	51	0.21	0.75	0.893	0.94	1	3320		sig=35%, lid=15%,
1216		REACTOME REGULATION OF FZD BY UBIQUITINATION	13	0.26	0.62	0.893	0.973	1	3927		sig=47%, lid=39%,
1193		REACTOME REGULATION OF IRF3 ACTIVITY THROUGH PHOSPHORYLATION	31	0.22	0.73	0.894	0.943	1	3130		sig=22%, lid=22%,
1186		RUAN RESPONSE TO TNF DN	51	0.22	0.72	0.894	0.944	1	3318		sig=16%, lid=20%,
1224		REACTOME O LINKED GLYCOSYLATION OF MUCINS	17	0.25	0.66	0.895	0.972	1	2597		sig=35%, lid=24%,
1190		IE EGR3 TARGETS UP	31	0.21	0.74	0.896	0.957	1	3107		sig=18%, lid=18%,
1198		KARLSSON TGFB1 TARGETS UP	110	0.21	0.75	0.897	0.937	1	3871		sig=38%, lid=38%,
1211		REACTOME INTRAFLAGELLAR TRANSPORT	35	0.21	0.67	0.897	0.972	1	3320		sig=38%, lid=23%,
1151		HANSON APC MYC TARGETS	149	0.21	0.75	0.898	0.914	1	3894		sig=38%, lid=37%,
1192		REACTOME RAC1 GTPASE CYCLE	85	0.21	0.73	0.898	0.937	1	3383		sig=27%, lid=28%,
1207		RUNINGER IGF1 VS PDGFB TARGETS UP	31	0.21	0.68	0.898	0.969	1	3316		sig=24%, lid=24%,
1206		REACTOME INITIATION OF NUCLEAR ENVELOPE NE REFORMATION	18	0.26	0.66	0.899	0.969	1	3936		sig=68%, lid=50%,
1193		MEYNER CORTICAL PLATE POSTMITOTIC NEURONS	58	0.22	0.73	0.9	0.92	1	3382		sig=31%, lid=37%,
1197		REACTOME HSP90 CHAPERONE CYCLE FOR STEROID HORMONE RECEPTORS SHR IN THE PRESENCE OF LIGANDS	38	0.22	0.7	0.9	0.963	1	3625		sig=42%, lid=35%,
1147		REACTOME MITOTIC G2 G2 M PHASES	139	0.21	0.72	0.901	0.926	1	3716		sig=27%, lid=27%,
1208		BIOCARTA DEATH PATHWAY	23	0.24	0.68	0.901	0.972	1	3190		sig=35%, lid=31%,
1176		KOHLAN MLL TELE MYELOMA C D UP	31	0.21	0.75	0.902	0.941	1	345		sig=25%, lid=3%, qval=7%
1204		REACTOME FGFR2 PKC SIGNALING VIA ATM NOT VIA NFKB DN	31	0.21	0.68	0.902	0.961	1	3313		sig=24%, lid=24%,
1200		BIOCARTA MAPK PATHWAY	31	0.22	0.68	0.902	0.972	1	3179		sig=35%, lid=3%, qval=10%
1198		HP CHE CARBON METABOLISM AND RELATED PATHWAYS	62	0.22	0.7	0.904	0.963	1	3236		sig=48%, lid=43%,
1219		MORI PLASMA CELL DN	31	0.24	0.63	0.904	0.973	1	3373		sig=67%, lid=53%,
1221		BIOCARTA MITOCHONDRIA PATHWAY	18	0.26	0.66	0.904	0.974	1	3977		sig=69%, lid=55%,
1201		BRACHAT RESPONSE TO CISPLATIN	35	0.24	0.68	0.909	0.972	1	3322		sig=35%, lid=32%,
1213		HP GLYCOGEN METABOLISM	26	0.23	0.65	0.91	0.973	1	3938		sig=35%, lid=35%,
1228		PLASARI TIPF1 TARGETS 1HR UP	13	0.21	0.63	0.911	0.973	1	1119		sig=7%, lid=7%, qval=7%
1222		REACTOME ACTIVATED TAK1 MEDIATES P38 MAPK ACTIVATION	13	0.25	0.65	0.911	0.973	1	3389		sig=38%, lid=21%,
1212		REACTOME PYRUVATE METABOLISM AND CITRIC ACID TCA CYCLE	35	0.21	0.67	0.912	0.973	1	3835		sig=46%, lid=46%,
1235		REACTOME TERMINATION OF TRANSLESION DNA SYNTHESIS	13	0.22	0.59	0.913	0.972	1	3389		sig=38%, lid=46%,
1235		BIOCARTA TNFR1 PATHWAY	24	0.22	0.64	0.913	0.973	1	3890		sig=25%, lid=25%,
1208		EMBELAN PAPR1 TARGETS UP	23	0.23	0.65	0.915	0.972	1	3391		sig=31%, lid=13%,
1218		REACTOME ENDOSOMAL SORTING COMPLEX REQUIRED FOR TRANSPORT ESCRT	35	0.23	0.65	0.917	0.972	1	3936		sig=43%, lid=43%,
1240		HP GLUTAMATE MYOSYNUCLEIN NETWORK	13	0.21	0.59	0.923	0.96	1	3320		sig=77%, lid=42%,
1201		BLANDES SERUM AND RAPAMYCIN SENSITIVE GENES	51	0.21	0.63	0.923	0.953	1	3301		sig=35%, lid=55%,
1223		HP IR SIGNALING PATHWAY	31	0.22	0.66	0.923	0.972	1	3894		sig=31%, lid=28%,
1224		REACTOME PYROPTOSIS	24	0.22	0.64	0.923	0.973	1	3934		sig=40%, lid=33%,
1227		LANDIS ERBB2 BREAST TUMORS 85 DN	23	0.22	0.65	0.923	0.973	1	1839		sig=17%, lid=18%,
1231		BIOCARTA RACCYCD PATHWAY	13	0.22	0.64	0.923	0.977	1	871		sig=10%, lid=5%, qval=10%
1238		REACTOME JNK C JUN KINASES PHOSPHORYLATION AND ACTIVATION MEDIATED BY ACTIVATED HUMAN TAK1	18	0.23	0.63	0.924	0.979	1	2102		sig=21%, lid=21%,
1241		REACTOME PCNA DEPENDENT LONG PATCH BASE EXCISION REPAIR	18	0.24	0.63	0.924	0.972	1	3896		sig=38%, lid=31%,
1237		HP SIGNAL TRANSDUCER	13	0.24	0.63	0.93	0.96	1	3177		sig=18%, lid=18%,
1237		REACTOME NUCLEOTIDE CATABOLISM	13	0.22	0.63	0.93	0.973	1	1319		sig=3%, lid=3%, qval=6%
1232		NEMETH INFLAMMATORY RESPONSE LPS DN	30	0.23	0.64	0.934	0.977	1	3384		sig=21%, lid=21%,
1242		MEISSNER NPC HCP WITH H3K4M3	18	0.21	0.61	0.94	0.973	1	3341		sig=21%, lid=21%,
1193		BERENZENO TRANSFORMED BY RHOA UP	100	0.21	0.61	0.94	0.895	1	3106		sig=22%, lid=21%,
1196		GOBERT OLIGODENDROCYTE DIFFERENTIATION UP	93	0.21	0.78	0.94	0.912	1	3323		sig=22%, lid=21%,
1219		REACTOME DUAL INCISION IN TC NER	35	0.2	0.65	0.94	0.973	1	3918		sig=38%, lid=32%,
1245		MEYNER INTERMEDIATE ZONE AND UP POSTMITOTIC PROJECTION NEURONS	58	0.21	0.61	0.942	0.95	1	3307		sig=22%, lid=24%,
1248		MEYNER CORTEX APICAL AND BASAL INTERMEDIATE PROGENITOR CELLS	58	0.2	0.6	0.944	0.955	1	3366		sig=21%, lid=21%,
1226		HP VMT SIGNALING PATHWAY AND PLURIPOTENCY	35	0.2	0.65	0.945	0.974	1	3172		sig=24%, lid=21%,
1245		REACTOME SIGNALING BY RETINOIC ACID	35	0.21	0.61	0.947	0.95	1	3313		sig=24%, lid=21%,
1233		REACTOME RHOD GTPASE CYCLE	62	0.2	0.54	0.948	0.976	1	3738		sig=21%, lid=27%,
1252		REACTOME LAGGING STRAND SYNTHESIS	13	0.22	0.59	0.949	0.947	1	3320		sig=35%, lid=22%,
1251		HP VMT SIGNALING IN KIDNEY DISEASE	22	0.22	0.6	0.953	0.964	1	3936		sig=41%, lid=40%,
1217		REACTOME TRANSLATION	216	0.2	0.74	0.95	0.941	1	3310		sig=24%, lid=21%,
1225		REACTOME CELLULAR RESPONSE TO HEAT STRESS	216	0.19	0.66	0.953	0.972	1	3236		sig=24%, lid=21%,
1174		LIM MAMMARY STEM CELL UP	23	0.2	0.74	0.961	0.942	1	3380		sig=21%, lid=21%,
1253		YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 10	79	0.22	0.55	0.963	0.969	1	3596		sig=24%, lid=24%,
1202		PAL PRMT5 TARGETS UP	139	0.19	0.65	0.968	0.963	1	3703		sig=31%, lid=27%,
1250		REACTOME FORMATION OF THE EARLY ELONGATION COMPLEX	35	0.2	0.6	0.968	0.965	1	3320		sig=31%, lid=21%,
1257		KOHOUTEK CDK12 TARGETS	23	0.2	0.52	0.97	0.969	1	3336		sig=22%, lid=22%,
1253		CAPELLA ZMPSTE24 TARGETS DN	42	0.19	0.58	0.971	0.968	1	3302		sig=24%, lid=24%,
1230		HANSON VMT PATHWAY REGULATE MYC	62	0.18	0.58	0.973	0.952	1	3730		sig=31%, lid=31%,
1256		REACTOME FORMATION OF INCISION COMPLEX IN GG NER	35	0.18	0.56	0.98	0.969	1	3697		sig=31%, lid=31%,
1259		MAGNA OPRA4 TARGETS	18	0.18	0.56	0.981	0.969	1	3894		sig=3%, lid=3%, qval=4%
1254		REACTOME REGULATION OF HSF1 MEDIATED HEAT SHOCK RESPONSE	58	0.18	0.55	0.983	0.96	1	3236		sig=24%, lid=24%,
1247		REACTOME GLYCOSAMINOGLYCAN METABOLISM	62	0.18	0.49	0.983	0.964	1	3533		sig=31%, lid=31%,
1248		BURTON ADIPOGENESIS 3	132	0.17	0.61	0.986	0.964	1	3327		sig=21%, lid=22%,
1236		IWAKABAYASHI ARPC5SENS PPARG RXRA BOUND 3HR	116	0.17	0.63	0.989	0.978	1	3322		sig=18%, lid=22%,
1244		LANDIS ERBB2 BREAST PRENEOPLASTIC DN	139	0.17	0.55	0.991	0.953	1	3318		sig=17%, lid=22%,
1260		MARTORIATI MDM4 TARGETS NEUROEPITHELIUM DN	139	0.17	0.61	0.993	0.983	1	3278		sig=24%, lid=24%,
1262		GAUSMANN MLL AF4 FUSION TARGETS A DN	68	0.17	0.54	0.993	0.994	1	3393		sig=31%, lid=31%,
1264		MORI MATURE B LYMPHOCYTE DN	93	0.16	0.49	0.993	0.987	1	3310		sig=24%, lid=24%,
1268		LEIN ASTROCYTE MARKERS	28	0.17	0.49	0.994	0.987	1	1795		sig=14%, lid=7%,
1257		REACTOME HDR THROUGH SINGLE STRAND ANNEALING SSA	23	0.2	0.47	0.995	0.987	1	3320		sig=24%, lid=24%,
1255		YANAGA CARCINOGENESIS BY KRAS PTEN DN	174	0.17	0.43	0.996	0.98	1	3370		sig=31%, lid=31%,
1265		MIKKELSEN MEF HCP WITH H3 UNMETHYLATED	93	0.17	0.51	0.998	0.998	1	3535		sig=24%, lid=24%,
1269		REACTOME NONSENSE MEDIATED DECAY NMD	93	0.16	0.37	0.998	0.991	1	3340		sig=24%, lid=24%,
1266		REACTOME MITOCHONDRIAL TRANSLATION	87	0.14	0.5	0.998	0.998	1	3700		sig=24%, lid=27%,
1210		STARK PREFRONTAL CORTEX 22Q11 DELETION DN	209	0.17	0.67	0.999	0.972	1	3318		sig=24%, lid=24%,
1217		REACTOME METABOLISM OF LIPIDS	492	0.17	0.62	0.999	0.972	1	3921		sig=22%, lid=23%,
1261		BURTON ADIPOGENESIS 4	116	0.14	0.54	1	0.995	1	3340		sig=24%, lid=24%,
1271		REACTOME COMPLEX I BIOGENESIS	58	0.12	0.44	1	0.998	1	3236		sig=24%, lid=24%,