Supplementary Table 7. Transcriptional effect induced by RZ-2994 vs. DMSO treatment at Day 1 and at Day 3 on KOPTK1 cells. This data is summarized in Figure 3 and Supplementary Figure 6.

Spreadsheet tabs

A Gene set enrichment for the transcriptional changes induced by RZ-2994 at Day 3 on KOPTK1 cells.
B Gene set enrichment for the transcriptional changes induced by RZ-2994 at Day 1 on KOPTK1 cells.
C Gene expression changes induced by RZ-2994 vs. DMSO at Day 3 on KOPTK1 cells.
D Gene expression changes induced by RZ-2994 vs. DMSO at Day 1 on KOPTK1 cells.

Supplementary Table 7A. Gene set enrichment for the transcriptional changes induced by RZ-2994 at Day 3 on KOPTK1 cells. MSigDB v7.0 collection, significance -log10(P-value+0.0001)>1. Effect of RZ-2994 on pathway based on Normalized Enrichment Score (NES): NES < -1.5 Repressed, NES > 1.5 Enhanced.

#	Gene set	Normalized Enrichment Score (NES) at Day 3	-log10 (P-value+0.0001) at Day 3	Amino Acid gene set signatures (1=yes, 0=no)	MYC gene set signatures (1=yes, 0=no)	Cell Cycle gene set signatures (1=yes, 0=no)	RZ-2994 vs. DMSO transcriptional effect on pathway at Day 3
1	MTOR_UP.N4.V1_UP	-3.01	4.00	0	0	0	Repressed
2	PENG_RAPAMYCIN_RESPONSE_DN	-2.97	4.00	0	0	0	Repressed
3	PENG_LEUCINE_DEPRIVATION_DN	-2.93	4.00	1	0	0	Repressed
4	PENG_GLUTAMINE_DEPRIVATION_DN	-2.90	4.00	1	0	0	Repressed
5	HALLMARK_MTORC1_SIGNALING	-2.74	4.00	0	0	0	Repressed
6	GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	-2.73	4.00	0	0	0	Repressed
7	GO_MITOCHONDRIAL_PROTEIN_COMPLEX	-2.73	4.00	0	0	0	Repressed
8	GARY_CD5_TARGETS_DN	-2.66	4.00	0	0	0	Repressed
9	RHODES_UNDIFFERENTIATED_CANCER	-2.63	4.00	0	0	0	Repressed
10	GO_RESPIRATORY_CHAIN_COMPLEX	-2.62	4.00	0	0	0	Repressed
11	MANALO_HYPOXIA_DN	-2.61	4.00	0	0	0	Repressed
12	REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G	-2.61	4.00	0	0	1	Repressed
13	TARTE_PLASMA_CELL_VS_PLASMABLAST_DN	-2.61	4.00	0	0	0	Repressed
14	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	-2.60	4.00	0	0	0	Repressed
15	TIEN_INTESTINE_PROBIOTICS_24HR_UP	-2.60	4.00	0	0	0	Repressed
16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	-2.59	4.00	0	0	0	Repressed
17	GO_OXIDATIVE_PHOSPHORYLATION	-2.58	4.00	0	0	0	Repressed
18	GO_ELECTRON_TRANSPORT_CHAIN	-2.57	4.00	0	0	0	Repressed
19	MOOTHA_VOXPHOS	-2.56	4.00	0	0	0	Repressed
20	GO_MITOCHONDRIAL_MEMBRANE_PART	-2.55	4.00	0	0	0	Repressed
21	GO_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN	-2.55	4.00	0	0	0	Repressed
22	WEI_MYCN_TARGETS_WITH_E_BOX	-2.55	4.00	0	1	0	Repressed
23	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN	-2.54	4.00	0	0	0	Repressed
24	KEGG_PROTEASOME	-2.50	4.00	0	0	0	Repressed
25	GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	-2.49	4.00	0	0	0	Repressed
26	GO_RESPIRASOME	-2.48	4.00	0	0	0	Repressed
27	REACTOME_ACTIVATION_OF_APC_C_AND_APC_C:CDC20_MEDIATED_DE	-2.48	4.00	0	0	0	Repressed
28	REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	-2.48	4.00	0	0	0	Repressed
29	GO_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT	-2.47	4.00	0	0	0	Repressed
30	GO_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS	-2.47	4.00	0	0	0	Repressed
31	GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROC	-2.46	4.00	0	0	0	Repressed
32	REACTOME_APC_C:CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_	-2.46	4.00	0	0	0	Repressed
33	REACTOME_METABOLISM_OF_POLYAMINES	-2.46	4.00	0	0	0	Repressed
34	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_	-2.46	4.00	0	0	0	Repressed
35	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_11	-2.46	4.00	0	0	0	Repressed
36	HALLMARK_MYC_TARGETS_V2	-2.45	4.00	0	1	0	Repressed
37	REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	-2.45	4.00	0	0	1	Repressed
38	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_DN	-2.45	4.00	0	1	0	Repressed
39	GO_TRANSLATIONAL_TERMINATION	-2.44	4.00	0	0	0	Repressed
40	REICHERT_MITOSIS_LIN9_TARGETS	-2.44	4.00	0	0	1	Repressed
41	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I	-2.43	4.00	0	0	0	Repressed
42	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_	-2.43	4.00	0	0	0	Repressed
43	REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIG	-2.43	4.00	0	0	0	Repressed
44	REACTOME_TRNA_AMINOACYLATION	-2.43	4.00	0	0	0	Repressed
45	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP	-2.43	4.00	0	0	0	Repressed
46	GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_NADH_TO_UBIQUINONE	-2.42	4.00	0	0	0	Repressed
47	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	-2.42	4.00	0	0	0	Repressed
48	GO_NADH_DEHYDROGENASE_ACTIVITY	-2.42	4.00	0	0	0	Repressed
49	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN	-2.42	4.00	0	0	0	Repressed
50	REACTOME_COMPLEX_I_BIOGENESIS	-2.42	4.00	0	0	0	Repressed
51	REACTOME_DEGRADATION_OF_GLI1_BY_THE_PROTEASOME	-2.41	4.00	0	0	0	Repressed
52	REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	-2.41	4.00	0	0	0	Repressed
53	GO_PRERIBOSOME	-2.40	4.00	0	0	0	Repressed
54	GO_ORGANELLAR_RIBOSOME	-2.39	4.00	0	0	0	Repressed
55	KARLSSON_TGFB1_TARGETS_UP	-2.39	4.00	0	0	0	Repressed
56	REACTOME_FBXL7_DOWN_REGULATES_AURKA_DURING_MITOTIC_ENTR	-2.39	4.00	0	0	0	Repressed
57	REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	-2.39	4.00	0	0	0	Repressed
58	GO_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY	-2.38	4.00	0	0	0	Repressed
59	BERENJENO_TRANSFORMED_BY_RHOA_UP	-2.37	4.00	0	0	0	Repressed
60	COLLER_MYC_TARGETS_UP	-2.37	4.00	0	1	0	Repressed
61	FOURNIER_ACINAR_DEVELOPMENT_LATE_2	-2.37	4.00	0	0	0	Repressed
62	GO_ELECTRON_TRANSFER_ACTIVITY	-2.37	4.00	0	0	0	Repressed
63	GO_MITOCHONDRIAL_GENE_EXPRESSION	-2.37	4.00	0	0	0	Repressed
64	REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTO	-2.36	4.00	0	0	0	Repressed
65	REACTOME_MITOCHONDRIAL_TRANSLATION	-2.36	4.00	0	0	0	Repressed
66	ELVIDGE_HYPOXIA_DN	-2.35	4.00	0	0	0	Repressed
67	GO_MITOCHONDRIAL_TRANSLATIONAL_TERMINATION	-2.35	4.00	0	0	0	Repressed
68	LEE_BMP2_TARGETS_DN	-2.35	4.00	0	0	0	Repressed
69	REACTOME_HIV_INFECTION	-2.35	4.00	0	0	0	Repressed
70	REACTOME_REGULATION_OF_RAS_BY_GAPS	-2.35	4.00	0	0	0	Repressed
71	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECT	-2.34	4.00	0	0	0	Repressed
72	SCHUHMACHER_MYC_TARGETS_UP	-2.34	4.00	0	1	0	Repressed
73	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEP	-2.33	4.00	0	0	0	Repressed
74	GO_ENDOPEPTIDASE_COMPLEX	-2.33	4.00	0	0	0	Repressed
75	HALLMARK_MYC_TARGETS_V1	-2.33	4.00	0	1	0	Repressed
76	REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	-2.33	4.00	0	0	0	Repressed
77	WONG_EMBRYONIC_STEM_CELL_CORE	-2.33	4.00	0	0	0	Repressed
78	HALLMARK_OXIDATIVE_PHOSPHORYLATION	-2.32	4.00	0	0	0	Repressed
79	REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	-2.32	4.00	0	0	0	Repressed
80	GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	-2.31	4.00	0	0	0	Repressed
81	PID_MYC_ACTIV_PATHWAY	-2.31	4.00	0	1	0	Repressed
82	REACTOME_REGULATION_OF_APOPTOSIS	-2.31	4.00	0	0	0	Repressed
83	YU_MYC_TARGETS_UP	-2.31	4.00	0	1	0	Repressed
84	GO_CELLULAR_RESPIRATION	-2.30	4.00	0	0	0	Repressed
85	GO_MITOCHONDRIAL_TRANSLATION	-2.30	4.00	0	0	0	Repressed
86	GO_PEPTIDASE_COMPLEX	-2.30	4.00	0	0	0	Repressed
87	NAKAMURA_CANCER_MICROENVIRONMENT_DN	-2.30	4.00	0	0	0	Repressed
88	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP	-2.30	4.00	0	0	0	Repressed
89	REACTOME_REGULATION_OF_RUNX2_EXPRESSION_AND_ACTIVITY	-2.30	4.00	0	0	0	Repressed
90	REACTOME_RRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL	-2.30	4.00	0	0	0	Repressed
91	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	-2.30	4.00	0	0	0	Repressed
92	TANG_SENESCENCE_TP53_TARGETS_DN	-2.30	4.00	0	0	0	Repressed
93	WINTER_HYPOXIA_UP	-2.30	4.00	0	0	0	Repressed
94	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	-2.29	4.00	0	0	0	Repressed
95	REACTOME_NEGATIVE_REGULATION_OF_NOTCH4_SIGNALING	-2.29	4.00	0	0	0	Repressed
96	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-2.29	4.00	0	0	0	Repressed
97	BASAKI_YBX1_TARGETS_UP	-2.28	4.00	0	0	0	Repressed

98	GO_PROTEASOME_ACCESSORY_COMPLEX	-2.28	4.00	0	0	0	Repressed
99	RAHMAN_TP53_TARGETS_PHOSPHORYLATED	-2.28	4.00	0	0	0	Repressed
100	GO_TRNA_METABOLIC_PROCESS	-2.27	4.00	1	0	0	Repressed
101	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGE	-2.26	4.00	0	0	0	Repressed
102	GO_MITOCHONDRIAL_MATRIX	-2.26	4.00	0	0	0	Repressed
103	GO_MITOCHONDRIAL_PART	-2.26	4.00	0	0	0	Repressed
104	GO_OXIDOREDUCTASE_COMPLEX	-2.26	4.00	0	0	0	Repressed
105	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	-2.26	4.00	1	0	0	Repressed
106	MOOTHA_HUMAN_MITODB_6_2002	-2.26	4.00	0	0	0	Repressed
107	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	-2.25	4.00	0	0	0	Repressed
108	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP	-2.25	4.00	0	0	0	Repressed
109	REACTOME_REGULATION_OF_RUNX3_EXPRESSION_AND_ACTIVITY	-2.25	4.00	0	0	0	Repressed
110	WONG_MITOCHONDRIA_GENE_MODULE	-2.25	4.00	0	0	0	Repressed
111	GO_CATALYTIC_ACTIVITY_ACTING_ON_A_TRNA	-2.24	4.00	0	0	0	Repressed
112	GO_SMALL_NUCLEOLAR_RIBONUCLEOPROTEIN_COMPLEX	-2.24	4.00	0	0	0	Repressed
113	LY_AGING_OLD_DN	-2.24	4.00	0	0	0	Repressed
114	SEMENZA_HIF1_TARGETS	-2.24	4.00	0	0	0	Repressed
115	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13	-2.24	4.00	0	0	0	Repressed
116	GO_SMALL_SUBUNIT_PROCESSOME	-2.23	4.00	0	0	0	Repressed
117	KEGG_OXIDATIVE_PHOSPHORYLATION	-2.23	4.00	0	0	0	Repressed
118	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP	-2.23	4.00	0	0	0	Repressed
119	PUJANA_CHEK2_PCC_NETWORK	-2.23	4.00	0	0	1	Repressed
120	REACTOME_CELLULAR_RESPONSE_TO_HYPOXIA	-2.23	4.00	0	0	0	Repressed
121	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR	-2.23	4.00	0	0	1	Repressed
122	GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PR	-2.22	4.00	0	0	0	Repressed
123	MENSSEN_MYC_TARGETS	-2.22	4.00	0	1	0	Repressed
124	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN	-2.22	4.00	0	0	0	Repressed
125	REACTOME_DOWNSTREAM_TCR_SIGNALING	-2.22	4.00	0	0	0	Repressed
126	GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	-2.21	4.00	0	0	0	Repressed
127	ONO_FOXP3_TARGETS_UP	-2.21	4.00	0	0	0	Repressed
128	REACTOME_DEGRADATION_OF_AXIN	-2.21	4.00	0	0	0	Repressed
129	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP	-2.21	4.00	0	0	0	Repressed
130	ELVIDGE_HIF1A_TARGETS_UP	-2.20	4.00	0	0	0	Repressed
131	GO_MITOCHONDRIAL_ENVELOPE	-2.20	4.00	0	0	0	Repressed
132	REACTOME_AUF1_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA	-2.19	4.00	0	0	0	Repressed
133	WINNEPENNINCKX_MELANOMA_METASTASIS_UP	-2.19	4.00	0	0	0	Repressed
134	FISCHER_G2_M_CELL_CYCLE	-2.18	4.00	0	0	1	Repressed
135	KANG_GIST_WITH_PDGFRA_UP	-2.18	4.00	0	0	0	Repressed
136	REACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING	-2.18	4.00	0	0	0	Repressed
137	REACTOME_DEGRADATION_OF_DVL	-2.18	4.00	0	0	0	Repressed
138	REACTOME_GLUCOSE_METABOLISM	-2.18	4.00	0	0	0	Repressed
139	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP	-2.17	4.00	0	0	0	Repressed
140	ELVIDGE_HYPOXIA_BY_DMOG_DN	-2.17	4.00	0	0	0	Repressed
141	GAVIN_FOXP3_TARGETS_CLUSTER_P6	-2.17	4.00	0	0	0	Repressed
142	GO_90S_PRERIBOSOME	-2.17	4.00	0	0	0	Repressed
143	REACTOME_ASYMMETRIC_LOCALIZATION_OF_PCP_PROTEINS	-2.17	4.00	0	0	0	Repressed
144	CROONQUIST_IL6_DEPRIVATION_DN	-2.16	4.00	0	0	0	Repressed
145	FARMER_BREAST_CANCER_CLUSTER_2	-2.16	4.00	0	0	0	Repressed
146	GO_AMINO_ACID_ACTIVATION	-2.16	4.00	0	0	0	Repressed
147	KIM_MYC_AMPLIFICATION_TARGETS_UP	-2.16	4.00	0	1	0	Repressed
148	CHANG_CORE_SERUM_RESPONSE_UP	-2.15	4.00	0	0	0	Repressed
149	GO_RNA_LOCALIZATION	-2.15	4.00	0	0	0	Repressed
150	GO_TRNA_METHYLATION	-2.15	4.00	0	0	0	Repressed
151	ODONNELL_TFRC_TARGETS_DN	-2.15	4.00	0	0	0	Repressed
152	REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_C	-2.15	4.00	0	0	0	Repressed
153	REACTOME_GLYCOLYSIS	-2.15	4.00	0	0	0	Repressed
154	REACTOME_TRNA_PROCESSING	-2.15	4.00	0	0	0	Repressed
155	WILLIAMS_ESR1_TARGETS_UP	-2.15	4.00	0	0	0	Repressed
156	BASSO_B_LYMPHOCYTE_NETWORK	-2.14	4.00	0	0	0	Repressed
157	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN	-2.14	4.00	0	0	0	Repressed
158	GO_CYTOKINE_RECEPTOR_ACTIVITY	-2.14	4.00	0	0	0	Repressed
159	GO_NCRNA_METABOLIC_PROCESS	-2.14	4.00	0	0	0	Repressed
160	KRIGE_AMINO_ACID_DEPRIVATION	-2.14	4.00	0	0	0	Repressed
161	MOOTHA_GLUCONEOGENESIS	-2.14	4.00	0	0	0	Repressed
162	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP	-2.14	4.00	0	0	0	Repressed
163	GO_NCRNA_PROCESSING	-2.13	4.00	0	0	0	Repressed
164	KEGG_GLYCOLYSIS_GLUCONEOGENESIS	-2.13	4.00	0	0	0	Repressed
165	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_UP	-2.13	4.00	0	0	0	Repressed
166	GO_ANAPHASE_PROMOTING_COMPLEX_BINDING	-2.12	4.00	0	0	0	Repressed
167	HALLMARK_UNFOLDED_PROTEIN_RESPONSE	-2.12	4.00	0	0	0	Repressed
168	BURTON_ADIPOGENESIS_PEAK_AT_24HR	-2.11	4.00	0	0	0	Repressed
169	GO_ORGANELLE_INNER_MEMBRANE	-2.11	4.00	0	0	0	Repressed
170	GO_TRNA_METHYLTRANSFERASE_ACTIVITY	-2.11	4.00	0	0	0	Repressed
171	MUELLER_PLURINET	-2.11	4.00	0	0	0	Repressed
172	REACTOME_FCERI_MEDIATED_NF_KB_ACTIVATION	-2.11	4.00	0	0	0	Repressed
173	REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21	-2.11	4.00	0	0	0	Repressed
174	REACTOME_TCR_SIGNALING	-2.11	4.00	0	0	0	Repressed
175	REACTOME_UCH_PROTEINASES	-2.11	4.00	0	0	0	Repressed
176	AMUNDSON_GAMMA_RADIATION_RESPONSE	-2.10	4.00	0	0	0	Repressed
177	GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	-2.10	4.00	0	0	0	Repressed
178	GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS	-2.10	4.00	0	0	0	Repressed
179	GO_RNA_MODIFICATION	-2.10	4.00	0	0	0	Repressed
180	REACTOME_MAPK6_MAPK4_SIGNALING	-2.10	4.00	0	0	0	Repressed
181	WEST_ADRENOCORTICAL_TUMOR_UP	-2.10	4.00	0	0	0	Repressed
182	GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE	-2.09	4.00	0	0	0	Repressed
183	GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE	-2.09	4.00	0	0	0	Repressed
184	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP	-2.09	4.00	0	0	0	Repressed
185	KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	-2.09	4.00	0	0	0	Repressed
186	MOOTHA_MITOCHONDRIA	-2.09	4.00	0	0	0	Repressed
187	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_DN	-2.09	4.00	0	0	0	Repressed
188	REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_C	-2.09	4.00	0	0	0	Repressed
189	SIMBULAN_PARP1_TARGETS_DN	-2.09	4.00	0	0	0	Repressed
190	VECCHI_GASTRIC_CANCER_EARLY_UP	-2.09	4.00	0	0	0	Repressed
191	GO_AMINE_METABOLIC_PROCESS	-2.08	4.00	0	0	0	Repressed
192	GO_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	-2.08	4.00	0	0	0	Repressed
193	GO_CYTOCHROME_COMPLEX	-2.08	4.00	0	0	0	Repressed
194	KEGG_PARKINSONS_DISEASE	-2.08	4.00	0	0	0	Repressed
195	KORKOLA_TERATOMA	-2.08	4.00	0	0	0	Repressed
196	LI_DCP2_BOUND_MRNA	-2.08	4.00	0	0	0	Repressed
197	MOOTHA_PGC	-2.08	4.00	0	0	0	Repressed
198	REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	-2.08	4.00	0	0	0	Repressed
199	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM	-2.08	4.00	0	1	0	Repressed
200	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14	-2.08	4.00	0	0	0	Repressed
201	BURTON_ADIPOGENESIS_5	-2.07	4.00	0	0	0	Repressed
202	GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	-2.07	4.00	0	0	0	Repressed
203	GO_INNATE_IMMUNE_RESPONSE_ACTIVATING_CELL_SURFACE_RECEPT	-2.07	4.00	0	0	0	Repressed
204	GO_MITOCHONDRION	-2.07	4.00	0	0	0	Repressed
205	HONMA_DOCETAXEL_RESISTANCE	-2.07	4.00	0	0	0	Repressed
206	REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SIGNALING	-2.07	4.00	0	0	0	Repressed

207	REACTOME_HEDGEHOG_LIGAND_BIOGENESIS	-2.07	4.00	0	0	0	Repressed
208	REACTOME_PCP_CE_PATHWAY	-2.07	4.00	0	0	0	Repressed
209	REACTOME_STABILIZATION_OF_P53	-2.07	4.00	0	0	0	Repressed
210	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN	-2.07	2.60	0	0	0	Repressed
211	BIOCARTA_IL12_PATHWAY	-2.06	4.00	0	0	0	Repressed
212	BMI1_DN.V1_DN	-2.06	4.00	0	0	0	Repressed
213	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN	-2.06	4.00	0	0	0	Repressed
214	CSR_EARLY_UP.V1_UP	-2.06	4.00	0	0	0	Repressed
215	GO_ESTABLISHMENT_OF_RNA_LOCALIZATION	-2.06	4.00	0	0	0	Repressed
216	GO_REGULATION_OF_CARDIAC_CONDUCTION	-2.06	4.00	0	0	0	Repressed
217	GO_TRNA_MODIFICATION	-2.06	4.00	0	0	0	Repressed
218	REACTOME_SIGNALING_BY_NOTCH4	-2.06	4.00	0	0	0	Repressed
219	SERVITJA_LIVER_HNF1A_TARGETS_UP	-2.06	4.00	0	0	0	Repressed
220	SHAFFER_IRF4_TARGETS_IN_ACTIVATED_B_LYMPHOCYTE	-2.06	4.00	0	0	0	Repressed
221	GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE	-2.05	4.00	0	0	0	Repressed
222	GO_REGULATION_OF_CELLULAR_KETONE_METABOLIC_PROCESS	-2.05	4.00	0	0	0	Repressed
223	HESS_TARGETS_OF_HOXA9_AND_MEIS1_UP	-2.05	4.00	0	0	0	Repressed
224	REACTOME_DEGRADATION_OF_BETA_CATENIN_BY_THE_DESTRUCTION	-2.05	4.00	0	0	0	Repressed
225	REACTOME_HEDGEHOG_OFF_STATE	-2.05	4.00	0	0	0	Repressed
226	REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION	-2.05	4.00	0	0	0	Repressed
227	GO_TRNA_PROCESSING	-2.04	4.00	0	0	0	Repressed
228	HALLMARK_G2M_CHECKPOINT	-2.04	4.00	0	0	1	Repressed
229	KEGG_ALZHEIMERS_DISEASE	-2.04	4.00	0	0	0	Repressed
230	KOBAYASHI_EGFR_SIGNALING_24HR_DN	-2.04	4.00	0	0	0	Repressed
231	MOOTHA_GLYCOLYSIS	-2.04	4.00	0	0	0	Repressed
232	OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_UP	-2.04	4.00	0	0	0	Repressed
233	REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	-2.04	4.00	0	0	0	Repressed
234	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP	-2.04	4.00	0	0	0	Repressed
235	CHR17Q24	-2.03	4.00	0	0	0	Repressed
236	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGE	-2.03	4.00	0	0	0	Repressed
237	GO_POSITIVE_REGULATION_OF_TELOMERASE_RNA_LOCALIZATION_TO	-2.03	4.00	0	0	0	Repressed
238	REACTOME_ABC_TRANSPORTER_DISORDERS	-2.03	4.00	0	0	0	Repressed
239	RHODES_CANCER_META_SIGNATURE	-2.03	4.00	0	0	0	Repressed
240	SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY	-2.03	4.00	0	1	0	Repressed
241	TOOKER_GEMCITABINE_RESISTANCE_DN	-2.03	4.00	0	0	0	Repressed
242	WINTER_HYPOXIA_METAGENE	-2.03	4.00	0	0	0	Repressed
243	CHEN_LUNG_CANCER_SURVIVAL	-2.02	4.00	0	0	0	Repressed
244	FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	-2.02	4.00	0	0	0	Repressed
245	GO_CELLULAR_KETONE_METABOLIC_PROCESS	-2.02	4.00	0	0	0	Repressed
246	GO_NEUTROPHIL_HOMEOSTASIS	-2.02	4.00	0	0	0	Repressed
247	GO_SNORNA_BINDING	-2.02	4.00	0	0	0	Repressed
248	REACTOME_CELL_CYCLE_CHECKPOINTS	-2.02	4.00	0	0	1	Repressed
249	REACTOME_METABOLISM_OF_NON_CODING_RNA	-2.02	4.00	0	0	0	Repressed
250	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN	-2.02	4.00	0	0	0	Repressed
251	WANG_SMARCE1_TARGETS_DN	-2.02	4.00	0	0	0	Repressed
252	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN	-2.02	2.62	0	0	0	Repressed
253	GO_RNA_METHYLTRANSFERASE_ACTIVITY	-2.01	4.00	0	0	0	Repressed
254	RB_P107_DN.V1_DN	-2.01	4.00	0	0	0	Repressed
255	REACTOME_HIV_LIFE_CYCLE	-2.01	4.00	0	0	0	Repressed
256	REACTOME_REGULATION_OF_PTEN_STABILITY_AND_ACTIVITY	-2.01	4.00	0	0	0	Repressed
257	GO_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	-2.00	4.00	0	0	0	Repressed
258	GO_REGULATION_OF_RIBOSOME_BIOGENESIS	-2.00	4.00	0	0	0	Repressed
259	GO_RIBOSOME_BIOGENESIS	-2.00	4.00	0	0	0	Repressed
260	KEGG_HUNTINGTONS_DISEASE	-2.00	4.00	0	0	0	Repressed
261	MALONEY_RESPONSE_TO_17AAG_DN	-2.00	4.00	0	0	0	Repressed
262	REACTOME_COOPERATION_OF_PREFOLDIN_AND_TRIC_CCT_IN_ACTIN_	-2.00	4.00	0	0	0	Repressed
263	REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_C	-2.00	4.00	0	0	0	Repressed
264	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17	-2.00	4.00	0	0	0	Repressed
265	GO_GLYCOLYTIC_PROCESS_THROUGH_FRUCTOSE_6_PHOSPHATE	-1.99	4.00	0	0	0	Repressed
266	GO_SCF_DEPENDENT_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEI	-1.99	4.00	0	0	0	Repressed
267	GOLDRATH_ANTIGEN_RESPONSE	-1.99	4.00	0	0	0	Repressed
268	NABA_ECM_AFFILIATED	-1.99	4.00	0	0	0	Repressed
269	REACTOME_HEDGEHOG_ON_STATE	-1.99	4.00	0	0	0	Repressed
270	REACTOME_HSP90_CHAPERONE_CYCLE_FOR_STEROID_HORMONE_RE	-1.99	4.00	0	0	0	Repressed
271	REACTOME_M_PHASE	-1.99	4.00	0	0	1	Repressed
272	REACTOME_METABOLISM_OF_COFACTORS	-1.99	4.00	0	0	0	Repressed
273	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX2	-1.99	4.00	0	0	0	Repressed
274	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX3	-1.99	4.00	0	0	0	Repressed
275	WANG_ADIPOGENIC_GENES_REPRESSED_BY_SIRT1	-1.99	4.00	0	0	0	Repressed
276	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	-1.99	2.63	0	0	0	Repressed
277	GO_RNA_EXPORT_FROM_NUCLEUS	-1.98	4.00	0	0	0	Repressed
278	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_PRE_INITIATION_AN	-1.98	4.00	0	0	0	Repressed
279	REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY	-1.98	4.00	0	0	0	Repressed
280	REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME	-1.98	4.00	0	0	0	Repressed
281	WANG_TUMOR_INVASIVENESS_UP	-1.98	4.00	0	0	0	Repressed
282	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_10	-1.98	4.00	0	0	0	Repressed
283	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_UP	-1.97	4.00	0	0	0	Repressed
284	GO_SARCOPLASMIC_RETICULUM_CALCIUM_ION_TRANSPORT	-1.97	4.00	0	0	0	Repressed
285	GO_TRNA_GUANINE_METHYLTRANSFERASE_ACTIVITY	-1.97	4.00	0	0	0	Repressed
286	KEGG_PPAR_SIGNALING_PATHWAY	-1.97	4.00	0	0	0	Repressed
287	MORI_IMMATURE_B_LYMPHOCYTE_DN	-1.97	4.00	0	0	0	Repressed
288	REACTOME_G_PROTEIN_MEDIATED_EVENTS	-1.97	4.00	0	0	0	Repressed
289	REACTOME_GENE_AND_PROTEIN_EXPRESSION_BY_JAK_STAT_SIGNALI	-1.97	4.00	0	0	0	Repressed
290	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_B	-1.97	4.00	0	0	0	Repressed
291	BOYAULT_LIVER_CANCER_SUBCLASS_G3_UP	-1.96	4.00	0	0	0	Repressed
292	CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_UP	-1.96	4.00	0	0	0	Repressed
293	GO_CYTOSOLIC_PROTEASOME_COMPLEX	-1.96	4.00	0	0	0	Repressed
294	GO_TRANSLATIONAL_ELONGATION	-1.96	4.00	0	0	0	Repressed
295	GO_TRNA_BINDING	-1.96	4.00	0	0	0	Repressed
296	GRUETZMANN_PANCREATIC_CANCER_UP	-1.96	4.00	0	0	0	Repressed
297	HORIUCHI_WTAP_TARGETS_DN	-1.96	4.00	0	0	0	Repressed
298	LY_AGING_MIDDLE_DN	-1.96	4.00	0	0	0	Repressed
299	REACTOME_MITOTIC_G2_G2_M_PHASES	-1.96	4.00	0	0	1	Repressed
300	REACTOME_MITOTIC_SPINDLE_CHECKPOINT	-1.96	4.00	0	0	1	Repressed
301	REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	-1.96	4.00	0	0	0	Repressed
302	REACTOME_REGULATION_OF_CHOLESTEROL_BIOSYNTHESIS_BY_SREB	-1.96	4.00	0	0	0	Repressed
303	REACTOME_SUMOYLATION_OF_DNA_REPLICATION_PROTEINS	-1.96	4.00	0	0	0	Repressed
304	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM3	-1.96	4.00	0	0	0	Repressed
305	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN	-1.96	4.00	0	0	0	Repressed
306	GO_MITOCHONDRIAL_RNA_PROCESSING	-1.96	2.61	0	0	0	Repressed
307	GO_RNA_POLYMERASE_II_GENERAL_TRANSCRIPTION_INITIATION_FACT	-1.96	2.61	0	0	0	Repressed
308	VALK_AML_CLUSTER_15	-1.96	2.33	0	0	0	Repressed
309	GO_ION_CHANNEL_BINDING	-1.95	4.00	0	0	0	Repressed
310	GO_MITOCHONDRIAL_RNA_METABOLIC_PROCESS	-1.95	4.00	0	0	0	Repressed
311	GO_ORGANELLE_ENVELOPE_LUMEN	-1.95	4.00	0	0	0	Repressed
312	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP	-1.95	4.00	0	0	0	Repressed
313	PID_AURORA_B_PATHWAY	-1.95	4.00	0	0	0	Repressed
314	POOLA_INVASIVE_BREAST_CANCER_UP	-1.95	4.00	0	0	0	Repressed
315	REACTOME_DEFECTIVE_CFTR_CAUSES_CYSTIC_FIBROSIS	-1.95	4.00	0	0	0	Repressed

316	REACTOME_RNA_POLYMERASE_II_PRE_TRANSCRIPTION_EVENTS	-1.95	4.00	0	0	0	Repressed
317	REACTOME_TRNA_PROCESSING_IN_THE_NUCLEUS	-1.95	4.00	0	0	0	Repressed
318	WONG_PROTEASOME_GENE_MODULE	-1.95	4.00	0	0	0	Repressed
319	GO_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL_BY_E	-1.95	2.61	0	0	0	Repressed
320	BENPORATH_PROLIFERATION	-1.94	4.00	0	0	0	Repressed
321	BIOCARTA_NO2IL12_PATHWAY	-1.94	4.00	0	0	0	Repressed
322	GO_ENVELOPE	-1.94	4.00	0	0	0	Repressed
323	GO_RRNA_METABOLIC_PROCESS	-1.94	4.00	0	0	0	Repressed
324	HALLMARK_E2F_TARGETS	-1.94	4.00	0	0	0	Repressed
325	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN	-1.94	4.00	0	0	0	Repressed
326	MOHANKUMAR_HOXA1_TARGETS_UP	-1.94	4.00	0	0	0	Repressed
327	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	-1.94	4.00	0	0	0	Repressed
328	SHEPARD_CRUSH_AND_BURN_MUTANT_UP	-1.94	4.00	0	0	0	Repressed
329	YANG_BREAST_CANCER_ESR1_LASER_DN	-1.94	4.00	0	0	0	Repressed
330	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53	-1.94	2.55	0	0	0	Repressed
331	GO_MYELOID_CELL_APOPTOTIC_PROCESS	-1.93	4.00	0	0	0	Repressed
332	GO_PLASMINOGEN_ACTIVATION	-1.93	4.00	0	0	0	Repressed
333	HALLMARK_GLYCOLYSIS	-1.93	4.00	0	0	0	Repressed
334	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP	-1.93	4.00	0	0	0	Repressed
335	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP	-1.93	4.00	0	0	0	Repressed
336	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_DN	-1.93	4.00	0	0	0	Repressed
337	REACTOME_GLUCONEOGENESIS	-1.93	4.00	0	0	0	Repressed
338	REACTOME_ION_HOMEOSTASIS	-1.93	4.00	0	0	0	Repressed
339	SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN	-1.93	4.00	0	0	0	Repressed
340	BLALOCK_ALZHEIMERS_DISEASE_DN	-1.92	4.00	0	0	0	Repressed
341	GO_ADP_BINDING	-1.92	4.00	0	0	0	Repressed
342	GO_CATALYTIC_ACTIVITY_ACTING_ON_RNA	-1.92	4.00	0	0	0	Repressed
343	GO_HEMATOPOIETIC_STEM_CELL_DIFFERENTIATION	-1.92	4.00	0	0	0	Repressed
344	GO_LYMPHOCYTE_CHEMOTAXIS	-1.92	4.00	0	0	0	Repressed
345	GO_PROTEIN_HETEROTETRAMERIZATION	-1.92	4.00	0	0	0	Repressed
346	GO_RESPIRATORY_CHAIN_COMPLEX_IV_ASSEMBLY	-1.92	4.00	0	0	0	Repressed
347	GRADE_COLON_AND_RECTAL_CANCER_UP	-1.92	4.00	0	0	0	Repressed
348	HWANG_PROSTATE_CANCER_MARKERS	-1.92	4.00	0	0	0	Repressed
349	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS	-1.92	4.00	0	0	0	Repressed
350	REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	-1.92	4.00	0	0	0	Repressed
351	REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE	-1.92	4.00	0	0	0	Repressed
352	SESTO_RESPONSE_TO_UV_C0	-1.92	4.00	0	0	0	Repressed
353	WHITFIELD_CELL_CYCLE_M_G1	-1.92	4.00	0	0	1	Repressed
354	COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_DN	-1.91	4.00	0	0	0	Repressed
355	CROONQUIST_NRAS_SIGNALING_DN	-1.91	4.00	0	0	0	Repressed
356	FARDIN_HYPOXIA_11	-1.91	4.00	0	0	0	Repressed
357	GILDEA_METASTASIS	-1.91	4.00	0	0	0	Repressed
358	GO_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	-1.91	4.00	0	0	0	Repressed
359	GO_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_BINDING	-1.91	4.00	0	0	0	Repressed
360	GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT	-1.91	4.00	0	0	0	Repressed
361	GO_RESPONSE_TO_KETONE	-1.91	4.00	0	0	0	Repressed
362	GO_THIOESTER_METABOLIC_PROCESS	-1.91	4.00	0	0	0	Repressed
363	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP	-1.91	4.00	0	0	0	Repressed
364	REACTOME_CLEC7A_DECTIN_1_SIGNALING	-1.91	4.00	0	0	0	Repressed
365	REACTOME_DISORDERS_OF_TRANSMEMBRANE_TRANSPORTERS	-1.91	4.00	0	0	0	Repressed
366	REACTOME_SIGNALING_BY_HEDGEHOG	-1.91	4.00	0	0	0	Repressed
367	ZHAN_MULTIPLE_MYELOMA_SUBGROUPS	-1.91	4.00	0	0	0	Repressed
368	GO_SYNAPSE_MATURATION	-1.91	2.36	0	0	0	Repressed
369	DAIRKEE_CANCER_PRONE_RESPONSE_BPA	-1.90	4.00	0	0	0	Repressed
370	GO_CYTOCHROME_COMPLEX_ASSEMBLY	-1.90	4.00	0	0	0	Repressed
371	GO_INTERLEUKIN_1_MEDIATED_SIGNALING_PATHWAY	-1.90	4.00	0	0	0	Repressed
372	GO_NUCLEAR_EXPORT	-1.90	4.00	0	0	0	Repressed
373	GO_PRERIBOSOME_LARGE_SUBUNIT_PRECURSOR	-1.90	4.00	0	0	0	Repressed
374	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER	-1.90	4.00	0	0	0	Repressed
375	REACTOME_COOPERATION_OF_PDCL_PHLP1_AND_TRIC_CCT_IN_G_PR	-1.90	4.00	0	0	0	Repressed
376	REACTOME_METABOLISM_OF_RNA	-1.90	4.00	0	0	0	Repressed
377	REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	-1.90	4.00	0	0	0	Repressed
378	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE	-1.90	4.00	0	0	0	Repressed
379	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN	-1.90	4.00	0	0	0	Repressed
380	ZHONG_SECRETOME_OF_LUNG_CANCER_AND_FIBROBLAST	-1.90	4.00	0	0	0	Repressed
381	REACTOME_KINESINS	-1.90	2.58	0	0	0	Repressed
382	GO_POSITIVE_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	-1.90	2.36	0	0	0	Repressed
383	BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE	-1.90	2.33	0	0	0	Repressed
384	DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2	-1.89	4.00	0	0	0	Repressed
385	GO_NCRNA_TRANSCRIPTION	-1.89	4.00	0	0	0	Repressed
386	MORI_PRE_BI_LYMPHOCYTE_UP	-1.89	4.00	0	0	0	Repressed
387	REACTOME_TRANSPORT_OF_CONNEXONS_TO_THE_PLASMA_MEMBRAN	-1.89	4.00	0	0	0	Repressed
388	GO_PROTEASOME_REGULATORY_PARTICLE_BASE_SUBCOMPLEX	-1.89	2.62	0	0	0	Repressed
389	GO_TIM23_MITOCHONDRIAL_IMPORT_INNER_MEMBRANE_TRANSLOCASE	-1.89	2.61	0	0	0	Repressed
390	GO_CALCIUM_DEPENDENT_PROTEIN_BINDING	-1.89	2.57	0	0	0	Repressed
391	ZHAN_MULTIPLE_MYELOMA_DN	-1.89	2.33	0	0	0	Repressed
392	CHANG_CYCLING_GENES	-1.88	4.00	0	0	0	Repressed
393	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN	-1.88	4.00	0	0	0	Repressed
394	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_UP	-1.88	4.00	0	0	0	Repressed
395	GO_CELLULAR_RESPONSE_TO_GLUCAGON_STIMULUS	-1.88	4.00	0	0	0	Repressed
396	GO_HEART_PROCESS	-1.88	4.00	0	0	0	Repressed
397	GO_LIPASE_INHIBITOR_ACTIVITY	-1.88	4.00	0	0	0	Repressed
398	GO_POSITIVE_REGULATION_OF_RIBOSOME_BIOGENESIS	-1.88	4.00	0	0	0	Repressed
399	GO_REGULATION_OF_CHOLESTEROL_BIOSYNTHETIC_PROCESS	-1.88	4.00	0	0	0	Repressed
400	GO_RESPONSE_TO_GLUCAGON	-1.88	4.00	0	0	0	Repressed
401	GO_RNA_BINDING	-1.88	4.00	0	0	0	Repressed
402	KANG_DOXORUBICIN_RESISTANCE_UP	-1.88	4.00	0	0	0	Repressed
403	KEGG_OOCYTE_MEIOSIS	-1.88	4.00	0	0	0	Repressed
404	MOHANKUMAR_TLX1_TARGETS_UP	-1.88	4.00	0	0	0	Repressed
405	REACTOME_PHOSPHORYLATION_OF_EMI1	-1.88	4.00	0	0	0	Repressed
406	RPS14_DN.V1_DN	-1.88	4.00	0	0	0	Repressed
407	REACTOME_INWARDLY_RECTIFYING_KPLUS_CHANNELS	-1.88	2.64	0	0	0	Repressed
408	GO_PODOSOME_ASSEMBLY	-1.88	2.32	0	0	0	Repressed
409	REACTOME_INTERLEUKIN_10_SIGNALING	-1.88	2.32	0	0	0	Repressed
410	GO_SPINDLE_MICROTUBULE	-1.88	2.29	0	0	0	Repressed
411	DELLA_RESPONSE_TO_TSA_AND_BUTYRATE	-1.87	4.00	0	0	0	Repressed
412	DOANE_BREAST_CANCER_ESR1_DN	-1.87	4.00	0	0	0	Repressed
413	GO_ANTIGEN_PROCESSING_AND_PRESENTATION	-1.87	4.00	0	0	0	Repressed
414	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITI	-1.87	4.00	0	0	0	Repressed
415	GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY	-1.87	4.00	0	0	0	Repressed
416	GO_STEROL_BIOSYNTHETIC_PROCESS	-1.87	4.00	0	0	0	Repressed
417	KAAB_HEART_ATRIUM_VS_VENTRICLE_DN	-1.87	4.00	0	0	0	Repressed
418	KORKOLA_SEMINOMA_UP	-1.87	4.00	0	0	0	Repressed
419	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN	-1.87	4.00	0	0	0	Repressed
420	QI_PLASMACYTOMA_UP	-1.87	4.00	0	0	0	Repressed
421	REACTOME_PROGRAMMED_CELL_DEATH	-1.87	4.00	0	0	0	Repressed
422	REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVE	-1.87	4.00	0	0	0	Repressed
423	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN	-1.87	2.61	0	0	0	Repressed
424	PID_RXR_VDR_PATHWAY	-1.87	2.61	0	0	0	Repressed

425	REACTOME_ACTIVATION_OF_NIMA_KINASES_NEK9_NEK6_NEK7	-1.87	2.34	0	0	0	Repressed
426	CYCLIN_D1_UP.V1_UP	-1.86	4.00	0	0	0	Repressed
427	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP	-1.86	4.00	0	0	0	Repressed
428	GO_CHROMOSOME_MOVEMENT_TOWARDS_SPINDLE_POLE	-1.86	4.00	0	0	0	Repressed
429	GO_VITAMIN_TRANSMEMBRANE_TRANSPORT	-1.86	4.00	0	0	0	Repressed
430	JAEGER_METASTASIS_UP	-1.86	4.00	0	0	0	Repressed
431	JISON_SICKLE_CELL_DISEASE_UP	-1.86	4.00	0	0	0	Repressed
432	KEGG_SPLICEOSOME	-1.86	4.00	0	0	0	Repressed
433	REACTOME_ATF6_ATF6_ALPHA_ACTIVATES_CHAPERONE_GENES	-1.86	4.00	0	0	0	Repressed
434	REACTOME_C_TYPE_LECTIN_RECEPTORS_CLRS	-1.86	4.00	0	0	0	Repressed
435	REACTOME_CELLULAR_RESPONSES_TO_STRESS	-1.86	4.00	0	0	0	Repressed
436	REACTOME_G2_M_CHECKPOINTS	-1.86	4.00	0	0	0	Repressed
437	REACTOME_HOST_INTERACTIONS_WITH_INFLUENZA_FACTORS	-1.86	4.00	0	0	0	Repressed
438	REACTOME_NUCLEAR_PORE_COMPLEX_NPC_DISASSEMBLY	-1.86	4.00	0	0	0	Repressed
439	REACTOME_REGULATION_OF_HSF1_MEDIATED_HEAT_SHOCK_RESPON	-1.86	4.00	0	0	0	Repressed
440	TAVOR_CEBPA_TARGETS_UP	-1.86	4.00	0	0	0	Repressed
441	VEGF_A_UP.V1_DN	-1.86	4.00	0	0	0	Repressed
442	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN	-1.86	4.00	0	0	0	Repressed
443	WHITFIELD_CELL_CYCLE_G2_M	-1.86	4.00	0	0	0	Repressed
444	FUNG_IL2_SIGNALING_1	-1.86	2.62	0	0	0	Repressed
445	GO_RNA_CAPPING	-1.86	2.60	0	0	0	Repressed
446	KEGG_CITRATE_CYCLE_TCA_CYCLE	-1.86	2.58	0	0	0	Repressed
447	BHAT_ESR1_TARGETS_NOT_VIA_AKT1_UP	-1.85	4.00	0	0	0	Repressed
448	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP_OF_DO	-1.85	4.00	0	0	0	Repressed
449	GO_RESPONSE_TO_CORTICOSTEROID	-1.85	4.00	0	0	0	Repressed
450	GO_T_CELL_CHEMOTAXIS	-1.85	4.00	0	0	0	Repressed
451	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN	-1.85	4.00	0	0	0	Repressed
452	LABBE_TARGETS_OF_TGFB1_AND_WNT3A_UP	-1.85	4.00	0	0	0	Repressed
453	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN	-1.85	4.00	0	0	0	Repressed
454	MEL18_DN.V1_DN	-1.85	4.00	0	0	0	Repressed
455	PUJANA_BRCA1_PCC_NETWORK	-1.85	4.00	0	0	0	Repressed
456	REACTOME_DNA_REPLICATION_PRE_INITIATION	-1.85	4.00	0	0	0	Repressed
457	REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS	-1.85	4.00	0	0	0	Repressed
458	REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_R	-1.85	4.00	0	0	0	Repressed
459	REACTOME_INTERLEUKIN_1_SIGNALING	-1.85	4.00	0	0	0	Repressed
460	WHITFIELD_CELL_CYCLE_LITERATURE	-1.85	4.00	0	0	0	Repressed
461	GREENBAUM_E2A_TARGETS_UP	-1.85	2.61	0	0	0	Repressed
462	FURUKAWA_DUSP6_TARGETS_PCI35_DN	-1.85	2.56	0	0	0	Repressed
463	GO_TOXIN_TRANSPORT	-1.85	2.31	0	0	0	Repressed
464	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_IV_ASSEMBLY	-1.85	2.15	0	0	0	Repressed
465	GO_RESPONSE_TO_MINERALOCORTICOID	-1.85	2.02	0	0	0	Repressed
466	CAIRO_HEPATOBLASTOMA_CLASSES_UP	-1.84	4.00	0	0	0	Repressed
467	GO_CELLULAR_RESPONSE_TO_HEAT	-1.84	4.00	0	0	0	Repressed
468	GO_OXIDOREDUCTASE_ACTIVITY	-1.84	4.00	0	0	0	Repressed
469	LABBE_WNT3A_TARGETS_UP	-1.84	4.00	0	0	0	Repressed
470	MIKKELSEN_MEF_LCP_WITH_H3K4ME3	-1.84	4.00	0	0	0	Repressed
471	REACTOME_UBIQUINOL_BIOSYNTHESIS	-1.84	4.00	0	0	0	Repressed
472	ZHONG_SECRETOME_OF_LUNG_CANCER_AND_MACROPHAGE	-1.84	4.00	0	0	0	Repressed
473	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	-1.84	2.64	0	0	0	Repressed
474	REACTOME_PHOSPHORYLATION_OF_THE_APC_C	-1.84	2.62	0	0	0	Repressed
475	NAGASHIMA_EGF_SIGNALING_UP	-1.84	2.59	0	0	0	Repressed
476	GO_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	-1.84	2.55	0	0	0	Repressed
477	REACTOME_GAP_JUNCTION_ASSEMBLY	-1.84	2.35	0	0	0	Repressed
478	GO_RESPONSE_TO_AMINE	-1.84	2.29	0	0	0	Repressed
479	BORCZUK_MALIGNANT_MESOTHELIOMA_UP	-1.83	4.00	0	0	0	Repressed
480	BURTON_ADIPOGENESIS_6	-1.83	4.00	0	0	0	Repressed
481	GO_MITOCHONDRION_MORPHOGENESIS	-1.83	4.00	0	0	0	Repressed
482	GO_MULTI_ORGANISM_MEMBRANE_ORGANIZATION	-1.83	4.00	0	0	0	Repressed
483	GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	-1.83	4.00	0	0	0	Repressed
484	GO_SNRNA_PROCESSING	-1.83	4.00	0	0	0	Repressed
485	GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	-1.83	4.00	0	0	0	Repressed
486	GO_TELOMERASE_RNA_LOCALIZATION	-1.83	4.00	0	0	0	Repressed
487	LE_EGR2_TARGETS_UP	-1.83	4.00	0	0	0	Repressed
488	PID_HIF1_TFPATHWAY	-1.83	4.00	0	0	0	Repressed
489	REACTOME_INTERACTIONS_OF_REV_WITH_HOST_CELLULAR_PROTEIN	-1.83	4.00	0	0	0	Repressed
490	REACTOME_INTERLEUKIN_12_SIGNALING	-1.83	4.00	0	0	0	Repressed
491	SESTO_RESPONSE_TO_UV_C7	-1.83	4.00	0	0	0	Repressed
492	GO_PHOSPHOLIPASE_INHIBITOR_ACTIVITY	-1.83	2.68	0	0	0	Repressed
493	BIOCARTA_MHC_PATHWAY	-1.83	2.66	0	0	0	Repressed
494	GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	-1.83	2.62	0	0	0	Repressed
495	GO_TBP_CLASS_PROTEIN_BINDING	-1.83	2.60	0	0	0	Repressed
496	FINETTI_BREAST_CANCER_KINOME_RED	-1.83	2.59	0	0	0	Repressed
497	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MITOCHONDRIAL	-1.83	2.16	0	0	0	Repressed
498	BLUM_RESPONSE_TO_SALIRASIB_DN	-1.82	4.00	0	0	0	Repressed
499	CAFFAREL_RESPONSE_TO_THC_8HR_3_DN	-1.82	4.00	0	0	0	Repressed
500	GO_CYTOKINE_BINDING	-1.82	4.00	0	0	0	Repressed
501	GO_MORPHOGENESIS_OF_A_POLARIZED_EPITHELIUM	-1.82	4.00	0	0	0	Repressed
502	GO_RESPIRATORY_CHAIN_COMPLEX_IV	-1.82	4.00	0	0	0	Repressed
503	GO_RNA_5_END_PROCESSING	-1.82	4.00	0	0	0	Repressed
504	REACTOME_MRNA_CAPPING	-1.82	4.00	0	0	0	Repressed
505	VANTVEER_BREAST_CANCER_METASTASIS_DN	-1.82	4.00	0	0	0	Repressed
506	DASU_IL6_SIGNALING_SCAR_UP	-1.82	2.64	0	0	0	Repressed
507	BIOCARTA_MPR_PATHWAY	-1.82	2.62	0	0	0	Repressed
508	MAGRANGEAS_MULTIPLE_MYELOMA_IGG_VS_IGA_UP	-1.82	2.62	0	0	0	Repressed
509	VANDESLUIS_COMMD1_TARGETS_GROUP_2_UP	-1.82	2.62	0	0	0	Repressed
510	REACTOME_ACTIVATION_OF_GENE_EXPRESSION_BY_SREBF_SREBP	-1.82	2.57	0	0	0	Repressed
511	LEE_NEURAL_CREST_STEM_CELL_UP	-1.82	2.56	0	0	0	Repressed
512	REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS	-1.82	2.55	0	0	0	Repressed
513	GO_G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_ACTIVITY	-1.82	2.13	0	0	0	Repressed
514	BIDUS_METASTASIS_UP	-1.81	4.00	0	0	0	Repressed
515	CAHOY_ASTROGLIAL	-1.81	4.00	0	0	0	Repressed
516	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP	-1.81	4.00	0	0	0	Repressed
517	GO_NUCLEOBASE_CONTAINING_COMPOUND_TRANSPORT	-1.81	4.00	0	0	0	Repressed
518	GO_ORGANIC_ACID_METABOLIC_PROCESS	-1.81	4.00	0	0	0	Repressed
519	GO_OXIDATION_REDUCTION_PROCESS	-1.81	4.00	0	0	0	Repressed
520	KIM_WT1_TARGETS_12HR_DN	-1.81	4.00	0	0	0	Repressed
521	REACTOME_ABORTIVE_ELONGATION_OF_HIV_1_TRANSCRIPT_IN_THE_A	-1.81	4.00	0	0	0	Repressed
522	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	-1.81	4.00	0	0	0	Repressed
523	REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	-1.81	4.00	0	0	0	Repressed
524	FARDIN_HYPOXIA_9	-1.81	2.64	0	0	0	Repressed
525	IVANOV_MUTATED_IN_COLON_CANCER	-1.81	2.64	0	0	0	Repressed
526	PID_CD8_TCR_DOWNSTREAM_PATHWAY	-1.81	2.28	0	0	0	Repressed
527	GO_SIRNA_BINDING	-1.81	2.17	0	0	0	Repressed
528	GO_RESPONSE_TO_MUSCLE_STRETCH	-1.81	2.16	0	0	0	Repressed
529	GO_RNA_POLYMERASE_III_COMPLEX	-1.81	2.04	0	0	0	Repressed
530	DAZARD_RESPONSE_TO_UV_SCC_UP	-1.80	4.00	0	0	0	Repressed
531	GO_AEROBIC_RESPIRATION	-1.80	4.00	0	0	0	Repressed
532	GO_CHAPERONE_MEDIATED_PROTEIN_FOLDING	-1.80	4.00	0	0	0	Repressed
533	GO_MRNA_EXPORT_FROM_NUCLEUS	-1.80	4.00	0	0	0	Repressed

534	GO_MULTI_ORGANISM_MEMBRANE_FUSION	-1.80	4.00	0	0	0	Repressed
535	GO_ORGANIC_ACID_BIOSYNTHETIC_PROCESS	-1.80	4.00	0	0	0	Repressed
536	GO_REGULATION_OF_SMALL_MOLECULE_METABOLIC_PROCESS	-1.80	4.00	0	0	0	Repressed
537	GO_RNA_METABOLIC_PROCESS	-1.80	4.00	0	0	0	Repressed
538	GO_SARCOPLASM	-1.80	4.00	0	0	0	Repressed
539	REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_COMPLEX	-1.80	4.00	0	0	0	Repressed
540	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	-1.80	4.00	0	0	0	Repressed
541	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2PLU	-1.80	4.00	0	0	0	Repressed
542	REACTOME_TRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL	-1.80	4.00	0	0	0	Repressed
543	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN	-1.80	4.00	0	0	0	Repressed
544	WHITEFORD_PEDIATRIC_CANCER_MARKERS	-1.80	4.00	0	0	0	Repressed
545	GO_ADENYLATE_CYCLASE_BINDING	-1.80	2.17	0	0	0	Repressed
546	DORN_ADENOVIRUS_INFECTION_12HR_DN	-1.80	2.15	0	0	0	Repressed
547	LIU_IL13_MEMORY_MODEL_UP	-1.80	2.14	0	0	0	Repressed
548	REACTOME_STING_MEDIATED_INDUCTION_OF_HOST_IMMUNE_RESPONS	-1.80	1.94	0	0	0	Repressed
549	GO_INTERACTION_WITH_SYMBIONT	-1.79	4.00	0	0	0	Repressed
550	GO_MRNA_TRANSPORT	-1.79	4.00	0	0	0	Repressed
551	GO_PEPTIDASE_ACTIVATOR_ACTIVITY	-1.79	4.00	0	0	0	Repressed
552	GO_PROTEIN_FOLDING	-1.79	4.00	0	0	0	Repressed
553	GO_RESPONSE_TO_ESTRADIOL	-1.79	4.00	0	0	0	Repressed
554	GO_RESPONSE_TO_INTERLEUKIN_12	-1.79	4.00	0	0	0	Repressed
555	REACTOME_CYCLIN_A:CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTR	-1.79	4.00	0	0	0	Repressed
556	REACTOME_NUCLEAR_ENVELOPE_BREAKDOWN	-1.79	4.00	0	0	0	Repressed
557	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM2	-1.79	4.00	0	0	0	Repressed
558	ZHANG_RESPONSE_TO_CANTHARIDIN_DN	-1.79	4.00	0	0	0	Repressed
559	GO_2_IRON_2_SULFUR_CLUSTER_BINDING	-1.79	2.62	0	0	0	Repressed
560	GO_THREONINE_TYPE_PEPTIDASE_ACTIVITY	-1.79	2.60	0	0	0	Repressed
561	REACTOME_RECYCLING_PATHWAY_OF_L1	-1.79	2.57	0	0	0	Repressed
562	SIG_CHEMOTAXIS	-1.79	2.56	0	0	0	Repressed
563	JEON_SMAD6_TARGETS_DN	-1.79	2.36	0	0	0	Repressed
564	BIOCARTA_RANMS_PATHWAY	-1.79	2.33	0	0	0	Repressed
565	GO_PROTEASOME_CORE_COMPLEX	-1.79	2.31	0	0	0	Repressed
566	GO_MATURATION_OF_5_8S_RRNA	-1.79	2.03	0	0	0	Repressed
567	GO_CADHERIN_BINDING_INVOLVED_IN_CELL_CELL_ADHESION	-1.79	1.86	0	0	0	Repressed
568	GO_POSITIVE_REGULATION_BY_HOST_OF_VIRAL_PROCESS	-1.79	1.69	0	0	0	Repressed
569	DODD_NASOPHARYNGEAL_CARCINOMA_DN	-1.78	4.00	0	0	0	Repressed
570	GO_ANIMAL_ORGAN_REGENERATION	-1.78	4.00	0	0	0	Repressed
571	GO_ISOMERASE_ACTIVITY	-1.78	4.00	0	0	0	Repressed
572	GO_MITOCHONDRION_ORGANIZATION	-1.78	4.00	0	0	0	Repressed
573	GO_SUPEROXIDE_METABOLIC_PROCESS	-1.78	4.00	0	0	0	Repressed
574	GO_VESICLE_LUMEN	-1.78	4.00	0	0	0	Repressed
575	LI_INDUCED_T_TO_NATURAL_KILLER_UP	-1.78	4.00	0	0	0	Repressed
576	ONDER_CDH1_TARGETS_1_DN	-1.78	4.00	0	0	0	Repressed
577	REACTOME_FC_EPSILON_RECEPTOR_FCERI_SIGNALING	-1.78	4.00	0	0	0	Repressed
578	REACTOME_MITOTIC_PROPHASE	-1.78	4.00	0	0	0	Repressed
579	REACTOME_MUSCLE_CONTRACTION	-1.78	4.00	0	0	0	Repressed
580	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRN	-1.78	4.00	0	0	0	Repressed
581	GO_ANATOMICAL_STRUCTURE_ARRANGEMENT	-1.78	2.64	0	0	0	Repressed
582	BIOCARTA_HIF_PATHWAY	-1.78	2.61	0	0	0	Repressed
583	KORKOLA_YOLK_SAC_TUMOR_UP	-1.78	2.61	0	0	0	Repressed
584	REACTOME_TRANSPORT_OF_THE_SLBP_DEPENDANT_MATURE_MRNA	-1.78	2.61	0	0	0	Repressed
585	SPIRA_SMOKERS_LUNG_CANCER_UP	-1.78	2.61	0	0	0	Repressed
586	GO_PROTEASOMAL_UBIQUITIN_INDEPENDENT_PROTEIN_CATABOLIC_PR	-1.78	2.60	0	0	0	Repressed
587	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT	-1.78	2.51	0	0	0	Repressed
588	GO_CHEMOKINE_BINDING	-1.78	2.30	0	0	0	Repressed
589	GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	-1.78	2.29	0	0	0	Repressed
590	HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_UP	-1.78	2.29	0	0	0	Repressed
591	REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	-1.78	2.28	0	0	0	Repressed
592	GO_ENDOCYTIC_VESICLE_LUMEN	-1.78	2.19	0	0	0	Repressed
593	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_RED_UP	-1.78	2.14	0	0	0	Repressed
594	GO_REGULATION_OF_SUPEROXIDE_METABOLIC_PROCESS	-1.78	2.12	0	0	0	Repressed
595	GO_DENDRITIC_CELL_MIGRATION	-1.78	2.05	0	0	0	Repressed
596	GO_CALCIUM_DEPENDENT_PHOSPHOLIPID_BINDING	-1.78	2.00	0	0	0	Repressed
597	GO_PROTEIN_IMPORT_INTO_MITOCHONDRIAL_MATRIX	-1.78	1.94	0	0	0	Repressed
598	GO_C_C_CHEMOKINE_BINDING	-1.78	1.78	0	0	0	Repressed
599	AMIT_EGF_RESPONSE_240_MCF10A	-1.77	4.00	0	0	0	Repressed
600	BHAT_ESR1_TARGETS_VIA_AKT1_UP	-1.77	4.00	0	0	0	Repressed
601	FERREIRA_EWINGS_SARCOMA_UNSTABLE_VS_STABLE_UP	-1.77	4.00	0	0	0	Repressed
602	GO_PROTEIN_CONTAINING_COMPLEX_DISASSEMBLY	-1.77	4.00	0	0	0	Repressed
603	GO_SARCOLEMMA	-1.77	4.00	0	0	0	Repressed
604	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	-1.77	4.00	0	0	0	Repressed
605	REACTOME_MRNA_SPLICING	-1.77	4.00	0	0	0	Repressed
606	REACTOME_RHO_GTPASES_ACTIVATE_FORMINS	-1.77	4.00	0	0	0	Repressed
607	SASAI_TARGETS_OF_CXCR6_AND_PTCH1_UP	-1.77	2.66	0	0	0	Repressed
608	GO_SMN_SM_PROTEIN_COMPLEX	-1.77	2.65	0	0	0	Repressed
609	GRATIAS_RETINOBLASTOMA_16Q24	-1.77	2.62	0	0	0	Repressed
610	GO_CARTILAGE_DEVELOPMENT_INVOLVED_IN_ENDOCHONDRAL_BONE_	-1.77	2.60	0	0	0	Repressed
611	ZHAN_MULTIPLE_MYELOMA_CD2_DN	-1.77	2.59	0	0	0	Repressed
612	FU_INTERACT_WITH_ALKBH8	-1.77	2.33	0	0	0	Repressed
613	GO_RESPONSE_TO_CHEMOKINE	-1.77	2.33	0	0	0	Repressed
614	GO_PROTEASOME_REGULATORY_PARTICLE_LID_SUBCOMPLEX	-1.77	2.18	0	0	0	Repressed
615	REACTOME_ACTIVATION_OF_AMPK_DOWNSTREAM_OF_NMDARS	-1.77	2.15	0	0	0	Repressed
616	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_BIOSYNTHESIS	-1.77	2.14	1	0	0	Repressed
617	REACTOME_ANTIMICROBIAL_PEPTIDES	-1.77	2.14	0	0	0	Repressed
618	REACTOME_MET_ACTIVATES_PTK2_SIGNALING	-1.77	1.98	0	0	0	Repressed
619	REACTOME_GOLGI_CISTERNAE_PERICENTRIOLAR_STACK_REORGANIZA	-1.77	1.92	0	0	0	Repressed
620	REACTOME_RHO_GTPASES_ACTIVATE_IQGAPS	-1.77	1.90	0	0	0	Repressed
621	NGO_MALIGNANT_GLIOMA_1P_LOH	-1.77	1.86	0	0	0	Repressed
622	ALFANO_MYC_TARGETS	-1.76	4.00	0	0	0	Repressed
623	SESTO_RESPONSE_TO_UV_C1	-1.76	4.00	0	0	0	Repressed
624	TAKAO_RESPONSE_TO_UVB_RADIATION_DN	-1.76	4.00	0	0	0	Repressed
625	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP	-1.76	4.00	0	0	0	Repressed
626	REACTOME_COPI_INDEPENDENT_GOLGI_TO_ER_RETROGRADE_TRAFF	-1.76	2.58	0	0	0	Repressed
627	GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	-1.76	2.53	0	0	0	Repressed
628	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN	-1.76	2.32	0	0	0	Repressed
629	MOOTHA_TCA	-1.76	2.32	0	0	0	Repressed
630	CHR5P15	-1.76	2.28	0	0	0	Repressed
631	GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	-1.76	2.28	0	0	0	Repressed
632	BIOCARTA_NPC_PATHWAY	-1.76	2.16	0	0	0	Repressed
633	GO_ARP2_3_PROTEIN_COMPLEX	-1.76	2.15	0	0	0	Repressed
634	GO_INNER_EAR_RECEPTOR_CELL_STEREOCILIUM_ORGANIZATION	-1.76	2.04	0	0	0	Repressed
635	GO_POSITIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	-1.76	2.01	0	0	0	Repressed
636	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTO	-1.76	1.99	0	0	0	Repressed
637	GO_NEUTRAL_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVIT	-1.76	1.93	0	0	0	Repressed
638	OXFORD_RALA_OR_RALB_TARGETS_DN	-1.76	1.92	0	0	0	Repressed
639	GO_RESPONSE_TO_HYPEROXIA	-1.76	1.87	0	0	0	Repressed
640	CHICAS_RB1_TARGETS_GROWING	-1.75	4.00	0	0	0	Repressed
641	FARMER_BREAST_CANCER_APOCRINE_VS_BASAL	-1.75	4.00	0	0	0	Repressed
642	GO_BOX_C_D_SNORNP_COMPLEX	-1.75	4.00	0	0	0	Repressed

643	GO_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	-1.75	4.00	0	0	0	Repressed
644	GO_POSITIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	-1.75	4.00	0	0	0	Repressed
645	GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROC	-1.75	4.00	0	0	0	Repressed
646	LAIHO_COLORECTAL_CANCER_SERRATED_UP	-1.75	4.00	0	0	0	Repressed
647	PEART_HDAC_PROLIFERATION_CLUSTER_DN	-1.75	4.00	0	0	0	Repressed
648	PUIFFE_INVASION_INHIBITED_BY_ASCITES_UP	-1.75	4.00	0	0	0	Repressed
649	REACTOME_BINDING_AND_UPTAKE_OF_LIGANDS_BY_SCAVENGER_REC	-1.75	4.00	0	0	0	Repressed
650	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_SMALL_RNAS	-1.75	4.00	0	0	0	Repressed
651	GO_PEPTIDE_RECEPTOR_ACTIVITY	-1.75	2.59	0	0	0	Repressed
652	GO_TRNA_TRANSPORT	-1.75	2.56	0	0	0	Repressed
653	REACTOME_THE_CANONICAL_RETINOID_CYCLE_IN_RODS_TWILIGHT_VI	-1.75	2.36	0	0	0	Repressed
654	GO_NUCLEAR_NUCLEOSOME	-1.75	2.31	0	0	0	Repressed
655	REACTOME_MRNA_SPLICING_MINOR_PATHWAY	-1.75	2.27	0	0	0	Repressed
656	GO_PEPTIDYL_ARGININE_MODIFICATION	-1.75	2.16	0	0	0	Repressed
657	GO_VITAMIN_TRANSPORT	-1.75	2.13	0	0	0	Repressed
658	KEGG_PROPANOATE_METABOLISM	-1.75	2.12	0	0	0	Repressed
659	REACTOME_EXPORT_OF_VIRAL_RIBONUCLEOPROTEINS_FROM_NUCLE	-1.75	2.10	0	0	0	Repressed
660	REACTOME_VASOPRESSIN_REGULATES_RENAL_WATER_HOMEOSTASIS	-1.75	2.00	0	0	0	Repressed
661	GO_ADENYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	-1.75	1.97	0	0	0	Repressed
662	ITO_PTTG1_TARGETS_DN	-1.75	1.96	0	0	0	Repressed
663	GO_REGULATION_OF_PROTON_TRANSPORT	-1.75	1.85	0	0	0	Repressed
664	LEE_INTRATHYMIC_T_PROGENITOR	-1.75	1.81	0	0	0	Repressed
665	SMID_BREAST_CANCER_LUMINAL_A_DN	-1.75	1.77	0	0	0	Repressed
666	DANG_MYC_TARGETS_UP	-1.74	4.00	0	0	0	Repressed
667	GO_S_ADENOSYLMETHIONINE_DEPENDENT_METHYLTRANSFERASE_AC	-1.74	4.00	0	0	0	Repressed
668	GO_SEQUESTERING_OF_CALCIUM_ION	-1.74	4.00	0	0	0	Repressed
669	MULLIGAN_NTF3_SIGNALING_VIA_INSR_AND_IGF1R_UP	-1.74	4.00	0	0	0	Repressed
670	PAL_PRMT5_TARGETS_UP	-1.74	4.00	0	0	0	Repressed
671	REACTOME_CELLULAR_RESPONSE_TO_HEAT_STRESS	-1.74	4.00	0	0	0	Repressed
672	REACTOME_TP53_REGULATES_METABOLIC_GENES	-1.74	4.00	0	0	0	Repressed
673	WANG_TARGETS_OF_MLL_CBP_FUSION_DN	-1.74	4.00	0	0	0	Repressed
674	GO_METHYLOSOME	-1.74	2.62	0	0	0	Repressed
675	CERVERA_SDHB_TARGETS_2	-1.74	2.55	0	0	0	Repressed
676	GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_II_PROMOT	-1.74	2.48	0	0	0	Repressed
677	GO_CELL_PROLIFERATION_INVOLVED_IN_METANEPHROS_DEVELOPME	-1.74	2.37	0	0	0	Repressed
678	GAJATE_RESPONSE_TO_TRABECTEDIN_DN	-1.74	2.33	0	0	0	Repressed
679	GO_MEMBRANE_RAFT_ASSEMBLY	-1.74	2.19	0	0	0	Repressed
680	WANG_NFKB_TARGETS	-1.74	2.18	0	0	0	Repressed
681	REACTOME_GLUCAGON_LIKE_PEPTIDE_1_GLP1_REGULATES_INSULIN_	-1.74	2.13	0	0	0	Repressed
682	GO_WATER_SOLUBLE_VITAMIN_BIOSYNTHETIC_PROCESS	-1.74	2.05	0	0	0	Repressed
683	GO_CELLULAR_RESPONSE_TO_DEXAMETHASONE_STIMULUS	-1.74	2.02	0	0	0	Repressed
684	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_CLEARANCE	-1.74	1.93	0	0	0	Repressed
685	GROSS_HIF1A_TARGETS_DN	-1.74	1.93	0	0	0	Repressed
686	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP	-1.73	4.00	0	0	0	Repressed
687	GO_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENT	-1.73	4.00	0	0	0	Repressed
688	HALLMARK_FATTY_ACID_METABOLISM	-1.73	4.00	0	0	0	Repressed
689	JUBAN_TARGETS_OF_SPI1_AND_FLI1_DN	-1.73	4.00	0	0	0	Repressed
690	NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_DN	-1.73	4.00	0	0	0	Repressed
691	REACTOME_DNA_REPLICATION	-1.73	4.00	0	0	0	Repressed
692	REACTOME_INTERLEUKIN_1_FAMILY_SIGNALING	-1.73	4.00	0	0	0	Repressed
693	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	-1.73	4.00	0	0	0	Repressed
694	VANTVEER_BREAST_CANCER_ESR1_DN	-1.73	4.00	0	0	0	Repressed
695	WELCSH_BRCA1_TARGETS_DN	-1.73	4.00	0	0	0	Repressed
696	ZHU_CMV_ALL_UP	-1.73	4.00	0	0	0	Repressed
697	GO_POSITIVE_REGULATION_OF_RYANODINE_SENSITIVE_CALCIUM_RELE	-1.73	2.66	0	0	0	Repressed
698	GO_AMINO_ACID_BINDING	-1.73	2.56	0	0	0	Repressed
699	SASAKI_ADULT_T_CELL_LEUKEMIA	-1.73	2.46	0	0	0	Repressed
700	KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS	-1.73	2.34	0	0	0	Repressed
701	GO_ACTIVATION_OF_ADENYLATE_CYCLASE_ACTIVITY	-1.73	2.32	0	0	0	Repressed
702	GO_REGULATION_OF_SECONDARY_METABOLIC_PROCESS	-1.73	2.32	0	0	0	Repressed
703	BASSO_HAIRY_CELL_LEUKEMIA_UP	-1.73	2.28	0	0	0	Repressed
704	REACTOME_OPIOID_SIGNALLING	-1.73	2.27	0	0	0	Repressed
705	GO_SNRNA_TRANSCRIPTION	-1.73	2.24	0	0	0	Repressed
706	XU_HGF_SIGNALING_NOT_VIA_AKT1_48HR_DN	-1.73	2.15	0	0	0	Repressed
707	GO_CELLULAR_RESPONSE_TO_ESTRADIOL_STIMULUS	-1.73	2.01	0	0	0	Repressed
708	HORTON_SREBF_TARGETS	-1.73	2.01	0	0	0	Repressed
709	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_DN	-1.73	1.97	0	0	0	Repressed
710	LINDGREN_BLADDER_CANCER_HIGH_RECURRENCE	-1.73	1.96	0	0	0	Repressed
711	REACTOME_ATF6_ATF6_ALPHA_ACTIVATES_CHAPERONES	-1.73	1.88	0	0	0	Repressed
712	REACTOME_SIGNALING_BY_FGFR2_IIIA_TM	-1.73	1.85	0	0	0	Repressed
713	GO_NEGATIVE_REGULATION_OF_LYASE_ACTIVITY	-1.73	1.81	0	0	0	Repressed
714	GO_POSITIVE_REGULATION_OF_VIRAL_PROCESS	-1.72	4.00	0	0	0	Repressed
715	GO_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	-1.72	4.00	0	0	0	Repressed
716	JOHANSSON_GLIOMAGENESIS_BY_PDGFB_UP	-1.72	4.00	0	0	0	Repressed
717	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP	-1.72	2.60	0	1	0	Repressed
718	GO_ENDOPLASMIC_RETICULUM_CHAPERONE_COMPLEX	-1.72	2.34	0	0	0	Repressed
719	GO_AMIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.72	2.30	0	0	0	Repressed
720	SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_UP	-1.72	2.30	0	0	0	Repressed
721	GO_MICROBODY_LUMEN	-1.72	2.29	0	0	0	Repressed
722	JIANG_AGING_CEREBRAL_CORTEX_DN	-1.72	2.29	0	0	0	Repressed
723	GO_PODOSOME	-1.72	2.28	0	0	0	Repressed
724	GO_NCRNA_3_END_PROCESSING	-1.72	2.13	0	0	0	Repressed
725	KEGG_FATTY_ACID_METABOLISM	-1.72	2.13	0	0	0	Repressed
726	GESERICK_TERT_TARGETS_DN	-1.72	2.04	0	0	0	Repressed
727	GO_REGULATION_OF_LOW_DENSITY_LIPOPROTEIN_PARTICLE_CLEARA	-1.72	2.04	0	0	0	Repressed
728	GO_RIBONUCLEASE_P_COMPLEX	-1.72	2.03	0	0	0	Repressed
729	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_ELONGATION	-1.72	1.88	0	0	0	Repressed
730	GO_DEFENSE_RESPONSE_TO_FUNGUS	-1.72	1.85	0	0	0	Repressed
731	GO_COENZYME_METABOLIC_PROCESS	-1.71	4.00	0	0	0	Repressed
732	GO_GLYCOLYTIC_PROCESS	-1.71	4.00	0	0	0	Repressed
733	GO_POSITIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	-1.71	4.00	0	0	0	Repressed
734	GO_REGULATION_OF_MRNA_CATABOLIC_PROCESS	-1.71	4.00	0	0	0	Repressed
735	GO_REGULATION_OF_STEM_CELL_DIFFERENTIATION	-1.71	4.00	0	0	0	Repressed
736	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN	-1.71	4.00	0	0	0	Repressed
737	PID_ILK_PATHWAY	-1.71	4.00	0	0	0	Repressed
738	REACTOME_VISUAL_PHOTOTRANSDUCTION	-1.71	4.00	0	0	0	Repressed
739	SANA_RESPONSE_TO_IFNG_DN	-1.71	4.00	0	0	0	Repressed
740	STEIN_ESRRA_TARGETS_UP	-1.71	4.00	0	0	0	Repressed
741	WIELAND_UP_BY_HBV_INFECTION	-1.71	4.00	0	0	0	Repressed
742	GO_STRUCTURAL_CONSTITUENT_OF_CYTOSKELETON	-1.71	2.59	0	0	0	Repressed
743	ZHONG_SECRETOME_OF_LUNG_CANCER_AND_ENDOTHELIUM	-1.71	2.59	0	0	0	Repressed
744	LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_UP	-1.71	2.58	0	0	0	Repressed
745	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_UP	-1.71	2.57	0	0	0	Repressed
746	GO_RNA_METHYLATION	-1.71	2.55	0	0	0	Repressed
747	REACTOME_RNA_POLYMERASE_II_TRANSCRIBES_SNRNA_GENES	-1.71	2.53	0	0	0	Repressed
748	GO_DOUBLE_STRANDED_RNA_BINDING	-1.71	2.52	0	0	0	Repressed
749	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN	-1.71	2.51	0	0	0	Repressed
750	HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_DN	-1.71	2.36	0	0	0	Repressed
751	ZHAN_MULTIPLE_MYELOMA_PR_UP	-1.71	2.28	0	0	0	Repressed

752	REACTOME_APC_C:CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	-1.71	2.27	0	0	0	Repressed
753	GO_NOSE_DEVELOPMENT	-1.71	2.22	0	0	0	Repressed
754	GO_INFLAMMATORY_CELL_APOPTOTIC_PROCESS	-1.71	2.18	0	0	0	Repressed
755	GO_PROTEASOME_ACTIVATING_ATPASE_ACTIVITY	-1.71	2.17	0	0	0	Repressed
756	GO_PARASYMPATHETIC_NERVOUS_SYSTEM_DEVELOPMENT	-1.71	2.16	0	0	0	Repressed
757	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_T	-1.71	2.12	0	0	0	Repressed
758	GO_INTERFERON_BETA_BIOSYNTHETIC_PROCESS	-1.71	2.06	0	0	0	Repressed
759	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_6	-1.71	2.03	0	0	0	Repressed
760	GO_VITAMIN_BIOSYNTHETIC_PROCESS	-1.71	2.02	0	0	0	Repressed
761	GO_DIGESTION	-1.71	1.98	0	0	0	Repressed
762	GO_BOX_H_ACA_RNP_COMPLEX	-1.71	1.97	0	0	0	Repressed
763	REACTOME_FORMATION_OF_HIV_ELONGATION_COMPLEX_IN_THE_ABSE	-1.71	1.97	0	0	0	Repressed
764	KEGG_BETA_ALANINE_METABOLISM	-1.71	1.94	0	0	0	Repressed
765	RODRIGUES_NTN1_TARGETS_UP	-1.71	1.86	0	0	0	Repressed
766	GO_RIBOSOMAL_LARGE_SUBUNIT_EXPORT_FROM_NUCLEUS	-1.71	1.84	0	0	0	Repressed
767	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN	-1.71	1.82	0	0	0	Repressed
768	GO_TRNA_5_END_PROCESSING	-1.71	1.80	0	0	0	Repressed
769	REACTOME_RECEPTOR_TYPE_TYROSINE_PROTEIN_PHOSPHATASES	-1.71	1.80	0	0	0	Repressed
770	GO_SEH1_ASSOCIATED_COMPLEX	-1.71	1.57	0	0	0	Repressed
771	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_DN	-1.70	4.00	0	0	0	Repressed
772	DELYS_THYROID_CANCER_UP	-1.70	4.00	0	0	0	Repressed
773	GO_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	-1.70	4.00	0	0	0	Repressed
774	IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR	-1.70	4.00	0	0	0	Repressed
775	LEI_MYB_TARGETS	-1.70	4.00	0	0	0	Repressed
776	PID_PLK1_PATHWAY	-1.70	4.00	0	0	0	Repressed
777	SMITH_TERT_TARGETS_UP	-1.70	4.00	0	0	0	Repressed
778	REACTOME_NUCLEAR_IMPORT_OF_REV_PROTEIN	-1.70	2.57	0	0	0	Repressed
779	HARRIS_HYPOXIA	-1.70	2.55	0	0	0	Repressed
780	LENAOUR_DENDRITIC_CELL_MATURATION_DN	-1.70	2.52	0	0	0	Repressed
781	EGUCHI_CELL_CYCLE_RB1_TARGETS	-1.70	2.31	0	0	0	Repressed
782	GO_FEMALE_GENITALIA_DEVELOPMENT	-1.70	2.19	0	0	0	Repressed
783	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN	-1.70	2.19	0	0	0	Repressed
784	GO_ACTIN_FILAMENT_BUNDLE	-1.70	2.15	0	0	0	Repressed
785	REACTOME_CRISTAE_FORMATION	-1.70	2.05	0	0	0	Repressed
786	REACTOME_CA_DEPENDENT_EVENTS	-1.70	2.00	0	0	0	Repressed
787	GO_NEGATIVE_REGULATION_OF_GLIAL_CELL_PROLIFERATION	-1.70	1.97	0	0	0	Repressed
788	GO_MITOTIC_NUCLEAR_ENVELOPE_DISASSEMBLY	-1.70	1.96	0	0	0	Repressed
789	REACTOME_FOLDING_OF_ACTIN_BY_CCT_TRIC	-1.70	1.96	0	0	0	Repressed
790	GO_NITRIC_OXIDE_SYNTHASE_BINDING	-1.70	1.95	0	0	0	Repressed
791	GO_BONE_GROWTH	-1.70	1.93	0	0	0	Repressed
792	REACTOME_GAP_JUNCTION_TRAFFICKING_AND_REGULATION	-1.70	1.93	0	0	0	Repressed
793	BIOCARTA_S1P_PATHWAY	-1.70	1.90	0	0	0	Repressed
794	GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_UBIQUINOL_TO_CYTOCH	-1.70	1.87	0	0	0	Repressed
795	GO_TRNA_CYTOSINE_METHYLTRANSFERASE_ACTIVITY	-1.70	1.83	1	0	0	Repressed
796	GO_LONG_CHAIN_FATTY_ACID_COA_LIGASE_ACTIVITY	-1.70	1.74	0	0	0	Repressed
797	GO_MITOCHONDRIAL_CALCIUM_ION_HOMEOSTASIS	-1.70	1.69	0	0	0	Repressed
798	BILD_MYC_ONCOGENIC_SIGNATURE	-1.69	4.00	0	1	0	Repressed
799	GO_POSITIVE_REGULATION_OF_ION_TRANSPORT	-1.69	4.00	0	0	0	Repressed
800	GO_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	-1.69	4.00	0	0	0	Repressed
801	REACTOME_SIGNALING_BY_WNT	-1.69	4.00	0	0	0	Repressed
802	REACTOME_TRANSPORT_OF_MATURE_MRNAS_DERIVED_FROM_INTRON	-1.69	4.00	0	0	0	Repressed
803	REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	-1.69	4.00	0	0	0	Repressed
804	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN	-1.69	2.55	0	0	0	Repressed
805	REACTOME_CYTOSOLIC_SENSORS_OF_PATHOGEN_ASSOCIATED_DNA	-1.69	2.54	0	0	0	Repressed
806	DANG_REGULATED_BY_MYC_UP	-1.69	2.53	0	0	0	Repressed
807	GO_DIAPHRAGM_DEVELOPMENT	-1.69	2.37	0	0	0	Repressed
808	GO_CHEMOATTRACTANT_ACTIVITY	-1.69	2.34	0	0	0	Repressed
809	GO_NCRNA_EXPORT_FROM_NUCLEUS	-1.69	2.28	0	0	0	Repressed
810	GO_OXIDOREDUCTASE_ACTIVITY_OXIDIZING_METAL_IONS	-1.69	2.20	0	0	0	Repressed
811	GO_REGENERATION	-1.69	2.20	0	0	0	Repressed
812	REACTOME_RRNA_PROCESSING_IN_THE_MITOCHONDRION	-1.69	2.15	0	0	0	Repressed
813	GRADE_METASTASIS_DN	-1.69	2.10	0	0	0	Repressed
814	GO_LOCOMOTOR_RHYTHM	-1.69	2.05	0	0	0	Repressed
815	GO_NEUROTRANSMITTER_BINDING	-1.69	2.04	0	0	0	Repressed
816	REACTOME_TRNA_MODIFICATION_IN_THE_MITOCHONDRION	-1.69	2.03	0	0	0	Repressed
817	REACTOME_CONVERSION_FROM_APC_C:CDC20_TO_APC_C:CDH1_IN_LA	-1.69	1.93	0	0	0	Repressed
818	GO_MACROLIDE_BINDING	-1.69	1.87	0	0	0	Repressed
819	GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_REGULATI	-1.69	1.86	0	0	0	Repressed
820	DORMOY_ELAVL1_TARGETS	-1.69	1.85	0	0	0	Repressed
821	GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TR	-1.69	1.80	0	0	0	Repressed
822	OXFORD_RALA_TARGETS_UP	-1.69	1.80	0	0	0	Repressed
823	PID_HNF3B_PATHWAY	-1.69	1.74	0	0	0	Repressed
824	GO_INTEGRATOR_COMPLEX	-1.69	1.70	0	0	0	Repressed
825	GO_MITOTIC_SPINDLE_ORGANIZATION	-1.68	4.00	0	0	0	Repressed
826	GO_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	-1.68	4.00	0	0	0	Repressed
827	HALLMARK_PI3K_AKT_MTOR_SIGNALING	-1.68	4.00	0	0	0	Repressed
828	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP	-1.68	4.00	0	0	0	Repressed
829	MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_UP	-1.68	4.00	0	0	0	Repressed
830	ROSS_LEUKEMIA_WITH_MLL_FUSIONS	-1.68	4.00	0	0	0	Repressed
831	GO_REGULATION_OF_SYNAPSE_MATURATION	-1.68	2.65	0	0	0	Repressed
832	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION	-1.68	2.56	0	0	0	Repressed
833	RAMASWAMY_METASTASIS_UP	-1.68	2.55	0	0	0	Repressed
834	GO_BRUSH_BORDER	-1.68	2.53	0	0	0	Repressed
835	ZHU_CMV_24_HR_UP	-1.68	2.52	0	0	0	Repressed
836	GO_POSITIVE_REGULATION_OF_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	-1.68	2.35	0	0	0	Repressed
837	FARMER_BREAST_CANCER_CLUSTER_1	-1.68	2.26	0	0	0	Repressed
838	WEST_ADRENOCORTICAL_TUMOR_MARKERS_UP	-1.68	2.15	0	0	0	Repressed
839	REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	-1.68	2.10	0	0	0	Repressed
840	REACTOME_ERKS_ARE_INACTIVATED	-1.68	2.05	0	0	0	Repressed
841	GO_FRUCTOSE_METABOLIC_PROCESS	-1.68	2.02	0	0	0	Repressed
842	GO_GROWTH_INVOLVED_IN_SYMBIOTIC_INTERACTION	-1.68	1.96	0	0	0	Repressed
843	GO_AMINOACYL_TRNA_SYNTHETASE_MULTIENZYME_COMPLEX	-1.68	1.94	0	0	0	Repressed
844	BIOCARTA_NDKDYNAMIN_PATHWAY	-1.68	1.93	0	0	0	Repressed
845	KANG_GLIS3_TARGETS	-1.68	1.85	0	0	0	Repressed
846	LANDIS_ERBB2_BREAST_TUMORS_65_UP	-1.68	1.85	0	0	0	Repressed
847	GO_CONDENSED_CHROMOSOME_OUTER_KINETOCHORE	-1.68	1.82	0	0	0	Repressed
848	GO_PROTEIN_ARGININE_N_METHYLTRANSFERASE_ACTIVITY	-1.68	1.80	0	0	0	Repressed
849	GO_TRNA_5_LEADER_REMOVAL	-1.68	1.76	0	0	0	Repressed
850	GO_REGULATION_OF_PROTEIN_FOLDING	-1.68	1.74	0	0	0	Repressed
851	GO_RESPONSE_TO_REDOX_STATE	-1.68	1.73	0	0	0	Repressed
852	BOYAULT_LIVER_CANCER_SUBCLASS_G2	-1.68	1.67	0	0	0	Repressed
853	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP	-1.68	1.63	0	0	0	Repressed
854	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP	-1.67	4.00	0	0	0	Repressed
855	GO_AZUROPHIL_GRANULE_LUMEN	-1.67	4.00	0	0	0	Repressed
856	GO_CELLULAR_COMPONENT_DISASSEMBLY	-1.67	4.00	0	0	0	Repressed
857	GO_COFACTOR_METABOLIC_PROCESS	-1.67	4.00	0	0	0	Repressed
858	GO_NUCLEAR_TRANSPORT	-1.67	4.00	0	0	0	Repressed
859	GO_NUCLEOLAR_PART	-1.67	4.00	0	0	0	Repressed
860	GO_RIBONUCLEOPROTEIN_COMPLEX_BINDING	-1.67	4.00	0	0	0	Repressed

861	LINDGREN_BLADDER_CANCER_CLUSTER_3_UP	-1.67	4.00	0	0	0	Repressed
862	WATANABE_RECTAL_CANCER_RADIOTHERAPY_RESPONSIVE_DN	-1.67	4.00	0	0	0	Repressed
863	ZHANG_TLX_TARGETS_36HR_DN	-1.67	4.00	0	0	0	Repressed
864	FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_DN	-1.67	2.54	0	0	0	Repressed
865	MORI_SMALL_PRE_BII_LYMPHOCYTE_DN	-1.67	2.53	0	0	0	Repressed
866	GO_MONOCARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	-1.67	2.51	0	0	0	Repressed
867	GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_2B_COMPLEX	-1.67	2.35	0	0	0	Repressed
868	CROMER_METASTASIS_DN	-1.67	2.30	0	0	0	Repressed
869	ALK_DN.V1_UP	-1.67	2.28	0	0	0	Repressed
870	ONO_AML1_TARGETS_DN	-1.67	2.13	0	0	0	Repressed
871	REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	-1.67	2.04	0	0	0	Repressed
872	BURTON_ADIPOGENESIS_4	-1.67	1.99	0	0	0	Repressed
873	GO_MODULATION_OF_GROWTH_OF_SYMBIONT_INVOLVED_IN_INTERAC	-1.67	1.94	0	0	0	Repressed
874	GO_ANTIBIOTIC_CATABOLIC_PROCESS	-1.67	1.91	0	0	0	Repressed
875	GO_FATTY_ACID_DERIVATIVE_BIOSYNTHETIC_PROCESS	-1.67	1.91	0	0	0	Repressed
876	GO_NEGATIVE_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	-1.67	1.87	0	0	0	Repressed
877	GO_MEMBRANE_DISASSEMBLY	-1.67	1.85	0	0	0	Repressed
878	BIOCARTA_SM_PATHWAY	-1.67	1.82	0	0	0	Repressed
879	GO_TFIID_CLASS_TRANSCRIPTION_FACTOR_COMPLEX_BINDING	-1.67	1.82	0	0	0	Repressed
880	BIOCARTA_GCR_PATHWAY	-1.67	1.80	0	0	0	Repressed
881	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED	-1.67	1.77	0	0	0	Repressed
882	REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	-1.67	1.75	0	0	0	Repressed
883	REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	-1.67	1.72	0	0	0	Repressed
884	GO_ENDOLYSOSOME_MEMBRANE	-1.67	1.69	0	0	0	Repressed
885	GO_GATOR2_COMPLEX	-1.67	1.69	0	0	0	Repressed
886	GO_PROTEIN_COFACTOR_LINKAGE	-1.67	1.68	0	0	0	Repressed
887	GO_REGULATION_OF_APOPTOTIC_DNA_FRAGMENTATION	-1.67	1.66	0	0	0	Repressed
888	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_5	-1.67	1.63	0	0	0	Repressed
889	GO_CELLULAR_RESPONSE_TO_OXYGEN_LEVELS	-1.66	4.00	0	0	0	Repressed
890	GO_NUCLEOTIDYLTRANSFERASE_ACTIVITY	-1.66	4.00	0	0	0	Repressed
891	GO_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	-1.66	4.00	0	0	0	Repressed
892	GO_NUCLEOSIDE_BISPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.66	2.56	0	0	0	Repressed
893	GO_NUCLEAR_PORE	-1.66	2.55	0	0	0	Repressed
894	GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_DN	-1.66	2.48	0	0	0	Repressed
895	HALLMARK_ADIPOGENESIS	-1.66	2.47	0	0	0	Repressed
896	WANG_CISPLATIN_RESPONSE_AND_XPC_UP	-1.66	2.46	0	0	0	Repressed
897	GO_TELOMERASE_RNA_BINDING	-1.66	2.31	0	0	0	Repressed
898	KEGG_RNA_POLYMERASE	-1.66	2.31	0	0	0	Repressed
899	GO_STRIATED_MUSCLE_CONTRACTION	-1.66	2.26	0	0	0	Repressed
900	REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	-1.66	2.25	0	0	0	Repressed
901	GO_CHROMOSOME_PASSENGER_COMPLEX	-1.66	2.06	0	0	0	Repressed
902	GO_BOX_H_ACA_SNORNA_BINDING	-1.66	2.04	0	0	0	Repressed
903	GO_ATP_DEPENDENT_5_3_DNA_HELICASE_ACTIVITY	-1.66	1.97	0	0	0	Repressed
904	GO_REGULATION_OF_CALCIUM_TRANSPORTING_ATPASE_ACTIVITY	-1.66	1.95	0	0	0	Repressed
905	GO_GLOMERULUS_DEVELOPMENT	-1.66	1.92	0	0	0	Repressed
906	PID_HDAC_CLASSIII_PATHWAY	-1.66	1.92	0	0	0	Repressed
907	REACTOME_DEFECTIVE_TPR_MAY_CONFER_SUSCEPTIBILITY_TOWARD	-1.66	1.90	0	0	0	Repressed
908	CAIRO_PML_TARGETS_BOUND_BY_MYC_UP	-1.66	1.86	0	0	0	Repressed
909	AMIT_SERUM_RESPONSE_240_MCF10A	-1.66	1.85	0	0	0	Repressed
910	GO_CHONDROITIN_SULFATE_BINDING	-1.66	1.84	0	0	0	Repressed
911	GO_RESPONSE_TO_DEXAMETHASONE	-1.66	1.80	0	0	0	Repressed
912	REACTOME_REGULATION_OF_GLYCOLYSIS_BY_FRUCTOSE_2_6_BISPH	-1.66	1.79	0	0	0	Repressed
913	BIOCARTA_G2_PATHWAY	-1.66	1.75	0	0	0	Repressed
914	BIOCARTA_EGFR_SMRTE_PATHWAY	-1.66	1.74	0	0	0	Repressed
915	GO_SERINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	-1.66	1.72	0	0	0	Repressed
916	KEGG_PRION_DISEASES	-1.66	1.72	0	0	0	Repressed
917	NIKOLSKY_OVERCONNECTED_IN_BREAST_CANCER	-1.66	1.72	0	0	0	Repressed
918	GO_POTASSIUM_ION_BINDING	-1.66	1.68	0	0	0	Repressed
919	GO_REGULATION_OF_LIPOPROTEIN_PARTICLE_CLEARANCE	-1.66	1.58	0	0	0	Repressed
920	GO_PEPTIDYL_ARGININE_N_METHYLATION	-1.66	1.55	0	0	0	Repressed
921	AFFAR_YY1_TARGETS_DN	-1.65	4.00	0	0	0	Repressed
922	GO_CADHERIN_BINDING	-1.65	4.00	0	0	0	Repressed
923	GO_CATALYTIC_STEP_2_SPLICEOSOME	-1.65	4.00	0	0	0	Repressed
924	GO_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	-1.65	4.00	0	0	0	Repressed
925	GO_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENCING	-1.65	4.00	0	0	0	Repressed
926	GO_REGULATION_OF_STEROID_BIOSYNTHETIC_PROCESS	-1.65	4.00	0	0	0	Repressed
927	GO_RESPONSE_TO_HEAT	-1.65	4.00	0	0	0	Repressed
928	GO_RESPONSE_TO_TEMPERATURE_STIMULUS	-1.65	4.00	0	0	0	Repressed
929	GO_SMALL_MOLECULE_METABOLIC_PROCESS	-1.65	4.00	0	0	0	Repressed
930	HELLER_HDAC_TARGETS_DN	-1.65	4.00	0	0	0	Repressed
931	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_UP	-1.65	4.00	0	0	0	Repressed
932	REACTOME_UB_SPECIFIC_PROCESSING_PROTEASES	-1.65	4.00	0	0	0	Repressed
933	GO_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	-1.65	2.58	0	0	0	Repressed
934	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_	-1.65	2.58	0	0	0	Repressed
935	MARTINEZ_RESPONSE_TO_TRABECTEDIN_UP	-1.65	2.55	0	0	0	Repressed
936	MARZEC_IL2_SIGNALING_UP	-1.65	2.54	0	0	0	Repressed
937	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP	-1.65	2.54	0	0	0	Repressed
938	GO_ORGANIC_ACID_BINDING	-1.65	2.53	0	0	0	Repressed
939	ANDERSEN_CHOLANGIOCARCINOMA_CLASS2	-1.65	2.26	0	0	0	Repressed
940	GO_NEUTROPHIL_APOPTOTIC_PROCESS	-1.65	2.18	0	0	0	Repressed
941	GO_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	-1.65	2.18	0	0	0	Repressed
942	GO_MOLECULAR_CARRIER_ACTIVITY	-1.65	2.13	0	0	0	Repressed
943	SERVITJA_ISLET_HNF1A_TARGETS_DN	-1.65	2.12	0	0	0	Repressed
944	REACTOME_INTRAFLAGELLAR_TRANSPORT	-1.65	2.10	0	0	0	Repressed
945	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_DN	-1.65	2.05	0	0	0	Repressed
946	GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSC	-1.65	1.99	0	0	0	Repressed
947	GO_RRNA_TRANSCRIPTION	-1.65	1.98	0	0	0	Repressed
948	KEGG_BASAL_TRANSCRIPTION_FACTORS	-1.65	1.97	0	0	0	Repressed
949	GO_RRNA_PSEUDOURIDINE_SYNTHESIS	-1.65	1.95	0	0	0	Repressed
950	REACTOME_G_PROTEIN_ACTIVATION	-1.65	1.93	0	0	0	Repressed
951	BIOCARTA_NKT_PATHWAY	-1.65	1.82	0	0	0	Repressed
952	REACTOME_SCAVENGING_BY_CLASS_F_RECEPTORS	-1.65	1.82	0	0	0	Repressed
953	GO_NADH_METABOLIC_PROCESS	-1.65	1.81	0	0	0	Repressed
954	GO_NITRIC_OXIDE_SYNTHASE_REGULATOR_ACTIVITY	-1.65	1.76	0	0	0	Repressed
955	GO_C_X_C_CHEMOKINE_RECEPTOR_ACTIVITY	-1.65	1.73	0	0	0	Repressed
956	CHR6P24	-1.65	1.72	0	0	0	Repressed
957	GO_ATF6_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	-1.65	1.69	0	0	0	Repressed
958	GO_COLLAGEN_FIBRIL_ORGANIZATION	-1.65	1.69	0	0	0	Repressed
959	GO_OLFACTORY_LOBE_DEVELOPMENT	-1.65	1.69	0	0	0	Repressed
960	KEGG_PHENYLALANINE_METABOLISM	-1.65	1.69	0	0	0	Repressed
961	REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION	-1.65	1.59	0	0	0	Repressed
962	GO_INTRACELLULAR_STEROL_TRANSPORT	-1.65	1.51	0	0	0	Repressed
963	BENPORATH_ES_1	-1.64	4.00	0	0	0	Repressed
964	BURTON_ADIPOGENESIS_3	-1.64	4.00	0	0	0	Repressed
965	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP	-1.64	4.00	0	0	0	Repressed
966	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN	-1.64	4.00	0	0	0	Repressed
967	GO_CELL_CYCLE_G2_M_PHASE_TRANSITION	-1.64	4.00	0	0	0	Repressed
968	GO_CONTRACTILE_FIBER	-1.64	4.00	0	0	0	Repressed
969	GO_FICOLIN_1_RICH_GRANULE	-1.64	4.00	0	0	0	Repressed

970	GO_REGULATION_OF_METAL_ION_TRANSPORT	-1.64	4.00	0	0	0	Repressed
971	GO_RESPONSE_TO_STEROID_HORMONE	-1.64	4.00	0	0	0	Repressed
972	GO_RNA_3_END_PROCESSING	-1.64	4.00	0	0	0	Repressed
973	GO_SULFUR_COMPOUND_METABOLIC_PROCESS	-1.64	4.00	0	0	0	Repressed
974	LINDGREN_BLADDER_CANCER_CLUSTER_1_DN	-1.64	4.00	0	0	0	Repressed
975	REACTOME_CELL_CYCLE_MITOTIC	-1.64	4.00	0	0	0	Repressed
976	REACTOME_PROTEIN_FOLDING	-1.64	4.00	0	0	0	Repressed
977	REACTOME_PROTEIN_LOCALIZATION	-1.64	4.00	0	0	0	Repressed
978	GO_DIGESTIVE_SYSTEM_PROCESS	-1.64	2.29	0	0	0	Repressed
979	REACTOME_REGULATION_OF_INSULIN_SECRETION	-1.64	2.29	0	0	0	Repressed
980	GO_NUCLEAR_RECEPTOR_TRANSCRIPTION_COACTIVATOR_ACTIVITY	-1.64	2.27	0	0	0	Repressed
981	GO_MATURATION_OF_SSU_RRNA	-1.64	2.02	0	0	0	Repressed
982	GO_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	-1.64	2.01	0	0	0	Repressed
983	GO_TRICARBOXYLIC_ACID_CYCLE	-1.64	1.98	0	0	0	Repressed
984	GO_HISTONE_SERINE_KINASE_ACTIVITY	-1.64	1.89	0	0	0	Repressed
985	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN	-1.64	1.89	0	0	0	Repressed
986	GO_CHROMATOID_BODY	-1.64	1.82	0	0	0	Repressed
987	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_1	-1.64	1.79	0	0	0	Repressed
988	REACTOME_AQUAPORIN_MEDIATED_TRANSPORT	-1.64	1.78	0	0	0	Repressed
989	GO_AEROBIC_ELECTRON_TRANSPORT_CHAIN	-1.64	1.75	0	0	0	Repressed
990	CHR8P23	-1.64	1.73	0	0	0	Repressed
991	DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN	-1.64	1.73	0	0	0	Repressed
992	GO_MITOCHONDRIAL_TRNA_PROCESSING	-1.64	1.73	0	0	0	Repressed
993	GO_PEROXIREDOXIN_ACTIVITY	-1.64	1.73	0	0	0	Repressed
994	GO_GOLGI_LOCALIZATION	-1.64	1.72	0	0	0	Repressed
995	GO_NEGATIVE_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	-1.64	1.72	0	0	0	Repressed
996	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_TERMINATION	-1.64	1.68	0	0	0	Repressed
997	GO_GROWTH_PLATE_CARTILAGE_DEVELOPMENT	-1.64	1.67	0	0	0	Repressed
998	GO_PSEUDOURIDINE_SYNTHESIS	-1.64	1.67	0	0	0	Repressed
999	GO_PEPTIDE_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	-1.64	1.66	0	0	0	Repressed
1000	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	-1.64	1.63	0	0	0	Repressed
1001	GO_NEGATIVE_REGULATION_OF_MEGAKARYOCYTE_DIFFERENTIATION	-1.64	1.62	0	0	0	Repressed
1002	REACTOME_IRF3_MEDIATED_INDUCTION_OF_TYPE_I_IFN	-1.64	1.60	0	0	0	Repressed
1003	KANG_FLUOROURACIL_RESISTANCE_DN	-1.64	1.59	0	0	0	Repressed
1004	GO_POSITIVE_REGULATION_OF_PODOSOME_ASSEMBLY	-1.64	1.58	0	0	0	Repressed
1005	REACTOME_FGFR2_MUTANT_RECEPTOR_ACTIVATION	-1.64	1.56	0	0	0	Repressed
1006	GO_HISTONE_ARGININE_N_METHYLTRANSFERASE_ACTIVITY	-1.64	1.52	0	0	0	Repressed
1007	BIOCARTA_ETC_PATHWAY	-1.64	1.47	0	0	0	Repressed
1008	DAZARD_RESPONSE_TO_UV_NHEK_UP	-1.63	4.00	0	0	0	Repressed
1009	GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MIT	-1.63	4.00	0	0	0	Repressed
1010	GO_POSITIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	-1.63	4.00	0	0	0	Repressed
1011	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	-1.63	4.00	0	0	0	Repressed
1012	RICKMAN_METASTASIS_DN	-1.63	4.00	0	0	0	Repressed
1013	ZHANG_BREAST_CANCER_PROGENITORS_UP	-1.63	4.00	0	0	0	Repressed
1014	KIM_MYCN_AMPLIFICATION_TARGETS_UP	-1.63	2.58	0	0	0	Repressed
1015	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_UP	-1.63	2.56	0	0	0	Repressed
1016	REACTOME_SUMOYLATION_OF_UBIQUITINYLATION_PROTEINS	-1.63	2.56	0	0	0	Repressed
1017	REACTOME_ACTIVATION_OF_HOX_GENES_DURING_DIFFERENTIATION	-1.63	2.54	0	0	0	Repressed
1018	GO_SM_LIKE_PROTEIN_FAMILY_COMPLEX	-1.63	2.52	0	0	0	Repressed
1019	REACTOME_COPI_DEPENDENT_GOLGI_TO_ER_RETROGRADE_TRAFFIC	-1.63	2.48	0	0	0	Repressed
1020	SU_TESTIS	-1.63	2.26	0	0	0	Repressed
1021	WAESCH_ANAPHASE_PROMOTING_COMPLEX	-1.63	2.15	0	0	0	Repressed
1022	GO_CARDIAC_MUSCLE_CONTRACTION	-1.63	2.10	0	0	0	Repressed
1023	TSENG_IRS1_TARGETS_UP	-1.63	2.08	0	0	0	Repressed
1024	GO_CELLULAR_RESPONSE_TO_UV_B	-1.63	1.91	0	0	0	Repressed
1025	GO_BOX_H_ACA_TELOMERASE_RNP_COMPLEX	-1.63	1.90	0	0	0	Repressed
1026	GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER	-1.63	1.88	0	0	0	Repressed
1027	GO_SPINDLE_LOCALIZATION	-1.63	1.88	0	0	0	Repressed
1028	LI_CISPLATIN_RESISTANCE_DN	-1.63	1.88	0	0	0	Repressed
1029	GO_MODULATION_BY_HOST_OF_VIRAL_PROCESS	-1.63	1.86	0	0	0	Repressed
1030	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_DN	-1.63	1.82	0	0	0	Repressed
1031	GO_TOLL_LIKE_RECEPTOR_9_SIGNALING_PATHWAY	-1.63	1.80	0	0	0	Repressed
1032	GROSS_ELK3_TARGETS_UP	-1.63	1.80	0	0	0	Repressed
1033	GO_HYDROGEN_PEROXIDE_CATABOLIC_PROCESS	-1.63	1.77	0	0	0	Repressed
1034	REACTOME_G_BETA:GAMMA_SIGNALLING_THROUGH_CDC42	-1.63	1.75	0	0	0	Repressed
1035	GO_DEAMINASE_ACTIVITY	-1.63	1.73	0	0	0	Repressed
1036	BIOCARTA_CTL_PATHWAY	-1.63	1.72	0	0	0	Repressed
1037	GO_REGULATION_OF_CARTILAGE_DEVELOPMENT	-1.63	1.72	0	0	0	Repressed
1038	BIOCARTA_MCALPAIN_PATHWAY	-1.63	1.70	0	0	0	Repressed
1039	GO_CELLULAR_RESPONSE_TO_CORTICOSTEROID_STIMULUS	-1.63	1.69	0	0	0	Repressed
1040	GO_SPLICEOSOMAL_TRI_SNRNP_COMPLEX	-1.63	1.69	0	0	0	Repressed
1041	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITORS_UP	-1.63	1.60	0	0	0	Repressed
1042	AMIT_DELAYED_EARLY_GENES	-1.63	1.59	0	0	0	Repressed
1043	MURAKAMI_UV_RESPONSE_6HR_DN	-1.63	1.42	0	0	0	Repressed
1044	GO_NEGATIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	-1.62	4.00	0	0	0	Repressed
1045	GO_POSTTRANSCRIPTIONAL_REGULATION_OF_GENE_EXPRESSION	-1.62	4.00	0	0	0	Repressed
1046	GO_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	-1.62	4.00	0	0	0	Repressed
1047	GO_REGULATION_OF_TRANSPORTER_ACTIVITY	-1.62	4.00	0	0	0	Repressed
1048	GO_RIBOSE_PHOSPHATE_BIOSYNTHETIC_PROCESS	-1.62	4.00	0	0	0	Repressed
1049	GO_RNA_DEPENDENT_DNA_BIOSYNTHETIC_PROCESS	-1.62	4.00	0	0	0	Repressed
1050	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ONE_CARBON_GROUPS	-1.62	4.00	0	0	0	Repressed
1051	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_UP	-1.62	4.00	0	0	0	Repressed
1052	SENESE_HDAC1_TARGETS_UP	-1.62	4.00	0	0	0	Repressed
1053	SMID_BREAST_CANCER_BASAL_UP	-1.62	4.00	0	0	0	Repressed
1054	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP	-1.62	4.00	0	0	0	Repressed
1055	GO_CARDIOCYTE_DIFFERENTIATION	-1.62	2.55	0	0	0	Repressed
1056	GO_CHANNEL_REGULATOR_ACTIVITY	-1.62	2.53	0	0	0	Repressed
1057	GO_CLUSTER_OF_ACTIN_BASED_CELL_PROJECTIONS	-1.62	2.52	0	0	0	Repressed
1058	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	-1.62	2.26	0	0	0	Repressed
1059	GO_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENG	-1.62	2.24	0	0	0	Repressed
1060	GO_LYASE_ACTIVITY	-1.62	2.22	0	0	0	Repressed
1061	BROWN_MYELOID_CELL_DEVELOPMENT_DN	-1.62	2.21	0	0	0	Repressed
1062	KEGG_CARDIAC_MUSCLE_CONTRACTION	-1.62	1.99	0	0	0	Repressed
1063	MARCHINI_TRABECTEDIN_RESISTANCE_DN	-1.62	1.98	0	0	0	Repressed
1064	GO_PROTEIN_TRANSPORTER_ACTIVITY	-1.62	1.96	0	0	0	Repressed
1065	GO_SUBSTANTIA_NIGRA_DEVELOPMENT	-1.62	1.92	0	0	0	Repressed
1066	GO_SECONDARY_METABOLIC_PROCESS	-1.62	1.83	0	0	0	Repressed
1067	LEE_LIVER_CANCER_E2F1_UP	-1.62	1.82	0	0	0	Repressed
1068	GO_REGULATION_OF_DNA_METHYLATION	-1.62	1.78	0	0	0	Repressed
1069	BIOCARTA_BCR_PATHWAY	-1.62	1.76	0	0	0	Repressed
1070	KEGG_ARGININE_AND_PROLINE_METABOLISM	-1.62	1.74	0	0	0	Repressed
1071	BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN	-1.62	1.67	0	0	0	Repressed
1072	GO_REGULATION_OF_OXIDATIVE_PHOSPHORYLATION	-1.62	1.67	0	0	0	Repressed
1073	GO_INTRACELLULAR_LIPID_TRANSPORT	-1.62	1.66	0	0	0	Repressed
1074	GO_NUCLEOCYTOPLASMIC_CARRIER_ACTIVITY	-1.62	1.62	0	0	0	Repressed
1075	PARK_HSC_VS_MULTIPOTENT_PROGENITORS_DN	-1.62	1.55	0	0	0	Repressed
1076	REACTOME_GABA_B_RECEPTOR_ACTIVATION	-1.62	1.55	0	0	0	Repressed
1077	AMIT_SERUM_RESPONSE_20_MCF10A	-1.62	1.53	0	0	0	Repressed
1078	GO_SUPEROXIDE_ANION_GENERATION	-1.62	1.53	0	0	0	Repressed

1079	REACTOME_ADRENALINE_NORADRENALINE_INHIBITS_INSULIN_SECRETIO	-1.62	1.50	0	0	0	Repressed
1080	GO_PYRUVATE_METABOLIC_PROCESS	-1.62	1.49	0	0	0	Repressed
1081	BIOCARTA_CCR5_PATHWAY	-1.62	1.47	0	0	0	Repressed
1082	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BROWN_UP	-1.62	1.45	0	0	0	Repressed
1083	GO_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	-1.61	4.00	0	0	0	Repressed
1084	GO_POSITIVE_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT	-1.61	4.00	0	0	0	Repressed
1085	GO_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	-1.61	4.00	0	0	0	Repressed
1086	GO_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.61	4.00	0	0	0	Repressed
1087	HOELZEL_NF1_TARGETS_UP	-1.61	4.00	0	0	0	Repressed
1088	MATTIOLI_MGUS_VS_PCL	-1.61	4.00	0	0	0	Repressed
1089	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP	-1.61	4.00	0	0	0	Repressed
1090	GO_LEUKOCYTE_CHEMOTAXIS	-1.61	2.55	0	0	0	Repressed
1091	GO_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	-1.61	2.55	0	0	0	Repressed
1092	GO_RESPONSE_TO_INTERLEUKIN_1	-1.61	2.50	0	0	0	Repressed
1093	GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-1.61	2.49	0	0	0	Repressed
1094	GO_REGULATION_OF_MUSCLE_SYSTEM_PROCESS	-1.61	2.49	0	0	0	Repressed
1095	SNF5_DN.V1_UP	-1.61	2.49	0	0	0	Repressed
1096	GO_ACTOMYOSIN	-1.61	2.25	0	0	0	Repressed
1097	NAGASHIMA_NRG1_SIGNALING_UP	-1.61	2.18	0	0	0	Repressed
1098	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN	-1.61	2.12	0	0	0	Repressed
1099	LEF1_UP.V1_UP	-1.61	2.08	0	0	0	Repressed
1100	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_7	-1.61	1.97	0	0	0	Repressed
1101	GO_REGULATION_OF_SISTER_CHROMATID_SEGREGATION	-1.61	1.95	0	0	0	Repressed
1102	GO_BOX_H_ACA_SNORNP_COMPLEX	-1.61	1.89	0	0	0	Repressed
1103	GO_NAD_METABOLIC_PROCESS	-1.61	1.85	0	0	0	Repressed
1104	GO_ESTABLISHMENT_OF_EPITHELIAL_CELL_POLARITY	-1.61	1.83	0	0	0	Repressed
1105	GO_MRNA_PSEUDOURIDINE_SYNTHESIS	-1.61	1.81	0	0	0	Repressed
1106	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQUOISE_D	-1.61	1.80	0	0	0	Repressed
1107	TERAMOTO_OPN_TARGETS_CLUSTER_1	-1.61	1.80	0	0	0	Repressed
1108	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREEN_UP	-1.61	1.77	0	0	0	Repressed
1109	GO_CRD_MEDIATED_MRNA_STABILITY_COMPLEX	-1.61	1.76	0	0	0	Repressed
1110	REACTOME_DAG_AND_IP3_SIGNALING	-1.61	1.76	0	0	0	Repressed
1111	GO_RNA_POLYMERASE_ACTIVITY	-1.61	1.75	0	0	0	Repressed
1112	PID_CXCR3_PATHWAY	-1.61	1.75	0	0	0	Repressed
1113	KEGG_RENIN_ANGIOTENSIN_SYSTEM	-1.61	1.71	0	0	0	Repressed
1114	LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_SMALL_VS_HUGE_UP	-1.61	1.69	0	0	0	Repressed
1115	GO_RRNA_MODIFICATION	-1.61	1.66	0	0	0	Repressed
1116	GO_UBIQUITIN_PROTEIN_TRANSFERASE_ACTIVATOR_ACTIVITY	-1.61	1.65	0	0	0	Repressed
1117	REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TR	-1.61	1.65	0	0	0	Repressed
1118	GO_REGULATION_OF_MAST_CELL_CHEMOTAXIS	-1.61	1.63	0	0	0	Repressed
1119	REACTOME_FGFR2_ALTERNATIVE_SPLICING	-1.61	1.61	0	0	0	Repressed
1120	GO_RNA_POLYMERASE_III_ACTIVITY	-1.61	1.60	0	0	0	Repressed
1121	GO_DOUBLE_STRANDED_METHYLATED_DNA_BINDING	-1.61	1.59	0	0	0	Repressed
1122	GO_PROTEIN_DISULFIDE_ISOMERASE_ACTIVITY	-1.61	1.54	0	0	0	Repressed
1123	BILANGES_SERUM_SENSITIVE_VIA_TSC1	-1.61	1.53	0	0	0	Repressed
1124	GO_RRNA_CONTAINING_RIBONUCLEOPROTEIN_COMPLEX_EXPORT_FRO	-1.61	1.52	0	0	0	Repressed
1125	BIOCARTA_RARRXR_PATHWAY	-1.61	1.51	0	0	0	Repressed
1126	GO_POSTTRANSLATIONAL_PROTEIN_TARGETING_TO_ENDOPLASMIC_RE	-1.61	1.45	0	0	0	Repressed
1127	ALCALAY_AML_BY_NPM1_LOCALIZATION_DN	-1.60	4.00	0	0	0	Repressed
1128	BENPORATH_MYC_MAX_TARGETS	-1.60	4.00	0	0	0	Repressed
1129	ERBB2_UP.V1_DN	-1.60	4.00	0	0	0	Repressed
1130	GO_MITOTIC_SISTER_CHROMATID_SEGREGATION	-1.60	4.00	0	0	0	Repressed
1131	GO_PROTEIN_TETRAMERIZATION	-1.60	4.00	0	0	0	Repressed
1132	IGLESIAS_E2F_TARGETS_UP	-1.60	4.00	0	0	0	Repressed
1133	KENNY_CTNNB1_TARGETS_UP	-1.60	4.00	0	0	0	Repressed
1134	MTOR_UP.V1_UP	-1.60	4.00	0	0	0	Repressed
1135	REACTOME_TCF_DEPENDENT_SIGNALING_IN_RESPONSE_TO_WNT	-1.60	4.00	0	0	0	Repressed
1136	ZHANG_TLX_TARGETS_60HR_DN	-1.60	4.00	0	0	0	Repressed
1137	GO_POSITIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	-1.60	2.27	0	0	0	Repressed
1138	GO_MYELIN_SHEATH_ADAXONAL_REGION	-1.60	2.17	0	0	0	Repressed
1139	GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STIMULUS	-1.60	1.91	0	0	0	Repressed
1140	GO_NEURAL_NUCLEUS_DEVELOPMENT	-1.60	1.87	0	0	0	Repressed
1141	GO_NUCLEOSOMAL_DNA_BINDING	-1.60	1.80	0	0	0	Repressed
1142	REACTOME_ANTIGEN_PRESENTATION:_FOLDING_ASSEMBLY_AND_PEPT	-1.60	1.78	0	0	0	Repressed
1143	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	-1.60	1.76	0	0	0	Repressed
1144	GO_SCAVENGER_RECEPTOR_ACTIVITY	-1.60	1.72	0	0	0	Repressed
1145	REACTOME_SUMOYLATION_OF_SUMOYLATION_PROTEINS	-1.60	1.71	0	0	0	Repressed
1146	GO_CHAPERONIN_CONTAINING_T_COMPLEX	-1.60	1.69	0	0	0	Repressed
1147	BIOCARTA_TCAPOPTOSIS_PATHWAY	-1.60	1.61	0	0	0	Repressed
1148	GO_TRNA_3_END_PROCESSING	-1.60	1.60	0	0	0	Repressed
1149	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN	-1.60	1.60	0	0	0	Repressed
1150	GO_CATALYTIC_ACTIVITY_ACTING_ON_A_RRNA	-1.60	1.59	0	0	0	Repressed
1151	GO_NUCLEAR_RECEPTOR_ACTIVITY	-1.60	1.57	0	0	0	Repressed
1152	GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANS	-1.60	1.57	0	0	0	Repressed
1153	SUZUKI_RESPONSE_TO_TSA	-1.60	1.56	0	0	0	Repressed
1154	GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANS	-1.60	1.55	0	0	0	Repressed
1155	GO_REGULATION_OF_TRANSLATIONAL_TERMINATION	-1.60	1.55	0	0	0	Repressed
1156	REACTOME_TIE2_SIGNALING	-1.60	1.55	0	0	0	Repressed
1157	GO_MITOCHONDRIAL_RNA_MODIFICATION	-1.60	1.54	0	0	0	Repressed
1158	MANN_RESPONSE_TO_AMIFOSTINE_DN	-1.60	1.54	0	0	0	Repressed
1159	REACTOME_ETHANOL_OXIDATION	-1.60	1.54	0	0	0	Repressed
1160	GO_MITOCHONDRIAL_TRANSCRIPTION	-1.60	1.50	0	0	0	Repressed
1161	TURJANSKI_MAPK8_AND_MAPK9_TARGETS	-1.60	1.49	0	0	0	Repressed
1162	GO_METHYL_CPG_BINDING	-1.60	1.47	0	0	0	Repressed
1163	GO_CELL_ADHESION_MOLECULE_BINDING	-1.59	4.00	0	0	0	Repressed
1164	GO_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	-1.59	4.00	0	0	0	Repressed
1165	GO_LIGASE_ACTIVITY	-1.59	4.00	0	0	0	Repressed
1166	GO_RESPONSE_TO_OXYGEN_LEVELS	-1.59	4.00	0	0	0	Repressed
1167	GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	-1.59	4.00	0	0	0	Repressed
1168	HALLMARK_HYPOXIA	-1.59	4.00	0	0	0	Repressed
1169	GO_OTHER_ORGANISM	-1.59	2.53	0	0	0	Repressed
1170	GO_PROTEIN_SERINE_THREONINE_PHOSPHATASE_COMPLEX	-1.59	2.30	0	0	0	Repressed
1171	GO_FATTY_ACID_BIOSYNTHETIC_PROCESS	-1.59	2.23	0	0	0	Repressed
1172	REACTOME_COPI_MEDIATED_ANTEROGRADE_TRANSPORT	-1.59	2.23	0	0	0	Repressed
1173	GO_FATTY_ACID_BETA_OXIDATION	-1.59	2.09	0	0	0	Repressed
1174	LEONARD_HYPOXIA	-1.59	2.08	0	0	0	Repressed
1175	GO_PROTEIN_TARGETING_TO_MITOCHONDRION	-1.59	2.05	0	0	0	Repressed
1176	MOHANKUMAR_TLX1_TARGETS_DN	-1.59	1.98	0	0	0	Repressed
1177	BIOCARTA_CELL2CELL_PATHWAY	-1.59	1.83	0	0	0	Repressed
1178	GO_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE	-1.59	1.79	0	0	0	Repressed
1179	SMITH_LIVER_CANCER	-1.59	1.75	0	0	0	Repressed
1180	REACTOME_MAP2K_AND_MAPK_ACTIVATION	-1.59	1.74	0	0	0	Repressed
1181	GO_ENUCLEATE_ERYTHROCYTE_DIFFERENTIATION	-1.59	1.73	0	0	0	Repressed
1182	GO_REGULATION_OF_TRIGLYCERIDE_BIOSYNTHETIC_PROCESS	-1.59	1.70	0	0	0	Repressed
1183	GO_RNA_POLYMERASE_II_CTD_HEPTAPEPTIDE_REPEAT_KINASE_ACTIV	-1.59	1.70	0	0	0	Repressed
1184	GO_REGULATION_OF_TELOMERASE_ACTIVITY	-1.59	1.69	0	0	0	Repressed
1185	BIOCARTA_CARM1_PATHWAY	-1.59	1.67	0	0	0	Repressed
1186	GO_TRNA_SPLICING_LIGASE_COMPLEX	-1.59	1.66	0	0	0	Repressed
1187	FARMER_BREAST_CANCER_CLUSTER_5	-1.59	1.63	0	0	0	Repressed

1188	GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS	-1.59	1.63	0	0	0	Repressed
1189	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_OF_NUCLEOLAR_LAR	-1.59	1.60	0	0	0	Repressed
1190	GO_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	-1.59	1.60	0	0	0	Repressed
1191	MCBRYAN_TERMINAL_END_BUD_DN	-1.59	1.56	0	0	0	Repressed
1192	VALK_AML_CLUSTER_16	-1.59	1.53	0	0	0	Repressed
1193	GO_PHOSPHATIDYLINOSITOL_3_KINASE_BINDING	-1.59	1.51	0	0	0	Repressed
1194	MACLACHLAN_BRCA1_TARGETS_UP	-1.59	1.49	0	0	0	Repressed
1195	VILIMAS_NOTCH1_TARGETS_DN	-1.59	1.49	0	0	0	Repressed
1196	GO_MICOS_COMPLEX	-1.59	1.48	0	0	0	Repressed
1197	GO_ESTABLISHMENT_OF_MITOTIC_SPINDLE_LOCALIZATION	-1.59	1.47	0	0	0	Repressed
1198	GO_GEMINI_OF_COILED_BODIES	-1.59	1.47	0	0	0	Repressed
1199	REACTOME_REGULATION_OF_CYTOSKELETAL_REMODELING_AND_CEL	-1.59	1.47	0	0	0	Repressed
1200	GO_RESPONSE_TO_FUNGUS	-1.59	1.46	0	0	0	Repressed
1201	GO_TAT_PROTEIN_BINDING	-1.59	1.44	0	0	0	Repressed
1202	GO_REGULATION_OF_TRANSLATIONAL_ELONGATION	-1.59	1.43	0	0	0	Repressed
1203	GO_TRNA_THREONYLCARBAMOYLADENOSINE_METABOLIC_PROCESS	-1.59	1.43	1	0	0	Repressed
1204	GO_PHOSPHOFRUCTOKINASE_ACTIVITY	-1.59	1.41	0	0	0	Repressed
1205	GO_SODIUM_CHANNEL_REGULATOR_ACTIVITY	-1.59	1.39	0	0	0	Repressed
1206	CHUANG_OXIDATIVE_STRESS_RESPONSE_DN	-1.59	1.34	0	0	0	Repressed
1207	GO_N6_METHYLADENOSINE_CONTAINING_RNA_BINDING	-1.59	1.34	0	0	0	Repressed
1208	GO_MULTIMERIC_RIBONUCLEASE_P_COMPLEX	-1.59	1.30	0	0	0	Repressed
1209	GO_MONOCYTE_CHEMOTAXIS	-1.59	1.22	0	0	0	Repressed
1210	DITTMER_PTHLH_TARGETS_UP	-1.58	4.00	0	0	0	Repressed
1211	FISCHER_DREAM_TARGETS	-1.58	4.00	0	0	0	Repressed
1212	GO_REGULATION_OF_SYMBIOSIS_ENCOMPASSING_MUTUALISM_THROU	-1.58	4.00	0	0	0	Repressed
1213	GO_RESPONSE_TO_HORMONE	-1.58	4.00	0	0	0	Repressed
1214	GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY	-1.58	4.00	0	0	0	Repressed
1215	QI_HYPOXIA	-1.58	4.00	0	0	0	Repressed
1216	REACTOME_CELL_CYCLE	-1.58	4.00	0	0	0	Repressed
1217	REACTOME_RHO_GTPASE_EFFECTORS	-1.58	4.00	0	0	0	Repressed
1218	SMIRNOV_RESPONSE_TO_IR_6HR_DN	-1.58	4.00	0	0	0	Repressed
1219	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DON	-1.58	2.51	0	0	0	Repressed
1220	GO_POSITIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	-1.58	2.22	0	0	0	Repressed
1221	GO_COFACTOR_BIOSYNTHETIC_PROCESS	-1.58	2.17	0	0	0	Repressed
1222	GO_MONOCARBOXYLIC_ACID_TRANSPORT	-1.58	2.05	0	0	0	Repressed
1223	GO_POSITIVE_REGULATION_OF_VIRAL_LIFE_CYCLE	-1.58	2.01	0	0	0	Repressed
1224	LU_IL4_SIGNALING	-1.58	1.96	0	0	0	Repressed
1225	GAURNIER_PSMD4_TARGETS	-1.58	1.84	0	0	0	Repressed
1226	HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_DN	-1.58	1.84	0	0	0	Repressed
1227	GO_NUCLEOID	-1.58	1.78	0	0	0	Repressed
1228	GO_EXTRACELLULAR_MATRIX_BINDING	-1.58	1.72	0	0	0	Repressed
1229	HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN	-1.58	1.72	0	0	0	Repressed
1230	GO_OXALOACETATE_METABOLIC_PROCESS	-1.58	1.71	0	0	0	Repressed
1231	GO_HORMONE_ACTIVITY	-1.58	1.64	0	0	0	Repressed
1232	GO_NEGATIVE_REGULATION_OF_LIPOPROTEIN_PARTICLE_CLEARANCE	-1.58	1.63	0	0	0	Repressed
1233	GO_DEFENSE_RESPONSE_TO_GRAM_NEGATIVE_BACTERIUM	-1.58	1.61	0	0	0	Repressed
1234	GO_STAT_FAMILY_PROTEIN_BINDING	-1.58	1.61	0	0	0	Repressed
1235	KEGG_LIMONENE_AND_PINENE_DEGRADATION	-1.58	1.61	0	0	0	Repressed
1236	GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_DEVELOPMENT	-1.58	1.58	0	0	0	Repressed
1237	FARMER_BREAST_CANCER_CLUSTER_4	-1.58	1.55	0	0	0	Repressed
1238	GO_CELL_PROLIFERATION_INVOLVED_IN_HEART_MORPHOGENESIS	-1.58	1.53	0	0	0	Repressed
1239	GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABO	-1.58	1.53	0	0	0	Repressed
1240	GO_RNA_POLYMERASE_II_PREINITIATION_COMPLEX_ASSEMBLY	-1.58	1.53	0	0	0	Repressed
1241	SCHUHMACHER_MYC_TARGETS_DN	-1.58	1.52	0	0	0	Repressed
1242	REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_BCR_LEADING_	-1.58	1.50	0	0	0	Repressed
1243	GO_CYSTEINE_METABOLIC_PROCESS	-1.58	1.49	0	0	0	Repressed
1244	KEGG_GALACTOSE_METABOLISM	-1.58	1.48	0	0	0	Repressed
1245	GO_RESPIRATORY_CHAIN_COMPLEX_III	-1.58	1.47	0	0	0	Repressed
1246	GO_TISSUE_REGENERATION	-1.58	1.47	0	0	0	Repressed
1247	GO_ENDOPEPTIDASE_ACTIVATOR_ACTIVITY	-1.58	1.46	0	0	0	Repressed
1248	GO_POSITIVE_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	-1.58	1.44	0	0	0	Repressed
1249	GO_POSITIVE_REGULATION_OF_STEROID_METABOLIC_PROCESS	-1.58	1.42	0	0	0	Repressed
1250	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_TRANSMEMBRANE_ELECT	-1.58	1.41	0	0	0	Repressed
1251	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN	-1.58	1.39	0	0	0	Repressed
1252	GO_PROTEIN_LOCALIZATION_TO_NUCLEAR_ENVELOPE	-1.58	1.37	0	0	0	Repressed
1253	GO_CELLULAR_RESPONSE_TO_FLUID_SHEAR_STRESS	-1.58	1.31	0	0	0	Repressed
1254	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP	-1.58	1.31	0	0	0	Repressed
1255	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP	-1.57	4.00	0	0	0	Repressed
1256	CHICAS_RB1_TARGETS_CONFLUENT	-1.57	4.00	0	0	0	Repressed
1257	GO_UNFOLDED_PROTEIN_BINDING	-1.57	4.00	0	0	0	Repressed
1258	JOHNSTONE_PARVB_TARGETS_3_DN	-1.57	4.00	0	0	0	Repressed
1259	RB_DN.V1_DN	-1.57	4.00	0	0	0	Repressed
1260	REACTOME_S_PHASE	-1.57	4.00	0	0	0	Repressed
1261	GO_VESICLE_BUDDING_FROM_MEMBRANE	-1.57	2.54	0	0	0	Repressed
1262	GO_MULTI_ORGANISM_LOCALIZATION	-1.57	2.53	0	0	0	Repressed
1263	LEE_LIVER_CANCER_SURVIVAL_UP	-1.57	2.52	0	0	0	Repressed
1264	GO_REGULATION_OF_TELOMERE_MAINTENANCE	-1.57	2.50	0	0	0	Repressed
1265	GO_REGULATION_OF_BLOOD_CIRCULATION	-1.57	2.48	0	0	0	Repressed
1266	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	-1.57	2.09	0	0	0	Repressed
1267	ALCALAY_AML_BY_NPM1_LOCALIZATION_UP	-1.57	1.96	0	0	0	Repressed
1268	CHR10Q23	-1.57	1.91	0	0	0	Repressed
1269	GO_CARDIAC_CONDUCTION	-1.57	1.88	0	0	0	Repressed
1270	REACTOME_SIGNALING_BY_RAS_MUTANTS	-1.57	1.80	0	0	0	Repressed
1271	SABATES_COLORECTAL_ADENOMA_UP	-1.57	1.80	0	0	0	Repressed
1272	GENTILE_UV_LOW_DOSE_DN	-1.57	1.74	0	0	0	Repressed
1273	GO_COFACTOR_CATABOLIC_PROCESS	-1.57	1.74	0	0	0	Repressed
1274	GO_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	-1.57	1.73	0	0	0	Repressed
1275	GO_PROTEIN_KINASE_A_BINDING	-1.57	1.73	0	0	0	Repressed
1276	GO_POSITIVE_REGULATION_OF_VOLTAGE_GATED_POTASSIUM_CHANN	-1.57	1.72	0	0	0	Repressed
1277	GO_STRUCTURAL_CONSTITUENT_OF_NUCLEAR_PORE	-1.57	1.72	0	0	0	Repressed
1278	REACTOME_CONDENSATION_OF_PROPHASE_CHROMOSOMES	-1.57	1.71	0	0	0	Repressed
1279	KONDO_HYPOXIA	-1.57	1.63	0	0	0	Repressed
1280	GO_DE_NOVO_PROTEIN_FOLDING	-1.57	1.62	0	0	0	Repressed
1281	REACTOME_METABOLISM_OF_INGESTED_SEMET_SEC_MESEC_INTO_H2	-1.57	1.62	0	0	0	Repressed
1282	REACTOME_HSF1_ACTIVATION	-1.57	1.59	0	0	0	Repressed
1283	PID_RETINOIC_ACID_PATHWAY	-1.57	1.58	0	0	0	Repressed
1284	CHR3P14	-1.57	1.57	0	0	0	Repressed
1285	LEE_LIVER_CANCER_DENA_UP	-1.57	1.56	0	0	0	Repressed
1286	GO_MATURE_RIBOSOME_ASSEMBLY	-1.57	1.55	0	0	0	Repressed
1287	GO_P_P_BOND_HYDROLYSIS_DRIVEN_PROTEIN_TRANSMEMBRANE_TRA	-1.57	1.55	0	0	0	Repressed
1288	GO_REGULATION_OF_SUPEROXIDE_ANION_GENERATION	-1.57	1.54	0	0	0	Repressed
1289	GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_CALCIUM_ION_CONCE	-1.57	1.52	0	0	0	Repressed
1290	GO_COMPACT_MYELIN	-1.57	1.51	0	0	0	Repressed
1291	REACTOME_ADP_SIGNALLING_THROUGH_P2Y_PURINOCEPTOR_12	-1.57	1.49	0	0	0	Repressed
1292	REACTOME_SEMA3A_PAK_DEPENDENT_AXON_REPULSION	-1.57	1.49	0	0	0	Repressed
1293	GO_POSITIVE_REGULATION_OF_STEROID_BIOSYNTHETIC_PROCESS	-1.57	1.48	0	0	0	Repressed
1294	REACTOME_ASPARTATE_AND_ASPARAGINE_METABOLISM	-1.57	1.48	0	0	0	Repressed
1295	GO_PEPTIDYL_ARGININE_METHYLATION	-1.57	1.47	0	0	0	Repressed
1296	REACTOME_CELLULAR_HEXOSE_TRANSPORT	-1.57	1.47	0	0	0	Repressed

1297	GO_THIOREDOXIN_PEROXIDASE_ACTIVITY	-1.57	1.46	0	0	0	Repressed
1298	PIEPOLI_LGI1_TARGETS_UP	-1.57	1.46	0	0	0	Repressed
1299	SUMI_HNF4A_TARGETS	-1.57	1.45	0	0	0	Repressed
1300	GO_POLY_G_BINDING	-1.57	1.44	0	0	0	Repressed
1301	GO_PSEUDOPODIUM	-1.57	1.44	0	0	0	Repressed
1302	GO_I_KAPPAB_PHOSPHORYLATION	-1.57	1.42	0	0	0	Repressed
1303	GO_L_SERINE_METABOLIC_PROCESS	-1.57	1.41	0	0	0	Repressed
1304	REACTOME_CHK1_CHK2_CDS1_MEDIATED_INACTIVATION_OF_CYCLIN_B	-1.57	1.41	0	0	0	Repressed
1305	GO_SHORT_CHAIN_FATTY_ACID_CATABOLIC_PROCESS	-1.57	1.38	0	0	0	Repressed
1306	DALESSIO_TSA_RESPONSE	-1.57	1.35	0	0	0	Repressed
1307	GO_RESPONSE_TO_CORTICOSTERONE	-1.57	1.30	0	0	0	Repressed
1308	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP	-1.56	4.00	0	0	0	Repressed
1309	GO_RESPONSE_TO_CYTOKINE	-1.56	4.00	0	0	0	Repressed
1310	GROSS_HYPOXIA_VIA_ELK3_UP	-1.56	4.00	0	0	0	Repressed
1311	MULLIGHAN_MLL_SIGNATURE_2_UP	-1.56	4.00	0	0	0	Repressed
1312	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN	-1.56	4.00	0	0	0	Repressed
1313	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	-1.56	4.00	0	0	0	Repressed
1314	SHEN_SMARCA2_TARGETS_DN	-1.56	4.00	0	0	0	Repressed
1315	HUANG_GATA2_TARGETS_DN	-1.56	2.55	0	0	0	Repressed
1316	GO_COENZYME_BIOSYNTHETIC_PROCESS	-1.56	2.50	0	0	0	Repressed
1317	HALLMARK_ESTROGEN_RESPONSE_EARLY	-1.56	2.50	0	0	0	Repressed
1318	CYCLIN_D1_KE_.V1_UP	-1.56	2.49	0	0	0	Repressed
1319	HALLMARK_ALLOGRAFT_REJECTION	-1.56	2.48	0	0	0	Repressed
1320	HALLMARK_ESTROGEN_RESPONSE_LATE	-1.56	2.48	0	0	0	Repressed
1321	CAHOY_ASTROCYTIC	-1.56	2.26	0	0	0	Repressed
1322	GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	-1.56	2.09	0	0	0	Repressed
1323	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	-1.56	2.07	0	0	0	Repressed
1324	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_DN	-1.56	2.06	0	0	0	Repressed
1325	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP	-1.56	1.97	0	0	0	Repressed
1326	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_TERMINATION	-1.56	1.81	0	0	0	Repressed
1327	GO_SPINDLE_MIDZONE	-1.56	1.78	0	0	0	Repressed
1328	GO_ENDOPEPTIDASE_REGULATOR_ACTIVITY	-1.56	1.76	0	0	0	Repressed
1329	GO_DNA_REPLICATION_DEPENDENT_NUCLEOSOME_ORGANIZATION	-1.56	1.69	0	0	0	Repressed
1330	HUANG_DASATINIB_RESISTANCE_UP	-1.56	1.69	0	0	0	Repressed
1331	GO_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	-1.56	1.68	0	0	0	Repressed
1332	GO_REGULATION_OF_INTRACELLULAR_LIPID_TRANSPORT	-1.56	1.65	0	0	0	Repressed
1333	GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANS	-1.56	1.62	0	0	0	Repressed
1334	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_UP	-1.56	1.62	0	0	0	Repressed
1335	GO_ENDOCHONDRAL_BONE_MORPHOGENESIS	-1.56	1.60	0	0	0	Repressed
1336	BIOCARTA_CALCINEURIN_PATHWAY	-1.56	1.58	0	0	0	Repressed
1337	GO_REGULATION_OF_VESICLE_FUSION	-1.56	1.58	0	0	0	Repressed
1338	LEIN_NEURON_MARKERS	-1.56	1.58	0	0	0	Repressed
1339	GO_NEGATIVE_REGULATION_OF_INSULIN_SECRETION	-1.56	1.54	0	0	0	Repressed
1340	GO_FRUCTOSE_1_6_BISPHOSPHATE_METABOLIC_PROCESS	-1.56	1.51	0	0	0	Repressed
1341	GO_PROSTATE_GLAND_DEVELOPMENT	-1.56	1.51	0	0	0	Repressed
1342	HE_PTEN_TARGETS_UP	-1.56	1.51	0	0	0	Repressed
1343	GO_NEGATIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_	-1.56	1.48	0	0	0	Repressed
1344	GO_PEBOW_COMPLEX	-1.56	1.48	0	0	0	Repressed
1345	GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	-1.56	1.48	0	0	0	Repressed
1346	MARCINIAK_ER_STRESS_RESPONSE_VIA_CHOP	-1.56	1.48	0	0	0	Repressed
1347	LEE_LIVER_CANCER_E2F1_DN	-1.56	1.47	0	0	0	Repressed
1348	GO_DNA_PROTECTION	-1.56	1.44	0	0	0	Repressed
1349	GO_POSITIVE_REGULATION_OF_SUPEROXIDE_ANION_GENERATION	-1.56	1.44	0	0	0	Repressed
1350	KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	-1.56	1.43	0	0	0	Repressed
1351	SUH_COEXPRESSED_WITH_ID1_AND_ID2_UP	-1.56	1.43	0	0	0	Repressed
1352	GO_FACIAL_NERVE_MORPHOGENESIS	-1.56	1.42	0	0	0	Repressed
1353	GO_MEDIUM_CHAIN_FATTY_ACID_COA_LIGASE_ACTIVITY	-1.56	1.42	0	0	0	Repressed
1354	GO_NEUTRAL_LIPID_BIOSYNTHETIC_PROCESS	-1.56	1.42	0	0	0	Repressed
1355	SCHURINGA_STAT5A_TARGETS_UP	-1.56	1.41	0	0	0	Repressed
1356	GO_CENTROMERIC_SISTER_CHROMATID_COHESION	-1.56	1.39	0	0	0	Repressed
1357	GO_CHOLESTEROL_CATABOLIC_PROCESS	-1.56	1.39	0	0	0	Repressed
1358	GO_MYOBLAST_MIGRATION	-1.56	1.39	0	0	0	Repressed
1359	GO_CARBONYL_REDUCTASE_NADPH_ACTIVITY	-1.56	1.36	0	0	0	Repressed
1360	GO_GDP_DISSOCIATION_INHIBITOR_ACTIVITY	-1.56	1.28	0	0	0	Repressed
1361	GO_CALCIUM_CHANNEL_INHIBITOR_ACTIVITY	-1.56	1.25	0	0	0	Repressed
1362	GO_FC_RECEPTOR_SIGNALING_PATHWAY	-1.55	4.00	0	0	0	Repressed
1363	GO_SPINDLE_POLE	-1.55	4.00	0	0	0	Repressed
1364	LEE_LIVER_CANCER_SURVIVAL_DN	-1.55	4.00	0	0	0	Repressed
1365	MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP	-1.55	4.00	0	0	0	Repressed
1366	REACTOME_CELLULAR_RESPONSES_TO_EXTERNAL_STIMULI	-1.55	4.00	0	0	0	Repressed
1367	REACTOME_MITOTIC_PROMETAPHASE	-1.55	4.00	0	0	0	Repressed
1368	SWEET_LUNG_CANCER_KRAS_UP	-1.55	4.00	0	0	0	Repressed
1369	ZHENG_GLIOBLASTOMA_PLASTICITY_UP	-1.55	2.45	0	0	0	Repressed
1370	GO_RESPIRATORY_SYSTEM_DEVELOPMENT	-1.55	2.23	0	0	0	Repressed
1371	HELLER_SILENCED_BY_METHYLATION_DN	-1.55	2.08	0	0	0	Repressed
1372	HALLMARK_PEROXISOME	-1.55	2.07	0	0	0	Repressed
1373	GO_HEPATICOBILIARY_SYSTEM_DEVELOPMENT	-1.55	2.06	0	0	0	Repressed
1374	GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	-1.55	2.06	0	0	0	Repressed
1375	LIN_APC_TARGETS	-1.55	1.96	0	0	0	Repressed
1376	HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_DN	-1.55	1.90	0	0	0	Repressed
1377	GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	-1.55	1.77	0	0	0	Repressed
1378	JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_DN	-1.55	1.70	0	0	0	Repressed
1379	SCHMIDT_POR_TARGETS_IN_LIMB_BUD_UP	-1.55	1.68	0	0	0	Repressed
1380	GO_STEREOCILIUM_TIP	-1.55	1.67	0	0	0	Repressed
1381	GO_EXTRACELLULAR_MATRIX_CONSTITUENT_CONFERRING_ELASTICITY	-1.55	1.63	0	0	0	Repressed
1382	LI_WILMS_TUMOR_ANAPLASTIC_UP	-1.55	1.63	0	0	0	Repressed
1383	GO_CELLULAR_RESPONSE_TO_FATTY_ACID	-1.55	1.62	0	0	0	Repressed
1384	GO_POSITIVE_REGULATION_OF_HORMONE_BIOSYNTHETIC_PROCESS	-1.55	1.58	0	0	0	Repressed
1385	GO_KINETOCHORE_BINDING	-1.55	1.54	0	0	0	Repressed
1386	GO_RNA_POLYMERASE_II_ACTIVITY	-1.55	1.53	0	0	0	Repressed
1387	NGUYEN_NOTCH1_TARGETS_UP	-1.55	1.53	0	0	0	Repressed
1388	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_DN	-1.55	1.49	0	0	0	Repressed
1389	WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLESTEROL_UP	-1.55	1.49	0	0	0	Repressed
1390	GO_MITOCHONDRIAL_RNA_3_END_PROCESSING	-1.55	1.46	0	0	0	Repressed
1391	GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_CALCIUM_	-1.55	1.46	0	0	0	Repressed
1392	REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES	-1.55	1.44	0	0	0	Repressed
1393	KAPOSI_LIVER_CANCER_MET_UP	-1.55	1.43	0	0	0	Repressed
1394	GO_SCHMIDT_LANTERMAN_INCISURE	-1.55	1.42	0	0	0	Repressed
1395	FUNG_IL2_TARGETS_WITH_STAT5_BINDING_SITES	-1.55	1.40	0	0	0	Repressed
1396	REACTOME_NOTCH2_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRI	-1.55	1.40	0	0	0	Repressed
1397	REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB	-1.55	1.40	0	0	0	Repressed
1398	COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_UP	-1.55	1.39	0	0	0	Repressed
1399	LIU_IL13_PRIMING_MODEL	-1.55	1.39	0	0	0	Repressed
1400	GO_CELLULAR_RESPONSE_TO_OXYGEN_RADICAL	-1.55	1.38	0	0	0	Repressed
1401	GO_PEPTIDE_CATABOLIC_PROCESS	-1.55	1.38	0	0	0	Repressed
1402	GO_PRERIBOSOME_SMALL_SUBUNIT_PRECURSOR	-1.55	1.37	0	0	0	Repressed
1403	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CHROMOSOME_TEL	-1.55	1.37	0	0	0	Repressed
1404	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_DRUG	-1.55	1.36	0	0	0	Repressed
1405	GO_NEGATIVE_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	-1.55	1.36	0	0	0	Repressed

1406	GO_PULMONARY_VALVE_DEVELOPMENT	-1.55	1.36	0	0	0	Repressed
1407	GO_EYELID_DEVELOPMENT_IN_CAMERA_TYPE_EYE	-1.55	1.34	0	0	0	Repressed
1408	GO_N_TERMINAL_PROTEIN_ACETYLTRANSFERASE_COMPLEX	-1.55	1.33	0	0	0	Repressed
1409	REACTOME_INTEGRATION_OF_PROVIRUS	-1.55	1.31	0	0	0	Repressed
1410	GO_PULMONARY_VALVE_MORPHOGENESIS	-1.55	1.30	0	0	0	Repressed
1411	GO_NEGATIVE_REGULATION_OF_TELOMERASE_ACTIVITY	-1.55	1.28	0	0	0	Repressed
1412	GO_POSITIVE_REGULATION_OF_OXIDATIVE_PHOSPHORYLATION	-1.55	1.27	0	0	0	Repressed
1413	GO_REGULATION_OF_UNSATURATED_FATTY_ACID_BIOSYNTHETIC_PRC	-1.55	1.21	0	0	0	Repressed
1414	GO_RESPONSE_TO_LIPID	-1.54	4.00	0	0	0	Repressed
1415	MULLIGHAN_MLL_SIGNATURE_1_UP	-1.54	4.00	0	0	0	Repressed
1416	REACTOME_INTERFERON_SIGNALING	-1.54	4.00	0	0	0	Repressed
1417	ELVIDGE_HIF1A_TARGETS_DN	-1.54	2.25	0	0	0	Repressed
1418	GO_COLLAGEN_CONTAINING_EXTRACELLULAR_MATRIX	-1.54	2.20	0	0	0	Repressed
1419	GRABARCZYK_BCL11B_TARGETS_UP	-1.54	2.07	0	0	0	Repressed
1420	LANDIS_ERBB2_BREAST_TUMORS_324_DN	-1.54	2.06	0	0	0	Repressed
1421	GO_TRANSCRIPTION_BY_RNA_POLYMERASE_I	-1.54	1.88	0	0	0	Repressed
1422	GO_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	-1.54	1.87	0	0	0	Repressed
1423	GO_RESPONSE_TO_AMINO_ACID	-1.54	1.86	0	0	0	Repressed
1424	VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_UP	-1.54	1.79	0	0	0	Repressed
1425	BRACHAT_RESPONSE_TO_CAMPTOTHECIN_DN	-1.54	1.77	0	0	0	Repressed
1426	GO_VENTRICULAR_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	-1.54	1.75	0	0	0	Repressed
1427	GO_MITOTIC_SPINDLE_ASSEMBLY	-1.54	1.72	0	0	0	Repressed
1428	KEGG_TYROSINE_METABOLISM	-1.54	1.55	0	0	0	Repressed
1429	GO_MYELIN_SHEATH	-1.54	1.54	0	0	0	Repressed
1430	GO_DICARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	-1.54	1.49	0	0	0	Repressed
1431	GO_NEGATIVE_REGULATION_OF_MRNA_PROCESSING	-1.54	1.49	0	0	0	Repressed
1432	SIG_REGULATION_OF_THE_ACTIN_CYTOSKELETON_BY_RHO_GTPASES	-1.54	1.49	0	0	0	Repressed
1433	CHR12Q22	-1.54	1.48	0	0	0	Repressed
1434	GO_OXIDATIVE_RNA_DEMETHYLASE_ACTIVITY	-1.54	1.48	0	0	0	Repressed
1435	GO_U2_TYPE_CATALYTIC_STEP_2_SPLICEOSOME	-1.54	1.47	0	0	0	Repressed
1436	GO_OXIDATIVE_RNA_DEMETHYLATION	-1.54	1.46	0	0	0	Repressed
1437	GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_	-1.54	1.45	0	0	0	Repressed
1438	GO_NECROPTOTIC_SIGNALING_PATHWAY	-1.54	1.45	0	0	0	Repressed
1439	NIELSEN_SCHWANNOMA_UP	-1.54	1.43	0	0	0	Repressed
1440	BIOCARTA_PRION_PATHWAY	-1.54	1.42	0	0	0	Repressed
1441	GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	-1.54	1.41	0	0	0	Repressed
1442	GO_EXTRACELLULAR_MATRIX_COMPONENT	-1.54	1.40	0	0	0	Repressed
1443	GO_POLYADENYLATION_DEPENDENT_RNA_CATABOLIC_PROCESS	-1.54	1.40	0	0	0	Repressed
1444	GO_TRACHEA_DEVELOPMENT	-1.54	1.39	0	0	0	Repressed
1445	REACTOME_IMPORT_OF_PALMITOYL_COA_INTO_THE_MITOCHONDRIAL_	-1.54	1.39	0	0	0	Repressed
1446	BIOCARTA_CDMAC_PATHWAY	-1.54	1.38	0	0	0	Repressed
1447	BIOCARTA_RAN_PATHWAY	-1.54	1.37	0	0	0	Repressed
1448	GO_SPECTRIN_BINDING	-1.54	1.34	0	0	0	Repressed
1449	BIOCARTA_TID_PATHWAY	-1.54	1.33	0	0	0	Repressed
1450	DAZARD_UV_RESPONSE_CLUSTER_G4	-1.54	1.33	0	0	0	Repressed
1451	GO_5_3_DNA_HELICASE_ACTIVITY	-1.54	1.32	0	0	0	Repressed
1452	GO_POSITIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_SIG	-1.54	1.29	0	0	0	Repressed
1453	REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_	-1.54	1.29	0	0	0	Repressed
1454	GO_CALCIUM_ION_EXPORT	-1.54	1.28	0	0	0	Repressed
1455	GO_VITAMIN_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.54	1.28	0	0	0	Repressed
1456	GO_EXONUCLEOLYTIC_TRIMMING_INVOLVED_IN_RRNA_PROCESSING	-1.54	1.24	0	0	0	Repressed
1457	CHEN_HOXA5_TARGETS_6HR_UP	-1.54	1.23	0	0	0	Repressed
1458	PLASARI_NFIC_TARGETS_BASAL_DN	-1.54	1.23	0	0	0	Repressed
1459	REACTOME_TETRAHYDROBIOPTERIN_BH4_SYNTHESIS_RECYCLING_SAL	-1.54	1.21	0	0	0	Repressed
1460	GO_ENDOLYSOSOME	-1.54	1.20	0	0	0	Repressed
1461	GO_U5_SNRNP	-1.54	1.19	0	0	0	Repressed
1462	GO_NIK_NF_KAPPAB_SIGNALING	-1.53	4.00	0	0	0	Repressed
1463	GO_SISTER_CHROMATID_SEGREGATION	-1.53	4.00	0	0	0	Repressed
1464	KRIEG_KDM3A_TARGETS_NOT_HYPOXIA	-1.53	4.00	0	0	0	Repressed
1465	MARKEY_RB1_ACUTE_LOF_UP	-1.53	4.00	0	0	0	Repressed
1466	MATSUDA_NATURAL_KILLER_DIFFERENTIATION	-1.53	4.00	0	0	0	Repressed
1467	REACTOME_MAPK_FAMILY_SIGNALING_CASCADES	-1.53	4.00	0	0	0	Repressed
1468	REACTOME_SIGNALING_BY_INTERLEUKINS	-1.53	4.00	0	0	0	Repressed
1469	SANSOM_APC_TARGETS_REQUIRE_MYC	-1.53	4.00	0	1	0	Repressed
1470	SERVITJA_ISLET_HNF1A_TARGETS_UP	-1.53	2.52	0	0	0	Repressed
1471	GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION	-1.53	2.51	0	0	0	Repressed
1472	EIF4E_UP	-1.53	2.22	0	0	0	Repressed
1473	GO_LEUKOCYTE_APOPTOTIC_PROCESS	-1.53	2.22	0	0	0	Repressed
1474	GO_STEROID_BIOSYNTHETIC_PROCESS	-1.53	2.20	0	0	0	Repressed
1475	REACTOME_GOLGI_TO_ER_RETROGRADE_TRANSPORT	-1.53	1.99	0	0	0	Repressed
1476	HU_ANGIOGENESIS_DN	-1.53	1.91	0	0	0	Repressed
1477	GO_CELLULAR_RESPONSE_TO_KETONE	-1.53	1.85	0	0	0	Repressed
1478	BOYAULT_LIVER_CANCER_SUBCLASS_G6_UP	-1.53	1.70	0	0	0	Repressed
1479	GO_CELLULAR_DETOXIFICATION	-1.53	1.68	0	0	0	Repressed
1480	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_UP	-1.53	1.61	0	0	0	Repressed
1481	HALLMARK_CHOLESTEROL_HOMEOSTASIS	-1.53	1.61	0	0	0	Repressed
1482	KEGG_PENTOSE_PHOSPHATE_PATHWAY	-1.53	1.49	0	0	0	Repressed
1483	GO_GENITALIA_DEVELOPMENT	-1.53	1.46	0	0	0	Repressed
1484	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRAN	-1.53	1.44	0	0	0	Repressed
1485	WILSON_PROTEASES_AT_TUMOR_BONE_INTERFACE_UP	-1.53	1.44	0	0	0	Repressed
1486	GO_CELLULAR_DEFENSE_RESPONSE	-1.53	1.42	0	0	0	Repressed
1487	GO_NEGATIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM	-1.53	1.42	0	0	0	Repressed
1488	REACTOME_THE_ROLE_OF_NEF_IN_HIV_1_REPLICATION_AND_DISEASE_	-1.53	1.42	0	0	0	Repressed
1489	GO_ETHANOL_OXIDATION	-1.53	1.41	0	0	0	Repressed
1490	MARIADASON_RESPONSE_TO_CURCUMIN_SULINDAC_5	-1.53	1.41	0	0	0	Repressed
1491	GO_ALDITOL_METABOLIC_PROCESS	-1.53	1.40	0	0	0	Repressed
1492	GO_MUSCLE_FILAMENT_SLIDING	-1.53	1.40	0	0	0	Repressed
1493	GO_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPRE	-1.53	1.40	0	0	0	Repressed
1494	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_IV	-1.53	1.38	0	0	0	Repressed
1495	BIOCARTA_ARENRF2_PATHWAY	-1.53	1.36	0	0	0	Repressed
1496	GO_AMP_BINDING	-1.53	1.36	0	0	0	Repressed
1497	GO_NEGATIVE_REGULATION_OF_PEPTIDE_HORMONE_SECRETION	-1.53	1.36	0	0	0	Repressed
1498	KIM_HYPOXIA	-1.53	1.36	0	0	0	Repressed
1499	REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RI	-1.53	1.36	0	0	0	Repressed
1500	GO_POSITIVE_REGULATION_OF_VESICLE_FUSION	-1.53	1.34	0	0	0	Repressed
1501	GO_MITOCHONDRIAL_TRNA_METHYLATION	-1.53	1.33	0	0	0	Repressed
1502	GO_REGULATION_OF_RYANODINE_SENSITIVE_CALCIUM_RELEASE_CHAN	-1.53	1.32	0	0	0	Repressed
1503	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_DN	-1.53	1.32	0	0	0	Repressed
1504	GO_TRANSLATION_TERMINATION_FACTOR_ACTIVITY	-1.53	1.31	0	0	0	Repressed
1505	REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS	-1.53	1.31	0	0	0	Repressed
1506	GO_ACYLGLYCEROL_HOMEOSTASIS	-1.53	1.29	0	0	0	Repressed
1507	YIH_RESPONSE_TO_ARSENITE_C1	-1.53	1.29	0	0	0	Repressed
1508	GO_BASE_CONVERSION_OR_SUBSTITUTION_EDITING	-1.53	1.28	0	0	0	Repressed
1509	GO_T_CELL_EXTRAVASATION	-1.53	1.27	0	0	0	Repressed
1510	LANDIS_ERBB2_BREAST_PRENEOPLASTIC_UP	-1.53	1.27	0	0	0	Repressed
1511	GO_SMN_COMPLEX	-1.53	1.25	0	0	0	Repressed
1512	GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_DRUG	-1.53	1.23	0	0	0	Repressed
1513	MCCLUNG_DELTA_FOSB_TARGETS_2WK	-1.53	1.22	0	0	0	Repressed
1514	LE_NEURONAL_DIFFERENTIATION_DN	-1.53	1.19	0	0	0	Repressed

1515	GO_RIBONUCLEOPROTEIN_COMPLEX	-1.52	4.00	0	0	0	Repressed
1516	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP	-1.52	4.00	0	0	0	Repressed
1517	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN	-1.52	4.00	0	0	0	Repressed
1518	MYC_UP.V1_UP	-1.52	2.49	0	0	0	Repressed
1519	FARMER_BREAST_CANCER_BASAL_VS_LULMINAL	-1.52	2.38	0	0	0	Repressed
1520	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_	-1.52	1.99	0	0	0	Repressed
1521	GO_HEAT_SHOCK_PROTEIN_BINDING	-1.52	1.95	0	0	0	Repressed
1522	GO_PEPTIDASE_REGULATOR_ACTIVITY	-1.52	1.95	0	0	0	Repressed
1523	GO_NON_CANONICAL_WNT_SIGNALING_PATHWAY	-1.52	1.91	0	0	0	Repressed
1524	OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_UP	-1.52	1.88	0	0	0	Repressed
1525	GO_REGULATION_OF_CHROMOSOME_SEPARATION	-1.52	1.86	0	0	0	Repressed
1526	DAZARD_UV_RESPONSE_CLUSTER_G1	-1.52	1.73	0	0	0	Repressed
1527	GO_ALPHA_AMINO_ACID_BIOSYNTHETIC_PROCESS	-1.52	1.73	0	0	0	Repressed
1528	KEGG_PEROXISOME	-1.52	1.73	0	0	0	Repressed
1529	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_UP	-1.52	1.71	0	1	0	Repressed
1530	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	-1.52	1.69	0	0	0	Repressed
1531	PID_AURORA_A_PATHWAY	-1.52	1.65	0	0	0	Repressed
1532	BERENJENO_ROCK_SIGNALING_NOT_VIA_RHOA_DN	-1.52	1.51	0	0	0	Repressed
1533	GO_MAINTENANCE_OF_DNA_REPEAT_ELEMENTS	-1.52	1.48	0	0	0	Repressed
1534	GO_RELAXATION_OF_SMOOTH_MUSCLE	-1.52	1.44	0	0	0	Repressed
1535	TSUNODA_CISPLATIN_RESISTANCE_DN	-1.52	1.43	0	0	0	Repressed
1536	KEGG_SELENOAMINO_ACID_METABOLISM	-1.52	1.39	0	0	0	Repressed
1537	GO_REGULATION_OF_PANCREATIC_JUICE_SECRETION	-1.52	1.37	0	0	0	Repressed
1538	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_8_SECRETION	-1.52	1.36	0	0	0	Repressed
1539	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN	-1.52	1.35	0	0	0	Repressed
1540	NAKAJIMA_EOSINOPHIL	-1.52	1.35	0	0	0	Repressed
1541	GO_CAMP_DEPENDENT_PROTEIN_KINASE_INHIBITOR_ACTIVITY	-1.52	1.34	0	0	0	Repressed
1542	BAFNA_MUC4_TARGETS_UP	-1.52	1.28	0	0	0	Repressed
1543	GO_HETEROTRIMERIC_G_PROTEIN_COMPLEX	-1.52	1.28	0	0	0	Repressed
1544	GO_NUCLEOLAR_LARGE_RRNA_TRANSCRIPTION_BY_RNA_POLYMERAS	-1.52	1.26	0	0	0	Repressed
1545	GO_IMMUNOLOGICAL_SYNAPSE_FORMATION	-1.52	1.24	0	0	0	Repressed
1546	GO_REGULATION_OF_RIBONUCLEASE_ACTIVITY	-1.52	1.24	0	0	0	Repressed
1547	GO_S100_PROTEIN_BINDING	-1.52	1.23	0	0	0	Repressed
1548	GO_PROTEIN_FOLDING_IN_ENDOPLASMIC_RETICULUM	-1.52	1.20	0	0	0	Repressed
1549	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP	-1.52	1.19	0	0	0	Repressed
1550	GO_CELL_CYCLE_PHASE_TRANSITION	-1.51	4.00	0	0	0	Repressed
1551	GO_CIRCULATORY_SYSTEM_PROCESS	-1.51	4.00	0	0	0	Repressed
1552	GO_REGULATION_OF_GENERATION_OF_PRECURSOR_METABOLITES_A	-1.51	4.00	0	0	0	Repressed
1553	HOSHIDA_LIVER_CANCER_SUBCLASS_S1	-1.51	4.00	0	0	0	Repressed
1554	GO_MODIFICATION_OF_MORPHOLOGY_OR_PHYSIOLOGY_OF_OTHER_C	-1.51	2.53	0	0	0	Repressed
1555	GO_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	-1.51	2.49	0	0	0	Repressed
1556	GO_MODIFICATION_OF_MORPHOLOGY_OR_PHYSIOLOGY_OF_OTHER_C	-1.51	2.22	0	0	0	Repressed
1557	GO_SKELETAL_MUSCLE_ORGAN_DEVELOPMENT	-1.51	2.22	0	0	0	Repressed
1558	HELLER_SILENCED_BY_METHYLATION_UP	-1.51	2.17	0	0	0	Repressed
1559	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP	-1.51	2.04	0	0	0	Repressed
1560	GO_CELLULAR_GLUCOSE_HOMEOSTASIS	-1.51	2.03	0	0	0	Repressed
1561	GO_PLATELET_DEGRANULATION	-1.51	1.97	0	0	0	Repressed
1562	MIKKELSEN_ES_LCP_WITH_H3K4ME3	-1.51	1.95	0	0	0	Repressed
1563	ATF2_S_UP.V1_UP	-1.51	1.83	0	0	0	Repressed
1564	BHATTACHARYA_EMBRYONIC_STEM_CELL	-1.51	1.76	0	0	0	Repressed
1565	PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_UP	-1.51	1.73	0	0	0	Repressed
1566	GO_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	-1.51	1.70	0	0	0	Repressed
1567	GROSS_HYPOXIA_VIA_HIF1A_UP	-1.51	1.56	0	0	0	Repressed
1568	GO_IMP_BIOSYNTHETIC_PROCESS	-1.51	1.52	0	0	0	Repressed
1569	DELPUECH_FOXO3_TARGETS_DN	-1.51	1.50	0	0	0	Repressed
1570	PID_PI3KCI_AKT_PATHWAY	-1.51	1.50	0	0	0	Repressed
1571	REACTOME_PHASE_II_CONJUGATION_OF_COMPOUNDS	-1.51	1.47	0	0	0	Repressed
1572	ASTIER_INTEGRIN_SIGNALING	-1.51	1.43	0	0	0	Repressed
1573	REACTOME_PROCESSING_OF_INTRONLESS_PRE_MRNAS	-1.51	1.41	0	0	0	Repressed
1574	GO_GLYCINE_BINDING	-1.51	1.40	0	0	0	Repressed
1575	GO_POSTTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE_TRAN	-1.51	1.38	0	0	0	Repressed
1576	GO_SARCOPLASMIC_RETICULUM_MEMBRANE	-1.51	1.37	0	0	0	Repressed
1577	REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEIN	-1.51	1.36	0	0	0	Repressed
1578	MCMURRAY_TP53_HRAS_COOPERATION_RESPONSE_DN	-1.51	1.34	0	0	0	Repressed
1579	GO_POTASSIUM_TRANSPORTING_ATPASE_ACTIVITY	-1.51	1.33	0	0	0	Repressed
1580	CAMPS_COLON_CANCER_COPY_NUMBER_DN	-1.51	1.31	0	0	0	Repressed
1581	GO_PROTEIN_PHOSPHATASE_TYPE_2A_COMPLEX	-1.51	1.30	0	0	0	Repressed
1582	AMIT_EGF_RESPONSE_40_MCF10A	-1.51	1.29	0	0	0	Repressed
1583	GO_RESPONSE_TO_THYROID_HORMONE	-1.51	1.29	0	0	0	Repressed
1584	GO_PROTEASOME_CORE_COMPLEX_BETA_SUBUNIT_COMPLEX	-1.51	1.28	0	0	0	Repressed
1585	GO_VESICLE_CARGO_LOADING	-1.51	1.28	0	0	0	Repressed
1586	PID_RANBP2_PATHWAY	-1.51	1.28	0	0	0	Repressed
1587	KERLEY_RESPONSE_TO_CISPLATIN_UP	-1.51	1.27	0	0	0	Repressed
1588	GO_PROTEIN_LIPOYLATION	-1.51	1.26	0	0	0	Repressed
1589	GO_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	-1.51	1.24	0	0	0	Repressed
1590	GO_CARBOHYDRATE_PHOSPHATASE_ACTIVITY	-1.51	1.23	0	0	0	Repressed
1591	XU_RESPONSE_TO_TRETINOIN_DN	-1.51	1.22	0	0	0	Repressed
1592	GO_LEUCINE_BINDING	-1.51	1.20	0	0	0	Repressed
1593	GO_OLIGOPEPTIDE_BINDING	-1.51	1.18	0	0	0	Repressed
1594	REACTOME_NEF_MEDIATED_CD4_DOWN_REGULATION	-1.51	1.16	0	0	0	Repressed
1595	KARAKAS_TGFB1_SIGNALING	-1.51	1.15	0	0	0	Repressed
1596	GO_ANATOMICAL_STRUCTURE_HOMEOSTASIS	-1.50	4.00	0	0	0	Repressed
1597	GO_CATALYTIC_COMPLEX	-1.50	4.00	0	0	0	Repressed
1598	GO_CELLULAR_RESPONSE_TO_OXIDATIVE_STRESS	-1.50	4.00	0	0	0	Repressed
1599	GO_COENZYME_BINDING	-1.50	4.00	0	0	0	Repressed
1600	GO_GTPASE_ACTIVITY	-1.50	4.00	0	0	0	Repressed
1601	GO_MITOCHONDRIAL_TRANSPORT	-1.50	4.00	0	0	0	Repressed
1602	GO_SUPRAMOLECULAR_COMPLEX	-1.50	4.00	0	0	0	Repressed
1603	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP	-1.50	4.00	0	0	0	Repressed
1604	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN	-1.50	4.00	0	0	0	Repressed
1605	GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	-1.50	2.49	0	0	0	Repressed
1606	REACTOME_ER_TO_GOLGI_ANTEROGRADE_TRANSPORT	-1.50	2.48	0	0	0	Repressed
1607	PGF_UP.V1_UP	-1.50	2.46	0	0	0	Repressed
1608	GO_CELLULAR_RESPONSE_TO_XENOBIOTIC_STIMULUS	-1.50	2.22	0	0	0	Repressed
1609	BOYLAN_MULTIPLE_MYELOMA_C_D_UP	-1.50	2.21	0	0	0	Repressed
1610	REACTOME_MITOTIC_G1_G1_S_PHASES	-1.50	2.18	0	0	0	Repressed
1611	GO_U2_TYPE_SPLICEOSOMAL_COMPLEX	-1.50	1.93	0	0	0	Repressed
1612	CAIRO_LIVER_DEVELOPMENT_DN	-1.50	1.90	0	0	0	Repressed
1613	REACTOME_DUAL_INCISION_IN_TC_NER	-1.50	1.77	0	0	0	Repressed
1614	KAYO_CALORIE_RESTRICTION_MUSCLE_UP	-1.50	1.76	0	0	0	Repressed
1615	GO_LIPID_OXIDATION	-1.50	1.71	0	0	0	Repressed
1616	MUNSHI_MULTIPLE_MYELOMA_UP	-1.50	1.71	0	0	0	Repressed
1617	SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_UP	-1.50	1.69	0	0	0	Repressed
1618	REACTOME_HIV_ELONGATION_ARREST_AND_RECOVERY	-1.50	1.67	0	0	0	Repressed
1619	GO_PROTEIN_SUMOYLATION	-1.50	1.66	0	0	0	Repressed
1620	REACTOME_FORMATION_OF_TC_NER_PRE_INCISION_COMPLEX	-1.50	1.60	0	0	0	Repressed
1621	GO_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	-1.50	1.59	0	0	0	Repressed
1622	GO_THIOESTER_BIOSYNTHETIC_PROCESS	-1.50	1.49	0	0	0	Repressed
1623	LINDSTEDT_DENDRITIC_CELL_MATURATION_A	-1.50	1.46	0	0	0	Repressed

1624	GO_FACE_DEVELOPMENT	-1.50	1.45	0	0	0	Repressed
1625	GO_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	-1.50	1.45	0	0	0	Repressed
1626	PLASARI_TGFB1_TARGETS_1HR_UP	-1.50	1.45	0	0	0	Repressed
1627	GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_F	-1.50	1.42	0	0	0	Repressed
1628	GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY	-1.50	1.38	0	0	0	Repressed
1629	GO_RAN_GTPASE_BINDING	-1.50	1.37	0	0	0	Repressed
1630	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER	-1.50	1.37	0	0	0	Repressed
1631	GO_RIBONUCLEASE_MRP_COMPLEX	-1.50	1.36	0	0	0	Repressed
1632	CHEOK_RESPONSE_TO_MERCAPTOPURINE_DN	-1.50	1.31	0	0	0	Repressed
1633	GO_POSITIVE_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	-1.50	1.30	0	0	0	Repressed
1634	HALLMARK_PANCREAS_BETA_CELLS	-1.50	1.29	0	0	0	Repressed
1635	GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALI	-1.50	1.28	0	0	0	Repressed
1636	ZEMBUTSU_SENSITIVITY_TO_DOXORUBICIN	-1.50	1.28	0	0	0	Repressed
1637	FARMER_BREAST_CANCER_CLUSTER_7	-1.50	1.27	0	0	0	Repressed
1638	BOYAULT_LIVER_CANCER_SUBCLASS_G12_DN	-1.50	1.26	0	0	0	Repressed
1639	GO_ACID_THIOL_LIGASE_ACTIVITY	-1.50	1.26	0	0	0	Repressed
1640	GO_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_I	-1.50	1.26	0	0	0	Repressed
1641	PID_IL12_STAT4_PATHWAY	-1.50	1.26	0	0	0	Repressed
1642	GO_REGULATION_OF_PODOSOME_ASSEMBLY	-1.50	1.22	0	0	0	Repressed
1643	GO_RESPONSE_TO_TUMOR_CELL	-1.50	1.22	0	0	0	Repressed
1644	GO_UBIQUITIN_RECYCLING	-1.50	1.21	0	0	0	Repressed
1645	GO_NLRP3_INFLAMMASOME_COMPLEX_ASSEMBLY	-1.50	1.20	0	0	0	Repressed
1646	GO_POSITIVE_REGULATION_OF_CHEMOKINE_PRODUCTION	-1.50	1.20	0	0	0	Repressed
1647	GO_PURINE_NUCLEOBASE_BIOSYNTHETIC_PROCESS	-1.50	1.20	0	0	0	Repressed
1648	GO_REGULATION_OF_HORMONE_BIOSYNTHETIC_PROCESS	-1.50	1.17	0	0	0	Repressed
1649	GO_PROTEASOME_CORE_COMPLEX_ALPHA_SUBUNIT_COMPLEX	-1.50	1.14	0	0	0	Repressed
1650	SANDERSON_PPARA_TARGETS	-1.50	1.14	0	0	0	Repressed
1651	GO_ORGANIC_HYDROXY_COMPOUND_TRANSMEMBRANE_TRANSPORTE	-1.50	1.08	0	0	0	Repressed
1652	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN	-1.49	4.00	0	0	0	not significant
1653	FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL	-1.49	4.00	0	0	0	not significant
1654	GO_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	-1.49	4.00	0	0	0	not significant
1655	GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	-1.49	4.00	0	0	0	not significant
1656	GO_CELLULAR_AMIDE_METABOLIC_PROCESS	-1.49	4.00	0	0	0	not significant
1657	GO_PROTEIN_CONTAINING_COMPLEX_BINDING	-1.49	4.00	0	0	0	not significant
1658	GO_RNA_SPLICING	-1.49	4.00	0	0	0	not significant
1659	REACTOME_ADAPTIVE_IMMUNE_SYSTEM	-1.49	4.00	0	0	0	not significant
1660	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP	-1.49	4.00	0	0	0	not significant
1661	GO_RESPONSE_TO_MECHANICAL_STIMULUS	-1.49	2.21	0	0	0	not significant
1662	GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	-1.49	2.17	0	0	0	not significant
1663	GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	-1.49	2.03	0	0	0	not significant
1664	GO_RNA_POLYMERASE_COMPLEX	-1.49	2.01	0	0	0	not significant
1665	GO_RESPONSE_TO_TYPE_I_INTERFERON	-1.49	1.94	0	0	0	not significant
1666	GO_SINGLE_STRANDED_RNA_BINDING	-1.49	1.85	0	0	0	not significant
1667	ROSS_AML_OF_FAB_M7_TYPE	-1.49	1.72	0	0	0	not significant
1668	GOZGIT_ESR1_TARGETS_UP	-1.49	1.63	0	0	0	not significant
1669	LANDIS_ERBB2_BREAST_PRENEOPLASTIC_DN	-1.49	1.61	0	0	0	not significant
1670	NADERI_BREAST_CANCER_PROGNOSIS_UP	-1.49	1.57	0	0	0	not significant
1671	GO_ION_CHANNEL_REGULATOR_ACTIVITY	-1.49	1.55	0	0	0	not significant
1672	GO_MITOTIC_METAPHASE_PLATE_CONGRESSION	-1.49	1.50	0	0	0	not significant
1673	GO_RUFFLE_ORGANIZATION	-1.49	1.48	0	0	0	not significant
1674	BYSTROEM_CORRELATED_WITH_IL5_UP	-1.49	1.46	0	0	0	not significant
1675	CORDENONSI_YAP_CONSERVED_SIGNATURE	-1.49	1.44	0	0	0	not significant
1676	KRAS.LUNG_UP.V1_DN	-1.49	1.43	0	0	0	not significant
1677	GO_MITOCHONDRIAL_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	-1.49	1.42	0	0	0	not significant
1678	REACTOME_SIGNAL_AMPLIFICATION	-1.49	1.42	0	0	0	not significant
1679	GO_REGULATION_OF_ER_TO_GOLGI_VESICLE_MEDIATED_TRANSPORT	-1.49	1.41	0	0	0	not significant
1680	GO_NEGATIVE_REGULATION_OF_HORMONE_SECRETION	-1.49	1.40	0	0	0	not significant
1681	MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_DN	-1.49	1.36	0	0	0	not significant
1682	GO_POSITIVE_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCES	-1.49	1.35	0	0	0	not significant
1683	GO_CHAPERONE_COMPLEX	-1.49	1.30	0	0	0	not significant
1684	GO_POSITIVE_REGULATION_OF_ANOIKIS	-1.49	1.30	0	0	0	not significant
1685	REACTOME_FOXO_MEDIATED_TRANSCRIPTION_OF_OXIDATIVE_STRESS	-1.49	1.28	0	0	0	not significant
1686	GO_PHOSPHOLIPASE_C_ACTIVITY	-1.49	1.25	0	0	0	not significant
1687	SHANK_TAL1_TARGETS_DN	-1.49	1.22	0	0	0	not significant
1688	GO_OUTER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	-1.49	1.21	0	0	0	not significant
1689	GO_RESPONSE_TO_LAMINAR_FLUID_SHEAR_STRESS	-1.49	1.21	0	0	0	not significant
1690	GO_STRUCTURAL_MOLECULE_ACTIVITY_CONFERRING_ELASTICITY	-1.49	1.21	0	0	0	not significant
1691	GO_ADENYLATE_KINASE_ACTIVITY	-1.49	1.20	0	0	0	not significant
1692	GO_ALDO_KETO_REDUCTASE_NADP_ACTIVITY	-1.49	1.20	0	0	0	not significant
1693	REACTOME_SCAVENGING_BY_CLASS_A_RECEPTORS	-1.49	1.20	0	0	0	not significant
1694	BIOCARTA_CPSF_PATHWAY	-1.49	1.17	0	0	0	not significant
1695	GO_3_PHOSPHOADENOSINE_5_PHOSPHOSULFATE_BIOSYNTHETIC_PRO	-1.49	1.16	0	0	0	not significant
1696	GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSPORT	-1.49	1.16	0	0	0	not significant
1697	GO_REGULATION_OF_MICROVILLUS_ORGANIZATION	-1.49	1.16	0	0	0	not significant
1698	GO_POSITIVE_REGULATION_OF_CHEMOKINE_BIOSYNTHETIC_PROCESS	-1.49	1.15	0	0	0	not significant
1699	GO_CELLULAR_RESPONSE_TO_LAMINAR_FLUID_SHEAR_STRESS	-1.49	1.14	0	0	0	not significant
1700	GO_PURINE_CONTAINING_COMPOUND_SALVAGE	-1.49	1.14	0	0	0	not significant
1701	REACTOME_TRAFFICKING_AND_PROCESSING_OF_ENDOSOMAL_TLR	-1.49	1.13	0	0	0	not significant
1702	GO_PEPTIDE_CROSS_LINKING	-1.49	1.11	0	0	0	not significant
1703	BERENJENO_TRANSFORMED_BY_RHOA_FOREVER_DN	-1.49	1.06	0	0	0	not significant
1704	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN	-1.48	4.00	0	0	0	not significant
1705	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP	-1.48	4.00	0	0	0	not significant
1706	ENK_UV_RESPONSE_KERATINOCYTE_UP	-1.48	4.00	0	0	0	not significant
1707	GO_RESPONSE_TO_TUMOR_NECROSIS_FACTOR	-1.48	4.00	0	0	0	not significant
1708	GO_TRANSMEMBRANE_TRANSPORT	-1.48	4.00	0	0	0	not significant
1709	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN	-1.48	4.00	0	0	0	not significant
1710	RUTELLA_RESPONSE_TO_HGF_UP	-1.48	4.00	0	0	0	not significant
1711	CSR_LATE_UP.V1_UP	-1.48	2.50	0	0	0	not significant
1712	GO_TELOMERE_ORGANIZATION	-1.48	2.48	0	0	0	not significant
1713	GO_ACTIN_FILAMENT_BUNDLE_ORGANIZATION	-1.48	2.23	0	0	0	not significant
1714	MCBRYAN_PUBERTAL_BREAST_4_5WK_DN	-1.48	2.20	0	0	0	not significant
1715	GO_ORGANIC_ACID_TRANSPORT	-1.48	2.19	0	0	0	not significant
1716	GO_CARBOHYDRATE_HOMEOSTASIS	-1.48	2.17	0	0	0	not significant
1717	UDAYAKUMAR_MED1_TARGETS_UP	-1.48	2.05	0	0	0	not significant
1718	GO_PIGMENT_GRANULE	-1.48	1.78	0	0	0	not significant
1719	KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	-1.48	1.77	0	0	0	not significant
1720	GO_LONG_CHAIN_FATTY_ACID_TRANSPORT	-1.48	1.64	0	0	0	not significant
1721	MOHANKUMAR_HOXA1_TARGETS_DN	-1.48	1.61	0	0	0	not significant
1722	GO_CELLULAR_AMINO_ACID_BIOSYNTHETIC_PROCESS	-1.48	1.60	0	0	0	not significant
1723	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN	-1.48	1.55	0	0	0	not significant
1724	GO_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	-1.48	1.55	0	0	0	not significant
1725	GO_RESPONSE_TO_CAMP	-1.48	1.55	0	0	0	not significant
1726	KEGG_PYRUVATE_METABOLISM	-1.48	1.54	0	0	0	not significant
1727	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	-1.48	1.53	0	0	0	not significant
1728	RUAN_RESPONSE_TO_TNF_DN	-1.48	1.50	0	0	0	not significant
1729	PENG_GLUCOSE_DEPRIVATION_UP	-1.48	1.43	0	0	0	not significant
1730	GO_TELOMERASE_HOLOENZYME_COMPLEX	-1.48	1.29	0	0	0	not significant
1731	PETRETTO_BLOOD_PRESSURE_UP	-1.48	1.27	0	0	0	not significant
1732	GO_PYRIMIDINE_RIBONUCLEOSIDE_CATABOLIC_PROCESS	-1.48	1.26	0	0	0	not significant

1733	PETRETTO_CARDIAC_HYPERTROPHY	-1.48	1.26	0	0	0	not significant
1734	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	-1.48	1.25	0	0	0	not significant
1735	GO_MULTICELLULAR_ORGANISM_AGING	-1.48	1.24	0	0	0	not significant
1736	GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PE	-1.48	1.22	0	0	0	not significant
1737	GO_SNRNA_3_END_PROCESSING	-1.48	1.22	0	0	0	not significant
1738	GO_GLUTAMINE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	-1.48	1.21	0	0	0	not significant
1739	MCBRYAN_TERMINAL_END_BUD_UP	-1.48	1.20	0	0	0	not significant
1740	GO_HEART_FORMATION	-1.48	1.16	0	0	0	not significant
1741	GO_PROTEIN_LOCALIZATION_TO_NUCLEOLUS	-1.48	1.16	0	0	0	not significant
1742	GO_T_HELPER_1_CELL_DIFFERENTIATION	-1.48	1.14	0	0	0	not significant
1743	YANG_MUC2_TARGETS_DUODENUM_6MO_DN	-1.48	1.13	0	0	0	not significant
1744	GO_REGULATION_OF_RECEPTOR_CATABOLIC_PROCESS	-1.48	1.10	0	0	0	not significant
1745	GO_POSITIVE_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONS	-1.48	1.06	0	0	0	not significant
1746	GAL_LEUKEMIC_STEM_CELL_DN	-1.47	4.00	0	0	0	not significant
1747	GO_INNATE_IMMUNE_RESPONSE	-1.47	4.00	0	0	0	not significant
1748	GO_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT	-1.47	4.00	0	0	0	not significant
1749	GO_REGULATION_OF_LIPID_METABOLIC_PROCESS	-1.47	4.00	0	0	0	not significant
1750	GO_RESPONSE_TO_DRUG	-1.47	4.00	0	0	0	not significant
1751	MILI_PSEUDOPODIA_HAPTOTAXIS_UP	-1.47	4.00	0	0	0	not significant
1752	ONDER_CDH1_TARGETS_2_DN	-1.47	4.00	0	0	0	not significant
1753	REACTOME_INNATE_IMMUNE_SYSTEM	-1.47	4.00	0	0	0	not significant
1754	GO_REGULATION_OF_VASCULATURE_DEVELOPMENT	-1.47	2.44	0	0	0	not significant
1755	CAMP_UP.V1_UP	-1.47	2.43	0	0	0	not significant
1756	MCLACHLAN_DENTAL_CARIES_UP	-1.47	2.21	0	0	0	not significant
1757	PID_ERBB1_DOWNSTREAM_PATHWAY	-1.47	2.02	0	0	0	not significant
1758	SHEPARD_BMYB_MORPHOLINO_DN	-1.47	2.02	0	0	0	not significant
1759	REACTOME_SIGNALING_BY_NUCLEAR_RECEPTORS	-1.47	1.96	0	0	0	not significant
1760	GO_PROTON_TRANSMEMBRANE_TRANSPORT	-1.47	1.89	0	0	0	not significant
1761	WILCOX_RESPONSE_TO_PROGESTERONE_UP	-1.47	1.89	0	0	0	not significant
1762	WOOD_EBV_EBNA1_TARGETS_UP	-1.47	1.75	0	0	0	not significant
1763	GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS	-1.47	1.70	0	0	0	not significant
1764	GO_CARBON_CARBON_LYASE_ACTIVITY	-1.47	1.57	0	0	0	not significant
1765	VANTVEER_BREAST_CANCER_BRCA1_UP	-1.47	1.57	0	0	0	not significant
1766	GO_NUCLEAR_ENVELOPE_ORGANIZATION	-1.47	1.55	0	0	0	not significant
1767	ZHOU_TNF_SIGNALING_30MIN	-1.47	1.55	0	0	0	not significant
1768	ZHAN_MULTIPLE_MYELOMA_CD1_UP	-1.47	1.49	0	0	0	not significant
1769	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_DN	-1.47	1.46	0	0	0	not significant
1770	REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	-1.47	1.46	0	0	0	not significant
1771	REACTOME_RMTS_METHYLATE_HISTONE_ARGININES	-1.47	1.46	0	0	0	not significant
1772	GO_ENDONUCLEASE_COMPLEX	-1.47	1.38	0	0	0	not significant
1773	GO_REGULATORY_RNA_BINDING	-1.47	1.36	0	0	0	not significant
1774	GO_CHANNEL_INHIBITOR_ACTIVITY	-1.47	1.35	0	0	0	not significant
1775	LEE_LIVER_CANCER_MYC_E2F1_UP	-1.47	1.35	0	0	0	not significant
1776	GO_UNSATURATED_FATTY_ACID_BIOSYNTHETIC_PROCESS	-1.47	1.33	0	0	0	not significant
1777	LY_AGING_PREMATURE_DN	-1.47	1.32	0	0	0	not significant
1778	GO_RESPONSE_TO_DSRNA	-1.47	1.29	0	0	0	not significant
1779	GO_TRNA_SPECIFIC_RIBONUCLEASE_ACTIVITY	-1.47	1.29	0	0	0	not significant
1780	GO_RNA_POLYMERASE_II_CORE_COMPLEX	-1.47	1.25	0	0	0	not significant
1781	GO_CELLULAR_RESPONSE_TO_GONADOTROPIN_STIMULUS	-1.47	1.24	0	0	0	not significant
1782	GO_RESPONSE_TO_IRON_III_ION	-1.47	1.24	0	0	0	not significant
1783	GO_FIBRINOLYSIS	-1.47	1.23	0	0	0	not significant
1784	GO_LEUCINE_CATABOLIC_PROCESS	-1.47	1.23	0	0	0	not significant
1785	LIANG_SILENCED_BY_METHYLATION_UP	-1.47	1.23	0	0	0	not significant
1786	GO_ACTIN_CROSSLINK_FORMATION	-1.47	1.20	0	0	0	not significant
1787	GO_ADENOSINE_RECEPTOR_SIGNALING_PATHWAY	-1.47	1.20	0	0	0	not significant
1788	GO_ADENYLATE_CYCLASE_ACTIVATOR_ACTIVITY	-1.47	1.20	0	0	0	not significant
1789	GO_LONG_CHAIN_FATTY_ACID_TRANSPORTER_ACTIVITY	-1.47	1.20	0	0	0	not significant
1790	GO_SINGLE_STRANDED_VIRAL_RNA_REPLICATION_VIA_DOUBLE_STRAN	-1.47	1.20	0	0	0	not significant
1791	BIOCARTA_NUCLEARRS_PATHWAY	-1.47	1.17	0	0	0	not significant
1792	GO_GLYCINE_TRANSPORT	-1.47	1.16	0	0	0	not significant
1793	GO_POSITIVE_REGULATION_OF_AMYLOID_PRECURSOR_PROTEIN_CATA	-1.47	1.16	0	0	0	not significant
1794	SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_UP	-1.47	1.16	0	0	0	not significant
1795	REACTOME_TRNA_PROCESSING_IN_THE_MITOCHONDRION	-1.47	1.14	0	0	0	not significant
1796	GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_BIOSYNTH	-1.47	1.13	0	0	0	not significant
1797	GO_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	-1.47	1.13	0	0	0	not significant
1798	ZHAN_V1_LATE_DIFFERENTIATION_GENES_DN	-1.47	1.13	0	0	0	not significant
1799	GO_FOREBRAIN_NEURON_DEVELOPMENT	-1.47	1.11	0	0	0	not significant
1800	ZERBINI_RESPONSE_TO_SULINDAC_DN	-1.47	1.11	0	0	0	not significant
1801	GO_PINOSOME	-1.47	1.08	0	0	0	not significant
1802	GO_POSITIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INIT	-1.47	1.08	0	0	0	not significant
1803	YANG_MUC2_TARGETS_DUODENUM_3MO_DN	-1.47	1.08	0	0	0	not significant
1804	GO_RENAL_ABSORPTION	-1.47	1.07	0	0	0	not significant
1805	GO_MAINTENANCE_OF_GASTROINTESTINAL_EPITHELIUM	-1.47	1.06	0	0	0	not significant
1806	GO_ACTIN_CYTOSKELETON	-1.46	4.00	0	0	0	not significant
1807	GO_CELLULAR_PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	-1.46	4.00	0	0	0	not significant
1808	GO_REGULATION_OF_SYSTEM_PROCESS	-1.46	4.00	0	0	0	not significant
1809	GO_RESPONSE_TO_ABIOTIC_STIMULUS	-1.46	4.00	0	0	0	not significant
1810	REACTOME_TRANSLATION	-1.46	4.00	0	0	0	not significant
1811	MEK_UP.V1_DN	-1.46	2.43	0	0	0	not significant
1812	KIM_WT1_TARGETS_DN	-1.46	2.25	0	0	0	not significant
1813	GO_CYTOSOLIC_CALCIUM_ION_TRANSPORT	-1.46	2.24	0	0	0	not significant
1814	RAMALHO_STEMNESS_UP	-1.46	2.10	0	0	0	not significant
1815	REACTOME_METABOLISM_OF_STEROIDS	-1.46	2.02	0	0	0	not significant
1816	EPPERT_PROGENITOR	-1.46	2.00	0	0	0	not significant
1817	REACTOME_AURKA_ACTIVATION_BY_TPX2	-1.46	1.94	0	0	0	not significant
1818	MACAEVA_PBMC_RESPONSE_TO_IR	-1.46	1.84	0	0	0	not significant
1819	REACTOME_CARDIAC_CONDUCTION	-1.46	1.75	0	0	0	not significant
1820	GO_I_BAND	-1.46	1.74	0	0	0	not significant
1821	REACTOME_INTERLEUKIN_12_FAMILY_SIGNALING	-1.46	1.73	0	0	0	not significant
1822	GO_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	-1.46	1.68	0	0	0	not significant
1823	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN	-1.46	1.63	0	0	0	not significant
1824	REACTOME_TRANSCRIPTIONAL_ACTIVATION_OF_MITOCHONDRIAL_BIOG	-1.46	1.63	0	0	0	not significant
1825	BROWNE_HCMV_INFECTION_20HR_DN	-1.46	1.60	0	0	0	not significant
1826	GO_MUSCLE_CELL_DEVELOPMENT	-1.46	1.57	0	0	0	not significant
1827	GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORT	-1.46	1.57	0	0	0	not significant
1828	GO_RESPONSE_TO_FATTY_ACID	-1.46	1.53	0	0	0	not significant
1829	HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_DN	-1.46	1.48	0	0	0	not significant
1830	GO_CELLULAR_RESPONSE_TO_MECHANICAL_STIMULUS	-1.46	1.44	0	0	0	not significant
1831	NAKAMURA_METASTASIS_MODEL_UP	-1.46	1.44	0	0	0	not significant
1832	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION	-1.46	1.41	0	0	0	not significant
1833	PID_BCR_5PATHWAY	-1.46	1.40	0	0	0	not significant
1834	REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	-1.46	1.33	0	0	0	not significant
1835	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_UP	-1.46	1.31	0	0	0	not significant
1836	GO_CIS_TRANS_ISOMERASE_ACTIVITY	-1.46	1.30	0	0	0	not significant
1837	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	-1.56	1.30	1	0	0	Repressed
1838	GENTILE_UV_RESPONSE_CLUSTER_D5	-1.46	1.29	0	0	0	not significant
1839	GO_SODIUM_POTASSIUM_EXCHANGING_ATPASE_COMPLEX	-1.46	1.29	0	0	0	not significant
1840	AMIT_EGF_RESPONSE_60_HELA	-1.46	1.27	0	0	0	not significant
1841	GO_SMALL_NUCLEOLAR_RIBONUCLEOPROTEIN_COMPLEX_ASSEMBLY	-1.46	1.22	0	0	0	not significant

1842	REACTOME_PKA_ACTIVATION_IN_GLUCAGON_SIGNALLING	-1.46	1.21	0	0	0	not significant
1843	GO_POSITIVE_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	-1.46	1.19	0	0	0	not significant
1844	GO_EXON_EXON_JUNCTION_COMPLEX	-1.46	1.18	0	0	0	not significant
1845	GO_QUINONE_BIOSYNTHETIC_PROCESS	-1.46	1.18	0	0	0	not significant
1846	MARCHINI_TRABECTEDIN_RESISTANCE_UP	-1.46	1.18	0	0	0	not significant
1847	STAMBOLSKY_BOUND_BY_MUTATED_TP53	-1.46	1.18	0	0	0	not significant
1848	GO_FATTY_ACYL_COA_BIOSYNTHETIC_PROCESS	-1.46	1.17	0	0	0	not significant
1849	GO_PWP2P_CONTAINING_SUBCOMPLEX_OF_90S_PRERIBOSOME	-1.46	1.16	0	0	0	not significant
1850	GO_DENDRITIC_TRANSPORT	-1.46	1.15	0	0	0	not significant
1851	KOBAYASHI_EGFR_SIGNALING_6HR_DN	-1.46	1.15	0	0	0	not significant
1852	REACTOME_G2_M_DNA_REPLICATION_CHECKPOINT	-1.46	1.15	0	0	0	not significant
1853	GO_CHAPERONE_MEDIATED_PROTEIN_COMPLEX_ASSEMBLY	-1.46	1.14	0	0	0	not significant
1854	GO_ENDONUCLEOLYTIC_CLEAVAGE_IN_5_ETS_OF_TRICISTRONIC_RRNA	-1.46	1.14	0	0	0	not significant
1855	GO_NEGATIVE_REGULATION_OF_CENTROSOME_CYCLE	-1.46	1.14	0	0	0	not significant
1856	GO_POSITIVE_REGULATION_OF_NAD_P_H_OXIDASE_ACTIVITY	-1.46	1.13	0	0	0	not significant
1857	SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_UP	-1.46	1.13	0	0	0	not significant
1858	GO_AMINOACYL_TRNA_EDITING_ACTIVITY	-1.46	1.12	0	0	0	not significant
1859	GO_POSITIVE_REGULATION_OF_MUSCLE_HYPERTROPHY	-1.46	1.12	0	0	0	not significant
1860	GO_AMINOACYL_TRNA_METABOLISM_INVOLVED_IN_TRANSLATIONAL_FI	-1.46	1.11	0	0	0	not significant
1861	GO_NUCLEAR_EXPORT_SIGNAL_RECEPTOR_ACTIVITY	-1.46	1.11	0	0	0	not significant
1862	GO_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	-1.46	1.10	0	0	0	not significant
1863	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_1_UP	-1.46	1.08	0	0	0	not significant
1864	HOWLIN_CITED1_TARGETS_2_DN	-1.46	1.08	0	0	0	not significant
1865	STEGER_ADIPOGENESIS_UP	-1.46	1.08	0	0	0	not significant
1866	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_DIPHENOLS_AND_RELATE	-1.46	1.05	0	0	0	not significant
1867	DANG_BOUND_BY_MYC	-1.45	4.00	0	0	0	not significant
1868	GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	-1.45	4.00	0	0	0	not significant
1869	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN	-1.45	4.00	0	0	0	not significant
1870	LOPEZ_MBD_TARGETS	-1.45	4.00	0	0	0	not significant
1871	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP	-1.45	4.00	0	0	0	not significant
1872	GO_SPLICEOSOMAL_COMPLEX	-1.45	2.40	0	0	0	not significant
1873	GO_MUSCLE_SYSTEM_PROCESS	-1.45	2.16	0	0	0	not significant
1874	GOLDRATH_HOMEOSTATIC_PROLIFERATION	-1.45	1.99	0	0	0	not significant
1875	PROVENZANI_METASTASIS_DN	-1.45	1.97	0	0	0	not significant
1876	GO_MICROBODY_PART	-1.45	1.96	0	0	0	not significant
1877	MISSIAGLIA_REGULATED_BY_METHYLATION_DN	-1.45	1.75	0	0	0	not significant
1878	CAFFAREL_RESPONSE_TO_THC_24HR_5_DN	-1.45	1.63	0	0	0	not significant
1879	FOSTER_TOLERANT_MACROPHAGE_UP	-1.45	1.62	0	0	0	not significant
1880	JAIN_NFKB_SIGNALING	-1.45	1.62	0	0	0	not significant
1881	REACTOME_RNA_POLYMERASE_I_PROMOTER_ESCAPE	-1.45	1.61	0	0	0	not significant
1882	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	-1.45	1.60	0	0	0	not significant
1883	REACTOME_POSITIVE_EPIGENETIC_REGULATION_OF_RRNA_EXPRESSIO	-1.45	1.60	0	0	0	not significant
1884	REACTOME_FORMATION_OF_THE_BETA_CATENIN:TCF_TRANSACTIVATI	-1.45	1.57	0	0	0	not significant
1885	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	-1.45	1.57	0	0	0	not significant
1886	GO_NAD_BINDING	-1.45	1.53	0	0	0	not significant
1887	FAELT_B_CLL_WITH_VH3_21_UP	-1.45	1.46	0	0	0	not significant
1888	ABRAMSON_INTERACT_WITH_AIRE	-1.45	1.44	0	0	0	not significant
1889	GO_PROTEIN_K11_LINKED_UBIQUITINATION	-1.45	1.39	0	0	0	not significant
1890	NAKAMURA_METASTASIS	-1.45	1.38	0	0	0	not significant
1891	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN	-1.45	1.38	0	0	0	not significant
1892	GO_MACROMOLECULE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.45	1.36	0	0	0	not significant
1893	GO_ESTABLISHMENT_OF_SPINDLE_ORIENTATION	-1.45	1.35	0	0	0	not significant
1894	JIANG_AGING_HYPOTHALAMUS_UP	-1.45	1.35	0	0	0	not significant
1895	REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	-1.45	1.31	0	0	0	not significant
1896	ROY_WOUND_BLOOD_VESSEL_UP	-1.45	1.27	0	0	0	not significant
1897	GO_FAD_BINDING	-1.45	1.26	0	0	0	not significant
1898	REACTOME_MET_PROMOTES_CELL_MOTILITY	-1.45	1.26	0	0	0	not significant
1899	ZHAN_VARIABLE_EARLY_DIFFERENTIATION_GENES_DN	-1.45	1.26	0	0	0	not significant
1900	GO_PROTEIN_SERINE_THREONINE_KINASE_ACTIVATOR_ACTIVITY	-1.45	1.25	0	0	0	not significant
1901	GNATENKO_PLATELET_SIGNATURE	-1.45	1.24	0	0	0	not significant
1902	GO_ANTIBACTERIAL_HUMORAL_RESPONSE	-1.45	1.22	0	0	0	not significant
1903	GO_POSITIVE_REGULATION_OF_TRANSLATIONAL_INITIATION	-1.45	1.22	0	0	0	not significant
1904	GO_PYRIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-1.45	1.22	0	0	0	not significant
1905	GO_SULFURTRANSFERASE_ACTIVITY	-1.45	1.17	0	0	0	not significant
1906	GO_CRISTAE_FORMATION	-1.45	1.16	0	0	0	not significant
1907	GO_PROTEIN_LOCALIZATION_TO_NUCLEOPLASM	-1.45	1.16	0	0	0	not significant
1908	GO_RNA_POLYMERASE_I_ACTIVITY	-1.45	1.15	0	0	0	not significant
1909	COLLIS_PRKDC_REGULATORS	-1.45	1.14	0	0	0	not significant
1910	GO_POSITIVE_REGULATION_OF_LAMELLIPODIUM_MORPHOGENESIS	-1.45	1.12	0	0	0	not significant
1911	ZHANG_GATA6_TARGETS_UP	-1.45	1.12	0	0	0	not significant
1912	BIOCARTA_MTA3_PATHWAY	-1.45	1.11	0	0	0	not significant
1913	GO_CELLULAR_LIPID_BIOSYNTHETIC_PROCESS	-1.45	1.10	0	0	0	not significant
1914	GO_PURINE_NUCLEOTIDE_SALVAGE	-1.45	1.10	0	0	0	not significant
1915	KEGG_FOLATE_BIOSYNTHESIS	-1.45	1.10	0	0	0	not significant
1916	LEE_METASTASIS_AND_RNA_PROCESSING_UP	-1.45	1.10	0	0	0	not significant
1917	WU_HBX_TARGETS_3_DN	-1.45	1.10	0	0	0	not significant
1918	GO_INFLAMMATORY_RESPONSE_TO_WOUNDING	-1.45	1.08	0	0	0	not significant
1919	CROSBY_E2F4_TARGETS	-1.45	1.07	0	0	0	not significant
1920	KRAS.50_UP.V1_UP	-1.45	1.07	0	0	0	not significant
1921	BIOCARTA_MEF2D_PATHWAY	-1.45	1.06	0	0	0	not significant
1922	GO_PYRAMIDAL_NEURON_DIFFERENTIATION	-1.45	1.06	0	0	0	not significant
1923	GO_RESPONSE_TO_GONADOTROPIN	-1.45	1.06	0	0	0	not significant
1924	GO_RETROGRADE_AXONAL_TRANSPORT	-1.45	1.06	0	0	0	not significant
1925	REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS	-1.45	1.05	0	0	0	not significant
1926	GO_LEUKOCYTE_ACTIVATION_INVOLVED_IN_INFLAMMATORY_RESPONSE	-1.45	1.04	0	0	0	not significant
1927	GO_PEPTIDYL_ARGININE_METHYLATION_TO_ASYMMETRICAL_DIMETHYL	-1.45	1.04	0	0	0	not significant
1928	GO_EPITHELIAL_TUBE_BRANCHING_INVOLVED_IN_LUNG_MORPHOGENES	-1.45	1.03	0	0	0	not significant
1929	REACTOME_BINDING_OF_TCF_LEF:CTNNB1_TO_TARGET_GENE_PROMO	-1.45	1.03	0	0	0	not significant
1930	GO_REGULATION_OF_VITAMIN_METABOLIC_PROCESS	-1.45	1.01	0	0	0	not significant
1931	YAMANAKA_GLIOBLASTOMA_SURVIVAL_UP	-1.45	1.01	0	0	0	not significant
1932	GO_HEART_TRABECULA_FORMATION	-1.45	0.99	0	0	0	not significant
1933	GO_HEPARAN_SULFATE_PROTEOGLYCAN_BINDING	-1.45	0.99	0	0	0	not significant
1934	GO_POSITIVE_REGULATION_OF_CELLULAR_RESPIRATION	-1.45	0.98	0	0	0	not significant
1935	GO_NEGATIVE_REGULATION_OF_DIGESTIVE_SYSTEM_PROCESS	-1.45	0.96	0	0	0	not significant
1936	COLINA_TARGETS_OF_4EBP1_AND_4EBP2	-1.44	4.00	0	0	0	not significant
1937	GO_AMIDE_BIOSYNTHETIC_PROCESS	-1.44	4.00	0	0	0	not significant
1938	GO_HYDROLASE_ACTIVITY_ACTING_ON_ACID_ANHYDRIDES	-1.44	4.00	0	0	0	not significant
1939	REACTOME_PTEN_REGULATION	-1.44	4.00	0	0	0	not significant
1940	KONG_E2F3_TARGETS	-1.44	2.52	0	0	0	not significant
1941	GO_ENZYME_INHIBITOR_ACTIVITY	-1.44	2.44	0	0	0	not significant
1942	IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR	-1.44	2.31	0	0	0	not significant
1943	GO_RESPONSE_TO_CARBOHYDRATE	-1.44	2.19	0	0	0	not significant
1944	GO_FATTY_ACID_CATABOLIC_PROCESS	-1.44	2.07	0	0	0	not significant
1945	GO_RESPONSE_TO_XENOBIOTIC_STIMULUS	-1.44	2.02	0	0	0	not significant
1946	BROWNE_HCMV_INFECTION_14HR_UP	-1.44	1.99	0	0	0	not significant
1947	GO_NUCLEUS_ORGANIZATION	-1.44	1.90	0	0	0	not significant
1948	REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS	-1.44	1.88	0	0	0	not significant
1949	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_UP	-1.44	1.80	0	0	0	not significant
1950	GO_CALCIUM_MEDIATED_SIGNALING	-1.44	1.80	0	0	0	not significant

1951	GO_NEPHRON_DEVELOPMENT	-1.44	1.57	0	0	0	not significant
1952	MORI_MATURE_B_LYMPHOCYTE_DN	-1.44	1.56	0	0	0	not significant
1953	CRX_DN.V1_UP	-1.44	1.55	0	0	0	not significant
1954	CHR1P32	-1.44	1.46	0	0	0	not significant
1955	GO_HORMONE_BINDING	-1.44	1.44	0	0	0	not significant
1956	GO_POSITIVE_REGULATION_OF_VIRAL_TRANSCRIPTION	-1.44	1.41	0	0	0	not significant
1957	GO_REGULATION_OF_PROTEIN_DEPOLYMERIZATION	-1.44	1.39	0	0	0	not significant
1958	PID_FOXM1_PATHWAY	-1.44	1.39	0	0	0	not significant
1959	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	-1.44	1.33	0	0	0	not significant
1960	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN	-1.44	1.32	0	0	0	not significant
1961	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP	-1.44	1.32	0	0	0	not significant
1962	CUI_GLUCOSE_DEPRIVATION	-1.44	1.31	0	0	0	not significant
1963	GO_REGULATION_OF_SISTER_CHROMATID_COHESION	-1.44	1.24	0	0	0	not significant
1964	GO_TERMINATION_OF_RNA_POLYMERASE_I_TRANSCRIPTION	-1.44	1.24	0	0	0	not significant
1965	GO_NEUROMUSCULAR_SYNAPTIC_TRANSMISSION	-1.44	1.22	0	0	0	not significant
1966	GO_CELLULAR_RESPONSE_TO_CAMP	-1.44	1.21	0	0	0	not significant
1967	GO_MATURATION_OF_LSU_RRNA	-1.44	1.21	0	0	0	not significant
1968	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	-1.44	1.21	0	0	0	not significant
1969	GO_ATP_DEPENDENT_MICROTUBULE_MOTOR_ACTIVITY_PLUS_END_DIF	-1.44	1.19	0	0	0	not significant
1970	GO_GLANDULAR_EPITHELIAL_CELL_DIFFERENTIATION	-1.44	1.19	0	0	0	not significant
1971	CROMER_TUMORIGENESIS_UP	-1.44	1.18	0	0	0	not significant
1972	GO_ANAPHASE_PROMOTING_COMPLEX	-1.44	1.18	0	0	0	not significant
1973	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN	-1.44	1.18	0	0	0	not significant
1974	GO_MONOCARBOXYLIC_ACID_BINDING	-1.44	1.17	0	0	0	not significant
1975	GO_KETONE_BIOSYNTHETIC_PROCESS	-1.44	1.16	0	0	0	not significant
1976	KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	-1.44	1.15	0	0	0	not significant
1977	REACTOME_CHOLESTEROL_BIOSYNTHESIS	-1.44	1.15	0	0	0	not significant
1978	GO_REGULATION_OF_LYASE_ACTIVITY	-1.44	1.14	0	0	0	not significant
1979	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_HO	-1.44	1.14	0	0	0	not significant
1980	GO_NEGATIVE_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_	-1.44	1.12	0	0	0	not significant
1981	GO_POSITIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	-1.44	1.12	0	0	0	not significant
1982	WANG_RESPONSE_TO_FORSKOLIN_UP	-1.44	1.12	0	0	0	not significant
1983	GO_REGULATION_OF_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	-1.44	1.11	0	0	0	not significant
1984	GO_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZATION	-1.44	1.08	0	0	0	not significant
1985	GO_CRANIAL_NERVE_MORPHOGENESIS	-1.44	1.08	0	0	0	not significant
1986	GO_INNATE_IMMUNE_RESPONSE_IN_MUCOSA	-1.44	1.08	0	0	0	not significant
1987	MURAKAMI_UV_RESPONSE_24HR	-1.44	1.07	0	0	0	not significant
1988	REACTOME_BETA_OXIDATION_OF_VERY_LONG_CHAIN_FATTY_ACIDS	-1.44	1.07	0	0	0	not significant
1989	GO_POSITIVE_REGULATION_OF_MRNA_3_END_PROCESSING	-1.44	1.06	0	0	0	not significant
1990	GO_PROTEIN_INSERTION_INTO_MITOCHONDRIAL_OUTER_MEMBRANE	-1.44	1.04	0	0	0	not significant
1991	REACTOME_PURINE_SALVAGE	-1.44	1.04	0	0	0	not significant
1992	GO_CYTIDINE_TO_URIDINE_EDITING	-1.44	1.03	0	0	0	not significant
1993	GO_EMBRYONIC_CLEAVAGE	-1.44	1.02	0	0	0	not significant
1994	GO_TROPHECTODERMAL_CELL_DIFFERENTIATION	-1.44	1.01	0	0	0	not significant
1995	GO_POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUN	-1.44	0.98	0	0	0	not significant
1996	GO_COFACTOR_BINDING	-1.43	4.00	0	0	0	not significant
1997	GO_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	-1.43	4.00	0	0	0	not significant
1998	GO_PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	-1.43	4.00	0	0	0	not significant
1999	GO_PROTEIN_CONTAINING_COMPLEX_LOCALIZATION	-1.43	4.00	0	0	0	not significant
2000	GO_REGULATION_OF_ION_TRANSPORT	-1.43	4.00	0	0	0	not significant
2001	ONKEN_UVEAL_MELANOMA_UP	-1.43	4.00	0	0	0	not significant
2002	STEIN_ESRRA_TARGETS	-1.43	4.00	0	0	0	not significant
2003	YOSHIMURA_MAPK8_TARGETS_DN	-1.43	4.00	0	0	0	not significant
2004	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP	-1.43	2.46	0	0	0	not significant
2005	IL2_UP.V1_UP	-1.43	2.18	0	0	0	not significant
2006	REACTOME_SIGNALING_BY_NOTCH	-1.43	1.98	0	0	0	not significant
2007	GO_PROTEIN_HETEROOLIGOMERIZATION	-1.43	1.92	0	0	0	not significant
2008	REACTOME_ESTROGEN_DEPENDENT_GENE_EXPRESSION	-1.43	1.89	0	0	0	not significant
2009	REACTOME_NUCLEOTIDE_EXCISION_REPAIR	-1.43	1.88	0	0	0	not significant
2010	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_DN	-1.43	1.86	0	0	0	not significant
2011	GO_RESPONSE_TO_PURINE_CONTAINING_COMPOUND	-1.43	1.85	0	0	0	not significant
2012	GO_EXTRACELLULAR_MATRIX	-1.43	1.78	0	0	0	not significant
2013	GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS	-1.43	1.72	0	0	0	not significant
2014	GO_CELLULAR_RESPONSE_TO_ACID_CHEMICAL	-1.43	1.65	0	0	0	not significant
2015	GO_CELL_REDOX_HOMEOSTASIS	-1.43	1.60	0	0	0	not significant
2016	HALLMARK_UV_RESPONSE_UP	-1.43	1.58	0	0	0	not significant
2017	GO_RNA_POLYMERASE_II_HOLOENZYME	-1.43	1.50	0	0	0	not significant
2018	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN	-1.43	1.46	0	0	0	not significant
2019	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_DN	-1.43	1.44	0	0	0	not significant
2020	GO_CHEMOKINE_PRODUCTION	-1.43	1.43	0	0	0	not significant
2021	KANG_IMMORTALIZED_BY_TERT_UP	-1.43	1.41	0	0	0	not significant
2022	APPIERTO_RESPONSE_TO_FENRETINIDE_DN	-1.43	1.35	0	0	0	not significant
2023	ZHAN_EARLY_DIFFERENTIATION_GENES_DN	-1.43	1.34	0	0	0	not significant
2024	MASSARWEH_RESPONSE_TO_ESTRADIOL	-1.43	1.33	0	0	0	not significant
2025	GO_PRECATALYTIC_SPLICEOSOME	-1.43	1.29	0	0	0	not significant
2026	REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	-1.43	1.29	0	0	0	not significant
2027	REACTOME_SIGNALING_BY_MODERATE_KINASE_ACTIVITY_BRAF_MUTAN	-1.43	1.29	0	0	0	not significant
2028	CHR2P22	-1.43	1.26	0	0	0	not significant
2029	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_UP	-1.43	1.26	0	0	0	not significant
2030	SESTO_RESPONSE_TO_UV_C4	-1.43	1.24	0	0	0	not significant
2031	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	-1.43	1.23	0	0	0	not significant
2032	YAMASHITA_LIVER_CANCER_STEM_CELL_UP	-1.43	1.22	0	0	0	not significant
2033	GO_SARCOMERE_ORGANIZATION	-1.43	1.17	0	0	0	not significant
2034	KEGG_PROTEIN_EXPORT	-1.43	1.17	0	0	0	not significant
2035	REACTOME_MOLECULES_ASSOCIATED_WITH_ELASTIC_FIBRES	-1.43	1.17	0	0	0	not significant
2036	GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION	-1.43	1.14	0	0	0	not significant
2037	HU_GENOTOXIC_DAMAGE_4HR	-1.43	1.14	0	0	0	not significant
2038	GO_REGULATION_OF_NAD_P_H_OXIDASE_ACTIVITY	-1.43	1.13	0	0	0	not significant
2039	GO_SERINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.43	1.13	0	0	0	not significant
2040	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_IL3RA	-1.43	1.12	0	0	0	not significant
2041	GO_ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_O	-1.43	1.12	0	0	0	not significant
2042	REACTOME_POTASSIUM_CHANNELS	-1.43	1.12	0	0	0	not significant
2043	GO_COA_HYDROLASE_ACTIVITY	-1.43	1.11	0	0	0	not significant
2044	GO_AZOLE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.43	1.10	0	0	0	not significant
2045	GO_MATURATION_OF_LSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSC	-1.43	1.10	0	0	0	not significant
2046	ROY_WOUND_BLOOD_VESSEL_DN	-1.43	1.10	0	0	0	not significant
2047	GO_DETECTION_OF_MECHANICAL_STIMULUS_INVOLVED_IN_SENSORY_F	-1.43	1.09	0	0	0	not significant
2048	GO_GLYCINE_METABOLIC_PROCESS	-1.43	1.08	0	0	0	not significant
2049	GO_NUCLEAR_NCRNA_SURVEILLANCE	-1.43	1.08	0	0	0	not significant
2050	GO_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	-1.43	1.08	0	0	0	not significant
2051	GO_MYELIN_ASSEMBLY	-1.43	1.07	0	0	0	not significant
2052	GO_STEREOCILIUM_BUNDLE	-1.43	1.07	0	0	0	not significant
2053	GO_GLUTATHIONE_TRANSFERASE_ACTIVITY	-1.43	1.06	0	0	0	not significant
2054	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SU	-1.43	1.06	0	0	0	not significant
2055	BIOCARTA_ECM_PATHWAY	-1.43	1.05	0	0	0	not significant
2056	GO_MULTI_ORGANISM_CELLULAR_LOCALIZATION	-1.43	1.05	0	0	0	not significant
2057	GO_REGULATION_OF_T_HELPER_1_CELL_DIFFERENTIATION	-1.43	1.05	0	0	0	not significant
2058	GO_CARBOHYDRATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.43	1.04	0	0	0	not significant
2059	GO_POTASSIUM_ION_IMPORT_ACROSS_PLASMA_MEMBRANE	-1.43	1.04	0	0	0	not significant

2060	GO_GLUCOSE_6_PHOSPHATE_METABOLIC_PROCESS	-1.43	1.03	0	0	0	not significant
2061	GO_NUCLEAR_PORE_CENTRAL_TRANSPORT_CHANNEL	-1.43	1.03	0	0	0	not significant
2062	GO_PSEUDOURIDINE_SYNTHASE_ACTIVITY	-1.43	1.02	0	0	0	not significant
2063	GO_CENTRAL_NERVOUS_SYSTEM_NEURON_AXONOGENESIS	-1.43	1.01	0	0	0	not significant
2064	FIGUEROA_AML_METHYLATION_CLUSTER_4_DN	-1.43	1.00	0	0	0	not significant
2065	CUI_TCF21_TARGETS_UP	-1.43	0.98	0	0	0	not significant
2066	GO_SUGAR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.43	0.98	0	0	0	not significant
2067	GO_DNA_CYTOSINE_DEAMINATION	-1.43	0.97	0	0	0	not significant
2068	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	-1.43	0.94	0	0	0	not significant
2069	GO_SYNAPTIC_VESICLE_BUDDING	-1.43	0.94	0	0	0	not significant
2070	GO_DNA_DEAMINATION	-1.43	0.91	0	0	0	not significant
2071	ENK_UV_RESPONSE_KERATINOCYTE_DN	-1.42	4.00	0	0	0	not significant
2072	GO_CELL_DIVISION	-1.42	4.00	0	0	0	not significant
2073	GO_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	-1.42	4.00	0	0	0	not significant
2074	GO_ENZYME_REGULATOR_ACTIVITY	-1.42	4.00	0	0	0	not significant
2075	GO_MORPHOGENESIS_OF_AN_EPITHELIUM	-1.42	4.00	0	0	0	not significant
2076	REACTOME_SIGNALING_BY_RHO_GTPASES	-1.42	4.00	0	0	0	not significant
2077	WIERENGA_STAT5A_TARGETS_DN	-1.42	2.49	0	0	0	not significant
2078	REACTOME_OTHER_INTERLEUKIN_SIGNALING	-1.42	2.43	0	0	0	not significant
2079	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN	-1.42	2.37	0	0	0	not significant
2080	GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	-1.42	2.20	0	0	0	not significant
2081	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM1	-1.42	2.18	0	0	0	not significant
2082	REACTOME_NEDDYLATION	-1.42	2.13	0	0	0	not significant
2083	GO_MEMBRANE_FUSION	-1.42	1.88	0	0	0	not significant
2084	GO_REGULATION_OF_CYTOKINESIS	-1.42	1.79	0	0	0	not significant
2085	KAAB_FAILED_HEART_ATRIUM_DN	-1.42	1.77	0	0	0	not significant
2086	RASHI_RESPONSE_TO_IONIZING_RADIATION_5	-1.42	1.74	0	0	0	not significant
2087	GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	-1.42	1.59	0	0	0	not significant
2088	REACTOME_MITOCHONDRIAL_BIOGENESIS	-1.42	1.54	0	0	0	not significant
2089	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G	-1.42	1.47	0	0	0	not significant
2090	GO_REGULATION_OF_STEROID_METABOLIC_PROCESS	-1.42	1.44	0	0	0	not significant
2091	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	-1.42	1.43	0	0	0	not significant
2092	LEE_AGING_NEOCORTEX_DN	-1.42	1.43	0	0	0	not significant
2093	GO_NEGATIVE_REGULATION_OF_PROTEIN_BINDING	-1.42	1.42	0	0	0	not significant
2094	GO_METAL_CLUSTER_BINDING	-1.42	1.40	0	0	0	not significant
2095	CHR14Q12	-1.42	1.39	0	0	0	not significant
2096	GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROM	-1.42	1.39	0	0	0	not significant
2097	GO_REGULATION_OF_MUSCLE_ADAPTATION	-1.42	1.38	0	0	0	not significant
2098	GO_MUSCLE_ADAPTATION	-1.42	1.36	0	0	0	not significant
2099	GO_NEGATIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	-1.42	1.31	0	0	0	not significant
2100	GO_PROTEIN_PEPTIDYL_PROLYL_ISOMERIZATION	-1.42	1.30	0	0	0	not significant
2101	QUINTENS_EMBRYONIC_BRAIN_RESPONSE_TO_IR	-1.42	1.29	0	0	0	not significant
2102	REACTOME_RAF_ACTIVATION	-1.42	1.29	0	0	0	not significant
2103	SMID_BREAST_CANCER_ERBB2_UP	-1.42	1.28	0	0	0	not significant
2104	REACTOME_SMOOTH_MUSCLE_CONTRACTION	-1.42	1.27	0	0	0	not significant
2105	PID_EPHB_FWD_PATHWAY	-1.42	1.23	0	0	0	not significant
2106	GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	-1.42	1.22	0	0	0	not significant
2107	CHR2Q32	-1.42	1.21	0	0	0	not significant
2108	GO_POSITIVE_REGULATION_OF_TELOMERASE_ACTIVITY	-1.42	1.21	0	0	0	not significant
2109	LI_LUNG_CANCER	-1.42	1.21	0	0	0	not significant
2110	CORRE_MULTIPLE_MYELOMA_UP	-1.42	1.20	0	0	0	not significant
2111	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	-1.42	1.20	0	0	0	not significant
2112	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERAS	-1.42	1.19	0	0	0	not significant
2113	TRACEY_RESISTANCE_TO_IFNA2_DN	-1.42	1.18	0	0	0	not significant
2114	GO_SECRETORY_GRANULE_ORGANIZATION	-1.42	1.17	0	0	0	not significant
2115	LINDSTEDT_DENDRITIC_CELL_MATURATION_D	-1.42	1.17	0	0	0	not significant
2116	REACTOME_STRIATED_MUSCLE_CONTRACTION	-1.42	1.17	0	0	0	not significant
2117	GO_LIGASE_ACTIVITY_FORMING_CARBON_SULFUR_BONDS	-1.42	1.16	0	0	0	not significant
2118	GO_RESPONSE_TO_ISCHEMIA	-1.42	1.16	0	0	0	not significant
2119	GO_REGULATION_OF_B_CELL_DIFFERENTIATION	-1.42	1.15	0	0	0	not significant
2120	REACTOME_TRANSPORT_AND_SYNTHESIS_OF_PAPS	-1.42	1.15	0	0	0	not significant
2121	GO_POSITIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	-1.42	1.14	0	0	0	not significant
2122	GO_TOLL_LIKE_RECEPTOR_7_SIGNALING_PATHWAY	-1.42	1.14	0	0	0	not significant
2123	PID_DELTA_NP63_PATHWAY	-1.42	1.12	0	0	0	not significant
2124	JIANG_TIP30_TARGETS_DN	-1.42	1.11	0	0	0	not significant
2125	GO_ZYMOGEN_ACTIVATION	-1.42	1.10	0	0	0	not significant
2126	KAMIKUBO_MYELOID_CEBPA_NETWORK	-1.42	1.10	0	0	0	not significant
2127	PARK_APL_PATHOGENESIS_UP	-1.42	1.10	0	0	0	not significant
2128	REACTOME_MITOTIC_TELOPHASE_CYTOKINESIS	-1.42	1.10	0	0	0	not significant
2129	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_UP	-1.42	1.09	0	0	0	not significant
2130	GO_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	-1.42	1.09	0	0	0	not significant
2131	ZWANG_EGF_PERSISTENTLY_UP	-1.42	1.09	0	0	0	not significant
2132	DAZARD_UV_RESPONSE_CLUSTER_G2	-1.42	1.08	0	0	0	not significant
2133	GO_PROTEASOME_ASSEMBLY	-1.42	1.08	0	0	0	not significant
2134	ZUCCHI_METASTASIS_DN	-1.42	1.08	0	0	0	not significant
2135	GO_COENZYME_A_BIOSYNTHETIC_PROCESS	-1.42	1.07	0	0	0	not significant
2136	GO_POSITIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	-1.42	1.07	0	0	0	not significant
2137	GO_RESPONSE_TO_ANGIOTENSIN	-1.42	1.07	0	0	0	not significant
2138	AKL_HTLV1_INFECTION_UP	-1.42	1.06	0	0	0	not significant
2139	GO_POSITIVE_REGULATION_OF_CALCINEURIN_MEDIATED_SIGNALING	-1.42	1.06	0	0	0	not significant
2140	MA_PITUITARY_FETAL_VS_ADULT_DN	-1.42	1.06	0	0	0	not significant
2141	GO_CELLULAR_RESPONSE_TO_PURINE_CONTAINING_COMPOUND	-1.42	1.05	0	0	0	not significant
2142	GO_POSITIVE_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRINSI	-1.42	1.05	0	0	0	not significant
2143	GO_ISOPRENOID_BINDING	-1.42	1.04	0	0	0	not significant
2144	GO_CYTIDINE_DEAMINASE_ACTIVITY	-1.42	1.03	0	0	0	not significant
2145	GO_MONONUCLEAR_CELL_MIGRATION	-1.42	1.03	0	0	0	not significant
2146	REACTOME_RECYCLING_OF_EIF2:GDP	-1.42	1.02	0	0	0	not significant
2147	LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_QTL	-1.42	1.01	0	0	0	not significant
2148	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_DN	-1.42	1.00	0	0	0	not significant
2149	GO_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING_INVOLVED_IN_	-1.42	0.99	0	0	0	not significant
2150	GO_HISTONE_SERINE_PHOSPHORYLATION	-1.42	0.99	0	0	0	not significant
2151	BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_DN	-1.42	0.98	0	0	0	not significant
2152	WIEMANN_TELOMERE_SHORTENING_AND_CHRONIC_LIVER_DAMAGE_UP	-1.42	0.98	0	0	0	not significant
2153	GO_NUCLEOLAR_RIBONUCLEASE_P_COMPLEX	-1.42	0.97	0	0	0	not significant
2154	GO_PROTEIN_K6_LINKED_UBIQUITINATION	-1.42	0.97	0	0	0	not significant
2155	GO_GLYCEROL_ETHER_BIOSYNTHETIC_PROCESS	-1.42	0.95	0	0	0	not significant
2156	BIOCARTA_UCALPAIN_PATHWAY	-1.42	0.94	0	0	0	not significant
2157	GO_RIBONUCLEASE_P_ACTIVITY	-1.42	0.93	0	0	0	not significant
2158	GO_DRUG_BINDING	-1.41	4.00	0	0	0	not significant
2159	GO_MITOTIC_CELL_CYCLE	-1.41	4.00	0	0	0	not significant
2160	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	-1.41	4.00	0	0	0	not significant
2161	GO_RESPONSE_TO_EXTRACELLULAR_STIMULUS	-1.41	4.00	0	0	0	not significant
2162	GO_RESPONSE_TO_OXIDATIVE_STRESS	-1.41	4.00	0	0	0	not significant
2163	GO_ACTIN_FILAMENT_BINDING	-1.41	2.47	0	0	0	not significant
2164	GO_NUCLEOSIDE_PHOSPHATE_METABOLIC_PROCESS	-1.41	2.46	0	0	0	not significant
2165	REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION	-1.41	2.35	0	0	0	not significant
2166	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_1	-1.41	2.29	0	0	0	not significant
2167	GO_CELLULAR_RESPONSE_TO_STEROID_HORMONE_STIMULUS	-1.41	2.17	0	0	0	not significant
2168	GO_POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND	-1.41	2.15	0	0	0	not significant

2169	GO_UROGENITAL_SYSTEM_DEVELOPMENT	-1.41	2.14	0	0	0	not significant
2170	REACTOME_DEUBIQUITINATION	-1.41	2.05	0	0	0	not significant
2171	HOSHIDA_LIVER_CANCER_SUBCLASS_S3	-1.41	2.01	0	0	0	not significant
2172	SMID_BREAST_CANCER_LUMINAL_B_UP	-1.41	1.67	0	0	0	not significant
2173	DARWICHE_SQUAMOUS_CELL_CARCINOMA_UP	-1.41	1.63	0	0	0	not significant
2174	MENSE_HYPOXIA_UP	-1.41	1.59	0	0	0	not significant
2175	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	-1.41	1.57	0	0	0	not significant
2176	WANG_ESOPHAGUS_CANCER_VS_NORMAL_DN	-1.41	1.57	0	0	0	not significant
2177	HSIAO_LIVER_SPECIFIC_GENES	-1.41	1.56	0	0	0	not significant
2178	IL21_UP.V1_UP	-1.41	1.52	0	0	0	not significant
2179	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	-1.41	1.49	0	0	0	not significant
2180	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP	-1.41	1.46	0	0	0	not significant
2181	GO_ORGANIC_HYDROXY_COMPOUND_CATABOLIC_PROCESS	-1.41	1.43	0	0	0	not significant
2182	GO_REGULATION_OF_MUSCLE_CONTRACTION	-1.41	1.40	0	0	0	not significant
2183	GO_RESPONSE_TO_AMMONIUM_ION	-1.41	1.40	0	0	0	not significant
2184	KEGG_GAP_JUNCTION	-1.41	1.37	0	0	0	not significant
2185	HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	-1.41	1.36	0	0	0	not significant
2186	PID_CDC42_PATHWAY	-1.41	1.35	0	0	0	not significant
2187	SHEPARD_BMYB_TARGETS	-1.41	1.35	0	0	0	not significant
2188	GO_CHROMOSOME_SEPARATION	-1.41	1.34	0	0	0	not significant
2189	GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	-1.41	1.32	0	0	0	not significant
2190	REACTOME_TRANSLOCATION_OF_SLC2A4_GLUT4_TO_THE_PLASMA_ME	-1.41	1.29	0	0	0	not significant
2191	GO_CARDIAC_CELL_DEVELOPMENT	-1.41	1.28	0	0	0	not significant
2192	AMIT_EGF_RESPONSE_480_MCF10A	-1.41	1.27	0	0	0	not significant
2193	REACTOME_EPH_EPHRIN_SIGNALING	-1.41	1.27	0	0	0	not significant
2194	GO_BODY_MORPHOGENESIS	-1.41	1.26	0	0	0	not significant
2195	PID_IL12_2PATHWAY	-1.41	1.25	0	0	0	not significant
2196	GO_ALCOHOL_CATABOLIC_PROCESS	-1.41	1.21	0	0	0	not significant
2197	GO_REGULATION_OF_PROTEIN_MATURATION	-1.41	1.21	0	0	0	not significant
2198	BROWNE_HCMV_INFECTION_6HR_UP	-1.41	1.20	0	0	0	not significant
2199	BURTON_ADIPOGENESIS_PEAK_AT_8HR	-1.41	1.19	0	0	0	not significant
2200	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP	-1.41	1.19	0	0	0	not significant
2201	GO_NUCLEAR_ENVELOPE_REASSEMBLY	-1.41	1.18	0	0	0	not significant
2202	GO_POSITIVE_REGULATION_OF_UBIQUITIN_PROTEIN_TRANSFERASE_AC	-1.41	1.18	0	0	0	not significant
2203	REACTOME_BMAL1:CLOCK_NPAS2_ACTIVATES_CIRCADIAN_GENE_EXPR	-1.41	1.17	0	0	0	not significant
2204	BIOCARTA_AKAP95_PATHWAY	-1.41	1.15	0	0	0	not significant
2205	GO_MICROVILLUS_ORGANIZATION	-1.41	1.15	0	0	0	not significant
2206	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_OX	-1.41	1.14	0	0	0	not significant
2207	GO_SKELETAL_MUSCLE_TISSUE_REGENERATION	-1.41	1.12	0	0	0	not significant
2208	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQO_IN_WS	-1.41	1.10	0	0	0	not significant
2209	GO_PROTEIN_KINASE_A_REGULATORY_SUBUNIT_BINDING	-1.41	1.08	0	0	0	not significant
2210	GO_RESPONSE_TO_MORPHINE	-1.41	1.08	0	0	0	not significant
2211	HOFMANN_CELL_LYMPHOMA_DN	-1.41	1.08	0	0	0	not significant
2212	DACOSTA_ERCC3_ALLELE_XPCS_VS_TTD_UP	-1.41	1.05	0	0	0	not significant
2213	GO_NUCLEAR_LOCALIZATION_SEQUENCE_BINDING	-1.41	1.05	0	0	0	not significant
2214	BIOCARTA_PPARG_PATHWAY	-1.41	1.04	0	0	0	not significant
2215	GO_CARBON_NITROGEN_LYASE_ACTIVITY	-1.41	1.03	0	0	0	not significant
2216	GO_NEGATIVE_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	-1.41	1.02	0	0	0	not significant
2217	GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_MEMBRA	-1.41	1.02	0	0	0	not significant
2218	GO_POSITIVE_REGULATION_OF_MONOOXYGENASE_ACTIVITY	-1.41	1.02	0	0	0	not significant
2219	PID_INTEGRIN_A9B1_PATHWAY	-1.41	1.01	0	0	0	not significant
2220	GO_NUCLEAR_POLYADENYLATION_DEPENDENT_TRNA_CATABOLIC_PRO	-1.41	0.99	0	0	0	not significant
2221	GO_ADULT_HEART_DEVELOPMENT	-1.41	0.97	0	0	0	not significant
2222	GO_MITOCHONDRIAL_ACETYL_COA_BIOSYNTHETIC_PROCESS_FROM_P	-1.41	0.97	0	0	0	not significant
2223	GO_REGULATION_OF_CARDIAC_MUSCLE_ADAPTATION	-1.41	0.97	0	0	0	not significant
2224	GO_POSITIVE_REGULATION_OF_MONOCYTE_CHEMOTAXIS	-1.41	0.96	0	0	0	not significant
2225	OXFORD_RALA_TARGETS_DN	-1.41	0.96	0	0	0	not significant
2226	SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_DN	-1.41	0.96	0	0	0	not significant
2227	GO_TOXIN_METABOLIC_PROCESS	-1.41	0.94	0	0	0	not significant
2228	OHASHI_AURKA_TARGETS	-1.41	0.93	0	0	0	not significant
2229	GO_FEMALE_MEIOSIS_I	-1.41	0.92	0	0	0	not significant
2230	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	-1.41	0.92	0	0	0	not significant
2231	REACTOME_WAX_AND_PLASMALOGEN_BIOSYNTHESIS	-1.41	0.92	0	0	0	not significant
2232	GO_HISTONE_H4_R3_METHYLATION	-1.41	0.90	0	0	0	not significant
2233	ACEVEDO_LIVER_CANCER_UP	-1.40	4.00	0	0	0	not significant
2234	CUI_TCF21_TARGETS_2_UP	-1.40	4.00	0	0	0	not significant
2235	GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	-1.40	4.00	0	0	0	not significant
2236	GO_MRNA_METABOLIC_PROCESS	-1.40	4.00	0	0	0	not significant
2237	YANG_BCL3_TARGETS_UP	-1.40	2.43	0	0	0	not significant
2238	NABA_MATRISOME_ASSOCIATED	-1.40	2.41	0	0	0	not significant
2239	ENK_UV_RESPONSE_EPIDERMIS_UP	-1.40	2.40	0	0	0	not significant
2240	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN	-1.40	2.00	0	0	0	not significant
2241	GO_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-1.40	1.80	0	0	0	not significant
2242	REACTOME_REGULATION_OF_LIPID_METABOLISM_BY_PEROXISOME_PR	-1.40	1.73	0	0	0	not significant
2243	SMITH_TERT_TARGETS_DN	-1.40	1.58	0	0	0	not significant
2244	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP	-1.40	1.53	0	0	0	not significant
2245	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_OR_POL	-1.40	1.53	0	0	0	not significant
2246	DER_IFN_ALPHA_RESPONSE_UP	-1.40	1.52	0	0	0	not significant
2247	GO_VESICLE_TARGETING_TO_FROM_OR_WITHIN_GOLGI	-1.40	1.44	0	0	0	not significant
2248	SUNG_METASTASIS_STROMA_UP	-1.40	1.42	0	0	0	not significant
2249	GO_DIGESTIVE_SYSTEM_DEVELOPMENT	-1.40	1.39	0	0	0	not significant
2250	GO_CELL_CELL_ADHERENS_JUNCTION	-1.40	1.37	0	0	0	not significant
2251	GO_NEGATIVE_REGULATION_OF_RNA_CATABOLIC_PROCESS	-1.40	1.36	0	0	0	not significant
2252	PID_HEDGEHOG_GLI_PATHWAY	-1.40	1.34	0	0	0	not significant
2253	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN	-1.40	1.27	0	0	0	not significant
2254	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_C	-1.40	1.26	0	0	0	not significant
2255	REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	-1.40	1.23	0	0	0	not significant
2256	GO_CARBOHYDRATE_KINASE_ACTIVITY	-1.40	1.22	0	0	0	not significant
2257	KORKOLA_EMBRYONAL_CARCINOMA_UP	-1.40	1.22	0	0	0	not significant
2258	GO_HOMOTYPIC_CELL_CELL_ADHESION	-1.40	1.21	0	0	0	not significant
2259	KAMMINGA_EZH2_TARGETS	-1.40	1.17	0	0	0	not significant
2260	REACTOME_MICRORNA_MIRNA_BIOGENESIS	-1.40	1.14	0	0	0	not significant
2261	BORLAK_LIVER_CANCER_EGF_UP	-1.40	1.13	0	0	0	not significant
2262	GO_MEMBRANE_REPOLARIZATION	-1.40	1.12	0	0	0	not significant
2263	GO_RESPONSE_TO_PROGESTERONE	-1.40	1.12	0	0	0	not significant
2264	OUYANG_PROSTATE_CANCER_PROGRESSION_DN	-1.40	1.12	0	0	0	not significant
2265	GO_MAIN_AXON	-1.40	1.11	0	0	0	not significant
2266	GO_POTASSIUM_CHANNEL_ACTIVITY	-1.40	1.11	0	0	0	not significant
2267	WANG_METASTASIS_OF_BREAST_CANCER_ESR1_UP	-1.40	1.10	0	0	0	not significant
2268	BIOCARTA_RHO_PATHWAY	-1.40	1.09	0	0	0	not significant
2269	PETRETTO_HEART_MASS_QTL_CIS_DN	-1.40	1.06	0	0	0	not significant
2270	RUAN_RESPONSE_TO_TROGLITAZONE_UP	-1.40	1.06	0	0	0	not significant
2271	MAGRANGEAS_MULTIPLE_MYELOMA_IGG_VS_IGA_DN	-1.40	1.05	0	0	0	not significant
2272	REACTOME_ATTENUATION_PHASE	-1.40	1.05	0	0	0	not significant
2273	GO_SEMI_LUNAR_VALVE_DEVELOPMENT	-1.40	1.04	0	0	0	not significant
2274	NEBEN_AML_WITH_FLT3_OR_NRAS_UP	-1.40	1.03	0	0	0	not significant
2275	GO_CALCIUM_IMPORT_INTO_THE_MITOCHONDRION	-1.40	1.02	0	0	0	not significant
2276	GO_SPINDLE_POLE_CENTROSOME	-1.40	1.02	0	0	0	not significant
2277	GO_ALDEHYDE_LYASE_ACTIVITY	-1.40	1.01	0	0	0	not significant

2278	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN	-1.40	1.01	0	0	0	not significant
2279	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_MONOPOLAR_CELL_POLA	-1.40	1.00	0	0	0	not significant
2280	MAHADEVAN_RESPONSE_TO_MP470_UP	-1.40	1.00	0	0	0	not significant
2281	GO_REGULATION_OF_T_HELPER_2_CELL_DIFFERENTIATION	-1.40	0.99	0	0	0	not significant
2282	NIELSEN_LEIOMYOSARCOMA_UP	-1.40	0.99	0	0	0	not significant
2283	GO_CARBON_NITROGEN_LIGASE_ACTIVITY_WITH_GLUTAMINE_AS_AMID	-1.40	0.98	0	0	0	not significant
2284	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_DN	-1.40	0.97	0	0	0	not significant
2285	TSAI_DNAJB4_TARGETS_UP	-1.40	0.97	0	0	0	not significant
2286	GAVIN_IL2_RESPONSIVE_FOXP3_TARGETS_UP	-1.40	0.96	0	0	0	not significant
2287	GO_PROTEIN_LOCALIZATION_TO_CYTOPLASMIC_STRESS_GRANULE	-1.40	0.96	0	0	0	not significant
2288	GO_NEGATIVE_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	-1.40	0.95	0	0	0	not significant
2289	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_15	-1.40	0.95	0	0	0	not significant
2290	GO_NEGATIVE_REGULATION_OF_CHOLESTEROL_STORAGE	-1.40	0.94	0	0	0	not significant
2291	REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	-1.40	0.94	0	0	0	not significant
2292	GO_DE_NOVO_PYRIMIDINE_NUCLEOBASE_BIOSYNTHETIC_PROCESS	-1.40	0.93	0	0	0	not significant
2293	GO_POSITIVE_REGULATION_OF_BEHAVIOR	-1.40	0.93	0	0	0	not significant
2294	GO_NUCLEAR_IMPORT_SIGNAL_RECEPTOR_ACTIVITY	-1.40	0.92	0	0	0	not significant
2295	GO_PTW_PP1_PHOSPHATASE_COMPLEX	-1.40	0.92	0	0	0	not significant
2296	SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1B	-1.40	0.92	0	0	0	not significant
2297	BIOCARTA_SALMONELLA_PATHWAY	-1.40	0.91	0	0	0	not significant
2298	GO_PROTEIN_INSERTION_INTO_MITOCHONDRIAL_INNER_MEMBRANE	-1.40	0.91	0	0	0	not significant
2299	GO_REGULATION_OF_SECONDARY_HEART_FIELD_CARDIOBLAST_PROL	-1.40	0.90	0	0	0	not significant
2300	CHEN_METABOLIC_SYNDROM_NETWORK	-1.39	4.00	0	0	0	not significant
2301	GO_METAL_ION_TRANSPORT	-1.39	4.00	0	0	0	not significant
2302	GO_PEPTIDE_BIOSYNTHETIC_PROCESS	-1.39	4.00	0	0	0	not significant
2303	GO_RESPONSE_TO_ENDOGENOUS_STIMULUS	-1.39	4.00	0	0	0	not significant
2304	GO_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	-1.39	4.00	0	0	0	not significant
2305	REACTOME_HEMOSTASIS	-1.39	4.00	0	0	0	not significant
2306	GCNP_SHH_UP_LATE.V1_UP	-1.39	2.16	0	0	0	not significant
2307	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP	-1.39	2.03	0	0	0	not significant
2308	GO_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	-1.39	1.89	0	0	0	not significant
2309	GO_GENE_SILENCING_BY_RNA	-1.39	1.88	0	0	0	not significant
2310	LTE2_UP.V1_DN	-1.39	1.88	0	0	0	not significant
2311	GO_RESPONSE_TO_INTERFERON_GAMMA	-1.39	1.81	0	0	0	not significant
2312	GO_ALCOHOL_BIOSYNTHETIC_PROCESS	-1.39	1.80	0	0	0	not significant
2313	HALLMARK_XENOBIOTIC_METABOLISM	-1.39	1.79	0	0	0	not significant
2314	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP	-1.39	1.73	0	0	0	not significant
2315	GO_CELLULAR_RESPONSE_TO_STARVATION	-1.39	1.72	0	0	0	not significant
2316	REACTOME_REGULATION_OF_PLK1_ACTIVITY_AT_G2_M_TRANSITION	-1.39	1.62	0	0	0	not significant
2317	TAKAO_RESPONSE_TO_UVB_RADIATION_UP	-1.39	1.57	0	0	0	not significant
2318	KIM_WT1_TARGETS_12HR_UP	-1.39	1.54	0	0	0	not significant
2319	GO_ACTIVATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVO	-1.39	1.40	0	0	0	not significant
2320	GO_TRANSCRIPTION_FACTOR_TFIID_COMPLEX	-1.39	1.37	0	0	0	not significant
2321	FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	-1.39	1.31	0	0	0	not significant
2322	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	-1.39	1.25	0	0	0	not significant
2323	GO_REGULATION_OF_SODIUM_ION_TRANSPORT	-1.39	1.23	0	0	0	not significant
2324	IRITANI_MAD1_TARGETS_DN	-1.39	1.21	0	0	0	not significant
2325	JOHANSSON_BRAIN_CANCER_EARLY_VS_LATE_DN	-1.39	1.12	0	0	0	not significant
2326	GO_EXOSOME_RNASE_COMPLEX_	-1.39	1.08	0	0	0	not significant
2327	GO_STEROL_HOMEOSTASIS	-1.39	1.07	0	0	0	not significant
2328	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN	-1.39	1.07	0	0	0	not significant
2329	GO_INNER_EAR_RECEPTOR_CELL_DEVELOPMENT	-1.39	1.04	0	0	0	not significant
2330	REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	-1.39	1.04	0	0	0	not significant
2331	GO_XENOBIOTIC_CATABOLIC_PROCESS	-1.39	1.03	0	0	0	not significant
2332	GO_CORECEPTOR_ACTIVITY	-1.39	1.02	0	0	0	not significant
2333	REACTOME_BASIGIN_INTERACTIONS	-1.39	1.02	0	0	0	not significant
2334	GO_NUCLEAR_PORE_OUTER_RING	-1.39	1.01	0	0	0	not significant
2335	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH_GROUP_OF_	-1.39	1.00	0	0	0	not significant
2336	GO_NEGATIVE_REGULATION_OF_NECROTIC_CELL_DEATH	-1.39	0.99	0	0	0	not significant
2337	GO_RIBONUCLEOSIDE_CATABOLIC_PROCESS	-1.39	0.98	0	0	0	not significant
2338	KYNG_DNA_DAMAGE_BY_4NQO_OR_GAMMA_RADIATION	-1.39	0.97	0	0	0	not significant
2339	GO_CARNITINE_SHUTTLE	-1.39	0.96	0	0	0	not significant
2340	GO_CHONDROCYTE_DIFFERENTIATION_INVOLVED_IN_ENDOCHONDRAL_	-1.39	0.96	0	0	0	not significant
2341	GO_F_ACTIN_CAPPING_PROTEIN_COMPLEX	-1.39	0.96	0	0	0	not significant
2342	GO_POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	-1.39	0.96	0	0	0	not significant
2343	GO_GLUCOSE_BINDING	-1.39	0.95	0	0	0	not significant
2344	NAKAYAMA_FGF2_TARGETS	-1.39	0.95	0	0	0	not significant
2345	GO_POSITIVE_REGULATION_OF_PHOSPHOLIPID_BIOSYNTHETIC_PROCE	-1.39	0.93	0	0	0	not significant
2346	GO_PRONUCLEUS	-1.39	0.93	0	0	0	not significant
2347	GO_VESICLE_FUSION_WITH_ENDOPLASMIC_RETICULUM_GOLGI_INTERM	-1.39	0.93	0	0	0	not significant
2348	HO_LIVER_CANCER_VASCULAR_INVASION	-1.39	0.92	0	0	0	not significant
2349	REACTOME_TRIGLYCERIDE_CATABOLISM	-1.39	0.92	0	0	0	not significant
2350	GO_PML_BODY_ORGANIZATION	-1.39	0.91	0	0	0	not significant
2351	GO_CYTOCHROME_B5_REDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	-1.39	0.90	0	0	0	not significant
2352	GO_SNRNA_MODIFICATION	-1.39	0.90	0	0	0	not significant
2353	REACTOME_TRANSLOCATION_OF_ZAP_70_TO_IMMUNOLOGICAL_SYNAP	-1.39	0.89	0	0	0	not significant
2354	GO_PYRIMIDINE_NUCLEOBASE_BIOSYNTHETIC_PROCESS	-1.39	0.86	0	0	0	not significant
2355	BRUINS_UVC_RESPONSE_LATE	-1.38	4.00	0	0	0	not significant
2356	GO_CELLULAR_RESPONSE_TO_HORMONE_STIMULUS	-1.38	4.00	0	0	0	not significant
2357	GO_DIVALENT_INORGANIC_CATION_TRANSPORT	-1.38	4.00	0	0	0	not significant
2358	GO_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	-1.38	4.00	0	0	0	not significant
2359	GRYDER_PAX3FOXO1_ENHANCERS_IN_TADS	-1.38	4.00	0	0	0	not significant
2360	KIM_ALL_DISORDERS_CALB1_CORR_UP	-1.38	4.00	0	0	0	not significant
2361	MARSON_BOUND_BY_E2F4_UNSTIMULATED	-1.38	4.00	0	0	0	not significant
2362	GO_ORGANIC_HYDROXY_COMPOUND_BIOSYNTHETIC_PROCESS	-1.38	2.49	0	0	0	not significant
2363	GO_PHAGOCYTOSIS	-1.38	2.43	0	0	0	not significant
2364	SMID_BREAST_CANCER_LUMINAL_B_DN	-1.38	2.40	0	0	0	not significant
2365	KIM_ALL_DISORDERS_DURATION_CORR_DN	-1.38	2.21	0	0	0	not significant
2366	HALLMARK_MITOTIC_SPINDLE	-1.38	1.73	0	0	0	not significant
2367	GO_REGULATION_OF_VIRAL_LIFE_CYCLE	-1.38	1.70	0	0	0	not significant
2368	GO_REGULATION_OF_CELL_DIVISION	-1.38	1.69	0	0	0	not significant
2369	P53_DN.V1_DN	-1.38	1.64	0	0	0	not significant
2370	KEEN_RESPONSE_TO_ROSIGLITAZONE_DN	-1.38	1.61	0	0	0	not significant
2371	KEGG_PURINE_METABOLISM	-1.51	1.61	1	0	0	Repressed
2372	GO_CARBOHYDRATE_CATABOLIC_PROCESS	-1.38	1.58	0	0	0	not significant
2373	REACTOME_FATTY_ACID_METABOLISM	-1.38	1.58	0	0	0	not significant
2374	GO_CARBON_OXYGEN_LYASE_ACTIVITY	-1.38	1.38	0	0	0	not significant
2375	JOHNSTONE_PARVB_TARGETS_2_UP	-1.38	1.33	0	0	0	not significant
2376	DORN_ADENOVIRUS_INFECTION_24HR_DN	-1.38	1.28	0	0	0	not significant
2377	ZAMORA_NOS2_TARGETS_DN	-1.38	1.27	0	0	0	not significant
2378	GO_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLATION	-1.38	1.26	0	0	0	not significant
2379	GO_ANTIOXIDANT_ACTIVITY	-1.38	1.24	0	0	0	not significant
2380	GO_TELOMERIC_DNA_BINDING	-1.38	1.22	0	0	0	not significant
2381	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_4	-1.38	1.22	0	0	0	not significant
2382	DOANE_BREAST_CANCER_CLASSES_UP	-1.38	1.21	0	0	0	not significant
2383	CHR15Q22	-1.38	1.19	0	0	0	not significant
2384	HU_GENOTOXIC_DAMAGE_24HR	-1.38	1.19	0	0	0	not significant
2385	CHIBA_RESPONSE_TO_TSA	-1.38	1.13	0	0	0	not significant
2386	SU_PANCREAS	-1.38	1.13	0	0	0	not significant

2387	ONGUSAHA_TP53_TARGETS	-1.38	1.09	0	0	0	not significant
2388	GO_STEROID_HORMONE_RECEPTOR_ACTIVITY	-1.38	1.08	0	0	0	not significant
2389	REACTOME_PYRUVATE_METABOLISM	-1.38	1.08	0	0	0	not significant
2390	GO_SIGNAL_SEQUENCE_BINDING	-1.38	1.07	0	0	0	not significant
2391	GO_PINOCYTOSIS	-1.38	1.06	0	0	0	not significant
2392	GO_FEEDING_BEHAVIOR	-1.38	1.05	0	0	0	not significant
2393	GO_POSITIVE_REGULATION_OF_LIPID_LOCALIZATION	-1.38	1.05	0	0	0	not significant
2394	IIZUKA_LIVER_CANCER_PROGRESSION_G1_G2_DN	-1.38	1.05	0	0	0	not significant
2395	LAMB_CCND1_TARGETS	-1.38	1.04	0	0	0	not significant
2396	PID_SYNDECAN_2_PATHWAY	-1.38	1.04	0	0	0	not significant
2397	GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	-1.38	1.03	0	0	0	not significant
2398	HOUSTIS_ROS	-1.38	1.03	0	0	0	not significant
2399	GO_ATP_BIOSYNTHETIC_PROCESS	-1.38	1.02	0	0	0	not significant
2400	GO_NEUROMUSCULAR_PROCESS_CONTROLLING_BALANCE	-1.38	1.02	0	0	0	not significant
2401	SEIDEN_MET_SIGNALING	-1.38	1.02	0	0	0	not significant
2402	GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK_BY_PHOTOPERIOD	-1.38	1.01	0	0	0	not significant
2403	GO_MRNA_MODIFICATION	-1.38	1.01	0	0	0	not significant
2404	GO_PORE_COMPLEX	-1.38	1.00	0	0	0	not significant
2405	GO_ORGAN_OR_TISSUE_SPECIFIC_IMMUNE_RESPONSE	-1.38	0.99	0	0	0	not significant
2406	NOUSHMEHR_GBM_SOMATIC_MUTATED	-1.38	0.99	0	0	0	not significant
2407	CHR2Q36	-1.38	0.98	0	0	0	not significant
2408	GO_FACE_MORPHOGENESIS	-1.38	0.98	0	0	0	not significant
2409	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON	-1.38	0.98	0	0	0	not significant
2410	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMEF	-1.38	0.97	0	0	0	not significant
2411	GO_REGULATION_OF_RNA_POLYMERASE_II_TRANSCRIPTIONAL_PREINIT	-1.38	0.97	0	0	0	not significant
2412	GO_NEGATIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_STRESS_II	-1.38	0.96	0	0	0	not significant
2413	GO_NUCLEOLUS_ORGANIZATION	-1.38	0.96	0	0	0	not significant
2414	GO_RENAL_SYSTEM_VASCULATURE_DEVELOPMENT	-1.38	0.95	0	0	0	not significant
2415	REACTOME_GDP_FUCOSE_BIOSYNTHESIS	-1.38	0.95	0	0	0	not significant
2416	STONER_ESOPHAGEAL_CARCINOGENESIS_DN	-1.38	0.95	0	0	0	not significant
2417	GO_POSITIVE_REGULATION_OF_VACUOLE_ORGANIZATION	-1.38	0.94	0	0	0	not significant
2418	GO_DNA_TOPOISOMERASE_ACTIVITY	-1.38	0.93	0	0	0	not significant
2419	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_CIF	-1.38	0.93	0	0	0	not significant
2420	PID_CONE_PATHWAY	-1.38	0.92	0	0	0	not significant
2421	GO_CATION_TRANSPORTING_ATPASE_COMPLEX	-1.38	0.91	0	0	0	not significant
2422	GO_INTESTINAL_ABSORPTION	-1.38	0.91	0	0	0	not significant
2423	GO_TYPE_I_INTERFERON_BIOSYNTHETIC_PROCESS	-1.38	0.91	0	0	0	not significant
2424	REACTOME_CREB1_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_C	-1.38	0.91	0	0	0	not significant
2425	REACTOME_TELOMERE_EXTENSION_BY_TELOMERASE	-1.38	0.91	0	0	0	not significant
2426	GO_ENOYL_COA_HYDRATASE_ACTIVITY	-1.38	0.90	0	0	0	not significant
2427	GO_FATTY_ACID_BINDING	-1.38	0.89	0	0	0	not significant
2428	GO_ALKALI_METAL_ION_BINDING	-1.38	0.88	0	0	0	not significant
2429	GO_REGULATION_OF_ISOMERASE_ACTIVITY	-1.38	0.88	0	0	0	not significant
2430	REACTOME_CLEC7A_DECTIN_1_INDUCES_NFAT_ACTIVATION	-1.38	0.88	0	0	0	not significant
2431	GO_U4_SNRNP	-1.38	0.87	0	0	0	not significant
2432	REACTOME_DNA_DAMAGE_REVERSAL	-1.38	0.87	0	0	0	not significant
2433	GO_GLOMERULAR_MESANGIUM_DEVELOPMENT	-1.38	0.81	0	0	0	not significant
2434	GO_ADENYL_NUCLEOTIDE_BINDING	-1.37	4.00	0	0	0	not significant
2435	GO_ATPASE_ACTIVITY_COUPLED	-1.37	4.00	0	0	0	not significant
2436	GO_HOMEOSTATIC_PROCESS	-1.37	4.00	0	0	0	not significant
2437	GO_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE	-1.37	4.00	0	0	0	not significant
2438	GO_REGULATION_OF_IMMUNE_RESPONSE	-1.37	4.00	0	0	0	not significant
2439	REACTOME_METABOLISM_OF_CARBOHYDRATES	-1.37	4.00	0	0	0	not significant
2440	MITSIADES_RESPONSE_TO_APLIDIN_DN	-1.37	1.92	0	0	0	not significant
2441	HALLMARK_IL2_STAT5_SIGNALING	-1.37	1.80	0	0	0	not significant
2442	DOANE_RESPONSE_TO_ANDROGEN_UP	-1.37	1.75	0	0	0	not significant
2443	GO_RESPONSE_TO_NUTRIENT	-1.37	1.73	0	0	0	not significant
2444	GO_SPINDLE_ORGANIZATION	-1.37	1.73	0	0	0	not significant
2445	HAMAI_APOPTOSIS_VIA_TRAIL_DN	-1.37	1.73	0	0	0	not significant
2446	GO_NEGATIVE_REGULATION_OF_BINDING	-1.37	1.70	0	0	0	not significant
2447	GO_STEM_CELL_DIFFERENTIATION	-1.37	1.69	0	0	0	not significant
2448	GO_RENAL_SYSTEM_DEVELOPMENT	-1.37	1.64	0	0	0	not significant
2449	LEE_EARLY_T_LYMPHOCYTE_UP	-1.37	1.64	0	0	0	not significant
2450	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION	-1.37	1.63	0	0	0	not significant
2451	SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_UP	-1.37	1.56	0	0	0	not significant
2452	E2F3_UP.V1_DN	-1.37	1.44	0	0	0	not significant
2453	GO_REGULATION_OF_TRANSLATIONAL_INITIATION	-1.37	1.42	0	0	0	not significant
2454	MCCLUNG_CREB1_TARGETS_UP	-1.37	1.30	0	0	0	not significant
2455	GO_REGULATION_OF_WOUND_HEALING	-1.37	1.27	0	0	0	not significant
2456	GO_MACROPHAGE_ACTIVATION	-1.37	1.22	0	0	0	not significant
2457	BURTON_ADIPOGENESIS_2	-1.37	1.18	0	0	0	not significant
2458	GO_BASAL_TRANSCRIPTION_MACHINERY_BINDING	-1.37	1.17	0	0	0	not significant
2459	WARTERS_IR_RESPONSE_5GY	-1.37	1.15	0	0	0	not significant
2460	GO_MRNA_CIS_SPLICING_VIA_SPLICEOSOME	-1.37	1.13	0	0	0	not significant
2461	GO_PLATELET_AGGREGATION	-1.37	1.10	0	0	0	not significant
2462	VILLANUEVA_LIVER_CANCER_KRT19_DN	-1.37	1.10	0	0	0	not significant
2463	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_TELOMERE	-1.37	1.09	0	0	0	not significant
2464	GO_POSITIVE_REGULATION_OF_LIPID_TRANSPORT	-1.37	1.07	0	0	0	not significant
2465	GO_REGULATION_OF_CELLULAR_RESPIRATION	-1.37	1.05	0	0	0	not significant
2466	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED	-1.37	1.05	0	0	0	not significant
2467	GO_REGULATION_OF_T_CELL_CHEMOTAXIS	-1.37	1.04	0	0	0	not significant
2468	GO_CALCIUM_CHANNEL_REGULATOR_ACTIVITY	-1.37	1.03	0	0	0	not significant
2469	GO_REGULATION_OF_MITOCHONDRIAL_TRANSLATION	-1.37	1.03	0	0	0	not significant
2470	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_SCP2_QTL_TRANS	-1.37	1.02	0	0	0	not significant
2471	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_CHROMOSOME	-1.37	1.01	0	0	0	not significant
2472	GO_LAMELLIPODIUM_MORPHOGENESIS	-1.37	1.01	0	0	0	not significant
2473	GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME_TELOMERIC_REGION	-1.37	1.01	0	0	0	not significant
2474	JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_UP	-1.37	1.01	0	0	0	not significant
2475	GO_REGULATION_OF_MYELINATION	-1.37	1.00	0	0	0	not significant
2476	GO_MHC_CLASS_I_PEPTIDE_LOADING_COMPLEX	-1.37	0.99	0	0	0	not significant
2477	GO_NEGATIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	-1.37	0.99	0	0	0	not significant
2478	GO_BRANCHED_CHAIN_AMINO_ACID_CATABOLIC_PROCESS	-1.37	0.98	0	0	0	not significant
2479	GO_REGULATION_OF_MACROPHAGE_ACTIVATION	-1.37	0.97	0	0	0	not significant
2480	GO_CENTROSOME_SEPARATION	-1.37	0.96	0	0	0	not significant
2481	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_	-1.37	0.96	0	0	0	not significant
2482	TERAO_AOX4_TARGETS_SKIN_DN	-1.37	0.96	0	0	0	not significant
2483	GO_HAIR_CELL_DIFFERENTIATION	-1.37	0.95	0	0	0	not significant
2484	GO_TRNA_WOBBLE_BASE_MODIFICATION	-1.37	0.95	0	0	0	not significant
2485	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_BINDING	-1.37	0.95	0	0	0	not significant
2486	MOOTHA_GLYCOGEN_METABOLISM	-1.37	0.95	0	0	0	not significant
2487	BIOCARTA_NO1_PATHWAY	-1.37	0.94	0	0	0	not significant
2488	GO_POSITIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	-1.37	0.94	0	0	0	not significant
2489	GO_RIBOSOMAL_SMALL_SUBUNIT_BINDING	-1.37	0.94	0	0	0	not significant
2490	GO_U4_SNRNA_BINDING	-1.37	0.94	0	0	0	not significant
2491	THUM_MIR21_TARGETS_HEART_DISEASE_DN	-1.37	0.93	0	0	0	not significant
2492	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_RE	-1.37	0.92	0	0	0	not significant
2493	GO_RNA_POLYMERASE_I_COMPLEX	-1.37	0.92	0	0	0	not significant
2494	ZHAN_MULTIPLE_MYELOMA_SPIKED	-1.37	0.92	0	0	0	not significant
2495	GO_CARDIOBLAST_PROLIFERATION	-1.37	0.91	0	0	0	not significant

2496	GO_COMMITMENT_COMPLEX	-1.37	0.90	0	0	0	not significant
2497	GO_PHOSPHATIDYLINOSITOL_3_KINASE_REGULATORY_SUBUNIT_BINDIN	-1.37	0.90	0	0	0	not significant
2498	GO_EMBRYONIC_CAMERA_TYPE_EYE_FORMATION	-1.37	0.89	0	0	0	not significant
2499	GO_POSITIVE_REGULATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	-1.37	0.89	0	0	0	not significant
2500	CHEN_ETV5_TARGETS_SERTOLI	-1.37	0.88	0	0	0	not significant
2501	GO_PEPTIDE_HORMONE_PROCESSING	-1.37	0.87	0	0	0	not significant
2502	GO_TRNA_CYTOSINE_5__METHYLTRANSFERASE_ACTIVITY	-1.37	0.87	0	0	0	not significant
2503	MIKKELSEN_ES_ICP_WITH_H3K27ME3	-1.37	0.87	0	0	0	not significant
2504	GO_NEGATIVE_REGULATION_OF_MACROPHAGE_ACTIVATION	-1.37	0.86	0	0	0	not significant
2505	FEVR_CTNNB1_TARGETS_DN	-1.36	4.00	0	0	0	not significant
2506	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PROCESS	-1.36	4.00	0	0	0	not significant
2507	GO_REGULATION_OF_INNATE_IMMUNE_RESPONSE	-1.36	4.00	0	0	0	not significant
2508	GO_RESPONSE_TO_NITROGEN_COMPOUND	-1.36	4.00	0	0	0	not significant
2509	GO_RIBONUCLEOTIDE_BINDING	-1.36	4.00	0	0	0	not significant
2510	HAMAI_APOPTOSIS_VIA_TRAIL_UP	-1.36	4.00	0	0	0	not significant
2511	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP	-1.36	4.00	0	0	0	not significant
2512	PATIL_LIVER_CANCER	-1.36	4.00	0	0	0	not significant
2513	REACTOME_INFECTIOUS_DISEASE	-1.36	4.00	0	0	0	not significant
2514	REACTOME_TRANSPORT_OF_SMALL_MOLECULES	-1.36	4.00	0	0	0	not significant
2515	NABA_MATRISOME	-1.36	1.91	0	0	0	not significant
2516	VERHAAK_GLIOBLASTOMA_MESENCHYMAL	-1.36	1.86	0	0	0	not significant
2517	UEDA_PERIFERAL_CLOCK	-1.36	1.74	0	0	0	not significant
2518	MARKEY_RB1_ACUTE_LOF_DN	-1.36	1.61	0	0	0	not significant
2519	CHR11P15	-1.36	1.60	0	0	0	not significant
2520	GO_RESPONSE_TO_ACID_CHEMICAL	-1.36	1.60	0	0	0	not significant
2521	GO_PEPTIDE_BINDING	-1.36	1.59	0	0	0	not significant
2522	CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_UP	-1.36	1.55	0	0	0	not significant
2523	GO_KINETOCHORE	-1.36	1.54	0	0	0	not significant
2524	OISHI_CHOLANGIOMA_STEM_CELL_LIKE_DN	-1.36	1.53	0	0	0	not significant
2525	GO_CIRCADIAN_RHYTHM	-1.36	1.50	0	0	0	not significant
2526	REACTOME_PROTEIN_UBIQUITINATION	-1.36	1.48	0	0	0	not significant
2527	GO_REGULATION_OF_CATION_CHANNEL_ACTIVITY	-1.36	1.46	0	0	0	not significant
2528	JIANG_HYPOXIA_CANCER	-1.36	1.35	0	0	0	not significant
2529	REACTOME_DISEASES_OF_GLYCOSYLATION	-1.36	1.30	0	0	0	not significant
2530	GO_CELL_DEATH_IN_RESPONSE_TO_OXIDATIVE_STRESS	-1.36	1.29	0	0	0	not significant
2531	GO_METAPHASE_PLATE_CONGRESSION	-1.36	1.22	0	0	0	not significant
2532	GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	-1.36	1.21	0	0	0	not significant
2533	GO_CELLULAR_RESPONSE_TO_AMMONIUM_ION	-1.36	1.17	0	0	0	not significant
2534	PID_RAS_PATHWAY	-1.36	1.14	0	0	0	not significant
2535	GO_NEGATIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	-1.36	1.13	0	0	0	not significant
2536	GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_I_PROMOTE	-1.36	1.13	0	0	0	not significant
2537	TBK1.DN.48HRS_UP	-1.36	1.12	0	0	0	not significant
2538	GO_CELLULAR_RESPONSE_TO_GLUCOSE_STARVATION	-1.36	1.09	0	0	0	not significant
2539	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN	-1.36	1.08	0	0	0	not significant
2540	DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_UP	-1.36	1.07	0	0	0	not significant
2541	GO_NEUTRAL_AMINO_ACID_TRANSPORT	-1.36	1.06	0	0	0	not significant
2542	GO_REGULATION_OF_ATTACHMENT_OF_SPINDLE_MICROTUBULES_TO_	-1.36	1.05	0	0	0	not significant
2543	SASAI_RESISTANCE_TO_NEOPLASTIC_TRANSFROMATION	-1.36	1.02	0	0	0	not significant
2544	EPPERT_CE_HSC_LSC	-1.36	1.01	0	0	0	not significant
2545	GO_COPPER_ION_TRANSPORT	-1.36	0.98	0	0	0	not significant
2546	GO_T_CELL_RECEPTOR_COMPLEX	-1.36	0.98	0	0	0	not significant
2547	GO_INTERFERON_ALPHA_PRODUCTION	-1.36	0.96	0	0	0	not significant
2548	REACTOME_GLUTATHIONE_CONJUGATION	-1.36	0.96	0	0	0	not significant
2549	REACTOME_PHOSPHORYLATION_SITE_MUTANTS_OF_CTNNB1_ARE_NOT	-1.36	0.95	0	0	0	not significant
2550	ALONSO_METASTASIS_EMT_UP	-1.36	0.93	0	0	0	not significant
2551	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_UP	-1.36	0.93	0	0	0	not significant
2552	GO_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFEREN	-1.36	0.93	0	0	0	not significant
2553	MIKKELSEN_MEF_LCP_WITH_H3K27ME3	-1.36	0.93	0	0	0	not significant
2554	GO_EMBRYONIC_HINDLIMB_MORPHOGENESIS	-1.36	0.92	0	0	0	not significant
2555	KEGG_TRYPTOPHAN_METABOLISM	-1.36	0.92	0	0	0	not significant
2556	STOSSI_RESPONSE_TO_ESTRADIOL	-1.36	0.92	0	0	0	not significant
2557	GLINSKY_CANCER_DEATH_UP	-1.36	0.91	0	0	0	not significant
2558	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYL	-1.36	0.91	0	0	0	not significant
2559	CHR5Q32	-1.36	0.90	0	0	0	not significant
2560	GO_MAINTENANCE_OF_ORGANELLE_LOCATION	-1.36	0.90	0	0	0	not significant
2561	REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES	-1.36	0.90	0	0	0	not significant
2562	REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_7ALPHA	-1.36	0.90	0	0	0	not significant
2563	GO_APOPTOTIC_DNA_FRAGMENTATION	-1.36	0.89	0	0	0	not significant
2564	GO_NEGATIVE_REGULATION_OF_LIPASE_ACTIVITY	-1.36	0.89	0	0	0	not significant
2565	IIZUKA_LIVER_CANCER_PROGRESSION_L0_L1_DN	-1.36	0.89	0	0	0	not significant
2566	REACTOME_CALCINEURIN_ACTIVATES_NFAT	-1.36	0.89	0	0	0	not significant
2567	GO_PYRUVATE_DEHYDROGENASE_ACTIVITY	-1.36	0.88	0	0	0	not significant
2568	GO_ASTROCYTE_PROJECTION	-1.36	0.87	0	0	0	not significant
2569	GO_CELLULAR_RESPONSE_TO_NICOTINE	-1.36	0.87	0	0	0	not significant
2570	GO_INDUCTION_OF_POSITIVE_CHEMOTAXIS	-1.36	0.87	0	0	0	not significant
2571	GO_DE_NOVO_IMP_BIOSYNTHETIC_PROCESS	-1.36	0.86	0	0	0	not significant
2572	LEI_HOXC8_TARGETS_DN	-1.36	0.86	0	0	0	not significant
2573	GO_ESTABLISHMENT_OF_EPITHELIAL_CELL_APICAL_BASAL_POLARITY	-1.36	0.85	0	0	0	not significant
2574	GO_TROPHOBLAST_CELL_MIGRATION	-1.36	0.85	0	0	0	not significant
2575	GO_AMIDINE_LYASE_ACTIVITY	-1.36	0.84	0	0	0	not significant
2576	GO_POSITIVE_REGULATION_OF_CELLULAR_EXTRAVASATION	-1.36	0.83	0	0	0	not significant
2577	REACTOME_G_PROTEIN_GATED_POTASSIUM_CHANNELS	-1.36	0.81	0	0	0	not significant
2578	GO_POSITIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	-1.35	4.00	0	0	0	not significant
2579	GO_REGULATION_OF_PROTEOLYSIS	-1.35	4.00	0	0	0	not significant
2580	GO_PROTEIN_DEPHOSPHORYLATION	-1.35	2.41	0	0	0	not significant
2581	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESEN	-1.35	2.35	0	0	0	not significant
2582	GO_CELLULAR_RESPONSE_TO_LIPID	-1.35	2.31	0	0	0	not significant
2583	REACTOME_NEUTROPHIL_DEGRANULATION	-1.35	2.30	0	0	0	not significant
2584	NFE2L2.V2	-1.35	2.16	0	0	0	not significant
2585	GO_CELL_CORTEX	-1.35	2.12	0	0	0	not significant
2586	GO_PHOSPHATASE_ACTIVITY	-1.35	1.85	0	0	0	not significant
2587	GO_MUSCLE_CONTRACTION	-1.35	1.63	0	0	0	not significant
2588	GO_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	-1.35	1.51	0	0	0	not significant
2589	GO_NEGATIVE_REGULATION_OF_SECRETION	-1.35	1.51	0	0	0	not significant
2590	AKT_UP.V1_UP	-1.35	1.49	0	0	0	not significant
2591	GO_LEARNING	-1.35	1.48	0	0	0	not significant
2592	DER_IFN_BETA_RESPONSE_UP	-1.35	1.46	0	0	0	not significant
2593	SENESE_HDAC2_TARGETS_UP	-1.35	1.46	0	0	0	not significant
2594	RUIZ_TNC_TARGETS_DN	-1.35	1.43	0	0	0	not significant
2595	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP	-1.35	1.37	0	0	0	not significant
2596	GO_CHROMOSOME_LOCALIZATION	-1.35	1.31	0	0	0	not significant
2597	APRELIKOVA_BRCA1_TARGETS	-1.35	1.20	0	0	0	not significant
2598	GO_TRANSCRIPTION_BY_RNA_POLYMERASE_III	-1.35	1.18	0	0	0	not significant
2599	LEE_LIVER_CANCER_MYC_TGFA_UP	-1.35	1.15	0	0	0	not significant
2600	GO_MUSCLE_HYPERTROPHY	-1.35	1.13	0	0	0	not significant
2601	GO_PEPTIDYL_PROLINE_MODIFICATION	-1.35	1.12	0	0	0	not significant
2602	GO_CARGO_RECEPTOR_ACTIVITY	-1.35	1.11	0	0	0	not significant
2603	NATSUME_RESPONSE_TO_INTERFERON_BETA_DN	-1.35	1.11	0	0	0	not significant
2604	PID_CDC42_REG_PATHWAY	-1.35	1.11	0	0	0	not significant

2605	GO_PLASMA_LIPOPROTEIN_PARTICLE_CLEARANCE	-1.35	1.09	0	0	0	not significant
2606	MCBRYAN_PUBERTAL_BREAST_6_7WK_DN	-1.35	1.08	0	0	0	not significant
2607	WHITEHURST_PACLITAXEL_SENSITIVITY	-1.35	1.08	0	0	0	not significant
2608	GO_PEPTIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.35	1.06	0	0	0	not significant
2609	YAMASHITA_LIVER_CANCER_STEM_CELL_DN	-1.35	1.04	0	0	0	not significant
2610	GO_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	-1.35	1.01	0	0	0	not significant
2611	GO_INNER_EAR_AUDITORY_RECEPTOR_CELL_DIFFERENTIATION	-1.35	0.99	0	0	0	not significant
2612	CAFFAREL_RESPONSE_TO_THC_DN	-1.35	0.98	0	0	0	not significant
2613	GO_CONDENSED_NUCLEAR_CHROMOSOME_CENTROMERIC_REGION	-1.35	0.98	0	0	0	not significant
2614	NIELSEN_SYNOVIAL_SARCOMA_DN	-1.35	0.98	0	0	0	not significant
2615	REACTOME_G_PROTEIN_BETA:GAMMA_SIGNALLING	-1.35	0.97	0	0	0	not significant
2616	GO_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	-1.35	0.95	0	0	0	not significant
2617	GO_HISTONE_KINASE_ACTIVITY	-1.35	0.95	0	0	0	not significant
2618	KIM_ALL_DISORDERS_CALB1_CORR_DN	-1.35	0.95	0	0	0	not significant
2619	KASLER_HDAC7_TARGETS_2_DN	-1.35	0.94	0	0	0	not significant
2620	GO_UREA_CYCLE	-1.35	0.92	0	0	0	not significant
2621	GO_MRNA_5_SPLICE_SITE_RECOGNITION	-1.35	0.91	0	0	0	not significant
2622	REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	-1.35	0.91	0	0	0	not significant
2623	GO_DETERMINATION_OF_ADULT_LIFESPAN	-1.35	0.89	0	0	0	not significant
2624	HOLLEMAN_DAUNORUBICIN_ALL_UP	-1.35	0.89	0	0	0	not significant
2625	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN	-1.35	0.89	0	0	0	not significant
2626	GLI1_UP.V1_DN	-1.35	0.88	0	0	0	not significant
2627	GO_CONDENSED_NUCLEAR_CHROMOSOME_KINETOCHORE	-1.35	0.88	0	0	0	not significant
2628	GO_NUCLEAR_PORE_NUCLEAR_BASKET	-1.35	0.88	0	0	0	not significant
2629	GO_PLATELET_DENSE_TUBULAR_NETWORK_MEMBRANE	-1.35	0.88	0	0	0	not significant
2630	TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_DN	-1.35	0.88	0	0	0	not significant
2631	GO_FATTY_ACID_LIGASE_ACTIVITY	-1.35	0.87	0	0	0	not significant
2632	GO_POSITIVE_REGULATION_OF_CELL_PROLIFERATION_INVOLVED_IN_H	-1.35	0.87	0	0	0	not significant
2633	GO_POSITIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	-1.35	0.87	0	0	0	not significant
2634	GO_UV_PROTECTION	-1.35	0.87	0	0	0	not significant
2635	GO_CELLULAR_RESPONSE_TO_CAFFEINE	-1.35	0.86	0	0	0	not significant
2636	GO_NEURON_NEURON_SYNAPTIC_TRANSMISSION	-1.35	0.86	0	0	0	not significant
2637	GO_PROTEIN_OXIDATION	-1.35	0.86	0	0	0	not significant
2638	SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_DN	-1.35	0.86	0	0	0	not significant
2639	GO_CHEMOKINE_BIOSYNTHETIC_PROCESS	-1.35	0.85	0	0	0	not significant
2640	GO_MITOCHONDRIAL_INTERMEMBRANE_SPACE_PROTEIN_TRANSPORTE	-1.35	0.85	0	0	0	not significant
2641	GO_POSITIVE_REGULATION_OF_NON_CANONICAL_WNT_SIGNALING_PAT	-1.35	0.84	0	0	0	not significant
2642	GO_ER_MEMBRANE_INSERTION_COMPLEX	-1.35	0.83	0	0	0	not significant
2643	GO_DEPYRIMIDINATION	-1.35	0.81	0	0	0	not significant
2644	GO_POSITIVE_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	-1.35	0.79	0	0	0	not significant
2645	GO_CATION_TRANSMEMBRANE_TRANSPORT	-1.34	4.00	0	0	0	not significant
2646	GO_CELLULAR_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	-1.34	4.00	0	0	0	not significant
2647	GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	-1.34	4.00	0	0	0	not significant
2648	GO_REGULATION_OF_MITOTIC_CELL_CYCLE	-1.34	4.00	0	0	0	not significant
2649	GRADE_COLON_CANCER_UP	-1.34	4.00	0	0	0	not significant
2650	MARTENS_TRETINOIN_RESPONSE_UP	-1.34	1.97	0	0	0	not significant
2651	GO_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	-1.34	1.80	0	0	0	not significant
2652	GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	-1.34	1.72	0	0	0	not significant
2653	GO_CELLULAR_RESPONSE_TO_CARBOHYDRATE_STIMULUS	-1.34	1.43	0	0	0	not significant
2654	REACTOME_NEGATIVE_EPIGENETIC_REGULATION_OF_RRNA_EXPRESSI	-1.34	1.41	0	0	0	not significant
2655	HALLMARK_PROTEIN_SECRETION	-1.34	1.37	0	0	0	not significant
2656	GO_CONDENSED_CHROMOSOME_CENTROMERIC_REGION	-1.34	1.33	0	0	0	not significant
2657	GO_CELLULAR_COMPONENT_ASSEMBLY_INVOLVED_IN_MORPHOGENES	-1.34	1.25	0	0	0	not significant
2658	PEART_HDAC_PROLIFERATION_CLUSTER_UP	-1.34	1.22	0	0	0	not significant
2659	GO_VESICLE_TARGETING	-1.34	1.21	0	0	0	not significant
2660	LIM_MAMMARY_LUMINAL_MATURE_UP	-1.34	1.21	0	0	0	not significant
2661	GO_REGULATION_OF_VIRAL_TRANSCRIPTION	-1.34	1.20	0	0	0	not significant
2662	GO_VESICLE_COAT	-1.34	1.19	0	0	0	not significant
2663	GO_KINASE_ACTIVATOR_ACTIVITY	-1.34	1.18	0	0	0	not significant
2664	OHGUCHI_LIVER_HNF4A_TARGETS_DN	-1.34	1.17	0	0	0	not significant
2665	REACTOME_RHO_GTPASES_ACTIVATE_PKNS	-1.34	1.15	0	0	0	not significant
2666	DURCHDEWALD_SKIN_CARCINOGENESIS_UP	-1.34	1.13	0	0	0	not significant
2667	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP	-1.34	1.11	0	0	0	not significant
2668	BOYLAN_MULTIPLE_MYELOMA_PCA1_UP	-1.34	1.10	0	0	0	not significant
2669	GO_HIPPOCAMPUS_DEVELOPMENT	-1.34	1.10	0	0	0	not significant
2670	GO_PROTEIN_TRANSMEMBRANE_IMPORT_INTO_INTRACELLULAR_ORGA	-1.34	1.10	0	0	0	not significant
2671	GO_RIBOSOME_BINDING	-1.34	1.09	0	0	0	not significant
2672	GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE	-1.34	1.08	0	0	0	not significant
2673	HEIDENBLAD_AMPLICON_12P11_12_UP	-1.34	1.08	0	0	0	not significant
2674	BIOCARTA_VEGF_PATHWAY	-1.34	1.06	0	0	0	not significant
2675	GO_RESPONSE_TO_AMINO_ACID_STARVATION	-1.34	1.06	0	0	0	not significant
2676	REACTOME_EPHB_MEDIATED_FORWARD_SIGNALING	-1.34	1.03	0	0	0	not significant
2677	GO_POSITIVE_REGULATION_OF_GLIOGENESIS	-1.34	1.01	0	0	0	not significant
2678	GEISS_RESPONSE_TO_DSRNA_UP	-1.34	1.00	0	0	0	not significant
2679	REACTOME_SIGNALING_BY_RETINOIC_ACID	-1.34	0.98	0	0	0	not significant
2680	BIOCARTA_FMLP_PATHWAY	-1.34	0.96	0	0	0	not significant
2681	GO_MHC_PROTEIN_COMPLEX_BINDING	-1.34	0.96	0	0	0	not significant
2682	GO_RESPONSE_TO_LITHIUM_ION	-1.34	0.95	0	0	0	not significant
2683	GO_A_BAND	-1.34	0.93	0	0	0	not significant
2684	GO_RESPONSE_TO_INCREASED_OXYGEN_LEVELS	-1.34	0.92	0	0	0	not significant
2685	KEGG_OLFACTORY_TRANSDUCTION	-1.34	0.92	0	0	0	not significant
2686	GO_REGULATION_OF_HORMONE_METABOLIC_PROCESS	-1.34	0.91	0	0	0	not significant
2687	GO_RESPONSE_TO_FLUID_SHEAR_STRESS	-1.34	0.91	0	0	0	not significant
2688	CAFFAREL_RESPONSE_TO_THC_24HR_3_DN	-1.34	0.89	0	0	0	not significant
2689	GO_ACTIN_MONOMER_BINDING	-1.34	0.89	0	0	0	not significant
2690	GO_REGULATION_OF_HIGH_VOLTAGE_GATED_CALCIUM_CHANNEL_ACT	-1.34	0.89	0	0	0	not significant
2691	GO_CELL_PROLIFERATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	-1.34	0.88	0	0	0	not significant
2692	GO_EPITHELIAL_STRUCTURE_MAINTENANCE	-1.34	0.88	0	0	0	not significant
2693	GO_NEGATIVE_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	-1.34	0.88	0	0	0	not significant
2694	GO_NEGATIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	-1.34	0.88	0	0	0	not significant
2695	GO_RELAXATION_OF_MUSCLE	-1.34	0.88	0	0	0	not significant
2696	BAKER_HEMATOPOIESIS_STAT3_TARGETS	-1.34	0.87	0	0	0	not significant
2697	GO_NONRIBOSOMAL_PEPTIDE_BIOSYNTHETIC_PROCESS	-1.34	0.87	0	0	0	not significant
2698	GO_PROTEASOME_BINDING	-1.34	0.87	0	0	0	not significant
2699	MATTHEWS_SKIN_CARCINOGENESIS_VIA_JUN	-1.34	0.87	0	0	0	not significant
2700	GO_REGULATION_OF_POTASSIUM_ION_IMPORT	-1.34	0.86	0	0	0	not significant
2701	HUNSBERGER_EXERCISE_REGULATED_GENES	-1.34	0.86	0	0	0	not significant
2702	GO_CHOLESTEROL_STORAGE	-1.34	0.85	0	0	0	not significant
2703	GO_NUCLEOTIDE_DIPHOSPHATASE_ACTIVITY	-1.34	0.84	0	0	0	not significant
2704	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_INITIATION_FROM_RN	-1.34	0.84	0	0	0	not significant
2705	GO_DSRNA_TRANSPORT	-1.34	0.83	0	0	0	not significant
2706	GO_MAST_CELL_GRANULE	-1.34	0.83	0	0	0	not significant
2707	GO_POSITIVE_REGULATION_OF_SPINDLE_CHECKPOINT	-1.34	0.83	0	0	0	not significant
2708	GO_RECEPTOR_SERINE_THREONINE_KINASE_BINDING	-1.34	0.83	0	0	0	not significant
2709	REACTOME_HUR_ELAVL1_BINDS_AND_STABILIZES_MRNA	-1.34	0.83	0	0	0	not significant
2710	GO_ATP_DEPENDENT_PEPTIDASE_ACTIVITY	-1.34	0.82	0	0	0	not significant
2711	GO_GLUTATHIONE_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	-1.34	0.82	0	0	0	not significant
2712	GO_NEGATIVE_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	-1.34	0.82	0	0	0	not significant
2713	GO_CELLULAR_RESPONSE_TO_LITHIUM_ION	-1.34	0.81	0	0	0	not significant

2714	GO_MEIOTIC_CELL_CYCLE_CHECKPOINT	-1.34	0.81	0	0	0	not significant
2715	GO_CALCINEURIN_COMPLEX	-1.34	0.80	0	0	0	not significant
2716	GO_COSTAMERE	-1.34	0.80	0	0	0	not significant
2717	MATZUK_IMPLANTATION_AND_UTERINE	-1.34	0.80	0	0	0	not significant
2718	GO_MIRNA_CATABOLIC_PROCESS	-1.34	0.79	0	0	0	not significant
2719	GO_MITOTIC_SPINDLE_MIDZONE_ASSEMBLY	-1.34	0.79	0	0	0	not significant
2720	MIKKELSEN_MCV6_LCP_WITH_H3K27ME3	-1.34	0.77	0	0	0	not significant
2721	GO_ANIMAL_ORGAN_MORPHOGENESIS	-1.33	4.00	0	0	0	not significant
2722	GO_EPITHELIUM_DEVELOPMENT	-1.33	4.00	0	0	0	not significant
2723	GO_TISSUE_MORPHOGENESIS	-1.33	4.00	0	0	0	not significant
2724	GO_TUBE_DEVELOPMENT	-1.33	2.26	0	0	0	not significant
2725	GO_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	-1.33	2.00	0	0	0	not significant
2726	SHAFFER_IRF4_TARGETS_IN_MYELOMA_VS_MATURE_B_LYMPHOCYTE	-1.33	1.59	0	0	0	not significant
2727	PENG_LEUCINE_DEPRIVATION_UP	-1.33	1.37	0	0	0	not significant
2728	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE	-1.33	1.32	0	0	0	not significant
2729	REACTOME_GENE_SILENCING_BY_RNA	-1.33	1.31	0	0	0	not significant
2730	BMI1_DN_MEL18_DN.V1_DN	-1.33	1.25	0	0	0	not significant
2731	PTEN_DN.V1_UP	-1.33	1.25	0	0	0	not significant
2732	GO_COPII_COATED_VESICLE_BUDDING	-1.33	1.23	0	0	0	not significant
2733	GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	-1.33	1.20	0	0	0	not significant
2734	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN	-1.33	1.17	0	0	0	not significant
2735	GO_DNA_GEOMETRIC_CHANGE	-1.33	1.16	0	0	0	not significant
2736	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	-1.33	1.16	0	0	0	not significant
2737	LABBE_TARGETS_OF_TGFB1_AND_WNT3A_DN	-1.33	1.15	0	0	0	not significant
2738	GO_INTRACELLULAR_PROTEIN_TRANSMEMBRANE_TRANSPORT	-1.33	1.13	0	0	0	not significant
2739	ANDERSEN_LIVER_CANCER_KRT19_DN	-1.33	1.09	0	0	0	not significant
2740	GO_FATTY_ACID_TRANSPORT	-1.33	1.08	0	0	0	not significant
2741	REACTOME_DNA_METHYLATION	-1.33	1.08	0	0	0	not significant
2742	OUILLETTE_CLL_13Q14_DELETION_DN	-1.33	1.07	0	0	0	not significant
2743	GO_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	-1.33	1.06	0	0	0	not significant
2744	BILANGES_SERUM_SENSITIVE_VIA_TSC2	-1.33	1.00	0	0	0	not significant
2745	GO_GLIAL_CELL_ACTIVATION	-1.33	0.99	0	0	0	not significant
2746	BEIER_GLIOMA_STEM_CELL_UP	-1.33	0.98	0	0	0	not significant
2747	GO_ACTIN_FILAMENT_DEPOLYMERIZATION	-1.33	0.97	0	0	0	not significant
2748	GO_RESPONSE_TO_TESTOSTERONE	-1.33	0.96	0	0	0	not significant
2749	KEEN_RESPONSE_TO_ROSIGLITAZONE_UP	-1.33	0.95	0	0	0	not significant
2750	GO_POSITIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	-1.33	0.94	0	0	0	not significant
2751	BARIS_THYROID_CANCER_UP	-1.33	0.93	0	0	0	not significant
2752	GO_LOW_DENSITY_LIPOPROTEIN_RECEPTOR_PARTICLE_METABOLIC_P	-1.33	0.91	0	0	0	not significant
2753	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION	-1.33	0.90	0	0	0	not significant
2754	REACTOME_ELASTIC_FIBRE_FORMATION	-1.33	0.90	0	0	0	not significant
2755	GO_LUNG_EPITHELIUM_DEVELOPMENT	-1.33	0.89	0	0	0	not significant
2756	GO_PEPTIDE_ANTIGEN_BINDING	-1.33	0.89	0	0	0	not significant
2757	GO_PHOTOPERIODISM	-1.33	0.88	0	0	0	not significant
2758	HASLINGER_B_CLL_WITH_17P13_DELETION	-1.33	0.88	0	0	0	not significant
2759	GO_REGULATION_OF_ANOIKIS	-1.33	0.87	0	0	0	not significant
2760	GO_AZOLE_TRANSPORT	-1.33	0.86	0	0	0	not significant
2761	GO_SERINE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	-1.33	0.86	0	0	0	not significant
2762	GO_SWR1_COMPLEX	-1.33	0.86	0	0	0	not significant
2763	RAMPON_ENRICHED_LEARNING_ENVIRONMENT_LATE_UP	-1.33	0.84	0	0	0	not significant
2764	GO_LONG_CHAIN_FATTY_ACYL_COA_BIOSYNTHETIC_PROCESS	-1.33	0.83	0	0	0	not significant
2765	KOINUMA_COLON_CANCER_MSI_UP	-1.33	0.83	0	0	0	not significant
2766	GO_BOX_C_D_SNORNP_ASSEMBLY	-1.33	0.82	0	0	0	not significant
2767	GO_IMMUNE_RESPONSE_TO_TUMOR_CELL	-1.33	0.82	0	0	0	not significant
2768	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_RECEPTOR_CATABOLIC_P	-1.33	0.82	0	0	0	not significant
2769	GO_RENAL_SODIUM_ION_TRANSPORT	-1.33	0.82	0	0	0	not significant
2770	GALI_TP53_TARGETS_APOPTOTIC_DN	-1.33	0.81	0	0	0	not significant
2771	GO_KINETOCHORE_MICROTUBULE	-1.33	0.81	0	0	0	not significant
2772	GO_REGULATION_OF_GROWTH_RATE	-1.33	0.81	0	0	0	not significant
2773	MACLACHLAN_BRCA1_TARGETS_DN	-1.33	0.81	0	0	0	not significant
2774	GO_CYTOSKELETAL_ADAPTOR_ACTIVITY	-1.33	0.80	0	0	0	not significant
2775	GO_PROTEIN_SERINE_THREONINE_PHOSPHATASE_INHIBITOR_ACTIVITY	-1.33	0.80	0	0	0	not significant
2776	MAINA_VHL_TARGETS_DN	-1.33	0.80	0	0	0	not significant
2777	GO_RESPONSE_TO_GRANULOCYTE_MACROPHAGE_COLONY_STIMULAT	-1.33	0.79	0	0	0	not significant
2778	GO_POSITIVE_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	-1.33	0.78	0	0	0	not significant
2779	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_HY	-1.33	0.75	0	0	0	not significant
2780	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_UP	-1.33	0.73	0	0	0	not significant
2781	GO_CYTOSKELETAL_PROTEIN_BINDING	-1.32	4.00	0	0	0	not significant
2782	GO_NUCLEOLUS	-1.32	4.00	0	0	0	not significant
2783	ROME_INSULIN_TARGETS_IN_MUSCLE_UP	-1.32	4.00	0	0	0	not significant
2784	GO_DEFENSE_RESPONSE_TO_OTHER_ORGANISM	-1.32	2.39	0	0	0	not significant
2785	GO_ATPASE_ACTIVITY	-1.32	2.35	0	0	0	not significant
2786	GO_RESPONSE_TO_WOUNDING	-1.32	2.32	0	0	0	not significant
2787	GO_TUBE_MORPHOGENESIS	-1.32	2.28	0	0	0	not significant
2788	GO_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.32	2.07	0	0	0	not significant
2789	GO_GUANYL_NUCLEOTIDE_BINDING	-1.32	2.04	0	0	0	not significant
2790	GO_SPINDLE	-1.32	1.94	0	0	0	not significant
2791	GO_REGULATION_OF_PEPTIDASE_ACTIVITY	-1.32	1.93	0	0	0	not significant
2792	GO_GLAND_DEVELOPMENT	-1.32	1.82	0	0	0	not significant
2793	HEDENFALK_BREAST_CANCER_BRCA1_VS_BRCA2	-1.32	1.77	0	0	0	not significant
2794	GO_CELL_SURFACE	-1.32	1.71	0	0	0	not significant
2795	GO_AMIDE_BINDING	-1.32	1.69	0	0	0	not significant
2796	CAIRO_HEPATOBLASTOMA_DN	-1.32	1.62	0	0	0	not significant
2797	LINDGREN_BLADDER_CANCER_WITH_LOH_IN_CHR9Q	-1.32	1.58	0	0	0	not significant
2798	KEGG_CHEMOKINE_SIGNALING_PATHWAY	-1.32	1.55	0	0	0	not significant
2799	GO_STRIATED_MUSCLE_CELL_DIFFERENTIATION	-1.32	1.48	0	0	0	not significant
2800	CHUNG_BLISTER_CYTOTOXICITY_UP	-1.32	1.40	0	0	0	not significant
2801	ESC_J1_UP_LATE.V1_DN	-1.32	1.37	0	0	0	not significant
2802	GO_POSITIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	-1.32	1.35	0	0	0	not significant
2803	GO_SINGLE_STRANDED_DNA_BINDING	-1.32	1.34	0	0	0	not significant
2804	BROWNE_HCMV_INFECTION_48HR_UP	-1.32	1.29	0	0	0	not significant
2805	REACTOME_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	-1.32	1.28	0	0	0	not significant
2806	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	-1.32	1.20	0	0	0	not significant
2807	DER_IFN_GAMMA_RESPONSE_UP	-1.32	1.17	0	0	0	not significant
2808	TBK1.DN.48HRS_DN	-1.32	1.13	0	0	0	not significant
2809	GO_LYMPHOCYTE_MIGRATION	-1.32	1.09	0	0	0	not significant
2810	FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN	-1.32	1.06	0	0	0	not significant
2811	GO_RESPONSE_TO_BRONCHODILATOR	-1.32	1.05	0	0	0	not significant
2812	COATES_MACROPHAGE_M1_VS_M2_DN	-1.32	1.04	0	0	0	not significant
2813	GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_ACTIVITY	-1.32	0.98	0	0	0	not significant
2814	REACTOME_PINK_PARKIN_MEDIATED_MITOPHAGY	-1.32	0.97	0	0	0	not significant
2815	KEGG_MTOR_SIGNALING_PATHWAY	-1.32	0.96	0	0	0	not significant
2816	REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRA	-1.32	0.96	0	0	0	not significant
2817	GO_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	-1.32	0.95	0	0	0	not significant
2818	GO_RNA_STABILIZATION	-1.32	0.95	0	0	0	not significant
2819	REACTOME_MITOCHONDRIAL_CALCIUM_ION_TRANSPORT	-1.32	0.94	0	0	0	not significant
2820	CEBALLOS_TARGETS_OF_TP53_AND_MYC_UP	-1.32	0.93	0	0	0	not significant
2821	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	-1.32	0.91	0	0	0	not significant
2822	GO_RNA_POLYMERASE_II_GENERAL_TRANSCRIPTION_INITIATION_FACTO	-1.32	0.91	0	0	0	not significant

2823	GO_GOLGI_LUMEN	-1.32	0.90	0	0	0	not significant
2824	NOUSHMEHR_GBM_SILENCED_BY_METHYLATION	-1.32	0.90	0	0	0	not significant
2825	GO_FATTY_ACID_DERIVATIVE_BINDING	-1.32	0.89	0	0	0	not significant
2826	GO_CULLIN_FAMILY_PROTEIN_BINDING	-1.32	0.88	0	0	0	not significant
2827	HALMOS_CEBPA_TARGETS_DN	-1.32	0.88	0	0	0	not significant
2828	REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM	-1.32	0.88	0	0	0	not significant
2829	REACTOME_VEGFR2_MEDIATED_CELL_PROLIFERATION	-1.32	0.88	0	0	0	not significant
2830	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH_GROUP_OF_	-1.32	0.87	0	0	0	not significant
2831	GO_REGULATION_OF_CELLULAR_EXTRAVASATION	-1.32	0.87	0	0	0	not significant
2832	BERENJENO_TRANSFORMED_BY_RHOA_REVERSIBLY_DN	-1.32	0.86	0	0	0	not significant
2833	GO_POSITIVE_REGULATION_OF_LIPID_STORAGE	-1.32	0.86	0	0	0	not significant
2834	GO_POSITIVE_REGULATION_OF_TRIGLYCERIDE_BIOSYNTHETIC_PROCE	-1.32	0.86	0	0	0	not significant
2835	GO_RIBOSOMAL_LARGE_SUBUNIT_BINDING	-1.32	0.85	0	0	0	not significant
2836	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGE	-1.32	0.84	0	0	0	not significant
2837	GO_PRENYLTRANSFERASE_ACTIVITY	-1.32	0.84	0	0	0	not significant
2838	CHUANG_OXIDATIVE_STRESS_RESPONSE_UP	-1.32	0.83	0	0	0	not significant
2839	DEMAGALHAES_AGING_DN	-1.32	0.83	0	0	0	not significant
2840	GO_LIPOPHAGY	-1.32	0.83	0	0	0	not significant
2841	GO_SECONDARY_METABOLITE_BIOSYNTHETIC_PROCESS	-1.32	0.82	0	0	0	not significant
2842	BIOCARTA_CDC25_PATHWAY	-1.32	0.81	0	0	0	not significant
2843	GO_CELLULAR_RESPONSE_TO_NITROGEN_STARVATION	-1.32	0.81	0	0	0	not significant
2844	GO_DNA_TOPOLOGICAL_CHANGE	-1.32	0.81	0	0	0	not significant
2845	GO_NEGATIVE_REGULATION_OF_CAMP_DEPENDENT_PROTEIN_KINASE_	-1.32	0.81	0	0	0	not significant
2846	BIOCARTA_FREE_PATHWAY	-1.32	0.80	0	0	0	not significant
2847	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_NITROGENOUS_GROUPS	-1.32	0.80	0	0	0	not significant
2848	BIOCARTA_CACAM_PATHWAY	-1.32	0.79	0	0	0	not significant
2849	GO_NEPHRON_TUBULE_EPITHELIAL_CELL_DIFFERENTIATION	-1.32	0.79	0	0	0	not significant
2850	GO_S_ADENOSYL_L_METHIONINE_BINDING	-1.32	0.79	0	0	0	not significant
2851	PHESSE_TARGETS_OF_APC_AND_MBD2_DN	-1.32	0.78	0	0	0	not significant
2852	GO_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_PROSTATE_GLA	-1.32	0.77	0	0	0	not significant
2853	GO_PRIMARY_ALCOHOL_CATABOLIC_PROCESS	-1.32	0.77	0	0	0	not significant
2854	REACTOME_SHC_RELATED_EVENTS_TRIGGERED_BY_IGF1R	-1.32	0.77	0	0	0	not significant
2855	WANG_CLASSIC_ADIPOGENIC_TARGETS_OF_PPARG	-1.32	0.77	0	0	0	not significant
2856	GO_DEPHOSPHORYLATION_OF_RNA_POLYMERASE_II_C_TERMINAL_DO	-1.32	0.74	0	0	0	not significant
2857	WU_APOPTOSIS_BY_CDKN1A_NOT_VIA_TP53	-1.32	0.74	0	0	0	not significant
2858	GO_CIRCULATORY_SYSTEM_DEVELOPMENT	-1.31	4.00	0	0	0	not significant
2859	GO_ESTABLISHMENT_OF_ORGANELLE_LOCALIZATION	-1.31	4.00	0	0	0	not significant
2860	GO_MOLECULAR_FUNCTION_REGULATOR	-1.31	4.00	0	0	0	not significant
2861	GO_MYELOID_LEUKOCYTE_ACTIVATION	-1.31	4.00	0	0	0	not significant
2862	GO_RESPONSE_TO_BIOTIC_STIMULUS	-1.31	4.00	0	0	0	not significant
2863	GO_CALCIUM_ION_BINDING	-1.31	2.35	0	0	0	not significant
2864	REACTOME_ESR_MEDIATED_SIGNALING	-1.31	1.98	0	0	0	not significant
2865	GO_RUFFLE	-1.31	1.75	0	0	0	not significant
2866	GO_FIBRILLAR_CENTER	-1.31	1.66	0	0	0	not significant
2867	GO_RESPONSE_TO_STARVATION	-1.31	1.57	0	0	0	not significant
2868	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	-1.31	1.55	0	0	0	not significant
2869	GO_INTERACTION_WITH_HOST	-1.31	1.55	0	0	0	not significant
2870	GO_FATTY_ACID_METABOLIC_PROCESS	-1.31	1.44	0	0	0	not significant
2871	MEK_UP.V1_UP	-1.31	1.43	0	0	0	not significant
2872	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM4	-1.31	1.43	0	0	0	not significant
2873	DARWICHE_SKIN_TUMOR_PROMOTER_UP	-1.31	1.35	0	0	0	not significant
2874	GO_CALCIUM_ION_TRANSMEMBRANE_IMPORT_INTO_CYTOSOL	-1.31	1.35	0	0	0	not significant
2875	GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS	-1.31	1.35	0	0	0	not significant
2876	GO_SULFUR_COMPOUND_BINDING	-1.31	1.30	0	0	0	not significant
2877	BROWN_MYELOID_CELL_DEVELOPMENT_UP	-1.31	1.23	0	0	0	not significant
2878	REACTOME_INTERFERON_GAMMA_SIGNALING	-1.31	1.21	0	0	0	not significant
2879	FOSTER_KDM1A_TARGETS_UP	-1.31	1.20	0	0	0	not significant
2880	REACTOME_NONHOMOLOGOUS_END_JOINING_NHEJ	-1.31	1.17	0	0	0	not significant
2881	UEDA_CENTRAL_CLOCK	-1.31	1.17	0	0	0	not significant
2882	GO_RESPONSE_TO_ALKALOID	-1.31	1.14	0	0	0	not significant
2883	ZHU_CMV_ALL_DN	-1.31	1.13	0	0	0	not significant
2884	GO_ATP_DEPENDENT_CHROMATIN_REMODELING	-1.31	1.10	0	0	0	not significant
2885	GO_DNA_PACKAGING_COMPLEX	-1.31	1.10	0	0	0	not significant
2886	HOOI_ST7_TARGETS_DN	-1.31	1.06	0	0	0	not significant
2887	GO_BONE_MORPHOGENESIS	-1.31	1.05	0	0	0	not significant
2888	GO_RENAL_TUBULE_DEVELOPMENT	-1.31	1.05	0	0	0	not significant
2889	GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	-1.31	1.04	0	0	0	not significant
2890	BROWNE_INTERFERON_RESPONSIVE_GENES	-1.31	1.03	0	0	0	not significant
2891	GO_REGULATION_OF_SPINDLE_ORGANIZATION	-1.31	1.03	0	0	0	not significant
2892	REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	-1.31	1.03	0	0	0	not significant
2893	HAHTOLA_SEZARY_SYNDROM_UP	-1.31	1.02	0	0	0	not significant
2894	GENTILE_UV_RESPONSE_CLUSTER_D4	-1.31	1.01	0	0	0	not significant
2895	HU_GENOTOXIN_ACTION_DIRECT_VS_INDIRECT_24HR	-1.31	1.00	0	0	0	not significant
2896	MEISSNER_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3	-1.31	0.98	0	0	0	not significant
2897	GO_POSITIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	-1.31	0.95	0	0	0	not significant
2898	VANDESLUIS_COMMD1_TARGETS_GROUP_3_UP	-1.31	0.95	0	0	0	not significant
2899	GO_REGULATION_OF_MONOOXYGENASE_ACTIVITY	-1.31	0.94	0	0	0	not significant
2900	GUTIERREZ_MULTIPLE_MYELOMA_UP	-1.31	0.94	0	0	0	not significant
2901	GO_EMBRYONIC_CAMERA_TYPE_EYE_DEVELOPMENT	-1.31	0.93	0	0	0	not significant
2902	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	-1.31	0.93	0	0	0	not significant
2903	MODY_HIPPOCAMPUS_NEONATAL	-1.31	0.93	0	0	0	not significant
2904	GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_STABILIZA	-1.31	0.92	0	0	0	not significant
2905	GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RE	-1.31	0.92	0	0	0	not significant
2906	PID_VEGFR1_PATHWAY	-1.31	0.92	0	0	0	not significant
2907	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_HD_MTX_DN	-1.31	0.91	0	0	0	not significant
2908	GO_ANTIBIOTIC_METABOLIC_PROCESS	-1.31	0.91	0	0	0	not significant
2909	WU_HBX_TARGETS_3_UP	-1.31	0.91	0	0	0	not significant
2910	GO_CELL_DEATH_IN_RESPONSE_TO_HYDROGEN_PEROXIDE	-1.31	0.89	0	0	0	not significant
2911	GO_REGULATION_OF_STEROL_TRANSPORT	-1.31	0.88	0	0	0	not significant
2912	GO_CALCIUM_RELEASE_CHANNEL_ACTIVITY	-1.31	0.87	0	0	0	not significant
2913	GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	-1.31	0.87	0	0	0	not significant
2914	GO_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWAY	-1.31	0.87	0	0	0	not significant
2915	GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_T	-1.31	0.84	0	0	0	not significant
2916	REACTOME_UREA_CYCLE	-1.31	0.83	0	0	0	not significant
2917	REACTOME_MASTL_FACILITATES_MITOTIC_PROGRESSION	-1.31	0.81	0	0	0	not significant
2918	REACTOME_RUNX1_REGULATES_ESTROGEN_RECEPTOR_MEDIATED_T	-1.31	0.80	0	0	0	not significant
2919	SA_TRKA_RECEPTOR	-1.31	0.80	0	0	0	not significant
2920	GO_DETECTION_OF_CALCIUM_ION	-1.31	0.79	0	0	0	not significant
2921	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_CYTOSKELETON_POLARIT	-1.31	0.79	0	0	0	not significant
2922	GO_FATTY_ACID_HOMEOSTASIS	-1.31	0.79	0	0	0	not significant
2923	GO_NUCLEOTIDE_SALVAGE	-1.31	0.79	0	0	0	not significant
2924	GO_RETINOL_DEHYDROGENASE_ACTIVITY	-1.31	0.79	0	0	0	not significant
2925	KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	-1.31	0.79	0	0	0	not significant
2926	GO_OXIDATIVE_DNA_DEMETHYLATION	-1.31	0.78	0	0	0	not significant
2927	GO_VINCULIN_BINDING	-1.31	0.78	0	0	0	not significant
2928	REACTOME_PRESYNAPTIC_FUNCTION_OF_KAINATE_RECEPTORS	-1.31	0.78	0	0	0	not significant
2929	GO_POSITIVE_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPRO	-1.31	0.77	0	0	0	not significant
2930	GO_REVERSE_CHOLESTEROL_TRANSPORT	-1.31	0.77	0	0	0	not significant
2931	GO_RIBOSOMAL_PROTEIN_S6_KINASE_ACTIVITY	-1.31	0.77	0	0	0	not significant

2932	GO_SEQUENCE_SPECIFIC_MRNA_BINDING	-1.31	0.77	0	0	0	not significant
2933	GO_DYSTROGLYCAN_BINDING	-1.31	0.76	0	0	0	not significant
2934	GO_POSITIVE_REGULATION_OF_DEACETYLASE_ACTIVITY	-1.31	0.76	0	0	0	not significant
2935	SHIN_B_CELL_LYMPHOMA_CLUSTER_3	-1.31	0.76	0	0	0	not significant
2936	GO_ARACHIDONIC_ACID_SECRETION	-1.31	0.75	0	0	0	not significant
2937	GO_EMBRYONIC_DIGESTIVE_TRACT_DEVELOPMENT	-1.31	0.75	0	0	0	not significant
2938	TSUDA_ALVEOLAR_SOFT_PART_SARCOMA	-1.31	0.75	0	0	0	not significant
2939	GO_7S_RNA_BINDING	-1.31	0.74	0	0	0	not significant
2940	CHR4Q23	-1.31	0.73	0	0	0	not significant
2941	GO_ACTIN_DEPENDENT_ATPASE_ACTIVITY	-1.31	0.73	0	0	0	not significant
2942	GO_REGULATION_OF_REMOVAL_OF_SUPEROXIDE_RADICALS	-1.31	0.73	0	0	0	not significant
2943	REACTOME_ACTIVATION_OF_RAC1_DOWNSTREAM_OF_NMDARS	-1.31	0.73	0	0	0	not significant
2944	GO_ACTIN_FILAMENT_BASED_PROCESS	-1.30	4.00	0	0	0	not significant
2945	GO_DEFENSE_RESPONSE	-1.30	4.00	0	0	0	not significant
2946	GO_ION_TRANSMEMBRANE_TRANSPORT	-1.30	4.00	0	0	0	not significant
2947	GO_REGULATION_OF_CELLULAR_CATABOLIC_PROCESS	-1.30	4.00	0	0	0	not significant
2948	GO_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	-1.30	4.00	0	0	0	not significant
2949	LIU_SOX4_TARGETS_DN	-1.30	2.37	0	0	0	not significant
2950	GO_SUPRAMOLECULAR_FIBER_ORGANIZATION	-1.30	2.26	0	0	0	not significant
2951	WANG_CLIM2_TARGETS_DN	-1.30	1.76	0	0	0	not significant
2952	GO_MUSCLE_TISSUE_DEVELOPMENT	-1.30	1.73	0	0	0	not significant
2953	GO_RESPONSE_TO_PEPTIDE_HORMONE	-1.30	1.71	0	0	0	not significant
2954	SHEPARD_BMYB_MORPHOLINO_UP	-1.30	1.60	0	0	0	not significant
2955	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4	-1.30	1.56	0	0	0	not significant
2956	HALLMARK_APICAL_JUNCTION	-1.30	1.51	0	0	0	not significant
2957	WHITFIELD_CELL_CYCLE_G2	-1.30	1.48	0	0	0	not significant
2958	ALONSO_METASTASIS_UP	-1.30	1.46	0	0	0	not significant
2959	GO_TISSUE_MIGRATION	-1.30	1.42	0	0	0	not significant
2960	GO_PROTEIN_IMPORT	-1.30	1.34	0	0	0	not significant
2961	GROSS_HYPOXIA_VIA_ELK3_AND_HIF1A_UP	-1.30	1.33	0	0	0	not significant
2962	GO_REGULATION_OF_GENE_SILENCING	-1.30	1.31	0	0	0	not significant
2963	ELVIDGE_HYPOXIA_BY_DMOG_UP	-1.30	1.26	0	0	0	not significant
2964	REACTOME_SUMOYLATION	-1.30	1.26	0	0	0	not significant
2965	GO_MRNA_3_END_PROCESSING	-1.30	1.23	0	0	0	not significant
2966	GO_PROTEIN_TYROSINE_PHOSPHATASE_ACTIVITY	-1.30	1.19	0	0	0	not significant
2967	GO_POSITIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	-1.30	1.18	0	0	0	not significant
2968	HALLMARK_MYOGENESIS	-1.30	1.18	0	0	0	not significant
2969	GO_NEGATIVE_REGULATION_OF_PEPTIDE_SECRETION	-1.30	1.17	0	0	0	not significant
2970	GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_P	-1.30	1.17	0	0	0	not significant
2971	DARWICHE_PAPILLOMA_RISK_LOW_UP	-1.30	1.16	0	0	0	not significant
2972	GO_ORGANELLE_MEMBRANE_FUSION	-1.30	1.12	0	0	0	not significant
2973	REACTOME_TELOMERE_MAINTENANCE	-1.30	1.10	0	0	0	not significant
2974	GO_PROTEIN_DEPOLYMERIZATION	-1.30	1.09	0	0	0	not significant
2975	KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	-1.30	1.08	0	0	0	not significant
2976	GO_REGULATION_OF_PLASMA_LIPOPROTEIN_PARTICLE_LEVELS	-1.30	1.06	0	0	0	not significant
2977	GO_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.30	1.05	0	0	0	not significant
2978	LEE_AGING_CEREBELLUM_DN	-1.30	1.05	0	0	0	not significant
2979	REACTOME_SUMOYLATION_OF_CHROMATIN_ORGANIZATION_PROTEINS	-1.30	1.05	0	0	0	not significant
2980	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_DNA_REPAIR_GEN	-1.30	1.05	0	0	0	not significant
2981	ESC_J1_UP_LATE.V1_UP	-1.30	1.04	0	0	0	not significant
2982	CHR7Q32	-1.30	0.97	0	0	0	not significant
2983	REN_BOUND_BY_E2F	-1.30	0.97	0	0	0	not significant
2984	REACTOME_SYNTHESIS_OF_ACTIVE_UBIQUITIN:_ROLES_OF_E1_AND_E2	-1.30	0.96	0	0	0	not significant
2985	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_TERMINATION	-1.30	0.95	0	0	0	not significant
2986	GO_TERTIARY_GRANULE_MEMBRANE	-1.30	0.94	0	0	0	not significant
2987	GO_KINESIN_COMPLEX	-1.30	0.93	0	0	0	not significant
2988	GO_MECHANORECEPTOR_DIFFERENTIATION	-1.30	0.92	0	0	0	not significant
2989	GO_RECEPTOR_CATABOLIC_PROCESS	-1.30	0.91	0	0	0	not significant
2990	PID_HIF2PATHWAY	-1.30	0.90	0	0	0	not significant
2991	LIANG_SILENCED_BY_METHYLATION_2	-1.30	0.89	0	0	0	not significant
2992	GO_POSITIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	-1.30	0.88	0	0	0	not significant
2993	KRASNOSELSKAYA_ILF3_TARGETS_DN	-1.30	0.88	0	0	0	not significant
2994	SCIAN_INVERSED_TARGETS_OF_TP53_AND_TP73_DN	-1.30	0.88	0	0	0	not significant
2995	YAO_HOXA10_TARGETS_VIA_PROGESTERONE_UP	-1.30	0.88	0	0	0	not significant
2996	GO_BETA_CATENIN_TCF_COMPLEX_ASSEMBLY	-1.30	0.87	0	0	0	not significant
2997	GO_SULFUR_COMPOUND_TRANSPORT	-1.30	0.87	0	0	0	not significant
2998	PID_ECADHERIN_STABILIZATION_PATHWAY	-1.30	0.87	0	0	0	not significant
2999	HAHTOLA_SEZARY_SYNDROM_DN	-1.30	0.86	0	0	0	not significant
3000	GO_ICOSANOID_BIOSYNTHETIC_PROCESS	-1.30	0.82	0	0	0	not significant
3001	GO_POSITIVE_REGULATION_OF_INTERFERON_ALPHA_PRODUCTION	-1.30	0.82	0	0	0	not significant
3002	GO_RHYTHMIC_BEHAVIOR	-1.30	0.82	0	0	0	not significant
3003	GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOM	-1.30	0.81	0	0	0	not significant
3004	GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_CATA	-1.30	0.81	0	0	0	not significant
3005	GO_U1_SNRNP	-1.30	0.81	0	0	0	not significant
3006	KIM_LRRC3B_TARGETS	-1.30	0.81	0	0	0	not significant
3007	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_LATE_STAGE_BRA	-1.30	0.81	0	0	0	not significant
3008	REACTOME_SYNTHESIS_OF_VERY_LONG_CHAIN_FATTY_ACYL_COAS	-1.30	0.81	0	0	0	not significant
3009	GHO_ATF5_TARGETS_DN	-1.30	0.80	0	0	0	not significant
3010	GO_DIGESTIVE_TRACT_MORPHOGENESIS	-1.30	0.80	0	0	0	not significant
3011	GO_INCLUSION_BODY_ASSEMBLY	-1.30	0.80	0	0	0	not significant
3012	REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS	-1.30	0.80	0	0	0	not significant
3013	GO_DNA_TOPOISOMERASE_BINDING	-1.30	0.79	0	0	0	not significant
3014	GO_NEGATIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC	-1.30	0.79	0	0	0	not significant
3015	GO_SIGNAL_RECOGNITION_PARTICLE_ENDOPLASMIC_RETICULUM_TAR	-1.30	0.78	0	0	0	not significant
3016	BIOCARTA_DREAM_PATHWAY	-1.30	0.77	0	0	0	not significant
3017	GO_NOTCH_BINDING	-1.30	0.77	0	0	0	not significant
3018	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_	-1.30	0.77	0	0	0	not significant
3019	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_2_BINDIN	-1.30	0.77	0	0	0	not significant
3020	KIM_PTEN_TARGETS_UP	-1.30	0.77	0	0	0	not significant
3021	REACTOME_NEF_MEDIATED_DOWNREGULATION_OF_MHC_CLASS_I_CO	-1.30	0.77	0	0	0	not significant
3022	REACTOME_LOSS_OF_MECP2_BINDING_ABILITY_TO_THE_NCOR_SMRT_	-1.30	0.76	0	0	0	not significant
3023	REACTOME_SYNTHESIS_OF_PYROPHOSPHATES_IN_THE_CYTOSOL	-1.30	0.76	0	0	0	not significant
3024	GO_AXO_DENDRITIC_PROTEIN_TRANSPORT	-1.30	0.75	0	0	0	not significant
3025	GO_CELLULAR_RESPONSE_TO_ALDEHYDE	-1.30	0.75	0	0	0	not significant
3026	GO_NATURAL_KILLER_CELL_DEGRANULATION	-1.30	0.75	0	0	0	not significant
3027	GO_PRE_SNORNP_COMPLEX	-1.30	0.75	0	0	0	not significant
3028	GO_REGULATION_OF_SKELETAL_MUSCLE_ADAPTATION	-1.30	0.75	0	0	0	not significant
3029	KRISHNAN_FURIN_TARGETS_DN	-1.30	0.75	0	0	0	not significant
3030	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_4	-1.30	0.75	0	0	0	not significant
3031	GO_ANNULATE_LAMELLAE	-1.30	0.74	0	0	0	not significant
3032	GO_NEGATIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	-1.30	0.74	0	0	0	not significant
3033	GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_9_SIGNALING_PATHWAY	-1.30	0.74	0	0	0	not significant
3034	REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE	-1.30	0.74	0	0	0	not significant
3035	GO_ESTABLISHMENT_OF_GOLGI_LOCALIZATION	-1.30	0.73	0	0	0	not significant
3036	GO_LACTATE_METABOLIC_PROCESS	-1.30	0.73	0	0	0	not significant
3037	LIU_CDX2_TARGETS_UP	-1.30	0.73	0	0	0	not significant
3038	GO_TRANSCRIPTION_FACTOR_TFIIH_CORE_COMPLEX	-1.30	0.72	0	0	0	not significant
3039	HOLLEMAN_DAUNORUBICIN_B_ALL_UP	-1.30	0.72	0	0	0	not significant
3040	GO_EMBRYONIC_VISCEROCRANIUM_MORPHOGENESIS	-1.30	0.69	0	0	0	not significant

3041	GO_MEMBRANE_ORGANIZATION	-1.29	4.00	0	0	0	not significant
3042	GO_PROTEIN_DIMERIZATION_ACTIVITY	-1.29	4.00	0	0	0	not significant
3043	GO_PROTEIN_HOMODIMERIZATION_ACTIVITY	-1.29	4.00	0	0	0	not significant
3044	GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	-1.29	1.97	0	0	0	not significant
3045	GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCE	-1.29	1.94	0	0	0	not significant
3046	GO_RESPONSE_TO_BACTERIUM	-1.29	1.86	0	0	0	not significant
3047	HUTTMANN_B_CLL_POOR_SURVIVAL_UP	-1.29	1.73	0	0	0	not significant
3048	GO_DEPHOSPHORYLATION	-1.29	1.67	0	0	0	not significant
3049	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP	-1.29	1.65	0	0	0	not significant
3050	GO_RHYTHMIC_PROCESS	-1.29	1.51	0	0	0	not significant
3051	GO_PROTEIN_HOMOOLIGOMERIZATION	-1.29	1.49	0	0	0	not significant
3052	GO_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	-1.29	1.39	0	0	0	not significant
3053	GO_CYTOKINESIS	-1.29	1.30	0	0	0	not significant
3054	GO_REGULATION_OF_PROTEIN_DEPHOSPHORYLATION	-1.29	1.20	0	0	0	not significant
3055	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN	-1.29	1.18	0	0	0	not significant
3056	RPS14_DN.V1_UP	-1.29	1.18	0	0	0	not significant
3057	REACTOME_BIOLOGICAL_OXIDATIONS	-1.29	1.17	0	0	0	not significant
3058	REACTOME_G2_M_DNA_DAMAGE_CHECKPOINT	-1.29	1.17	0	0	0	not significant
3059	PID_P73PATHWAY	-1.29	1.15	0	0	0	not significant
3060	GO_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	-1.29	1.13	0	0	0	not significant
3061	GO_RESPONSE_TO_ORGANOPHOSPHORUS	-1.29	1.10	0	0	0	not significant
3062	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR	-1.29	1.10	0	0	0	not significant
3063	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_UP	-1.29	1.04	0	0	0	not significant
3064	PRAMOONJAGO_SOX4_TARGETS_DN	-1.29	1.04	0	0	0	not significant
3065	CHR12Q23	-1.29	1.03	0	0	0	not significant
3066	GAJATE_RESPONSE_TO_TRABECTEDIN_UP	-1.29	1.02	0	0	0	not significant
3067	BIOCARTA_TCR_PATHWAY	-1.29	0.94	0	0	0	not significant
3068	CERVERA_SDHB_TARGETS_1_UP	-1.29	0.94	0	0	0	not significant
3069	GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DEVELOPMENT	-1.29	0.93	0	0	0	not significant
3070	GO_NEGATIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.29	0.93	0	0	0	not significant
3071	GO_OVULATION_CYCLE	-1.29	0.90	0	0	0	not significant
3072	GO_SKELETAL_MUSCLE_CELL_DIFFERENTIATION	-1.29	0.88	0	0	0	not significant
3073	REACTOME_DISEASES_ASSOCIATED_WITH_O_GLYCOSYLATION_OF_PR	-1.29	0.88	0	0	0	not significant
3074	REACTOME_SIGNALING_BY_FGFR2_IN_DISEASE	-1.29	0.88	0	0	0	not significant
3075	BIOCARTA_INTEGRIN_PATHWAY	-1.29	0.87	0	0	0	not significant
3076	GO_MODULATION_BY_SYMBIONT_OF_HOST_CELLULAR_PROCESS	-1.29	0.87	0	0	0	not significant
3077	PETROVA_PROX1_TARGETS_DN	-1.29	0.87	0	0	0	not significant
3078	GO_POSITIVE_REGULATION_OF_STEROL_TRANSPORT	-1.29	0.85	0	0	0	not significant
3079	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_DN	-1.29	0.85	0	0	0	not significant
3080	XU_AKT1_TARGETS_6HR	-1.29	0.85	0	0	0	not significant
3081	GO_RESPONSE_TO_INTERFERON_BETA	-1.29	0.82	0	0	0	not significant
3082	GO_ATP_DEPENDENT_MICROTUBULE_MOTOR_ACTIVITY	-1.29	0.81	0	0	0	not significant
3083	GRANDVAUX_IRF3_TARGETS_UP	-1.29	0.81	0	0	0	not significant
3084	SINGH_NFE2L2_TARGETS	-1.29	0.81	0	0	0	not significant
3085	GO_KILLING_OF_CELLS_OF_OTHER_ORGANISM	-1.29	0.80	0	0	0	not significant
3086	GO_RENAL_WATER_HOMEOSTASIS	-1.29	0.80	0	0	0	not significant
3087	REACTOME_SEMA3A_PLEXIN_REPULSION_SIGNALING_BY_INHIBITING_INT	-1.29	0.80	0	0	0	not significant
3088	VERRECCHIA_RESPONSE_TO_TGFB1_C3	-1.29	0.79	0	0	0	not significant
3089	MATTIOLI_MGUS_VS_MULTIPLE_MYELOMA	-1.29	0.78	0	0	0	not significant
3090	GO_MUSCLE_HYPERTROPHY_IN_RESPONSE_TO_STRESS	-1.29	0.77	0	0	0	not significant
3091	BIOCARTA_EFP_PATHWAY	-1.29	0.76	0	0	0	not significant
3092	CHR14Q13	-1.29	0.76	0	0	0	not significant
3093	EHRLICH_ICF_SYNDROM_DN	-1.29	0.75	0	0	0	not significant
3094	GO_INTEGRIN_ACTIVATION	-1.29	0.75	0	0	0	not significant
3095	GO_PANCREATIC_JUICE_SECRETION	-1.29	0.75	0	0	0	not significant
3096	JOHANSSON_BRAIN_CANCER_EARLY_VS_LATE_UP	-1.29	0.75	0	0	0	not significant
3097	REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVE	-1.29	0.75	0	0	0	not significant
3098	SHIN_B_CELL_LYMPHOMA_CLUSTER_9	-1.29	0.75	0	0	0	not significant
3099	WANG_RECURRENT_LIVER_CANCER_DN	-1.29	0.75	0	0	0	not significant
3100	GO_SNRNP_BINDING	-1.29	0.74	0	0	0	not significant
3101	KEGG_GRAFT_VERSUS_HOST_DISEASE	-1.29	0.74	0	0	0	not significant
3102	GO_G_PROTEIN_BETA_GAMMA_SUBUNIT_COMPLEX_BINDING	-1.29	0.73	0	0	0	not significant
3103	GO_NEGATIVE_REGULATION_OF_SINGLE_STRANDED_VIRAL_RNA_REPL	-1.29	0.73	0	0	0	not significant
3104	GO_PEPTIDE_ALPHA_N_ACETYLTRANSFERASE_ACTIVITY	-1.29	0.73	0	0	0	not significant
3105	GO_REGULATION_OF_TAU_PROTEIN_KINASE_ACTIVITY	-1.29	0.73	0	0	0	not significant
3106	BIOCARTA_EIF2_PATHWAY	-1.29	0.72	0	0	0	not significant
3107	GO_BARBED_END_ACTIN_FILAMENT_CAPPING	-1.29	0.72	0	0	0	not significant
3108	GO_WD40_REPEAT_DOMAIN_BINDING	-1.29	0.70	0	0	0	not significant
3109	MURAKAMI_UV_RESPONSE_1HR_UP	-1.29	0.70	0	0	0	not significant
3110	DOUGLAS_BMI1_TARGETS_UP	-1.28	4.00	0	0	0	not significant
3111	GO_CATION_TRANSPORT	-1.28	4.00	0	0	0	not significant
3112	GO_CHEMICAL_HOMEOSTASIS	-1.28	4.00	0	0	0	not significant
3113	GO_EXOCYTOSIS	-1.28	4.00	0	0	0	not significant
3114	REACTOME_DISEASE	-1.28	4.00	0	0	0	not significant
3115	GO_REGULATION_OF_CELL_CYCLE_PROCESS	-1.28	2.12	0	0	0	not significant
3116	GO_RESPONSE_TO_TOXIC_SUBSTANCE	-1.28	2.06	0	0	0	not significant
3117	GO_NEGATIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	-1.28	1.88	0	0	0	not significant
3118	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP	-1.28	1.68	0	0	0	not significant
3119	BENPORATH_MYC_TARGETS_WITH_EBOX	-1.28	1.65	0	0	0	not significant
3120	GO_NEGATIVE_REGULATION_OF_TRANSPORT	-1.28	1.61	0	0	0	not significant
3121	GO_AMEBOIDAL_TYPE_CELL_MIGRATION	-1.28	1.43	0	0	0	not significant
3122	GO_CHROMOSOME_CENTROMERIC_REGION	-1.28	1.37	0	0	0	not significant
3123	GO_ACTIN_BINDING	-1.28	1.31	0	0	0	not significant
3124	EGFR_UP.V1_UP	-1.28	1.30	0	0	0	not significant
3125	GO_CELL_CHEMOTAXIS	-1.28	1.30	0	0	0	not significant
3126	GO_MULTI_MULTICELLULAR_ORGANISM_PROCESS	-1.28	1.28	0	0	0	not significant
3127	KYNG_DNA_DAMAGE_DN	-1.28	1.28	0	0	0	not significant
3128	GO_POSITIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	-1.28	1.25	0	0	0	not significant
3129	GO_NEGATIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCAL	-1.28	1.17	0	0	0	not significant
3130	GO_PEPTIDYL_TYROSINE_DEPHOSPHORYLATION	-1.28	1.17	0	0	0	not significant
3131	DARWICHE_PAPILLOMA_RISK_HIGH_UP	-1.28	1.16	0	0	0	not significant
3132	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_12	-1.28	1.07	0	0	0	not significant
3133	GROSS_HYPOXIA_VIA_ELK3_AND_HIF1A_DN	-1.28	1.06	0	0	0	not significant
3134	GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	-1.28	1.04	0	0	0	not significant
3135	GO_REGULATION_OF_GLIOGENESIS	-1.28	1.04	0	0	0	not significant
3136	GO_NEURON_PROJECTION_CYTOPLASM	-1.28	1.03	0	0	0	not significant
3137	REACTOME_HDACS_DEACETYLATE_HISTONES	-1.28	1.02	0	0	0	not significant
3138	REACTOME_SUMOYLATION_OF_RNA_BINDING_PROTEINS	-1.28	1.00	0	0	0	not significant
3139	GO_ER_TO_GOLGI_TRANSPORT_VESICLE_MEMBRANE	-1.28	0.99	0	0	0	not significant
3140	GO_RESPONSE_TO_ANTINEOPLASTIC_AGENT	-1.28	0.99	0	0	0	not significant
3141	MODY_HIPPOCAMPUS_POSTNATAL	-1.28	0.98	0	0	0	not significant
3142	CHR6Q21	-1.28	0.95	0	0	0	not significant
3143	CHR1P22	-1.28	0.94	0	0	0	not significant
3144	DASU_IL6_SIGNALING_UP	-1.28	0.93	0	0	0	not significant
3145	REACTOME_HSF1_DEPENDENT_TRANSACTIVATION	-1.28	0.92	0	0	0	not significant
3146	NIKOLSKY_BREAST_CANCER_12Q13_Q21_AMPLICON	-1.28	0.91	0	0	0	not significant
3147	STAMBOLSKY_TARGETS_OF_MUTATED_TP53_UP	-1.28	0.91	0	0	0	not significant
3148	GO_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.28	0.90	0	0	0	not significant
3149	GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	-1.28	0.90	0	0	0	not significant

3150	BIOCARTA_GPCR_PATHWAY	-1.28	0.89	0	0	0	not significant
3151	GERHOLD_ADIPOGENESIS_UP	-1.28	0.89	0	0	0	not significant
3152	GO_PLATELET_ALPHA_GRANULE_LUMEN	-1.28	0.88	0	0	0	not significant
3153	GO_REGULATION_OF_LAMELLIPODIUM_ORGANIZATION	-1.28	0.88	0	0	0	not significant
3154	EINAV_INTERFERON_SIGNATURE_IN_CANCER	-1.28	0.86	0	0	0	not significant
3155	GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOM	-1.28	0.86	0	0	0	not significant
3156	HEIDENBLAD_AMPLICON_8Q24_UP	-1.28	0.85	0	0	0	not significant
3157	GO_REGULATION_OF_CYTOPLASMIC_TRANSLATION	-1.28	0.84	0	0	0	not significant
3158	REACTOME_SIGNALING_BY_WNT_IN_CANCER	-1.28	0.84	0	0	0	not significant
3159	GO_TRANSCRIPTION_PREINITIATION_COMPLEX_ASSEMBLY	-1.28	0.83	0	0	0	not significant
3160	SU_LIVER	-1.28	0.83	0	0	0	not significant
3161	WANG_RECURRENT_LIVER_CANCER_UP	-1.28	0.83	0	0	0	not significant
3162	GO_CLATHRIN_VESICLE_COAT	-1.28	0.82	0	0	0	not significant
3163	REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	-1.28	0.81	0	0	0	not significant
3164	CEBALLOS_TARGETS_OF_TP53_AND_MYC_DN	-1.28	0.80	0	0	0	not significant
3165	BIOCARTA_NGF_PATHWAY	-1.28	0.79	0	0	0	not significant
3166	GO_INACTIVATION_OF_MAPK_ACTIVITY	-1.28	0.79	0	0	0	not significant
3167	GO_MUSCLE_FIBER_DEVELOPMENT	-1.28	0.78	0	0	0	not significant
3168	GO_CRANIAL_NERVE_DEVELOPMENT	-1.28	0.77	0	0	0	not significant
3169	GO_FEMALE_MEIOTIC_NUCLEAR_DIVISION	-1.28	0.77	0	0	0	not significant
3170	GO_PHOTORECEPTOR_INNER_SEGMENT	-1.28	0.77	0	0	0	not significant
3171	LI_ADIPOGENESIS_BY_ACTIVATED_PPARG	-1.28	0.77	0	0	0	not significant
3172	YANG_BREAST_CANCER_ESR1_BULK_DN	-1.28	0.77	0	0	0	not significant
3173	GO_MICRO_RIBONUCLEOPROTEIN_COMPLEX	-1.28	0.76	0	0	0	not significant
3174	GO_MYELIN_MAINTENANCE	-1.28	0.76	0	0	0	not significant
3175	WANG_LSD1_TARGETS_UP	-1.28	0.76	0	0	0	not significant
3176	KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	-1.28	0.75	0	0	0	not significant
3177	WHITESIDE_CISPLATIN_RESISTANCE_UP	-1.28	0.75	0	0	0	not significant
3178	GO_MITOCHONDRIAL_RNA_CATABOLIC_PROCESS	-1.28	0.74	0	0	0	not significant
3179	VALK_AML_CLUSTER_13	-1.28	0.74	0	0	0	not significant
3180	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_CHROMATIN	-1.28	0.73	0	0	0	not significant
3181	GO_MAP_KINASE_PHOSPHATASE_ACTIVITY	-1.28	0.73	0	0	0	not significant
3182	GO_REGULATION_OF_DIGESTIVE_SYSTEM_PROCESS	-1.28	0.73	0	0	0	not significant
3183	GO_TRNA_SPECIFIC_ADENOSINE_DEAMINASE_ACTIVITY	-1.28	0.73	0	0	0	not significant
3184	GO_WIDE_PORE_CHANNEL_ACTIVITY	-1.28	0.73	0	0	0	not significant
3185	REACTOME_CREB1_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_	-1.28	0.73	0	0	0	not significant
3186	GO_EOSINOPHIL_ACTIVATION	-1.28	0.72	0	0	0	not significant
3187	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP	-1.28	0.72	0	0	0	not significant
3188	GO_NEGATIVE_REGULATION_OF_GLUCOSE_TRANSMEMBRANE_TRANSP	-1.28	0.71	0	0	0	not significant
3189	GO_SMOOTH_MUSCLE_TISSUE_DEVELOPMENT	-1.28	0.70	0	0	0	not significant
3190	CERVERA_SDHB_TARGETS_1_DN	-1.28	0.69	0	0	0	not significant
3191	GO_BEHAVIORAL_RESPONSE_TO_COCAINE	-1.28	0.69	0	0	0	not significant
3192	REACTOME_SYNTHESIS_OF_KETONE_BODIES	-1.28	0.69	0	0	0	not significant
3193	GO_REGULATION_OF_MICROGLIAL_CELL_ACTIVATION	-1.28	0.68	0	0	0	not significant
3194	GO_REGULATION_BY_VIRUS_OF_VIRAL_PROTEIN_LEVELS_IN_HOST_CE	-1.28	0.67	0	0	0	not significant
3195	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP	-1.27	4.00	0	0	0	not significant
3196	GO_ION_TRANSPORT	-1.27	4.00	0	0	0	not significant
3197	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_TP53	-1.27	2.03	0	0	0	not significant
3198	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3	-1.27	2.00	0	0	0	not significant
3199	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN	-1.27	1.88	0	0	0	not significant
3200	GO_IMMUNE_EFFECTOR_PROCESS	-1.27	1.74	0	0	0	not significant
3201	DAIRKEE_TERT_TARGETS_UP	-1.27	1.67	0	0	0	not significant
3202	GO_CELLULAR_RESPONSE_TO_DRUG	-1.27	1.66	0	0	0	not significant
3203	GO_MITOTIC_NUCLEAR_DIVISION	-1.27	1.55	0	0	0	not significant
3204	GO_PHOSPHORIC_ESTER_HYDROLASE_ACTIVITY	-1.27	1.37	0	0	0	not significant
3205	GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_DN	-1.27	1.34	0	0	0	not significant
3206	GO_MIDBODY	-1.27	1.23	0	0	0	not significant
3207	GO_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	-1.27	1.23	0	0	0	not significant
3208	GO_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	-1.27	1.21	0	0	0	not significant
3209	PRC2_EZH2_UP.V1_UP	-1.27	1.20	0	0	0	not significant
3210	SASSON_RESPONSE_TO_FORSKOLIN_UP	-1.27	1.20	0	0	0	not significant
3211	GO_ORGANELLE_FUSION	-1.27	1.12	0	0	0	not significant
3212	GO_ENDOTHELIAL_CELL_MIGRATION	-1.27	1.11	0	0	0	not significant
3213	GO_HISTONE_DEACETYLASE_BINDING	-1.27	1.10	0	0	0	not significant
3214	WIERENGA_STAT5A_TARGETS_GROUP1	-1.27	1.05	0	0	0	not significant
3215	P53_DN.V2_DN	-1.27	1.03	0	0	0	not significant
3216	TOOKER_GEMCITABINE_RESISTANCE_UP	-1.27	1.00	0	0	0	not significant
3217	GO_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS	-1.27	0.99	0	0	0	not significant
3218	CHR9Q33	-1.27	0.98	0	0	0	not significant
3219	COLDREN_GEFITINIB_RESISTANCE_UP	-1.27	0.97	0	0	0	not significant
3220	KAUFFMANN_MELANOMA_RELAPSE_UP	-1.27	0.96	0	0	0	not significant
3221	GO_NEUROMUSCULAR_PROCESS	-1.27	0.94	0	0	0	not significant
3222	PTEN_DN.V1_DN	-1.27	0.94	0	0	0	not significant
3223	GO_MICROBODY_MEMBRANE	-1.27	0.93	0	0	0	not significant
3224	LUCAS_HNF4A_TARGETS_UP	-1.27	0.92	0	0	0	not significant
3225	KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	-1.27	0.89	0	0	0	not significant
3226	ZHU_CMV_24_HR_DN	-1.27	0.89	0	0	0	not significant
3227	BARRIER_COLON_CANCER_RECURRENCE_UP	-1.27	0.88	0	0	0	not significant
3228	GO_HEAD_MORPHOGENESIS	-1.27	0.86	0	0	0	not significant
3229	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYME	-1.27	0.86	0	0	0	not significant
3230	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRAN	-1.27	0.85	0	0	0	not significant
3231	PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_UP	-1.27	0.84	0	0	0	not significant
3232	CHR12Q14	-1.27	0.83	0	0	0	not significant
3233	GO_POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	-1.27	0.83	0	0	0	not significant
3234	GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	-1.27	0.83	0	0	0	not significant
3235	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	-1.27	0.83	0	0	0	not significant
3236	GO_FATTY_ACYL_COA_BINDING	-1.27	0.81	0	0	0	not significant
3237	GO_MEMBRANE_RAFT_ORGANIZATION	-1.27	0.81	0	0	0	not significant
3238	GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_I_PROM	-1.27	0.81	0	0	0	not significant
3239	GO_POTASSIUM_CHANNEL_COMPLEX	-1.27	0.80	0	0	0	not significant
3240	OSADA_ASCL1_TARGETS_UP	-1.27	0.80	0	0	0	not significant
3241	GO_NEURON_CELLULAR_HOMEOSTASIS	-1.27	0.79	0	0	0	not significant
3242	GO_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_	-1.27	0.79	0	0	0	not significant
3243	GO_SUMO_BINDING	-1.27	0.79	0	0	0	not significant
3244	REACTOME_NON_INTEGRIN_MEMBRANE_ECM_INTERACTIONS	-1.27	0.79	0	0	0	not significant
3245	GO_NCRNA_CATABOLIC_PROCESS	-1.27	0.78	0	0	0	not significant
3246	GO_ADENYLYLTRANSFERASE_ACTIVITY	-1.27	0.77	0	0	0	not significant
3247	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_DRUG	-1.27	0.76	0	0	0	not significant
3248	GO_OUTER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	-1.27	0.75	0	0	0	not significant
3249	GO_MITOCHONDRIAL_OUTER_MEMBRANE_TRANSLOCASE_COMPLEX	-1.27	0.74	0	0	0	not significant
3250	GO_POSITIVE_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLA	-1.27	0.74	0	0	0	not significant
3251	GO_POSITIVE_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION	-1.27	0.74	0	0	0	not significant
3252	GO_PTERIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-1.27	0.74	0	0	0	not significant
3253	GO_AP_2_ADAPTOR_COMPLEX_BINDING	-1.27	0.73	0	0	0	not significant
3254	PODAR_RESPONSE_TO_ADAPHOSTIN_DN	-1.27	0.73	0	0	0	not significant
3255	REACTOME_RNF_MUTANTS_SHOW_ENHANCED_WNT_SIGNALING_AND_P	-1.27	0.73	0	0	0	not significant
3256	GO_COPII_COATED_VESICLE_CARGO_LOADING	-1.27	0.72	0	0	0	not significant
3257	GO_REGULATION_OF_PINOCYTOSIS	-1.27	0.72	0	0	0	not significant
3258	KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS_AND_CYCLIC_RGD	-1.27	0.72	0	0	0	not significant

3259	GO_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	-1.27	0.71	0	0	0	not significant
3260	REACTOME_2_LTR_CIRCLE_FORMATION	-1.27	0.71	0	0	0	not significant
3261	REACTOME_METHYLATION	-1.27	0.71	0	0	0	not significant
3262	GO_EPITHELIAL_CELL_FATE_COMMITMENT	-1.27	0.70	0	0	0	not significant
3263	GO_CDP_DIACYLGLYCEROL_BIOSYNTHETIC_PROCESS	-1.27	0.69	0	0	0	not significant
3264	GO_NEGATIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	-1.27	0.69	0	0	0	not significant
3265	GO_SPINDLE_MIDZONE_ASSEMBLY	-1.27	0.69	0	0	0	not significant
3266	GO_BRANCH_ELONGATION_OF_AN_EPITHELIUM	-1.27	0.68	0	0	0	not significant
3267	GO_MEIOTIC_SPINDLE	-1.27	0.68	0	0	0	not significant
3268	GO_SMALL_PROTEIN_ACTIVATING_ENZYME_BINDING	-1.27	0.68	0	0	0	not significant
3269	REACTOME_ACTIVATION_OF_RAS_IN_B_CELLS	-1.27	0.68	0	0	0	not significant
3270	GO_MACROPHAGE_APOPTOTIC_PROCESS	-1.27	0.67	0	0	0	not significant
3271	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	-1.27	0.67	0	0	0	not significant
3272	GO_RAGE_RECEPTOR_BINDING	-1.27	0.67	0	0	0	not significant
3273	GO_RESPONSE_TO_ISOLATION_STRESS	-1.27	0.67	0	0	0	not significant
3274	GO_PROTEIN_NITROSYLATION	-1.27	0.66	0	0	0	not significant
3275	GO_TRANSCRIPTIONAL_PREINITIATION_COMPLEX	-1.27	0.63	0	0	0	not significant
3276	GO_NEGATIVE_REGULATION_OF_MOLECULAR_FUNCTION	-1.26	4.00	0	0	0	not significant
3277	GO_INORGANIC_ION_TRANSMEMBRANE_TRANSPORT	-1.26	2.01	0	0	0	not significant
3278	RODWELL_AGING_KIDNEY_UP	-1.26	1.78	0	0	0	not significant
3279	GO_POLYMERIC_CYTOSKELETAL_FIBER	-1.26	1.76	0	0	0	not significant
3280	GO_BLOOD_VESSEL_MORPHOGENESIS	-1.26	1.56	0	0	0	not significant
3281	RIGGI_EWING_SARCOMA_PROGENITOR_UP	-1.26	1.42	0	0	0	not significant
3282	GO_MEMBRANE_REGION	-1.26	1.41	0	0	0	not significant
3283	GO_CELLULAR_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	-1.26	1.37	0	0	0	not significant
3284	YAMAZAKI_TCEB3_TARGETS_DN	-1.26	1.37	0	0	0	not significant
3285	WALLACE_PROSTATE_CANCER_RACE_UP	-1.26	1.27	0	0	0	not significant
3286	CHR3P21	-1.26	1.25	0	0	0	not significant
3287	PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_DN	-1.26	1.25	0	0	0	not significant
3288	REACTOME_ONCOGENIC_MAPK_SIGNALING	-1.26	1.08	0	0	0	not significant
3289	GO_MULTICELLULAR_ORGANISMAL_SIGNALING	-1.26	1.05	0	0	0	not significant
3290	MILI_PSEUDOPODIA_CHEMOTAXIS_UP	-1.26	1.05	0	0	0	not significant
3291	SEIDEN_ONCOGENESIS_BY_MET	-1.26	1.03	0	0	0	not significant
3292	LANDIS_ERBB2_BREAST_TUMORS_324_UP	-1.26	1.00	0	0	0	not significant
3293	GO_CYTOSKELETON_DEPENDENT_CYTOKINESIS	-1.26	0.98	0	0	0	not significant
3294	GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIA	-1.26	0.98	0	0	0	not significant
3295	MAYBURD_RESPONSE_TO_L663536_DN	-1.26	0.98	0	0	0	not significant
3296	GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY	-1.26	0.94	0	0	0	not significant
3297	GO_ATPASE_REGULATOR_ACTIVITY	-1.26	0.93	0	0	0	not significant
3298	PID_THROMBIN_PAR1_PATHWAY	-1.26	0.93	0	0	0	not significant
3299	BERNARD_PPAPDC1B_TARGETS_DN	-1.26	0.92	0	0	0	not significant
3300	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_DN	-1.26	0.92	0	0	0	not significant
3301	KEGG_TYPE_II_DIABETES_MELLITUS	-1.26	0.91	0	0	0	not significant
3302	GAUSSMANN_MLL_AF4_FUSION_TARGETS_A_DN	-1.26	0.89	0	0	0	not significant
3303	GO_HISTONE_EXCHANGE	-1.26	0.83	0	0	0	not significant
3304	GO_NEGATIVE_REGULATION_OF_TOR_SIGNALING	-1.26	0.83	0	0	0	not significant
3305	HINATA_NFKB_TARGETS_KERATINOCYTE_UP	-1.26	0.83	0	0	0	not significant
3306	GALLUZZI_PERMEABILIZE_MITOCHONDRIA	-1.26	0.82	0	0	0	not significant
3307	GO_NEGATIVE_REGULATION_OF_RNA_SPLICING	-1.26	0.81	0	0	0	not significant
3308	GO_PROTEIN_REFOLDING	-1.26	0.81	0	0	0	not significant
3309	YIH_RESPONSE_TO_ARSENITE_C3	-1.26	0.81	0	0	0	not significant
3310	BROWNE_HCMV_INFECTION_1HR_UP	-1.26	0.80	0	0	0	not significant
3311	GO_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPROUTING_AN	-1.26	0.80	0	0	0	not significant
3312	SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER	-1.26	0.80	0	0	0	not significant
3313	GO_ENDOCRINE_PANCREAS_DEVELOPMENT	-1.26	0.79	0	0	0	not significant
3314	REACTOME_SYNDECAN_INTERACTIONS	-1.26	0.78	0	0	0	not significant
3315	VALK_AML_CLUSTER_11	-1.26	0.78	0	0	0	not significant
3316	CERIBELLI_PROMOTERS_INACTIVE_AND_BOUND_BY_NFY	-1.26	0.77	0	0	0	not significant
3317	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	-1.26	0.77	0	0	0	not significant
3318	GO_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRINSIC_APOPT	-1.26	0.76	0	0	0	not significant
3319	HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_UP	-1.26	0.76	0	0	0	not significant
3320	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_DN	-1.26	0.76	0	0	0	not significant
3321	GO_MYOFIBRIL_ASSEMBLY	-1.26	0.75	0	0	0	not significant
3322	GO_POSITIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PA	-1.26	0.75	0	0	0	not significant
3323	REACTOME_RORA_ACTIVATES_GENE_EXPRESSION	-1.26	0.75	0	0	0	not significant
3324	GO_ACETYLCHOLINE_GATED_CHANNEL_COMPLEX	-1.26	0.74	0	0	0	not significant
3325	GO_FOREBRAIN_NEURON_DIFFERENTIATION	-1.26	0.74	0	0	0	not significant
3326	GO_PSEUDOPODIUM_ORGANIZATION	-1.26	0.74	0	0	0	not significant
3327	GO_POLYAMINE_BIOSYNTHETIC_PROCESS	-1.26	0.73	0	0	0	not significant
3328	GO_TRNA_CATABOLIC_PROCESS	-1.26	0.73	0	0	0	not significant
3329	GO_RESPONSE_TO_CAFFEINE	-1.26	0.72	0	0	0	not significant
3330	GO_MODIFIED_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVI	-1.26	0.71	0	0	0	not significant
3331	GO_RESPONSE_TO_L_GLUTAMATE	-1.26	0.71	0	0	0	not significant
3332	KUROKAWA_LIVER_CANCER_CHEMOTHERAPY_UP	-1.26	0.71	0	0	0	not significant
3333	ZIRN_TRETINOIN_RESPONSE_UP	-1.26	0.70	0	0	0	not significant
3334	GO_CHEMOKINE_C_C_MOTIF_LIGAND_2_SECRETION	-1.26	0.69	0	0	0	not significant
3335	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_HEME_PROTE	-1.26	0.69	0	0	0	not significant
3336	GO_PROSTANOID_BIOSYNTHETIC_PROCESS	-1.26	0.69	0	0	0	not significant
3337	REACTOME_SHC1_EVENTS_IN_EGFR_SIGNALING	-1.26	0.69	0	0	0	not significant
3338	GO_MITOTIC_NUCLEAR_ENVELOPE_REASSEMBLY	-1.26	0.68	0	0	0	not significant
3339	GO_NEGATIVE_REGULATION_OF_PROGRAMMED_NECROTIC_CELL_DEA	-1.26	0.68	0	0	0	not significant
3340	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEOLUS	-1.26	0.68	0	0	0	not significant
3341	GO_POSITIVE_REGULATION_OF_MUSCLE_ADAPTATION	-1.26	0.67	0	0	0	not significant
3342	REACTOME_KETONE_BODY_METABOLISM	-1.26	0.67	0	0	0	not significant
3343	GO_REGULATION_OF_PROTEIN_HETERODIMERIZATION_ACTIVITY	-1.26	0.66	0	0	0	not significant
3344	GO_SODIUM_ION_EXPORT_ACROSS_PLASMA_MEMBRANE	-1.26	0.65	0	0	0	not significant
3345	GO_MAINTENANCE_OF_CENTROSOME_LOCATION	-1.26	0.64	0	0	0	not significant
3346	REACTOME_ACTIVATED_NTRK3_SIGNALS_THROUGH_RAS	-1.26	0.63	0	0	0	not significant
3347	REACTOME_P75NTR_REGULATES_AXONOGENESIS	-1.26	0.63	0	0	0	not significant
3348	GO_L_PHENYLALANINE_CATABOLIC_PROCESS	-1.26	0.62	0	0	0	not significant
3349	GO_REGULATION_OF_CATABOLIC_PROCESS	-1.25	4.00	0	0	0	not significant
3350	MARTINEZ_RB1_TARGETS_UP	-1.25	4.00	0	0	0	not significant
3351	GO_NEGATIVE_REGULATION_OF_CATALYTIC_ACTIVITY	-1.25	2.29	0	0	0	not significant
3352	GO_METHYLATION	-1.25	1.68	0	0	0	not significant
3353	GO_MICROTUBULE	-1.25	1.68	0	0	0	not significant
3354	GO_ACTIVATION_OF_IMMUNE_RESPONSE	-1.25	1.60	0	0	0	not significant
3355	GO_CHROMOSOMAL_REGION	-1.25	1.58	0	0	0	not significant
3356	GO_ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS	-1.25	1.56	0	0	0	not significant
3357	GO_POSITIVE_REGULATION_OF_PROTEOLYSIS	-1.25	1.53	0	0	0	not significant
3358	GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SI	-1.25	1.52	0	0	0	not significant
3359	GO_VIRAL_LIFE_CYCLE	-1.25	1.49	0	0	0	not significant
3360	GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_REMOVAL	-1.25	1.48	0	0	0	not significant
3361	GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	-1.25	1.32	0	0	0	not significant
3362	GO_MRNA_BINDING	-1.25	1.28	0	0	0	not significant
3363	GO_RESPONSE_TO_ALCOHOL	-1.25	1.18	0	0	0	not significant
3364	MASSARWEH_TAMOXIFEN_RESISTANCE_DN	-1.25	1.18	0	0	0	not significant
3365	SHEPARD_CRUSH_AND_BURN_MUTANT_DN	-1.25	1.16	0	0	0	not significant
3366	HALLMARK_KRAS_SIGNALING_UP	-1.25	1.15	0	0	0	not significant
3367	KUMAR_PATHOGEN_LOAD_BY_MACROPHAGES	-1.25	1.12	0	0	0	not significant

3368	RODRIGUES_NTN1_TARGETS_DN	-1.25	1.11	0	0	0	not significant
3369	REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT	-1.25	1.10	0	0	0	not significant
3370	WIERENGA_STAT5A_TARGETS_UP	-1.25	1.10	0	0	0	not significant
3371	GUO_TARGETS_OF_IRS1_AND_IRS2	-1.25	1.08	0	0	0	not significant
3372	GO_POSITIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	-1.25	1.05	0	0	0	not significant
3373	YAMAZAKI_TCEB3_TARGETS_UP	-1.25	1.04	0	0	0	not significant
3374	GO_TISSUE_HOMEOSTASIS	-1.25	1.02	0	0	0	not significant
3375	CHENG_IMPRINTED_BY_ESTRADIOL	-1.25	0.98	0	0	0	not significant
3376	GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME	-1.25	0.98	0	0	0	not significant
3377	KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	-1.25	0.97	0	0	0	not significant
3378	GO_REGULATION_OF_REPRODUCTIVE_PROCESS	-1.25	0.96	0	0	0	not significant
3379	GO_NUCLEOSOME_BINDING	-1.25	0.94	0	0	0	not significant
3380	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN	-1.25	0.92	0	0	0	not significant
3381	GO_NEPHRON_EPITHELIUM_DEVELOPMENT	-1.25	0.91	0	0	0	not significant
3382	ISHIDA_E2F_TARGETS	-1.25	0.86	0	0	0	not significant
3383	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP	-1.25	0.86	0	0	0	not significant
3384	GO_SISTER_CHROMATID_COHESION	-1.25	0.85	0	0	0	not significant
3385	GO_PROTEIN_TYROSINE_SERINE_THREONINE_PHOSPHATASE_ACTIVITY	-1.25	0.84	0	0	0	not significant
3386	REACTOME_CA2PLUS_PATHWAY	-1.25	0.84	0	0	0	not significant
3387	GO_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	-1.25	0.83	0	0	0	not significant
3388	MALONEY_RESPONSE_TO_17AAG_UP	-1.25	0.83	0	0	0	not significant
3389	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_UF	-1.25	0.83	0	0	0	not significant
3390	ZHU_CMV_8_HR_UP	-1.25	0.83	0	0	0	not significant
3391	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP	-1.25	0.82	0	0	0	not significant
3392	PID_RET_PATHWAY	-1.25	0.80	0	0	0	not significant
3393	DORN_ADENOVIRUS_INFECTION_48HR_DN	-1.25	0.79	0	0	0	not significant
3394	GO_ANCHORED_COMPONENT_OF_PLASMA_MEMBRANE	-1.25	0.79	0	0	0	not significant
3395	GO_POSITIVE_CHEMOTAXIS	-1.25	0.79	0	0	0	not significant
3396	GO_RESPONSE_TO_ANESTHETIC	-1.25	0.78	0	0	0	not significant
3397	REACTOME_SUMOYLATION_OF_INTRACELLULAR_RECEPTORS	-1.25	0.78	0	0	0	not significant
3398	KEGG_BUTANOATE_METABOLISM	-1.25	0.77	0	0	0	not significant
3399	GO_POSITIVE_REGULATION_OF_LAMELLIPODIUM_ORGANIZATION	-1.25	0.76	0	0	0	not significant
3400	GO_REGULATION_OF_HELICASE_ACTIVITY	-1.25	0.76	0	0	0	not significant
3401	REACTOME_CARBOXYTERMINAL_POST_TRANSLATIONAL_MODIFICATION	-1.25	0.76	0	0	0	not significant
3402	REACTOME_RHO_GTPASES_ACTIVATE_ROCKS	-1.25	0.76	0	0	0	not significant
3403	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE	-1.25	0.75	0	0	0	not significant
3404	GO_RESPONSE_TO_VITAMIN_D	-1.25	0.75	0	0	0	not significant
3405	GO_ALPHA_LINOLENIC_ACID_METABOLIC_PROCESS	-1.25	0.73	0	0	0	not significant
3406	GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK	-1.25	0.73	0	0	0	not significant
3407	GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATI	-1.25	0.73	0	0	0	not significant
3408	GO_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING	-1.25	0.72	0	0	0	not significant
3409	GO_EYE_PHOTORECEPTOR_CELL_DEVELOPMENT	-1.25	0.72	0	0	0	not significant
3410	GO_NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_IN_ABSENCE_	-1.25	0.72	0	0	0	not significant
3411	GO_REGULATION_OF_MICROTUBULE_DEPOLYMERIZATION	-1.25	0.72	0	0	0	not significant
3412	REACTOME_ZINC_INFLUX_INTO_CELLS_BY_THE_SLC39_GENE_FAMILY	-1.25	0.71	0	0	0	not significant
3413	GO_PROTEIN_KINASE_A_CATALYTIC_SUBUNIT_BINDING	-1.25	0.70	0	0	0	not significant
3414	GO_RESPONSE_TO_PLATELET_DERIVED_GROWTH_FACTOR	-1.25	0.70	0	0	0	not significant
3415	GO_RESPONSE_TO_OLEIC_ACID	-1.25	0.69	0	0	0	not significant
3416	GO_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	-1.25	0.68	0	0	0	not significant
3417	GO_NEGATIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	-1.25	0.68	0	0	0	not significant
3418	GO_PROTEIN_CONTAINING_COMPLEX_REMODELING	-1.25	0.68	0	0	0	not significant
3419	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_DN	-1.25	0.67	0	0	0	not significant
3420	GAUTSCHI_SRC_SIGNALING	-1.25	0.67	0	0	0	not significant
3421	GO_POSITIVE_REGULATION_OF_MONOCYTE_DIFFERENTIATION	-1.25	0.67	0	0	0	not significant
3422	GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHET	-1.25	0.67	0	0	0	not significant
3423	BIOCARTA_RB_PATHWAY	-1.25	0.66	0	0	0	not significant
3424	GO_S_SHAPED_BODY_MORPHOGENESIS	-1.25	0.65	0	0	0	not significant
3425	WORSCHECH_TUMOR_REJECTION_DN	-1.25	0.65	0	0	0	not significant
3426	GO_REGULATION_OF_DNA_CATABOLIC_PROCESS	-1.25	0.64	0	0	0	not significant
3427	REACTOME_PHENYLALANINE_AND_TYROSINE_METABOLISM	-1.25	0.64	0	0	0	not significant
3428	GO_ACTIVATION_INDUCED_CELL_DEATH_OF_T_CELLS	-1.25	0.63	0	0	0	not significant
3429	GO_REGULATION_OF_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_ELE	-1.25	0.63	0	0	0	not significant
3430	GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_REMODELING	-1.25	0.62	0	0	0	not significant
3431	REACTOME_ACTIVATED_NTRK2_SIGNALS_THROUGH_RAS	-1.25	0.62	0	0	0	not significant
3432	GO_ENDOCYTIC_ADAPTOR_ACTIVITY	-1.25	0.60	0	0	0	not significant
3433	PILON_KLF1_TARGETS_DN	-1.24	4.00	0	0	0	not significant
3434	GO_MEMBRANE_PROTEIN_COMPLEX	-1.24	2.14	0	0	0	not significant
3435	GO_REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHOGENESIS	-1.24	2.14	0	0	0	not significant
3436	GO_SECRETION	-1.24	1.92	0	0	0	not significant
3437	WANG_LMO4_TARGETS_DN	-1.24	1.61	0	0	0	not significant
3438	GO_ACTIN_FILAMENT_ORGANIZATION	-1.24	1.52	0	0	0	not significant
3439	GO_REGULATION_OF_BINDING	-1.24	1.50	0	0	0	not significant
3440	GO_SMALL_MOLECULE_CATABOLIC_PROCESS	-1.24	1.43	0	0	0	not significant
3441	GO_REGULATION_OF_MULTI_ORGANISM_PROCESS	-1.24	1.42	0	0	0	not significant
3442	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP	-1.24	1.42	0	0	0	not significant
3443	GO_MUSCLE_ORGAN_DEVELOPMENT	-1.24	1.31	0	0	0	not significant
3444	GO_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	-1.24	1.26	0	0	0	not significant
3445	GO_REGULATION_OF_PROTEIN_STABILITY	-1.24	1.26	0	0	0	not significant
3446	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_UP	-1.24	1.22	0	0	0	not significant
3447	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP	-1.24	1.21	0	0	0	not significant
3448	FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP	-1.24	1.19	0	0	0	not significant
3449	GO_ORGANIC_ANION_TRANSPORT	-1.24	1.18	0	0	0	not significant
3450	GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	-1.24	1.15	0	0	0	not significant
3451	ESC_J1_UP_EARLY.V1_DN	-1.24	1.10	0	0	0	not significant
3452	GO_CELLULAR_RESPONSE_TO_TOXIC_SUBSTANCE	-1.24	1.10	0	0	0	not significant
3453	TIEN_INTESTINE_PROBIOTICS_6HR_DN	-1.24	1.10	0	0	0	not significant
3454	GO_LIPID_HOMEOSTASIS	-1.24	1.01	0	0	0	not significant
3455	LU_AGING_BRAIN_DN	-1.24	1.00	0	0	0	not significant
3456	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP	-1.24	0.94	0	0	0	not significant
3457	GO_PERIKARYON	-1.24	0.93	0	0	0	not significant
3458	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN	-1.24	0.92	0	0	0	not significant
3459	GO_INTEGRIN_BINDING	-1.24	0.89	0	0	0	not significant
3460	GO_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	-1.24	0.89	0	0	0	not significant
3461	GO_MONOSACCHARIDE_BINDING	-1.24	0.88	0	0	0	not significant
3462	GO_ACID_SECRETION	-1.24	0.86	0	0	0	not significant
3463	GO_DRUG_CATABOLIC_PROCESS	-1.24	0.86	0	0	0	not significant
3464	REACTOME_NEGATIVE_REGULATION_OF_MAPK_PATHWAY	-1.24	0.86	0	0	0	not significant
3465	BOSCO_TH1_CYTOTOXIC_MODULE	-1.24	0.84	0	0	0	not significant
3466	GO_INTERLEUKIN_1_PRODUCTION	-1.24	0.84	0	0	0	not significant
3467	REACTOME_DNA_DOUBLE_STRAND_BREAK_RESPONSE	-1.24	0.84	0	0	0	not significant
3468	GO_CARDIAC_VENTRICLE_DEVELOPMENT	-1.24	0.82	0	0	0	not significant
3469	HUTTMANN_B_CLL_POOR_SURVIVAL_DN	-1.24	0.82	0	0	0	not significant
3470	GO_SOMATIC_STEM_CELL_POPULATION_MAINTENANCE	-1.24	0.81	0	0	0	not significant
3471	SESTO_RESPONSE_TO_UV_C2	-1.24	0.81	0	0	0	not significant
3472	GO_CHROMATIN_SILENCING_AT_RDNA	-1.24	0.80	0	0	0	not significant
3473	GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	-1.24	0.80	0	0	0	not significant
3474	CHR7P15	-1.24	0.79	0	0	0	not significant
3475	GO_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	-1.24	0.79	0	0	0	not significant
3476	REACTOME_BASE_EXCISION_REPAIR_AP_SITE_FORMATION	-1.24	0.79	0	0	0	not significant

3477	REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATE	-1.24	0.79	0	0	0	not significant
3478	LABBE_TGFB1_TARGETS_UP	-1.24	0.78	0	0	0	not significant
3479	GO_INORGANIC_ION_IMPORT_ACROSS_PLASMA_MEMBRANE	-1.24	0.77	0	0	0	not significant
3480	BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP	-1.24	0.76	0	0	0	not significant
3481	GO_CELLULAR_RESPONSE_TO_ALKALOID	-1.24	0.76	0	0	0	not significant
3482	GO_DITERPENOID_METABOLIC_PROCESS	-1.24	0.76	0	0	0	not significant
3483	GO_VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	-1.24	0.75	0	0	0	not significant
3484	WEINMANN_ADAPTATION_TO_HYPOXIA_DN	-1.24	0.74	0	0	0	not significant
3485	GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOM	-1.24	0.73	0	0	0	not significant
3486	TOMIDA_METASTASIS_UP	-1.24	0.73	0	0	0	not significant
3487	GO_COPPER_ION_HOMEOSTASIS	-1.24	0.72	0	0	0	not significant
3488	GO_COPII_VESICLE_COAT	-1.24	0.71	0	0	0	not significant
3489	GO_POSITIVE_REGULATION_OF_MRNA_PROCESSING	-1.24	0.71	0	0	0	not significant
3490	GO_VITAMIN_B6_BINDING	-1.24	0.71	0	0	0	not significant
3491	REACTOME_EPHA_MEDIATED_GROWTH_CONE_COLLAPSE	-1.24	0.71	0	0	0	not significant
3492	BIOCARTA_PML_PATHWAY	-1.24	0.70	0	0	0	not significant
3493	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	-1.24	0.70	0	0	0	not significant
3494	VALK_AML_CLUSTER_9	-1.24	0.70	0	0	0	not significant
3495	GO_CELL_CORTEX_REGION	-1.24	0.69	0	0	0	not significant
3496	GO_GLUTATHIONE_PEROXIDASE_ACTIVITY	-1.24	0.69	0	0	0	not significant
3497	GO_M_BAND	-1.24	0.69	0	0	0	not significant
3498	GO_MUSCLE_CELL_CELLULAR_HOMEOSTASIS	-1.24	0.69	0	0	0	not significant
3499	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_MEDIAT	-1.24	0.69	0	0	0	not significant
3500	GO_NEGATIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_	-1.24	0.68	0	0	0	not significant
3501	GO_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_TRANSP	-1.24	0.68	0	0	0	not significant
3502	GO_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY	-1.24	0.68	0	0	0	not significant
3503	GO_CELLULAR_RESPONSE_TO_THYROID_HORMONE_STIMULUS	-1.24	0.67	0	0	0	not significant
3504	GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATION	-1.24	0.67	0	0	0	not significant
3505	GO_REGULATION_OF_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	-1.24	0.67	0	0	0	not significant
3506	LIANG_SILENCED_BY_METHYLATION_DN	-1.24	0.67	0	0	0	not significant
3507	REACTOME_GLUTAMATE_AND_GLUTAMINE_METABOLISM	-1.24	0.67	0	0	0	not significant
3508	GO_TRABECULA_FORMATION	-1.24	0.66	0	0	0	not significant
3509	REACTOME_SYNTHESIS_OF_IP2_IP_AND_INS_IN_THE_CYTOSOL	-1.24	0.66	0	0	0	not significant
3510	IWANAGA_E2F1_TARGETS_NOT_INDUCED_BY_SERUM	-1.24	0.65	0	0	0	not significant
3511	REACTOME_ADP_SIGNALLING_THROUGH_P2Y_PURINOCEPTOR_1	-1.24	0.65	0	0	0	not significant
3512	REACTOME_ALPHA_LINOLENIC_OMEGA3_AND_LINOLEIC_OMEGA6_ACID_	-1.24	0.65	0	0	0	not significant
3513	GO_CELLULAR_RESPONSE_TO_MANGANESE_ION	-1.24	0.64	0	0	0	not significant
3514	GO_G_PROTEIN_COUPLED_PURINERGIC_RECEPTOR_SIGNALING_PATHW	-1.24	0.64	0	0	0	not significant
3515	GO_POSITIVE_REGULATION_OF_METANEPHROS_DEVELOPMENT	-1.24	0.64	0	0	0	not significant
3516	GO_TRNA_THIO_MODIFICATION	-1.24	0.64	0	0	0	not significant
3517	BIOCARTA_DNAFRAGMENT_PATHWAY	-1.24	0.63	0	0	0	not significant
3518	GO_CYTIDYLYLTRANSFERASE_ACTIVITY	-1.24	0.63	0	0	0	not significant
3519	GO_REGULATION_OF_MACROPHAGE_APOPTOTIC_PROCESS	-1.24	0.63	0	0	0	not significant
3520	GO_IMPORTIN_ALPHA_FAMILY_PROTEIN_BINDING	-1.24	0.62	0	0	0	not significant
3521	REACTOME_APOBEC3G_MEDIATED_RESISTANCE_TO_HIV_1_INFECTION	-1.24	0.62	0	0	0	not significant
3522	GO_AMP_METABOLIC_PROCESS	-1.24	0.61	0	0	0	not significant
3523	GO_SULFUR_AMINO_ACID_CATABOLIC_PROCESS	-1.24	0.61	0	0	0	not significant
3524	GO_ANATOMICAL_STRUCTURE_REGRESSION	-1.24	0.59	0	0	0	not significant
3525	GO_CELLULAR_HOMEOSTASIS	-1.23	4.00	0	0	0	not significant
3526	GO_ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	-1.23	4.00	0	0	0	not significant
3527	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_8D	-1.23	2.15	0	0	0	not significant
3528	GO_CELL_SUBSTRATE_JUNCTION	-1.23	2.06	0	0	0	not significant
3529	GRYDER_PAX3FOXO1_TOP_ENHANCERS	-1.23	1.84	0	0	0	not significant
3530	MARTENS_BOUND_BY_PML_RARA_FUSION	-1.23	1.66	0	0	0	not significant
3531	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER	-1.23	1.51	0	0	0	not significant
3532	GO_DEFENSE_RESPONSE_TO_VIRUS	-1.23	1.47	0	0	0	not significant
3533	GO_WOUND_HEALING	-1.23	1.41	0	0	0	not significant
3534	REACTOME_ANTIGEN_PROCESSING:_UBIQUITINATION_PROTEASOME_DE	-1.23	1.39	0	0	0	not significant
3535	GO_NEURON_DEATH	-1.23	1.34	0	0	0	not significant
3536	GO_LEUKOCYTE_MIGRATION	-1.23	1.32	0	0	0	not significant
3537	BROWNE_HCMV_INFECTION_14HR_DN	-1.23	1.25	0	0	0	not significant
3538	REACTOME_RRNA_PROCESSING	-1.23	1.21	0	0	0	not significant
3539	SWEET_LUNG_CANCER_KRAS_DN	-1.23	1.17	0	0	0	not significant
3540	PDGF_UP.V1_UP	-1.23	1.06	0	0	0	not significant
3541	REACTOME_EPIGENETIC_REGULATION_OF_GENE_EXPRESSION	-1.23	1.03	0	0	0	not significant
3542	MIKKELSEN_MCV6_LCP_WITH_H3K4ME3	-1.23	1.02	0	0	0	not significant
3543	GO_ALPHA_AMINO_ACID_METABOLIC_PROCESS	-1.23	1.01	0	0	0	not significant
3544	GO_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	-1.23	1.00	0	0	0	not significant
3545	WARTERS_RESPONSE_TO_IR_SKIN	-1.23	1.00	0	0	0	not significant
3546	BRUECKNER_TARGETS_OF_MIRLET7A3_UP	-1.23	0.96	0	0	0	not significant
3547	PLASARI_TGFB1_TARGETS_10HR_UP	-1.23	0.96	0	0	0	not significant
3548	GO_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	-1.23	0.94	0	0	0	not significant
3549	REACTOME_GPCR_LIGAND_BINDING	-1.23	0.94	0	0	0	not significant
3550	SRC_UP.V1_DN	-1.23	0.93	0	0	0	not significant
3551	GO_DNA_DEPENDENT_ATPASE_ACTIVITY	-1.23	0.92	0	0	0	not significant
3552	REACTOME_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR_GG_NE	-1.23	0.89	0	0	0	not significant
3553	KEGG_TIGHT_JUNCTION	-1.23	0.88	0	0	0	not significant
3554	BREDEMEYER_RAG_SIGNALING_NOT_VIA_ATM_UP	-1.23	0.87	0	0	0	not significant
3555	GO_TRANSPORT_OF_VIRUS	-1.23	0.87	0	0	0	not significant
3556	REACTOME_CIRCADIAN_CLOCK	-1.23	0.87	0	0	0	not significant
3557	GO_CAJAL_BODY	-1.23	0.86	0	0	0	not significant
3558	GO_DRUG_TRANSMEMBRANE_TRANSPORT	-1.23	0.86	0	0	0	not significant
3559	GO_FLAVIN_ADENINE_DINUCLEOTIDE_BINDING	-1.23	0.86	0	0	0	not significant
3560	GO_PROTEIN_TRANSMEMBRANE_TRANSPORT	-1.23	0.86	0	0	0	not significant
3561	GO_GDP_BINDING	-1.23	0.85	0	0	0	not significant
3562	GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL	-1.23	0.84	0	0	0	not significant
3563	LIN_NPAS4_TARGETS_DN	-1.23	0.84	0	0	0	not significant
3564	GO_INOSITOL_PHOSPHATE_MEDIATED_SIGNALING	-1.23	0.83	0	0	0	not significant
3565	GO_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_CELL_DEATH	-1.23	0.83	0	0	0	not significant
3566	REACTOME_REGULATION_OF_ACTIN_DYNAMICS_FOR_PHAGOCYTIC_CU	-1.23	0.82	0	0	0	not significant
3567	BRUECKNER_TARGETS_OF_MIRLET7A3_DN	-1.23	0.81	0	0	0	not significant
3568	GO_CELL_CELL_RECOGNITION	-1.23	0.80	0	0	0	not significant
3569	GO_MIDBRAIN_DEVELOPMENT	-1.23	0.79	0	0	0	not significant
3570	GO_STRIATED_MUSCLE_ADAPTATION	-1.23	0.78	0	0	0	not significant
3571	NADLER_OBESITY_DN	-1.23	0.78	0	0	0	not significant
3572	GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_	-1.23	0.77	0	0	0	not significant
3573	GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	-1.23	0.77	0	0	0	not significant
3574	GO_REGULATION_OF_MUSCLE_HYPERTROPHY	-1.23	0.76	0	0	0	not significant
3575	GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS_WITHIN_A_TISSUE	-1.23	0.75	0	0	0	not significant
3576	GO_RETINA_HOMEOSTASIS	-1.23	0.75	0	0	0	not significant
3577	ROSS_AML_WITH_CBFB_MYH11_FUSION	-1.23	0.75	0	0	0	not significant
3578	GO_METANEPHROS_DEVELOPMENT	-1.23	0.74	0	0	0	not significant
3579	GO_LIVER_REGENERATION	-1.23	0.72	0	0	0	not significant
3580	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_UP	-1.23	0.72	0	0	0	not significant
3581	GO_POSITIVE_REGULATION_OF_CYTOKINESIS	-1.23	0.71	0	0	0	not significant
3582	TIAN_TNF_SIGNALING_NOT_VIA_NFKB	-1.23	0.71	0	0	0	not significant
3583	YORDY_RECIPROCAL_REGULATION_BY_ETS1_AND_SP100_UP	-1.23	0.70	0	0	0	not significant
3584	BIOCARTA_CSK_PATHWAY	-1.23	0.69	0	0	0	not significant
3585	GO_AUTONOMIC_NERVOUS_SYSTEM_DEVELOPMENT	-1.23	0.69	0	0	0	not significant

3586	GO_DNA_DEALKYLATION	-1.23	0.69	0	0	0	not significant
3587	GO_REGULATION_OF_GLIAL_CELL_PROLIFERATION	-1.23	0.69	0	0	0	not significant
3588	GO_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVEL	-1.23	0.67	0	0	0	not significant
3589	REACTOME_NUCLEAR_ENVELOPE_REASSEMBLY	-1.23	0.67	0	0	0	not significant
3590	REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION_IN_TLR7_8_OR_9_SIG	-1.23	0.67	0	0	0	not significant
3591	GO_MEIOTIC_SPINDLE_ORGANIZATION	-1.23	0.66	0	0	0	not significant
3592	GO_PLATELET_MORPHOGENESIS	-1.23	0.66	0	0	0	not significant
3593	RAMPON_ENRICHED_LEARNING_ENVIRONMENT_EARLY_DN	-1.23	0.66	0	0	0	not significant
3594	BIOCARTA_PTC1_PATHWAY	-1.23	0.65	0	0	0	not significant
3595	GO_C_ACETYLTRANSFERASE_ACTIVITY	-1.23	0.65	0	0	0	not significant
3596	REACTOME_REDUCTION_OF_CYTOSOLIC_CAPLUSPLUS_LEVELS	-1.23	0.65	0	0	0	not significant
3597	GO_AGGREPHAGY	-1.23	0.64	0	0	0	not significant
3598	GO_CORONARY_VASCULATURE_MORPHOGENESIS	-1.23	0.64	0	0	0	not significant
3599	GO_MEMBRANE_DEPOLARIZATION_DURING_CARDIAC_MUSCLE_CELL_A	-1.23	0.64	0	0	0	not significant
3600	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_	-1.23	0.64	0	0	0	not significant
3601	GO_PROTEOGLYCAN_BINDING	-1.23	0.64	0	0	0	not significant
3602	GO_REGULATION_OF_MEMBRANE_REPOLARIZATION	-1.23	0.64	0	0	0	not significant
3603	GO_SNORNA_3_END_PROCESSING	-1.23	0.64	0	0	0	not significant
3604	HOFMANN_MYELODYSPLASTIC_SYNDROM_HIGH_RISK_DN	-1.23	0.64	0	0	0	not significant
3605	REACTOME_VLDLR_INTERNALISATION_AND_DEGRADATION	-1.23	0.64	0	0	0	not significant
3606	GO_DOLICHYL_DIPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.23	0.63	0	0	0	not significant
3607	GO_POTASSIUM_CHANNEL_INHIBITOR_ACTIVITY	-1.23	0.63	0	0	0	not significant
3608	REACTOME_GRB2:SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FO	-1.23	0.63	0	0	0	not significant
3609	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP	-1.23	0.63	0	0	0	not significant
3610	GO_NEGATIVE_REGULATION_OF_HELICASE_ACTIVITY	-1.23	0.62	0	0	0	not significant
3611	GO_REGULATION_OF_DNA_DUPLEX_UNWINDING	-1.23	0.62	0	0	0	not significant
3612	FRIDMAN_SENESCENCE_DN	-1.23	0.61	0	0	0	not significant
3613	GO_CAMERA_TYPE_EYE_PHOTORECEPTOR_CELL_DIFFERENTIATION	-1.23	0.61	0	0	0	not significant
3614	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_III_ASSEMBLY	-1.23	0.61	0	0	0	not significant
3615	GO_POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_SECRETION	-1.23	0.60	0	0	0	not significant
3616	GO_SPERMATOPROTEASOME_COMPLEX	-1.23	0.60	0	0	0	not significant
3617	REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	-1.23	0.60	0	0	0	not significant
3618	GO_IDENTICAL_PROTEIN_BINDING	-1.22	4.00	0	0	0	not significant
3619	GO_LEUKOCYTE_MEDIATED_IMMUNITY	-1.22	4.00	0	0	0	not significant
3620	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN	-1.22	4.00	0	0	0	not significant
3621	SCHLOSSER_SERUM_RESPONSE_DN	-1.22	1.82	0	0	0	not significant
3622	GO_HEART_DEVELOPMENT	-1.22	1.63	0	0	0	not significant
3623	GO_IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY	-1.22	1.63	0	0	0	not significant
3624	DELACROIX_RARG_BOUND_MEF	-1.22	1.31	0	0	0	not significant
3625	GO_REGULATION_OF_CELL_ADHESION	-1.22	1.31	0	0	0	not significant
3626	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX1	-1.22	1.31	0	0	0	not significant
3627	HOLLMANN_APOPTOSIS_VIA_CD40_UP	-1.22	1.29	0	0	0	not significant
3628	GO_EPITHELIAL_TUBE_MORPHOGENESIS	-1.22	1.23	0	0	0	not significant
3629	MEISSNER_NPC_HCP_WITH_H3K4ME2	-1.22	1.23	0	0	0	not significant
3630	REACTOME_SIGNALING_BY_GPCR	-1.22	1.23	0	0	0	not significant
3631	GO_DNA_CONFORMATION_CHANGE	-1.22	1.19	0	0	0	not significant
3632	PURBEY_TARGETS_OF_CTBP1_NOT_SATB1_UP	-1.22	1.15	0	0	0	not significant
3633	GO_PROTEIN_MATURATION	-1.22	1.13	0	0	0	not significant
3634	REACTOME_NEURONAL_SYSTEM	-1.22	1.12	0	0	0	not significant
3635	GO_REGULATION_OF_RNA_METABOLIC_PROCESS	-1.22	1.09	0	0	0	not significant
3636	GO_CONNECTIVE_TISSUE_DEVELOPMENT	-1.22	1.08	0	0	0	not significant
3637	GO_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	-1.22	1.08	0	0	0	not significant
3638	GO_REGULATION_OF_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS	-1.22	1.06	0	0	0	not significant
3639	GRUETZMANN_PANCREATIC_CANCER_DN	-1.22	1.04	0	0	0	not significant
3640	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_UP	-1.22	1.00	0	0	0	not significant
3641	GO_VACUOLAR_LUMEN	-1.22	1.00	0	0	0	not significant
3642	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN	-1.22	0.99	0	0	0	not significant
3643	GO_MICROTUBULE_ASSOCIATED_COMPLEX	-1.22	0.98	0	0	0	not significant
3644	KIM_WT1_TARGETS_8HR_UP	-1.22	0.97	0	0	0	not significant
3645	GO_MYELOID_CELL_HOMEOSTASIS	-1.22	0.90	0	0	0	not significant
3646	GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.22	0.90	0	0	0	not significant
3647	GO_PURINE_NTP_DEPENDENT_HELICASE_ACTIVITY	-1.22	0.90	0	0	0	not significant
3648	GO_PROTEIN_SERINE_THREONINE_PHOSPHATASE_ACTIVITY	-1.22	0.89	0	0	0	not significant
3649	GO_REGULATION_OF_RESPONSE_TO_WOUNDING	-1.22	0.89	0	0	0	not significant
3650	CHR10Q22	-1.22	0.88	0	0	0	not significant
3651	GO_GOLGI_VESICLE_BUDDING	-1.22	0.86	0	0	0	not significant
3652	CHANG_IMMORTALIZED_BY_HPV31_UP	-1.22	0.85	0	0	0	not significant
3653	GO_PLATELET_ALPHA_GRANULE	-1.22	0.84	0	0	0	not significant
3654	HUMMERICH_SKIN_CANCER_PROGRESSION_UP	-1.22	0.84	0	0	0	not significant
3655	SCIBETTA_KDM5B_TARGETS_DN	-1.22	0.84	0	0	0	not significant
3656	REACTOME_ACTIVATED_PKN1_STIMULATES_TRANSCRIPTION_OF_AR_A	-1.22	0.83	0	0	0	not significant
3657	NUTT_GBM_VS_AO_GLIOMA_UP	-1.22	0.81	0	0	0	not significant
3658	GO_IMPORT_ACROSS_PLASMA_MEMBRANE	-1.22	0.80	0	0	0	not significant
3659	MA_MYELOID_DIFFERENTIATION_UP	-1.22	0.80	0	0	0	not significant
3660	MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_DN	-1.22	0.79	0	0	0	not significant
3661	REACTOME_IRE1ALPHA_ACTIVATES_CHAPERONES	-1.22	0.79	0	0	0	not significant
3662	GO_POSITIVE_REGULATION_OF_FIBROBLAST_PROLIFERATION	-1.22	0.78	0	0	0	not significant
3663	LINDVALL_IMMORTALIZED_BY_TERT_DN	-1.22	0.78	0	0	0	not significant
3664	PID_HIV_NEF_PATHWAY	-1.22	0.77	0	0	0	not significant
3665	GO_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	-1.22	0.76	0	0	0	not significant
3666	ZHAN_MULTIPLE_MYELOMA_MF_UP	-1.22	0.75	0	0	0	not significant
3667	GO_NEUROTROPHIN_SIGNALING_PATHWAY	-1.22	0.74	0	0	0	not significant
3668	GAVIN_FOXP3_TARGETS_CLUSTER_P2	-1.22	0.71	0	0	0	not significant
3669	GO_DNA_DEMETHYLATION	-1.22	0.71	0	0	0	not significant
3670	GO_DNA_HELICASE_COMPLEX	-1.22	0.71	0	0	0	not significant
3671	GO_NUCLEOSIDE_MONOPHOSPHATE_KINASE_ACTIVITY	-1.22	0.71	0	0	0	not significant
3672	GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	-1.22	0.71	0	0	0	not significant
3673	WILCOX_RESPONSE_TO_PROGESTERONE_DN	-1.22	0.70	0	0	0	not significant
3674	GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	-1.22	0.69	0	0	0	not significant
3675	PID_UPA_UPAR_PATHWAY	-1.22	0.69	0	0	0	not significant
3676	GO_DENDRITE_CYTOPLASM	-1.22	0.67	0	0	0	not significant
3677	GO_FOAM_CELL_DIFFERENTIATION	-1.22	0.67	0	0	0	not significant
3678	GO_POSITIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	-1.22	0.67	0	0	0	not significant
3679	GO_POSITIVE_REGULATION_OF_HEART_GROWTH	-1.22	0.67	0	0	0	not significant
3680	GO_PROTEIN_HOMOTRIMERIZATION	-1.22	0.67	0	0	0	not significant
3681	BIOCARTA_TCRA_PATHWAY	-1.22	0.66	0	0	0	not significant
3682	GO_GLUTATHIONE_DERIVATIVE_BIOSYNTHETIC_PROCESS	-1.22	0.66	0	0	0	not significant
3683	GO_ANKYRIN_BINDING	-1.22	0.64	0	0	0	not significant
3684	GO_GLUTAMINE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	-1.22	0.64	0	0	0	not significant
3685	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_ACTIN_CYTOSKELETON_P	-1.22	0.63	0	0	0	not significant
3686	GO_ESTROUS_CYCLE	-1.22	0.63	0	0	0	not significant
3687	GO_MHC_CLASS_I_PROTEIN_COMPLEX	-1.22	0.63	0	0	0	not significant
3688	GO_TRNA_AMINOACYLATION_FOR_MITOCHONDRIAL_PROTEIN_TRANSL	-1.22	0.63	0	0	0	not significant
3689	OHASHI_AURKB_TARGETS	-1.22	0.62	0	0	0	not significant
3690	VALK_AML_CLUSTER_5	-1.22	0.62	0	0	0	not significant
3691	GO_ALANINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.22	0.61	0	0	0	not significant
3692	GO_CYTOPLASMIC_TRANSLATIONAL_ELONGATION	-1.22	0.61	0	0	0	not significant
3693	GO_GALACTOSE_CATABOLIC_PROCESS_VIA_UDP_GALACTOSE	-1.22	0.61	0	0	0	not significant
3694	GO_SPERM_MIDPIECE	-1.22	0.61	0	0	0	not significant

3695	GO_NEGATIVE_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_STR	-1.22	0.60	0	0	0	not significant
3696	GO_PRESYNAPTIC_ACTIVE_ZONE_CYTOPLASMIC_COMPONENT	-1.22	0.60	0	0	0	not significant
3697	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27	-1.22	0.60	0	0	0	not significant
3698	REACTOME_PP2A_MEDIATED_DEPHOSPHORYLATION_OF_KEY_METABO	-1.22	0.60	0	0	0	not significant
3699	GO_L_ALANINE_TRANSPORT	-1.22	0.58	0	0	0	not significant
3700	GO_POSITIVE_REGULATION_OF_URINE_VOLUME	-1.22	0.57	0	0	0	not significant
3701	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP	-1.22	0.57	0	0	0	not significant
3702	GO_PHOSPHATIDYLCHOLINE_CATABOLIC_PROCESS	-1.22	0.56	0	0	0	not significant
3703	GO_ZONA_PELLUCIDA_RECEPTOR_COMPLEX	-1.22	0.55	0	0	0	not significant
3704	GO_NEGATIVE_REGULATION_OF_CELL_DEATH	-1.21	2.14	0	0	0	not significant
3705	GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	-1.21	1.95	0	0	0	not significant
3706	GO_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS	-1.21	1.94	0	0	0	not significant
3707	GO_CELLULAR_RESPONSE_TO_ENDOGENOUS_STIMULUS	-1.21	1.78	0	0	0	not significant
3708	GO_PROTEIN_COMPLEX_OLIGOMERIZATION	-1.21	1.70	0	0	0	not significant
3709	GO_ENZYME_ACTIVATOR_ACTIVITY	-1.21	1.56	0	0	0	not significant
3710	GO_CYTOPLASMIC_REGION	-1.21	1.54	0	0	0	not significant
3711	GO_LIPID_BIOSYNTHETIC_PROCESS	-1.21	1.51	0	0	0	not significant
3712	MARTINEZ_RESPONSE_TO_TRABECTEDIN_DN	-1.21	1.36	0	0	0	not significant
3713	FORTSCHEGGER_PHF8_TARGETS_UP	-1.21	1.20	0	0	0	not significant
3714	WELCSH_BRCA1_TARGETS_UP	-1.21	1.12	0	0	0	not significant
3715	GO_REGULATION_OF_CELL_SHAPE	-1.21	1.03	0	0	0	not significant
3716	GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	-1.21	1.01	0	0	0	not significant
3717	GO_MICROBODY	-1.21	0.98	0	0	0	not significant
3718	GO_ERK1_AND_ERK2_CASCADE	-1.21	0.97	0	0	0	not significant
3719	BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE	-1.21	0.96	0	0	0	not significant
3720	GO_SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS	-1.21	0.96	0	0	0	not significant
3721	GO_NUCLEAR_CHROMOSOME_TELOMERIC_REGION	-1.21	0.92	0	0	0	not significant
3722	GO_SERINE_HYDROLASE_ACTIVITY	-1.21	0.88	0	0	0	not significant
3723	GO_ORGAN_GROWTH	-1.21	0.85	0	0	0	not significant
3724	GO_ACTIN_FILAMENT	-1.21	0.84	0	0	0	not significant
3725	GO_REGULATION_OF_VIRAL_GENOME_REPLICATION	-1.21	0.84	0	0	0	not significant
3726	GEORGES_CELL_CYCLE_MIR192_TARGETS	-1.21	0.81	0	0	0	not significant
3727	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_E	-1.21	0.81	0	0	0	not significant
3728	GO_AXON_CYTOPLASM	-1.21	0.80	0	0	0	not significant
3729	LEE_EARLY_T_LYMPHOCYTE_DN	-1.21	0.80	0	0	0	not significant
3730	CHR11Q14	-1.21	0.79	0	0	0	not significant
3731	LEE_CALORIE_RESTRICTION_NEOCORTEX_DN	-1.21	0.79	0	0	0	not significant
3732	PID_NFAT_3PATHWAY	-1.21	0.77	0	0	0	not significant
3733	GO_RUFFLE_ASSEMBLY	-1.21	0.76	0	0	0	not significant
3734	JIANG_AGING_CEREBRAL_CORTEX_UP	-1.21	0.76	0	0	0	not significant
3735	SMIRNOV_RESPONSE_TO_IR_2HR_UP	-1.21	0.75	0	0	0	not significant
3736	GO_POSITIVE_REGULATION_OF_ATPASE_ACTIVITY	-1.21	0.74	0	0	0	not significant
3737	GO_COLUMNAR_CUBOIDAL_EPITHELIAL_CELL_DIFFERENTIATION	-1.21	0.73	0	0	0	not significant
3738	GO_HYDRO_LYASE_ACTIVITY	-1.21	0.73	0	0	0	not significant
3739	GO_T_CELL_MIGRATION	-1.21	0.72	0	0	0	not significant
3740	GO_TIGHT_JUNCTION_ORGANIZATION	-1.21	0.72	0	0	0	not significant
3741	GO_CARDIAC_MUSCLE_TISSUE_MORPHOGENESIS	-1.21	0.71	0	0	0	not significant
3742	PID_ARF6_PATHWAY	-1.21	0.71	0	0	0	not significant
3743	GO_MEMBRANE_BIOGENESIS	-1.21	0.70	0	0	0	not significant
3744	WESTON_VEGFA_TARGETS_3HR	-1.21	0.69	0	0	0	not significant
3745	GO_LIPOPROTEIN_PARTICLE_RECEPTOR_BINDING	-1.21	0.68	0	0	0	not significant
3746	GO_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	-1.21	0.68	0	0	0	not significant
3747	GO_BILE_ACID_BIOSYNTHETIC_PROCESS	-1.21	0.67	0	0	0	not significant
3748	GO_REGULATION_OF_HISTONE_UBIQUITINATION	-1.21	0.66	0	0	0	not significant
3749	VISALA_RESPONSE_TO_HEAT_SHOCK_AND_AGING_DN	-1.21	0.65	0	0	0	not significant
3750	GO_ANNEALING_ACTIVITY	-1.21	0.64	0	0	0	not significant
3751	GO_CARBOHYDRATE_PHOSPHORYLATION	-1.21	0.64	0	0	0	not significant
3752	ONDER_CDH1_TARGETS_3_UP	-1.21	0.64	0	0	0	not significant
3753	REACTOME_NEF_MEDIATED_CD8_DOWN_REGULATION	-1.21	0.64	0	0	0	not significant
3754	REACTOME_RUNX3_REGULATES_NOTCH_SIGNALING	-1.21	0.64	0	0	0	not significant
3755	GO_CYTOPLASMIC_EXOSOME_RNASE_COMPLEX_	-1.21	0.63	0	0	0	not significant
3756	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_UP	-1.21	0.63	0	0	0	not significant
3757	REACTOME_PROCESSING_OF_SMDT1	-1.21	0.63	0	0	0	not significant
3758	GO_ASPARTATE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	-1.21	0.62	0	0	0	not significant
3759	GO_MHC_PROTEIN_COMPLEX	-1.21	0.62	0	0	0	not significant
3760	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_DN	-1.21	0.61	0	0	0	not significant
3761	GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY_TRANSPOSING_C	-1.21	0.60	0	0	0	not significant
3762	GO_NEGATIVE_REGULATION_OF_CELL_GROWTH_INVOLVED_IN_CARDIA	-1.21	0.60	0	0	0	not significant
3763	GO_NOTOCHORD_DEVELOPMENT	-1.21	0.60	0	0	0	not significant
3764	GO_PROTEIN_MATURATION_BY_PROTEIN_FOLDING	-1.21	0.60	0	0	0	not significant
3765	GO_MITOCHONDRIAL_DNA_REPLICATION	-1.21	0.59	0	0	0	not significant
3766	GO_NEGATIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_CALCIUM_	-1.21	0.59	0	0	0	not significant
3767	GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PA	-1.21	0.59	0	0	0	not significant
3768	GO_HISTONE_METHYLTRANSFERASE_BINDING	-1.21	0.58	0	0	0	not significant
3769	GO_REGULATION_OF_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	-1.21	0.58	0	0	0	not significant
3770	GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	-1.21	0.58	0	0	0	not significant
3771	GO_WASH_COMPLEX	-1.21	0.58	0	0	0	not significant
3772	REACTOME_CAMK_IV_MEDIATED_PHOSPHORYLATION_OF_CREB	-1.21	0.58	0	0	0	not significant
3773	REACTOME_COENZYME_A_BIOSYNTHESIS	-1.21	0.58	0	0	0	not significant
3774	GO_ALDITOL_CATABOLIC_PROCESS	-1.21	0.57	0	0	0	not significant
3775	GO_CLEAVAGE_FURROW_FORMATION	-1.21	0.57	0	0	0	not significant
3776	GO_L_GLUTAMATE_IMPORT	-1.21	0.57	0	0	0	not significant
3777	GO_PORIN_ACTIVITY	-1.21	0.57	0	0	0	not significant
3778	GO_NEGATIVE_REGULATION_OF_RNA_POLYMERASE_II_REGULATORY_	-1.21	0.56	0	0	0	not significant
3779	GO_CELL_CYCLE_PROCESS	-1.20	4.00	0	0	0	not significant
3780	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN	-1.20	1.30	0	0	0	not significant
3781	GO_CELL_LEADING_EDGE	-1.20	1.29	0	0	0	not significant
3782	GO_CELL_CYCLE_G1_S_PHASE_TRANSITION	-1.20	1.24	0	0	0	not significant
3783	CHYLA_CBFA2T3_TARGETS_UP	-1.20	1.06	0	0	0	not significant
3784	REACTOME_INTRA_GOLGI_AND_RETROGRADE_GOLGI_TO_ER_TRAFFIC	-1.20	1.05	0	0	0	not significant
3785	GO_DRUG_METABOLIC_PROCESS	-1.20	1.01	0	0	0	not significant
3786	GO_HELICASE_ACTIVITY	-1.20	0.97	0	0	0	not significant
3787	GO_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	-1.20	0.94	0	0	0	not significant
3788	GO_OSTEOBLAST_DIFFERENTIATION	-1.20	0.89	0	0	0	not significant
3789	P53_DN.V1_UP	-1.20	0.89	0	0	0	not significant
3790	GO_POSITIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	-1.20	0.88	0	0	0	not significant
3791	BURTON_ADIPOGENESIS_8	-1.20	0.84	0	0	0	not significant
3792	GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	-1.20	0.84	0	0	0	not significant
3793	CHR2P13	-1.20	0.82	0	0	0	not significant
3794	REACTOME_COPII_MEDIATED_VESICLE_TRANSPORT	-1.20	0.82	0	0	0	not significant
3795	BASSO_CD40_SIGNALING_DN	-1.20	0.81	0	0	0	not significant
3796	GROSS_HYPOXIA_VIA_HIF1A_DN	-1.20	0.81	0	0	0	not significant
3797	HOEBEKE_LYMPHOID_STEM_CELL_DN	-1.20	0.81	0	0	0	not significant
3798	BURTON_ADIPOGENESIS_PEAK_AT_16HR	-1.20	0.78	0	0	0	not significant
3799	GO_DNA_HELICASE_ACTIVITY	-1.20	0.78	0	0	0	not significant
3800	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_UP	-1.20	0.77	0	0	0	not significant
3801	GO_ATP_DEPENDENT_DNA_HELICASE_ACTIVITY	-1.20	0.74	0	0	0	not significant
3802	GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.20	0.74	0	0	0	not significant
3803	GO_NERVE_DEVELOPMENT	-1.20	0.73	0	0	0	not significant

3804	REACTOME_PEROXISOMAL_PROTEIN_IMPORT	-1.20	0.72	0	0	0	not significant
3805	GO_MUSCLE_CELL_MIGRATION	-1.20	0.71	0	0	0	not significant
3806	GO_TERTIARY_GRANULE_LUMEN	-1.20	0.71	0	0	0	not significant
3807	HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_UP	-1.20	0.71	0	0	0	not significant
3808	BECKER_TAMOXIFEN_RESISTANCE_UP	-1.20	0.70	0	0	0	not significant
3809	GO_BLOOD_MICROPARTICLE	-1.20	0.70	0	0	0	not significant
3810	GO_NEURAL_CREST_CELL_DIFFERENTIATION	-1.20	0.69	0	0	0	not significant
3811	GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_UP	-1.20	0.68	0	0	0	not significant
3812	GO_U12_TYPE_SPLICEOSOMAL_COMPLEX	-1.20	0.68	0	0	0	not significant
3813	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_48HR_DN	-1.20	0.67	0	0	0	not significant
3814	GO_CELLULAR_RESPONSE_TO_GAMMA_RADIATION	-1.20	0.67	0	0	0	not significant
3815	GO_ONE_CARBON_METABOLIC_PROCESS	-1.20	0.67	0	0	0	not significant
3816	REACTOME_MITOPHAGY	-1.20	0.67	0	0	0	not significant
3817	GO_CELLULAR_RESPONSE_TO_DSRNA	-1.20	0.66	0	0	0	not significant
3818	REACTOME_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE	-1.20	0.66	0	0	0	not significant
3819	APPIERTO_RESPONSE_TO_FENRETINIDE_UP	-1.20	0.65	0	0	0	not significant
3820	GO_FATTY_ACID_TRANSMEMBRANE_TRANSPORT	-1.20	0.65	0	0	0	not significant
3821	GO_SPLICEOSOMAL_TRI_SNRNP_COMPLEX_ASSEMBLY	-1.20	0.65	0	0	0	not significant
3822	MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_DN	-1.20	0.65	0	0	0	not significant
3823	CHOI_ATL_CHRONIC_VS_ACUTE_DN	-1.20	0.64	0	0	0	not significant
3824	LIAO_HAVE_SOX4_BINDING_SITES	-1.20	0.64	0	0	0	not significant
3825	GO_T_CELL_CYTOKINE_PRODUCTION	-1.20	0.63	0	0	0	not significant
3826	REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	-1.20	0.63	0	0	0	not significant
3827	REACTOME_REGULATION_OF_FZD_BY_UBIQUITINATION	-1.20	0.63	0	0	0	not significant
3828	DEN_INTERACT_WITH_LCA5	-1.20	0.62	0	0	0	not significant
3829	GO_GOLGI_TO_VACUOLE_TRANSPORT	-1.20	0.62	0	0	0	not significant
3830	GO_LINOLEIC_ACID_METABOLIC_PROCESS	-1.20	0.62	0	0	0	not significant
3831	GO_NEGATIVE_REGULATION_OF_PROTEIN_KINASE_ACTIVITY_BY_REGUL	-1.20	0.62	0	0	0	not significant
3832	GO_PROTEIN_DENEDDYLATION	-1.20	0.62	0	0	0	not significant
3833	HAHTOLA_CTCL_PATHOGENESIS	-1.20	0.62	0	0	0	not significant
3834	GO_TRNA_WOBBLE_URIDINE_MODIFICATION	-1.20	0.61	0	0	0	not significant
3835	GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZAT	-1.20	0.61	0	0	0	not significant
3836	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_ASSOCIATION_	-1.20	0.61	0	0	0	not significant
3837	GO_POLYAMINE_METABOLIC_PROCESS	-1.20	0.60	0	0	0	not significant
3838	GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_TRANSLATION	-1.20	0.60	0	0	0	not significant
3839	KEGG_RETINOL_METABOLISM	-1.20	0.60	0	0	0	not significant
3840	ANASTASSIOU_MULTICANCER_INVASIVENESS_SIGNATURE	-1.20	0.59	0	0	0	not significant
3841	GO_HEPATOCYTE_DIFFERENTIATION	-1.20	0.59	0	0	0	not significant
3842	GO_POSITIVE_REGULATION_OF_GONAD_DEVELOPMENT	-1.20	0.59	0	0	0	not significant
3843	GO_SUCCINATE_METABOLIC_PROCESS	-1.20	0.58	0	0	0	not significant
3844	NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP	-1.20	0.58	0	0	0	not significant
3845	REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	-1.20	0.58	0	0	0	not significant
3846	SHIRAISHI_PLZF_TARGETS_UP	-1.20	0.58	0	0	0	not significant
3847	GO_ANGIOTENSIN_ACTIVATED_SIGNALING_PATHWAY	-1.20	0.57	0	0	0	not significant
3848	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_OXYGEN_AS_A	-1.20	0.57	0	0	0	not significant
3849	GO_PURINE_RIBONUCLEOSIDE_SALVAGE	-1.20	0.57	0	0	0	not significant
3850	GO_RIBOSOMAL_SMALL_SUBUNIT_EXPORT_FROM_NUCLEUS	-1.20	0.56	0	0	0	not significant
3851	GO_SERINE_TRANSPORT	-1.20	0.56	0	0	0	not significant
3852	CHR2Q13	-1.20	0.55	0	0	0	not significant
3853	GO_NEGATIVE_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOP	-1.20	0.55	0	0	0	not significant
3854	GO_POSITIVE_REGULATION_OF_ATTACHMENT_OF_SPINDLE_MICROTUB	-1.20	0.54	0	0	0	not significant
3855	GO_RESPONSE_TO_MUSCLE_INACTIVITY	-1.20	0.54	0	0	0	not significant
3856	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN	-1.19	4.00	0	0	0	not significant
3857	GO_STRUCTURAL_MOLECULE_ACTIVITY	-1.19	1.45	0	0	0	not significant
3858	GO_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS	-1.19	1.33	0	0	0	not significant
3859	MARTINEZ_TP53_TARGETS_UP	-1.19	1.30	0	0	0	not significant
3860	GO_NEGATIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	-1.19	1.25	0	0	0	not significant
3861	GO_CHROMOSOME_SEGREGATION	-1.19	1.16	0	0	0	not significant
3862	GO_NUCLEAR_CHROMOSOME_SEGREGATION	-1.19	1.05	0	0	0	not significant
3863	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	-1.19	1.05	0	0	0	not significant
3864	REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICA	-1.19	0.96	0	0	0	not significant
3865	GO_TELENCEPHALON_DEVELOPMENT	-1.19	0.95	0	0	0	not significant
3866	GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	-1.19	0.94	0	0	0	not significant
3867	KRAS.DF.V1_UP	-1.19	0.94	0	0	0	not significant
3868	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	-1.19	0.93	0	0	0	not significant
3869	GO_VIRAL_GENOME_REPLICATION	-1.19	0.89	0	0	0	not significant
3870	ELVIDGE_HYPOXIA_UP	-1.19	0.88	0	0	0	not significant
3871	GO_EPIDERMAL_CELL_DIFFERENTIATION	-1.19	0.88	0	0	0	not significant
3872	GO_POSITIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACT	-1.19	0.88	0	0	0	not significant
3873	RODWELL_AGING_KIDNEY_NO_BLOOD_DN	-1.19	0.88	0	0	0	not significant
3874	GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	-1.19	0.85	0	0	0	not significant
3875	GALE_APL_WITH_FLT3_MUTATED_UP	-1.19	0.80	0	0	0	not significant
3876	GO_NUCLEOSIDE_PHOSPHATE_CATABOLIC_PROCESS	-1.19	0.80	0	0	0	not significant
3877	GO_REGULATION_OF_LIPID_LOCALIZATION	-1.19	0.80	0	0	0	not significant
3878	GO_NEGATIVE_REGULATION_OF_NUCLEAR_DIVISION	-1.19	0.78	0	0	0	not significant
3879	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_UP	-1.19	0.75	0	0	0	not significant
3880	GO_NECROTIC_CELL_DEATH	-1.19	0.74	0	0	0	not significant
3881	GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	-1.19	0.74	0	0	0	not significant
3882	GO_POSITIVE_REGULATION_OF_DNA_BINDING	-1.19	0.74	0	0	0	not significant
3883	CHR11Q23	-1.19	0.73	0	0	0	not significant
3884	GO_WATER_SOLUBLE_VITAMIN_METABOLIC_PROCESS	-1.19	0.72	0	0	0	not significant
3885	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP	-1.19	0.72	0	0	0	not significant
3886	LINDVALL_IMMORTALIZED_BY_TERT_UP	-1.19	0.71	0	0	0	not significant
3887	GO_REGULATION_OF_LIPID_TRANSPORT	-1.19	0.70	0	0	0	not significant
3888	GO_TRANSLATION_INITIATION_FACTOR_ACTIVITY	-1.19	0.70	0	0	0	not significant
3889	PID_ERBB1_INTERNALIZATION_PATHWAY	-1.19	0.70	0	0	0	not significant
3890	GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	-1.19	0.69	0	0	0	not significant
3891	GO_NADP_BINDING	-1.19	0.69	0	0	0	not significant
3892	HALLMARK_NOTCH_SIGNALING	-1.19	0.69	0	0	0	not significant
3893	ASTON_MAJOR_DEPRESSIVE_DISORDER_UP	-1.19	0.68	0	0	0	not significant
3894	GO_CELLULAR_MODIFIED_AMINO_ACID_BIOSYNTHETIC_PROCESS	-1.19	0.68	0	0	0	not significant
3895	GO_EXTRINSIC_COMPONENT_OF_ORGANELLE_MEMBRANE	-1.19	0.68	0	0	0	not significant
3896	GO_NEGATIVE_REGULATION_OF_METAPHASE_ANAPHASE_TRANSITION_	-1.19	0.68	0	0	0	not significant
3897	GO_RESPONSE_TO_COLD	-1.19	0.68	0	0	0	not significant
3898	BIOCARTA_FCER1_PATHWAY	-1.19	0.67	0	0	0	not significant
3899	ZHANG_GATA6_TARGETS_DN	-1.19	0.67	0	0	0	not significant
3900	BROWNE_HCMV_INFECTION_4HR_UP	-1.19	0.66	0	0	0	not significant
3901	GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_INTERCONVERSION	-1.19	0.66	0	0	0	not significant
3902	GO_POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	-1.19	0.66	0	0	0	not significant
3903	GO_REGULATION_OF_TRANSLATIONAL_FIDELITY	-1.19	0.66	0	0	0	not significant
3904	MCCLUNG_DELTA_FOSB_TARGETS_8WK	-1.19	0.65	0	0	0	not significant
3905	CHR5Q12	-1.19	0.64	0	0	0	not significant
3906	DORN_ADENOVIRUS_INFECTION_32HR_DN	-1.19	0.64	0	0	0	not significant
3907	GO_RESPONSE_TO_X_RAY	-1.19	0.64	0	0	0	not significant
3908	PID_LIS1_PATHWAY	-1.19	0.64	0	0	0	not significant
3909	GO_EMBRYONIC_EYE_MORPHOGENESIS	-1.19	0.63	0	0	0	not significant
3910	GO_MHC_CLASS_II_PROTEIN_COMPLEX_BINDING	-1.19	0.63	0	0	0	not significant
3911	GO_NEGATIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	-1.19	0.63	0	0	0	not significant
3912	GRADE_COLON_CANCER_DN	-1.19	0.63	0	0	0	not significant

3913	GO_ASYMMETRIC_CELL_DIVISION	-1.19	0.62	0	0	0	not significant
3914	GO_MONOCARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIV	-1.19	0.62	0	0	0	not significant
3915	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_2_DN	-1.19	0.62	0	0	0	not significant
3916	GO_DYNEIN_INTERMEDIATE_CHAIN_BINDING	-1.19	0.61	0	0	0	not significant
3917	GO_FATTY_ACID_DERIVATIVE_CATABOLIC_PROCESS	-1.19	0.61	0	0	0	not significant
3918	GO_REGULATION_OF_CELL_MATURATION	-1.19	0.61	0	0	0	not significant
3919	REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLUCOSE_	-1.19	0.61	0	0	0	not significant
3920	WENG_POR_TARGETS_GLOBAL_DN	-1.19	0.60	0	0	0	not significant
3921	GO_POSITIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_UNFOLDED	-1.19	0.59	0	0	0	not significant
3922	GO_SNORNA_PROCESSING	-1.19	0.59	0	0	0	not significant
3923	GO_G_QUADRUPLEX_DNA_BINDING	-1.19	0.58	0	0	0	not significant
3924	GO_JUN_KINASE_KINASE_KINASE_ACTIVITY	-1.19	0.58	0	0	0	not significant
3925	GO_NUCLEAR_CYCLIN_DEPENDENT_PROTEIN_KINASE_HOLOENZYME_C	-1.19	0.58	0	0	0	not significant
3926	GO_RESPONSE_TO_MANGANESE_ION	-1.19	0.58	0	0	0	not significant
3927	GO_TRANSLOCATION_OF_MOLECULES_INTO_HOST	-1.19	0.58	0	0	0	not significant
3928	GOLUB_ALL_VS_AML_DN	-1.19	0.58	0	0	0	not significant
3929	KEGG_STEROID_HORMONE_BIOSYNTHESIS	-1.19	0.58	0	0	0	not significant
3930	MIKKELSEN_IPS_WITH_HCP_H3K27ME3	-1.19	0.58	0	0	0	not significant
3931	GO_EXTRINSIC_COMPONENT_OF_ENDOSOME_MEMBRANE	-1.19	0.57	0	0	0	not significant
3932	GO_KINETOCHORE_ASSEMBLY	-1.19	0.57	0	0	0	not significant
3933	GO_STEROL_IMPORT	-1.19	0.57	0	0	0	not significant
3934	GO_STRESS_INDUCED_PREMATURE_SENESCENCE	-1.19	0.57	0	0	0	not significant
3935	GO_UTERUS_DEVELOPMENT	-1.19	0.57	0	0	0	not significant
3936	REACTOME_ROBO_RECEPTORS_BIND_AKAP5	-1.19	0.57	0	0	0	not significant
3937	REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_27_HYD	-1.19	0.57	0	0	0	not significant
3938	GO_SECRETION_OF_LYSOSOMAL_ENZYMES	-1.19	0.56	0	0	0	not significant
3939	KUWANO_RNA_STABILIZED_BY_NO	-1.19	0.56	0	0	0	not significant
3940	DELASERNA_TARGETS_OF_MYOD_AND_SMARCA4	-1.19	0.55	0	0	0	not significant
3941	GO_ESTABLISHMENT_OF_CENTROSOME_LOCALIZATION	-1.19	0.55	0	0	0	not significant
3942	GO_POSITIVE_REGULATION_OF_RECEPTOR_BIOSYNTHETIC_PROCESS	-1.19	0.55	0	0	0	not significant
3943	GO_SEX_CHROMATIN	-1.19	0.55	0	0	0	not significant
3944	GO_SIGNAL_PEPTIDASE_COMPLEX	-1.19	0.55	0	0	0	not significant
3945	GO_SUCCINYL_COA_METABOLIC_PROCESS	-1.19	0.55	0	0	0	not significant
3946	GO_EARLY_ENDOSOME_TO_GOLGI_TRANSPORT	-1.19	0.54	0	0	0	not significant
3947	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_CYSTEINE_S_NITROSYLATI	-1.19	0.54	0	0	0	not significant
3948	GO_PERICHROMATIN_FIBRILS	-1.19	0.54	0	0	0	not significant
3949	GO_POSITIVE_REGULATION_OF_NEURON_PROJECTION_REGENERATIO	-1.19	0.54	0	0	0	not significant
3950	GO_REGULATION_OF_DEVELOPMENT_HETEROCHRONIC	-1.19	0.54	0	0	0	not significant
3951	GO_REGULATION_OF_NEUROMUSCULAR_JUNCTION_DEVELOPMENT	-1.19	0.54	0	0	0	not significant
3952	GO_REGULATION_OF_WNT_SIGNALING_PATHWAY_PLANAR_CELL_POLA	-1.19	0.54	0	0	0	not significant
3953	GO_U1_SNRNP_BINDING	-1.19	0.54	0	0	0	not significant
3954	REACTOME_TYSND1_CLEAVES_PEROXISOMAL_PROTEINS	-1.19	0.53	0	0	0	not significant
3955	GO_MECHANOSENSORY_BEHAVIOR	-1.19	0.52	0	0	0	not significant
3956	GO_FEMALE_MEIOSIS_CHROMOSOME_SEGREGATION	-1.19	0.51	0	0	0	not significant
3957	GO_POSITIVE_REGULATION_OF_ER_ASSOCIATED_UBIQUITIN_DEPENDE	-1.19	0.51	0	0	0	not significant
3958	GO_SECRETORY_GRANULE	-1.18	1.96	0	0	0	not significant
3959	GO_REGULATION_OF_CELL_DEATH	-1.18	1.91	0	0	0	not significant
3960	PUJANA_ATM_PCC_NETWORK	-1.18	1.82	0	0	0	not significant
3961	GO_SECRETORY_VESICLE	-1.18	1.68	0	0	0	not significant
3962	BENPORATH_CYCLING_GENES	-1.18	1.59	0	0	0	not significant
3963	GO_CARDIOVASCULAR_SYSTEM_DEVELOPMENT	-1.18	1.46	0	0	0	not significant
3964	GO_SIGNAL_TRANSDUCTION_BY_PROTEIN_PHOSPHORYLATION	-1.18	1.36	0	0	0	not significant
3965	GO_IMPORT_INTO_CELL	-1.18	1.34	0	0	0	not significant
3966	GO_CELLULAR_CHEMICAL_HOMEOSTASIS	-1.18	1.29	0	0	0	not significant
3967	GO_NUCLEAR_ENVELOPE	-1.18	1.29	0	0	0	not significant
3968	GO_REGULATION_OF_DEFENSE_RESPONSE	-1.18	1.25	0	0	0	not significant
3969	GO_MULTICELLULAR_ORGANISMAL_HOMEOSTASIS	-1.18	1.20	0	0	0	not significant
3970	GO_RESPONSE_TO_PEPTIDE	-1.18	1.18	0	0	0	not significant
3971	GO_EPITHELIAL_CELL_DIFFERENTIATION	-1.18	1.17	0	0	0	not significant
3972	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	-1.18	1.15	0	0	0	not significant
3973	GO_MONOVALENT_INORGANIC_CATION_TRANSPORT	-1.18	1.07	0	0	0	not significant
3974	REACTOME_INTRACELLULAR_SIGNALING_BY_SECOND_MESSENGERS	-1.18	1.07	0	0	0	not significant
3975	GO_PROTEIN_LOCALIZATION_TO_NUCLEUS	-1.18	1.04	0	0	0	not significant
3976	GO_SECOND_MESSENGER_MEDIATED_SIGNALING	-1.18	0.98	0	0	0	not significant
3977	GO_NEGATIVE_REGULATION_OF_CELL_MOTILITY	-1.18	0.97	0	0	0	not significant
3978	HOXA9_DN.V1_DN	-1.18	0.97	0	0	0	not significant
3979	GO_DNA_BIOSYNTHETIC_PROCESS	-1.18	0.96	0	0	0	not significant
3980	GO_NEGATIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.18	0.95	0	0	0	not significant
3981	SANSOM_APC_TARGETS	-1.18	0.92	0	0	0	not significant
3982	GO_REGULATION_OF_PROTEIN_BINDING	-1.18	0.91	0	0	0	not significant
3983	GO_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION	-1.18	0.89	0	0	0	not significant
3984	GO_ADAPTIVE_THERMOGENESIS	-1.18	0.88	0	0	0	not significant
3985	GO_TEMPERATURE_HOMEOSTASIS	-1.18	0.87	0	0	0	not significant
3986	CHR14Q24	-1.18	0.85	0	0	0	not significant
3987	GO_ESTABLISHMENT_OF_CELL_POLARITY	-1.18	0.83	0	0	0	not significant
3988	ROESSLER_LIVER_CANCER_METASTASIS_UP	-1.18	0.83	0	0	0	not significant
3989	GO_ENTRY_INTO_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERA	-1.18	0.81	0	0	0	not significant
3990	GO_MICROTUBULE_MOTOR_ACTIVITY	-1.18	0.80	0	0	0	not significant
3991	GO_SPINDLE_ASSEMBLY	-1.18	0.78	0	0	0	not significant
3992	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP	-1.18	0.76	0	0	0	not significant
3993	GO_CHAPERONE_BINDING	-1.18	0.75	0	0	0	not significant
3994	GO_KIDNEY_EPITHELIUM_DEVELOPMENT	-1.18	0.75	0	0	0	not significant
3995	REACTOME_RECRUITMENT_OF_NUMA_TO_MITOTIC_CENTROSOMES	-1.18	0.75	0	0	0	not significant
3996	CARD_MIR302A_TARGETS	-1.18	0.74	0	0	0	not significant
3997	REACTOME_NUCLEOSOME_ASSEMBLY	-1.18	0.74	0	0	0	not significant
3998	RASHI_RESPONSE_TO_IONIZING_RADIATION_6	-1.18	0.73	0	0	0	not significant
3999	BRUNO_HEMATOPOIESIS	-1.18	0.71	0	0	0	not significant
4000	DOANE_BREAST_CANCER_ESR1_UP	-1.18	0.70	0	0	0	not significant
4001	GO_ALCOHOL_BINDING	-1.18	0.70	0	0	0	not significant
4002	GO_RESPONSE_TO_NERVE_GROWTH_FACTOR	-1.18	0.69	0	0	0	not significant
4003	GO_DICARBOXYLIC_ACID_TRANSPORT	-1.18	0.68	0	0	0	not significant
4004	NADLER_OBESITY_UP	-1.18	0.68	0	0	0	not significant
4005	YORDY_RECIPROCAL_REGULATION_BY_ETS1_AND_SP100_DN	-1.18	0.68	0	0	0	not significant
4006	LANDIS_BREAST_CANCER_PROGRESSION_UP	-1.18	0.66	0	0	0	not significant
4007	LEE_CALORIE_RESTRICTION_MUSCLE_UP	-1.18	0.65	0	0	0	not significant
4008	PID_AR_NONGENOMIC_PATHWAY	-1.18	0.65	0	0	0	not significant
4009	REACTOME_DAP12_INTERACTIONS	-1.18	0.65	0	0	0	not significant
4010	TERAO_AOX4_TARGETS_HG_UP	-1.18	0.65	0	0	0	not significant
4011	GO_NEGATIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	-1.18	0.64	0	0	0	not significant
4012	GO_OLIGOSACCHARIDE_LIPID_INTERMEDIATE_BIOSYNTHETIC_PROCES	-1.18	0.64	0	0	0	not significant
4013	GO_VIRAL_RNA_GENOME_REPLICATION	-1.18	0.64	0	0	0	not significant
4014	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_DN	-1.18	0.64	0	0	0	not significant
4015	GO_MAMMARY_GLAND_MORPHOGENESIS	-1.18	0.63	0	0	0	not significant
4016	GO_PROTEIN_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	-1.18	0.63	0	0	0	not significant
4017	GO_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	-1.18	0.63	0	0	0	not significant
4018	GO_REGULATION_OF_CYCLASE_ACTIVITY	-1.18	0.63	0	0	0	not significant
4019	CHR6Q16	-1.18	0.62	0	0	0	not significant
4020	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_DN	-1.18	0.62	0	0	0	not significant
4021	SA_CASPASE_CASCADE	-1.18	0.62	0	0	0	not significant

4022	GO_NUCLEAR_PORE_ORGANIZATION	-1.18	0.61	0	0	0	not significant
4023	GO_POSITIVE_REGULATION_OF_INTERFERON_BETA_PRODUCTION	-1.18	0.61	0	0	0	not significant
4024	REACTOME_PENTOSE_PHOSPHATE_PATHWAY	-1.18	0.61	0	0	0	not significant
4025	CHEOK_RESPONSE_TO_HD_MTX_UP	-1.18	0.60	0	0	0	not significant
4026	GO_NUCLEAR_BODY_ORGANIZATION	-1.18	0.60	0	0	0	not significant
4027	WATANABE_ULCERATIVE_COLITIS_WITH_CANCER_DN	-1.18	0.60	0	0	0	not significant
4028	GO_CLATHRIN_COAT_OF_ENDOCYTIC_VESICLE	-1.18	0.59	0	0	0	not significant
4029	REACTOME_REGULATION_OF_LOCALIZATION_OF_FOXO_TRANSCRIPTIO	-1.18	0.59	0	0	0	not significant
4030	SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_UP	-1.18	0.59	0	0	0	not significant
4031	GO_HOST_CELL_PART	-1.18	0.58	0	0	0	not significant
4032	GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	-1.18	0.58	0	0	0	not significant
4033	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_DN	-1.18	0.58	0	0	0	not significant
4034	SA_G2_AND_M_PHASES	-1.18	0.58	0	0	0	not significant
4035	GO_ACTIVATION_OF_PROTEIN_KINASE_A_ACTIVITY	-1.18	0.57	0	0	0	not significant
4036	GO_MOTILE_CILIUM_ASSEMBLY	-1.18	0.57	0	0	0	not significant
4037	GO_ALCOHOL_DEHYDROGENASE_NADPPLUS_ACTIVITY	-1.18	0.56	0	0	0	not significant
4038	GO_CELLULAR_RESPONSE_TO_EXOGENOUS_DSRNA	-1.18	0.56	0	0	0	not significant
4039	GO_HOST_INTRACELLULAR_PART	-1.18	0.56	0	0	0	not significant
4040	GO_NEGATIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	-1.18	0.56	0	0	0	not significant
4041	GO_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	-1.18	0.56	0	0	0	not significant
4042	GO_POSITIVE_REGULATION_OF_AMYLOID_BETA_FORMATION	-1.18	0.56	0	0	0	not significant
4043	GO_TPR_DOMAIN_BINDING	-1.18	0.56	0	0	0	not significant
4044	GO_TRACHEA_MORPHOGENESIS	-1.18	0.56	0	0	0	not significant
4045	GO_TROPOMYOSIN_BINDING	-1.18	0.56	0	0	0	not significant
4046	GO_POSITIVE_REGULATION_OF_MACROPHAGE_DIFFERENTIATION	-1.18	0.55	0	0	0	not significant
4047	REACTOME_CONDENSATION_OF_PROMETAPHASE_CHROMOSOMES	-1.18	0.55	0	0	0	not significant
4048	BIOCARTA_TSP1_PATHWAY	-1.18	0.54	0	0	0	not significant
4049	GO_NERVE_GROWTH_FACTOR_SIGNALING_PATHWAY	-1.18	0.54	0	0	0	not significant
4050	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_UP	-1.18	0.54	0	0	0	not significant
4051	REACTOME_DECTIN_2_FAMILY	-1.18	0.54	0	0	0	not significant
4052	GO_EUKARYOTIC_INITIATION_FACTOR_4E_BINDING	-1.18	0.53	0	0	0	not significant
4053	GO_REGULATION_OF_MACROPHAGE_DIFFERENTIATION	-1.18	0.53	0	0	0	not significant
4054	GO_NEGATIVE_REGULATION_OF_FIBROBLAST_APOPTOTIC_PROCESS	-1.18	0.51	0	0	0	not significant
4055	GO_REGULATION_OF_VITAMIN_D_RECEPTOR_SIGNALING_PATHWAY	-1.18	0.51	0	0	0	not significant
4056	GO_HEART_FIELD_SPECIFICATION	-1.18	0.50	0	0	0	not significant
4057	GO_HYDROLASE_ACTIVITY_ACTING_ON_ESTER_BONDS	-1.17	2.21	0	0	0	not significant
4058	GO_POSITIVE_REGULATION_OF_CATALYTIC_ACTIVITY	-1.17	1.97	0	0	0	not significant
4059	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	-1.17	1.92	0	0	0	not significant
4060	GO_REGULATION_OF_HYDROLASE_ACTIVITY	-1.17	1.76	0	0	0	not significant
4061	GO_APOPTOTIC_PROCESS	-1.17	1.74	0	0	0	not significant
4062	MARTINEZ_RB1_AND_TP53_TARGETS_UP	-1.17	1.50	0	0	0	not significant
4063	SENESE_HDAC3_TARGETS_UP	-1.17	1.15	0	0	0	not significant
4064	GO_CELL_BODY	-1.17	1.11	0	0	0	not significant
4065	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP	-1.17	1.03	0	0	0	not significant
4066	HALLMARK_INTERFERON_GAMMA_RESPONSE	-1.17	0.98	0	0	0	not significant
4067	GO_CANONICAL_WNT_SIGNALING_PATHWAY	-1.17	0.94	0	0	0	not significant
4068	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	-1.17	0.93	0	0	0	not significant
4069	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_2G	-1.17	0.92	0	0	0	not significant
4070	FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_UP	-1.17	0.91	0	0	0	not significant
4071	JIANG_HYPOXIA_NORMAL	-1.17	0.88	0	0	0	not significant
4072	IWANAGA_CARCINOGENESIS_BY_KRAS_UP	-1.17	0.87	0	0	0	not significant
4073	FERNANDEZ_BOUND_BY_MYC	-1.17	0.83	0	0	0	not significant
4074	GO_T_CELL_MEDIATED_IMMUNITY	-1.17	0.80	0	0	0	not significant
4075	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	-1.17	0.77	0	0	0	not significant
4076	XU_GH1_AUTOCRINE_TARGETS_UP	-1.17	0.76	0	0	0	not significant
4077	GO_GLUTAMINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	-1.17	0.74	0	0	0	not significant
4078	KEGG_RNA_DEGRADATION	-1.17	0.74	0	0	0	not significant
4079	GO_LEUKOCYTE_HOMEOSTASIS	-1.17	0.73	0	0	0	not significant
4080	GO_NEGATIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	-1.17	0.73	0	0	0	not significant
4081	GO_POSITIVE_REGULATION_OF_SMALL_MOLECULE_METABOLIC_PROC	-1.17	0.73	0	0	0	not significant
4082	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PE	-1.17	0.71	0	0	0	not significant
4083	STARK_HYPPOCAMPUS_22Q11_DELETION_UP	-1.17	0.69	0	0	0	not significant
4084	ROVERSI_GLIOMA_COPY_NUMBER_DN	-1.17	0.68	0	0	0	not significant
4085	GO_PEROXISOMAL_TRANSPORT	-1.17	0.67	0	0	0	not significant
4086	GO_POLYOL_METABOLIC_PROCESS	-1.17	0.67	0	0	0	not significant
4087	GO_POSITIVE_REGULATION_OF_G1_S_TRANSITION_OF_MITOTIC_CELL_	-1.17	0.67	0	0	0	not significant
4088	GO_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHO	-1.17	0.67	0	0	0	not significant
4089	BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN	-1.17	0.66	0	0	0	not significant
4090	GO_REGULATION_OF_SPROUTING_ANGIOGENESIS	-1.17	0.66	0	0	0	not significant
4091	JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER	-1.17	0.66	0	0	0	not significant
4092	GO_9PLUS2_MOTILE_CILIUM	-1.17	0.65	0	0	0	not significant
4093	GO_INTERLEUKIN_12_PRODUCTION	-1.17	0.64	0	0	0	not significant
4094	MA_MYELOID_DIFFERENTIATION_DN	-1.17	0.64	0	0	0	not significant
4095	GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	-1.17	0.63	0	0	0	not significant
4096	MOREIRA_RESPONSE_TO_TSA_UP	-1.17	0.63	0	0	0	not significant
4097	NEMETH_INFLAMMATORY_RESPONSE_LPS_DN	-1.17	0.63	0	0	0	not significant
4098	REACTOME_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHA	-1.17	0.62	0	0	0	not significant
4099	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	-1.17	0.61	0	0	0	not significant
4100	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	-1.17	0.61	0	0	0	not significant
4101	GO_NUCLEAR_EXOSOME_RNASE_COMPLEX_	-1.17	0.60	0	0	0	not significant
4102	NAKAMURA_METASTASIS_MODEL_DN	-1.17	0.60	0	0	0	not significant
4103	GO_ACETYL_COA_BIOSYNTHETIC_PROCESS	-1.17	0.59	0	0	0	not significant
4104	GO_CHONDROCYTE_DEVELOPMENT	-1.17	0.59	0	0	0	not significant
4105	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_RECEPTOR_BINDING	-1.17	0.59	0	0	0	not significant
4106	GO_MAP_KINASE_KINASE_ACTIVITY	-1.17	0.59	0	0	0	not significant
4107	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLE	-1.17	0.59	0	0	0	not significant
4108	GO_PHAGOCYTIC_CUP	-1.17	0.59	0	0	0	not significant
4109	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYME	-1.17	0.59	0	0	0	not significant
4110	GO_PROTEIN_DESTABILIZATION	-1.17	0.59	0	0	0	not significant
4111	GO_CELLULAR_MODIFIED_AMINO_ACID_CATABOLIC_PROCESS	-1.17	0.58	0	0	0	not significant
4112	GO_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	-1.17	0.58	0	0	0	not significant
4113	GROSS_ELK3_TARGETS_DN	-1.17	0.58	0	0	0	not significant
4114	GO_CELLULAR_RESPONSE_TO_LEUCINE_STARVATION	-1.17	0.56	0	0	0	not significant
4115	GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_OXIDASE	-1.17	0.55	0	0	0	not significant
4116	GO_KERATINOCYTE_MIGRATION	-1.17	0.55	0	0	0	not significant
4117	GO_NEGATIVE_REGULATION_OF_RYANODINE_SENSITIVE_CALCIUM_REL	-1.17	0.55	0	0	0	not significant
4118	GO_POSITIVE_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	-1.17	0.55	0	0	0	not significant
4119	GO_SPERM_PRINCIPAL_PIECE	-1.17	0.55	0	0	0	not significant
4120	GO_VITAMIN_D_RECEPTOR_SIGNALING_PATHWAY	-1.17	0.55	0	0	0	not significant
4121	GO_ACETYLCHOLINE_GATED_CATION_SELECTIVE_CHANNEL_ACTIVITY	-1.17	0.54	0	0	0	not significant
4122	REACTOME_ABC_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	-1.17	0.54	0	0	0	not significant
4123	REACTOME_GP1B_IX_V_ACTIVATION_SIGNALLING	-1.17	0.54	0	0	0	not significant
4124	GO_NEGATIVE_REGULATION_OF_METANEPHROS_DEVELOPMENT	-1.17	0.53	0	0	0	not significant
4125	GO_REGULATION_OF_WOUND_HEALING_SPREADING_OF_EPIDERMAL_C	-1.17	0.53	0	0	0	not significant
4126	GO_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	-1.17	0.53	0	0	0	not significant
4127	GO_TETRAHYDROBIOPTERIN_BIOSYNTHETIC_PROCESS	-1.17	0.53	0	0	0	not significant
4128	REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	-1.17	0.53	0	0	0	not significant
4129	CHR5Q34	-1.17	0.52	0	0	0	not significant
4130	GO_KETONE_BODY_BIOSYNTHETIC_PROCESS	-1.17	0.52	0	0	0	not significant

4131	GO_MODULATION_OF_MOLECULAR_FUNCTION_IN_OTHER_ORGANISM	-1.17	0.52	0	0	0	not significant
4132	GO_SERINE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	-1.17	0.52	0	0	0	not significant
4133	GO_PRE_MIRNA_BINDING	-1.17	0.51	0	0	0	not significant
4134	GO_SECONDARY_HEART_FIELD_SPECIFICATION	-1.17	0.51	0	0	0	not significant
4135	GO_SERINE_TYPE_EXOPEPTIDASE_ACTIVITY	-1.17	0.51	0	0	0	not significant
4136	GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SU	-1.17	0.50	0	0	0	not significant
4137	GO_POSITIVE_REGULATION_OF_MOLECULAR_FUNCTION	-1.16	1.96	0	0	0	not significant
4138	GO_INTERSPECIES_INTERACTION_BETWEEN_ORGANISMS	-1.16	1.75	0	0	0	not significant
4139	GO_REGULATION_OF_RESPONSE_TO_STRESS	-1.16	1.71	0	0	0	not significant
4140	GO_CELL_ACTIVATION	-1.16	1.69	0	0	0	not significant
4141	GO_GROWTH	-1.16	1.52	0	0	0	not significant
4142	GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCE	-1.16	1.47	0	0	0	not significant
4143	GO_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	-1.16	1.17	0	0	0	not significant
4144	GO_REGULATION_OF_CYTOSKELETON_ORGANIZATION	-1.16	1.15	0	0	0	not significant
4145	LIM_MAMMARY_STEM_CELL_UP	-1.16	0.99	0	0	0	not significant
4146	GO_COGNITION	-1.16	0.92	0	0	0	not significant
4147	GO_ORGANIC_ACID_CATABOLIC_PROCESS	-1.16	0.88	0	0	0	not significant
4148	WANG_TUMOR_INVASIVENESS_DN	-1.16	0.88	0	0	0	not significant
4149	GO_PROTEIN_STABILIZATION	-1.16	0.87	0	0	0	not significant
4150	GO_RESPONSE_TO_VIRUS	-1.16	0.87	0	0	0	not significant
4151	REACTOME_TOLL_LIKE_RECEPTOR_CASCADES	-1.16	0.84	0	0	0	not significant
4152	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	-1.16	0.83	0	0	0	not significant
4153	GO_NUCLEOTIDE_EXCISION_REPAIR	-1.16	0.79	0	0	0	not significant
4154	KEGG_CELL_CYCLE	-1.16	0.79	0	0	0	not significant
4155	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_DN	-1.16	0.79	0	0	0	not significant
4156	GO_CHROMATIN_DNA_BINDING	-1.16	0.78	0	0	0	not significant
4157	GO_RIBONUCLEASE_ACTIVITY	-1.16	0.78	0	0	0	not significant
4158	REACTOME_CHROMOSOME_MAINTENANCE	-1.16	0.77	0	0	0	not significant
4159	REACTOME_SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE_SAS	-1.16	0.77	0	0	0	not significant
4160	GO_CARBOHYDRATE_TRANSMEMBRANE_TRANSPORT	-1.16	0.76	0	0	0	not significant
4161	GO_IMPORT_INTO_NUCLEUS	-1.16	0.76	0	0	0	not significant
4162	NGUYEN_NOTCH1_TARGETS_DN	-1.16	0.76	0	0	0	not significant
4163	BMI1_DN_MEL18_DN.V1_UP	-1.16	0.75	0	0	0	not significant
4164	GO_AMINO_ACID_TRANSPORT	-1.16	0.75	0	0	0	not significant
4165	GO_REGULATION_OF_MRNA_PROCESSING	-1.16	0.75	0	0	0	not significant
4166	GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_BIOSYNTHETIC_PRC	-1.16	0.74	0	0	0	not significant
4167	GO_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING	-1.16	0.74	0	0	0	not significant
4168	GROSS_HYPOXIA_VIA_ELK3_DN	-1.16	0.73	0	0	0	not significant
4169	DE_YY1_TARGETS_DN	-1.16	0.72	0	0	0	not significant
4170	GO_N_METHYLTRANSFERASE_ACTIVITY	-1.16	0.71	0	0	0	not significant
4171	GO_CARDIAC_CHAMBER_MORPHOGENESIS	-1.16	0.69	0	0	0	not significant
4172	GO_EPHRIN_RECEPTOR_SIGNALING_PATHWAY	-1.16	0.69	0	0	0	not significant
4173	KAYO_CALORIE_RESTRICTION_MUSCLE_DN	-1.16	0.69	0	0	0	not significant
4174	ZHANG_PROLIFERATING_VS_QUIESCENT	-1.16	0.69	0	0	0	not significant
4175	BMI1_DN.V1_UP	-1.16	0.68	0	0	0	not significant
4176	DIRMEIER_LMP1_RESPONSE_LATE_UP	-1.16	0.68	0	0	0	not significant
4177	GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEI	-1.16	0.68	0	0	0	not significant
4178	GO_PROTEIN_HOMOTETRAMERIZATION	-1.16	0.68	0	0	0	not significant
4179	GO_MODIFICATION_BY_SYMBIONT_OF_HOST_MORPHOLOGY_OR_PHYSI	-1.16	0.67	0	0	0	not significant
4180	PID_RAC1_PATHWAY	-1.16	0.66	0	0	0	not significant
4181	GO_EXOGENOUS_PROTEIN_BINDING	-1.16	0.65	0	0	0	not significant
4182	GO_HISTONE_PHOSPHORYLATION	-1.16	0.65	0	0	0	not significant
4183	GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_INCISION	-1.16	0.65	0	0	0	not significant
4184	GO_T_CELL_APOPTOTIC_PROCESS	-1.16	0.65	0	0	0	not significant
4185	MARSON_FOXP3_TARGETS_UP	-1.16	0.65	0	0	0	not significant
4186	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP	-1.16	0.64	0	0	0	not significant
4187	GO_ACIDIC_AMINO_ACID_TRANSPORT	-1.16	0.63	0	0	0	not significant
4188	GUO_HEX_TARGETS_DN	-1.16	0.63	0	0	0	not significant
4189	PID_RHOA_PATHWAY	-1.16	0.63	0	0	0	not significant
4190	CHR12P12	-1.16	0.62	0	0	0	not significant
4191	COLLIS_PRKDC_SUBSTRATES	-1.16	0.62	0	0	0	not significant
4192	WILLERT_WNT_SIGNALING	-1.16	0.62	0	0	0	not significant
4193	GO_POSITIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	-1.16	0.61	0	0	0	not significant
4194	KEGG_GLUTATHIONE_METABOLISM	-1.16	0.61	0	0	0	not significant
4195	CROONQUIST_NRAS_SIGNALING_UP	-1.16	0.60	0	0	0	not significant
4196	GO_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GROWTH_FA	-1.16	0.60	0	0	0	not significant
4197	GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	-1.16	0.60	0	0	0	not significant
4198	HARRIS_BRAIN_CANCER_PROGENITORS	-1.16	0.60	0	0	0	not significant
4199	STEIN_ESRRA_TARGETS_RESPONSIVE_TO_ESTROGEN_DN	-1.16	0.60	0	0	0	not significant
4200	BERENJENO_ROCK_SIGNALING_NOT_VIA_RHOA_UP	-1.16	0.59	0	0	0	not significant
4201	GUILLAUMOND_KLF10_TARGETS_DN	-1.16	0.59	0	0	0	not significant
4202	GENTILE_UV_LOW_DOSE_UP	-1.16	0.58	0	0	0	not significant
4203	GO_ANTERIOR_POSTERIOR_AXIS_SPECIFICATION	-1.16	0.58	0	0	0	not significant
4204	GO_ANTIMICROBIAL_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_ANT	-1.16	0.58	0	0	0	not significant
4205	REACTOME_PROTEIN_METHYLATION	-1.16	0.58	0	0	0	not significant
4206	VARELA_ZMPSTE24_TARGETS_DN	-1.16	0.58	0	0	0	not significant
4207	GO_ASTROCYTE_DEVELOPMENT	-1.16	0.57	0	0	0	not significant
4208	GO_HISTONE_H2A_K63_LINKED_UBIQUITINATION	-1.16	0.57	0	0	0	not significant
4209	GO_RESPONSE_TO_OXYGEN_RADICAL	-1.16	0.57	0	0	0	not significant
4210	BIOCARTA_RANBP2_PATHWAY	-1.16	0.56	0	0	0	not significant
4211	GO_REGULATION_OF_METANEPHROS_DEVELOPMENT	-1.16	0.56	0	0	0	not significant
4212	SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_DN	-1.16	0.56	0	0	0	not significant
4213	DE_YY1_TARGETS_UP	-1.16	0.55	0	0	0	not significant
4214	GO_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYS	-1.16	0.55	0	0	0	not significant
4215	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP	-1.16	0.55	0	0	0	not significant
4216	REACTOME_OAS_ANTIVIRAL_RESPONSE	-1.16	0.55	0	0	0	not significant
4217	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR	-1.16	0.55	0	0	0	not significant
4218	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	-1.16	0.54	0	0	0	not significant
4219	GO_POSITIVE_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PI	-1.16	0.54	0	0	0	not significant
4220	BIOCARTA_SRCRPTP_PATHWAY	-1.16	0.53	0	0	0	not significant
4221	GO_ADENOSINE_DEAMINASE_ACTIVITY	-1.16	0.53	0	0	0	not significant
4222	GO_DEATH_DOMAIN_BINDING	-1.16	0.53	0	0	0	not significant
4223	GO_GERM_CELL_NUCLEUS	-1.16	0.53	0	0	0	not significant
4224	GO_LUNG_CELL_DIFFERENTIATION	-1.16	0.53	0	0	0	not significant
4225	GO_MAST_CELL_MIGRATION	-1.16	0.53	0	0	0	not significant
4226	GO_L_SERINE_BIOSYNTHETIC_PROCESS	-1.16	0.52	0	0	0	not significant
4227	GO_MORPHOGENESIS_OF_AN_EPITHELIAL_FOLD	-1.16	0.52	0	0	0	not significant
4228	GO_OBSERVATIONAL_LEARNING	-1.16	0.51	0	0	0	not significant
4229	GO_PLATELET_DENSE_GRANULE_MEMBRANE	-1.16	0.51	0	0	0	not significant
4230	GO_LSM1_7_PAT1_COMPLEX	-1.16	0.50	0	0	0	not significant
4231	GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_BIOSYNTHETIC_I	-1.16	0.50	0	0	0	not significant
4232	GO_TELOMERASE_ACTIVITY	-1.16	0.50	0	0	0	not significant
4233	GO_L_GLUTAMATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.16	0.49	0	0	0	not significant
4234	GO_POSITIVE_REGULATION_OF_HISTONE_UBIQUITINATION	-1.16	0.48	0	0	0	not significant
4235	INAMURA_LUNG_CANCER_SCC_DN	-1.16	0.48	0	0	0	not significant
4236	GO_CELL_CYCLE	-1.15	4.00	0	0	0	not significant
4237	GO_REGULATION_OF_CELL_CYCLE	-1.15	4.00	0	0	0	not significant
4238	GO_CYTOPLASMIC_VESICLE_PART	-1.15	1.60	0	0	0	not significant
4239	GO_POSITIVE_REGULATION_OF_TRANSPORT	-1.15	1.39	0	0	0	not significant

4240	GO_NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATI	-1.15	1.25	0	0	0	not significant
4241	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3	-1.15	1.25	0	0	0	not significant
4242	GO_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.15	1.23	0	0	0	not significant
4243	GO_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABO	-1.15	1.22	0	0	0	not significant
4244	TOYOTA_TARGETS_OF_MIR34B_AND_MIR34C	-1.15	1.19	0	0	0	not significant
4245	GO_MUSCLE_STRUCTURE_DEVELOPMENT	-1.15	1.18	0	0	0	not significant
4246	GO_DEVELOPMENTAL_GROWTH	-1.15	1.14	0	0	0	not significant
4247	SMID_BREAST_CANCER_NORMAL_LIKE_UP	-1.15	1.05	0	0	0	not significant
4248	GO_REGULATION_OF_BODY_FLUID_LEVELS	-1.15	0.95	0	0	0	not significant
4249	GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	-1.15	0.95	0	0	0	not significant
4250	GO_RESPONSE_TO_ANTIBIOTIC	-1.15	0.90	0	0	0	not significant
4251	E2F1_UP.V1_UP	-1.15	0.85	0	0	0	not significant
4252	GO_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	-1.15	0.85	0	0	0	not significant
4253	GO_OUTER_MEMBRANE	-1.15	0.84	0	0	0	not significant
4254	WANG_MLL_TARGETS	-1.15	0.83	0	0	0	not significant
4255	HALLMARK_DNA_REPAIR	-1.15	0.81	0	0	0	not significant
4256	PENG_GLUCOSE_DEPRIVATION_DN	-1.15	0.77	0	0	0	not significant
4257	ZHANG_TLX_TARGETS_DN	-1.15	0.76	0	0	0	not significant
4258	GO_REGULATION_OF_LEUKOCYTE_MIGRATION	-1.15	0.75	0	0	0	not significant
4259	SAFFORD_T_LYMPHOCYTE_ANERGY	-1.15	0.72	0	0	0	not significant
4260	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_INITIATION	-1.15	0.70	0	0	0	not significant
4261	GO_PROTON_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.15	0.69	0	0	0	not significant
4262	HALLMARK_BILE_ACID_METABOLISM	-1.15	0.69	0	0	0	not significant
4263	GO_EYE_MORPHOGENESIS	-1.15	0.68	0	0	0	not significant
4264	GO_REGULATION_OF_UBIQUITIN_PROTEIN_TRANSFERASE_ACTIVITY	-1.15	0.68	0	0	0	not significant
4265	REACTOME_FCGAMMA_RECEPTOR_FCGR_DEPENDENT_PHAGOCYTOSI	-1.15	0.68	0	0	0	not significant
4266	ROSS_ACUTE_MYELOID_LEUKEMIA_CBF	-1.15	0.68	0	0	0	not significant
4267	GAVIN_FOXP3_TARGETS_CLUSTER_T4	-1.15	0.67	0	0	0	not significant
4268	RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POORLY_UP	-1.15	0.67	0	0	0	not significant
4269	ROSS_AML_WITH_MLL_FUSIONS	-1.15	0.67	0	0	0	not significant
4270	GO_LYMPHOCYTE_APOPTOTIC_PROCESS	-1.15	0.66	0	0	0	not significant
4271	GO_FIBROBLAST_PROLIFERATION	-1.15	0.65	0	0	0	not significant
4272	GO_IRE1_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	-1.15	0.65	0	0	0	not significant
4273	REACTOME_INOSITOL_PHOSPHATE_METABOLISM	-1.15	0.65	0	0	0	not significant
4274	REACTOME_DNA_DAMAGE_RECOGNITION_IN_GG_NER	-1.15	0.62	0	0	0	not significant
4275	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_UP	-1.15	0.62	0	0	0	not significant
4276	GO_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	-1.15	0.61	0	0	0	not significant
4277	REACTOME_SIGNALING_BY_FGFR2	-1.15	0.61	0	0	0	not significant
4278	GO_CHAPERONE_COFACTOR_DEPENDENT_PROTEIN_REFOLDING	-1.15	0.59	0	0	0	not significant
4279	GO_MOVEMENT_IN_ENVIRONMENT_OF_OTHER_ORGANISM_INVOLVED_I	-1.15	0.59	0	0	0	not significant
4280	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OX	-1.15	0.59	0	0	0	not significant
4281	REACTOME_GABA_RECEPTOR_ACTIVATION	-1.15	0.59	0	0	0	not significant
4282	GO_GLANDULAR_EPITHELIAL_CELL_DEVELOPMENT	-1.15	0.58	0	0	0	not significant
4283	GO_QUINONE_BINDING	-1.15	0.58	0	0	0	not significant
4284	GO_RESPONSE_TO_AUDITORY_STIMULUS	-1.15	0.58	0	0	0	not significant
4285	VALK_AML_WITH_FLT3_ITD	-1.15	0.58	0	0	0	not significant
4286	VANASSE_BCL2_TARGETS_DN	-1.15	0.58	0	0	0	not significant
4287	ZHU_CMV_8_HR_DN	-1.15	0.58	0	0	0	not significant
4288	BURTON_ADIPOGENESIS_PEAK_AT_2HR	-1.15	0.57	0	0	0	not significant
4289	GO_NEGATIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	-1.15	0.57	0	0	0	not significant
4290	GO_NEGATIVE_REGULATION_OF_GLIOGENESIS	-1.15	0.57	0	0	0	not significant
4291	GO_RESPONSE_TO_AMPHETAMINE	-1.15	0.57	0	0	0	not significant
4292	TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_UP	-1.15	0.57	0	0	0	not significant
4293	CHR2Q21	-1.15	0.56	0	0	0	not significant
4294	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_P	-1.15	0.56	0	0	0	not significant
4295	GO_MELANIN_BIOSYNTHETIC_PROCESS	-1.15	0.56	0	0	0	not significant
4296	GO_NEGATIVE_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	-1.15	0.56	0	0	0	not significant
4297	GO_POSITIVE_REGULATION_OF_B_CELL_DIFFERENTIATION	-1.15	0.56	0	0	0	not significant
4298	GO_DEATH_RECEPTOR_BINDING	-1.15	0.55	0	0	0	not significant
4299	GO_EXTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE	-1.15	0.55	0	0	0	not significant
4300	GO_RESPONSE_TO_NICOTINE	-1.15	0.55	0	0	0	not significant
4301	GO_MITOCHONDRIAL_FRAGMENTATION_INVOLVED_IN_APOPTOTIC_PRO	-1.15	0.54	0	0	0	not significant
4302	TERAMOTO_OPN_TARGETS_CLUSTER_6	-1.15	0.54	0	0	0	not significant
4303	FIGUEROA_AML_METHYLATION_CLUSTER_5_UP	-1.15	0.53	0	0	0	not significant
4304	GO_BETA_CATENIN_DESTRUCTION_COMPLEX	-1.15	0.53	0	0	0	not significant
4305	GO_CELLULAR_RESPONSE_TO_INTERFERON_BETA	-1.15	0.53	0	0	0	not significant
4306	GO_NADH_PYROPHOSPHATASE_ACTIVITY	-1.15	0.53	0	0	0	not significant
4307	GO_PHOTORECEPTOR_CONNECTING_CILIUM	-1.15	0.53	0	0	0	not significant
4308	GO_PRESPLICEOSOME	-1.15	0.53	0	0	0	not significant
4309	GO_EXTRINSIC_COMPONENT_OF_POSTSYNAPTIC_MEMBRANE	-1.15	0.52	0	0	0	not significant
4310	GO_NEGATIVE_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	-1.15	0.52	0	0	0	not significant
4311	GO_POSITIVE_REGULATION_OF_BLOOD_PRESSURE	-1.15	0.52	0	0	0	not significant
4312	PID_S1P_S1P4_PATHWAY	-1.15	0.52	0	0	0	not significant
4313	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_UP	-1.15	0.52	0	0	0	not significant
4314	GO_CELLULAR_SODIUM_ION_HOMEOSTASIS	-1.15	0.51	0	0	0	not significant
4315	PHONG_TNF_TARGETS_DN	-1.15	0.51	0	0	0	not significant
4316	REACTOME_LINOLEIC_ACID_LA_METABOLISM	-1.15	0.51	0	0	0	not significant
4317	FUKUSHIMA_TNFSF11_TARGETS	-1.15	0.50	0	0	0	not significant
4318	GO_CHROMO_SHADOW_DOMAIN_BINDING	-1.15	0.50	0	0	0	not significant
4319	GO_NEGATIVE_REGULATION_OF_MEMBRANE_POTENTIAL	-1.15	0.50	0	0	0	not significant
4320	GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_4_SIGNALING_PATHWAY	-1.15	0.50	0	0	0	not significant
4321	GO_U4_SNRNA_3_END_PROCESSING	-1.15	0.50	0	0	0	not significant
4322	REICHERT_G1S_REGULATORS_AS_PI3K_TARGETS	-1.15	0.50	0	0	0	not significant
4323	GO_ASTROCYTE_CELL_MIGRATION	-1.15	0.49	0	0	0	not significant
4324	KIM_RESPONSE_TO_TSA_AND_DECITABINE_DN	-1.15	0.49	0	0	0	not significant
4325	GO_POSITIVE_REGULATION_OF_PROTEIN_MONOUBIQUITINATION	-1.15	0.48	0	0	0	not significant
4326	GO_PURINE_NUCLEOSIDE_DIPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.15	0.48	0	0	0	not significant
4327	GO_REGULATION_OF_CATECHOLAMINE_METABOLIC_PROCESS	-1.15	0.48	0	0	0	not significant
4328	GO_REGULATION_OF_PEPTIDYL_CYSTEINE_S_NITROSYLATION	-1.15	0.48	0	0	0	not significant
4329	REACTOME_INTERLEUKIN_1_PROCESSING	-1.15	0.48	0	0	0	not significant
4330	GO_INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	-1.15	0.47	0	0	0	not significant
4331	BENPORATH_NANOG_TARGETS	-1.14	1.72	0	0	0	not significant
4332	GO_CELL_MOTILITY	-1.14	1.72	0	0	0	not significant
4333	GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	-1.14	1.17	0	0	0	not significant
4334	REACTOME_DNA_REPAIR	-1.14	1.13	0	0	0	not significant
4335	PHONG_TNF_RESPONSE_NOT_VIA_P38	-1.14	1.10	0	0	0	not significant
4336	GO_RESPONSE_TO_INORGANIC_SUBSTANCE	-1.14	1.04	0	0	0	not significant
4337	GRYDER_PAX3FOXO1_ENHANCERS_KO_DOWN	-1.14	1.00	0	0	0	not significant
4338	GO_REGULATION_OF_HEMOPOIESIS	-1.14	0.94	0	0	0	not significant
4339	GO_SIDE_OF_MEMBRANE	-1.14	0.93	0	0	0	not significant
4340	GO_MACROMOLECULE_METHYLATION	-1.14	0.92	0	0	0	not significant
4341	GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	-1.14	0.92	0	0	0	not significant
4342	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP	-1.14	0.91	0	0	0	not significant
4343	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN	-1.14	0.89	0	0	0	not significant
4344	GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	-1.14	0.86	0	0	0	not significant
4345	GO_AGING	-1.14	0.83	0	0	0	not significant
4346	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_UP	-1.14	0.82	0	0	0	not significant
4347	SRC_UP.V1_UP	-1.14	0.77	0	0	0	not significant
4348	GO_RECEPTOR_MEDIATED_ENDOCYTOSIS	-1.14	0.76	0	0	0	not significant

4349	GO_REGULATION_OF_DEPHOSPHORYLATION	-1.14	0.74	0	0	0	not significant
4350	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	-1.14	0.73	0	0	0	not significant
4351	LI_AMPLIFIED_IN_LUNG_CANCER	-1.14	0.73	0	0	0	not significant
4352	IWANAGA_CARCINOGENESIS_BY_KRAS_PTEN_UP	-1.14	0.72	0	0	0	not significant
4353	KEGG_PYRIMIDINE_METABOLISM	-1.14	0.70	0	0	0	not significant
4354	TSAI_RESPONSE_TO_IONIZING_RADIATION	-1.14	0.70	0	0	0	not significant
4355	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN	-1.14	0.69	0	0	0	not significant
4356	GO_MRNA_3_UTR_BINDING	-1.14	0.69	0	0	0	not significant
4357	GO_VITAMIN_METABOLIC_PROCESS	-1.14	0.69	0	0	0	not significant
4358	WATANABE_RECTAL_CANCER_RADIOTHERAPY_RESPONSIVE_UP	-1.14	0.69	0	0	0	not significant
4359	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	-1.14	0.66	0	0	0	not significant
4360	GO_CARDIAC_CHAMBER_DEVELOPMENT	-1.14	0.65	0	0	0	not significant
4361	REACTOME_PI_METABOLISM	-1.14	0.65	0	0	0	not significant
4362	GO_ACTIN_MEDIATED_CELL_CONTRACTION	-1.14	0.64	0	0	0	not significant
4363	GO_NEGATIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	-1.14	0.64	0	0	0	not significant
4364	GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	-1.14	0.64	0	0	0	not significant
4365	LEE_NEURAL_CREST_STEM_CELL_DN	-1.14	0.64	0	0	0	not significant
4366	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE_D	-1.14	0.64	0	0	0	not significant
4367	BIOCARTA_HIVNEF_PATHWAY	-1.14	0.63	0	0	0	not significant
4368	GO_ACTIN_FILAMENT_BASED_MOVEMENT	-1.14	0.63	0	0	0	not significant
4369	PID_CASPASE_PATHWAY	-1.14	0.63	0	0	0	not significant
4370	PTEN_DN.V2_UP	-1.14	0.63	0	0	0	not significant
4371	GO_POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	-1.14	0.62	0	0	0	not significant
4372	GO_PROTEIN_TRANSPORT_ALONG_MICROTUBULE	-1.14	0.62	0	0	0	not significant
4373	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN	-1.14	0.62	0	0	0	not significant
4374	NEMETH_INFLAMMATORY_RESPONSE_LPS_UP	-1.14	0.62	0	0	0	not significant
4375	FONTAINE_PAPILLARY_THYROID_CARCINOMA_UP	-1.14	0.61	0	0	0	not significant
4376	GO_T_CELL_MEDIATED_CYTOTOXICITY	-1.14	0.61	0	0	0	not significant
4377	GO_VISUAL_BEHAVIOR	-1.14	0.61	0	0	0	not significant
4378	BROWNE_HCMV_INFECTION_2HR_DN	-1.14	0.60	0	0	0	not significant
4379	GO_REGULATION_OF_BEHAVIOR	-1.14	0.60	0	0	0	not significant
4380	GO_REGULATION_OF_HEART_GROWTH	-1.14	0.60	0	0	0	not significant
4381	GO_REGULATION_OF_LIPID_STORAGE	-1.14	0.60	0	0	0	not significant
4382	GO_DICARBOXYLIC_ACID_METABOLIC_PROCESS	-1.14	0.59	0	0	0	not significant
4383	GO_MHC_PROTEIN_BINDING	-1.14	0.59	0	0	0	not significant
4384	REACTOME_PERK_REGULATES_GENE_EXPRESSION	-1.14	0.59	0	0	0	not significant
4385	GO_DOPAMINE_RECEPTOR_SIGNALING_PATHWAY	-1.14	0.58	0	0	0	not significant
4386	GO_L_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.14	0.58	0	0	0	not significant
4387	GO_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	-1.14	0.58	0	0	0	not significant
4388	BIOCARTA_TNFR1_PATHWAY	-1.14	0.57	0	0	0	not significant
4389	BRACHAT_RESPONSE_TO_METHOTREXATE_DN	-1.14	0.57	0	0	0	not significant
4390	GO_PROTEIN_LOCALIZATION_TO_CHROMATIN	-1.14	0.57	0	0	0	not significant
4391	GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	-1.14	0.57	0	0	0	not significant
4392	CHR17Q22	-1.14	0.56	0	0	0	not significant
4393	HUANG_FOXA2_TARGETS_DN	-1.14	0.56	0	0	0	not significant
4394	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_15	-1.14	0.56	0	0	0	not significant
4395	CHR4Q25	-1.14	0.55	0	0	0	not significant
4396	GO_INTERCALATED_DISC	-1.14	0.55	0	0	0	not significant
4397	GO_NEUROMUSCULAR_PROCESS_CONTROLLING_POSTURE	-1.14	0.55	0	0	0	not significant
4398	GO_REGULATION_OF_MRNA_3_END_PROCESSING	-1.14	0.55	0	0	0	not significant
4399	KEGG_TYPE_I_DIABETES_MELLITUS	-1.14	0.55	0	0	0	not significant
4400	LEE_LIVER_CANCER_MYC_TGFA_DN	-1.14	0.55	0	0	0	not significant
4401	PID_NECTIN_PATHWAY	-1.14	0.55	0	0	0	not significant
4402	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN	-1.14	0.55	0	0	0	not significant
4403	BIOCARTA_CDK5_PATHWAY	-1.14	0.54	0	0	0	not significant
4404	GO_PLASMA_MEMBRANE_TUBULATION	-1.14	0.54	0	0	0	not significant
4405	GO_NEURON_PROJECTION_MEMBRANE	-1.14	0.53	0	0	0	not significant
4406	GO_O_METHYLTRANSFERASE_ACTIVITY	-1.14	0.53	0	0	0	not significant
4407	KEGG_STEROID_BIOSYNTHESIS	-1.14	0.53	0	0	0	not significant
4408	MIKKELSEN_MEF_ICP_WITH_H3K4ME3_AND_H3K27ME3	-1.14	0.53	0	0	0	not significant
4409	PID_HIF1A_PATHWAY	-1.14	0.53	0	0	0	not significant
4410	REACTOME_DISEASES_ASSOCIATED_WITH_GLYCOSYLATION_PRECURS	-1.14	0.53	0	0	0	not significant
4411	RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POORLY_DN	-1.14	0.53	0	0	0	not significant
4412	GO_CALCIUM_MEDIATED_SIGNALING_USING_INTRACELLULAR_CALCIUM_	-1.14	0.52	0	0	0	not significant
4413	GO_N_TERMINAL_PEPTIDYL_METHIONINE_ACETYLATION	-1.14	0.52	0	0	0	not significant
4414	GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATI	-1.14	0.52	0	0	0	not significant
4415	KEGG_RIBOFLAVIN_METABOLISM	-1.14	0.52	0	0	0	not significant
4416	REACTOME_ENOS_ACTIVATION	-1.14	0.52	0	0	0	not significant
4417	SESTO_RESPONSE_TO_UV_C3	-1.14	0.52	0	0	0	not significant
4418	GO_CHEMOKINE_SECRETION	-1.14	0.51	0	0	0	not significant
4419	GO_NEURAL_CREST_FORMATION	-1.14	0.51	0	0	0	not significant
4420	GO_PHOSPHATIDYLETHANOLAMINE_BIOSYNTHETIC_PROCESS	-1.14	0.51	0	0	0	not significant
4421	GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_DEHYDROGENAS	-1.14	0.50	0	0	0	not significant
4422	GO_FRUCTOSE_6_PHOSPHATE_METABOLIC_PROCESS	-1.14	0.50	0	0	0	not significant
4423	GO_MOTOR_NEURON_APOPTOTIC_PROCESS	-1.14	0.50	0	0	0	not significant
4424	GO_REGULATION_OF_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_AC	-1.14	0.50	0	0	0	not significant
4425	GO_REGULATION_OF_RECEPTOR_CLUSTERING	-1.14	0.50	0	0	0	not significant
4426	REACTOME_REGULATION_OF_GENE_EXPRESSION_BY_HYPOXIA_INDUCI	-1.14	0.50	0	0	0	not significant
4427	GO_GLOMERULAR_EPITHELIUM_DEVELOPMENT	-1.14	0.49	0	0	0	not significant
4428	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DEGRANULATION	-1.14	0.49	0	0	0	not significant
4429	GO_NEGATIVE_REGULATION_OF_RETINOIC_ACID_RECEPTOR_SIGNALIN	-1.14	0.49	0	0	0	not significant
4430	GO_POSITIVE_REGULATION_OF_NEURON_MIGRATION	-1.14	0.49	0	0	0	not significant
4431	GO_RESPONSE_TO_NITROSATIVE_STRESS	-1.14	0.49	0	0	0	not significant
4432	GO_RNA_DIRECTED_DNA_POLYMERASE_ACTIVITY	-1.14	0.49	0	0	0	not significant
4433	BIOCARTA_DSP_PATHWAY	-1.14	0.48	0	0	0	not significant
4434	TAGHAVI_NEOPLASTIC_TRANSFORMATION	-1.14	0.48	0	0	0	not significant
4435	GO_NUCLEAR_RETENTION_OF_PRE_MRNA_AT_THE_SITE_OF_TRANSCR	-1.14	0.46	0	0	0	not significant
4436	GO_REGULATION_OF_GOLGI_TO_PLASMA_MEMBRANE_PROTEIN_TRAN	-1.14	0.44	0	0	0	not significant
4437	GO_HYDROXYMETHYL__FORMYL_AND_RELATED_TRANSFERASE_ACTIV	-1.14	0.43	0	0	0	not significant
4438	GO_POSITIVE_REGULATION_OF_PROTEIN_METABOLIC_PROCESS	-1.13	1.94	0	0	0	not significant
4439	GO_PROTEOLYSIS	-1.13	1.70	0	0	0	not significant
4440	GO_REGULATION_OF_TRANSPORT	-1.13	1.28	0	0	0	not significant
4441	GO_BIOLOGICAL_ADHESION	-1.13	1.25	0	0	0	not significant
4442	GO_ORGANELLE_LOCALIZATION	-1.13	0.99	0	0	0	not significant
4443	GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	-1.13	0.98	0	0	0	not significant
4444	GO_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	-1.13	0.94	0	0	0	not significant
4445	GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_UP	-1.13	0.92	0	0	0	not significant
4446	GO_MYELOID_CELL_DIFFERENTIATION	-1.13	0.90	0	0	0	not significant
4447	GO_VESICLE_ORGANIZATION	-1.13	0.84	0	0	0	not significant
4448	GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS	-1.13	0.83	0	0	0	not significant
4449	VANOEVELEN_MYOGENESIS_SIN3A_TARGETS	-1.13	0.79	0	0	0	not significant
4450	GO_CARBOHYDRATE_BINDING	-1.13	0.77	0	0	0	not significant
4451	GO_NEGATIVE_REGULATION_OF_CELL_ADHESION	-1.13	0.77	0	0	0	not significant
4452	YAGI_AML_FAB_MARKERS	-1.13	0.77	0	0	0	not significant
4453	GO_CELL_CELL_JUNCTION	-1.13	0.74	0	0	0	not significant
4454	GO_PHAGOCYTIC_VESICLE	-1.13	0.73	0	0	0	not significant
4455	STK33_SKM_DN	-1.13	0.73	0	0	0	not significant
4456	RIZKI_TUMOR_INVASIVENESS_3D_DN	-1.13	0.72	0	0	0	not significant
4457	GO_REGULATION_OF_CIRCADIAN_RHYTHM	-1.13	0.68	0	0	0	not significant

4458	SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC	-1.13	0.68	0	0	0	not significant
4459	GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	-1.13	0.67	0	0	0	not significant
4460	GO_HEART_MORPHOGENESIS	-1.13	0.66	0	0	0	not significant
4461	GO_P_BODY	-1.13	0.66	0	0	0	not significant
4462	REACTOME_TOLL_LIKE_RECEPTOR_9_TLR9_CASCADE	-1.13	0.66	0	0	0	not significant
4463	GO_INOSITOL_PHOSPHATE_METABOLIC_PROCESS	-1.13	0.65	0	0	0	not significant
4464	REACTOME_PROCESSING_OF_DNA_DOUBLE_STRAND_BREAK_ENDS	-1.13	0.65	0	0	0	not significant
4465	MEL18_DN.V1_UP	-1.13	0.64	0	0	0	not significant
4466	HUANG_DASATINIB_RESISTANCE_DN	-1.13	0.63	0	0	0	not significant
4467	FAELT_B_CLL_WITH_VH_REARRANGEMENTS_DN	-1.13	0.62	0	0	0	not significant
4468	GO_MEMORY	-1.13	0.62	0	0	0	not significant
4469	MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_DN	-1.13	0.62	0	0	0	not significant
4470	PID_TGFBR_PATHWAY	-1.13	0.62	0	0	0	not significant
4471	GO_MICROVILLUS	-1.13	0.61	0	0	0	not significant
4472	HUMMEL_BURKITTS_LYMPHOMA_UP	-1.13	0.61	0	0	0	not significant
4473	GO_ASSOCIATIVE_LEARNING	-1.13	0.60	0	0	0	not significant
4474	GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	-1.13	0.60	0	0	0	not significant
4475	REACTOME_SIGNALING_BY_FGFR	-1.13	0.60	0	0	0	not significant
4476	GO_ATTACHMENT_OF_SPINDLE_MICROTUBULES_TO_KINETOCHORE	-1.13	0.59	0	0	0	not significant
4477	GO_GLYCOSYL_COMPOUND_METABOLIC_PROCESS	-1.13	0.59	0	0	0	not significant
4478	GO_PROTEIN_LOCALIZATION_TO_GOLGI_APPARATUS	-1.13	0.59	0	0	0	not significant
4479	GO_REGULATION_OF_ATPASE_ACTIVITY	-1.13	0.59	0	0	0	not significant
4480	ROSS_AML_WITH_AML1_ETO_FUSION	-1.13	0.59	0	0	0	not significant
4481	GO_BODY_FLUID_SECRETION	-1.13	0.58	0	0	0	not significant
4482	GO_CENTROMERE_COMPLEX_ASSEMBLY	-1.13	0.58	0	0	0	not significant
4483	REACTOME_SIRT1_NEGATIVELY_REGULATES_RRNA_EXPRESSION	-1.13	0.58	0	0	0	not significant
4484	CAFFAREL_RESPONSE_TO_THC_24HR_5_UP	-1.13	0.56	0	0	0	not significant
4485	STEARMAN_LUNG_CANCER_EARLY_VS_LATE_DN	-1.13	0.56	0	0	0	not significant
4486	VARELA_ZMPSTE24_TARGETS_UP	-1.13	0.56	0	0	0	not significant
4487	BURTON_ADIPOGENESIS_10	-1.13	0.55	0	0	0	not significant
4488	GO_GUANOSINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-1.13	0.55	0	0	0	not significant
4489	GO_LUNG_ALVEOLUS_DEVELOPMENT	-1.13	0.55	0	0	0	not significant
4490	PID_ATR_PATHWAY	-1.13	0.55	0	0	0	not significant
4491	REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	-1.13	0.55	0	0	0	not significant
4492	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_8	-1.13	0.55	0	0	0	not significant
4493	BIOCARTA_SET_PATHWAY	-1.13	0.54	0	0	0	not significant
4494	GO_ANIMAL_ORGAN_FORMATION	-1.13	0.54	0	0	0	not significant
4495	GO_BONE_CELL_DEVELOPMENT	-1.13	0.54	0	0	0	not significant
4496	GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	-1.13	0.54	0	0	0	not significant
4497	GO_POTASSIUM_CHANNEL_REGULATOR_ACTIVITY	-1.13	0.54	0	0	0	not significant
4498	GO_REGULATION_OF_NUCLEASE_ACTIVITY	-1.13	0.54	0	0	0	not significant
4499	RUAN_RESPONSE_TO_TNF_TROGLITAZONE_DN	-1.13	0.54	0	0	0	not significant
4500	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP	-1.13	0.54	0	0	0	not significant
4501	YE_METASTATIC_LIVER_CANCER	-1.13	0.54	0	0	0	not significant
4502	CHR2P14	-1.13	0.53	0	0	0	not significant
4503	GO_BRANCHING_INVOLVED_IN_MAMMARY_GLAND_DUCT_MORPHOGENE	-1.13	0.53	0	0	0	not significant
4504	GO_RESPIRATORY_BURST	-1.13	0.53	0	0	0	not significant
4505	ROZANOV_MMP14_TARGETS_SUBSET	-1.13	0.53	0	0	0	not significant
4506	AZARE_STAT3_TARGETS	-1.13	0.52	0	0	0	not significant
4507	CHR2P15	-1.13	0.52	0	0	0	not significant
4508	GO_RECEPTOR_BIOSYNTHETIC_PROCESS	-1.13	0.52	0	0	0	not significant
4509	REACTOME_SYNTHESIS_OF_PIPS_AT_THE_EARLY_ENDOSOME_MEMBRA	-1.13	0.52	0	0	0	not significant
4510	YANG_BREAST_CANCER_ESR1_UP	-1.13	0.52	0	0	0	not significant
4511	CHRXQ21	-1.13	0.51	0	0	0	not significant
4512	GO_IMMUNOGLOBULIN_SECRETION	-1.13	0.51	0	0	0	not significant
4513	GO_PALMITOYL_COA_HYDROLASE_ACTIVITY	-1.13	0.51	0	0	0	not significant
4514	GO_REGULATION_OF_INCLUSION_BODY_ASSEMBLY	-1.13	0.51	0	0	0	not significant
4515	GO_REGULATION_OF_THE_FORCE_OF_HEART_CONTRACTION	-1.13	0.51	0	0	0	not significant
4516	GO_FATTY_ACID_DERIVATIVE_TRANSPORT	-1.13	0.50	0	0	0	not significant
4517	GO_NEGATIVE_REGULATION_OF_CENTRIOLE_REPLICATION	-1.13	0.50	0	0	0	not significant
4518	LIU_VAV3_PROSTATE_CARCINOGENESIS_DN	-1.13	0.50	0	0	0	not significant
4519	PID_ARF_3PATHWAY	-1.13	0.50	0	0	0	not significant
4520	REACTOME_G_BETA:GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	-1.13	0.50	0	0	0	not significant
4521	GO_CYCLIN_DEPENDENT_PROTEIN_SERINE_THREONINE_KINASE_ACTIVA	-1.13	0.49	0	0	0	not significant
4522	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_IN_WS	-1.13	0.49	0	0	0	not significant
4523	REACTOME_DARPP_32_EVENTS	-1.13	0.49	0	0	0	not significant
4524	GO_ADENOSINE_TO_INOSINE_EDITING	-1.13	0.48	0	0	0	not significant
4525	GO_BILE_ACID_AND_BILE_SALT_TRANSPORT	-1.13	0.48	0	0	0	not significant
4526	GO_CELLULAR_KETONE_BODY_METABOLIC_PROCESS	-1.13	0.48	0	0	0	not significant
4527	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	-1.13	0.48	0	0	0	not significant
4528	GO_REGULATION_OF_KERATINOCYTE_MIGRATION	-1.13	0.48	0	0	0	not significant
4529	BIOCARTA_MALATEX_PATHWAY	-1.13	0.47	0	0	0	not significant
4530	GO_AXONEMAL_DYNEIN_COMPLEX	-1.13	0.47	0	0	0	not significant
4531	GO_NEGATIVE_REGULATION_OF_NUCLEASE_ACTIVITY	-1.13	0.47	0	0	0	not significant
4532	GO_REGULATION_OF_DNA_TOPOISOMERASE_ATP_HYDROLYZING_ACTI	-1.13	0.47	0	0	0	not significant
4533	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP	-1.13	0.47	0	0	0	not significant
4534	GO_RRNA_ADENINE_METHYLTRANSFERASE_ACTIVITY	-1.13	0.46	0	0	0	not significant
4535	GO_RESPONSE_TO_VITAMIN_E	-1.13	0.45	0	0	0	not significant
4536	REACTOME_SYNTHESIS_OF_DOLICHYL_PHOSPHATE	-1.13	0.45	0	0	0	not significant
4537	GO_MALE_GENITALIA_DEVELOPMENT	-1.13	0.44	0	0	0	not significant
4538	GO_NEGATIVE_REGULATION_OF_VESICLE_FUSION	-1.13	0.42	0	0	0	not significant
4539	GO_REGULATION_OF_ORGANELLE_ORGANIZATION	-1.12	1.49	0	0	0	not significant
4540	NUYTTEN_EZH2_TARGETS_UP	-1.12	1.24	0	0	0	not significant
4541	GO_POSITIVE_REGULATION_OF_HYDROLASE_ACTIVITY	-1.12	1.22	0	0	0	not significant
4542	REACTOME_METABOLISM_OF_LIPIDS	-1.12	1.21	0	0	0	not significant
4543	REACTOME_VESICLE_MEDIATED_TRANSPORT	-1.12	1.07	0	0	0	not significant
4544	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE	-1.12	1.06	0	0	0	not significant
4545	GO_PERINUCLEAR_REGION_OF_CYTOPLASM	-1.12	1.02	0	0	0	not significant
4546	MASSARWEH_TAMOXIFEN_RESISTANCE_UP	-1.12	0.95	0	0	0	not significant
4547	GO_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	-1.12	0.88	0	0	0	not significant
4548	PASINI_SUZ12_TARGETS_DN	-1.12	0.84	0	0	0	not significant
4549	GENTILE_UV_HIGH_DOSE_DN	-1.12	0.79	0	0	0	not significant
4550	GO_MUSCLE_CELL_DIFFERENTIATION	-1.12	0.77	0	0	0	not significant
4551	KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	-1.12	0.74	0	0	0	not significant
4552	GO_ENDOPLASMIC_RETICULUM_TO_GOLGI_VESICLE_MEDIATED_TRANS	-1.12	0.73	0	0	0	not significant
4553	GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	-1.12	0.73	0	0	0	not significant
4554	GO_NEGATIVE_REGULATION_OF_NEURON_DIFFERENTIATION	-1.12	0.72	0	0	0	not significant
4555	GO_ALCOHOL_METABOLIC_PROCESS	-1.12	0.71	0	0	0	not significant
4556	GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	-1.12	0.71	0	0	0	not significant
4557	ROZANOV_MMP14_TARGETS_UP	-1.12	0.71	0	0	0	not significant
4558	GO_REGULATION_OF_CELL_SUBSTRATE_ADHESION	-1.12	0.69	0	0	0	not significant
4559	GO_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_COMPLEX	-1.12	0.69	0	0	0	not significant
4560	IGARASHI_ATF4_TARGETS_DN	-1.12	0.67	0	0	0	not significant
4561	CHR21Q22	-1.12	0.66	0	0	0	not significant
4562	GO_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	-1.12	0.66	0	0	0	not significant
4563	IL15_UP.V1_UP	-1.12	0.66	0	0	0	not significant
4564	ONDER_CDH1_TARGETS_1_UP	-1.12	0.66	0	0	0	not significant
4565	GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IM	-1.12	0.62	0	0	0	not significant
4566	GO_POTASSIUM_ION_TRANSPORT	-1.12	0.61	0	0	0	not significant

4567	GO_REGULATION_OF_CARBOHYDRATE_CATABOLIC_PROCESS	-1.12	0.61	0	0	0	not significant
4568	REACTOME_ACTIVATION_OF_NMDA_RECEPTORS_AND_POSTSYNAPTIC_	-1.12	0.61	0	0	0	not significant
4569	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN	-1.12	0.59	0	0	0	not significant
4570	DAUER_STAT3_TARGETS_DN	-1.12	0.59	0	0	0	not significant
4571	GO_ER_NUCLEUS_SIGNALING_PATHWAY	-1.12	0.59	0	0	0	not significant
4572	KYNG_DNA_DAMAGE_BY_UV	-1.12	0.59	0	0	0	not significant
4573	MARTINEZ_RESPONSE_TO_TRABECTEDIN	-1.12	0.59	0	0	0	not significant
4574	REACTOME_E3_UBIQUITIN_LIGASES_UBIQUITINATE_TARGET_PROTEINS	-1.12	0.59	0	0	0	not significant
4575	CHR1Q42	-1.12	0.58	0	0	0	not significant
4576	GO_REGULATION_OF_PROTEIN_EXPORT_FROM_NUCLEUS	-1.12	0.58	0	0	0	not significant
4577	SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_UP	-1.12	0.58	0	0	0	not significant
4578	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_16	-1.12	0.58	0	0	0	not significant
4579	CHR1Q25	-1.12	0.57	0	0	0	not significant
4580	ZHAN_MULTIPLE_MYELOMA_LB_UP	-1.12	0.57	0	0	0	not significant
4581	GO_CIRCADIAN_REGULATION_OF_GENE_EXPRESSION	-1.12	0.56	0	0	0	not significant
4582	GO_PHAGOCYTIC_VESICLE_MEMBRANE	-1.12	0.56	0	0	0	not significant
4583	GO_CYTOKINETIC_PROCESS	-1.12	0.55	0	0	0	not significant
4584	GO_E_BOX_BINDING	-1.12	0.55	0	0	0	not significant
4585	GO_NEGATIVE_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	-1.12	0.55	0	0	0	not significant
4586	GO_NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	-1.12	0.55	0	0	0	not significant
4587	GO_T_TUBULE	-1.12	0.55	0	0	0	not significant
4588	REACTOME_RHO_GTPASES_ACTIVATE_WASPS_AND_WAVES	-1.12	0.55	0	0	0	not significant
4589	BIOCARTA_PYK2_PATHWAY	-1.12	0.54	0	0	0	not significant
4590	GO_REGULATION_OF_COLLAGEN_BIOSYNTHETIC_PROCESS	-1.12	0.54	0	0	0	not significant
4591	HOWLIN_PUBERTAL_MAMMARY_GLAND	-1.12	0.54	0	0	0	not significant
4592	ZHAN_LATE_DIFFERENTIATION_GENES_UP	-1.12	0.54	0	0	0	not significant
4593	GO_ESTABLISHMENT_OF_MITOCHONDRION_LOCALIZATION	-1.12	0.53	0	0	0	not significant
4594	GO_INO80_TYPE_COMPLEX	-1.12	0.53	0	0	0	not significant
4595	JAZAG_TGFB1_SIGNALING_DN	-1.12	0.53	0	0	0	not significant
4596	LEE_LIVER_CANCER_MYC_DN	-1.12	0.53	0	0	0	not significant
4597	PID_ALPHA_SYNUCLEIN_PATHWAY	-1.12	0.53	0	0	0	not significant
4598	GO_MODIFIED_AMINO_ACID_TRANSPORT	-1.12	0.52	0	0	0	not significant
4599	PID_INSULIN_GLUCOSE_PATHWAY	-1.12	0.52	0	0	0	not significant
4600	GO_RESPONSE_TO_UV_B	-1.12	0.51	0	0	0	not significant
4601	GO_TOLL_LIKE_RECEPTOR_4_SIGNALING_PATHWAY	-1.12	0.51	0	0	0	not significant
4602	REACTOME_EXTENSION_OF_TELOMERES	-1.12	0.51	0	0	0	not significant
4603	GO_NEGATIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	-1.12	0.50	0	0	0	not significant
4604	LEE_LIVER_CANCER	-1.12	0.50	0	0	0	not significant
4605	REACTOME_NEPHRIN_FAMILY_INTERACTIONS	-1.12	0.50	0	0	0	not significant
4606	ROETH_TERT_TARGETS_UP	-1.12	0.50	0	0	0	not significant
4607	GO_RESPONSE_TO_INSECTICIDE	-1.12	0.49	0	0	0	not significant
4608	REACTOME_NOTCH3_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRI	-1.12	0.49	0	0	0	not significant
4609	GO_CLATHRIN_HEAVY_CHAIN_BINDING	-1.12	0.48	0	0	0	not significant
4610	GO_NEGATIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFE	-1.12	0.48	0	0	0	not significant
4611	GO_NEGATIVE_REGULATION_OF_PROTEIN_EXPORT_FROM_NUCLEUS	-1.12	0.48	0	0	0	not significant
4612	GO_TYPE_B_PANCREATIC_CELL_APOPTOTIC_PROCESS	-1.12	0.48	0	0	0	not significant
4613	MATZUK_OVULATION	-1.12	0.48	0	0	0	not significant
4614	OXFORD_RALB_TARGETS_DN	-1.12	0.48	0	0	0	not significant
4615	REACTOME_SYNTHESIS_OF_PE	-1.12	0.48	0	0	0	not significant
4616	GO_CAMP_DEPENDENT_PROTEIN_KINASE_COMPLEX	-1.12	0.47	0	0	0	not significant
4617	GO_DNA_REPAIR_COMPLEX_ASSEMBLY	-1.12	0.47	0	0	0	not significant
4618	GO_GLUCOSE_CATABOLIC_PROCESS	-1.12	0.47	0	0	0	not significant
4619	GO_PRESYNAPTIC_ENDOCYTIC_ZONE	-1.12	0.47	0	0	0	not significant
4620	GO_REGULATION_OF_CELL_PROLIFERATION_INVOLVED_IN_KIDNEY_DEV	-1.12	0.47	0	0	0	not significant
4621	GO_NEGATIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCAL	-1.12	0.46	0	0	0	not significant
4622	NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON	-1.12	0.46	0	0	0	not significant
4623	GO_METANEPHRIC_EPITHELIUM_DEVELOPMENT	-1.12	0.45	0	0	0	not significant
4624	GO_POSITIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_4_SIGNALING_P	-1.12	0.45	0	0	0	not significant
4625	MOOTHA_PYR	-1.12	0.45	0	0	0	not significant
4626	REACTOME_LRR_FLII_INTERACTING_PROTEIN_1_LRRFIP1_ACTIVATES_T	-1.12	0.45	0	0	0	not significant
4627	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_HY	-1.12	0.44	0	0	0	not significant
4628	GO_MODULATION_OF_SIGNAL_TRANSDUCTION_IN_OTHER_ORGANISM	-1.12	0.43	0	0	0	not significant
4629	VICENT_METASTASIS_UP	-1.12	0.43	0	0	0	not significant
4630	GO_CYTOSKELETON_ORGANIZATION	-1.11	1.36	0	0	0	not significant
4631	YOSHIMURA_MAPK8_TARGETS_UP	-1.11	1.26	0	0	0	not significant
4632	GO_CELLULAR_PROTEIN_CATABOLIC_PROCESS	-1.11	1.15	0	0	0	not significant
4633	GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATIO	-1.11	1.11	0	0	0	not significant
4634	GO_ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	-1.11	1.07	0	0	0	not significant
4635	GO_ANCHORING_JUNCTION	-1.11	0.90	0	0	0	not significant
4636	MARTINEZ_RB1_AND_TP53_TARGETS_DN	-1.11	0.87	0	0	0	not significant
4637	GO_NEGATIVE_REGULATION_OF_CELL_POPULATION_PROLIFERATION	-1.11	0.80	0	0	0	not significant
4638	GO_TRANSFERASE_COMPLEX_TRANSFERRING_PHOSPHORUS_CONTAIN	-1.11	0.79	0	0	0	not significant
4639	GO_POSITIVE_REGULATION_OF_CELL_ADHESION	-1.11	0.77	0	0	0	not significant
4640	REACTOME_ORGANELLE_BIOGENESIS_AND_MAINTENANCE	-1.11	0.76	0	0	0	not significant
4641	GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	-1.11	0.75	0	0	0	not significant
4642	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN	-1.11	0.73	0	0	0	not significant
4643	GO_RESPONSE_TO_INSULIN	-1.11	0.72	0	0	0	not significant
4644	GO_COATED_VESICLE_MEMBRANE	-1.11	0.69	0	0	0	not significant
4645	GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	-1.11	0.68	0	0	0	not significant
4646	GO_PROTEIN_PROCESSING	-1.11	0.68	0	0	0	not significant
4647	AKT_UP_MTOR_DN.V1_UP	-1.11	0.67	0	0	0	not significant
4648	GO_MYELOID_LEUKOCYTE_DIFFERENTIATION	-1.11	0.67	0	0	0	not significant
4649	GO_POSITIVE_REGULATION_OF_BINDING	-1.11	0.67	0	0	0	not significant
4650	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_DN	-1.11	0.66	0	0	0	not significant
4651	GO_BONE_DEVELOPMENT	-1.11	0.66	0	0	0	not significant
4652	GO_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN	-1.11	0.66	0	0	0	not significant
4653	RAF_UP.V1_DN	-1.11	0.66	0	0	0	not significant
4654	BOQUEST_STEM_CELL_DN	-1.11	0.64	0	0	0	not significant
4655	GO_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	-1.11	0.64	0	0	0	not significant
4656	GAVIN_FOXP3_TARGETS_CLUSTER_T7	-1.11	0.62	0	0	0	not significant
4657	GO_COATED_MEMBRANE	-1.11	0.62	0	0	0	not significant
4658	SASSON_RESPONSE_TO_GONADOTROPHINS_UP	-1.11	0.62	0	0	0	not significant
4659	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_UP	-1.11	0.60	0	0	0	not significant
4660	ATF2_UP.V1_UP	-1.11	0.60	0	0	0	not significant
4661	GO_PEROXISOME_ORGANIZATION	-1.11	0.60	0	0	0	not significant
4662	GO_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	-1.11	0.60	0	0	0	not significant
4663	MARKEY_RB1_CHRONIC_LOF_UP	-1.11	0.60	0	0	0	not significant
4664	PUJANA_BRCA_CENTERED_NETWORK	-1.11	0.60	0	0	0	not significant
4665	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_48HR_DN	-1.11	0.59	0	0	0	not significant
4666	NIKOLSKY_BREAST_CANCER_17Q11_Q21_AMPLICON	-1.11	0.58	0	0	0	not significant
4667	VANLOO_SP3_TARGETS_DN	-1.11	0.58	0	0	0	not significant
4668	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP	-1.11	0.57	0	0	0	not significant
4669	GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	-1.11	0.56	0	0	0	not significant
4670	GO_REGULATION_OF_CELL_MATRIX_ADHESION	-1.11	0.56	0	0	0	not significant
4671	KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	-1.11	0.56	0	0	0	not significant
4672	KEGG_NUCLEOTIDE_EXCISION_REPAIR	-1.11	0.56	0	0	0	not significant
4673	KRAS.300_UP.V1_UP	-1.11	0.56	0	0	0	not significant
4674	REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	-1.11	0.56	0	0	0	not significant
4675	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_DN	-1.11	0.55	0	0	0	not significant

4676	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	-1.11	0.54	0	0	0	not significant
4677	GO_OLIGODENDROCYTE_DEVELOPMENT	-1.11	0.54	0	0	0	not significant
4678	SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_UP	-1.11	0.54	0	0	0	not significant
4679	GO_MRNA_CLEAVAGE_FACTOR_COMPLEX	-1.11	0.53	0	0	0	not significant
4680	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_ENDOPLASMIC_RETICU	-1.11	0.53	0	0	0	not significant
4681	GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	-1.11	0.53	0	0	0	not significant
4682	PID_MYC_REPRESS_PATHWAY	-1.11	0.53	0	0	0	not significant
4683	REACTOME_THE_PHOTOTRANSDUCTION_CASCADE	-1.11	0.53	0	0	0	not significant
4684	GO_POSITIVE_REGULATION_OF_WOUND_HEALING	-1.11	0.52	0	0	0	not significant
4685	GO_PROTEIN_INSERTION_INTO_MITOCHONDRIAL_MEMBRANE	-1.11	0.52	0	0	0	not significant
4686	GO_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	-1.11	0.52	0	0	0	not significant
4687	PID_S1P_S1P2_PATHWAY	-1.11	0.52	0	0	0	not significant
4688	WANG_LSD1_TARGETS_DN	-1.11	0.52	0	0	0	not significant
4689	GO_HISTONE_MRNA_METABOLIC_PROCESS	-1.11	0.51	0	0	0	not significant
4690	GO_NEGATIVE_REGULATION_OF_COAGULATION	-1.11	0.51	0	0	0	not significant
4691	GO_PEPTIDYL_METHIONINE_MODIFICATION	-1.11	0.51	0	0	0	not significant
4692	GO_PHOTORECEPTOR_CELL_MAINTENANCE	-1.11	0.51	0	0	0	not significant
4693	GO_POSITIVE_REGULATION_OF_SPROUTING_ANGIOGENESIS	-1.11	0.51	0	0	0	not significant
4694	LEIN_LOCALIZED_TO_PROXIMAL_DENDRITES	-1.11	0.51	0	0	0	not significant
4695	REACTOME_DISEASES_ASSOCIATED_WITH_N_GLYCOSYLATION_OF_PR	-1.11	0.51	0	0	0	not significant
4696	AMIT_SERUM_RESPONSE_480_MCF10A	-1.11	0.50	0	0	0	not significant
4697	GO_L_AMINO_ACID_TRANSPORT	-1.11	0.50	0	0	0	not significant
4698	GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_S	-1.11	0.50	0	0	0	not significant
4699	GO_REGULATION_OF_GRANULOCYTE_DIFFERENTIATION	-1.11	0.50	0	0	0	not significant
4700	KIM_LIVER_CANCER_POOR_SURVIVAL_DN	-1.11	0.50	0	0	0	not significant
4701	PID_MAPK_TRK_PATHWAY	-1.11	0.50	0	0	0	not significant
4702	REACTOME_REGULATION_OF_INNATE_IMMUNE_RESPONSES_TO_CYTOS	-1.11	0.50	0	0	0	not significant
4703	SESTO_RESPONSE_TO_UV_C6	-1.11	0.50	0	0	0	not significant
4704	GO_DOUBLE_STRANDED_TELOMERIC_DNA_BINDING	-1.11	0.49	0	0	0	not significant
4705	GO_GLUTAMATE_SECRETION	-1.11	0.49	0	0	0	not significant
4706	GO_REGULATION_OF_ER_ASSOCIATED_UBIQUITIN_DEPENDENT_PROTE	-1.11	0.49	0	0	0	not significant
4707	REACTOME_GLUTATHIONE_SYNTHESIS_AND_RECYCLING	-1.11	0.49	0	0	0	not significant
4708	YUAN_ZNF143_PARTNERS	-1.11	0.49	0	0	0	not significant
4709	FARMER_BREAST_CANCER_CLUSTER_3	-1.11	0.48	0	0	0	not significant
4710	GO_CHEMOKINE_RECEPTOR_BINDING	-1.11	0.48	0	0	0	not significant
4711	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_OF_NOTCH_RECEPT	-1.11	0.48	0	0	0	not significant
4712	GO_RESPONSE_TO_NITRIC_OXIDE	-1.11	0.48	0	0	0	not significant
4713	GO_RETINOIC_ACID_RECEPTOR_BINDING	-1.11	0.48	0	0	0	not significant
4714	REACTOME_MOLYBDENUM_COFACTOR_BIOSYNTHESIS	-1.11	0.48	0	0	0	not significant
4715	REACTOME_RAP1_SIGNALLING	-1.11	0.48	0	0	0	not significant
4716	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP	-1.11	0.48	0	0	0	not significant
4717	BIOCARTA_STATHMIN_PATHWAY	-1.11	0.47	0	0	0	not significant
4718	GO_RESPONSE_TO_PH	-1.11	0.47	0	0	0	not significant
4719	REACTOME_METABOLISM_OF_PORPHYRINS	-1.11	0.47	0	0	0	not significant
4720	GO_GOLGI_TRANSPORT_COMPLEX	-1.11	0.46	0	0	0	not significant
4721	TOMLINS_METASTASIS_UP	-1.11	0.46	0	0	0	not significant
4722	CAIRO_HEPATOBLASTOMA_POOR_SURVIVAL	-1.11	0.45	0	0	0	not significant
4723	GO_CARDIAC_MUSCLE_FIBER_DEVELOPMENT	-1.11	0.45	0	0	0	not significant
4724	GO_GAS_HOMEOSTASIS	-1.11	0.45	0	0	0	not significant
4725	GO_GLOMERULAR_EPITHELIAL_CELL_DIFFERENTIATION	-1.11	0.45	0	0	0	not significant
4726	GO_INTERLEUKIN_2_SECRETION	-1.11	0.45	0	0	0	not significant
4727	GO_MIDGUT_DEVELOPMENT	-1.11	0.45	0	0	0	not significant
4728	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZ	-1.11	0.45	0	0	0	not significant
4729	GO_INTERFERON_RECEPTOR_ACTIVITY	-1.11	0.44	0	0	0	not significant
4730	GO_MEIOSIS_II_CELL_CYCLE_PROCESS	-1.11	0.44	0	0	0	not significant
4731	GO_REGULATION_OF_RESPIRATORY_GASEOUS_EXCHANGE_BY_NEURO	-1.11	0.43	0	0	0	not significant
4732	LU_TUMOR_VASCULATURE_DN	-1.11	0.43	0	0	0	not significant
4733	GO_ROSTROCAUDAL_NEURAL_TUBE_PATTERNING	-1.11	0.42	0	0	0	not significant
4734	NUYTTEN_EZH2_TARGETS_DN	-1.10	1.52	0	0	0	not significant
4735	GO_PROTEIN_PHOSPHORYLATION	-1.10	1.30	0	0	0	not significant
4736	GO_SIGNALING_RECEPTOR_BINDING	-1.10	0.97	0	0	0	not significant
4737	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR	-1.10	0.94	0	0	0	not significant
4738	GO_ORGANOPHOSPHATE_METABOLIC_PROCESS	-1.10	0.90	0	0	0	not significant
4739	GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	-1.10	0.83	0	0	0	not significant
4740	GO_INFLAMMATORY_RESPONSE	-1.10	0.80	0	0	0	not significant
4741	BRUINS_UVC_RESPONSE_EARLY_LATE	-1.10	0.78	0	0	0	not significant
4742	MULLIGHAN_NPM1_SIGNATURE_3_UP	-1.10	0.76	0	0	0	not significant
4743	GO_LEUKOCYTE_CELL_CELL_ADHESION	-1.10	0.72	0	0	0	not significant
4744	GO_SENSORY_SYSTEM_DEVELOPMENT	-1.10	0.71	0	0	0	not significant
4745	REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	-1.10	0.71	0	0	0	not significant
4746	GO_LIPID_LOCALIZATION	-1.10	0.69	0	0	0	not significant
4747	GO_REPRODUCTIVE_SYSTEM_DEVELOPMENT	-1.10	0.68	0	0	0	not significant
4748	GO_STEROID_METABOLIC_PROCESS	-1.10	0.67	0	0	0	not significant
4749	PRC2_EZH2_UP.V1_DN	-1.10	0.67	0	0	0	not significant
4750	GARCIA_TARGETS_OF_FLI1_AND_DAX1_DN	-1.10	0.66	0	0	0	not significant
4751	GO_REGULATION_OF_MEMBRANE_POTENTIAL	-1.10	0.66	0	0	0	not significant
4752	HALLMARK_P53_PATHWAY	-1.10	0.65	0	0	0	not significant
4753	GO_ENDOCYTIC_VESICLE	-1.10	0.64	0	0	0	not significant
4754	GO_REGULATION_OF_INFLAMMATORY_RESPONSE	-1.10	0.64	0	0	0	not significant
4755	REACTOME_RRNA_PROCESSING_IN_THE_NUCLEUS_AND_CYTOSOL	-1.10	0.64	0	0	0	not significant
4756	GO_MEMBRANE_DOCKING	-1.10	0.63	0	0	0	not significant
4757	KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	-1.10	0.63	0	0	0	not significant
4758	GO_CARBOHYDRATE_TRANSPORT	-1.10	0.62	0	0	0	not significant
4759	GO_ACTOMYOSIN_STRUCTURE_ORGANIZATION	-1.10	0.61	0	0	0	not significant
4760	GO_CYTOKINE_RECEPTOR_BINDING	-1.10	0.61	0	0	0	not significant
4761	GO_CYTOKINE_SECRETION	-1.10	0.60	0	0	0	not significant
4762	BROWNE_HCMV_INFECTION_12HR_UP	-1.10	0.58	0	0	0	not significant
4763	GO_BETA_CATENIN_BINDING	-1.10	0.58	0	0	0	not significant
4764	GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	-1.10	0.58	0	0	0	not significant
4765	GO_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	-1.10	0.58	0	0	0	not significant
4766	GO_VITAMIN_BINDING	-1.10	0.58	0	0	0	not significant
4767	ONDER_CDH1_SIGNALING_VIA_CTNNB1	-1.10	0.58	0	0	0	not significant
4768	GO_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN	-1.10	0.56	0	0	0	not significant
4769	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	-1.10	0.55	0	0	0	not significant
4770	GO_4_IRON_4_SULFUR_CLUSTER_BINDING	-1.10	0.54	0	0	0	not significant
4771	GO_CELL_ADHESION_MEDIATOR_ACTIVITY	-1.10	0.54	0	0	0	not significant
4772	GO_FEMALE_SEX_DIFFERENTIATION	-1.10	0.54	0	0	0	not significant
4773	GO_GLIAL_CELL_DEVELOPMENT	-1.10	0.54	0	0	0	not significant
4774	GO_NEGATIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN	-1.10	0.54	0	0	0	not significant
4775	GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_	-1.10	0.54	0	0	0	not significant
4776	GO_CHONDROCYTE_DIFFERENTIATION	-1.10	0.53	0	0	0	not significant
4777	GO_CLATHRIN_COAT	-1.10	0.53	0	0	0	not significant
4778	GO_LIPID_DROPLET	-1.10	0.53	0	0	0	not significant
4779	GO_MUSCLE_ORGAN_MORPHOGENESIS	-1.10	0.53	0	0	0	not significant
4780	GO_PHOTORECEPTOR_OUTER_SEGMENT	-1.10	0.53	0	0	0	not significant
4781	HUMMERICH_SKIN_CANCER_PROGRESSION_DN	-1.10	0.53	0	0	0	not significant
4782	REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RR	-1.10	0.53	0	0	0	not significant
4783	LIN_MELANOMA_COPY_NUMBER_DN	-1.10	0.52	0	0	0	not significant
4784	REACTOME_DEPURINATION	-1.10	0.52	0	0	0	not significant

4785	GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	-1.10	0.51	0	0	0	not significant
4786	GO_RRNA_METHYLATION	-1.10	0.51	0	0	0	not significant
4787	WEIGEL_OXIDATIVE_STRESS_RESPONSE	-1.10	0.51	0	0	0	not significant
4788	CHR7P21	-1.10	0.50	0	0	0	not significant
4789	REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE	-1.10	0.50	0	0	0	not significant
4790	CHR4Q28	-1.10	0.49	0	0	0	not significant
4791	GO_INTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	-1.10	0.49	0	0	0	not significant
4792	GO_POSITIVE_REGULATION_OF_VIRAL_RELEASE_FROM_HOST_CELL	-1.10	0.49	0	0	0	not significant
4793	GO_REGULATION_OF_TRANSCRIPTION_INITIATION_FROM_RNA_POLYME	-1.10	0.49	0	0	0	not significant
4794	GO_REGULATION_OF_VACUOLE_ORGANIZATION	-1.10	0.49	0	0	0	not significant
4795	GREENBAUM_E2A_TARGETS_DN	-1.10	0.49	0	0	0	not significant
4796	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	-1.10	0.49	0	0	0	not significant
4797	WEIGEL_OXIDATIVE_STRESS_BY_TBH_AND_H2O2	-1.10	0.49	0	0	0	not significant
4798	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVATOR_ACTIVITY_INVOLVED	-1.10	0.48	0	0	0	not significant
4799	GO_POSITIVE_REGULATION_OF_CAMP_MEDIATED_SIGNALING	-1.10	0.48	0	0	0	not significant
4800	GO_TELENCEPHALON_GLIAL_CELL_MIGRATION	-1.10	0.48	0	0	0	not significant
4801	TRAYNOR_RETT_SYNDROM_DN	-1.10	0.48	0	0	0	not significant
4802	VERNELL_RETINOBLASTOMA_PATHWAY_DN	-1.10	0.48	0	0	0	not significant
4803	BARRIER_CANCER_RELAPSE_TUMOR_SAMPLE_UP	-1.10	0.47	0	0	0	not significant
4804	CHR1Q43	-1.10	0.47	0	0	0	not significant
4805	GO_ADRENAL_GLAND_DEVELOPMENT	-1.10	0.47	0	0	0	not significant
4806	GO_ASTROCYTE_ACTIVATION	-1.10	0.47	0	0	0	not significant
4807	GO_CELL_CELL_SIGNALING_INVOLVED_IN_CARDIAC_CONDUCTION	-1.10	0.47	0	0	0	not significant
4808	GO_POLARIZED_EPITHELIAL_CELL_DIFFERENTIATION	-1.10	0.47	0	0	0	not significant
4809	GO_PROTEIN_FOLDING_CHAPERONE	-1.10	0.47	0	0	0	not significant
4810	GO_RESPONSE_TO_FOOD	-1.10	0.47	0	0	0	not significant
4811	TANG_SENESCENCE_TP53_TARGETS_UP	-1.10	0.47	0	0	0	not significant
4812	WALLACE_PROSTATE_CANCER_UP	-1.10	0.47	0	0	0	not significant
4813	BIOCARTA_EPONFKB_PATHWAY	-1.10	0.46	0	0	0	not significant
4814	GHO_ATF5_TARGETS_UP	-1.10	0.46	0	0	0	not significant
4815	GO_GLIAL_CELL_MIGRATION	-1.10	0.46	0	0	0	not significant
4816	GO_RESPONSE_TO_INACTIVITY	-1.10	0.46	0	0	0	not significant
4817	GO_RNA_CAP_BINDING	-1.10	0.46	0	0	0	not significant
4818	NELSON_RESPONSE_TO_ANDROGEN_DN	-1.10	0.46	0	0	0	not significant
4819	RAMPON_ENRICHED_LEARNING_ENVIRONMENT_EARLY_UP	-1.10	0.46	0	0	0	not significant
4820	GO_CARDIAC_CONDUCTION_SYSTEM_DEVELOPMENT	-1.10	0.45	0	0	0	not significant
4821	GO_MATING	-1.10	0.45	0	0	0	not significant
4822	GO_NUCLEOTIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.10	0.45	0	0	0	not significant
4823	GO_REGULATION_OF_CAMP_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-1.10	0.45	0	0	0	not significant
4824	CHR13Q31	-1.10	0.44	0	0	0	not significant
4825	GO_1_PHOSPHATIDYLINOSITOL_3_KINASE_REGULATOR_ACTIVITY	-1.10	0.44	0	0	0	not significant
4826	GO_2_OXOGLUTARATE_METABOLIC_PROCESS	-1.10	0.44	0	0	0	not significant
4827	GO_DICARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.10	0.44	0	0	0	not significant
4828	GO_DNA_UNWINDING_INVOLVED_IN_DNA_REPLICATION	-1.10	0.44	0	0	0	not significant
4829	GO_POSITIVE_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATION	-1.10	0.44	0	0	0	not significant
4830	GO_POSITIVE_REGULATION_OF_PROTEIN_DEPOLYMERIZATION	-1.10	0.44	0	0	0	not significant
4831	GO_REGULATION_OF_HISTONE_H4_K16_ACETYLATION	-1.10	0.44	0	0	0	not significant
4832	GO_MODULATION_OF_AGE_RELATED_BEHAVIORAL_DECLINE	-1.10	0.43	0	0	0	not significant
4833	GO_REGULATION_OF_PSEUDOPODIUM_ASSEMBLY	-1.10	0.43	0	0	0	not significant
4834	LUI_THYROID_CANCER_CLUSTER_5	-1.10	0.42	0	0	0	not significant
4835	GO_DENSE_CORE_GRANULE_TRANSPORT	-1.10	0.40	0	0	0	not significant
4836	GO_CYTOSKELETAL_PART	-1.09	1.27	0	0	0	not significant
4837	GO_CHROMOSOME	-1.09	1.05	0	0	0	not significant
4838	GO_MODIFICATION_DEPENDENT_MACROMOLECULE_CATABOLIC_PROCE	-1.09	0.92	0	0	0	not significant
4839	HSIAO_HOUSEKEEPING_GENES	-1.09	0.82	0	0	0	not significant
4840	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN	-1.09	0.77	0	0	0	not significant
4841	GO_ENDOCYTOSIS	-1.09	0.76	0	0	0	not significant
4842	DELACROIX_RAR_BOUND_ES	-1.09	0.75	0	0	0	not significant
4843	FISCHER_DIRECT_P53_TARGETS_META_ANALYSIS	-1.09	0.73	0	0	0	not significant
4844	GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	-1.09	0.73	0	0	0	not significant
4845	GO_MAINTENANCE_OF_LOCATION	-1.09	0.69	0	0	0	not significant
4846	GO_REGULATION_OF_HORMONE_LEVELS	-1.09	0.68	0	0	0	not significant
4847	GO_CHROMOSOME_TELOMERIC_REGION	-1.09	0.64	0	0	0	not significant
4848	CHR1P34	-1.09	0.61	0	0	0	not significant
4849	GO_ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.09	0.61	0	0	0	not significant
4850	SENESE_HDAC1_AND_HDAC2_TARGETS_UP	-1.09	0.61	0	0	0	not significant
4851	KAAB_HEART_ATRIUM_VS_VENTRICLE_UP	-1.09	0.59	0	0	0	not significant
4852	NOTCH_DN.V1_DN	-1.09	0.58	0	0	0	not significant
4853	GO_RESPONSE_TO_HYDROGEN_PEROXIDE	-1.09	0.55	0	0	0	not significant
4854	GO_RNA_HELICASE_ACTIVITY	-1.09	0.55	0	0	0	not significant
4855	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_GRANULOPOIESIS	-1.09	0.55	0	0	0	not significant
4856	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	-1.09	0.54	0	0	0	not significant
4857	CYCLIN_D1_KE_.V1_DN	-1.09	0.53	0	0	0	not significant
4858	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	-1.09	0.53	0	0	0	not significant
4859	GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATIO	-1.09	0.52	0	0	0	not significant
4860	GO_REGULATION_OF_HEART_RATE	-1.09	0.52	0	0	0	not significant
4861	GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO	-1.09	0.52	0	0	0	not significant
4862	SESTO_RESPONSE_TO_UV_C5	-1.09	0.52	0	0	0	not significant
4863	CHR15Q25	-1.09	0.51	0	0	0	not significant
4864	GO_NLS_BEARING_PROTEIN_IMPORT_INTO_NUCLEUS	-1.09	0.51	0	0	0	not significant
4865	GO_SENSORY_PERCEPTION_OF_MECHANICAL_STIMULUS	-1.09	0.51	0	0	0	not significant
4866	HALLMARK_COAGULATION	-1.09	0.51	0	0	0	not significant
4867	CHR5Q13	-1.09	0.50	0	0	0	not significant
4868	GO_MRNA_CLEAVAGE	-1.09	0.50	0	0	0	not significant
4869	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATI	-1.09	0.50	0	0	0	not significant
4870	GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.09	0.50	0	0	0	not significant
4871	GO_CARBOHYDRATE_DERIVATIVE_TRANSPORT	-1.09	0.49	0	0	0	not significant
4872	GO_ENDOSOME_LUMEN	-1.09	0.49	0	0	0	not significant
4873	GO_INTERLEUKIN_1_SECRETION	-1.09	0.49	0	0	0	not significant
4874	GO_MULTICELLULAR_ORGANISMAL_MOVEMENT	-1.09	0.49	0	0	0	not significant
4875	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	-1.09	0.49	0	0	0	not significant
4876	GO_SULFUR_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.09	0.49	0	0	0	not significant
4877	JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_DN	-1.09	0.49	0	0	0	not significant
4878	LANDIS_BREAST_CANCER_PROGRESSION_DN	-1.09	0.49	0	0	0	not significant
4879	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_DN	-1.09	0.48	0	0	0	not significant
4880	GO_ANION_HOMEOSTASIS	-1.09	0.48	0	0	0	not significant
4881	GO_ISOPRENOID_BIOSYNTHETIC_PROCESS	-1.09	0.48	0	0	0	not significant
4882	GO_PRIMARY_ALCOHOL_METABOLIC_PROCESS	-1.09	0.48	0	0	0	not significant
4883	GO_REGULATION_OF_GOLGI_ORGANIZATION	-1.09	0.48	0	0	0	not significant
4884	GO_AMINO_SUGAR_METABOLIC_PROCESS	-1.09	0.47	0	0	0	not significant
4885	GO_NADPH_BINDING	-1.09	0.47	0	0	0	not significant
4886	GO_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE	-1.09	0.47	0	0	0	not significant
4887	GO_THIOLESTER_HYDROLASE_ACTIVITY	-1.09	0.47	0	0	0	not significant
4888	HAHTOLA_CTCL_CUTANEOUS	-1.09	0.47	0	0	0	not significant
4889	GO_AMYLOID_FIBRIL_FORMATION	-1.09	0.46	0	0	0	not significant
4890	GO_NEGATIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_	-1.09	0.46	0	0	0	not significant
4891	GO_NUCLEOTIDE_TRANSPORT	-1.09	0.46	0	0	0	not significant
4892	TERAMOTO_OPN_TARGETS_CLUSTER_7	-1.09	0.46	0	0	0	not significant
4893	BIOCARTA_IL17_PATHWAY	-1.09	0.45	0	0	0	not significant

4894	BIOCARTA_TRKA_PATHWAY	-1.09	0.45	0	0	0	not significant
4895	GO_FATTY_ACID_ELONGATION	-1.09	0.45	0	0	0	not significant
4896	GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEU	-1.09	0.45	0	0	0	not significant
4897	GO_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	-1.09	0.45	0	0	0	not significant
4898	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PE	-1.09	0.44	0	0	0	not significant
4899	GO_MODULATION_BY_HOST_OF_VIRAL_GENOME_REPLICATION	-1.09	0.44	0	0	0	not significant
4900	GO_NADP_RETINOL_DEHYDROGENASE_ACTIVITY	-1.09	0.44	0	0	0	not significant
4901	GO_NEGATIVE_REGULATION_OF_ATPASE_ACTIVITY	-1.09	0.44	0	0	0	not significant
4902	RICKMAN_HEAD_AND_NECK_CANCER_E	-1.09	0.44	0	0	0	not significant
4903	GO_ACROSOME_ASSEMBLY	-1.09	0.43	0	0	0	not significant
4904	GO_CAMP_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-1.09	0.43	0	0	0	not significant
4905	GO_MITOCHONDRIAL_RIBOSOME_ASSEMBLY	-1.09	0.43	0	0	0	not significant
4906	GO_MYOFILAMENT	-1.09	0.43	0	0	0	not significant
4907	GO_TELENCEPHALON_REGIONALIZATION	-1.09	0.43	0	0	0	not significant
4908	REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYCLE	-1.09	0.43	0	0	0	not significant
4909	REACTOME_RHO_GTPASES_ACTIVATE_KTN1	-1.09	0.43	0	0	0	not significant
4910	REACTOME_SLBP_DEPENDENT_PROCESSING_OF_REPLICATION_DEPEN	-1.09	0.43	0	0	0	not significant
4911	WILLIAMS_ESR2_TARGETS_UP	-1.09	0.43	0	0	0	not significant
4912	GO_PEPTIDYL_HISTIDINE_MODIFICATION	-1.09	0.42	0	0	0	not significant
4913	GO_SERINE_TYPE_CARBOXYPEPTIDASE_ACTIVITY	-1.09	0.42	0	0	0	not significant
4914	NIELSEN_LEIOMYOSARCOMA_CNN1_UP	-1.09	0.42	0	0	0	not significant
4915	GO_POSTSYNAPTIC_SIGNAL_TRANSDUCTION	-1.09	0.41	0	0	0	not significant
4916	GO_PERIPHERAL_NERVOUS_SYSTEM_MYELIN_MAINTENANCE	-1.09	0.40	0	0	0	not significant
4917	GO_EXTRACELLULAR_MATRIX_CONSTITUENT_SECRETION	-1.09	0.39	0	0	0	not significant
4918	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	-1.08	1.01	0	0	0	not significant
4919	REACTOME_DEVELOPMENTAL_BIOLOGY	-1.08	0.88	0	0	0	not significant
4920	GO_RESPONSE_TO_GROWTH_FACTOR	-1.08	0.84	0	0	0	not significant
4921	GO_TRANSPORTER_ACTIVITY	-1.08	0.83	0	0	0	not significant
4922	GO_APOPTOTIC_SIGNALING_PATHWAY	-1.08	0.76	0	0	0	not significant
4923	GO_CELL_CELL_ADHESION	-1.08	0.72	0	0	0	not significant
4924	GO_NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	-1.08	0.68	0	0	0	not significant
4925	SANSOM_APC_TARGETS_DN	-1.08	0.68	0	0	0	not significant
4926	GO_NEGATIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	-1.08	0.65	0	0	0	not significant
4927	GO_NEGATIVE_REGULATION_OF_LOCOMOTION	-1.08	0.64	0	0	0	not significant
4928	GO_NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	-1.08	0.63	0	0	0	not significant
4929	GO_MONOVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORT	-1.08	0.62	0	0	0	not significant
4930	GO_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_C	-1.08	0.60	0	0	0	not significant
4931	SANSOM_APC_MYC_TARGETS	-1.08	0.60	0	0	0	not significant
4932	GO_RESPONSE_TO_IONIZING_RADIATION	-1.08	0.59	0	0	0	not significant
4933	GCNP_SHH_UP_LATE.V1_DN	-1.08	0.57	0	0	0	not significant
4934	GO_KINASE_REGULATOR_ACTIVITY	-1.08	0.57	0	0	0	not significant
4935	MANALO_HYPOXIA_UP	-1.08	0.55	0	0	0	not significant
4936	REACTOME_NEUROTRANSMITTER_RECEPTORS_AND_POSTSYNAPTIC_S	-1.08	0.55	0	0	0	not significant
4937	GO_PROTEIN_DNA_COMPLEX	-1.08	0.54	0	0	0	not significant
4938	GRABARCZYK_BCL11B_TARGETS_DN	-1.08	0.54	0	0	0	not significant
4939	JAEGER_METASTASIS_DN	-1.08	0.54	0	0	0	not significant
4940	NAKAMURA_ADIPOGENESIS_LATE_UP	-1.08	0.54	0	0	0	not significant
4941	REACTOME_SLC_TRANSPORTER_DISORDERS	-1.08	0.54	0	0	0	not significant
4942	AKL_HTLV1_INFECTION_DN	-1.08	0.53	0	0	0	not significant
4943	PURBEY_TARGETS_OF_CTBP1_AND_SATB1_UP	-1.08	0.53	0	0	0	not significant
4944	AMUNDSON_GENOTOXIC_SIGNATURE	-1.08	0.52	0	0	0	not significant
4945	GO_RIBOSOME_ASSEMBLY	-1.08	0.52	0	0	0	not significant
4946	GO_HORMONE_METABOLIC_PROCESS	-1.08	0.51	0	0	0	not significant
4947	GO_PLASMA_MEMBRANE_ORGANIZATION	-1.08	0.51	0	0	0	not significant
4948	GO_POSITIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	-1.08	0.51	0	0	0	not significant
4949	GO_MULTI_ORGANISM_CELLULAR_PROCESS	-1.08	0.50	0	0	0	not significant
4950	GO_MYELOID_LEUKOCYTE_MIGRATION	-1.08	0.50	0	0	0	not significant
4951	GO_POSITIVE_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	-1.08	0.50	0	0	0	not significant
4952	GO_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	-1.08	0.50	0	0	0	not significant
4953	HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGENESIS	-1.08	0.50	0	0	0	not significant
4954	REACTOME_MTOR_SIGNALLING	-1.08	0.50	0	0	0	not significant
4955	REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	-1.08	0.50	0	0	0	not significant
4956	CHR2Q35	-1.08	0.49	0	0	0	not significant
4957	GO_ENDORIBONUCLEASE_ACTIVITY_PRODUCING_5_PHOSPHOMONOES	-1.08	0.49	0	0	0	not significant
4958	GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PA	-1.08	0.49	0	0	0	not significant
4959	GO_POSITIVE_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE	-1.08	0.49	0	0	0	not significant
4960	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_REGULATOR_ACTIVITY_INVOLVE	-1.08	0.48	0	0	0	not significant
4961	GO_EXTRACELLULAR_MATRIX_DISASSEMBLY	-1.08	0.48	0	0	0	not significant
4962	GO_INTERLEUKIN_1_BETA_SECRETION	-1.08	0.48	0	0	0	not significant
4963	LEE_LIVER_CANCER_DENA_DN	-1.08	0.48	0	0	0	not significant
4964	SHAFFER_IRF4_TARGETS_IN_ACTIVATED_DENDRITIC_CELL	-1.08	0.48	0	0	0	not significant
4965	GO_CARBOXY_LYASE_ACTIVITY	-1.08	0.47	0	0	0	not significant
4966	GO_CELL_CELL_ADHESION_MEDIATOR_ACTIVITY	-1.08	0.47	0	0	0	not significant
4967	GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	-1.08	0.47	0	0	0	not significant
4968	GO_REGULATION_OF_KERATINOCYTE_DIFFERENTIATION	-1.08	0.47	0	0	0	not significant
4969	LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_DN	-1.08	0.47	0	0	0	not significant
4970	REACTOME_GLYOXYLATE_METABOLISM_AND_GLYCINE_DEGRADATION	-1.08	0.47	0	0	0	not significant
4971	YU_BAP1_TARGETS	-1.08	0.47	0	0	0	not significant
4972	BIOCARTA_STRESS_PATHWAY	-1.08	0.46	0	0	0	not significant
4973	GO_MATERNAL_PLACENTA_DEVELOPMENT	-1.08	0.46	0	0	0	not significant
4974	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRA	-1.08	0.46	0	0	0	not significant
4975	GO_OXIDATIVE_DEMETHYLATION	-1.08	0.46	0	0	0	not significant
4976	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_17	-1.08	0.46	0	0	0	not significant
4977	REACTOME_PEPTIDE_HORMONE_METABOLISM	-1.08	0.46	0	0	0	not significant
4978	GO_CEREBELLAR_PURKINJE_CELL_LAYER_DEVELOPMENT	-1.08	0.45	0	0	0	not significant
4979	GO_RNA_INTERFERENCE	-1.08	0.45	0	0	0	not significant
4980	GO_TELOMERE_CAP_COMPLEX	-1.08	0.45	0	0	0	not significant
4981	REACTOME_MTORC1_MEDIATED_SIGNALLING	-1.08	0.45	0	0	0	not significant
4982	REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS	-1.08	0.45	0	0	0	not significant
4983	CAVARD_LIVER_CANCER_MALIGNANT_VS_BENIGN	-1.08	0.44	0	0	0	not significant
4984	GO_CILIARY_TRANSITION_FIBER	-1.08	0.44	0	0	0	not significant
4985	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYME	-1.08	0.44	0	0	0	not significant
4986	GO_REGULATION_OF_CELL_GROWTH_INVOLVED_IN_CARDIAC_MUSCLE	-1.08	0.44	0	0	0	not significant
4987	KIM_GLIS2_TARGETS_UP	-1.08	0.44	0	0	0	not significant
4988	REACTOME_PLATELET_SENSITIZATION_BY_LDL	-1.08	0.44	0	0	0	not significant
4989	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_UP	-1.08	0.44	0	0	0	not significant
4990	GO_EPITHELIAL_CELL_MATURATION	-1.08	0.43	0	0	0	not significant
4991	GO_RETINOID_X_RECEPTOR_BINDING	-1.08	0.43	0	0	0	not significant
4992	GO_SAGA_COMPLEX	-1.08	0.43	0	0	0	not significant
4993	GO_U7_SNRNP	-1.08	0.43	0	0	0	not significant
4994	REACTOME_REGULATED_NECROSIS	-1.08	0.43	0	0	0	not significant
4995	GO_CYCLIC_NUCLEOTIDE_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-1.08	0.42	0	0	0	not significant
4996	GO_NEDD8_SPECIFIC_PROTEASE_ACTIVITY	-1.08	0.42	0	0	0	not significant
4997	GO_PLATELET_DENSE_TUBULAR_NETWORK	-1.08	0.42	0	0	0	not significant
4998	GO_RECEPTOR_RECYCLING	-1.08	0.42	0	0	0	not significant
4999	REACTOME_ESTROGEN_STIMULATED_SIGNALING_THROUGH_PRKCZ	-1.08	0.42	0	0	0	not significant
5000	GO_POSITIVE_REGULATION_OF_GLIAL_CELL_MIGRATION	-1.08	0.41	0	0	0	not significant
5001	HASINA_NOL7_TARGETS_DN	-1.08	0.41	0	0	0	not significant
5002	GO_GALACTOSE_CATABOLIC_PROCESS	-1.08	0.40	0	0	0	not significant

5003	GO_POSITIVE_REGULATION_OF_CHEMOKINE_C_X_C_MOTIF_LIGAND_2_	-1.08	0.40	0	0	0	not significant
5004	REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVE	-1.08	0.40	0	0	0	not significant
5005	GO_REGULATION_OF_KETONE_BIOSYNTHETIC_PROCESS	-1.08	0.39	0	0	0	not significant
5006	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_TRANS	-1.07	0.81	0	0	0	not significant
5007	GO_NUCLEAR_CHROMOSOME	-1.07	0.74	0	0	0	not significant
5008	BAELDE_DIABETIC_NEPHROPATHY_DN	-1.07	0.70	0	0	0	not significant
5009	SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_DN	-1.07	0.67	0	0	0	not significant
5010	SENESE_HDAC3_TARGETS_DN	-1.07	0.63	0	0	0	not significant
5011	GO_REGULATION_OF_DNA_METABOLIC_PROCESS	-1.07	0.59	0	0	0	not significant
5012	GO_CELLULAR_RESPONSE_TO_PEPTIDE_HORMONE_STIMULUS	-1.07	0.58	0	0	0	not significant
5013	GO_NUCLEOSIDE_TRIPHOSPHATASE_REGULATOR_ACTIVITY	-1.07	0.58	0	0	0	not significant
5014	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP	-1.07	0.58	0	0	0	not significant
5015	GO_ENDOPEPTIDASE_ACTIVITY	-1.07	0.57	0	0	0	not significant
5016	GO_NEGATIVE_REGULATION_OF_CELLULAR_CATABOLIC_PROCESS	-1.07	0.56	0	0	0	not significant
5017	GO_POSITIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	-1.07	0.56	0	0	0	not significant
5018	ERBB2_UP.V1_UP	-1.07	0.55	0	0	0	not significant
5019	GO_NEGATIVE_REGULATION_OF_CELL_DEVELOPMENT	-1.07	0.55	0	0	0	not significant
5020	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	-1.07	0.55	0	0	0	not significant
5021	GO_CELL_CORTEX_PART	-1.07	0.54	0	0	0	not significant
5022	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	-1.07	0.53	0	0	0	not significant
5023	VILLANUEVA_LIVER_CANCER_KRT19_UP	-1.07	0.53	0	0	0	not significant
5024	GO_CELL_KILLING	-1.07	0.52	0	0	0	not significant
5025	GO_LARGE_RIBOSOMAL_SUBUNIT	-1.07	0.52	0	0	0	not significant
5026	IKEDA_MIR133_TARGETS_UP	-1.07	0.52	0	0	0	not significant
5027	CHR2Q31	-1.07	0.51	0	0	0	not significant
5028	GO_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	-1.07	0.51	0	0	0	not significant
5029	GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	-1.07	0.51	0	0	0	not significant
5030	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN	-1.07	0.51	0	0	0	not significant
5031	GO_ASTROCYTE_DIFFERENTIATION	-1.07	0.50	0	0	0	not significant
5032	GO_DRUG_TRANSPORT	-1.07	0.50	0	0	0	not significant
5033	KEGG_APOPTOSIS	-1.07	0.50	0	0	0	not significant
5034	GO_PHOSPHOLIPASE_ACTIVITY	-1.07	0.49	0	0	0	not significant
5035	GO_RESPONSE_TO_VITAMIN	-1.07	0.49	0	0	0	not significant
5036	KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_DN	-1.07	0.49	0	0	0	not significant
5037	HINATA_NFKB_TARGETS_FIBROBLAST_UP	-1.07	0.48	0	0	0	not significant
5038	KRAS.KIDNEY_UP.V1_DN	-1.07	0.48	0	0	0	not significant
5039	REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	-1.07	0.48	0	0	0	not significant
5040	GO_BRANCHING_MORPHOGENESIS_OF_AN_EPITHELIAL_TUBE	-1.07	0.47	0	0	0	not significant
5041	GO_NEUROINFLAMMATORY_RESPONSE	-1.07	0.47	0	0	0	not significant
5042	GO_POSITIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	-1.07	0.47	0	0	0	not significant
5043	GO_POSITIVE_REGULATION_OF_STRESS_FIBER_ASSEMBLY	-1.07	0.47	0	0	0	not significant
5044	BIOCARTA_AT1R_PATHWAY	-1.07	0.46	0	0	0	not significant
5045	CHR1P35	-1.07	0.46	0	0	0	not significant
5046	GO_GRANULOCYTE_MIGRATION	-1.07	0.46	0	0	0	not significant
5047	GO_PHOSPHOTRANSFERASE_ACTIVITY_PHOSPHATE_GROUP_AS_ACCE	-1.07	0.46	0	0	0	not significant
5048	GO_PROGRAMMED_NECROTIC_CELL_DEATH	-1.07	0.46	0	0	0	not significant
5049	GO_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	-1.07	0.46	0	0	0	not significant
5050	LEE_LIVER_CANCER_MYC_UP	-1.07	0.46	0	0	0	not significant
5051	LEIN_MEDULLA_MARKERS	-1.07	0.46	0	0	0	not significant
5052	REACTOME_EXTRA_NUCLEAR_ESTROGEN_SIGNALING	-1.07	0.46	0	0	0	not significant
5053	ZHAN_MULTIPLE_MYELOMA_HP_DN	-1.07	0.46	0	0	0	not significant
5054	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	-1.07	0.45	0	0	0	not significant
5055	PID_ANTHRAX_PATHWAY	-1.07	0.45	0	0	0	not significant
5056	REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_K	-1.07	0.45	0	0	0	not significant
5057	TOMIDA_METASTASIS_DN	-1.07	0.45	0	0	0	not significant
5058	GO_CCR4_NOT_COMPLEX	-1.07	0.44	0	0	0	not significant
5059	GO_PEPTIDASE_ACTIVATOR_ACTIVITY_INVOLVED_IN_APOPTOTIC_PROC	-1.07	0.44	0	0	0	not significant
5060	GO_PERK_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	-1.07	0.44	0	0	0	not significant
5061	GO_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	-1.07	0.44	0	0	0	not significant
5062	REACTOME_APOPTOSIS_INDUCED_DNA_FRAGMENTATION	-1.07	0.44	0	0	0	not significant
5063	REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	-1.07	0.44	0	0	0	not significant
5064	REACTOME_UPTAKE_AND_FUNCTION_OF_ANTHRAX_TOXINS	-1.07	0.44	0	0	0	not significant
5065	XU_HGF_SIGNALING_NOT_VIA_AKT1_6HR	-1.07	0.44	0	0	0	not significant
5066	CHIN_BREAST_CANCER_COPY_NUMBER_UP	-1.07	0.43	0	0	0	not significant
5067	GO_LUNG_MORPHOGENESIS	-1.07	0.43	0	0	0	not significant
5068	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_ARREST	-1.07	0.43	0	0	0	not significant
5069	GO_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_STRESS	-1.07	0.43	0	0	0	not significant
5070	GO_SNRNA_BINDING	-1.07	0.43	0	0	0	not significant
5071	STREICHER_LSM1_TARGETS_DN	-1.07	0.43	0	0	0	not significant
5072	ALONSO_METASTASIS_NEURAL_UP	-1.07	0.42	0	0	0	not significant
5073	BIOCARTA_CDC42RAC_PATHWAY	-1.07	0.42	0	0	0	not significant
5074	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_P	-1.07	0.42	0	0	0	not significant
5075	GO_GMP_METABOLIC_PROCESS	-1.07	0.42	0	0	0	not significant
5076	GO_GOLGI_TO_LYSOSOME_TRANSPORT	-1.07	0.42	0	0	0	not significant
5077	GO_NEUROTROPHIN_TRK_RECEPTOR_SIGNALING_PATHWAY	-1.07	0.42	0	0	0	not significant
5078	GO_PEPTIDYL_DIPHTHAMIDE_BIOSYNTHETIC_PROCESS_FROM_PEPTIDY	-1.07	0.42	0	0	0	not significant
5079	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_UP	-1.07	0.42	0	0	0	not significant
5080	PARK_HSC_VS_MULTIPOTENT_PROGENITORS_UP	-1.07	0.42	0	0	0	not significant
5081	REACTOME_SHC_MEDIATED_CASCADE:FGFR3	-1.07	0.42	0	0	0	not significant
5082	VIETOR_IFRD1_TARGETS	-1.07	0.42	0	0	0	not significant
5083	GO_CELLULAR_RESPONSE_TO_EPINEPHRINE_STIMULUS	-1.07	0.41	0	0	0	not significant
5084	GO_CORNIFIED_ENVELOPE	-1.07	0.41	0	0	0	not significant
5085	GO_NONHOMOLOGOUS_END_JOINING_COMPLEX	-1.07	0.41	0	0	0	not significant
5086	GO_CHLORIDE_CHANNEL_INHIBITOR_ACTIVITY	-1.07	0.40	0	0	0	not significant
5087	GO_ELASTIC_FIBER_ASSEMBLY	-1.07	0.40	0	0	0	not significant
5088	GO_FATTY_ACID_SYNTHASE_ACTIVITY	-1.07	0.40	0	0	0	not significant
5089	GO_G_PROTEIN_BETA_SUBUNIT_BINDING	-1.07	0.40	0	0	0	not significant
5090	GO_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	-1.07	0.40	0	0	0	not significant
5091	GO_POSITIVE_REGULATION_OF_HORMONE_METABOLIC_PROCESS	-1.07	0.40	0	0	0	not significant
5092	GO_UBIQUINONE_BINDING	-1.07	0.40	0	0	0	not significant
5093	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_FLI1	-1.07	0.39	0	0	0	not significant
5094	GO_PROTEIN_O_LINKED_FUCOSYLATION	-1.07	0.39	0	0	0	not significant
5095	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_CORTEX	-1.07	0.39	0	0	0	not significant
5096	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13	-1.07	0.39	0	0	0	not significant
5097	GO_CARNITINE_O_ACYLTRANSFERASE_ACTIVITY	-1.07	0.38	0	0	0	not significant
5098	GO_REGULATION_OF_ASPARTIC_TYPE_ENDOPEPTIDASE_ACTIVITY_INV	-1.07	0.38	0	0	0	not significant
5099	GO_REGULATION_OF_HYALURONAN_BIOSYNTHETIC_PROCESS	-1.07	0.36	0	0	0	not significant
5100	GO_DNA_METABOLIC_PROCESS	-1.06	0.82	0	0	0	not significant
5101	GO_REGULATION_OF_CELL_DEVELOPMENT	-1.06	0.73	0	0	0	not significant
5102	GO_LIPID_METABOLIC_PROCESS	-1.06	0.72	0	0	0	not significant
5103	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_STRESS	-1.06	0.70	0	0	0	not significant
5104	GO_PROTEIN_POLYUBIQUITINATION	-1.06	0.64	0	0	0	not significant
5105	GO_REGULATION_OF_GROWTH	-1.06	0.63	0	0	0	not significant
5106	GO_PROTEIN_CATABOLIC_PROCESS	-1.06	0.62	0	0	0	not significant
5107	GO_CELLULAR_RESPONSE_TO_ABIOTIC_STIMULUS	-1.06	0.60	0	0	0	not significant
5108	GO_RIBONUCLEOPROTEIN_GRANULE	-1.06	0.58	0	0	0	not significant
5109	GO_RNA_CATABOLIC_PROCESS	-1.06	0.58	0	0	0	not significant
5110	GO_LIPID_MODIFICATION	-1.06	0.56	0	0	0	not significant
5111	GO_OSSIFICATION	-1.06	0.56	0	0	0	not significant

5112	GO_POSITIVE_REGULATION_OF_CELL_CYCLE	-1.06	0.56	0	0	0	not significant
5113	GO_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	-1.06	0.56	0	0	0	not significant
5114	MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_UP	-1.06	0.54	0	0	0	not significant
5115	FUJII_YBX1_TARGETS_DN	-1.06	0.53	0	0	0	not significant
5116	GO_POSITIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.06	0.53	0	0	0	not significant
5117	GO_REGULATION_OF_CELL_CELL_ADHESION	-1.06	0.53	0	0	0	not significant
5118	STK33_DN	-1.06	0.53	0	0	0	not significant
5119	GO_CELL_SUBSTRATE_ADHESION	-1.06	0.52	0	0	0	not significant
5120	GO_RECEPTOR_METABOLIC_PROCESS	-1.06	0.51	0	0	0	not significant
5121	GO_REGULATION_OF_CELL_CYCLE_ARREST	-1.06	0.51	0	0	0	not significant
5122	GO_BASOLATERAL_PLASMA_MEMBRANE	-1.06	0.50	0	0	0	not significant
5123	GO_IMMUNOGLOBULIN_PRODUCTION	-1.06	0.50	0	0	0	not significant
5124	PROVENZANI_METASTASIS_UP	-1.06	0.50	0	0	0	not significant
5125	GO_PRIMARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.06	0.48	0	0	0	not significant
5126	CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_DN	-1.06	0.47	0	0	0	not significant
5127	GO_ISOPRENOID_METABOLIC_PROCESS	-1.06	0.47	0	0	0	not significant
5128	GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_ASSEMBL	-1.06	0.47	0	0	0	not significant
5129	HALLMARK_INFLAMMATORY_RESPONSE	-1.06	0.47	0	0	0	not significant
5130	IKEDA_MIR1_TARGETS_UP	-1.06	0.46	0	0	0	not significant
5131	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP	-1.06	0.46	0	0	0	not significant
5132	MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_UP	-1.06	0.46	0	0	0	not significant
5133	WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT	-1.06	0.46	0	0	0	not significant
5134	CHESLER_BRAIN_QTL_CIS	-1.06	0.45	0	0	0	not significant
5135	GO_MITOTIC_CYTOKINESIS	-1.06	0.45	0	0	0	not significant
5136	GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PA	-1.06	0.45	0	0	0	not significant
5137	GO_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	-1.06	0.45	0	0	0	not significant
5138	GO_SIGNAL_TRANSDUCTION_INVOLVED_IN_CELL_CYCLE_CHECKPOINT	-1.06	0.45	0	0	0	not significant
5139	KEGG_LYSINE_DEGRADATION	-1.06	0.45	0	0	0	not significant
5140	RB_P130_DN.V1_UP	-1.06	0.45	0	0	0	not significant
5141	REACTOME_RET_SIGNALING	-1.06	0.45	0	0	0	not significant
5142	REACTOME_SEMAPHORIN_INTERACTIONS	-1.06	0.45	0	0	0	not significant
5143	SWEET_KRAS_TARGETS_DN	-1.06	0.45	0	0	0	not significant
5144	CHR10P15	-1.06	0.44	0	0	0	not significant
5145	GO_REGULATION_OF_POTASSIUM_ION_TRANSPORT	-1.06	0.44	0	0	0	not significant
5146	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	-1.06	0.44	0	0	0	not significant
5147	TERAO_AOX4_TARGETS_SKIN_UP	-1.06	0.44	0	0	0	not significant
5148	GO_C2H2_ZINC_FINGER_DOMAIN_BINDING	-1.06	0.43	0	0	0	not significant
5149	GO_POSITIVE_REGULATION_OF_GLYCOLYTIC_PROCESS	-1.06	0.43	0	0	0	not significant
5150	GO_REGULATION_OF_ACTOMYOSIN_STRUCTURE_ORGANIZATION	-1.06	0.43	0	0	0	not significant
5151	JOHANSSON_GLIOMAGENESIS_BY_PDGFB_DN	-1.06	0.43	0	0	0	not significant
5152	KEGG_DRUG_METABOLISM_OTHER_ENZYMES	-1.06	0.43	0	0	0	not significant
5153	REACTOME_REGULATION_OF_FOXO_TRANSCRIPTIONAL_ACTIVITY_BY_	-1.06	0.43	0	0	0	not significant
5154	ZHAN_V2_LATE_DIFFERENTIATION_GENES	-1.06	0.43	0	0	0	not significant
5155	BIOCARTA_ACTINY_PATHWAY	-1.06	0.42	0	0	0	not significant
5156	CHEN_PDGF_TARGETS	-1.06	0.42	0	0	0	not significant
5157	CHOW_RASSF1_TARGETS_UP	-1.06	0.42	0	0	0	not significant
5158	GO_COP9_SIGNALOSOME	-1.06	0.42	0	0	0	not significant
5159	GO_DISRUPTION_OF_CELLS_OF_OTHER_ORGANISM_INVOLVED_IN_SYM	-1.06	0.42	0	0	0	not significant
5160	GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATIO	-1.06	0.42	0	0	0	not significant
5161	GO_NEUROTRANSMITTER_TRANSPORTER_ACTIVITY	-1.06	0.42	0	0	0	not significant
5162	GO_PHYSIOLOGICAL_CARDIAC_MUSCLE_HYPERTROPHY	-1.06	0.42	0	0	0	not significant
5163	GO_POSITIVE_REGULATION_OF_MEMBRANE_POTENTIAL	-1.06	0.42	0	0	0	not significant
5164	GO_POSITIVE_REGULATION_OF_ORGAN_GROWTH	-1.06	0.42	0	0	0	not significant
5165	REACTOME_ECM_PROTEOGLYCANS	-1.06	0.42	0	0	0	not significant
5166	GO_CAMP_RESPONSE_ELEMENT_BINDING_PROTEIN_BINDING	-1.06	0.41	0	0	0	not significant
5167	GO_CHEMOKINE_C_X_C_MOTIF_LIGAND_2_PRODUCTION	-1.06	0.41	0	0	0	not significant
5168	GO_GUANYLATE_KINASE_ACTIVITY	-1.06	0.41	0	0	0	not significant
5169	GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_OUTER_MEMBRANE	-1.06	0.41	0	0	0	not significant
5170	GO_NEGATIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATH	-1.06	0.41	0	0	0	not significant
5171	GO_REGULATION_OF_NEUTROPHIL_ACTIVATION	-1.06	0.41	0	0	0	not significant
5172	GO_TRANSCRIPTION_DEPENDENT_TETHERING_OF_RNA_POLYMERASE_	-1.06	0.41	0	0	0	not significant
5173	REACTOME_METABOLISM_OF_FAT_SOLUBLE_VITAMINS	-1.06	0.41	0	0	0	not significant
5174	GO_GROWTH_PLATE_CARTILAGE_CHONDROCYTE_DIFFERENTIATION	-1.06	0.40	0	0	0	not significant
5175	GO_HINDBRAIN_RADIAL_GLIA_GUIDED_CELL_MIGRATION	-1.06	0.40	0	0	0	not significant
5176	GO_MOLYBDOPTERIN_COFACTOR_BIOSYNTHETIC_PROCESS	-1.06	0.40	0	0	0	not significant
5177	GO_NUCLEOSIDE_CATABOLIC_PROCESS	-1.06	0.40	0	0	0	not significant
5178	GO_POSITIVE_REGULATION_OF_HELICASE_ACTIVITY	-1.06	0.40	0	0	0	not significant
5179	GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_CYTOKINE_PRO	-1.06	0.40	0	0	0	not significant
5180	GO_RRNA_TRANSPORT	-1.06	0.40	0	0	0	not significant
5181	GO_STEROID_ESTERIFICATION	-1.06	0.40	0	0	0	not significant
5182	HUPER_BREAST_BASAL_VS_LUMINAL_UP	-1.06	0.40	0	0	0	not significant
5183	REACTOME_TRIGLYCERIDE_METABOLISM	-1.06	0.40	0	0	0	not significant
5184	BIOCARTA_LONGEVITY_PATHWAY	-1.06	0.39	0	0	0	not significant
5185	GO_DOPAMINE_METABOLIC_PROCESS	-1.06	0.39	0	0	0	not significant
5186	GO_LONG_CHAIN_FATTY_ACID_BINDING	-1.06	0.39	0	0	0	not significant
5187	GO_PROTEIN_INSERTION_INTO_ER_MEMBRANE	-1.06	0.39	0	0	0	not significant
5188	GO_TETRAHYDROFOLATE_BIOSYNTHETIC_PROCESS	-1.06	0.39	0	0	0	not significant
5189	GO_POSITIVE_REGULATION_OF_CHEMOKINE_SECRETION	-1.06	0.38	0	0	0	not significant
5190	WACKER_HYPOXIA_TARGETS_OF_VHL	-1.06	0.38	0	0	0	not significant
5191	GO_ETHER_METABOLIC_PROCESS	-1.06	0.37	0	0	0	not significant
5192	GO_GLUTAMATE_CATABOLIC_PROCESS	-1.06	0.37	0	0	0	not significant
5193	GO_CDC42_PROTEIN_SIGNAL_TRANSDUCTION	-1.06	0.36	0	0	0	not significant
5194	REACTOME_PRE_NOTCH_PROCESSING_IN_THE_ENDOPLASMIC_RETICU	-1.06	0.36	0	0	0	not significant
5195	GO_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	-1.05	0.79	0	0	0	not significant
5196	GO_NEGATIVE_REGULATION_OF_SIGNALING	-1.05	0.67	0	0	0	not significant
5197	MARTINEZ_TP53_TARGETS_DN	-1.05	0.64	0	0	0	not significant
5198	NUYTTEN_NIPP1_TARGETS_UP	-1.05	0.64	0	0	0	not significant
5199	MARTINEZ_RB1_TARGETS_DN	-1.05	0.56	0	0	0	not significant
5200	GO_PEPTIDASE_ACTIVITY	-1.05	0.55	0	0	0	not significant
5201	GO_LAMELLIPODIUM	-1.05	0.54	0	0	0	not significant
5202	CHR6P21	-1.05	0.53	0	0	0	not significant
5203	GO_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	-1.05	0.53	0	0	0	not significant
5204	GO_VESICLE_LOCALIZATION	-1.05	0.53	0	0	0	not significant
5205	KEGG_ENDOCYTOSIS	-1.05	0.53	0	0	0	not significant
5206	GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	-1.05	0.52	0	0	0	not significant
5207	GO_REGULATION_OF_WNT_SIGNALING_PATHWAY	-1.05	0.52	0	0	0	not significant
5208	YAGI_AML_WITH_11Q23_REARRANGED	-1.05	0.52	0	0	0	not significant
5209	BILD_HRAS_ONCOGENIC_SIGNATURE	-1.05	0.50	0	0	0	not significant
5210	BROWNE_HCMV_INFECTION_24HR_UP	-1.05	0.50	0	0	0	not significant
5211	THUM_SYSTOLIC_HEART_FAILURE_UP	-1.05	0.50	0	0	0	not significant
5212	GO_AZUROPHIL_GRANULE	-1.05	0.49	0	0	0	not significant
5213	KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_UP	-1.05	0.49	0	0	0	not significant
5214	GO_CONDENSED_CHROMOSOME	-1.05	0.48	0	0	0	not significant
5215	GO_MONOSACCHARIDE_METABOLIC_PROCESS	-1.05	0.48	0	0	0	not significant
5216	GO_NEGATIVE_REGULATION_OF_MAPK_CASCADE	-1.05	0.48	0	0	0	not significant
5217	GO_TYPE_I_INTERFERON_PRODUCTION	-1.05	0.48	0	0	0	not significant
5218	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP	-1.05	0.48	0	0	0	not significant
5219	REACTOME_CENTROSOME_MATURATION	-1.05	0.47	0	0	0	not significant
5220	REACTOME_PRC2_METHYLATES_HISTONES_AND_DNA	-1.05	0.47	0	0	0	not significant

5221	GAVIN_FOXP3_TARGETS_CLUSTER_P3	-1.05	0.46	0	0	0	not significant
5222	GO_NEGATIVE_REGULATION_OF_PROTEOLYSIS	-1.05	0.46	0	0	0	not significant
5223	NABA_ECM_GLYCOPROTEINS	-1.05	0.46	0	0	0	not significant
5224	FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_UP	-1.05	0.45	0	0	0	not significant
5225	GERY_CEBP_TARGETS	-1.05	0.45	0	0	0	not significant
5226	GO_KINESIN_BINDING	-1.05	0.45	0	0	0	not significant
5227	GO_TRANSLATION_REGULATOR_ACTIVITY	-1.05	0.45	0	0	0	not significant
5228	GRADE_COLON_VS_RECTAL_CANCER_UP	-1.05	0.45	0	0	0	not significant
5229	BROWNE_HCMV_INFECTION_16HR_DN	-1.05	0.44	0	0	0	not significant
5230	GO_EAR_DEVELOPMENT	-1.05	0.44	0	0	0	not significant
5231	GO_GROWTH_FACTOR_ACTIVITY	-1.05	0.44	0	0	0	not significant
5232	GO_PURINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	-1.05	0.44	0	0	0	not significant
5233	KALMA_E2F1_TARGETS	-1.05	0.44	0	0	0	not significant
5234	KEGG_ABC_TRANSPORTERS	-1.05	0.44	0	0	0	not significant
5235	KEGG_ECM_RECEPTOR_INTERACTION	-1.05	0.44	0	0	0	not significant
5236	KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	-1.05	0.44	0	0	0	not significant
5237	LEE_AGING_NEOCORTEX_UP	-1.05	0.44	0	0	0	not significant
5238	REACTOME_SIGNALING_BY_EGFR	-1.05	0.44	0	0	0	not significant
5239	ROSS_AML_WITH_PML_RARA_FUSION	-1.05	0.44	0	0	0	not significant
5240	GO_CYCLIN_DEPENDENT_PROTEIN_KINASE_HOLOENZYME_COMPLEX	-1.05	0.43	0	0	0	not significant
5241	GO_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	-1.05	0.43	0	0	0	not significant
5242	MARSON_FOXP3_CORE_DIRECT_TARGETS	-1.05	0.43	0	0	0	not significant
5243	BIOCARTA_CARDIACEGF_PATHWAY	-1.05	0.42	0	0	0	not significant
5244	GO_CELLULAR_COMPONENT_DISASSEMBLY_INVOLVED_IN_EXECUTION_	-1.05	0.42	0	0	0	not significant
5245	GO_EMBRYONIC_CAMERA_TYPE_EYE_MORPHOGENESIS	-1.05	0.42	0	0	0	not significant
5246	GO_H4_H2A_HISTONE_ACETYLTRANSFERASE_COMPLEX	-1.05	0.42	0	0	0	not significant
5247	GO_MITOTIC_SPINDLE_POLE	-1.05	0.42	0	0	0	not significant
5248	GO_PROTEIN_PHOSPHATASE_ACTIVATOR_ACTIVITY	-1.05	0.42	0	0	0	not significant
5249	GO_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGNALING_PAT	-1.05	0.42	0	0	0	not significant
5250	RASHI_RESPONSE_TO_IONIZING_RADIATION_1	-1.05	0.42	0	0	0	not significant
5251	REACTOME_ACTIVATION_OF_BAD_AND_TRANSLOCATION_TO_MITOCHO	-1.05	0.42	0	0	0	not significant
5252	REACTOME_LDL_CLEARANCE	-1.05	0.42	0	0	0	not significant
5253	BOYAULT_LIVER_CANCER_SUBCLASS_G5_DN	-1.05	0.41	0	0	0	not significant
5254	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_BINDING	-1.05	0.41	0	0	0	not significant
5255	GO_NEGATIVE_REGULATION_OF_MUSCLE_HYPERTROPHY	-1.05	0.41	0	0	0	not significant
5256	KUROKAWA_LIVER_CANCER_CHEMOTHERAPY_DN	-1.05	0.41	0	0	0	not significant
5257	POS_RESPONSE_TO_HISTAMINE_UP	-1.05	0.41	0	0	0	not significant
5258	RICKMAN_HEAD_AND_NECK_CANCER_C	-1.05	0.41	0	0	0	not significant
5259	BIOCARTA_VDR_PATHWAY	-1.05	0.40	0	0	0	not significant
5260	GO_GLUTATHIONE_METABOLIC_PROCESS	-1.05	0.40	0	0	0	not significant
5261	GO_NEGATIVE_REGULATION_OF_PROTEIN_MATURATION	-1.05	0.40	0	0	0	not significant
5262	GO_POSITIVE_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	-1.05	0.40	0	0	0	not significant
5263	GO_RESPONSE_TO_STEROL	-1.05	0.40	0	0	0	not significant
5264	GO_UBIQUITIN_CONJUGATING_ENZYME_COMPLEX	-1.05	0.40	0	0	0	not significant
5265	HENDRICKS_SMARCA4_TARGETS_DN	-1.05	0.40	0	0	0	not significant
5266	KORKOLA_TERATOMA_UP	-1.05	0.40	0	0	0	not significant
5267	REACTOME_METABOLISM_OF_NITRIC_OXIDE:_ENOS_ACTIVATION_AND_	-1.05	0.40	0	0	0	not significant
5268	BIOCARTA_MITOCHONDRIA_PATHWAY	-1.05	0.39	0	0	0	not significant
5269	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN	-1.05	0.39	0	0	0	not significant
5270	GO_3_5_CYCLIC_GMP_PHOSPHODIESTERASE_ACTIVITY	-1.05	0.39	0	0	0	not significant
5271	GO_CCR_CHEMOKINE_RECEPTOR_BINDING	-1.05	0.39	0	0	0	not significant
5272	GO_LIPID_DROPLET_ORGANIZATION	-1.05	0.39	0	0	0	not significant
5273	GO_MEGAKARYOCYTE_DEVELOPMENT	-1.05	0.39	0	0	0	not significant
5274	GO_MITOCHONDRIAL_GENOME_MAINTENANCE	-1.05	0.39	0	0	0	not significant
5275	GO_NEGATIVE_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_	-1.05	0.39	0	0	0	not significant
5276	GO_PHOSPHORYLATION_OF_RNA_POLYMERASE_II_C_TERMINAL_DOMAI	-1.05	0.39	0	0	0	not significant
5277	GO_POSITIVE_REGULATION_OF_IRE1_MEDIATED_UNFOLDED_PROTEIN_	-1.05	0.39	0	0	0	not significant
5278	GO_POSITIVE_REGULATION_OF_PHOSPHOLIPID_TRANSPORT	-1.05	0.39	0	0	0	not significant
5279	GO_RESPONSE_TO_ETHER	-1.05	0.39	0	0	0	not significant
5280	HOEGERKORP_CD44_TARGETS_TEMPORAL_DN	-1.05	0.39	0	0	0	not significant
5281	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_24	-1.05	0.39	0	0	0	not significant
5282	GO_ALANINE_TRANSPORT	-1.05	0.38	0	0	0	not significant
5283	GO_CALCIUM_TRANSPORTING_ATPASE_ACTIVITY	-1.05	0.38	0	0	0	not significant
5284	GO_CLATHRIN_COMPLEX	-1.05	0.38	0	0	0	not significant
5285	GO_PHOSPHOSERINE_RESIDUE_BINDING	-1.05	0.38	0	0	0	not significant
5286	GO_REGULATION_OF_LAMELLIPODIUM_MORPHOGENESIS	-1.05	0.38	0	0	0	not significant
5287	GO_POLYNUCLEOTIDE_ADENYLYLTRANSFERASE_ACTIVITY	-1.05	0.37	0	0	0	not significant
5288	REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS	-1.05	0.36	0	0	0	not significant
5289	ZEILSTRA_CD44_TARGETS_DN	-1.05	0.36	0	0	0	not significant
5290	GO_REGULATION_OF_GLOMERULUS_DEVELOPMENT	-1.05	0.34	0	0	0	not significant
5291	GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION	-1.04	0.86	0	0	0	not significant
5292	GO_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	-1.04	0.68	0	0	0	not significant
5293	GO_HEAD_DEVELOPMENT	-1.04	0.51	0	0	0	not significant
5294	GO_LIPID_CATABOLIC_PROCESS	-1.04	0.51	0	0	0	not significant
5295	GO_CARTILAGE_DEVELOPMENT	-1.04	0.48	0	0	0	not significant
5296	GO_POSITIVE_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	-1.04	0.48	0	0	0	not significant
5297	BONOME_OVARIAN_CANCER_SURVIVAL_OPTIMAL_DEBULKING	-1.04	0.47	0	0	0	not significant
5298	HOLLMANN_APOPTOSIS_VIA_CD40_DN	-1.04	0.47	0	0	0	not significant
5299	ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP	-1.04	0.47	0	0	0	not significant
5300	GO_DNA_REPLICATION_INDEPENDENT_NUCLEOSOME_ORGANIZATION	-1.04	0.46	0	0	0	not significant
5301	GO_LAMELLIPODIUM_ORGANIZATION	-1.04	0.46	0	0	0	not significant
5302	GO_ORGANOPHOSPHATE_CATABOLIC_PROCESS	-1.04	0.46	0	0	0	not significant
5303	KEGG_VIRAL_MYOCARDITIS	-1.04	0.46	0	0	0	not significant
5304	GO_CLATHRIN_COATED_PIT	-1.04	0.45	0	0	0	not significant
5305	GO_COPII_COATED_ER_TO_GOLGI_TRANSPORT_VESICLE	-1.04	0.45	0	0	0	not significant
5306	PURBEY_TARGETS_OF_CTBP1_AND_SATB1_DN	-1.04	0.45	0	0	0	not significant
5307	CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_DN	-1.04	0.44	0	0	0	not significant
5308	DANG_REGULATED_BY_MYC_DN	-1.04	0.44	0	0	0	not significant
5309	GO_CELLULAR_RESPONSE_TO_IONIZING_RADIATION	-1.04	0.44	0	0	0	not significant
5310	GO_POSITIVE_REGULATION_OF_CELL_DIVISION	-1.04	0.44	0	0	0	not significant
5311	GO_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	-1.04	0.44	0	0	0	not significant
5312	GO_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	-1.04	0.44	0	0	0	not significant
5313	REACTOME_TRIF_TICAM1_MEDIATED_TLR4_SIGNALING	-1.04	0.44	0	0	0	not significant
5314	REACTOME_UNFOLDED_PROTEIN_RESPONSE_UPR	-1.04	0.44	0	0	0	not significant
5315	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP	-1.04	0.43	0	0	0	not significant
5316	GO_DETECTION_OF_LIGHT_STIMULUS	-1.04	0.43	0	0	0	not significant
5317	GO_PROTEIN_TYROSINE_KINASE_BINDING	-1.04	0.43	0	0	0	not significant
5318	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	-1.04	0.43	0	0	0	not significant
5319	LANG_MYB_FAMILY_TARGETS	-1.04	0.43	0	0	0	not significant
5320	LEE_CALORIE_RESTRICTION_MUSCLE_DN	-1.04	0.43	0	0	0	not significant
5321	REACTOME_ANCHORING_OF_THE_BASAL_BODY_TO_THE_PLASMA_MEM	-1.04	0.43	0	0	0	not significant
5322	GO_INTERFERON_BETA_PRODUCTION	-1.04	0.42	0	0	0	not significant
5323	GO_REGULATION_OF_CALCINEURIN_MEDIATED_SIGNALING	-1.04	0.42	0	0	0	not significant
5324	GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS	-1.04	0.42	0	0	0	not significant
5325	CAHOY_OLIGODENDROCUTIC	-1.04	0.41	0	0	0	not significant
5326	GENTILE_UV_RESPONSE_CLUSTER_D1	-1.04	0.41	0	0	0	not significant
5327	GO_HSP90_PROTEIN_BINDING	-1.04	0.41	0	0	0	not significant
5328	GO_MYOSIN_BINDING	-1.04	0.41	0	0	0	not significant
5329	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLE	-1.04	0.41	0	0	0	not significant

5330	GO_POSITIVE_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOP	-1.04	0.41	0	0	0	not significant
5331	GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFA	-1.04	0.41	0	0	0	not significant
5332	GO_REGULATION_OF_RUFFLE_ASSEMBLY	-1.04	0.41	0	0	0	not significant
5333	GO_SKELETAL_MUSCLE_CONTRACTION	-1.04	0.41	0	0	0	not significant
5334	HAN_JNK_SINGALING_DN	-1.04	0.41	0	0	0	not significant
5335	KYNG_RESPONSE_TO_H2O2_VIA_ERCC6_UP	-1.04	0.41	0	0	0	not significant
5336	SANA_TNF_SIGNALING_UP	-1.04	0.41	0	0	0	not significant
5337	GO_AXIS_ELONGATION	-1.04	0.40	0	0	0	not significant
5338	GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	-1.04	0.40	0	0	0	not significant
5339	GO_OUTFLOW_TRACT_MORPHOGENESIS	-1.04	0.40	0	0	0	not significant
5340	GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	-1.04	0.40	0	0	0	not significant
5341	GO_PROTEIN_K63_LINKED_UBIQUITINATION	-1.04	0.40	0	0	0	not significant
5342	GO_REGULATION_OF_SYNAPTIC_VESICLE_TRANSPORT	-1.04	0.40	0	0	0	not significant
5343	RASHI_RESPONSE_TO_IONIZING_RADIATION_3	-1.04	0.40	0	0	0	not significant
5344	VALK_AML_WITH_CEBPA	-1.04	0.40	0	0	0	not significant
5345	ABE_VEGFA_TARGETS_2HR	-1.04	0.39	0	0	0	not significant
5346	BIOCARTA_IGF1_PATHWAY	-1.04	0.39	0	0	0	not significant
5347	GO_NEGATIVE_REGULATION_OF_LIPID_STORAGE	-1.04	0.39	0	0	0	not significant
5348	GO_NUCLEOSIDE_DIPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.04	0.39	0	0	0	not significant
5349	GO_PENTOSE_PHOSPHATE_SHUNT	-1.04	0.39	0	0	0	not significant
5350	GO_REGULATION_OF_ALKALINE_PHOSPHATASE_ACTIVITY	-1.04	0.39	0	0	0	not significant
5351	GO_RESPONSE_TO_ACIDIC_PH	-1.04	0.39	0	0	0	not significant
5352	GO_RESPONSE_TO_EPINEPHRINE	-1.04	0.39	0	0	0	not significant
5353	GO_TRANSFERRIN_RECEPTOR_BINDING	-1.04	0.39	0	0	0	not significant
5354	MCBRYAN_PUBERTAL_BREAST_3_4WK_DN	-1.04	0.39	0	0	0	not significant
5355	REACTOME_DEFECTIVE_EXT2_CAUSES_EXOSTOSES_2	-1.04	0.39	0	0	0	not significant
5356	BIOCARTA_RNA_PATHWAY	-1.04	0.38	0	0	0	not significant
5357	GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_4_PHOSPHATASE_ACTIVITY	-1.04	0.38	0	0	0	not significant
5358	GO_POSITIVE_REGULATION_OF_HISTONE_DEACETYLATION	-1.04	0.38	0	0	0	not significant
5359	GO_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STIMULUS	-1.04	0.38	0	0	0	not significant
5360	REACTOME_SIGNALING_BY_NTRK3_TRKC	-1.04	0.38	0	0	0	not significant
5361	RUAN_RESPONSE_TO_TNF_TROGLITAZONE_UP	-1.04	0.38	0	0	0	not significant
5362	GO_ANTEROGRADE_AXONAL_PROTEIN_TRANSPORT	-1.04	0.37	0	0	0	not significant
5363	GO_CELL_MIGRATION_IN_HINDBRAIN	-1.04	0.37	0	0	0	not significant
5364	GO_CELLULAR_RESPONSE_TO_BRAIN_DERIVED_NEUROTROPHIC_FACT	-1.04	0.37	0	0	0	not significant
5365	GO_CHEMOKINE_C_C_MOTIF_LIGAND_5_PRODUCTION	-1.04	0.37	0	0	0	not significant
5366	GO_DOUBLE_STRAND_BREAK_REPAIR_VIA_SYNTHESIS_DEPENDENT_ST	-1.04	0.37	0	0	0	not significant
5367	GO_PHOSPHATIDYLINOSITOL_3_5_BISPHOSPHATE_PHOSPHATASE_ACTI	-1.04	0.37	0	0	0	not significant
5368	GO_POSITIVE_REGULATION_BY_HOST_OF_VIRAL_GENOME_REPLICATIO	-1.04	0.37	0	0	0	not significant
5369	GO_SCARNA_LOCALIZATION_TO_CAJAL_BODY	-1.04	0.37	0	0	0	not significant
5370	BIOCARTA_AGPCR_PATHWAY	-1.04	0.36	0	0	0	not significant
5371	GO_5_3_EXODEOXYRIBONUCLEASE_ACTIVITY	-1.04	0.36	0	0	0	not significant
5372	GO_NEGATIVE_REGULATION_OF_PROTEIN_FOLDING	-1.04	0.36	0	0	0	not significant
5373	GO_PROSTAGLANDIN_TRANSPORT	-1.04	0.36	0	0	0	not significant
5374	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_DN	-1.04	0.36	0	0	0	not significant
5375	MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA_VHL_DN	-1.04	0.36	0	0	0	not significant
5376	REACTOME_PLASMA_LIPOPROTEIN_ASSEMBLY	-1.04	0.36	0	0	0	not significant
5377	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_HD_MTX_UP	-1.04	0.35	0	0	0	not significant
5378	GO_AMYLOID_BETA_CLEARANCE_BY_CELLULAR_CATABOLIC_PROCESS	-1.04	0.35	0	0	0	not significant
5379	GO_RS_DOMAIN_BINDING	-1.04	0.35	0	0	0	not significant
5380	NAKAMURA_CANCER_MICROENVIRONMENT_UP	-1.04	0.35	0	0	0	not significant
5381	REACTOME_PD_1_SIGNALING	-1.04	0.35	0	0	0	not significant
5382	GO_REGULATION_OF_PROTEIN_LOCALIZATION	-1.03	0.60	0	0	0	not significant
5383	GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	-1.03	0.53	0	0	0	not significant
5384	GO_GOLGI_VESICLE_TRANSPORT	-1.03	0.49	0	0	0	not significant
5385	GO_ANION_TRANSPORT	-1.03	0.48	0	0	0	not significant
5386	KOYAMA_SEMA3B_TARGETS_DN	-1.03	0.47	0	0	0	not significant
5387	GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_ENDONUCLEOLYTIC	-1.03	0.45	0	0	0	not significant
5388	LU_AGING_BRAIN_UP	-1.03	0.45	0	0	0	not significant
5389	ACEVEDO_LIVER_CANCER_DN	-1.03	0.44	0	0	0	not significant
5390	PKCA_DN.V1_DN	-1.03	0.44	0	0	0	not significant
5391	GO_APICAL_PART_OF_CELL	-1.03	0.43	0	0	0	not significant
5392	GO_INTERLEUKIN_1_BETA_PRODUCTION	-1.03	0.43	0	0	0	not significant
5393	GO_NEGATIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	-1.03	0.43	0	0	0	not significant
5394	GO_RESPONSE_TO_METAL_ION	-1.03	0.43	0	0	0	not significant
5395	GO_SIGNAL_TRANSDUCTION_IN_RESPONSE_TO_DNA_DAMAGE	-1.03	0.43	0	0	0	not significant
5396	PID_AR_TF_PATHWAY	-1.03	0.43	0	0	0	not significant
5397	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_VIA_MHC_CLASS_IB	-1.03	0.42	0	0	0	not significant
5398	GO_CALCIUM_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-1.03	0.42	0	0	0	not significant
5399	GO_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	-1.03	0.42	0	0	0	not significant
5400	GO_EMBRYONIC_ORGAN_MORPHOGENESIS	-1.03	0.42	0	0	0	not significant
5401	GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY_COUPLED	-1.03	0.42	0	0	0	not significant
5402	GO_NEPHRON_MORPHOGENESIS	-1.03	0.42	0	0	0	not significant
5403	GO_NEURON_APOPTOTIC_PROCESS	-1.03	0.42	0	0	0	not significant
5404	GO_NUCLEAR_TRANSCRIPTION_FACTOR_COMPLEX	-1.03	0.42	0	0	0	not significant
5405	REACTOME_PLATELET_HOMEOSTASIS	-1.03	0.42	0	0	0	not significant
5406	GO_PEPTIDYL_THREONINE_MODIFICATION	-1.03	0.41	0	0	0	not significant
5407	GO_PYRIMIDINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	-1.03	0.41	0	0	0	not significant
5408	GO_REGULATION_OF_ERBB_SIGNALING_PATHWAY	-1.03	0.41	0	0	0	not significant
5409	GO_REGULATION_OF_HORMONE_SECRETION	-1.03	0.41	0	0	0	not significant
5410	LABBE_WNT3A_TARGETS_DN	-1.03	0.41	0	0	0	not significant
5411	LEE_AGING_CEREBELLUM_UP	-1.03	0.41	0	0	0	not significant
5412	REACTOME_SULFUR_AMINO_ACID_METABOLISM	-1.03	0.41	0	0	0	not significant
5413	TAVAZOIE_METASTASIS	-1.03	0.41	0	0	0	not significant
5414	BAE_BRCA1_TARGETS_UP	-1.03	0.40	0	0	0	not significant
5415	GO_CENTRAL_NERVOUS_SYSTEM_PROJECTION_NEURON_AXONOGENES	-1.03	0.40	0	0	0	not significant
5416	GO_MITOTIC_CYTOKINETIC_PROCESS	-1.03	0.40	0	0	0	not significant
5417	GO_PHOTOTRANSDUCTION	-1.03	0.40	0	0	0	not significant
5418	GO_RNA_SURVEILLANCE	-1.03	0.40	0	0	0	not significant
5419	HOSHIDA_LIVER_CANCER_SURVIVAL_UP	-1.03	0.40	0	0	0	not significant
5420	KEGG_FOCAL_ADHESION	-1.03	0.40	0	0	0	not significant
5421	MORI_MATURE_B_LYMPHOCYTE_UP	-1.03	0.40	0	0	0	not significant
5422	REACTOME_GAP_JUNCTION_DEGRADATION	-1.03	0.40	0	0	0	not significant
5423	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	-1.03	0.40	0	0	0	not significant
5424	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM	-1.03	0.40	0	0	0	not significant
5425	REN_ALVEOLAR_RHABDOMYOSARCOMA_UP	-1.03	0.40	0	0	0	not significant
5426	SATO_SILENCED_EPIGENETICALLY_IN_PANCREATIC_CANCER	-1.03	0.40	0	0	0	not significant
5427	ZWANG_EGF_INTERVAL_UP	-1.03	0.40	0	0	0	not significant
5428	GO_HISTONE_METHYLTRANSFERASE_ACTIVITY	-1.03	0.39	0	0	0	not significant
5429	GO_MOTOR_ACTIVITY	-1.03	0.39	0	0	0	not significant
5430	GO_NEGATIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SI	-1.03	0.39	0	0	0	not significant
5431	GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYME	-1.03	0.39	0	0	0	not significant
5432	GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	-1.03	0.39	0	0	0	not significant
5433	GO_REGULATION_OF_MITOTIC_CENTROSOME_SEPARATION	-1.03	0.39	0	0	0	not significant
5434	GO_RUFFLE_MEMBRANE	-1.03	0.39	0	0	0	not significant
5435	HONRADO_BREAST_CANCER_BRCA1_VS_BRCA2	-1.03	0.39	0	0	0	not significant
5436	MCCLUNG_COCAIN_REWARD_4WK	-1.03	0.39	0	0	0	not significant
5437	OHGUCHI_LIVER_HNF4A_TARGETS_UP	-1.03	0.39	0	0	0	not significant
5438	REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	-1.03	0.39	0	0	0	not significant

5439	FINETTI_BREAST_CANCER_KINOME_GREEN	-1.03	0.38	0	0	0	not significant
5440	GO_CELL_COMMUNICATION_INVOLVED_IN_CARDIAC_CONDUCTION	-1.03	0.38	0	0	0	not significant
5441	GO_CHEMICAL_HOMEOSTASIS_WITHIN_A_TISSUE	-1.03	0.38	0	0	0	not significant
5442	GO_NEGATIVE_REGULATION_OF_MUSCLE_CONTRACTION	-1.03	0.38	0	0	0	not significant
5443	GO_PLASMA_MEMBRANE_TO_ENDOSOME_TRANSPORT	-1.03	0.38	0	0	0	not significant
5444	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYT	-1.03	0.38	0	0	0	not significant
5445	GO_POSITIVE_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	-1.03	0.38	0	0	0	not significant
5446	GO_REGULATION_OF_TRANSCRIPTION_ELONGATION_FROM_RNA_POLY	-1.03	0.38	0	0	0	not significant
5447	GO_RESPONSE_TO_GAMMA_RADIATION	-1.03	0.38	0	0	0	not significant
5448	MOOTHA_FFA_OXYDATION	-1.03	0.38	0	0	0	not significant
5449	REACTOME_FCERI_MEDIATED_MAPK_ACTIVATION	-1.03	0.38	0	0	0	not significant
5450	XU_HGF_TARGETS_REPRESSED_BY_AKT1_UP	-1.03	0.38	0	0	0	not significant
5451	GO_INOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	-1.03	0.37	0	0	0	not significant
5452	GO_INWARD_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	-1.03	0.37	0	0	0	not significant
5453	GO_REGULATION_OF_RNA_BINDING	-1.03	0.37	0	0	0	not significant
5454	GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	-1.03	0.37	0	0	0	not significant
5455	GO_REGULATION_OF_URINE_VOLUME	-1.03	0.37	0	0	0	not significant
5456	GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	-1.03	0.37	0	0	0	not significant
5457	LEIN_PONS_MARKERS	-1.03	0.37	0	0	0	not significant
5458	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN	-1.03	0.37	0	0	0	not significant
5459	GO_INTRINSIC_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_MEMBR	-1.03	0.36	0	0	0	not significant
5460	GO_LAYER_FORMATION_IN_CEREBRAL_CORTEX	-1.03	0.36	0	0	0	not significant
5461	GO_REPLICATION_FORK_PROTECTION_COMPLEX	-1.03	0.36	0	0	0	not significant
5462	GO_SERTOLI_CELL_DIFFERENTIATION	-1.03	0.36	0	0	0	not significant
5463	REACTOME_MITOCHONDRIAL_IRON_SULFUR_CLUSTER_BIOGENESIS	-1.03	0.36	0	0	0	not significant
5464	BIOCARTA_HES_PATHWAY	-1.03	0.35	0	0	0	not significant
5465	CORRADETTI_MTOR_PATHWAY_REGULATORS_DN	-1.03	0.35	0	0	0	not significant
5466	GENTLES_LEUKEMIC_STEM_CELL_DN	-1.03	0.35	0	0	0	not significant
5467	GO_CORTICAL_ENDOPLASMIC_RETICULUM	-1.03	0.35	0	0	0	not significant
5468	REACTOME_ARMS_MEDIATED_ACTIVATION	-1.03	0.35	0	0	0	not significant
5469	GO_NUCLEAR_STRESS_GRANULE	-1.03	0.34	0	0	0	not significant
5470	GO_TRNA_PSEUDOURIDINE_SYNTHESIS	-1.03	0.34	0	0	0	not significant
5471	PID_P38_MK2_PATHWAY	-1.03	0.34	0	0	0	not significant
5472	GO_NEGATIVE_REGULATION_OF_PROTEIN_METABOLIC_PROCESS	-1.02	0.52	0	0	0	not significant
5473	GO_EMBRYONIC_ORGAN_DEVELOPMENT	-1.02	0.45	0	0	0	not significant
5474	GO_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	-1.02	0.45	0	0	0	not significant
5475	GO_CELLULAR_MACROMOLECULE_LOCALIZATION	-1.02	0.42	0	0	0	not significant
5476	GO_PEPTIDE_METABOLIC_PROCESS	-1.02	0.42	0	0	0	not significant
5477	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_ARREST	-1.02	0.42	0	0	0	not significant
5478	GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	-1.02	0.42	0	0	0	not significant
5479	GO_HEART_GROWTH	-1.02	0.41	0	0	0	not significant
5480	GO_NEGATIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	-1.02	0.41	0	0	0	not significant
5481	GO_REGULATION_OF_CELLULAR_LOCALIZATION	-1.02	0.41	0	0	0	not significant
5482	MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_UP	-1.02	0.41	0	0	0	not significant
5483	PID_IL8_CXCR2_PATHWAY	-1.02	0.41	0	0	0	not significant
5484	CHR4Q32	-1.02	0.40	0	0	0	not significant
5485	DING_LUNG_CANCER_EXPRESSION_BY_COPY_NUMBER	-1.02	0.40	0	0	0	not significant
5486	JAK2_DN.V1_UP	-1.02	0.40	0	0	0	not significant
5487	REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDUCED_SENESCENC	-1.02	0.40	0	0	0	not significant
5488	REACTOME_SIGNALING_BY_BRAF_AND_RAF_FUSIONS	-1.02	0.40	0	0	0	not significant
5489	ATF2_UP.V1_DN	-1.02	0.39	0	0	0	not significant
5490	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP	-1.02	0.39	0	0	0	not significant
5491	GO_CEREBRAL_CORTEX_RADIALLY_ORIENTED_CELL_MIGRATION	-1.02	0.39	0	0	0	not significant
5492	GO_DENDRITIC_CELL_DIFFERENTIATION	-1.02	0.39	0	0	0	not significant
5493	GO_DNA_METHYLATION_OR_DEMETHYLATION	-1.02	0.39	0	0	0	not significant
5494	GO_POSITIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.02	0.39	0	0	0	not significant
5495	GO_PROTEIN_METHYLTRANSFERASE_ACTIVITY	-1.02	0.39	0	0	0	not significant
5496	REACTOME_RHO_GTPASES_ACTIVATE_NADPH_OXIDASES	-1.02	0.39	0	0	0	not significant
5497	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP	-1.02	0.39	0	0	0	not significant
5498	CHR9Q22	-1.02	0.38	0	0	0	not significant
5499	GO_CELL_ADHESION_MEDIATED_BY_INTEGRIN	-1.02	0.38	0	0	0	not significant
5500	GO_CYTOPLASMIC_STRESS_GRANULE	-1.02	0.38	0	0	0	not significant
5501	GO_FILOPODIUM_ASSEMBLY	-1.02	0.38	0	0	0	not significant
5502	GO_MICROTUBULE_DEPOLYMERIZATION	-1.02	0.38	0	0	0	not significant
5503	GO_NEGATIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	-1.02	0.38	0	0	0	not significant
5504	GO_NEGATIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION	-1.02	0.38	0	0	0	not significant
5505	GO_PIGMENT_BIOSYNTHETIC_PROCESS	-1.02	0.38	0	0	0	not significant
5506	GO_PIGMENT_METABOLIC_PROCESS	-1.02	0.38	0	0	0	not significant
5507	GO_POSITIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	-1.02	0.38	0	0	0	not significant
5508	GO_REGULATION_OF_RECEPTOR_RECYCLING	-1.02	0.38	0	0	0	not significant
5509	GO_RESPONSE_TO_ESTROGEN	-1.02	0.38	0	0	0	not significant
5510	GO_VESICLE_DOCKING	-1.02	0.38	0	0	0	not significant
5511	HOWLIN_CITED1_TARGETS_1_DN	-1.02	0.38	0	0	0	not significant
5512	PID_ARF6_DOWNSTREAM_PATHWAY	-1.02	0.38	0	0	0	not significant
5513	REACTOME_FORMATION_OF_SENESCENCE_ASSOCIATED_HETEROCHR	-1.02	0.38	0	0	0	not significant
5514	REACTOME_NEURODEGENERATIVE_DISEASES	-1.02	0.38	0	0	0	not significant
5515	GO_CARDIAC_VENTRICLE_MORPHOGENESIS	-1.02	0.37	0	0	0	not significant
5516	GO_CLATHRIN_COAT_OF_COATED_PIT	-1.02	0.37	0	0	0	not significant
5517	GO_INSULIN_SECRETION	-1.02	0.37	0	0	0	not significant
5518	GO_NEGATIVE_REGULATION_OF_TORC1_SIGNALING	-1.02	0.37	0	0	0	not significant
5519	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_ADHESION_TO_VASCULA	-1.02	0.37	0	0	0	not significant
5520	GO_VESICLE_DOCKING_INVOLVED_IN_EXOCYTOSIS	-1.02	0.37	0	0	0	not significant
5521	REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	-1.02	0.37	0	0	0	not significant
5522	STANELLE_E2F1_TARGETS	-1.02	0.37	0	0	0	not significant
5523	VANDESLUIS_COMMD1_TARGETS_GROUP_4_UP	-1.02	0.37	0	0	0	not significant
5524	ZUCCHI_METASTASIS_UP	-1.02	0.37	0	0	0	not significant
5525	BIOCARTA_IGF1MTOR_PATHWAY	-1.02	0.36	0	0	0	not significant
5526	GO_ARTERY_MORPHOGENESIS	-1.02	0.36	0	0	0	not significant
5527	GO_EXOCYTIC_PROCESS	-1.02	0.36	0	0	0	not significant
5528	GO_GLUCAN_CATABOLIC_PROCESS	-1.02	0.36	0	0	0	not significant
5529	GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	-1.02	0.36	0	0	0	not significant
5530	GO_SEMAPHORIN_RECEPTOR_ACTIVITY	-1.02	0.36	0	0	0	not significant
5531	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_DN	-1.02	0.36	0	0	0	not significant
5532	REACTOME_CHREBP_ACTIVATES_METABOLIC_GENE_EXPRESSION	-1.02	0.36	0	0	0	not significant
5533	GO_METALLOCHAPERONE_ACTIVITY	-1.02	0.35	0	0	0	not significant
5534	GO_NK_T_CELL_DIFFERENTIATION	-1.02	0.35	0	0	0	not significant
5535	GO_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY_INVOLVED_IN_NEURON	-1.02	0.35	0	0	0	not significant
5536	GO_ATRIAL_CARDIAC_MUSCLE_CELL_TO_AV_NODE_CELL_SIGNALING	-1.02	0.34	0	0	0	not significant
5537	GO_ICOSANOID_RECEPTOR_ACTIVITY	-1.02	0.34	0	0	0	not significant
5538	GO_NEGATIVE_REGULATION_OF_PROTEIN_IMPORT_INTO_NUCLEUS	-1.02	0.34	0	0	0	not significant
5539	GO_POSITIVE_REGULATION_OF_CELL_MATURATION	-1.02	0.34	0	0	0	not significant
5540	LEIN_MIDBRAIN_MARKERS	-1.02	0.34	0	0	0	not significant
5541	GO_AXON_INITIAL_SEGMENT	-1.02	0.33	0	0	0	not significant
5542	GO_CARDIAC_LEFT_VENTRICLE_MORPHOGENESIS	-1.02	0.33	0	0	0	not significant
5543	GO_REGULATION_OF_NEUROTROPHIN_TRK_RECEPTOR_SIGNALING_PA	-1.02	0.33	0	0	0	not significant
5544	GO_ACTIN_BASED_CELL_PROJECTION	-1.01	0.42	0	0	0	not significant
5545	GO_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.01	0.42	0	0	0	not significant
5546	CHR12Q13	-1.01	0.40	0	0	0	not significant
5547	GO_REGULATION_OF_ORGAN_GROWTH	-1.01	0.40	0	0	0	not significant

5548	GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_SUPERFAMILY_BINDING	-1.01	0.40	0	0	0	not significant
5549	GO_CELLULAR_MACROMOLECULE_CATABOLIC_PROCESS	-1.01	0.39	0	0	0	not significant
5550	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	-1.01	0.39	0	0	0	not significant
5551	GO_MAINTENANCE_OF_CELL_NUMBER	-1.01	0.39	0	0	0	not significant
5552	GO_MICROTUBULE_BASED_PROCESS	-1.01	0.39	0	0	0	not significant
5553	JAZAG_TGFB1_SIGNALING_UP	-1.01	0.39	0	0	0	not significant
5554	JIANG_VHL_TARGETS	-1.01	0.39	0	0	0	not significant
5555	KEGG_THYROID_CANCER	-1.01	0.39	0	0	0	not significant
5556	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_TRANS	-1.01	0.38	0	0	0	not significant
5557	GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_DN	-1.01	0.38	0	0	0	not significant
5558	GO_POSITIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	-1.01	0.38	0	0	0	not significant
5559	GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN	-1.01	0.38	0	0	0	not significant
5560	GO_REGULATION_OF_AMYLOID_PRECURSOR_PROTEIN_CATABOLIC_PR	-1.01	0.38	0	0	0	not significant
5561	GO_REGULATION_OF_DEVELOPMENTAL_GROWTH	-1.01	0.38	0	0	0	not significant
5562	GO_REGULATION_OF_SUPRAMOLECULAR_FIBER_ORGANIZATION	-1.01	0.38	0	0	0	not significant
5563	GO_SKELETAL_SYSTEM_MORPHOGENESIS	-1.01	0.38	0	0	0	not significant
5564	AMIT_EGF_RESPONSE_480_HELA	-1.01	0.37	0	0	0	not significant
5565	BIOCARTA_FAS_PATHWAY	-1.01	0.37	0	0	0	not significant
5566	CROMER_TUMORIGENESIS_DN	-1.01	0.37	0	0	0	not significant
5567	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_STIMULUS	-1.01	0.37	0	0	0	not significant
5568	GO_REGION_OF_CYTOSOL	-1.01	0.37	0	0	0	not significant
5569	GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN	-1.01	0.37	0	0	0	not significant
5570	GO_REGULATION_OF_INTRACELLULAR_TRANSPORT	-1.01	0.37	0	0	0	not significant
5571	KEGG_INSULIN_SIGNALING_PATHWAY	-1.01	0.37	0	0	0	not significant
5572	KUNINGER_IGF1_VS_PDGFB_TARGETS_DN	-1.01	0.37	0	0	0	not significant
5573	OKUMURA_INFLAMMATORY_RESPONSE_LPS	-1.01	0.37	0	0	0	not significant
5574	PID_VEGFR1_2_PATHWAY	-1.01	0.37	0	0	0	not significant
5575	RHEIN_ALL_GLUCOCORTICOID_THERAPY_UP	-1.01	0.37	0	0	0	not significant
5576	RIGGINS_TAMOXIFEN_RESISTANCE_DN	-1.01	0.37	0	0	0	not significant
5577	TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA	-1.01	0.37	0	0	0	not significant
5578	BIOCARTA_RAC1_PATHWAY	-1.01	0.36	0	0	0	not significant
5579	BLUM_RESPONSE_TO_SALIRASIB_UP	-1.01	0.36	0	0	0	not significant
5580	BOYLAN_MULTIPLE_MYELOMA_D_UP	-1.01	0.36	0	0	0	not significant
5581	CHENG_RESPONSE_TO_NICKEL_ACETATE	-1.01	0.36	0	0	0	not significant
5582	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_DN	-1.01	0.36	0	0	0	not significant
5583	CHR3P25	-1.01	0.36	0	0	0	not significant
5584	CHR9Q21	-1.01	0.36	0	0	0	not significant
5585	E2F1_UP.V1_DN	-1.01	0.36	0	0	0	not significant
5586	GO_CATALYTIC_ACTIVITY_ACTING_ON_DNA	-1.01	0.36	0	0	0	not significant
5587	GO_ENDOCARDIUM_DEVELOPMENT	-1.01	0.36	0	0	0	not significant
5588	GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_CATABOLIC_PROCE	-1.01	0.36	0	0	0	not significant
5589	GO_NUCLEOSOME_ORGANIZATION	-1.01	0.36	0	0	0	not significant
5590	GO_POSITIVE_REGULATION_OF_PROTEIN_DEPHOSPHORYLATION	-1.01	0.36	0	0	0	not significant
5591	GO_POSITIVE_REGULATION_OF_T_CELL_MIGRATION	-1.01	0.36	0	0	0	not significant
5592	GO_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	-1.01	0.36	0	0	0	not significant
5593	GO_TAU_PROTEIN_BINDING	-1.01	0.36	0	0	0	not significant
5594	REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR	-1.01	0.36	0	0	0	not significant
5595	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CELL_CYCLE_GEN	-1.01	0.36	0	0	0	not significant
5596	TSENG_IRS1_TARGETS_DN	-1.01	0.36	0	0	0	not significant
5597	YAP1_UP	-1.01	0.36	0	0	0	not significant
5598	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN	-1.01	0.35	0	0	0	not significant
5599	CASTELLANO_NRAS_TARGETS_DN	-1.01	0.35	0	0	0	not significant
5600	GO_ALPHA_ACTININ_BINDING	-1.01	0.35	0	0	0	not significant
5601	GO_COLLAGEN_BIOSYNTHETIC_PROCESS	-1.01	0.35	0	0	0	not significant
5602	GO_DISORDERED_DOMAIN_SPECIFIC_BINDING	-1.01	0.35	0	0	0	not significant
5603	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_DEADENYL	-1.01	0.35	0	0	0	not significant
5604	GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATIO	-1.01	0.35	0	0	0	not significant
5605	GO_REGULATION_OF_RECEPTOR_BIOSYNTHETIC_PROCESS	-1.01	0.35	0	0	0	not significant
5606	GO_RESPONSE_TO_PROSTAGLANDIN	-1.01	0.35	0	0	0	not significant
5607	GO_SEMAPHORIN_RECEPTOR_COMPLEX	-1.01	0.35	0	0	0	not significant
5608	KANNAN_TP53_TARGETS_UP	-1.01	0.35	0	0	0	not significant
5609	LABBE_TGFB1_TARGETS_DN	-1.01	0.35	0	0	0	not significant
5610	OUYANG_PROSTATE_CANCER_MARKERS	-1.01	0.35	0	0	0	not significant
5611	PHONG_TNF_RESPONSE_VIA_P38_COMPLETE	-1.01	0.35	0	0	0	not significant
5612	CHR8P21	-1.01	0.34	0	0	0	not significant
5613	GCNP_SHH_UP_EARLY.V1_DN	-1.01	0.34	0	0	0	not significant
5614	GO_COENZYME_CATABOLIC_PROCESS	-1.01	0.34	0	0	0	not significant
5615	GO_ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	-1.01	0.34	0	0	0	not significant
5616	GO_MATING_BEHAVIOR	-1.01	0.34	0	0	0	not significant
5617	GO_NEGATIVE_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDEN	-1.01	0.34	0	0	0	not significant
5618	GO_NEUROPEPTIDE_RECEPTOR_BINDING	-1.01	0.34	0	0	0	not significant
5619	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_	-1.01	0.34	0	0	0	not significant
5620	GO_POSITIVE_REGULATION_OF_RNA_BINDING	-1.01	0.34	0	0	0	not significant
5621	GO_POSITIVE_REGULATION_OF_RUFFLE_ASSEMBLY	-1.01	0.34	0	0	0	not significant
5622	GO_REGULATION_OF_OOCYTE_MATURATION	-1.01	0.34	0	0	0	not significant
5623	GO_SMOOTH_MUSCLE_CELL_PROLIFERATION	-1.01	0.34	0	0	0	not significant
5624	REACTOME_INTERLEUKIN_17_SIGNALING	-1.01	0.34	0	0	0	not significant
5625	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR	-1.01	0.34	0	0	0	not significant
5626	GO_CHLORIDE_ION_BINDING	-1.01	0.33	0	0	0	not significant
5627	GO_POSITIVE_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	-1.01	0.33	0	0	0	not significant
5628	GO_QUINONE_METABOLIC_PROCESS	-1.01	0.33	0	0	0	not significant
5629	JOHNSTONE_PARVB_TARGETS_2_DN	-1.01	0.33	0	0	0	not significant
5630	KANG_GIST_WITH_PDGFRA_DN	-1.01	0.33	0	0	0	not significant
5631	REACTOME_SYNTHESIS_SECRETION_AND_DEACYLATION_OF_GHRELIN	-1.01	0.33	0	0	0	not significant
5632	GO_POSITIVE_REGULATION_OF_DENDRITIC_CELL_CYTOKINE_PRODUCT	-1.01	0.32	0	0	0	not significant
5633	REACTOME_CGMP_EFFECTS	-1.01	0.32	0	0	0	not significant
5634	EPPERT_LSC_R	-1.01	0.31	0	0	0	not significant
5635	MATZUK_LUTEAL_GENES	-1.01	0.30	0	0	0	not significant
5636	GO_DNA_DEALKYLATION_INVOLVED_IN_DNA_REPAIR	-1.00	0.37	0	0	0	not significant
5637	GO_POSITIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	-1.00	0.37	0	0	0	not significant
5638	GO_REGULATION_OF_INSULIN_SECRETION	-1.00	0.37	0	0	0	not significant
5639	GO_REGULATION_OF_LONG_TERM_NEURONAL_SYNAPTIC_PLASTICITY	-1.00	0.37	0	0	0	not significant
5640	KIM_WT1_TARGETS_8HR_DN	-1.00	0.37	0	0	0	not significant
5641	BIOCARTA_MTOR_PATHWAY	-1.00	0.36	0	0	0	not significant
5642	GO_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	-1.00	0.36	0	0	0	not significant
5643	GO_APOPTOTIC_MITOCHONDRIAL_CHANGES	-1.00	0.36	0	0	0	not significant
5644	GO_CEREBELLAR_CORTEX_DEVELOPMENT	-1.00	0.36	0	0	0	not significant
5645	GO_L_GLUTAMATE_TRANSMEMBRANE_TRANSPORT	-1.00	0.36	0	0	0	not significant
5646	GO_MEMBRANE_FISSION	-1.00	0.36	0	0	0	not significant
5647	GO_NEURONAL_STEM_CELL_POPULATION_MAINTENANCE	-1.00	0.36	0	0	0	not significant
5648	GO_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX	-1.00	0.36	0	0	0	not significant
5649	GO_REGULATION_OF_MICROTUBULE_BASED_PROCESS	-1.00	0.36	0	0	0	not significant
5650	GO_TRANSCRIPTION_FACTOR_TFTC_COMPLEX	-1.00	0.36	0	0	0	not significant
5651	GO_TRANSLATION_REPRESSOR_ACTIVITY	-1.00	0.36	0	0	0	not significant
5652	LU_EZH2_TARGETS_UP	-1.00	0.36	0	0	0	not significant
5653	PID_ENDOTHELIN_PATHWAY	-1.00	0.36	0	0	0	not significant
5654	REACTOME_DISEASES_OF_METABOLISM	-1.00	0.36	0	0	0	not significant
5655	REACTOME_METABOLIC_DISORDERS_OF_BIOLOGICAL_OXIDATION_ENZ	-1.00	0.36	0	0	0	not significant
5656	REACTOME_SIGNALING_BY_VEGF	-1.00	0.36	0	0	0	not significant

5657	REACTOME_ZBP1_DAI_MEDIATED_INDUCTION_OF_TYPE_I_IFNS	-1.00	0.36	0	0	0	not significant
5658	RIZ_ERYTHROID_DIFFERENTIATION_CCNE1	-1.00	0.36	0	0	0	not significant
5659	CHR2Q12	-1.00	0.35	0	0	0	not significant
5660	GO_NEGATIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	-1.00	0.35	0	0	0	not significant
5661	GO_NEGATIVE_REGULATION_OF_THYMOCYTE_APOPTOTIC_PROCESS	-1.00	0.35	0	0	0	not significant
5662	GO_NEURON_PROJECTION_MAINTENANCE	-1.00	0.35	0	0	0	not significant
5663	GO_POSITIVE_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_CELL_D	-1.00	0.35	0	0	0	not significant
5664	GO_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	-1.00	0.35	0	0	0	not significant
5665	GO_REGULATION_OF_NMDA_RECEPTOR_ACTIVITY	-1.00	0.35	0	0	0	not significant
5666	GO_REGULATION_OF_PERK_MEDIATED_UNFOLDED_PROTEIN_RESPONS	-1.00	0.35	0	0	0	not significant
5667	GO_REGULATION_OF_PROTEIN_DEACETYLATION	-1.00	0.35	0	0	0	not significant
5668	GO_SULFUR_COMPOUND_CATABOLIC_PROCESS	-1.00	0.35	0	0	0	not significant
5669	GROSS_HYPOXIA_VIA_ELK3_ONLY_DN	-1.00	0.35	0	0	0	not significant
5670	KAYO_AGING_MUSCLE_UP	-1.00	0.35	0	0	0	not significant
5671	NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON	-1.00	0.35	0	0	0	not significant
5672	BIOCARTA_P35ALZHEIMERS_PATHWAY	-1.00	0.34	0	0	0	not significant
5673	BOCHKIS_FOXA2_TARGETS	-1.00	0.34	0	0	0	not significant
5674	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX	-1.00	0.34	0	0	0	not significant
5675	BROWNE_HCMV_INFECTION_16HR_UP	-1.00	0.34	0	0	0	not significant
5676	CHR6P22	-1.00	0.34	0	0	0	not significant
5677	GO_ACUTE_PHASE_RESPONSE	-1.00	0.34	0	0	0	not significant
5678	GO_AMINO_ACID_IMPORT	-1.00	0.34	0	0	0	not significant
5679	GO_CILIARY_BASAL_BODY_PLASMA_MEMBRANE_DOCKING	-1.00	0.34	0	0	0	not significant
5680	GO_CORE_MEDIATOR_COMPLEX	-1.00	0.34	0	0	0	not significant
5681	GO_EYE_PHOTORECEPTOR_CELL_DIFFERENTIATION	-1.00	0.34	0	0	0	not significant
5682	GO_HORMONE_BIOSYNTHETIC_PROCESS	-1.00	0.34	0	0	0	not significant
5683	GO_NEGATIVE_REGULATION_OF_CELL_DIVISION	-1.00	0.34	0	0	0	not significant
5684	GO_NEGATIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_EL	-1.00	0.34	0	0	0	not significant
5685	GO_NUCLEAR_OUTER_MEMBRANE_ENDOPLASMIC_RETICULUM_MEMBRA	-1.00	0.34	0	0	0	not significant
5686	GO_NUCLEOTIDE_PHOSPHORYLATION	-1.00	0.34	0	0	0	not significant
5687	GO_ORGANIC_HYDROXY_COMPOUND_TRANSPORT	-1.00	0.34	0	0	0	not significant
5688	GO_PALLIUM_DEVELOPMENT	-1.00	0.34	0	0	0	not significant
5689	GO_POSITIVE_REGULATION_OF_RECEPTOR_RECYCLING	-1.00	0.34	0	0	0	not significant
5690	GO_REGULATION_OF_ENDOPLASMIC_RETICULUM_UNFOLDED_PROTEIN	-1.00	0.34	0	0	0	not significant
5691	GO_SKIN_DEVELOPMENT	-1.00	0.34	0	0	0	not significant
5692	GO_SNAP_RECEPTOR_ACTIVITY	-1.00	0.34	0	0	0	not significant
5693	GO_TOR_COMPLEX	-1.00	0.34	0	0	0	not significant
5694	KEGG_SULFUR_METABOLISM	-1.00	0.34	0	0	0	not significant
5695	REACTOME_PURINE_CATABOLISM	-1.00	0.34	0	0	0	not significant
5696	STEIN_ESTROGEN_RESPONSE_NOT_VIA_ESRRA	-1.00	0.34	0	0	0	not significant
5697	CHR5Q31	-1.00	0.33	0	0	0	not significant
5698	GO_DRUG_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.00	0.33	0	0	0	not significant
5699	GO_LEADING_EDGE_MEMBRANE	-1.00	0.33	0	0	0	not significant
5700	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION_IN	-1.00	0.33	0	0	0	not significant
5701	GO_POSITIVE_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	-1.00	0.33	0	0	0	not significant
5702	GO_PROTON_EXPORTING_ATPASE_ACTIVITY_PHOSPHORYLATIVE_MEC	-1.00	0.33	0	0	0	not significant
5703	GO_PROTOPORPHYRINOGEN_IX_BIOSYNTHETIC_PROCESS	-1.00	0.33	0	0	0	not significant
5704	GO_REGULATION_OF_NUCLEAR_DIVISION	-1.00	0.33	0	0	0	not significant
5705	GO_RNA_7_METHYLGUANOSINE_CAP_BINDING	-1.00	0.33	0	0	0	not significant
5706	GO_TRANS_GOLGI_NETWORK_TRANSPORT_VESICLE_MEMBRANE	-1.00	0.33	0	0	0	not significant
5707	MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA_VHL_UP	-1.00	0.33	0	0	0	not significant
5708	PID_CMYB_PATHWAY	-1.00	0.33	0	0	0	not significant
5709	REACTOME_CTLA4_INHIBITORY_SIGNALING	-1.00	0.33	0	0	0	not significant
5710	REACTOME_PHASE_I_FUNCTIONALIZATION_OF_COMPOUNDS	-1.00	0.33	0	0	0	not significant
5711	GO_AP_3_ADAPTOR_COMPLEX	-1.00	0.32	0	0	0	not significant
5712	GO_CRANIAL_SUTURE_MORPHOGENESIS	-1.00	0.32	0	0	0	not significant
5713	GO_POSITIVE_REGULATION_OF_MACROPHAGE_ACTIVATION	-1.00	0.32	0	0	0	not significant
5714	GO_PYRIMIDINE_NUCLEOSIDE_CATABOLIC_PROCESS	-1.00	0.32	0	0	0	not significant
5715	GO_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	-1.00	0.32	0	0	0	not significant
5716	GO_RNA_CAP_BINDING_COMPLEX	-1.00	0.32	0	0	0	not significant
5717	MARSON_BOUND_BY_FOXP3_STIMULATED	-1.00	0.32	0	0	0	not significant
5718	PURBEY_TARGETS_OF_CTBP1_NOT_SATB1_DN	-1.00	0.32	0	0	0	not significant
5719	REACTOME_DAP12_SIGNALING	-1.00	0.32	0	0	0	not significant
5720	ZHU_SKIL_TARGETS_UP	-1.00	0.32	0	0	0	not significant
5721	GO_CALMODULIN_DEPENDENT_PROTEIN_PHOSPHATASE_ACTIVITY	-1.00	0.31	0	0	0	not significant
5722	GO_CAMERA_TYPE_EYE_DEVELOPMENT	-1.00	0.31	0	0	0	not significant
5723	GO_ANDROGEN_BIOSYNTHETIC_PROCESS	-1.00	0.30	0	0	0	not significant
5724	PID_ANGIOPOIETIN_RECEPTOR_PATHWAY	-0.99	0.37	0	0	0	not significant
5725	CHR4Q24	-0.99	0.36	0	0	0	not significant
5726	GO_POSITIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE	-0.99	0.36	0	0	0	not significant
5727	REACTOME_APOPTOTIC_FACTOR_MEDIATED_RESPONSE	-0.99	0.36	0	0	0	not significant
5728	THILLAINADESAN_ZNF217_TARGETS_UP	-0.99	0.36	0	0	0	not significant
5729	EPPERT_HSC_R	-0.99	0.35	0	0	0	not significant
5730	GO_POSITIVE_REGULATION_OF_CELL_MATRIX_ADHESION	-0.99	0.35	0	0	0	not significant
5731	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	-0.99	0.35	0	0	0	not significant
5732	GO_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	-0.99	0.35	0	0	0	not significant
5733	AIYAR_COBRA1_TARGETS_DN	-0.99	0.34	0	0	0	not significant
5734	BILBAN_B_CLL_LPL_UP	-0.99	0.34	0	0	0	not significant
5735	FRASOR_RESPONSE_TO_ESTRADIOL_UP	-0.99	0.34	0	0	0	not significant
5736	GLI1_UP.V1_UP	-0.99	0.34	0	0	0	not significant
5737	GO_APOPTOTIC_CELL_CLEARANCE	-0.99	0.34	0	0	0	not significant
5738	GO_GLUCOSE_IMPORT	-0.99	0.34	0	0	0	not significant
5739	GO_MACROPHAGE_DIFFERENTIATION	-0.99	0.34	0	0	0	not significant
5740	GO_RESPONSE_TO_AXON_INJURY	-0.99	0.34	0	0	0	not significant
5741	GO_RESPONSE_TO_IRON_ION	-0.99	0.34	0	0	0	not significant
5742	GO_RNA_POLYADENYLATION	-0.99	0.34	0	0	0	not significant
5743	GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING	-0.99	0.34	0	0	0	not significant
5744	GO_VITAMIN_D_BIOSYNTHETIC_PROCESS	-0.99	0.34	0	0	0	not significant
5745	KEGG_GNRH_SIGNALING_PATHWAY	-0.99	0.34	0	0	0	not significant
5746	KOMMAGANI_TP63_GAMMA_TARGETS	-0.99	0.34	0	0	0	not significant
5747	REACTOME_INTEGRIN_SIGNALING	-0.99	0.34	0	0	0	not significant
5748	REACTOME_RA_BIOSYNTHESIS_PATHWAY	-0.99	0.34	0	0	0	not significant
5749	TONG_INTERACT_WITH_PTTG1	-0.99	0.34	0	0	0	not significant
5750	WU_HBX_TARGETS_1_DN	-0.99	0.34	0	0	0	not significant
5751	BIOCARTA_KERATINOCYTE_PATHWAY	-0.99	0.33	0	0	0	not significant
5752	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3	-0.99	0.33	0	0	0	not significant
5753	GO_CELLULAR_LIPID_CATABOLIC_PROCESS	-0.99	0.33	0	0	0	not significant
5754	GO_INTERLEUKIN_1_RECEPTOR_BINDING	-0.99	0.33	0	0	0	not significant
5755	GO_LAMININ_BINDING	-0.99	0.33	0	0	0	not significant
5756	GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	-0.99	0.33	0	0	0	not significant
5757	GO_POSITIVE_REGULATION_OF_EPIDERMIS_DEVELOPMENT	-0.99	0.33	0	0	0	not significant
5758	GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS	-0.99	0.33	0	0	0	not significant
5759	GO_POSITIVE_REGULATION_OF_PROTEIN_MATURATION	-0.99	0.33	0	0	0	not significant
5760	GO_POSITIVE_REGULATION_OF_SMAD_PROTEIN_SIGNAL_TRANSDUCTI	-0.99	0.33	0	0	0	not significant
5761	GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	-0.99	0.33	0	0	0	not significant
5762	GO_RESPONSE_TO_LEUKEMIA_INHIBITORY_FACTOR	-0.99	0.33	0	0	0	not significant
5763	GO_TRACHEA_FORMATION	-0.99	0.33	0	0	0	not significant
5764	HEIDENBLAD_AMPLIFIED_IN_PANCREATIC_CANCER	-0.99	0.33	0	0	0	not significant
5765	LEE_LIVER_CANCER_MYC_E2F1_DN	-0.99	0.33	0	0	0	not significant

5766	PID_MET_PATHWAY	-0.99	0.33	0	0	0	not significant
5767	REACTOME_DEPOLYMERISATION_OF_THE_NUCLEAR_LAMINA	-0.99	0.33	0	0	0	not significant
5768	REACTOME_SUMOYLATION_OF_IMMUNE_RESPONSE_PROTEINS	-0.99	0.33	0	0	0	not significant
5769	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX4_DN	-0.99	0.33	0	0	0	not significant
5770	CHANG_IMMORTALIZED_BY_HPV31_DN	-0.99	0.32	0	0	0	not significant
5771	FONTAINE_FOLLICULAR_THYROID_ADENOMA_DN	-0.99	0.32	0	0	0	not significant
5772	GO_C21_STEROID_HORMONE_METABOLIC_PROCESS	-0.99	0.32	0	0	0	not significant
5773	GO_CELL_CELL_SIGNALING_BY_WNT	-0.99	0.32	0	0	0	not significant
5774	GO_CELL_MIGRATION_INVOLVED_IN_GASTRULATION	-0.99	0.32	0	0	0	not significant
5775	GO_CELLULAR_COPPER_ION_HOMEOSTASIS	-0.99	0.32	0	0	0	not significant
5776	GO_COAGULATION	-0.99	0.32	0	0	0	not significant
5777	GO_DNA_PACKAGING	-0.99	0.32	0	0	0	not significant
5778	GO_FOLIC_ACID_METABOLIC_PROCESS	-0.99	0.32	0	0	0	not significant
5779	GO_LIPASE_ACTIVATOR_ACTIVITY	-0.99	0.32	0	0	0	not significant
5780	GO_MLL1_2_COMPLEX	-0.99	0.32	0	0	0	not significant
5781	GO_NEGATIVE_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	-0.99	0.32	0	0	0	not significant
5782	GO_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	-0.99	0.32	0	0	0	not significant
5783	PID_BETA_CATENIN_NUC_PATHWAY	-0.99	0.32	0	0	0	not significant
5784	REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE	-0.99	0.32	0	0	0	not significant
5785	REACTOME_PERVASIVE_DEVELOPMENTAL_DISORDERS	-0.99	0.32	0	0	0	not significant
5786	REACTOME_SUMOYLATION_OF_DNA_DAMAGE_RESPONSE_AND_REPAIR	-0.99	0.32	0	0	0	not significant
5787	SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_DN	-0.99	0.32	0	0	0	not significant
5788	GO_INTRACELLULAR_MRNA_LOCALIZATION	-0.99	0.31	0	0	0	not significant
5789	GO_NEGATIVE_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_	-0.99	0.31	0	0	0	not significant
5790	GO_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	-0.99	0.31	0	0	0	not significant
5791	GO_POSITIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM	-0.99	0.31	0	0	0	not significant
5792	GO_PROGESTERONE_RECEPTOR_SIGNALING_PATHWAY	-0.99	0.31	0	0	0	not significant
5793	GO_PROSTATE_GLAND_MORPHOGENESIS	-0.99	0.31	0	0	0	not significant
5794	GO_TELOMERE_CAPPING	-0.99	0.31	0	0	0	not significant
5795	GO_ZYMOGEN_INHIBITION	-0.99	0.31	0	0	0	not significant
5796	HILLION_HMGA1B_TARGETS	-0.99	0.31	0	0	0	not significant
5797	KANG_DOXORUBICIN_RESISTANCE_DN	-0.99	0.31	0	0	0	not significant
5798	MANTOVANI_VIRAL_GPCR_SIGNALING_DN	-0.99	0.31	0	0	0	not significant
5799	PID_RHODOPSIN_PATHWAY	-0.99	0.31	0	0	0	not significant
5800	ZHAN_MULTIPLE_MYELOMA_UP	-0.99	0.31	0	0	0	not significant
5801	GO_AXO_DENDRITIC_TRANSPORT	-0.99	0.30	0	0	0	not significant
5802	GO_CARBONATE_DEHYDRATASE_ACTIVITY	-0.99	0.30	0	0	0	not significant
5803	GO_G_PROTEIN_COUPLED_SEROTONIN_RECEPTOR_BINDING	-0.99	0.30	0	0	0	not significant
5804	GO_REGULATION_OF_TRANSFERASE_ACTIVITY	-0.99	0.30	0	0	0	not significant
5805	HUMMERICH_BENIGN_SKIN_TUMOR_DN	-0.99	0.30	0	0	0	not significant
5806	SMID_BREAST_CANCER_LUMINAL_A_UP	-0.99	0.30	0	0	0	not significant
5807	GO_NEGATIVE_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	-0.99	0.29	0	0	0	not significant
5808	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DEGRANULATION	-0.99	0.29	0	0	0	not significant
5809	LI_WILMS_TUMOR_ANAPLASTIC_DN	-0.99	0.29	0	0	0	not significant
5810	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN	-0.98	0.34	0	0	0	not significant
5811	GO_DNA_APURINIC_OR_APYRIMIDINIC_SITE_ENDONUCLEASE_ACTIVITY	-0.98	0.34	0	0	0	not significant
5812	GO_INTESTINAL_EPITHELIAL_CELL_DEVELOPMENT	-0.98	0.34	0	0	0	not significant
5813	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITI	-0.98	0.34	0	0	0	not significant
5814	GO_NUCLEAR_PORE_COMPLEX_ASSEMBLY	-0.98	0.34	0	0	0	not significant
5815	GO_PURINE_NUCLEOSIDE_METABOLIC_PROCESS	-0.98	0.34	0	0	0	not significant
5816	GO_REGULATION_OF_T_CELL_MIGRATION	-0.98	0.34	0	0	0	not significant
5817	GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	-0.98	0.34	0	0	0	not significant
5818	CHR10P13	-0.98	0.33	0	0	0	not significant
5819	CHR2P25	-0.98	0.33	0	0	0	not significant
5820	GO_ADA2_GCN5_ADA3_TRANSCRIPTION_ACTIVATOR_COMPLEX	-0.98	0.33	0	0	0	not significant
5821	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_A	-0.98	0.33	0	0	0	not significant
5822	GO_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_ACTIVITY	-0.98	0.33	0	0	0	not significant
5823	GO_MITOCHONDRIAL_PROTEIN_PROCESSING	-0.98	0.33	0	0	0	not significant
5824	GO_NEURON_DEATH_IN_RESPONSE_TO_OXIDATIVE_STRESS	-0.98	0.33	0	0	0	not significant
5825	GO_POSITIVE_REGULATION_OF_FILOPODIUM_ASSEMBLY	-0.98	0.33	0	0	0	not significant
5826	GO_POSITIVE_REGULATION_OF_RNA_SPLICING	-0.98	0.33	0	0	0	not significant
5827	GO_POSTREPLICATION_REPAIR	-0.98	0.33	0	0	0	not significant
5828	GO_RESPONSE_TO_PROSTAGLANDIN_E	-0.98	0.33	0	0	0	not significant
5829	GO_RNA_STEM_LOOP_BINDING	-0.98	0.33	0	0	0	not significant
5830	LANDIS_ERBB2_BREAST_TUMORS_65_DN	-0.98	0.33	0	0	0	not significant
5831	PID_AVB3_INTEGRIN_PATHWAY	-0.98	0.33	0	0	0	not significant
5832	AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP	-0.98	0.32	0	0	0	not significant
5833	CHASSOT_SKIN_WOUND	-0.98	0.32	0	0	0	not significant
5834	FIGUEROA_AML_METHYLATION_CLUSTER_2_DN	-0.98	0.32	0	0	0	not significant
5835	GO_CELLULAR_RESPONSE_TO_LOW_DENSITY_LIPOPROTEIN_PARTICLE	-0.98	0.32	0	0	0	not significant
5836	GO_HISTONE_H4_DEACETYLATION	-0.98	0.32	0	0	0	not significant
5837	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_O	-0.98	0.32	0	0	0	not significant
5838	GO_MITOTIC_SISTER_CHROMATID_COHESION	-0.98	0.32	0	0	0	not significant
5839	GO_NEGATIVE_REGULATION_OF_ION_TRANSPORT	-0.98	0.32	0	0	0	not significant
5840	GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_ELONGATION_FROM_	-0.98	0.32	0	0	0	not significant
5841	GO_NEUROTRANSMITTER_BIOSYNTHETIC_PROCESS	-0.98	0.32	0	0	0	not significant
5842	GO_OUTFLOW_TRACT_SEPTUM_MORPHOGENESIS	-0.98	0.32	0	0	0	not significant
5843	GO_POSITIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRAN	-0.98	0.32	0	0	0	not significant
5844	GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_OUTER_MEMBRANE_	-0.98	0.32	0	0	0	not significant
5845	GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_ASSE	-0.98	0.32	0	0	0	not significant
5846	GO_REGULATION_OF_HEART_MORPHOGENESIS	-0.98	0.32	0	0	0	not significant
5847	GO_REGULATION_OF_MEIOTIC_CELL_CYCLE	-0.98	0.32	0	0	0	not significant
5848	GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PR	-0.98	0.32	0	0	0	not significant
5849	KAUFFMANN_DNA_REPLICATION_GENES	-0.98	0.32	0	0	0	not significant
5850	MANN_RESPONSE_TO_AMIFOSTINE_UP	-0.98	0.32	0	0	0	not significant
5851	PIEPOLI_LGI1_TARGETS_DN	-0.98	0.32	0	0	0	not significant
5852	REACTOME_NUCLEOTIDE_SALVAGE	-0.98	0.32	0	0	0	not significant
5853	REACTOME_SHC_MEDIATED_CASCADE:FGFR4	-0.98	0.32	0	0	0	not significant
5854	ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_UP	-0.98	0.32	0	0	0	not significant
5855	BOYAULT_LIVER_CANCER_SUBCLASS_G6_DN	-0.98	0.31	0	0	0	not significant
5856	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP	-0.98	0.31	0	0	0	not significant
5857	GO_CORONARY_VASCULATURE_DEVELOPMENT	-0.98	0.31	0	0	0	not significant
5858	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH2_GROUP_O	-0.98	0.31	0	0	0	not significant
5859	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	-0.98	0.31	0	0	0	not significant
5860	GO_POSITIVE_REGULATION_OF_PROTEIN_DEACETYLATION	-0.98	0.31	0	0	0	not significant
5861	GO_PROSTANOID_RECEPTOR_ACTIVITY	-0.98	0.31	0	0	0	not significant
5862	GO_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	-0.98	0.31	0	0	0	not significant
5863	GO_REGULATION_OF_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTI	-0.98	0.31	0	0	0	not significant
5864	GO_REGULATION_OF_NUCLEAR_TRANSCRIBED_MRNA_POLY_A_TAIL_S	-0.98	0.31	0	0	0	not significant
5865	GO_REGULATION_OF_PHOSPHATASE_ACTIVITY	-0.98	0.31	0	0	0	not significant
5866	MARKEY_RB1_CHRONIC_LOF_DN	-0.98	0.31	0	0	0	not significant
5867	PID_MTOR_4PATHWAY	-0.98	0.31	0	0	0	not significant
5868	REACTOME_FBXW7_MUTANTS_AND_NOTCH1_IN_CANCER	-0.98	0.31	0	0	0	not significant
5869	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CELL_DEATH_GEN	-0.98	0.31	0	0	0	not significant
5870	GENTILE_UV_RESPONSE_CLUSTER_D7	-0.98	0.30	0	0	0	not significant
5871	GO_ASPARTATE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	-0.98	0.30	0	0	0	not significant
5872	GO_CAMERA_TYPE_EYE_MORPHOGENESIS	-0.98	0.30	0	0	0	not significant
5873	GO_CELLULAR_RESPONSE_TO_RADIATION	-0.98	0.30	0	0	0	not significant
5874	GO_COPPER_CHAPERONE_ACTIVITY	-0.98	0.30	0	0	0	not significant

5875	GO_MODIFICATION_OF_POSTSYNAPTIC_ACTIN_CYTOSKELETON	-0.98	0.30	0	0	0	not significant
5876	GO_NEGATIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_AC	-0.98	0.30	0	0	0	not significant
5877	GO_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	-0.98	0.30	0	0	0	not significant
5878	GO_NEGATIVE_REGULATION_OF_PHOSPHORYLATION	-0.98	0.30	0	0	0	not significant
5879	GO_REGULATION_OF_GLUCOCORTICOID_RECEPTOR_SIGNALING_PATH	-0.98	0.30	0	0	0	not significant
5880	GO_SULFURIC_ESTER_HYDROLASE_ACTIVITY	-0.98	0.30	0	0	0	not significant
5881	GO_TORC1_COMPLEX	-0.98	0.30	0	0	0	not significant
5882	GO_TRANSCRIPTION_FACTOR_TFIIH_HOLO_COMPLEX	-0.98	0.30	0	0	0	not significant
5883	GO_TRANSPORT_VESICLE_MEMBRANE	-0.98	0.30	0	0	0	not significant
5884	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES	-0.98	0.30	0	0	0	not significant
5885	ONDER_CDH1_TARGETS_2_UP	-0.98	0.30	0	0	0	not significant
5886	REACTOME_SHC_MEDIATED_CASCADE:FGFR2	-0.98	0.30	0	0	0	not significant
5887	SA_G1_AND_S_PHASES	-0.98	0.30	0	0	0	not significant
5888	SESTO_RESPONSE_TO_UV_C8	-0.98	0.30	0	0	0	not significant
5889	GO_ALDEHYDE_BIOSYNTHETIC_PROCESS	-0.98	0.29	0	0	0	not significant
5890	GO_FOREBRAIN_RADIAL_GLIAL_CELL_DIFFERENTIATION	-0.98	0.29	0	0	0	not significant
5891	GO_NEDD8_TRANSFERASE_ACTIVITY	-0.98	0.29	0	0	0	not significant
5892	GO_PHOTORECEPTOR_CELL_DEVELOPMENT	-0.98	0.29	0	0	0	not significant
5893	GO_REGULATION_OF_IRE1_MEDIATED_UNFOLDED_PROTEIN_RESPONS	-0.98	0.29	0	0	0	not significant
5894	GO_REGULATION_OF_LEUKOCYTE_ADHESION_TO_VASCULAR_ENDOTH	-0.98	0.29	0	0	0	not significant
5895	LOPEZ_MESOTHELIOMA_SURVIVAL_DN	-0.98	0.29	0	0	0	not significant
5896	TGFB_UP.V1_UP	-0.98	0.29	0	0	0	not significant
5897	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP	-0.98	0.29	0	0	0	not significant
5898	GO_BEHAVIOR	-0.98	0.28	0	0	0	not significant
5899	GO_CARBOHYDRATE_METABOLIC_PROCESS	-0.98	0.28	0	0	0	not significant
5900	GO_MESENCHYMAL_CELL_DIFFERENTIATION	-0.98	0.28	0	0	0	not significant
5901	GO_NEGATIVE_REGULATION_OF_CATABOLIC_PROCESS	-0.98	0.28	0	0	0	not significant
5902	GO_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	-0.98	0.28	0	0	0	not significant
5903	GO_RIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	-0.98	0.28	0	0	0	not significant
5904	GO_TOR_SIGNALING	-0.98	0.28	0	0	0	not significant
5905	REACTOME_METABOLISM_OF_NUCLEOTIDES	-0.98	0.28	0	0	0	not significant
5906	WANG_RESPONSE_TO_ANDROGEN_UP	-0.98	0.28	0	0	0	not significant
5907	GO_REGULATION_OF_CELLULAR_COMPONENT_SIZE	-0.98	0.27	0	0	0	not significant
5908	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_DN	-0.98	0.27	0	0	0	not significant
5909	GO_RESPONSE_TO_RADIATION	-0.98	0.26	0	0	0	not significant
5910	GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	-0.98	0.25	0	0	0	not significant
5911	GO_NEURON_PROJECTION	-0.98	0.24	0	0	0	not significant
5912	GO_POSITIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	-0.98	0.23	0	0	0	not significant
5913	GO_POSITIVE_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	-0.98	0.18	0	0	0	not significant
5914	GO_INTRACELLULAR_TRANSPORT	-0.98	0.15	0	0	0	not significant
5915	GO_CYTOPLASMIC_DYNEIN_COMPLEX	-0.97	0.34	0	0	0	not significant
5916	PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION	-0.97	0.34	0	0	0	not significant
5917	GO_REGULATION_OF_BLOOD_PRESSURE	-0.97	0.33	0	0	0	not significant
5918	CHEOK_RESPONSE_TO_MERCAPTOPURINE_UP	-0.97	0.32	0	0	0	not significant
5919	GO_ATPASE_ACTIVITY_COUPLED_TO_MOVEMENT_OF_SUBSTANCES	-0.97	0.32	0	0	0	not significant
5920	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_ELONGATION_FROM_	-0.97	0.32	0	0	0	not significant
5921	GO_REGULATION_OF_EPIDERMAL_CELL_DIFFERENTIATION	-0.97	0.32	0	0	0	not significant
5922	REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	-0.97	0.32	0	0	0	not significant
5923	REACTOME_WNT5A_DEPENDENT_INTERNALIZATION_OF_FZD4	-0.97	0.32	0	0	0	not significant
5924	GO_ACETYL_COA_METABOLIC_PROCESS	-0.97	0.31	0	0	0	not significant
5925	GO_CHROMOCENTER	-0.97	0.31	0	0	0	not significant
5926	GO_FOREBRAIN_REGIONALIZATION	-0.97	0.31	0	0	0	not significant
5927	GO_GLIAL_CELL_PROLIFERATION	-0.97	0.31	0	0	0	not significant
5928	GO_IRON_SULFUR_CLUSTER_ASSEMBLY	-0.97	0.31	0	0	0	not significant
5929	GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PRO	-0.97	0.31	0	0	0	not significant
5930	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPOR	-0.97	0.31	0	0	0	not significant
5931	GO_NEGATIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_	-0.97	0.31	0	0	0	not significant
5932	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	-0.97	0.31	0	0	0	not significant
5933	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	-0.97	0.31	0	0	0	not significant
5934	GO_POSITIVE_REGULATION_OF_SUPRAMOLECULAR_FIBER_ORGANIZAT	-0.97	0.31	0	0	0	not significant
5935	GO_RENAL_SYSTEM_PROCESS	-0.97	0.31	0	0	0	not significant
5936	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ADAPT	-0.97	0.31	0	0	0	not significant
5937	OZANNE_AP1_TARGETS_UP	-0.97	0.31	0	0	0	not significant
5938	PID_SYNDECAN_1_PATHWAY	-0.97	0.31	0	0	0	not significant
5939	REACTOME_FREE_FATTY_ACIDS_REGULATE_INSULIN_SECRETION	-0.97	0.31	0	0	0	not significant
5940	REACTOME_PTK6_REGULATES_RHO_GTPASES_RAS_GTPASE_AND_MAP	-0.97	0.31	0	0	0	not significant
5941	REACTOME_TOLL_LIKE_RECEPTOR_4_TLR4_CASCADE	-0.97	0.31	0	0	0	not significant
5942	YANG_BREAST_CANCER_ESR1_BULK_UP	-0.97	0.31	0	0	0	not significant
5943	BIOCARTA_RELA_PATHWAY	-0.97	0.30	0	0	0	not significant
5944	BIOCARTA_TEL_PATHWAY	-0.97	0.30	0	0	0	not significant
5945	CAIRO_LIVER_DEVELOPMENT_UP	-0.97	0.30	0	0	0	not significant
5946	CHR4Q27	-0.97	0.30	0	0	0	not significant
5947	GALINDO_IMMUNE_RESPONSE_TO_ENTEROTOXIN	-0.97	0.30	0	0	0	not significant
5948	GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	-0.97	0.30	0	0	0	not significant
5949	GO_BLOOD_COAGULATION_INTRINSIC_PATHWAY	-0.97	0.30	0	0	0	not significant
5950	GO_CAP_INDEPENDENT_TRANSLATIONAL_INITIATION	-0.97	0.30	0	0	0	not significant
5951	GO_ESTABLISHMENT_OF_LYMPHOCYTE_POLARITY	-0.97	0.30	0	0	0	not significant
5952	GO_INOSITOL_METABOLIC_PROCESS	-0.97	0.30	0	0	0	not significant
5953	GO_NEGATIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGN	-0.97	0.30	0	0	0	not significant
5954	GO_POSITIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	-0.97	0.30	0	0	0	not significant
5955	GO_POSITIVE_REGULATION_OF_PROTEIN_SUMOYLATION	-0.97	0.30	0	0	0	not significant
5956	GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	-0.97	0.30	0	0	0	not significant
5957	GO_REGULATION_OF_PROTEIN_TARGETING	-0.97	0.30	0	0	0	not significant
5958	GO_RESPONSE_TO_GROWTH_HORMONE	-0.97	0.30	0	0	0	not significant
5959	GO_SITE_OF_DOUBLE_STRAND_BREAK	-0.97	0.30	0	0	0	not significant
5960	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN	-0.97	0.30	0	0	0	not significant
5961	PID_CERAMIDE_PATHWAY	-0.97	0.30	0	0	0	not significant
5962	QI_PLASMACYTOMA_DN	-0.97	0.30	0	0	0	not significant
5963	REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_ZBP1	-0.97	0.30	0	0	0	not significant
5964	TING_SILENCED_BY_DICER	-0.97	0.30	0	0	0	not significant
5965	VALK_AML_WITH_11Q23_REARRANGED	-0.97	0.30	0	0	0	not significant
5966	WU_HBX_TARGETS_2_DN	-0.97	0.30	0	0	0	not significant
5967	ALONSO_METASTASIS_DN	-0.97	0.29	0	0	0	not significant
5968	BROWNE_HCMV_INFECTION_1HR_DN	-0.97	0.29	0	0	0	not significant
5969	CHOI_ATL_STAGE_PREDICTOR	-0.97	0.29	0	0	0	not significant
5970	GO_BINDING_OF_SPERM_TO_ZONA_PELLUCIDA	-0.97	0.29	0	0	0	not significant
5971	GO_CHROMOSOME_CONDENSATION	-0.97	0.29	0	0	0	not significant
5972	GO_COLUMNAR_CUBOIDAL_EPITHELIAL_CELL_DEVELOPMENT	-0.97	0.29	0	0	0	not significant
5973	GO_CORONARY_ARTERY_MORPHOGENESIS	-0.97	0.29	0	0	0	not significant
5974	GO_ENDONUCLEOLYTIC_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	-0.97	0.29	0	0	0	not significant
5975	GO_GLUTAMINE_TRANSPORT	-0.97	0.29	0	0	0	not significant
5976	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_LYSINE_ACETYLATION	-0.97	0.29	0	0	0	not significant
5977	GO_NEURON_REMODELING	-0.97	0.29	0	0	0	not significant
5978	GO_NITRIC_OXIDE_BIOSYNTHETIC_PROCESS	-0.97	0.29	0	0	0	not significant
5979	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_MEMBRAN	-0.97	0.29	0	0	0	not significant
5980	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_DRUG	-0.97	0.29	0	0	0	not significant
5981	GO_POSTSYNAPTIC_CYTOSKELETON_ORGANIZATION	-0.97	0.29	0	0	0	not significant
5982	GO_REGULATION_OF_PHOSPHOLIPID_BIOSYNTHETIC_PROCESS	-0.97	0.29	0	0	0	not significant
5983	GO_RESPONSE_TO_OXYGEN_GLUCOSE_DEPRIVATION	-0.97	0.29	0	0	0	not significant

5984	REACTOME_INTRINSIC_PATHWAY_OF_FIBRIN_CLOT_FORMATION	-0.97	0.29	0	0	0	not significant
5985	CHR20P13	-0.97	0.28	0	0	0	not significant
5986	GO_COATED_VESICLE	-0.97	0.28	0	0	0	not significant
5987	GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PRO	-0.97	0.28	0	0	0	not significant
5988	GO_PROTEIN_C_TERMINUS_BINDING	-0.97	0.28	0	0	0	not significant
5989	GO_RESPONSE_TO_BMP	-0.97	0.28	0	0	0	not significant
5990	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER	-0.97	0.28	0	0	0	not significant
5991	MIKKELSEN_MCV6_ICP_WITH_H3K27ME3	-0.97	0.28	0	0	0	not significant
5992	EGFR_UP.V1_DN	-0.97	0.26	0	0	0	not significant
5993	ESC_V6.5_UP_LATE.V1_DN	-0.97	0.26	0	0	0	not significant
5994	GO_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	-0.97	0.26	0	0	0	not significant
5995	GO_EPIDERMIS_DEVELOPMENT	-0.97	0.26	0	0	0	not significant
5996	GO_PROTEIN_N_TERMINUS_BINDING	-0.97	0.26	0	0	0	not significant
5997	REACTOME_MEIOTIC_RECOMBINATION	-0.97	0.26	0	0	0	not significant
5998	BROWNE_HCMV_INFECTION_20HR_UP	-0.97	0.25	0	0	0	not significant
5999	GO_POSITIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	-0.97	0.25	0	0	0	not significant
6000	FORTSCHEGGER_PHF8_TARGETS_DN	-0.97	0.20	0	0	0	not significant
6001	GO_CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	-0.97	0.17	0	0	0	not significant
6002	GO_REGULATION_OF_AMINO_ACID_TRANSPORT	-0.96	0.32	0	0	0	not significant
6003	TURJANSKI_MAPK14_TARGETS	-0.96	0.32	0	0	0	not significant
6004	AMIT_EGF_RESPONSE_60_MCF10A	-0.96	0.31	0	0	0	not significant
6005	GO_G_PROTEIN_COUPLED_ACETYLCHOLINE_RECEPTOR_SIGNALING_P	-0.96	0.31	0	0	0	not significant
6006	GO_ISOCITRATE_DEHYDROGENASE_ACTIVITY	-0.96	0.31	0	0	0	not significant
6007	GO_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	-0.96	0.31	0	0	0	not significant
6008	GO_MRNA_CLEAVAGE_INVOLVED_IN_MRNA_PROCESSING	-0.96	0.31	0	0	0	not significant
6009	GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_MEDIATE	-0.96	0.31	0	0	0	not significant
6010	GO_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	-0.96	0.31	0	0	0	not significant
6011	GO_PROTEIN_TRIMERIZATION	-0.96	0.31	0	0	0	not significant
6012	GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	-0.96	0.31	0	0	0	not significant
6013	GO_RIBOSOMAL_PROTEIN_IMPORT_INTO_NUCLEUS	-0.96	0.31	0	0	0	not significant
6014	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION_OF_SATU	-0.96	0.31	0	0	0	not significant
6015	GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE_MEMBRANE	-0.96	0.30	0	0	0	not significant
6016	GO_ENDORIBONUCLEASE_ACTIVITY	-0.96	0.30	0	0	0	not significant
6017	GO_MYELOID_DENDRITIC_CELL_ACTIVATION	-0.96	0.30	0	0	0	not significant
6018	GO_MYOSIN_FILAMENT	-0.96	0.30	0	0	0	not significant
6019	GO_NEGATIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_P	-0.96	0.30	0	0	0	not significant
6020	GO_NEURAL_CREST_CELL_MIGRATION	-0.96	0.30	0	0	0	not significant
6021	GO_NEURON_CELL_CELL_ADHESION	-0.96	0.30	0	0	0	not significant
6022	GO_PHOSPHOLIPASE_ACTIVATOR_ACTIVITY	-0.96	0.30	0	0	0	not significant
6023	GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	-0.96	0.30	0	0	0	not significant
6024	GO_POSITIVE_REGULATION_OF_SISTER_CHROMATID_COHESION	-0.96	0.30	0	0	0	not significant
6025	GO_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	-0.96	0.30	0	0	0	not significant
6026	GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	-0.96	0.30	0	0	0	not significant
6027	JACKSON_DNMT1_TARGETS_DN	-0.96	0.30	0	0	0	not significant
6028	SCHRAETS_MLL_TARGETS_DN	-0.96	0.30	0	0	0	not significant
6029	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_DN	-0.96	0.29	0	0	0	not significant
6030	GO_CELL_CELL_CONTACT_ZONE	-0.96	0.29	0	0	0	not significant
6031	GO_CELLULAR_HORMONE_METABOLIC_PROCESS	-0.96	0.29	0	0	0	not significant
6032	GO_NEGATIVE_REGULATION_OF_MICROTUBULE_DEPOLYMERIZATION	-0.96	0.29	0	0	0	not significant
6033	GO_POSTSYNAPTIC_ACTIN_CYTOSKELETON_ORGANIZATION	-0.96	0.29	0	0	0	not significant
6034	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	-0.96	0.29	0	0	0	not significant
6035	GO_REGULATION_OF_CHEMOKINE_C_X_C_MOTIF_LIGAND_2_PRODUCTI	-0.96	0.29	0	0	0	not significant
6036	GO_REGULATION_OF_COLLATERAL_SPROUTING	-0.96	0.29	0	0	0	not significant
6037	GO_REGULATION_OF_GASTRULATION	-0.96	0.29	0	0	0	not significant
6038	GO_RESPONSE_TO_ACETYLCHOLINE	-0.96	0.29	0	0	0	not significant
6039	GO_U6_SNRNA_BINDING	-0.96	0.29	0	0	0	not significant
6040	KRIEG_HYPOXIA_VIA_KDM3A	-0.96	0.29	0	0	0	not significant
6041	REACTOME_BASE_EXCISION_REPAIR	-0.96	0.29	0	0	0	not significant
6042	REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MA	-0.96	0.29	0	0	0	not significant
6043	REACTOME_SIGNALING_BY_NTRK1_TRKA	-0.96	0.29	0	0	0	not significant
6044	RIZ_ERYTHROID_DIFFERENTIATION	-0.96	0.29	0	0	0	not significant
6045	SCHAVOLT_TARGETS_OF_TP53_AND_TP63	-0.96	0.29	0	0	0	not significant
6046	VANASSE_BCL2_TARGETS_UP	-0.96	0.29	0	0	0	not significant
6047	WENG_POR_DOSAGE	-0.96	0.29	0	0	0	not significant
6048	GO_EPHRIN_RECEPTOR_ACTIVITY	-0.96	0.28	0	0	0	not significant
6049	GO_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	-0.96	0.28	0	0	0	not significant
6050	GO_POLYSACCHARIDE_BINDING	-0.96	0.28	0	0	0	not significant
6051	GO_POST_EMBRYONIC_CAMERA_TYPE_EYE_DEVELOPMENT	-0.96	0.28	0	0	0	not significant
6052	GO_PURINE_NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	-0.96	0.28	0	0	0	not significant
6053	GO_REGULATION_OF_OOGENESIS	-0.96	0.28	0	0	0	not significant
6054	GO_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	-0.96	0.28	0	0	0	not significant
6055	GO_SNORNA_LOCALIZATION	-0.96	0.28	0	0	0	not significant
6056	GO_SPERM_CHROMATIN_CONDENSATION	-0.96	0.28	0	0	0	not significant
6057	GO_STEROL_TRANSPORT	-0.96	0.28	0	0	0	not significant
6058	HOOI_ST7_TARGETS_UP	-0.96	0.28	0	0	0	not significant
6059	MAYBURD_RESPONSE_TO_L663536_UP	-0.96	0.28	0	0	0	not significant
6060	MORI_PLASMA_CELL_UP	-0.96	0.28	0	0	0	not significant
6061	NAM_FXYD5_TARGETS_DN	-0.96	0.28	0	0	0	not significant
6062	REACTOME_EGFR_TRANSACTIVATION_BY_GASTRIN	-0.96	0.28	0	0	0	not significant
6063	REACTOME_REPRESSION_OF_WNT_TARGET_GENES	-0.96	0.28	0	0	0	not significant
6064	SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES	-0.96	0.28	0	0	0	not significant
6065	ZAMORA_NOS2_TARGETS_UP	-0.96	0.28	0	0	0	not significant
6066	BOYLAN_MULTIPLE_MYELOMA_PCA3_DN	-0.96	0.27	0	0	0	not significant
6067	GO_LIMBIC_SYSTEM_DEVELOPMENT	-0.96	0.27	0	0	0	not significant
6068	GO_NURD_COMPLEX	-0.96	0.27	0	0	0	not significant
6069	GO_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEI	-0.96	0.27	0	0	0	not significant
6070	GO_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALIN	-0.96	0.27	0	0	0	not significant
6071	GO_RRNA_3_END_PROCESSING	-0.96	0.27	0	0	0	not significant
6072	HOLLERN_EMT_BREAST_TUMOR_UP	-0.96	0.27	0	0	0	not significant
6073	MCCLUNG_COCAINE_REWARD_5D	-0.96	0.27	0	0	0	not significant
6074	MELLMAN_TUT1_TARGETS_DN	-0.96	0.27	0	0	0	not significant
6075	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN	-0.96	0.27	0	0	0	not significant
6076	PID_LKB1_PATHWAY	-0.96	0.27	0	0	0	not significant
6077	VETTER_TARGETS_OF_PRKCA_AND_ETS1_UP	-0.96	0.27	0	0	0	not significant
6078	BROWNE_HCMV_INFECTION_10HR_DN	-0.96	0.26	0	0	0	not significant
6079	CASTELLANO_NRAS_TARGETS_UP	-0.96	0.26	0	0	0	not significant
6080	GO_BIOMINERAL_TISSUE_DEVELOPMENT	-0.96	0.26	0	0	0	not significant
6081	GO_PROTEIN_TAG	-0.96	0.26	0	0	0	not significant
6082	HALLMARK_SPERMATOGENESIS	-0.96	0.26	0	0	0	not significant
6083	RAF_UP.V1_UP	-0.96	0.26	0	0	0	not significant
6084	GO_NUCLEAR_PERIPHERY	-0.96	0.25	0	0	0	not significant
6085	KATSANOU_ELAVL1_TARGETS_DN	-0.96	0.25	0	0	0	not significant
6086	SANSOM_WNT_PATHWAY_REQUIRE_MYC	-0.96	0.25	0	0	0	not significant
6087	REACTOME_CILIUM_ASSEMBLY	-0.96	0.24	0	0	0	not significant
6088	GO_NEGATIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	-0.96	0.22	0	0	0	not significant
6089	GO_POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	-0.96	0.22	0	0	0	not significant
6090	GO_PROTEIN_DOMAIN_SPECIFIC_BINDING	-0.96	0.22	0	0	0	not significant
6091	PILON_KLF1_TARGETS_UP	-0.96	0.22	0	0	0	not significant
6092	GO_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.96	0.21	0	0	0	not significant

6093	GO_ORGANELLE_FISSION	-0.96	0.21	0	0	0	not significant
6094	GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION	-0.96	0.20	0	0	0	not significant
6095	YAGI_AML_WITH_INV_16_TRANSLOCATION	-0.96	0.20	0	0	0	not significant
6096	HAN_SATB1_TARGETS_UP	-0.96	0.19	0	0	0	not significant
6097	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	-0.96	0.17	0	0	0	not significant
6098	GO_REGULATION_OF_KINASE_ACTIVITY	-0.96	0.12	0	0	0	not significant
6099	GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_BIOSYNTHETIC_PROCES	-0.95	0.31	0	0	0	not significant
6100	GO_FATTY_ACID_DERIVATIVE_METABOLIC_PROCESS	-0.95	0.30	0	0	0	not significant
6101	GO_NEGATIVE_REGULATION_OF_CYTOKINE_SECRETION	-0.95	0.30	0	0	0	not significant
6102	GO_NUCLEOSIDE_TRIPHOSPHATE_DIPHOSPHATASE_ACTIVITY	-0.95	0.30	0	0	0	not significant
6103	GO_PROTEIN_LOCALIZATION_TO_PRESYNAPSE	-0.95	0.30	0	0	0	not significant
6104	GO_SYNAPTIC_TRANSMISSION_CHOLINERGIC	-0.95	0.30	0	0	0	not significant
6105	MCGARVEY_SILENCED_BY_METHYLATION_IN_COLON_CANCER	-0.95	0.30	0	0	0	not significant
6106	NAGY_PCAF_COMPONENTS_HUMAN	-0.95	0.30	0	0	0	not significant
6107	BILBAN_B_CLL_LPL_DN	-0.95	0.29	0	0	0	not significant
6108	CHR1P12	-0.95	0.29	0	0	0	not significant
6109	GO_ACTIVATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVO	-0.95	0.29	0	0	0	not significant
6110	GO_LIPOPOLYSACCHARIDE_BINDING	-0.95	0.29	0	0	0	not significant
6111	GO_REGULATION_OF_EPIDERMIS_DEVELOPMENT	-0.95	0.29	0	0	0	not significant
6112	GO_SURFACTANT_HOMEOSTASIS	-0.95	0.29	0	0	0	not significant
6113	GO_UBIQUITINATION_LIKE_MODIFICATION_DEPENDENT_PROTEIN_BINDIN	-0.95	0.29	0	0	0	not significant
6114	GO_V_D_J_RECOMBINATION	-0.95	0.29	0	0	0	not significant
6115	KEGG_HISTIDINE_METABOLISM	-0.95	0.29	0	0	0	not significant
6116	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAMMA_IN_WS	-0.95	0.29	0	0	0	not significant
6117	WEINMANN_ADAPTATION_TO_HYPOXIA_UP	-0.95	0.29	0	0	0	not significant
6118	AMIT_EGF_RESPONSE_40_HELA	-0.95	0.28	0	0	0	not significant
6119	GO_9PLUS0_NON_MOTILE_CILIUM	-0.95	0.28	0	0	0	not significant
6120	GO_CHLORIDE_CHANNEL_REGULATOR_ACTIVITY	-0.95	0.28	0	0	0	not significant
6121	GO_EKC_KEOPS_COMPLEX	-0.95	0.28	0	0	0	not significant
6122	GO_REGULATION_OF_MRNA_BINDING	-0.95	0.28	0	0	0	not significant
6123	GO_TORC2_COMPLEX	-0.95	0.28	0	0	0	not significant
6124	GO_TRANSLESION_SYNTHESIS	-0.95	0.28	0	0	0	not significant
6125	HUPER_BREAST_BASAL_VS_LUMINAL_DN	-0.95	0.28	0	0	0	not significant
6126	KONDO_PROSTATE_CANCER_HCP_WITH_H3K27ME3	-0.95	0.28	0	0	0	not significant
6127	KRASNOSELSKAYA_ILF3_TARGETS_UP	-0.95	0.28	0	0	0	not significant
6128	BIOCARTA_AHSP_PATHWAY	-0.95	0.27	0	0	0	not significant
6129	GO_MYOSIN_FILAMENT_ORGANIZATION	-0.95	0.27	0	0	0	not significant
6130	GO_REGULATION_OF_GLIAL_CELL_MIGRATION	-0.95	0.27	0	0	0	not significant
6131	GO_SOLUTE_PROTON_SYMPORTER_ACTIVITY	-0.95	0.27	0	0	0	not significant
6132	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	-0.95	0.27	0	0	0	not significant
6133	MODY_HIPPOCAMPUS_PRENATAL	-0.95	0.27	0	0	0	not significant
6134	REACTOME_GAB1_SIGNALOSOME	-0.95	0.27	0	0	0	not significant
6135	REACTOME_MET_ACTIVATES_RAS_SIGNALING	-0.95	0.27	0	0	0	not significant
6136	ROZANOV_MMP14_CORRELATED	-0.95	0.27	0	0	0	not significant
6137	TSAI_RESPONSE_TO_RADIATION_THERAPY	-0.95	0.27	0	0	0	not significant
6138	WIERENGA_STAT5A_TARGETS_GROUP2	-0.95	0.27	0	0	0	not significant
6139	GO_DNA_MODIFICATION	-0.95	0.26	0	0	0	not significant
6140	GO_N_TERMINAL_PROTEIN_AMINO_ACID_MODIFICATION	-0.95	0.26	0	0	0	not significant
6141	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	-0.95	0.26	0	0	0	not significant
6142	GO_REGULATION_OF_SPINDLE_ASSEMBLY	-0.95	0.26	0	0	0	not significant
6143	GO_VENTRICULAR_SEPTUM_DEVELOPMENT	-0.95	0.26	0	0	0	not significant
6144	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN	-0.95	0.26	0	0	0	not significant
6145	XU_GH1_EXOGENOUS_TARGETS_DN	-0.95	0.26	0	0	0	not significant
6146	AUNG_GASTRIC_CANCER	-0.95	0.25	0	0	0	not significant
6147	GO_POSITIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_	-0.95	0.25	0	0	0	not significant
6148	GO_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_	-0.95	0.25	0	0	0	not significant
6149	GO_TERTIARY_GRANULE	-0.95	0.25	0	0	0	not significant
6150	INGA_TP53_TARGETS	-0.95	0.25	0	0	0	not significant
6151	KRAS.KIDNEY_UP.V1_UP	-0.95	0.25	0	0	0	not significant
6152	PUJANA_XPRSS_INT_NETWORK	-0.95	0.25	0	0	0	not significant
6153	REACTOME_DISEASES_ASSOCIATED_WITH_GLYCOSAMINOGLYCAN_MET	-0.95	0.25	0	0	0	not significant
6154	GO_FAT_CELL_DIFFERENTIATION	-0.95	0.24	0	0	0	not significant
6155	GO_L_GLUTAMINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.95	0.24	0	0	0	not significant
6156	GO_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	-0.95	0.24	0	0	0	not significant
6157	GO_CLATHRIN_COATED_VESICLE	-0.95	0.23	0	0	0	not significant
6158	GO_INSULIN_RECEPTOR_SIGNALING_PATHWAY	-0.95	0.23	0	0	0	not significant
6159	GO_GOLGI_ASSOCIATED_VESICLE_MEMBRANE	-0.95	0.22	0	0	0	not significant
6160	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN	-0.95	0.17	0	0	0	not significant
6161	GO_GTPASE_REGULATOR_ACTIVITY	-0.95	0.16	0	0	0	not significant
6162	GO_CELLULAR_COMPONENT_MORPHOGENESIS	-0.95	0.14	0	0	0	not significant
6163	GO_ENDOPLASMIC_RETICULUM_PART	-0.95	0.10	0	0	0	not significant
6164	GO_MACROMOLECULE_CATABOLIC_PROCESS	-0.95	0.10	0	0	0	not significant
6165	GO_NEURON_PART	-0.95	0.09	0	0	0	not significant
6166	GO_NEURAL_RETINA_DEVELOPMENT	-0.94	0.30	0	0	0	not significant
6167	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN	-0.94	0.29	0	0	0	not significant
6168	FERRARI_RESPONSE_TO_FENRETINIDE_UP	-0.94	0.29	0	0	0	not significant
6169	GO_MODIFICATION_OF_POSTSYNAPTIC_STRUCTURE	-0.94	0.29	0	0	0	not significant
6170	GO_NEGATIVE_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILEN	-0.94	0.29	0	0	0	not significant
6171	GO_T_CELL_HOMEOSTASIS	-0.94	0.29	0	0	0	not significant
6172	TSUNODA_CISPLATIN_RESISTANCE_UP	-0.94	0.29	0	0	0	not significant
6173	ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE	-0.94	0.29	0	0	0	not significant
6174	GENTILE_UV_RESPONSE_CLUSTER_D9	-0.94	0.28	0	0	0	not significant
6175	GO_CLASS_I_DNA_APURINIC_OR_APYRIMIDINIC_SITE_ENDONUCLEASE_A	-0.94	0.28	0	0	0	not significant
6176	GO_REGULATION_OF_HISTONE_DEACETYLATION	-0.94	0.28	0	0	0	not significant
6177	GO_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	-0.94	0.28	0	0	0	not significant
6178	HOFMANN_CELL_LYMPHOMA_UP	-0.94	0.28	0	0	0	not significant
6179	REACTOME_CROSSLINKING_OF_COLLAGEN_FIBRILS	-0.94	0.28	0	0	0	not significant
6180	REACTOME_SYNTHESIS_OF_WYBUTOSINE_AT_G37_OF_TRNA_PHE	-0.94	0.28	0	0	0	not significant
6181	ZEMBUTSU_SENSITIVITY_TO_VINCRISTINE	-0.94	0.28	0	0	0	not significant
6182	BIOCARTA_LIS1_PATHWAY	-0.94	0.27	0	0	0	not significant
6183	GERHOLD_ADIPOGENESIS_DN	-0.94	0.27	0	0	0	not significant
6184	GO_AMYLOID_BETA_CLEARANCE_BY_TRANSCYTOSIS	-0.94	0.27	0	0	0	not significant
6185	GO_CALCINEURIN_MEDIATED_SIGNALING	-0.94	0.27	0	0	0	not significant
6186	GO_CELL_MOTILITY_INVOLVED_IN_CEREBRAL_CORTEX_RADIAL_GLIA_	-0.94	0.27	0	0	0	not significant
6187	GO_LATERAL_PLASMA_MEMBRANE	-0.94	0.27	0	0	0	not significant
6188	GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE	-0.94	0.27	0	0	0	not significant
6189	GO_NUCLEOTIDE_ACTIVATED_PROTEIN_KINASE_COMPLEX	-0.94	0.27	0	0	0	not significant
6190	GO_PHOSPHATIDYLINOSITOL_BISPHOSPHATE_PHOSPHATASE_ACTIVITY	-0.94	0.27	0	0	0	not significant
6191	GO_POSITIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	-0.94	0.27	0	0	0	not significant
6192	GO_REGULATION_OF_FEEDING_BEHAVIOR	-0.94	0.27	0	0	0	not significant
6193	GO_REGULATION_OF_NECROTIC_CELL_DEATH	-0.94	0.27	0	0	0	not significant
6194	GO_REGULATION_OF_TRANSMISSION_OF_NERVE_IMPULSE	-0.94	0.27	0	0	0	not significant
6195	KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	-0.94	0.27	0	0	0	not significant
6196	ROZANOV_MMP14_TARGETS_DN	-0.94	0.27	0	0	0	not significant
6197	ZHU_SKIL_TARGETS_DN	-0.94	0.27	0	0	0	not significant
6198	ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_DN	-0.94	0.26	0	0	0	not significant
6199	BROWNE_HCMV_INFECTION_30MIN_DN	-0.94	0.26	0	0	0	not significant
6200	DAWSON_METHYLATED_IN_LYMPHOMA_TCL1	-0.94	0.26	0	0	0	not significant
6201	FINETTI_BREAST_CANCERS_KINOME_BLUE	-0.94	0.26	0	0	0	not significant

6202	GO_MYD88_DEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	-0.94	0.26	0	0	0	not significant
6203	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_	-0.94	0.26	0	0	0	not significant
6204	GO_NUCLEOBASE_CONTAINING_COMPOUND_KINASE_ACTIVITY	-0.94	0.26	0	0	0	not significant
6205	GO_REGULATION_OF_BONE_DEVELOPMENT	-0.94	0.26	0	0	0	not significant
6206	GO_REGULATION_OF_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLI	-0.94	0.26	0	0	0	not significant
6207	GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	-0.94	0.26	0	0	0	not significant
6208	KANG_FLUOROURACIL_RESISTANCE_UP	-0.94	0.26	0	0	0	not significant
6209	KIM_LIVER_CANCER_POOR_SURVIVAL_UP	-0.94	0.26	0	0	0	not significant
6210	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP	-0.94	0.26	0	0	0	not significant
6211	MARSON_FOXP3_TARGETS_STIMULATED_UP	-0.94	0.26	0	0	0	not significant
6212	REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	-0.94	0.26	0	0	0	not significant
6213	CHR11P11	-0.94	0.25	0	0	0	not significant
6214	CHR1P13	-0.94	0.25	0	0	0	not significant
6215	GO_NEGATIVE_REGULATION_OF_SYNAPSE_ORGANIZATION	-0.94	0.25	0	0	0	not significant
6216	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITIO	-0.94	0.25	0	0	0	not significant
6217	GO_PROTEIN_LIPID_COMPLEX_SUBUNIT_ORGANIZATION	-0.94	0.25	0	0	0	not significant
6218	GO_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	-0.94	0.25	0	0	0	not significant
6219	PID_TAP63_PATHWAY	-0.94	0.25	0	0	0	not significant
6220	PUJANA_BREAST_CANCER_LIT_INT_NETWORK	-0.94	0.25	0	0	0	not significant
6221	REACTOME_PLASMA_LIPOPROTEIN_CLEARANCE	-0.94	0.25	0	0	0	not significant
6222	GO_HEART_VALVE_DEVELOPMENT	-0.94	0.24	0	0	0	not significant
6223	GO_MITOTIC_SPINDLE	-0.94	0.24	0	0	0	not significant
6224	GO_POSITIVE_REGULATION_OF_PROTEOLYSIS_INVOLVED_IN_CELLULA	-0.94	0.24	0	0	0	not significant
6225	REACTOME_METABOLISM_OF_WATER_SOLUBLE_VITAMINS_AND_COFA	-0.94	0.24	0	0	0	not significant
6226	SIRNA_EIF4GI_UP	-0.94	0.24	0	0	0	not significant
6227	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_CIS	-0.94	0.23	0	0	0	not significant
6228	DITTMER_PTHLH_TARGETS_DN	-0.94	0.23	0	0	0	not significant
6229	GO_NEGATIVE_REGULATION_OF_DNA_BINDING_TRANSCRIPTION_FACT	-0.94	0.23	0	0	0	not significant
6230	GO_NUCLEOSIDE_METABOLIC_PROCESS	-0.94	0.23	0	0	0	not significant
6231	HOSHIDA_LIVER_CANCER_SURVIVAL_DN	-0.94	0.23	0	0	0	not significant
6232	GO_GLUCOSE_METABOLIC_PROCESS	-0.94	0.22	0	0	0	not significant
6233	GO_POSITIVE_REGULATION_OF_JNK_CASCADE	-0.94	0.22	0	0	0	not significant
6234	GO_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	-0.94	0.22	0	0	0	not significant
6235	GO_REGULATION_OF_NEUROTRANSMITTER_LEVELS	-0.94	0.22	0	0	0	not significant
6236	GO_SPECIFIC_GRANULE	-0.94	0.22	0	0	0	not significant
6237	NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON	-0.94	0.22	0	0	0	not significant
6238	RAY_TUMORIGENESIS_BY_ERBB2_CDC25A_UP	-0.94	0.22	0	0	0	not significant
6239	REACTOME_RHO_GTPASE_CYCLE	-0.94	0.22	0	0	0	not significant
6240	SMIRNOV_RESPONSE_TO_IR_6HR_UP	-0.94	0.22	0	0	0	not significant
6241	GO_CELL_PROJECTION_MEMBRANE	-0.94	0.21	0	0	0	not significant
6242	GO_MULTICELLULAR_ORGANISM_GROWTH	-0.94	0.21	0	0	0	not significant
6243	GO_NEGATIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	-0.94	0.21	0	0	0	not significant
6244	GO_POSITIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	-0.94	0.21	0	0	0	not significant
6245	PID_TELOMERASE_PATHWAY	-0.94	0.21	0	0	0	not significant
6246	GO_TRANSPORT_VESICLE	-0.94	0.20	0	0	0	not significant
6247	GCNP_SHH_UP_EARLY.V1_UP	-0.94	0.19	0	0	0	not significant
6248	GO_STEROID_HORMONE_MEDIATED_SIGNALING_PATHWAY	-0.94	0.19	0	0	0	not significant
6249	GO_CELLULAR_RESPONSE_TO_PEPTIDE	-0.94	0.18	0	0	0	not significant
6250	GO_MAGNESIUM_ION_BINDING	-0.94	0.18	0	0	0	not significant
6251	GO_POSITIVE_REGULATION_OF_KINASE_ACTIVITY	-0.94	0.17	0	0	0	not significant
6252	LU_EZH2_TARGETS_DN	-0.94	0.16	0	0	0	not significant
6253	OSMAN_BLADDER_CANCER_UP	-0.94	0.15	0	0	0	not significant
6254	GO_CHROMOSOME_ORGANIZATION	-0.94	0.07	0	0	0	not significant
6255	GO_CALCIUM_DEPENDENT_PROTEIN_SERINE_THREONINE_PHOSPHATAS	-0.93	0.29	0	0	0	not significant
6256	GO_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMM	-0.93	0.28	0	0	0	not significant
6257	GO_POLY_PURINE_TRACT_BINDING	-0.93	0.28	0	0	0	not significant
6258	LEE_NAIVE_T_LYMPHOCYTE	-0.93	0.28	0	0	0	not significant
6259	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_DN	-0.93	0.28	0	0	0	not significant
6260	BIOCARTA_THELPER_PATHWAY	-0.93	0.27	0	0	0	not significant
6261	CHR10Q11	-0.93	0.27	0	0	0	not significant
6262	GO_DNA_METHYLTRANSFERASE_ACTIVITY	-0.93	0.27	0	0	0	not significant
6263	GO_LABYRINTHINE_LAYER_BLOOD_VESSEL_DEVELOPMENT	-0.93	0.27	0	0	0	not significant
6264	GO_NEGATIVE_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRINS	-0.93	0.27	0	0	0	not significant
6265	GO_STRIATUM_DEVELOPMENT	-0.93	0.27	0	0	0	not significant
6266	GO_TRANSLATIONAL_READTHROUGH	-0.93	0.27	0	0	0	not significant
6267	NIELSEN_LEIOMYOSARCOMA_CNN1_DN	-0.93	0.27	0	0	0	not significant
6268	NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	-0.93	0.27	0	0	0	not significant
6269	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN	-0.93	0.27	0	0	0	not significant
6270	REACTOME_CASPASE_ACTIVATION_VIA_DEATH_RECEPTORS_IN_THE_PI	-0.93	0.27	0	0	0	not significant
6271	BIOCARTA_P53HYPOXIA_PATHWAY	-0.93	0.26	0	0	0	not significant
6272	FIRESTEIN_CTNNB1_PATHWAY_AND_PROLIFERATION	-0.93	0.26	0	0	0	not significant
6273	GO_ARTERY_DEVELOPMENT	-0.93	0.26	0	0	0	not significant
6274	GO_CAMP_DEPENDENT_PROTEIN_KINASE_REGULATOR_ACTIVITY	-0.93	0.26	0	0	0	not significant
6275	GO_EPITHELIAL_CELL_PROLIFERATION_INVOLVED_IN_PROSTATE_GLAN	-0.93	0.26	0	0	0	not significant
6276	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_BIPOLAR_CELL_POLARITY	-0.93	0.26	0	0	0	not significant
6277	GO_FOLIC_ACID_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-0.93	0.26	0	0	0	not significant
6278	GO_FUCOSYLATION	-0.93	0.26	0	0	0	not significant
6279	GO_MICROTUBULE_ORGANIZING_CENTER_LOCALIZATION	-0.93	0.26	0	0	0	not significant
6280	GO_NEGATIVE_REGULATION_OF_KERATINOCYTE_PROLIFERATION	-0.93	0.26	0	0	0	not significant
6281	GO_NEGATIVE_REGULATION_OF_MONOOXYGENASE_ACTIVITY	-0.93	0.26	0	0	0	not significant
6282	GO_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_BINDING	-0.93	0.26	0	0	0	not significant
6283	GO_POSITIVE_REGULATION_OF_BONE_RESORPTION	-0.93	0.26	0	0	0	not significant
6284	GO_PURINE_NUCLEOSIDE_TRIPHOSPHATE_CATABOLIC_PROCESS	-0.93	0.26	0	0	0	not significant
6285	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HYPOXIA	-0.93	0.26	0	0	0	not significant
6286	GO_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_ENDOPLASMIC_	-0.93	0.26	0	0	0	not significant
6287	GO_SINGLE_STRANDED_DNA_DEPENDENT_ATPASE_ACTIVITY	-0.93	0.26	0	0	0	not significant
6288	REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	-0.93	0.26	0	0	0	not significant
6289	REACTOME_INACTIVATION_OF_CDC42_AND_RAC1	-0.93	0.26	0	0	0	not significant
6290	REACTOME_SENSING_OF_DNA_DOUBLE_STRAND_BREAKS	-0.93	0.26	0	0	0	not significant
6291	REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING	-0.93	0.26	0	0	0	not significant
6292	WANG_METASTASIS_OF_BREAST_CANCER_ESR1_DN	-0.93	0.26	0	0	0	not significant
6293	BOWIE_RESPONSE_TO_TAMOXIFEN	-0.93	0.25	0	0	0	not significant
6294	GO_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR	-0.93	0.25	0	0	0	not significant
6295	GO_HINDLIMB_MORPHOGENESIS	-0.93	0.25	0	0	0	not significant
6296	GO_POSITIVE_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECE	-0.93	0.25	0	0	0	not significant
6297	GO_REGULATION_OF_COENZYME_METABOLIC_PROCESS	-0.93	0.25	0	0	0	not significant
6298	GO_SYNAPTIC_CLEFT	-0.93	0.25	0	0	0	not significant
6299	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	-0.93	0.25	0	0	0	not significant
6300	KOHOUTEK_CCNT1_TARGETS	-0.93	0.25	0	0	0	not significant
6301	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHY_UP	-0.93	0.25	0	0	0	not significant
6302	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_23	-0.93	0.25	0	0	0	not significant
6303	REACTOME_DEFECTIVE_B4GALT7_CAUSES_EDS_PROGEROID_TYPE	-0.93	0.25	0	0	0	not significant
6304	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_2	-0.93	0.25	0	0	0	not significant
6305	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_TOP20_UP	-0.93	0.25	0	0	0	not significant
6306	BIOCARTA_PELP1_PATHWAY	-0.93	0.24	0	0	0	not significant
6307	GO_AMYLOID_BETA_BINDING	-0.93	0.24	0	0	0	not significant
6308	GO_CLEAVAGE_FURROW	-0.93	0.24	0	0	0	not significant
6309	GO_ORGANOPHOSPHATE_ESTER_TRANSMEMBRANE_TRANSPORTER_A	-0.93	0.24	0	0	0	not significant
6310	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OX	-0.93	0.24	0	0	0	not significant

6311	GO_PHOSPHATIDYLCHOLINE_BIOSYNTHETIC_PROCESS	-0.93	0.24	0	0	0	not significant
6312	GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNT	-0.93	0.24	0	0	0	not significant
6313	GO_REGULATION_OF_FILOPODIUM_ASSEMBLY	-0.93	0.24	0	0	0	not significant
6314	REACTOME_SIGNALING_BY_MET	-0.93	0.24	0	0	0	not significant
6315	CHR11Q12	-0.93	0.23	0	0	0	not significant
6316	CHR5Q33	-0.93	0.23	0	0	0	not significant
6317	GO_CALCIUM_CHANNEL_COMPLEX	-0.93	0.23	0	0	0	not significant
6318	GO_EXOPEPTIDASE_ACTIVITY	-0.93	0.23	0	0	0	not significant
6319	GO_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	-0.93	0.23	0	0	0	not significant
6320	GO_REGULATION_OF_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABIL	-0.93	0.23	0	0	0	not significant
6321	GO_VESICLE_CYTOSKELETAL_TRAFFICKING	-0.93	0.23	0	0	0	not significant
6322	MINGUEZ_LIVER_CANCER_VASCULAR_INVASION_UP	-0.93	0.23	0	0	0	not significant
6323	PASINI_SUZ12_TARGETS_UP	-0.93	0.23	0	0	0	not significant
6324	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN	-0.93	0.22	0	0	0	not significant
6325	GO_ATPASE_BINDING	-0.93	0.22	0	0	0	not significant
6326	GO_CELL_DIVISION_SITE	-0.93	0.22	0	0	0	not significant
6327	GO_REGULATION_OF_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRE	-0.93	0.22	0	0	0	not significant
6328	REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHO	-0.93	0.22	0	0	0	not significant
6329	REACTOME_DUAL_INCISION_IN_GG_NER	-0.93	0.22	0	0	0	not significant
6330	SASSON_RESPONSE_TO_FORSKOLIN_DN	-0.93	0.22	0	0	0	not significant
6331	GO_CONDENSED_NUCLEAR_CHROMOSOME	-0.93	0.21	0	0	0	not significant
6332	REACTOME_HATS_ACETYLATE_HISTONES	-0.93	0.21	0	0	0	not significant
6333	GO_ATPASE_COMPLEX	-0.93	0.20	0	0	0	not significant
6334	GO_MYELOID_CELL_DEVELOPMENT	-0.93	0.20	0	0	0	not significant
6335	GO_PEPTIDE_HORMONE_SECRETION	-0.93	0.20	0	0	0	not significant
6336	NRL_DN.V1_DN	-0.93	0.20	0	0	0	not significant
6337	REACTOME_RUNX1_REGULATES_GENES_INVOLVED_IN_MEGAKARYOCYT	-0.93	0.20	0	0	0	not significant
6338	GO_NEGATIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_	-0.93	0.18	0	0	0	not significant
6339	REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	-0.93	0.18	0	0	0	not significant
6340	GO_GLUTAMATERGIC_SYNAPSE	-0.93	0.16	0	0	0	not significant
6341	GO_UBIQUITIN_LIKE_PROTEIN_LIGASE_BINDING	-0.93	0.16	0	0	0	not significant
6342	GO_CELL_GROWTH	-0.93	0.15	0	0	0	not significant
6343	GO_POSITIVE_REGULATION_OF_CATABOLIC_PROCESS	-0.93	0.15	0	0	0	not significant
6344	OISHI_CHOLANGIOMA_STEM_CELL_LIKE_UP	-0.93	0.14	0	0	0	not significant
6345	GO_CELLULAR_LIPID_METABOLIC_PROCESS	-0.93	0.11	0	0	0	not significant
6346	GO_MICROTUBULE_CYTOSKELETON	-0.93	0.08	0	0	0	not significant
6347	GO_CELL_PROJECTION_ORGANIZATION	-0.93	0.04	0	0	0	not significant
6348	MARSON_BOUND_BY_FOXP3_UNSTIMULATED	-0.93	0.03	0	0	0	not significant
6349	GO_WHOLE_MEMBRANE	-0.93	0.02	0	0	0	not significant
6350	GO_AMINE_CATABOLIC_PROCESS	-0.92	0.28	0	0	0	not significant
6351	CHR3P26	-0.92	0.27	0	0	0	not significant
6352	GO_BASE_EXCISION_REPAIR_AP_SITE_FORMATION	-0.92	0.27	0	0	0	not significant
6353	GO_CLATHRIN_ADAPTOR_COMPLEX	-0.92	0.27	0	0	0	not significant
6354	GO_PHOSPHATASE_ACTIVATOR_ACTIVITY	-0.92	0.27	0	0	0	not significant
6355	GO_PROTEIN_ACTIVATION_CASCADE	-0.92	0.27	0	0	0	not significant
6356	PID_RHOA_REG_PATHWAY	-0.92	0.27	0	0	0	not significant
6357	BIOCARTA_EIF_PATHWAY	-0.92	0.26	0	0	0	not significant
6358	CONRAD_STEM_CELL	-0.92	0.26	0	0	0	not significant
6359	GO_CELLULAR_TRIGLYCERIDE_HOMEOSTASIS	-0.92	0.26	0	0	0	not significant
6360	GO_CHAPERONE_MEDIATED_PROTEIN_TRANSPORT	-0.92	0.26	0	0	0	not significant
6361	GO_GOLGI_RIBBON_FORMATION	-0.92	0.26	0	0	0	not significant
6362	GO_MYOSIN_V_BINDING	-0.92	0.26	0	0	0	not significant
6363	GO_RNA_SPLICING_VIA_ENDONUCLEOLYTIC_CLEAVAGE_AND_LIGATION	-0.92	0.26	0	0	0	not significant
6364	GO_SUBPALLIUM_DEVELOPMENT	-0.92	0.26	0	0	0	not significant
6365	SCHLINGEMANN_SKIN_CARCINOGENESIS_TPA_UP	-0.92	0.26	0	0	0	not significant
6366	YIH_RESPONSE_TO_ARSENITE_C4	-0.92	0.26	0	0	0	not significant
6367	ZHENG_RESPONSE_TO_ARSENITE_DN	-0.92	0.26	0	0	0	not significant
6368	BIOCARTA_REELIN_PATHWAY	-0.92	0.25	0	0	0	not significant
6369	GO_BROWN_FAT_CELL_DIFFERENTIATION	-0.92	0.25	0	0	0	not significant
6370	GO_FMN_BINDING	-0.92	0.25	0	0	0	not significant
6371	GO_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_BINDING	-0.92	0.25	0	0	0	not significant
6372	GO_NEGATIVE_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATH	-0.92	0.25	0	0	0	not significant
6373	GO_NEURON_FATE_COMMITMENT	-0.92	0.25	0	0	0	not significant
6374	GO_PHOSPHATIDYLINOSITOL_MONOPHOSPHATE_PHOSPHATASE_ACTIVI	-0.92	0.25	0	0	0	not significant
6375	GO_POLAR_MICROTUBULE	-0.92	0.25	0	0	0	not significant
6376	GO_POSITIVE_REGULATION_OF_COLLATERAL_SPROUTING	-0.92	0.25	0	0	0	not significant
6377	GO_POSITIVE_REGULATION_OF_DNA_DAMAGE_RESPONSE_SIGNAL_TRA	-0.92	0.25	0	0	0	not significant
6378	GO_PROTEIN_LOCALIZATION_TO_MEMBRANE_RAFT	-0.92	0.25	0	0	0	not significant
6379	GO_REGULATION_OF_POSITIVE_CHEMOTAXIS	-0.92	0.25	0	0	0	not significant
6380	GO_RIBOSOME_DISASSEMBLY	-0.92	0.25	0	0	0	not significant
6381	IIZUKA_LIVER_CANCER_PROGRESSION_G1_G2_UP	-0.92	0.25	0	0	0	not significant
6382	KEGG_NITROGEN_METABOLISM	-0.92	0.25	0	0	0	not significant
6383	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_UP	-0.92	0.25	0	0	0	not significant
6384	LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS	-0.92	0.25	0	0	0	not significant
6385	REACTOME_SIGNALLING_TO_ERKS	-0.92	0.25	0	0	0	not significant
6386	REACTOME_SYNTHESIS_OF_PIPS_AT_THE_LATE_ENDOSOME_MEMBRAN	-0.92	0.25	0	0	0	not significant
6387	SCHRAETS_MLL_TARGETS_UP	-0.92	0.25	0	0	0	not significant
6388	BOYLAN_MULTIPLE_MYELOMA_C_UP	-0.92	0.24	0	0	0	not significant
6389	GO_COPPER_ION_BINDING	-0.92	0.24	0	0	0	not significant
6390	GO_MIRNA_BINDING	-0.92	0.24	0	0	0	not significant
6391	GO_NEGATIVE_REGULATION_OF_MACROAUTOPHAGY	-0.92	0.24	0	0	0	not significant
6392	GO_POSITIVE_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	-0.92	0.24	0	0	0	not significant
6393	GO_POSITIVE_REGULATION_OF_ERAD_PATHWAY	-0.92	0.24	0	0	0	not significant
6394	GO_REGULATION_OF_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLI	-0.92	0.24	0	0	0	not significant
6395	REACTOME_EICOSANOID_LIGAND_BINDING_RECEPTORS	-0.92	0.24	0	0	0	not significant
6396	FRASOR_TAMOXIFEN_RESPONSE_UP	-0.92	0.23	0	0	0	not significant
6397	GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PA	-0.92	0.23	0	0	0	not significant
6398	GO_POSITIVE_REGULATION_OF_COLLAGEN_BIOSYNTHETIC_PROCESS	-0.92	0.23	0	0	0	not significant
6399	GO_REGULATION_OF_MEIOTIC_NUCLEAR_DIVISION	-0.92	0.23	0	0	0	not significant
6400	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CANCER	-0.92	0.23	0	0	0	not significant
6401	GO_NEGATIVE_REGULATION_OF_PROTEIN_DEPHOSPHORYLATION	-0.92	0.22	0	0	0	not significant
6402	GO_RETROGRADE_VESICLE_MEDIATED_TRANSPORT_GOLGI_TO_ENDO	-0.92	0.22	0	0	0	not significant
6403	KEGG_STARCH_AND_SUCROSE_METABOLISM	-0.92	0.22	0	0	0	not significant
6404	KONDO_COLON_CANCER_HCP_WITH_H3K27ME1	-0.92	0.22	0	0	0	not significant
6405	REACTOME_POST_TRANSLATIONAL_MODIFICATION:_SYNTHESIS_OF_GF	-0.92	0.22	0	0	0	not significant
6406	RIZKI_TUMOR_INVASIVENESS_2D_UP	-0.92	0.22	0	0	0	not significant
6407	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_UP	-0.92	0.22	0	0	0	not significant
6408	CRX_NRL_DN.V1_UP	-0.92	0.21	0	0	0	not significant
6409	GO_SMAD_BINDING	-0.92	0.21	0	0	0	not significant
6410	REACTOME_EPH_EPHRIN_MEDIATED_REPULSION_OF_CELLS	-0.92	0.21	0	0	0	not significant
6411	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_CIS	-0.92	0.20	0	0	0	not significant
6412	GO_CELLULAR_RESPONSE_TO_HYDROGEN_PEROXIDE	-0.92	0.20	0	0	0	not significant
6413	GO_NEUROTRANSMITTER_METABOLIC_PROCESS	-0.92	0.20	0	0	0	not significant
6414	SASSON_RESPONSE_TO_GONADOTROPHINS_DN	-0.92	0.20	0	0	0	not significant
6415	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_UP	-0.92	0.19	0	0	0	not significant
6416	GO_NEGATIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION	-0.92	0.19	0	0	0	not significant
6417	SONG_TARGETS_OF_IE86_CMV_PROTEIN	-0.92	0.19	0	0	0	not significant
6418	ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION	-0.92	0.19	0	0	0	not significant
6419	GO_CYTOSKELETON_DEPENDENT_INTRACELLULAR_TRANSPORT	-0.92	0.18	0	0	0	not significant

6420	GO_CULLIN_RING_UBIQUITIN_LIGASE_COMPLEX	-0.92	0.17	0	0	0	not significant
6421	GO_NUCLEAR_MATRIX	-0.92	0.17	0	0	0	not significant
6422	GO_SODIUM_ION_TRANSPORT	-0.92	0.17	0	0	0	not significant
6423	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP	-0.92	0.13	0	0	0	not significant
6424	GO_POSITIVE_REGULATION_OF_GTPASE_ACTIVITY	-0.92	0.13	0	0	0	not significant
6425	GO_PROTEIN_HETERODIMERIZATION_ACTIVITY	-0.92	0.12	0	0	0	not significant
6426	GO_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	-0.92	0.07	0	0	0	not significant
6427	GO_NEURON_DEVELOPMENT	-0.92	0.06	0	0	0	not significant
6428	GO_NUCLEAR_BODY	-0.92	0.05	0	0	0	not significant
6429	GO_ENDOPLASMIC_RETICULUM	-0.92	0.03	0	0	0	not significant
6430	GO_NUCLEOSIDE_DIPHOSPHATE_KINASE_ACTIVITY	-0.91	0.27	0	0	0	not significant
6431	REACTOME_REGULATION_BY_C_FLIP	-0.91	0.27	0	0	0	not significant
6432	GO_HAIR_FOLLICLE_MATURATION	-0.91	0.26	0	0	0	not significant
6433	GO_REPLICATIVE_SENESCENCE	-0.91	0.26	0	0	0	not significant
6434	INAMURA_LUNG_CANCER_SCC_UP	-0.91	0.26	0	0	0	not significant
6435	REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_F	-0.91	0.26	0	0	0	not significant
6436	REACTOME_LOSS_OF_FUNCTION_OF_TGFBR1_IN_CANCER	-0.91	0.26	0	0	0	not significant
6437	VALK_AML_CLUSTER_6	-0.91	0.26	0	0	0	not significant
6438	CHR11P12	-0.91	0.25	0	0	0	not significant
6439	GO_CELLULAR_RESPONSE_TO_LEUCINE	-0.91	0.25	0	0	0	not significant
6440	GO_ORGANELLE_INHERITANCE	-0.91	0.25	0	0	0	not significant
6441	GO_POSTSYNAPTIC_CYTOSOL	-0.91	0.25	0	0	0	not significant
6442	GO_REGULATION_OF_PLATELET_DERIVED_GROWTH_FACTOR_RECEPT	-0.91	0.25	0	0	0	not significant
6443	HESSON_TUMOR_SUPPRESSOR_CLUSTER_3P21_3	-0.91	0.25	0	0	0	not significant
6444	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_UP	-0.91	0.25	0	0	0	not significant
6445	WEBER_METHYLATED_IN_COLON_CANCER	-0.91	0.25	0	0	0	not significant
6446	BIOCARTA_ERK_PATHWAY	-0.91	0.24	0	0	0	not significant
6447	CARDOSO_RESPONSE_TO_GAMMA_RADIATION_AND_3AB	-0.91	0.24	0	0	0	not significant
6448	CHESLER_BRAIN_HIGHEST_GENETIC_VARIANCE	-0.91	0.24	0	0	0	not significant
6449	GO_ACTIVATION_OF_JNKK_ACTIVITY	-0.91	0.24	0	0	0	not significant
6450	GO_DYNACTIN_COMPLEX	-0.91	0.24	0	0	0	not significant
6451	GO_HISTONE_H3_K36_METHYLATION	-0.91	0.24	0	0	0	not significant
6452	GO_LONG_CHAIN_FATTY_ACID_IMPORT_INTO_CELL	-0.91	0.24	0	0	0	not significant
6453	GO_MAMMARY_GLAND_ALVEOLUS_DEVELOPMENT	-0.91	0.24	0	0	0	not significant
6454	GO_MICROFILAMENT_MOTOR_ACTIVITY	-0.91	0.24	0	0	0	not significant
6455	GO_MITOCHONDRIAL_DNA_METABOLIC_PROCESS	-0.91	0.24	0	0	0	not significant
6456	GO_NEGATIVE_REGULATION_OF_AMINE_TRANSPORT	-0.91	0.24	0	0	0	not significant
6457	GO_NEGATIVE_REGULATION_OF_PROTEIN_ACETYLATION	-0.91	0.24	0	0	0	not significant
6458	GO_NEGATIVE_REGULATION_OF_SPROUTING_ANGIOGENESIS	-0.91	0.24	0	0	0	not significant
6459	GO_POLYADENYLATION_DEPENDENT_SNORNA_3_END_PROCESSING	-0.91	0.24	0	0	0	not significant
6460	GO_POSITIVE_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHW	-0.91	0.24	0	0	0	not significant
6461	GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPM	-0.91	0.24	0	0	0	not significant
6462	GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PAT	-0.91	0.24	0	0	0	not significant
6463	GO_RESPIRATORY_SYSTEM_PROCESS	-0.91	0.24	0	0	0	not significant
6464	GO_SIGNAL_TRANSDUCTION_INVOLVED_IN_G2_DNA_DAMAGE_CHECKPO	-0.91	0.24	0	0	0	not significant
6465	GO_UDP_GLUCOSYLTRANSFERASE_ACTIVITY	-0.91	0.24	0	0	0	not significant
6466	PID_EPHA_FWDPATHWAY	-0.91	0.24	0	0	0	not significant
6467	AMIT_EGF_RESPONSE_20_MCF10A	-0.91	0.23	0	0	0	not significant
6468	GO_ARP2_3_COMPLEX_MEDIATED_ACTIN_NUCLEATION	-0.91	0.23	0	0	0	not significant
6469	GO_ASPARTATE_METABOLIC_PROCESS	-0.91	0.23	0	0	0	not significant
6470	GO_DIACYLGLYCEROL_BINDING	-0.91	0.23	0	0	0	not significant
6471	GO_NEGATIVE_REGULATION_OF_INCLUSION_BODY_ASSEMBLY	-0.91	0.23	0	0	0	not significant
6472	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPT	-0.91	0.23	0	0	0	not significant
6473	GO_NEGATIVE_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CAT	-0.91	0.23	0	0	0	not significant
6474	GO_PEPTIDYL_CYSTEINE_MODIFICATION	-0.91	0.23	0	0	0	not significant
6475	GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MIRNAS_INVOLVED_I	-0.91	0.23	0	0	0	not significant
6476	GO_REGULATION_OF_TRANSLATIONAL_INITIATION_IN_RESPONSE_TO_S	-0.91	0.23	0	0	0	not significant
6477	CHR6Q25	-0.91	0.22	0	0	0	not significant
6478	ELLWOOD_MYC_TARGETS_DN	-0.91	0.22	0	0	0	not significant
6479	FIGUEROA_AML_METHYLATION_CLUSTER_5_DN	-0.91	0.22	0	0	0	not significant
6480	GO_MEMBRANE_PROTEIN_PROTEOLYSIS	-0.91	0.22	0	0	0	not significant
6481	GO_NEGATIVE_REGULATION_OF_SODIUM_ION_TRANSPORT	-0.91	0.22	0	0	0	not significant
6482	GO_REGULATION_OF_ENDOPLASMIC_RETICULUM_STRESS_INDUCED_IN	-0.91	0.22	0	0	0	not significant
6483	GO_REGULATION_OF_GLUCOSE_TRANSMEMBRANE_TRANSPORT	-0.91	0.22	0	0	0	not significant
6484	GO_REGULATION_OF_MITOTIC_SPINDLE_ASSEMBLY	-0.91	0.22	0	0	0	not significant
6485	GO_SCHWANN_CELL_DEVELOPMENT	-0.91	0.22	0	0	0	not significant
6486	GO_WOUND_HEALING_SPREADING_OF_EPIDERMAL_CELLS	-0.91	0.22	0	0	0	not significant
6487	GENTILE_UV_RESPONSE_CLUSTER_D2	-0.91	0.21	0	0	0	not significant
6488	GO_MEGAKARYOCYTE_DIFFERENTIATION	-0.91	0.21	0	0	0	not significant
6489	GO_RAC_GTPASE_BINDING	-0.91	0.21	0	0	0	not significant
6490	REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES	-0.91	0.21	0	0	0	not significant
6491	COATES_MACROPHAGE_M1_VS_M2_UP	-0.91	0.20	0	0	0	not significant
6492	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREY_DN	-0.91	0.20	0	0	0	not significant
6493	GO_CONTRACTILE_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	-0.91	0.20	0	0	0	not significant
6494	GO_CORTICAL_ACTIN_CYTOSKELETON	-0.91	0.20	0	0	0	not significant
6495	GO_G1_DNA_DAMAGE_CHECKPOINT	-0.91	0.20	0	0	0	not significant
6496	GO_PROTEIN_CONTAINING_COMPLEX_SCAFFOLD_ACTIVITY	-0.91	0.20	0	0	0	not significant
6497	GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO	-0.91	0.20	0	0	0	not significant
6498	CHR15Q15	-0.91	0.19	0	0	0	not significant
6499	GO_EXONUCLEASE_ACTIVITY	-0.91	0.19	0	0	0	not significant
6500	GO_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	-0.91	0.19	0	0	0	not significant
6501	GO_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	-0.91	0.19	0	0	0	not significant
6502	ALCALA_APOPTOSIS	-0.91	0.18	0	0	0	not significant
6503	CHR9Q34	-0.91	0.18	0	0	0	not significant
6504	GO_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	-0.91	0.18	0	0	0	not significant
6505	GO_MESENCHYME_DEVELOPMENT	-0.91	0.17	0	0	0	not significant
6506	MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_DN	-0.91	0.17	0	0	0	not significant
6507	NIKOLSKY_BREAST_CANCER_11Q12_Q14_AMPLICON	-0.91	0.16	0	0	0	not significant
6508	GO_POSITIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION	-0.91	0.15	0	0	0	not significant
6509	GO_REGULATION_OF_ENDOCYTOSIS	-0.91	0.15	0	0	0	not significant
6510	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINAS	-0.91	0.14	0	0	0	not significant
6511	GO_AXON_PART	-0.91	0.13	0	0	0	not significant
6512	GO_DENDRITE_DEVELOPMENT	-0.91	0.12	0	0	0	not significant
6513	GO_EARLY_ENDOSOME	-0.91	0.12	0	0	0	not significant
6514	GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	-0.91	0.11	0	0	0	not significant
6515	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP	-0.91	0.10	0	0	0	not significant
6516	GO_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	-0.91	0.10	0	0	0	not significant
6517	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCT	-0.91	0.09	0	0	0	not significant
6518	MIKKELSEN_NPC_ICP_WITH_H3K4ME3	-0.91	0.09	0	0	0	not significant
6519	GO_ORGANELLE_ASSEMBLY	-0.91	0.04	0	0	0	not significant
6520	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINI	-0.91	0.04	0	0	0	not significant
6521	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRAN	-0.90	0.25	0	0	0	not significant
6522	GO_REGULATION_OF_NEUROTRANSMITTER_UPTAKE	-0.90	0.25	0	0	0	not significant
6523	GO_VIRAL_TRANSLATION	-0.90	0.25	0	0	0	not significant
6524	REACTOME_SIGNALLING_TO_RAS	-0.90	0.25	0	0	0	not significant
6525	GO_CGMP_MEDIATED_SIGNALING	-0.90	0.24	0	0	0	not significant
6526	GO_GTP_DEPENDENT_PROTEIN_BINDING	-0.90	0.24	0	0	0	not significant
6527	GO_MAINTENANCE_OF_SYNAPSE_STRUCTURE	-0.90	0.24	0	0	0	not significant
6528	GO_NUCLEOSIDE_MONOPHOSPHATE_PHOSPHORYLATION	-0.90	0.24	0	0	0	not significant

6529	REACTOME_BETA_OXIDATION_OF_PRISTANOYL_COA	-0.90	0.24	0	0	0	not significant
6530	WOTTON_RUNX_TARGETS_DN	-0.90	0.24	0	0	0	not significant
6531	BIOCARTA_RAS_PATHWAY	-0.90	0.23	0	0	0	not significant
6532	CHR3Q24	-0.90	0.23	0	0	0	not significant
6533	GAUSSMANN_MLL_AF4_FUSION_TARGETS_C_DN	-0.90	0.23	0	0	0	not significant
6534	GO_ADIPONECTIN_ACTIVATED_SIGNALING_PATHWAY	-0.90	0.23	0	0	0	not significant
6535	GO_GLUCOSAMINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-0.90	0.23	0	0	0	not significant
6536	GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_P38_BINDING	-0.90	0.23	0	0	0	not significant
6537	GO_NEGATIVE_REGULATION_OF_FIBROBLAST_MIGRATION	-0.90	0.23	0	0	0	not significant
6538	GO_OUTER_DYNEIN_ARM_ASSEMBLY	-0.90	0.23	0	0	0	not significant
6539	GO_POSITIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTE	-0.90	0.23	0	0	0	not significant
6540	GO_PROTEIN_SERINE_THREONINE_KINASE_INHIBITOR_ACTIVITY	-0.90	0.23	0	0	0	not significant
6541	GO_REGULATION_OF_LYSOSOMAL_PROTEIN_CATABOLIC_PROCESS	-0.90	0.23	0	0	0	not significant
6542	GO_REGULATION_OF_MONOCYTE_DIFFERENTIATION	-0.90	0.23	0	0	0	not significant
6543	GO_STRUCTURAL_CONSTITUENT_OF_MUSCLE	-0.90	0.23	0	0	0	not significant
6544	MELLMAN_TUT1_TARGETS_UP	-0.90	0.23	0	0	0	not significant
6545	NUMATA_CSF3_SIGNALING_VIA_STAT3	-0.90	0.23	0	0	0	not significant
6546	PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN	-0.90	0.23	0	0	0	not significant
6547	AIYAR_COBRA1_TARGETS_UP	-0.90	0.22	0	0	0	not significant
6548	ANDERSEN_CHOLANGIOCARCINOMA_CLASS1	-0.90	0.22	0	0	0	not significant
6549	CHR2P16	-0.90	0.22	0	0	0	not significant
6550	GO_AMYLOID_PRECURSOR_PROTEIN_CATABOLIC_PROCESS	-0.90	0.22	0	0	0	not significant
6551	GO_ANOIKIS	-0.90	0.22	0	0	0	not significant
6552	GO_DYNEIN_COMPLEX_BINDING	-0.90	0.22	0	0	0	not significant
6553	GO_HSP70_PROTEIN_BINDING	-0.90	0.22	0	0	0	not significant
6554	GO_INTERLEUKIN_8_SECRETION	-0.90	0.22	0	0	0	not significant
6555	GO_OSTEOCLAST_DEVELOPMENT	-0.90	0.22	0	0	0	not significant
6556	GO_REGULATION_OF_GLIAL_CELL_APOPTOTIC_PROCESS	-0.90	0.22	0	0	0	not significant
6557	GO_REGULATION_OF_KIDNEY_DEVELOPMENT	-0.90	0.22	0	0	0	not significant
6558	MADAN_DPPA4_TARGETS	-0.90	0.22	0	0	0	not significant
6559	PID_INTEGRIN1_PATHWAY	-0.90	0.22	0	0	0	not significant
6560	REACTOME_SYNTHESIS_OF_IP3_AND_IP4_IN_THE_CYTOSOL	-0.90	0.22	0	0	0	not significant
6561	GO_BASEMENT_MEMBRANE	-0.90	0.21	0	0	0	not significant
6562	GO_CALMODULIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-0.90	0.21	0	0	0	not significant
6563	GO_ESTROGEN_RECEPTOR_BINDING	-0.90	0.21	0	0	0	not significant
6564	GO_NEGATIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METAB	-0.90	0.21	0	0	0	not significant
6565	GO_NUCLEAR_UBIQUITIN_LIGASE_COMPLEX	-0.90	0.21	0	0	0	not significant
6566	GO_POSITIVE_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	-0.90	0.21	0	0	0	not significant
6567	GO_POST_EMBRYONIC_ANIMAL_ORGAN_DEVELOPMENT	-0.90	0.21	0	0	0	not significant
6568	GO_SECRETION_BY_TISSUE	-0.90	0.21	0	0	0	not significant
6569	NUTT_GBM_VS_AO_GLIOMA_DN	-0.90	0.21	0	0	0	not significant
6570	CHR3Q29	-0.90	0.20	0	0	0	not significant
6571	GO_EXORIBONUCLEASE_ACTIVITY	-0.90	0.20	0	0	0	not significant
6572	GO_POSITIVE_REGULATION_OF_P38MAPK_CASCADE	-0.90	0.20	0	0	0	not significant
6573	GO_THYMOCYTE_APOPTOTIC_PROCESS	-0.90	0.20	0	0	0	not significant
6574	VANTVEER_BREAST_CANCER_POOR_PROGNOSIS	-0.90	0.20	0	0	0	not significant
6575	CHR22Q12	-0.90	0.19	0	0	0	not significant
6576	GO_CELLULAR_EXTRAVASATION	-0.90	0.19	0	0	0	not significant
6577	GO_RECEPTOR_INTERNALIZATION	-0.90	0.19	0	0	0	not significant
6578	GO_SITE_OF_DNA_DAMAGE	-0.90	0.19	0	0	0	not significant
6579	GO_SPECIFIC_GRANULE_MEMBRANE	-0.90	0.19	0	0	0	not significant
6580	KEGG_DILATED_CARDIOMYOPATHY	-0.90	0.19	0	0	0	not significant
6581	KYNG_DNA_DAMAGE_BY_GAMMA_RADIATION	-0.90	0.19	0	0	0	not significant
6582	PID_P53_REGULATION_PATHWAY	-0.90	0.19	0	0	0	not significant
6583	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	-0.90	0.18	0	0	0	not significant
6584	GO_TISSUE_REMODELING	-0.90	0.18	0	0	0	not significant
6585	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALI	-0.90	0.18	0	0	0	not significant
6586	KEGG_LONG_TERM_POTENTIATION	-0.90	0.18	0	0	0	not significant
6587	STEIN_ESR1_TARGETS	-0.90	0.18	0	0	0	not significant
6588	GO_CARDIAC_SEPTUM_DEVELOPMENT	-0.90	0.17	0	0	0	not significant
6589	GO_PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	-0.90	0.17	0	0	0	not significant
6590	KEGG_RENAL_CELL_CARCINOMA	-0.90	0.17	0	0	0	not significant
6591	GO_CELLULAR_RESPONSE_TO_LIGHT_STIMULUS	-0.90	0.16	0	0	0	not significant
6592	NOTCH_DN.V1_UP	-0.90	0.16	0	0	0	not significant
6593	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	-0.90	0.15	0	0	0	not significant
6594	FIRESTEIN_PROLIFERATION	-0.90	0.13	0	0	0	not significant
6595	GO_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIAT	-0.90	0.13	0	0	0	not significant
6596	GO_PEPTIDYL_SERINE_MODIFICATION	-0.90	0.12	0	0	0	not significant
6597	GO_POSITIVE_REGULATION_OF_GROWTH	-0.90	0.12	0	0	0	not significant
6598	GO_FOREBRAIN_DEVELOPMENT	-0.90	0.10	0	0	0	not significant
6599	GO_POSITIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	-0.90	0.10	0	0	0	not significant
6600	GO_RESPONSE_TO_LIGHT_STIMULUS	-0.90	0.09	0	0	0	not significant
6601	TBK1.DF_DN	-0.90	0.09	0	0	0	not significant
6602	GO_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.90	0.06	0	0	0	not significant
6603	GO_NEGATIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	-0.90	0.06	0	0	0	not significant
6604	GO_I_SMAD_BINDING	-0.89	0.24	0	0	0	not significant
6605	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_CHECKPOINT	-0.89	0.24	0	0	0	not significant
6606	GO_RESPONSE_TO_LEUCINE	-0.89	0.24	0	0	0	not significant
6607	GO_TRANSLATION_REPRESSOR_ACTIVITY_MRNA_REGULATORY_ELEME	-0.89	0.24	0	0	0	not significant
6608	GO_VOLUNTARY_MUSCULOSKELETAL_MOVEMENT	-0.89	0.24	0	0	0	not significant
6609	YAMASHITA_METHYLATED_IN_PROSTATE_CANCER	-0.89	0.24	0	0	0	not significant
6610	GO_AP_1_ADAPTOR_COMPLEX	-0.89	0.23	0	0	0	not significant
6611	GO_AXONEMAL_DYNEIN_COMPLEX_ASSEMBLY	-0.89	0.23	0	0	0	not significant
6612	GO_CELLULAR_ALDEHYDE_METABOLIC_PROCESS	-0.89	0.23	0	0	0	not significant
6613	GO_FLOTILLIN_COMPLEX	-0.89	0.23	0	0	0	not significant
6614	GO_LSM2_8_COMPLEX	-0.89	0.23	0	0	0	not significant
6615	GO_REGULATION_OF_GLYCOGEN_CATABOLIC_PROCESS	-0.89	0.23	0	0	0	not significant
6616	GO_REGULATION_OF_HISTONE_DEACETYLASE_ACTIVITY	-0.89	0.23	0	0	0	not significant
6617	GO_WOUND_HEALING_INVOLVED_IN_INFLAMMATORY_RESPONSE	-0.89	0.23	0	0	0	not significant
6618	ONDER_CDH1_TARGETS_3_DN	-0.89	0.23	0	0	0	not significant
6619	REACTOME_NOTCH4_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRI	-0.89	0.23	0	0	0	not significant
6620	WIERENGA_PML_INTERACTOME	-0.89	0.23	0	0	0	not significant
6621	ZHAN_MULTIPLE_MYELOMA_MS_UP	-0.89	0.23	0	0	0	not significant
6622	BIOCARTA_CCR3_PATHWAY	-0.89	0.22	0	0	0	not significant
6623	DAZARD_UV_RESPONSE_CLUSTER_G28	-0.89	0.22	0	0	0	not significant
6624	GO_ACETYLCHOLINE_BINDING	-0.89	0.22	0	0	0	not significant
6625	GO_CHONDROCYTE_DEVELOPMENT_INVOLVED_IN_ENDOCHONDRAL_B	-0.89	0.22	0	0	0	not significant
6626	GO_POLY_PYRIMIDINE_TRACT_BINDING	-0.89	0.22	0	0	0	not significant
6627	GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_ORGANIZATION	-0.89	0.22	0	0	0	not significant
6628	GO_REGULATION_OF_RESPIRATORY_SYSTEM_PROCESS	-0.89	0.22	0	0	0	not significant
6629	GO_RESPONSE_TO_IMMOBILIZATION_STRESS	-0.89	0.22	0	0	0	not significant
6630	GO_VENTRAL_SPINAL_CORD_DEVELOPMENT	-0.89	0.22	0	0	0	not significant
6631	IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_UP	-0.89	0.22	0	0	0	not significant
6632	MCCABE_HOXC6_TARGETS_CANCER_DN	-0.89	0.22	0	0	0	not significant
6633	NEWMAN_ERCC6_TARGETS_UP	-0.89	0.22	0	0	0	not significant
6634	REACTOME_CRMPS_IN_SEMA3A_SIGNALING	-0.89	0.22	0	0	0	not significant
6635	REACTOME_METABOLISM_OF_FOLATE_AND_PTERINES	-0.89	0.22	0	0	0	not significant
6636	SA_PTEN_PATHWAY	-0.89	0.22	0	0	0	not significant
6637	GO_CELLULAR_RESPONSE_TO_REACTIVE_NITROGEN_SPECIES	-0.89	0.21	0	0	0	not significant

6638	GO_NEGATIVE_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTI	-0.89	0.21	0	0	0	not significant
6639	GO_NEGATIVE_REGULATION_OF_T_CELL_DIFFERENTIATION	-0.89	0.21	0	0	0	not significant
6640	GO_PEPTIDYL_LYSINE_DIMETHYLATION	-0.89	0.21	0	0	0	not significant
6641	GO_POSITIVE_REGULATION_OF_CHOLESTEROL_EFFLUX	-0.89	0.21	0	0	0	not significant
6642	GO_PRIMARY_MIRNA_PROCESSING	-0.89	0.21	0	0	0	not significant
6643	GO_REGULATION_OF_GRANULOCYTE_CHEMOTAXIS	-0.89	0.21	0	0	0	not significant
6644	GO_REGULATION_OF_PRODUCTION_OF_SMALL_RNA_INVOLVED_IN_GEN	-0.89	0.21	0	0	0	not significant
6645	GO_RESPONSE_TO_COCAINE	-0.89	0.21	0	0	0	not significant
6646	GO_STEROID_HORMONE_SECRETION	-0.89	0.21	0	0	0	not significant
6647	GO_TUBULIN_COMPLEX_ASSEMBLY	-0.89	0.21	0	0	0	not significant
6648	GO_VESICLE_TRANSPORT_ALONG_ACTIN_FILAMENT	-0.89	0.21	0	0	0	not significant
6649	HASLINGER_B_CLL_WITH_13Q14_DELETION	-0.89	0.21	0	0	0	not significant
6650	REACTOME_PLATELET_CALCIUM_HOMEOSTASIS	-0.89	0.21	0	0	0	not significant
6651	REACTOME_RHO_GTPASES_ACTIVATE_CIT	-0.89	0.21	0	0	0	not significant
6652	ULE_SPLICING_VIA_NOVA2	-0.89	0.21	0	0	0	not significant
6653	ZEMBUTSU_SENSITIVITY_TO_VINBLASTINE	-0.89	0.21	0	0	0	not significant
6654	GO_LIPASE_ACTIVITY	-0.89	0.20	0	0	0	not significant
6655	GO_PROTEIN_QUALITY_CONTROL_FOR_MISFOLDED_OR_INCOMPLETEL	-0.89	0.20	0	0	0	not significant
6656	GO_RESPIRATORY_GASEOUS_EXCHANGE	-0.89	0.20	0	0	0	not significant
6657	GO_U2_SNRNP	-0.89	0.20	0	0	0	not significant
6658	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_UP	-0.89	0.20	0	0	0	not significant
6659	BIOCARTA_TOLL_PATHWAY	-0.89	0.19	0	0	0	not significant
6660	GO_AMINOPEPTIDASE_ACTIVITY	-0.89	0.19	0	0	0	not significant
6661	GO_CHROMATIN_REMODELING_AT_CENTROMERE	-0.89	0.19	0	0	0	not significant
6662	GO_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNAL	-0.89	0.19	0	0	0	not significant
6663	AMIT_EGF_RESPONSE_120_MCF10A	-0.89	0.18	0	0	0	not significant
6664	GAVIN_FOXP3_TARGETS_CLUSTER_P7	-0.89	0.18	0	0	0	not significant
6665	GO_REGULATION_OF_PROTEIN_TARGETING_TO_MITOCHONDRION	-0.89	0.18	0	0	0	not significant
6666	GO_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	-0.89	0.18	0	0	0	not significant
6667	NELSON_RESPONSE_TO_ANDROGEN_UP	-0.89	0.18	0	0	0	not significant
6668	ZHOU_TNF_SIGNALING_4HR	-0.89	0.18	0	0	0	not significant
6669	CADWELL_ATG16L1_TARGETS_DN	-0.89	0.17	0	0	0	not significant
6670	HILLION_HMGA1_TARGETS	-0.89	0.17	0	0	0	not significant
6671	GO_REGULATION_OF_FAT_CELL_DIFFERENTIATION	-0.89	0.16	0	0	0	not significant
6672	GO_CELLULAR_RESPONSE_TO_UV	-0.89	0.15	0	0	0	not significant
6673	GO_CLATHRIN_COATED_VESICLE_MEMBRANE	-0.89	0.15	0	0	0	not significant
6674	GO_UBIQUITIN_LIKE_PROTEIN_BINDING	-0.89	0.15	0	0	0	not significant
6675	GO_NEUROTRANSMITTER_TRANSPORT	-0.89	0.14	0	0	0	not significant
6676	GO_REGULATION_OF_DENDRITE_DEVELOPMENT	-0.89	0.14	0	0	0	not significant
6677	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_DN	-0.89	0.11	0	0	0	not significant
6678	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_B	-0.89	0.06	0	0	0	not significant
6679	GO_GTPASE_BINDING	-0.89	0.04	0	0	0	not significant
6680	GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION	-0.89	0.02	0	0	0	not significant
6681	GO_NUCLEOPLASM_PART	-0.89	0.00	0	0	0	not significant
6682	GO_RIBONUCLEOPROTEIN_COMPLEX_DISASSEMBLY	-0.88	0.24	0	0	0	not significant
6683	BIOCARTA_LAIR_PATHWAY	-0.88	0.23	0	0	0	not significant
6684	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_	-0.88	0.23	0	0	0	not significant
6685	RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP	-0.88	0.23	0	0	0	not significant
6686	WU_HBX_TARGETS_1_UP	-0.88	0.23	0	0	0	not significant
6687	GO_AMPA_GLUTAMATE_RECEPTOR_CLUSTERING	-0.88	0.22	0	0	0	not significant
6688	GO_COENZYME_A_METABOLIC_PROCESS	-0.88	0.22	0	0	0	not significant
6689	GO_HISTONE_PRE_MRNA_3_END_PROCESSING_COMPLEX	-0.88	0.22	0	0	0	not significant
6690	GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_KINASE_KINASE_BINDING	-0.88	0.22	0	0	0	not significant
6691	GO_O_ACETYLTRANSFERASE_ACTIVITY	-0.88	0.22	0	0	0	not significant
6692	GO_REGULATION_OF_SKELETAL_MUSCLE_FIBER_DEVELOPMENT	-0.88	0.22	0	0	0	not significant
6693	REACTOME_REGULATION_OF_PYRUVATE_DEHYDROGENASE_PDH_COM	-0.88	0.22	0	0	0	not significant
6694	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN	-0.88	0.21	0	0	0	not significant
6695	GO_ACETYLCHOLINE_RECEPTOR_ACTIVITY	-0.88	0.21	0	0	0	not significant
6696	GO_HISTONE_H2B_UBIQUITINATION	-0.88	0.21	0	0	0	not significant
6697	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH2_GROUP_O	-0.88	0.21	0	0	0	not significant
6698	GO_PERICARDIUM_DEVELOPMENT	-0.88	0.21	0	0	0	not significant
6699	GO_POSITIVE_REGULATION_OF_CELL_MIGRATION_BY_VASCULAR_END	-0.88	0.21	0	0	0	not significant
6700	GO_REGULATION_OF_NEUTROPHIL_MIGRATION	-0.88	0.21	0	0	0	not significant
6701	GO_TRICARBOXYLIC_ACID_METABOLIC_PROCESS	-0.88	0.21	0	0	0	not significant
6702	PID_HES_HEY_PATHWAY	-0.88	0.21	0	0	0	not significant
6703	GO_ARGININE_CATABOLIC_PROCESS	-0.88	0.20	0	0	0	not significant
6704	GO_CHAPERONE_MEDIATED_AUTOPHAGY	-0.88	0.20	0	0	0	not significant
6705	GO_NUCLEOTIDE_SUGAR_METABOLIC_PROCESS	-0.88	0.20	0	0	0	not significant
6706	GO_POSITIVE_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACT	-0.88	0.20	0	0	0	not significant
6707	GO_POSITIVE_REGULATION_OF_SYNAPSE_ASSEMBLY	-0.88	0.20	0	0	0	not significant
6708	REACTOME_INTERLEUKIN_37_SIGNALING	-0.88	0.20	0	0	0	not significant
6709	REACTOME_INTERLEUKIN_RECEPTOR_SHC_SIGNALING	-0.88	0.20	0	0	0	not significant
6710	SCHWAB_TARGETS_OF_BMYB_POLYMORPHIC_VARIANTS_UP	-0.88	0.20	0	0	0	not significant
6711	STEINER_ERYTHROCYTE_MEMBRANE_GENES	-0.88	0.20	0	0	0	not significant
6712	TSENG_ADIPOGENIC_POTENTIAL_UP	-0.88	0.20	0	0	0	not significant
6713	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_DN	-0.88	0.20	0	0	0	not significant
6714	ZHAN_VARIABLE_EARLY_DIFFERENTIATION_GENES_UP	-0.88	0.20	0	0	0	not significant
6715	GO_POSITIVE_REGULATION_OF_PROTEIN_EXPORT_FROM_NUCLEUS	-0.88	0.19	0	0	0	not significant
6716	GO_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	-0.88	0.19	0	0	0	not significant
6717	GO_SKELETAL_MUSCLE_ADAPTATION	-0.88	0.19	0	0	0	not significant
6718	JIANG_TIP30_TARGETS_UP	-0.88	0.19	0	0	0	not significant
6719	MARTIN_NFKB_TARGETS_UP	-0.88	0.19	0	0	0	not significant
6720	BURTON_ADIPOGENESIS_7	-0.88	0.18	0	0	0	not significant
6721	GO_ENDOCRINE_PROCESS	-0.88	0.18	0	0	0	not significant
6722	GO_MONONUCLEAR_CELL_DIFFERENTIATION	-0.88	0.18	0	0	0	not significant
6723	GO_NEGATIVE_REGULATION_OF_DNA_BINDING	-0.88	0.18	0	0	0	not significant
6724	GO_POLYOL_CATABOLIC_PROCESS	-0.88	0.18	0	0	0	not significant
6725	GO_PROTEIN_INSERTION_INTO_MEMBRANE	-0.88	0.18	0	0	0	not significant
6726	GO_SAGA_TYPE_COMPLEX	-0.88	0.18	0	0	0	not significant
6727	JIANG_AGING_HYPOTHALAMUS_DN	-0.88	0.18	0	0	0	not significant
6728	KAAB_FAILED_HEART_VENTRICLE_DN	-0.88	0.18	0	0	0	not significant
6729	PID_IGF1_PATHWAY	-0.88	0.18	0	0	0	not significant
6730	REACTOME_PLASMA_LIPOPROTEIN_ASSEMBLY_REMODELING_AND_CLE	-0.88	0.18	0	0	0	not significant
6731	BIOCARTA_EIF4_PATHWAY	-0.88	0.17	0	0	0	not significant
6732	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_DN	-0.88	0.17	0	0	0	not significant
6733	GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR	-0.88	0.16	0	0	0	not significant
6734	GO_REGULATION_OF_PROTEIN_IMPORT	-0.88	0.15	0	0	0	not significant
6735	BOUDOUKHA_BOUND_BY_IGF2BP2	-0.88	0.14	0	0	0	not significant
6736	GO_DEVELOPMENTAL_CELL_GROWTH	-0.88	0.12	0	0	0	not significant
6737	GO_ACETYLTRANSFERASE_ACTIVITY	-0.88	0.10	0	0	0	not significant
6738	ZHOU_INFLAMMATORY_RESPONSE_LIVE_DN	-0.88	0.06	0	0	0	not significant
6739	GO_CENTROSOME	-0.88	0.03	0	0	0	not significant
6740	GO_REGULATION_OF_MIRNA_METABOLIC_PROCESS	-0.87	0.23	0	0	0	not significant
6741	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY_INVOLVED_	-0.87	0.22	0	0	0	not significant
6742	GO_POSITIVE_REGULATION_OF_HEART_RATE	-0.87	0.22	0	0	0	not significant
6743	GO_REGULATION_OF_RENAL_SYSTEM_PROCESS	-0.87	0.22	0	0	0	not significant
6744	GO_RESPONSE_TO_MERCURY_ION	-0.87	0.22	0	0	0	not significant
6745	GO_UBIQUITIN_LIKE_MODIFIER_ACTIVATING_ENZYME_ACTIVITY	-0.87	0.22	0	0	0	not significant
6746	OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN	-0.87	0.22	0	0	0	not significant

6747	BIOCARTA_SODD_PATHWAY	-0.87	0.21	0	0	0	not significant
6748	GO_ACETYL_COA_BIOSYNTHETIC_PROCESS_FROM_PYRUVATE	-0.87	0.21	0	0	0	not significant
6749	GO_LIPOPROTEIN_LOCALIZATION	-0.87	0.21	0	0	0	not significant
6750	GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_CELL_DIFFERENTI	-0.87	0.21	0	0	0	not significant
6751	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_SECRETION	-0.87	0.21	0	0	0	not significant
6752	GO_PROTEIN_LOCALIZATION_TO_CELL_CORTEX	-0.87	0.21	0	0	0	not significant
6753	GO_REGULATION_OF_PRESYNAPTIC_CYTOSOLIC_CALCIUM_ION_CONCE	-0.87	0.21	0	0	0	not significant
6754	GO_REGULATION_OF_T_CIRCLE_FORMATION	-0.87	0.21	0	0	0	not significant
6755	GO_SUCKLING_BEHAVIOR	-0.87	0.21	0	0	0	not significant
6756	GO_SULFUR_AMINO_ACID_METABOLIC_PROCESS	-0.87	0.21	0	0	0	not significant
6757	GO_U6_SNRNP	-0.87	0.21	0	0	0	not significant
6758	VALK_AML_CLUSTER_1	-0.87	0.21	0	0	0	not significant
6759	YANAGIHARA_ESX1_TARGETS	-0.87	0.21	0	0	0	not significant
6760	GO_DEOXYRIBOSE_PHOSPHATE_CATABOLIC_PROCESS	-0.87	0.20	0	0	0	not significant
6761	GO_DOPAMINERGIC_NEURON_DIFFERENTIATION	-0.87	0.20	0	0	0	not significant
6762	GO_HEPATOCYTE_APOPTOTIC_PROCESS	-0.87	0.20	0	0	0	not significant
6763	GO_MYOBLAST_PROLIFERATION	-0.87	0.20	0	0	0	not significant
6764	GO_PLUS_END_DIRECTED_ORGANELLE_TRANSPORT_ALONG_MICROTU	-0.87	0.20	0	0	0	not significant
6765	GO_REGULATION_OF_ACTION_POTENTIAL	-0.87	0.20	0	0	0	not significant
6766	GO_THIOESTERASE_BINDING	-0.87	0.20	0	0	0	not significant
6767	GO_U1_SNRNA_BINDING	-0.87	0.20	0	0	0	not significant
6768	HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_UP	-0.87	0.20	0	0	0	not significant
6769	INAMURA_LUNG_CANCER_SCC_SUBTYPES_UP	-0.87	0.20	0	0	0	not significant
6770	BIOCARTA_NKCELLS_PATHWAY	-0.87	0.19	0	0	0	not significant
6771	BURTON_ADIPOGENESIS_1	-0.87	0.19	0	0	0	not significant
6772	GO_LIPOPROTEIN_CATABOLIC_PROCESS	-0.87	0.19	0	0	0	not significant
6773	GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTI	-0.87	0.19	0	0	0	not significant
6774	GO_REGULATION_OF_ANIMAL_ORGAN_FORMATION	-0.87	0.19	0	0	0	not significant
6775	GO_REGULATION_OF_NEUROBLAST_PROLIFERATION	-0.87	0.19	0	0	0	not significant
6776	REACTOME_GLYCOGEN_STORAGE_DISEASES	-0.87	0.19	0	0	0	not significant
6777	REACTOME_ROLE_OF_PHOSPHOLIPIDS_IN_PHAGOCYTOSIS	-0.87	0.19	0	0	0	not significant
6778	WANG_RESPONSE_TO_BEXAROTENE_DN	-0.87	0.19	0	0	0	not significant
6779	WENG_POR_TARGETS_GLOBAL_UP	-0.87	0.19	0	0	0	not significant
6780	YAP1_DN	-0.87	0.19	0	0	0	not significant
6781	GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMU	-0.87	0.18	0	0	0	not significant
6782	LIU_LIVER_CANCER	-0.87	0.18	0	0	0	not significant
6783	PARENT_MTOR_SIGNALING_DN	-0.87	0.18	0	0	0	not significant
6784	PARK_HSC_AND_MULTIPOTENT_PROGENITORS	-0.87	0.18	0	0	0	not significant
6785	PETROVA_PROX1_TARGETS_UP	-0.87	0.18	0	0	0	not significant
6786	REACTOME_PIWI_INTERACTING_RNA_PIRNA_BIOGENESIS	-0.87	0.18	0	0	0	not significant
6787	CHR8Q21	-0.87	0.17	0	0	0	not significant
6788	GO_CELLULAR_METABOLIC_COMPOUND_SALVAGE	-0.87	0.17	0	0	0	not significant
6789	GO_MRNA_5_UTR_BINDING	-0.87	0.17	0	0	0	not significant
6790	PID_ER_NONGENOMIC_PATHWAY	-0.87	0.17	0	0	0	not significant
6791	GUO_HEX_TARGETS_UP	-0.87	0.16	0	0	0	not significant
6792	LEE_TARGETS_OF_PTCH1_AND_SUFU_UP	-0.87	0.16	0	0	0	not significant
6793	GO_APICAL_JUNCTION_ASSEMBLY	-0.87	0.15	0	0	0	not significant
6794	GO_POSITIVE_REGULATION_OF_ENDOCYTOSIS	-0.87	0.15	0	0	0	not significant
6795	GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PAT	-0.87	0.15	0	0	0	not significant
6796	GO_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	-0.87	0.15	0	0	0	not significant
6797	REACTOME_AMYLOID_FIBER_FORMATION	-0.87	0.15	0	0	0	not significant
6798	ZHAN_MULTIPLE_MYELOMA_CD1_AND_CD2_DN	-0.87	0.15	0	0	0	not significant
6799	GO_CORTICAL_CYTOSKELETON	-0.87	0.14	0	0	0	not significant
6800	GO_RECYCLING_ENDOSOME_MEMBRANE	-0.87	0.14	0	0	0	not significant
6801	GO_SPLICEOSOMAL_COMPLEX_ASSEMBLY	-0.87	0.14	0	0	0	not significant
6802	GO_SYNAPTIC_VESICLE_EXOCYTOSIS	-0.87	0.14	0	0	0	not significant
6803	PRC1_BMI_UP.V1_DN	-0.87	0.14	0	0	0	not significant
6804	REACTOME_TOLL_LIKE_RECEPTOR_TLR1:TLR2_CASCADE	-0.87	0.14	0	0	0	not significant
6805	GO_ENSHEATHMENT_OF_NEURONS	-0.87	0.13	0	0	0	not significant
6806	GO_POSITIVE_REGULATION_OF_NEURON_DEATH	-0.87	0.13	0	0	0	not significant
6807	GO_EARLY_ENDOSOME_MEMBRANE	-0.87	0.12	0	0	0	not significant
6808	GO_CALCIUM_ION_REGULATED_EXOCYTOSIS	-0.87	0.11	0	0	0	not significant
6809	REACTOME_CLATHRIN_MEDIATED_ENDOCYTOSIS	-0.87	0.11	0	0	0	not significant
6810	GO_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS_IN_THE_VACUOL	-0.86	0.22	0	0	0	not significant
6811	RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_MAPK1_DN	-0.86	0.22	0	0	0	not significant
6812	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_UP	-0.86	0.21	0	0	0	not significant
6813	KOINUMA_COLON_CANCER_MSI_DN	-0.86	0.21	0	0	0	not significant
6814	MCMURRAY_TP53_HRAS_COOPERATION_RESPONSE_UP	-0.86	0.21	0	0	0	not significant
6815	BIOCARTA_VIP_PATHWAY	-0.86	0.20	0	0	0	not significant
6816	CHR9P21	-0.86	0.20	0	0	0	not significant
6817	DASU_IL6_SIGNALING_SCAR_DN	-0.86	0.20	0	0	0	not significant
6818	GO_CELLULAR_RESPONSE_TO_IRON_ION	-0.86	0.20	0	0	0	not significant
6819	GO_CYTOPLASMIC_SEQUESTERING_OF_NF_KAPPAB	-0.86	0.20	0	0	0	not significant
6820	GO_POSITIVE_REGULATION_BY_HOST_OF_VIRAL_TRANSCRIPTION	-0.86	0.20	0	0	0	not significant
6821	GO_POSITIVE_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	-0.86	0.20	0	0	0	not significant
6822	GO_POSITIVE_REGULATION_OF_AMINE_TRANSPORT	-0.86	0.20	0	0	0	not significant
6823	GO_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	-0.86	0.20	0	0	0	not significant
6824	STEGMEIER_PREMITOTIC_CELL_CYCLE_REGULATORS	-0.86	0.20	0	0	0	not significant
6825	GO_ATPASE_ACTIVATOR_ACTIVITY	-0.86	0.19	0	0	0	not significant
6826	GO_CD95_DEATH_INDUCING_SIGNALING_COMPLEX	-0.86	0.19	0	0	0	not significant
6827	GO_ENDOPLASMIC_RETICULUM_SUBCOMPARTMENT	-0.86	0.19	0	0	0	not significant
6828	GO_FEMALE_PRONUCLEUS	-0.86	0.19	0	0	0	not significant
6829	GO_NEGATIVE_REGULATION_OF_HISTONE_ACETYLATION	-0.86	0.19	0	0	0	not significant
6830	GO_NEUROTRANSMITTER_UPTAKE	-0.86	0.19	0	0	0	not significant
6831	GO_NUCLEAR_TRANSCRIPTIONAL_REPRESSOR_COMPLEX	-0.86	0.19	0	0	0	not significant
6832	GO_PROTEIN_LOCALIZATION_TO_MICROTUBULE	-0.86	0.19	0	0	0	not significant
6833	GO_RESPONSE_TO_HYDROPEROXIDE	-0.86	0.19	0	0	0	not significant
6834	MARKS_ACETYLATED_NON_HISTONE_PROTEINS	-0.86	0.19	0	0	0	not significant
6835	ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_DN	-0.86	0.19	0	0	0	not significant
6836	GO_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_BINDING	-0.86	0.18	0	0	0	not significant
6837	GO_EPSILON_DNA_POLYMERASE_COMPLEX	-0.86	0.18	0	0	0	not significant
6838	GO_FERRIC_IRON_BINDING	-0.86	0.18	0	0	0	not significant
6839	GO_G_QUADRUPLEX_DNA_UNWINDING	-0.86	0.18	0	0	0	not significant
6840	GO_MITOTIC_SPINDLE_MIDZONE	-0.86	0.18	0	0	0	not significant
6841	GO_OLIGOSACCHARYLTRANSFERASE_COMPLEX	-0.86	0.18	0	0	0	not significant
6842	GO_PHOSPHATIDYLINOSITOL_3_KINASE_REGULATOR_ACTIVITY	-0.86	0.18	0	0	0	not significant
6843	GO_REGULATION_OF_HISTONE_H3_K36_METHYLATION	-0.86	0.18	0	0	0	not significant
6844	GO_REGULATION_OF_NEURON_MIGRATION	-0.86	0.18	0	0	0	not significant
6845	GO_REGULATION_OF_RHODOPSIN_MEDIATED_SIGNALING_PATHWAY	-0.86	0.18	0	0	0	not significant
6846	MIKKELSEN_NPC_LCP_WITH_H3K4ME3	-0.86	0.18	0	0	0	not significant
6847	SHI_SPARC_TARGETS_UP	-0.86	0.18	0	0	0	not significant
6848	CHR16Q23	-0.86	0.17	0	0	0	not significant
6849	CHR1Q31	-0.86	0.17	0	0	0	not significant
6850	CHR5Q11	-0.86	0.17	0	0	0	not significant
6851	GO_ENDOPLASMIC_RETICULUM_CALCIUM_ION_HOMEOSTASIS	-0.86	0.17	0	0	0	not significant
6852	GO_IRES_DEPENDENT_VIRAL_TRANSLATIONAL_INITIATION	-0.86	0.17	0	0	0	not significant
6853	GO_LABYRINTHINE_LAYER_DEVELOPMENT	-0.86	0.17	0	0	0	not significant
6854	GO_PRE_MRNA_BINDING	-0.86	0.17	0	0	0	not significant
6855	KEGG_REGULATION_OF_AUTOPHAGY	-0.86	0.17	0	0	0	not significant

6856	MATZUK_CENTRAL_FOR_FEMALE_FERTILITY	-0.86	0.17	0	0	0	not significant
6857	QI_HYPOXIA_TARGETS_OF_HIF1A_AND_FOXA2	-0.86	0.17	0	0	0	not significant
6858	BIOCARTA_P38MAPK_PATHWAY	-0.86	0.16	0	0	0	not significant
6859	CHR2Q24	-0.86	0.16	0	0	0	not significant
6860	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREEN_DN	-0.86	0.16	0	0	0	not significant
6861	GO_KINETOCHORE_ORGANIZATION	-0.86	0.16	0	0	0	not significant
6862	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	-0.86	0.16	0	0	0	not significant
6863	LEE_LIVER_CANCER_ACOX1_UP	-0.86	0.16	0	0	0	not significant
6864	GO_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	-0.86	0.15	0	0	0	not significant
6865	AMIT_SERUM_RESPONSE_120_MCF10A	-0.86	0.14	0	0	0	not significant
6866	GO_REGULATION_OF_CENTROSOME_CYCLE	-0.86	0.14	0	0	0	not significant
6867	GO_REGULATION_OF_RESPONSE_TO_DRUG	-0.86	0.14	0	0	0	not significant
6868	MILI_PSEUDOPODIA	-0.86	0.14	0	0	0	not significant
6869	PID_FAK_PATHWAY	-0.86	0.14	0	0	0	not significant
6870	REACTOME_FOXO_MEDIATED_TRANSCRIPTION	-0.86	0.14	0	0	0	not significant
6871	LIU_COMMON_CANCER_GENES	-0.86	0.13	0	0	0	not significant
6872	REACTOME_STIMULI_SENSING_CHANNELS	-0.86	0.13	0	0	0	not significant
6873	GO_POSITIVE_REGULATION_OF_ORGANELLE_ASSEMBLY	-0.86	0.12	0	0	0	not significant
6874	REACTOME_MYD88_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	-0.86	0.11	0	0	0	not significant
6875	GO_TUBE_FORMATION	-0.86	0.10	0	0	0	not significant
6876	MCBRYAN_PUBERTAL_TGFB1_TARGETS_UP	-0.86	0.10	0	0	0	not significant
6877	GO_HORMONE_MEDIATED_SIGNALING_PATHWAY	-0.86	0.09	0	0	0	not significant
6878	KAYO_AGING_MUSCLE_DN	-0.86	0.09	0	0	0	not significant
6879	MCBRYAN_PUBERTAL_BREAST_6_7WK_UP	-0.86	0.09	0	0	0	not significant
6880	GO_NUCLEASE_ACTIVITY	-0.86	0.08	0	0	0	not significant
6881	GO_GLYCEROLIPID_BIOSYNTHETIC_PROCESS	-0.86	0.07	0	0	0	not significant
6882	GO_NUCLEAR_CHROMATIN	-0.86	0.04	0	0	0	not significant
6883	GO_REGULATION_OF_MAPK_CASCADE	-0.86	0.04	0	0	0	not significant
6884	GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY_PHOSPHOTRANSFERA	-0.85	0.22	0	0	0	not significant
6885	GO_IRON_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.85	0.20	0	0	0	not significant
6886	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYT	-0.85	0.20	0	0	0	not significant
6887	GO_POSITIVE_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	-0.85	0.20	0	0	0	not significant
6888	GO_REGULATION_OF_NEUROINFLAMMATORY_RESPONSE	-0.85	0.20	0	0	0	not significant
6889	REACTOME_NOREPINEPHRINE_NEUROTRANSMITTER_RELEASE_CYCLE	-0.85	0.20	0	0	0	not significant
6890	REACTOME_SYNTHESIS_OF_PIPS_AT_THE_GOLGI_MEMBRANE	-0.85	0.20	0	0	0	not significant
6891	REACTOME_TRISTETRAPROLIN_TTP_ZFP36_BINDS_AND_DESTABILIZES_	-0.85	0.20	0	0	0	not significant
6892	GO_3_HYDROXYACYL_COA_DEHYDROGENASE_ACTIVITY	-0.85	0.19	0	0	0	not significant
6893	GO_MALE_MATING_BEHAVIOR	-0.85	0.19	0	0	0	not significant
6894	GO_METANEPHRIC_NEPHRON_EPITHELIUM_DEVELOPMENT	-0.85	0.19	0	0	0	not significant
6895	GO_MUTLALPHA_COMPLEX_BINDING	-0.85	0.19	0	0	0	not significant
6896	GO_NEGATIVE_REGULATION_OF_ANDROGEN_RECEPTOR_SIGNALING_P	-0.85	0.19	0	0	0	not significant
6897	GO_NEGATIVE_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTR	-0.85	0.19	0	0	0	not significant
6898	GO_PROTEIN_MEMBRANE_ANCHOR	-0.85	0.19	0	0	0	not significant
6899	GO_RAGULATOR_COMPLEX	-0.85	0.19	0	0	0	not significant
6900	MURAKAMI_UV_RESPONSE_1HR_DN	-0.85	0.19	0	0	0	not significant
6901	REACTOME_HEME_BIOSYNTHESIS	-0.85	0.19	0	0	0	not significant
6902	GO_BETA_CATENIN_TCF_COMPLEX	-0.85	0.18	0	0	0	not significant
6903	GO_CATALYTIC_STEP_1_SPLICEOSOME	-0.85	0.18	0	0	0	not significant
6904	GO_DEATH_INDUCING_SIGNALING_COMPLEX	-0.85	0.18	0	0	0	not significant
6905	GO_NEGATIVE_REGULATION_OF_ANOIKIS	-0.85	0.18	0	0	0	not significant
6906	GO_NEGATIVE_REGULATION_OF_CARDIOCYTE_DIFFERENTIATION	-0.85	0.18	0	0	0	not significant
6907	GO_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	-0.85	0.18	0	0	0	not significant
6908	GO_REGULATION_OF_THYMOCYTE_APOPTOTIC_PROCESS	-0.85	0.18	0	0	0	not significant
6909	REACTOME_ACTIVATION_OF_MATRIX_METALLOPROTEINASES	-0.85	0.18	0	0	0	not significant
6910	REACTOME_DEFECTS_IN_BIOTIN_BTN_METABOLISM	-0.85	0.18	0	0	0	not significant
6911	REACTOME_HS_GAG_BIOSYNTHESIS	-0.85	0.18	0	0	0	not significant
6912	REACTOME_RAF_INDEPENDENT_MAPK1_3_ACTIVATION	-0.85	0.18	0	0	0	not significant
6913	SA_B_CELL_RECEPTOR_COMPLEXES	-0.85	0.18	0	0	0	not significant
6914	YIH_RESPONSE_TO_ARSENITE_C2	-0.85	0.18	0	0	0	not significant
6915	CUI_TCF21_TARGETS_DN	-0.85	0.17	0	0	0	not significant
6916	GO_FEAR_RESPONSE	-0.85	0.17	0	0	0	not significant
6917	GO_NEGATIVE_REGULATION_OF_JNK_CASCADE	-0.85	0.17	0	0	0	not significant
6918	GO_NEURON_PROJECTION_EXTENSION_INVOLVED_IN_NEURON_PROJEC	-0.85	0.17	0	0	0	not significant
6919	GO_OOCYTE_MATURATION	-0.85	0.17	0	0	0	not significant
6920	GO_PROTEIN_PHOSPHATASE_TYPE_1_COMPLEX	-0.85	0.17	0	0	0	not significant
6921	GO_TRANSFERRIN_TRANSPORT	-0.85	0.17	0	0	0	not significant
6922	GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_BINDING	-0.85	0.17	0	0	0	not significant
6923	REACTOME_AKT_PHOSPHORYLATES_TARGETS_IN_THE_NUCLEUS	-0.85	0.17	0	0	0	not significant
6924	GO_MODIFICATION_OF_SYNAPTIC_STRUCTURE	-0.85	0.16	0	0	0	not significant
6925	GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIA	-0.85	0.16	0	0	0	not significant
6926	LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_SMALL_VS_HUGE_DN	-0.85	0.16	0	0	0	not significant
6927	PID_MYC_PATHWAY	-0.85	0.16	0	0	0	not significant
6928	REACTOME_ELEVATION_OF_CYTOSOLIC_CA2PLUS_LEVELS	-0.85	0.16	0	0	0	not significant
6929	GO_ATP_METABOLIC_PROCESS	-0.85	0.15	0	0	0	not significant
6930	GO_ZINC_ION_TRANSMEMBRANE_TRANSPORT	-0.85	0.15	0	0	0	not significant
6931	LEE_TARGETS_OF_PTCH1_AND_SUFU_DN	-0.85	0.15	0	0	0	not significant
6932	REACTOME_TRANSLESION_SYNTHESIS_BY_Y_FAMILY_DNA_POLYMERAS	-0.85	0.15	0	0	0	not significant
6933	GENTILE_UV_RESPONSE_CLUSTER_D8	-0.85	0.14	0	0	0	not significant
6934	GO_MATERNAL_PROCESS_INVOLVED_IN_FEMALE_PREGNANCY	-0.85	0.14	0	0	0	not significant
6935	GO_MONOSACCHARIDE_CATABOLIC_PROCESS	-0.85	0.14	0	0	0	not significant
6936	GO_MYOBLAST_DIFFERENTIATION	-0.85	0.14	0	0	0	not significant
6937	GO_SMOOTH_MUSCLE_CELL_MIGRATION	-0.85	0.14	0	0	0	not significant
6938	KENNY_CTNNB1_TARGETS_DN	-0.85	0.14	0	0	0	not significant
6939	MAHAJAN_RESPONSE_TO_IL1A_DN	-0.85	0.14	0	0	0	not significant
6940	GO_BLASTOCYST_FORMATION	-0.85	0.13	0	0	0	not significant
6941	GO_REGULATION_OF_TORC1_SIGNALING	-0.85	0.13	0	0	0	not significant
6942	GO_NEGATIVE_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT	-0.85	0.12	0	0	0	not significant
6943	GO_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	-0.85	0.12	0	0	0	not significant
6944	GO_SWI_SNF_SUPERFAMILY_TYPE_COMPLEX	-0.85	0.12	0	0	0	not significant
6945	GO_NEUTRAL_LIPID_METABOLIC_PROCESS	-0.85	0.11	0	0	0	not significant
6946	GO_P53_BINDING	-0.85	0.11	0	0	0	not significant
6947	GO_CEREBRAL_CORTEX_DEVELOPMENT	-0.85	0.10	0	0	0	not significant
6948	PID_HDAC_CLASSI_PATHWAY	-0.85	0.10	0	0	0	not significant
6949	GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	-0.85	0.08	0	0	0	not significant
6950	GO_MICROTUBULE_BASED_MOVEMENT	-0.85	0.05	0	0	0	not significant
6951	LINSLEY_MIR16_TARGETS	-0.85	0.04	0	0	0	not significant
6952	PUJANA_BRCA2_PCC_NETWORK	-0.85	0.02	0	0	0	not significant
6953	GO_REGULATION_OF_GTPASE_ACTIVITY	-0.85	0.01	0	0	0	not significant
6954	GO_CELLULAR_RESPONSE_TO_DNA_DAMAGE_STIMULUS	-0.85	0.00	0	0	0	not significant
6955	GO_CHROMATIN	-0.85	0.00	0	0	0	not significant
6956	NADERI_BREAST_CANCER_PROGNOSIS_DN	-0.84	0.20	0	0	0	not significant
6957	GO_DISTAL_TUBULE_DEVELOPMENT	-0.84	0.19	0	0	0	not significant
6958	GO_ENDORIBONUCLEASE_ACTIVITY_PRODUCING_3_PHOSPHOMONOEST	-0.84	0.19	0	0	0	not significant
6959	GO_ER_OVERLOAD_RESPONSE	-0.84	0.19	0	0	0	not significant
6960	GO_GALACTOSE_METABOLIC_PROCESS	-0.84	0.19	0	0	0	not significant
6961	GO_MACROPINOCYTOSIS	-0.84	0.19	0	0	0	not significant
6962	GO_NEGATIVE_REGULATION_OF_PRI_MIRNA_TRANSCRIPTION_BY_RNA_	-0.84	0.19	0	0	0	not significant
6963	REACTOME_METHIONINE_SALVAGE_PATHWAY	-0.84	0.19	0	0	0	not significant
6964	REACTOME_SYNTHESIS_OF_GDP_MANNOSE	-0.84	0.19	0	0	0	not significant

6965	REACTOME_SYNTHESIS_OF_PIPS_AT_THE_ER_MEMBRANE	-0.84	0.19	0	0	0	not significant
6966	BIOCARTA_PKC_PATHWAY	-0.84	0.18	0	0	0	not significant
6967	BRUNEAU_SEPTATION_VENTRICULAR	-0.84	0.18	0	0	0	not significant
6968	GO_EXTRACELLULAR_MATRIX_ASSEMBLY	-0.84	0.18	0	0	0	not significant
6969	GO_MAINTENANCE_OF_PROTEIN_LOCALIZATION_IN_ENDOPLASMIC_RET	-0.84	0.18	0	0	0	not significant
6970	GO_MICROTUBULE_SEVERING	-0.84	0.18	0	0	0	not significant
6971	GO_PHOSPHATIDYLGLYCEROL_BIOSYNTHETIC_PROCESS	-0.84	0.18	0	0	0	not significant
6972	GO_POSITIVE_REGULATION_OF_AMINO_ACID_TRANSPORT	-0.84	0.18	0	0	0	not significant
6973	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_	-0.84	0.18	0	0	0	not significant
6974	PID_SYNDECAN_4_PATHWAY	-0.84	0.18	0	0	0	not significant
6975	REACTOME_SUMO_IS_CONJUGATED_TO_E1_UBA2:SAE1	-0.84	0.18	0	0	0	not significant
6976	GO_ACTIVATION_OF_MAPKKK_ACTIVITY	-0.84	0.17	0	0	0	not significant
6977	GO_CILIARY_BASE	-0.84	0.17	0	0	0	not significant
6978	GO_FAT_SOLUBLE_VITAMIN_BIOSYNTHETIC_PROCESS	-0.84	0.17	0	0	0	not significant
6979	GO_MIDBODY_ABSCISSION	-0.84	0.17	0	0	0	not significant
6980	GO_N_TERMINAL_PROTEIN_AMINO_ACID_ACETYLATION	-0.84	0.17	0	0	0	not significant
6981	GO_TRANSLOCON_COMPLEX	-0.84	0.17	0	0	0	not significant
6982	HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_DN	-0.84	0.17	0	0	0	not significant
6983	KIM_MYCL1_AMPLIFICATION_TARGETS_DN	-0.84	0.17	0	0	0	not significant
6984	PID_NETRIN_PATHWAY	-0.84	0.17	0	0	0	not significant
6985	WIKMAN_ASBESTOS_LUNG_CANCER_DN	-0.84	0.17	0	0	0	not significant
6986	GO_3_UTR_MEDIATED_MRNA_STABILIZATION	-0.84	0.16	0	0	0	not significant
6987	GO_FOREBRAIN_GENERATION_OF_NEURONS	-0.84	0.16	0	0	0	not significant
6988	GO_PHOSPHATIDYLINOSITOL_3_5_BISPHOSPHATE_BINDING	-0.84	0.16	0	0	0	not significant
6989	GO_SERINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	-0.84	0.16	0	0	0	not significant
6990	REACTOME_SIGNALING_BY_EGFRVIII_IN_CANCER	-0.84	0.16	0	0	0	not significant
6991	GO_ATP_HYDROLYSIS_COUPLED_TRANSMEMBRANE_TRANSPORT	-0.84	0.15	0	0	0	not significant
6992	KEGG_MISMATCH_REPAIR	-0.84	0.15	0	0	0	not significant
6993	OZEN_MIR125B1_TARGETS	-0.84	0.15	0	0	0	not significant
6994	REACTOME_BBSOME_MEDIATED_CARGO_TARGETING_TO_CILIUM	-0.84	0.15	0	0	0	not significant
6995	CHR15Q24	-0.84	0.14	0	0	0	not significant
6996	GO_CYCLIN_BINDING	-0.84	0.14	0	0	0	not significant
6997	GO_NEGATIVE_REGULATION_OF_CELL_MATRIX_ADHESION	-0.84	0.14	0	0	0	not significant
6998	LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_DN	-0.84	0.14	0	0	0	not significant
6999	WIEDERSCHAIN_TARGETS_OF_BMI1_AND_PCGF2	-0.84	0.14	0	0	0	not significant
7000	BOYLAN_MULTIPLE_MYELOMA_C_CLUSTER_UP	-0.84	0.13	0	0	0	not significant
7001	GO_INTERCELLULAR_BRIDGE	-0.84	0.13	0	0	0	not significant
7002	NIKOLSKY_BREAST_CANCER_20Q11_AMPLICON	-0.84	0.13	0	0	0	not significant
7003	WOO_LIVER_CANCER_RECURRENCE_DN	-0.84	0.13	0	0	0	not significant
7004	DUTTA_APOPTOSIS_VIA_NFKB	-0.84	0.12	0	0	0	not significant
7005	GO_MANGANESE_ION_BINDING	-0.84	0.12	0	0	0	not significant
7006	GO_REGULATION_OF_BMP_SIGNALING_PATHWAY	-0.84	0.12	0	0	0	not significant
7007	NABA_ECM_REGULATORS	-0.84	0.12	0	0	0	not significant
7008	GO_GLAND_MORPHOGENESIS	-0.84	0.11	0	0	0	not significant
7009	GO_METENCEPHALON_DEVELOPMENT	-0.84	0.11	0	0	0	not significant
7010	LE_EGR2_TARGETS_DN	-0.84	0.11	0	0	0	not significant
7011	SIG_PIP3_SIGNALING_IN_CARDIAC_MYOCTES	-0.84	0.11	0	0	0	not significant
7012	GO_HISTONE_DEACETYLASE_COMPLEX	-0.84	0.10	0	0	0	not significant
7013	GO_METALLOPEPTIDASE_ACTIVITY	-0.84	0.10	0	0	0	not significant
7014	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_	-0.84	0.10	0	0	0	not significant
7015	GO_REGULATION_OF_DNA_BINDING	-0.84	0.08	0	0	0	not significant
7016	REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	-0.84	0.08	0	0	0	not significant
7017	GO_CHROMATIN_ASSEMBLY	-0.84	0.07	0	0	0	not significant
7018	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_WITH_H4K20ME1_	-0.84	0.07	0	0	0	not significant
7019	REACTOME_HOMOLOGY_DIRECTED_REPAIR	-0.84	0.06	0	0	0	not significant
7020	GO_INTRACELLULAR_RECEPTOR_SIGNALING_PATHWAY	-0.84	0.03	0	0	0	not significant
7021	GO_DNA_REPAIR	-0.84	0.01	0	0	0	not significant
7022	WAKABAYASHI_ADIPOGENESIS_PPARG_BOUND_8D	-0.84	0.01	0	0	0	not significant
7023	GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_F	-0.84	0.00	0	0	0	not significant
7024	GO_CELLULAR_RESPONSE_TO_NITROSATIVE_STRESS	-0.83	0.19	0	0	0	not significant
7025	GO_GATOR1_COMPLEX	-0.83	0.19	0	0	0	not significant
7026	GO_CELL_TRAILING_EDGE	-0.83	0.18	0	0	0	not significant
7027	GO_CELLULAR_RESPONSE_TO_ACIDIC_PH	-0.83	0.18	0	0	0	not significant
7028	GO_REGULATION_OF_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	-0.83	0.18	0	0	0	not significant
7029	GO_TRAIL_ACTIVATED_APOPTOTIC_SIGNALING_PATHWAY	-0.83	0.18	0	0	0	not significant
7030	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_5	-0.83	0.18	0	0	0	not significant
7031	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_DEATH_RECEPTOF	-0.83	0.18	0	0	0	not significant
7032	STEGMEIER_PRE-MITOTIC_CELL_CYCLE_REGULATORS	-0.83	0.18	0	0	0	not significant
7033	BIOCARTA_MAL_PATHWAY	-0.83	0.17	0	0	0	not significant
7034	DAZARD_UV_RESPONSE_CLUSTER_G5	-0.83	0.17	0	0	0	not significant
7035	GO_EGO_COMPLEX	-0.83	0.17	0	0	0	not significant
7036	GO_NEGATIVE_REGULATION_OF_EPIDERMIS_DEVELOPMENT	-0.83	0.17	0	0	0	not significant
7037	GO_PEPTIDYL_LYSINE_MONOMETHYLATION	-0.83	0.17	0	0	0	not significant
7038	GO_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX_CLASS_I	-0.83	0.17	0	0	0	not significant
7039	GO_POSITIVE_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIG	-0.83	0.17	0	0	0	not significant
7040	GO_POSITIVE_REGULATION_OF_MEIOTIC_CELL_CYCLE	-0.83	0.17	0	0	0	not significant
7041	GO_POSITIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	-0.83	0.17	0	0	0	not significant
7042	GO_REGULATION_OF_DEACETYLASE_ACTIVITY	-0.83	0.17	0	0	0	not significant
7043	GO_REGULATION_OF_PROTEIN_KINASE_C_SIGNALING	-0.83	0.17	0	0	0	not significant
7044	GO_SEQUENCE_SPECIFIC_SINGLE_STRANDED_DNA_BINDING	-0.83	0.17	0	0	0	not significant
7045	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_DN	-0.83	0.17	0	0	0	not significant
7046	REACTOME_ENDOSOMAL_VACUOLAR_PATHWAY	-0.83	0.17	0	0	0	not significant
7047	REACTOME_HYALURONAN_UPTAKE_AND_DEGRADATION	-0.83	0.17	0	0	0	not significant
7048	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED	-0.83	0.17	0	0	0	not significant
7049	CHR12Q15	-0.83	0.16	0	0	0	not significant
7050	GO_ENDOPLASMIC_RETICULUM_EXIT_SITE	-0.83	0.16	0	0	0	not significant
7051	GO_PTERIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-0.83	0.16	0	0	0	not significant
7052	GO_RAC_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	-0.83	0.16	0	0	0	not significant
7053	GO_REGULATION_OF_CHOLESTEROL_EFFLUX	-0.83	0.16	0	0	0	not significant
7054	GO_RESOLUTION_OF_MEIOTIC_RECOMBINATION_INTERMEDIATES	-0.83	0.16	0	0	0	not significant
7055	GO_RRNA_CATABOLIC_PROCESS	-0.83	0.16	0	0	0	not significant
7056	GO_VERY_LOW_DENSITY_LIPOPROTEIN_PARTICLE_ASSEMBLY	-0.83	0.16	0	0	0	not significant
7057	NAGY_TFTC_COMPONENTS_HUMAN	-0.83	0.16	0	0	0	not significant
7058	REACTOME_CYTOCHROME_C_MEDIATED_APOPTOTIC_RESPONSE	-0.83	0.16	0	0	0	not significant
7059	REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	-0.83	0.16	0	0	0	not significant
7060	REACTOME_SEROTONIN_NEUROTRANSMITTER_RELEASE_CYCLE	-0.83	0.16	0	0	0	not significant
7061	FOURNIER_ACINAR_DEVELOPMENT_EARLY_UP	-0.83	0.15	0	0	0	not significant
7062	GO_POSITIVE_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	-0.83	0.15	0	0	0	not significant
7063	GO_POSITIVE_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	-0.83	0.15	0	0	0	not significant
7064	GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	-0.83	0.15	0	0	0	not significant
7065	GO_REGULATION_OF_EXTRACELLULAR_MATRIX_DISASSEMBLY	-0.83	0.15	0	0	0	not significant
7066	GO_REGULATION_OF_MYOBLAST_DIFFERENTIATION	-0.83	0.15	0	0	0	not significant
7067	GO_REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	-0.83	0.15	0	0	0	not significant
7068	PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_DN	-0.83	0.15	0	0	0	not significant
7069	SIMBULAN_UV_RESPONSE_NORMAL_DN	-0.83	0.15	0	0	0	not significant
7070	BIOCARTA_HSP27_PATHWAY	-0.83	0.14	0	0	0	not significant
7071	GO_HISTONE_H2A_ACETYLATION	-0.83	0.14	0	0	0	not significant
7072	GO_PRODUCTION_OF_SMALL_RNA_INVOLVED_IN_GENE_SILENCING_BY_	-0.83	0.14	0	0	0	not significant
7073	CHR4Q31	-0.83	0.13	0	0	0	not significant

7074	GO_MODULATION_OF_TRANSCRIPTION_IN_OTHER_ORGANISM_INVOLVE	-0.83	0.13	0	0	0	not significant
7075	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	-0.83	0.13	0	0	0	not significant
7076	GO_OVULATION_CYCLE_PROCESS	-0.83	0.13	0	0	0	not significant
7077	GO_POSITIVE_REGULATION_OF_ANION_TRANSPORT	-0.83	0.13	0	0	0	not significant
7078	GO_REGULATION_OF_HISTONE_H4_ACETYLATION	-0.83	0.13	0	0	0	not significant
7079	PID_FOXO_PATHWAY	-0.83	0.13	0	0	0	not significant
7080	GO_PHOSPHATIDYLINOSITOL_4_5_BISPHOSPHATE_BINDING	-0.83	0.12	0	0	0	not significant
7081	GO_POSITIVE_REGULATION_OF_MEMBRANE_PERMEABILITY	-0.83	0.12	0	0	0	not significant
7082	GO_TETHERING_COMPLEX	-0.83	0.12	0	0	0	not significant
7083	PID_ERBB2_ERBB3_PATHWAY	-0.83	0.12	0	0	0	not significant
7084	GO_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNALING_PATHWAY	-0.83	0.11	0	0	0	not significant
7085	WENG_POR_TARGETS_LIVER_UP	-0.83	0.11	0	0	0	not significant
7086	GO_CILIARY_TRANSITION_ZONE	-0.83	0.10	0	0	0	not significant
7087	GO_EXONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYR	-0.83	0.10	0	0	0	not significant
7088	HALLMARK_ANDROGEN_RESPONSE	-0.83	0.10	0	0	0	not significant
7089	HOEBEKE_LYMPHOID_STEM_CELL_UP	-0.83	0.10	0	0	0	not significant
7090	DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_DN	-0.83	0.09	0	0	0	not significant
7091	GO_MACROMOLECULE_DEACYLATION	-0.83	0.09	0	0	0	not significant
7092	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	-0.83	0.09	0	0	0	not significant
7093	IKEDA_MIR30_TARGETS_UP	-0.83	0.08	0	0	0	not significant
7094	REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	-0.83	0.08	0	0	0	not significant
7095	GO_TRANSITION_METAL_ION_TRANSPORT	-0.83	0.07	0	0	0	not significant
7096	GO_UBIQUITIN_LIKE_PROTEIN_SPECIFIC_PROTEASE_ACTIVITY	-0.83	0.07	0	0	0	not significant
7097	GO_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	-0.83	0.06	0	0	0	not significant
7098	GO_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PR	-0.83	0.06	0	0	0	not significant
7099	BENPORATH_OCT4_TARGETS	-0.83	0.04	0	0	0	not significant
7100	CHR12Q24	-0.83	0.03	0	0	0	not significant
7101	GO_ALDEHYDE_CATABOLIC_PROCESS	-0.82	0.18	0	0	0	not significant
7102	GO_PARASPECKLES	-0.82	0.18	0	0	0	not significant
7103	GO_PROGRAMMED_CELL_DEATH_IN_RESPONSE_TO_REACTIVE_OXYGE	-0.82	0.18	0	0	0	not significant
7104	CHR16Q11	-0.82	0.17	0	0	0	not significant
7105	GO_MEMBRANOUS_SEPTUM_MORPHOGENESIS	-0.82	0.17	0	0	0	not significant
7106	GO_NEGATIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_F	-0.82	0.17	0	0	0	not significant
7107	GO_SPERM_CAPACITATION	-0.82	0.17	0	0	0	not significant
7108	HINATA_NFKB_TARGETS_KERATINOCYTE_DN	-0.82	0.17	0	0	0	not significant
7109	GO_ACTIVATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	-0.82	0.16	0	0	0	not significant
7110	GO_HYALURONAN_CATABOLIC_PROCESS	-0.82	0.16	0	0	0	not significant
7111	GO_INNER_CELL_MASS_CELL_PROLIFERATION	-0.82	0.16	0	0	0	not significant
7112	GO_MEMBRANE_REPOLARIZATION_DURING_ACTION_POTENTIAL	-0.82	0.16	0	0	0	not significant
7113	GO_MITOTIC_CELL_CYCLE_ARREST	-0.82	0.16	0	0	0	not significant
7114	GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PA	-0.82	0.16	0	0	0	not significant
7115	GO_PARTURITION	-0.82	0.16	0	0	0	not significant
7116	GO_PHOSPHORYLASE_ACTIVITY	-0.82	0.16	0	0	0	not significant
7117	GO_REGULATION_OF_AMINO_ACID_IMPORT_ACROSS_PLASMA_MEMBRA	-0.82	0.16	0	0	0	not significant
7118	GO_REGULATION_OF_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWA	-0.82	0.16	0	0	0	not significant
7119	GO_RESPONSE_TO_FOLLICLE_STIMULATING_HORMONE	-0.82	0.16	0	0	0	not significant
7120	GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_III_PROMOT	-0.82	0.16	0	0	0	not significant
7121	GO_TYPE_I_INTERFERON_SECRETION	-0.82	0.16	0	0	0	not significant
7122	GO_WALKING_BEHAVIOR	-0.82	0.16	0	0	0	not significant
7123	LI_CYTIDINE_ANALOGS_CYCTOTOXICITY	-0.82	0.16	0	0	0	not significant
7124	LUND_SILENCED_BY_METHYLATION	-0.82	0.16	0	0	0	not significant
7125	REACTOME_BETA_OXIDATION_OF_DECANOYL_COA_TO_OCTANOYL_CC	-0.82	0.16	0	0	0	not significant
7126	SA_FAS_SIGNALING	-0.82	0.16	0	0	0	not significant
7127	BIOCARTA_SPPA_PATHWAY	-0.82	0.15	0	0	0	not significant
7128	GO_ANDROGEN_METABOLIC_PROCESS	-0.82	0.15	0	0	0	not significant
7129	GO_APOLIPOPROTEIN_BINDING	-0.82	0.15	0	0	0	not significant
7130	GO_CELLULAR_RESPONSE_TO_FOLLICLE_STIMULATING_HORMONE_ST	-0.82	0.15	0	0	0	not significant
7131	GO_CELLULAR_RESPONSE_TO_LIPOPROTEIN_PARTICLE_STIMULUS	-0.82	0.15	0	0	0	not significant
7132	GO_LATERAL_VENTRICLE_DEVELOPMENT	-0.82	0.15	0	0	0	not significant
7133	GO_PHOSPHATIDYLINOSITOL_3_5_BISPHOSPHATE_3_PHOSPHATASE_AC	-0.82	0.15	0	0	0	not significant
7134	GO_POSTSYNAPTIC_ENDOCYTIC_ZONE	-0.82	0.15	0	0	0	not significant
7135	REACTOME_SYNTHESIS_OF_PA	-0.82	0.15	0	0	0	not significant
7136	RICKMAN_HEAD_AND_NECK_CANCER_B	-0.82	0.15	0	0	0	not significant
7137	BIOCARTA_HSWI_SNF_PATHWAY	-0.82	0.14	0	0	0	not significant
7138	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_DN	-0.82	0.14	0	0	0	not significant
7139	GO_BILE_ACID_METABOLIC_PROCESS	-0.82	0.14	0	0	0	not significant
7140	GO_CORTICOSTEROID_RECEPTOR_SIGNALING_PATHWAY	-0.82	0.14	0	0	0	not significant
7141	GO_ERROR_FREE_TRANSLESION_SYNTHESIS	-0.82	0.14	0	0	0	not significant
7142	GO_HEXOSE_CATABOLIC_PROCESS	-0.82	0.14	0	0	0	not significant
7143	GO_ISOCITRATE_METABOLIC_PROCESS	-0.82	0.14	0	0	0	not significant
7144	GO_PURINE_NUCLEOTIDE_TRANSPORT	-0.82	0.14	0	0	0	not significant
7145	GO_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	-0.82	0.14	0	0	0	not significant
7146	HOLLEMAN_PREDNISOLONE_RESISTANCE_B_ALL_UP	-0.82	0.14	0	0	0	not significant
7147	MURAKAMI_UV_RESPONSE_6HR_UP	-0.82	0.14	0	0	0	not significant
7148	PARK_HSC_MARKERS	-0.82	0.14	0	0	0	not significant
7149	REACTOME_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_AR	-0.82	0.14	0	0	0	not significant
7150	CHR12P11	-0.82	0.13	0	0	0	not significant
7151	GO_AXONAL_TRANSPORT	-0.82	0.13	0	0	0	not significant
7152	GO_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	-0.82	0.13	0	0	0	not significant
7153	HOLLERN_MICROACINAR_BREAST_TUMOR_UP	-0.82	0.13	0	0	0	not significant
7154	PID_AVB3_OPN_PATHWAY	-0.82	0.13	0	0	0	not significant
7155	GO_INTRA_GOLGI_VESICLE_MEDIATED_TRANSPORT	-0.82	0.12	0	0	0	not significant
7156	GO_REGULATION_OF_LIPID_KINASE_ACTIVITY	-0.82	0.12	0	0	0	not significant
7157	GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_EXONUCLEOLYTIC	-0.82	0.12	0	0	0	not significant
7158	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_9	-0.82	0.11	0	0	0	not significant
7159	CHR16P12	-0.82	0.10	0	0	0	not significant
7160	GO_H4_HISTONE_ACETYLTRANSFERASE_COMPLEX	-0.82	0.10	0	0	0	not significant
7161	GO_L_ALPHA_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	-0.82	0.10	0	0	0	not significant
7162	GO_LIPID_STORAGE	-0.82	0.10	0	0	0	not significant
7163	GO_NUCLEAR_REPLICATION_FORK	-0.82	0.10	0	0	0	not significant
7164	GO_PHOSPHATASE_REGULATOR_ACTIVITY	-0.82	0.10	0	0	0	not significant
7165	SWEET_KRAS_TARGETS_UP	-0.82	0.10	0	0	0	not significant
7166	CHRXQ28	-0.82	0.09	0	0	0	not significant
7167	GO_NEGATIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PA	-0.82	0.09	0	0	0	not significant
7168	GO_NEGATIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR	-0.82	0.09	0	0	0	not significant
7169	RELA_DN.V1_UP	-0.82	0.08	0	0	0	not significant
7170	BROWNE_HCMV_INFECTION_12HR_DN	-0.82	0.07	0	0	0	not significant
7171	GO_REGULATION_OF_MUSCLE_ORGAN_DEVELOPMENT	-0.82	0.07	0	0	0	not significant
7172	PDGF_ERK_DN.V1_UP	-0.82	0.06	0	0	0	not significant
7173	RAY_TUMORIGENESIS_BY_ERBB2_CDC25A_DN	-0.82	0.03	0	0	0	not significant
7174	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_UP	-0.82	0.02	0	0	0	not significant
7175	GO_TRANSFERASE_COMPLEX	-0.82	0.00	0	0	0	not significant
7176	GO_PROTEIN_PHOSPHATASE_2B_BINDING	-0.81	0.18	0	0	0	not significant
7177	GO_CELLULAR_RESPONSE_TO_ESTROGEN_STIMULUS	-0.81	0.17	0	0	0	not significant
7178	REACTOME_GALACTOSE_CATABOLISM	-0.81	0.17	0	0	0	not significant
7179	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN	-0.81	0.16	0	0	0	not significant
7180	GO_ACTIN_POLYMERIZATION_DEPENDENT_CELL_MOTILITY	-0.81	0.16	0	0	0	not significant
7181	GO_CONNECTIVE_TISSUE_REPLACEMENT	-0.81	0.16	0	0	0	not significant
7182	GO_FILOPODIUM_TIP	-0.81	0.16	0	0	0	not significant

7183	GO_VESICLE_FUSION_WITH_GOLGI_APPARATUS	-0.81	0.16	0	0	0	not significant
7184	YEMELYANOV_GR_TARGETS_DN	-0.81	0.16	0	0	0	not significant
7185	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN	-0.81	0.15	0	0	0	not significant
7186	GHANDHI_BYSTANDER_IRRADIATION_DN	-0.81	0.15	0	0	0	not significant
7187	GO_CARBON_SULFUR_LYASE_ACTIVITY	-0.81	0.15	0	0	0	not significant
7188	GO_CELLULAR_RESPONSE_TO_NITRIC_OXIDE	-0.81	0.15	0	0	0	not significant
7189	GO_INTESTINAL_EPITHELIAL_CELL_DIFFERENTIATION	-0.81	0.15	0	0	0	not significant
7190	GO_NADP_METABOLIC_PROCESS	-0.81	0.15	0	0	0	not significant
7191	GO_PIGMENT_GRANULE_MATURATION	-0.81	0.15	0	0	0	not significant
7192	GO_PURINE_NUCLEOTIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.81	0.15	0	0	0	not significant
7193	REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	-0.81	0.15	0	0	0	not significant
7194	REACTOME_MISCELLANEOUS_SUBSTRATES	-0.81	0.15	0	0	0	not significant
7195	VERNOCHET_ADIPOGENESIS	-0.81	0.15	0	0	0	not significant
7196	BIOCARTA_EPHA4_PATHWAY	-0.81	0.14	0	0	0	not significant
7197	CHANG_POU5F1_TARGETS_UP	-0.81	0.14	0	0	0	not significant
7198	CHR5Q23	-0.81	0.14	0	0	0	not significant
7199	GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_COMPLEX	-0.81	0.14	0	0	0	not significant
7200	PID_SMAD2_3PATHWAY	-0.81	0.14	0	0	0	not significant
7201	REACTOME_NEF_AND_SIGNAL_TRANSDUCTION	-0.81	0.14	0	0	0	not significant
7202	XU_AKT1_TARGETS_48HR	-0.81	0.14	0	0	0	not significant
7203	GO_AU_RICH_ELEMENT_BINDING	-0.81	0.13	0	0	0	not significant
7204	GO_CARBOXY_TERMINAL_DOMAIN_PROTEIN_KINASE_COMPLEX	-0.81	0.13	0	0	0	not significant
7205	GO_POSITIVE_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	-0.81	0.13	0	0	0	not significant
7206	GO_POSITIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	-0.81	0.13	0	0	0	not significant
7207	GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_DN	-0.81	0.13	0	0	0	not significant
7208	REACTOME_TRANSLESION_SYNTHESIS_BY_POLH	-0.81	0.13	0	0	0	not significant
7209	GO_EXIT_FROM_MITOSIS	-0.81	0.12	0	0	0	not significant
7210	REACTOME_LYSOSOME_VESICLE_BIOGENESIS	-0.81	0.12	0	0	0	not significant
7211	BREDEMEYER_RAG_SIGNALING_NOT_VIA_ATM_DN	-0.81	0.10	0	0	0	not significant
7212	GO_BONE_REMODELING	-0.81	0.10	0	0	0	not significant
7213	GO_CELLULAR_PIGMENTATION	-0.81	0.10	0	0	0	not significant
7214	GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	-0.81	0.10	0	0	0	not significant
7215	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_	-0.81	0.10	0	0	0	not significant
7216	GO_PYRIMIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-0.81	0.10	0	0	0	not significant
7217	MAHAJAN_RESPONSE_TO_IL1A_UP	-0.81	0.10	0	0	0	not significant
7218	REACTOME_PKMTS_METHYLATE_HISTONE_LYSINES	-0.81	0.10	0	0	0	not significant
7219	KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	-0.81	0.09	0	0	0	not significant
7220	REACTOME_TRANSPORT_OF_BILE_SALTS_AND_ORGANIC_ACIDS_META	-0.81	0.09	0	0	0	not significant
7221	GO_DEVELOPMENT_OF_PRIMARY_FEMALE_SEXUAL_CHARACTERISTICS	-0.81	0.08	0	0	0	not significant
7222	KEGG_AXON_GUIDANCE	-0.81	0.07	0	0	0	not significant
7223	REACTOME_ION_CHANNEL_TRANSPORT	-0.81	0.05	0	0	0	not significant
7224	GO_CALMODULIN_BINDING	-0.81	0.04	0	0	0	not significant
7225	GO_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS	-0.81	0.02	0	0	0	not significant
7226	GO_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	-0.81	0.02	0	0	0	not significant
7227	GO_NUCLEAR_MEMBRANE	-0.81	0.01	0	0	0	not significant
7228	GO_PHOSPHOLIPID_BIOSYNTHETIC_PROCESS	-0.81	0.01	0	0	0	not significant
7229	GO_ENDOMEMBRANE_SYSTEM_ORGANIZATION	-0.81	0.00	0	0	0	not significant
7230	GO_PEPTIDYL_AMINO_ACID_MODIFICATION	-0.81	0.00	0	0	0	not significant
7231	GO_GDP_METABOLIC_PROCESS	-0.80	0.17	0	0	0	not significant
7232	GO_POSITIVE_REGULATION_OF_DNA_CATABOLIC_PROCESS	-0.80	0.17	0	0	0	not significant
7233	GO_SUPERCOILED_DNA_BINDING	-0.80	0.17	0	0	0	not significant
7234	GO_HISTONE_THREONINE_PHOSPHORYLATION	-0.80	0.16	0	0	0	not significant
7235	GO_N_ACETYLGLUCOSAMINE_METABOLIC_PROCESS	-0.80	0.16	0	0	0	not significant
7236	GO_NEGATIVE_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	-0.80	0.16	0	0	0	not significant
7237	GO_CELL_AGGREGATION	-0.80	0.15	0	0	0	not significant
7238	GO_CELLULAR_RESPONSE_TO_LEPTIN_STIMULUS	-0.80	0.15	0	0	0	not significant
7239	GO_ESTABLISHMENT_OF_VIRAL_LATENCY	-0.80	0.15	0	0	0	not significant
7240	GO_LONG_CHAIN_FATTY_ACID_BIOSYNTHETIC_PROCESS	-0.80	0.15	0	0	0	not significant
7241	GO_MORPHOGENESIS_OF_AN_ENDOTHELIUM	-0.80	0.15	0	0	0	not significant
7242	GO_PIGMENT_ACCUMULATION	-0.80	0.15	0	0	0	not significant
7243	GO_REGULATION_OF_LYSOSOMAL_LUMEN_PH	-0.80	0.15	0	0	0	not significant
7244	GO_TRAPP_COMPLEX	-0.80	0.15	0	0	0	not significant
7245	MUNSHI_MULTIPLE_MYELOMA_DN	-0.80	0.15	0	0	0	not significant
7246	REACTOME_E2F_ENABLED_INHIBITION_OF_PRE_REPLICATION_COMPLE	-0.80	0.15	0	0	0	not significant
7247	REACTOME_SYNTHESIS_OF_DIPHTHAMIDE_EEF2	-0.80	0.15	0	0	0	not significant
7248	GO_CELLULAR_RESPONSE_TO_INCREASED_OXYGEN_LEVELS	-0.80	0.14	0	0	0	not significant
7249	GO_HISTONE_THREONINE_KINASE_ACTIVITY	-0.80	0.14	0	0	0	not significant
7250	GO_METALLOAMINOPEPTIDASE_ACTIVITY	-0.80	0.14	0	0	0	not significant
7251	GO_PYRUVATE_DEHYDROGENASE_COMPLEX	-0.80	0.14	0	0	0	not significant
7252	MIKKELSEN_ES_HCP_WITH_H3_UNMETHYLATED	-0.80	0.14	0	0	0	not significant
7253	REACTOME_RHO_GTPASES_ACTIVATE_PAKS	-0.80	0.14	0	0	0	not significant
7254	GO_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTION_RESULTING_IN_	-0.80	0.13	0	0	0	not significant
7255	GO_POSITIVE_REGULATION_OF_VASCULAR_SMOOTH_MUSCLE_CELL_P	-0.80	0.13	0	0	0	not significant
7256	GO_SIN3_TYPE_COMPLEX	-0.80	0.13	0	0	0	not significant
7257	GO_STABILIZATION_OF_MEMBRANE_POTENTIAL	-0.80	0.13	0	0	0	not significant
7258	HOEGERKORP_CD44_TARGETS_DIRECT_DN	-0.80	0.13	0	0	0	not significant
7259	KORKOLA_CORRELATED_WITH_POU5F1	-0.80	0.13	0	0	0	not significant
7260	BIOCARTA_CARM_ER_PATHWAY	-0.80	0.12	0	0	0	not significant
7261	GO_PHOSPHATASE_INHIBITOR_ACTIVITY	-0.80	0.12	0	0	0	not significant
7262	GO_REGULATION_OF_CARDIOCYTE_DIFFERENTIATION	-0.80	0.12	0	0	0	not significant
7263	GO_REGULATION_OF_PROTEIN_SUMOYLATION	-0.80	0.12	0	0	0	not significant
7264	REACTOME_GLYCOGEN_METABOLISM	-0.80	0.12	0	0	0	not significant
7265	REACTOME_METALLOPROTEASE_DUBS	-0.80	0.12	0	0	0	not significant
7266	GO_MACROPHAGE_MIGRATION	-0.80	0.11	0	0	0	not significant
7267	GO_NEGATIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	-0.80	0.11	0	0	0	not significant
7268	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	-0.80	0.11	0	0	0	not significant
7269	GO_CARDIAC_SEPTUM_MORPHOGENESIS	-0.80	0.10	0	0	0	not significant
7270	GO_CRANIAL_SKELETAL_SYSTEM_DEVELOPMENT	-0.80	0.10	0	0	0	not significant
7271	GO_INTRACILIARY_TRANSPORT_INVOLVED_IN_CILIUM_ASSEMBLY	-0.80	0.10	0	0	0	not significant
7272	GOLUB_ALL_VS_AML_UP	-0.80	0.10	0	0	0	not significant
7273	GO_PLASMA_MEMBRANE_RAFT	-0.80	0.09	0	0	0	not significant
7274	GO_SIGNALING_ADAPTOR_ACTIVITY	-0.80	0.09	0	0	0	not significant
7275	PID_S1P_S1P3_PATHWAY	-0.80	0.09	0	0	0	not significant
7276	REACTOME_IRON_UPTAKE_AND_TRANSPORT	-0.80	0.09	0	0	0	not significant
7277	HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_DN	-0.80	0.08	0	0	0	not significant
7278	KYNG_DNA_DAMAGE_BY_4NQO_OR_UV	-0.80	0.08	0	0	0	not significant
7279	GO_INCLUSION_BODY	-0.80	0.07	0	0	0	not significant
7280	GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	-0.80	0.07	0	0	0	not significant
7281	GO_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTO	-0.80	0.07	0	0	0	not significant
7282	GO_TETRAPYRROLE_BINDING	-0.80	0.07	0	0	0	not significant
7283	CHEN_HOXA5_TARGETS_9HR_UP	-0.80	0.02	0	0	0	not significant
7284	GO_REGULATION_OF_MACROAUTOPHAGY	-0.80	0.02	0	0	0	not significant
7285	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP	-0.80	0.02	0	0	0	not significant
7286	GO_NUCLEAR_SPECK	-0.80	0.01	0	0	0	not significant
7287	GO_TRANSCRIPTION_FACTOR_COMPLEX	-0.80	0.01	0	0	0	not significant
7288	GO_ENDOSOMAL_PART	-0.80	0.00	0	0	0	not significant
7289	GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY_INVOLVE	-0.79	0.16	0	0	0	not significant
7290	GO_NEGATIVE_REGULATION_OF_HORMONE_METABOLIC_PROCESS	-0.79	0.16	0	0	0	not significant
7291	GO_AMINO_ACID_BETAINE_METABOLIC_PROCESS	-0.79	0.15	0	0	0	not significant

7292	GO_ATP_TRANSPORT	-0.79	0.15	0	0	0	not significant
7293	GO_GLYOXYLATE_METABOLIC_PROCESS	-0.79	0.15	0	0	0	not significant
7294	GO_MEIOTIC_CHROMOSOME_SEPARATION	-0.79	0.15	0	0	0	not significant
7295	REACTOME_ADVANCED_GLYCOSYLATION_ENDPRODUCT_RECEPTOR_S	-0.79	0.15	0	0	0	not significant
7296	BIOCARTA_IRES_PATHWAY	-0.79	0.14	0	0	0	not significant
7297	BIOCARTA_SUMO_PATHWAY	-0.79	0.14	0	0	0	not significant
7298	GO_CELLULAR_HYPEROSMOTIC_RESPONSE	-0.79	0.14	0	0	0	not significant
7299	GO_EMBRYONIC_NEUROCRANIUM_MORPHOGENESIS	-0.79	0.14	0	0	0	not significant
7300	GO_ENDOPLASMIC_RETICULUM_PALMITOYLTRANSFERASE_COMPLEX	-0.79	0.14	0	0	0	not significant
7301	GO_MRNA_METHYLTRANSFERASE_ACTIVITY	-0.79	0.14	0	0	0	not significant
7302	GO_MYOSIN_II_BINDING	-0.79	0.14	0	0	0	not significant
7303	GO_NEGATIVE_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPRO	-0.79	0.14	0	0	0	not significant
7304	GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	-0.79	0.14	0	0	0	not significant
7305	GO_NUCLEOSIDE_DIPHOSPHATASE_ACTIVITY	-0.79	0.14	0	0	0	not significant
7306	GO_PHOSPHATIDYLCHOLINE_ACYL_CHAIN_REMODELING	-0.79	0.14	0	0	0	not significant
7307	GO_SYNAPTIC_VESICLE_MATURATION	-0.79	0.14	0	0	0	not significant
7308	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON	-0.79	0.14	0	0	0	not significant
7309	BIOCARTA_IGF1R_PATHWAY	-0.79	0.13	0	0	0	not significant
7310	GO_CARBOHYDRATE_CATION_SYMPORTER_ACTIVITY	-0.79	0.13	0	0	0	not significant
7311	GO_CELLULAR_RESPONSE_TO_COLD	-0.79	0.13	0	0	0	not significant
7312	GO_HYDROLASE_ACTIVITY_ACTING_ON_ETHER_BONDS	-0.79	0.13	0	0	0	not significant
7313	GO_MRNA_3_UTR_AU_RICH_REGION_BINDING	-0.79	0.13	0	0	0	not significant
7314	GO_NEGATIVE_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_NEURO	-0.79	0.13	0	0	0	not significant
7315	GO_PEPTIDE_HORMONE_RECEPTOR_BINDING	-0.79	0.13	0	0	0	not significant
7316	GO_REGULATION_OF_RNA_POLYMERASE_II_REGULATORY_REGION_SE	-0.79	0.13	0	0	0	not significant
7317	GO_REPLICATIVE_CELL_AGING	-0.79	0.13	0	0	0	not significant
7318	KEGG_CIRCADIAN_RHYTHM_MAMMAL	-0.79	0.13	0	0	0	not significant
7319	REACTOME_RUNX3_REGULATES_P14_ARF	-0.79	0.13	0	0	0	not significant
7320	REACTOME_UNWINDING_OF_DNA	-0.79	0.13	0	0	0	not significant
7321	WIKMAN_ASBESTOS_LUNG_CANCER_UP	-0.79	0.13	0	0	0	not significant
7322	BIOCARTA_PTEN_PATHWAY	-0.79	0.12	0	0	0	not significant
7323	GO_VESICLE_FUSION_TO_PLASMA_MEMBRANE	-0.79	0.12	0	0	0	not significant
7324	GO_MYOSIN_COMPLEX	-0.79	0.11	0	0	0	not significant
7325	GO_TRANS_GOLGI_NETWORK_TRANSPORT_VESICLE	-0.79	0.11	0	0	0	not significant
7326	KEGG_HOMOLOGOUS_RECOMBINATION	-0.79	0.11	0	0	0	not significant
7327	BROWNE_HCMV_INFECTION_30MIN_UP	-0.79	0.10	0	0	0	not significant
7328	GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VI	-0.79	0.10	0	0	0	not significant
7329	GO_THYMUS_DEVELOPMENT	-0.79	0.10	0	0	0	not significant
7330	HASLINGER_B_CLL_WITH_CHROMOSOME_12_TRISOMY	-0.79	0.10	0	0	0	not significant
7331	SILIGAN_BOUND_BY_EWS_FLT1_FUSION	-0.79	0.10	0	0	0	not significant
7332	GO_3_5_EXONUCLEASE_ACTIVITY	-0.79	0.09	0	0	0	not significant
7333	GO_PHOSPHOLIPID_CATABOLIC_PROCESS	-0.79	0.09	0	0	0	not significant
7334	GO_POSITIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	-0.79	0.09	0	0	0	not significant
7335	GO_RNA_POLYMERASE_CORE_ENZYME_BINDING	-0.79	0.09	0	0	0	not significant
7336	GO_SIGNAL_TRANSDUCTION_IN_ABSENCE_OF_LIGAND	-0.79	0.09	0	0	0	not significant
7337	STONER_ESOPHAGEAL_CARCINOGENESIS_UP	-0.79	0.09	0	0	0	not significant
7338	GO_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	-0.79	0.08	0	0	0	not significant
7339	GO_XENOBIOTIC_METABOLIC_PROCESS	-0.79	0.08	0	0	0	not significant
7340	GO_DETECTION_OF_ABIOTIC_STIMULUS	-0.79	0.07	0	0	0	not significant
7341	GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_P	-0.79	0.06	0	0	0	not significant
7342	GO_STEM_CELL_PROLIFERATION	-0.79	0.06	0	0	0	not significant
7343	KEGG_COLORECTAL_CANCER	-0.79	0.06	0	0	0	not significant
7344	GO_NEGATIVE_REGULATION_OF_DEPHOSPHORYLATION	-0.79	0.05	0	0	0	not significant
7345	GO_NON_MOTILE_CILIUM	-0.79	0.05	0	0	0	not significant
7346	GO_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYME	-0.79	0.05	0	0	0	not significant
7347	GO_JNK_CASCADE	-0.79	0.02	0	0	0	not significant
7348	KAUFFMANN_DNA_REPAIR_GENES	-0.79	0.01	0	0	0	not significant
7349	GO_THO_COMPLEX	-0.78	0.15	0	0	0	not significant
7350	REACTOME_RSK_ACTIVATION	-0.78	0.15	0	0	0	not significant
7351	GO_ATP_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.78	0.14	0	0	0	not significant
7352	GO_DNA_REPLICATION_FACTOR_C_COMPLEX	-0.78	0.14	0	0	0	not significant
7353	GO_NEGATIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENT	-0.78	0.14	0	0	0	not significant
7354	GO_PRE_MRNA_INTRONIC_BINDING	-0.78	0.14	0	0	0	not significant
7355	REACTOME_RUNX3_REGULATES_CDKN1A_TRANSCRIPTION	-0.78	0.14	0	0	0	not significant
7356	EHRLICH_ICF_SYNDROM_UP	-0.78	0.13	0	0	0	not significant
7357	GO_CELLULAR_RESPONSE_TO_INSULIN_LIKE_GROWTH_FACTOR_STIMU	-0.78	0.13	0	0	0	not significant
7358	GO_CYTOPLASMIC_UBIQUITIN_LIGASE_COMPLEX	-0.78	0.13	0	0	0	not significant
7359	GO_HOST_INTRACELLULAR_ORGANELLE	-0.78	0.13	0	0	0	not significant
7360	GO_NEGATIVE_REGULATION_OF_CHOLESTEROL_BIOSYNTHETIC_PROC	-0.78	0.13	0	0	0	not significant
7361	GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGN	-0.78	0.13	0	0	0	not significant
7362	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM_EXIT_SITE	-0.78	0.13	0	0	0	not significant
7363	GO_REGULATION_OF_BICELLULAR_TIGHT_JUNCTION_ASSEMBLY	-0.78	0.13	0	0	0	not significant
7364	GO_REGULATION_OF_MALE_GONAD_DEVELOPMENT	-0.78	0.13	0	0	0	not significant
7365	GO_SPERMATID_NUCLEUS_DIFFERENTIATION	-0.78	0.13	0	0	0	not significant
7366	BIOCARTA_RAB_PATHWAY	-0.78	0.12	0	0	0	not significant
7367	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_UP	-0.78	0.12	0	0	0	not significant
7368	GO_ASPARTATE_TRANSMEMBRANE_TRANSPORT	-0.78	0.12	0	0	0	not significant
7369	GO_MAMMARY_GLAND_EPITHELIAL_CELL_PROLIFERATION	-0.78	0.12	0	0	0	not significant
7370	GO_MINUS_END_DIRECTED_ORGANELLE_TRANSPORT_ALONG_MICROT	-0.78	0.12	0	0	0	not significant
7371	GO_MITOCHONDRIAL_DEPOLARIZATION	-0.78	0.12	0	0	0	not significant
7372	GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CEL	-0.78	0.12	0	0	0	not significant
7373	GO_UBIQUITIN_PROTEIN_TRANSFERASE_REGULATOR_ACTIVITY	-0.78	0.12	0	0	0	not significant
7374	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	-0.78	0.12	0	0	0	not significant
7375	NEBEN_AML_WITH_FLT3_OR_NRAS_DN	-0.78	0.12	0	0	0	not significant
7376	PETRETTO_LEFT_VENTRICLE_MASS_QTL_CIS_DN	-0.78	0.12	0	0	0	not significant
7377	PID_EPHA2_FWD_PATHWAY	-0.78	0.12	0	0	0	not significant
7378	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN	-0.78	0.12	0	0	0	not significant
7379	WAGNER_APO2_SENSITIVITY	-0.78	0.12	0	0	0	not significant
7380	BIOCARTA_AKT_PATHWAY	-0.78	0.11	0	0	0	not significant
7381	BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_UP	-0.78	0.11	0	0	0	not significant
7382	GO_RACEMASE_AND_EPIMERASE_ACTIVITY	-0.78	0.11	0	0	0	not significant
7383	GO_VASODILATION	-0.78	0.11	0	0	0	not significant
7384	NIKOLSKY_BREAST_CANCER_6P24_P22_AMPLICON	-0.78	0.11	0	0	0	not significant
7385	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_3	-0.78	0.11	0	0	0	not significant
7386	WELCH_GATA1_TARGETS	-0.78	0.11	0	0	0	not significant
7387	GO_NEGATIVE_REGULATION_OF_LIPID_LOCALIZATION	-0.78	0.10	0	0	0	not significant
7388	GO_SMOOTH_ENDOPLASMIC_RETICULUM	-0.78	0.10	0	0	0	not significant
7389	REACTOME_ATF4_ACTIVATES_GENES_IN_RESPONSE_TO_ENDOPLASMI	-0.78	0.10	0	0	0	not significant
7390	REACTOME_CONSTITUTIVE_SIGNALING_BY_AKT1_E17K_IN_CANCER	-0.78	0.10	0	0	0	not significant
7391	GO_NEGATIVE_REGULATION_OF_ORGANELLE_ASSEMBLY	-0.78	0.09	0	0	0	not significant
7392	GO_RESPONSE_TO_EPIDERMAL_GROWTH_FACTOR	-0.78	0.09	0	0	0	not significant
7393	GO_SCHWANN_CELL_DIFFERENTIATION	-0.78	0.09	0	0	0	not significant
7394	XU_HGF_SIGNALING_NOT_VIA_AKT1_48HR_UP	-0.78	0.09	0	0	0	not significant
7395	GO_ACTIVE_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.78	0.08	0	0	0	not significant
7396	GO_TORC1_SIGNALING	-0.78	0.08	0	0	0	not significant
7397	PID_IL2_PI3K_PATHWAY	-0.78	0.08	0	0	0	not significant
7398	PID_SHP2_PATHWAY	-0.78	0.08	0	0	0	not significant
7399	CHR18Q21	-0.78	0.07	0	0	0	not significant
7400	GO_INTRACILIARY_TRANSPORT	-0.78	0.07	0	0	0	not significant

7401	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	-0.78	0.07	0	0	0	not significant
7402	GO_SNARE_COMPLEX	-0.78	0.07	0	0	0	not significant
7403	NADLER_HYPERGLYCEMIA_AT_OBESITY	-0.78	0.07	0	0	0	not significant
7404	REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRI	-0.78	0.07	0	0	0	not significant
7405	TCGA_GLIOBLASTOMA_COPY_NUMBER_UP	-0.78	0.07	0	0	0	not significant
7406	GO_IRON_ION_BINDING	-0.78	0.06	0	0	0	not significant
7407	CHRXP22	-0.78	0.05	0	0	0	not significant
7408	GO_PROTEIN_N_LINKED_GLYCOSYLATION	-0.78	0.05	0	0	0	not significant
7409	GO_NEGATIVE_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCE	-0.78	0.04	0	0	0	not significant
7410	REACTOME_MACROAUTOPHAGY	-0.78	0.04	0	0	0	not significant
7411	DARWICHE_PAPILLOMA_RISK_HIGH_DN	-0.78	0.02	0	0	0	not significant
7412	GO_TRANSCRIPTION_FACTOR_TFIIIC_COMPLEX	-0.77	0.15	0	0	0	not significant
7413	CHR19Q12	-0.77	0.14	0	0	0	not significant
7414	GO_NEUROTRANSMITTER_GATED_ION_CHANNEL_CLUSTERING	-0.77	0.14	0	0	0	not significant
7415	GO_RESPIRATORY_BURST_INVOLVED_IN_DEFENSE_RESPONSE	-0.77	0.14	0	0	0	not significant
7416	GO_SPINDLE_ELONGATION	-0.77	0.14	0	0	0	not significant
7417	REACTOME_SIGNAL_REGULATORY_PROTEIN_FAMILY_INTERACTIONS	-0.77	0.14	0	0	0	not significant
7418	GO_KIDNEY_MESENCHYME_DEVELOPMENT	-0.77	0.13	0	0	0	not significant
7419	GO_MUCOSAL_ASSOCIATED_LYMPHOID_TISSUE_DEVELOPMENT	-0.77	0.13	0	0	0	not significant
7420	GO_POLYAMINE_TRANSPORT	-0.77	0.13	0	0	0	not significant
7421	LU_TUMOR_ENDOTHELIAL_MARKERS_UP	-0.77	0.13	0	0	0	not significant
7422	PID_VEGF_VEGFR_PATHWAY	-0.77	0.13	0	0	0	not significant
7423	REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX_IN_CANC	-0.77	0.13	0	0	0	not significant
7424	REACTOME_SUMO_IS_TRANSFERRED_FROM_E1_TO_E2_UBE2I_UBC9	-0.77	0.13	0	0	0	not significant
7425	BIOCARTA_D4GDI_PATHWAY	-0.77	0.12	0	0	0	not significant
7426	CAFFAREL_RESPONSE_TO_THC_8HR_5_DN	-0.77	0.12	0	0	0	not significant
7427	GALE_APL_WITH_FLT3_MUTATED_DN	-0.77	0.12	0	0	0	not significant
7428	GO_DNA_REPLICATION_PREINITIATION_COMPLEX	-0.77	0.12	0	0	0	not significant
7429	GO_REGULATION_OF_STEROID_HORMONE_BIOSYNTHETIC_PROCESS	-0.77	0.12	0	0	0	not significant
7430	REACTOME_GLYCEROPHOSPHOLIPID_CATABOLISM	-0.77	0.12	0	0	0	not significant
7431	WESTON_VEGFA_TARGETS_12HR	-0.77	0.12	0	0	0	not significant
7432	GO_C_ACYLTRANSFERASE_ACTIVITY	-0.77	0.11	0	0	0	not significant
7433	GO_MAMMARY_GLAND_DUCT_MORPHOGENESIS	-0.77	0.11	0	0	0	not significant
7434	GO_MISMATCHED_DNA_BINDING	-0.77	0.11	0	0	0	not significant
7435	REACTOME_RETROGRADE_NEUROTROPHIN_SIGNALLING	-0.77	0.11	0	0	0	not significant
7436	REACTOME_SODIUM_PROTON_EXCHANGERS	-0.77	0.11	0	0	0	not significant
7437	ZEMBUTSU_SENSITIVITY_TO_CYCLOPHOSPHAMIDE	-0.77	0.11	0	0	0	not significant
7438	GO_CELLULAR_BIOGENIC_AMINE_METABOLIC_PROCESS	-0.77	0.10	0	0	0	not significant
7439	GO_FERROUS_IRON_BINDING	-0.77	0.10	0	0	0	not significant
7440	GO_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	-0.77	0.10	0	0	0	not significant
7441	GO_MISFOLDED_PROTEIN_BINDING	-0.77	0.10	0	0	0	not significant
7442	GO_NEGATIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	-0.77	0.10	0	0	0	not significant
7443	GO_NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLAS	-0.77	0.10	0	0	0	not significant
7444	GO_PEROXISOME_PROLIFERATOR_ACTIVATED_RECEPTOR_SIGNALING_	-0.77	0.10	0	0	0	not significant
7445	GO_TRANSCRIPTIONALLY_ACTIVE_CHROMATIN	-0.77	0.10	0	0	0	not significant
7446	BIOCARTA_AGR_PATHWAY	-0.77	0.09	0	0	0	not significant
7447	DEMAGALHAES_AGING_UP	-0.77	0.09	0	0	0	not significant
7448	GO_DENDRITE_EXTENSION	-0.77	0.09	0	0	0	not significant
7449	GO_GLYCOSYL_COMPOUND_CATABOLIC_PROCESS	-0.77	0.09	0	0	0	not significant
7450	GO_NEGATIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENT	-0.77	0.09	0	0	0	not significant
7451	GU_PDEF_TARGETS_UP	-0.77	0.09	0	0	0	not significant
7452	REACTOME_DISEASES_OF_CARBOHYDRATE_METABOLISM	-0.77	0.09	0	0	0	not significant
7453	BIOCARTA_INSULIN_PATHWAY	-0.77	0.08	0	0	0	not significant
7454	CHR6P25	-0.77	0.08	0	0	0	not significant
7455	GO_DETECTION_OF_VISIBLE_LIGHT	-0.77	0.08	0	0	0	not significant
7456	LUI_THYROID_CANCER_CLUSTER_1	-0.77	0.07	0	0	0	not significant
7457	PID_LYSOPHOSPHOLIPID_PATHWAY	-0.77	0.06	0	0	0	not significant
7458	WAKASUGI_HAVE_ZNF143_BINDING_SITES	-0.77	0.06	0	0	0	not significant
7459	GO_RETROGRADE_TRANSPORT_ENDOSOME_TO_GOLGI	-0.77	0.05	0	0	0	not significant
7460	GO_HISTONE_DEACETYLATION	-0.77	0.04	0	0	0	not significant
7461	GO_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	-0.77	0.04	0	0	0	not significant
7462	GO_RNA_POLYMERASE_II_SPECIFIC_DNA_BINDING_TRANSCRIPTION_FAC	-0.77	0.01	0	0	0	not significant
7463	NOUZOVA_TRETINOIN_AND_H4_ACETYLATION	-0.77	0.01	0	0	0	not significant
7464	SHEN_SMARCA2_TARGETS_UP	-0.77	0.00	0	0	0	not significant
7465	CHESLER_BRAIN_QTL_TRANS	-0.76	0.13	0	0	0	not significant
7466	GO_METANEPHRIC_MESENCHYME_DEVELOPMENT	-0.76	0.13	0	0	0	not significant
7467	GO_NEGATIVE_REGULATION_OF_PRODUCTION_OF_MIRNAS_INVOLVED_	-0.76	0.13	0	0	0	not significant
7468	GO_POSITIVE_REGULATION_OF_NON_MOTILE_CILIUM_ASSEMBLY	-0.76	0.13	0	0	0	not significant
7469	GO_REGULATION_OF_GTP_BINDING	-0.76	0.13	0	0	0	not significant
7470	GO_REGULATION_OF_LIPOPROTEIN_LIPASE_ACTIVITY	-0.76	0.13	0	0	0	not significant
7471	GO_UTP_BIOSYNTHETIC_PROCESS	-0.76	0.13	0	0	0	not significant
7472	LIM_MAMMARY_LUMINAL_PROGENITOR_DN	-0.76	0.13	0	0	0	not significant
7473	REACTOME_PHOSPHATE_BOND_HYDROLYSIS_BY_NUDT_PROTEINS	-0.76	0.13	0	0	0	not significant
7474	BALLIF_DEVELOPMENTAL_DISABILITY_P16_P12_DELETION	-0.76	0.12	0	0	0	not significant
7475	GO_GABA_RECEPTOR_BINDING	-0.76	0.12	0	0	0	not significant
7476	GO_LYS48_SPECIFIC_DEUBIQUITINASE_ACTIVITY	-0.76	0.12	0	0	0	not significant
7477	GO_OLIGOPEPTIDE_TRANSPORT	-0.76	0.12	0	0	0	not significant
7478	GO_PHOSPHATIDYLINOSITOL_BISPHOSPHATE_KINASE_ACTIVITY	-0.76	0.12	0	0	0	not significant
7479	GO_POSITIVE_REGULATION_OF_PROTEIN_DEUBIQUITINATION	-0.76	0.12	0	0	0	not significant
7480	GO_REGULATION_OF_HYDROGEN_PEROXIDE_METABOLIC_PROCESS	-0.76	0.12	0	0	0	not significant
7481	GO_SINGLE_STRANDED_DNA_ENDODEOXYRIBONUCLEASE_ACTIVITY	-0.76	0.12	0	0	0	not significant
7482	GO_TRANSLATION_ACTIVATOR_ACTIVITY	-0.76	0.12	0	0	0	not significant
7483	REACTOME_VEGF_LIGAND_RECEPTOR_INTERACTIONS	-0.76	0.12	0	0	0	not significant
7484	SEMBA_FHIT_TARGETS_DN	-0.76	0.12	0	0	0	not significant
7485	ZHAN_EARLY_DIFFERENTIATION_GENES_UP	-0.76	0.12	0	0	0	not significant
7486	BIOCARTA_LEPTIN_PATHWAY	-0.76	0.11	0	0	0	not significant
7487	DORN_ADENOVIRUS_INFECTION_48HR_UP	-0.76	0.11	0	0	0	not significant
7488	GEISS_RESPONSE_TO_DSRNA_DN	-0.76	0.11	0	0	0	not significant
7489	GO_DENDRITIC_CELL_CYTOKINE_PRODUCTION	-0.76	0.11	0	0	0	not significant
7490	GO_ER_MEMBRANE_PROTEIN_COMPLEX	-0.76	0.11	0	0	0	not significant
7491	GO_LIGASE_ACTIVITY_FORMING_CARBON_CARBON_BONDS	-0.76	0.11	0	0	0	not significant
7492	GO_PALMITOYLTRANSFERASE_COMPLEX	-0.76	0.11	0	0	0	not significant
7493	GO_POSITIVE_REGULATION_OF_HEART_CONTRACTION	-0.76	0.11	0	0	0	not significant
7494	GO_POSITIVE_REGULATION_OF_HISTONE_PHOSPHORYLATION	-0.76	0.11	0	0	0	not significant
7495	GO_PURINERGIC_RECEPTOR_ACTIVITY	-0.76	0.11	0	0	0	not significant
7496	GO_REGULATION_OF_CELL_CELL_ADHESION_MEDIATED_BY_CADHERIN	-0.76	0.11	0	0	0	not significant
7497	GO_RESPONSE_TO_LEPTIN	-0.76	0.11	0	0	0	not significant
7498	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_2HR	-0.76	0.11	0	0	0	not significant
7499	GO_GTP_METABOLIC_PROCESS	-0.76	0.10	0	0	0	not significant
7500	GO_NEUROPEPTIDE_SIGNALING_PATHWAY	-0.76	0.10	0	0	0	not significant
7501	GO_PLACENTA_BLOOD_VESSEL_DEVELOPMENT	-0.76	0.10	0	0	0	not significant
7502	REACTOME_MECP2_REGULATES_NEURONAL_RECEPTORS_AND_CHANN	-0.76	0.10	0	0	0	not significant
7503	GO_LEUKOCYTE_ADHESION_TO_VASCULAR_ENDOTHELIAL_CELL	-0.76	0.09	0	0	0	not significant
7504	REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI	-0.76	0.09	0	0	0	not significant
7505	WANG_BARRETTS_ESOPHAGUS_DN	-0.76	0.09	0	0	0	not significant
7506	GO_NEUROBLAST_PROLIFERATION	-0.76	0.08	0	0	0	not significant
7507	GO_POSITIVE_REGULATION_OF_GLUCOSE_TRANSMEMBRANE_TRANSPO	-0.76	0.08	0	0	0	not significant
7508	GO_REGULATION_OF_ORGANIC_ACID_TRANSPORT	-0.76	0.08	0	0	0	not significant
7509	REACTOME_CARGO_CONCENTRATION_IN_THE_ER	-0.76	0.08	0	0	0	not significant

7510	REACTOME_PEROXISOMAL_LIPID_METABOLISM	-0.76	0.08	0	0	0	not significant
7511	BURTON_ADIPOGENESIS_12	-0.76	0.07	0	0	0	not significant
7512	GO_LAMELLIPODIUM_ASSEMBLY	-0.76	0.07	0	0	0	not significant
7513	GO_REGULATION_OF_VASCULAR_SMOOTH_MUSCLE_CELL_PROLIFERA	-0.76	0.07	0	0	0	not significant
7514	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP	-0.76	0.07	0	0	0	not significant
7515	BIOCARTA_NFAT_PATHWAY	-0.76	0.06	0	0	0	not significant
7516	GO_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	-0.76	0.06	0	0	0	not significant
7517	CHR3Q13	-0.76	0.05	0	0	0	not significant
7518	GO_REGULATION_OF_SYNAPSE_ASSEMBLY	-0.76	0.05	0	0	0	not significant
7519	REACTOME_MEIOTIC_SYNAPSIS	-0.76	0.05	0	0	0	not significant
7520	GO_NEURAL_TUBE_FORMATION	-0.76	0.04	0	0	0	not significant
7521	GO_POSITIVE_REGULATION_OF_PROTEIN_BINDING	-0.76	0.04	0	0	0	not significant
7522	YEGNASUBRAMANIAN_PROSTATE_CANCER	-0.76	0.04	0	0	0	not significant
7523	GO_NUCLEAR_RECEPTOR_BINDING	-0.76	0.03	0	0	0	not significant
7524	GO_GOLGI_ASSOCIATED_VESICLE	-0.76	0.02	0	0	0	not significant
7525	GO_PROTEIN_KINASE_B_SIGNALING	-0.76	0.02	0	0	0	not significant
7526	GO_SYNAPTIC_VESICLE_CYCLE	-0.76	0.02	0	0	0	not significant
7527	GO_HORMONE_RECEPTOR_BINDING	-0.76	0.01	0	0	0	not significant
7528	CHR20Q12	-0.75	0.13	0	0	0	not significant
7529	GO_SUSCEPTIBILITY_TO_NATURAL_KILLER_CELL_MEDIATED_CYTOTOX	-0.75	0.12	0	0	0	not significant
7530	BAUS_TFF2_TARGETS_DN	-0.75	0.11	0	0	0	not significant
7531	GO_BIOTIN_METABOLIC_PROCESS	-0.75	0.11	0	0	0	not significant
7532	GO_DEOXYRIBOSE_PHOSPHATE_BIOSYNTHETIC_PROCESS	-0.75	0.11	0	0	0	not significant
7533	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_RECEPTOR_ACTIVITY	-0.75	0.11	0	0	0	not significant
7534	GO_NEGATIVE_REGULATION_OF_MACROPHAGE_MIGRATION	-0.75	0.11	0	0	0	not significant
7535	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERAS	-0.75	0.11	0	0	0	not significant
7536	GO_POSTSYNAPTIC_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	-0.75	0.11	0	0	0	not significant
7537	GO_REGULATION_OF_AEROBIC_RESPIRATION	-0.75	0.11	0	0	0	not significant
7538	GO_REGULATION_OF_ATP_BIOSYNTHETIC_PROCESS	-0.75	0.11	0	0	0	not significant
7539	GO_REGULATION_OF_HEART_RATE_BY_CHEMICAL_SIGNAL	-0.75	0.11	0	0	0	not significant
7540	GO_TRANSCYTOSIS	-0.75	0.11	0	0	0	not significant
7541	MIKKELSEN_IPS_ICP_WITH_H3K27ME3	-0.75	0.11	0	0	0	not significant
7542	ZHENG_FOXP3_TARGETS_IN_T_LYMPHOCYTE_UP	-0.75	0.11	0	0	0	not significant
7543	GO_COMMON_PARTNER_SMAD_PROTEIN_PHOSPHORYLATION	-0.75	0.10	0	0	0	not significant
7544	GO_GLYCOGEN_GRANULE	-0.75	0.10	0	0	0	not significant
7545	HAHTOLA_MYCOSIS_FUNGOIDES_UP	-0.75	0.10	0	0	0	not significant
7546	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_UP	-0.75	0.10	0	0	0	not significant
7547	BIOCARTA_HCMV_PATHWAY	-0.75	0.09	0	0	0	not significant
7548	GO_CEREBRAL_CORTEX_CELL_MIGRATION	-0.75	0.09	0	0	0	not significant
7549	REACTOME_BIOTIN_TRANSPORT_AND_METABOLISM	-0.75	0.09	0	0	0	not significant
7550	GO_EXODEOXYRIBONUCLEASE_ACTIVITY	-0.75	0.08	0	0	0	not significant
7551	GO_MITOCHONDRIAL_FUSION	-0.75	0.08	0	0	0	not significant
7552	GO_NEGATIVE_REGULATION_OF_BLOOD_PRESSURE	-0.75	0.08	0	0	0	not significant
7553	GO_ENDODERM_FORMATION	-0.75	0.07	0	0	0	not significant
7554	GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	-0.75	0.07	0	0	0	not significant
7555	REACTOME_CASPASE_ACTIVATION_VIA_EXTRINSIC_APOPTOTIC_SIGNAL	-0.75	0.07	0	0	0	not significant
7556	REACTOME_EGFR_DOWNREGULATION	-0.75	0.07	0	0	0	not significant
7557	CHANGOLKAR_H2AFY_TARGETS_UP	-0.75	0.06	0	0	0	not significant
7558	SUBTIL_PROGESTIN_TARGETS	-0.75	0.06	0	0	0	not significant
7559	BOYAULT_LIVER_CANCER_SUBCLASS_G12_UP	-0.75	0.05	0	0	0	not significant
7560	GO_SCF_UBIQUITIN_LIGASE_COMPLEX	-0.75	0.05	0	0	0	not significant
7561	KEGG_VEGF_SIGNALING_PATHWAY	-0.75	0.05	0	0	0	not significant
7562	PID_PI3KCI_PATHWAY	-0.75	0.05	0	0	0	not significant
7563	RIZKI_TUMOR_INVASIVENESS_2D_DN	-0.75	0.05	0	0	0	not significant
7564	GO_REGULATION_OF_EMBRYONIC_DEVELOPMENT	-0.75	0.04	0	0	0	not significant
7565	GO_NEURAL_PRECURSOR_CELL_PROLIFERATION	-0.75	0.03	0	0	0	not significant
7566	BROWNE_HCMV_INFECTION_18HR_UP	-0.75	0.01	0	0	0	not significant
7567	GO_DNA_BINDING_TRANSCRIPTION_FACTOR_BINDING	-0.75	0.00	0	0	0	not significant
7568	GO_MACROAUTOPHAGY	-0.75	0.00	0	0	0	not significant
7569	GO_REGULATION_OF_AUTOPHAGY	-0.75	0.00	0	0	0	not significant
7570	GO_COPPER_ION_TRANSMEMBRANE_TRANSPORT	-0.74	0.13	0	0	0	not significant
7571	DONATO_CELL_CYCLE_TRETINOIN	-0.74	0.12	0	0	0	not significant
7572	GO_IKAPPAB_KINASE_COMPLEX	-0.74	0.12	0	0	0	not significant
7573	GO_PERIPHERAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	-0.74	0.12	0	0	0	not significant
7574	GO_POSITIVE_REGULATION_OF_PROTEIN_EXIT_FROM_ENDOPLASMIC_	-0.74	0.12	0	0	0	not significant
7575	GO_RNA_POLYMERASE_II_CTD_HEPTAPEPTIDE_REPEAT_PHOSPHATAS	-0.74	0.12	0	0	0	not significant
7576	GO_AROMATIC_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVI	-0.74	0.11	0	0	0	not significant
7577	GO_FATTY_ACYL_COA_METABOLIC_PROCESS	-0.74	0.11	0	0	0	not significant
7578	GO_GLYCOPROTEIN_CATABOLIC_PROCESS	-0.74	0.11	0	0	0	not significant
7579	GO_GUANYLYLTRANSFERASE_ACTIVITY	-0.74	0.11	0	0	0	not significant
7580	GO_INTERLEUKIN_35_MEDIATED_SIGNALING_PATHWAY	-0.74	0.11	0	0	0	not significant
7581	GO_INTERMEDIATE_FILAMENT_BINDING	-0.74	0.11	0	0	0	not significant
7582	GO_MONOVALENT_CATION_PROTON_ANTIPORTER_ACTIVITY	-0.74	0.11	0	0	0	not significant
7583	GO_NEPHRIC_DUCT_MORPHOGENESIS	-0.74	0.11	0	0	0	not significant
7584	GO_RNA_POLYMERASE_III_TRANSCRIPTION_FACTOR_COMPLEX	-0.74	0.11	0	0	0	not significant
7585	GO_TELOMERASE_HOLOENZYME_COMPLEX_ASSEMBLY	-0.74	0.11	0	0	0	not significant
7586	REACTOME_DCC_MEDIATED_ATTRACTIVE_SIGNALING	-0.74	0.11	0	0	0	not significant
7587	REACTOME_NONCANONICAL_ACTIVATION_OF_NOTCH3	-0.74	0.11	0	0	0	not significant
7588	BIOCARTA_SPRY_PATHWAY	-0.74	0.10	0	0	0	not significant
7589	GO_ACETYL_COA_C_ACYLTRANSFERASE_ACTIVITY	-0.74	0.10	0	0	0	not significant
7590	GO_AORTIC_VALVE_DEVELOPMENT	-0.74	0.10	0	0	0	not significant
7591	GO_POSITIVE_REGULATION_OF_ATP_BIOSYNTHETIC_PROCESS	-0.74	0.10	0	0	0	not significant
7592	GO_POSITIVE_REGULATION_OF_TELOMERE_CAPPING	-0.74	0.10	0	0	0	not significant
7593	HOLLERN_MICROACINAR_BREAST_TUMOR_DN	-0.74	0.10	0	0	0	not significant
7594	NIKOLSKY_BREAST_CANCER_10Q22_AMPLICON	-0.74	0.10	0	0	0	not significant
7595	PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP	-0.74	0.10	0	0	0	not significant
7596	REACTOME_JOSEPHIN_DOMAIN_DUBS	-0.74	0.10	0	0	0	not significant
7597	GO_UMP_BIOSYNTHETIC_PROCESS	-0.74	0.09	0	0	0	not significant
7598	MAGRANGEAS_MULTIPLE_MYELOMA_IGLL_VS_IGLK_DN	-0.74	0.09	0	0	0	not significant
7599	REACTOME_PROCESSING_AND_ACTIVATION_OF_SUMO	-0.74	0.09	0	0	0	not significant
7600	CHR17P12	-0.74	0.08	0	0	0	not significant
7601	GO_CHOLESTEROL_EFFLUX	-0.74	0.08	0	0	0	not significant
7602	GO_GLUTAMATE_METABOLIC_PROCESS	-0.74	0.08	0	0	0	not significant
7603	GO_INTRACILIARY_TRANSPORT_PARTICLE_B	-0.74	0.08	0	0	0	not significant
7604	GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING	-0.74	0.08	0	0	0	not significant
7605	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	-0.74	0.08	0	0	0	not significant
7606	GO_PYRIMIDINE_NUCLEOTIDE_CATABOLIC_PROCESS	-0.74	0.08	0	0	0	not significant
7607	GO_SPERM_EGG_RECOGNITION	-0.74	0.08	0	0	0	not significant
7608	REACTOME_DEFECTS_IN_VITAMIN_AND_COFACTOR_METABOLISM	-0.74	0.08	0	0	0	not significant
7609	GO_POSITIVE_REGULATION_OF_TOR_SIGNALING	-0.74	0.07	0	0	0	not significant
7610	KAAB_FAILED_HEART_ATRIUM_UP	-0.74	0.07	0	0	0	not significant
7611	PID_RAC1_REG_PATHWAY	-0.74	0.07	0	0	0	not significant
7612	ENGELMANN_CANCER_PROGENITORS_DN	-0.74	0.06	0	0	0	not significant
7613	GO_AMMONIUM_ION_BINDING	-0.74	0.06	0	0	0	not significant
7614	GO_PERICENTRIOLAR_MATERIAL	-0.74	0.06	0	0	0	not significant
7615	CHR1P31	-0.74	0.05	0	0	0	not significant
7616	CHR2P11	-0.74	0.05	0	0	0	not significant
7617	JI_RESPONSE_TO_FSH_DN	-0.74	0.05	0	0	0	not significant
7618	KEGG_DNA_REPLICATION	-0.74	0.05	0	0	0	not significant

7619	PID_INSULIN_PATHWAY	-0.74	0.05	0	0	0	not significant
7620	RASHI_RESPONSE_TO_IONIZING_RADIATION_4	-0.74	0.05	0	0	0	not significant
7621	GO_HETEROCHROMATIN	-0.74	0.03	0	0	0	not significant
7622	GO_POSITIVE_REGULATION_OF_PLASMA_MEMBRANE_BOUNDED_CELL_	-0.74	0.03	0	0	0	not significant
7623	KEGG_MAPK_SIGNALING_PATHWAY	-0.74	0.00	0	0	0	not significant
7624	GO_PONS_DEVELOPMENT	-0.73	0.12	0	0	0	not significant
7625	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOS	-0.73	0.11	0	0	0	not significant
7626	GO_REGULATION_OF_RESPONSE_TO_TUMOR_CELL	-0.73	0.11	0	0	0	not significant
7627	MINGUEZ_LIVER_CANCER_VASCULAR_INVASION_DN	-0.73	0.11	0	0	0	not significant
7628	AMIT_EGF_RESPONSE_20_HELA	-0.73	0.10	0	0	0	not significant
7629	GO_AT_DNA_BINDING	-0.73	0.10	0	0	0	not significant
7630	GO_CELLULAR_RESPONSE_TO_ATP	-0.73	0.10	0	0	0	not significant
7631	GO_DIPHOSPHOTRANSFERASE_ACTIVITY	-0.73	0.10	0	0	0	not significant
7632	REACTOME_RECEPTOR_MEDIATED_MITOPHAGY	-0.73	0.10	0	0	0	not significant
7633	GO_5S_RRNA_BINDING	-0.73	0.09	0	0	0	not significant
7634	GO_LEUKOCYTE_AGGREGATION	-0.73	0.09	0	0	0	not significant
7635	GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BIOSYNTHETIC_PROCESS	-0.73	0.09	0	0	0	not significant
7636	GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_CELL_DIFFERENTIA	-0.73	0.09	0	0	0	not significant
7637	GO_PROTEIN_PROCESSING_INVOLVED_IN_PROTEIN_TARGETING_TO_MI	-0.73	0.09	0	0	0	not significant
7638	GO_PYRIMIDINE_RIBONUCLEOTIDE_BIOSYNTHETIC_PROCESS	-0.73	0.09	0	0	0	not significant
7639	BIOCARTA_RANKL_PATHWAY	-0.73	0.08	0	0	0	not significant
7640	GO_WW_DOMAIN_BINDING	-0.73	0.08	0	0	0	not significant
7641	KEGG_ONE_CARBON_POOL_BY_FOLATE	-0.73	0.08	0	0	0	not significant
7642	REACTOME_TICAM1_DEPENDENT_ACTIVATION_OF_IRF3_IRF7	-0.73	0.08	0	0	0	not significant
7643	WATANABE_COLON_CANCER_MSI_VS_MSS_DN	-0.73	0.08	0	0	0	not significant
7644	GO_BHLH_TRANSCRIPTION_FACTOR_BINDING	-0.73	0.07	0	0	0	not significant
7645	GO_SODIUM_ION_HOMEOSTASIS	-0.73	0.07	0	0	0	not significant
7646	GO_VIRAL_LATENCY	-0.73	0.07	0	0	0	not significant
7647	LEE_AGING_MUSCLE_DN	-0.73	0.07	0	0	0	not significant
7648	CHESLER_BRAIN_HIGHEST_EXPRESSION	-0.73	0.06	0	0	0	not significant
7649	GO_MICROTUBULE_PLUS_END	-0.73	0.06	0	0	0	not significant
7650	GO_REGULATION_OF_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	-0.73	0.06	0	0	0	not significant
7651	GO_LYSOSOME_LOCALIZATION	-0.73	0.04	0	0	0	not significant
7652	GO_MICROTUBULE_ORGANIZING_CENTER_ORGANIZATION	-0.73	0.02	0	0	0	not significant
7653	GO_NEURON_MIGRATION	-0.73	0.02	0	0	0	not significant
7654	GO_POST_GOLGI_VESICLE_MEDIATED_TRANSPORT	-0.73	0.02	0	0	0	not significant
7655	GO_UBIQUITIN_BINDING	-0.73	0.02	0	0	0	not significant
7656	REACTOME_SIGNALING_BY_NTRKS	-0.73	0.02	0	0	0	not significant
7657	GO_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	-0.73	0.01	0	0	0	not significant
7658	GO_PEPTIDYL_LYSINE_MODIFICATION	-0.73	0.00	0	0	0	not significant
7659	GO_REGULATION_OF_ORGANELLE_ASSEMBLY	-0.73	0.00	0	0	0	not significant
7660	GO_PEPTIDYL_LYSINE_HYDROXYLATION	-0.72	0.11	0	0	0	not significant
7661	DING_LUNG_CANCER_MUTATED_FREQUENTLY	-0.72	0.10	0	0	0	not significant
7662	GO_DEOXYRIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-0.72	0.10	0	0	0	not significant
7663	GO_HISTONE_METHYLTRANSFERASE_ACTIVITY_H3_K36_SPECIFIC_	-0.72	0.10	0	0	0	not significant
7664	GO_POSITIVE_REGULATION_OF_PINOCYTOSIS	-0.72	0.10	0	0	0	not significant
7665	GO_PROTON_TRANSPORTING_V_TYPE_ATPASE_V1_DOMAIN	-0.72	0.10	0	0	0	not significant
7666	GO_REGULATION_OF_NEUTROPHIL_DEGRANULATION	-0.72	0.10	0	0	0	not significant
7667	GO_REGULATION_OF_PROTEIN_K63_LINKED_UBIQUITINATION	-0.72	0.10	0	0	0	not significant
7668	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_16	-0.72	0.10	0	0	0	not significant
7669	REACTOME_INTERLEUKIN_35_SIGNALLING	-0.72	0.10	0	0	0	not significant
7670	CHR7P11	-0.72	0.09	0	0	0	not significant
7671	GO_CALYX_OF_HELD	-0.72	0.09	0	0	0	not significant
7672	GO_CILIARY_ROOTLET	-0.72	0.09	0	0	0	not significant
7673	GO_POLYPEPTIDE_N_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVIT	-0.72	0.09	0	0	0	not significant
7674	GO_PROTEIN_LIPID_COMPLEX_BINDING	-0.72	0.09	0	0	0	not significant
7675	RAFFEL_VEGFA_TARGETS_UP	-0.72	0.09	0	0	0	not significant
7676	SCHMAHL_PDGF_SIGNALING	-0.72	0.09	0	0	0	not significant
7677	GO_BLOC_1_COMPLEX	-0.72	0.08	0	0	0	not significant
7678	GO_HYDROGEN_PEROXIDE_METABOLIC_PROCESS	-0.72	0.08	0	0	0	not significant
7679	GO_REGULATION_OF_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	-0.72	0.08	0	0	0	not significant
7680	GO_REGULATION_OF_PROGRAMMED_NECROTIC_CELL_DEATH	-0.72	0.08	0	0	0	not significant
7681	REACTOME_SIGNALING_BY_LIGAND_RESPONSIVE_EGFR_VARIANTS_IN_	-0.72	0.08	0	0	0	not significant
7682	GO_DNA_POLYMERASE_COMPLEX	-0.72	0.07	0	0	0	not significant
7683	GO_DNA_REPLICATION_FACTOR_A_COMPLEX	-0.72	0.07	0	0	0	not significant
7684	GO_LATE_ENDOSOME_TO_VACUOLE_TRANSPORT	-0.72	0.07	0	0	0	not significant
7685	GO_MRNA_METHYLATION	-0.72	0.07	0	0	0	not significant
7686	GO_NEGATIVE_REGULATION_OF_TRANSLATIONAL_INITIATION	-0.72	0.07	0	0	0	not significant
7687	GO_REGULATION_OF_PROTEIN_HOMODIMERIZATION_ACTIVITY	-0.72	0.07	0	0	0	not significant
7688	REACTOME_SIGNALING_BY_EGFR_IN_CANCER	-0.72	0.07	0	0	0	not significant
7689	REACTOME_TERMINATION_OF_TRANSLESION_DNA_SYNTHESIS	-0.72	0.05	0	0	0	not significant
7690	GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE	-0.72	0.04	0	0	0	not significant
7691	GO_METALLOENDOPEPTIDASE_ACTIVITY	-0.72	0.04	0	0	0	not significant
7692	GO_P38MAPK_CASCADE	-0.72	0.04	0	0	0	not significant
7693	PID_FAS_PATHWAY	-0.72	0.04	0	0	0	not significant
7694	BYSTROEM_CORRELATED_WITH_IL5_DN	-0.72	0.03	0	0	0	not significant
7695	GO_PHOSPHATIDYLINOSITOL_PHOSPHORYLATION	-0.72	0.03	0	0	0	not significant
7696	GO_ACTIVATION_OF_GTPASE_ACTIVITY	-0.72	0.02	0	0	0	not significant
7697	GO_N_ACETYLTRANSFERASE_ACTIVITY	-0.72	0.02	0	0	0	not significant
7698	GO_PROTEIN_ACETYLTRANSFERASE_COMPLEX	-0.72	0.02	0	0	0	not significant
7699	RB_P130_DN.V1_DN	-0.72	0.02	0	0	0	not significant
7700	KESHELAVA_MULTIPLE_DRUG_RESISTANCE	-0.72	0.01	0	0	0	not significant
7701	SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B_LYMPHOCY	-0.72	0.01	0	0	0	not significant
7702	GO_NEGATIVE_REGULATION_OF_GLUCOSE_IMPORT	-0.71	0.10	0	0	0	not significant
7703	GO_PENTOSE_PHOSPHATE_SHUNT_NON_OXIDATIVE_BRANCH	-0.71	0.10	0	0	0	not significant
7704	GO_REGULATION_OF_ENDOSOME_SIZE	-0.71	0.10	0	0	0	not significant
7705	CHR13Q21	-0.71	0.09	0	0	0	not significant
7706	DORN_ADENOVIRUS_INFECTION_24HR_UP	-0.71	0.09	0	0	0	not significant
7707	GO_4_HYDROXYPROLINE_METABOLIC_PROCESS	-0.71	0.09	0	0	0	not significant
7708	GO_BONE_MARROW_DEVELOPMENT	-0.71	0.09	0	0	0	not significant
7709	GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_E_STIMULUS	-0.71	0.09	0	0	0	not significant
7710	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_RECEPTOR_BIOSYNTHETI	-0.71	0.09	0	0	0	not significant
7711	GO_NEGATIVE_REGULATION_OF_MITOCHONDRIAL_FUSION	-0.71	0.09	0	0	0	not significant
7712	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STI	-0.71	0.09	0	0	0	not significant
7713	GO_PENTOSE_CATABOLIC_PROCESS	-0.71	0.09	0	0	0	not significant
7714	GO_PICLN_SM_PROTEIN_COMPLEX	-0.71	0.09	0	0	0	not significant
7715	BIOCARTA_CTBP1_PATHWAY	-0.71	0.08	0	0	0	not significant
7716	BIOCARTA_PLCE_PATHWAY	-0.71	0.08	0	0	0	not significant
7717	GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_STIMULUS	-0.71	0.08	0	0	0	not significant
7718	OXFORD_RALA_AND_RALB_TARGETS_UP	-0.71	0.08	0	0	0	not significant
7719	PID_BETA_CATENIN_DEG_PATHWAY	-0.71	0.08	0	0	0	not significant
7720	TAKADA_GASTRIC_CANCER_COPY_NUMBER_DN	-0.71	0.08	0	0	0	not significant
7721	CHR3Q12	-0.71	0.07	0	0	0	not significant
7722	FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_DN	-0.71	0.07	0	0	0	not significant
7723	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_MAGENTA_DN	-0.71	0.07	0	0	0	not significant
7724	GO_C21_STEROID_HORMONE_BIOSYNTHETIC_PROCESS	-0.71	0.07	0	0	0	not significant
7725	GO_DOPAMINE_RECEPTOR_BINDING	-0.71	0.07	0	0	0	not significant
7726	GO_EXOCYST	-0.71	0.07	0	0	0	not significant
7727	GO_NEGATIVE_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	-0.71	0.07	0	0	0	not significant

7728	GO_POLYSACCHARIDE_CATABOLIC_PROCESS	-0.71	0.07	0	0	0	not significant
7729	GO_POSITIVE_REGULATION_OF_CARDIOCYTE_DIFFERENTIATION	-0.71	0.07	0	0	0	not significant
7730	GO_TELOMERE_MAINTENANCE_VIA_RECOMBINATION	-0.71	0.07	0	0	0	not significant
7731	JEPSEN_SMRT_TARGETS	-0.71	0.07	0	0	0	not significant
7732	MUELLER_METHYLATED_IN_GLIOBLASTOMA	-0.71	0.07	0	0	0	not significant
7733	GO_AMYLOID_BETA_METABOLIC_PROCESS	-0.71	0.06	0	0	0	not significant
7734	GO_REGULATION_OF_PRESYNAPSE_ORGANIZATION	-0.71	0.06	0	0	0	not significant
7735	GO_ZINC_ION_TRANSPORT	-0.71	0.06	0	0	0	not significant
7736	ZHENG_IL22_SIGNALING_UP	-0.71	0.06	0	0	0	not significant
7737	BREDEMEYER_RAG_SIGNALING_VIA_ATM_NOT_VIA_NFKB_DN	-0.71	0.05	0	0	0	not significant
7738	GO_DNA_CATABOLIC_PROCESS_ENDONUCLEOLYTIC	-0.71	0.05	0	0	0	not significant
7739	GO_MITOCHONDRION_LOCALIZATION	-0.71	0.05	0	0	0	not significant
7740	GO_RETROMER_COMPLEX	-0.71	0.05	0	0	0	not significant
7741	CHR14Q22	-0.71	0.04	0	0	0	not significant
7742	BCAT_BILD_ET_AL_UP	-0.71	0.03	0	0	0	not significant
7743	HEDENFALK_BREAST_CANCER_HEREDITARY_VS_SPORADIC	-0.71	0.03	0	0	0	not significant
7744	CHR2P23	-0.71	0.02	0	0	0	not significant
7745	GO_POSITIVE_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	-0.71	0.02	0	0	0	not significant
7746	GO_RNA_POLYMERASE_BINDING	-0.71	0.02	0	0	0	not significant
7747	GO_SYNAPTIC_VESICLE_LOCALIZATION	-0.71	0.01	0	0	0	not significant
7748	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYL	-0.71	0.01	0	0	0	not significant
7749	GO_DNA_REPLICATION	-0.71	0.00	0	0	0	not significant
7750	GO_LATE_ENDOSOME	-0.71	0.00	0	0	0	not significant
7751	REACTOME_CHROMATIN_ORGANIZATION	-0.71	0.00	0	0	0	not significant
7752	GO_COPPER_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.70	0.09	0	0	0	not significant
7753	GO_DNA_RECOMBINASE_MEDIATOR_COMPLEX	-0.70	0.09	0	0	0	not significant
7754	GO_POSITIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_2_SIGNALING_	-0.70	0.09	0	0	0	not significant
7755	GO_STRESS_GRANULE_DISASSEMBLY	-0.70	0.09	0	0	0	not significant
7756	GO_BETA_CATENIN_DESTRUCTION_COMPLEX_ASSEMBLY	-0.70	0.08	0	0	0	not significant
7757	GO_CELLULAR_RESPONSE_TO_TESTOSTERONE_STIMULUS	-0.70	0.08	0	0	0	not significant
7758	GO_LENS_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	-0.70	0.08	0	0	0	not significant
7759	GO_POSITIVE_REGULATION_OF_LYASE_ACTIVITY	-0.70	0.08	0	0	0	not significant
7760	GO_POSITIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	-0.70	0.08	0	0	0	not significant
7761	GO_PROTEIN_LOCALIZATION_TO_NON_MOTILE_CILIUM	-0.70	0.08	0	0	0	not significant
7762	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS	-0.70	0.08	0	0	0	not significant
7763	REACTOME_DISEASES_OF_MISMATCH_REPAIR_MMR	-0.70	0.08	0	0	0	not significant
7764	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_UP	-0.70	0.07	0	0	0	not significant
7765	FARMER_BREAST_CANCER_CLUSTER_6	-0.70	0.07	0	0	0	not significant
7766	GO_CDP_CHOLINE_PATHWAY	-0.70	0.07	0	0	0	not significant
7767	GO_EPHRIN_RECEPTOR_BINDING	-0.70	0.07	0	0	0	not significant
7768	GO_FUCOSE_METABOLIC_PROCESS	-0.70	0.07	0	0	0	not significant
7769	GO_INVADOPODIUM	-0.70	0.07	0	0	0	not significant
7770	GO_PHARYNGEAL_ARCH_ARTERY_MORPHOGENESIS	-0.70	0.07	0	0	0	not significant
7771	GO_SODIUM_ION_IMPORT_ACROSS_PLASMA_MEMBRANE	-0.70	0.07	0	0	0	not significant
7772	GO_BLASTOCYST_GROWTH	-0.70	0.06	0	0	0	not significant
7773	GO_NEGATIVE_REGULATION_OF_HISTONE_H3_K9_METHYLATION	-0.70	0.06	0	0	0	not significant
7774	GO_NEUROTROPHIN_RECEPTOR_BINDING	-0.70	0.06	0	0	0	not significant
7775	GO_REGULATION_OF_DNA_DAMAGE_CHECKPOINT	-0.70	0.06	0	0	0	not significant
7776	PID_HNF3A_PATHWAY	-0.70	0.06	0	0	0	not significant
7777	BIOCARTA_CASPASE_PATHWAY	-0.70	0.05	0	0	0	not significant
7778	GO_REGULATION_OF_MYOTUBE_DIFFERENTIATION	-0.70	0.05	0	0	0	not significant
7779	ISSAEVA_MLL2_TARGETS	-0.70	0.05	0	0	0	not significant
7780	PID_NEPHRIN_NEPH1_PATHWAY	-0.70	0.05	0	0	0	not significant
7781	GO_EMBRYO_IMPLANTATION	-0.70	0.04	0	0	0	not significant
7782	REACTOME_TRAF6_MEDIATED_NF_KB_ACTIVATION	-0.70	0.04	0	0	0	not significant
7783	GO_MEDIATOR_COMPLEX	-0.70	0.03	0	0	0	not significant
7784	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLAT	-0.70	0.03	0	0	0	not significant
7785	GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_PERMEABILITY_INV	-0.70	0.03	0	0	0	not significant
7786	REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_ST	-0.70	0.03	0	0	0	not significant
7787	SIG_BCR_SIGNALING_PATHWAY	-0.70	0.03	0	0	0	not significant
7788	GO_DENDRITIC_SPINE_DEVELOPMENT	-0.70	0.02	0	0	0	not significant
7789	GO_IRON_ION_HOMEOSTASIS	-0.70	0.02	0	0	0	not significant
7790	GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_CLEARANCE	-0.69	0.09	0	0	0	not significant
7791	GO_NEUROTROPHIN_TRK_RECEPTOR_BINDING	-0.69	0.09	0	0	0	not significant
7792	REACTOME_TIGHT_JUNCTION_INTERACTIONS	-0.69	0.09	0	0	0	not significant
7793	GO_CDC73_PAF1_COMPLEX	-0.69	0.08	0	0	0	not significant
7794	GO_ENDONUCLEOLYTIC_CLEAVAGE_IN_ITS1_TO_SEPARATE_SSU_RRN	-0.69	0.08	0	0	0	not significant
7795	GO_HISTONE_H3_K9_DIMETHYLATION	-0.69	0.08	0	0	0	not significant
7796	GO_REGULATION_OF_ODONTOGENESIS	-0.69	0.08	0	0	0	not significant
7797	GO_TOLL_LIKE_RECEPTOR_2_SIGNALING_PATHWAY	-0.69	0.08	0	0	0	not significant
7798	GO_XYLULOSE_5_PHOSPHATE_BIOSYNTHETIC_PROCESS	-0.69	0.08	0	0	0	not significant
7799	MIKKELSEN_PLURIPOTENT_STATE_UP	-0.69	0.08	0	0	0	not significant
7800	REACTOME_REGULATION_OF_PTEN_LOCALIZATION	-0.69	0.08	0	0	0	not significant
7801	GO_NEGATIVE_REGULATION_OF_JUN_KINASE_ACTIVITY	-0.69	0.07	0	0	0	not significant
7802	GO_OLIGOSACCHARYL_TRANSFERASE_ACTIVITY	-0.69	0.07	0	0	0	not significant
7803	GO_REGULATION_OF_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	-0.69	0.07	0	0	0	not significant
7804	GO_SEQUESTERING_OF_TRIGLYCERIDE	-0.69	0.07	0	0	0	not significant
7805	GO_SOMATIC_DIVERSIFICATION_OF_T_CELL_RECEPTOR_GENES	-0.69	0.07	0	0	0	not significant
7806	WU_ALZHEIMER_DISEASE_DN	-0.69	0.07	0	0	0	not significant
7807	CHR18Q22	-0.69	0.06	0	0	0	not significant
7808	GO_PIGMENT_GRANULE_LOCALIZATION	-0.69	0.06	0	0	0	not significant
7809	GO_PLATELET_DENSE_GRANULE	-0.69	0.06	0	0	0	not significant
7810	GO_REGULATION_OF_AUTOPHAGOSOME_MATURATION	-0.69	0.06	0	0	0	not significant
7811	LU_TUMOR_VASCULATURE_UP	-0.69	0.06	0	0	0	not significant
7812	REACTOME_TGF_BETA_RECEPTOR_SIGNALING_IN_EMT_EPITHELIAL_T	-0.69	0.06	0	0	0	not significant
7813	GO_CARBOXYPEPTIDASE_ACTIVITY	-0.69	0.05	0	0	0	not significant
7814	GO_POSITIVE_REGULATION_OF_NEUROBLAST_PROLIFERATION	-0.69	0.05	0	0	0	not significant
7815	CHR20P12	-0.69	0.04	0	0	0	not significant
7816	GO_NUCLEAR_HETEROCHROMATIN	-0.69	0.04	0	0	0	not significant
7817	GO_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	-0.69	0.04	0	0	0	not significant
7818	GO_AP_TYPE_MEMBRANE_COAT_ADAPTOR_COMPLEX	-0.69	0.03	0	0	0	not significant
7819	GO_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABILIZATION	-0.69	0.03	0	0	0	not significant
7820	GO_POSITIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	-0.69	0.02	0	0	0	not significant
7821	GO_REGULATION_OF_HISTONE_MODIFICATION	-0.69	0.01	0	0	0	not significant
7822	GO_REGULATION_OF_POSTSYNAPSE_ORGANIZATION	-0.69	0.01	0	0	0	not significant
7823	GO_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALING_PAT	-0.69	0.00	0	0	0	not significant
7824	GO_NEGATIVE_REGULATION_OF_NEURON_DEATH	-0.69	0.00	0	0	0	not significant
7825	GO_NUCLEAR_HORMONE_RECEPTOR_BINDING	-0.69	0.00	0	0	0	not significant
7826	GO_RAB_GTPASE_BINDING	-0.69	0.00	0	0	0	not significant
7827	REACTOME_REGULATION_OF_TP53_ACTIVITY	-0.69	0.00	0	0	0	not significant
7828	ITO_PTTG1_TARGETS_UP	-0.68	0.09	0	0	0	not significant
7829	REACTOME_FORMATION_OF_XYLULOSE_5_PHOSPHATE	-0.68	0.08	0	0	0	not significant
7830	CHR8P22	-0.68	0.07	0	0	0	not significant
7831	GO_ATG1_ULK1_KINASE_COMPLEX	-0.68	0.07	0	0	0	not significant
7832	GO_ER_ASSOCIATED_MISFOLDED_PROTEIN_CATABOLIC_PROCESS	-0.68	0.07	0	0	0	not significant
7833	GO_ESCRT_COMPLEX_DISASSEMBLY	-0.68	0.07	0	0	0	not significant
7834	GO_MITOCHONDRIAL_DNA_REPAIR	-0.68	0.07	0	0	0	not significant
7835	GO_NEUROTRANSMITTER_CATABOLIC_PROCESS	-0.68	0.07	0	0	0	not significant
7836	GO_NODE_OF_RANVIER	-0.68	0.07	0	0	0	not significant

7837	GO_PHAGOLYSOSOME_ASSEMBLY	-0.68	0.07	0	0	0	not significant
7838	GO_PROLINE_RICH_REGION_BINDING	-0.68	0.07	0	0	0	not significant
7839	GO_RESPONSE_TO_MACROPHAGE_COLONY_STIMULATING_FACTOR	-0.68	0.07	0	0	0	not significant
7840	GO_TRNA_TRANSCRIPTION	-0.68	0.07	0	0	0	not significant
7841	TERAMOTO_OPN_TARGETS_CLUSTER_4	-0.68	0.07	0	0	0	not significant
7842	CHR18Q23	-0.68	0.06	0	0	0	not significant
7843	GO_RNA_POLYMERASE_I_REGULATORY_REGION_DNA_BINDING	-0.68	0.06	0	0	0	not significant
7844	GO_VASCULAR_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	-0.68	0.06	0	0	0	not significant
7845	HEIDENBLAD_AMPLIFIED_IN_SOFT_TISSUE_CANCER	-0.68	0.06	0	0	0	not significant
7846	BENPORATH_ES_2	-0.68	0.05	0	0	0	not significant
7847	GO_MYOTUBE_CELL_DEVELOPMENT	-0.68	0.05	0	0	0	not significant
7848	GO_PHOTOTRANSDUCTION_VISIBLE_LIGHT	-0.68	0.05	0	0	0	not significant
7849	GO_PROTEIN_NEDDYLATION	-0.68	0.05	0	0	0	not significant
7850	HOEGERKORP_CD44_TARGETS_DIRECT_UP	-0.68	0.05	0	0	0	not significant
7851	WOOD_EBV_EBNA1_TARGETS_DN	-0.68	0.05	0	0	0	not significant
7852	BIOCARTA_ALK_PATHWAY	-0.68	0.04	0	0	0	not significant
7853	BIOCARTA_IL1R_PATHWAY	-0.68	0.04	0	0	0	not significant
7854	CHANGOLKAR_H2AFY_TARGETS_DN	-0.68	0.04	0	0	0	not significant
7855	GO_NEGATIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PA	-0.68	0.04	0	0	0	not significant
7856	GO_NUCLEAR_TRANSCRIBED_MRNA_POLY_A_TAIL_SHORTENING	-0.68	0.04	0	0	0	not significant
7857	HASLINGER_B_CLL_WITH_11Q23_DELETION	-0.68	0.04	0	0	0	not significant
7858	GO_AMYLOID_PRECURSOR_PROTEIN_METABOLIC_PROCESS	-0.68	0.03	0	0	0	not significant
7859	GO_MISMATCH_REPAIR	-0.68	0.03	0	0	0	not significant
7860	GO_WATER_HOMEOSTASIS	-0.68	0.03	0	0	0	not significant
7861	KEGG_INOSITOL_PHOSPHATE_METABOLISM	-0.68	0.03	0	0	0	not significant
7862	REACTOME_DNA_DAMAGE_BYPASS	-0.68	0.02	0	0	0	not significant
7863	GO_FILOPODIUM	-0.68	0.01	0	0	0	not significant
7864	GO_PROTEIN_METHYLATION	-0.68	0.00	0	0	0	not significant
7865	GO_VESICLE_MEDIATED_TRANSPORT_IN_SYNAPSE	-0.68	0.00	0	0	0	not significant
7866	REACTOME_MEIOSIS	-0.68	0.00	0	0	0	not significant
7867	REACTOME_VITAMIN_C_ASCORBATE_METABOLISM	-0.67	0.09	0	0	0	not significant
7868	GO_REGULATION_OF_HISTONE_H2B_UBIQUITINATION	-0.67	0.08	0	0	0	not significant
7869	GO_SATELLITE_DNA_BINDING	-0.67	0.08	0	0	0	not significant
7870	FUJIWARA_PARK2_HEPATOCYTE_PROLIFERATION_DN	-0.67	0.07	0	0	0	not significant
7871	GO_DEOXYRIBONUCLEOSIDE_TRIPHOSPHATE_CATABOLIC_PROCESS	-0.67	0.07	0	0	0	not significant
7872	GO_NEGATIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	-0.67	0.07	0	0	0	not significant
7873	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTC	-0.67	0.07	0	0	0	not significant
7874	GO_PROTEIN_DESUMOYLATION	-0.67	0.07	0	0	0	not significant
7875	GO_REGULATION_OF_BROWN_FAT_CELL_DIFFERENTIATION	-0.67	0.07	0	0	0	not significant
7876	GO_REGULATION_OF_GLUCONEOGENESIS_BY_REGULATION_OF_TRANS	-0.67	0.07	0	0	0	not significant
7877	GO_SNRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_III	-0.67	0.07	0	0	0	not significant
7878	REACTOME_SODIUM_CALCIUM_EXCHANGERS	-0.67	0.07	0	0	0	not significant
7879	GO_POSITIVE_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZAT	-0.67	0.06	0	0	0	not significant
7880	GO_S_ADENOSYLMETHIONINE_METABOLIC_PROCESS	-0.67	0.06	0	0	0	not significant
7881	GO_STAGA_COMPLEX	-0.67	0.06	0	0	0	not significant
7882	REACTOME_MAPK3_ERK1_ACTIVATION	-0.67	0.06	0	0	0	not significant
7883	REACTOME_WNT5A_DEPENDENT_INTERNALIZATION_OF_FZD2_FZD5_AN	-0.67	0.06	0	0	0	not significant
7884	WOTTON_RUNX_TARGETS_UP	-0.67	0.06	0	0	0	not significant
7885	FRIDMAN_IMMORTALIZATION_DN	-0.67	0.05	0	0	0	not significant
7886	GO_3_UTR_MEDIATED_MRNA_DESTABILIZATION	-0.67	0.05	0	0	0	not significant
7887	GO_LYSINE_ACETYLATED_HISTONE_BINDING	-0.67	0.05	0	0	0	not significant
7888	GO_NUCLEAR_EUCHROMATIN	-0.67	0.05	0	0	0	not significant
7889	GO_REGULATION_OF_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PRO	-0.67	0.05	0	0	0	not significant
7890	OUYANG_PROSTATE_CANCER_PROGRESSION_UP	-0.67	0.05	0	0	0	not significant
7891	WALLACE_JAK2_TARGETS_UP	-0.67	0.05	0	0	0	not significant
7892	CHR1Q41	-0.67	0.04	0	0	0	not significant
7893	GO_LONG_TERM_MEMORY	-0.67	0.04	0	0	0	not significant
7894	STEIN_ESRRA_TARGETS_RESPONSIVE_TO_ESTROGEN_UP	-0.67	0.04	0	0	0	not significant
7895	GO_AXON_REGENERATION	-0.67	0.03	0	0	0	not significant
7896	GO_DNA_REPLICATION_ORIGIN_BINDING	-0.67	0.03	0	0	0	not significant
7897	REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTI	-0.67	0.03	0	0	0	not significant
7898	GO_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	-0.67	0.01	0	0	0	not significant
7899	TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP	-0.67	0.01	0	0	0	not significant
7900	GO_CYTOSOLIC_TRANSPORT	-0.67	0.00	0	0	0	not significant
7901	GO_METHYLTRANSFERASE_COMPLEX	-0.67	0.00	0	0	0	not significant
7902	GO_REGULATION_OF_PROTEIN_MONOUBIQUITINATION	-0.66	0.08	0	0	0	not significant
7903	GO_INDOLE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-0.66	0.07	0	0	0	not significant
7904	GO_SKELETAL_MYOFIBRIL_ASSEMBLY	-0.66	0.07	0	0	0	not significant
7905	GO_MAINTENANCE_OF_DNA_METHYLATION	-0.66	0.06	0	0	0	not significant
7906	GO_PHOSPHORYLATED_CARBOHYDRATE_DEPHOSPHORYLATION	-0.66	0.06	0	0	0	not significant
7907	GO_REGULATION_OF_TRANSLATION_AT_SYNAPSE_MODULATING_SYNA	-0.66	0.06	0	0	0	not significant
7908	GO_SECRETORY_GRANULE_LOCALIZATION	-0.66	0.06	0	0	0	not significant
7909	GO_CELLULAR_RESPONSE_TO_PH	-0.66	0.05	0	0	0	not significant
7910	GO_CHROMATIN_SILENCING_AT_TELOMERE	-0.66	0.05	0	0	0	not significant
7911	GO_GOLGI_DISASSEMBLY	-0.66	0.05	0	0	0	not significant
7912	GO_NEGATIVE_REGULATION_OF_STEROID_METABOLIC_PROCESS	-0.66	0.05	0	0	0	not significant
7913	GO_POSITIVE_REGULATION_OF_HISTONE_H3_K4_METHYLATION	-0.66	0.05	0	0	0	not significant
7914	GO_PROTEIN_KINASE_B_BINDING	-0.66	0.05	0	0	0	not significant
7915	GO_PYRIMIDINE_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PRO	-0.66	0.05	0	0	0	not significant
7916	HUMMERICH_BENIGN_SKIN_TUMOR_UP	-0.66	0.05	0	0	0	not significant
7917	AMIT_SERUM_RESPONSE_40_MCF10A	-0.66	0.04	0	0	0	not significant
7918	GO_GALACTOSYLTRANSFERASE_ACTIVITY	-0.66	0.04	0	0	0	not significant
7919	GO_PHOSPHATIDYLINOSITOL_DEPHOSPHORYLATION	-0.66	0.04	0	0	0	not significant
7920	GO_POSITIVE_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENC	-0.66	0.04	0	0	0	not significant
7921	GO_PROTEIN_HYDROXYLATION	-0.66	0.04	0	0	0	not significant
7922	GO_SMOOTH_MUSCLE_CELL_APOPTOTIC_PROCESS	-0.66	0.04	0	0	0	not significant
7923	PID_IL1_PATHWAY	-0.66	0.04	0	0	0	not significant
7924	REACTOME_PCNA_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR	-0.66	0.04	0	0	0	not significant
7925	REACTOME_TICAM1_RIP1_MEDIATED_IKK_COMPLEX_RECRUITMENT	-0.66	0.04	0	0	0	not significant
7926	REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	-0.66	0.04	0	0	0	not significant
7927	KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	-0.66	0.03	0	0	0	not significant
7928	REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_A	-0.66	0.03	0	0	0	not significant
7929	SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN	-0.66	0.03	0	0	0	not significant
7930	ZEMBUTSU_SENSITIVITY_TO_METHOTREXATE	-0.66	0.03	0	0	0	not significant
7931	GO_TRANSCRIPTION_ELONGATION_FACTOR_COMPLEX	-0.66	0.02	0	0	0	not significant
7932	PID_ATM_PATHWAY	-0.66	0.02	0	0	0	not significant
7933	GO_REGULATION_OF_MAINTENANCE_OF_SISTER_CHROMATID_COHESIC	-0.65	0.08	0	0	0	not significant
7934	GO_INSULIN_BINDING	-0.65	0.06	0	0	0	not significant
7935	GO_METHIONINE_BIOSYNTHETIC_PROCESS	-0.65	0.06	0	0	0	not significant
7936	GO_NEGATIVE_REGULATION_OF_HISTONE_H3_K4_METHYLATION	-0.65	0.06	0	0	0	not significant
7937	GO_NEGATIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION	-0.65	0.06	0	0	0	not significant
7938	GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_DEPHOSPHORYLATION	-0.65	0.06	0	0	0	not significant
7939	GO_SPHINGOMYELIN_BIOSYNTHETIC_PROCESS	-0.65	0.06	0	0	0	not significant
7940	REACTOME_FRS2_MEDIATED_ACTIVATION	-0.65	0.06	0	0	0	not significant
7941	GO_INTERLEUKIN_6_BIOSYNTHETIC_PROCESS	-0.65	0.05	0	0	0	not significant
7942	GO_LATE_ENDOSOME_TO_VACUOLE_TRANSPORT_VIA_MULTIVESICULA	-0.65	0.05	0	0	0	not significant
7943	GO_MONOUBIQUITINATED_PROTEIN_DEUBIQUITINATION	-0.65	0.05	0	0	0	not significant
7944	GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	-0.65	0.05	0	0	0	not significant
7945	GO_CHROMATIN_DISASSEMBLY	-0.65	0.04	0	0	0	not significant

7946	GO_CLATHRIN_COAT_ASSEMBLY	-0.65	0.04	0	0	0	not significant
7947	GO_DEOXYRIBONUCLEOTIDE_BIOSYNTHETIC_PROCESS	-0.65	0.04	0	0	0	not significant
7948	GO_ESCRT_III_COMPLEX	-0.65	0.04	0	0	0	not significant
7949	GO_FILOPODIUM_MEMBRANE	-0.65	0.04	0	0	0	not significant
7950	GO_MICROTUBULE_PLUS_END_BINDING	-0.65	0.03	0	0	0	not significant
7951	GO_RESPONSE_TO_CATECHOLAMINE	-0.65	0.03	0	0	0	not significant
7952	GO_SOLUTE_PROTON_ANTIPORTER_ACTIVITY	-0.65	0.03	0	0	0	not significant
7953	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_UP	-0.65	0.03	0	0	0	not significant
7954	PID_AMB2_NEUTROPHILS_PATHWAY	-0.65	0.03	0	0	0	not significant
7955	TAVOR_CEBPA_TARGETS_DN	-0.65	0.03	0	0	0	not significant
7956	GO_MITOCHONDRIAL_FISSION	-0.65	0.02	0	0	0	not significant
7957	GO_NF_KAPPAB_BINDING	-0.65	0.02	0	0	0	not significant
7958	PID_REELIN_PATHWAY	-0.65	0.02	0	0	0	not significant
7959	GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN	-0.65	0.01	0	0	0	not significant
7960	GO_ORGANELLE_TRANSPORT_ALONG_MICROTUBULE	-0.65	0.01	0	0	0	not significant
7961	GO_PIGMENTATION	-0.65	0.01	0	0	0	not significant
7962	DAZARD_RESPONSE_TO_UV_NHEK_DN	-0.65	0.00	0	0	0	not significant
7963	REACTOME_PHOSPHOLIPID_METABOLISM	-0.65	0.00	0	0	0	not significant
7964	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	-0.64	0.06	0	0	0	not significant
7965	GO_PHOSPHATE_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.64	0.06	0	0	0	not significant
7966	GO_REGULATION_OF_RIBONUCLEOPROTEIN_COMPLEX_LOCALIZATION	-0.64	0.06	0	0	0	not significant
7967	GO_ENDOPLASMIC_RETICULUM_LOCALIZATION	-0.64	0.05	0	0	0	not significant
7968	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	-0.64	0.05	0	0	0	not significant
7969	GO_NEGATIVE_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_S	-0.64	0.05	0	0	0	not significant
7970	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_S	-0.64	0.05	0	0	0	not significant
7971	GO_ZINC_ION_IMPORT_ACROSS_PLASMA_MEMBRANE	-0.64	0.05	0	0	0	not significant
7972	GO_ZYMOGEN_GRANULE	-0.64	0.05	0	0	0	not significant
7973	HUMMERICH_MALIGNANT_SKIN_TUMOR_DN	-0.64	0.05	0	0	0	not significant
7974	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	-0.64	0.05	0	0	0	not significant
7975	FIGUEROA_AML_METHYLATION_CLUSTER_6_DN	-0.64	0.04	0	0	0	not significant
7976	GO_CELLULAR_RESPONSE_TO_VITAMIN_D	-0.64	0.04	0	0	0	not significant
7977	GO_EPITHELIAL_CELL_MORPHOGENESIS	-0.64	0.04	0	0	0	not significant
7978	GO_G_RICH_STRAND_TELOMERIC_DNA_BINDING	-0.64	0.04	0	0	0	not significant
7979	GO_NEGATIVE_REGULATION_OF_CIRCADIAN_RHYTHM	-0.64	0.04	0	0	0	not significant
7980	GO_POSITIVE_REGULATION_OF_EPIDERMAL_CELL_DIFFERENTIATION	-0.64	0.04	0	0	0	not significant
7981	GO_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_	-0.64	0.04	0	0	0	not significant
7982	GO_VITAMIN_D_RECEPTOR_BINDING	-0.64	0.04	0	0	0	not significant
7983	GO_ACTIN_CORTICAL_PATCH	-0.64	0.03	0	0	0	not significant
7984	GO_RESPONSE_TO_MISFOLDED_PROTEIN	-0.64	0.03	0	0	0	not significant
7985	REACTOME_AKT_PHOSPHORYLATES_TARGETS_IN_THE_CYTOSOL	-0.64	0.03	0	0	0	not significant
7986	CHR14Q23	-0.64	0.02	0	0	0	not significant
7987	GO_PHOSPHATIDIC_ACID_BIOSYNTHETIC_PROCESS	-0.64	0.02	0	0	0	not significant
7988	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_UP	-0.64	0.01	0	0	0	not significant
7989	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_MECP2	-0.64	0.01	0	0	0	not significant
7990	GO_REPLICATION_FORK	-0.64	0.00	0	0	0	not significant
7991	GO_DEATH_INDUCING_SIGNALING_COMPLEX_ASSEMBLY	-0.63	0.06	0	0	0	not significant
7992	GO_NEGATIVE_REGULATION_OF_MYELINATION	-0.63	0.06	0	0	0	not significant
7993	GO_POSITIVE_REGULATION_OF_DEOXYRIBONUCLEASE_ACTIVITY	-0.63	0.06	0	0	0	not significant
7994	REACTOME_PREGNENOLONE_BIOSYNTHESIS	-0.63	0.06	0	0	0	not significant
7995	DER_IFN_GAMMA_RESPONSE_DN	-0.63	0.05	0	0	0	not significant
7996	GO_LYSOSOMAL_PROTEIN_CATABOLIC_PROCESS	-0.63	0.05	0	0	0	not significant
7997	GO_POSITIVE_REGULATION_OF_SYNAPTIC_VESICLE_RECYCLING	-0.63	0.05	0	0	0	not significant
7998	GO_REGULATION_OF_NON_MOTILE_CILIUM_ASSEMBLY	-0.63	0.05	0	0	0	not significant
7999	GO_RNA_POLYMERASE_III_TYPE_3_PROMOTER_DNA_BINDING	-0.63	0.05	0	0	0	not significant
8000	PID_P38_GAMMA_DELTA_PATHWAY	-0.63	0.05	0	0	0	not significant
8001	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX1_DN	-0.63	0.05	0	0	0	not significant
8002	BIOCARTA_BARR_MAPK_PATHWAY	-0.63	0.04	0	0	0	not significant
8003	GO_ENDOSOME_TO_LYSOSOME_TRANSPORT_VIA_MULTIVESICULAR_B	-0.63	0.04	0	0	0	not significant
8004	GO_MEIOTIC_CHROMOSOME_CONDENSATION	-0.63	0.04	0	0	0	not significant
8005	GO_POSITIVE_REGULATION_OF_NUCLEASE_ACTIVITY	-0.63	0.04	0	0	0	not significant
8006	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_DN	-0.63	0.04	0	0	0	not significant
8007	REACTOME_ROLE_OF_ABL_IN_ROBO_SLIT_SIGNALING	-0.63	0.04	0	0	0	not significant
8008	ZHENG_IL22_SIGNALING_DN	-0.63	0.04	0	0	0	not significant
8009	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN	-0.63	0.03	0	0	0	not significant
8010	GO_CELLULAR_PROTEIN_CONTAINING_COMPLEX_LOCALIZATION	-0.63	0.03	0	0	0	not significant
8011	GO_NUCLEAR_INCLUSION_BODY	-0.63	0.03	0	0	0	not significant
8012	GO_TETRAHYDROFOLATE_METABOLIC_PROCESS	-0.63	0.03	0	0	0	not significant
8013	HU_ANGIOGENESIS_UP	-0.63	0.03	0	0	0	not significant
8014	ROVERSI_GLIOMA_LOH_REGIONS	-0.63	0.03	0	0	0	not significant
8015	GO_MICROTUBULE_END	-0.63	0.02	0	0	0	not significant
8016	GO_PROTEIN_DNA_COMPLEX_DISASSEMBLY	-0.63	0.02	0	0	0	not significant
8017	GO_RAB_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	-0.63	0.02	0	0	0	not significant
8018	REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS	-0.63	0.02	0	0	0	not significant
8019	GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	-0.63	0.01	0	0	0	not significant
8020	KEGG_GLIOMA	-0.63	0.01	0	0	0	not significant
8021	GO_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	-0.63	0.00	0	0	0	not significant
8022	GO_POSITIVE_REGULATION_OF_AUTOPHAGY	-0.63	0.00	0	0	0	not significant
8023	GO_ANGIOGENESIS_INVOLVED_IN_WOUND_HEALING	-0.62	0.05	0	0	0	not significant
8024	GO_AUTOPHAGY_OF_PEROXISOME	-0.62	0.05	0	0	0	not significant
8025	GO_GLYCOPROTEIN_COMPLEX	-0.62	0.05	0	0	0	not significant
8026	GO_NUCLEOSIDE_TRIPHOSPHATE_CATABOLIC_PROCESS	-0.62	0.05	0	0	0	not significant
8027	GO_TETRAHYDROFOLATE_INTERCONVERSION	-0.62	0.05	0	0	0	not significant
8028	REACTOME_DOWNREGULATION_OF_ERBB4_SIGNALING	-0.62	0.05	0	0	0	not significant
8029	GO_CONTRACTILE_RING	-0.62	0.04	0	0	0	not significant
8030	GO_POLYOL_TRANSPORT	-0.62	0.04	0	0	0	not significant
8031	GO_REGULATION_OF_DENDRITIC_SPINE_MAINTENANCE	-0.62	0.04	0	0	0	not significant
8032	GO_SMC5_SMC6_COMPLEX	-0.62	0.04	0	0	0	not significant
8033	GO_SYNAPTIC_VESICLE_ENDOSOMAL_PROCESSING	-0.62	0.04	0	0	0	not significant
8034	BIOCARTA_ERK5_PATHWAY	-0.62	0.03	0	0	0	not significant
8035	DING_LUNG_CANCER_MUTATED_SIGNIFICANTLY	-0.62	0.03	0	0	0	not significant
8036	GO_POSITIVE_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEG	-0.62	0.03	0	0	0	not significant
8037	GO_RDNA_BINDING	-0.62	0.03	0	0	0	not significant
8038	GO_TRANSCRIPTION_EXPORT_COMPLEX	-0.62	0.03	0	0	0	not significant
8039	BIOCARTA_CTCF_PATHWAY	-0.62	0.02	0	0	0	not significant
8040	GO_NEGATIVE_REGULATION_OF_FIBROBLAST_PROLIFERATION	-0.62	0.02	0	0	0	not significant
8041	CHR10Q26	-0.62	0.01	0	0	0	not significant
8042	GO_MUSCLE_CELL_APOPTOTIC_PROCESS	-0.62	0.01	0	0	0	not significant
8043	GO_OVARIAN_FOLLICLE_DEVELOPMENT	-0.62	0.01	0	0	0	not significant
8044	REACTOME_APOPTOTIC_EXECUTION_PHASE	-0.62	0.01	0	0	0	not significant
8045	GO_DOLICHYL_PHOSPHATE_MANNOSE_PROTEIN_MANNOSYLTRANSFER	-0.61	0.05	0	0	0	not significant
8046	GO_L_ASCORBIC_ACID_METABOLIC_PROCESS	-0.61	0.05	0	0	0	not significant
8047	REACTOME_TRAIL_SIGNALING	-0.61	0.05	0	0	0	not significant
8048	GO_LATE_ENDOSOME_TO_LYSOSOME_TRANSPORT	-0.61	0.04	0	0	0	not significant
8049	GO_NEGATIVE_REGULATION_OF_DNA_DAMAGE_RESPONSE_SIGNAL_TR	-0.61	0.04	0	0	0	not significant
8050	GO_NUCLEAR_MEMBRANE_ORGANIZATION	-0.61	0.04	0	0	0	not significant
8051	CHRXQ23	-0.61	0.03	0	0	0	not significant
8052	GO_LATERAL_ELEMENT	-0.61	0.03	0	0	0	not significant
8053	GO_NUCLEOSOME_POSITIONING	-0.61	0.03	0	0	0	not significant
8054	KEGG_ETHER_LIPID_METABOLISM	-0.61	0.03	0	0	0	not significant

8055	REACTOME_ACTIVATION_OF_IRF3_IRF7_MEDIATED_BY_TBK1_IKK_EPSIL	-0.61	0.03	0	0	0	not significant
8056	TURJANSKI_MAPK7_TARGETS	-0.61	0.03	0	0	0	not significant
8057	WENDT_COHESIN_TARGETS_UP	-0.61	0.02	0	0	0	not significant
8058	GO_CUL4_RING_E3_UBIQUITIN_LIGASE_COMPLEX	-0.61	0.01	0	0	0	not significant
8059	GO_NEGATIVE_REGULATION_OF_DNA_REPLICATION	-0.61	0.01	0	0	0	not significant
8060	GO_THYROID_HORMONE_RECEPTOR_BINDING	-0.61	0.01	0	0	0	not significant
8061	REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACT	-0.61	0.01	0	0	0	not significant
8062	BIOCARTA_MAPK_PATHWAY	-0.61	0.00	0	0	0	not significant
8063	GO_ACTIN_FILAMENT_SEVERING	-0.60	0.05	0	0	0	not significant
8064	GO_GROWTH_HORMONE_SECRETION	-0.60	0.04	0	0	0	not significant
8065	GO_MANGANESE_ION_TRANSPORT	-0.60	0.04	0	0	0	not significant
8066	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_EARLY_EI	-0.60	0.04	0	0	0	not significant
8067	GO_POTASSIUM_ION_ANTIPORTER_ACTIVITY	-0.60	0.04	0	0	0	not significant
8068	GO_1_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_3_KINASE_ACTIVITY	-0.60	0.03	0	0	0	not significant
8069	GO_CEREBRAL_CORTEX_NEURON_DIFFERENTIATION	-0.60	0.03	0	0	0	not significant
8070	GO_CONDENSIN_COMPLEX	-0.60	0.03	0	0	0	not significant
8071	GO_INTRINSIC_COMPONENT_OF_PEROXISOMAL_MEMBRANE	-0.60	0.03	0	0	0	not significant
8072	GO_MALE_GERM_CELL_NUCLEUS	-0.60	0.03	0	0	0	not significant
8073	GO_NUCLEAR_LAMINA	-0.60	0.03	0	0	0	not significant
8074	GO_RAL_GTPASE_BINDING	-0.60	0.03	0	0	0	not significant
8075	GO_REGULATION_OF_PLASMA_MEMBRANE_ORGANIZATION	-0.60	0.03	0	0	0	not significant
8076	GO_RESPONSE_TO_CELL_CYCLE_CHECKPOINT_SIGNALING	-0.60	0.03	0	0	0	not significant
8077	REACTOME_GLYCOGEN_SYNTHESIS	-0.60	0.03	0	0	0	not significant
8078	ZEMBUTSU_SENSITIVITY_TO_FLUOROURACIL	-0.60	0.03	0	0	0	not significant
8079	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_SALMON_DN	-0.60	0.02	0	0	0	not significant
8080	GO_CATECHOLAMINE_METABOLIC_PROCESS	-0.60	0.02	0	0	0	not significant
8081	GO_MAINTENANCE_OF_CELL_POLARITY	-0.60	0.02	0	0	0	not significant
8082	GO_NEURON_PROJECTION_REGENERATION	-0.60	0.02	0	0	0	not significant
8083	GO_PERICENTRIC_HETEROCHROMATIN	-0.60	0.02	0	0	0	not significant
8084	GO_VIRAL_BUDDING_VIA_HOST_ESCRT_COMPLEX	-0.60	0.02	0	0	0	not significant
8085	REACTOME_IKK_COMPLEX_RECRUITMENT_MEDIATED_BY_RIP1	-0.60	0.02	0	0	0	not significant
8086	BIOCARTA_BAD_PATHWAY	-0.60	0.01	0	0	0	not significant
8087	BIOCARTA_CREB_PATHWAY	-0.60	0.01	0	0	0	not significant
8088	GO_PHOSPHOLIPID_DEPHOSPHORYLATION	-0.60	0.01	0	0	0	not significant
8089	GO_REGULATION_OF_CENTROSOME_DUPLICATION	-0.60	0.01	0	0	0	not significant
8090	GO_CHROMATIN_REMODELING	-0.60	0.00	0	0	0	not significant
8091	REACTOME_RAB_GEFS_EXCHANGE_GTP_FOR_GDP_ON_RABS	-0.60	0.00	0	0	0	not significant
8092	GO_NEGATIVE_REGULATION_OF_DNA_ENDOREDUPLICATION	-0.59	0.05	0	0	0	not significant
8093	BIOCARTA_VITCB_PATHWAY	-0.59	0.03	0	0	0	not significant
8094	GO_MACROMOLECULE_DEPALMITOYLATION	-0.59	0.03	0	0	0	not significant
8095	GO_NEGATIVE_REGULATION_OF_VOLTAGE_GATED_CALCIUM_CHANNEL	-0.59	0.03	0	0	0	not significant
8096	JI_METASTASIS_REPRESSED_BY_STK11	-0.59	0.03	0	0	0	not significant
8097	GO_MITOTIC_RECOMBINATION	-0.59	0.02	0	0	0	not significant
8098	GO_PHOSPHOTRANSFERASE_ACTIVITY_FOR_OTHER_SUBSTITUTED_PH	-0.59	0.02	0	0	0	not significant
8099	GO_THYROID_GLAND_DEVELOPMENT	-0.59	0.02	0	0	0	not significant
8100	REACTOME_MISMATCH_REPAIR	-0.59	0.02	0	0	0	not significant
8101	GO_SELECTIVE_AUTOPHAGY	-0.59	0.01	0	0	0	not significant
8102	DAZARD_UV_RESPONSE_CLUSTER_G6	-0.59	0.00	0	0	0	not significant
8103	GO_GLYCOLIPID_TRANSPORT	-0.58	0.04	0	0	0	not significant
8104	HEIDENBLAD_AMPLIFIED_IN_BONE_CANCER	-0.58	0.04	0	0	0	not significant
8105	GO_LYSOSOMAL_LUMEN_ACIDIFICATION	-0.58	0.03	0	0	0	not significant
8106	GO_PLATELET_DENSE_GRANULE_ORGANIZATION	-0.58	0.03	0	0	0	not significant
8107	GO_POSITIVE_REGULATION_OF_NEUROTRANSMITTER_SECRETION	-0.58	0.03	0	0	0	not significant
8108	GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS_ENGULFMENT	-0.58	0.03	0	0	0	not significant
8109	GO_PRIMARY_AMINO_COMPOUND_METABOLIC_PROCESS	-0.58	0.03	0	0	0	not significant
8110	GO_PROTEIN_LOCALIZATION_TO_EARLY_ENDOSOME	-0.58	0.03	0	0	0	not significant
8111	GO_REGULATION_OF_MRNA_EXPORT_FROM_NUCLEUS	-0.58	0.03	0	0	0	not significant
8112	GO_RETINAL_GANGLION_CELL_AXON_GUIDANCE	-0.58	0.03	0	0	0	not significant
8113	GO_RNA_POLYMERASE_III_REGULATORY_REGION_DNA_BINDING	-0.58	0.03	0	0	0	not significant
8114	SINGH_KRAS_DEPENDENCY_SIGNATURE_	-0.58	0.03	0	0	0	not significant
8115	BIOCARTA_MYOSIN_PATHWAY	-0.58	0.02	0	0	0	not significant
8116	CHR13Q22	-0.58	0.02	0	0	0	not significant
8117	GO_ESTABLISHMENT_OF_ENDOTHELIAL_INTESTINAL_BARRIER	-0.58	0.02	0	0	0	not significant
8118	GO_INTERLEUKIN_12_BIOSYNTHETIC_PROCESS	-0.58	0.02	0	0	0	not significant
8119	GO_PALMITOYL_PROTEIN_HYDROLASE_ACTIVITY	-0.58	0.02	0	0	0	not significant
8120	GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_ST	-0.58	0.02	0	0	0	not significant
8121	GO_POSITIVE_REGULATION_OF_EARLY_ENDOSOME_TO_LATE_ENDOSC	-0.58	0.02	0	0	0	not significant
8122	GO_POSITIVE_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	-0.58	0.02	0	0	0	not significant
8123	GO_PREFOLDIN_COMPLEX	-0.58	0.02	0	0	0	not significant
8124	GO_PRODUCTION_OF_SIRNA_INVOLVED_IN_RNA_INTERFERENCE	-0.58	0.02	0	0	0	not significant
8125	NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON	-0.58	0.02	0	0	0	not significant
8126	REACTOME_SUMO_IS_PROTEOLYTICALLY_PROCESSED	-0.58	0.02	0	0	0	not significant
8127	BIOCARTA_CXCR4_PATHWAY	-0.58	0.01	0	0	0	not significant
8128	BIOCARTA_GSK3_PATHWAY	-0.58	0.01	0	0	0	not significant
8129	ZHANG_ADIPOGENESIS_BY_BMP7	-0.58	0.01	0	0	0	not significant
8130	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN	-0.58	0.00	0	0	0	not significant
8131	GO_CARDIOLIPIN_BINDING	-0.57	0.03	0	0	0	not significant
8132	GO_CUL4B_RING_E3_UBIQUITIN_LIGASE_COMPLEX	-0.57	0.03	0	0	0	not significant
8133	GO_EIF2ALPHA_PHOSPHORYLATION_IN_RESPONSE_TO_ENDOPLASMIC_	-0.57	0.03	0	0	0	not significant
8134	GO_ORGANIC_ACID_SODIUM_SYMPORTER_ACTIVITY	-0.57	0.03	0	0	0	not significant
8135	GO_S_ADENOSYLMETHIONINE_CYCLE	-0.57	0.03	0	0	0	not significant
8136	CHR8Q11	-0.57	0.02	0	0	0	not significant
8137	GO_ACTIN_FILAMENT_BASED_TRANSPORT	-0.57	0.02	0	0	0	not significant
8138	GO_C4_DICARBOXYLATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.57	0.02	0	0	0	not significant
8139	GO_DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATION	-0.57	0.02	0	0	0	not significant
8140	GO_NEGATIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_AC	-0.57	0.02	0	0	0	not significant
8141	GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_MEMBRANI	-0.57	0.02	0	0	0	not significant
8142	IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_DN	-0.57	0.02	0	0	0	not significant
8143	SHIRAISHI_PLZF_TARGETS_DN	-0.57	0.02	0	0	0	not significant
8144	GO_DYNEIN_COMPLEX	-0.57	0.01	0	0	0	not significant
8145	GO_ERROR_PRONE_TRANSLESION_SYNTHESIS	-0.57	0.01	0	0	0	not significant
8146	GO_PROTEIN_PHOSPHORYLATED_AMINO_ACID_BINDING	-0.57	0.01	0	0	0	not significant
8147	GO_REGULATION_OF_MRNA_POLYADENYLATION	-0.57	0.01	0	0	0	not significant
8148	HEDENFALK_BREAST_CANCER_BRACX_DN	-0.57	0.01	0	0	0	not significant
8149	KYNG_WERNER_SYNDROM_UP	-0.57	0.01	0	0	0	not significant
8150	PID_INTEGRIN_A4B1_PATHWAY	-0.57	0.01	0	0	0	not significant
8151	GO_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	-0.57	0.00	0	0	0	not significant
8152	GO_TRANSCRIPTIONAL_REPRESSOR_COMPLEX	-0.57	0.00	0	0	0	not significant
8153	GO_ESTROGEN_METABOLIC_PROCESS	-0.56	0.03	0	0	0	not significant
8154	GO_SPLICEOSOMAL_CONFORMATIONAL_CHANGES_TO_GENERATE_CAT	-0.56	0.03	0	0	0	not significant
8155	GO_TRANSCRIPTION_FACTOR_AP_1_COMPLEX	-0.56	0.03	0	0	0	not significant
8156	REACTOME_MET_ACTIVATES_RAP1_AND_RAC1	-0.56	0.03	0	0	0	not significant
8157	CHR11P14	-0.56	0.02	0	0	0	not significant
8158	CHR4Q34	-0.56	0.02	0	0	0	not significant
8159	GO_ASTRAL_MICROTUBULE_ORGANIZATION	-0.56	0.02	0	0	0	not significant
8160	GO_REGULATION_OF_HETEROTYPIC_CELL_CELL_ADHESION	-0.56	0.02	0	0	0	not significant
8161	GO_VERY_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	-0.56	0.02	0	0	0	not significant
8162	INAMURA_LUNG_CANCER_SCC_SUBTYPES_DN	-0.56	0.02	0	0	0	not significant
8163	LIU_CMYB_TARGETS_DN	-0.56	0.02	0	0	0	not significant

8164	REACTOME_PHASE_2_PLATEAU_PHASE	-0.56	0.02	0	0	0	not significant
8165	BIOCARTA_CERAMIDE_PATHWAY	-0.56	0.01	0	0	0	not significant
8166	GO_REGULATION_OF_MYOBLAST_FUSION	-0.56	0.01	0	0	0	not significant
8167	GO_TELOMERE_MAINTENANCE_VIA_SEMI_CONSERVATIVE_REPLICATION	-0.56	0.01	0	0	0	not significant
8168	MOREIRA_RESPONSE_TO_TSA_DN	-0.56	0.01	0	0	0	not significant
8169	REACTOME_THE_NLRP3_INFLAMMASOME	-0.56	0.01	0	0	0	not significant
8170	GO_DNA_INSERTION_OR_DELETION_BINDING	-0.55	0.03	0	0	0	not significant
8171	GO_NEGATIVE_REGULATION_OF_HEART_RATE	-0.55	0.02	0	0	0	not significant
8172	GO_NEGATIVE_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	-0.55	0.02	0	0	0	not significant
8173	GO_POSITIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_3_SIGNALING_	-0.55	0.02	0	0	0	not significant
8174	GO_REGULATION_OF_MYOSIN_LIGHT_CHAIN_PHOSPHATASE_ACTIVITY	-0.55	0.02	0	0	0	not significant
8175	GO_SEQUESTERING_OF_METAL_ION	-0.55	0.02	0	0	0	not significant
8176	GO_SKELETAL_MUSCLE_ACETYLCHOLINE_GATED_CHANNEL_CLUSTERI	-0.55	0.02	0	0	0	not significant
8177	PID_THROMBIN_PAR4_PATHWAY	-0.55	0.02	0	0	0	not significant
8178	REACTOME_DEGRADATION_OF_CYSTEINE_AND_HOMOCYSTEINE	-0.55	0.02	0	0	0	not significant
8179	REACTOME_ZINC_TRANSPORTERS	-0.55	0.02	0	0	0	not significant
8180	GO_NEGATIVE_REGULATION_OF_VIRAL_TRANSCRIPTION	-0.55	0.01	0	0	0	not significant
8181	GO_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	-0.55	0.01	0	0	0	not significant
8182	REACTOME_SYNTHESIS_OF_PC	-0.55	0.01	0	0	0	not significant
8183	REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS	-0.55	0.01	0	0	0	not significant
8184	REACTOME_UPTAKE_AND_ACTIONS_OF_BACTERIAL_TOXINS	-0.55	0.01	0	0	0	not significant
8185	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_DN	-0.55	0.00	0	0	0	not significant
8186	KEGG_ENDOMETRIAL_CANCER	-0.55	0.00	0	0	0	not significant
8187	GO_MONOCYTE_CHEMOTACTIC_PROTEIN_1_PRODUCTION	-0.54	0.03	0	0	0	not significant
8188	GO_REGULATION_OF_XENOPHAGY	-0.54	0.03	0	0	0	not significant
8189	GO_COPI_COATED_VESICLE_BUDDING	-0.54	0.02	0	0	0	not significant
8190	GO_COPI_VESICLE_COAT	-0.54	0.02	0	0	0	not significant
8191	GO_GAMMA_AMINOBUTYRIC_ACID_SECRETION	-0.54	0.02	0	0	0	not significant
8192	GO_MEIOTIC_COHESIN_COMPLEX	-0.54	0.02	0	0	0	not significant
8193	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OX	-0.54	0.02	0	0	0	not significant
8194	GO_PURINE_NUCLEOSIDE_CATABOLIC_PROCESS	-0.54	0.02	0	0	0	not significant
8195	GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_LOCALIZATION	-0.54	0.02	0	0	0	not significant
8196	SUZUKI_AMPLIFIED_IN_ORAL_CANCER	-0.54	0.02	0	0	0	not significant
8197	GO_ENDOPLASMIC_RETICULUM_TUBULAR_NETWORK	-0.54	0.01	0	0	0	not significant
8198	GO_INTRACELLULAR_DISTRIBUTION_OF_MITOCHONDRIA	-0.54	0.01	0	0	0	not significant
8199	GO_NEGATIVE_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCES	-0.54	0.01	0	0	0	not significant
8200	GO_PYRIMIDINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROC	-0.54	0.01	0	0	0	not significant
8201	GO_REGULATION_OF_TRANSLATIONAL_INITIATION_BY_EIF2_ALPHA_PH	-0.54	0.01	0	0	0	not significant
8202	MATZUK_SPERMATOGONIA	-0.54	0.01	0	0	0	not significant
8203	REACTOME_TRANSLESION_SYNTHESIS_BY_POLK	-0.54	0.01	0	0	0	not significant
8204	GO_BLOC_COMPLEX	-0.54	0.00	0	0	0	not significant
8205	GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	-0.54	0.00	0	0	0	not significant
8206	BIOCARTA_BARRESTIN_PATHWAY	-0.53	0.02	0	0	0	not significant
8207	GO_GAMMA_AMINOBUTYRIC_ACID_TRANSPORT	-0.53	0.02	0	0	0	not significant
8208	GO_HISTONE_H3_K27_TRIMETHYLATION	-0.53	0.02	0	0	0	not significant
8209	GO_MSL_COMPLEX	-0.53	0.02	0	0	0	not significant
8210	GO_NEGATIVE_REGULATION_OF_PROTEIN_K63_LINKED_UBIQUITINATIO	-0.53	0.02	0	0	0	not significant
8211	GO_SHELTERIN_COMPLEX	-0.53	0.02	0	0	0	not significant
8212	GO_SPANNING_COMPONENT_OF_MEMBRANE	-0.53	0.02	0	0	0	not significant
8213	GO_SUMO_SPECIFIC_PROTEASE_ACTIVITY	-0.53	0.02	0	0	0	not significant
8214	RUAN_RESPONSE_TO_TROGLITAZONE_DN	-0.53	0.02	0	0	0	not significant
8215	BENPORATH_ES_CORE_NINE	-0.53	0.01	0	0	0	not significant
8216	GO_DEOXYRIBONUCLEOTIDE_BINDING	-0.53	0.01	0	0	0	not significant
8217	GO_ESTABLISHMENT_OF_PIGMENT_GRANULE_LOCALIZATION	-0.53	0.01	0	0	0	not significant
8218	GO_LEWY_BODY	-0.53	0.01	0	0	0	not significant
8219	GO_POSITIVE_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	-0.53	0.01	0	0	0	not significant
8220	GO_POSITIVE_REGULATION_OF_CENTROSOME_CYCLE	-0.53	0.01	0	0	0	not significant
8221	GO_POSITIVE_REGULATION_OF_MYELINATION	-0.53	0.01	0	0	0	not significant
8222	GO_VASCULAR_ASSOCIATED_SMOOTH_MUSCLE_CELL_MIGRATION	-0.53	0.01	0	0	0	not significant
8223	GO_CELLULAR_RESPONSE_TO_VITAMIN	-0.53	0.00	0	0	0	not significant
8224	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITI	-0.53	0.00	0	0	0	not significant
8225	GO_TRANSITION_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIV	-0.53	0.00	0	0	0	not significant
8226	GO_RESPONSE_TO_LIGHT_INTENSITY	-0.52	0.02	0	0	0	not significant
8227	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION_OF_UNSA	-0.52	0.02	0	0	0	not significant
8228	CHR4Q35	-0.52	0.01	0	0	0	not significant
8229	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_DN	-0.52	0.01	0	0	0	not significant
8230	GO_ACTIVATION_OF_NF_KAPPAB_INDUCING_KINASE_ACTIVITY	-0.52	0.01	0	0	0	not significant
8231	GO_ZINC_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.52	0.01	0	0	0	not significant
8232	REACTOME_REGULATION_OF_IFNG_SIGNALING	-0.52	0.01	0	0	0	not significant
8233	GO_2_OXOGLUTARATE_DEPENDENT_DIOXYGENASE_ACTIVITY	-0.52	0.00	0	0	0	not significant
8234	CHR4P13	-0.51	0.02	0	0	0	not significant
8235	GO_TRANSCRIPTION_FACTOR_TFIIIB_COMPLEX	-0.51	0.02	0	0	0	not significant
8236	BIOCARTA_BCELLSURVIVAL_PATHWAY	-0.51	0.01	0	0	0	not significant
8237	GO_CARDIAC_MYOFIBRIL_ASSEMBLY	-0.51	0.01	0	0	0	not significant
8238	GO_COMMON_MYELOID_PROGENITOR_CELL_PROLIFERATION	-0.51	0.01	0	0	0	not significant
8239	GO_NEGATIVE_REGULATION_OF_PLATELET_DERIVED_GROWTH_FACT	-0.51	0.01	0	0	0	not significant
8240	GO_REGULATION_OF_HEXOKINASE_ACTIVITY	-0.51	0.01	0	0	0	not significant
8241	GO_RESPONSE_TO_LEAD_ION	-0.51	0.01	0	0	0	not significant
8242	GO_TYPE_B_PANCREATIC_CELL_PROLIFERATION	-0.51	0.01	0	0	0	not significant
8243	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_DN	-0.51	0.01	0	0	0	not significant
8244	CHR5P13	-0.51	0.00	0	0	0	not significant
8245	GENTILE_RESPONSE_CLUSTER_D3	-0.51	0.00	0	0	0	not significant
8246	GO_FOLIC_ACID_BINDING	-0.51	0.00	0	0	0	not significant
8247	GO_NEGATIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	-0.51	0.00	0	0	0	not significant
8248	PID_TRAIL_PATHWAY	-0.51	0.00	0	0	0	not significant
8249	REACTOME_RECOGNITION_OF_DNA_DAMAGE_BY_PCNA_CONTAINING_R	-0.51	0.00	0	0	0	not significant
8250	GO_1_ACYLGLYCEROPHOSPHOCHOLINE_O_ACYLTRANSFERASE_ACTIV	-0.50	0.02	0	0	0	not significant
8251	BIOCARTA_CK1_PATHWAY	-0.50	0.01	0	0	0	not significant
8252	BIOCARTA_RNAPOL3_PATHWAY	-0.50	0.01	0	0	0	not significant
8253	GO_CD4_RECEPTOR_BINDING	-0.50	0.01	0	0	0	not significant
8254	GO_MRE11_COMPLEX	-0.50	0.01	0	0	0	not significant
8255	GO_NEURON_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPON	-0.50	0.01	0	0	0	not significant
8256	GO_PEPTIDYL_PROLINE_4_DIOXYGENASE_ACTIVITY	-0.50	0.01	0	0	0	not significant
8257	GO_PEPTIDYL_PROLINE_HYDROXYLATION_TO_4_HYDROXY_L_PROLINE	-0.50	0.01	0	0	0	not significant
8258	GO_POSITIVE_REGULATION_OF_PROTEIN_HOMODIMERIZATION_ACTIVIT	-0.50	0.01	0	0	0	not significant
8259	GO_REGULATION_OF_NEURON_PROJECTION_REGENERATION	-0.50	0.01	0	0	0	not significant
8260	GO_SUMO_POLYMER_BINDING	-0.50	0.01	0	0	0	not significant
8261	NAGY_STAGA_COMPONENTS_HUMAN	-0.50	0.01	0	0	0	not significant
8262	WEBER_METHYLATED_HCP_IN_SPERM_UP	-0.50	0.01	0	0	0	not significant
8263	FINETTI_BREAST_CANCERS_KINOME_GRAY	-0.50	0.00	0	0	0	not significant
8264	GO_ENDODERMAL_CELL_FATE_COMMITMENT	-0.50	0.00	0	0	0	not significant
8265	GO_POLY_A_PLUS_MRNA_EXPORT_FROM_NUCLEUS	-0.50	0.00	0	0	0	not significant
8266	GO_UV_DAMAGE_EXCISION_REPAIR	-0.50	0.00	0	0	0	not significant
8267	CHR14Q31	-0.49	0.01	0	0	0	not significant
8268	GO_NEGATIVE_REGULATION_OF_CELL_SIZE	-0.49	0.01	0	0	0	not significant
8269	GO_NEUROPEPTIDE_RECEPTOR_ACTIVITY	-0.49	0.01	0	0	0	not significant
8270	GO_PANTOTHENATE_METABOLIC_PROCESS	-0.49	0.01	0	0	0	not significant
8271	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX4_UP	-0.49	0.01	0	0	0	not significant
8272	GO_ENDOSOME_TRANSPORT_VIA_MULTIVESICULAR_BODY_SORTING_P	-0.49	0.00	0	0	0	not significant

8273	GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_KINASE_ACTIVITY	-0.49	0.00	0	0	0	not significant
8274	REACTOME_CLASS_I_PEROXISOMAL_MEMBRANE_PROTEIN_IMPORT	-0.49	0.00	0	0	0	not significant
8275	GO_RESPONSE_TO_DEFENSES_OF_OTHER_ORGANISM_INVOLVED_IN_S	-0.48	0.01	0	0	0	not significant
8276	BIOCARTA_PLC_PATHWAY	-0.48	0.00	0	0	0	not significant
8277	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN	-0.48	0.00	0	0	0	not significant
8278	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_RED_DN	-0.48	0.00	0	0	0	not significant
8279	GO_DNA_STRAND_ELONGATION	-0.48	0.00	0	0	0	not significant
8280	GO_PROTEIN_LOCALIZATION_TO_CILIARY_MEMBRANE	-0.48	0.00	0	0	0	not significant
8281	GO_REGULATION_OF_RESPONSE_TO_FOOD	-0.48	0.00	0	0	0	not significant
8282	GO_SEX_CHROMOSOME	-0.48	0.00	0	0	0	not significant
8283	GO_INTRACILIARY_TRANSPORT_PARTICLE	-0.47	0.01	0	0	0	not significant
8284	GO_MITOCHONDRIAL_TRICARBOXYLIC_ACID_CYCLE_ENZYME_COMPLEX	-0.47	0.01	0	0	0	not significant
8285	REACTOME_RUNX2_REGULATES_GENES_INVOLVED_IN_CELL_MIGRATIO	-0.47	0.01	0	0	0	not significant
8286	GO_GENITALIA_MORPHOGENESIS	-0.47	0.00	0	0	0	not significant
8287	GO_MULTI_ORGANISM_BEHAVIOR	-0.47	0.00	0	0	0	not significant
8288	GO_PEPTIDYL_PROLINE_DIOXYGENASE_ACTIVITY	-0.47	0.00	0	0	0	not significant
8289	GO_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	-0.47	0.00	0	0	0	not significant
8290	GO_POSITIVE_REGULATION_OF_HISTONE_H4_ACETYLATION	-0.47	0.00	0	0	0	not significant
8291	REACTOME_INFLAMMASOMES	-0.47	0.00	0	0	0	not significant
8292	GO_3_5_DNA_HELICASE_ACTIVITY	-0.46	0.00	0	0	0	not significant
8293	GO_REGULATION_OF_CENTRIOLE_REPLICATION	-0.46	0.00	0	0	0	not significant
8294	GO_REGULATION_OF_MDA_5_SIGNALING_PATHWAY	-0.46	0.00	0	0	0	not significant
8295	GO_CHROMATIN_SILENCING_COMPLEX	-0.44	0.00	0	0	0	not significant
8296	GO_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHWAY	-0.44	0.00	0	0	0	not significant
8297	GO_REGULATION_OF_NEURON_MATURATION	-0.44	0.00	0	0	0	not significant
8298	PID_ERB_GENOMIC_PATHWAY	-0.44	0.00	0	0	0	not significant
8299	REACTOME_TBC_RABGAPS	-0.44	0.00	0	0	0	not significant
8300	GO_POSITIVE_REGULATION_OF_KERATINOCYTE_DIFFERENTIATION	-0.43	0.00	0	0	0	not significant
8301	GO_REGULATION_OF_APPETITE	-0.43	0.00	0	0	0	not significant
8302	GO_GABA_ERGIC_SYNAPSE	-0.42	0.00	0	0	0	not significant
8303	GO_LYSOPHOSPHOLIPASE_ACTIVITY	-0.42	0.00	0	0	0	not significant
8304	GO_NEGATIVE_REGULATION_OF_PROTEIN_POLYUBIQUITINATION	-0.42	0.00	0	0	0	not significant
8305	GO_MCM_COMPLEX	-0.41	0.00	0	0	0	not significant
8306	GO_NEGATIVE_REGULATION_OF_MYOSIN_LIGHT_CHAIN_PHOSPHATASE_	-0.41	0.00	0	0	0	not significant
8307	REACTOME_ESTABLISHMENT_OF_SISTER_CHROMATID_COHESION	-0.41	0.00	0	0	0	not significant
8308	REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_C_STRAND_OF_THE_TE	-0.41	0.00	0	0	0	not significant
8309	GO_PROTEIN_HEXAMERIZATION	-0.40	0.00	0	0	0	not significant
8310	GO_TUBULAR_ENDOSOME	-0.40	0.00	0	0	0	not significant
8311	GO_METHIONINE_METABOLIC_PROCESS	-0.39	0.00	0	0	0	not significant
8312	GO_NUCLEAR_OUTER_MEMBRANE	-0.39	0.00	0	0	0	not significant
8313	REACTOME_DNA_STRAND_ELONGATION	-0.36	0.00	0	0	0	not significant
8314	GO_PROTEIN_LOCALIZATION_TO_CELL_JUNCTION	-0.35	0.00	0	0	0	not significant
8315	GO_MAINTENANCE_OF_SISTER_CHROMATID_COHESION	0.34	0.00	0	0	0	not significant
8316	GO_MISMATCH_REPAIR_COMPLEX_BINDING	0.38	0.00	0	0	0	not significant
8317	GO_CARD_DOMAIN_BINDING	0.39	0.00	0	0	0	not significant
8318	GO_HISTONE_METHYLTRANSFERASE_ACTIVITY_H3_K27_SPECIFIC_	0.40	0.00	0	0	0	not significant
8319	GO_MITOTIC_CHROMOSOME_CONDENSATION	0.40	0.00	0	0	0	not significant
8320	GO_NEGATIVE_REGULATION_OF_MUSCLE_ADAPTATION	0.41	0.00	0	0	0	not significant
8321	GO_POSITIVE_REGULATION_OF_AUTOPHAGY_OF_MITOCHONDRION	0.41	0.00	0	0	0	not significant
8322	GO_REGULATION_OF_MITOCHONDRIAL_FUSION	0.41	0.00	0	0	0	not significant
8323	GO_MESSENGER_RIBONUCLEOPROTEIN_COMPLEX	0.42	0.00	0	0	0	not significant
8324	GO_MUTSALPHA_COMPLEX_BINDING	0.42	0.00	0	0	0	not significant
8325	GO_NEGATIVE_REGULATION_OF_HISTONE_H3_K9_TRIMETHYLATION	0.42	0.00	0	0	0	not significant
8326	GO_OLIGOSACCHARIDE_BIOSYNTHETIC_PROCESS	0.42	0.00	0	0	0	not significant
8327	GO_PYRIMIDINE_NUCLEOTIDE_SALVAGE	0.42	0.00	0	0	0	not significant
8328	GO_REGULATION_OF_CILIUM_BEAT_FREQUENCY_INVOLVED_IN_CILIARY	0.42	0.00	0	0	0	not significant
8329	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CILIUM	0.42	0.00	0	0	0	not significant
8330	GO_SULFATE_TRANSPORT	0.42	0.00	0	0	0	not significant
8331	GO_BRCA1_A_COMPLEX	0.43	0.00	0	0	0	not significant
8332	GO_PHOTORECEPTOR_DISC_MEMBRANE	0.43	0.00	0	0	0	not significant
8333	GO_REGULATION_OF_MITOTIC_RECOMBINATION	0.43	0.00	0	0	0	not significant
8334	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	0.43	0.00	0	0	0	not significant
8335	GO_INTRASPECIES_INTERACTION_BETWEEN_ORGANISMS	0.44	0.00	0	0	0	not significant
8336	GO_NEGATIVE_REGULATION_OF_HISTONE_METHYLATION	0.44	0.00	0	0	0	not significant
8337	ONGUSAHA_BRCA1_TARGETS_DN	0.44	0.00	0	0	0	not significant
8338	BILD_CTNNB1_ONCOGENIC_SIGNATURE	0.45	0.00	0	0	0	not significant
8339	GO_ACYL_COA_DEHYDROGENASE_ACTIVITY	0.45	0.00	0	0	0	not significant
8340	GO_ATP_DEPENDENT_MICROTUBULE_MOTOR_ACTIVITY_MINUS_END_DI	0.45	0.00	0	0	0	not significant
8341	GO_CELL_CELL_ADHESION_INVOLVED_IN_GASTRULATION	0.45	0.00	0	0	0	not significant
8342	GO_CHOLINE_TRANSPORT	0.45	0.00	0	0	0	not significant
8343	GO_INSULIN_RESPONSIVE_COMPARTMENT	0.45	0.00	0	0	0	not significant
8344	GO_NEGATIVE_REGULATION_OF_HISTONE_MODIFICATION	0.45	0.00	0	0	0	not significant
8345	GO_REPLICATION_FORK_PROCESSING	0.45	0.00	0	0	0	not significant
8346	GO_3_PHOSPHOADENOSINE_5_PHOSPHOSULFATE_METABOLIC_PROCES	0.46	0.01	0	0	0	not significant
8347	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_SINGLE_DONORS_WITH_	0.46	0.01	0	0	0	not significant
8348	GO_HETEROCHROMATIN_ORGANIZATION	0.46	0.00	0	0	0	not significant
8349	GO_REGULATION_OF_INTERLEUKIN_2_SECRETION	0.46	0.00	0	0	0	not significant
8350	GO_REGULATION_OF_WATER_LOSS_VIA_SKIN	0.46	0.00	0	0	0	not significant
8351	GO_REPLISOME	0.46	0.00	0	0	0	not significant
8352	GO_SYNTAXIN_1_BINDING	0.46	0.00	0	0	0	not significant
8353	GO_UDP_N_ACETYLGLUCOSAMINE_METABOLIC_PROCESS	0.46	0.00	0	0	0	not significant
8354	REACTOME_ATTACHMENT_OF_GPI_ANCHOR_TO_UPAR	0.46	0.00	0	0	0	not significant
8355	REACTOME_PECAM1_INTERACTIONS	0.46	0.00	0	0	0	not significant
8356	GO_AUDITORY_RECEPTOR_CELL_MORPHOGENESIS	0.47	0.01	0	0	0	not significant
8357	GO_CENTROMERIC_DNA_BINDING	0.47	0.01	0	0	0	not significant
8358	GO_CIRCADIAN_SLEEP_WAKE_CYCLE	0.47	0.01	0	0	0	not significant
8359	GO_PLATELET_ALPHA_GRANULE_MEMBRANE	0.47	0.01	0	0	0	not significant
8360	GO_POSITIVE_REGULATION_OF_GLUCOKINASE_ACTIVITY	0.47	0.00	0	0	0	not significant
8361	GO_POSITIVE_REGULATION_OF_HEXOKINASE_ACTIVITY	0.47	0.00	0	0	0	not significant
8362	GO_SULFATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.47	0.00	0	0	0	not significant
8363	GO_SYMMETRIC_SYNAPSE	0.47	0.00	0	0	0	not significant
8364	ELLWOOD_MYC_TARGETS_UP	0.48	0.01	0	0	0	not significant
8365	GO_ASYMMETRIC_STEM_CELL_DIVISION	0.48	0.01	0	0	0	not significant
8366	GO_CARDIOLIPIN_METABOLIC_PROCESS	0.48	0.01	0	0	0	not significant
8367	GO_HISTONE_METHYLTRANSFERASE_ACTIVITY_H3_K4_SPECIFIC_	0.48	0.01	0	0	0	not significant
8368	GO_CELL_CELL_JUNCTION_MAINTENANCE	0.48	0.00	0	0	0	not significant
8369	GO_NEGATIVE_REGULATION_OF_VIRAL_RELEASE_FROM_HOST_CELL	0.48	0.00	0	0	0	not significant
8370	GO_REGULATION_OF_HISTONE_H3_K9_TRIMETHYLATION	0.48	0.00	0	0	0	not significant
8371	GO_REGULATION_OF_PROTEIN_POLYUBIQUITINATION	0.48	0.00	0	0	0	not significant
8372	GO_CUL4A_RING_E3_UBIQUITIN_LIGASE_COMPLEX	0.49	0.01	0	0	0	not significant
8373	GO_FUCOSYLTRANSFERASE_ACTIVITY	0.49	0.01	0	0	0	not significant
8374	GO_MIRNA_METABOLIC_PROCESS	0.49	0.01	0	0	0	not significant
8375	GO_POSITIVE_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATI	0.49	0.01	0	0	0	not significant
8376	GO_PROTEIN_O_LINKED_MANNOSYLATION	0.49	0.01	0	0	0	not significant
8377	GO_FLEMMING_BODY	0.49	0.00	0	0	0	not significant
8378	GO_HEPARAN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	0.49	0.00	0	0	0	not significant
8379	GO_NEGATIVE_REGULATION_OF_MRNA_3_END_PROCESSING	0.49	0.00	0	0	0	not significant
8380	REACTOME_GAP_FILLING_DNA_REPAIR_SYNTHESIS_AND_LIGATION_IN_	0.49	0.00	0	0	0	not significant
8381	REACTOME_LAGGING_STRAND_SYNTHESIS	0.49	0.00	0	0	0	not significant

8382	BIOCARTA_SAM68_PATHWAY	0.50	0.01	0	0	0	not significant
8383	GO_BETA_2_ADRENERGIC_RECEPTOR_BINDING	0.50	0.01	0	0	0	not significant
8384	GO_CAVEOLIN_MEDIATED_ENDOCYTOSIS	0.50	0.01	0	0	0	not significant
8385	GO_NEURON_FATE_SPECIFICATION	0.50	0.01	0	0	0	not significant
8386	GO_PERINUCLEAR_ENDOPLASMIC_RETICULUM	0.50	0.01	0	0	0	not significant
8387	GO_PROTEIN_LOCALIZATION_TO_ENDOSOME	0.50	0.01	0	0	0	not significant
8388	GO_TELOMERIC_LOOP_DISASSEMBLY	0.50	0.01	0	0	0	not significant
8389	GO_XENOPHAGY	0.50	0.01	0	0	0	not significant
8390	REACTOME_BETA_OXIDATION_OF_OCTANOYL_COA_TO_HEXANOYL_CO	0.50	0.01	0	0	0	not significant
8391	REACTOME_COHESIN_LOADING_ONTO_CHROMATIN	0.50	0.01	0	0	0	not significant
8392	REACTOME_VITAMIN_D_CALCIFEROL_METABOLISM	0.50	0.01	0	0	0	not significant
8393	CHR13Q34	0.50	0.00	0	0	0	not significant
8394	GO_R_SMAD_BINDING	0.50	0.00	0	0	0	not significant
8395	GO_AMINO_ACID_SALVAGE	0.51	0.02	0	0	0	not significant
8396	GO_ATP_DEPENDENT_3_5_DNA_HELICASE_ACTIVITY	0.51	0.01	0	0	0	not significant
8397	GO_AUDITORY_RECEPTOR_CELL_STEREOCILIUM_ORGANIZATION	0.51	0.01	0	0	0	not significant
8398	GO_L_METHIONINE_SALVAGE_FROM_METHYLTHIOADENOSINE	0.51	0.01	0	0	0	not significant
8399	GO_POSITIVE_REGULATION_OF_AUTOPHAGOSOME_MATURATION	0.51	0.01	0	0	0	not significant
8400	GO_PURINE_DEOXYRIBONUCLEOTIDE_CATABOLIC_PROCESS	0.51	0.01	0	0	0	not significant
8401	GO_REGULATION_OF_FERTILIZATION	0.51	0.01	0	0	0	not significant
8402	GO_REGULATION_OF_HISTONE_H3_K9_METHYLATION	0.51	0.01	0	0	0	not significant
8403	REACTOME_NEGATIVE_FEEDBACK_REGULATION_OF_MAPK_PATHWAY	0.51	0.01	0	0	0	not significant
8404	REACTOME_PROTON_COUPLED_MONOCARBOXYLATE_TRANSPORT	0.51	0.01	0	0	0	not significant
8405	GO_DNA_DAMAGE_RESPONSE_DETECTION_OF_DNA_DAMAGE	0.51	0.00	0	0	0	not significant
8406	GO_HISTONE_LYSINE_N_METHYLTRANSFERASE_ACTIVITY	0.51	0.00	0	0	0	not significant
8407	GO_PEROXISOMAL_MEMBRANE_TRANSPORT	0.51	0.00	0	0	0	not significant
8408	PID_ERBB1_RECEPTOR_PROXIMAL_PATHWAY	0.51	0.00	0	0	0	not significant
8409	GO_D1_DOPAMINE_RECEPTOR_BINDING	0.52	0.02	0	0	0	not significant
8410	GO_NEGATIVE_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZAT	0.52	0.02	0	0	0	not significant
8411	GO_REGULATION_OF_CELL_CELL_ADHESION_MEDIATED_BY_INTEGRIN	0.52	0.02	0	0	0	not significant
8412	CHR7Q33	0.52	0.01	0	0	0	not significant
8413	GO_PEPTIDYL_THREONINE_DEPHOSPHORYLATION	0.52	0.01	0	0	0	not significant
8414	GO_POSITIVE_REGULATION_OF_ERBB_SIGNALING_PATHWAY	0.52	0.01	0	0	0	not significant
8415	GO_POSITIVE_REGULATION_OF_MACROPHAGE_MIGRATION	0.52	0.01	0	0	0	not significant
8416	GO_RESPONSE_TO_STIMULUS_INVOLVED_IN_REGULATION_OF_MUSCLE	0.52	0.01	0	0	0	not significant
8417	REACTOME_ALPHA_OXIDATION_OF_PHYTANATE	0.52	0.01	0	0	0	not significant
8418	GO_PHOSPHATIDYLINOSITOL_METABOLIC_PROCESS	0.52	0.00	0	0	0	not significant
8419	LEE_CALORIE_RESTRICTION_NEOCORTEX_UP	0.52	0.00	0	0	0	not significant
8420	SCHEIDEREIT_IKK_TARGETS	0.52	0.00	0	0	0	not significant
8421	GO_GPI_ANCHOR_TRANSAMIDASE_ACTIVITY	0.53	0.02	0	0	0	not significant
8422	GO_RNA_DNA_HYBRID_RIBONUCLEASE_ACTIVITY	0.53	0.02	0	0	0	not significant
8423	ASGHARZADEH_NEUROBLASTOMA_POOR_SURVIVAL_DN	0.53	0.01	0	0	0	not significant
8424	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_YELLOW_UP	0.53	0.01	0	0	0	not significant
8425	GO_DYNEIN_HEAVY_CHAIN_BINDING	0.53	0.01	0	0	0	not significant
8426	GO_ENDONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXY	0.53	0.01	0	0	0	not significant
8427	GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGN	0.53	0.01	0	0	0	not significant
8428	GO_POSITIVE_REGULATION_OF_TOLERANCE_INDUCTION	0.53	0.01	0	0	0	not significant
8429	GO_SIN3_COMPLEX	0.53	0.01	0	0	0	not significant
8430	GO_TRICARBOXYLIC_ACID_CYCLE_ENZYME_COMPLEX	0.53	0.01	0	0	0	not significant
8431	REACTOME_LEADING_STRAND_SYNTHESIS	0.53	0.01	0	0	0	not significant
8432	REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND	0.53	0.01	0	0	0	not significant
8433	REACTOME_RETROGRADE_TRANSPORT_AT_THE_TRANS_GOLGI_NETW	0.53	0.00	0	0	0	not significant
8434	GO_PRE_MRNA_3_SPLICE_SITE_BINDING	0.54	0.03	0	0	0	not significant
8435	CHR11Q25	0.54	0.02	0	0	0	not significant
8436	GO_COLLAGEN_METABOLIC_PROCESS	0.54	0.02	0	0	0	not significant
8437	GO_EMBRYONIC_BODY_MORPHOGENESIS	0.54	0.02	0	0	0	not significant
8438	GO_GPI_ANCHOR_TRANSAMIDASE_COMPLEX	0.54	0.02	0	0	0	not significant
8439	GO_MACROPHAGE_CYTOKINE_PRODUCTION	0.54	0.02	0	0	0	not significant
8440	GO_PEPTIDYL_LYSINE_DEACETYLATION	0.54	0.02	0	0	0	not significant
8441	GO_PROTEIN_PHOSPHATASE_1_BINDING	0.54	0.02	0	0	0	not significant
8442	GO_RNA_POLYMERASE_I_PREINITIATION_COMPLEX_ASSEMBLY	0.54	0.02	0	0	0	not significant
8443	MCCABE_HOXC6_TARGETS_UP	0.54	0.02	0	0	0	not significant
8444	GO_HISTONE_H3_K9_TRIMETHYLATION	0.54	0.01	0	0	0	not significant
8445	GO_NEGATIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	0.54	0.01	0	0	0	not significant
8446	GO_REGULATION_OF_EARLY_ENDOSOME_TO_LATE_ENDOSOME_TRAN	0.54	0.01	0	0	0	not significant
8447	REACTOME_BETA_OXIDATION_OF_HEXANOYL_COA_TO_BUTANOYL_CO	0.54	0.01	0	0	0	not significant
8448	REACTOME_SPRY_REGULATION_OF_FGF_SIGNALING	0.54	0.01	0	0	0	not significant
8449	CHR3Q26	0.54	0.00	0	0	0	not significant
8450	GO_LYSINE_N_METHYLTRANSFERASE_ACTIVITY	0.54	0.00	0	0	0	not significant
8451	NIKOLSKY_MUTATED_AND_AMPLIFIED_IN_BREAST_CANCER	0.54	0.00	0	0	0	not significant
8452	GO_ELONGATOR_HOLOENZYME_COMPLEX	0.55	0.02	0	0	0	not significant
8453	GO_EMBRYONIC_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	0.55	0.02	0	0	0	not significant
8454	GO_REGULATION_OF_METHYLATION_DEPENDENT_CHROMATIN_SILENCI	0.55	0.02	0	0	0	not significant
8455	GO_TELOMERIC_D_LOOP_DISASSEMBLY	0.55	0.02	0	0	0	not significant
8456	BIOCARTA_DEATH_PATHWAY	0.55	0.01	0	0	0	not significant
8457	GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGI	0.55	0.01	0	0	0	not significant
8458	GO_POSITIVE_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	0.55	0.01	0	0	0	not significant
8459	GO_REGULATION_OF_HISTONE_H3_K4_METHYLATION	0.55	0.01	0	0	0	not significant
8460	KRAS.50_UP.V1_DN	0.55	0.01	0	0	0	not significant
8461	REACTOME_REGULATION_OF_MECP2_EXPRESSION_AND_ACTIVITY	0.55	0.01	0	0	0	not significant
8462	GO_MORPHOGENESIS_OF_AN_EPITHELIAL_SHEET	0.55	0.00	0	0	0	not significant
8463	GO_PEPTIDE_N_ACETYLTRANSFERASE_ACTIVITY	0.55	0.00	0	0	0	not significant
8464	REACTOME_RAB_REGULATION_OF_TRAFFICKING	0.55	0.00	0	0	0	not significant
8465	GO_CYCLOHYDROLASE_ACTIVITY	0.56	0.03	0	0	0	not significant
8466	GO_NPBAF_COMPLEX	0.56	0.03	0	0	0	not significant
8467	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF	0.56	0.03	0	0	0	not significant
8468	LIU_TARGETS_OF_VMYB_VS_CMYB_UP	0.56	0.03	0	0	0	not significant
8469	REACTOME_PI5P_REGULATES_TP53_ACETYLATION	0.56	0.03	0	0	0	not significant
8470	DAVIES_MULTIPLE_MYELOMA_VS_MGUS_UP	0.56	0.02	0	0	0	not significant
8471	GO_ATTACHMENT_OF_GPI_ANCHOR_TO_PROTEIN	0.56	0.02	0	0	0	not significant
8472	GO_CATION_CATION_ANTIPORTER_ACTIVITY	0.56	0.02	0	0	0	not significant
8473	GO_GTPASE_INHIBITOR_ACTIVITY	0.56	0.02	0	0	0	not significant
8474	GO_LARGE_RIBOSOMAL_SUBUNIT_RRNA_BINDING	0.56	0.02	0	0	0	not significant
8475	GO_NEGATIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	0.56	0.02	0	0	0	not significant
8476	GO_NEUROTRANSMITTER_RECEPTOR_LOCALIZATION_TO_POSTSYNAPT	0.56	0.02	0	0	0	not significant
8477	GO_PHOSPHATIDYLGLYCEROL_BINDING	0.56	0.02	0	0	0	not significant
8478	GO_PHOSPHATIDYLINOSITOL_4_5_BISPHOSPHATE_PHOSPHATASE_ACTI	0.56	0.02	0	0	0	not significant
8479	GO_PHOTORECEPTOR_OUTER_SEGMENT_MEMBRANE	0.56	0.02	0	0	0	not significant
8480	GO_REGULATION_OF_EXTRACELLULAR_MATRIX_ASSEMBLY	0.56	0.02	0	0	0	not significant
8481	REACTOME_CREB_PHOSPHORYLATION	0.56	0.02	0	0	0	not significant
8482	VISALA_AGING_LYMPHOCYTE_DN	0.56	0.02	0	0	0	not significant
8483	ZAIDI_OSTEOBLAST_TRANSCRIPTION_FACTORS	0.56	0.02	0	0	0	not significant
8484	GO_SOLUTE_CATION_ANTIPORTER_ACTIVITY	0.56	0.01	0	0	0	not significant
8485	TOMLINS_PROSTATE_CANCER_UP	0.56	0.01	0	0	0	not significant
8486	ODONNELL_METASTASIS_UP	0.56	0.00	0	0	0	not significant
8487	PID_FANCONI_PATHWAY	0.56	0.00	0	0	0	not significant
8488	GO_MYOSIN_II_COMPLEX	0.57	0.03	0	0	0	not significant
8489	GO_POSITIVE_REGULATION_OF_COAGULATION	0.57	0.03	0	0	0	not significant
8490	NIELSEN_LIPOSARCOMA_DN	0.57	0.03	0	0	0	not significant

8491	REACTOME_DNA_REPLICATION_INITIATION	0.57	0.03	0	0	0	not significant
8492	BIOCARTA_PTDINS_PATHWAY	0.57	0.02	0	0	0	not significant
8493	GO_CYCLIN_CDK_POSITIVE_TRANSCRIPTION_ELONGATION_FACTOR_C	0.57	0.02	0	0	0	not significant
8494	GO_DECIDUALIZATION	0.57	0.02	0	0	0	not significant
8495	GO_FOUR_WAY_JUNCTION_DNA_BINDING	0.57	0.02	0	0	0	not significant
8496	GO_INTRA_S_DNA_DAMAGE_CHECKPOINT	0.57	0.02	0	0	0	not significant
8497	GO_NEGATIVE_REGULATION_BY_HOST_OF_VIRAL_TRANSCRIPTION	0.57	0.02	0	0	0	not significant
8498	GO_NEGATIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	0.57	0.02	0	0	0	not significant
8499	GO_POSITIVE_REGULATION_OF_MYOTUBE_DIFFERENTIATION	0.57	0.02	0	0	0	not significant
8500	GO_PROTEIN_CATABOLIC_PROCESS_IN_THE_VACUOLE	0.57	0.02	0	0	0	not significant
8501	GO_REPLACEMENT_OSSIFICATION	0.57	0.02	0	0	0	not significant
8502	GO_SECONDARY_LYSOSOME	0.57	0.02	0	0	0	not significant
8503	WORSCHECH_TUMOR_REJECTION_UP	0.57	0.02	0	0	0	not significant
8504	CHR9Q32	0.57	0.01	0	0	0	not significant
8505	GO_COPI_COATED_VESICLE	0.57	0.01	0	0	0	not significant
8506	GO_GOLGI_TO_PLASMA_MEMBRANE_TRANSPORT	0.57	0.01	0	0	0	not significant
8507	GO_PIGMENT_GRANULE_ORGANIZATION	0.57	0.01	0	0	0	not significant
8508	GO_ENDOPLASMIC_RETICULUM_ORGANIZATION	0.57	0.00	0	0	0	not significant
8509	GO_APICAL_DENDRITE	0.58	0.03	0	0	0	not significant
8510	GO_APICAL_PROTEIN_LOCALIZATION	0.58	0.03	0	0	0	not significant
8511	GO_BRANCHING_INVOLVED_IN_BLOOD_VESSEL_MORPHOGENESIS	0.58	0.03	0	0	0	not significant
8512	GO_EPOXIDE_HYDROLASE_ACTIVITY	0.58	0.03	0	0	0	not significant
8513	GO_GLIAL_CELL_APOPTOTIC_PROCESS	0.58	0.03	0	0	0	not significant
8514	GO_ISWI_TYPE_COMPLEX	0.58	0.03	0	0	0	not significant
8515	GO_PEROXISOME_PROLIFERATOR_ACTIVATED_RECEPTOR_BINDING	0.58	0.03	0	0	0	not significant
8516	GO_RRNA_BASE_METHYLATION	0.58	0.03	0	0	0	not significant
8517	GO_VESICLE_TETHERING	0.58	0.03	0	0	0	not significant
8518	GU_PDEF_TARGETS_DN	0.58	0.03	0	0	0	not significant
8519	BIOCARTA_HBX_PATHWAY	0.58	0.02	0	0	0	not significant
8520	CHR4Q13	0.58	0.02	0	0	0	not significant
8521	GO_INOSITOL_PHOSPHATE_CATABOLIC_PROCESS	0.58	0.02	0	0	0	not significant
8522	GO_INSULIN_RECEPTOR_SUBSTRATE_BINDING	0.58	0.02	0	0	0	not significant
8523	GO_METHYLATION_DEPENDENT_CHROMATIN_SILENCING	0.58	0.02	0	0	0	not significant
8524	GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	0.58	0.02	0	0	0	not significant
8525	GO_PROTEIN_LIPID_COMPLEX_ASSEMBLY	0.58	0.02	0	0	0	not significant
8526	GO_REGULATION_OF_FATTY_ACID_BETA_OXIDATION	0.58	0.02	0	0	0	not significant
8527	PID_IL8_CXCR1_PATHWAY	0.58	0.02	0	0	0	not significant
8528	CHIARETTI_T_ALL_RELAPSE_PROGNOSIS	0.58	0.01	0	0	0	not significant
8529	FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN	0.58	0.01	0	0	0	not significant
8530	GO_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	0.58	0.01	0	0	0	not significant
8531	CHR1Q24	0.58	0.00	0	0	0	not significant
8532	GO_NEGATIVE_REGULATION_OF_AUTOPHAGY	0.58	0.00	0	0	0	not significant
8533	KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	0.58	0.00	0	0	0	not significant
8534	KEGG_PANCREATIC_CANCER	0.58	0.00	0	0	0	not significant
8535	GO_NEUROTRANSMITTER_REUPTAKE	0.59	0.04	0	0	0	not significant
8536	CHIN_BREAST_CANCER_COPY_NUMBER_DN	0.59	0.03	0	0	0	not significant
8537	CHR10P14	0.59	0.03	0	0	0	not significant
8538	GO_DNA_REPLICATION_SYNTHESIS_OF_RNA_PRIMER	0.59	0.03	0	0	0	not significant
8539	GO_ORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.59	0.03	0	0	0	not significant
8540	GO_POSITIVE_REGULATION_OF_CREB_TRANSCRIPTION_FACTOR_ACTI	0.59	0.03	0	0	0	not significant
8541	GO_POSITIVE_REGULATION_OF_METHYLATION_DEPENDENT_CHROMAT	0.59	0.03	0	0	0	not significant
8542	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_APOPTOTIC_	0.59	0.03	0	0	0	not significant
8543	GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCES	0.59	0.03	0	0	0	not significant
8544	IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_DN	0.59	0.03	0	0	0	not significant
8545	GO_FORMATION_OF_EXTRACHROMOSOMAL_CIRCULAR_DNA	0.59	0.02	0	0	0	not significant
8546	GO_MISMATCH_REPAIR_COMPLEX	0.59	0.02	0	0	0	not significant
8547	GO_PHOSPHATIDYLGLYCEROL_METABOLIC_PROCESS	0.59	0.02	0	0	0	not significant
8548	GO_PIGMENT_CELL_DIFFERENTIATION	0.59	0.02	0	0	0	not significant
8549	GO_POSITIVE_REGULATION_OF_BLOOD_CIRCULATION	0.59	0.02	0	0	0	not significant
8550	GO_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_	0.59	0.02	0	0	0	not significant
8551	GROSS_HYPOXIA_VIA_ELK3_ONLY_UP	0.59	0.02	0	0	0	not significant
8552	REACTOME_REGULATION_OF_SIGNALING_BY_CBL	0.59	0.02	0	0	0	not significant
8553	GO_CELLULAR_IRON_ION_HOMEOSTASIS	0.59	0.01	0	0	0	not significant
8554	GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_GAP_FILLING	0.59	0.01	0	0	0	not significant
8555	GO_OOCYTE_DIFFERENTIATION	0.59	0.01	0	0	0	not significant
8556	GO_ENDOSOMAL_TRANSPORT	0.59	0.00	0	0	0	not significant
8557	GO_LIPID_PHOSPHORYLATION	0.59	0.00	0	0	0	not significant
8558	GO_TRANS_GOLGI_NETWORK_MEMBRANE	0.59	0.00	0	0	0	not significant
8559	KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	0.60	0.05	0	0	0	not significant
8560	GO_ADAPTATION_OF_SIGNALING_PATHWAY	0.60	0.04	0	0	0	not significant
8561	GO_PHOSPHATIDYLGLYCEROL_ACYL_CHAIN_REMODELING	0.60	0.04	0	0	0	not significant
8562	GO_PROTEIN_HETEROTRIMERIZATION	0.60	0.04	0	0	0	not significant
8563	GO_REGULATION_OF_CHAPERONE_MEDIATED_AUTOPHAGY	0.60	0.04	0	0	0	not significant
8564	GO_REGULATION_OF_SEQUESTERING_OF_TRIGLYCERIDE	0.60	0.04	0	0	0	not significant
8565	REACTOME_ERYTHROPOIETIN_ACTIVATES_RAS	0.60	0.04	0	0	0	not significant
8566	REACTOME_SIGNALING_BY_FGFR4_IN_DISEASE	0.60	0.04	0	0	0	not significant
8567	DARWICHE_PAPILLOMA_RISK_HIGH_VS_LOW_UP	0.60	0.03	0	0	0	not significant
8568	GO_BASEMENT_MEMBRANE_ASSEMBLY	0.60	0.03	0	0	0	not significant
8569	GO_MRNA_3_SPLICE_SITE_RECOGNITION	0.60	0.03	0	0	0	not significant
8570	CHR13Q32	0.60	0.02	0	0	0	not significant
8571	GO_5_3_EXONUCLEASE_ACTIVITY	0.60	0.02	0	0	0	not significant
8572	GO_CILIUM_OR_FLAGELLUM_DEPENDENT_CELL_MOTILITY	0.60	0.02	0	0	0	not significant
8573	GO_PEPTIDYL_ASPARAGINE_MODIFICATION	0.60	0.02	0	0	0	not significant
8574	GO_POSITIVE_REGULATION_OF_BLOOD_VESSEL_DIAMETER	0.60	0.02	0	0	0	not significant
8575	GO_WNT_SIGNALING_PATHWAY_CALCIUM_MODULATING_PATHWAY	0.60	0.02	0	0	0	not significant
8576	HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_DN	0.60	0.02	0	0	0	not significant
8577	LIU_BREAST_CANCER	0.60	0.02	0	0	0	not significant
8578	GO_VESICLE_MEDIATED_TRANSPORT_BETWEEN_ENDOSOMAL_COMPA	0.60	0.01	0	0	0	not significant
8579	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_UP	0.60	0.00	0	0	0	not significant
8580	SIRNA_EIF4GI_DN	0.60	0.00	0	0	0	not significant
8581	GO_RNA_POLYMERASE_II_C_TERMINAL_DOMAIN_BINDING	0.61	0.06	0	0	0	not significant
8582	GO_COENZYME_TRANSPORT	0.61	0.04	0	0	0	not significant
8583	GO_DORSAL_VENTRAL_AXIS_SPECIFICATION	0.61	0.04	0	0	0	not significant
8584	GO_NEGATIVE_REGULATION_OF_VIRAL_INDUCED_CYTOPLASMIC_PATT	0.61	0.04	0	0	0	not significant
8585	GO_POSITIVE_REGULATION_OF_CYTOPLASMIC_TRANSLATION	0.61	0.04	0	0	0	not significant
8586	GO_REPLICATION_FORK_ARREST	0.61	0.04	0	0	0	not significant
8587	GO_RNA_POLYMERASE_III_GENERAL_TRANSCRIPTION_INITIATION_FACT	0.61	0.04	0	0	0	not significant
8588	GO_SYNAPTIC_VESICLE_PRIMING	0.61	0.04	0	0	0	not significant
8589	GO_COPI_COATED_VESICLE_MEMBRANE	0.61	0.03	0	0	0	not significant
8590	GO_NEGATIVE_REGULATION_OF_ANION_TRANSMEMBRANE_TRANSPOR	0.61	0.03	0	0	0	not significant
8591	GO_NEGATIVE_REGULATION_OF_HEART_CONTRACTION	0.61	0.03	0	0	0	not significant
8592	GO_POSITIVE_REGULATION_OF_VASCULAR_ASSOCIATED_SMOOTH_MU	0.61	0.03	0	0	0	not significant
8593	GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_F	0.61	0.03	0	0	0	not significant
8594	GO_RESPONSE_TO_FOLIC_ACID	0.61	0.03	0	0	0	not significant
8595	GO_SWI_SNF_COMPLEX	0.61	0.03	0	0	0	not significant
8596	REACTOME_EPHRIN_SIGNALING	0.61	0.03	0	0	0	not significant
8597	SAGIV_CD24_TARGETS_UP	0.61	0.03	0	0	0	not significant
8598	BIOCARTA_IL6_PATHWAY	0.61	0.02	0	0	0	not significant
8599	CHR8Q12	0.61	0.02	0	0	0	not significant

8600	GO_DNA_DOUBLE_STRAND_BREAK_PROCESSING	0.61	0.02	0	0	0	not significant
8601	KEGG_DORSO_VENTRAL_AXIS_FORMATION	0.61	0.02	0	0	0	not significant
8602	REACTOME_SIGNALING_BY_FGFR3_FUSIONS_IN_CANCER	0.61	0.02	0	0	0	not significant
8603	GO_CORTICAL_CYTOSKELETON_ORGANIZATION	0.61	0.01	0	0	0	not significant
8604	GO_POSITIVE_REGULATION_OF_MACROAUTOPHAGY	0.61	0.01	0	0	0	not significant
8605	GO_PROTEIN_LOCALIZATION_TO_CILIUM	0.61	0.01	0	0	0	not significant
8606	GO_VIRION_ASSEMBLY	0.61	0.01	0	0	0	not significant
8607	KEGG_BASE_EXCISION_REPAIR	0.61	0.01	0	0	0	not significant
8608	PID_IFNG_PATHWAY	0.61	0.01	0	0	0	not significant
8609	GO_AUTOPHAGOSOME_ORGANIZATION	0.61	0.00	0	0	0	not significant
8610	GO_GOLGI_ORGANIZATION	0.61	0.00	0	0	0	not significant
8611	GO_TRANS_GOLGI_NETWORK	0.61	0.00	0	0	0	not significant
8612	CLAUS_PGR_POSITIVE_MENINGIOMA_UP	0.62	0.05	0	0	0	not significant
8613	GO_REGULATION_OF_OSTEOCLAST_DEVELOPMENT	0.62	0.05	0	0	0	not significant
8614	GO_REGULATION_OF_SMAD_PROTEIN_COMPLEX_ASSEMBLY	0.62	0.05	0	0	0	not significant
8615	REACTOME_SMAC_XIAP_REGULATED_APOPTOTIC_RESPONSE	0.62	0.05	0	0	0	not significant
8616	GO_BBSOME	0.62	0.04	0	0	0	not significant
8617	GO_C4_DICARBOXYLATE_TRANSPORT	0.62	0.04	0	0	0	not significant
8618	GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_PROLIFERATION	0.62	0.04	0	0	0	not significant
8619	GO_LIPOPROTEIN_PARTICLE_RECEPTOR_ACTIVITY	0.62	0.04	0	0	0	not significant
8620	GO_MUSCLE_ALPHA_ACTININ_BINDING	0.62	0.04	0	0	0	not significant
8621	GO_REGULATION_OF_SKELETAL_MUSCLE_CELL_DIFFERENTIATION	0.62	0.04	0	0	0	not significant
8622	GO_SYNAPTIC_VESICLE_DOCKING	0.62	0.04	0	0	0	not significant
8623	RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_SMAD4_DN	0.62	0.04	0	0	0	not significant
8624	SYED_ESTRADIOL_RESPONSE	0.62	0.04	0	0	0	not significant
8625	CHEN_ETV5_TARGETS_TESTIS	0.62	0.03	0	0	0	not significant
8626	GO_AMINO_SUGAR_BIOSYNTHETIC_PROCESS	0.62	0.03	0	0	0	not significant
8627	GO_DIVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_	0.62	0.03	0	0	0	not significant
8628	GO_LYSOPHOSPHOLIPID_ACYLTRANSFERASE_ACTIVITY	0.62	0.03	0	0	0	not significant
8629	GO_MLL3_4_COMPLEX	0.62	0.03	0	0	0	not significant
8630	GO_POSITIVE_REGULATION_OF_LIPID_KINASE_ACTIVITY	0.62	0.03	0	0	0	not significant
8631	GO_RESPONSE_TO_INTERFERON_ALPHA	0.62	0.03	0	0	0	not significant
8632	GO_SUMO_TRANSFERASE_ACTIVITY	0.62	0.03	0	0	0	not significant
8633	REACTOME_NUCLEOBASE_CATABOLISM	0.62	0.03	0	0	0	not significant
8634	BIOCARTA_ATM_PATHWAY	0.62	0.02	0	0	0	not significant
8635	GAZIN_EPIGENETIC_SILENCING_BY_KRAS	0.62	0.02	0	0	0	not significant
8636	GO_DEVELOPMENTAL_PIGMENTATION	0.62	0.02	0	0	0	not significant
8637	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	0.62	0.02	0	0	0	not significant
8638	REACTOME_BUDDING_AND_MATURATION_OF_HIV_VIRION	0.62	0.02	0	0	0	not significant
8639	REACTOME_SIGNALING_BY_FGFR3	0.62	0.02	0	0	0	not significant
8640	GO_PH_REDUCTION	0.62	0.01	0	0	0	not significant
8641	GO_REGULATION_OF_PROTEIN_ACETYLATION	0.62	0.01	0	0	0	not significant
8642	REACTOME_HDR_THROUGH_HOMOLOGOUS_RECOMBINATION_HRR	0.62	0.00	0	0	0	not significant
8643	GO_DETECTION_OF_TEMPERATURE_STIMULUS	0.63	0.05	0	0	0	not significant
8644	GO_HYALURONAN_BIOSYNTHETIC_PROCESS	0.63	0.05	0	0	0	not significant
8645	GO_LRR_DOMAIN_BINDING	0.63	0.04	0	0	0	not significant
8646	GO_POSITIVE_REGULATION_OF_CYCLASE_ACTIVITY	0.63	0.04	0	0	0	not significant
8647	GO_POSITIVE_REGULATION_OF_PROTEIN_POLYUBIQUITINATION	0.63	0.04	0	0	0	not significant
8648	GO_POSITIVE_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_STRE	0.63	0.04	0	0	0	not significant
8649	GO_PRE_MIRNA_PROCESSING	0.63	0.04	0	0	0	not significant
8650	GO_REGULATION_OF_RESPONSE_TO_INTERFERON_GAMMA	0.63	0.04	0	0	0	not significant
8651	GO_SENSORY_PERCEPTION_OF_TEMPERATURE_STIMULUS	0.63	0.04	0	0	0	not significant
8652	GO_SIGNAL_PEPTIDE_PROCESSING	0.63	0.04	0	0	0	not significant
8653	KYNG_NORMAL_AGING_UP	0.63	0.04	0	0	0	not significant
8654	BCAT.100_UP.V1_UP	0.63	0.03	0	0	0	not significant
8655	CHIBA_RESPONSE_TO_TSA_DN	0.63	0.03	0	0	0	not significant
8656	CHR9Q31	0.63	0.03	0	0	0	not significant
8657	GO_DNA_LIGATION	0.63	0.03	0	0	0	not significant
8658	GO_MAGNESIUM_DEPENDENT_PROTEIN_SERINE_THREONINE_PHOSPHAT	0.63	0.03	0	0	0	not significant
8659	GO_NUCLEOSIDE_SALVAGE	0.63	0.03	0	0	0	not significant
8660	GO_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	0.63	0.03	0	0	0	not significant
8661	GO_CUL3_RING_UBIQUITIN_LIGASE_COMPLEX	0.63	0.02	0	0	0	not significant
8662	GO_DNA_REPAIR_COMPLEX	0.63	0.02	0	0	0	not significant
8663	GO_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDI	0.63	0.02	0	0	0	not significant
8664	REACTOME_RESOLUTION_OF_ABASIC_SITES_AP_SITES	0.63	0.02	0	0	0	not significant
8665	GO_CILIARY_TIP	0.63	0.01	0	0	0	not significant
8666	GO_DAMAGED_DNA_BINDING	0.63	0.01	0	0	0	not significant
8667	GO_REGULATION_OF_PEPTIDYL_LYSINE_ACETYLATION	0.63	0.01	0	0	0	not significant
8668	CHR13Q14	0.63	0.00	0	0	0	not significant
8669	GO_REGULATION_OF_CHROMATIN_ORGANIZATION	0.63	0.00	0	0	0	not significant
8670	RAO_BOUND_BY_SALL4_ISOFORM_A	0.63	0.00	0	0	0	not significant
8671	GO_DETECTION_OF_TEMPERATURE_STIMULUS_INVOLVED_IN_SENSORY	0.64	0.06	0	0	0	not significant
8672	GO_DOUBLE_STRAND_BREAK_REPAIR_VIA_SINGLE_STRAND_ANNEALIN	0.64	0.06	0	0	0	not significant
8673	GO_FILTRATION_DIAPHRAGM	0.64	0.06	0	0	0	not significant
8674	GO_LAGGING_STRAND_ELONGATION	0.64	0.06	0	0	0	not significant
8675	GO_MELANOSOME_MEMBRANE	0.64	0.06	0	0	0	not significant
8676	BIOCARTA_CHREBP_PATHWAY	0.64	0.05	0	0	0	not significant
8677	CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_UP	0.64	0.05	0	0	0	not significant
8678	GO_AXONAL_TRANSPORT_OF_MITOCHONDRION	0.64	0.05	0	0	0	not significant
8679	GO_CARDIOBLAST_DIFFERENTIATION	0.64	0.05	0	0	0	not significant
8680	GO_DENDRITE_TERMINUS	0.64	0.05	0	0	0	not significant
8681	GO_GOLGI_MEDIAL_CISTERNA	0.64	0.05	0	0	0	not significant
8682	GO_INTRACILIARY_RETROGRADE_TRANSPORT	0.64	0.05	0	0	0	not significant
8683	GO_MAP_KINASE_SCAFFOLD_ACTIVITY	0.64	0.05	0	0	0	not significant
8684	GO_SPHINGOMYELIN_CATABOLIC_PROCESS	0.64	0.05	0	0	0	not significant
8685	MATZUK_EARLY_ANTRAL_FOLLICLE	0.64	0.05	0	0	0	not significant
8686	NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON	0.64	0.05	0	0	0	not significant
8687	REACTOME_IKBA_VARIANT_LEADS_TO_EDA_ID	0.64	0.05	0	0	0	not significant
8688	GO_CELL_CELL_ADHESION_MEDIATED_BY_INTEGRIN	0.64	0.04	0	0	0	not significant
8689	GO_OSTEOBLAST_DEVELOPMENT	0.64	0.04	0	0	0	not significant
8690	GO_PORE_COMPLEX_ASSEMBLY	0.64	0.04	0	0	0	not significant
8691	GO_REGULATION_OF_MICROTUBULE_MOTOR_ACTIVITY	0.64	0.04	0	0	0	not significant
8692	REACTOME_SIGNALING_BY_HIPPO	0.64	0.04	0	0	0	not significant
8693	REACTOME_TRP_CHANNELS	0.64	0.04	0	0	0	not significant
8694	BERNARD_PPAPDC1B_TARGETS_UP	0.64	0.03	0	0	0	not significant
8695	GO_CRANIOFACIAL_SUTURE_MORPHOGENESIS	0.64	0.03	0	0	0	not significant
8696	GO_NEGATIVE_REGULATION_OF_GENE_SILENCING	0.64	0.03	0	0	0	not significant
8697	GO_POSITIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_EL	0.64	0.03	0	0	0	not significant
8698	GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME_CENTROMERIC_REGI	0.64	0.03	0	0	0	not significant
8699	GO_SNARE_COMPLEX_ASSEMBLY	0.64	0.03	0	0	0	not significant
8700	REACTOME_INSERTION_OF_TAIL_ANCHORED_PROTEINS_INTO_THE_EN	0.64	0.03	0	0	0	not significant
8701	BCAT_BILD_ET_AL_DN	0.64	0.02	0	0	0	not significant
8702	GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_UP	0.64	0.02	0	0	0	not significant
8703	GO_CORE_PROMOTER_SEQUENCE_SPECIFIC_DNA_BINDING	0.64	0.02	0	0	0	not significant
8704	GO_DNA_SECONDARY_STRUCTURE_BINDING	0.64	0.02	0	0	0	not significant
8705	WNT_SIGNALING	0.64	0.02	0	0	0	not significant
8706	GO_NEGATIVE_REGULATION_OF_CHROMATIN_ORGANIZATION	0.64	0.01	0	0	0	not significant
8707	GO_TUBE_CLOSURE	0.64	0.01	0	0	0	not significant
8708	KEGG_NON_SMALL_CELL_LUNG_CANCER	0.64	0.01	0	0	0	not significant

8709	GO_HISTONE_METHYLATION	0.64	0.00	0	0	0	not significant
8710	GO_VACUOLE_ORGANIZATION	0.64	0.00	0	0	0	not significant
8711	REACTOME_AUTOPHAGY	0.64	0.00	0	0	0	not significant
8712	GO_APOPTOTIC_PROCESS_INVOLVED_IN_MORPHOGENESIS	0.65	0.06	0	0	0	not significant
8713	GO_AUTOLYSOSOME	0.65	0.06	0	0	0	not significant
8714	GO_NEGATIVE_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATIO	0.65	0.06	0	0	0	not significant
8715	GO_POSTSYNAPTIC_MEMBRANE_ASSEMBLY	0.65	0.06	0	0	0	not significant
8716	REACTOME_ACTIVATED_NTRK2_SIGNALS_THROUGH_FRS2_AND_FRS3	0.65	0.06	0	0	0	not significant
8717	REACTOME_ESTROGEN_DEPENDENT_NUCLEAR_EVENTS_DOWNSTREA	0.65	0.06	0	0	0	not significant
8718	BIOCARTA_ERAD_PATHWAY	0.65	0.05	0	0	0	not significant
8719	DORN_ADENOVIRUS_INFECTION_32HR_UP	0.65	0.05	0	0	0	not significant
8720	FRASOR_TAMOXIFEN_RESPONSE_DN	0.65	0.05	0	0	0	not significant
8721	GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_ASSEMBLY	0.65	0.05	0	0	0	not significant
8722	GO_NEGATIVE_REGULATION_OF_AMYLOID_PRECURSOR_PROTEIN_BIO	0.65	0.05	0	0	0	not significant
8723	GO_NEGATIVE_REGULATION_OF_PROTEIN_HOMOOLIGOMERIZATION	0.65	0.05	0	0	0	not significant
8724	GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_DRUG	0.65	0.05	0	0	0	not significant
8725	GO_POSITIVE_REGULATION_OF_FATTY_ACID_BETA_OXIDATION	0.65	0.05	0	0	0	not significant
8726	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CHROMATIN	0.65	0.05	0	0	0	not significant
8727	GO_REGULATION_OF_RESPIRATORY_BURST	0.65	0.05	0	0	0	not significant
8728	SAENZ_DETOX_PATHWAY_AND_CARCINOGENESIS_DN	0.65	0.05	0	0	0	not significant
8729	GO_CENTRIOLE_CENTRIOLE_COHESION	0.65	0.04	0	0	0	not significant
8730	GO_PHOSPHATIDIC_ACID_BINDING	0.65	0.04	0	0	0	not significant
8731	KEGG_BLADDER_CANCER	0.65	0.04	0	0	0	not significant
8732	PID_WNT_CANONICAL_PATHWAY	0.65	0.04	0	0	0	not significant
8733	CHR11P13	0.65	0.03	0	0	0	not significant
8734	DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_UP	0.65	0.03	0	0	0	not significant
8735	GO_AUTOPHAGOSOME_MATURATION	0.65	0.03	0	0	0	not significant
8736	GO_ENDONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXY	0.65	0.03	0	0	0	not significant
8737	GO_ENDOPLASMIC_RETICULUM_TO_CYTOSOL_TRANSPORT	0.65	0.03	0	0	0	not significant
8738	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_G	0.65	0.03	0	0	0	not significant
8739	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_1_DN	0.65	0.03	0	0	0	not significant
8740	KIM_TIAL1_TARGETS	0.65	0.03	0	0	0	not significant
8741	XU_CREBBP_TARGETS_DN	0.65	0.03	0	0	0	not significant
8742	GO_CELLULAR_RESPONSE_TO_NUTRIENT	0.65	0.02	0	0	0	not significant
8743	GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFO	0.65	0.02	0	0	0	not significant
8744	GO_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGION_DNA_BIN	0.65	0.02	0	0	0	not significant
8745	GO_ROOF_OF_MOUTH_DEVELOPMENT	0.65	0.02	0	0	0	not significant
8746	REACTOME_HOMOLOGOUS_DNA_PAIRING_AND_STRAND_EXCHANGE	0.65	0.02	0	0	0	not significant
8747	GO_ANDROGEN_RECEPTOR_BINDING	0.65	0.01	0	0	0	not significant
8748	GO_PHOSPHOPROTEIN_BINDING	0.65	0.01	0	0	0	not significant
8749	TIEN_INTESTINE_PROBIOTICS_2HR_DN	0.65	0.01	0	0	0	not significant
8750	GO_CENTRIOLE_ELONGATION	0.66	0.07	0	0	0	not significant
8751	GO_VASCULAR_ASSOCIATED_SMOOTH_MUSCLE_CELL_APOPTOTIC_PR	0.66	0.07	0	0	0	not significant
8752	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_2	0.66	0.07	0	0	0	not significant
8753	BOYERINAS_ONCOFETAL_TARGETS_OF_LET7A1	0.66	0.06	0	0	0	not significant
8754	GO_COBALAMIN_BINDING	0.66	0.06	0	0	0	not significant
8755	GO_G1_TO_G0_TRANSITION	0.66	0.06	0	0	0	not significant
8756	GO_HEMIDESMOSOME_ASSEMBLY	0.66	0.06	0	0	0	not significant
8757	GO_NEGATIVE_REGULATION_OF_CHEMOKINE_PRODUCTION	0.66	0.06	0	0	0	not significant
8758	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_DEADENYL	0.66	0.06	0	0	0	not significant
8759	GO_POSITIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	0.66	0.06	0	0	0	not significant
8760	GO_REGULATION_OF_DEOXYRIBONUCLEASE_ACTIVITY	0.66	0.06	0	0	0	not significant
8761	PLASARI_NFIC_TARGETS_BASAL_UP	0.66	0.06	0	0	0	not significant
8762	REACTOME_TYPE_I_HEMIDESMOSOME_ASSEMBLY	0.66	0.06	0	0	0	not significant
8763	GO_GLUCOSYLTRANSFERASE_ACTIVITY	0.66	0.05	0	0	0	not significant
8764	GO_RESPONSE_TO_HEPATOCYTE_GROWTH_FACTOR	0.66	0.05	0	0	0	not significant
8765	GO_EMBRYONIC_CRANIAL_SKELETON_MORPHOGENESIS	0.66	0.04	0	0	0	not significant
8766	GO_INSULIN_RECEPTOR_BINDING	0.66	0.04	0	0	0	not significant
8767	GO_MICROTUBULE_ANCHORING	0.66	0.04	0	0	0	not significant
8768	PID_PDGFRA_PATHWAY	0.66	0.04	0	0	0	not significant
8769	SHIN_B_CELL_LYMPHOMA_CLUSTER_7	0.66	0.04	0	0	0	not significant
8770	GO_HISTONE_H3_K4_TRIMETHYLATION	0.66	0.03	0	0	0	not significant
8771	GO_PHOSPHOTYROSINE_RESIDUE_BINDING	0.66	0.03	0	0	0	not significant
8772	GO_CYTOPLASMIC_MICROTUBULE_ORGANIZATION	0.66	0.02	0	0	0	not significant
8773	GO_POSITIVE_REGULATION_OF_MRNA_CATABOLIC_PROCESS	0.66	0.02	0	0	0	not significant
8774	GRADE_COLON_VS_RECTAL_CANCER_DN	0.66	0.02	0	0	0	not significant
8775	KEGG_N_GLYCAN_BIOSYNTHESIS	0.66	0.02	0	0	0	not significant
8776	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_UP	0.66	0.02	0	0	0	not significant
8777	PID_CD8_TCR_PATHWAY	0.66	0.02	0	0	0	not significant
8778	RADMACHER_AML_PROGNOSIS	0.66	0.02	0	0	0	not significant
8779	GO_CHROMATIN_ORGANIZATION_INVOLVED_IN_REGULATION_OF_TRANS	0.66	0.01	0	0	0	not significant
8780	GO_ENERGY_RESERVE_METABOLIC_PROCESS	0.66	0.01	0	0	0	not significant
8781	GO_REGULATION_OF_DNA_REPLICATION	0.66	0.01	0	0	0	not significant
8782	GO_PROTEIN_ACETYLATION	0.66	0.00	0	0	0	not significant
8783	GO_POSITIVE_REGULATION_OF_CELL_SIZE	0.67	0.08	0	0	0	not significant
8784	GO_DENDRITE_SELF_AVOIDANCE	0.67	0.07	0	0	0	not significant
8785	GO_MYELIN_SHEATH_ABAXONAL_REGION	0.67	0.07	0	0	0	not significant
8786	GO_NEGATIVE_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	0.67	0.07	0	0	0	not significant
8787	GO_NUCLEOTIDE_TRANSMEMBRANE_TRANSPORT	0.67	0.07	0	0	0	not significant
8788	REACTOME_INLA_MEDIATED_ENTRY_OF_LISTERIA_MONOCYTOGENES_I	0.67	0.07	0	0	0	not significant
8789	CHR5Q15	0.67	0.06	0	0	0	not significant
8790	GO_HISTONE_MRNA_CATABOLIC_PROCESS	0.67	0.06	0	0	0	not significant
8791	GO_NEUROTRANSMITTER_SODIUM_SYMPORTER_ACTIVITY	0.67	0.06	0	0	0	not significant
8792	BIOCARTA_HDAC_PATHWAY	0.67	0.05	0	0	0	not significant
8793	GO_DYNEIN_LIGHT_CHAIN_BINDING	0.67	0.05	0	0	0	not significant
8794	GO_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	0.67	0.05	0	0	0	not significant
8795	GO_NEGATIVE_REGULATION_OF_UBIQUITIN_PROTEIN_TRANSFERASE_A	0.67	0.05	0	0	0	not significant
8796	GO_POSITIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGN	0.67	0.05	0	0	0	not significant
8797	GO_REGULATION_OF_CYTOPLASMIC_TRANSPORT	0.67	0.05	0	0	0	not significant
8798	GO_REGULATION_OF_FIBROBLAST_MIGRATION	0.67	0.05	0	0	0	not significant
8799	PID_ALK1_PATHWAY	0.67	0.05	0	0	0	not significant
8800	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR3	0.67	0.05	0	0	0	not significant
8801	CHR8P12	0.67	0.04	0	0	0	not significant
8802	GO_AMINE_BIOSYNTHETIC_PROCESS	0.67	0.04	0	0	0	not significant
8803	GO_NEGATIVE_REGULATION_OF_GTPASE_ACTIVITY	0.67	0.04	0	0	0	not significant
8804	GO_NEGATIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	0.67	0.04	0	0	0	not significant
8805	GO_PRI_MIRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	0.67	0.04	0	0	0	not significant
8806	GO_PEPTIDYL_LYSINE_TRIMETHYLATION	0.67	0.03	0	0	0	not significant
8807	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_ACETYLATION	0.67	0.03	0	0	0	not significant
8808	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_DN	0.67	0.03	0	0	0	not significant
8809	GO_CYTOPLASMIC_MICROTUBULE	0.67	0.02	0	0	0	not significant
8810	GO_HISTONE_H4_ACETYLATION	0.67	0.02	0	0	0	not significant
8811	GO_LYTIC_VACUOLE_ORGANIZATION	0.67	0.02	0	0	0	not significant
8812	MCCLUNG_CREB1_TARGETS_DN	0.67	0.02	0	0	0	not significant
8813	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	0.67	0.02	0	0	0	not significant
8814	FIGUEROA_AML_METHYLATION_CLUSTER_7_UP	0.67	0.01	0	0	0	not significant
8815	GO_NON_RECOMBINATIONAL_REPAIR	0.67	0.01	0	0	0	not significant
8816	GO_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	0.67	0.01	0	0	0	not significant
8817	LIN_NPAS4_TARGETS_UP	0.67	0.01	0	0	0	not significant

8818	REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING	0.67	0.01	0	0	0	not significant
8819	GO_PEPTIDYL_LYSINE_ACETYLATION	0.67	0.00	0	0	0	not significant
8820	CHR8Q23	0.68	0.08	0	0	0	not significant
8821	GO_CALCIUM_ION_IMPORT_INTO_CYTOSOL	0.68	0.08	0	0	0	not significant
8822	GO_CROSSOVER_JUNCTION_ENDODEOXYRIBONUCLEASE_ACTIVITY	0.68	0.08	0	0	0	not significant
8823	GO_POSITIVE_REGULATION_OF_HETEROTYPIC_CELL_CELL_ADHESION	0.68	0.08	0	0	0	not significant
8824	GO_PRESYNAPTIC_CYTOSOL	0.68	0.08	0	0	0	not significant
8825	GO_NEUTROPHIL_DIFFERENTIATION	0.68	0.07	0	0	0	not significant
8826	GO_POST_MRNA_RELEASE_SPLICEOSOMAL_COMPLEX	0.68	0.07	0	0	0	not significant
8827	GO_RESPONSE_TO_DOPAMINE	0.68	0.07	0	0	0	not significant
8828	GO_RIPOPTOSOME	0.68	0.07	0	0	0	not significant
8829	MOOTHA_ROS	0.68	0.07	0	0	0	not significant
8830	PID_FRA_PATHWAY	0.68	0.07	0	0	0	not significant
8831	REACTOME_TRANSPORT_OF_NUCLEOTIDE_SUGARS	0.68	0.07	0	0	0	not significant
8832	REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	0.68	0.07	0	0	0	not significant
8833	DORN_ADENOVIRUS_INFECTION_12HR_UP	0.68	0.06	0	0	0	not significant
8834	GO_CALCIUM_DEPENDENT_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	0.68	0.06	0	0	0	not significant
8835	GO_COLLAGEN_CATABOLIC_PROCESS	0.68	0.06	0	0	0	not significant
8836	GO_DEADENYLATION_DEPENDENT_DECAPPING_OF_NUCLEAR_TRANSC	0.68	0.06	0	0	0	not significant
8837	GO_FORMATION_OF_TRANSLATION_PREINITIATION_COMPLEX	0.68	0.06	0	0	0	not significant
8838	GO_MICROTUBULE_ANCHORING_AT_MICROTUBULE_ORGANIZING_CENTE	0.68	0.06	0	0	0	not significant
8839	GO_NEGATIVE_REGULATION_OF_MYOTUBE_DIFFERENTIATION	0.68	0.06	0	0	0	not significant
8840	GO_POSITIVE_REGULATION_OF_GRANULOCYTE_CHEMOTAXIS	0.68	0.06	0	0	0	not significant
8841	GO_POSITIVE_REGULATION_OF_NEUTROPHIL_MIGRATION	0.68	0.06	0	0	0	not significant
8842	KAMIKUBO_MYELOID_MN1_NETWORK	0.68	0.06	0	0	0	not significant
8843	LI_CYTIDINE_ANALOG_PATHWAY	0.68	0.06	0	0	0	not significant
8844	BIOCARTA_ARF_PATHWAY	0.68	0.05	0	0	0	not significant
8845	BIOCARTA_BARRESTIN_SRC_PATHWAY	0.68	0.05	0	0	0	not significant
8846	CHR7P14	0.68	0.05	0	0	0	not significant
8847	GO_MAST_CELL_MEDIATED_IMMUNITY	0.68	0.04	0	0	0	not significant
8848	GO_SH2_DOMAIN_BINDING	0.68	0.04	0	0	0	not significant
8849	REACTOME_SIGNALING_BY_FGFR4	0.68	0.04	0	0	0	not significant
8850	SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES	0.68	0.04	0	0	0	not significant
8851	GO_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	0.68	0.03	0	0	0	not significant
8852	REACTOME_INTRA_GOLGI_TRAFFIC	0.68	0.03	0	0	0	not significant
8853	GO_PML_BODY	0.68	0.02	0	0	0	not significant
8854	GO_UBIQUITIN_DEPENDENT_ERAD_PATHWAY	0.68	0.02	0	0	0	not significant
8855	DARWICHE_PAPILLOMA_RISK_LOW_DN	0.68	0.01	0	0	0	not significant
8856	GAUSSMANN_MLL_AF4_FUSION_TARGETS_A_UP	0.68	0.01	0	0	0	not significant
8857	GO_CENTRIOLE	0.68	0.01	0	0	0	not significant
8858	GO_PROTEIN_MONOUBIQUITINATION	0.68	0.01	0	0	0	not significant
8859	GO_STEROID_HORMONE_RECEPTOR_BINDING	0.68	0.01	0	0	0	not significant
8860	HOSHIDA_LIVER_CANCER_SUBCLASS_S2	0.68	0.01	0	0	0	not significant
8861	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON	0.68	0.01	0	0	0	not significant
8862	GO_DOUBLE_STRAND_BREAK_REPAIR	0.68	0.00	0	0	0	not significant
8863	GO_MUTLALPHA_COMPLEX	0.69	0.09	0	0	0	not significant
8864	GO_THIAMINE_PYROPHOSPHATE_BINDING	0.69	0.09	0	0	0	not significant
8865	GO_ENDOSOMAL_VESICLE_FUSION	0.69	0.08	0	0	0	not significant
8866	GO_GLYCOSYLCERAMIDE_CATABOLIC_PROCESS	0.69	0.08	0	0	0	not significant
8867	GO_HYPOTONIC_RESPONSE	0.69	0.08	0	0	0	not significant
8868	GO_LYSINE_CATABOLIC_PROCESS	0.69	0.08	0	0	0	not significant
8869	GO_MITOTIC_SPINDLE_ASTRAL_MICROTUBULE	0.69	0.08	0	0	0	not significant
8870	GO_POSITIVE_REGULATION_OF_SYNAPTIC_VESICLE_TRANSPORT	0.69	0.08	0	0	0	not significant
8871	GO_RADIAL_GLIAL_CELL_DIFFERENTIATION	0.69	0.08	0	0	0	not significant
8872	SABATES_COLORECTAL_ADENOMA_SIZE_DN	0.69	0.08	0	0	0	not significant
8873	BIOCARTA_TERC_PATHWAY	0.69	0.07	0	0	0	not significant
8874	GO_GAMMA_SECRETASE_COMPLEX	0.69	0.07	0	0	0	not significant
8875	GO_HETEROCHROMATIN_ASSEMBLY	0.69	0.07	0	0	0	not significant
8876	GO_HYPEROSMOTIC_RESPONSE	0.69	0.07	0	0	0	not significant
8877	GO_MICROTUBULE_ANCHORING_AT_CENTROSOME	0.69	0.07	0	0	0	not significant
8878	GO_MYOBLAST_FUSION	0.69	0.07	0	0	0	not significant
8879	GO_NEGATIVE_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	0.69	0.07	0	0	0	not significant
8880	GO_REGULATION_OF_AMYLOID_BETA_FORMATION	0.69	0.07	0	0	0	not significant
8881	GO_SYNAPTIC_MEMBRANE_ADHESION	0.69	0.07	0	0	0	not significant
8882	MEISSNER_BRAIN_HCP_WITH_H3_UNMETHYLATED	0.69	0.07	0	0	0	not significant
8883	GO_POSITIVE_REGULATION_OF_CHROMATIN_SILENCING	0.69	0.06	0	0	0	not significant
8884	GO_REGULATION_OF_TELOMERE_CAPPING	0.69	0.06	0	0	0	not significant
8885	CHEOK_RESPONSE_TO_HD_MTX_DN	0.69	0.05	0	0	0	not significant
8886	GO_MAST_CELL_ACTIVATION	0.69	0.05	0	0	0	not significant
8887	GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION	0.69	0.05	0	0	0	not significant
8888	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAMMA_IN_OLD	0.69	0.05	0	0	0	not significant
8889	LUI_THYROID_CANCER_CLUSTER_2	0.69	0.05	0	0	0	not significant
8890	GO_ADENYLATE_CYCLASE_ACTIVATING_G_PROTEIN_COUPLED_RECEP	0.69	0.04	0	0	0	not significant
8891	GO_DEMETHYLATION	0.69	0.04	0	0	0	not significant
8892	KOHOUTEK_CCNT2_TARGETS	0.69	0.04	0	0	0	not significant
8893	REACTOME_NOTCH_HLH_TRANSCRIPTION_PATHWAY	0.69	0.04	0	0	0	not significant
8894	CHEN_HOXA5_TARGETS_9HR_DN	0.69	0.03	0	0	0	not significant
8895	GO_DENDRITIC_SPINE_MORPHOGENESIS	0.69	0.03	0	0	0	not significant
8896	PID_TXA2PATHWAY	0.69	0.03	0	0	0	not significant
8897	GO_BLASTOCYST_DEVELOPMENT	0.69	0.02	0	0	0	not significant
8898	GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT	0.69	0.01	0	0	0	not significant
8899	GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	0.69	0.01	0	0	0	not significant
8900	GO_RAS_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	0.69	0.01	0	0	0	not significant
8901	CLIMENT_BREAST_CANCER_COPY_NUMBER_DN	0.70	0.10	0	0	0	not significant
8902	BIOCARTA_PLK3_PATHWAY	0.70	0.09	0	0	0	not significant
8903	GO_CUL7_RING_UBIQUITIN_LIGASE_COMPLEX	0.70	0.09	0	0	0	not significant
8904	GO_DENDRITIC_GROWTH_CONE	0.70	0.09	0	0	0	not significant
8905	GO_PROTEIN_GERANYLGERANYLTRANSFERASE_ACTIVITY	0.70	0.09	0	0	0	not significant
8906	GO_REGULATION_OF_PLATELET_AGGREGATION	0.70	0.09	0	0	0	not significant
8907	REACTOME_LYSINE_CATABOLISM	0.70	0.09	0	0	0	not significant
8908	GO_METANEPHRIC_COLLECTING_DUCT_DEVELOPMENT	0.70	0.08	0	0	0	not significant
8909	GO_NUCLEAR_ENVELOPE_LUMEN	0.70	0.08	0	0	0	not significant
8910	GO_PROTEIN_GLYCOSYLATION_IN_GOLGI	0.70	0.08	0	0	0	not significant
8911	GO_REGULATION_OF_MICROTUBULE_BINDING	0.70	0.08	0	0	0	not significant
8912	GO_RESPONSE_TO_VITAMIN_A	0.70	0.08	0	0	0	not significant
8913	GO_RISC_LOADING_COMPLEX	0.70	0.08	0	0	0	not significant
8914	GO_SERTOLI_CELL_DEVELOPMENT	0.70	0.08	0	0	0	not significant
8915	GO_SMALL_RNA_LOADING_ONTO_RISC	0.70	0.08	0	0	0	not significant
8916	CROONQUIST_STROMAL_STIMULATION_DN	0.70	0.07	0	0	0	not significant
8917	GO_COENZYME_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.70	0.07	0	0	0	not significant
8918	GO_EXTRINSIC_COMPONENT_OF_SYNAPTIC_MEMBRANE	0.70	0.07	0	0	0	not significant
8919	GO_NEGATIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	0.70	0.07	0	0	0	not significant
8920	GO_NEGATIVE_T_CELL_SELECTION	0.70	0.07	0	0	0	not significant
8921	GO_UBIQUITIN_SPECIFIC_PROTEASE_BINDING	0.70	0.07	0	0	0	not significant
8922	REACTOME_FCGR_ACTIVATION	0.70	0.07	0	0	0	not significant
8923	ABBUD_LIF_SIGNALING_1_DN	0.70	0.06	0	0	0	not significant
8924	CHR3Q23	0.70	0.06	0	0	0	not significant
8925	CHR4P14	0.70	0.06	0	0	0	not significant
8926	GO_PHOSPHOLIPID_TRANSLOCATING_ATPASE_ACTIVITY	0.70	0.06	0	0	0	not significant

8927	GO_REGULATION_OF_MEMBRANE_LIPID_DISTRIBUTION	0.70	0.06	0	0	0	not significant
8928	REACTOME_BETA_CATENIN_PHOSPHORYLATION_CASCADE	0.70	0.06	0	0	0	not significant
8929	REACTOME_METAL_ION_SLC_TRANSPORTERS	0.70	0.06	0	0	0	not significant
8930	GO_MULTIVESICULAR_BODY_ORGANIZATION	0.70	0.05	0	0	0	not significant
8931	GO_NEGATIVE_REGULATION_OF_CHEMOTAXIS	0.70	0.05	0	0	0	not significant
8932	GO_RNA_DESTABILIZATION	0.70	0.05	0	0	0	not significant
8933	GO_VENTRICULAR_SYSTEM_DEVELOPMENT	0.70	0.05	0	0	0	not significant
8934	MCDOWELL_ACUTE_LUNG_INJURY_UP	0.70	0.05	0	0	0	not significant
8935	REACTOME_DEADENYLATION_OF_MRNA	0.70	0.05	0	0	0	not significant
8936	REACTOME_SIGNALING_BY_NOTCH3	0.70	0.05	0	0	0	not significant
8937	WANG_TARGETS_OF_MLL_CBP_FUSION_UP	0.70	0.05	0	0	0	not significant
8938	ZHANG_INTERFERON_RESPONSE	0.70	0.05	0	0	0	not significant
8939	GO_PROTEIN_SELF_ASSOCIATION	0.70	0.04	0	0	0	not significant
8940	PID_BARD1_PATHWAY	0.70	0.04	0	0	0	not significant
8941	GO_REGULATION_OF_TUBE_SIZE	0.70	0.03	0	0	0	not significant
8942	GO_REGULATION_OF_CELL_PROJECTION_ASSEMBLY	0.70	0.02	0	0	0	not significant
8943	GO_SMOOTHENED_SIGNALING_PATHWAY	0.70	0.02	0	0	0	not significant
8944	GO_VESICLE_MEDIATED_TRANSPORT_TO_THE_PLASMA_MEMBRANE	0.70	0.02	0	0	0	not significant
8945	CHANDRAN_METASTASIS_UP	0.70	0.00	0	0	0	not significant
8946	GO_NEGATIVE_REGULATION_OF_MEIOTIC_NUCLEAR_DIVISION	0.71	0.10	0	0	0	not significant
8947	REACTOME_ACTIVATION_OF_CASPASES_THROUGH_APOPTOSOME_MED	0.71	0.10	0	0	0	not significant
8948	BIOCARTA_IFNG_PATHWAY	0.71	0.09	0	0	0	not significant
8949	GO_1_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_5_KINASE_ACTIVITY	0.71	0.09	0	0	0	not significant
8950	GO_NEGATIVE_REGULATION_OF_RIG_I_SIGNALING_PATHWAY	0.71	0.09	0	0	0	not significant
8951	GO_NUCLEOBASE_METABOLIC_PROCESS	0.71	0.09	0	0	0	not significant
8952	GO_POSITIVE_REGULATION_OF_VASCULAR_ASSOCIATED_SMOOTH_MU	0.71	0.09	0	0	0	not significant
8953	REACTOME_NAPLUS_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPOR	0.71	0.09	0	0	0	not significant
8954	BIOCARTA_TGFB_PATHWAY	0.71	0.08	0	0	0	not significant
8955	GO_ACTININ_BINDING	0.71	0.08	0	0	0	not significant
8956	GO_ENTEROENDOCRINE_CELL_DIFFERENTIATION	0.71	0.08	0	0	0	not significant
8957	GO_GLUCOSIDASE_ACTIVITY	0.71	0.08	0	0	0	not significant
8958	GO_REGULATION_OF_ENDODEOXYRIBONUCLEASE_ACTIVITY	0.71	0.08	0	0	0	not significant
8959	GO_REGULATION_OF_PROTEIN_DEUBIQUITINATION	0.71	0.08	0	0	0	not significant
8960	GO_REGULATION_OF_SNARE_COMPLEX_ASSEMBLY	0.71	0.08	0	0	0	not significant
8961	GO_TYPE_I_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BIN	0.71	0.08	0	0	0	not significant
8962	LEE_LIVER_CANCER_HEPATOBLAST	0.71	0.08	0	0	0	not significant
8963	REACTOME_BUTYROPHILIN_BTN_FAMILY_INTERACTIONS	0.71	0.08	0	0	0	not significant
8964	REACTOME_DEFECTS_IN_COBALAMIN_B12_METABOLISM	0.71	0.08	0	0	0	not significant
8965	REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIUM_MOBILIZATION	0.71	0.08	0	0	0	not significant
8966	SA_PROGRAMMED_CELL_DEATH	0.71	0.08	0	0	0	not significant
8967	GO_ENDOPLASMIC_RETICULUM_QUALITY_CONTROL_COMPARTMENT	0.71	0.07	0	0	0	not significant
8968	GO_MKS_COMPLEX	0.71	0.07	0	0	0	not significant
8969	GO_RECEPTOR_INHIBITOR_ACTIVITY	0.71	0.07	0	0	0	not significant
8970	GO_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS_BY_REG	0.71	0.07	0	0	0	not significant
8971	GO_RESPONSE_TO_ANTIMETABOLITE	0.71	0.07	0	0	0	not significant
8972	GO_SYNAPTIC_VESICLE_CYTOSKELETAL_TRANSPORT	0.71	0.07	0	0	0	not significant
8973	GO_VIRAL_BUDDING	0.71	0.07	0	0	0	not significant
8974	HASLINGER_B_CLL_WITH_6Q21_DELETION	0.71	0.07	0	0	0	not significant
8975	JIANG_HYPOXIA_VIA_VHL	0.71	0.07	0	0	0	not significant
8976	MATZUK_EMBRYONIC_GERM_CELL	0.71	0.07	0	0	0	not significant
8977	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR4	0.71	0.07	0	0	0	not significant
8978	REACTOME_MISCELLANEOUS_TRANSPORT_AND_BINDING_EVENTS	0.71	0.07	0	0	0	not significant
8979	REACTOME_PHASE_0_RAPID_DEPOLARISATION	0.71	0.07	0	0	0	not significant
8980	REACTOME_TRANSCRIPTION_OF_E2F_TARGETS_UNDER_NEGATIVE_CO	0.71	0.07	0	0	0	not significant
8981	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX1_UP	0.71	0.07	0	0	0	not significant
8982	BIOCARTA_ATRBRCA_PATHWAY	0.71	0.06	0	0	0	not significant
8983	GO_CERAMIDE_METABOLIC_PROCESS	0.71	0.06	0	0	0	not significant
8984	GO_MICROTUBULE_NUCLEATION	0.71	0.06	0	0	0	not significant
8985	GO_MYELOID_LEUKOCYTE_CYTOKINE_PRODUCTION	0.71	0.06	0	0	0	not significant
8986	GO_REGULATION_OF_EXIT_FROM_MITOSIS	0.71	0.06	0	0	0	not significant
8987	PETRETTO_HEART_MASS_QTL_CIS_UP	0.71	0.06	0	0	0	not significant
8988	REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	0.71	0.06	0	0	0	not significant
8989	ZHAN_MULTIPLE_MYELOMA_CD1_DN	0.71	0.06	0	0	0	not significant
8990	GO_CAVEOLA	0.71	0.05	0	0	0	not significant
8991	GO_ENDODERM_DEVELOPMENT	0.71	0.05	0	0	0	not significant
8992	GO_NEGATIVE_REGULATION_OF_BLOOD_CIRCULATION	0.71	0.05	0	0	0	not significant
8993	GO_REGULATION_OF_CELL_CYCLE_CHECKPOINT	0.71	0.05	0	0	0	not significant
8994	KEGG_MELANOMA	0.71	0.05	0	0	0	not significant
8995	KYNG_RESPONSE_TO_H2O2_VIA_ERCC6_DN	0.71	0.05	0	0	0	not significant
8996	REACTOME_SIGNALING_BY_ERBB2	0.71	0.05	0	0	0	not significant
8997	GO_ATP_HYDROLYSIS_COUPLED_CATION_TRANSMEMBRANE_TRANSPO	0.71	0.04	0	0	0	not significant
8998	REACTOME_REPRODUCTION	0.71	0.03	0	0	0	not significant
8999	GO_LATE_ENDOSOME_MEMBRANE	0.71	0.02	0	0	0	not significant
9000	GO_NEGATIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	0.71	0.02	0	0	0	not significant
9001	IVANOVSKA_MIR106B_TARGETS	0.71	0.02	0	0	0	not significant
9002	GO_NEGATIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUN	0.71	0.01	0	0	0	not significant
9003	REACTOME_CELLULAR_SENESCENCE	0.71	0.01	0	0	0	not significant
9004	GO_CHROMATIN_ORGANIZATION	0.71	0.00	0	0	0	not significant
9005	GO_MICROTUBULE_ORGANIZING_CENTER	0.71	0.00	0	0	0	not significant
9006	GO_PYRIMIDINE_DEOXYRIBONUCLEOTIDE_BIOSYNTHETIC_PROCESS	0.72	0.10	0	0	0	not significant
9007	GO_Y_FORM_DNA_BINDING	0.72	0.10	0	0	0	not significant
9008	VANDESLUIS_COMMD1_TARGETS_GROUP_4_DN	0.72	0.10	0	0	0	not significant
9009	GO_DYNACTIN_BINDING	0.72	0.09	0	0	0	not significant
9010	GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN	0.72	0.09	0	0	0	not significant
9011	GO_PROTEIN_AUTOPROCESSING	0.72	0.09	0	0	0	not significant
9012	GO_REGULATION_OF_METAPHASE_PLATE_CONGRESSION	0.72	0.09	0	0	0	not significant
9013	GO_REGULATION_OF_VIRAL_INDUCED_CYTOPLASMIC_PATTERN_RECO	0.72	0.09	0	0	0	not significant
9014	GO_RNA_POLYMERASE_III_PREINITIATION_COMPLEX_ASSEMBLY	0.72	0.09	0	0	0	not significant
9015	GO_SMAD_PROTEIN_COMPLEX_ASSEMBLY	0.72	0.09	0	0	0	not significant
9016	KONG_E2F1_TARGETS	0.72	0.09	0	0	0	not significant
9017	MIKKELSEN_PLURIPOTENT_STATE_DN	0.72	0.09	0	0	0	not significant
9018	BIOCARTA_PITX2_PATHWAY	0.72	0.08	0	0	0	not significant
9019	GO_ATPASE_DEPENDENT_TRANSMEMBRANE_TRANSPORT_COMPLEX	0.72	0.08	0	0	0	not significant
9020	GO_LIVER_MORPHOGENESIS	0.72	0.08	0	0	0	not significant
9021	GO_MICROVILLUS_MEMBRANE	0.72	0.08	0	0	0	not significant
9022	GO_NEGATIVE_REGULATION_OF_ANION_TRANSPORT	0.72	0.08	0	0	0	not significant
9023	GO_REGULATION_OF_EPIDERMAL_GROWTH_FACTOR_ACTIVATED_REC	0.72	0.08	0	0	0	not significant
9024	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CENTROSOME	0.72	0.08	0	0	0	not significant
9025	GO_SEX_DETERMINATION	0.72	0.08	0	0	0	not significant
9026	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR2	0.72	0.08	0	0	0	not significant
9027	STARK_HYPPOCAMPUS_22Q11_DELETION_DN	0.72	0.08	0	0	0	not significant
9028	BIOCARTA_CHEMICAL_PATHWAY	0.72	0.07	0	0	0	not significant
9029	BIOCARTA_NFKB_PATHWAY	0.72	0.07	0	0	0	not significant
9030	CHR18Q12	0.72	0.07	0	0	0	not significant
9031	GO_ORGANIC_CATION_TRANSPORT	0.72	0.07	0	0	0	not significant
9032	GO_PYRIMIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	0.72	0.07	0	0	0	not significant
9033	GO_REGULATION_OF_FATTY_ACID_OXIDATION	0.72	0.07	0	0	0	not significant
9034	PID_A6B1_A6B4_INTEGRIN_PATHWAY	0.72	0.07	0	0	0	not significant
9035	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_ADDITIONAL_CELL_	0.72	0.07	0	0	0	not significant

9036	CHRXQ22	0.72	0.06	0	0	0	not significant
9037	GO_S_ACYLTRANSFERASE_ACTIVITY	0.72	0.06	0	0	0	not significant
9038	REACTOME_IRAK1_RECRUITS_IKK_COMPLEX	0.72	0.06	0	0	0	not significant
9039	AMIT_EGF_RESPONSE_240_HELA	0.72	0.05	0	0	0	not significant
9040	CHEN_NEUROBLASTOMA_COPY_NUMBER_GAINS	0.72	0.05	0	0	0	not significant
9041	GO_CENTRIOLE_ASSEMBLY	0.72	0.05	0	0	0	not significant
9042	GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT_	0.72	0.05	0	0	0	not significant
9043	GO_NEUTROPHIL_MIGRATION	0.72	0.05	0	0	0	not significant
9044	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN	0.72	0.05	0	0	0	not significant
9045	PID_TRKR_PATHWAY	0.72	0.05	0	0	0	not significant
9046	GO_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	0.72	0.04	0	0	0	not significant
9047	GO_REGULATION_OF_HISTONE_METHYLATION	0.72	0.04	0	0	0	not significant
9048	OUILLETTE_CLL_13Q14_DELETION_UP	0.72	0.04	0	0	0	not significant
9049	PID_P75_NTR_PATHWAY	0.72	0.04	0	0	0	not significant
9050	GO_ALTERNATIVE_MRNA_SPLICING_VIA_SPLICEOSOME	0.72	0.03	0	0	0	not significant
9051	DARWICHE_SKIN_TUMOR_PROMOTER_DN	0.72	0.02	0	0	0	not significant
9052	GO_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNALING_PATHWAY	0.72	0.02	0	0	0	not significant
9053	WEI_MIR34A_TARGETS	0.72	0.02	0	0	0	not significant
9054	GABRIELY_MIR21_TARGETS	0.72	0.00	0	0	0	not significant
9055	GO_PROCESS_UTILIZING_AUTOPHAGIC_MECHANISM	0.72	0.00	0	0	0	not significant
9056	REACTOME_IL_6_TYPE_CYTOKINE_RECEPTOR_LIGAND_INTERACTIONS	0.73	0.12	0	0	0	not significant
9057	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_DIFFERENTIA	0.73	0.11	0	0	0	not significant
9058	GO_RNA_POLYMERASE_III_TYPE_1_PROMOTER_DNA_BINDING	0.73	0.11	0	0	0	not significant
9059	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_25	0.73	0.11	0	0	0	not significant
9060	CHR3P13	0.73	0.10	0	0	0	not significant
9061	GO_MAINTENANCE_OF_APICAL_BASAL_CELL_POLARITY	0.73	0.10	0	0	0	not significant
9062	GO_MUCUS_SECRETION	0.73	0.10	0	0	0	not significant
9063	GO_NURF_COMPLEX	0.73	0.10	0	0	0	not significant
9064	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_ENDOSOME	0.73	0.10	0	0	0	not significant
9065	GO_SIGNAL_COMPLEX_ASSEMBLY	0.73	0.10	0	0	0	not significant
9066	HOWLIN_CITED1_TARGETS_2_UP	0.73	0.10	0	0	0	not significant
9067	REACTOME_ACYL_CHAIN_REMODELLING_OF_PG	0.73	0.10	0	0	0	not significant
9068	GENTILE_UV_HIGH_DOSE_UP	0.73	0.09	0	0	0	not significant
9069	GO_ATTACHMENT_OF_MITOTIC_SPINDLE_MICROTUBULES_TO_KINETOC	0.73	0.09	0	0	0	not significant
9070	GO_KERATINOCYTE_PROLIFERATION	0.73	0.09	0	0	0	not significant
9071	GO_MITOCHONDRION_DISTRIBUTION	0.73	0.09	0	0	0	not significant
9072	GO_NEGATIVE_REGULATION_OF_BONE_MINERALIZATION	0.73	0.09	0	0	0	not significant
9073	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_	0.73	0.09	0	0	0	not significant
9074	GO_OXOGLUTARATE_DEHYDROGENASE_COMPLEX	0.73	0.09	0	0	0	not significant
9075	GO_PROTEIN_LOCALIZATION_TO_KINETOCHORE	0.73	0.09	0	0	0	not significant
9076	GO_UBIQUITIN_UBIQUITIN_LIGASE_ACTIVITY	0.73	0.09	0	0	0	not significant
9077	GROSS_HYPOXIA_VIA_HIF1A_ONLY	0.73	0.09	0	0	0	not significant
9078	NIELSEN_SYNOVIAL_SARCOMA_UP	0.73	0.09	0	0	0	not significant
9079	REACTOME_MYOCLONIC_EPILEPSY_OF_LAFORA	0.73	0.09	0	0	0	not significant
9080	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_TOP20_DN	0.73	0.09	0	0	0	not significant
9081	GO_G_PROTEIN_COUPLED_RECEPTOR_INTERNALIZATION	0.73	0.08	0	0	0	not significant
9082	GO_MEMBRANE_PROTEIN_INTRACELLULAR_DOMAIN_PROTEOLYSIS	0.73	0.08	0	0	0	not significant
9083	GO_NBAF_COMPLEX	0.73	0.08	0	0	0	not significant
9084	GO_PRIMITIVE_HEMOPOIESIS	0.73	0.08	0	0	0	not significant
9085	GO_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS	0.73	0.08	0	0	0	not significant
9086	GO_REGULATION_OF_INTEGRIN_ACTIVATION	0.73	0.08	0	0	0	not significant
9087	SCHLINGEMANN_SKIN_CARCINOGENESIS_TPA_DN	0.73	0.08	0	0	0	not significant
9088	GO_HISTONE_H3_K9_METHYLATION	0.73	0.06	0	0	0	not significant
9089	GO_INTERSTRAND_CROSS_LINK_REPAIR	0.73	0.06	0	0	0	not significant
9090	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.73	0.06	0	0	0	not significant
9091	GO_DNA_DEPENDENT_DNA_REPLICATION_MAINTENANCE_OF_FIDELITY	0.73	0.05	0	0	0	not significant
9092	REACTOME_HDR_THROUGH_SINGLE_STRAND_ANNEALING_SSA	0.73	0.05	0	0	0	not significant
9093	BROWNE_HCMV_INFECTION_8HR_UP	0.73	0.04	0	0	0	not significant
9094	GO_MYOTUBE_DIFFERENTIATION	0.73	0.04	0	0	0	not significant
9095	GO_REGULATION_OF_MEMBRANE_PERMEABILITY	0.73	0.04	0	0	0	not significant
9096	CHR1Q32	0.73	0.03	0	0	0	not significant
9097	GO_POSITIVE_REGULATION_OF_CHROMATIN_ORGANIZATION	0.73	0.03	0	0	0	not significant
9098	DAZARD_RESPONSE_TO_UV_SCC_DN	0.73	0.02	0	0	0	not significant
9099	GO_PRESYNAPSE	0.73	0.01	0	0	0	not significant
9100	GO_COVALENT_CHROMATIN_MODIFICATION	0.73	0.00	0	0	0	not significant
9101	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN	0.73	0.00	0	0	0	not significant
9102	MILI_PSEUDOPODIA_HAPTOTAXIS_DN	0.73	0.00	0	0	0	not significant
9103	GO_CDP_ALCOHOL_PHOSPHATIDYLTRANSFERASE_ACTIVITY	0.74	0.13	0	0	0	not significant
9104	GO_CUL2_RING_UBIQUITIN_LIGASE_COMPLEX	0.74	0.12	0	0	0	not significant
9105	GO_INTERLEUKIN_4_MEDIATED_SIGNALING_PATHWAY	0.74	0.11	0	0	0	not significant
9106	GO_REGULATION_OF_DENDRITIC_CELL_DIFFERENTIATION	0.74	0.11	0	0	0	not significant
9107	GO_T_CELL_TOLERANCE_INDUCTION	0.74	0.11	0	0	0	not significant
9108	CHANG_POU5F1_TARGETS_DN	0.74	0.10	0	0	0	not significant
9109	GO_DNA_N_GLYCOSYLASE_ACTIVITY	0.74	0.10	0	0	0	not significant
9110	GO_LEPTIN_MEDIATED_SIGNALING_PATHWAY	0.74	0.10	0	0	0	not significant
9111	GO_MESENCHYMAL_TO_EPITHELIAL_TRANSITION_INVOLVED_IN_METANE	0.74	0.10	0	0	0	not significant
9112	GO_NEGATIVE_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	0.74	0.10	0	0	0	not significant
9113	GO_PHOSPHATIDYLINOSITOL_KINASE_ACTIVITY	0.74	0.10	0	0	0	not significant
9114	GO_POSITIVE_REGULATION_OF_RECEPTOR_INTERNALIZATION	0.74	0.10	0	0	0	not significant
9115	PID_ALK2_PATHWAY	0.74	0.10	0	0	0	not significant
9116	REACTOME_KSRP_KHSRP_BINDS_AND_DESTABILIZES_MRNA	0.74	0.10	0	0	0	not significant
9117	REACTOME_NOTCH4_ACTIVATION_AND_TRANSMISSION_OF_SIGNAL_TO_	0.74	0.10	0	0	0	not significant
9118	REACTOME_RUNX3_REGULATES_WNT_SIGNALING	0.74	0.10	0	0	0	not significant
9119	REACTOME_SOS_MEDIATED_SIGNALLING	0.74	0.10	0	0	0	not significant
9120	GO_DIOL_BIOSYNTHETIC_PROCESS	0.74	0.09	0	0	0	not significant
9121	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_IN_OLD	0.74	0.09	0	0	0	not significant
9122	PIONTEK_PKD1_TARGETS_UP	0.74	0.09	0	0	0	not significant
9123	REACTOME_FRS_MEDIATED_FGFR3_SIGNALING	0.74	0.09	0	0	0	not significant
9124	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN	0.74	0.09	0	0	0	not significant
9125	CHR3P24	0.74	0.08	0	0	0	not significant
9126	GO_AMYLOID_BETA_FORMATION	0.74	0.08	0	0	0	not significant
9127	GO_PHENOL_CONTAINING_COMPOUND_METABOLIC_PROCESS	0.74	0.08	0	0	0	not significant
9128	GO_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	0.74	0.08	0	0	0	not significant
9129	GO_REGULATION_OF_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	0.74	0.08	0	0	0	not significant
9130	WONG_IFNA2_RESISTANCE_UP	0.74	0.08	0	0	0	not significant
9131	XU_CREBBP_TARGETS_UP	0.74	0.08	0	0	0	not significant
9132	GO_O_ACYLTRANSFERASE_ACTIVITY	0.74	0.07	0	0	0	not significant
9133	GO_PROTEIN_INSERTION_INTO_MITOCHONDRIAL_MEMBRANE_INVOLVED	0.74	0.07	0	0	0	not significant
9134	HU_GENOTOXIN_ACTION_DIRECT_VS_INDIRECT_4HR	0.74	0.07	0	0	0	not significant
9135	MIZUSHIMA_AUTOPHAGOSOME_FORMATION	0.74	0.07	0	0	0	not significant
9136	REACTOME_NEGATIVE_REGULATION_OF_FGFR3_SIGNALING	0.74	0.07	0	0	0	not significant
9137	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_DN	0.74	0.07	0	0	0	not significant
9138	SHIPP_DLBCL_CURED_VS_FATAL_DN	0.74	0.07	0	0	0	not significant
9139	GO_DNA_CATABOLIC_PROCESS	0.74	0.06	0	0	0	not significant
9140	GO_HISTONE_UBIQUITINATION	0.74	0.06	0	0	0	not significant
9141	GO_NEGATIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	0.74	0.06	0	0	0	not significant
9142	REACTOME_FANCONI_ANEMIA_PATHWAY	0.74	0.06	0	0	0	not significant
9143	GO_DNA_METHYLATION	0.74	0.05	0	0	0	not significant
9144	REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	0.74	0.05	0	0	0	not significant

9145	ROPERO_HDAC2_TARGETS	0.74	0.05	0	0	0	not significant
9146	GO_CARBOXYLIC_ESTER_HYDROLASE_ACTIVITY	0.74	0.04	0	0	0	not significant
9147	GO_MORPHOGENESIS_OF_EMBRYONIC_EPITHELIUM	0.74	0.04	0	0	0	not significant
9148	GO_SH3_DOMAIN_BINDING	0.74	0.04	0	0	0	not significant
9149	JNK_DN.V1_UP	0.74	0.04	0	0	0	not significant
9150	VERHAAK_GLIOBLASTOMA_NEURAL	0.74	0.04	0	0	0	not significant
9151	GO_NEGATIVE_REGULATION_OF_CELL_GROWTH	0.74	0.03	0	0	0	not significant
9152	THUM_SYSTOLIC_HEART_FAILURE_DN	0.74	0.02	0	0	0	not significant
9153	GO_UBIQUITIN_LIGASE_COMPLEX	0.74	0.00	0	0	0	not significant
9154	GO_MUCOPOLYSACCHARIDE_METABOLIC_PROCESS	0.75	0.13	0	0	0	not significant
9155	GO_MITOCHONDRIAL_ALPHA_KETOGLUTARATE_DEHYDROGENASE_COM	0.75	0.12	0	0	0	not significant
9156	GO_MUSCLE_MYOSIN_COMPLEX	0.75	0.12	0	0	0	not significant
9157	GO_NEGATIVE_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS	0.75	0.12	0	0	0	not significant
9158	GO_PHOSPHATIDYLINOSITOL_TRANSPORTER_ACTIVITY	0.75	0.12	0	0	0	not significant
9159	GO_ARF_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	0.75	0.11	0	0	0	not significant
9160	GO_GLYCEROPHOSPHOLIPID_CATABOLIC_PROCESS	0.75	0.11	0	0	0	not significant
9161	GO_IRON_ION_TRANSMEMBRANE_TRANSPORT	0.75	0.11	0	0	0	not significant
9162	GO_MDA_5_SIGNALING_PATHWAY	0.75	0.11	0	0	0	not significant
9163	GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_	0.75	0.11	0	0	0	not significant
9164	GO_REGULATION_OF_CYTOPLASMIC_TRANSLATIONAL_INITIATION	0.75	0.11	0	0	0	not significant
9165	GO_REGULATION_OF_DENDRITE_EXTENSION	0.75	0.11	0	0	0	not significant
9166	ABDELMOHSEN_ELAVL4_TARGETS	0.75	0.10	0	0	0	not significant
9167	CHR6Q27	0.75	0.10	0	0	0	not significant
9168	GO_CELL_DIFFERENTIATION_INVOLVED_IN_METANEPHROS_DEVELOPME	0.75	0.10	0	0	0	not significant
9169	GO_ENDODEOXYRIBONUCLEASE_ACTIVITY_PRODUCING_3_PHOSPHOM	0.75	0.10	0	0	0	not significant
9170	GO_FIBROBLAST_ACTIVATION	0.75	0.10	0	0	0	not significant
9171	GO_NEURON_RECOGNITION	0.75	0.10	0	0	0	not significant
9172	GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_FISSION	0.75	0.10	0	0	0	not significant
9173	GO_POSITIVE_REGULATION_OF_MITOTIC_SISTER_CHROMATID_SEGRE	0.75	0.10	0	0	0	not significant
9174	GO_POSITIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHW	0.75	0.10	0	0	0	not significant
9175	GO_RAP_PROTEIN_SIGNAL_TRANSDUCTION	0.75	0.10	0	0	0	not significant
9176	GO_REGULATION_OF_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNA	0.75	0.10	0	0	0	not significant
9177	GO_REGULATION_OF_TUBULIN_DEACETYLATION	0.75	0.10	0	0	0	not significant
9178	GO_RESPONSE_TO_SALT	0.75	0.10	0	0	0	not significant
9179	GO_SODIUM_ION_BINDING	0.75	0.10	0	0	0	not significant
9180	MIKKELSEN_IPS_LCP_WITH_H3K27ME3	0.75	0.10	0	0	0	not significant
9181	REACTOME_P38MAPK_EVENTS	0.75	0.10	0	0	0	not significant
9182	GO_AMYLOID_BETA_CLEARANCE	0.75	0.09	0	0	0	not significant
9183	GO_EATING_BEHAVIOR	0.75	0.09	0	0	0	not significant
9184	GO_MULTIVESICULAR_BODY	0.75	0.09	0	0	0	not significant
9185	LIU_SMARCA4_TARGETS	0.75	0.09	0	0	0	not significant
9186	GO_DNA_POLYMERASE_ACTIVITY	0.75	0.08	0	0	0	not significant
9187	GO_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWA	0.75	0.08	0	0	0	not significant
9188	GO_REGULATION_OF_MAST_CELL_ACTIVATION	0.75	0.08	0	0	0	not significant
9189	GO_VENTRICULAR_SEPTUM_MORPHOGENESIS	0.75	0.08	0	0	0	not significant
9190	SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_DN	0.75	0.08	0	0	0	not significant
9191	WAKABAYASHI_ADIPOGENESIS_PPARG_BOUND_36HR	0.75	0.08	0	0	0	not significant
9192	GO_NEGATIVE_REGULATION_OF_AXONOGENESIS	0.75	0.07	0	0	0	not significant
9193	GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	0.75	0.07	0	0	0	not significant
9194	REACTOME_OVARIAN_TUMOR_DOMAIN_PROTEASES	0.75	0.07	0	0	0	not significant
9195	ROESSLER_LIVER_CANCER_METASTASIS_DN	0.75	0.07	0	0	0	not significant
9196	BROWNE_HCMV_INFECTION_10HR_UP	0.75	0.05	0	0	0	not significant
9197	CAMPS_COLON_CANCER_COPY_NUMBER_UP	0.75	0.05	0	0	0	not significant
9198	GO_FEMALE_GAMETE_GENERATION	0.75	0.05	0	0	0	not significant
9199	GO_NEGATIVE_REGULATION_OF_PROTEOLYSIS_INVOLVED_IN_CELLULA	0.75	0.05	0	0	0	not significant
9200	GO_POSITIVE_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATA	0.75	0.05	0	0	0	not significant
9201	GO_PROTEIN_LOCALIZATION_TO_CYTOSKELETON	0.75	0.05	0	0	0	not significant
9202	GO_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOSIS	0.75	0.05	0	0	0	not significant
9203	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	0.75	0.04	0	0	0	not significant
9204	GO_ERAD_PATHWAY	0.75	0.04	0	0	0	not significant
9205	GO_NEGATIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	0.75	0.04	0	0	0	not significant
9206	GO_CELLULAR_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN	0.75	0.03	0	0	0	not significant
9207	CHR1P36	0.75	0.01	0	0	0	not significant
9208	GO_SMALL_GTPASE_BINDING	0.75	0.01	0	0	0	not significant
9209	GO_BLOOD_VESSEL_REMODELING	0.76	0.13	0	0	0	not significant
9210	GO_NEGATIVE_REGULATION_OF_ACTIN_NUCLEATION	0.76	0.13	0	0	0	not significant
9211	REACTOME_TRIF_MEDIATED_PROGRAMMED_CELL_DEATH	0.76	0.13	0	0	0	not significant
9212	GO_NEGATIVE_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	0.76	0.12	0	0	0	not significant
9213	GO_PROTEIN_PRENYLTRANSFERASE_ACTIVITY	0.76	0.12	0	0	0	not significant
9214	GO_RNA_POLYMERASE_I_CORE_BINDING	0.76	0.12	0	0	0	not significant
9215	REACTOME_ACTIVATION_OF_RAC1	0.76	0.12	0	0	0	not significant
9216	BIOCARTA_EICOSANOID_PATHWAY	0.76	0.11	0	0	0	not significant
9217	GO_ANTIBIOTIC_BIOSYNTHETIC_PROCESS	0.76	0.11	0	0	0	not significant
9218	GO_BASAL_PLASMA_MEMBRANE	0.76	0.11	0	0	0	not significant
9219	GO_COLLECTING_DUCT_DEVELOPMENT	0.76	0.11	0	0	0	not significant
9220	GO_DIACYLGLYCEROL_KINASE_ACTIVITY	0.76	0.11	0	0	0	not significant
9221	GO_EXCITATORY_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACT	0.76	0.11	0	0	0	not significant
9222	GO_KERATINOCYTE_DEVELOPMENT	0.76	0.11	0	0	0	not significant
9223	GO_POSITIVE_REGULATION_OF_FC_RECEPTOR_MEDIATED_STIMULATO	0.76	0.11	0	0	0	not significant
9224	GO_POSTSYNAPTIC_NEUROTRANSMITTER_RECEPTOR_INTERNALIZATIO	0.76	0.11	0	0	0	not significant
9225	GO_PROTEIN_IMPORT_INTO_PEROXISOME_MEMBRANE	0.76	0.11	0	0	0	not significant
9226	GO_REGULATION_OF_AXON_GUIDANCE	0.76	0.11	0	0	0	not significant
9227	GO_REGULATION_OF_EXOSOMAL_SECRETION	0.76	0.11	0	0	0	not significant
9228	GO_TRIGLYCERIDE_RICH_PLASMA_LIPOPROTEIN_PARTICLE	0.76	0.11	0	0	0	not significant
9229	GO_UDP_GALACTOSYLTRANSFERASE_ACTIVITY	0.76	0.11	0	0	0	not significant
9230	LI_CISPLATIN_RESISTANCE_UP	0.76	0.11	0	0	0	not significant
9231	REACTOME_ACTIVATION_OF_SMO	0.76	0.11	0	0	0	not significant
9232	REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION	0.76	0.11	0	0	0	not significant
9233	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN	0.76	0.11	0	0	0	not significant
9234	BIOCARTA_41BB_PATHWAY	0.76	0.10	0	0	0	not significant
9235	BIOCARTA_RACCYCD_PATHWAY	0.76	0.10	0	0	0	not significant
9236	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP	0.76	0.10	0	0	0	not significant
9237	CHR21Q21	0.76	0.10	0	0	0	not significant
9238	CHR2Q23	0.76	0.10	0	0	0	not significant
9239	FIGUEROA_AML_METHYLATION_CLUSTER_3_DN	0.76	0.10	0	0	0	not significant
9240	GO_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY	0.76	0.10	0	0	0	not significant
9241	GO_AORTA_DEVELOPMENT	0.76	0.10	0	0	0	not significant
9242	GO_CATALYTIC_ACTIVITY_ACTING_ON_A_GLYCOPROTEIN	0.76	0.10	0	0	0	not significant
9243	GO_MESENCHYMAL_TO_EPITHELIAL_TRANSITION	0.76	0.10	0	0	0	not significant
9244	GO_NEUROTRANSMITTER_RECEPTOR_INTERNALIZATION	0.76	0.10	0	0	0	not significant
9245	GO_POSITIVE_THYMIC_T_CELL_SELECTION	0.76	0.10	0	0	0	not significant
9246	GO_REGULATION_OF_PLATELET_DERIVED_GROWTH_FACTOR_RECEPT	0.76	0.10	0	0	0	not significant
9247	GO_TETRAPYRROLE_METABOLIC_PROCESS	0.76	0.10	0	0	0	not significant
9248	REACTOME_BUTYRATE_RESPONSE_FACTOR_1_BRF1_BINDS_AND_DES	0.76	0.10	0	0	0	not significant
9249	CASORELLI_APL_SECONDARY_VS_DE_NOVO_UP	0.76	0.09	0	0	0	not significant
9250	CERIBELLI_GENES_INACTIVE_AND_BOUND_BY_NFY	0.76	0.09	0	0	0	not significant
9251	CHANDRAN_METASTASIS_TOP50_UP	0.76	0.09	0	0	0	not significant
9252	GO_AGGRESOME	0.76	0.09	0	0	0	not significant
9253	GO_AXONAL_GROWTH_CONE	0.76	0.09	0	0	0	not significant

9254	GO_HEME_BIOSYNTHETIC_PROCESS	0.76	0.09	0	0	0	not significant
9255	GO_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_III	0.76	0.09	0	0	0	not significant
9256	REACTOME_INSULIN_PROCESSING	0.76	0.09	0	0	0	not significant
9257	SHAFFER_IRF4_MULTIPLE_MYELOMA_PROGRAM	0.76	0.09	0	0	0	not significant
9258	WU_HBX_TARGETS_2_UP	0.76	0.09	0	0	0	not significant
9259	GO_ENDOCYTIC_RECYCLING	0.76	0.08	0	0	0	not significant
9260	GO_HISTONE_MONOUBIQUITINATION	0.76	0.08	0	0	0	not significant
9261	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_ENDOPLASMIC_RETIC	0.76	0.08	0	0	0	not significant
9262	PID_PI3K_PLC_TRK_PATHWAY	0.76	0.08	0	0	0	not significant
9263	GO_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	0.76	0.07	0	0	0	not significant
9264	GO_OOGENESIS	0.76	0.07	0	0	0	not significant
9265	JOHNSTONE_PARVB_TARGETS_1_DN	0.76	0.07	0	0	0	not significant
9266	LUI_TARGETS_OF_PAX8_PPARG_FUSION	0.76	0.07	0	0	0	not significant
9267	PID_AR_PATHWAY	0.76	0.07	0	0	0	not significant
9268	ZHAN_MULTIPLE_MYELOMA_MF_DN	0.76	0.07	0	0	0	not significant
9269	GO_CELL_RECOGNITION	0.76	0.06	0	0	0	not significant
9270	GO_GLUCAN_METABOLIC_PROCESS	0.76	0.06	0	0	0	not significant
9271	GO_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	0.76	0.06	0	0	0	not significant
9272	KEGG_TGF_BETA_SIGNALING_PATHWAY	0.76	0.06	0	0	0	not significant
9273	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.76	0.06	0	0	0	not significant
9274	PID_TCR_PATHWAY	0.76	0.06	0	0	0	not significant
9275	PKCA_DN.V1_UP	0.76	0.06	0	0	0	not significant
9276	REACTOME_G_ALPHA_12_13_SIGNALLING_EVENTS	0.76	0.06	0	0	0	not significant
9277	GO_ORGANELLE_DISASSEMBLY	0.76	0.04	0	0	0	not significant
9278	REACTOME_SIGNALING_BY_TGF_BETA_FAMILY_MEMBERS	0.76	0.04	0	0	0	not significant
9279	DARWICHE_SQUAMOUS_CELL_CARCINOMA_DN	0.76	0.03	0	0	0	not significant
9280	GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	0.76	0.03	0	0	0	not significant
9281	GO_RECYCLING_ENDOSOME	0.76	0.02	0	0	0	not significant
9282	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_UP	0.76	0.02	0	0	0	not significant
9283	WANG_CISPLATIN_RESPONSE_AND_XPC_DN	0.76	0.02	0	0	0	not significant
9284	GO_PEROXISOME_FISSION	0.77	0.14	0	0	0	not significant
9285	GO_HEMATOPOIETIC_STEM_CELL_PROLIFERATION	0.77	0.13	0	0	0	not significant
9286	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQO_IN_OLD	0.77	0.13	0	0	0	not significant
9287	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_DN	0.77	0.13	0	0	0	not significant
9288	BIOCARTA_PAR1_PATHWAY	0.77	0.12	0	0	0	not significant
9289	GO_ACTIVATION_OF_PROTEIN_KINASE_B_ACTIVITY	0.77	0.12	0	0	0	not significant
9290	GO_DNA_BINDING_BENDING	0.77	0.12	0	0	0	not significant
9291	GO_INOSITOL_TRISPHOSPHATE_PHOSPHATASE_ACTIVITY	0.77	0.12	0	0	0	not significant
9292	GO_MODULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	0.77	0.12	0	0	0	not significant
9293	GO_POSITIVE_REGULATION_OF_MICROTUBULE_BINDING	0.77	0.12	0	0	0	not significant
9294	GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	0.77	0.12	0	0	0	not significant
9295	WILLIAMS_ESR2_TARGETS_DN	0.77	0.12	0	0	0	not significant
9296	GHANDHI_DIRECT_IRRADIATION_DN	0.77	0.11	0	0	0	not significant
9297	GO_CYTOPLASMIC_MRNA_PROCESSING_BODY_ASSEMBLY	0.77	0.11	0	0	0	not significant
9298	GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_KINASE_BINDING	0.77	0.11	0	0	0	not significant
9299	GO_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE_TO_ANTIGE	0.77	0.11	0	0	0	not significant
9300	GO_REGULATION_OF_MITOCHONDRIAL_FISSION	0.77	0.11	0	0	0	not significant
9301	GO_RESPONSE_TO_FUNGICIDE	0.77	0.11	0	0	0	not significant
9302	GO_RNAI_EFFECTOR_COMPLEX	0.77	0.11	0	0	0	not significant
9303	KEGG_DRUG_METABOLISM_CYTOCHROME_P450	0.77	0.11	0	0	0	not significant
9304	OLSSON_E2F3_TARGETS_UP	0.77	0.11	0	0	0	not significant
9305	REACTOME_DOWNREGULATION_OF_ERBB2_SIGNALING	0.77	0.11	0	0	0	not significant
9306	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_DN	0.77	0.10	0	0	0	not significant
9307	GO_CENTRIOLAR_SUBDISTAL_APPENDAGE	0.77	0.10	0	0	0	not significant
9308	GO_CYTOPLASMIC_TRANSLATIONAL_INITIATION	0.77	0.10	0	0	0	not significant
9309	GO_MULTIVESICULAR_BODY_SORTING_PATHWAY	0.77	0.10	0	0	0	not significant
9310	GO_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIAT	0.77	0.10	0	0	0	not significant
9311	GO_TOLL_LIKE_RECEPTOR_3_SIGNALING_PATHWAY	0.77	0.10	0	0	0	not significant
9312	REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	0.77	0.10	0	0	0	not significant
9313	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_UP	0.77	0.09	0	0	0	not significant
9314	CHR8P11	0.77	0.09	0	0	0	not significant
9315	GO_FIBROBLAST_MIGRATION	0.77	0.09	0	0	0	not significant
9316	GO_ION_ANTIPORTER_ACTIVITY	0.77	0.09	0	0	0	not significant
9317	GO_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	0.77	0.09	0	0	0	not significant
9318	GO_REGULATION_OF_ERAD_PATHWAY	0.77	0.09	0	0	0	not significant
9319	KEGG_NOTCH_SIGNALING_PATHWAY	0.77	0.09	0	0	0	not significant
9320	CHANDRAN_METASTASIS_TOP50_DN	0.77	0.08	0	0	0	not significant
9321	CHEBOTAEV_GR_TARGETS_UP	0.77	0.08	0	0	0	not significant
9322	GO_ACTIVATION_OF_MAPKK_ACTIVITY	0.77	0.08	0	0	0	not significant
9323	GO_IRON_ION_TRANSPORT	0.77	0.08	0	0	0	not significant
9324	GO_NEUROMUSCULAR_JUNCTION	0.77	0.08	0	0	0	not significant
9325	GO_PROMOTER_SPECIFIC_CHROMATIN_BINDING	0.77	0.08	0	0	0	not significant
9326	LUI_THYROID_CANCER_PAX8_PPARG_DN	0.77	0.08	0	0	0	not significant
9327	PID_ERA_GENOMIC_PATHWAY	0.77	0.08	0	0	0	not significant
9328	REACTOME_REGULATION_OF_TP53_EXPRESSION_AND_DEGRADATION	0.77	0.08	0	0	0	not significant
9329	REACTOME_SIGNALING_BY_NOTCH1_IN_CANCER	0.77	0.08	0	0	0	not significant
9330	CHR1Q23	0.77	0.07	0	0	0	not significant
9331	GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	0.77	0.07	0	0	0	not significant
9332	GO_NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	0.77	0.07	0	0	0	not significant
9333	KEGG_VIBRIO_CHOLERAE_INFECTION	0.77	0.07	0	0	0	not significant
9334	AMIT_EGF_RESPONSE_120_HELA	0.77	0.06	0	0	0	not significant
9335	CROMER_METASTASIS_UP	0.77	0.06	0	0	0	not significant
9336	ZHAN_MULTIPLE_MYELOMA_CD1_AND_CD2_UP	0.77	0.06	0	0	0	not significant
9337	GO_POSITIVE_REGULATION_OF_CELL_GROWTH	0.77	0.05	0	0	0	not significant
9338	REACTOME_DEATH_RECEPTOR_SIGNALLING	0.77	0.04	0	0	0	not significant
9339	GO_CELL_CYCLE_CHECKPOINT	0.77	0.03	0	0	0	not significant
9340	GO_CYSTEINE_TYPE_PEPTIDASE_ACTIVITY	0.77	0.03	0	0	0	not significant
9341	GO_CILIUM	0.77	0.01	0	0	0	not significant
9342	GO_COMMISSURAL_NEURON_AXON_GUIDANCE	0.78	0.14	0	0	0	not significant
9343	GO_NEGATIVE_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY_	0.78	0.14	0	0	0	not significant
9344	GO_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX_CLASS_III	0.78	0.14	0	0	0	not significant
9345	EHLERS_ANEUPLOIDY_DN	0.78	0.13	0	0	0	not significant
9346	GO_NEGATIVE_REGULATION_OF_LIPID_TRANSPORT	0.78	0.13	0	0	0	not significant
9347	GO_PEPTIDYL_PROLINE_HYDROXYLATION	0.78	0.13	0	0	0	not significant
9348	GO_VIRAL_TRANSLATIONAL_TERMINATION_REINITIATION	0.78	0.13	0	0	0	not significant
9349	REACTOME_SIGNALING_BY_NTRK2_TRKB	0.78	0.13	0	0	0	not significant
9350	GO_DENDRITE_MEMBRANE	0.78	0.12	0	0	0	not significant
9351	GO_DIHYDROLIPOYL_DEHYDROGENASE_COMPLEX	0.78	0.12	0	0	0	not significant
9352	GO_INSULIN_LIKE_GROWTH_FACTOR_BINDING	0.78	0.12	0	0	0	not significant
9353	GO_POSITIVE_REGULATION_OF_TORC1_SIGNALING	0.78	0.12	0	0	0	not significant
9354	GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_	0.78	0.12	0	0	0	not significant
9355	GO_RETINAL_METABOLIC_PROCESS	0.78	0.12	0	0	0	not significant
9356	REACTOME_PLATELET_ADHESION_TO_EXPOSED_COLLAGEN	0.78	0.12	0	0	0	not significant
9357	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_SEVERAL_ADDITIO	0.78	0.12	0	0	0	not significant
9358	REACTOME_TRAF3_DEPENDENT_IRF_ACTIVATION_PATHWAY	0.78	0.12	0	0	0	not significant
9359	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP	0.78	0.12	0	0	0	not significant
9360	SPIRA_SMOKERS_LUNG_CANCER_DN	0.78	0.12	0	0	0	not significant
9361	GO_HISTONE_H4_K16_ACETYLATION	0.78	0.11	0	0	0	not significant
9362	GO_NEGATIVE_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CE	0.78	0.11	0	0	0	not significant

9363	GO_PHOTORECEPTOR_CELL_DIFFERENTIATION	0.78	0.11	0	0	0	not significant
9364	GO_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	0.78	0.11	0	0	0	not significant
9365	PID_GLYPICAN_1PATHWAY	0.78	0.11	0	0	0	not significant
9366	BROWNE_HCMV_INFECTION_8HR_DN	0.78	0.10	0	0	0	not significant
9367	BURTON_ADIPOGENESIS_PEAK_AT_0HR	0.78	0.10	0	0	0	not significant
9368	GO_CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS	0.78	0.10	0	0	0	not significant
9369	GO_DETECTION_OF_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION	0.78	0.10	0	0	0	not significant
9370	GO_HISTONE_ACETYLTRANSFERASE_BINDING	0.78	0.10	0	0	0	not significant
9371	GO_PALMITOYLTRANSFERASE_ACTIVITY	0.78	0.10	0	0	0	not significant
9372	GO_POSITIVE_REGULATION_OF_PROTEIN_IMPORT	0.78	0.10	0	0	0	not significant
9373	GO_PROTEIN_DEACETYLASE_ACTIVITY	0.78	0.10	0	0	0	not significant
9374	GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.78	0.10	0	0	0	not significant
9375	REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANS	0.78	0.10	0	0	0	not significant
9376	GO_RECEPTOR_CLUSTERING	0.78	0.09	0	0	0	not significant
9377	GO_SCAFFOLD_PROTEIN_BINDING	0.78	0.09	0	0	0	not significant
9378	PID_NOTCH_PATHWAY	0.78	0.09	0	0	0	not significant
9379	LEIN_CHOROID_PLEXUS_MARKERS	0.78	0.08	0	0	0	not significant
9380	POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN	0.78	0.08	0	0	0	not significant
9381	REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYTHESIS	0.78	0.08	0	0	0	not significant
9382	DCA_UP.V1_UP	0.78	0.06	0	0	0	not significant
9383	GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_	0.78	0.06	0	0	0	not significant
9384	GO_LIPID_TRANSPORTER_ACTIVITY	0.78	0.06	0	0	0	not significant
9385	FIGUEROA_AML_METHYLATION_CLUSTER_3_UP	0.78	0.05	0	0	0	not significant
9386	GO_PLATELET_ACTIVATION	0.78	0.05	0	0	0	not significant
9387	REACTOME_OXIDATIVE_STRESS_INDUCED_SENESCENCE	0.78	0.05	0	0	0	not significant
9388	BAKKER_FOXO3_TARGETS_DN	0.78	0.04	0	0	0	not significant
9389	GO_PLASMA_MEMBRANE_BOUNDED_CELL_PROJECTION_CYTOPLASM	0.78	0.04	0	0	0	not significant
9390	GO_REGULATION_OF_RNA_SPLICING	0.78	0.04	0	0	0	not significant
9391	GO_MICROTUBULE_BINDING	0.78	0.03	0	0	0	not significant
9392	GO_MICROTUBULE_ORGANIZING_CENTER_PART	0.78	0.03	0	0	0	not significant
9393	GO_REGULATION_OF_MITOCHONDRION_ORGANIZATION	0.78	0.03	0	0	0	not significant
9394	HALLMARK_HEME_METABOLISM	0.78	0.03	0	0	0	not significant
9395	DURCHDEWALD_SKIN_CARCINOGENESIS_DN	0.78	0.02	0	0	0	not significant
9396	GO_INTRINSIC_COMPONENT_OF_ORGANELLE_MEMBRANE	0.78	0.02	0	0	0	not significant
9397	GO_TRANSITION_METAL_ION_BINDING	0.78	0.00	0	0	0	not significant
9398	CHRXQ11	0.79	0.15	0	0	0	not significant
9399	GO_AP_1_ADAPTOR_COMPLEX_BINDING	0.79	0.15	0	0	0	not significant
9400	GO_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	0.79	0.15	0	0	0	not significant
9401	GO_NUCLEAR_PERICENTRIC_HETEROCHROMATIN	0.79	0.15	0	0	0	not significant
9402	REACTOME_PI3K_AKT_ACTIVATION	0.79	0.15	0	0	0	not significant
9403	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_24HR_DN	0.79	0.14	0	0	0	not significant
9404	GO_ENDOPLASMIC_RETICULUM_TUBULAR_NETWORK_ORGANIZATION	0.79	0.14	0	0	0	not significant
9405	GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_4F_COMPLEX	0.79	0.14	0	0	0	not significant
9406	GO_FATTY_ACID_ALPHA_OXIDATION	0.79	0.14	0	0	0	not significant
9407	GO_NEGATIVE_REGULATION_OF_BEHAVIOR	0.79	0.14	0	0	0	not significant
9408	GO_POSITIVE_REGULATION_OF_CHROMOSOME_SEPARATION	0.79	0.14	0	0	0	not significant
9409	GO_REGULATION_OF_MESONEPHROS_DEVELOPMENT	0.79	0.14	0	0	0	not significant
9410	GO_REGULATION_OF_SYNAPTIC_VESICLE_FUSION_TO_PRESYNAPTIC_A	0.79	0.14	0	0	0	not significant
9411	HINATA_NFKB_IMMU_INF	0.79	0.14	0	0	0	not significant
9412	ZHENG_FOXP3_TARGETS_IN_THYMUS_DN	0.79	0.14	0	0	0	not significant
9413	CHRXQ24	0.79	0.13	0	0	0	not significant
9414	GO_CELL_FATE_DETERMINATION	0.79	0.13	0	0	0	not significant
9415	GO_LEUKOCYTE_TETHERING_OR_ROLLING	0.79	0.13	0	0	0	not significant
9416	GO_LYMPH_NODE_DEVELOPMENT	0.79	0.13	0	0	0	not significant
9417	GO_MANNOSYL_OLIGOSACCHARIDE_1_2_ALPHA_MANNOSIDASE_ACTIVIT	0.79	0.13	0	0	0	not significant
9418	GO_POSITIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	0.79	0.13	0	0	0	not significant
9419	GO_POSITIVE_REGULATION_OF_ISOTYPE_SWITCHING	0.79	0.13	0	0	0	not significant
9420	GO_PROTEIN_MATURATION_BY_IRON_SULFUR_CLUSTER_TRANSFER	0.79	0.13	0	0	0	not significant
9421	GO_REGULATION_OF_KERATINOCYTE_PROLIFERATION	0.79	0.13	0	0	0	not significant
9422	MANTOVANI_NFKB_TARGETS_UP	0.79	0.13	0	0	0	not significant
9423	REACTOME_CD28_DEPENDENT_VAV1_PATHWAY	0.79	0.13	0	0	0	not significant
9424	REACTOME_MAP3K8_TPL2_DEPENDENT_MAPK1_3_ACTIVATION	0.79	0.13	0	0	0	not significant
9425	GO_DOSAGE_COMPENSATION	0.79	0.12	0	0	0	not significant
9426	GO_HYDROLASE_ACTIVITY_HYDROLYZING_N_GLYCOSYL_COMPOUNDS	0.79	0.12	0	0	0	not significant
9427	GO_MAGNESIUM_ION_TRANSPORT	0.79	0.12	0	0	0	not significant
9428	GO_NEGATIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	0.79	0.12	0	0	0	not significant
9429	GO_POSTSYNAPTIC_MEMBRANE_ORGANIZATION	0.79	0.12	0	0	0	not significant
9430	GO_REPRODUCTIVE_BEHAVIOR	0.79	0.12	0	0	0	not significant
9431	GO_STRESS_GRANULE_ASSEMBLY	0.79	0.12	0	0	0	not significant
9432	LEE_AGING_MUSCLE_UP	0.79	0.12	0	0	0	not significant
9433	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	0.79	0.12	0	0	0	not significant
9434	REACTOME_MAPK1_ERK2_ACTIVATION	0.79	0.12	0	0	0	not significant
9435	REACTOME_SIGNALING_BY_NOTCH2	0.79	0.12	0	0	0	not significant
9436	VALK_AML_CLUSTER_7	0.79	0.12	0	0	0	not significant
9437	GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNALING_P	0.79	0.11	0	0	0	not significant
9438	REACTOME_SIGNALING_BY_FGFR1	0.79	0.11	0	0	0	not significant
9439	DELASERNA_MYOD_TARGETS_DN	0.79	0.10	0	0	0	not significant
9440	FIGUEROA_AML_METHYLATION_CLUSTER_1_DN	0.79	0.10	0	0	0	not significant
9441	GO_CERAMIDE_BIOSYNTHETIC_PROCESS	0.79	0.10	0	0	0	not significant
9442	GO_EMBRYONIC_PLACENTA_DEVELOPMENT	0.79	0.10	0	0	0	not significant
9443	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	0.79	0.10	0	0	0	not significant
9444	NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON	0.79	0.10	0	0	0	not significant
9445	STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN	0.79	0.10	0	0	0	not significant
9446	CHRXQ26	0.79	0.09	0	0	0	not significant
9447	GO_NEGATIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_T	0.79	0.09	0	0	0	not significant
9448	KEGG_LONG_TERM_DEPRESSION	0.79	0.09	0	0	0	not significant
9449	LIN_MELANOMA_COPY_NUMBER_UP	0.79	0.09	0	0	0	not significant
9450	CHEN_LIVER_METABOLISM_QTL_CIS	0.79	0.08	0	0	0	not significant
9451	GO_CELLULAR_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	0.79	0.08	0	0	0	not significant
9452	GO_NEURON_PROJECTION_ORGANIZATION	0.79	0.08	0	0	0	not significant
9453	GOLDRATH_IMMUNE_MEMORY	0.79	0.08	0	0	0	not significant
9454	REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMIN	0.79	0.08	0	0	0	not significant
9455	PID_CXCR4_PATHWAY	0.79	0.07	0	0	0	not significant
9456	GO_N_ACYLTRANSFERASE_ACTIVITY	0.79	0.06	0	0	0	not significant
9457	GO_SEX_DIFFERENTIATION	0.79	0.05	0	0	0	not significant
9458	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ACYL_GROUPS	0.79	0.04	0	0	0	not significant
9459	IVANOVA_HEMATOPOIESIS_MATURE_CELL	0.79	0.03	0	0	0	not significant
9460	DOUGLAS_BMI1_TARGETS_DN	0.79	0.02	0	0	0	not significant
9461	GO_ENDOSOME	0.79	0.00	0	0	0	not significant
9462	GO_ACTOMYOSIN_CONTRACTILE_RING_ORGANIZATION	0.80	0.16	0	0	0	not significant
9463	GO_POSITIVE_REGULATION_OF_ARP2_3_COMPLEX_MEDIATED_ACTIN_	0.80	0.16	0	0	0	not significant
9464	GO_REGULATION_OF_CHOLESTEROL_METABOLIC_PROCESS	0.80	0.15	0	0	0	not significant
9465	GO_REGULATION_OF_VASCULAR_SMOOTH_MUSCLE_CELL_DIFFERENT	0.80	0.15	0	0	0	not significant
9466	BIOCARTA_PDZS_PATHWAY	0.80	0.14	0	0	0	not significant
9467	BIOCARTA_PGC1A_PATHWAY	0.80	0.14	0	0	0	not significant
9468	CHR3Q25	0.80	0.14	0	0	0	not significant
9469	FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_DN	0.80	0.14	0	0	0	not significant
9470	GO_ACTIVIN_BINDING	0.80	0.14	0	0	0	not significant
9471	GO_COBALAMIN_METABOLIC_PROCESS	0.80	0.14	0	0	0	not significant

9472	GO_ENDOTHELIAL_CELL_CHEMOTAXIS	0.80	0.14	0	0	0	not significant
9473	GO_EPIBOLY	0.80	0.14	0	0	0	not significant
9474	GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_3_COMPLEX_EIF3	0.80	0.14	0	0	0	not significant
9475	GO_HIPPOCAMPAL_MOSSY_FIBER_TO_CA3_SYNAPSE	0.80	0.14	0	0	0	not significant
9476	GO_LYS63_SPECIFIC_DEUBIQUITINASE_ACTIVITY	0.80	0.14	0	0	0	not significant
9477	GO_NEGATIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	0.80	0.14	0	0	0	not significant
9478	GO_POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE_T	0.80	0.14	0	0	0	not significant
9479	GO_RESPONSE_TO_DIETARY_EXCESS	0.80	0.14	0	0	0	not significant
9480	GO_STORE_OPERATED_CALCIUM_CHANNEL_ACTIVITY	0.80	0.14	0	0	0	not significant
9481	GOUYER_TATI_TARGETS_DN	0.80	0.14	0	0	0	not significant
9482	REACTOME_DOPAMINE_NEUROTRANSMITTER_RELEASE_CYCLE	0.80	0.14	0	0	0	not significant
9483	REACTOME_TRANSCRIPTION_OF_E2F_TARGETS_UNDER_NEGATIVE_CO	0.80	0.14	0	0	0	not significant
9484	SASSON_FSH_RESPONSE	0.80	0.14	0	0	0	not significant
9485	SCIAN_INVERSED_TARGETS_OF_TP53_AND_TP73_UP	0.80	0.14	0	0	0	not significant
9486	AMUNDSON_DNA_DAMAGE_RESPONSE_TP53	0.80	0.13	0	0	0	not significant
9487	GO_HISTONE_H3_DEACETYLATION	0.80	0.13	0	0	0	not significant
9488	GO_PHENOL_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	0.80	0.13	0	0	0	not significant
9489	GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	0.80	0.13	0	0	0	not significant
9490	HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_UP	0.80	0.13	0	0	0	not significant
9491	REACTOME_ACYL_CHAIN_REMODELLING_OF_PC	0.80	0.13	0	0	0	not significant
9492	BAUS_TFF2_TARGETS_UP	0.80	0.12	0	0	0	not significant
9493	CHR14Q21	0.80	0.12	0	0	0	not significant
9494	GO_PROTON_EXPORTING_ATPASE_ACTIVITY	0.80	0.12	0	0	0	not significant
9495	GO_RIBONUCLEOTIDE_CATABOLIC_PROCESS	0.80	0.12	0	0	0	not significant
9496	SIG_IL4RECEPTOR_IN_B_LYPHOCYTES	0.80	0.12	0	0	0	not significant
9497	PHONG_TNF_TARGETS_UP	0.80	0.11	0	0	0	not significant
9498	REACTOME_MICROAUTOPHAGY	0.80	0.11	0	0	0	not significant
9499	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_UP	0.80	0.10	0	0	0	not significant
9500	GO_REGULATION_OF_AUTOPHAGY_OF_MITOCHONDRION	0.80	0.10	0	0	0	not significant
9501	KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFEC	0.80	0.10	0	0	0	not significant
9502	MARIADASON_REGULATED_BY_HISTONE_ACETYLATION_DN	0.80	0.10	0	0	0	not significant
9503	MARIADASON_REGULATED_BY_HISTONE_ACETYLATION_UP	0.80	0.10	0	0	0	not significant
9504	GO_REGULATION_OF_NEUROTRANSMITTER_SECRETION	0.80	0.09	0	0	0	not significant
9505	OXFORD_RALA_OR_RALB_TARGETS_UP	0.80	0.09	0	0	0	not significant
9506	GO_REGULATION_OF_MEGAKARYOCYTE_DIFFERENTIATION	0.80	0.08	0	0	0	not significant
9507	GO_NEGATIVE_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	0.80	0.07	0	0	0	not significant
9508	KRAS.DF.V1_DN	0.80	0.07	0	0	0	not significant
9509	LINDGREN_BLADDER_CANCER_CLUSTER_1_UP	0.80	0.06	0	0	0	not significant
9510	GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	0.80	0.05	0	0	0	not significant
9511	GO_PROTEIN_ACYLATION	0.80	0.05	0	0	0	not significant
9512	RIZKI_TUMOR_INVASIVENESS_3D_UP	0.80	0.05	0	0	0	not significant
9513	GO_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	0.80	0.02	0	0	0	not significant
9514	RAO_BOUND_BY_SALL4_ISOFORM_B	0.80	0.02	0	0	0	not significant
9515	GO_ECTODERMAL_PLACODE_DEVELOPMENT	0.81	0.17	0	0	0	not significant
9516	BARRIER_CANCER_RELAPSE_TUMOR_SAMPLE_DN	0.81	0.16	0	0	0	not significant
9517	GO_REGULATION_OF_STEM_CELL_DIVISION	0.81	0.16	0	0	0	not significant
9518	GO_ZYMOGEN_GRANULE_MEMBRANE	0.81	0.16	0	0	0	not significant
9519	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_22	0.81	0.16	0	0	0	not significant
9520	NIKOLSKY_BREAST_CANCER_14Q22_AMPLICON	0.81	0.16	0	0	0	not significant
9521	REACTOME_FRS_MEDIATED_FGFR2_SIGNALING	0.81	0.16	0	0	0	not significant
9522	REACTOME_TLR3_MEDIATED_TICAM1_DEPENDENT_PROGRAMMED_CEL	0.81	0.16	0	0	0	not significant
9523	GO_ALDEHYDE_DEHYDROGENASE_NAD_ACTIVITY	0.81	0.15	0	0	0	not significant
9524	GO_AORTA_MORPHOGENESIS	0.81	0.15	0	0	0	not significant
9525	GO_ARRESTIN_FAMILY_PROTEIN_BINDING	0.81	0.15	0	0	0	not significant
9526	GO_HISTONE_DEMETHYLASE_ACTIVITY_H3_K4_SPECIFIC_	0.81	0.15	0	0	0	not significant
9527	GO_MAGNESIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.81	0.15	0	0	0	not significant
9528	GO_NEGATIVE_REGULATION_OF_MAST_CELL_ACTIVATION	0.81	0.15	0	0	0	not significant
9529	GO_NEGATIVE_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_I	0.81	0.15	0	0	0	not significant
9530	GO_NEGATIVE_REGULATION_OF_VASCULAR_SMOOTH_MUSCLE_CELL_	0.81	0.15	0	0	0	not significant
9531	GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIU	0.81	0.15	0	0	0	not significant
9532	GO_PYRIMIDINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	0.81	0.15	0	0	0	not significant
9533	GO_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY_INVOLVED_	0.81	0.15	0	0	0	not significant
9534	REACTOME_PHASE_4_RESTING_MEMBRANE_POTENTIAL	0.81	0.15	0	0	0	not significant
9535	WANG_RESPONSE_TO_FORSKOLIN_DN	0.81	0.15	0	0	0	not significant
9536	CHR4Q12	0.81	0.14	0	0	0	not significant
9537	CHR6P23	0.81	0.14	0	0	0	not significant
9538	FINAK_BREAST_CANCER_SDPP_SIGNATURE	0.81	0.14	0	0	0	not significant
9539	GO_1_PHOSPHATIDYLINOSITOL_4_KINASE_ACTIVITY	0.81	0.14	0	0	0	not significant
9540	GO_CELL_BODY_MEMBRANE	0.81	0.14	0	0	0	not significant
9541	GO_INTERLEUKIN_21_MEDIATED_SIGNALING_PATHWAY	0.81	0.14	0	0	0	not significant
9542	GO_NUCLEOTIDE_SUGAR_TRANSMEMBRANE_TRANSPORT	0.81	0.14	0	0	0	not significant
9543	GO_REGULATION_OF_BILE_ACID_METABOLIC_PROCESS	0.81	0.14	0	0	0	not significant
9544	GO_REGULATION_OF_ENDOTHELIAL_CELL_CHEMOTAXIS	0.81	0.14	0	0	0	not significant
9545	GO_SMALL_RIBOSOMAL_SUBUNIT_RRNA_BINDING	0.81	0.14	0	0	0	not significant
9546	PATTERSON_DOCETAXEL_RESISTANCE	0.81	0.14	0	0	0	not significant
9547	REACTOME_FRS_MEDIATED_FGFR4_SIGNALING	0.81	0.14	0	0	0	not significant
9548	REACTOME_NEGATIVE_REGULATION_OF_FGFR2_SIGNALING	0.81	0.14	0	0	0	not significant
9549	STAMBOLSKY_RESPONSE_TO_VITAMIN_D3_DN	0.81	0.14	0	0	0	not significant
9550	BRIDEAU_IMPRINTED_GENES	0.81	0.13	0	0	0	not significant
9551	GO_DORSAL_VENTRAL_NEURAL_TUBE_PATTERNING	0.81	0.13	0	0	0	not significant
9552	GO_ESTABLISHMENT_OF_ENDOTHELIAL_BARRIER	0.81	0.13	0	0	0	not significant
9553	GO_HEART_TRABECULA_MORPHOGENESIS	0.81	0.13	0	0	0	not significant
9554	GO_POLY_A_SPECIFIC_RIBONUCLEASE_ACTIVITY	0.81	0.13	0	0	0	not significant
9555	GO_POSITIVE_REGULATION_OF_FOCAL_ADHESION_ASSEMBLY	0.81	0.13	0	0	0	not significant
9556	GO_POSITIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_	0.81	0.13	0	0	0	not significant
9557	PID_CIRCADIAN_PATHWAY	0.81	0.13	0	0	0	not significant
9558	REACTOME_MYOGENESIS	0.81	0.13	0	0	0	not significant
9559	CORRE_MULTIPLE_MYELOMA_DN	0.81	0.12	0	0	0	not significant
9560	ENGELMANN_CANCER_PROGENITORS_UP	0.81	0.12	0	0	0	not significant
9561	GO_COFACTOR_TRANSPORT	0.81	0.12	0	0	0	not significant
9562	GO_ENDOTHELIAL_CELL_DEVELOPMENT	0.81	0.12	0	0	0	not significant
9563	GO_G0_TO_G1_TRANSITION	0.81	0.12	0	0	0	not significant
9564	GO_NEGATIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	0.81	0.12	0	0	0	not significant
9565	GO_NEGATIVE_REGULATION_OF_OSSIFICATION	0.81	0.12	0	0	0	not significant
9566	GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	0.81	0.12	0	0	0	not significant
9567	GO_RAC_PROTEIN_SIGNAL_TRANSDUCTION	0.81	0.12	0	0	0	not significant
9568	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_PENTOSYL_GROUPS	0.81	0.12	0	0	0	not significant
9569	GO_UNSATURATED_FATTY_ACID_METABOLIC_PROCESS	0.81	0.12	0	0	0	not significant
9570	LASTOWSKA_COAMPLIFIED_WITH_MYCN	0.81	0.12	0	0	0	not significant
9571	WEIGEL_OXIDATIVE_STRESS_BY_HNE_AND_TBH	0.81	0.12	0	0	0	not significant
9572	GO_CELLULAR_RESPONSE_TO_VIRUS	0.81	0.11	0	0	0	not significant
9573	GO_ESCRT_COMPLEX	0.81	0.11	0	0	0	not significant
9574	GO_HISTONE_H3_K4_METHYLATION	0.81	0.11	0	0	0	not significant
9575	GO_ODONTOGENESIS	0.81	0.11	0	0	0	not significant
9576	GO_REGULATION_OF_LIPID_CATABOLIC_PROCESS	0.81	0.11	0	0	0	not significant
9577	KRAS.LUNG.BREAST_UP.V1_UP	0.81	0.10	0	0	0	not significant
9578	GO_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	0.81	0.09	0	0	0	not significant
9579	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMUL	0.81	0.09	0	0	0	not significant
9580	GO_SPERM_PART	0.81	0.09	0	0	0	not significant

9581	KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_UP	0.81	0.08	0	0	0	not significant
9582	GO_RECOMBINATIONAL_REPAIR	0.81	0.07	0	0	0	not significant
9583	FOSTER_KDM1A_TARGETS_DN	0.81	0.06	0	0	0	not significant
9584	GO_DEVELOPMENTAL_PROCESS_INVOLVED_IN_REPRODUCTION	0.81	0.03	0	0	0	not significant
9585	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_A	0.81	0.01	0	0	0	not significant
9586	GO_NUCLEOTIDE_SUGAR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.82	0.18	0	0	0	not significant
9587	CHR4P12	0.82	0.17	0	0	0	not significant
9588	GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_PROLIFERATION_INVOLVED_I	0.82	0.17	0	0	0	not significant
9589	GO_CELLULAR_RESPONSE_TO_INTERFERON_ALPHA	0.82	0.17	0	0	0	not significant
9590	GO_ELL_EAF_COMPLEX	0.82	0.17	0	0	0	not significant
9591	GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY_INTERCONVERTIN	0.82	0.17	0	0	0	not significant
9592	GO_MHC_CLASS_II_BIOSYNTHETIC_PROCESS	0.82	0.17	0	0	0	not significant
9593	GO_MOTOR_BEHAVIOR	0.82	0.17	0	0	0	not significant
9594	GO_SPECIFICATION_OF_ANIMAL_ORGAN_IDENTITY	0.82	0.17	0	0	0	not significant
9595	KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	0.82	0.17	0	0	0	not significant
9596	PID_TOLL_ENDOGENOUS_PATHWAY	0.82	0.17	0	0	0	not significant
9597	REACTOME_EICOSANOIDS	0.82	0.17	0	0	0	not significant
9598	REACTOME_POLB_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR	0.82	0.17	0	0	0	not significant
9599	REACTOME_SYNTHESIS_OF_PG	0.82	0.17	0	0	0	not significant
9600	CHR13Q13	0.82	0.16	0	0	0	not significant
9601	GO_1_PHOSPHATIDYLINOSITOL_BINDING	0.82	0.16	0	0	0	not significant
9602	GO_DOPAMINERGIC_SYNAPSE	0.82	0.16	0	0	0	not significant
9603	GO_INNERVATION	0.82	0.16	0	0	0	not significant
9604	GO_L_ASCORBIC_ACID_BINDING	0.82	0.16	0	0	0	not significant
9605	GO_POSITIVE_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN	0.82	0.16	0	0	0	not significant
9606	GO_VERY_LONG_CHAIN_FATTY_ACID_COA_LIGASE_ACTIVITY	0.82	0.16	0	0	0	not significant
9607	GO_VOCALIZATION_BEHAVIOR	0.82	0.16	0	0	0	not significant
9608	REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS	0.82	0.16	0	0	0	not significant
9609	GO_CORNIFICATION	0.82	0.15	0	0	0	not significant
9610	GO_ENERGY_COUPLED_PROTON_TRANSMEMBRANE_TRANSPORT_AGA	0.82	0.15	0	0	0	not significant
9611	GO_GLIAL_CELL_PROJECTION	0.82	0.15	0	0	0	not significant
9612	GO_MICROTUBULE_MINUS_END_BINDING	0.82	0.15	0	0	0	not significant
9613	GO_NEGATIVE_REGULATION_OF_PLASMA_MEMBRANE_BOUNDED_CELL_	0.82	0.15	0	0	0	not significant
9614	GO_NEUROPILIN_BINDING	0.82	0.15	0	0	0	not significant
9615	GO_PEPTIDYL_L_CYSTEINE_S_PALMITOYLATION	0.82	0.15	0	0	0	not significant
9616	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_BIOSYNTHETIC_PROCE	0.82	0.15	0	0	0	not significant
9617	GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION	0.82	0.15	0	0	0	not significant
9618	GO_THYMIC_T_CELL_SELECTION	0.82	0.15	0	0	0	not significant
9619	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12	0.82	0.15	0	0	0	not significant
9620	REACTOME_NEGATIVE_REGULATION_OF_FGFR4_SIGNALING	0.82	0.15	0	0	0	not significant
9621	GO_CELLULAR_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE	0.82	0.14	0	0	0	not significant
9622	GO_NEGATIVE_REGULATION_OF_ENDOCYTOSIS	0.82	0.14	0	0	0	not significant
9623	GO_POLY_A_BINDING	0.82	0.14	0	0	0	not significant
9624	GO_POSITIVE_REGULATION_OF_CYTOPLASMIC_TRANSPORT	0.82	0.14	0	0	0	not significant
9625	GO_PRESYNAPSE_ORGANIZATION	0.82	0.14	0	0	0	not significant
9626	GO_REGULATION_OF_COAGULATION	0.82	0.14	0	0	0	not significant
9627	GO_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INV	0.82	0.14	0	0	0	not significant
9628	REACTOME_ROS_AND_RNS_PRODUCTION_IN_PHAGOCYTES	0.82	0.14	0	0	0	not significant
9629	REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	0.82	0.14	0	0	0	not significant
9630	REACTOME_VXPX_CARGO_TARGETING_TO_CILIUM	0.82	0.14	0	0	0	not significant
9631	WEIGEL_OXIDATIVE_STRESS_BY_HNE_AND_H2O2	0.82	0.14	0	0	0	not significant
9632	ZHAN_V1_LATE_DIFFERENTIATION_GENES_UP	0.82	0.14	0	0	0	not significant
9633	GO_LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	0.82	0.13	0	0	0	not significant
9634	GO_NEGATIVE_REGULATION_OF_ERBB_SIGNALING_PATHWAY	0.82	0.13	0	0	0	not significant
9635	GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_INVOLVED_IN_INFLAMM	0.82	0.13	0	0	0	not significant
9636	MOSERLE_IFNA_RESPONSE	0.82	0.13	0	0	0	not significant
9637	ALK_DN.V1_DN	0.82	0.12	0	0	0	not significant
9638	CHR17Q12	0.82	0.12	0	0	0	not significant
9639	GO_CIS_GOLGI_NETWORK	0.82	0.12	0	0	0	not significant
9640	GO_INNER_EAR_MORPHOGENESIS	0.82	0.12	0	0	0	not significant
9641	MORI_IMMATURE_B_LYMPHOCYTE_UP	0.82	0.12	0	0	0	not significant
9642	REACTOME_G1_PHASE	0.82	0.12	0	0	0	not significant
9643	DIRMEIER_LMP1_RESPONSE_LATE_DN	0.82	0.11	0	0	0	not significant
9644	GO_PROTEASE_BINDING	0.82	0.11	0	0	0	not significant
9645	GO_SH3_SH2_ADAPTOR_ACTIVITY	0.82	0.11	0	0	0	not significant
9646	KYNG_DNA_DAMAGE_BY_GAMMA_AND_UV_RADIATION	0.82	0.11	0	0	0	not significant
9647	MORI_SMALL_PRE_BII_LYMPHOCYTE_UP	0.82	0.11	0	0	0	not significant
9648	GO_CELL_AGING	0.82	0.10	0	0	0	not significant
9649	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMUL	0.82	0.10	0	0	0	not significant
9650	CHR1Q21	0.82	0.09	0	0	0	not significant
9651	GO_ACTIN_CYTOSKELETON_REORGANIZATION	0.82	0.09	0	0	0	not significant
9652	GO_EXOCYTIC_VESICLE	0.82	0.09	0	0	0	not significant
9653	VERHAAK_GLIOBLASTOMA_CLASSICAL	0.82	0.09	0	0	0	not significant
9654	PUIFFE_INVASION_INHIBITED_BY_ASCITES_DN	0.82	0.08	0	0	0	not significant
9655	GO_DNA_DEPENDENT_DNA_REPLICATION	0.82	0.07	0	0	0	not significant
9656	GO_ENDOCYTIC_VESICLE_MEMBRANE	0.82	0.07	0	0	0	not significant
9657	GO_MOLECULAR_ADAPTOR_ACTIVITY	0.82	0.07	0	0	0	not significant
9658	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_UP	0.82	0.04	0	0	0	not significant
9659	GO_CILIARY_PART	0.82	0.04	0	0	0	not significant
9660	GO_TRANSCRIPTION_COACTIVATOR_ACTIVITY	0.82	0.04	0	0	0	not significant
9661	GO_REGULATION_OF_NEURON_DIFFERENTIATION	0.82	0.03	0	0	0	not significant
9662	GO_GOLGI_APPARATUS_PART	0.82	0.01	0	0	0	not significant
9663	GO_POSITIVE_REGULATION_OF_RNA_BIOSYNTHETIC_PROCESS	0.82	0.01	0	0	0	not significant
9664	FLORIO_HUMAN_NEOCORTEX	0.83	0.18	0	0	0	not significant
9665	GO_MACROPHAGE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	0.83	0.18	0	0	0	not significant
9666	GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_BINDING	0.83	0.18	0	0	0	not significant
9667	GO_POSITIVE_REGULATION_OF_MITOTIC_SISTER_CHROMATID_SEPARA	0.83	0.18	0	0	0	not significant
9668	GO_POSTSYNAPTIC_MODULATION_OF_CHEMICAL_SYNAPTIC_TRANSMIS	0.83	0.18	0	0	0	not significant
9669	GO_REGULATION_OF_ENDOTHELIAL_CELL_DEVELOPMENT	0.83	0.18	0	0	0	not significant
9670	NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_DN	0.83	0.18	0	0	0	not significant
9671	REACTOME_SMALL_INTERFERING_RNA_SIRNA_BIOGENESIS	0.83	0.18	0	0	0	not significant
9672	DACOSTA_ERCC3_ALLELE_XPCS_VS_TTD_DN	0.83	0.17	0	0	0	not significant
9673	GO_PARKIN_MEDIATED_STIMULATION_OF_MITOPHAGY_IN_RESPONSE_T	0.83	0.17	0	0	0	not significant
9674	GO_POSITIVE_REGULATION_OF_CELL_AGING	0.83	0.17	0	0	0	not significant
9675	GO_POSITIVE_REGULATION_OF_FC_GAMMA_RECEPTOR_SIGNALING_P	0.83	0.17	0	0	0	not significant
9676	GO_POST_EMBRYONIC_EYE_MORPHOGENESIS	0.83	0.17	0	0	0	not significant
9677	KYNG_DNA_DAMAGE_BY_4NQO	0.83	0.17	0	0	0	not significant
9678	REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS	0.83	0.17	0	0	0	not significant
9679	ABE_INNER_EAR	0.83	0.16	0	0	0	not significant
9680	BIOCARTA_RECK_PATHWAY	0.83	0.16	0	0	0	not significant
9681	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	0.83	0.16	0	0	0	not significant
9682	REACTOME_BLOOD_GROUP_SYSTEMS_BIOSYNTHESIS	0.83	0.16	0	0	0	not significant
9683	REACTOME_NF_KB_ACTIVATION_THROUGH_FADD_RIP_1_PATHWAY_ME	0.83	0.16	0	0	0	not significant
9684	SHIPP_DLBCL_CURED_VS_FATAL_UP	0.83	0.16	0	0	0	not significant
9685	VALK_AML_CLUSTER_8	0.83	0.16	0	0	0	not significant
9686	GO_B_CELL_APOPTOTIC_PROCESS	0.83	0.15	0	0	0	not significant
9687	GO_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	0.83	0.15	0	0	0	not significant
9688	GO_EMBRYONIC_SKELETAL_JOINT_DEVELOPMENT	0.83	0.15	0	0	0	not significant
9689	GO_GLYCEROLIPID_CATABOLIC_PROCESS	0.83	0.15	0	0	0	not significant

9690	GO_HOLLIDAY_JUNCTION_RESOLVASE_COMPLEX	0.83	0.15	0	0	0	not significant
9691	GO_KERATINIZATION	0.83	0.15	0	0	0	not significant
9692	GO_MOLTING_CYCLE_PROCESS	0.83	0.15	0	0	0	not significant
9693	GO_NEGATIVE_REGULATION_OF_SYNAPTIC_VESICLE_TRANSPORT	0.83	0.15	0	0	0	not significant
9694	GO_NUCLEOTIDE_SUGAR_BIOSYNTHETIC_PROCESS	0.83	0.15	0	0	0	not significant
9695	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_	0.83	0.15	0	0	0	not significant
9696	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_BIOSYNTHETIC_PROCE	0.83	0.15	0	0	0	not significant
9697	GO_PROTEIN_HORMONE_RECEPTOR_ACTIVITY	0.83	0.15	0	0	0	not significant
9698	GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY_	0.83	0.15	0	0	0	not significant
9699	GO_REGULATION_OF_MICROTUBULE_POLYMERIZATION	0.83	0.15	0	0	0	not significant
9700	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_AMINO_ACYL_GROUPS	0.83	0.15	0	0	0	not significant
9701	LEE_LIVER_CANCER_ACOX1_DN	0.83	0.15	0	0	0	not significant
9702	BIOCARTA_CBL_PATHWAY	0.83	0.14	0	0	0	not significant
9703	GO_BONE_MINERALIZATION	0.83	0.14	0	0	0	not significant
9704	GO_ERYTHROCYTE_DEVELOPMENT	0.83	0.14	0	0	0	not significant
9705	GO_EXTRINSIC_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_PLASMA_ME	0.83	0.14	0	0	0	not significant
9706	GO_GOLGI_TO_PLASMA_MEMBRANE_PROTEIN_TRANSPORT	0.83	0.14	0	0	0	not significant
9707	PID_EPHRINB_REV_PATHWAY	0.83	0.14	0	0	0	not significant
9708	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_UP	0.83	0.13	0	0	0	not significant
9709	GO_EMBRYONIC_SKELETAL_SYSTEM_MORPHOGENESIS	0.83	0.12	0	0	0	not significant
9710	GO_NEGATIVE_REGULATION_OF_PROTEASOMAL_PROTEIN_CATABOLIC	0.83	0.12	0	0	0	not significant
9711	GO_PRESYNAPTIC_MEMBRANE	0.83	0.12	0	0	0	not significant
9712	MCLACHLAN_DENTAL_CARIES_DN	0.83	0.12	0	0	0	not significant
9713	WINTER_HYPOXIA_DN	0.83	0.12	0	0	0	not significant
9714	AMBROSINI_FLAVOPIRIDOL_TREATMENT_TP53	0.83	0.10	0	0	0	not significant
9715	CHR20Q11	0.83	0.10	0	0	0	not significant
9716	GO_ENDONUCLEASE_ACTIVITY	0.83	0.09	0	0	0	not significant
9717	GO_LOCALIZATION_WITHIN_MEMBRANE	0.83	0.09	0	0	0	not significant
9718	GO_PHOSPHATASE_BINDING	0.83	0.09	0	0	0	not significant
9719	GO_PHOSPHATIDYLINOSITOL_BIOSYNTHETIC_PROCESS	0.83	0.09	0	0	0	not significant
9720	GO_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	0.83	0.09	0	0	0	not significant
9721	GO_SIGNAL_RELEASE_FROM_SYNAPSE	0.83	0.09	0	0	0	not significant
9722	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_UP	0.83	0.09	0	0	0	not significant
9723	GO_POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNAL	0.83	0.07	0	0	0	not significant
9724	GO_DNA_RECOMBINATION	0.83	0.06	0	0	0	not significant
9725	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_PROCESS	0.83	0.06	0	0	0	not significant
9726	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN	0.83	0.05	0	0	0	not significant
9727	GO_POSITIVE_REGULATION_OF_MAPK_CASCADE	0.83	0.05	0	0	0	not significant
9728	GO_CELL_PROJECTION_ASSEMBLY	0.83	0.04	0	0	0	not significant
9729	GO_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	0.83	0.03	0	0	0	not significant
9730	GO_KINASE_BINDING	0.83	0.02	0	0	0	not significant
9731	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERAS	0.83	0.02	0	0	0	not significant
9732	GO_TRANSCRIPTION_FACTOR_BINDING	0.83	0.02	0	0	0	not significant
9733	GO_CELL_PROJECTION_PART	0.83	0.01	0	0	0	not significant
9734	GO_INTRACELLULAR_PROTEIN_TRANSPORT	0.83	0.01	0	0	0	not significant
9735	GO_RACEMASE_AND_EPIMERASE_ACTIVITY_ACTING_ON_CARBOHYDRA	0.84	0.19	0	0	0	not significant
9736	GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_SOMATI	0.84	0.19	0	0	0	not significant
9737	GO_LUTEINIZATION	0.84	0.18	0	0	0	not significant
9738	GO_LYMPH_VESSEL_MORPHOGENESIS	0.84	0.18	0	0	0	not significant
9739	GO_MHC_CLASS_I_PROTEIN_BINDING	0.84	0.18	0	0	0	not significant
9740	GO_NEGATIVE_REGULATION_OF_NEUROINFLAMMATORY_RESPONSE	0.84	0.18	0	0	0	not significant
9741	HE_PTEN_TARGETS_DN	0.84	0.18	0	0	0	not significant
9742	WANG_IMMORTALIZED_BY_HOXA9_AND_MEIS1_UP	0.84	0.18	0	0	0	not significant
9743	WENG_POR_TARGETS_LIVER_DN	0.84	0.18	0	0	0	not significant
9744	DING_LUNG_CANCER_MUTATED_RECURRENTLY	0.84	0.17	0	0	0	not significant
9745	GO_CYTOPLASMIC_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_P	0.84	0.17	0	0	0	not significant
9746	GO_EMBRYONIC_HEMOPOIESIS	0.84	0.17	0	0	0	not significant
9747	GO_HINDBRAIN_MORPHOGENESIS	0.84	0.17	0	0	0	not significant
9748	GO_HOPS_COMPLEX	0.84	0.17	0	0	0	not significant
9749	GO_POSITIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	0.84	0.17	0	0	0	not significant
9750	GO_POSITIVE_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_	0.84	0.17	0	0	0	not significant
9751	GO_POSITIVE_REGULATION_OF_GRANULOCYTE_DIFFERENTIATION	0.84	0.17	0	0	0	not significant
9752	GO_RIBOSOMAL_SMALL_SUBUNIT_ASSEMBLY	0.84	0.17	0	0	0	not significant
9753	GO_TITIN_BINDING	0.84	0.17	0	0	0	not significant
9754	GO_WNT_SIGNALOSOME	0.84	0.17	0	0	0	not significant
9755	KANG_CISPLATIN_RESISTANCE_DN	0.84	0.17	0	0	0	not significant
9756	MIKKELSEN_MCV6_ICP_WITH_H3K4ME3_AND_H3K27ME3	0.84	0.17	0	0	0	not significant
9757	NABA_BASEMENT_MEMBRANES	0.84	0.17	0	0	0	not significant
9758	REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	0.84	0.17	0	0	0	not significant
9759	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CASPASE_ACTIVA	0.84	0.17	0	0	0	not significant
9760	ZHANG_RESPONSE_TO_CANTHARIDIN_UP	0.84	0.17	0	0	0	not significant
9761	CHR6Q14	0.84	0.16	0	0	0	not significant
9762	GO_DNA_DIRECTED_DNA_POLYMERASE_ACTIVITY	0.84	0.16	0	0	0	not significant
9763	GO_GUANOSINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	0.84	0.16	0	0	0	not significant
9764	GO_MYELOID_DENDRITIC_CELL_DIFFERENTIATION	0.84	0.16	0	0	0	not significant
9765	GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFOR	0.84	0.16	0	0	0	not significant
9766	GO_POSITIVE_REGULATION_OF_HISTONE_METHYLATION	0.84	0.16	0	0	0	not significant
9767	GO_RESPONSE_TO_SODIUM_ARSENITE	0.84	0.16	0	0	0	not significant
9768	MEISSNER_BRAIN_ICP_WITH_H3K4ME3	0.84	0.16	0	0	0	not significant
9769	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5	0.84	0.16	0	0	0	not significant
9770	PID_TCR_RAS_PATHWAY	0.84	0.16	0	0	0	not significant
9771	POS_HISTAMINE_RESPONSE_NETWORK	0.84	0.16	0	0	0	not significant
9772	REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	0.84	0.16	0	0	0	not significant
9773	BIOCARTA_IL2RB_PATHWAY	0.84	0.15	0	0	0	not significant
9774	CHR17Q23	0.84	0.15	0	0	0	not significant
9775	DARWICHE_PAPILLOMA_PROGRESSION_RISK	0.84	0.15	0	0	0	not significant
9776	GO_LAMELLIPODIUM_MEMBRANE	0.84	0.15	0	0	0	not significant
9777	GO_POLYOL_BIOSYNTHETIC_PROCESS	0.84	0.15	0	0	0	not significant
9778	GO_POLYUBIQUITIN_MODIFICATION_DEPENDENT_PROTEIN_BINDING	0.84	0.15	0	0	0	not significant
9779	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_UP	0.84	0.14	0	0	0	not significant
9780	GO_EMBRYONIC_HEART_TUBE_DEVELOPMENT	0.84	0.14	0	0	0	not significant
9781	GO_PROTEIN_K48_LINKED_UBIQUITINATION	0.84	0.14	0	0	0	not significant
9782	GO_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	0.84	0.14	0	0	0	not significant
9783	HOLLERN_SQUAMOUS_BREAST_TUMOR	0.84	0.14	0	0	0	not significant
9784	PID_NFKAPPAB_CANONICAL_PATHWAY	0.84	0.14	0	0	0	not significant
9785	PRAMOONJAGO_SOX4_TARGETS_UP	0.84	0.14	0	0	0	not significant
9786	GO_REGULATION_OF_SYNAPTIC_PLASTICITY	0.84	0.13	0	0	0	not significant
9787	GO_RESPONSE_TO_ETHANOL	0.84	0.13	0	0	0	not significant
9788	KEGG_ADHERENS_JUNCTION	0.84	0.13	0	0	0	not significant
9789	PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_DN	0.84	0.13	0	0	0	not significant
9790	FALVELLA_SMOKERS_WITH_LUNG_CANCER	0.84	0.12	0	0	0	not significant
9791	GO_MOTILE_CILIUM	0.84	0.12	0	0	0	not significant
9792	GO_NUCLEAR_DNA_REPLICATION	0.84	0.12	0	0	0	not significant
9793	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	0.84	0.11	0	0	0	not significant
9794	GO_SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.84	0.11	0	0	0	not significant
9795	REACTOME_CARGO_RECOGNITION_FOR_CLATHRIN_MEDIATED_ENDOC	0.84	0.11	0	0	0	not significant
9796	GO_ERBB_SIGNALING_PATHWAY	0.84	0.10	0	0	0	not significant
9797	RB_DN.V1_UP	0.84	0.10	0	0	0	not significant
9798	CAIRO_HEPATOBLASTOMA_UP	0.84	0.08	0	0	0	not significant

9799	GO_ANION_TRANSMEMBRANE_TRANSPORT	0.84	0.08	0	0	0	not significant
9800	GO_CILIUM_ORGANIZATION	0.84	0.07	0	0	0	not significant
9801	GO_POSITIVE_REGULATION_OF_LOCOMOTION	0.84	0.07	0	0	0	not significant
9802	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP	0.84	0.06	0	0	0	not significant
9803	GO_ORGANELLE_SUBCOMPARTMENT	0.84	0.06	0	0	0	not significant
9804	GO_REGULATION_OF_CELL_MORPHOGENESIS	0.84	0.06	0	0	0	not significant
9805	GO_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	0.84	0.04	0	0	0	not significant
9806	GO_SYNAPSE	0.84	0.02	0	0	0	not significant
9807	NUYTTEN_NIPP1_TARGETS_DN	0.84	0.02	0	0	0	not significant
9808	GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_PHOSPHATASE_A	0.85	0.20	0	0	0	not significant
9809	ZEMBUTSU_SENSITIVITY_TO_MITOMYCIN	0.85	0.20	0	0	0	not significant
9810	GO_CELLULAR_POTASSIUM_ION_HOMEOSTASIS	0.85	0.19	0	0	0	not significant
9811	GO_EXTRACELLULAR_VESICLE_BIOGENESIS	0.85	0.19	0	0	0	not significant
9812	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE	0.85	0.19	0	0	0	not significant
9813	GO_NEGATIVE_REGULATION_OF_CYTOPLASMIC_TRANSLATION	0.85	0.19	0	0	0	not significant
9814	GO_NEGATIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_UNFOLDE	0.85	0.19	0	0	0	not significant
9815	GO_POSITIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFE	0.85	0.19	0	0	0	not significant
9816	GO_TELOMERE_MAINTENANCE_IN_RESPONSE_TO_DNA_DAMAGE	0.85	0.19	0	0	0	not significant
9817	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY	0.85	0.19	0	0	0	not significant
9818	GO_VENOUS_BLOOD_VESSEL_MORPHOGENESIS	0.85	0.19	0	0	0	not significant
9819	REACTOME_APEX1_INDEPENDENT_RESOLUTION_OF_AP_SITES_VIA_THE	0.85	0.19	0	0	0	not significant
9820	VANLOO_SP3_TARGETS_UP	0.85	0.19	0	0	0	not significant
9821	BCAT.100_UP.V1_DN	0.85	0.18	0	0	0	not significant
9822	GO_ACTIN_CORTICAL_PATCH_LOCALIZATION	0.85	0.18	0	0	0	not significant
9823	GO_DEVELOPMENT_OF_SECONDARY_SEXUAL_CHARACTERISTICS	0.85	0.18	0	0	0	not significant
9824	GO_PHOSPHORUS_OXYGEN_LYASE_ACTIVITY	0.85	0.18	0	0	0	not significant
9825	GO_POSITIVE_REGULATION_OF_HEAT_GENERATION	0.85	0.18	0	0	0	not significant
9826	GO_PROTEIN_PHOSPHATASE_2A_BINDING	0.85	0.18	0	0	0	not significant
9827	GO_PYRIMIDINE_NUCLEOSIDE_METABOLIC_PROCESS	0.85	0.18	0	0	0	not significant
9828	GO_REGULATION_OF_T_CELL_TOLERANCE_INDUCTION	0.85	0.18	0	0	0	not significant
9829	GO_UDP_N_ACETYLGLUCOSAMINE_BIOSYNTHETIC_PROCESS	0.85	0.18	0	0	0	not significant
9830	HOEGERKORP_CD44_TARGETS_TEMPORAL_UP	0.85	0.18	0	0	0	not significant
9831	REACTOME_O_GLYCOSYLATION_OF_TSR_DOMAIN_CONTAINING_PROTE	0.85	0.18	0	0	0	not significant
9832	BIOCARTA_GRANULOCYTES_PATHWAY	0.85	0.17	0	0	0	not significant
9833	DELACROIX_RAR_TARGETS_UP	0.85	0.17	0	0	0	not significant
9834	GO_CALCIUM_ACTIVATED_CATION_CHANNEL_ACTIVITY	0.85	0.17	0	0	0	not significant
9835	GO_CELLULAR_RESPONSE_TO_SODIUM_ARSENITE	0.85	0.17	0	0	0	not significant
9836	GO_METALLOENDOPEPTIDASE_INHIBITOR_ACTIVITY	0.85	0.17	0	0	0	not significant
9837	GO_POSITIVE_REGULATION_OF_AXON_EXTENSION	0.85	0.17	0	0	0	not significant
9838	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_CHEMOTAXIS	0.85	0.17	0	0	0	not significant
9839	GO_POSITIVE_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATIO	0.85	0.17	0	0	0	not significant
9840	GO_POSITIVE_REGULATION_OF_PEPTIDYL_LYSINE_ACETYLATION	0.85	0.17	0	0	0	not significant
9841	GO_REGULATION_OF_BILE_ACID_BIOSYNTHETIC_PROCESS	0.85	0.17	0	0	0	not significant
9842	GO_RNA_SECONDARY_STRUCTURE_UNWINDING	0.85	0.17	0	0	0	not significant
9843	KEGG_O_GLYCAN_BIOSYNTHESIS	0.85	0.17	0	0	0	not significant
9844	OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_UP	0.85	0.17	0	0	0	not significant
9845	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	0.85	0.17	0	0	0	not significant
9846	REACTOME_ENDOGENOUS_STEROLS	0.85	0.17	0	0	0	not significant
9847	REACTOME_HYALURONAN_METABOLISM	0.85	0.17	0	0	0	not significant
9848	REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	0.85	0.17	0	0	0	not significant
9849	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP	0.85	0.16	0	0	0	not significant
9850	GO_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	0.85	0.16	0	0	0	not significant
9851	MMS_MOUSE_LYMPH_HIGH_4HRS_UP	0.85	0.16	0	0	0	not significant
9852	SEKI_INFLAMMATORY_RESPONSE_LPS_UP	0.85	0.16	0	0	0	not significant
9853	CHR16Q21	0.85	0.15	0	0	0	not significant
9854	DUAN_PRDM5_TARGETS	0.85	0.15	0	0	0	not significant
9855	GO_NEGATIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_SI	0.85	0.15	0	0	0	not significant
9856	GO_PROTEIN_SERINE_THREONINE_TYROSINE_KINASE_ACTIVITY	0.85	0.15	0	0	0	not significant
9857	GO_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	0.85	0.15	0	0	0	not significant
9858	GO_SOMITOGENESIS	0.85	0.15	0	0	0	not significant
9859	PID_HDAC_CLASSII_PATHWAY	0.85	0.15	0	0	0	not significant
9860	GO_INTRINSIC_COMPONENT_OF_POSTSYNAPTIC_MEMBRANE	0.85	0.14	0	0	0	not significant
9861	GO_MICROTUBULE_POLYMERIZATION	0.85	0.14	0	0	0	not significant
9862	GO_POSITIVE_REGULATION_OF_DNA_REPAIR	0.85	0.14	0	0	0	not significant
9863	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN	0.85	0.13	0	0	0	not significant
9864	GO_CILIARY_BASAL_BODY	0.85	0.13	0	0	0	not significant
9865	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY	0.85	0.13	0	0	0	not significant
9866	HALLMARK_UV_RESPONSE_DN	0.85	0.12	0	0	0	not significant
9867	DCA_UP.V1_DN	0.85	0.11	0	0	0	not significant
9868	GO_ENDOPLASMIC_RETICULUM_UNFOLDED_PROTEIN_RESPONSE	0.85	0.11	0	0	0	not significant
9869	MULLIGHAN_NPM1_SIGNATURE_3_DN	0.85	0.10	0	0	0	not significant
9870	CHR17P13	0.85	0.09	0	0	0	not significant
9871	GO_ACTIVATION_OF_PROTEIN_KINASE_ACTIVITY	0.85	0.09	0	0	0	not significant
9872	GO_PROTEIN_AUTOPHOSPHORYLATION	0.85	0.09	0	0	0	not significant
9873	GO_POSITIVE_REGULATION_OF_NEURON_DIFFERENTIATION	0.85	0.08	0	0	0	not significant
9874	GO_TUBULIN_BINDING	0.85	0.08	0	0	0	not significant
9875	GO_KINASE_ACTIVITY	0.85	0.04	0	0	0	not significant
9876	GO_PHARYNGEAL_SYSTEM_DEVELOPMENT	0.86	0.20	0	0	0	not significant
9877	GO_PROTEIN_KINASE_C_ACTIVITY	0.86	0.20	0	0	0	not significant
9878	GO_QUATERNARY_AMMONIUM_GROUP_BINDING	0.86	0.20	0	0	0	not significant
9879	GO_REGULATION_OF_CILIUM_BEAT_FREQUENCY	0.86	0.20	0	0	0	not significant
9880	GO_REGULATION_OF_CILIUM_MOVEMENT	0.86	0.20	0	0	0	not significant
9881	GO_RESPONSE_TO_HYDROXYUREA	0.86	0.20	0	0	0	not significant
9882	GO_SEMINIFEROUS_TUBULE_DEVELOPMENT	0.86	0.20	0	0	0	not significant
9883	NEWMAN_ERCC6_TARGETS_DN	0.86	0.20	0	0	0	not significant
9884	RADAEVA_RESPONSE_TO_IFNA1_DN	0.86	0.20	0	0	0	not significant
9885	REACTOME_TNFR1_MEDIATED_CERAMIDE_PRODUCTION	0.86	0.20	0	0	0	not significant
9886	GO_ALPHA_DNA_POLYMERASE_PRIMASE_COMPLEX	0.86	0.19	0	0	0	not significant
9887	GO_ARF_PROTEIN_SIGNAL_TRANSDUCTION	0.86	0.19	0	0	0	not significant
9888	GO_CELL_PROLIFERATION_IN_HINDBRAIN	0.86	0.19	0	0	0	not significant
9889	GO_JUN_KINASE_BINDING	0.86	0.19	0	0	0	not significant
9890	GO_MULTIVESICULAR_BODY_MEMBRANE	0.86	0.19	0	0	0	not significant
9891	GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	0.86	0.19	0	0	0	not significant
9892	GO_NEGATIVE_REGULATION_OF_RECEPTOR_BINDING	0.86	0.19	0	0	0	not significant
9893	GO_REGULATION_OF_ANION_TRANSMEMBRANE_TRANSPORT	0.86	0.19	0	0	0	not significant
9894	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHE	0.86	0.19	0	0	0	not significant
9895	GO_REGULATION_OF_DNA_DEMETHYLATION	0.86	0.19	0	0	0	not significant
9896	GO_REGULATION_OF_HIPPO_SIGNALING	0.86	0.19	0	0	0	not significant
9897	GO_REGULATION_OF_HISTONE_PHOSPHORYLATION	0.86	0.19	0	0	0	not significant
9898	GO_T_CELL_ACTIVATION_VIA_T_CELL_RECEPTOR_CONTACT_WITH_AN	0.86	0.19	0	0	0	not significant
9899	REACTOME_COLLAGEN_DEGRADATION	0.86	0.19	0	0	0	not significant
9900	REACTOME_FCERI_MEDIATED_CAPLUS2_MOBILIZATION	0.86	0.19	0	0	0	not significant
9901	VETTER_TARGETS_OF_PRKCA_AND_ETS1_DN	0.86	0.19	0	0	0	not significant
9902	BALDWIN_PRKCI_TARGETS_UP	0.86	0.18	0	0	0	not significant
9903	BIOCARTA_MET_PATHWAY	0.86	0.18	0	0	0	not significant
9904	CHR3Q22	0.86	0.18	0	0	0	not significant
9905	GO_BRAIN_MORPHOGENESIS	0.86	0.18	0	0	0	not significant
9906	GO_CYCLOOXYGENASE_PATHWAY	0.86	0.18	0	0	0	not significant
9907	GO_ERBB2_SIGNALING_PATHWAY	0.86	0.18	0	0	0	not significant

9908	GO_GOLGI_TRANS_CISTERNA	0.86	0.18	0	0	0	not significant
9909	GO_HEXOSAMINIDASE_ACTIVITY	0.86	0.18	0	0	0	not significant
9910	GO_MRNA_TRANSCRIPTION	0.86	0.18	0	0	0	not significant
9911	PID_AJDISS_2PATHWAY	0.86	0.18	0	0	0	not significant
9912	REACTOME_REGULATED_PROTEOLYSIS_OF_P75NTR	0.86	0.18	0	0	0	not significant
9913	REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_	0.86	0.18	0	0	0	not significant
9914	GO_ANTIPORTER_ACTIVITY	0.86	0.17	0	0	0	not significant
9915	GO_AXIS_SPECIFICATION	0.86	0.17	0	0	0	not significant
9916	GO_NUCLEOSIDE_KINASE_ACTIVITY	0.86	0.17	0	0	0	not significant
9917	GO_POSITIVE_REGULATION_OF_PROTEIN_ACETYLATION	0.86	0.17	0	0	0	not significant
9918	GO_REGULATION_OF_CHROMATIN_BINDING	0.86	0.17	0	0	0	not significant
9919	REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	0.86	0.17	0	0	0	not significant
9920	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS	0.86	0.17	0	0	0	not significant
9921	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_DN	0.86	0.17	0	0	0	not significant
9922	CHR2Q14	0.86	0.16	0	0	0	not significant
9923	GO_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	0.86	0.16	0	0	0	not significant
9924	GO_REGULATION_OF_PHAGOCYTOSIS	0.86	0.16	0	0	0	not significant
9925	KRAS.AMP.LUNG_UP.V1_UP	0.86	0.16	0	0	0	not significant
9926	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5	0.86	0.16	0	0	0	not significant
9927	CHIBA_RESPONSE_TO_TSA_UP	0.86	0.15	0	0	0	not significant
9928	GAL_LEUKEMIC_STEM_CELL_UP	0.86	0.15	0	0	0	not significant
9929	GO_PROTEIN_AUTOUBIQUITINATION	0.86	0.15	0	0	0	not significant
9930	NIELSEN_GIST	0.86	0.15	0	0	0	not significant
9931	RAGHAVACHARI_PLATELET_SPECIFIC_GENES	0.86	0.15	0	0	0	not significant
9932	CHR14Q32	0.86	0.14	0	0	0	not significant
9933	COULOUARN_TEMPORAL_TGFB1_SIGNATURE_DN	0.86	0.14	0	0	0	not significant
9934	GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PR	0.86	0.14	0	0	0	not significant
9935	GO_SERINE_THREONINE_PROTEIN_KINASE_COMPLEX	0.86	0.14	0	0	0	not significant
9936	NATSUME_RESPONSE_TO_INTERFERON_BETA_UP	0.86	0.14	0	0	0	not significant
9937	GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	0.86	0.13	0	0	0	not significant
9938	GO_REGULATION_OF_PEPTIDE_HORMONE_SECRETION	0.86	0.13	0	0	0	not significant
9939	RODWELL_AGING_KIDNEY_DN	0.86	0.13	0	0	0	not significant
9940	GO_INTRINSIC_COMPONENT_OF_ENDOPLASMIC_RETICULUM_MEMBRAN	0.86	0.12	0	0	0	not significant
9941	GO_POSITIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	0.86	0.12	0	0	0	not significant
9942	PRC2_EED_UP.V1_DN	0.86	0.12	0	0	0	not significant
9943	VERHAAK_AML_WITH_NPM1_MUTATED_UP	0.86	0.12	0	0	0	not significant
9944	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_D	0.86	0.11	0	0	0	not significant
9945	GO_DEVELOPMENT_OF_PRIMARY_SEXUAL_CHARACTERISTICS	0.86	0.11	0	0	0	not significant
9946	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_S	0.86	0.11	0	0	0	not significant
9947	KASLER_HDAC7_TARGETS_1_UP	0.86	0.10	0	0	0	not significant
9948	GO_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	0.86	0.09	0	0	0	not significant
9949	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_7	0.86	0.07	0	0	0	not significant
9950	MIKKELSEN_ES_ICP_WITH_H3K4ME3	0.86	0.06	0	0	0	not significant
9951	GO_SOMATODENDRITIC_COMPARTMENT	0.86	0.05	0	0	0	not significant
9952	GO_C_TERMINAL_PROTEIN_LIPIDATION	0.87	0.22	0	0	0	not significant
9953	GO_CYTOKINE_SECRETION_INVOLVED_IN_IMMUNE_RESPONSE	0.87	0.22	0	0	0	not significant
9954	FERRANDO_TAL1_NEIGHBORS	0.87	0.21	0	0	0	not significant
9955	GO_CHRONIC_INFLAMMATORY_RESPONSE	0.87	0.21	0	0	0	not significant
9956	GO_HISTONE_H4_K20_METHYLATION	0.87	0.21	0	0	0	not significant
9957	GO_INHIBITORY_POSTSYNAPTIC_POTENTIAL	0.87	0.21	0	0	0	not significant
9958	GO_MATURE_B_CELL_DIFFERENTIATION	0.87	0.21	0	0	0	not significant
9959	GO_MATURE_B_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPO	0.87	0.21	0	0	0	not significant
9960	GO_MICROTUBULE_SEVERING_ATPASE_ACTIVITY	0.87	0.21	0	0	0	not significant
9961	GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_T	0.87	0.21	0	0	0	not significant
9962	PARK_TRETINOIN_RESPONSE	0.87	0.21	0	0	0	not significant
9963	GENTLES_LEUKEMIC_STEM_CELL_UP	0.87	0.20	0	0	0	not significant
9964	GO_CYCLOSPORIN_A_BINDING	0.87	0.20	0	0	0	not significant
9965	GO_FLUID_TRANSPORT	0.87	0.20	0	0	0	not significant
9966	GO_LYMPHOID_PROGENITOR_CELL_DIFFERENTIATION	0.87	0.20	0	0	0	not significant
9967	GO_NEURAL_TUBE_PATTERNING	0.87	0.20	0	0	0	not significant
9968	GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_5_PHOSPHATASE_ACTIVITY	0.87	0.20	0	0	0	not significant
9969	GO_POSITIVE_REGULATION_OF_GLIAL_CELL_PROLIFERATION	0.87	0.20	0	0	0	not significant
9970	GO_PRIMARY_MIRNA_BINDING	0.87	0.20	0	0	0	not significant
9971	GO_SCHWANN_CELL_PROLIFERATION	0.87	0.20	0	0	0	not significant
9972	GO_SMOOTHENED_SIGNALING_PATHWAY_INVOLVED_IN_DORSAL_VENT	0.87	0.20	0	0	0	not significant
9973	REACTOME_BIOSYNTHESIS_OF_SPECIALIZED_PRORESOLVING_MEDIAT	0.87	0.20	0	0	0	not significant
9974	REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS	0.87	0.20	0	0	0	not significant
9975	REACTOME_FORMATION_OF_THE_CORNIFIED_ENVELOPE	0.87	0.20	0	0	0	not significant
9976	REACTOME_SYNTHESIS_OF_PROSTAGLANDINS_PG_AND_THROMBOXAN	0.87	0.20	0	0	0	not significant
9977	RIZ_ERYTHROID_DIFFERENTIATION_6HR	0.87	0.20	0	0	0	not significant
9978	YAMANAKA_GLIOBLASTOMA_SURVIVAL_DN	0.87	0.20	0	0	0	not significant
9979	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_48HR_UP	0.87	0.19	0	0	0	not significant
9980	BIOCARTA_PRC2_PATHWAY	0.87	0.19	0	0	0	not significant
9981	CHR16Q12	0.87	0.19	0	0	0	not significant
9982	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP	0.87	0.19	0	0	0	not significant
9983	GALLUZZI_PREVENT_MITOCHONDIAL_PERMEABILIZATION	0.87	0.19	0	0	0	not significant
9984	GO_DNA_POLYMERASE_BINDING	0.87	0.19	0	0	0	not significant
9985	GO_ENDOTHELIAL_CELL_MORPHOGENESIS	0.87	0.19	0	0	0	not significant
9986	GO_ISG15_PROTEIN_CONJUGATION	0.87	0.19	0	0	0	not significant
9987	GO_NUCLEOBASE_TRANSPORT	0.87	0.19	0	0	0	not significant
9988	GO_POSITIVE_REGULATION_OF_MESONEPHROS_DEVELOPMENT	0.87	0.19	0	0	0	not significant
9989	GO_POSITIVE_REGULATION_OF_STEM_CELL_PROLIFERATION	0.87	0.19	0	0	0	not significant
9990	GO_PRP19_COMPLEX	0.87	0.19	0	0	0	not significant
9991	GO_REGULATION_OF_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	0.87	0.19	0	0	0	not significant
9992	GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_	0.87	0.19	0	0	0	not significant
9993	REACTOME_INHIBITION_OF_REPLICATION_INITIATION_OF_DAMAGED_DN	0.87	0.19	0	0	0	not significant
9994	REACTOME_KERATINIZATION	0.87	0.19	0	0	0	not significant
9995	WANG_RESPONSE_TO_BEXAROTENE_UP	0.87	0.19	0	0	0	not significant
9996	FIGUEROA_AML_METHYLATION_CLUSTER_2_UP	0.87	0.18	0	0	0	not significant
9997	FRIDMAN_SENESCENCE_UP	0.87	0.18	0	0	0	not significant
9998	GO_PHAGOSOME_ACIDIFICATION	0.87	0.18	0	0	0	not significant
9999	GO_POSTSYNAPTIC_SPECIALIZATION_INTRACELLULAR_COMPONENT	0.87	0.18	0	0	0	not significant
10000	GO_REGULATION_OF_RAC_PROTEIN_SIGNAL_TRANSDUCTION	0.87	0.18	0	0	0	not significant
10001	HEIDENBLAD_AMPLICON_8Q24_DN	0.87	0.18	0	0	0	not significant
10002	NAGASHIMA_NRG1_SIGNALING_DN	0.87	0.18	0	0	0	not significant
10003	ONO_FOXP3_TARGETS_DN	0.87	0.18	0	0	0	not significant
10004	PID_P38_MKK3_6PATHWAY	0.87	0.18	0	0	0	not significant
10005	REACTOME_CARGO_TRAFFICKING_TO_THE_PERICILIARY_MEMBRANE	0.87	0.18	0	0	0	not significant
10006	REACTOME_HDMS_DEMETHYLATE_HISTONES	0.87	0.18	0	0	0	not significant
10007	GO_CENTRIOLAR_SATELLITE	0.87	0.17	0	0	0	not significant
10008	GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	0.87	0.17	0	0	0	not significant
10009	GO_POSITIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	0.87	0.17	0	0	0	not significant
10010	GO_CENTROSOME_DUPLICATION	0.87	0.16	0	0	0	not significant
10011	GO_REGULATION_OF_SYNAPTIC_VESICLE_CYCLE	0.87	0.16	0	0	0	not significant
10012	GO_RNA_POLYMERASE_II_CORE_PROMOTER_SEQUENCE_SPECIFIC_DN	0.87	0.16	0	0	0	not significant
10013	LIU_PROSTATE_CANCER_UP	0.87	0.16	0	0	0	not significant
10014	DELASERNA_MYOD_TARGETS_UP	0.87	0.15	0	0	0	not significant
10015	GO_ANTERIOR_POSTERIOR_PATTERN_SPECIFICATION	0.87	0.15	0	0	0	not significant
10016	GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROT	0.87	0.15	0	0	0	not significant

10017	GO_OSTEOCLAST_DIFFERENTIATION	0.87	0.15	0	0	0	not significant
10018	REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	0.87	0.15	0	0	0	not significant
10019	GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_	0.87	0.14	0	0	0	not significant
10020	PID_PDGFRB_PATHWAY	0.87	0.14	0	0	0	not significant
10021	RAPA_EARLY_UP.V1_DN	0.87	0.14	0	0	0	not significant
10022	REACTOME_SIGNALING_BY_NOTCH1	0.87	0.14	0	0	0	not significant
10023	GO_EPITHELIAL_CELL_DEVELOPMENT	0.87	0.13	0	0	0	not significant
10024	GO_EXTRINSIC_COMPONENT_OF_MEMBRANE	0.87	0.12	0	0	0	not significant
10025	GO_PHOSPHATIDYLINOSITOL_BINDING	0.87	0.12	0	0	0	not significant
10026	PDGF_ERK_DN.V1_DN	0.87	0.12	0	0	0	not significant
10027	BOYLAN_MULTIPLE_MYELOMA_C_D_DN	0.87	0.11	0	0	0	not significant
10028	CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_DN	0.87	0.11	0	0	0	not significant
10029	GO_HORMONE_TRANSPORT	0.87	0.11	0	0	0	not significant
10030	GO_IN_UTERO_EMBRYONIC_DEVELOPMENT	0.87	0.10	0	0	0	not significant
10031	GO_POSITIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_	0.87	0.10	0	0	0	not significant
10032	GO_UBIQUITIN_LIKE_PROTEIN_LIGASE_ACTIVITY	0.87	0.10	0	0	0	not significant
10033	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN	0.87	0.10	0	0	0	not significant
10034	GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	0.87	0.09	0	0	0	not significant
10035	GO_UBIQUITIN_LIKE_PROTEIN_TRANSFERASE_ACTIVITY	0.87	0.08	0	0	0	not significant
10036	GO_CHROMATIN_BINDING	0.87	0.07	0	0	0	not significant
10037	GO_ENDOTHELIAL_CELL_ACTIVATION	0.88	0.22	0	0	0	not significant
10038	GO_LABYRINTHINE_LAYER_MORPHOGENESIS	0.88	0.22	0	0	0	not significant
10039	GO_REGULATION_OF_LIGASE_ACTIVITY	0.88	0.22	0	0	0	not significant
10040	GO_UDP_XYLOSYLTRANSFERASE_ACTIVITY	0.88	0.22	0	0	0	not significant
10041	BIOCARTA_TERT_PATHWAY	0.88	0.21	0	0	0	not significant
10042	BREUHAHN_GROWTH_FACTOR_SIGNALING_IN_LIVER_CANCER	0.88	0.21	0	0	0	not significant
10043	GO_7SK_SNRNA_BINDING	0.88	0.21	0	0	0	not significant
10044	GO_ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_O	0.88	0.21	0	0	0	not significant
10045	GO_AXON_ENSHEATHMENT_IN_CENTRAL_NERVOUS_SYSTEM	0.88	0.21	0	0	0	not significant
10046	GO_EMBRYONIC_FORELIMB_MORPHOGENESIS	0.88	0.21	0	0	0	not significant
10047	GO_EXCITATORY_SYNAPSE_ASSEMBLY	0.88	0.21	0	0	0	not significant
10048	GO_NEGATIVE_REGULATION_OF_B_CELL_APOPTOTIC_PROCESS	0.88	0.21	0	0	0	not significant
10049	GO_NEGATIVE_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEG	0.88	0.21	0	0	0	not significant
10050	GO_NEGATIVE_REGULATION_OF_CHROMATIN_SILENCING	0.88	0.21	0	0	0	not significant
10051	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CENTROS	0.88	0.21	0	0	0	not significant
10052	GO_PRE_B_CELL_DIFFERENTIATION	0.88	0.21	0	0	0	not significant
10053	GO_REGULATION_OF_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	0.88	0.21	0	0	0	not significant
10054	GO_REGULATION_OF_SPINDLE_CHECKPOINT	0.88	0.21	0	0	0	not significant
10055	GO_SUMO_LIGASE_ACTIVITY	0.88	0.21	0	0	0	not significant
10056	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP	0.88	0.21	0	0	0	not significant
10057	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP	0.88	0.21	0	0	0	not significant
10058	KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	0.88	0.21	0	0	0	not significant
10059	MARKS_HDAC_TARGETS_UP	0.88	0.21	0	0	0	not significant
10060	REACTOME_BH3_ONLY_PROTEINS_ASSOCIATE_WITH_AND_INACTIVATE_	0.88	0.21	0	0	0	not significant
10061	CHR6Q23	0.88	0.20	0	0	0	not significant
10062	GO_DEVELOPMENT_OF_SECONDARY_FEMALE_SEXUAL_CHARACTERIST	0.88	0.20	0	0	0	not significant
10063	GO_MONOOXYGENASE_ACTIVITY	0.88	0.20	0	0	0	not significant
10064	GO_POSITIVE_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR	0.88	0.20	0	0	0	not significant
10065	GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	0.88	0.20	0	0	0	not significant
10066	GO_PROTECTION_FROM_NON_HOMOLOGOUS_END_JOINING_AT_TELOM	0.88	0.20	0	0	0	not significant
10067	GO_PROTON_TRANSPORTING_ATPASE_ACTIVITY_ROTATIONAL_MECHAI	0.88	0.20	0	0	0	not significant
10068	GO_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PA	0.88	0.20	0	0	0	not significant
10069	GO_REGULATION_OF_RESPIRATORY_GASEOUS_EXCHANGE	0.88	0.20	0	0	0	not significant
10070	REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DU	0.88	0.20	0	0	0	not significant
10071	BIOCARTA_TNFR2_PATHWAY	0.88	0.19	0	0	0	not significant
10072	GO_CLATHRIN_DEPENDENT_ENDOCYTOSIS	0.88	0.19	0	0	0	not significant
10073	GO_DIAPEDESIS	0.88	0.19	0	0	0	not significant
10074	GO_GAMMA_CATENIN_BINDING	0.88	0.19	0	0	0	not significant
10075	GO_PHOSPHATIDYLCHOLINE_TRANSPORTER_ACTIVITY	0.88	0.19	0	0	0	not significant
10076	GO_POSITIVE_REGULATION_OF_T_CELL_DIFFERENTIATION_IN_THYMUS	0.88	0.19	0	0	0	not significant
10077	GO_PROTEIN_POLYUFMYLATION	0.88	0.19	0	0	0	not significant
10078	GO_REGULATION_OF_CILIUM_ASSEMBLY	0.88	0.19	0	0	0	not significant
10079	GO_REGULATION_OF_RECEPTOR_INTERNALIZATION	0.88	0.19	0	0	0	not significant
10080	GO_SMOOTH_MUSCLE_CONTRACTION	0.88	0.19	0	0	0	not significant
10081	GO_XENOBIOTIC_TRANSPORT	0.88	0.19	0	0	0	not significant
10082	KAMMINGA_SENESCENCE	0.88	0.19	0	0	0	not significant
10083	PID_TNF_PATHWAY	0.88	0.19	0	0	0	not significant
10084	PIONTEK_PKD1_TARGETS_DN	0.88	0.19	0	0	0	not significant
10085	REACTOME_DEACTIVATION_OF_THE_BETA_CATENIN_TRANSACTIVATING	0.88	0.19	0	0	0	not significant
10086	REACTOME_O_LINKED_GLYCOSYLATION	0.88	0.19	0	0	0	not significant
10087	ROVERSI_GLIOMA_COPY_NUMBER_UP	0.88	0.19	0	0	0	not significant
10088	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_DN	0.88	0.18	0	0	0	not significant
10089	GEORGANTAS_HSC_MARKERS	0.88	0.18	0	0	0	not significant
10090	GO_LUMENAL_SIDE_OF_MEMBRANE	0.88	0.18	0	0	0	not significant
10091	GO_POSITIVE_REGULATION_OF_NUCLEAR_DIVISION	0.88	0.18	0	0	0	not significant
10092	GO_PROTEIN_K48_LINKED_DEUBIQUITINATION	0.88	0.18	0	0	0	not significant
10093	GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	0.88	0.18	0	0	0	not significant
10094	DIRMEIER_LMP1_RESPONSE_EARLY	0.88	0.17	0	0	0	not significant
10095	GO_METALLOEXOPEPTIDASE_ACTIVITY	0.88	0.17	0	0	0	not significant
10096	KATSANOU_ELAVL1_TARGETS_UP	0.88	0.17	0	0	0	not significant
10097	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_DN	0.88	0.17	0	0	0	not significant
10098	EIF4E_DN	0.88	0.16	0	0	0	not significant
10099	GO_ACTION_POTENTIAL	0.88	0.16	0	0	0	not significant
10100	GO_ANCHORED_COMPONENT_OF_MEMBRANE	0.88	0.16	0	0	0	not significant
10101	GO_ENDOSOME_ORGANIZATION	0.88	0.16	0	0	0	not significant
10102	LIU_VMYB_TARGETS_UP	0.88	0.16	0	0	0	not significant
10103	MCBRYAN_PUBERTAL_BREAST_5_6WK_UP	0.88	0.16	0	0	0	not significant
10104	GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_	0.88	0.15	0	0	0	not significant
10105	GO_SENSORY_PERCEPTION_OF_LIGHT_STIMULUS	0.88	0.15	0	0	0	not significant
10106	GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_	0.88	0.15	0	0	0	not significant
10107	MCBRYAN_PUBERTAL_BREAST_5_6WK_DN	0.88	0.15	0	0	0	not significant
10108	GO_HINDBRAIN_DEVELOPMENT	0.88	0.14	0	0	0	not significant
10109	GO_MUSCLE_CELL_PROLIFERATION	0.88	0.13	0	0	0	not significant
10110	GO_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	0.88	0.13	0	0	0	not significant
10111	GO_DNA_BINDING_TRANSCRIPTION_ACTIVATOR_ACTIVITY	0.88	0.12	0	0	0	not significant
10112	GO_AXON	0.88	0.10	0	0	0	not significant
10113	GO_CELL_PART_MORPHOGENESIS	0.88	0.09	0	0	0	not significant
10114	GO_VESICLE_MEMBRANE	0.88	0.09	0	0	0	not significant
10115	GO_NERVOUS_SYSTEM_PROCESS	0.88	0.08	0	0	0	not significant
10116	MILI_PSEUDOPODIA_CHEMOTAXIS_DN	0.88	0.08	0	0	0	not significant
10117	BENPORATH_SOX2_TARGETS	0.88	0.07	0	0	0	not significant
10118	GO_ZINC_ION_BINDING	0.88	0.07	0	0	0	not significant
10119	KRIEG_HYPOXIA_NOT_VIA_KDM3A	0.88	0.07	0	0	0	not significant
10120	ODONNELL_METASTASIS_DN	0.89	0.24	0	0	0	not significant
10121	GO_CELLULAR_ANION_HOMEOSTASIS	0.89	0.23	0	0	0	not significant
10122	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	0.89	0.23	0	0	0	not significant
10123	GO_REGULATION_OF_RECEPTOR_BINDING	0.89	0.23	0	0	0	not significant
10124	GO_SLEEP	0.89	0.23	0	0	0	not significant
10125	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	0.89	0.23	0	0	0	not significant

10126	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_PLURIPOTENT_STEM_	0.89	0.23	0	0	0	not significant
10127	DISTECHE_ESCAPED_FROM_X_INACTIVATION	0.89	0.22	0	0	0	not significant
10128	GO_DNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC	0.89	0.22	0	0	0	not significant
10129	GO_HETEROPHILIC_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_C	0.89	0.22	0	0	0	not significant
10130	GO_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	0.89	0.22	0	0	0	not significant
10131	GO_ORIGIN_RECOGNITION_COMPLEX	0.89	0.22	0	0	0	not significant
10132	GO_PHOSPHATIDYLINOSITOL_4_5_BISPHOSPHATE_5_PHOSPHATASE_AC	0.89	0.22	0	0	0	not significant
10133	GO_POSITIVE_REGULATION_OF_CHROMATIN_BINDING	0.89	0.22	0	0	0	not significant
10134	GO_POSITIVE_REGULATION_OF_HISTONE_H3_K9_ACETYLATION	0.89	0.22	0	0	0	not significant
10135	GO_REGULATION_OF_ARP2_3_COMPLEX_MEDIATED_ACTIN_NUCLEATIO	0.89	0.22	0	0	0	not significant
10136	GO_REGULATION_OF_AUTOPHAGY_OF_MITOCHONDRION_IN_RESPONS	0.89	0.22	0	0	0	not significant
10137	SAKAI_TUMOR_INFILTRATING_MONOCYTES_UP	0.89	0.22	0	0	0	not significant
10138	BURTON_ADIPOGENESIS_9	0.89	0.21	0	0	0	not significant
10139	CHR8Q22	0.89	0.21	0	0	0	not significant
10140	GO_GLYCOSYLPHOSPHATIDYLINOSITOL_N_ACETYLGLUCOSAMINYLTRA	0.89	0.21	0	0	0	not significant
10141	GO_RENAL_SYSTEM_PROCESS_INVOLVED_IN_REGULATION_OF_SYSTE	0.89	0.21	0	0	0	not significant
10142	GO_SEGMENT_SPECIFICATION	0.89	0.21	0	0	0	not significant
10143	GO_UNCONVENTIONAL_MYOSIN_COMPLEX	0.89	0.21	0	0	0	not significant
10144	KEGG_HEDGEHOG_SIGNALING_PATHWAY	0.89	0.21	0	0	0	not significant
10145	PAL_PRMT5_TARGETS_DN	0.89	0.21	0	0	0	not significant
10146	PARK_TRETINOIN_RESPONSE_AND_RARA_PLZF_FUSION	0.89	0.21	0	0	0	not significant
10147	REACTOME_PLASMA_LIPOPROTEIN_REMODELING	0.89	0.21	0	0	0	not significant
10148	SHIN_B_CELL_LYMPHOMA_CLUSTER_8	0.89	0.21	0	0	0	not significant
10149	ZHAN_MULTIPLE_MYELOMA_MS_DN	0.89	0.21	0	0	0	not significant
10150	BIOCARTA_DC_PATHWAY	0.89	0.20	0	0	0	not significant
10151	FIRESTEIN_CTNNB1_PATHWAY	0.89	0.20	0	0	0	not significant
10152	GO_CARBOHYDRATE_DERIVATIVE_TRANSMEMBRANE_TRANSPORTER_	0.89	0.20	0	0	0	not significant
10153	GO_GALACTOSIDASE_ACTIVITY	0.89	0.20	0	0	0	not significant
10154	GO_NEGATIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS	0.89	0.20	0	0	0	not significant
10155	GO_POLYSACCHARIDE_METABOLIC_PROCESS	0.89	0.20	0	0	0	not significant
10156	GO_POSITIVE_REGULATION_OF_CIRCADIAN_RHYTHM	0.89	0.20	0	0	0	not significant
10157	GO_PRESYNAPTIC_ACTIVE_ZONE	0.89	0.20	0	0	0	not significant
10158	GO_REGULATION_OF_MEMBRANE_TUBULATION	0.89	0.20	0	0	0	not significant
10159	GO_RETINAL_ROD_CELL_DEVELOPMENT	0.89	0.20	0	0	0	not significant
10160	REACTOME_NOTCH3_ACTIVATION_AND_TRANSMISSION_OF_SIGNAL_TO	0.89	0.20	0	0	0	not significant
10161	REACTOME_SUMOYLATION_OF_TRANSCRIPTION_COFACTORS	0.89	0.20	0	0	0	not significant
10162	VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_DN	0.89	0.20	0	0	0	not significant
10163	ZEMBUTSU_SENSITIVITY_TO_CISPLATIN	0.89	0.20	0	0	0	not significant
10164	BILD_SRC_ONCOGENIC_SIGNATURE	0.89	0.19	0	0	0	not significant
10165	CHUNG_BLISTER_CYTOTOXICITY_DN	0.89	0.19	0	0	0	not significant
10166	GO_CILIARY_MEMBRANE	0.89	0.19	0	0	0	not significant
10167	GO_KINASE_INHIBITOR_ACTIVITY	0.89	0.19	0	0	0	not significant
10168	GO_NUCLEOBASE_CONTAINING_COMPOUND_TRANSMEMBRANE_TRANS	0.89	0.19	0	0	0	not significant
10169	GO_O_GLYCAN_PROCESSING	0.89	0.19	0	0	0	not significant
10170	GO_PLACENTA_DEVELOPMENT	0.89	0.19	0	0	0	not significant
10171	HALLMARK_TGF_BETA_SIGNALING	0.89	0.19	0	0	0	not significant
10172	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	0.89	0.19	0	0	0	not significant
10173	RIGGINS_TAMOXIFEN_RESISTANCE_UP	0.89	0.19	0	0	0	not significant
10174	GO_AUTOPHAGY_OF_MITOCHONDRION	0.89	0.18	0	0	0	not significant
10175	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GR	0.89	0.18	0	0	0	not significant
10176	POOLA_INVASIVE_BREAST_CANCER_DN	0.89	0.18	0	0	0	not significant
10177	GO_ACTIVATION_OF_MAPK_ACTIVITY	0.89	0.17	0	0	0	not significant
10178	GO_ERYTHROCYTE_HOMEOSTASIS	0.89	0.17	0	0	0	not significant
10179	GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	0.89	0.17	0	0	0	not significant
10180	GO_NEURON_PROJECTION_EXTENSION	0.89	0.17	0	0	0	not significant
10181	GO_NOTCH_SIGNALING_PATHWAY	0.89	0.17	0	0	0	not significant
10182	GO_REGULATION_OF_LIPASE_ACTIVITY	0.89	0.17	0	0	0	not significant
10183	GREGORY_SYNTHETIC_LETHAL_WITH_IMATINIB	0.89	0.16	0	0	0	not significant
10184	YAGI_AML_WITH_T_9_11_TRANSLOCATION	0.89	0.16	0	0	0	not significant
10185	GO_MITOTIC_CELL_CYCLE_CHECKPOINT	0.89	0.14	0	0	0	not significant
10186	MONNIER_POSTRADIATION_TUMOR_ESCAPE_DN	0.89	0.10	0	0	0	not significant
10187	GO_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	0.89	0.08	0	0	0	not significant
10188	MARKS_HDAC_TARGETS_DN	0.90	0.25	0	0	0	not significant
10189	GO_FOREBRAIN_MORPHOGENESIS	0.90	0.24	0	0	0	not significant
10190	GO_THROMBIN_ACTIVATED_RECEPTOR_SIGNALING_PATHWAY	0.90	0.24	0	0	0	not significant
10191	NOJIMA_SFRP2_TARGETS_DN	0.90	0.24	0	0	0	not significant
10192	REACTOME_NF_KB_IS_ACTIVATED_AND_SIGNALS_SURVIVAL	0.90	0.24	0	0	0	not significant
10193	GO_INOSITOL_TRISPHOSPHATE_BIOSYNTHETIC_PROCESS	0.90	0.23	0	0	0	not significant
10194	GO_MICROTUBULE_MINUS_END	0.90	0.23	0	0	0	not significant
10195	GO_PEPTIDYL_SERINE_DEPHOSPHORYLATION	0.90	0.23	0	0	0	not significant
10196	GO_PHAGOPHORE_ASSEMBLY_SITE_MEMBRANE	0.90	0.23	0	0	0	not significant
10197	GO_POSITIVE_REGULATION_OF_GLYCOPROTEIN_BIOSYNTHETIC_PROC	0.90	0.23	0	0	0	not significant
10198	GO_REGULATION_OF_ACTIN_FILAMENT_BASED_MOVEMENT	0.90	0.23	0	0	0	not significant
10199	GO_TORC2_SIGNALING	0.90	0.23	0	0	0	not significant
10200	GO_TRANSEPITHELIAL_TRANSPORT	0.90	0.23	0	0	0	not significant
10201	GO_VOLTAGE_GATED_ANION_CHANNEL_ACTIVITY	0.90	0.23	0	0	0	not significant
10202	HASINA_NOL7_TARGETS_UP	0.90	0.23	0	0	0	not significant
10203	MCGOWAN_RSP6_TARGETS_UP	0.90	0.23	0	0	0	not significant
10204	WANG_TNF_TARGETS	0.90	0.23	0	0	0	not significant
10205	BIOCARTA_GABA_PATHWAY	0.90	0.22	0	0	0	not significant
10206	GO_ATP_DEPENDENT_PROTEIN_BINDING	0.90	0.22	0	0	0	not significant
10207	GO_BONE_RESORPTION	0.90	0.22	0	0	0	not significant
10208	GO_CILIUM_MOVEMENT_INVOLVED_IN_CELL_MOTILITY	0.90	0.22	0	0	0	not significant
10209	GO_FRIZZLED_BINDING	0.90	0.22	0	0	0	not significant
10210	GO_MUSCLE_ATROPHY	0.90	0.22	0	0	0	not significant
10211	GO_NOTCH_RECEPTOR_PROCESSING_LIGAND_DEPENDENT	0.90	0.22	0	0	0	not significant
10212	GO_NUCLEOTIDE_EXCISION_REPAIR_COMPLEX	0.90	0.22	0	0	0	not significant
10213	GO_RELAXATION_OF_CARDIAC_MUSCLE	0.90	0.22	0	0	0	not significant
10214	GO_RESPONSE_TO_COBALT_ION	0.90	0.22	0	0	0	not significant
10215	GO_STEM_CELL_DIVISION	0.90	0.22	0	0	0	not significant
10216	GO_SYNAPTIC_GROWTH_AT_NEUROMUSCULAR_JUNCTION	0.90	0.22	0	0	0	not significant
10217	HALLMARK_HEDGEHOG_SIGNALING	0.90	0.22	0	0	0	not significant
10218	HUI_MAPK14_TARGETS_UP	0.90	0.22	0	0	0	not significant
10219	WANG_METASTASIS_OF_BREAST_CANCER	0.90	0.22	0	0	0	not significant
10220	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_UP	0.90	0.21	0	0	0	not significant
10221	GO_EXCRETION	0.90	0.21	0	0	0	not significant
10222	GO_FORMATION_OF_PRIMARY_GERM_LAYER	0.90	0.21	0	0	0	not significant
10223	GO_IMMUNOLOGICAL_SYNAPSE	0.90	0.21	0	0	0	not significant
10224	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_BETA_PRODUCTION	0.90	0.21	0	0	0	not significant
10225	GO_POSITIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_AC	0.90	0.21	0	0	0	not significant
10226	GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	0.90	0.21	0	0	0	not significant
10227	GO_REGULATION_OF_LYMPHOID_PROGENITOR_CELL_DIFFERENTIATIO	0.90	0.21	0	0	0	not significant
10228	GO_RESPONSE_TO_INTERLEUKIN_4	0.90	0.21	0	0	0	not significant
10229	LUI_THYROID_CANCER_PAX8_PPARG_UP	0.90	0.21	0	0	0	not significant
10230	REACTOME_ACTIVATION_OF_THE_TFAP2_AP_2_FAMILY_OF_TRANSCRI	0.90	0.21	0	0	0	not significant
10231	REACTOME_CELL_CELL_COMMUNICATION	0.90	0.21	0	0	0	not significant
10232	REACTOME_SHC_MEDIATED_CASCADE:FGFR1	0.90	0.21	0	0	0	not significant
10233	REACTOME_TNFR1_INDUCED_NFKAPPAB_SIGNALING_PATHWAY	0.90	0.21	0	0	0	not significant
10234	SCIBETTA_KDM5B_TARGETS_UP	0.90	0.21	0	0	0	not significant

10235	WESTON_VEGFA_TARGETS	0.90	0.21	0	0	0	not significant
10236	GO_BETA_TUBULIN_BINDING	0.90	0.20	0	0	0	not significant
10237	GO_MEIOTIC_CHROMOSOME_SEGREGATION	0.90	0.20	0	0	0	not significant
10238	GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	0.90	0.20	0	0	0	not significant
10239	GO_RRNA_BINDING	0.90	0.20	0	0	0	not significant
10240	GO_SYNAPTONEMAL_STRUCTURE	0.90	0.20	0	0	0	not significant
10241	HENDRICKS_SMARCA4_TARGETS_UP	0.90	0.20	0	0	0	not significant
10242	REACTOME_REGULATION_OF_PTEN_GENE_TRANSCRIPTION	0.90	0.20	0	0	0	not significant
10243	GO_RESPONSE_TO_ACTIVITY	0.90	0.19	0	0	0	not significant
10244	KEGG_SMALL_CELL_LUNG_CANCER	0.90	0.19	0	0	0	not significant
10245	KEGG_WNT_SIGNALING_PATHWAY	0.90	0.19	0	0	0	not significant
10246	XU_HGF_TARGETS_REPRESSED_BY_AKT1_DN	0.90	0.19	0	0	0	not significant
10247	GO_PEPTIDYL_LYSINE_METHYLATION	0.90	0.18	0	0	0	not significant
10248	GO_REGULATION_OF_CELL_SIZE	0.90	0.18	0	0	0	not significant
10249	GO_REGULATION_OF_PH	0.90	0.18	0	0	0	not significant
10250	SANSOM_APC_TARGETS_UP	0.90	0.18	0	0	0	not significant
10251	GO_MAMMARY_GLAND_DEVELOPMENT	0.90	0.17	0	0	0	not significant
10252	GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	0.90	0.17	0	0	0	not significant
10253	KYNG_DNA_DAMAGE_UP	0.90	0.17	0	0	0	not significant
10254	PECE_MAMMARY_STEM_CELL_DN	0.90	0.17	0	0	0	not significant
10255	BROWNE_HCMV_INFECTION_4HR_DN	0.90	0.16	0	0	0	not significant
10256	GO_DNA_INTEGRITY_CHECKPOINT	0.90	0.16	0	0	0	not significant
10257	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	0.90	0.16	0	0	0	not significant
10258	GO_RESPONSE_TO_UV	0.90	0.16	0	0	0	not significant
10259	GO_POSITIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	0.90	0.15	0	0	0	not significant
10260	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP	0.90	0.15	0	0	0	not significant
10261	GO_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	0.90	0.14	0	0	0	not significant
10262	GO_SENSORY_ORGAN_DEVELOPMENT	0.90	0.14	0	0	0	not significant
10263	RATTENBACHER_BOUND_BY_CELF1	0.90	0.13	0	0	0	not significant
10264	GO_DENDRITIC_TREE	0.90	0.12	0	0	0	not significant
10265	GO_SIGNAL_RELEASE	0.90	0.12	0	0	0	not significant
10266	GO_VACUOLAR_PART	0.90	0.12	0	0	0	not significant
10267	PARENT_MTOR_SIGNALING_UP	0.90	0.11	0	0	0	not significant
10268	GO_CARBOHYDRATE_DERIVATIVE_BIOSYNTHETIC_PROCESS	0.90	0.10	0	0	0	not significant
10269	GO_PLASMA_MEMBRANE_REGION	0.90	0.10	0	0	0	not significant
10270	GO_EMBRYO_DEVELOPMENT	0.90	0.09	0	0	0	not significant
10271	GO_POSITIVE_REGULATION_OF_SIGNALING	0.90	0.07	0	0	0	not significant
10272	REACTOME_GENE_EXPRESSION_TRANSCRIPTION	0.90	0.07	0	0	0	not significant
10273	GO_ADRENERGIC_RECEPTOR_BINDING	0.91	0.25	0	0	0	not significant
10274	GO_INTERLEUKIN_17_PRODUCTION	0.91	0.25	0	0	0	not significant
10275	GO_ARMADILLO_REPEAT_DOMAIN_BINDING	0.91	0.24	0	0	0	not significant
10276	GO_ESCRT_I_COMPLEX	0.91	0.24	0	0	0	not significant
10277	GO_EXPLORATION_BEHAVIOR	0.91	0.24	0	0	0	not significant
10278	GO_GTP_BIOSYNTHETIC_PROCESS	0.91	0.24	0	0	0	not significant
10279	GO_HEPARIN_BIOSYNTHETIC_PROCESS	0.91	0.24	0	0	0	not significant
10280	REACTOME_COBALAMIN_CBL_VITAMIN_B12_TRANSPORT_AND_METABO	0.91	0.24	0	0	0	not significant
10281	REACTOME_HS_GAG_DEGRADATION	0.91	0.24	0	0	0	not significant
10282	REACTOME_P75NTR_SIGNALS_VIA_NF_KB	0.91	0.24	0	0	0	not significant
10283	SUZUKI_CTCFL_TARGETS_UP	0.91	0.24	0	0	0	not significant
10284	ZERBINI_RESPONSE_TO_SULINDAC_UP	0.91	0.24	0	0	0	not significant
10285	BIOCARTA_BTG2_PATHWAY	0.91	0.23	0	0	0	not significant
10286	CHOW_RASSF1_TARGETS_DN	0.91	0.23	0	0	0	not significant
10287	GO_14_3_3_PROTEIN_BINDING	0.91	0.23	0	0	0	not significant
10288	GO_CORE_PROMOTER_BINDING	0.91	0.23	0	0	0	not significant
10289	GO_NADPLUS_BINDING	0.91	0.23	0	0	0	not significant
10290	GO_NEGATIVE_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	0.91	0.23	0	0	0	not significant
10291	GO_NEGATIVE_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSU	0.91	0.23	0	0	0	not significant
10292	GO_POSITIVE_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	0.91	0.23	0	0	0	not significant
10293	GO_PRO_B_CELL_DIFFERENTIATION	0.91	0.23	0	0	0	not significant
10294	GO_PROTEIN_TRANSPORT_WITHIN_LIPID_BILAYER	0.91	0.23	0	0	0	not significant
10295	GO_RESPONSE_TO_INTERLEUKIN_6	0.91	0.23	0	0	0	not significant
10296	GO_TROPHOBLAST_GIANT_CELL_DIFFERENTIATION	0.91	0.23	0	0	0	not significant
10297	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_UP	0.91	0.23	0	0	0	not significant
10298	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS	0.91	0.23	0	0	0	not significant
10299	KRAS.BREAST_UP.V1_UP	0.91	0.23	0	0	0	not significant
10300	LIN_TUMOR_ESCAPE_FROM_IMMUNE_ATTACK	0.91	0.23	0	0	0	not significant
10301	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_DN	0.91	0.23	0	0	0	not significant
10302	REACTOME_G0_AND_EARLY_G1	0.91	0.23	0	0	0	not significant
10303	SANCHEZ_MDM2_TARGETS	0.91	0.23	0	0	0	not significant
10304	ZHAN_LATE_DIFFERENTIATION_GENES_DN	0.91	0.23	0	0	0	not significant
10305	BCAT_GDS748_UP	0.91	0.22	0	0	0	not significant
10306	GO_ADHERENS_JUNCTION_ASSEMBLY	0.91	0.22	0	0	0	not significant
10307	GO_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.91	0.22	0	0	0	not significant
10308	GO_CELL_DIFFERENTIATION_INVOLVED_IN_EMBRYONIC_PLACENTA_DEV	0.91	0.22	0	0	0	not significant
10309	GO_HEART_VALVE_FORMATION	0.91	0.22	0	0	0	not significant
10310	GO_N_TERMINAL_PROTEIN_LIPIDATION	0.91	0.22	0	0	0	not significant
10311	GO_PROTEIN_GERANYLGERANYLATION	0.91	0.22	0	0	0	not significant
10312	GO_RESPONSE_TO_AMYLOID_BETA	0.91	0.22	0	0	0	not significant
10313	GO_SCAR_COMPLEX	0.91	0.22	0	0	0	not significant
10314	GRANDVAUX_IRF3_TARGETS_DN	0.91	0.22	0	0	0	not significant
10315	GUILLAUMOND_KLF10_TARGETS_UP	0.91	0.22	0	0	0	not significant
10316	REACTOME_FATTY_ACIDS_BOUND_TO_GPR40_FFAR1_REGULATE_INSU	0.91	0.22	0	0	0	not significant
10317	GO_CELLULAR_RESPONSE_TO_ANTIBIOTIC	0.91	0.21	0	0	0	not significant
10318	GO_GROWTH_FACTOR_BINDING	0.91	0.21	0	0	0	not significant
10319	GO_NAD_DEPENDENT_PROTEIN_DEACETYLASE_ACTIVITY	0.91	0.21	0	0	0	not significant
10320	GO_PHOSPHATIDYLINOSITOL_BISPHOSPHATE_BINDING	0.91	0.21	0	0	0	not significant
10321	PID_RB_1PATHWAY	0.91	0.21	0	0	0	not significant
10322	REACTOME_L1CAM_INTERACTIONS	0.91	0.21	0	0	0	not significant
10323	BONCI_TARGETS_OF_MIR15A_AND_MIR16_1	0.91	0.20	0	0	0	not significant
10324	GO_MEIOTIC_CELL_CYCLE_PROCESS	0.91	0.20	0	0	0	not significant
10325	PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP	0.91	0.20	0	0	0	not significant
10326	PID_FCER1_PATHWAY	0.91	0.20	0	0	0	not significant
10327	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_UP	0.91	0.20	0	0	0	not significant
10328	GO_CELL_CYCLE_DNA_REPLICATION	0.91	0.19	0	0	0	not significant
10329	GO_CYTOPLASMIC_SIDE_OF_MEMBRANE	0.91	0.19	0	0	0	not significant
10330	GO_RNA_POLYMERASE_II_DISTAL_ENHANCER_SEQUENCE_SPECIFIC_DN	0.91	0.19	0	0	0	not significant
10331	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP	0.91	0.19	0	0	0	not significant
10332	GO_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.91	0.17	0	0	0	not significant
10333	GO_GERM_CELL_DEVELOPMENT	0.91	0.17	0	0	0	not significant
10334	KARLSSON_TGFB1_TARGETS_DN	0.91	0.17	0	0	0	not significant
10335	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN	0.91	0.15	0	0	0	not significant
10336	GO_EMBRYONIC_MORPHOGENESIS	0.91	0.15	0	0	0	not significant
10337	KUMAR_TARGETS_OF_MLL_AF9_FUSION	0.91	0.15	0	0	0	not significant
10338	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN	0.91	0.14	0	0	0	not significant
10339	GO_VACUOLE	0.91	0.13	0	0	0	not significant
10340	GO_POSITIVE_REGULATION_OF_CELL_DEATH	0.91	0.12	0	0	0	not significant
10341	GO_SYNAPSE_PART	0.91	0.11	0	0	0	not significant
10342	GO_PROTEIN_LOCALIZATION_TO_ORGANELLE	0.91	0.10	0	0	0	not significant
10343	GO_REGULATION_OF_STORE_OPERATED_CALCIUM_CHANNEL_ACTIVITY	0.92	0.27	0	0	0	not significant

10344	VANDESLUIS_COMMD1_TARGETS_GROUP_3_DN	0.92	0.27	0	0	0	not significant
10345	CHR7P13	0.92	0.26	0	0	0	not significant
10346	GO_ANION_ANION_ANTIPORTER_ACTIVITY	0.92	0.26	0	0	0	not significant
10347	GO_NEGATIVE_REGULATION_OF_ORGAN_GROWTH	0.92	0.26	0	0	0	not significant
10348	GO_NEGATIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE	0.92	0.26	0	0	0	not significant
10349	GO_SINGLE_STRAND_BREAK_REPAIR	0.92	0.26	0	0	0	not significant
10350	TSENG_ADIPOGENIC_POTENTIAL_DN	0.92	0.26	0	0	0	not significant
10351	ABDULRAHMAN_KIDNEY_CANCER_VHL_UP	0.92	0.25	0	0	0	not significant
10352	GO_FOREBRAIN_CELL_MIGRATION	0.92	0.25	0	0	0	not significant
10353	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_D	0.92	0.25	0	0	0	not significant
10354	GO_PHOSPHATIDYLINOSITOL_5_PHOSPHATE_BINDING	0.92	0.25	0	0	0	not significant
10355	GO_POSITIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLAS	0.92	0.25	0	0	0	not significant
10356	GO_PROSTANOID_METABOLIC_PROCESS	0.92	0.25	0	0	0	not significant
10357	GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	0.92	0.25	0	0	0	not significant
10358	GO_REGULATION_OF_STEM_CELL_PROLIFERATION	0.92	0.25	0	0	0	not significant
10359	GO_REPLICATION_FORK_PROTECTION	0.92	0.25	0	0	0	not significant
10360	GO_SYNAPTONEMAL_COMPLEX_ORGANIZATION	0.92	0.25	0	0	0	not significant
10361	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_UP	0.92	0.25	0	0	0	not significant
10362	HOLLERN_PAPILLARY_BREAST_TUMOR	0.92	0.25	0	0	0	not significant
10363	MARIADASON_RESPONSE_TO_CURCUMIN_SULINDAC_7	0.92	0.25	0	0	0	not significant
10364	PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_UP	0.92	0.25	0	0	0	not significant
10365	REACTOME_PTK6_REGULATES_RTKS_AND_THEIR_EFFECTORS_AKT1_	0.92	0.25	0	0	0	not significant
10366	REACTOME_REGULATION_OF_KIT_SIGNALING	0.92	0.25	0	0	0	not significant
10367	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_	0.92	0.25	0	0	0	not significant
10368	VERRECCHIA_RESPONSE_TO_TGFB1_C1	0.92	0.25	0	0	0	not significant
10369	VILIMAS_NOTCH1_TARGETS_UP	0.92	0.25	0	0	0	not significant
10370	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_MAGENTA_UP	0.92	0.24	0	0	0	not significant
10371	GO_CELL_SUBSTRATE_JUNCTION_ASSEMBLY	0.92	0.24	0	0	0	not significant
10372	GO_FIBRONECTIN_BINDING	0.92	0.24	0	0	0	not significant
10373	GO_MICROVILLUS_ASSEMBLY	0.92	0.24	0	0	0	not significant
10374	GO_NOTCH_RECEPTOR_PROCESSING	0.92	0.24	0	0	0	not significant
10375	GO_PROTEIN_KINASE_A_SIGNALING	0.92	0.24	0	0	0	not significant
10376	GO_REGULATION_OF_FEMALE_GONAD_DEVELOPMENT	0.92	0.24	0	0	0	not significant
10377	GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_CELL_FATE_COM	0.92	0.24	0	0	0	not significant
10378	PID_INTEGRIN_CS_PATHWAY	0.92	0.24	0	0	0	not significant
10379	REACTOME_CHAPERONE_MEDIATED_AUTOPHAGY	0.92	0.24	0	0	0	not significant
10380	REACTOME_RUNX2_REGULATES_OSTEOBLAST_DIFFERENTIATION	0.92	0.24	0	0	0	not significant
10381	CHR7P22	0.92	0.23	0	0	0	not significant
10382	GO_ANGIOTENSIN_RECEPTOR_BINDING	0.92	0.23	0	0	0	not significant
10383	GO_BASEMENT_MEMBRANE_ORGANIZATION	0.92	0.23	0	0	0	not significant
10384	GO_BLEB	0.92	0.23	0	0	0	not significant
10385	GO_CELLULAR_RESPONSE_TO_X_RAY	0.92	0.23	0	0	0	not significant
10386	GO_NEGATIVE_REGULATION_OF_HIPPO_SIGNALING	0.92	0.23	0	0	0	not significant
10387	GO_POSITIVE_REGULATION_OF_AXONOGENESIS	0.92	0.23	0	0	0	not significant
10388	GO_PROTEIN_LOCALIZATION_TO_VACUOLE	0.92	0.23	0	0	0	not significant
10389	LUI_THYROID_CANCER_CLUSTER_4	0.92	0.23	0	0	0	not significant
10390	PID_P38_ALPHA_BETA_DOWNSTREAM_PATHWAY	0.92	0.23	0	0	0	not significant
10391	REACTOME_BICARBONATE_TRANSPORTERS	0.92	0.23	0	0	0	not significant
10392	GO_INTRINSIC_COMPONENT_OF_GOLGI_MEMBRANE	0.92	0.22	0	0	0	not significant
10393	GO_OMEGA_PEPTIDASE_ACTIVITY	0.92	0.22	0	0	0	not significant
10394	GO_POSITIVE_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	0.92	0.22	0	0	0	not significant
10395	GO_REGULATION_OF_EXOCYTOSIS	0.92	0.22	0	0	0	not significant
10396	GO_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR	0.92	0.22	0	0	0	not significant
10397	PID_ARF6_TRAFFICKING_PATHWAY	0.92	0.22	0	0	0	not significant
10398	YU_MYC_TARGETS_DN	0.92	0.22	0	0	0	not significant
10399	ZHAN_MULTIPLE_MYELOMA_LB_DN	0.92	0.22	0	0	0	not significant
10400	GO_DENDRITE_MORPHOGENESIS	0.92	0.21	0	0	0	not significant
10401	GO_DIOXYGENASE_ACTIVITY	0.92	0.21	0	0	0	not significant
10402	GO_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	0.92	0.21	0	0	0	not significant
10403	REACTOME_GLUTAMATE_BINDING_ACTIVATION_OF_AMPA_RECEPTORS_	0.92	0.21	0	0	0	not significant
10404	STEARMAN_LUNG_CANCER_EARLY_VS_LATE_UP	0.92	0.21	0	0	0	not significant
10405	GO_APICAL_PLASMA_MEMBRANE	0.92	0.20	0	0	0	not significant
10406	GO_CELL_JUNCTION_ORGANIZATION	0.92	0.20	0	0	0	not significant
10407	GO_POSITIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION	0.92	0.20	0	0	0	not significant
10408	REACTOME_DDX58_IFIH1_MEDIATED_INDUCTION_OF_INTERFERON_ALP	0.92	0.20	0	0	0	not significant
10409	WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN	0.92	0.20	0	0	0	not significant
10410	ZHANG_BREAST_CANCER_PROGENITORS_DN	0.92	0.20	0	0	0	not significant
10411	GO_REGULATION_OF_ACTIN_FILAMENT_ORGANIZATION	0.92	0.19	0	0	0	not significant
10412	KEGG_PATHWAYS_IN_CANCER	0.92	0.18	0	0	0	not significant
10413	GO_NEGATIVE_REGULATION_OF_CELL_DIFFERENTIATION	0.92	0.17	0	0	0	not significant
10414	GO_RAS_PROTEIN_SIGNAL_TRANSDUCTION	0.92	0.17	0	0	0	not significant
10415	GO_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFEREN	0.92	0.17	0	0	0	not significant
10416	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_DN	0.92	0.17	0	0	0	not significant
10417	GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_C	0.92	0.16	0	0	0	not significant
10418	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF	0.92	0.16	0	0	0	not significant
10419	GO_REGULATION_OF_SECRETION	0.92	0.14	0	0	0	not significant
10420	GO_CELL_CELL_SIGNALING	0.92	0.12	0	0	0	not significant
10421	GO_REPRODUCTION	0.92	0.11	0	0	0	not significant
10422	GO_REGULATION_OF_CELL_DIFFERENTIATION	0.92	0.10	0	0	0	not significant
10423	FERRANDO_HOX11_NEIGHBORS	0.93	0.27	0	0	0	not significant
10424	GO_AMYLOID_PRECURSOR_PROTEIN_BIOSYNTHETIC_PROCESS	0.93	0.27	0	0	0	not significant
10425	GO_CHOLESTEROL_TRANSPORTER_ACTIVITY	0.93	0.27	0	0	0	not significant
10426	GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	0.93	0.27	0	0	0	not significant
10427	GO_SPINAL_CORD_PATTERNING	0.93	0.27	0	0	0	not significant
10428	KHETCHOUMIAN_TRIM24_TARGETS_UP	0.93	0.27	0	0	0	not significant
10429	MULLIGAN_NTF3_SIGNALING_VIA_INSR_AND_IGF1R_DN	0.93	0.27	0	0	0	not significant
10430	WHITE_NEUROBLASTOMA_WITH_1P36.3_DELETION	0.93	0.27	0	0	0	not significant
10431	BAELDE_DIABETIC_NEPHROPATHY_UP	0.93	0.26	0	0	0	not significant
10432	GO_CORPUS_CALLOSUM_DEVELOPMENT	0.93	0.26	0	0	0	not significant
10433	GO_HAUS_COMPLEX	0.93	0.26	0	0	0	not significant
10434	GO_PHOSPHODIESTERASE_I_ACTIVITY	0.93	0.26	0	0	0	not significant
10435	GO_POSITIVE_REGULATION_OF_PRI_MIRNA_TRANSCRIPTION_BY_RNA_	0.93	0.26	0	0	0	not significant
10436	GO_PROTEIN_KINASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTO	0.93	0.26	0	0	0	not significant
10437	GO_PYRIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	0.93	0.26	0	0	0	not significant
10438	GO_SALIVARY_GLAND_DEVELOPMENT	0.93	0.26	0	0	0	not significant
10439	PID_ATF2_PATHWAY	0.93	0.26	0	0	0	not significant
10440	REACTOME_NEGATIVE_REGULATION_OF_MET_ACTIVITY	0.93	0.26	0	0	0	not significant
10441	RODRIGUES_THYROID_CARCINOMA_UP	0.93	0.26	0	0	0	not significant
10442	DAIRKEE_TERT_TARGETS_DN	0.93	0.25	0	0	0	not significant
10443	GO_ACUTE_INFLAMMATORY_RESPONSE	0.93	0.25	0	0	0	not significant
10444	GO_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMATORY_RESPONSE	0.93	0.25	0	0	0	not significant
10445	GO_FLAP_ENDONUCLEASE_ACTIVITY	0.93	0.25	0	0	0	not significant
10446	GO_HEPARAN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS_P	0.93	0.25	0	0	0	not significant
10447	GO_HOMOCYSTEINE_METABOLIC_PROCESS	0.93	0.25	0	0	0	not significant
10448	GO_NEGATIVE_REGULATION_OF_PERK_MEDIATED_UNFOLDED_PROTEI	0.93	0.25	0	0	0	not significant
10449	GO_NEUROMUSCULAR_JUNCTION_DEVELOPMENT	0.93	0.25	0	0	0	not significant
10450	GO_PEPTIDE_HORMONE_BINDING	0.93	0.25	0	0	0	not significant
10451	GO_POSITIVE_REGULATION_OF_LIGASE_ACTIVITY	0.93	0.25	0	0	0	not significant
10452	GO_POSITIVE_REGULATION_OF_SPHINGOLIPID_BIOSYNTHETIC_PROCES	0.93	0.25	0	0	0	not significant

10453	GO_RIG_I_SIGNALING_PATHWAY	0.93	0.25	0	0	0	not significant
10454	GO_TUBULIN_DEACETYLATION	0.93	0.25	0	0	0	not significant
10455	KORKOLA_YOLK_SAC_TUMOR	0.93	0.25	0	0	0	not significant
10456	ONO_AML1_TARGETS_UP	0.93	0.25	0	0	0	not significant
10457	STAMBOLSKY_RESPONSE_TO_VITAMIN_D3_UP	0.93	0.25	0	0	0	not significant
10458	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_2	0.93	0.25	0	0	0	not significant
10459	BIOCARTA_CELLCYCLE_PATHWAY	0.93	0.24	0	0	0	not significant
10460	GO_MOLTING_CYCLE	0.93	0.24	0	0	0	not significant
10461	GO_POSITIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	0.93	0.24	0	0	0	not significant
10462	GO_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_BINDING	0.93	0.24	0	0	0	not significant
10463	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_SIGNALING_PATHWA	0.93	0.24	0	0	0	not significant
10464	CHR10Q24	0.93	0.23	0	0	0	not significant
10465	GO_MIDBRAIN_DOPAMINERGIC_NEURON_DIFFERENTIATION	0.93	0.23	0	0	0	not significant
10466	GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	0.93	0.23	0	0	0	not significant
10467	GO_ORGANOPHOSPHATE_ESTER_TRANSPORT	0.93	0.23	0	0	0	not significant
10468	GO_PROTEIN_LOCALIZATION_TO_SYNAPSE	0.93	0.23	0	0	0	not significant
10469	GO_REGULATION_OF_ANION_TRANSPORT	0.93	0.23	0	0	0	not significant
10470	GO_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	0.93	0.22	0	0	0	not significant
10471	GO_GLIOGENESIS	0.93	0.22	0	0	0	not significant
10472	GO_MODIFICATION_DEPENDENT_PROTEIN_BINDING	0.93	0.22	0	0	0	not significant
10473	GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	0.93	0.22	0	0	0	not significant
10474	HALLMARK_APOPTOSIS	0.93	0.22	0	0	0	not significant
10475	JNK_DN.V1_DN	0.93	0.22	0	0	0	not significant
10476	KEGG_MELANOGENESIS	0.93	0.22	0	0	0	not significant
10477	KUMAR_AUTOPHAGY_NETWORK	0.93	0.22	0	0	0	not significant
10478	LTE2_UP.V1_UP	0.93	0.22	0	0	0	not significant
10479	DOANE_RESPONSE_TO_ANDROGEN_DN	0.93	0.21	0	0	0	not significant
10480	GO_AXON_DEVELOPMENT	0.93	0.19	0	0	0	not significant
10481	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN	0.93	0.18	0	0	0	not significant
10482	GO_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.93	0.18	0	0	0	not significant
10483	GO_REGULATION_OF_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVIT	0.93	0.18	0	0	0	not significant
10484	CHICAS_RB1_TARGETS_SENESCENT	0.93	0.17	0	0	0	not significant
10485	GO_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	0.93	0.17	0	0	0	not significant
10486	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNA	0.93	0.17	0	0	0	not significant
10487	GO_GOLGI_APPARATUS	0.93	0.13	0	0	0	not significant
10488	GO_NEUROGENESIS	0.93	0.13	0	0	0	not significant
10489	GO_NEURON_DIFFERENTIATION	0.93	0.12	0	0	0	not significant
10490	GO_GAMMA_AMINOBUTYRIC_ACID_SIGNALING_PATHWAY	0.94	0.29	0	0	0	not significant
10491	LI_PROSTATE_CANCER_EPIGENETIC	0.94	0.29	0	0	0	not significant
10492	ABE_VEGFA_TARGETS_30MIN	0.94	0.28	0	0	0	not significant
10493	GO_GAMMA_TUBULIN_COMPLEX	0.94	0.28	0	0	0	not significant
10494	GO_GLUCOCORTICOID_RECEPTOR_BINDING	0.94	0.28	0	0	0	not significant
10495	GO_MESONEPHRIC_TUBULE_MORPHOGENESIS	0.94	0.28	0	0	0	not significant
10496	GO_PROTEIN_LOCALIZATION_TO_POSTSYNAPTIC_MEMBRANE	0.94	0.28	0	0	0	not significant
10497	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.94	0.27	0	0	0	not significant
10498	BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE	0.94	0.27	0	0	0	not significant
10499	GO_ADRENERGIC_RECEPTOR_SIGNALING_PATHWAY	0.94	0.27	0	0	0	not significant
10500	GO_BICARBONATE_TRANSPORT	0.94	0.27	0	0	0	not significant
10501	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMB	0.94	0.27	0	0	0	not significant
10502	GO_GLYCOLIPID_CATABOLIC_PROCESS	0.94	0.27	0	0	0	not significant
10503	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	0.94	0.27	0	0	0	not significant
10504	GO_NEGATIVE_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	0.94	0.27	0	0	0	not significant
10505	GO_REGULATION_OF_CHROMATIN_SILENCING	0.94	0.27	0	0	0	not significant
10506	REACTOME_RESOLUTION_OF_D_LOOP_STRUCTURES_THROUGH_SYNT	0.94	0.27	0	0	0	not significant
10507	ATM_DN.V1_UP	0.94	0.26	0	0	0	not significant
10508	FUJII_YBX1_TARGETS_UP	0.94	0.26	0	0	0	not significant
10509	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_YELLOW_DN	0.94	0.26	0	0	0	not significant
10510	GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_H	0.94	0.26	0	0	0	not significant
10511	GO_CHEMOSENSORY_BEHAVIOR	0.94	0.26	0	0	0	not significant
10512	GO_GROWTH_FACTOR_RECEPTOR_BINDING	0.94	0.26	0	0	0	not significant
10513	GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE	0.94	0.26	0	0	0	not significant
10514	GO_INTRACILIARY_TRANSPORT_PARTICLE_A	0.94	0.26	0	0	0	not significant
10515	GO_NEGATIVE_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_REC	0.94	0.26	0	0	0	not significant
10516	GO_NEGATIVE_REGULATION_OF_MEMBRANE_PERMEABILITY	0.94	0.26	0	0	0	not significant
10517	GO_POSITIVE_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCE	0.94	0.26	0	0	0	not significant
10518	GO_POSITIVE_REGULATION_OF_FIBROBLAST_MIGRATION	0.94	0.26	0	0	0	not significant
10519	GO_POSITIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	0.94	0.26	0	0	0	not significant
10520	GO_POSITIVE_REGULATION_OF_MITOPHAGY	0.94	0.26	0	0	0	not significant
10521	GO_PROTEIN_RETENTION_IN_ER_LUMEN	0.94	0.26	0	0	0	not significant
10522	GO_REGULATION_OF_HAIR_FOLLICLE_DEVELOPMENT	0.94	0.26	0	0	0	not significant
10523	GO_REGULATION_OF_PEROXISOME_PROLIFERATOR_ACTIVATED_RECE	0.94	0.26	0	0	0	not significant
10524	GO_TRANSLATION_INITIATION_FACTOR_BINDING	0.94	0.26	0	0	0	not significant
10525	GO_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS_VIA_THE_	0.94	0.26	0	0	0	not significant
10526	INGRAM_SHH_TARGETS_UP	0.94	0.26	0	0	0	not significant
10527	MATTIOLI_MULTIPLE_MYELOMA_WITH_14Q32_TRANSLOCATIONS	0.94	0.26	0	0	0	not significant
10528	PID_PS1_PATHWAY	0.94	0.26	0	0	0	not significant
10529	REACTOME_FERTILIZATION	0.94	0.26	0	0	0	not significant
10530	GO_CEREBELLAR_CORTEX_FORMATION	0.94	0.25	0	0	0	not significant
10531	GO_COCHLEA_DEVELOPMENT	0.94	0.25	0	0	0	not significant
10532	GO_NEGATIVE_CHEMOTAXIS	0.94	0.25	0	0	0	not significant
10533	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	0.94	0.25	0	0	0	not significant
10534	GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_	0.94	0.25	0	0	0	not significant
10535	GO_RETINOL_METABOLIC_PROCESS	0.94	0.25	0	0	0	not significant
10536	GO_SPHINGOSINE_N_ACYLTRANSFERASE_ACTIVITY	0.94	0.25	0	0	0	not significant
10537	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_UP	0.94	0.25	0	0	0	not significant
10538	LENAOUR_DENDRITIC_CELL_MATURATION_UP	0.94	0.25	0	0	0	not significant
10539	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED	0.94	0.25	0	0	0	not significant
10540	REACTOME_NRIF_SIGNALS_CELL_DEATH_FROM_THE_NUCLEUS	0.94	0.25	0	0	0	not significant
10541	TIEN_INTESTINE_PROBIOTICS_2HR_UP	0.94	0.25	0	0	0	not significant
10542	GO_FIBROBLAST_GROWTH_FACTOR_PRODUCTION	0.94	0.24	0	0	0	not significant
10543	GO_REGULATION_OF_B_CELL_ACTIVATION	0.94	0.24	0	0	0	not significant
10544	GO_RIBOSOME	0.94	0.24	0	0	0	not significant
10545	GOTTWEIN_TARGETS_OF_KSHV_MIR_K12_11	0.94	0.24	0	0	0	not significant
10546	PID_P53_DOWNSTREAM_PATHWAY	0.94	0.24	0	0	0	not significant
10547	GO_CELLULAR_SENESCENCE	0.94	0.23	0	0	0	not significant
10548	JUBAN_TARGETS_OF_SPI1_AND_FLI1_UP	0.94	0.23	0	0	0	not significant
10549	KYNG_RESPONSE_TO_H2O2	0.94	0.23	0	0	0	not significant
10550	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN	0.94	0.23	0	0	0	not significant
10551	BROWNE_HCMV_INFECTION_6HR_DN	0.94	0.22	0	0	0	not significant
10552	GO_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.94	0.22	0	0	0	not significant
10553	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	0.94	0.22	0	0	0	not significant
10554	GO_REGULATION_OF_NUCLEOTIDE_BINDING_OLIGOMERIZATION_DOMA	0.94	0.22	0	0	0	not significant
10555	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1	0.94	0.22	0	0	0	not significant
10556	GO_PROTEIN_KINASE_ACTIVITY	0.94	0.19	0	0	0	not significant
10557	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5	0.94	0.18	0	0	0	not significant
10558	GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	0.94	0.18	0	0	0	not significant
10559	GO_GOLGI_MEMBRANE	0.94	0.17	0	0	0	not significant
10560	GO_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	0.94	0.13	0	0	0	not significant
10561	GO_SPECIFIC_GRANULE_LUMEN	0.95	0.30	0	0	0	not significant

10562	BIOCARTA_ETS_PATHWAY	0.95	0.29	0	0	0	not significant
10563	BIOCARTA_NTHI_PATHWAY	0.95	0.29	0	0	0	not significant
10564	CHR10Q25	0.95	0.29	0	0	0	not significant
10565	DANG_MYC_TARGETS_DN	0.95	0.29	0	0	0	not significant
10566	GO_PROTEIN_COMPLEX_INVOLVED_IN_CELL_ADHESION	0.95	0.29	0	0	0	not significant
10567	GO_PROTEIN_KINASE_C_SIGNALING	0.95	0.29	0	0	0	not significant
10568	PID_TCR_JNK_PATHWAY	0.95	0.29	0	0	0	not significant
10569	CHR7Q11	0.95	0.28	0	0	0	not significant
10570	CHRXQ13	0.95	0.28	0	0	0	not significant
10571	GO_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL_INVOLVED_IN_CONT	0.95	0.28	0	0	0	not significant
10572	GO_EUKARYOTIC_48S_PREINITIATION_COMPLEX	0.95	0.28	0	0	0	not significant
10573	GO_H4_HISTONE_ACETYLTRANSFERASE_ACTIVITY	0.95	0.28	0	0	0	not significant
10574	GO_LIGAND_GATED_CATION_CHANNEL_ACTIVITY	0.95	0.28	0	0	0	not significant
10575	GO_POSITIVE_REGULATION_OF_PEROXISOME_PROLIFERATOR_ACTIVA	0.95	0.28	0	0	0	not significant
10576	GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	0.95	0.28	0	0	0	not significant
10577	GO_SPHINGOLIPID_BIOSYNTHETIC_PROCESS	0.95	0.28	0	0	0	not significant
10578	HUANG_FOXA2_TARGETS_UP	0.95	0.28	0	0	0	not significant
10579	KANNAN_TP53_TARGETS_DN	0.95	0.28	0	0	0	not significant
10580	LA_MEN1_TARGETS	0.95	0.28	0	0	0	not significant
10581	LAU_APOPTOSIS_CDKN2A_UP	0.95	0.28	0	0	0	not significant
10582	MCCABE_HOXC6_TARGETS_DN	0.95	0.28	0	0	0	not significant
10583	BROWNE_HCMV_INFECTION_2HR_UP	0.95	0.27	0	0	0	not significant
10584	GO_COLLATERAL_SPROUTING	0.95	0.27	0	0	0	not significant
10585	GO_INTERLEUKIN_8_BIOSYNTHETIC_PROCESS	0.95	0.27	0	0	0	not significant
10586	GO_NEGATIVE_REGULATION_OF_SUPRAMOLECULAR_FIBER_ORGANIZA	0.95	0.27	0	0	0	not significant
10587	GO_POSITIVE_REGULATION_OF_GLUCONEOGENESIS	0.95	0.27	0	0	0	not significant
10588	GO_POSITIVE_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION	0.95	0.27	0	0	0	not significant
10589	GO_REGULATION_OF_HEPATOCYTE_PROLIFERATION	0.95	0.27	0	0	0	not significant
10590	GO_URIDYLYLTRANSFERASE_ACTIVITY	0.95	0.27	0	0	0	not significant
10591	GO_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	0.95	0.27	0	0	0	not significant
10592	JEON_SMAD6_TARGETS_UP	0.95	0.27	0	0	0	not significant
10593	KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_DN	0.95	0.27	0	0	0	not significant
10594	PID_TCR_CALCIUM_PATHWAY	0.95	0.27	0	0	0	not significant
10595	TCGA_GLIOBLASTOMA_COPY_NUMBER_DN	0.95	0.27	0	0	0	not significant
10596	WALLACE_PROSTATE_CANCER_RACE_DN	0.95	0.27	0	0	0	not significant
10597	ZWANG_CLASS_2_TRANSIENTLY_INDUCED_BY_EGF	0.95	0.27	0	0	0	not significant
10598	CHR11Q22	0.95	0.26	0	0	0	not significant
10599	CHR3Q11	0.95	0.26	0	0	0	not significant
10600	GO_DEOXYRIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCE	0.95	0.26	0	0	0	not significant
10601	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_5_PRODUCTION	0.95	0.26	0	0	0	not significant
10602	GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATE	0.95	0.26	0	0	0	not significant
10603	GO_PRESYNAPTIC_ENDOCYTOSIS	0.95	0.26	0	0	0	not significant
10604	GO_PROTEIN_PHOSPHATASE_BINDING	0.95	0.26	0	0	0	not significant
10605	GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	0.95	0.26	0	0	0	not significant
10606	GO_RESPONSE_TO_HERBICIDE	0.95	0.26	0	0	0	not significant
10607	GO_SYNAPTIC_VESICLE_RECYCLING	0.95	0.26	0	0	0	not significant
10608	GO_UBIQUITIN_PROTEIN_TRANSFERASE_INHIBITOR_ACTIVITY	0.95	0.26	0	0	0	not significant
10609	GO_VASCULAR_PROCESS_IN_CIRCULATORY_SYSTEM	0.95	0.26	0	0	0	not significant
10610	JACKSON_DNMT1_TARGETS_UP	0.95	0.26	0	0	0	not significant
10611	LIU_NASOPHARYNGEAL_CARCINOMA	0.95	0.26	0	0	0	not significant
10612	REACTOME_ACTIVATION_OF_NOXA_AND_TRANSLOCATION_TO_MITOCH	0.95	0.26	0	0	0	not significant
10613	WANG_IMMORTALIZED_BY_HOXA9_AND_MEIS1_DN	0.95	0.26	0	0	0	not significant
10614	GO_DEVELOPMENTAL_GROWTH_INVOLVED_IN_MORPHOGENESIS	0.95	0.25	0	0	0	not significant
10615	GO_NEPHRIC_DUCT_DEVELOPMENT	0.95	0.25	0	0	0	not significant
10616	GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_BINDING	0.95	0.25	0	0	0	not significant
10617	GO_POSITIVE_REGULATION_OF_DNA_REPLICATION	0.95	0.25	0	0	0	not significant
10618	GO_PYROPTOSIS	0.95	0.25	0	0	0	not significant
10619	GO_SENSORY_ORGAN_MORPHOGENESIS	0.95	0.25	0	0	0	not significant
10620	REACTOME_DISEASES_OF_IMMUNE_SYSTEM	0.95	0.25	0	0	0	not significant
10621	REACTOME_SYNTHESIS_OF_5_EICOSATETRAENOIC_ACIDS	0.95	0.25	0	0	0	not significant
10622	ZHOU_INFLAMMATORY_RESPONSE_LPS_UP	0.95	0.25	0	0	0	not significant
10623	GO_CLATHRIN_LIGHT_CHAIN_BINDING	0.95	0.24	0	0	0	not significant
10624	GO_NEGATIVE_REGULATION_OF_GROWTH	0.95	0.24	0	0	0	not significant
10625	GO_SYNAPSE_ORGANIZATION	0.95	0.24	0	0	0	not significant
10626	HOXA9_DN.V1_UP	0.95	0.24	0	0	0	not significant
10627	GO_TRANSCRIPTION_COREGULATOR_ACTIVITY	0.95	0.23	0	0	0	not significant
10628	TBK1.DF_UP	0.95	0.23	0	0	0	not significant
10629	BONOME_OVARIAN_CANCER_SURVIVAL_SUBOPTIMAL_DEBULKING	0.95	0.21	0	0	0	not significant
10630	GO_CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT	0.95	0.21	0	0	0	not significant
10631	GO_LACTATION	0.96	0.32	0	0	0	not significant
10632	BRACHAT_RESPONSE_TO_CAMPTOTHECIN_UP	0.96	0.31	0	0	0	not significant
10633	FONTAINE_FOLLICULAR_THYROID_ADENOMA_UP	0.96	0.31	0	0	0	not significant
10634	GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALI	0.96	0.31	0	0	0	not significant
10635	GO_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	0.96	0.30	0	0	0	not significant
10636	GO_CALCIUM_ION_IMPORT	0.96	0.30	0	0	0	not significant
10637	GO_EARLY_PHAGOSOME	0.96	0.30	0	0	0	not significant
10638	GO_HEPARIN_BINDING	0.96	0.30	0	0	0	not significant
10639	GO_RESPONSE_TO_RETINOIC_ACID	0.96	0.30	0	0	0	not significant
10640	PID_PRL_SIGNALING_EVENTS_PATHWAY	0.96	0.30	0	0	0	not significant
10641	REACTOME_GLUCURONIDATION	0.96	0.30	0	0	0	not significant
10642	REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI	0.96	0.30	0	0	0	not significant
10643	BIOCARTA_TALL1_PATHWAY	0.96	0.29	0	0	0	not significant
10644	CHR2Q37	0.96	0.29	0	0	0	not significant
10645	GO_ACYLGLYCEROL_O_ACYLTRANSFERASE_ACTIVITY	0.96	0.29	0	0	0	not significant
10646	GO_HISTONE_DEACETYLASE_ACTIVITY_H3_K14_SPECIFIC_	0.96	0.29	0	0	0	not significant
10647	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	0.96	0.29	0	0	0	not significant
10648	GO_NEGATIVE_REGULATION_OF_PROTEIN_OLIGOMERIZATION	0.96	0.29	0	0	0	not significant
10649	GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BINDING	0.96	0.29	0	0	0	not significant
10650	GO_PHOSPHOLIPASE_BINDING	0.96	0.29	0	0	0	not significant
10651	GO_POSITIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_STRESS_IN	0.96	0.29	0	0	0	not significant
10652	GO_POSITIVE_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS	0.96	0.29	0	0	0	not significant
10653	GO_POSITIVE_REGULATION_OF_EXOCYTOSIS	0.96	0.29	0	0	0	not significant
10654	GO_POSTSYNAPTIC_DENSITY_INTRACELLULAR_COMPONENT	0.96	0.29	0	0	0	not significant
10655	GO_PRENYLATION	0.96	0.29	0	0	0	not significant
10656	GRADE_COLON_AND_RECTAL_CANCER_DN	0.96	0.29	0	0	0	not significant
10657	HAN_JNK_SINGALING_UP	0.96	0.29	0	0	0	not significant
10658	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN	0.96	0.29	0	0	0	not significant
10659	CHEMELLO_SOLEUS_VS_EDL_MYOFIBERS_UP	0.96	0.28	0	0	0	not significant
10660	CHR8Q13	0.96	0.28	0	0	0	not significant
10661	GO_CARDIAC_MUSCLE_CELL_PROLIFERATION	0.96	0.28	0	0	0	not significant
10662	GO_EMBRYONIC_AXIS_SPECIFICATION	0.96	0.28	0	0	0	not significant
10663	GO_HISTONE_H3_K9_MODIFICATION	0.96	0.28	0	0	0	not significant
10664	GO_INORGANIC_ANION_EXCHANGER_ACTIVITY	0.96	0.28	0	0	0	not significant
10665	GO_NAD_BIOSYNTHESIS_VIA_NICOTINAMIDE_RIBOSIDE_SALVAGE_PATHW	0.96	0.28	0	0	0	not significant
10666	GO_NEGATIVE_REGULATION_OF_PROTEIN_SUMOYLATION	0.96	0.28	0	0	0	not significant
10667	GO_NEGATIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRAN	0.96	0.28	0	0	0	not significant
10668	GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	0.96	0.28	0	0	0	not significant
10669	GO_PYRIMIDINE_DEOXYRIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTH	0.96	0.28	0	0	0	not significant
10670	GO_REGULATION_OF_DNA_REPAIR	0.96	0.28	0	0	0	not significant

10671	GO_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIM	0.96	0.28	0	0	0	not significant
10672	GO_SEGMENTATION	0.96	0.28	0	0	0	not significant
10673	GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS	0.96	0.28	0	0	0	not significant
10674	GO_SPERM_MOTILITY	0.96	0.28	0	0	0	not significant
10675	GO_STEROL_METABOLIC_PROCESS	0.96	0.28	0	0	0	not significant
10676	GO_WNT_SIGNALING_PATHWAY_INVOLVED_IN_MIDBRAIN_DOPAMINERGI	0.96	0.28	0	0	0	not significant
10677	KIM_WT1_TARGETS_UP	0.96	0.28	0	0	0	not significant
10678	REACTOME_ACETYLCHOLINE_REGULATES_INSULIN_SECRETION	0.96	0.28	0	0	0	not significant
10679	REACTOME_AFLATOXIN_ACTIVATION_AND_DETOXIFICATION	0.96	0.28	0	0	0	not significant
10680	REACTOME_COLLAGEN_CHAIN_TRIMERIZATION	0.96	0.28	0	0	0	not significant
10681	REACTOME_MUCOPOLYSACCHARIDOSES	0.96	0.28	0	0	0	not significant
10682	REACTOME_N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CALRETI	0.96	0.28	0	0	0	not significant
10683	WATANABE_ULCERATIVE_COLITIS_WITH_CANCER_UP	0.96	0.28	0	0	0	not significant
10684	CAMP_UP.V1_DN	0.96	0.27	0	0	0	not significant
10685	CHR20Q13	0.96	0.27	0	0	0	not significant
10686	GO_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTION_BY_P53_CLASS	0.96	0.27	0	0	0	not significant
10687	GO_ENDOCRINE_SYSTEM_DEVELOPMENT	0.96	0.27	0	0	0	not significant
10688	GO_GLUCURONOSYLTRANSFERASE_ACTIVITY	0.96	0.27	0	0	0	not significant
10689	GO_LEUCINE_ZIPPER_DOMAIN_BINDING	0.96	0.27	0	0	0	not significant
10690	GO_NEGATIVE_REGULATION_OF_NEURON_PROJECTION_REGENERATIO	0.96	0.27	0	0	0	not significant
10691	GO_REGULATION_OF_ICOSANOID_SECRETION	0.96	0.27	0	0	0	not significant
10692	GO_REGULATION_OF_JUN_KINASE_ACTIVITY	0.96	0.27	0	0	0	not significant
10693	GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_2_SIGNALING_PATHWAY	0.96	0.27	0	0	0	not significant
10694	GO_SYMPATHETIC_NERVOUS_SYSTEM_DEVELOPMENT	0.96	0.27	0	0	0	not significant
10695	HALLMARK_INTERFERON_ALPHA_RESPONSE	0.96	0.27	0	0	0	not significant
10696	HECKER_IFNB1_TARGETS	0.96	0.27	0	0	0	not significant
10697	KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_AF	0.96	0.27	0	0	0	not significant
10698	REACTOME_DEX_H_BOX_HELICASES_ACTIVATE_TYPE_I_IFN_AND_INFLA	0.96	0.27	0	0	0	not significant
10699	REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	0.96	0.27	0	0	0	not significant
10700	BIOCARTA_PS1_PATHWAY	0.96	0.26	0	0	0	not significant
10701	GO_NEGATIVE_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	0.96	0.26	0	0	0	not significant
10702	SCHEIDEREIT_IKK_INTERACTING_PROTEINS	0.96	0.26	0	0	0	not significant
10703	GO_RECEPTOR_ANTAGONIST_ACTIVITY	0.96	0.25	0	0	0	not significant
10704	JOHNSTONE_PARVB_TARGETS_3_UP	0.96	0.25	0	0	0	not significant
10705	MULLIGHAN_MLL_SIGNATURE_2_DN	0.96	0.25	0	0	0	not significant
10706	GO_CELL_CYCLE_ARREST	0.96	0.23	0	0	0	not significant
10707	ENK_UV_RESPONSE_EPIDERMIS_DN	0.96	0.22	0	0	0	not significant
10708	GO_EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG_HATCHING	0.96	0.22	0	0	0	not significant
10709	GO_CELL_JUNCTION	0.96	0.20	0	0	0	not significant
10710	GO_LOCOMOTION	0.96	0.20	0	0	0	not significant
10711	GO_MRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	0.97	0.33	0	0	0	not significant
10712	BIOCARTA_EGF_PATHWAY	0.97	0.32	0	0	0	not significant
10713	GO_3_5_RNA_HELICASE_ACTIVITY	0.97	0.32	0	0	0	not significant
10714	GO_POSITIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	0.97	0.32	0	0	0	not significant
10715	RAMALHO_STEMNESS_DN	0.97	0.32	0	0	0	not significant
10716	REACTOME_REGULATION_OF_IFNA_SIGNALING	0.97	0.32	0	0	0	not significant
10717	GO_KERATAN_SULFATE_BIOSYNTHETIC_PROCESS	0.97	0.31	0	0	0	not significant
10718	GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_H	0.97	0.31	0	0	0	not significant
10719	GO_REGULATION_OF_PROTEIN_HOMOOLIGOMERIZATION	0.97	0.31	0	0	0	not significant
10720	KEGG_GLYCEROLIPID_METABOLISM	0.97	0.31	0	0	0	not significant
10721	MARIADASON_RESPONSE_TO_BUTYRATE_SULINDAC_6	0.97	0.31	0	0	0	not significant
10722	PRC2_SUZ12_UP.V1_DN	0.97	0.31	0	0	0	not significant
10723	YOSHIOKA_LIVER_CANCER_EARLY_RECURRENCE_UP	0.97	0.31	0	0	0	not significant
10724	BIOCARTA_WNT_PATHWAY	0.97	0.30	0	0	0	not significant
10725	GO_ASTER	0.97	0.30	0	0	0	not significant
10726	GO_CARDIAC_MUSCLE_CELL_CONTRACTION	0.97	0.30	0	0	0	not significant
10727	GO_GLIAL_CELL_DIFFERENTIATION	0.97	0.30	0	0	0	not significant
10728	GO_GROWTH_CONE_PART	0.97	0.30	0	0	0	not significant
10729	GO_NEGATIVE_REGULATION_OF_CILIUM_ASSEMBLY	0.97	0.30	0	0	0	not significant
10730	GO_NEGATIVE_REGULATION_OF_TISSUE_REMODELING	0.97	0.30	0	0	0	not significant
10731	GO_NEUROEPITHELIAL_CELL_DIFFERENTIATION	0.97	0.30	0	0	0	not significant
10732	GO_PROTEIN_IMPORT_INTO_PEROXISOME_MATRIX	0.97	0.30	0	0	0	not significant
10733	GO_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	0.97	0.30	0	0	0	not significant
10734	GO_TRANSLATION_PREINITIATION_COMPLEX	0.97	0.30	0	0	0	not significant
10735	GO_TRIGLYCERIDE_CATABOLIC_PROCESS	0.97	0.30	0	0	0	not significant
10736	KASLER_HDAC7_TARGETS_1_DN	0.97	0.30	0	0	0	not significant
10737	MATZUK_SPERMATOCYTE	0.97	0.30	0	0	0	not significant
10738	NABA_COLLAGENS	0.97	0.30	0	0	0	not significant
10739	PID_LPA4_PATHWAY	0.97	0.30	0	0	0	not significant
10740	CHR22Q11	0.97	0.29	0	0	0	not significant
10741	FAELT_B_CLL_WITH_VH3_21_DN	0.97	0.29	0	0	0	not significant
10742	GO_3_5_EXODEOXYRIBONUCLEASE_ACTIVITY	0.97	0.29	0	0	0	not significant
10743	GO_ACTIN_NUCLEATION	0.97	0.29	0	0	0	not significant
10744	GO_AROMATIC_AMINO_ACID_TRANSPORT	0.97	0.29	0	0	0	not significant
10745	GO_CARBOHYDRATE_DERIVATIVE_CATABOLIC_PROCESS	0.97	0.29	0	0	0	not significant
10746	GO_DERLIN_1_RETROTRANSLOCATION_COMPLEX	0.97	0.29	0	0	0	not significant
10747	GO_EQUATORIAL_MICROTUBULE_ORGANIZING_CENTER	0.97	0.29	0	0	0	not significant
10748	GO_GTPASE_ACTIVATING_PROTEIN_BINDING	0.97	0.29	0	0	0	not significant
10749	GO_HISTONE_H3_K9_ACETYLATION	0.97	0.29	0	0	0	not significant
10750	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	0.97	0.29	0	0	0	not significant
10751	GO_REGULATION_OF_B_CELL_PROLIFERATION	0.97	0.29	0	0	0	not significant
10752	GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	0.97	0.29	0	0	0	not significant
10753	GO_SINGLE_STRANDED_DNA_EXODEOXYRIBONUCLEASE_ACTIVITY	0.97	0.29	0	0	0	not significant
10754	LINDSTEDT_DENDRITIC_CELL_MATURATION_C	0.97	0.29	0	0	0	not significant
10755	MIKKELSEN_IPS_LCP_WITH_H3K4ME3	0.97	0.29	0	0	0	not significant
10756	NRL_DN.V1_UP	0.97	0.29	0	0	0	not significant
10757	REACTOME_HDR_THROUGH_MMEJ_ALT_NHEJ	0.97	0.29	0	0	0	not significant
10758	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM5	0.97	0.29	0	0	0	not significant
10759	FRASOR_RESPONSE_TO_ESTRADIOL_DN	0.97	0.28	0	0	0	not significant
10760	GO_CARDIAC_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	0.97	0.28	0	0	0	not significant
10761	GO_NEGATIVE_REGULATION_OF_AUTOPHAGY_OF_MITOCHONDRION	0.97	0.28	0	0	0	not significant
10762	GO_REGULATION_OF_CELLULAR_CARBOHYDRATE_CATABOLIC_PROCE	0.97	0.28	0	0	0	not significant
10763	HAN_SATB1_TARGETS_DN	0.97	0.28	0	0	0	not significant
10764	IWANAGA_CARCINOGENESIS_BY_KRAS_PTEN_DN	0.97	0.28	0	0	0	not significant
10765	KEGG_TASTE_TRANSDUCTION	0.97	0.28	0	0	0	not significant
10766	REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS	0.97	0.28	0	0	0	not significant
10767	SMIRNOV_RESPONSE_TO_IR_2HR_DN	0.97	0.28	0	0	0	not significant
10768	VANTVEER_BREAST_CANCER_BRCA1_DN	0.97	0.28	0	0	0	not significant
10769	GO_BETA_2_MICROGLOBULIN_BINDING	0.97	0.27	0	0	0	not significant
10770	GO_TAXIS	0.97	0.27	0	0	0	not significant
10771	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP	0.97	0.27	0	0	0	not significant
10772	GRESHOCK_CANCER_COPY_NUMBER_UP	0.97	0.26	0	0	0	not significant
10773	GO_CELL_MORPHOGENESIS_INVOLVED_IN_NEURON_DIFFERENTIATION	0.97	0.24	0	0	0	not significant
10774	GO_ION_HOMEOSTASIS	0.97	0.24	0	0	0	not significant
10775	GO_MULTI_ORGANISM_REPRODUCTIVE_PROCESS	0.97	0.24	0	0	0	not significant
10776	HALLMARK_WNT_BETA_CATENIN_SIGNALING	0.98	0.34	0	0	0	not significant
10777	DING_LUNG_CANCER_BY_MUTATION_RATE	0.98	0.33	0	0	0	not significant
10778	GO_LIGAND_GATED_ION_CHANNEL_ACTIVITY	0.98	0.33	0	0	0	not significant
10779	PID_GMCSF_PATHWAY	0.98	0.33	0	0	0	not significant

10780	BIOCARTA_IL4_PATHWAY	0.98	0.32	0	0	0	not significant
10781	GO_FIBROBLAST_APOPTOTIC_PROCESS	0.98	0.32	0	0	0	not significant
10782	GO_INTERLEUKIN_5_PRODUCTION	0.98	0.32	0	0	0	not significant
10783	GO_PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY	0.98	0.32	0	0	0	not significant
10784	GO_POSITIVE_REGULATION_OF_B_CELL_PROLIFERATION	0.98	0.32	0	0	0	not significant
10785	GO_POSITIVE_REGULATION_OF_DNA_RECOMBINATION	0.98	0.32	0	0	0	not significant
10786	GO_POST_EMBRYONIC_ANIMAL_MORPHOGENESIS	0.98	0.32	0	0	0	not significant
10787	GO_REGULATION_OF_GONAD_DEVELOPMENT	0.98	0.32	0	0	0	not significant
10788	GO_XY_BODY	0.98	0.32	0	0	0	not significant
10789	LEE_LIVER_CANCER_CIPROFIBRATE_UP	0.98	0.32	0	0	0	not significant
10790	BASSO_CD40_SIGNALING_UP	0.98	0.31	0	0	0	not significant
10791	DURAND_STROMA_NS_UP	0.98	0.31	0	0	0	not significant
10792	GO_DETECTION_OF_MECHANICAL_STIMULUS	0.98	0.31	0	0	0	not significant
10793	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERAT	0.98	0.31	0	0	0	not significant
10794	GO_PHOSPHOLIPID_METABOLIC_PROCESS	0.98	0.31	0	0	0	not significant
10795	GO_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	0.98	0.31	0	0	0	not significant
10796	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IM	0.98	0.31	0	0	0	not significant
10797	GO_PRESYNAPTIC_MEMBRANE_ORGANIZATION	0.98	0.31	0	0	0	not significant
10798	GO_PYRIMIDINE_DIMER_REPAIR	0.98	0.31	0	0	0	not significant
10799	GO_SYNCYTIUM_FORMATION	0.98	0.31	0	0	0	not significant
10800	GO_TERPENOID_BIOSYNTHETIC_PROCESS	0.98	0.31	0	0	0	not significant
10801	GO_VENTRICULAR_TRABECULA_MYOCARDIUM_MORPHOGENESIS	0.98	0.31	0	0	0	not significant
10802	KONDO_EZH2_TARGETS	0.98	0.31	0	0	0	not significant
10803	LOPEZ_TRANSLATION_VIA_FN1_SIGNALING	0.98	0.31	0	0	0	not significant
10804	PRC1_BMI_UP.V1_UP	0.98	0.31	0	0	0	not significant
10805	REACTOME_NETRIN_1_SIGNALING	0.98	0.31	0	0	0	not significant
10806	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_DN	0.98	0.31	0	0	0	not significant
10807	WATTEL_AUTONOMOUS_THYROID_ADENOMA_DN	0.98	0.31	0	0	0	not significant
10808	BIOCARTA_CFTR_PATHWAY	0.98	0.30	0	0	0	not significant
10809	FAELT_B_CLL_WITH_VH_REARRANGEMENTS_UP	0.98	0.30	0	0	0	not significant
10810	GO_ACTIVATION_OF_JUN_KINASE_ACTIVITY	0.98	0.30	0	0	0	not significant
10811	GO_CALCIUM_ACTIVATED_POTASSIUM_CHANNEL_ACTIVITY	0.98	0.30	0	0	0	not significant
10812	GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.98	0.30	0	0	0	not significant
10813	GO_DETECTION_OF_STIMULUS	0.98	0.30	0	0	0	not significant
10814	GO_EXECUTION_PHASE_OF_APOPTOSIS	0.98	0.30	0	0	0	not significant
10815	GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT_CONFERRI	0.98	0.30	0	0	0	not significant
10816	GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	0.98	0.30	0	0	0	not significant
10817	GO_NEGATIVE_REGULATION_OF_PROTEIN_POLYMERIZATION	0.98	0.30	0	0	0	not significant
10818	GO_NEGATIVE_REGULATION_OF_VASCULAR_SMOOTH_MUSCLE_CELL_	0.98	0.30	0	0	0	not significant
10819	GO_NODAL_SIGNALING_PATHWAY	0.98	0.30	0	0	0	not significant
10820	GO_POSITIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	0.98	0.30	0	0	0	not significant
10821	GO_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION_INITIATION	0.98	0.30	0	0	0	not significant
10822	GO_REGULATION_OF_SKELETAL_MUSCLE_CONTRACTION	0.98	0.30	0	0	0	not significant
10823	GO_RETINA_LAYER_FORMATION	0.98	0.30	0	0	0	not significant
10824	GO_SODIUM_BICARBONATE_SYMPORTER_ACTIVITY	0.98	0.30	0	0	0	not significant
10825	GO_VITAMIN_CATABOLIC_PROCESS	0.98	0.30	0	0	0	not significant
10826	HALLMARK_APICAL_SURFACE	0.98	0.30	0	0	0	not significant
10827	LEIN_ASTROCYTE_MARKERS	0.98	0.30	0	0	0	not significant
10828	LINDGREN_BLADDER_CANCER_CLUSTER_2B	0.98	0.30	0	0	0	not significant
10829	MARTIN_VIRAL_GPCR_SIGNALING_DN	0.98	0.30	0	0	0	not significant
10830	PID_REG_GR_PATHWAY	0.98	0.30	0	0	0	not significant
10831	RAPA_EARLY_UP.V1_UP	0.98	0.30	0	0	0	not significant
10832	REACTOME_SYNTHESIS_OF_LEUKOTRIENES_LT_AND_EOXINS_EX	0.98	0.30	0	0	0	not significant
10833	REACTOME_TICAM1_TRAF6_DEPENDENT_INDUCTION_OF_TAK1_COMPL	0.98	0.30	0	0	0	not significant
10834	ZHOU_INFLAMMATORY_RESPONSE_FIMA_DN	0.98	0.30	0	0	0	not significant
10835	GO_CHROMAFFIN_GRANULE_MEMBRANE	0.98	0.29	0	0	0	not significant
10836	GO_CORECEPTOR_ACTIVITY_INVOLVED_IN_WNT_SIGNALING_PATHWAY	0.98	0.29	0	0	0	not significant
10837	GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	0.98	0.29	0	0	0	not significant
10838	GO_NEGATIVE_REGULATION_OF_MITOPHAGY	0.98	0.29	0	0	0	not significant
10839	KREPPEL_CD99_TARGETS_DN	0.98	0.29	0	0	0	not significant
10840	NAKAMURA_ADIPOGENESIS_LATE_DN	0.98	0.29	0	0	0	not significant
10841	SANA_TNF_SIGNALING_DN	0.98	0.29	0	0	0	not significant
10842	SU_THYMUS	0.98	0.29	0	0	0	not significant
10843	CAFFAREL_RESPONSE_TO_THC_24HR_3_UP	0.98	0.28	0	0	0	not significant
10844	GO_HISTONE_BINDING	0.98	0.28	0	0	0	not significant
10845	GO_IMMUNE_SYSTEM_DEVELOPMENT	0.98	0.28	0	0	0	not significant
10846	GO_LIPID_GLYCOSYLATION	0.98	0.28	0	0	0	not significant
10847	GO_METAL_ION_HOMEOSTASIS	0.98	0.28	0	0	0	not significant
10848	GO_MRNA_SPLICE_SITE_SELECTION	0.98	0.28	0	0	0	not significant
10849	FEVR_CTNNB1_TARGETS_UP	0.98	0.26	0	0	0	not significant
10850	CHR12Q12	0.99	0.35	0	0	0	not significant
10851	GO_POSTSYNAPSE_ORGANIZATION	0.99	0.35	0	0	0	not significant
10852	GO_CELL_MATRIX_ADHESION	0.99	0.34	0	0	0	not significant
10853	GO_NEGATIVE_REGULATION_OF_GLYCOPROTEIN_BIOSYNTHETIC_PROC	0.99	0.34	0	0	0	not significant
10854	GO_PHOSPHOLIPID_TRANSPORTER_ACTIVITY	0.99	0.34	0	0	0	not significant
10855	GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATIO	0.99	0.34	0	0	0	not significant
10856	GO_SPROUTING_ANGIOGENESIS	0.99	0.34	0	0	0	not significant
10857	CHEBOTAEV_GR_TARGETS_DN	0.99	0.33	0	0	0	not significant
10858	GO_DEOXYRIBONUCLEASE_ACTIVITY	0.99	0.33	0	0	0	not significant
10859	GO_MAP_KINASE_KINASE_KINASE_ACTIVITY	0.99	0.33	0	0	0	not significant
10860	GO_NON_MOTILE_CILIUM_ASSEMBLY	0.99	0.33	0	0	0	not significant
10861	GO_POSITIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_	0.99	0.33	0	0	0	not significant
10862	GO_STEROL_BINDING	0.99	0.33	0	0	0	not significant
10863	KANG_AR_TARGETS_DN	0.99	0.33	0	0	0	not significant
10864	REACTOME_RUNX2_REGULATES_BONE_DEVELOPMENT	0.99	0.33	0	0	0	not significant
10865	SENGUPTA_EBNA1_ANTICORRELATED	0.99	0.33	0	0	0	not significant
10866	ATF2_S_UP.V1_DN	0.99	0.32	0	0	0	not significant
10867	BIOCARTA_IFNA_PATHWAY	0.99	0.32	0	0	0	not significant
10868	BIOCARTA_SKP2E2F_PATHWAY	0.99	0.32	0	0	0	not significant
10869	CHR16Q22	0.99	0.32	0	0	0	not significant
10870	CHR9P13	0.99	0.32	0	0	0	not significant
10871	GO_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	0.99	0.32	0	0	0	not significant
10872	GO_NEGATIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDI	0.99	0.32	0	0	0	not significant
10873	GO_POSITIVE_REGULATION_OF_FATTY_ACID_TRANSPORT	0.99	0.32	0	0	0	not significant
10874	GO_POSTSYNAPTIC_SPECIALIZATION_ASSEMBLY	0.99	0.32	0	0	0	not significant
10875	GO_RETINA_DEVELOPMENT_IN_CAMERA_TYPE_EYE	0.99	0.32	0	0	0	not significant
10876	GO_VACUOLAR_MEMBRANE	0.99	0.32	0	0	0	not significant
10877	HOWLIN_CITED1_TARGETS_1_UP	0.99	0.32	0	0	0	not significant
10878	HUMMERICH_MALIGNANT_SKIN_TUMOR_UP	0.99	0.32	0	0	0	not significant
10879	KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	0.99	0.32	0	0	0	not significant
10880	PARK_APL_PATHOGENESIS_DN	0.99	0.32	0	0	0	not significant
10881	REACTOME_ER_QUALITY_CONTROL_COMPARTMENT_ERQC	0.99	0.32	0	0	0	not significant
10882	REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	0.99	0.32	0	0	0	not significant
10883	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP	0.99	0.32	0	0	0	not significant
10884	WHITESIDE_CISPLATIN_RESISTANCE_DN	0.99	0.32	0	0	0	not significant
10885	WONG_IFNA2_RESISTANCE_DN	0.99	0.32	0	0	0	not significant
10886	ZHANG_TLX_TARGETS_36HR_UP	0.99	0.32	0	0	0	not significant
10887	BIOCARTA_ACH_PATHWAY	0.99	0.31	0	0	0	not significant
10888	GO_ESTABLISHMENT_OF_SISTER_CHROMATID_COHESION	0.99	0.31	0	0	0	not significant

10889	GO_LEUKOTRIENE_METABOLIC_PROCESS	0.99	0.31	0	0	0	not significant
10890	GO_MICROTUBULE_NUCLEATION_BY_INTERPHASE_MICROTUBULE_ORG	0.99	0.31	0	0	0	not significant
10891	GO_NEGATIVE_REGULATION_OF_METALLOPEPTIDASE_ACTIVITY	0.99	0.31	0	0	0	not significant
10892	GO_POSITIVE_REGULATION_OF_ACTIVATED_T_CELL_PROLIFERATION	0.99	0.31	0	0	0	not significant
10893	GO_POSITIVE_REGULATION_OF_VASOCONSTRICTION	0.99	0.31	0	0	0	not significant
10894	GO_PROTEIN_KINASE_COMPLEX	0.99	0.31	0	0	0	not significant
10895	GO_REGULATION_OF_DEVELOPMENTAL_PIGMENTATION	0.99	0.31	0	0	0	not significant
10896	GO_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	0.99	0.31	0	0	0	not significant
10897	GO_REGULATION_OF_SPHINGOLIPID_BIOSYNTHETIC_PROCESS	0.99	0.31	0	0	0	not significant
10898	GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_3_SIGNALING_PATHWAY	0.99	0.31	0	0	0	not significant
10899	REACTOME_CALNEXIN_CALRETICULIN_CYCLE	0.99	0.31	0	0	0	not significant
10900	REACTOME_SEMA4D_MEDIATED_INHIBITION_OF_CELL_ATTACHMENT_AN	0.99	0.31	0	0	0	not significant
10901	GO_BASIC_AMINO_ACID_TRANSPORT	0.99	0.30	0	0	0	not significant
10902	GO_POSITIVE_REGULATION_OF_CENTRIOLE_REPLICATION	0.99	0.30	0	0	0	not significant
10903	GO_REGULATION_OF_CELL_POPULATION_PROLIFERATION	0.99	0.30	0	0	0	not significant
10904	GO_REGULATION_OF_HISTONE_H3_K9_ACETYLATION	0.99	0.30	0	0	0	not significant
10905	MARIADASON_RESPONSE_TO_BUTYRATE_CURCUMIN_SULINDAC_TSA_2	0.99	0.30	0	0	0	not significant
10906	MCDOWELL_ACUTE_LUNG_INJURY_DN	0.99	0.30	0	0	0	not significant
10907	REACTOME_AXON_GUIDANCE	0.99	0.30	0	0	0	not significant
10908	REACTOME_NEUROTOXICITY_OF_CLOSTRIDIUM_TOXINS	0.99	0.30	0	0	0	not significant
10909	STARK_BRAIN_22Q11_DELETION	0.99	0.30	0	0	0	not significant
10910	VEGF_A_UP.V1_UP	0.99	0.30	0	0	0	not significant
10911	GO_PROTEIN_O_LINKED_GLYCOSYLATION	0.99	0.29	0	0	0	not significant
10912	REACTOME_ARYL_HYDROCARBON_RECEPTOR_SIGNALLING	0.99	0.29	0	0	0	not significant
10913	REACTOME_CASPASE_ACTIVATION_VIA_DEPENDENCE_RECEPTORS_IN	0.99	0.28	0	0	0	not significant
10914	CRX_DN.V1_DN	1.00	0.36	0	0	0	not significant
10915	GO_CELLULAR_MODIFIED_AMINO_ACID_METABOLIC_PROCESS	1.00	0.36	0	0	0	not significant
10916	GO_REGULATION_OF_AXONOGENESIS	1.00	0.36	0	0	0	not significant
10917	MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3	1.00	0.36	0	0	0	not significant
10918	BIOCARTA_P27_PATHWAY	1.00	0.35	0	0	0	not significant
10919	DOANE_BREAST_CANCER_CLASSES_DN	1.00	0.35	0	0	0	not significant
10920	GO_ANTIGEN_BINDING	1.00	0.35	0	0	0	not significant
10921	GO_C_TERMINAL_PROTEIN_AMINO_ACID_MODIFICATION	1.00	0.35	0	0	0	not significant
10922	GO_MEMBRANE_DEPOLARIZATION	1.00	0.35	0	0	0	not significant
10923	GO_NEGATIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCES	1.00	0.35	0	0	0	not significant
10924	GO_SPERMATID_DIFFERENTIATION	1.00	0.35	0	0	0	not significant
10925	GO_TRANSCRIPTION_COACTIVATOR_BINDING	1.00	0.35	0	0	0	not significant
10926	HOLLEMAN_ASPARAGINASE_RESISTANCE_B_ALL_DN	1.00	0.35	0	0	0	not significant
10927	OKAWA_NEUROBLASTOMA_1P36_31_DELETION	1.00	0.35	0	0	0	not significant
10928	VANTVEER_BREAST_CANCER_ESR1_UP	1.00	0.35	0	0	0	not significant
10929	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_1	1.00	0.35	0	0	0	not significant
10930	ZWANG_EGF_PERSISTENTLY_DN	1.00	0.35	0	0	0	not significant
10931	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN	1.00	0.34	0	0	0	not significant
10932	CHR1Q22	1.00	0.34	0	0	0	not significant
10933	CHR5Q14	1.00	0.34	0	0	0	not significant
10934	GO_CELL_CELL_ADHESION_MEDIATED_BY_CADHERIN	1.00	0.34	0	0	0	not significant
10935	GO_CELLULAR_ION_HOMEOSTASIS	1.00	0.34	0	0	0	not significant
10936	GO_DENDRITIC_SHAFT	1.00	0.34	0	0	0	not significant
10937	GO_EMBRYONIC_SKELETAL_SYSTEM_DEVELOPMENT	1.00	0.34	0	0	0	not significant
10938	GO_POSITIVE_REGULATION_OF_MUSCLE_CONTRACTION	1.00	0.34	0	0	0	not significant
10939	GO_PREASSEMBLY_OF_GPI_ANCHOR_IN_ER_MEMBRANE	1.00	0.34	0	0	0	not significant
10940	GO_REGULATION_OF_MAP_KINASE_ACTIVITY	1.00	0.34	0	0	0	not significant
10941	GO_REGULATION_OF_PROTEIN_COMPLEX_STABILITY	1.00	0.34	0	0	0	not significant
10942	GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PR	1.00	0.34	0	0	0	not significant
10943	GO_RESPONSE_TO_OSMOTIC_STRESS	1.00	0.34	0	0	0	not significant
10944	GO_SIGNAL_RECOGNITION_PARTICLE	1.00	0.34	0	0	0	not significant
10945	GO_TRANSITION_METAL_ION_HOMEOSTASIS	1.00	0.34	0	0	0	not significant
10946	GO_VACUOLAR_ACIDIFICATION	1.00	0.34	0	0	0	not significant
10947	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN	1.00	0.34	0	0	0	not significant
10948	VANDESLUIS_NORMAL_EMBRYOS_DN	1.00	0.34	0	0	0	not significant
10949	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_36HR	1.00	0.34	0	0	0	not significant
10950	YOSHIOKA_LIVER_CANCER_EARLY_RECURRENCE_DN	1.00	0.34	0	0	0	not significant
10951	AMUNDSON_RESPONSE_TO_ARSENITE	1.00	0.33	0	0	0	not significant
10952	CADWELL_ATG16L1_TARGETS_UP	1.00	0.33	0	0	0	not significant
10953	DAZARD_UV_RESPONSE_CLUSTER_G3	1.00	0.33	0	0	0	not significant
10954	GO_HORMONE_CATABOLIC_PROCESS	1.00	0.33	0	0	0	not significant
10955	GO_NEGATIVE_REGULATION_OF_CELL_AGING	1.00	0.33	0	0	0	not significant
10956	GO_OTIC_VESICLE_DEVELOPMENT	1.00	0.33	0	0	0	not significant
10957	GO_PHOSPHOLIPID_BINDING	1.00	0.33	0	0	0	not significant
10958	GO_REGULATION_OF_BONE_REMODELING	1.00	0.33	0	0	0	not significant
10959	GO_REGULATION_OF_FC_GAMMA_RECEPTOR_SIGNALING_PATHWAY_IN	1.00	0.33	0	0	0	not significant
10960	GO_RHO_PROTEIN_SIGNAL_TRANSDUCTION	1.00	0.33	0	0	0	not significant
10961	GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	1.00	0.33	0	0	0	not significant
10962	LIU_CMYB_TARGETS_UP	1.00	0.33	0	0	0	not significant
10963	PENG_GLUTAMINE_DEPRIVATION_UP	1.00	0.33	0	0	0	not significant
10964	REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES	1.00	0.33	0	0	0	not significant
10965	VALK_AML_CLUSTER_3	1.00	0.33	0	0	0	not significant
10966	CAFFAREL_RESPONSE_TO_THC_8HR_5_UP	1.00	0.32	0	0	0	not significant
10967	GEORGES_TARGETS_OF_MIR192_AND_MIR215	1.00	0.32	0	0	0	not significant
10968	GO_AXON_EXTENSION	1.00	0.32	0	0	0	not significant
10969	GO_BH_DOMAIN_BINDING	1.00	0.32	0	0	0	not significant
10970	GO_ESC_E_Z_COMPLEX	1.00	0.32	0	0	0	not significant
10971	GO_NEGATIVE_REGULATION_OF_FATTY_ACID_OXIDATION	1.00	0.32	0	0	0	not significant
10972	GO_POSITIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENT	1.00	0.32	0	0	0	not significant
10973	GO_POSITIVE_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	1.00	0.32	0	0	0	not significant
10974	GO_REGULATION_OF_ISOTYPE_SWITCHING	1.00	0.32	0	0	0	not significant
10975	JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN	1.00	0.32	0	0	0	not significant
10976	PEDRIOLI_MIR31_TARGETS_DN	1.00	0.32	0	0	0	not significant
10977	REACTOME_DISPLACEMENT_OF_DNA_GLYCOSYLASE_BY_APEX1	1.00	0.32	0	0	0	not significant
10978	GO_INSULIN_LIKE_GROWTH_FACTOR_I_BINDING	1.00	0.31	0	0	0	not significant
10979	GO_LIPOXYGENASE_PATHWAY	1.00	0.31	0	0	0	not significant
10980	GO_POSITIVE_REGULATION_OF_MAST_CELL_ACTIVATION	1.00	0.31	0	0	0	not significant
10981	GO_REGULATION_OF_ANTIGEN_PROCESSING_AND_PRESENTATION	1.00	0.31	0	0	0	not significant
10982	GO_3_PHOSPHOADENOSINE_5_PHOSPHOSULFATE_BINDING	1.00	0.30	0	0	0	not significant
10983	GO_CHROMAFFIN_GRANULE	1.00	0.30	0	0	0	not significant
10984	KORKOLA_EMBRYONAL_CARCINOMA	1.00	0.28	0	0	0	not significant
10985	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	1.01	0.38	0	0	0	not significant
10986	GO_MITOCHONDRIA_ASSOCIATED_ENDOPLASMIC_RETICULUM_MEMBRA	1.01	0.38	0	0	0	not significant
10987	BROWNE_HCMV_INFECTION_24HR_DN	1.01	0.37	0	0	0	not significant
10988	GO_RAB_PROTEIN_SIGNAL_TRANSDUCTION	1.01	0.37	0	0	0	not significant
10989	GO_VACUOLAR_TRANSPORT	1.01	0.37	0	0	0	not significant
10990	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_UP	1.01	0.37	0	0	0	not significant
10991	HATADA_METHYLATED_IN_LUNG_CANCER_UP	1.01	0.37	0	0	0	not significant
10992	PID_IL23_PATHWAY	1.01	0.37	0	0	0	not significant
10993	REACTOME_SMAD2_SMAD3:SMAD4_HETEROTRIMER_REGULATES_TRAN	1.01	0.37	0	0	0	not significant
10994	RUTELLA_RESPONSE_TO_HGF_DN	1.01	0.37	0	0	0	not significant
10995	VALK_AML_CLUSTER_12	1.01	0.37	0	0	0	not significant
10996	BIOCARTA_FBW7_PATHWAY	1.01	0.36	0	0	0	not significant
10997	GO_NEGATIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_	1.01	0.36	0	0	0	not significant

10998	GO_POSITIVE_REGULATION_OF_JUN_KINASE_ACTIVITY	1.01	0.36	0	0	0	not significant
10999	GO_REGULATION_OF_CELLULAR_COMPONENT_MOVEMENT	1.01	0.36	0	0	0	not significant
11000	RODRIGUES_DCC_TARGETS_DN	1.01	0.36	0	0	0	not significant
11001	SNF5_DN.V1_DN	1.01	0.36	0	0	0	not significant
11002	URS_ADIPOCYTE_DIFFERENTIATION_DN	1.01	0.36	0	0	0	not significant
11003	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_UP	1.01	0.35	0	0	0	not significant
11004	ESC_V6.5_UP_EARLY.V1_DN	1.01	0.35	0	0	0	not significant
11005	GO_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLE	1.01	0.35	0	0	0	not significant
11006	GO_HISTONE_H3_ACETYLATION	1.01	0.35	0	0	0	not significant
11007	GO_HISTONE_METHYLTRANSFERASE_ACTIVITY_H3_K9_SPECIFIC_	1.01	0.35	0	0	0	not significant
11008	GO_HISTONE_METHYLTRANSFERASE_COMPLEX	1.01	0.35	0	0	0	not significant
11009	GO_INTERLEUKIN_2_PRODUCTION	1.01	0.35	0	0	0	not significant
11010	GO_LIGAND_GATED_CALCIUM_CHANNEL_ACTIVITY	1.01	0.35	0	0	0	not significant
11011	GO_LYMPHANGIOGENESIS	1.01	0.35	0	0	0	not significant
11012	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	1.01	0.35	0	0	0	not significant
11013	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGIO	1.01	0.35	0	0	0	not significant
11014	GO_REGULATION_OF_RETROGRADE_PROTEIN_TRANSPORT_ER_TO_CY	1.01	0.35	0	0	0	not significant
11015	GO_REPRESSING_TRANSCRIPTION_FACTOR_BINDING	1.01	0.35	0	0	0	not significant
11016	GO_SYMPORTER_ACTIVITY	1.01	0.35	0	0	0	not significant
11017	GO_TYPE_B_PANCREATIC_CELL_DEVELOPMENT	1.01	0.35	0	0	0	not significant
11018	REACTOME_FOXO_MEDIATED_TRANSCRIPTION_OF_CELL_DEATH_GENE	1.01	0.35	0	0	0	not significant
11019	REACTOME_SUMOYLATION_OF_DNA_METHYLATION_PROTEINS	1.01	0.35	0	0	0	not significant
11020	REACTOME_VEGFR2_MEDIATED_VASCULAR_PERMEABILITY	1.01	0.35	0	0	0	not significant
11021	BIOCARTA_PCAF_PATHWAY	1.01	0.34	0	0	0	not significant
11022	GO_ACUTE_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	1.01	0.34	0	0	0	not significant
11023	GO_ADULT_LOCOMOTORY_BEHAVIOR	1.01	0.34	0	0	0	not significant
11024	GO_CEREBELLAR_CORTEX_MORPHOGENESIS	1.01	0.34	0	0	0	not significant
11025	GO_COHESIN_LOADING	1.01	0.34	0	0	0	not significant
11026	GO_DIPEPTIDYL_PEPTIDASE_ACTIVITY	1.01	0.34	0	0	0	not significant
11027	GO_DNA_DAMAGE_INDUCED_PROTEIN_PHOSPHORYLATION	1.01	0.34	0	0	0	not significant
11028	GO_GLYCEROPHOSPHOLIPID_METABOLIC_PROCESS	1.01	0.34	0	0	0	not significant
11029	GO_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLU	1.01	0.34	0	0	0	not significant
11030	GO_METANEPHRIC_NEPHRON_DEVELOPMENT	1.01	0.34	0	0	0	not significant
11031	GO_NEGATIVE_REGULATION_OF_BLOOD_VESSEL_DIAMETER	1.01	0.34	0	0	0	not significant
11032	GO_POSITIVE_REGULATION_OF_DNA_BINDING_TRANSCRIPTION_FACTO	1.01	0.34	0	0	0	not significant
11033	GO_RESPONSE_TO_WATER	1.01	0.34	0	0	0	not significant
11034	GO_SYNAPTIC_VESICLE_MEMBRANE	1.01	0.34	0	0	0	not significant
11035	GO_T_HELPER_2_CELL_DIFFERENTIATION	1.01	0.34	0	0	0	not significant
11036	GO_TYPE_2_IMMUNE_RESPONSE	1.01	0.34	0	0	0	not significant
11037	MEISSNER_NPC_ICP_WITH_H3K4ME3	1.01	0.34	0	0	0	not significant
11038	PID_IL6_7_PATHWAY	1.01	0.34	0	0	0	not significant
11039	REACTOME_NCAM1_INTERACTIONS	1.01	0.34	0	0	0	not significant
11040	REACTOME_SIGNALING_BY_TYPE_1_INSULIN_LIKE_GROWTH_FACTOR_1	1.01	0.34	0	0	0	not significant
11041	ZHENG_GLIOBLASTOMA_PLASTICITY_DN	1.01	0.34	0	0	0	not significant
11042	BRACHAT_RESPONSE_TO_METHOTREXATE_UP	1.01	0.33	0	0	0	not significant
11043	GO_CYCLIC_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	1.01	0.33	0	0	0	not significant
11044	GO_REGULATION_OF_MAMMARY_GLAND_EPITHELIAL_CELL_PROLIFERA	1.01	0.33	0	0	0	not significant
11045	GO_WNT_ACTIVATED_RECEPTOR_ACTIVITY	1.01	0.33	0	0	0	not significant
11046	LIAN_LIPA_TARGETS_6M	1.01	0.33	0	0	0	not significant
11047	MARTIN_NFKB_TARGETS_DN	1.01	0.33	0	0	0	not significant
11048	NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON	1.01	0.33	0	0	0	not significant
11049	PID_INTEGRIN2_PATHWAY	1.01	0.33	0	0	0	not significant
11050	GO_CERAMIDE_1_PHOSPHATE_BINDING	1.01	0.32	0	0	0	not significant
11051	GO_PHOSPHATIDYLINOSITOL_N_ACETYLGLUCOSAMINYLTRANSFERASE_	1.01	0.32	0	0	0	not significant
11052	GO_REGULATION_OF_INORGANIC_ANION_TRANSMEMBRANE_TRANSPO	1.01	0.32	0	0	0	not significant
11053	GO_NEGATIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	1.01	0.31	0	0	0	not significant
11054	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP	1.01	0.30	0	0	0	not significant
11055	GO_GLUCOCORTICOID_METABOLIC_PROCESS	1.01	0.29	0	0	0	not significant
11056	WONG_ADULT_TISSUE_STEM_MODULE	1.02	0.41	0	0	0	not significant
11057	ESC_V6.5_UP_EARLY.V1_UP	1.02	0.39	0	0	0	not significant
11058	GO_CELL_JUNCTION_ASSEMBLY	1.02	0.39	0	0	0	not significant
11059	GO_MEIOTIC_CELL_CYCLE	1.02	0.39	0	0	0	not significant
11060	GO_PEPTIDE_SECRETION	1.02	0.39	0	0	0	not significant
11061	GO_POSITIVE_REGULATION_OF_SECRETION	1.02	0.39	0	0	0	not significant
11062	GO_T_CELL_PROLIFERATION	1.02	0.39	0	0	0	not significant
11063	CAIRO_HEPATOBLASTOMA_CLASSES_DN	1.02	0.38	0	0	0	not significant
11064	CHYLA_CBFA2T3_TARGETS_DN	1.02	0.38	0	0	0	not significant
11065	FOSTER_TOLERANT_MACROPHAGE_DN	1.02	0.38	0	0	0	not significant
11066	GO_LEUKOCYTE_PROLIFERATION	1.02	0.38	0	0	0	not significant
11067	GO_PHOSPHOLIPID_TRANSPORT	1.02	0.38	0	0	0	not significant
11068	GO_RESPONSE_TO_INTERLEUKIN_15	1.02	0.38	0	0	0	not significant
11069	MITSIADES_RESPONSE_TO_APLIDIN_UP	1.02	0.38	0	0	0	not significant
11070	SMID_BREAST_CANCER_RELAPSE_IN_BONE_UP	1.02	0.38	0	0	0	not significant
11071	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_UP	1.02	0.37	0	0	0	not significant
11072	CHR11Q24	1.02	0.37	0	0	0	not significant
11073	CHRXP11	1.02	0.37	0	0	0	not significant
11074	GO_MITOTIC_DNA_INTEGRITY_CHECKPOINT	1.02	0.37	0	0	0	not significant
11075	GO_MOTOR_NEURON_AXON_GUIDANCE	1.02	0.37	0	0	0	not significant
11076	GO_ODONTOGENESIS_OF_DENTIN_CONTAINING_TOOTH	1.02	0.37	0	0	0	not significant
11077	GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION	1.02	0.37	0	0	0	not significant
11078	GO_POSITIVE_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	1.02	0.37	0	0	0	not significant
11079	GO_PRESYNAPTIC_MEMBRANE_ASSEMBLY	1.02	0.37	0	0	0	not significant
11080	GO_RECEPTOR_TYROSINE_KINASE_BINDING	1.02	0.37	0	0	0	not significant
11081	GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	1.02	0.37	0	0	0	not significant
11082	GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_NEUROTRANSMITTE	1.02	0.37	0	0	0	not significant
11083	PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_DN	1.02	0.37	0	0	0	not significant
11084	REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM	1.02	0.37	0	0	0	not significant
11085	RODRIGUES_THYROID_CARCINOMA_DN	1.02	0.37	0	0	0	not significant
11086	BARIS_THYROID_CANCER_DN	1.02	0.36	0	0	0	not significant
11087	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_UP	1.02	0.36	0	0	0	not significant
11088	GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	1.02	0.36	0	0	0	not significant
11089	GO_GLUTAMATE_RECEPTOR_BINDING	1.02	0.36	0	0	0	not significant
11090	GO_NEGATIVE_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA	1.02	0.36	0	0	0	not significant
11091	GO_REGULATION_OF_CHEMOTAXIS	1.02	0.36	0	0	0	not significant
11092	KEGG_P53_SIGNALING_PATHWAY	1.02	0.36	0	0	0	not significant
11093	MARTIN_INTERACT_WITH_HDAC	1.02	0.36	0	0	0	not significant
11094	NIKOLSKY_BREAST_CANCER_8Q23_Q24_AMPLICON	1.02	0.36	0	0	0	not significant
11095	REACTOME_SURFACTANT_METABOLISM	1.02	0.36	0	0	0	not significant
11096	BIOCARTA_BIOPEPTIDES_PATHWAY	1.02	0.35	0	0	0	not significant
11097	GO_MIRNA_MEDIATED_INHIBITION_OF_TRANSLATION	1.02	0.35	0	0	0	not significant
11098	GO_NEGATIVE_REGULATION_OF_EPIDERMAL_GROWTH_FACTOR_ACTI	1.02	0.35	0	0	0	not significant
11099	GO_NEUREXIN_FAMILY_PROTEIN_BINDING	1.02	0.35	0	0	0	not significant
11100	GO_PROTEIN_LOCALIZATION_TO_LYSOSOME	1.02	0.35	0	0	0	not significant
11101	GO_SET1C_COMPASS_COMPLEX	1.02	0.35	0	0	0	not significant
11102	PID_S1P_S1P1_PATHWAY	1.02	0.35	0	0	0	not significant
11103	REACTOME_SYNTHESIS_OF_UDP_N_ACETYL_GLUCOSAMINE	1.02	0.35	0	0	0	not significant
11104	GO_CELLULAR_RESPONSE_TO_OSMOTIC_STRESS	1.02	0.34	0	0	0	not significant
11105	GO_HISTONE_H3_K9_DEMETHYLATION	1.02	0.34	0	0	0	not significant
11106	GO_LAMELLAR_BODY	1.02	0.34	0	0	0	not significant

11107	GO_NATURAL_KILLER_CELL_LECTIN_LIKE_RECEPTOR_BINDING	1.02	0.34	0	0	0	not significant
11108	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	1.02	0.34	0	0	0	not significant
11109	GO_PROTEIN_K11_LINKED_DEUBIQUITINATION	1.02	0.34	0	0	0	not significant
11110	NAKAMURA_ADIPOGENESIS_EARLY_DN	1.02	0.34	0	0	0	not significant
11111	PETRETTO_BLOOD_PRESSURE_DN	1.02	0.34	0	0	0	not significant
11112	REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS	1.02	0.34	0	0	0	not significant
11113	GO_DNA_LIGATION_INVOLVED_IN_DNA_REPAIR	1.02	0.33	0	0	0	not significant
11114	GO_G_QUADRUPLEX_RNA_BINDING	1.02	0.33	0	0	0	not significant
11115	GO_INTERLEUKIN_12_SECRETION	1.02	0.33	0	0	0	not significant
11116	GO_OLIGOSACCHARIDE_BINDING	1.02	0.33	0	0	0	not significant
11117	GO_REGULATION_OF_METALLOENDOPEPTIDASE_ACTIVITY	1.02	0.33	0	0	0	not significant
11118	GO_RESPONSE_TO_MUSCLE_ACTIVITY	1.02	0.33	0	0	0	not significant
11119	PID_P38_ALPHA_BETA_PATHWAY	1.02	0.33	0	0	0	not significant
11120	GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_CYTOKINE_PRODUCTION	1.02	0.32	0	0	0	not significant
11121	GO_NEGATIVE_REGULATION_OF_ARP2_3_COMPLEX_MEDIATED_ACTIN_	1.02	0.32	0	0	0	not significant
11122	GO_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCT	1.03	0.43	0	0	0	not significant
11123	GOZGIT_ESR1_TARGETS_DN	1.03	0.43	0	0	0	not significant
11124	GO_LIPID_BINDING	1.03	0.42	0	0	0	not significant
11125	BERENJENO_TRANSFORMED_BY_RHOA_DN	1.03	0.41	0	0	0	not significant
11126	CHR4P16	1.03	0.41	0	0	0	not significant
11127	GO_ANATOMICAL_STRUCTURE_FORMATION_INVOLVED_IN_MORPHOGE	1.03	0.41	0	0	0	not significant
11128	GO_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	1.03	0.41	0	0	0	not significant
11129	GO_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	1.03	0.41	0	0	0	not significant
11130	GO_MAINTENANCE_OF_LOCATION_IN_CELL	1.03	0.41	0	0	0	not significant
11131	GO_NEGATIVE_REGULATION_OF_DNA_REPAIR	1.03	0.41	0	0	0	not significant
11132	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	1.03	0.41	0	0	0	not significant
11133	KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	1.03	0.41	0	0	0	not significant
11134	AKT_UP_MTOR_DN.V1_DN	1.03	0.40	0	0	0	not significant
11135	BIOCARTA_PPARA_PATHWAY	1.03	0.40	0	0	0	not significant
11136	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	1.03	0.40	0	0	0	not significant
11137	GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERA	1.03	0.40	0	0	0	not significant
11138	GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	1.03	0.40	0	0	0	not significant
11139	GO_RHO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	1.03	0.40	0	0	0	not significant
11140	GO_RNA_POLYMERASE_II_REPRESSING_TRANSCRIPTION_FACTOR_BIND	1.03	0.40	0	0	0	not significant
11141	MULLIGHAN_MLL_SIGNATURE_1_DN	1.03	0.40	0	0	0	not significant
11142	PHONG_TNF_RESPONSE_VIA_P38_PARTIAL	1.03	0.40	0	0	0	not significant
11143	PID_WNT_NONCANONICAL_PATHWAY	1.03	0.40	0	0	0	not significant
11144	SANA_RESPONSE_TO_IFNG_UP	1.03	0.40	0	0	0	not significant
11145	SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_UP	1.03	0.40	0	0	0	not significant
11146	VANTVEER_BREAST_CANCER_METASTASIS_UP	1.03	0.40	0	0	0	not significant
11147	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_UP	1.03	0.39	0	0	0	not significant
11148	CHR6Q15	1.03	0.39	0	0	0	not significant
11149	CHR7Q22	1.03	0.39	0	0	0	not significant
11150	GO_POSITIVE_REGULATION_OF_B_CELL_ACTIVATION	1.03	0.39	0	0	0	not significant
11151	GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	1.03	0.39	0	0	0	not significant
11152	GO_PROTEIN_POLYMERIZATION	1.03	0.39	0	0	0	not significant
11153	GO_PROTON_TRANSPORTING_V_TYPE_ATPASE_COMPLEX	1.03	0.39	0	0	0	not significant
11154	GO_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	1.03	0.39	0	0	0	not significant
11155	GO_SYNAPTIC_SIGNALING	1.03	0.39	0	0	0	not significant
11156	REACTOME_DISASSEMBLY_OF_THE_DESTRUCTION_COMPLEX_AND_RE	1.03	0.39	0	0	0	not significant
11157	GO_HIPPO_SIGNALING	1.03	0.38	0	0	0	not significant
11158	GO_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAININ	1.03	0.38	0	0	0	not significant
11159	GO_REGULATION_OF_MITOPHAGY	1.03	0.38	0	0	0	not significant
11160	REACTOME_CELL_JUNCTION_ORGANIZATION	1.03	0.38	0	0	0	not significant
11161	CHR14Q11	1.03	0.37	0	0	0	not significant
11162	CYCLIN_D1_UP.V1_DN	1.03	0.37	0	0	0	not significant
11163	GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_3_COMPLEX	1.03	0.37	0	0	0	not significant
11164	GO_KERATAN_SULFATE_CATABOLIC_PROCESS	1.03	0.37	0	0	0	not significant
11165	GO_PEPTIDYL_GLUTAMIC_ACID_MODIFICATION	1.03	0.37	0	0	0	not significant
11166	GO_RESPONSE_TO_SALT_STRESS	1.03	0.37	0	0	0	not significant
11167	GO_SOMITE_DEVELOPMENT	1.03	0.37	0	0	0	not significant
11168	GO_UDP_GLYCOSYLTRANSFERASE_ACTIVITY	1.03	0.37	0	0	0	not significant
11169	REACTOME_ASSEMBLY_OF_THE_HIV_VIRION	1.03	0.37	0	0	0	not significant
11170	REACTOME_ASSEMBLY_OF_THE_ORC_COMPLEX_AT_THE_ORIGIN_OF_	1.03	0.37	0	0	0	not significant
11171	REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3:SMAD4_H	1.03	0.37	0	0	0	not significant
11172	WNT_UP.V1_DN	1.03	0.37	0	0	0	not significant
11173	GO_BASIC_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.03	0.36	0	0	0	not significant
11174	GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOP	1.03	0.36	0	0	0	not significant
11175	GO_NEGATIVE_REGULATION_OF_GLYCOLYTIC_PROCESS	1.03	0.36	0	0	0	not significant
11176	GO_OLIGOSACCHARIDE_METABOLIC_PROCESS	1.03	0.36	0	0	0	not significant
11177	GO_PYRIMIDINE_CONTAINING_COMPOUND_SALVAGE	1.03	0.36	0	0	0	not significant
11178	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_TRANS	1.03	0.36	0	0	0	not significant
11179	LANDEMAINE_LUNG_METASTASIS	1.03	0.36	0	0	0	not significant
11180	NOJIMA_SFRP2_TARGETS_UP	1.03	0.36	0	0	0	not significant
11181	REACTOME_CASPASE_MEDIATED_CLEAVAGE_OF_CYTOSKELETAL_PR	1.03	0.36	0	0	0	not significant
11182	ABE_VEGFA_TARGETS	1.03	0.35	0	0	0	not significant
11183	GO_POSITIVE_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_	1.03	0.35	0	0	0	not significant
11184	GO_RESPONSE_TO_STEROL_DEPLETION	1.03	0.35	0	0	0	not significant
11185	IIZUKA_LIVER_CANCER_PROGRESSION_L0_L1_UP	1.03	0.35	0	0	0	not significant
11186	GO_CERAMIDE_1_PHOSPHATE_TRANSPORT	1.03	0.34	0	0	0	not significant
11187	GO_CHEMOREPELLENT_ACTIVITY	1.03	0.34	0	0	0	not significant
11188	GO_REGULATION_OF_ACYL_COA_BIOSYNTHETIC_PROCESS	1.03	0.34	0	0	0	not significant
11189	GO_SULFATION	1.03	0.34	0	0	0	not significant
11190	GO_UBIQUITIN_DEPENDENT_ENDOCYTOSIS	1.03	0.34	0	0	0	not significant
11191	MANTOVANI_NFKB_TARGETS_DN	1.03	0.34	0	0	0	not significant
11192	BIOCARTA_INFLAM_PATHWAY	1.03	0.33	0	0	0	not significant
11193	GO_CONVERGENT_EXTENSION_INVOLVED_IN_GASTRULATION	1.03	0.33	0	0	0	not significant
11194	REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTORS	1.03	0.32	0	0	0	not significant
11195	GO_MULTICELLULAR_ORGANISM_REPRODUCTION	1.04	0.48	0	0	0	not significant
11196	GO_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	1.04	0.44	0	0	0	not significant
11197	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTI	1.04	0.44	0	0	0	not significant
11198	GO_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	1.04	0.44	0	0	0	not significant
11199	GO_SITE_OF_POLARIZED_GROWTH	1.04	0.44	0	0	0	not significant
11200	HALLMARK_COMPLEMENT	1.04	0.44	0	0	0	not significant
11201	CHR12P13	1.04	0.42	0	0	0	not significant
11202	CHR17Q25	1.04	0.42	0	0	0	not significant
11203	FIGUEROA_AML_METHYLATION_CLUSTER_6_UP	1.04	0.42	0	0	0	not significant
11204	GHANDHI_DIRECT_IRRADIATION_UP	1.04	0.42	0	0	0	not significant
11205	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPOR	1.04	0.42	0	0	0	not significant
11206	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	1.04	0.42	0	0	0	not significant
11207	MIKKELSEN_MEF_HCP_WITH_H3K27ME3	1.04	0.42	0	0	0	not significant
11208	RIGGI_EWING_SARCOMA_PROGENITOR_DN	1.04	0.42	0	0	0	not significant
11209	BIDUS_METASTASIS_DN	1.04	0.41	0	0	0	not significant
11210	CSR_LATE_UP.V1_DN	1.04	0.41	0	0	0	not significant
11211	GO_POSITIVE_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	1.04	0.41	0	0	0	not significant
11212	GO_PROTEIN_K63_LINKED_DEUBIQUITINATION	1.04	0.41	0	0	0	not significant
11213	GO_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	1.04	0.41	0	0	0	not significant
11214	GO_SENSORY_PERCEPTION_OF_PAIN	1.04	0.41	0	0	0	not significant
11215	MAGRANGEAS_MULTIPLE_MYELOMA_IGLL_VS_IGLK_UP	1.04	0.41	0	0	0	not significant

11216	RASHI_RESPONSE_TO_IONIZING_RADIATION_2	1.04	0.41	0	0	0	not significant
11217	REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIME	1.04	0.41	0	0	0	not significant
11218	REACTOME_INSULIN_RECEPTOR_RECYCLING	1.04	0.41	0	0	0	not significant
11219	REACTOME_SIGNALING_BY_ERBB4	1.04	0.41	0	0	0	not significant
11220	FERRANDO_LYL1_NEIGHBORS	1.04	0.40	0	0	0	not significant
11221	IKEDA_MIR30_TARGETS_DN	1.04	0.40	0	0	0	not significant
11222	KRAS.PROSTATE_UP.V1_UP	1.04	0.40	0	0	0	not significant
11223	MYC_UP.V1_DN	1.04	0.40	0	0	0	not significant
11224	PID_E2F_PATHWAY	1.04	0.40	0	0	0	not significant
11225	PID_KIT_PATHWAY	1.04	0.40	0	0	0	not significant
11226	REACTOME_NUCLEOBASE_BIOSYNTHESIS	1.04	0.40	0	0	0	not significant
11227	YOKOE_CANCER_TESTIS_ANTIGENS	1.04	0.40	0	0	0	not significant
11228	BIOCARTA_IL2_PATHWAY	1.04	0.39	0	0	0	not significant
11229	GO_CELLULAR_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	1.04	0.39	0	0	0	not significant
11230	GO_NEGATIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNT	1.04	0.39	0	0	0	not significant
11231	GO_STEROL_TRANSPORTER_ACTIVITY	1.04	0.39	0	0	0	not significant
11232	OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_DN	1.04	0.39	0	0	0	not significant
11233	REACTOME_COLLAGEN_FORMATION	1.04	0.39	0	0	0	not significant
11234	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1	1.04	0.39	0	0	0	not significant
11235	CHR15Q23	1.04	0.38	0	0	0	not significant
11236	GO_NEGATIVE_REGULATION_OF_PROTEIN_EXIT_FROM_ENDOPLASMIC_	1.04	0.38	0	0	0	not significant
11237	GO_POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	1.04	0.38	0	0	0	not significant
11238	GO_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATION	1.04	0.38	0	0	0	not significant
11239	GO_REGULATION_OF_PROTEIN_OLIGOMERIZATION	1.04	0.38	0	0	0	not significant
11240	HALLMARK_ANGIOGENESIS	1.04	0.38	0	0	0	not significant
11241	PID_PTP1B_PATHWAY	1.04	0.38	0	0	0	not significant
11242	REACTOME_PI_3K_CASCADE:FGFR3	1.04	0.38	0	0	0	not significant
11243	GO_BLEB_ASSEMBLY	1.04	0.37	0	0	0	not significant
11244	GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT_VIA_HIGH_VOLTAGE	1.04	0.37	0	0	0	not significant
11245	GO_CYCLIC_NUCLEOTIDE_CATABOLIC_PROCESS	1.04	0.37	0	0	0	not significant
11246	GO_HISTONE_DEMETHYLASE_ACTIVITY_H3_K36_SPECIFIC_	1.04	0.37	0	0	0	not significant
11247	GO_PHOSPHATIDYLETHANOLAMINE_BINDING	1.04	0.37	0	0	0	not significant
11248	GO_POSITIVE_REGULATION_OF_TISSUE_REMODELING	1.04	0.37	0	0	0	not significant
11249	GO_POSTSYNAPSE_ASSEMBLY	1.04	0.37	0	0	0	not significant
11250	GO_POSTSYNAPTIC_DENSITY_ASSEMBLY	1.04	0.37	0	0	0	not significant
11251	GO_SERINE_PHOSPHORYLATION_OF_STAT_PROTEIN	1.04	0.37	0	0	0	not significant
11252	GO_SPECTRIN	1.04	0.37	0	0	0	not significant
11253	BIOCARTA_CTLA4_PATHWAY	1.04	0.36	0	0	0	not significant
11254	GO_G_PROTEIN_COUPLED_GLUTAMATE_RECEPTOR_BINDING	1.04	0.36	0	0	0	not significant
11255	GO_RESPONSE_TO_PROTOZOAN	1.04	0.36	0	0	0	not significant
11256	GO_VCP_NPL4_UFD1_AAA_ATPASE_COMPLEX	1.04	0.36	0	0	0	not significant
11257	GO_VENOUS_BLOOD_VESSEL_DEVELOPMENT	1.04	0.36	0	0	0	not significant
11258	GO_CYCLASE_ACTIVITY	1.04	0.35	0	0	0	not significant
11259	GO_HISTONE_H3_K4_DEMETHYLATION	1.04	0.35	0	0	0	not significant
11260	GO_NUCLEOTIDASE_ACTIVITY	1.04	0.35	0	0	0	not significant
11261	MARSON_FOXP3_TARGETS_STIMULATED_DN	1.04	0.35	0	0	0	not significant
11262	REACTOME_KERATAN_SULFATE_DEGRADATION	1.04	0.35	0	0	0	not significant
11263	REACTOME_SERINE_BIOSYNTHESIS	1.04	0.35	0	0	0	not significant
11264	REACTOME_SIGNALING_BY_BMP	1.04	0.35	0	0	0	not significant
11265	GO_LIPID_KINASE_ACTIVITY	1.04	0.34	0	0	0	not significant
11266	GO_NLRP3_INFLAMMASOME_COMPLEX	1.04	0.34	0	0	0	not significant
11267	GO_REGULATION_OF_POSTSYNAPTIC_SPECIALIZATION_ASSEMBLY	1.04	0.34	0	0	0	not significant
11268	MARTENS_TRETINOIN_RESPONSE_DN	1.05	0.53	0	0	0	not significant
11269	GO_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROC	1.05	0.50	0	0	0	not significant
11270	GO_TRANSCRIPTION_COREPRESSOR_ACTIVITY	1.05	0.49	0	0	0	not significant
11271	STK33_NOMO_DN	1.05	0.49	0	0	0	not significant
11272	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF	1.05	0.49	0	0	0	not significant
11273	TIEN_INTESTINE_PROBIOTICS_24HR_DN	1.05	0.48	0	0	0	not significant
11274	GO_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	1.05	0.47	0	0	0	not significant
11275	GO_PLASMA_MEMBRANE_PROTEIN_COMPLEX	1.05	0.47	0	0	0	not significant
11276	GO_REGULATION_OF_LYMPHOCYTE_ACTIVATION	1.05	0.46	0	0	0	not significant
11277	GO_RIBOSOMAL_SUBUNIT	1.05	0.46	0	0	0	not significant
11278	ASTON_MAJOR_DEPRESSIVE_DISORDER_DN	1.05	0.45	0	0	0	not significant
11279	GO_EPITHELIAL_CELL_PROLIFERATION	1.05	0.45	0	0	0	not significant
11280	GO_LOCOMOTORY_BEHAVIOR	1.05	0.45	0	0	0	not significant
11281	BENPORATH_NOS_TARGETS	1.05	0.44	0	0	0	not significant
11282	GO_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	1.05	0.44	0	0	0	not significant
11283	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_2_UP	1.05	0.44	0	0	0	not significant
11284	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP	1.05	0.44	0	0	0	not significant
11285	GO_CYTOPLASMIC_TRANSLATION	1.05	0.43	0	0	0	not significant
11286	GO_EXTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	1.05	0.43	0	0	0	not significant
11287	YAGI_AML_SURVIVAL	1.05	0.43	0	0	0	not significant
11288	CHR3Q21	1.05	0.42	0	0	0	not significant
11289	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_CYAN_UP	1.05	0.42	0	0	0	not significant
11290	GO_AMMONIUM_ION_METABOLIC_PROCESS	1.05	0.42	0	0	0	not significant
11291	GO_POSITIVE_REGULATION_OF_PEPTIDE_HORMONE_SECRETION	1.05	0.42	0	0	0	not significant
11292	GO_REGULATION_OF_MACROPHAGE_MIGRATION	1.05	0.42	0	0	0	not significant
11293	SHIN_B_CELL_LYMPHOMA_CLUSTER_2	1.05	0.42	0	0	0	not significant
11294	STEIN_ESRRA_TARGETS_DN	1.05	0.42	0	0	0	not significant
11295	BIOCARTA_HER2_PATHWAY	1.05	0.41	0	0	0	not significant
11296	GO_INTERLEUKIN_6_PRODUCTION	1.05	0.41	0	0	0	not significant
11297	GO_NEGATIVE_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	1.05	0.41	0	0	0	not significant
11298	GO_POSITIVE_REGULATION_OF_CENTROSOME_DUPLICATION	1.05	0.41	0	0	0	not significant
11299	GO_POSITIVE_REGULATION_OF_HORMONE_SECRETION	1.05	0.41	0	0	0	not significant
11300	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	1.05	0.41	0	0	0	not significant
11301	GO_REGULATION_OF_B_CELL_APOPTOTIC_PROCESS	1.05	0.41	0	0	0	not significant
11302	REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	1.05	0.41	0	0	0	not significant
11303	URS_ADIPOCYTE_DIFFERENTIATION_UP	1.05	0.41	0	0	0	not significant
11304	BCAT_GDS748_DN	1.05	0.40	0	0	0	not significant
11305	BIOCARTA_TFF_PATHWAY	1.05	0.40	0	0	0	not significant
11306	GO_BRUSH_BORDER_MEMBRANE	1.05	0.40	0	0	0	not significant
11307	GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	1.05	0.40	0	0	0	not significant
11308	GO_PANCREAS_DEVELOPMENT	1.05	0.40	0	0	0	not significant
11309	GO_REGULATION_OF_GENE_EXPRESSION_BY_GENETIC_IMPRINTING	1.05	0.40	0	0	0	not significant
11310	GO_TRANSLATION_ELONGATION_FACTOR_ACTIVITY	1.05	0.40	0	0	0	not significant
11311	LOPEZ_MESOTHELIOMA_SURVIVAL_UP	1.05	0.40	0	0	0	not significant
11312	SWEET_KRAS_ONCOGENIC_SIGNATURE	1.05	0.40	0	0	0	not significant
11313	WINZEN_DEGRADED_VIA_KHSRP	1.05	0.40	0	0	0	not significant
11314	CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70	1.05	0.39	0	0	0	not significant
11315	GO_CERAMIDE_TRANSPORT	1.05	0.39	0	0	0	not significant
11316	GO_MITOTIC_DNA_REPLICATION_CHECKPOINT	1.05	0.39	0	0	0	not significant
11317	GO_NADPLUS_KINASE_ACTIVITY	1.05	0.39	0	0	0	not significant
11318	GO_NEUTRAL_LIPID_CATABOLIC_PROCESS	1.05	0.39	0	0	0	not significant
11319	GO_POSITIVE_REGULATION_OF_PROTEIN_GLYCOSYLATION	1.05	0.39	0	0	0	not significant
11320	GO_POST_EMBRYONIC_ANIMAL_ORGAN_MORPHOGENESIS	1.05	0.39	0	0	0	not significant
11321	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	1.05	0.39	0	0	0	not significant
11322	MARIADASON_RESPONSE_TO_BUTYRATE_CURCUMIN_SULINDAC_TSA_8	1.05	0.39	0	0	0	not significant
11323	MEISSNER_BRAIN_HCP_WITH_H3K4ME2	1.05	0.39	0	0	0	not significant
11324	REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	1.05	0.39	0	0	0	not significant

11325	REACTOME_RESOLUTION_OF_D_LOOP_STRUCTURES	1.05	0.39	0	0	0	not significant
11326	SA_MMP_CYTOKINE_CONNECTION	1.05	0.39	0	0	0	not significant
11327	CLAUS_PGR_POSITIVE_MENINGIOMA_DN	1.05	0.38	0	0	0	not significant
11328	GO_CELL_JUNCTION_MAINTENANCE	1.05	0.38	0	0	0	not significant
11329	GO_CYTOPLASM_ORGANIZATION	1.05	0.38	0	0	0	not significant
11330	GO_HISTONE_H3_K36_DEMETHYLATION	1.05	0.38	0	0	0	not significant
11331	GO_CTF18_RFC_LIKE_COMPLEX	1.05	0.37	0	0	0	not significant
11332	GO_MEMBRANE_HYPERPOLARIZATION	1.05	0.37	0	0	0	not significant
11333	GO_NATURAL_KILLER_CELL_CYTOKINE_PRODUCTION	1.05	0.37	0	0	0	not significant
11334	HAHTOLA_MYCOSIS_FUNGOIDES_DN	1.05	0.37	0	0	0	not significant
11335	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX5_UP	1.05	0.37	0	0	0	not significant
11336	TERAMOTO_OPN_TARGETS_CLUSTER_5	1.05	0.37	0	0	0	not significant
11337	YANAGISAWA_LUNG_CANCER_RECURRENCE	1.05	0.37	0	0	0	not significant
11338	GO_HYPERSENSITIVITY	1.05	0.36	0	0	0	not significant
11339	GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVATING_G_PROTEIN_	1.05	0.36	0	0	0	not significant
11340	GO_AMINO_SUGAR_CATABOLIC_PROCESS	1.05	0.35	0	0	0	not significant
11341	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP	1.06	0.59	0	0	0	not significant
11342	ZHANG_TLX_TARGETS_60HR_UP	1.06	0.51	0	0	0	not significant
11343	GO_REGULATION_OF_PEPTIDE_SECRETION	1.06	0.50	0	0	0	not significant
11344	LIU_PROSTATE_CANCER_DN	1.06	0.50	0	0	0	not significant
11345	UDAYAKUMAR_MED1_TARGETS_DN	1.06	0.50	0	0	0	not significant
11346	CHR17Q11	1.06	0.49	0	0	0	not significant
11347	YAGI_AML_WITH_T_8_21_TRANSLOCATION	1.06	0.49	0	0	0	not significant
11348	GO_SKELETAL_SYSTEM_DEVELOPMENT	1.06	0.48	0	0	0	not significant
11349	PEREZ_TP63_TARGETS	1.06	0.48	0	0	0	not significant
11350	WANG_HCP_PROSTATE_CANCER	1.06	0.48	0	0	0	not significant
11351	XU_GH1_AUTOCRINE_TARGETS_DN	1.06	0.48	0	0	0	not significant
11352	CTIP_DN.V1_DN	1.06	0.46	0	0	0	not significant
11353	GO_CATION_CHANNEL_ACTIVITY	1.06	0.46	0	0	0	not significant
11354	GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_	1.06	0.46	0	0	0	not significant
11355	GO_OLIGODENDROCYTE_DIFFERENTIATION	1.06	0.46	0	0	0	not significant
11356	CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_UP	1.06	0.45	0	0	0	not significant
11357	MARTIN_VIRAL_GPCR_SIGNALING_UP	1.06	0.45	0	0	0	not significant
11358	PGF_UP.V1_DN	1.06	0.45	0	0	0	not significant
11359	VERNELL_RETINOBLASTOMA_PATHWAY_UP	1.06	0.45	0	0	0	not significant
11360	PRC2_SUZ12_UP.V1_UP	1.06	0.44	0	0	0	not significant
11361	GO_K63_LINKED_POLYUBIQUITIN_MODIFICATION_DEPENDENT_PROTEIN_	1.06	0.43	0	0	0	not significant
11362	GO_KIDNEY_MORPHOGENESIS	1.06	0.43	0	0	0	not significant
11363	GO_SECONDARY_ALCOHOL_METABOLIC_PROCESS	1.06	0.43	0	0	0	not significant
11364	GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_GERMLI	1.06	0.43	0	0	0	not significant
11365	GO_TIGHT_JUNCTION	1.06	0.43	0	0	0	not significant
11366	KIM_GERMINAL_CENTER_T_HELPER_DN	1.06	0.43	0	0	0	not significant
11367	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPH	1.06	0.43	0	0	0	not significant
11368	REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	1.06	0.43	0	0	0	not significant
11369	CAFFAREL_RESPONSE_TO_THC_UP	1.06	0.42	0	0	0	not significant
11370	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_DN	1.06	0.42	0	0	0	not significant
11371	CHR15Q14	1.06	0.42	0	0	0	not significant
11372	GO_REGULATION_OF_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_P	1.06	0.42	0	0	0	not significant
11373	KANG_CISPLATIN_RESISTANCE_UP	1.06	0.42	0	0	0	not significant
11374	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR1	1.06	0.42	0	0	0	not significant
11375	CHR15Q13	1.06	0.41	0	0	0	not significant
11376	CHR4Q21	1.06	0.41	0	0	0	not significant
11377	GO_ATRIOVENTRICULAR_VALVE_DEVELOPMENT	1.06	0.41	0	0	0	not significant
11378	GO_CELL_FATE_COMMITMENT_INVOLVED_IN_FORMATION_OF_PRIMARY	1.06	0.41	0	0	0	not significant
11379	GO_CELL_PROLIFERATION_IN_FOREBRAIN	1.06	0.41	0	0	0	not significant
11380	GO_CELLULAR_RESPONSE_TO_ETHANOL	1.06	0.41	0	0	0	not significant
11381	GO_COHESIN_COMPLEX	1.06	0.41	0	0	0	not significant
11382	GO_INTERMEDIATE_FILAMENT_BASED_PROCESS	1.06	0.41	0	0	0	not significant
11383	GO_LYMPH_VESSEL_DEVELOPMENT	1.06	0.41	0	0	0	not significant
11384	GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	1.06	0.41	0	0	0	not significant
11385	GO_PROTEIN_DEMANNOSYLATION	1.06	0.41	0	0	0	not significant
11386	GO_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	1.06	0.41	0	0	0	not significant
11387	PID_INTEGRIN3_PATHWAY	1.06	0.41	0	0	0	not significant
11388	GO_NEGATIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	1.06	0.40	0	0	0	not significant
11389	GO_SENSORY_PERCEPTION_OF_TASTE	1.06	0.40	0	0	0	not significant
11390	GO_SPINAL_CORD_MOTOR_NEURON_DIFFERENTIATION	1.06	0.40	0	0	0	not significant
11391	HANSON_HRAS_SIGNALING_VIA_NFKB	1.06	0.40	0	0	0	not significant
11392	KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	1.06	0.40	0	0	0	not significant
11393	SU_PLACENTA	1.06	0.40	0	0	0	not significant
11394	GO_ARYL_HYDROCARBON_RECEPTOR_BINDING	1.06	0.39	0	0	0	not significant
11395	GO_MEMBRANE_DEPOLARIZATION_DURING_ACTION_POTENTIAL	1.06	0.39	0	0	0	not significant
11396	GO_POSTSYNAPTIC_RECYCLING_ENDOSOME	1.06	0.39	0	0	0	not significant
11397	GO_RESPONSE_TO_POTASSIUM_ION	1.06	0.39	0	0	0	not significant
11398	GO_KETONE_CATABOLIC_PROCESS	1.06	0.38	0	0	0	not significant
11399	GO_MEMBRANE_RAFT_DISTRIBUTION	1.06	0.38	0	0	0	not significant
11400	HOLLEMAN_PREDNISOLONE_RESISTANCE_B_ALL_DN	1.06	0.38	0	0	0	not significant
11401	GO_CELL_MIGRATION_INVOLVED_IN_HEART_DEVELOPMENT	1.06	0.37	0	0	0	not significant
11402	GO_FAT_CELL_PROLIFERATION	1.06	0.37	0	0	0	not significant
11403	GO_HYALURONIC_ACID_BINDING	1.06	0.37	0	0	0	not significant
11404	GO_LOCOMOTION_INVOLVED_IN_LOCOMOTORY_BEHAVIOR	1.06	0.37	0	0	0	not significant
11405	GO_NEGATIVE_REGULATION_OF_B_CELL_PROLIFERATION	1.06	0.37	0	0	0	not significant
11406	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_SECRETION	1.06	0.37	0	0	0	not significant
11407	GO_POSITIVE_REGULATION_OF_CELL_POPULATION_PROLIFERATION	1.07	0.55	0	0	0	not significant
11408	BROWNE_HCMV_INFECTION_48HR_DN	1.07	0.54	0	0	0	not significant
11409	GO_REGULATION_OF_CELL_ACTIVATION	1.07	0.53	0	0	0	not significant
11410	TGFB_UP.V1_DN	1.07	0.51	0	0	0	not significant
11411	GO_PASSIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.07	0.50	0	0	0	not significant
11412	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_HEXOSYL_GROUPS	1.07	0.50	0	0	0	not significant
11413	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	1.07	0.49	0	0	0	not significant
11414	GO_REGULATION_OF_OSSIFICATION	1.07	0.49	0	0	0	not significant
11415	GO_REGULATION_OF_PROTEIN_POLYMERIZATION	1.07	0.49	0	0	0	not significant
11416	ESC_V6.5_UP_LATE.V1_UP	1.07	0.48	0	0	0	not significant
11417	GO_DEACETYLASE_ACTIVITY	1.07	0.47	0	0	0	not significant
11418	REACTOME_TRAF6_MEDIATED_INDUCTION_OF_TAK1_COMPLEX_WITHIN	1.07	0.46	0	0	0	not significant
11419	GO_HISTONE_H2A_MONOUBIQUITINATION	1.07	0.45	0	0	0	not significant
11420	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY_P53_CLASS_MED	1.07	0.45	0	0	0	not significant
11421	TAYLOR_METHYLATED_IN_ACUTE_LYMPHOBLASTIC_LEUKEMIA	1.07	0.45	0	0	0	not significant
11422	BHAT_ESR1_TARGETS_NOT_VIA_AKT1_DN	1.07	0.44	0	0	0	not significant
11423	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_VACUOLE	1.07	0.44	0	0	0	not significant
11424	GO_MAINTENANCE_OF_PROTEIN_LOCALIZATION_IN_ORGANELLE	1.07	0.44	0	0	0	not significant
11425	GO_SEMAPHORIN_RECEPTOR_BINDING	1.07	0.44	0	0	0	not significant
11426	MIKKELSEN_IPS_HCP_WITH_H3_UNMETHYLATED	1.07	0.44	0	0	0	not significant
11427	REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	1.07	0.44	0	0	0	not significant
11428	REACTOME_IRS_MEDIATED_SIGNALLING	1.07	0.44	0	0	0	not significant
11429	CHR10P12	1.07	0.43	0	0	0	not significant
11430	GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN	1.07	0.43	0	0	0	not significant
11431	GO_POSITIVE_REGULATION_OF_PROTEIN_POLYMERIZATION	1.07	0.43	0	0	0	not significant
11432	GO_PROTEIN_TARGETING_TO_VACUOLE	1.07	0.43	0	0	0	not significant
11433	GO_REGULATION_OF_GLYCOPROTEIN_BIOSYNTHETIC_PROCESS	1.07	0.43	0	0	0	not significant

11434	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_8	1.07	0.43	0	0	0	not significant
11435	POMEROY_MEDULLOBLASTOMA_PROGNOSIS_UP	1.07	0.43	0	0	0	not significant
11436	REACTOME TRANSCRIPTIONAL REGULATION BY THE AP 2 TFAP2 FA	1.07	0.43	0	0	0	not significant
11437	GO_CYTOPLASMIC_SEQUESTERING_OF_PROTEIN	1.07	0.42	0	0	0	not significant
11438	GO FORMATION OF CYTOPLASMIC TRANSLATION INITIATION COMPLE	1.07	0.42	0	0	0	not significant
11439	GO_GENETIC_IMPRINTING	1.07	0.42	0	0	0	not significant
11440	GO_HISTONE_H2A_UBIQUITINATION	1.07	0.42	0	0	0	not significant
11441	GO INTRINSIC COMPONENT OF POSTSYNAPTIC SPECIALIZATION MEMI	1.07	0.42	0	0	0	not significant
11442	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	1.07	0.42	0	0	0	not significant
11443	GO_OVULATION	1.07	0.42	0	0	0	not significant
11444	GO_REGULATION_OF_ENDOCYTIC_RECYCLING	1.07	0.42	0	0	0	not significant
11445	LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_UP	1.07	0.42	0	0	0	not significant
11446	MAEKAWA_ATF2_TARGETS	1.07	0.42	0	0	0	not significant
11447	XU_GH1_EXOGENOUS_TARGETS_UP	1.07	0.42	0	0	0	not significant
11448	GO_CONVERGENT_EXTENSION	1.07	0.41	0	0	0	not significant
11449	GO_NEURONAL_ION_CHANNEL_CLUSTERING	1.07	0.41	0	0	0	not significant
11450	GO_POSITIVE_REGULATION_OF_KILLING_OF_CELLS_OF_OTHER_ORGAI	1.07	0.41	0	0	0	not significant
11451	MATZUK_MEIOTIC_AND_DNA_REPAIR	1.07	0.41	0	0	0	not significant
11452	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_3	1.07	0.41	0	0	0	not significant
11453	GO_CEREBELLAR_PURKINJE_CELL_LAYER_MORPHOGENESIS	1.07	0.40	0	0	0	not significant
11454	GO_INTERMEDIATE_FILAMENT_ORGANIZATION	1.07	0.40	0	0	0	not significant
11455	GO NEGATIVE REGULATION OF PATHWAY RESTRICTED SMAD PROTI	1.07	0.40	0	0	0	not significant
11456	GO_STEROID_DEHYDROGENASE_ACTIVITY	1.07	0.40	0	0	0	not significant
11457	GO_STRAND_INVASION	1.07	0.40	0	0	0	not significant
11458	GYORFFY_DOXORUBICIN_RESISTANCE	1.07	0.40	0	0	0	not significant
11459	BAKER_HEMATOPOESIS_STAT1_TARGETS	1.07	0.39	0	0	0	not significant
11460	GO_NEGATIVE_REGULATION_OF_T_CELL_DIFFERENTIATION_IN_THYMUS	1.07	0.39	0	0	0	not significant
11461	GO POSITIVE REGULATION OF MAMMARY GLAND EPITHELIAL CELL F	1.07	0.39	0	0	0	not significant
11462	LIU_TOPBP1_TARGETS	1.07	0.39	0	0	0	not significant
11463	GO_ALPHA_BETA_T_CELL_RECEPTOR_COMPLEX	1.07	0.38	0	0	0	not significant
11464	REACTOME_MET_RECEPTOR_RECYCLING	1.07	0.38	0	0	0	not significant
11465	GO_QUATERNARY_AMMONIUM_GROUP_TRANSPORT	1.07	0.37	0	0	0	not significant
11466	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP	1.08	0.66	0	0	0	not significant
11467	GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALI	1.08	0.57	0	0	0	not significant
11468	GO_POSITIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	1.08	0.55	0	0	0	not significant
11469	MEISSNER_NPC_HCP_WITH_H3_UNMETHYLATED	1.08	0.54	0	0	0	not significant
11470	GO_SENSORY_PERCEPTION	1.08	0.52	0	0	0	not significant
11471	GO_RECEPTOR_REGULATOR_ACTIVITY	1.08	0.51	0	0	0	not significant
11472	REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	1.08	0.50	0	0	0	not significant
11473	REACTOME_NEGATIVE_REGULATORS_OF_DDX58_IFIH1_SIGNALING	1.08	0.49	0	0	0	not significant
11474	BILANGES_RAPAMYCIN_SENSITIVE_GENES	1.08	0.48	0	0	0	not significant
11475	BROCKE_APOPTOSIS_REVERSED_BY_IL6	1.08	0.48	0	0	0	not significant
11476	GO_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	1.08	0.48	0	0	0	not significant
11477	GO CYTOPLASMIC PATTERN RECOGNITION RECEPTOR SIGNALING PA	1.08	0.48	0	0	0	not significant
11478	GO_EAR_MORPHOGENESIS	1.08	0.48	0	0	0	not significant
11479	GO_REGULATION_OF_DENDRITE_MORPHOGENESIS	1.08	0.48	0	0	0	not significant
11480	GO_REGULATION_OF_EXTENT_OF_CELL_GROWTH	1.08	0.48	0	0	0	not significant
11481	CHR12Q21	1.08	0.47	0	0	0	not significant
11482	GO_LIPOPROTEIN_METABOLIC_PROCESS	1.08	0.47	0	0	0	not significant
11483	GO_NEGATIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNAI	1.08	0.47	0	0	0	not significant
11484	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	1.08	0.46	0	0	0	not significant
11485	GO_REGULATION_OF_GLUCONEOGENESIS	1.08	0.46	0	0	0	not significant
11486	GO_ACETYLGLUCOSAMINYLTRANSFERASE_ACTIVITY	1.08	0.45	0	0	0	not significant
11487	GO_AMINE_TRANSPORT	1.08	0.45	0	0	0	not significant
11488	GO_CYTOPLASMIC_SEQUESTERING_OF_TRANSCRIPTION_FACTOR	1.08	0.45	0	0	0	not significant
11489	GO_G_PROTEIN_ALPHA_SUBUNIT_BINDING	1.08	0.45	0	0	0	not significant
11490	GO_PROTEIN_ADP_RIBOSYLATION	1.08	0.45	0	0	0	not significant
11491	GO_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATION	1.08	0.45	0	0	0	not significant
11492	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	1.08	0.45	0	0	0	not significant
11493	KEGG_PRIMARY_IMMUNODEFICIENCY	1.08	0.45	0	0	0	not significant
11494	GO_ENDOCARDIAL_CUSHION_DEVELOPMENT	1.08	0.44	0	0	0	not significant
11495	GO POSITIVE REGULATION OF CALCIUM ION DEPENDENT EXOCYTOS	1.08	0.44	0	0	0	not significant
11496	GO_STEROID_DEHYDROGENASE_ACTIVITY_ACTING_ON_THE_CH_OH_GI	1.08	0.44	0	0	0	not significant
11497	GO_STRIATED_MUSCLE_CELL_PROLIFERATION	1.08	0.44	0	0	0	not significant
11498	GO_TRANSFORMING_GROWTH_FACTOR_BETA_BINDING	1.08	0.44	0	0	0	not significant
11499	REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	1.08	0.44	0	0	0	not significant
11500	REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	1.08	0.44	0	0	0	not significant
11501	GO_NEGATIVE_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	1.08	0.43	0	0	0	not significant
11502	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_BETA_SECRETION	1.08	0.43	0	0	0	not significant
11503	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_DN	1.08	0.42	0	0	0	not significant
11504	GO_FAT_SOLUBLE_VITAMIN_METABOLIC_PROCESS	1.08	0.42	0	0	0	not significant
11505	GO_NEGATIVE_REGULATION_OF_MEIOTIC_CELL_CYCLE	1.08	0.42	0	0	0	not significant
11506	GO_SREBP_SIGNALING_PATHWAY	1.08	0.42	0	0	0	not significant
11507	REACTOME_COLLAGEN_BIOSYNTHESIS_AND_MODIFYING_ENZYMES	1.08	0.42	0	0	0	not significant
11508	GO_CHROMATIN_MEDIATED_MAINTENANCE_OF_TRANSCRIPTION	1.08	0.41	0	0	0	not significant
11509	GO_DOUBLE_STRAND_BREAK_REPAIR_VIA_BREAK_INDUCED_REPLICATI	1.08	0.41	0	0	0	not significant
11510	GO NEGATIVE REGULATION OF NITRIC OXIDE BIOSYNTHETIC PROCES	1.08	0.41	0	0	0	not significant
11511	GO_NEGATIVE_REGULATION_OF_RECEPTOR_INTERNALIZATION	1.08	0.41	0	0	0	not significant
11512	GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION_INVOLVED_IN_II	1.08	0.41	0	0	0	not significant
11513	GO_STRIATED_MUSCLE_ATROPHY	1.08	0.41	0	0	0	not significant
11514	REACTOME ACTIVATION OF PUMA AND TRANSLOCATION TO MITOCH	1.08	0.41	0	0	0	not significant
11515	GO_AUTOPHAGY_OF_NUCLEUS	1.08	0.40	0	0	0	not significant
11516	GO_MELANOSOME_ASSEMBLY	1.08	0.40	0	0	0	not significant
11517	GO_VITAMIN_D_METABOLIC_PROCESS	1.08	0.40	0	0	0	not significant
11518	GO_LOCOMOTORY_EXPLORATION_BEHAVIOR	1.08	0.39	0	0	0	not significant
11519	GO_PLATELET_DENSE_GRANULE_LUMEN	1.08	0.39	0	0	0	not significant
11520	GO_REELIN_MEDIATED_SIGNALING_PATHWAY	1.08	0.39	0	0	0	not significant
11521	GO_X_CHROMOSOME	1.08	0.39	0	0	0	not significant
11522	GO_INTERLEUKIN_13_SECRETION	1.08	0.38	0	0	0	not significant
11523	GO_REGULATION_OF_TRIGLYCERIDE_METABOLIC_PROCESS	1.08	0.38	0	0	0	not significant
11524	GO_NEGATIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	1.09	0.74	0	0	0	not significant
11525	LIAO_METASTASIS	1.09	0.62	0	0	0	not significant
11526	BENPORATH_EED_TARGETS	1.09	0.60	0	0	0	not significant
11527	GO CELLULAR PROCESS INVOLVED IN REPRODUCTION IN MULTICELL	1.09	0.59	0	0	0	not significant
11528	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP	1.09	0.57	0	0	0	not significant
11529	GO_GLYCOSYLATION	1.09	0.56	0	0	0	not significant
11530	GO_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	1.09	0.54	0	0	0	not significant
11531	GO_NEGATIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	1.09	0.54	0	0	0	not significant
11532	SENESE_HDAC1_AND_HDAC2_TARGETS_DN	1.09	0.54	0	0	0	not significant
11533	GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	1.09	0.53	0	0	0	not significant
11534	GO_NEURON_PROJECTION_GUIDANCE	1.09	0.53	0	0	0	not significant
11535	GO_RESPONSE_TO_CALCIUM_ION	1.09	0.53	0	0	0	not significant
11536	CHR2Q11	1.09	0.51	0	0	0	not significant
11537	GO_CELL_CELL_JUNCTION_ORGANIZATION	1.09	0.51	0	0	0	not significant
11538	GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	1.09	0.51	0	0	0	not significant
11539	MISSIAGLIA_REGULATED_BY_METHYLATION_UP	1.09	0.51	0	0	0	not significant
11540	SERVITJA_LIVER_HNF1A_TARGETS_DN	1.09	0.51	0	0	0	not significant
11541	BOQUEST_STEM_CELL_UP	1.09	0.49	0	0	0	not significant
11542	GO_IMMUNOGLOBULIN_PRODUCTION_INVOLVED_IN_IMMUNOGLOBULIN_I	1.09	0.49	0	0	0	not significant

11543	GO_MAMMARY_GLAND_EPITHELIUM_DEVELOPMENT	1.09	0.49	0	0	0	not significant
11544	GO_PDZ_DOMAIN_BINDING	1.09	0.49	0	0	0	not significant
11545	GO_POSITIVE_REGULATION_OF_OSSIFICATION	1.09	0.49	0	0	0	not significant
11546	GO_POSITIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	1.09	0.49	0	0	0	not significant
11547	GO_SNARE_BINDING	1.09	0.49	0	0	0	not significant
11548	GO_STEROID_BINDING	1.09	0.49	0	0	0	not significant
11549	GO_T_CELL_DIFFERENTIATION_IN_THYMUS	1.09	0.49	0	0	0	not significant
11550	INGRAM_SHH_TARGETS_DN	1.09	0.49	0	0	0	not significant
11551	CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_DN	1.09	0.48	0	0	0	not significant
11552	GO_INOSITOL_PHOSPHATE_BIOSYNTHETIC_PROCESS	1.09	0.48	0	0	0	not significant
11553	GO_POSITIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PAT	1.09	0.48	0	0	0	not significant
11554	GO_TRANSCRIPTION_COFACTOR_BINDING	1.09	0.48	0	0	0	not significant
11555	MANTOVANI_VIRAL_GPCR_SIGNALING_UP	1.09	0.48	0	0	0	not significant
11556	OLSSON_E2F3_TARGETS_DN	1.09	0.48	0	0	0	not significant
11557	GO_COLLAGEN_TRIMER	1.09	0.47	0	0	0	not significant
11558	GO_ENDOSOME_TO_LYSOSOME_TRANSPORT	1.09	0.47	0	0	0	not significant
11559	GO_ENERGY_HOMEOSTASIS	1.09	0.47	0	0	0	not significant
11560	WILENSKY_RESPONSE_TO_DARAPLADIB	1.09	0.47	0	0	0	not significant
11561	CHR4P15	1.09	0.46	0	0	0	not significant
11562	GO_RESPONSE_TO_ATP	1.09	0.46	0	0	0	not significant
11563	CHR5Q21	1.09	0.45	0	0	0	not significant
11564	GO_CERAMIDE_CATABOLIC_PROCESS	1.09	0.45	0	0	0	not significant
11565	GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_GROWTH	1.09	0.45	0	0	0	not significant
11566	GO_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	1.09	0.45	0	0	0	not significant
11567	GO_TAU_PROTEIN_KINASE_ACTIVITY	1.09	0.45	0	0	0	not significant
11568	WANG_METHYLATED_IN_BREAST_CANCER	1.09	0.45	0	0	0	not significant
11569	BRACHAT_RESPONSE_TO_CISPLATIN	1.09	0.44	0	0	0	not significant
11570	GO_REGULATION_OF_PROTEIN_GLYCOSYLATION	1.09	0.44	0	0	0	not significant
11571	SIMBULAN_PARP1_TARGETS_UP	1.09	0.44	0	0	0	not significant
11572	BIOCARTA_AKAPCENTROSOME_PATHWAY	1.09	0.43	0	0	0	not significant
11573	GO_CELLULAR_RESPONSE_TO_MURAMYL_DIPEPTIDE	1.09	0.43	0	0	0	not significant
11574	GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_BETA_SIGNAL	1.09	0.43	0	0	0	not significant
11575	GO_REGULATION_OF_CALCIUM_ION_IMPORT	1.09	0.43	0	0	0	not significant
11576	BIOCARTA_IL10_PATHWAY	1.09	0.42	0	0	0	not significant
11577	GO_ACTIN_FILAMENT_REORGANIZATION	1.09	0.42	0	0	0	not significant
11578	GO_CERAMIDE_TRANSPORTER_ACTIVITY	1.09	0.42	0	0	0	not significant
11579	GO_EUCHROMATIN	1.09	0.42	0	0	0	not significant
11580	GO_RNA_POLYMERASE_II_INTRONIC_TRANSCRIPTION_REGULATORY_RE	1.09	0.42	0	0	0	not significant
11581	WEBER_METHYLATED_HCP_IN_FIBROBLAST_DN	1.09	0.42	0	0	0	not significant
11582	GO_NEUROBLAST_DIVISION	1.09	0.41	0	0	0	not significant
11583	GO_MITRAL_VALVE_DEVELOPMENT	1.09	0.40	0	0	0	not significant
11584	GO_THALAMUS_DEVELOPMENT	1.09	0.40	0	0	0	not significant
11585	BIOCARTA_NOTCH_PATHWAY	1.09	0.39	0	0	0	not significant
11586	BLALOCK_ALZHEIMERS_DISEASE_UP	1.10	0.93	0	0	0	not significant
11587	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	1.10	0.81	0	0	0	not significant
11588	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP	1.10	0.68	0	0	0	not significant
11589	LIM_MAMMARY_STEM_CELL_DN	1.10	0.64	0	0	0	not significant
11590	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN	1.10	0.63	0	0	0	not significant
11591	GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	1.10	0.62	0	0	0	not significant
11592	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	1.10	0.60	0	0	0	not significant
11593	HADDAD_B_LYMPHOCYTE_PROGENITOR	1.10	0.60	0	0	0	not significant
11594	SMID_BREAST_CANCER_BASAL_DN	1.10	0.60	0	0	0	not significant
11595	MCCABE_BOUND_BY_HOXC6	1.10	0.58	0	0	0	not significant
11596	CHR17Q21	1.10	0.57	0	0	0	not significant
11597	PLASARI_TGFB1_TARGETS_10HR_DN	1.10	0.57	0	0	0	not significant
11598	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12	1.10	0.57	0	0	0	not significant
11599	GO_ENDOPLASMIC_RETICULUM_LUMEN	1.10	0.56	0	0	0	not significant
11600	HUANG_GATA2_TARGETS_UP	1.10	0.55	0	0	0	not significant
11601	GO_G_PROTEIN_COUPLED_RECEPTOR_BINDING	1.10	0.54	0	0	0	not significant
11602	GO_MALE_SEX_DIFFERENTIATION	1.10	0.53	0	0	0	not significant
11603	ZHANG_TLX_TARGETS_UP	1.10	0.53	0	0	0	not significant
11604	GO_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION	1.10	0.52	0	0	0	not significant
11605	GO_SINGLE_FERTILIZATION	1.10	0.52	0	0	0	not significant
11606	GENTILE_UV_RESPONSE_CLUSTER_D6	1.10	0.51	0	0	0	not significant
11607	GO_GLYCOGEN_BIOSYNTHETIC_PROCESS	1.10	0.51	0	0	0	not significant
11608	GO_RECEPTOR_LOCALIZATION_TO_SYNAPSE	1.10	0.51	0	0	0	not significant
11609	GO_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	1.10	0.51	0	0	0	not significant
11610	GO_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	1.10	0.51	0	0	0	not significant
11611	CHR18P11	1.10	0.50	0	0	0	not significant
11612	KRAS.LUNG.BREAST_UP.V1_DN	1.10	0.50	0	0	0	not significant
11613	CHR20P11	1.10	0.49	0	0	0	not significant
11614	GO_POLYSACCHARIDE_BIOSYNTHETIC_PROCESS	1.10	0.49	0	0	0	not significant
11615	REACTOME_SIGNAL_TRANSDUCTION_BY_L1	1.10	0.49	0	0	0	not significant
11616	CHR1Q44	1.10	0.48	0	0	0	not significant
11617	GO_UBIQUITIN_CONJUGATING_ENZYME_BINDING	1.10	0.48	0	0	0	not significant
11618	KEGG_BASAL_CELL_CARCINOMA	1.10	0.48	0	0	0	not significant
11619	REACTOME_ASSEMBLY_AND_CELL_SURFACE_PRESENTATION_OF_NMD	1.10	0.48	0	0	0	not significant
11620	CHR9P24	1.10	0.47	0	0	0	not significant
11621	GO_ENDOPLASMIC_RETICULUM_MANNOSE_TRIMMING	1.10	0.47	0	0	0	not significant
11622	GO_INTERLEUKIN_6_SECRETION	1.10	0.47	0	0	0	not significant
11623	GO_MACROPHAGE_CHEMOTAXIS	1.10	0.47	0	0	0	not significant
11624	GO_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	1.10	0.47	0	0	0	not significant
11625	GO_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	1.10	0.47	0	0	0	not significant
11626	KYNG_RESPONSE_TO_H2O2_VIA_ERCC6	1.10	0.47	0	0	0	not significant
11627	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT	1.10	0.47	0	0	0	not significant
11628	REACTOME_LISTERIA_MONOCYTOGENES_ENTRY_INTO_HOST_CELLS	1.10	0.47	0	0	0	not significant
11629	GO_HEPATOCYTE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWA	1.10	0.46	0	0	0	not significant
11630	GO_NEGATIVE_REGULATION_OF_B_CELL_ACTIVATION	1.10	0.46	0	0	0	not significant
11631	GO_POSITIVE_REGULATION_OF_PROTEIN_OLIGOMERIZATION	1.10	0.46	0	0	0	not significant
11632	GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENT	1.10	0.46	0	0	0	not significant
11633	GO_STEROID_CATABOLIC_PROCESS	1.10	0.46	0	0	0	not significant
11634	REACTOME_LAMININ_INTERACTIONS	1.10	0.46	0	0	0	not significant
11635	GO_CHORION_DEVELOPMENT	1.10	0.45	0	0	0	not significant
11636	GO_LONG_TERM_SYNAPTIC_DEPRESSION	1.10	0.45	0	0	0	not significant
11637	GO_NATURAL_KILLER_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPO	1.10	0.45	0	0	0	not significant
11638	GO_PHOSPHATE_ION_TRANSMEMBRANE_TRANSPORT	1.10	0.45	0	0	0	not significant
11639	REACTOME_DOWNREGULATION_OF_ERBB2:ERBB3_SIGNALING	1.10	0.45	0	0	0	not significant
11640	REACTOME_SHC1_EVENTS_IN_ERBB2_SIGNALING	1.10	0.45	0	0	0	not significant
11641	GO_MANNOSE_BINDING	1.10	0.44	0	0	0	not significant
11642	GO_NEGATIVE_REGULATION_OF_CALCINEURIN_MEDIATED_SIGNALING	1.10	0.44	0	0	0	not significant
11643	GO_OXIDIZED_BASE_LESION_DNA_N_GLYCOSYLASE_ACTIVITY	1.10	0.44	0	0	0	not significant
11644	GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIG	1.10	0.44	0	0	0	not significant
11645	RUNNE_GENDER_EFFECT_UP	1.10	0.44	0	0	0	not significant
11646	GO_CALCIUM_CATION_ANTIPORTER_ACTIVITY	1.10	0.43	0	0	0	not significant
11647	GO_EXTRAEMBRYONIC_MEMBRANE_DEVELOPMENT	1.10	0.43	0	0	0	not significant
11648	GO_MARGINAL_ZONE_B_CELL_DIFFERENTIATION	1.10	0.43	0	0	0	not significant
11649	GO_REGULATION_OF_KILLING_OF_CELLS_OF_OTHER_ORGANISM	1.10	0.43	0	0	0	not significant
11650	GO_REGULATION_OF_POSTSYNAPTIC_NEUROTRANSMITTER_RECEPTO	1.10	0.42	0	0	0	not significant
11651	GO_ADP_RIBOSYLATION_FACTOR_BINDING	1.10	0.41	0	0	0	not significant

11652	GO_CYTOSKELETAL_ANCHORING_AT_PLASMA_MEMBRANE	1.10	0.41	0	0	0	not significant
11653	GO_HISTONE_H3_K27_DEMETHYLATION	1.10	0.40	0	0	0	not significant
11654	GO_REGULATION_OF_BLOOD_VESSEL_REMODELING	1.10	0.40	0	0	0	not significant
11655	GO_PROTEIN_LOCALIZATION_TO_MEMBRANE	1.11	0.74	0	0	0	not significant
11656	GO_LYMPHOCYTE_ACTIVATION	1.11	0.72	0	0	0	not significant
11657	CHR22Q13	1.11	0.63	0	0	0	not significant
11658	GO_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	1.11	0.61	0	0	0	not significant
11659	KEGG_CALCIUM_SIGNALING_PATHWAY	1.11	0.60	0	0	0	not significant
11660	CHR8Q24	1.11	0.59	0	0	0	not significant
11661	CHR11Q13	1.11	0.57	0	0	0	not significant
11662	GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE	1.11	0.56	0	0	0	not significant
11663	RB_P107_DN.V1_UP	1.11	0.56	0	0	0	not significant
11664	GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	1.11	0.55	0	0	0	not significant
11665	GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	1.11	0.54	0	0	0	not significant
11666	REACTOME_NEGATIVE_REGULATION_OF_THE_PI3K_AKT_NETWORK	1.11	0.54	0	0	0	not significant
11667	BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_UP	1.11	0.53	0	0	0	not significant
11668	PID_AP1_PATHWAY	1.11	0.53	0	0	0	not significant
11669	PID_ECADHERIN_NASCENT_AJ_PATHWAY	1.11	0.53	0	0	0	not significant
11670	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_E2F6	1.11	0.53	0	0	0	not significant
11671	GO_BASE_EXCISION_REPAIR	1.11	0.52	0	0	0	not significant
11672	GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_BINDING	1.11	0.52	0	0	0	not significant
11673	GO_REGULATION_OF_POLYSACCHARIDE_METABOLIC_PROCESS	1.11	0.52	0	0	0	not significant
11674	KONDO_PROSTATE_CANCER_WITH_H3K27ME3	1.11	0.52	0	0	0	not significant
11675	WANG_BARRETTS_ESOPHAGUS_UP	1.11	0.52	0	0	0	not significant
11676	GO_DETOXIFICATION	1.11	0.51	0	0	0	not significant
11677	GO_NEGATIVE_REGULATION_OF_GLUCONEOGENESIS	1.11	0.51	0	0	0	not significant
11678	GO_NEGATIVE_REGULATION_OF_SMALL_MOLECULE_METABOLIC_PROC	1.11	0.51	0	0	0	not significant
11679	GO_POSITIVE_REGULATION_OF_CILIUM_ASSEMBLY	1.11	0.51	0	0	0	not significant
11680	VANHARANTA_UTERINE_FIBROID_DN	1.11	0.51	0	0	0	not significant
11681	CHR11Q21	1.11	0.50	0	0	0	not significant
11682	GO_DNA_REPLICATION_INITIATION	1.11	0.50	0	0	0	not significant
11683	GO_PROTEIN_PALMITOYLATION	1.11	0.50	0	0	0	not significant
11684	PID_BMP_PATHWAY	1.11	0.50	0	0	0	not significant
11685	GO_GTP_RHO_BINDING	1.11	0.49	0	0	0	not significant
11686	REACTOME_INLB_MEDIATED_ENTRY_OF_LISTERIA_MONOCYTOGENES_I	1.11	0.49	0	0	0	not significant
11687	GO_APOPTOTIC_PROCESS_INVOLVED_IN_DEVELOPMENT	1.11	0.48	0	0	0	not significant
11688	GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	1.11	0.48	0	0	0	not significant
11689	GO_PROTEIN_POLY_ADP_RIBOSYLATION	1.11	0.48	0	0	0	not significant
11690	GO_METALLOCARBOXYPEPTIDASE_ACTIVITY	1.11	0.47	0	0	0	not significant
11691	GO_PHOSPHATIDYLCHOLINE_METABOLIC_PROCESS	1.11	0.47	0	0	0	not significant
11692	GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_UP	1.11	0.47	0	0	0	not significant
11693	REACTOME_SIGNAL_ATTENUATION	1.11	0.47	0	0	0	not significant
11694	CHR13Q33	1.11	0.46	0	0	0	not significant
11695	GO_EMBRYONIC_PLACENTA_MORPHOGENESIS	1.11	0.46	0	0	0	not significant
11696	GO_EXPORT_ACROSS_PLASMA_MEMBRANE	1.11	0.46	0	0	0	not significant
11697	GO_NEGATIVE_REGULATION_OF_PLATELET_ACTIVATION	1.11	0.46	0	0	0	not significant
11698	GO_PROTEIN_LOCALIZATION_TO_BASOLATERAL_PLASMA_MEMBRANE	1.11	0.46	0	0	0	not significant
11699	GO_CEREBELLAR_PURKINJE_CELL_LAYER_FORMATION	1.11	0.44	0	0	0	not significant
11700	GO_RNA_STRAND_ANNEALING_ACTIVITY	1.11	0.44	0	0	0	not significant
11701	GO_T_CELL_RECEPTOR_BINDING	1.11	0.44	0	0	0	not significant
11702	GO_TRANSFORMING_GROWTH_FACTOR_BETA_ACTIVATION	1.11	0.44	0	0	0	not significant
11703	ONGUSAHA_BRCA1_TARGETS_UP	1.11	0.44	0	0	0	not significant
11704	GO_DENSE_CORE_GRANULE	1.11	0.43	0	0	0	not significant
11705	GO_HISTONE_DEMETHYLASE_ACTIVITY_H3_K27_SPECIFIC_	1.11	0.43	0	0	0	not significant
11706	GO_NEGATIVE_REGULATION_OF_ACTIVIN_RECEPTOR_SIGNALING_PATH	1.11	0.43	0	0	0	not significant
11707	REACTOME_CDC6_ASSOCIATION_WITH_THE_ORC:ORIGIN_COMPLEX	1.11	0.43	0	0	0	not significant
11708	GO_CELLULAR_RESPONSE_TO_POTASSIUM_ION	1.11	0.39	0	0	0	not significant
11709	GO_REGULATION_OF_TRANS_SYNAPTIC_SIGNALING	1.12	0.72	0	0	0	not significant
11710	GO_PROXIMAL_PROMOTER_SEQUENCE_SPECIFIC_DNA_BINDING	1.12	0.69	0	0	0	not significant
11711	GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	1.12	0.69	0	0	0	not significant
11712	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP	1.12	0.68	0	0	0	not significant
11713	STK33_NOMO_UP	1.12	0.68	0	0	0	not significant
11714	GO_REGULATION_OF_T_CELL_ACTIVATION	1.12	0.66	0	0	0	not significant
11715	LEE_DIFFERENTIATING_T_LYMPHOCYTE	1.12	0.63	0	0	0	not significant
11716	PODAR_RESPONSE_TO_ADAPHOSTIN_UP	1.12	0.60	0	0	0	not significant
11717	GO_B_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	1.12	0.58	0	0	0	not significant
11718	GO_G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	1.12	0.58	0	0	0	not significant
11719	GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	1.12	0.58	0	0	0	not significant
11720	HALLMARK_KRAS_SIGNALING_DN	1.12	0.58	0	0	0	not significant
11721	GO_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	1.12	0.57	0	0	0	not significant
11722	GO_CELLULAR_RESPONSE_TO_ALCOHOL	1.12	0.56	0	0	0	not significant
11723	RADAEVA_RESPONSE_TO_IFNA1_UP	1.12	0.56	0	0	0	not significant
11724	GO_LYMPHOCYTE_HOMEOSTASIS	1.12	0.55	0	0	0	not significant
11725	GO_POSITIVE_REGULATION_OF_CELL_KILLING	1.12	0.55	0	0	0	not significant
11726	GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTENTIAL	1.12	0.55	0	0	0	not significant
11727	GO_MEMBRANE_INVAGINATION	1.12	0.54	0	0	0	not significant
11728	GO_NEGATIVE_REGULATION_OF_T_CELL_PROLIFERATION	1.12	0.54	0	0	0	not significant
11729	RELA_DN.V1_DN	1.12	0.54	0	0	0	not significant
11730	GO_REGULATION_OF_CELL_AGING	1.12	0.53	0	0	0	not significant
11731	REACTOME_RUNX1_INTERACTS_WITH_CO_FACTORS_WHOSE_PRECISE_	1.12	0.53	0	0	0	not significant
11732	GO_CELLULAR_RESPONSE_TO_RETINOIC_ACID	1.12	0.52	0	0	0	not significant
11733	GO_GOLGI_TO_ENDOSOME_TRANSPORT	1.12	0.52	0	0	0	not significant
11734	GO_SOMATIC_RECOMBINATION_OF_IMMUNOGLOBULIN_GENE_SEGMENT	1.12	0.52	0	0	0	not significant
11735	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_DN	1.12	0.52	0	0	0	not significant
11736	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_TR	1.12	0.52	0	0	0	not significant
11737	GO_NADPLUS_ADP_RIBOSYLTRANSFERASE_ACTIVITY	1.12	0.51	0	0	0	not significant
11738	GO_POSITIVE_REGULATION_OF_PROTEIN_TARGETING_TO_MITOCHOND	1.12	0.51	0	0	0	not significant
11739	GO_AXONAL_FASCICULATION	1.12	0.50	0	0	0	not significant
11740	GO_ORGANELLE_MEMBRANE_CONTACT_SITE	1.12	0.50	0	0	0	not significant
11741	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	1.12	0.50	0	0	0	not significant
11742	GO_PROTEIN_MANNOSYLATION	1.12	0.50	0	0	0	not significant
11743	GO_PROTEIN_TRANSPORT_WITHIN_PLASMA_MEMBRANE	1.12	0.50	0	0	0	not significant
11744	GO_REGULATION_OF_T_CELL_DIFFERENTIATION_IN_THYMUS	1.12	0.50	0	0	0	not significant
11745	MEISSNER_ES_ICP_WITH_H3K4ME3	1.12	0.50	0	0	0	not significant
11746	BIOCARTA_P53_PATHWAY	1.12	0.49	0	0	0	not significant
11747	GO_CYCLIC_NUCLEOTIDE_BINDING	1.12	0.49	0	0	0	not significant
11748	KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	1.12	0.49	0	0	0	not significant
11749	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_UP	1.12	0.48	0	0	0	not significant
11750	GO_DICARBOXYLIC_ACID_CATABOLIC_PROCESS	1.12	0.48	0	0	0	not significant
11751	GO_METANEPHROS_MORPHOGENESIS	1.12	0.48	0	0	0	not significant
11752	GO_TRANSPOSITION	1.12	0.48	0	0	0	not significant
11753	GO_WHITE_FAT_CELL_DIFFERENTIATION	1.12	0.48	0	0	0	not significant
11754	MATHEW_FANCONI_ANEMIA_GENES	1.12	0.48	0	0	0	not significant
11755	REACTOME_SUMOYLATION_OF_TRANSCRIPTION_FACTORS	1.12	0.48	0	0	0	not significant
11756	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_DN	1.12	0.48	0	0	0	not significant
11757	YANG_BREAST_CANCER_ESR1_DN	1.12	0.48	0	0	0	not significant
11758	GO_PROTEIN_POLYGLUTAMYLATION	1.12	0.47	0	0	0	not significant
11759	GO_REGULATION_OF_DNA_LIGATION	1.12	0.47	0	0	0	not significant
11760	GO_AMMONIUM_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.12	0.46	0	0	0	not significant

11761	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_LIPID_ANTIGEN_V	1.12	0.46	0	0	0	not significant
11762	GO_MEMBRANE_RAFT_LOCALIZATION	1.12	0.46	0	0	0	not significant
11763	GO_MICROFIBRIL	1.12	0.46	0	0	0	not significant
11764	GO_SPONGIOTROPHOBLAST_LAYER_DEVELOPMENT	1.12	0.46	0	0	0	not significant
11765	GO_NEGATIVE_REGULATION_OF_ACTIVATED_T_CELL_PROLIFERATION	1.12	0.45	0	0	0	not significant
11766	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_9	1.12	0.45	0	0	0	not significant
11767	REACTOME_CLEC7A_INFLAMMASOME_PATHWAY	1.12	0.44	0	0	0	not significant
11768	CUI_TCF21_TARGETS_2_DN	1.13	0.86	0	0	0	not significant
11769	GO_SEXUAL_REPRODUCTION	1.13	0.85	0	0	0	not significant
11770	GO_GAMETE_GENERATION	1.13	0.79	0	0	0	not significant
11771	ZHENG_BOUND_BY_FOXP3	1.13	0.78	0	0	0	not significant
11772	HELLER_HDAC_TARGETS_UP	1.13	0.76	0	0	0	not significant
11773	STK33_UP	1.13	0.70	0	0	0	not significant
11774	GO_PLASMA_MEMBRANE_RECEPTOR_COMPLEX	1.13	0.65	0	0	0	not significant
11775	GO_DEVELOPMENTAL_MATURATION	1.13	0.64	0	0	0	not significant
11776	LIU_SOX4_TARGETS_UP	1.13	0.64	0	0	0	not significant
11777	GO_ACTIN_FILAMENT_POLYMERIZATION	1.13	0.63	0	0	0	not significant
11778	GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	1.13	0.62	0	0	0	not significant
11779	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP	1.13	0.59	0	0	0	not significant
11780	GO_CELL_MATURATION	1.13	0.59	0	0	0	not significant
11781	FIGUEROA_AML_METHYLATION_CLUSTER_4_UP	1.13	0.58	0	0	0	not significant
11782	REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	1.13	0.58	0	0	0	not significant
11783	GO_PROTEIN_LOCALIZATION_TO_MICROTUBULE_ORGANIZING_CENTER	1.13	0.56	0	0	0	not significant
11784	KEGG_ACUTE_MYELOID_LEUKEMIA	1.13	0.56	0	0	0	not significant
11785	BIOCARTA_PDGF_PATHWAY	1.13	0.55	0	0	0	not significant
11786	GO_MESONEPHROS_DEVELOPMENT	1.13	0.55	0	0	0	not significant
11787	GO_NEURON_MATURATION	1.13	0.54	0	0	0	not significant
11788	RAMASWAMY_METASTASIS_DN	1.13	0.54	0	0	0	not significant
11789	REACTOME_SIGNALING_BY_NON_RECEPTOR_TYROSINE_KINASES	1.13	0.54	0	0	0	not significant
11790	DARWICHE_PAPILLOMA_RISK_HIGH_VS_LOW_DN	1.13	0.53	0	0	0	not significant
11791	GO_COLLAGEN_BINDING	1.13	0.53	0	0	0	not significant
11792	GO_RESPONSE_TO_ELECTRICAL_STIMULUS	1.13	0.53	0	0	0	not significant
11793	GO_RETROGRADE_TRANSPORT_ENDOSOME_TO_PLASMA_MEMBRANE	1.13	0.53	0	0	0	not significant
11794	KYNG_NORMAL_AGING_DN	1.13	0.53	0	0	0	not significant
11795	REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	1.13	0.53	0	0	0	not significant
11796	GO_COFACTOR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.13	0.52	0	0	0	not significant
11797	GO_ERYTHROCYTE_MATURATION	1.13	0.52	0	0	0	not significant
11798	GO_HISTONE_DEUBIQUITINATION	1.13	0.52	0	0	0	not significant
11799	GO_TRABECULA_MORPHOGENESIS	1.13	0.52	0	0	0	not significant
11800	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN	1.13	0.52	0	0	0	not significant
11801	BOYLAN_MULTIPLE_MYELOMA_D_CLUSTER_UP	1.13	0.51	0	0	0	not significant
11802	CHR6Q24	1.13	0.51	0	0	0	not significant
11803	GO_NEGATIVE_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	1.13	0.51	0	0	0	not significant
11804	GO_PROTEIN_LIPID_COMPLEX	1.13	0.51	0	0	0	not significant
11805	GO_ACROSOME_REACTION	1.13	0.50	0	0	0	not significant
11806	GO_CD40_RECEPTOR_COMPLEX	1.13	0.50	0	0	0	not significant
11807	GO_DYNEIN_LIGHT_INTERMEDIATE_CHAIN_BINDING	1.13	0.50	0	0	0	not significant
11808	GO_MONOVALENT_INORGANIC_ANION_HOMEOSTASIS	1.13	0.50	0	0	0	not significant
11809	PID_LYMPH_ANGIOGENESIS_PATHWAY	1.13	0.50	0	0	0	not significant
11810	REACTOME_NEGATIVE_REGULATION_OF_FGFR1_SIGNALING	1.13	0.50	0	0	0	not significant
11811	BIOCARTA_STAT3_PATHWAY	1.13	0.49	0	0	0	not significant
11812	COURTOIS_SENESCENCE_TRIGGERS	1.13	0.49	0	0	0	not significant
11813	NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_UP	1.13	0.49	0	0	0	not significant
11814	GO_NEGATIVE_REGULATION_OF_TELOMERE_CAPPING	1.13	0.48	0	0	0	not significant
11815	GO_SKELETAL_MUSCLE_CELL_PROLIFERATION	1.13	0.48	0	0	0	not significant
11816	GO_REGULATION_OF_PROTEIN_ADP_RIBOSYLATION	1.13	0.47	0	0	0	not significant
11817	BIOCARTA_ASBCELL_PATHWAY	1.13	0.46	0	0	0	not significant
11818	GO_DETECTION_OF_BIOTIC_STIMULUS	1.13	0.46	0	0	0	not significant
11819	GO_NEGATIVE_REGULATION_OF_BONE_REMODELING	1.13	0.46	0	0	0	not significant
11820	REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	1.13	0.46	0	0	0	not significant
11821	GO_MRNA_EDITING_COMPLEX	1.13	0.45	0	0	0	not significant
11822	PALOMERO_GSI_SENSITIVITY_UP	1.13	0.45	0	0	0	not significant
11823	SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1A	1.13	0.45	0	0	0	not significant
11824	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP	1.14	1.01	0	0	0	not significant
11825	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN	1.14	0.72	0	0	0	not significant
11826	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP	1.14	0.69	0	0	0	not significant
11827	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN	1.14	0.67	0	0	0	not significant
11828	CHR16P11	1.14	0.66	0	0	0	not significant
11829	LAIHO_COLORECTAL_CANCER_SERRATED_DN	1.14	0.65	0	0	0	not significant
11830	GO_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	1.14	0.64	0	0	0	not significant
11831	RAO_BOUND_BY_SALL4	1.14	0.64	0	0	0	not significant
11832	HALLMARK_IL6_JAK_STAT3_SIGNALING	1.14	0.63	0	0	0	not significant
11833	FIGUEROA_AML_METHYLATION_CLUSTER_1_UP	1.14	0.62	0	0	0	not significant
11834	HOLLERN_EMT_BREAST_TUMOR_DN	1.14	0.61	0	0	0	not significant
11835	GO_CHEMICAL_SYNAPTIC_TRANSMISSION_POSTSYNAPTIC	1.14	0.60	0	0	0	not significant
11836	REACTOME_TNF_SIGNALING	1.14	0.60	0	0	0	not significant
11837	BREDEMEYER_RAG_SIGNALING_VIA_ATM_NOT_VIA_NFKB_UP	1.14	0.59	0	0	0	not significant
11838	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	1.14	0.59	0	0	0	not significant
11839	GO_REGULATION_OF_ACTIN_NUCLEATION	1.14	0.58	0	0	0	not significant
11840	REACTOME_CD28_CO_STIMULATION	1.14	0.58	0	0	0	not significant
11841	GO_CLATHRIN_BINDING	1.14	0.57	0	0	0	not significant
11842	GO_DEMETHYLASE_ACTIVITY	1.14	0.57	0	0	0	not significant
11843	GO_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	1.14	0.57	0	0	0	not significant
11844	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM6	1.14	0.57	0	0	0	not significant
11845	GO_G2_DNA_DAMAGE_CHECKPOINT	1.14	0.56	0	0	0	not significant
11846	GO_GAMMA_TUBULIN_BINDING	1.14	0.56	0	0	0	not significant
11847	GO_B_CELL_HOMEOSTASIS	1.14	0.55	0	0	0	not significant
11848	GO_POSITIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	1.14	0.55	0	0	0	not significant
11849	GO_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	1.14	0.55	0	0	0	not significant
11850	GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_BINDING	1.14	0.55	0	0	0	not significant
11851	GO_FILAMENTOUS_ACTIN	1.14	0.53	0	0	0	not significant
11852	GO_METANEPHRIC_NEPHRON_MORPHOGENESIS	1.14	0.53	0	0	0	not significant
11853	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_DIFFERENTIA	1.14	0.53	0	0	0	not significant
11854	GO_REGULATION_OF_TRANSPOSITION	1.14	0.53	0	0	0	not significant
11855	RIZ_ERYTHROID_DIFFERENTIATION_12HR	1.14	0.53	0	0	0	not significant
11856	GO_NEGATIVE_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTIO	1.14	0.52	0	0	0	not significant
11857	GO_AUTOPHAGOSOME_MEMBRANE	1.14	0.51	0	0	0	not significant
11858	GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS	1.14	0.51	0	0	0	not significant
11859	GO_INFLAMMASOME_COMPLEX	1.14	0.51	0	0	0	not significant
11860	GO_MELANOCYTE_DIFFERENTIATION	1.14	0.51	0	0	0	not significant
11861	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	1.14	0.51	0	0	0	not significant
11862	MARIADASON_RESPONSE_TO_BUTYRATE_SULINDAC_4	1.14	0.51	0	0	0	not significant
11863	REACTOME_INTERLEUKIN_6_FAMILY_SIGNALING	1.14	0.51	0	0	0	not significant
11864	REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHES	1.14	0.51	0	0	0	not significant
11865	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP	1.14	0.50	0	0	0	not significant
11866	GO_PARAXIAL_MESODERM_MORPHOGENESIS	1.14	0.50	0	0	0	not significant
11867	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_SECRETION	1.14	0.50	0	0	0	not significant
11868	GO_REGULATION_OF_AMYLOID_BETA_CLEARANCE	1.14	0.50	0	0	0	not significant
11869	GO_REGULATION_OF_TOLERANCE_INDUCTION	1.14	0.50	0	0	0	not significant

11870	REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	1.14	0.50	0	0	0	not significant
11871	UROSEVIC_RESPONSE_TO_IMIQUIMOD	1.14	0.50	0	0	0	not significant
11872	GO_CELLULAR_RESPONSE_TO_SALT_STRESS	1.14	0.49	0	0	0	not significant
11873	GO_CORPUS_CALLOSUM_MORPHOGENESIS	1.14	0.49	0	0	0	not significant
11874	GO_DNA_CLAMP_LOADER_ACTIVITY	1.14	0.49	0	0	0	not significant
11875	REACTOME_IRAK2_MEDIATED_ACTIVATION_OF_TAK1_COMPLEX	1.14	0.49	0	0	0	not significant
11876	GO_BETA_GALACTOSIDASE_ACTIVITY	1.14	0.48	0	0	0	not significant
11877	GO_MANNOSE_METABOLIC_PROCESS	1.14	0.48	0	0	0	not significant
11878	GO_POLE_PLASM	1.14	0.48	0	0	0	not significant
11879	GO_DNA_ENDOREDUPLICATION	1.14	0.47	0	0	0	not significant
11880	REACTOME_PI_3K_CASCADE:FGFR2	1.14	0.46	0	0	0	not significant
11881	GO_SEQUENCE_SPECIFIC_DNA_BINDING	1.15	0.99	0	0	0	not significant
11882	GO_INTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	1.15	0.97	0	0	0	not significant
11883	RICKMAN_METASTASIS_UP	1.15	0.87	0	0	0	not significant
11884	GO_T_CELL_ACTIVATION	1.15	0.80	0	0	0	not significant
11885	GO_RECEPTOR_COMPLEX	1.15	0.77	0	0	0	not significant
11886	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN	1.15	0.76	0	0	0	not significant
11887	STK33_SKM_UP	1.15	0.74	0	0	0	not significant
11888	COLDREN_GEFITINIB_RESISTANCE_DN	1.15	0.71	0	0	0	not significant
11889	IVANOVA_HEMATOPOIESIS_STEM_CELL_LONG_TERM	1.15	0.71	0	0	0	not significant
11890	BROWNE_HCMV_INFECTION_18HR_DN	1.15	0.69	0	0	0	not significant
11891	GO_MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS	1.15	0.69	0	0	0	not significant
11892	AKT_UP.V1_DN	1.15	0.66	0	0	0	not significant
11893	GO_CELLULAR_TRANSITION_METAL_ION_HOMEOSTASIS	1.15	0.65	0	0	0	not significant
11894	GO_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	1.15	0.64	0	0	0	not significant
11895	BRUINS_UVC_RESPONSE_MIDDLE	1.15	0.63	0	0	0	not significant
11896	GO_LYSOSOMAL_TRANSPORT	1.15	0.63	0	0	0	not significant
11897	REACTOME_RAB_GERANYLGERANYLATION	1.15	0.61	0	0	0	not significant
11898	CHR13Q12	1.15	0.60	0	0	0	not significant
11899	GO_SOLUTE_CATION_SYMPORTER_ACTIVITY	1.15	0.60	0	0	0	not significant
11900	GO_SYNTAXIN_BINDING	1.15	0.60	0	0	0	not significant
11901	GO_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	1.15	0.58	0	0	0	not significant
11902	SENESE_HDAC2_TARGETS_DN	1.15	0.58	0	0	0	not significant
11903	CHR2P21	1.15	0.57	0	0	0	not significant
11904	GO_MANNOSYLATION	1.15	0.57	0	0	0	not significant
11905	GO_CYCLIN_DEPENDENT_PROTEIN_SERINE_THREONINE_KINASE_REGUL	1.15	0.56	0	0	0	not significant
11906	GO_PROTEIN_ADP_RIBOSYLASE_ACTIVITY	1.15	0.56	0	0	0	not significant
11907	LIAN_LIPA_TARGETS_3M	1.15	0.56	0	0	0	not significant
11908	BIOCARTA_EPO_PATHWAY	1.15	0.55	0	0	0	not significant
11909	GO_REGULATION_OF_MORPHOGENESIS_OF_A_BRANCHING_STRUCTUR	1.15	0.55	0	0	0	not significant
11910	GO_SOLUTE_SODIUM_SYMPORTER_ACTIVITY	1.15	0.55	0	0	0	not significant
11911	LOPES_METHYLATED_IN_COLON_CANCER_DN	1.15	0.55	0	0	0	not significant
11912	REACTOME_DOWNREGULATION_OF_SMAD2_3:SMAD4_TRANSCRIPTION	1.15	0.55	0	0	0	not significant
11913	GO_INTERLEUKIN_6_MEDIATED_SIGNALING_PATHWAY	1.15	0.54	0	0	0	not significant
11914	GO_NEGATIVE_REGULATION_OF_ERAD_PATHWAY	1.15	0.54	0	0	0	not significant
11915	GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	1.15	0.54	0	0	0	not significant
11916	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_PINK_DN	1.15	0.53	0	0	0	not significant
11917	GO_GAMMA_TUBULIN_LARGE_COMPLEX	1.15	0.53	0	0	0	not significant
11918	GO_INOSITOL_1_4_5_TRISPHOSPHATE_BINDING	1.15	0.53	0	0	0	not significant
11919	GO_NEGATIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_	1.15	0.53	0	0	0	not significant
11920	GO_OPSONIN_BINDING	1.15	0.53	0	0	0	not significant
11921	GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_I	1.15	0.51	0	0	0	not significant
11922	GO_REGULATION_OF_ISOTYPE_SWITCHING_TO_IGE_ISOTYPES	1.15	0.51	0	0	0	not significant
11923	GO_RETINA_VASCULATURE_DEVELOPMENT_IN_CAMERA_TYPE_EYE	1.15	0.51	0	0	0	not significant
11924	GO_GLYCOSIDE_CATABOLIC_PROCESS	1.15	0.50	0	0	0	not significant
11925	REACTOME_LIPOPHAGY	1.15	0.50	0	0	0	not significant
11926	REACTOME_PI_3K_CASCADE:FGFR4	1.15	0.50	0	0	0	not significant
11927	GO_DEAD_H_BOX_RNA_HELICASE_BINDING	1.15	0.49	0	0	0	not significant
11928	GO_REGULATION_OF_GASTRIC_ACID_SECRETION	1.15	0.49	0	0	0	not significant
11929	GO_UBIQUITIN_LIGASE_INHIBITOR_ACTIVITY	1.15	0.49	0	0	0	not significant
11930	TCGA_GLIOBLASTOMA_MUTATED	1.15	0.49	0	0	0	not significant
11931	GO_DOUBLE_STRANDED_DNA_BINDING	1.16	1.05	0	0	0	not significant
11932	BASAKI_YBX1_TARGETS_DN	1.16	0.84	0	0	0	not significant
11933	GO_SECRETORY_GRANULE_MEMBRANE	1.16	0.77	0	0	0	not significant
11934	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	1.16	0.75	0	0	0	not significant
11935	GO_POSITIVE_REGULATION_OF_PEPTIDE_SECRETION	1.16	0.74	0	0	0	not significant
11936	GO_REGIONALIZATION	1.16	0.74	0	0	0	not significant
11937	HALLMARK_TNFA_SIGNALING_VIA_NFKB	1.16	0.71	0	0	0	not significant
11938	MATZUK_SPERMATOZOA	1.16	0.70	0	0	0	not significant
11939	GO_INTERMEDIATE_FILAMENT_CYTOSKELETON	1.16	0.67	0	0	0	not significant
11940	MCBRYAN_PUBERTAL_BREAST_3_4WK_UP	1.16	0.67	0	0	0	not significant
11941	REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CC	1.16	0.66	0	0	0	not significant
11942	CHR17P11	1.16	0.65	0	0	0	not significant
11943	WNT_UP.V1_UP	1.16	0.65	0	0	0	not significant
11944	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQUOISE_	1.16	0.64	0	0	0	not significant
11945	GO_ADHERENS_JUNCTION_ORGANIZATION	1.16	0.64	0	0	0	not significant
11946	CHR3P22	1.16	0.63	0	0	0	not significant
11947	GO_EMBRYONIC_PATTERN_SPECIFICATION	1.16	0.61	0	0	0	not significant
11948	GO_MESODERM_DEVELOPMENT	1.16	0.61	0	0	0	not significant
11949	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	1.16	0.61	0	0	0	not significant
11950	GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	1.16	0.61	0	0	0	not significant
11951	SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN	1.16	0.61	0	0	0	not significant
11952	GO_ACROSOMAL_VESICLE	1.16	0.60	0	0	0	not significant
11953	GO_INTRINSIC_COMPONENT_OF_SYNAPTIC_MEMBRANE	1.16	0.60	0	0	0	not significant
11954	CHR1P21	1.16	0.59	0	0	0	not significant
11955	GO_FICOLIN_1_RICH_GRANULE_MEMBRANE	1.16	0.59	0	0	0	not significant
11956	GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_NONHOM	1.16	0.59	0	0	0	not significant
11957	GO_NEGATIVE_REGULATION_OF_AXON_EXTENSION	1.16	0.58	0	0	0	not significant
11958	GO_POSITIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	1.16	0.58	0	0	0	not significant
11959	GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	1.16	0.58	0	0	0	not significant
11960	GO_RESPONSE_TO_INTERLEUKIN_7	1.16	0.58	0	0	0	not significant
11961	NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	1.16	0.57	0	0	0	not significant
11962	GO_POSITIVE_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	1.16	0.56	0	0	0	not significant
11963	GO_RESPONSE_TO_MITOCHONDRIAL_DEPOLARISATION	1.16	0.56	0	0	0	not significant
11964	REACTOME_CYTOSOLIC_IRON_SULFUR_CLUSTER_ASSEMBLY	1.16	0.56	0	0	0	not significant
11965	GO_ENTRY_OF_BACTERIUM_INTO_HOST_CELL	1.16	0.53	0	0	0	not significant
11966	GO_PEPTIDYL_SERINE_AUTOPHOSPHORYLATION	1.16	0.53	0	0	0	not significant
11967	GO_REGULATION_OF_EXCITATORY_SYNAPSE_ASSEMBLY	1.16	0.53	0	0	0	not significant
11968	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_S	1.16	0.53	0	0	0	not significant
11969	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTGREEN_	1.16	0.52	0	0	0	not significant
11970	GO_SENSORY_PERCEPTION_OF_BITTER_TASTE	1.16	0.52	0	0	0	not significant
11971	GO_VOLTAGE_GATED_SODIUM_CHANNEL_ACTIVITY	1.16	0.52	0	0	0	not significant
11972	IRITANI_MAD1_TARGETS_UP	1.16	0.52	0	0	0	not significant
11973	KEGG_NON_HOMOLOGOUS_END_JOINING	1.16	0.52	0	0	0	not significant
11974	REACTOME_PYRIMIDINE_CATABOLISM	1.16	0.52	0	0	0	not significant
11975	GO_MRNA_3_END_PROCESSING_BY_STEM_LOOP_BINDING_AND_CLEAV	1.16	0.51	0	0	0	not significant
11976	GO_REGULATION_OF_PROTEIN_KINASE_A_SIGNALING	1.16	0.51	0	0	0	not significant
11977	GO_REGULATION_OF_TYPE_B_PANCREATIC_CELL_DEVELOPMENT	1.16	0.51	0	0	0	not significant
11978	HOLLEMAN_DAUNORUBICIN_ALL_DN	1.16	0.51	0	0	0	not significant

11979	GO_LIGASE_ACTIVITY_FORMING_PHOSPHORIC_ESTER_BONDS	1.16	0.50	0	0	0	not significant
11980	COULOUARN_TEMPORAL_TGFB1_SIGNATURE_UP	1.17	0.73	0	0	0	not significant
11981	KEGG_JAK_STAT_SIGNALING_PATHWAY	1.17	0.73	0	0	0	not significant
11982	GO_CELLULAR_RESPONSE_TO_INORGANIC_SUBSTANCE	1.17	0.71	0	0	0	not significant
11983	GO_GASTRULATION	1.17	0.71	0	0	0	not significant
11984	LI_INDUCED_T_TO_NATURAL_KILLER_DN	1.17	0.71	0	0	0	not significant
11985	GO_ADULT_BEHAVIOR	1.17	0.69	0	0	0	not significant
11986	GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR	1.17	0.67	0	0	0	not significant
11987	GO_AMINOGLYCAN_CATABOLIC_PROCESS	1.17	0.64	0	0	0	not significant
11988	GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_ACTIVITY	1.17	0.64	0	0	0	not significant
11989	GO_POST_EMBRYONIC_DEVELOPMENT	1.17	0.63	0	0	0	not significant
11990	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_6	1.17	0.63	0	0	0	not significant
11991	GO_POSITIVE_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA	1.17	0.62	0	0	0	not significant
11992	MATZUK_SPERMATID_DIFFERENTIATION	1.17	0.61	0	0	0	not significant
11993	ABBUD_LIF_SIGNALING_1_UP	1.17	0.59	0	0	0	not significant
11994	CHR6P12	1.17	0.59	0	0	0	not significant
11995	GO_ADIPOSE_TISSUE_DEVELOPMENT	1.17	0.59	0	0	0	not significant
11996	GYORFFY_MITOXANTRONE_RESISTANCE	1.17	0.59	0	0	0	not significant
11997	VANHARANTA_UTERINE_FIBROID_UP	1.17	0.59	0	0	0	not significant
11998	CHR4Q22	1.17	0.58	0	0	0	not significant
11999	GO_REGULATION_OF_FATTY_ACID_TRANSPORT	1.17	0.58	0	0	0	not significant
12000	RICKMAN_HEAD_AND_NECK_CANCER_F	1.17	0.58	0	0	0	not significant
12001	GO_CELLULAR_RESPONSE_TO_STEROL	1.17	0.56	0	0	0	not significant
12002	GO_NEGATIVE_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE	1.17	0.56	0	0	0	not significant
12003	GO_PROTEIN_AUTO_ADP_RIBOSYLATION	1.17	0.56	0	0	0	not significant
12004	STEARMAN_TUMOR_FIELD_EFFECT_UP	1.17	0.56	0	0	0	not significant
12005	GO_INOSITOL_TRISPHOSPHATE_KINASE_ACTIVITY	1.17	0.55	0	0	0	not significant
12006	GO_NEGATIVE_REGULATION_OF_AMYLOID_PRECURSOR_PROTEIN_CAT	1.17	0.55	0	0	0	not significant
12007	SCHURINGA_STAT5A_TARGETS_DN	1.17	0.55	0	0	0	not significant
12008	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_UP	1.17	0.54	0	0	0	not significant
12009	GO_POSITIVE_REGULATION_OF_HISTONE_H3_K27_METHYLATION	1.17	0.54	0	0	0	not significant
12010	KYNG_WERNER_SYNDROM_DN	1.17	0.54	0	0	0	not significant
12011	MAHADEVAN_IMATINIB_RESISTANCE_DN	1.17	0.54	0	0	0	not significant
12012	NIKOLSKY_BREAST_CANCER_22Q13_AMPLICON	1.17	0.54	0	0	0	not significant
12013	GO_NK_T_CELL_ACTIVATION	1.17	0.53	0	0	0	not significant
12014	GO_PROTEIN_TYROSINE_KINASE_ACTIVATOR_ACTIVITY	1.17	0.53	0	0	0	not significant
12015	BIOCARTA_NEUTROPHIL_PATHWAY	1.17	0.52	0	0	0	not significant
12016	GO_MAINTENANCE_OF_POSTSYNAPTIC_SPECIALIZATION_STRUCTURE	1.17	0.52	0	0	0	not significant
12017	GO_REGULATION_OF_ANION_CHANNEL_ACTIVITY	1.17	0.51	0	0	0	not significant
12018	GO_HMG_BOX_DOMAIN_BINDING	1.17	0.50	0	0	0	not significant
12019	GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_	1.17	0.50	0	0	0	not significant
12020	REACTOME_ACYL_CHAIN_REMODELING_OF_CL	1.17	0.50	0	0	0	not significant
12021	HEDVAT_ELF4_TARGETS_UP	1.17	0.48	0	0	0	not significant
12022	GO_NEGATIVE_REGULATION_OF_RNA_BIOSYNTHETIC_PROCESS	1.18	1.40	0	0	0	not significant
12023	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN	1.18	1.19	0	0	0	not significant
12024	GO_MOLECULAR_TRANSDUCER_ACTIVITY	1.18	1.03	0	0	0	not significant
12025	GO_GLYCOPROTEIN_BIOSYNTHETIC_PROCESS	1.18	0.94	0	0	0	not significant
12026	LINDGREN_BLADDER_CANCER_CLUSTER_3_DN	1.18	0.83	0	0	0	not significant
12027	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP	1.18	0.82	0	0	0	not significant
12028	WANG_SMARCE1_TARGETS_UP	1.18	0.76	0	0	0	not significant
12029	PRC2_EED_UP.V1_UP	1.18	0.74	0	0	0	not significant
12030	GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	1.18	0.72	0	0	0	not significant
12031	GO_NEURON_SPINE	1.18	0.71	0	0	0	not significant
12032	NABA_CORE_MATRISOME	1.18	0.70	0	0	0	not significant
12033	GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.18	0.69	0	0	0	not significant
12034	KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	1.18	0.69	0	0	0	not significant
12035	BORCZUK_MALIGNANT_MESOTHELIOMA_DN	1.18	0.68	0	0	0	not significant
12036	GO_NEURON_PROJECTION_TERMINUS	1.18	0.68	0	0	0	not significant
12037	CHR2Q33	1.18	0.64	0	0	0	not significant
12038	GO_PRESYNAPTIC_ACTIVE_ZONE_MEMBRANE	1.18	0.63	0	0	0	not significant
12039	GO_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_COUPLED_RECEPT	1.18	0.62	0	0	0	not significant
12040	REACTOME_CD209_DC_SIGN_SIGNALING	1.18	0.61	0	0	0	not significant
12041	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_UP	1.18	0.61	0	0	0	not significant
12042	GO_REGULATION_OF_ENDOCRINE_PROCESS	1.18	0.60	0	0	0	not significant
12043	GO_REGULATION_OF_NON_CANONICAL_WNT_SIGNALING_PATHWAY	1.18	0.59	0	0	0	not significant
12044	LEIN_LOCALIZED_TO_DISTAL_AND_PROXIMAL_DENDRITES	1.18	0.59	0	0	0	not significant
12045	GO_BICARBONATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.18	0.58	0	0	0	not significant
12046	GO_INTERLEUKIN_27_MEDIATED_SIGNALING_PATHWAY	1.18	0.58	0	0	0	not significant
12047	GO_NEGATIVE_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA	1.18	0.58	0	0	0	not significant
12048	REACTOME_P75NTR_RECRUITS_SIGNALLING_COMPLEXES	1.18	0.58	0	0	0	not significant
12049	GO_AMP_BIOSYNTHETIC_PROCESS	1.18	0.57	0	0	0	not significant
12050	GO_MAP_KINASE_ACTIVITY	1.18	0.57	0	0	0	not significant
12051	MALIK_REPRESSED_BY_ESTROGEN	1.18	0.57	0	0	0	not significant
12052	CAIRO_PML_TARGETS_BOUND_BY_MYC_DN	1.18	0.56	0	0	0	not significant
12053	GO_EPITHELIAL_CELL_CELL_ADHESION	1.18	0.56	0	0	0	not significant
12054	GO_REGULATION_OF_MESODERM_DEVELOPMENT	1.18	0.56	0	0	0	not significant
12055	GO_REGULATION_OF_STEM_CELL_POPULATION_MAINTENANCE	1.18	0.56	0	0	0	not significant
12056	GO_STRUCTURAL_CONSTITUENT_OF_SYNAPSE	1.18	0.56	0	0	0	not significant
12057	REACTOME_TNFR1_INDUCED_PROAPOPTOTIC_SIGNALING	1.18	0.56	0	0	0	not significant
12058	GO_RESPONSE_TO_CAMPTOTHECIN	1.18	0.54	0	0	0	not significant
12059	REACTOME_REACTIONS_SPECIFIC_TO_THE_COMPLEX_N_GLYCAN_SYN	1.18	0.54	0	0	0	not significant
12060	GO_MIRNA_LOADING_ONTO_RISC_INVOLVED_IN_GENE_SILENCING_BY_	1.18	0.53	0	0	0	not significant
12061	SHIN_B_CELL_LYMPHOMA_CLUSTER_1	1.18	0.53	0	0	0	not significant
12062	GO_SEQUENCE_SPECIFIC_DOUBLE_STRANDED_DNA_BINDING	1.19	1.20	0	0	0	not significant
12063	BENPORATH_PRC2_TARGETS	1.19	0.91	0	0	0	not significant
12064	GO_SYNAPTIC_MEMBRANE	1.19	0.91	0	0	0	not significant
12065	KOYAMA_SEMA3B_TARGETS_UP	1.19	0.87	0	0	0	not significant
12066	LEE_RECENT_THYMIC_EMIGRANT	1.19	0.85	0	0	0	not significant
12067	ROME_INSULIN_TARGETS_IN_MUSCLE_DN	1.19	0.83	0	0	0	not significant
12068	GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	1.19	0.82	0	0	0	not significant
12069	GO_REGULATION_OF_RAS_PROTEIN_SIGNAL_TRANSDUCTION	1.19	0.82	0	0	0	not significant
12070	PEDRIOLI_MIR31_TARGETS_UP	1.19	0.78	0	0	0	not significant
12071	GO_CYCLIC_NUCLEOTIDE_MEDIATED_SIGNALING	1.19	0.76	0	0	0	not significant
12072	KIM_MYCN_AMPLIFICATION_TARGETS_DN	1.19	0.76	0	0	0	not significant
12073	GO_MAINTENANCE_OF_PROTEIN_LOCATION	1.19	0.75	0	0	0	not significant
12074	BRCA1_DN.V1_DN	1.19	0.73	0	0	0	not significant
12075	GO_EPITHELIAL_CELL_APOPTOTIC_PROCESS	1.19	0.71	0	0	0	not significant
12076	GO_HOMOLOGOUS_RECOMBINATION	1.19	0.70	0	0	0	not significant
12077	KEGG_ERBB_SIGNALING_PATHWAY	1.19	0.70	0	0	0	not significant
12078	REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	1.19	0.70	0	0	0	not significant
12079	BIOCARTA_ARAP_PATHWAY	1.19	0.67	0	0	0	not significant
12080	CHR10P11	1.19	0.67	0	0	0	not significant
12081	GO_MESODERM_MORPHOGENESIS	1.19	0.67	0	0	0	not significant
12082	GO_ROUGH_ENDOPLASMIC_RETICULUM_MEMBRANE	1.19	0.66	0	0	0	not significant
12083	REACTOME_REGULATION_OF_TNFR1_SIGNALING	1.19	0.66	0	0	0	not significant
12084	MORI_PLASMA_CELL_DN	1.19	0.64	0	0	0	not significant
12085	BIOCARTA_TOB1_PATHWAY	1.19	0.62	0	0	0	not significant
12086	GO_POSITIVE_REGULATION_OF_ACTIN_NUCLEATION	1.19	0.61	0	0	0	not significant
12087	GO_REGULATION_OF_MEMBRANE_INVAGINATION	1.19	0.60	0	0	0	not significant

12088	GO_REGULATION_OF_RECEPTOR_LOCALIZATION_TO_SYNAPSE	1.19	0.60	0	0	0	not significant
12089	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP	1.19	0.60	0	0	0	not significant
12090	GO_DENTATE_GYRUS_DEVELOPMENT	1.19	0.59	0	0	0	not significant
12091	GO_REGULATION_OF_MODIFICATION_OF_SYNAPTIC_STRUCTURE	1.19	0.59	0	0	0	not significant
12092	KEGG_ALLOGRAFT_REJECTION	1.19	0.59	0	0	0	not significant
12093	REACTOME_SIGNALING_BY_ACTIVIN	1.19	0.59	0	0	0	not significant
12094	GO_NEGATIVE_REGULATION_OF_INTERFERON_BETA_PRODUCTION	1.19	0.58	0	0	0	not significant
12095	GO_POSITIVE_REGULATION_OF_CYTOPLASMIC_MRNA_PROCESSING_BC	1.19	0.57	0	0	0	not significant
12096	GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_MEDIATED	1.19	0.57	0	0	0	not significant
12097	GO_WATER_TRANSPORT	1.19	0.57	0	0	0	not significant
12098	ABBUD_LIF_SIGNALING_2_UP	1.19	0.56	0	0	0	not significant
12099	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	1.19	0.56	0	0	0	not significant
12100	ZHENG_FOXP3_TARGETS_DN	1.19	0.56	0	0	0	not significant
12101	GO_DETECTION_OF_VIRUS	1.19	0.55	0	0	0	not significant
12102	GO_POSITIVE_REGULATION_OF_ACTIVIN_RECEPTOR_SIGNALING_PATHW	1.19	0.55	0	0	0	not significant
12103	GO_POSITIVE_REGULATION_OF_NUCLEAR_CELL_CYCLE_DNA_REPLICAT	1.19	0.55	0	0	0	not significant
12104	GO_REGULATION_OF_CYTOPLASMIC_MRNA_PROCESSING_BODY_ASSEM	1.19	0.55	0	0	0	not significant
12105	BIOCARTA_DICER_PATHWAY	1.19	0.54	0	0	0	not significant
12106	GO_NEGATIVE_REGULATION_OF_CYTOKINESIS	1.19	0.54	0	0	0	not significant
12107	REACTOME_ERYTHROPOIETIN_ACTIVATES_PHOSPHOLIPASE_C_GAMMA_	1.19	0.54	0	0	0	not significant
12108	GO_POSITIVE_REGULATION_OF_PROTEIN_HOMOOLIGOMERIZATION	1.19	0.53	0	0	0	not significant
12109	GO_THYROID_HORMONE_METABOLIC_PROCESS	1.19	0.53	0	0	0	not significant
12110	GO_CYTOKINE_PRODUCTION	1.20	1.20	0	0	0	not significant
12111	GO_PROTEIN_TARGETING	1.20	1.16	0	0	0	not significant
12112	GO_POSTSYNAPSE	1.20	1.04	0	0	0	not significant
12113	CHANDRAN_METASTASIS_DN	1.20	0.92	0	0	0	not significant
12114	GO_GLYCEROLIPID_METABOLIC_PROCESS	1.20	0.91	0	0	0	not significant
12115	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN	1.20	0.87	0	0	0	not significant
12116	GO_RHO_GTPASE_BINDING	1.20	0.86	0	0	0	not significant
12117	GO_GATED_CHANNEL_ACTIVITY	1.20	0.85	0	0	0	not significant
12118	PEREZ_TP53_AND_TP63_TARGETS	1.20	0.82	0	0	0	not significant
12119	GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	1.20	0.81	0	0	0	not significant
12120	GO_DEFENSE_RESPONSE_TO_BACTERIUM	1.20	0.80	0	0	0	not significant
12121	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	1.20	0.80	0	0	0	not significant
12122	BENPORATH_ES_CORE_NINE_CORRELATED	1.20	0.79	0	0	0	not significant
12123	CHR16Q24	1.20	0.79	0	0	0	not significant
12124	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DN	1.20	0.79	0	0	0	not significant
12125	IVANOVA_HEMATOPOIESIS_STEM_CELL	1.20	0.77	0	0	0	not significant
12126	REACTOME_PI3K_AKT_SIGNALING_IN_CANCER	1.20	0.76	0	0	0	not significant
12127	GO_GLYCOSAMINOGLYCAN_BINDING	1.20	0.75	0	0	0	not significant
12128	GO_MAINTENANCE_OF_PROTEIN_LOCATION_IN_CELL	1.20	0.72	0	0	0	not significant
12129	GO_PROTEIN_KINASE_C_BINDING	1.20	0.72	0	0	0	not significant
12130	YAGI_AML_RELAPSE_PROGNOSIS	1.20	0.69	0	0	0	not significant
12131	ZHAN_MULTIPLE_MYELOMA_PR_DN	1.20	0.66	0	0	0	not significant
12132	GO_ACTIVATED_T_CELL_PROLIFERATION	1.20	0.64	0	0	0	not significant
12133	GO_GRANULOCYTE_DIFFERENTIATION	1.20	0.64	0	0	0	not significant
12134	GO_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	1.20	0.64	0	0	0	not significant
12135	GO_POSITIVE_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	1.20	0.63	0	0	0	not significant
12136	KEGG_AUTOIMMUNE_THYROID_DISEASE	1.20	0.63	0	0	0	not significant
12137	PID_SYNDECAN_3_PATHWAY	1.20	0.61	0	0	0	not significant
12138	XU_RESPONSE_TO_TRETINOIN_UP	1.20	0.61	0	0	0	not significant
12139	GO_REGULATION_OF_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SI	1.20	0.60	0	0	0	not significant
12140	GO_TRIGLYCERIDE_METABOLIC_PROCESS	1.20	0.60	0	0	0	not significant
12141	HOLLERN_SOLID_NODULAR_BREAST_TUMOR_DN	1.20	0.60	0	0	0	not significant
12142	COWLING_MYCN_TARGETS	1.20	0.59	0	0	0	not significant
12143	GO_PYRIMIDINE_NUCLEOBASE_METABOLIC_PROCESS	1.20	0.59	0	0	0	not significant
12144	GO_REGULATION_OF_POSTSYNAPTIC_DENSITY_ORGANIZATION	1.20	0.59	0	0	0	not significant
12145	REACTOME_WNT_MEDIATED_ACTIVATION_OF_DVL	1.20	0.59	0	0	0	not significant
12146	RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_DN	1.20	0.59	0	0	0	not significant
12147	BOYAULT_LIVER_CANCER_SUBCLASS_G56_UP	1.20	0.58	0	0	0	not significant
12148	GO_DNA_INTEGRATION	1.20	0.58	0	0	0	not significant
12149	GO_HISTONE_DEMETHYLASE_ACTIVITY_H3_K9_SPECIFIC_	1.20	0.58	0	0	0	not significant
12150	GO_MALE_SEX_DETERMINATION	1.20	0.58	0	0	0	not significant
12151	GO_POSITIVE_REGULATION_OF_DNA_LIGATION	1.20	0.58	0	0	0	not significant
12152	GO_CHANGES_TO_DNA_METHYLATION_INVOLVED_IN_EMBRYO_DEVELO	1.20	0.57	0	0	0	not significant
12153	GO_SPHINGOLIPID_TRANSPORTER_ACTIVITY	1.20	0.57	0	0	0	not significant
12154	GO_HIGH_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	1.20	0.56	0	0	0	not significant
12155	GO_VOLTAGE_GATED_SODIUM_CHANNEL_COMPLEX	1.20	0.56	0	0	0	not significant
12156	GO_BONE_TRABECULA_MORPHOGENESIS	1.20	0.53	0	0	0	not significant
12157	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN	1.21	1.26	0	0	0	not significant
12158	WANG_LMO4_TARGETS_UP	1.21	1.08	0	0	0	not significant
12159	GO_MALE_GAMETE_GENERATION	1.21	1.06	0	0	0	not significant
12160	REACTOME_SIGNALING_BY_ROBO_RECEPTORS	1.21	1.01	0	0	0	not significant
12161	GO_NEURAL_TUBE_DEVELOPMENT	1.21	0.90	0	0	0	not significant
12162	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP	1.21	0.90	0	0	0	not significant
12163	DELYS_THYROID_CANCER_DN	1.21	0.88	0	0	0	not significant
12164	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A4	1.21	0.87	0	0	0	not significant
12165	KRAS.600_UP.V1_UP	1.21	0.82	0	0	0	not significant
12166	GO_APICAL_JUNCTION_COMPLEX	1.21	0.81	0	0	0	not significant
12167	GO_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTIO	1.21	0.79	0	0	0	not significant
12168	NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON	1.21	0.76	0	0	0	not significant
12169	YAUCH_HEDGEHOG_SIGNALING_PARACRINE_UP	1.21	0.76	0	0	0	not significant
12170	GO_REGULATION_OF_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALIN	1.21	0.75	0	0	0	not significant
12171	GO_PROTEOGLYCAN_METABOLIC_PROCESS	1.21	0.73	0	0	0	not significant
12172	KEGG_CELL_ADHESION_MOLECULES_CAMS	1.21	0.73	0	0	0	not significant
12173	GO_CELLULAR_RESPONSE_TO_CALCIUM_ION	1.21	0.72	0	0	0	not significant
12174	MARSON_FOXP3_TARGETS_DN	1.21	0.72	0	0	0	not significant
12175	BOYLAN_MULTIPLE_MYELOMA_D_CLUSTER_DN	1.21	0.70	0	0	0	not significant
12176	GO_ANTIMICROBIAL_HUMORAL_RESPONSE	1.21	0.70	0	0	0	not significant
12177	FONTAINE_PAPILLARY_THYROID_CARCINOMA_DN	1.21	0.69	0	0	0	not significant
12178	GO_GPI_ANCHOR_BIOSYNTHETIC_PROCESS	1.21	0.68	0	0	0	not significant
12179	GO_IONOTROPIC_GLUTAMATE_RECEPTOR_BINDING	1.21	0.68	0	0	0	not significant
12180	GO_STORE_OPERATED_CALCIUM_ENTRY	1.21	0.68	0	0	0	not significant
12181	DAIRKEE_CANCER_PRONE_RESPONSE_E2	1.21	0.67	0	0	0	not significant
12182	STREICHER_LSM1_TARGETS_UP	1.21	0.66	0	0	0	not significant
12183	GO_T_CELL_SELECTION	1.21	0.65	0	0	0	not significant
12184	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTYELLOW	1.21	0.64	0	0	0	not significant
12185	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_BACTERIUM	1.21	0.64	0	0	0	not significant
12186	LE_NEURONAL_DIFFERENTIATION_UP	1.21	0.64	0	0	0	not significant
12187	VALK_AML_CLUSTER_10	1.21	0.64	0	0	0	not significant
12188	GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SECRETIO	1.21	0.63	0	0	0	not significant
12189	GO_REGULATION_OF_SYNAPTIC_VESICLE_ENDOCYTOSIS	1.21	0.63	0	0	0	not significant
12190	MARSHALL_VIRAL_INFECTION_RESPONSE_DN	1.21	0.63	0	0	0	not significant
12191	REACTOME_NOTCH2_ACTIVATION_AND_TRANSMISSION_OF_SIGNAL_TO_	1.21	0.63	0	0	0	not significant
12192	GO_FANCONI_ANAEMIA_NUCLEAR_COMPLEX	1.21	0.62	0	0	0	not significant
12193	GO_IMMATURE_B_CELL_DIFFERENTIATION	1.21	0.62	0	0	0	not significant
12194	GO_NUCLEOTIDE_RECEPTOR_ACTIVITY	1.21	0.62	0	0	0	not significant
12195	GO_NEGATIVE_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	1.21	0.61	0	0	0	not significant
12196	GO_VOLTAGE_GATED_CHLORIDE_CHANNEL_ACTIVITY	1.21	0.61	0	0	0	not significant

12197	PID_HEDGEHOG_2PATHWAY	1.21	0.61	0	0	0	not significant
12198	REACTOME_PYRIMIDINE_SALVAGE	1.21	0.61	0	0	0	not significant
12199	SEKI_INFLAMMATORY_RESPONSE_LPS_DN	1.21	0.60	0	0	0	not significant
12200	MATZUK_POST-IMPLANTATION_AND_POST-PARTUM	1.21	0.59	0	0	0	not significant
12201	PID_WNT_SIGNALING_PATHWAY	1.21	0.59	0	0	0	not significant
12202	GO_CALCIUM_ION_REGULATED_EXOCYTOSIS_OF_NEUROTRANSMITTER	1.21	0.58	0	0	0	not significant
12203	GO_INTERLEUKIN_10_SECRETION	1.21	0.58	0	0	0	not significant
12204	GO_ORGAN_INDUCTION	1.21	0.58	0	0	0	not significant
12205	WANG_NEOPLASTIC_TRANSFORMATION_BY_CCND1_MYC	1.21	0.58	0	0	0	not significant
12206	REACTOME_INTERLEUKIN_27_SIGNALING	1.21	0.57	0	0	0	not significant
12207	SHI_SPARC_TARGETS_DN	1.21	0.57	0	0	0	not significant
12208	GO_SPECTRIN_ASSOCIATED_CYTOSKELETON	1.21	0.56	0	0	0	not significant
12209	MARSHALL_VIRAL_INFECTION_RESPONSE_UP	1.21	0.56	0	0	0	not significant
12210	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7	1.21	0.56	0	0	0	not significant
12211	GO_SEQUESTERING_OF_EXTRACELLULAR_LIGAND_FROM_RECEPTOR	1.21	0.54	0	0	0	not significant
12212	GO_REGULATORY_REGION_NUCLEIC_ACID_BINDING	1.22	1.38	0	0	0	not significant
12213	GO_TRANSMEMBRANE_SIGNALING_RECEPTOR_ACTIVITY	1.22	1.21	0	0	0	not significant
12214	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP	1.22	1.12	0	0	0	not significant
12215	WANG_CLIM2_TARGETS_UP	1.22	1.07	0	0	0	not significant
12216	LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN	1.22	0.98	0	0	0	not significant
12217	GO_DISTAL_AXON	1.22	0.97	0	0	0	not significant
12218	PID_SMAD2_3NUCLEAR_PATHWAY	1.22	0.88	0	0	0	not significant
12219	BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP	1.22	0.86	0	0	0	not significant
12220	GO_REGULATION_OF_DNA_RECOMBINATION	1.22	0.86	0	0	0	not significant
12221	GO_CYTOKINE_ACTIVITY	1.22	0.81	0	0	0	not significant
12222	CRX_NRL_DN.V1_DN	1.22	0.80	0	0	0	not significant
12223	GO_PHAGOSOME_MATURATION	1.22	0.77	0	0	0	not significant
12224	GO_CELLULAR_COMPONENT_MAINTENANCE	1.22	0.73	0	0	0	not significant
12225	GO_NATURAL_KILLER_CELL_ACTIVATION	1.22	0.73	0	0	0	not significant
12226	LINDSTEDT_DENDRITIC_CELL_MATURATION_B	1.22	0.72	0	0	0	not significant
12227	BIOCARTA_GLEEVEC_PATHWAY	1.22	0.71	0	0	0	not significant
12228	GO_INTERLEUKIN_8_PRODUCTION	1.22	0.70	0	0	0	not significant
12229	REACTOME_NICOTINATE_METABOLISM	1.22	0.70	0	0	0	not significant
12230	MURATA_VIRULENCE_OF_H_PILORI	1.22	0.68	0	0	0	not significant
12231	GO_ENDOCRINE_HORMONE_SECRETION	1.22	0.67	0	0	0	not significant
12232	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_24HR_UP	1.22	0.65	0	0	0	not significant
12233	CHR7P12	1.22	0.65	0	0	0	not significant
12234	GO_EPITHELIAL_CILIUM_MOVEMENT	1.22	0.65	0	0	0	not significant
12235	GO_CLATHRIN_SCULPTED_GAMMA_AMINOBUTYRIC_ACID_TRANSPORT_	1.22	0.64	0	0	0	not significant
12236	GO_MANNOSYL_OLIGOSACCHARIDE_MANNOSIDASE_ACTIVITY	1.22	0.64	0	0	0	not significant
12237	GO_GLYCOSPHINGOLIPID_BIOSYNTHETIC_PROCESS	1.22	0.63	0	0	0	not significant
12238	GO_NEGATIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	1.22	0.63	0	0	0	not significant
12239	GO_NUCLEAR_MEMBRANE_PART	1.22	0.63	0	0	0	not significant
12240	GO_DETECTION_OF_EXTERNAL_BIOTIC_STIMULUS	1.22	0.62	0	0	0	not significant
12241	GO_GASTRIC_ACID_SECRETION	1.22	0.62	0	0	0	not significant
12242	GO_IRON_COORDINATION_ENTITY_TRANSPORT	1.22	0.62	0	0	0	not significant
12243	GO_NEGATIVE_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATIO	1.22	0.62	0	0	0	not significant
12244	BIOCARTA_CIRCADIAN_PATHWAY	1.22	0.61	0	0	0	not significant
12245	GO_INTERMEMBRANE_LIPID_TRANSFER	1.22	0.61	0	0	0	not significant
12246	GO_MAMMARY_GLAND_EPITHELIAL_CELL_DIFFERENTIATION	1.22	0.61	0	0	0	not significant
12247	GO_NEURAL_PLATE_REGIONALIZATION	1.22	0.61	0	0	0	not significant
12248	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3	1.22	0.61	0	0	0	not significant
12249	MATZUK_PREOVULATORY_FOLLICLE	1.22	0.61	0	0	0	not significant
12250	TURJANSKI_MAPK1_AND_MAPK2_TARGETS	1.22	0.61	0	0	0	not significant
12251	GO_BERGMANN_GLIAL_CELL_DIFFERENTIATION	1.22	0.60	0	0	0	not significant
12252	GO_PROTEIN_UFMYLATION	1.22	0.60	0	0	0	not significant
12253	REACTOME_THE_ACTIVATION_OF_ARYLSULFATASES	1.22	0.59	0	0	0	not significant
12254	ZIRN_TRETINOIN_RESPONSE_WT1_DN	1.22	0.59	0	0	0	not significant
12255	GO_PHOTORECEPTOR_CELL_OUTER_SEGMENT_ORGANIZATION	1.22	0.56	0	0	0	not significant
12256	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY	1.23	2.01	0	0	0	not significant
12257	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_GLYCOSYL_GROUPS	1.23	1.04	0	0	0	not significant
12258	GO_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	1.23	1.01	0	0	0	not significant
12259	GO_APPENDAGE_DEVELOPMENT	1.23	0.89	0	0	0	not significant
12260	GO_ENDOTHELIAL_CELL_PROLIFERATION	1.23	0.84	0	0	0	not significant
12261	PEDERSEN_TARGETS_OF_611CTF_ISOFORM_OF_ERBB2	1.23	0.81	0	0	0	not significant
12262	GO_AMINOGLYCAN_BIOSYNTHETIC_PROCESS	1.23	0.80	0	0	0	not significant
12263	KEGG_CHRONIC_MYELOID_LEUKEMIA	1.23	0.80	0	0	0	not significant
12264	GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	1.23	0.78	0	0	0	not significant
12265	GO_VOLTAGE_GATED_CATION_CHANNEL_ACTIVITY	1.23	0.75	0	0	0	not significant
12266	WINNEPENNINCKX_MELANOMA_METASTASIS_DN	1.23	0.75	0	0	0	not significant
12267	GO_POSITIVE_REGULATION_OF_BONE_MINERALIZATION	1.23	0.72	0	0	0	not significant
12268	REACTOME_SIALIC_ACID_METABOLISM	1.23	0.72	0	0	0	not significant
12269	BIOCARTA_TPO_PATHWAY	1.23	0.70	0	0	0	not significant
12270	GO_LEFT_RIGHT_PATTERN_FORMATION	1.23	0.70	0	0	0	not significant
12271	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN	1.23	0.70	0	0	0	not significant
12272	PID_IL2_STAT5_PATHWAY	1.23	0.70	0	0	0	not significant
12273	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_DN	1.23	0.69	0	0	0	not significant
12274	GO_CAMP_RESPONSE_ELEMENT_BINDING	1.23	0.69	0	0	0	not significant
12275	HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_UP	1.23	0.69	0	0	0	not significant
12276	GO_TRANSCRIPTION_COREPRESSOR_BINDING	1.23	0.68	0	0	0	not significant
12277	HATADA_METHYLATED_IN_LUNG_CANCER_DN	1.23	0.68	0	0	0	not significant
12278	REACTOME_RHO_GTPASES_ACTIVATE_RHOTEKIN_AND_RHOPHILINS	1.23	0.67	0	0	0	not significant
12279	WESTON_VEGFA_TARGETS_6HR	1.23	0.67	0	0	0	not significant
12280	GO_REGULATION_OF_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	1.23	0.66	0	0	0	not significant
12281	GO_SMAD_PROTEIN_COMPLEX	1.23	0.66	0	0	0	not significant
12282	GO_ACROSOMAL_MEMBRANE	1.23	0.65	0	0	0	not significant
12283	BIOCARTA_SHH_PATHWAY	1.23	0.64	0	0	0	not significant
12284	GO_ARP2_3_COMPLEX_BINDING	1.23	0.64	0	0	0	not significant
12285	GO_MALE_MEIOSIS_I	1.23	0.64	0	0	0	not significant
12286	GO_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	1.23	0.63	0	0	0	not significant
12287	GO_CELLULAR_RESPONSE_TO_CHOLESTEROL	1.23	0.62	0	0	0	not significant
12288	GO_FOUR_WAY_JUNCTION_HELICASE_ACTIVITY	1.23	0.61	0	0	0	not significant
12289	REACTOME_FRS_MEDIATED_FGFR1_SIGNALING	1.23	0.61	0	0	0	not significant
12290	REACTOME_TFAP2_AP_2_FAMILY_REGULATES_TRANSCRIPTION_OF_G	1.23	0.61	0	0	0	not significant
12291	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_POSTSYNAPTIC_	1.23	0.59	0	0	0	not significant
12292	GARY_CD5_TARGETS_UP	1.24	1.49	0	0	0	not significant
12293	GO_LEUKOCYTE_DIFFERENTIATION	1.24	1.33	0	0	0	not significant
12294	PENG_RAPAMYCIN_RESPONSE_UP	1.24	1.00	0	0	0	not significant
12295	GAVIN_FOXP3_TARGETS_CLUSTER_P4	1.24	0.84	0	0	0	not significant
12296	GO_REGULATION_OF_BONE_MINERALIZATION	1.24	0.79	0	0	0	not significant
12297	HOLLEMAN_VINCRISTINE_RESISTANCE_B_ALL_UP	1.24	0.79	0	0	0	not significant
12298	GO_DETERMINATION_OF_HEART_LEFT_RIGHT_ASYMMETRY	1.24	0.78	0	0	0	not significant
12299	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP	1.24	0.78	0	0	0	not significant
12300	GO_MEMBRANE_LIPID_CATABOLIC_PROCESS	1.24	0.75	0	0	0	not significant
12301	BIOCARTA_G1_PATHWAY	1.24	0.74	0	0	0	not significant
12302	GO_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	1.24	0.74	0	0	0	not significant
12303	YANG_BREAST_CANCER_ESR1_LASER_UP	1.24	0.73	0	0	0	not significant
12304	GO_MAINTENANCE_OF_PROTEIN_LOCATION_IN_NUCLEUS	1.24	0.72	0	0	0	not significant
12305	GO_NAD_BIOSYNTHETIC_PROCESS	1.24	0.71	0	0	0	not significant

12306	MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3	1.24	0.70	0	0	0	not significant
12307	GO_HEPARAN_SULFATE_SULFOTRANSFERASE_ACTIVITY	1.24	0.69	0	0	0	not significant
12308	REACTOME_ERYTHROPOIETIN_ACTIVATES_PHOSPHOINOSITIDE_3_KINAS	1.24	0.69	0	0	0	not significant
12309	GO_MITOTIC_DNA_REPLICATION	1.24	0.67	0	0	0	not significant
12310	GO_PHOSPHORYLASE_KINASE_COMPLEX	1.24	0.67	0	0	0	not significant
12311	GO_REGULATION_OF_DNA_DIRECTED_DNA_POLYMERASE_ACTIVITY	1.24	0.67	0	0	0	not significant
12312	VALK_AML_CLUSTER_2	1.24	0.67	0	0	0	not significant
12313	CHR4Q26	1.24	0.66	0	0	0	not significant
12314	BAKER_HEMATOPOESIS_STAT5_TARGETS	1.24	0.65	0	0	0	not significant
12315	GO_INTRINSIC_COMPONENT_OF_POSTSYNAPTIC_DENSITY_MEMBRANE	1.24	0.65	0	0	0	not significant
12316	GO_MESODERMAL_CELL_DIFFERENTIATION	1.24	0.65	0	0	0	not significant
12317	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINAS	1.24	0.65	0	0	0	not significant
12318	GO_RESPONSE_TO_CISPLATIN	1.24	0.64	0	0	0	not significant
12319	GO_ATP_BINDING_CASSETTE_ABC_TRANSPORTER_COMPLEX	1.24	0.63	0	0	0	not significant
12320	GO_VESICLE_UNCOATING	1.24	0.63	0	0	0	not significant
12321	GO_REGULATION_OF_CARDIAC_EPITHELIAL_TO_MESENCHYMAL_TRANS	1.24	0.62	0	0	0	not significant
12322	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_DN	1.25	1.17	0	0	0	not significant
12323	GO_LYMPHOCYTE_MEDIATED_IMMUNITY	1.25	1.10	0	0	0	not significant
12324	SENESE_HDAC1_TARGETS_DN	1.25	1.08	0	0	0	not significant
12325	REACTOME_REGULATION_OF_EXPRESSION_OF_SLITS_AND_ROBOS	1.25	1.00	0	0	0	not significant
12326	GO_FERTILIZATION	1.25	0.89	0	0	0	not significant
12327	GO_AUTOPHAGOSOME	1.25	0.87	0	0	0	not significant
12328	GO_CYTOKINE_METABOLIC_PROCESS	1.25	0.86	0	0	0	not significant
12329	KRAS.PROSTATE_UP.V1_DN	1.25	0.86	0	0	0	not significant
12330	GO_INTERFERON_GAMMA_PRODUCTION	1.25	0.84	0	0	0	not significant
12331	JI_RESPONSE_TO_FSH_UP	1.25	0.83	0	0	0	not significant
12332	REACTOME_INTERLEUKIN_3_INTERLEUKIN_5_AND_GM_CSF_SIGNALING	1.25	0.81	0	0	0	not significant
12333	KRAS.300_UP.V1_DN	1.25	0.80	0	0	0	not significant
12334	BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_DN	1.25	0.76	0	0	0	not significant
12335	GO_PROTEIN_TARGETING_TO_LYSOSOME	1.25	0.76	0	0	0	not significant
12336	GO_HEME_TRANSPORTER_ACTIVITY	1.25	0.74	0	0	0	not significant
12337	GO_INTEGRAL_COMPONENT_OF_SYNAPTIC_VESICLE_MEMBRANE	1.25	0.74	0	0	0	not significant
12338	GO_NEGATIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	1.25	0.74	0	0	0	not significant
12339	GO_RESPONSE_TO_ZINC_ION	1.25	0.74	0	0	0	not significant
12340	RIZ_ERYTHROID_DIFFERENTIATION_HBZ	1.25	0.74	0	0	0	not significant
12341	REACTOME_DSCAM_INTERACTIONS	1.25	0.72	0	0	0	not significant
12342	REACTOME_REGULATION_OF_RUNX1_EXPRESSION_AND_ACTIVITY	1.25	0.71	0	0	0	not significant
12343	BARRIER_COLON_CANCER_RECURRENCE_DN	1.25	0.70	0	0	0	not significant
12344	GO_SULFOTRANSFERASE_ACTIVITY	1.25	0.70	0	0	0	not significant
12345	GO_BETA_CATENIN_DESTRUCTION_COMPLEX_DISASSEMBLY	1.25	0.69	0	0	0	not significant
12346	REACTOME_ACTIVATION_OF_THE_AP_1_FAMILY_OF_TRANSCRIPTION_F	1.25	0.69	0	0	0	not significant
12347	GO_CYCLIN_DEPENDENT_PROTEIN_SERINE_THREONINE_KINASE_INHIBIT	1.25	0.68	0	0	0	not significant
12348	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTO	1.25	0.68	0	0	0	not significant
12349	GO_NEGATIVE_REGULATION_OF_PHAGOCYTOSIS	1.25	0.68	0	0	0	not significant
12350	GO_POSITIVE_REGULATION_OF_GRANULOCYTE_MACROPHAGE_COLON	1.25	0.68	0	0	0	not significant
12351	GO_POSITIVE_REGULATION_OF_HISTONE_H3_K9_METHYLATION	1.25	0.68	0	0	0	not significant
12352	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	1.25	0.68	0	0	0	not significant
12353	GO_REGULATION_OF_CD8_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENT	1.25	0.68	0	0	0	not significant
12354	GO_CERAMIDE_BINDING	1.25	0.67	0	0	0	not significant
12355	GO_NEGATIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	1.25	0.67	0	0	0	not significant
12356	REACTOME_FOXO_MEDIATED_TRANSCRIPTION_OF_CELL_CYCLE_GENE	1.25	0.67	0	0	0	not significant
12357	GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	1.25	0.66	0	0	0	not significant
12358	GO_RESPONSE_TO_MURAMYL_DIPEPTIDE	1.25	0.66	0	0	0	not significant
12359	MATZUK_POSTIMPLANTATION_AND_POSTPARTUM	1.25	0.66	0	0	0	not significant
12360	SCHOEN_NFKB_SIGNALING	1.25	0.66	0	0	0	not significant
12361	GO_REGULATION_OF_HAIR_CYCLE	1.25	0.65	0	0	0	not significant
12362	GO_PLASMA_MEMBRANE_PHOSPHOLIPID_SCRAMBLING	1.25	0.64	0	0	0	not significant
12363	LIEN_BREAST_CARCINOMA_METAPLASTIC	1.25	0.64	0	0	0	not significant
12364	REACTOME_INTERLEUKIN_6_SIGNALING	1.25	0.64	0	0	0	not significant
12365	GO_POSITIVE_REGULATION_OF_INTEGRIN_ACTIVATION	1.25	0.63	0	0	0	not significant
12366	GO_POLYNUCLEOTIDE_DEPHOSPHORYLATION	1.25	0.62	0	0	0	not significant
12367	GO_PARENTAL_BEHAVIOR	1.25	0.60	0	0	0	not significant
12368	GO_PEPTIDYL_TYROSINE_MODIFICATION	1.26	1.15	0	0	0	not significant
12369	GO_B_CELL_ACTIVATION	1.26	1.09	0	0	0	not significant
12370	SCHLOSSER_SERUM_RESPONSE_UP	1.26	1.01	0	0	0	not significant
12371	GAUSSMANN_MLL_AF4_FUSION_TARGETS_C_UP	1.26	0.99	0	0	0	not significant
12372	GO_LIPOPROTEIN_BIOSYNTHETIC_PROCESS	1.26	0.95	0	0	0	not significant
12373	RUIZ_TNC_TARGETS_UP	1.26	0.95	0	0	0	not significant
12374	KEGG_PROSTATE_CANCER	1.26	0.93	0	0	0	not significant
12375	BOYLAN_MULTIPLE_MYELOMA_C_DN	1.26	0.90	0	0	0	not significant
12376	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP	1.26	0.89	0	0	0	not significant
12377	GO_VOLTAGE_GATED_ION_CHANNEL_ACTIVITY	1.26	0.87	0	0	0	not significant
12378	GO_B_CELL_PROLIFERATION	1.26	0.86	0	0	0	not significant
12379	BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AND_TSC2	1.26	0.85	0	0	0	not significant
12380	DELPUECH_FOXO3_TARGETS_UP	1.26	0.85	0	0	0	not significant
12381	FURUKAWA_DUSP6_TARGETS_PCI35_UP	1.26	0.83	0	0	0	not significant
12382	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN	1.26	0.81	0	0	0	not significant
12383	LIM_MAMMARY_LUMINAL_PROGENITOR_UP	1.26	0.77	0	0	0	not significant
12384	BECKER_TAMOXIFEN_RESISTANCE_DN	1.26	0.76	0	0	0	not significant
12385	GO_PITUITARY_GLAND_DEVELOPMENT	1.26	0.76	0	0	0	not significant
12386	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_SYNAPSE	1.26	0.75	0	0	0	not significant
12387	GO_REGULATION_OF_CLATHRIN_DEPENDENT_ENDOCYTOSIS	1.26	0.74	0	0	0	not significant
12388	APPEL_IMATINIB_RESPONSE	1.26	0.73	0	0	0	not significant
12389	KEGG_ARACHIDONIC_ACID_METABOLISM	1.26	0.73	0	0	0	not significant
12390	BIOCARTA_GH_PATHWAY	1.26	0.72	0	0	0	not significant
12391	GO_FIBROBLAST_GROWTH_FACTOR_BINDING	1.26	0.72	0	0	0	not significant
12392	GO_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	1.26	0.72	0	0	0	not significant
12393	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TAN_DN	1.26	0.71	0	0	0	not significant
12394	GO_CYTOLYSIS	1.26	0.71	0	0	0	not significant
12395	SA_REG_CASCADE_OF_CYCLIN_EXPR	1.26	0.71	0	0	0	not significant
12396	TOMLINS_METASTASIS_DN	1.26	0.71	0	0	0	not significant
12397	GO_NEGATIVE_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIG	1.26	0.70	0	0	0	not significant
12398	WU_ALZHEIMER_DISEASE_UP	1.26	0.70	0	0	0	not significant
12399	AMUNDSON_GAMMA_RADIATION_RESISTANCE	1.26	0.69	0	0	0	not significant
12400	GO_CD8_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	1.26	0.69	0	0	0	not significant
12401	GO_REGULATION_OF_STORE_OPERATED_CALCIUM_ENTRY	1.26	0.69	0	0	0	not significant
12402	GO_SINGLE_STRANDED_DNA_3_5_EXODEOXYRIBONUCLEASE_ACTIVITY	1.26	0.69	0	0	0	not significant
12403	GO_NEGATIVE_REGULATION_OF_OSTEOBLAST_PROLIFERATION	1.26	0.68	0	0	0	not significant
12404	REACTOME_INTERLEUKIN_23_SIGNALING	1.26	0.68	0	0	0	not significant
12405	CHR4P11	1.26	0.67	0	0	0	not significant
12406	GO_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_INVOLVED_IN_ENDOCA	1.26	0.67	0	0	0	not significant
12407	GO_PROTEIN_CARBOXYL_O_METHYLTRANSFERASE_ACTIVITY	1.26	0.67	0	0	0	not significant
12408	GO_BUBBLE_DNA_BINDING	1.26	0.66	0	0	0	not significant
12409	GO_NUCLEAR_MEMBRANE_PROTEIN_COMPLEX	1.26	0.66	0	0	0	not significant
12410	GO_ACYLGLYCEROL_LIPASE_ACTIVITY	1.26	0.65	0	0	0	not significant
12411	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP	1.27	1.10	0	0	0	not significant
12412	GO_REGULATION_OF_T_CELL_DIFFERENTIATION	1.27	1.00	0	0	0	not significant
12413	PTEN_DN.V2_DN	1.27	1.00	0	0	0	not significant
12414	GO_CELL_CELL_JUNCTION_ASSEMBLY	1.27	0.93	0	0	0	not significant

12415	GO_GLYCOLIPID_BIOSYNTHETIC_PROCESS	1.27	0.91	0	0	0	not significant
12416	GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	1.27	0.90	0	0	0	not significant
12417	GO_REGULATION_OF_TISSUE_REMODELING	1.27	0.89	0	0	0	not significant
12418	CHR15Q26	1.27	0.88	0	0	0	not significant
12419	DORSAM_HOXA9_TARGETS_DN	1.27	0.86	0	0	0	not significant
12420	EHLERS_ANEUPLOIDY_UP	1.27	0.85	0	0	0	not significant
12421	GO_HOMOLOGOUS_CHROMOSOME_SEGREGATION	1.27	0.85	0	0	0	not significant
12422	KEGG_LEISHMANIA_INFECTION	1.27	0.83	0	0	0	not significant
12423	NICK_RESPONSE_TO_PROC_TREATMENT_DN	1.27	0.83	0	0	0	not significant
12424	PID_NFAT_TFPATHWAY	1.27	0.83	0	0	0	not significant
12425	GO_MANNOSYLTRANSFERASE_ACTIVITY	1.27	0.82	0	0	0	not significant
12426	GO_NEGATIVE_REGULATION_OF_DNA_RECOMBINATION	1.27	0.82	0	0	0	not significant
12427	DAUER_STAT3_TARGETS_UP	1.27	0.81	0	0	0	not significant
12428	LUI_THYROID_CANCER_CLUSTER_3	1.27	0.79	0	0	0	not significant
12429	ZHAN_MULTIPLE_MYELOMA_CD2_UP	1.27	0.79	0	0	0	not significant
12430	GO_BCL_2_FAMILY_PROTEIN_COMPLEX	1.27	0.78	0	0	0	not significant
12431	GO_PHOSPHORYLASE_KINASE_ACTIVITY	1.27	0.78	0	0	0	not significant
12432	SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS	1.27	0.78	0	0	0	not significant
12433	BOYLAN_MULTIPLE_MYELOMA_C_CLUSTER_DN	1.27	0.77	0	0	0	not significant
12434	BIOCARTA_CYTOKINE_PATHWAY	1.27	0.76	0	0	0	not significant
12435	GILMORE_CORE_NFKB_PATHWAY	1.27	0.75	0	0	0	not significant
12436	GO_PROTEIN_DEGLYCOSYLATION	1.27	0.75	0	0	0	not significant
12437	PID_IL3_PATHWAY	1.27	0.75	0	0	0	not significant
12438	BIOCARTA_MONOCYTE_PATHWAY	1.27	0.74	0	0	0	not significant
12439	GO_POSITIVE_REGULATION_OF_REGULATORY_T_CELL_DIFFERENTIATI	1.27	0.73	0	0	0	not significant
12440	GO_REGULATION_OF_OVARIAN_FOLLICLE_DEVELOPMENT	1.27	0.73	0	0	0	not significant
12441	REACTOME_INTERLEUKIN_2_SIGNALING	1.27	0.73	0	0	0	not significant
12442	SEMBA_FHIT_TARGETS_UP	1.27	0.73	0	0	0	not significant
12443	VERRECCHIA_RESPONSE_TO_TGFB1_C2	1.27	0.73	0	0	0	not significant
12444	BIOCARTA_LYM_PATHWAY	1.27	0.72	0	0	0	not significant
12445	REACTOME_PRESYNAPTIC_DEPOLARIZATION_AND_CALCIUM_CHANNEL_	1.27	0.72	0	0	0	not significant
12446	SASAKI_TARGETS_OF_TP73_AND_TP63	1.27	0.72	0	0	0	not significant
12447	GO_ASPARTIC_ENDOPEPTIDASE_ACTIVITY_INTRAMEMBRANE_CLEAVING	1.27	0.71	0	0	0	not significant
12448	GO_TRIGLYCERIDE_LIPASE_ACTIVITY	1.27	0.71	0	0	0	not significant
12449	GO_INTERLEUKIN_23_MEDIATED_SIGNALING_PATHWAY	1.27	0.70	0	0	0	not significant
12450	GO_INTRINSIC_COMPONENT_OF_VACUOLAR_MEMBRANE	1.27	0.69	0	0	0	not significant
12451	GO_NEGATIVE_REGULATION_OF_NEUROTRANSMITTER_SECRETION	1.27	0.67	0	0	0	not significant
12452	GO_ADAPTIVE_IMMUNE_RESPONSE	1.28	1.33	0	0	0	not significant
12453	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP	1.28	1.07	0	0	0	not significant
12454	GO_POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATI	1.28	0.92	0	0	0	not significant
12455	BILANGES_SERUM_SENSITIVE_GENES	1.28	0.90	0	0	0	not significant
12456	GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_T	1.28	0.89	0	0	0	not significant
12457	GO_REGULATION_OF_CELL_KILLING	1.28	0.89	0	0	0	not significant
12458	GO_PHAGOPHORE_ASSEMBLY_SITE	1.28	0.88	0	0	0	not significant
12459	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	1.28	0.88	0	0	0	not significant
12460	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	1.28	0.80	0	0	0	not significant
12461	GO_PROTON_TRANSPORTING_V_TYPE_ATPASE_V0_DOMAIN	1.28	0.78	0	0	0	not significant
12462	HOLLEMAN_DAUNORUBICIN_B_ALL_DN	1.28	0.78	0	0	0	not significant
12463	GO_SODIUM_CHANNEL_COMPLEX	1.28	0.77	0	0	0	not significant
12464	GO_HISTONE_H3_K27_METHYLATION	1.28	0.76	0	0	0	not significant
12465	TIAN_TNF_SIGNALING_VIA_NFKB	1.28	0.76	0	0	0	not significant
12466	GO_HYPOTHALAMUS_DEVELOPMENT	1.28	0.75	0	0	0	not significant
12467	GO_NEGATIVE_REGULATION_OF_CELL_KILLING	1.28	0.75	0	0	0	not significant
12468	GO_REGULATION_OF_INOSITOL_PHOSPHATE_BIOSYNTHETIC_PROCESS	1.28	0.75	0	0	0	not significant
12469	CHR2Q34	1.28	0.74	0	0	0	not significant
12470	GO_PHOSPHATE_ION_BINDING	1.28	0.74	0	0	0	not significant
12471	GO_SPHINGOID_BIOSYNTHETIC_PROCESS	1.28	0.74	0	0	0	not significant
12472	GO_GRANULOCYTE_MACROPHAGE_COLONY_STIMULATING_FACTOR_P	1.28	0.73	0	0	0	not significant
12473	GO_NEGATIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	1.28	0.73	0	0	0	not significant
12474	GO_NEGATIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IM	1.28	0.73	0	0	0	not significant
12475	GO_SODIUM_CHANNEL_ACTIVITY	1.28	0.73	0	0	0	not significant
12476	GO_SENSORY_PERCEPTION_OF_SMELL	1.28	0.72	0	0	0	not significant
12477	REACTOME_ASSEMBLY_OF_ACTIVE_LPL_AND_LIPC_LIPASE_COMPLEXE	1.28	0.72	0	0	0	not significant
12478	CONRAD_GERMLINE_STEM_CELL	1.28	0.71	0	0	0	not significant
12479	YAO_HOXA10_TARGETS_VIA_PROGESTERONE_DN	1.28	0.71	0	0	0	not significant
12480	CASTELLANO_HRAS_AND_NRAS_TARGETS_DN	1.28	0.69	0	0	0	not significant
12481	GO_POTASSIUM_ION_LEAK_CHANNEL_ACTIVITY	1.28	0.69	0	0	0	not significant
12482	THILLAINADESAN_ZNF217_TARGETS_DN	1.28	0.68	0	0	0	not significant
12483	GO_CELL_FATE_COMMITMENT	1.29	1.11	0	0	0	not significant
12484	KRAS.600.LUNG.BREAST_UP.V1_UP	1.29	1.07	0	0	0	not significant
12485	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP	1.29	1.07	0	0	0	not significant
12486	KRAS.600.LUNG.BREAST_UP.V1_DN	1.29	1.04	0	0	0	not significant
12487	GO_ENDOTHELIUM_DEVELOPMENT	1.29	1.01	0	0	0	not significant
12488	KIM_MYC_AMPLIFICATION_TARGETS_DN	1.29	0.96	0	0	0	not significant
12489	CHR7Q21	1.29	0.95	0	0	0	not significant
12490	GO_AMINOGLYCAN_METABOLIC_PROCESS	1.29	0.95	0	0	0	not significant
12491	AMIT_SERUM_RESPONSE_60_MCF10A	1.29	0.94	0	0	0	not significant
12492	GO_POLYSOME	1.29	0.94	0	0	0	not significant
12493	JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	1.29	0.91	0	0	0	not significant
12494	GO_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	1.29	0.90	0	0	0	not significant
12495	REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	1.29	0.88	0	0	0	not significant
12496	CAHOY_NEURONAL	1.29	0.85	0	0	0	not significant
12497	GO_MESENCHYMAL_CELL_PROLIFERATION	1.29	0.85	0	0	0	not significant
12498	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	1.29	0.85	0	0	0	not significant
12499	HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_UP	1.29	0.84	0	0	0	not significant
12500	GO_MITOPHAGY	1.29	0.83	0	0	0	not significant
12501	CHR9P22	1.29	0.81	0	0	0	not significant
12502	GO_LENS_FIBER_CELL_DIFFERENTIATION	1.29	0.81	0	0	0	not significant
12503	GO_MICROTUBULE_NUCLEATION_BY_MICROTUBULE_ORGANIZING_CENT	1.29	0.81	0	0	0	not significant
12504	ISHIKAWA_STING_SIGNALING	1.29	0.81	0	0	0	not significant
12505	GO_NEGATIVE_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	1.29	0.80	0	0	0	not significant
12506	GO_RECEPTOR_SIGNALING_COMPLEX_SCAFFOLD_ACTIVITY	1.29	0.80	0	0	0	not significant
12507	HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_UP	1.29	0.80	0	0	0	not significant
12508	RASHI_NFKB1_TARGETS	1.29	0.79	0	0	0	not significant
12509	GO_NATURAL_KILLER_CELL_DIFFERENTIATION	1.29	0.78	0	0	0	not significant
12510	GO_NUCLEOTIDE_BINDING_OLIGOMERIZATION_DOMAIN_CONTAINING_2_	1.29	0.78	0	0	0	not significant
12511	GO_SOMATIC_STEM_CELL_DIVISION	1.29	0.78	0	0	0	not significant
12512	GO_WNT_PROTEIN_BINDING	1.29	0.78	0	0	0	not significant
12513	GO_PROTEIN_BINDING_BRIDGING_INVOLVED_IN_SUBSTRATE_RECOGNIT	1.29	0.77	0	0	0	not significant
12514	GO_VOLTAGE_GATED_CALCIUM_CHANNEL_COMPLEX	1.29	0.77	0	0	0	not significant
12515	ZIRN_TRETINOIN_RESPONSE_WT1_UP	1.29	0.77	0	0	0	not significant
12516	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTYELLOW	1.29	0.76	0	0	0	not significant
12517	GO_BASIC_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	1.29	0.76	0	0	0	not significant
12518	GO_INHIBITORY_SYNAPSE	1.29	0.76	0	0	0	not significant
12519	GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	1.29	0.75	0	0	0	not significant
12520	BIOCARTA_TCYTOTOXIC_PATHWAY	1.29	0.74	0	0	0	not significant
12521	GO_ALPHA_CATENIN_BINDING	1.29	0.74	0	0	0	not significant
12522	GO_DIACYLGLYCEROL_METABOLIC_PROCESS	1.29	0.74	0	0	0	not significant
12523	GO_HISTONE_H3_K14_ACETYLATION	1.29	0.74	0	0	0	not significant

12524	GO_REGULATION_OF_HEAT_GENERATION	1.29	0.74	0	0	0	not significant
12525	REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	1.29	0.74	0	0	0	not significant
12526	GO_GAP_JUNCTION	1.29	0.73	0	0	0	not significant
12527	CHR5P12	1.29	0.72	0	0	0	not significant
12528	KIM_ALL_DISORDERS_DURATION_CORR_UP	1.29	0.72	0	0	0	not significant
12529	REACTOME_NEGATIVE_REGULATION_OF_ACTIVITY_OF_TFAP2_AP_2_F	1.29	0.72	0	0	0	not significant
12530	LEI_HOXC8_TARGETS_UP	1.29	0.70	0	0	0	not significant
12531	BENPORATH_ES_WITH_H3K27ME3	1.30	1.53	0	0	0	not significant
12532	GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINAT	1.30	1.23	0	0	0	not significant
12533	KEGG_LYSOSOME	1.30	1.15	0	0	0	not significant
12534	MTOR_UP.V1_DN	1.30	1.15	0	0	0	not significant
12535	NABA_SECRETED_FACTORS	1.30	1.09	0	0	0	not significant
12536	GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	1.30	1.08	0	0	0	not significant
12537	GO_B_CELL_DIFFERENTIATION	1.30	1.04	0	0	0	not significant
12538	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN	1.30	1.03	0	0	0	not significant
12539	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_UP	1.30	1.01	0	0	0	not significant
12540	KIM_GERMINAL_CENTER_T_HELPER_UP	1.30	0.98	0	0	0	not significant
12541	GO_LENS_DEVELOPMENT_IN_CAMERA_TYPE_EYE	1.30	0.94	0	0	0	not significant
12542	ZHAN_MULTIPLE_MYELOMA_HP_UP	1.30	0.93	0	0	0	not significant
12543	GO_ENDODEOXYRIBONUCLEASE_ACTIVITY	1.30	0.90	0	0	0	not significant
12544	SUNG_METASTASIS_STROMA_DN	1.30	0.90	0	0	0	not significant
12545	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY	1.30	0.88	0	0	0	not significant
12546	CHR7Q34	1.30	0.86	0	0	0	not significant
12547	CHR10Q21	1.30	0.85	0	0	0	not significant
12548	CHR6Q22	1.30	0.85	0	0	0	not significant
12549	GO_INTRINSIC_COMPONENT_OF_PRESYNAPTIC_MEMBRANE	1.30	0.83	0	0	0	not significant
12550	HEIDENBLAD_AMPLICON_12P11_12_DN	1.30	0.83	0	0	0	not significant
12551	PID_DNA_PK_PATHWAY	1.30	0.83	0	0	0	not significant
12552	GO_GLUTAMINE_METABOLIC_PROCESS	1.30	0.82	0	0	0	not significant
12553	GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	1.30	0.81	0	0	0	not significant
12554	REACTOME_TRANSPORT_OF_NUCLEOSIDES_AND_FREE_PURINE_AND_	1.30	0.81	0	0	0	not significant
12555	GO_ENDOCARDIAL_CUSHION_MORPHOGENESIS	1.30	0.80	0	0	0	not significant
12556	GO_INTERMEMBRANE_LIPID_TRANSFER_ACTIVITY	1.30	0.79	0	0	0	not significant
12557	GO_SECONDARY_PALATE_DEVELOPMENT	1.30	0.78	0	0	0	not significant
12558	GO_CARDIAC_RIGHT_VENTRICLE_MORPHOGENESIS	1.30	0.76	0	0	0	not significant
12559	GO_N_ACETYLNEURAMINATE_CATABOLIC_PROCESS	1.30	0.76	0	0	0	not significant
12560	GO_TELOMERE_LOCALIZATION	1.30	0.76	0	0	0	not significant
12561	GO_POSITIVE_REGULATION_OF_AMYLOID_BETA_CLEARANCE	1.30	0.75	0	0	0	not significant
12562	KOBAYASHI_EGFR_SIGNALING_6HR_UP	1.30	0.75	0	0	0	not significant
12563	REACTOME_SIGNALING_BY_NODAL	1.30	0.75	0	0	0	not significant
12564	CHRXQ25	1.30	0.74	0	0	0	not significant
12565	GO_RESPONSE_TO_INTERLEUKIN_2	1.30	0.70	0	0	0	not significant
12566	ONKEN_UVEAL_MELANOMA_DN	1.31	1.96	0	0	0	not significant
12567	GO_T_CELL_DIFFERENTIATION	1.31	1.43	0	0	0	not significant
12568	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP	1.31	1.20	0	0	0	not significant
12569	GO_MEIOSIS_I_CELL_CYCLE_PROCESS	1.31	1.12	0	0	0	not significant
12570	GO_HUMORAL_IMMUNE_RESPONSE	1.31	1.11	0	0	0	not significant
12571	GO_ROUGH_ENDOPLASMIC_RETICULUM	1.31	1.04	0	0	0	not significant
12572	CROONQUIST_STROMAL_STIMULATION_UP	1.31	0.97	0	0	0	not significant
12573	GO_POSITIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCES	1.31	0.95	0	0	0	not significant
12574	KRAS.LUNG_UP.V1_UP	1.31	0.95	0	0	0	not significant
12575	LIM_MAMMARY_LUMINAL_MATURE_DN	1.31	0.95	0	0	0	not significant
12576	GO_MODIFIED_AMINO_ACID_BINDING	1.31	0.93	0	0	0	not significant
12577	CHR15Q11	1.31	0.91	0	0	0	not significant
12578	REACTOME_PROLACTIN_RECEPTOR_SIGNALING	1.31	0.91	0	0	0	not significant
12579	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVI	1.31	0.90	0	0	0	not significant
12580	PID_TCPTP_PATHWAY	1.31	0.90	0	0	0	not significant
12581	GO_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	1.31	0.88	0	0	0	not significant
12582	GO_PROTEIN_DEMETHYLATION	1.31	0.88	0	0	0	not significant
12583	MCBRYAN_PUBERTAL_TGFB1_TARGETS_DN	1.31	0.88	0	0	0	not significant
12584	REACTOME_ARACHIDONIC_ACID_METABOLISM	1.31	0.87	0	0	0	not significant
12585	ZHENG_FOXP3_TARGETS_UP	1.31	0.87	0	0	0	not significant
12586	GO_ALPHA_BETA_T_CELL_PROLIFERATION	1.31	0.86	0	0	0	not significant
12587	GO_ARACHIDONIC_ACID_METABOLIC_PROCESS	1.31	0.86	0	0	0	not significant
12588	GO_DETERMINATION_OF_DORSAL_VENTRAL_ASYMMETRY	1.31	0.86	0	0	0	not significant
12589	HOQUE_METHYLATED_IN_CANCER	1.31	0.86	0	0	0	not significant
12590	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_METHYLATION	1.31	0.86	0	0	0	not significant
12591	BIOCARTA_LYMPHOCYTE_PATHWAY	1.31	0.85	0	0	0	not significant
12592	GO_CELL_FATE_SPECIFICATION	1.31	0.85	0	0	0	not significant
12593	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN	1.31	0.82	0	0	0	not significant
12594	GO_NEGATIVE_REGULATION_OF_AXON_GUIDANCE	1.31	0.82	0	0	0	not significant
12595	GO_REGULATION_OF_HISTONE_H3_K27_METHYLATION	1.31	0.82	0	0	0	not significant
12596	GO_ARGININE_TRANSPORT	1.31	0.80	0	0	0	not significant
12597	GO_POSITIVE_REGULATION_OF_FIBROBLAST_APOPTOTIC_PROCESS	1.31	0.80	0	0	0	not significant
12598	GO_ANTIBIOTIC_TRANSPORT	1.31	0.78	0	0	0	not significant
12599	GO_ENDOSOME_TO_PLASMA_MEMBRANE_PROTEIN_TRANSPORT	1.31	0.78	0	0	0	not significant
12600	GO_NARROW_PORE_CHANNEL_ACTIVITY	1.31	0.77	0	0	0	not significant
12601	GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROT	1.31	0.77	0	0	0	not significant
12602	GO_ANCHORED_COMPONENT_OF_SYNAPTIC_VESICLE_MEMBRANE	1.31	0.76	0	0	0	not significant
12603	GO_INTRONIC_TRANSCRIPTION_REGULATORY_REGION_DNA_BINDING	1.31	0.76	0	0	0	not significant
12604	GO_SEQUESTERING_OF_ACTIN_MONOMERS	1.31	0.76	0	0	0	not significant
12605	GO_POST_ANAL_TAIL_MORPHOGENESIS	1.31	0.75	0	0	0	not significant
12606	REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATI	1.31	0.73	0	0	0	not significant
12607	GO_DIPEPTIDASE_ACTIVITY	1.31	0.72	0	0	0	not significant
12608	CHR19P13	1.32	1.94	0	0	0	not significant
12609	DURAND_STROMA_S_UP	1.32	1.36	0	0	0	not significant
12610	GO_POSTSYNAPTIC_MEMBRANE	1.32	1.27	0	0	0	not significant
12611	ZWANG_EGF_INTERVAL_DN	1.32	1.27	0	0	0	not significant
12612	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP	1.32	1.18	0	0	0	not significant
12613	AFFAR_YY1_TARGETS_UP	1.32	1.14	0	0	0	not significant
12614	GO_CILIARY_PLASM	1.32	1.11	0	0	0	not significant
12615	GO_SYNAPSE_ASSEMBLY	1.32	1.06	0	0	0	not significant
12616	GO_APPENDAGE_MORPHOGENESIS	1.32	1.05	0	0	0	not significant
12617	GO_GLYCOPROTEIN_METABOLIC_PROCESS	1.32	1.04	0	0	0	not significant
12618	GO_DORSAL_VENTRAL_PATTERN_FORMATION	1.32	1.02	0	0	0	not significant
12619	REACTOME_NOD1_2_SIGNALING_PATHWAY	1.32	1.00	0	0	0	not significant
12620	GO_AMMONIUM_TRANSPORT	1.32	0.97	0	0	0	not significant
12621	LIU_TARGETS_OF_VMYB_VS_CMYB_DN	1.32	0.96	0	0	0	not significant
12622	DORSAM_HOXA9_TARGETS_UP	1.32	0.93	0	0	0	not significant
12623	GO_RESPONSE_TO_SORBITOL	1.32	0.93	0	0	0	not significant
12624	KUUSELO_PANCREATIC_CANCER_19Q13_AMPLIFICATION	1.32	0.92	0	0	0	not significant
12625	GO_HISTONE_DEMETHYLASE_ACTIVITY	1.32	0.89	0	0	0	not significant
12626	GO_REGULATION_OF_SYNAPTIC_VESICLE_RECYCLING	1.32	0.89	0	0	0	not significant
12627	GO_CARDIAC_ATRIUM_DEVELOPMENT	1.32	0.87	0	0	0	not significant
12628	OHM_METHYLATED_IN_ADULT_CANCERS	1.32	0.86	0	0	0	not significant
12629	PID_IL5_PATHWAY	1.32	0.86	0	0	0	not significant
12630	GO_CELL_VOLUME_HOMEOSTASIS	1.32	0.85	0	0	0	not significant
12631	MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_UP	1.32	0.85	0	0	0	not significant
12632	TUOMISTO_TUMOR_SUPPRESSION_BY_COL13A1_UP	1.32	0.85	0	0	0	not significant

12633	GO_COMPLEMENT_ACTIVATION_ALTERNATIVE_PATHWAY	1.32	0.83	0	0	0	not significant
12634	GO_NEGATIVE_REGULATION_OF_CELLULAR_SENESCENCE	1.32	0.83	0	0	0	not significant
12635	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_DIFFERENTIAT	1.32	0.82	0	0	0	not significant
12636	REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE	1.32	0.82	0	0	0	not significant
12637	GO_INTERLEUKIN_13_PRODUCTION	1.32	0.81	0	0	0	not significant
12638	GO_MESODERMAL_CELL_FATE_COMMITMENT	1.32	0.81	0	0	0	not significant
12639	MATZUK_MALE_REPRODUCTION_SERTOLI	1.32	0.81	0	0	0	not significant
12640	GO_POSITIVE_REGULATION_OF_CD8_POSITIVE_ALPHA_BETA_T_CELL_	1.32	0.79	0	0	0	not significant
12641	GO_LYMPHOCYTE_DIFFERENTIATION	1.33	1.56	0	0	0	not significant
12642	ODONNELL_TFRC_TARGETS_UP	1.33	1.49	0	0	0	not significant
12643	GO_PATTERN_SPECIFICATION_PROCESS	1.33	1.44	0	0	0	not significant
12644	GO_ENHANCER_BINDING	1.33	1.30	0	0	0	not significant
12645	GO_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	1.33	1.13	0	0	0	not significant
12646	GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	1.33	1.11	0	0	0	not significant
12647	KRAS.AMP.LUNG_UP.V1_DN	1.33	1.05	0	0	0	not significant
12648	WATTEL_AUTONOMOUS_THYROID_ADENOMA_UP	1.33	1.03	0	0	0	not significant
12649	REACTOME_SIGNALING_BY_PDGF	1.33	1.01	0	0	0	not significant
12650	GO_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	1.33	1.00	0	0	0	not significant
12651	BEIER_GLIOMA_STEM_CELL_DN	1.33	0.99	0	0	0	not significant
12652	BURTON_ADIPOGENESIS_11	1.33	0.95	0	0	0	not significant
12653	GO_MEIOTIC_TELOMERE_CLUSTERING	1.33	0.94	0	0	0	not significant
12654	GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	1.33	0.94	0	0	0	not significant
12655	SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_DN	1.33	0.90	0	0	0	not significant
12656	GO_NEGATIVE_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	1.33	0.88	0	0	0	not significant
12657	GOBERT_CORE_OLIGODENDROCYTE_DIFFERENTIATION	1.33	0.88	0	0	0	not significant
12658	GO_LEFT_RIGHT_AXIS_SPECIFICATION	1.33	0.87	0	0	0	not significant
12659	BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_UP	1.33	0.85	0	0	0	not significant
12660	GO_NEURAL_PLATE_MORPHOGENESIS	1.33	0.84	0	0	0	not significant
12661	CLIMENT_BREAST_CANCER_COPY_NUMBER_UP	1.33	0.82	0	0	0	not significant
12662	GO_BRANCHING_INVOLVED_IN_SALIVARY_GLAND_MORPHOGENESIS	1.33	0.82	0	0	0	not significant
12663	IGLESIAS_E2F_TARGETS_DN	1.33	0.79	0	0	0	not significant
12664	REACTOME_ACYL_CHAIN_REMODELLING_OF_PS	1.33	0.79	0	0	0	not significant
12665	GO_NEURON_TO_NEURON_SYNAPSE	1.34	1.56	0	0	0	not significant
12666	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_UP	1.34	1.45	0	0	0	not significant
12667	GO_LYSOSOMAL_LUMEN	1.34	1.22	0	0	0	not significant
12668	GO_SMALL_RIBOSOMAL_SUBUNIT	1.34	1.14	0	0	0	not significant
12669	KANG_IMMORTALIZED_BY_TERT_DN	1.34	1.14	0	0	0	not significant
12670	LEF1_UP.V1_DN	1.34	1.13	0	0	0	not significant
12671	GO_MICROTUBULE_BUNDLE_FORMATION	1.34	1.06	0	0	0	not significant
12672	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_DN	1.34	1.06	0	0	0	not significant
12673	GO_CHLORIDE_TRANSPORT	1.34	1.04	0	0	0	not significant
12674	GO_MALE_MEIOTIC_NUCLEAR_DIVISION	1.34	0.97	0	0	0	not significant
12675	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON	1.34	0.97	0	0	0	not significant
12676	GO_BASAL_PART_OF_CELL	1.34	0.96	0	0	0	not significant
12677	GO_NEGATIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	1.34	0.95	0	0	0	not significant
12678	RODRIGUES_NTN1_AND_DCC_TARGETS	1.34	0.94	0	0	0	not significant
12679	GO_SYNAPTIC_TRANSMISSION_GABAERGIC	1.34	0.93	0	0	0	not significant
12680	ZEILSTRA_CD44_TARGETS_UP	1.34	0.92	0	0	0	not significant
12681	HEDENFALK_BREAST_CANCER_BRACX_UP	1.34	0.91	0	0	0	not significant
12682	GO_DEATH_RECEPTOR_ACTIVITY	1.34	0.90	0	0	0	not significant
12683	GO_IMMUNOLOGICAL_MEMORY_FORMATION_PROCESS	1.34	0.90	0	0	0	not significant
12684	GO_CELLULAR_RESPONSE_TO_GROWTH_HORMONE_STIMULUS	1.34	0.89	0	0	0	not significant
12685	GO_ARGININE_TRANSMEMBRANE_TRANSPORT	1.34	0.88	0	0	0	not significant
12686	BUSA_SAM68_TARGETS_UP	1.34	0.86	0	0	0	not significant
12687	GO_PHOSPHATIDYLSERINE_ACYL_CHAIN_REMODELING	1.34	0.86	0	0	0	not significant
12688	STAEGE_EWING_FAMILY_TUMOR	1.34	0.86	0	0	0	not significant
12689	VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1	1.34	0.86	0	0	0	not significant
12690	GO_PARAXIAL_MESODERM_DEVELOPMENT	1.34	0.85	0	0	0	not significant
12691	DAZARD_UV_RESPONSE_CLUSTER_G24	1.34	0.84	0	0	0	not significant
12692	GO_PURINERGIC_NUCLEOTIDE_RECEPTOR_SIGNALING_PATHWAY	1.34	0.84	0	0	0	not significant
12693	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_CHECKPOINT	1.34	0.83	0	0	0	not significant
12694	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_13_PRODUCTION	1.34	0.83	0	0	0	not significant
12695	PID_INTEGRIN5_PATHWAY	1.34	0.83	0	0	0	not significant
12696	VERHAAK_AML_WITH_NPM1_MUTATED_DN	1.35	1.54	0	0	0	not significant
12697	GO_CYTOSOLIC_PART	1.35	1.52	0	0	0	not significant
12698	ZWANG_DOWN_BY_2ND_EGF_PULSE	1.35	1.46	0	0	0	not significant
12699	GO_ALPHA_BETA_T_CELL_ACTIVATION	1.35	1.35	0	0	0	not significant
12700	CHICAS_RB1_TARGETS_LOW_SERUM	1.35	1.29	0	0	0	not significant
12701	PID_IL2_1PATHWAY	1.35	1.13	0	0	0	not significant
12702	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINDED_IN_ERYT	1.35	1.07	0	0	0	not significant
12703	GO_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	1.35	1.03	0	0	0	not significant
12704	GO_CELL_DIFFERENTIATION_IN_SPINAL_CORD	1.35	0.99	0	0	0	not significant
12705	GO_POSITIVE_T_CELL_SELECTION	1.35	0.99	0	0	0	not significant
12706	RICKMAN_HEAD_AND_NECK_CANCER_A	1.35	0.98	0	0	0	not significant
12707	GO_SENSORY_PERCEPTION_OF_CHEMICAL_STIMULUS	1.35	0.95	0	0	0	not significant
12708	KAUFFMANN_MELANOMA_RELAPSE_DN	1.35	0.92	0	0	0	not significant
12709	GO_FOREBRAIN_NEUROBLAST_DIVISION	1.35	0.90	0	0	0	not significant
12710	GO_HEME_TRANSPORT	1.35	0.89	0	0	0	not significant
12711	REACTOME_P2Y_RECEPTORS	1.35	0.88	0	0	0	not significant
12712	GO_COMPLEMENT_BINDING	1.35	0.87	0	0	0	not significant
12713	BIOCARTA_IL3_PATHWAY	1.35	0.86	0	0	0	not significant
12714	GO_HEAT_GENERATION	1.35	0.86	0	0	0	not significant
12715	GO_POSITIVE_REGULATION_OF_RIG_I_SIGNALING_PATHWAY	1.35	0.86	0	0	0	not significant
12716	GO_LENS_FIBER_CELL_DEVELOPMENT	1.35	0.85	0	0	0	not significant
12717	GO_PROFILIN_BINDING	1.35	0.85	0	0	0	not significant
12718	REACTOME_CATION_COUPLED_CHLORIDE_COTRANSPORTERS	1.35	0.85	0	0	0	not significant
12719	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPT	1.35	0.84	0	0	0	not significant
12720	GO_HISTONE_H4_K12_ACETYLATION	1.35	0.84	0	0	0	not significant
12721	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_SYNAPSE	1.35	0.84	0	0	0	not significant
12722	REACTOME_OLFACTORY_SIGNALING_PATHWAY	1.35	0.84	0	0	0	not significant
12723	GO_ARGININE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.35	0.82	0	0	0	not significant
12724	WEST_ADRENOCORTICAL_TUMOR_DN	1.36	1.99	0	0	0	not significant
12725	GO_MEMBRANE_LIPID_METABOLIC_PROCESS	1.36	1.48	0	0	0	not significant
12726	VECCHI_GASTRIC_CANCER_EARLY_DN	1.36	1.43	0	0	0	not significant
12727	REACTOME_SPHINGOLIPID_METABOLISM	1.36	1.38	0	0	0	not significant
12728	GO_GOLGI_STACK	1.36	1.34	0	0	0	not significant
12729	RODWELL_AGING_KIDNEY_NO_BLOOD_UP	1.36	1.30	0	0	0	not significant
12730	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION	1.36	1.20	0	0	0	not significant
12731	ATM_DN.V1_DN	1.36	1.13	0	0	0	not significant
12732	GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	1.36	1.10	0	0	0	not significant
12733	GO_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE	1.36	1.04	0	0	0	not significant
12734	GO_REGULATION_OF_VASOCONSTRICTION	1.36	0.99	0	0	0	not significant
12735	REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	1.36	0.97	0	0	0	not significant
12736	IWANAGA_E2F1_TARGETS_INDUCED_BY_SERUM	1.36	0.96	0	0	0	not significant
12737	GO_CELLULAR_RESPONSE_TO_OXIDISED_LOW_DENSITY_LIPOPROTEIN_	1.36	0.95	0	0	0	not significant
12738	TOMLINS_PROSTATE_CANCER_DN	1.36	0.94	0	0	0	not significant
12739	GO_SPERM_AXONEME_ASSEMBLY	1.36	0.93	0	0	0	not significant
12740	GALI_TP53_TARGETS_APOPTOTIC_UP	1.36	0.92	0	0	0	not significant
12741	GO_CALCIUM_DEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMB	1.36	0.92	0	0	0	not significant

12742	GO_FOREGUT_MORPHOGENESIS	1.36	0.91	0	0	0	not significant
12743	GO_URETER_DEVELOPMENT	1.36	0.91	0	0	0	not significant
12744	GO_SIGNAL_RECOGNITION_PARTICLE_RECEPTOR_COMPLEX	1.36	0.90	0	0	0	not significant
12745	REACTOME_RUNX3_REGULATES_BCL2L11_BIM_TRANSCRIPTION	1.36	0.89	0	0	0	not significant
12746	GO_PROXIMAL_DISTAL_PATTERN_FORMATION	1.36	0.88	0	0	0	not significant
12747	REACTOME_WNT_LIGAND_BIOGENESIS_AND_TRAFFICKING	1.36	0.88	0	0	0	not significant
12748	BIOCARTA_GATA3_PATHWAY	1.36	0.86	0	0	0	not significant
12749	BIOCARTA_BARD1_PATHWAY	1.36	0.85	0	0	0	not significant
12750	GO_NEGATIVE_REGULATION_OF_P38MAPK_CASCADE	1.36	0.84	0	0	0	not significant
12751	GO_PRESYNAPTIC_MODULATION_OF_CHEMICAL_SYNAPTIC_TRANSMISS	1.36	0.83	0	0	0	not significant
12752	GO_AUTOPHAGIC_CELL_DEATH	1.36	0.82	0	0	0	not significant
12753	JAATINEN_HEMATOPOIETIC_STEM_CELL_UP	1.37	1.65	0	0	0	not significant
12754	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP	1.37	1.65	0	0	0	not significant
12755	NAKAMURA_ADIPOGENESIS_EARLY_UP	1.37	1.16	0	0	0	not significant
12756	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN	1.37	1.15	0	0	0	not significant
12757	CTIP_DN.V1_UP	1.37	1.10	0	0	0	not significant
12758	GO_POSITIVE_REGULATION_OF_CELLULAR_CARBOHYDRATE_METABOL	1.37	1.06	0	0	0	not significant
12759	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCE	1.37	1.03	0	0	0	not significant
12760	REACTOME_ACTIVATION_OF_PPARGC1A_PGC_1ALPHA_BY_PHOSPHOR	1.37	1.03	0	0	0	not significant
12761	GO_PHOSPHATE_ION_TRANSPORT	1.37	1.02	0	0	0	not significant
12762	GO_EXTRACELLULAR_REGULATION_OF_SIGNAL_TRANSDUCTION	1.37	1.00	0	0	0	not significant
12763	GO_LAMIN_BINDING	1.37	0.99	0	0	0	not significant
12764	GO_POTASSIUM_ION_HOMEOSTASIS	1.37	0.97	0	0	0	not significant
12765	GO_REGULATION_OF_SYNAPTIC_VESICLE_CLUSTERING	1.37	0.96	0	0	0	not significant
12766	GO_ENDODEOXYRIBONUCLEASE_ACTIVITY_PRODUCING_5_PHOSPHOM	1.37	0.95	0	0	0	not significant
12767	GO_FORELIMB_MORPHOGENESIS	1.37	0.95	0	0	0	not significant
12768	GO_CELLULAR_RESPONSE_TO_ELECTRICAL_STIMULUS	1.37	0.94	0	0	0	not significant
12769	GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_CYTOPLAS	1.37	0.93	0	0	0	not significant
12770	KIM_GLIS2_TARGETS_DN	1.37	0.93	0	0	0	not significant
12771	GO_ALPHA_BETA_T_CELL_LINEAGE_COMMITMENT	1.37	0.91	0	0	0	not significant
12772	MEISSNER_NPC_ICP_WITH_H3_UNMETHYLATED	1.37	0.91	0	0	0	not significant
12773	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_DN	1.37	0.89	0	0	0	not significant
12774	SHIN_B_CELL_LYMPHOMA_CLUSTER_5	1.37	0.88	0	0	0	not significant
12775	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN	1.38	2.91	0	0	0	not significant
12776	BENPORATH_SUZ12_TARGETS	1.38	2.04	0	0	0	not significant
12777	CHR5Q35	1.38	1.34	0	0	0	not significant
12778	GO_REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	1.38	1.29	0	0	0	not significant
12779	BOYLAN_MULTIPLE_MYELOMA_PCA3_UP	1.38	1.28	0	0	0	not significant
12780	LEIN_CEREBELLUM_MARKERS	1.38	1.15	0	0	0	not significant
12781	REACTOME_CONSTITUTIVE_SIGNALING_BY_ABERRANT_PI3K_IN_CANCE	1.38	1.13	0	0	0	not significant
12782	GO_POTASSIUM_CHLORIDE_SYMPORTER_ACTIVITY	1.38	1.11	0	0	0	not significant
12783	GO_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	1.38	1.06	0	0	0	not significant
12784	GO_CELL_DIFFERENTIATION_IN_HINDBRAIN	1.38	1.00	0	0	0	not significant
12785	GO_POSITIVE_REGULATION_OF_T_HELPER_17_CELL_DIFFERENTIATION	1.38	0.99	0	0	0	not significant
12786	GO_GLYCOLIPID_BINDING	1.38	0.98	0	0	0	not significant
12787	GO_RENAL_VESICLE_DEVELOPMENT	1.38	0.98	0	0	0	not significant
12788	CHR2P24	1.38	0.97	0	0	0	not significant
12789	GO_DNA_REPLICATION_CHECKPOINT	1.38	0.97	0	0	0	not significant
12790	GO_OLIGOSACCHARIDE_CATABOLIC_PROCESS	1.38	0.96	0	0	0	not significant
12791	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCE	1.38	0.96	0	0	0	not significant
12792	FOURNIER_ACINAR_DEVELOPMENT_EARLY_DN	1.38	0.95	0	0	0	not significant
12793	GO_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	1.38	0.94	0	0	0	not significant
12794	REACTOME_SIGNALING_BY_ERYTHROPOIETIN	1.38	0.94	0	0	0	not significant
12795	GO_NEURAL_PLATE_PATTERN_SPECIFICATION	1.38	0.93	0	0	0	not significant
12796	GO_PHOSPHATIDYLETHANOLAMINE_ACYL_CHAIN_REMODELING	1.38	0.92	0	0	0	not significant
12797	REACTOME_ACYL_CHAIN_REMODELLING_OF_PE	1.38	0.92	0	0	0	not significant
12798	HOFMANN_MYELODYSPLASTIC_SYNDROM_HIGH_RISK_UP	1.38	0.91	0	0	0	not significant
12799	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	1.38	0.83	0	0	0	not significant
12800	IVANOVA_HEMATOPOIESIS_STEM_CELL_AND_PROGENITOR	1.39	2.30	0	0	0	not significant
12801	GO_DNA_BINDING_TRANSCRIPTION_REPRESSOR_ACTIVITY_RNA_POLY	1.39	1.73	0	0	0	not significant
12802	YAUCH_HEDGEHOG_SIGNALING_PARACRINE_DN	1.39	1.41	0	0	0	not significant
12803	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN	1.39	1.33	0	0	0	not significant
12804	MORI_PRE_BI_LYMPHOCYTE_DN	1.39	1.33	0	0	0	not significant
12805	GO_METHYLATED_HISTONE_BINDING	1.39	1.22	0	0	0	not significant
12806	IL21_UP.V1_DN	1.39	1.22	0	0	0	not significant
12807	GO_REGULATION_OF_NEURON_PROJECTION_ARBORIZATION	1.39	1.20	0	0	0	not significant
12808	GO_CHROMOSOME_ORGANIZATION_INVOLVED_IN_MEIOTIC_CELL_CYCL	1.39	1.18	0	0	0	not significant
12809	GO_HETEROTYPIC_CELL_CELL_ADHESION	1.39	1.18	0	0	0	not significant
12810	REACTOME_SIGNALING_BY_SCF_KIT	1.39	1.12	0	0	0	not significant
12811	GO_NUCLEAR_MIGRATION	1.39	1.08	0	0	0	not significant
12812	GO_GOLGI_CIS_CISTERNA	1.39	1.07	0	0	0	not significant
12813	GO_METANEPHRIC_RENAL_VESICLE_MORPHOGENESIS	1.39	1.06	0	0	0	not significant
12814	GO_CYTOPLASMIC_SIDE_OF_ENDOPLASMIC_RETICULUM_MEMBRANE	1.39	1.05	0	0	0	not significant
12815	GO_TRANSMITTER_GATED_CHANNEL_ACTIVITY	1.39	1.05	0	0	0	not significant
12816	BIOCARTA_NOS1_PATHWAY	1.39	1.04	0	0	0	not significant
12817	GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	1.39	1.04	0	0	0	not significant
12818	CHO_NR4A1_TARGETS	1.39	1.03	0	0	0	not significant
12819	GO_T_HELPER_17_CELL_LINEAGE_COMMITMENT	1.39	1.01	0	0	0	not significant
12820	GO_LIPID_ANTIGEN_BINDING	1.39	1.00	0	0	0	not significant
12821	REACTOME_PI_3K_CASCADE:FGFR1	1.39	0.99	0	0	0	not significant
12822	VALK_AML_WITH_EVI1	1.39	0.99	0	0	0	not significant
12823	BIOCARTA_CD40_PATHWAY	1.39	0.98	0	0	0	not significant
12824	GO_NEURON_PROJECTION_ARBORIZATION	1.39	0.97	0	0	0	not significant
12825	REACTOME_INTERLEUKIN_20_FAMILY_SIGNALING	1.39	0.97	0	0	0	not significant
12826	MEISSNER_NPC_HCP_WITH_H3K27ME3	1.39	0.96	0	0	0	not significant
12827	PID_IL27_PATHWAY	1.39	0.96	0	0	0	not significant
12828	VERRECCHIA_RESPONSE_TO_TGFB1_C5	1.39	0.96	0	0	0	not significant
12829	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_ENDOGENOUS_LIPID	1.39	0.95	0	0	0	not significant
12830	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREY_UP	1.39	0.93	0	0	0	not significant
12831	GO_HISTONE_H2A_K119_MONOUBIQUITINATION	1.39	0.92	0	0	0	not significant
12832	GO_PROTEIN_TYROSINE_KINASE_ACTIVITY	1.40	1.68	0	0	0	not significant
12833	GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	1.40	1.39	0	0	0	not significant
12834	GO_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	1.40	1.39	0	0	0	not significant
12835	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN	1.40	1.20	0	0	0	not significant
12836	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	1.40	1.20	0	0	0	not significant
12837	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	1.40	1.18	0	0	0	not significant
12838	GO_ENDOCARDIAL_CUSHION_FORMATION	1.40	1.14	0	0	0	not significant
12839	GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_HOMOLO	1.40	1.14	0	0	0	not significant
12840	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_DN	1.40	1.14	0	0	0	not significant
12841	GO_PROTEIN_RETENTION_IN_GOLGI_APPARATUS	1.40	1.12	0	0	0	not significant
12842	GO_CLATHRIN_SCULPTED_VESICLE	1.40	1.10	0	0	0	not significant
12843	GO_SYNAPTIC_VESICLE_CLUSTERING	1.40	1.10	0	0	0	not significant
12844	VISALA_RESPONSE_TO_HEAT_SHOCK_AND_AGING_UP	1.40	1.09	0	0	0	not significant
12845	GO_DIENCEPHALON_DEVELOPMENT	1.40	1.08	0	0	0	not significant
12846	MEDINA_SMARCA4_TARGETS	1.40	1.08	0	0	0	not significant
12847	GO_REGULATION_OF_CD40_SIGNALING_PATHWAY	1.40	1.07	0	0	0	not significant
12848	GO_T_CELL_LINEAGE_COMMITMENT	1.40	1.07	0	0	0	not significant
12849	REACTOME_CELL_CELL_JUNCTION_ORGANIZATION	1.40	1.07	0	0	0	not significant
12850	GO_ALPHA_TUBULIN_BINDING	1.40	1.06	0	0	0	not significant

12851	GO_TOOTH_MINERALIZATION	1.40	1.04	0	0	0	not significant
12852	REACTOME_TNF_RECEPTOR_SUPERFAMILY_TNFSF_MEMBERS_MEDIAT	1.40	1.04	0	0	0	not significant
12853	GO_NEPHRON_TUBULE_FORMATION	1.40	1.03	0	0	0	not significant
12854	GO_CO_SMAD_BINDING	1.40	1.02	0	0	0	not significant
12855	MARIADASON_RESPONSE_TO_BUTYRATE_CURCUMIN_SULINDAC_TSA_1	1.40	1.02	0	0	0	not significant
12856	GO_EPIDERMIS_MORPHOGENESIS	1.40	1.01	0	0	0	not significant
12857	GO_PROTEIN_LOCALIZATION_TO_PHAGOPHORE_ASSEMBLY_SITE	1.40	1.01	0	0	0	not significant
12858	GO_INTEGRAL_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_ENDOPLASMI	1.40	1.00	0	0	0	not significant
12859	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_PURPLE_DN	1.40	0.99	0	0	0	not significant
12860	CASORELLI_APL_SECONDARY_VS_DE_NOVO_DN	1.40	0.98	0	0	0	not significant
12861	CHR1P33	1.40	0.96	0	0	0	not significant
12862	GO_PHOSPHOLIPASE_A2_ACTIVITY_CONSUMING_1_2_DIPALMITOYLPHOS	1.40	0.95	0	0	0	not significant
12863	GO_DNA_STRAND_RENATURATION	1.40	0.94	0	0	0	not significant
12864	GO_PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	1.40	0.93	0	0	0	not significant
12865	GO_AUDITORY_RECEPTOR_CELL_DEVELOPMENT	1.40	0.89	0	0	0	not significant
12866	PEREZ_TP53_TARGETS	1.41	2.90	0	0	0	not significant
12867	GO_VASCULOGENESIS	1.41	1.43	0	0	0	not significant
12868	IWANAGA_CARCINOGENESIS_BY_KRAS_DN	1.41	1.40	0	0	0	not significant
12869	GO_NUCLEAR_INNER_MEMBRANE	1.41	1.25	0	0	0	not significant
12870	CHR15Q21	1.41	1.20	0	0	0	not significant
12871	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_48HR_UP	1.41	1.17	0	0	0	not significant
12872	GO_ICOSANOID_METABOLIC_PROCESS	1.41	1.17	0	0	0	not significant
12873	GO_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	1.41	1.14	0	0	0	not significant
12874	REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	1.41	1.12	0	0	0	not significant
12875	REACTOME_INTERLEUKIN_2_FAMILY_SIGNALING	1.41	1.10	0	0	0	not significant
12876	REACTOME_ONCOGENE_INDUCED_SENESCENCE	1.41	1.10	0	0	0	not significant
12877	GO_HISTONE_ACETYLTRANSFERASE_ACTIVITY_H4_K5_SPECIFIC_	1.41	1.09	0	0	0	not significant
12878	GO_TRANSMISSION_OF_NERVE_IMPULSE	1.41	1.09	0	0	0	not significant
12879	ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_UP	1.41	1.08	0	0	0	not significant
12880	GO_EMBRYONIC_BRAIN_DEVELOPMENT	1.41	1.05	0	0	0	not significant
12881	REACTOME_SIGNALING_BY_NOTCH1_HD_DOMAIN_MUTANTS_IN_CANCER	1.41	1.05	0	0	0	not significant
12882	GO_POSITIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PAT	1.41	1.04	0	0	0	not significant
12883	GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GABAERGIC	1.41	1.04	0	0	0	not significant
12884	GO_ENGULFMENT_OF_APOPTOTIC_CELL	1.41	1.03	0	0	0	not significant
12885	GO_REGULATION_OF_METALLOPEPTIDASE_ACTIVITY	1.41	1.02	0	0	0	not significant
12886	BERENJENO_TRANSFORMED_BY_RHOA_FOREVER_UP	1.41	1.01	0	0	0	not significant
12887	GO_AMELOGENESIS	1.41	1.01	0	0	0	not significant
12888	BIOCARTA_RACC_PATHWAY	1.41	1.00	0	0	0	not significant
12889	GO_ACID_AMINO_ACID_LIGASE_ACTIVITY	1.41	0.99	0	0	0	not significant
12890	GO_ATRIAL_SEPTUM_MORPHOGENESIS	1.41	0.97	0	0	0	not significant
12891	GO_REGULATION_OF_CD8_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	1.41	0.96	0	0	0	not significant
12892	BIOCARTA_AKAP13_PATHWAY	1.41	0.94	0	0	0	not significant
12893	DODD_NASOPHARYNGEAL_CARCINOMA_UP	1.42	4.00	0	0	0	not significant
12894	TARTE_PLASMA_CELL_VS_PLASMABLAST_UP	1.42	2.08	0	0	0	not significant
12895	GO_ANATOMICAL_STRUCTURE_MATURATION	1.42	1.59	0	0	0	not significant
12896	KUNINGER_IGF1_VS_PDGFB_TARGETS_UP	1.42	1.36	0	0	0	not significant
12897	GO_LIPOSACCHARIDE_METABOLIC_PROCESS	1.42	1.33	0	0	0	not significant
12898	GO_AZUROPHIL_GRANULE_MEMBRANE	1.42	1.30	0	0	0	not significant
12899	GO_PEPTIDYL_TYROSINE_AUTOPHOSPHORYLATION	1.42	1.24	0	0	0	not significant
12900	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP	1.42	1.24	0	0	0	not significant
12901	GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_G1_S_TRANSITION	1.42	1.21	0	0	0	not significant
12902	GO_ACYLGLYCEROL_METABOLIC_PROCESS	1.42	1.17	0	0	0	not significant
12903	GO_SCHAFFER_COLLATERAL__CA1_SYNAPSE	1.42	1.17	0	0	0	not significant
12904	GO_ORGANISM_EMERGENCE_FROM_PROTECTIVE_STRUCTURE	1.42	1.14	0	0	0	not significant
12905	GO_MONOCYTE_ACTIVATION	1.42	1.10	0	0	0	not significant
12906	GO_REGULATION_OF_CYTOLYSIS	1.42	1.09	0	0	0	not significant
12907	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	1.42	1.09	0	0	0	not significant
12908	GO_GPI_ANCHOR_BINDING	1.42	1.08	0	0	0	not significant
12909	GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PRO	1.42	1.05	0	0	0	not significant
12910	GO_MODULATION_OF_PROGRAMMED_CELL_DEATH_IN_OTHER_ORGANI	1.42	1.00	0	0	0	not significant
12911	GO_RESPONSE_TO_PAIN	1.42	0.96	0	0	0	not significant
12912	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN	1.43	2.88	0	0	0	not significant
12913	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP	1.43	2.10	0	0	0	not significant
12914	VERHAAK_GLIOBLASTOMA_PRONEURAL	1.43	1.66	0	0	0	not significant
12915	GO_CATION_CHANNEL_COMPLEX	1.43	1.55	0	0	0	not significant
12916	BOYLAN_MULTIPLE_MYELOMA_D_DN	1.43	1.42	0	0	0	not significant
12917	KOBAYASHI_EGFR_SIGNALING_24HR_UP	1.43	1.39	0	0	0	not significant
12918	SABATES_COLORECTAL_ADENOMA_DN	1.43	1.37	0	0	0	not significant
12919	GO_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	1.43	1.33	0	0	0	not significant
12920	GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	1.43	1.33	0	0	0	not significant
12921	GO_CD8_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	1.43	1.20	0	0	0	not significant
12922	REACTOME_INTERLEUKIN_15_SIGNALING	1.43	1.20	0	0	0	not significant
12923	GO_MESENCHYME_MORPHOGENESIS	1.43	1.17	0	0	0	not significant
12924	GO_REGULATION_OF_NUCLEAR_CELL_CYCLE_DNA_REPLICATION	1.43	1.17	0	0	0	not significant
12925	GO_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	1.43	1.15	0	0	0	not significant
12926	GO_POSTSYNAPTIC_SPECIALIZATION_ORGANIZATION	1.43	1.11	0	0	0	not significant
12927	GO_NITRIC_OXIDE_MEDIATED_SIGNAL_TRANSDUCTION	1.43	1.10	0	0	0	not significant
12928	GO_VACUOLAR_PROTON_TRANSPORTING_V_TYPE_ATPASE_COMPLEX	1.43	1.10	0	0	0	not significant
12929	REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEU	1.43	1.10	0	0	0	not significant
12930	GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_LINEAGE_COMMITMENT	1.43	1.09	0	0	0	not significant
12931	GO_VOLUME_SENSITIVE_ANION_CHANNEL_ACTIVITY	1.43	1.09	0	0	0	not significant
12932	GO_CD40_SIGNALING_PATHWAY	1.43	1.08	0	0	0	not significant
12933	GO_REGULATION_OF_SENSORY_PERCEPTION	1.43	1.08	0	0	0	not significant
12934	GO_LIPOPEPTIDE_BINDING	1.43	1.07	0	0	0	not significant
12935	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN	1.43	1.04	0	0	0	not significant
12936	GO_PHOSPHATIDYLSERINE_BINDING	1.43	1.04	0	0	0	not significant
12937	GO_ISOTYPE_SWITCHING_TO_IGG_ISOTYPES	1.43	1.02	0	0	0	not significant
12938	THEODOROU_MAMMARY_TUMORIGENESIS	1.43	1.00	0	0	0	not significant
12939	GO_TRANSPORTER_COMPLEX	1.44	1.84	0	0	0	not significant
12940	MIKKELSEN_NPC_HCP_WITH_H3K27ME3	1.44	1.52	0	0	0	not significant
12941	SIG_CD40PATHWAYMAP	1.44	1.39	0	0	0	not significant
12942	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3	1.44	1.38	0	0	0	not significant
12943	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	1.44	1.31	0	0	0	not significant
12944	REACTOME_PROTEIN_PROTEIN_INTERACTIONS_AT_SYNAPSES	1.44	1.31	0	0	0	not significant
12945	GO_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	1.44	1.30	0	0	0	not significant
12946	PID_EPO_PATHWAY	1.44	1.29	0	0	0	not significant
12947	GHANDHI_BYSTANDER_IRRADIATION_UP	1.44	1.24	0	0	0	not significant
12948	REACTOME_POST_TRANSCRIPTIONAL_SILENCING_BY_SMALL_RNAS	1.44	1.17	0	0	0	not significant
12949	GO_CATECHOLAMINE_SECRETION	1.44	1.16	0	0	0	not significant
12950	GO_DERMATAN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	1.44	1.16	0	0	0	not significant
12951	GO_GLYCOSPHINGOLIPID_BINDING	1.44	1.15	0	0	0	not significant
12952	GO_EXOCRINE_SYSTEM_DEVELOPMENT	1.44	1.14	0	0	0	not significant
12953	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	1.44	1.14	0	0	0	not significant
12954	GO_CYTOPLASMIC_SIDE_OF_ROUGH_ENDOPLASMIC_RETICULUM_MEMB	1.44	1.13	0	0	0	not significant
12955	MOTAMED_RESPONSE_TO_ANDROGEN_DN	1.44	1.13	0	0	0	not significant
12956	BIOCARTA_TH1TH2_PATHWAY	1.44	1.12	0	0	0	not significant
12957	SCHWAB_TARGETS_OF_BMYB_POLYMORPHIC_VARIANTS_DN	1.44	1.10	0	0	0	not significant
12958	GO_ATP_GATED_ION_CHANNEL_ACTIVITY	1.44	1.09	0	0	0	not significant
12959	GO_NEURONAL_ACTION_POTENTIAL	1.44	1.09	0	0	0	not significant

12960	REACTOME_N_GLYCAN_ANTENNAE_ELONGATION	1.44	1.09	0	0	0	not significant
12961	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_UP	1.44	1.09	0	0	0	not significant
12962	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_MONOC	1.44	1.08	0	0	0	not significant
12963	HORIUCHI_WTAP_TARGETS_UP	1.45	1.97	0	0	0	not significant
12964	ESC_J1_UP_EARLY.V1_UP	1.45	1.75	0	0	0	not significant
12965	CHR7Q36	1.45	1.59	0	0	0	not significant
12966	GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	1.45	1.48	0	0	0	not significant
12967	TIEN_INTESTINE_PROBIOTICS_6HR_UP	1.45	1.38	0	0	0	not significant
12968	GO_ECTODERM_DEVELOPMENT	1.45	1.29	0	0	0	not significant
12969	REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRAN	1.45	1.27	0	0	0	not significant
12970	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN	1.45	1.26	0	0	0	not significant
12971	GO_INTRINSIC_COMPONENT_OF_SYNAPTIC_VESICLE_MEMBRANE	1.45	1.24	0	0	0	not significant
12972	REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLIS	1.45	1.22	0	0	0	not significant
12973	DELACROIX_RAR_TARGETS_DN	1.45	1.17	0	0	0	not significant
12974	GO_INHIBITORY_SYNAPSE_ASSEMBLY	1.45	1.16	0	0	0	not significant
12975	REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING	1.45	1.14	0	0	0	not significant
12976	GO_CYTOSKELETAL_ANCHORING_AT_NUCLEAR_MEMBRANE	1.45	1.13	0	0	0	not significant
12977	GO_REGULATION_OF_VASCULAR_PERMEABILITY	1.45	1.13	0	0	0	not significant
12978	PASTURAL_RIZ1_TARGETS_UP	1.45	1.12	0	0	0	not significant
12979	GO_RESPONSE_TO_UV_C	1.45	1.11	0	0	0	not significant
12980	OSADA_ASCL1_TARGETS_DN	1.45	1.11	0	0	0	not significant
12981	GO_REGULATION_OF_AMPA_RECEPTOR_ACTIVITY	1.45	1.10	0	0	0	not significant
12982	TIAN_BHLHA15_TARGETS	1.45	1.10	0	0	0	not significant
12983	GO_PIRNA_METABOLIC_PROCESS	1.45	1.08	0	0	0	not significant
12984	KOBAYASHI_RESPONSE_TO_ROMIDEPSIN	1.45	1.06	0	0	0	not significant
12985	GO_OXIDIZED_DNA_BINDING	1.45	1.00	0	0	0	not significant
12986	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP	1.46	4.00	0	0	0	not significant
12987	GO_HYDROLASE_ACTIVITY_ACTING_ON_GLYCOSYL_BONDS	1.46	1.61	0	0	0	not significant
12988	GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	1.46	1.46	0	0	0	not significant
12989	GO_RESPONSE_TO_CADMIUM_ION	1.46	1.43	0	0	0	not significant
12990	KLEIN_TARGETS_OF_BCR_ABL1_FUSION	1.46	1.38	0	0	0	not significant
12991	GO_ANNEALING_HELICASE_ACTIVITY	1.46	1.37	0	0	0	not significant
12992	GO_PCG_PROTEIN_COMPLEX	1.46	1.30	0	0	0	not significant
12993	PID_ERBB4_PATHWAY	1.46	1.28	0	0	0	not significant
12994	GO_INTERLEUKIN_4_PRODUCTION	1.46	1.27	0	0	0	not significant
12995	GO_NEGATIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	1.46	1.26	0	0	0	not significant
12996	SAGIV_CD24_TARGETS_DN	1.46	1.25	0	0	0	not significant
12997	GO_POSITIVE_REGULATION_OF_T_HELPER_17_TYPE_IMMUNE_RESPONS	1.46	1.23	0	0	0	not significant
12998	GAVIN_PDE3B_TARGETS	1.46	1.22	0	0	0	not significant
12999	GO_INTERLEUKIN_7_MEDIATED_SIGNALING_PATHWAY	1.46	1.22	0	0	0	not significant
13000	GO_POSITIVE_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	1.46	1.22	0	0	0	not significant
13001	MAHADEVAN_RESPONSE_TO_MP470_DN	1.46	1.21	0	0	0	not significant
13002	GO_CD4_POSITIVE_OR_CD8_POSITIVE_ALPHA_BETA_T_CELL_LINEAGE_	1.46	1.18	0	0	0	not significant
13003	GO_CELLULAR_RESPONSE_TO_SALT	1.46	1.17	0	0	0	not significant
13004	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GLOBO_SERIES	1.46	1.17	0	0	0	not significant
13005	GO_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIG	1.46	1.16	0	0	0	not significant
13006	TRAYNOR_RETT_SYNDROM_UP	1.46	1.16	0	0	0	not significant
13007	REACTOME_NICOTINAMIDE_SALVAGING	1.46	1.15	0	0	0	not significant
13008	GO_COCHLEA_MORPHOGENESIS	1.46	1.13	0	0	0	not significant
13009	NABA_PROTEOGLYCANS	1.46	1.13	0	0	0	not significant
13010	GO_DEVELOPMENTAL_INDUCTION	1.46	1.12	0	0	0	not significant
13011	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	1.47	2.25	0	0	0	not significant
13012	REACTOME_INFLUENZA_INFECTION	1.47	1.99	0	0	0	not significant
13013	GO_REGULATION_OF_CELLULAR_CARBOHYDRATE_METABOLIC_PROCE	1.47	1.71	0	0	0	not significant
13014	BHAT_ESR1_TARGETS_VIA_AKT1_DN	1.47	1.58	0	0	0	not significant
13015	FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_UP	1.47	1.41	0	0	0	not significant
13016	GO_ENAMEL_MINERALIZATION	1.47	1.39	0	0	0	not significant
13017	BRCA1_DN.V1_UP	1.47	1.34	0	0	0	not significant
13018	GO_CHLORIDE_CHANNEL_COMPLEX	1.47	1.33	0	0	0	not significant
13019	PID_FGF_PATHWAY	1.47	1.31	0	0	0	not significant
13020	GO_REGULATION_OF_NATURAL_KILLER_CELL_DIFFERENTIATION	1.47	1.30	0	0	0	not significant
13021	PID_S1P_META_PATHWAY	1.47	1.29	0	0	0	not significant
13022	GO_REGULATION_OF_HEART_RATE_BY_CARDIAC_CONDUCTION	1.47	1.25	0	0	0	not significant
13023	POS_RESPONSE_TO_HISTAMINE_DN	1.47	1.25	0	0	0	not significant
13024	REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	1.47	1.25	0	0	0	not significant
13025	GO_POSITIVE_REGULATION_OF_METALLOPEPTIDASE_ACTIVITY	1.47	1.24	0	0	0	not significant
13026	GO_POSITIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BI	1.47	1.22	0	0	0	not significant
13027	WONG_ENDMETRIUM_CANCER_DN	1.47	1.20	0	0	0	not significant
13028	GO_H3_HISTONE_ACETYLTRANSFERASE_COMPLEX	1.47	1.18	0	0	0	not significant
13029	GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION_CELL_EXTENSION	1.47	1.16	0	0	0	not significant
13030	AIGNER_ZEB1_TARGETS	1.47	1.15	0	0	0	not significant
13031	GO_POSITIVE_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	1.47	1.09	0	0	0	not significant
13032	GO_INOSITOL_LIPID_MEDIATED_SIGNALING	1.48	1.87	0	0	0	not significant
13033	KEGG_HEMATOPOIETIC_CELL_LINEAGE	1.48	1.48	0	0	0	not significant
13034	GO_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	1.48	1.41	0	0	0	not significant
13035	NOUZOVA_METHYLATED_IN_APL	1.48	1.39	0	0	0	not significant
13036	GO_NSL_COMPLEX	1.48	1.35	0	0	0	not significant
13037	GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CI	1.48	1.32	0	0	0	not significant
13038	MA_PITUITARY_FETAL_VS_ADULT_UP	1.48	1.29	0	0	0	not significant
13039	VALK_AML_CLUSTER_4	1.48	1.27	0	0	0	not significant
13040	GO_REGULATION_OF_MICROTUBULE_BASED_MOVEMENT	1.48	1.25	0	0	0	not significant
13041	KEGG_OTHER_GLYCAN_DEGRADATION	1.48	1.23	0	0	0	not significant
13042	CHR6Q13	1.48	1.22	0	0	0	not significant
13043	REACTOME_INTERLEUKIN_21_SIGNALING	1.48	1.21	0	0	0	not significant
13044	GO_CAMP_BINDING	1.48	1.14	0	0	0	not significant
13045	CHANG_CORE_SERUM_RESPONSE_DN	1.49	2.15	0	0	0	not significant
13046	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	1.49	1.86	0	0	0	not significant
13047	GO_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	1.49	1.64	0	0	0	not significant
13048	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN	1.49	1.58	0	0	0	not significant
13049	PID_IL4_2PATHWAY	1.49	1.49	0	0	0	not significant
13050	CHR5Q22	1.49	1.45	0	0	0	not significant
13051	GO_LONG_TERM_SYNAPTIC_POTENTIATION	1.49	1.43	0	0	0	not significant
13052	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN	1.49	1.42	0	0	0	not significant
13053	GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	1.49	1.39	0	0	0	not significant
13054	REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	1.49	1.36	0	0	0	not significant
13055	REACTOME_SIGNALING_BY_CYTOSOLIC_FGFR1_FUSION_MUTANTS	1.49	1.28	0	0	0	not significant
13056	GO_POSITIVE_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	1.49	1.27	0	0	0	not significant
13057	GO_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	1.49	1.26	0	0	0	not significant
13058	IIZUKA_LIVER_CANCER_EARLY_RECURRENCE	1.49	1.25	0	0	0	not significant
13059	KEGG_SPHINGOLIPID_METABOLISM	1.49	1.25	0	0	0	not significant
13060	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	1.49	1.23	0	0	0	not significant
13061	LU_TUMOR_ANGIOGENESIS_UP	1.49	1.22	0	0	0	not significant
13062	GO_COBALAMIN_TRANSPORT	1.49	1.21	0	0	0	not significant
13063	GO_ANION_CATION_SYMPORTER_ACTIVITY	1.49	1.20	0	0	0	not significant
13064	GO_DENDRITIC_SPINE_MAINTENANCE	1.49	1.20	0	0	0	not significant
13065	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	1.50	2.85	0	0	0	Enhanced
13066	KRAS.600_UP.V1_DN	1.50	2.04	0	0	0	Enhanced
13067	REACTOME_INTERLEUKIN_7_SIGNALING	1.50	1.39	0	0	0	Enhanced
13068	REACTOME_CREB3_FACTORS_ACTIVATE_GENES	1.50	1.36	0	0	0	Enhanced

13069	GO_TOLERANCE_INDUCTION	1.50	1.34	0	0	0	Enhanced
13070	SCHRAMM_INHBA_TARGETS_DN	1.50	1.28	0	0	0	Enhanced
13071	HOLLEMAN_VINCRISTINE_RESISTANCE_B_ALL_DN	1.50	1.21	0	0	0	Enhanced
13072	REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	1.50	1.20	0	0	0	Enhanced
13073	GO_GOLGI_CISTERNA	1.51	1.84	0	0	0	Enhanced
13074	P53_DN.V2_UP	1.51	1.80	0	0	0	Enhanced
13075	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	1.51	1.77	0	0	0	Enhanced
13076	GO_SPINAL_CORD_DEVELOPMENT	1.51	1.68	0	0	0	Enhanced
13077	GO_LYMPHOCYTE_COSTIMULATION	1.51	1.60	0	0	0	Enhanced
13078	GO_REGULATION_OF_PLATELET_ACTIVATION	1.51	1.50	0	0	0	Enhanced
13079	GO_PROTEIN_C_LINKED_GLYCOSYLATION	1.51	1.48	0	0	0	Enhanced
13080	GO_DOPAMINE_SECRETION	1.51	1.38	0	0	0	Enhanced
13081	GO_POSTSYNAPTIC_ENDOSOME	1.51	1.36	0	0	0	Enhanced
13082	YAGUE_PRETUMOR_DRUG_RESISTANCE_DN	1.51	1.36	0	0	0	Enhanced
13083	GO_LATERAL_MESODERM_DEVELOPMENT	1.51	1.30	0	0	0	Enhanced
13084	GO_ESTROGEN_BIOSYNTHETIC_PROCESS	1.51	1.27	0	0	0	Enhanced
13085	GO_CATION_CHLORIDE_SYMPORTER_ACTIVITY	1.51	1.26	0	0	0	Enhanced
13086	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	1.51	1.21	0	0	0	Enhanced
13087	GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	1.52	2.55	0	0	0	Enhanced
13088	CHR16P13	1.52	2.38	0	0	0	Enhanced
13089	MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_DN	1.52	2.10	0	0	0	Enhanced
13090	PDGF_UP.V1_DN	1.52	1.83	0	0	0	Enhanced
13091	GO_REGULATION_OF_POSTSYNAPTIC_NEUROTRANSMITTER_RECEPTO	1.52	1.47	0	0	0	Enhanced
13092	LOPES_METHYLATED_IN_COLON_CANCER_UP	1.52	1.44	0	0	0	Enhanced
13093	MEISSNER_BRAIN_HCP_WITH_H3K4ME2_AND_H3K27ME3	1.52	1.42	0	0	0	Enhanced
13094	BIOCARTA_BLYMPHOCYTE_PATHWAY	1.52	1.40	0	0	0	Enhanced
13095	GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	1.52	1.39	0	0	0	Enhanced
13096	GO_MITOTIC_G2_DNA_DAMAGE_CHECKPOINT	1.52	1.33	0	0	0	Enhanced
13097	GO_CHLORIDE_ION_HOMEOSTASIS	1.52	1.28	0	0	0	Enhanced
13098	REACTOME_REGULATION_OF_PTEN_MRNA_TRANSLATION	1.52	1.28	0	0	0	Enhanced
13099	REACTOME_CREB1_PHOSPHORYLATION_THROUGH_NMDA_RECEPTOR_	1.52	1.27	0	0	0	Enhanced
13100	CHRYQ11	1.52	1.26	0	0	0	Enhanced
13101	GERHOLD_RESPONSE_TO_TZD_DN	1.52	1.26	0	0	0	Enhanced
13102	NIELSEN_LEIOMYOSARCOMA_DN	1.52	1.26	0	0	0	Enhanced
13103	FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP	1.53	2.11	0	0	0	Enhanced
13104	FERREIRA_EWINGS_SARCOMA_UNSTABLE_VS_STABLE_DN	1.53	1.95	0	0	0	Enhanced
13105	PECE_MAMMARY_STEM_CELL_UP	1.53	1.89	0	0	0	Enhanced
13106	BAKKER_FOXO3_TARGETS_UP	1.53	1.86	0	0	0	Enhanced
13107	CHR3Q27	1.53	1.64	0	0	0	Enhanced
13108	GO_ACTIVATION_OF_JANUS_KINASE_ACTIVITY	1.53	1.61	0	0	0	Enhanced
13109	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_6_SECRETION	1.53	1.60	0	0	0	Enhanced
13110	LE_SKI_TARGETS_UP	1.53	1.55	0	0	0	Enhanced
13111	ANDERSEN_LIVER_CANCER_KRT19_UP	1.53	1.54	0	0	0	Enhanced
13112	PHESSE_TARGETS_OF_APC_AND_MBD2_UP	1.53	1.53	0	0	0	Enhanced
13113	GO_MITOTIC_G2_M_TRANSITION_CHECKPOINT	1.53	1.52	0	0	0	Enhanced
13114	GO_IMMUNOLOGICAL_MEMORY_PROCESS	1.53	1.51	0	0	0	Enhanced
13115	DORSEY_GAB2_TARGETS	1.53	1.44	0	0	0	Enhanced
13116	GO_NUCLEUS_LOCALIZATION	1.53	1.41	0	0	0	Enhanced
13117	GO_REGULATION_OF_T_HELPER_17_TYPE_IMMUNE_RESPONSE	1.53	1.40	0	0	0	Enhanced
13118	REACTOME_GLYCOSPHINGOLIPID_METABOLISM	1.53	1.40	0	0	0	Enhanced
13119	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_SECRETION	1.53	1.36	0	0	0	Enhanced
13120	LEE_DOUBLE_POLAR_THYMOCYTE	1.53	1.36	0	0	0	Enhanced
13121	GO_ESTABLISHMENT_OF_PLANAR_POLARITY_INVOLVED_IN_NEURAL_TU	1.53	1.34	0	0	0	Enhanced
13122	BIOCARTA_MCM_PATHWAY	1.53	1.32	0	0	0	Enhanced
13123	FISCHER_G1_S_CELL_CYCLE	1.54	2.83	0	0	0	Enhanced
13124	GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	1.54	1.96	0	0	0	Enhanced
13125	GO_ANION_CHANNEL_ACTIVITY	1.54	1.82	0	0	0	Enhanced
13126	GO_CAMP_CATABOLIC_PROCESS	1.54	1.73	0	0	0	Enhanced
13127	GO_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	1.54	1.57	0	0	0	Enhanced
13128	GO_ESTRADIOL_17_BETA_DEHYDROGENASE_ACTIVITY	1.54	1.49	0	0	0	Enhanced
13129	GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCES	1.54	1.48	0	0	0	Enhanced
13130	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	1.54	1.42	0	0	0	Enhanced
13131	HUMMEL_BURKITTS_LYMPHOMA_DN	1.54	1.41	0	0	0	Enhanced
13132	REACTOME_RAS_ACTIVATION_UPON_CA2PLUS_INFLUX_THROUGH_NMD	1.54	1.41	0	0	0	Enhanced
13133	GO_MIDDLE_EAR_MORPHOGENESIS	1.54	1.40	0	0	0	Enhanced
13134	REACTOME_COMPETING_ENDOGENOUS_RNAS_CERNAS_REGULATE_PT	1.54	1.39	0	0	0	Enhanced
13135	GO_DEFINITIVE_HEMOPOIESIS	1.54	1.38	0	0	0	Enhanced
13136	GO_INTERFERON_GAMMA_SECRETION	1.54	1.32	0	0	0	Enhanced
13137	GO_VIRAL_GENE_EXPRESSION	1.55	4.00	0	0	0	Enhanced
13138	WHITFIELD_CELL_CYCLE_G1_S	1.55	2.52	0	0	0	Enhanced
13139	GO_INORGANIC_ANION_TRANSPORT	1.55	1.96	0	0	0	Enhanced
13140	BAE_BRCA1_TARGETS_DN	1.55	1.64	0	0	0	Enhanced
13141	GO_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	1.55	1.63	0	0	0	Enhanced
13142	GO_SIGNAL_TRANSDUCTION_INVOLVED_IN_REGULATION_OF_GENE_EX	1.55	1.61	0	0	0	Enhanced
13143	GO_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTO	1.55	1.58	0	0	0	Enhanced
13144	GO_SIALYLTRANSFERASE_ACTIVITY	1.55	1.55	0	0	0	Enhanced
13145	PID_ECADHERIN_KERATINOCYTE_PATHWAY	1.55	1.55	0	0	0	Enhanced
13146	GO_NATURAL_KILLER_CELL_PROLIFERATION	1.55	1.53	0	0	0	Enhanced
13147	GO_PHOSPHOLIPASE_A2_ACTIVITY	1.55	1.52	0	0	0	Enhanced
13148	LEE_LIVER_CANCER_CIPROFIBRATE_DN	1.55	1.50	0	0	0	Enhanced
13149	GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	1.55	1.49	0	0	0	Enhanced
13150	GO_DNA_METHYLATION_INVOLVED_IN_GAMETE_GENERATION	1.55	1.44	0	0	0	Enhanced
13151	GO_MANNOSIDASE_ACTIVITY	1.55	1.39	0	0	0	Enhanced
13152	GO_OSTEOBLAST_PROLIFERATION	1.55	1.35	0	0	0	Enhanced
13153	LEE_BMP2_TARGETS_UP	1.56	4.00	0	0	0	Enhanced
13154	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY	1.56	4.00	0	0	0	Enhanced
13155	WOO_LIVER_CANCER_RECURRENCE_UP	1.56	2.02	0	0	0	Enhanced
13156	GO_SPHINGOLIPID_METABOLIC_PROCESS	1.56	1.84	0	0	0	Enhanced
13157	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_PROLIFERATI	1.56	1.69	0	0	0	Enhanced
13158	CHR7Q31	1.56	1.65	0	0	0	Enhanced
13159	GO_GOLGI_CISTERNA_MEMBRANE	1.56	1.63	0	0	0	Enhanced
13160	REACTOME_UNBLOCKING_OF_NMDA_RECEPTORS_GLUTAMATE_BINDIN	1.56	1.63	0	0	0	Enhanced
13161	GO_GAMMA_DELTA_T_CELL_DIFFERENTIATION	1.56	1.57	0	0	0	Enhanced
13162	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	1.56	1.54	0	0	0	Enhanced
13163	GO_INTERLEUKIN_10_PRODUCTION	1.56	1.53	0	0	0	Enhanced
13164	GO_POSITIVE_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_ST	1.56	1.51	0	0	0	Enhanced
13165	GO_T_HELPER_17_TYPE_IMMUNE_RESPONSE	1.56	1.51	0	0	0	Enhanced
13166	GO_CHONDROITIN_SULFATE_BIOSYNTHETIC_PROCESS	1.56	1.50	0	0	0	Enhanced
13167	GO_TUMOR_NECROSIS_FACTOR_SECRETION	1.56	1.50	0	0	0	Enhanced
13168	GO_POSITIVE_REGULATION_OF_ISOTYPE_SWITCHING_TO_IGG_ISOTYP	1.56	1.49	0	0	0	Enhanced
13169	CROONQUIST_IL6_DEPRIVATION_UP	1.56	1.45	0	0	0	Enhanced
13170	REACTOME_METABOLISM_OF_STEROID_HORMONES	1.56	1.45	0	0	0	Enhanced
13171	BIOCARTA_AMAN_PATHWAY	1.56	1.44	0	0	0	Enhanced
13172	GO_ATRIAL_SEPTUM_DEVELOPMENT	1.56	1.41	0	0	0	Enhanced
13173	GO_REGULATION_OF_EPITHELIAL_TUBE_FORMATION	1.56	1.40	0	0	0	Enhanced
13174	GO_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCTION	1.56	1.39	0	0	0	Enhanced
13175	REACTOME_SIGNALING_BY_FGFR1_IN_DISEASE	1.56	1.38	0	0	0	Enhanced
13176	GO_DESMOSOME	1.56	1.35	0	0	0	Enhanced
13177	CHR19Q13	1.57	4.00	0	0	0	Enhanced

13178	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP	1.57	2.14	0	0	0	Enhanced
13179	MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_UP	1.57	1.89	0	0	0	Enhanced
13180	GO_INORGANIC_ANION_TRANSMEMBRANE_TRANSPORT	1.57	1.87	0	0	0	Enhanced
13181	KANG_AR_TARGETS_UP	1.57	1.72	0	0	0	Enhanced
13182	GO_REGULATION_OF_CAMP_MEDIATED_SIGNALING	1.57	1.66	0	0	0	Enhanced
13183	GO_HISTONE_H4_K5_ACETYLATION	1.57	1.59	0	0	0	Enhanced
13184	GO_NEURAL_PLATE_DEVELOPMENT	1.57	1.50	0	0	0	Enhanced
13185	GO_TERMINAL_BOUTON	1.57	1.47	0	0	0	Enhanced
13186	IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_UP	1.57	1.47	0	0	0	Enhanced
13187	REACTOME_STAT5_ACTIVATION	1.57	1.44	0	0	0	Enhanced
13188	ZHENG_RESPONSE_TO_ARSENITE_UP	1.57	1.44	0	0	0	Enhanced
13189	GO_BONE_MATURATION	1.57	1.43	0	0	0	Enhanced
13190	GO_TRANSLATIONAL_INITIATION	1.58	2.83	0	0	0	Enhanced
13191	WU_CELL_MIGRATION	1.58	2.78	0	0	0	Enhanced
13192	GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_SECRETION	1.58	1.95	0	0	0	Enhanced
13193	PYEON_HPV_POSITIVE_TUMORS_UP	1.58	1.82	0	0	0	Enhanced
13194	GO_ESTABLISHMENT_OF_PLANAR_POLARITY_OF_EMBRYONIC_EPITHEL	1.58	1.64	0	0	0	Enhanced
13195	GO_EXCITATORY_SYNAPSE	1.58	1.59	0	0	0	Enhanced
13196	GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT_CONFERRI	1.58	1.58	0	0	0	Enhanced
13197	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	1.58	1.58	0	0	0	Enhanced
13198	PID_NFKAPPAB_ATYPICAL_PATHWAY	1.58	1.58	0	0	0	Enhanced
13199	GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERAT	1.58	1.56	0	0	0	Enhanced
13200	BIOCARTA_IL7_PATHWAY	1.58	1.53	0	0	0	Enhanced
13201	GO_SIALYLATION	1.58	1.51	0	0	0	Enhanced
13202	RIZ_ERYTHROID_DIFFERENTIATION_HEMGN	1.58	1.46	0	0	0	Enhanced
13203	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PRO	1.58	1.39	0	0	0	Enhanced
13204	REACTOME_ERYTHROPOIETIN_ACTIVATES_STAT5	1.59	2.12	0	0	0	Enhanced
13205	JAK2_DN.V1_DN	1.59	2.06	0	0	0	Enhanced
13206	TERAMOTO_OPN_TARGETS_CLUSTER_3	1.59	1.95	0	0	0	Enhanced
13207	REACTOME_NEGATIVE_REGULATION_OF_NMDA_RECEPTOR_MEDIATED_	1.59	1.67	0	0	0	Enhanced
13208	MCCABE_HOXC6_TARGETS_CANCER_UP	1.59	1.64	0	0	0	Enhanced
13209	BIOCARTA_EDG1_PATHWAY	1.59	1.62	0	0	0	Enhanced
13210	SABATES_COLORECTAL_ADENOMA_SIZE_UP	1.59	1.61	0	0	0	Enhanced
13211	NIKOLSKY_BREAST_CANCER_19Q13.1_AMPLICON	1.59	1.58	0	0	0	Enhanced
13212	GO_INTRINSIC_COMPONENT_OF_PRESYNAPTIC_ACTIVE_ZONE_MEMBRA	1.59	1.56	0	0	0	Enhanced
13213	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN	1.59	1.52	0	0	0	Enhanced
13214	JISON_SICKLE_CELL_DISEASE_DN	1.60	4.00	0	0	0	Enhanced
13215	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP	1.60	2.10	0	0	0	Enhanced
13216	KRAS.BREAST_UP.V1_DN	1.60	1.96	0	0	0	Enhanced
13217	GO_POTASSIUM_ION_EXPORT_ACROSS_PLASMA_MEMBRANE	1.60	1.88	0	0	0	Enhanced
13218	PID_NCADHERIN_PATHWAY	1.60	1.70	0	0	0	Enhanced
13219	GO_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	1.60	1.69	0	0	0	Enhanced
13220	GO_GASTRULATION_WITH_MOUTH_FORMING_SECOND	1.60	1.64	0	0	0	Enhanced
13221	GO_REGULATORY_T_CELL_DIFFERENTIATION	1.60	1.64	0	0	0	Enhanced
13222	RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_SMAD4_UP	1.60	1.55	0	0	0	Enhanced
13223	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN	1.61	2.33	0	0	0	Enhanced
13224	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP	1.61	2.07	0	0	0	Enhanced
13225	MIKKELSEN_IPS_ICP_WITH_H3K4ME3_AND_H327ME3	1.61	1.87	0	0	0	Enhanced
13226	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	1.61	1.86	0	0	0	Enhanced
13227	REACTOME_FGFR1_MUTANT_RECEPTOR_ACTIVATION	1.61	1.79	0	0	0	Enhanced
13228	GO_INTEGRAL_COMPONENT_OF_PRESYNAPTIC_ACTIVE_ZONE_MEMBR	1.61	1.78	0	0	0	Enhanced
13229	WEBER_METHYLATED_HCP_IN_SPERM_DN	1.61	1.75	0	0	0	Enhanced
13230	REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	1.61	1.66	0	0	0	Enhanced
13231	GO_DOPAMINE_TRANSPORT	1.61	1.59	0	0	0	Enhanced
13232	MIKKELSEN_MEF_ICP_WITH_H3K27ME3	1.62	2.30	0	0	0	Enhanced
13233	GO_INORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.62	2.13	0	0	0	Enhanced
13234	GO_INTRACELLULAR_CALCIUM_ACTIVATED_CHLORIDE_CHANNEL_ACTIV	1.62	1.95	0	0	0	Enhanced
13235	KEGG_ASTHMA	1.62	1.85	0	0	0	Enhanced
13236	GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	1.62	1.80	0	0	0	Enhanced
13237	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	1.62	1.72	0	0	0	Enhanced
13238	REACTOME_LONG_TERM_POTENTIATION	1.62	1.49	0	0	0	Enhanced
13239	GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	1.63	1.98	0	0	0	Enhanced
13240	MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN	1.63	1.88	0	0	0	Enhanced
13241	REACTOME_SIGNALING_BY_LEPTIN	1.63	1.74	0	0	0	Enhanced
13242	GO_3_5_CYCLIC_AMP_PHOSPHODIESTERASE_ACTIVITY	1.63	1.72	0	0	0	Enhanced
13243	RIZ_ERYTHROID_DIFFERENTIATION_APOBEC2	1.63	1.71	0	0	0	Enhanced
13244	GO_POSITIVE_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	1.63	1.70	0	0	0	Enhanced
13245	GO_AMPA_GLUTAMATE_RECEPTOR_COMPLEX	1.63	1.47	0	0	0	Enhanced
13246	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_0	1.64	2.31	0	0	0	Enhanced
13247	CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY	1.64	1.99	0	0	0	Enhanced
13248	HALMOS_CEBPA_TARGETS_UP	1.64	1.99	0	0	0	Enhanced
13249	GO_SPHINGOLIPID_BINDING	1.64	1.75	0	0	0	Enhanced
13250	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP	1.64	1.75	0	0	0	Enhanced
13251	GO_IONOTROPIC_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	1.64	1.69	0	0	0	Enhanced
13252	GO_COMPLEMENT_ACTIVATION	1.64	1.68	0	0	0	Enhanced
13253	CHR16Q13	1.64	1.65	0	0	0	Enhanced
13254	GO_N_GLYCAN_PROCESSING	1.64	1.60	0	0	0	Enhanced
13255	GO_HYDROLASE_ACTIVITY_HYDROLYZING_O_GLYCOSYL_COMPOUNDS	1.65	2.49	0	0	0	Enhanced
13256	IL15_UP.V1_DN	1.65	2.49	0	0	0	Enhanced
13257	GO_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SI	1.65	2.48	0	0	0	Enhanced
13258	GO_REGULATION_OF_INTERFERON_GAMMA_SECRETION	1.65	2.27	0	0	0	Enhanced
13259	WILLIAMS_ESR1_TARGETS_DN	1.65	2.11	0	0	0	Enhanced
13260	GO_CHLORIDE_CHANNEL_ACTIVITY	1.65	1.97	0	0	0	Enhanced
13261	REACTOME_CS_DS_DEGRADATION	1.65	1.96	0	0	0	Enhanced
13262	GO_CHLORIDE_TRANSMEMBRANE_TRANSPORT	1.65	1.82	0	0	0	Enhanced
13263	GO_MONOAMINE_TRANSPORT	1.65	1.81	0	0	0	Enhanced
13264	BIOCARTA_IL22BP_PATHWAY	1.65	1.75	0	0	0	Enhanced
13265	GO_POSTSYNAPTIC_DENSITY_MEMBRANE	1.65	1.73	0	0	0	Enhanced
13266	GO_POSITIVE_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	1.66	1.90	0	0	0	Enhanced
13267	GO_REGULATION_OF_CELL_FATE_COMMITMENT	1.66	1.65	0	0	0	Enhanced
13268	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP	1.67	2.81	0	0	0	Enhanced
13269	GO_APICOLATERAL_PLASMA_MEMBRANE	1.67	2.42	0	0	0	Enhanced
13270	GO_RESPONSE_TO_COPPER_ION	1.67	2.17	0	0	0	Enhanced
13271	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP	1.68	4.00	0	0	0	Enhanced
13272	HOELZEL_NF1_TARGETS_DN	1.68	2.48	0	0	0	Enhanced
13273	GO_EMBRYONIC_DIGIT_MORPHOGENESIS	1.68	2.17	0	0	0	Enhanced
13274	GO_REGULATION_OF_GERMINAL_CENTER_FORMATION	1.68	2.13	0	0	0	Enhanced
13275	STEGER_ADIPOGENESIS_DN	1.68	2.12	0	0	0	Enhanced
13276	GO_FAT_PAD_DEVELOPMENT	1.68	1.95	0	0	0	Enhanced
13277	MATTHEWS_AP1_TARGETS	1.68	1.89	0	0	0	Enhanced
13278	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP	1.69	4.00	0	0	0	Enhanced
13279	GO_CHONDROITIN_SULFATE_CATABOLIC_PROCESS	1.69	2.24	0	0	0	Enhanced
13280	GO_SPLEEN_DEVELOPMENT	1.69	2.17	0	0	0	Enhanced
13281	GO_RESPONSE_TO_INTERLEUKIN_9	1.69	2.13	0	0	0	Enhanced
13282	GO_STRESS_RESPONSE_TO_METAL_ION	1.69	2.13	0	0	0	Enhanced
13283	GO_GAMMA_DELTA_T_CELL_ACTIVATION	1.69	1.96	0	0	0	Enhanced
13284	GO_CILIUM_MOVEMENT	1.69	1.92	0	0	0	Enhanced
13285	REACTOME_COMPLEMENT_CASCADE	1.69	1.90	0	0	0	Enhanced
13286	REACTOME_INTERLEUKIN_9_SIGNALING	1.70	2.43	0	0	0	Enhanced

13287	GO_DORSAL_SPINAL_CORD_DEVELOPMENT	1.70	2.42	0	0	0	Enhanced
13288	GO_CELLULAR_RESPONSE_TO_CADMIUM_ION	1.70	2.29	0	0	0	Enhanced
13289	GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_CELL_PROL	1.70	2.25	0	0	0	Enhanced
13290	GO_CATENIN_COMPLEX	1.70	2.13	0	0	0	Enhanced
13291	GO_VASCULAR_ENDOTHELIAL_CELL_PROLIFERATION	1.70	2.04	0	0	0	Enhanced
13292	WHITFIELD_CELL_CYCLE_S	1.71	4.00	0	0	0	Enhanced
13293	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	1.71	2.79	0	0	0	Enhanced
13294	GO_STARTLE_RESPONSE	1.71	2.26	0	0	0	Enhanced
13295	GO_NEGATIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	1.71	2.14	0	0	0	Enhanced
13296	LEIN_OLIGODENDROCYTE_MARKERS	1.71	2.08	0	0	0	Enhanced
13297	REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES	1.71	1.97	0	0	0	Enhanced
13298	GO_GROWTH_HORMONE_RECEPTOR_SIGNALING_PATHWAY_VIA_JAK_S	1.72	2.73	0	0	0	Enhanced
13299	GO_POLYSOMAL_RIBOSOME	1.72	2.28	0	0	0	Enhanced
13300	CHR18Q11	1.72	2.16	0	0	0	Enhanced
13301	BILD_E2F3_ONCOGENIC_SIGNATURE	1.73	4.00	0	0	0	Enhanced
13302	OSMAN_BLADDER_CANCER_DN	1.73	4.00	0	0	0	Enhanced
13303	GO_NEGATIVE_REGULATION_OF_CAMP_MEDIATED_SIGNALING	1.73	2.26	0	0	0	Enhanced
13304	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_GRANU	1.73	2.13	0	0	0	Enhanced
13305	ZHENG_FOXP3_TARGETS_IN_T_LYMPHOCYTE_DN	1.74	4.00	0	0	0	Enhanced
13306	GO_POSITIVE_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTR	1.74	2.74	0	0	0	Enhanced
13307	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN	1.74	2.74	0	0	0	Enhanced
13308	GO_ZINC_ION_HOMEOSTASIS	1.74	2.44	0	0	0	Enhanced
13309	REACTOME_METALLOTHIONEINS_BIND_METALS	1.74	2.25	0	0	0	Enhanced
13310	GO_AXONEME_PART	1.74	1.96	0	0	0	Enhanced
13311	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN	1.76	4.00	0	0	0	Enhanced
13312	YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP	1.76	2.76	0	0	0	Enhanced
13313	PID_CD40_PATHWAY	1.76	2.75	0	0	0	Enhanced
13314	WATANABE_COLON_CANCER_MSI_VS_MSS_UP	1.76	2.27	0	0	0	Enhanced
13315	GO_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	1.77	4.00	0	0	0	Enhanced
13316	IL2_UP.V1_DN	1.77	4.00	0	0	0	Enhanced
13317	REACTOME_SELENOAMINO_ACID_METABOLISM	1.77	4.00	0	0	0	Enhanced
13318	GO_PRC1_COMPLEX	1.77	2.27	0	0	0	Enhanced
13319	GO_REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	1.77	2.00	0	0	0	Enhanced
13320	GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	1.78	4.00	0	0	0	Enhanced
13321	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN	1.78	4.00	0	0	0	Enhanced
13322	GO_SPHINGOLIPID_MEDIATED_SIGNALING_PATHWAY	1.79	4.00	0	0	0	Enhanced
13323	IVANOVA_HEMATOPOIESIS_STEM_CELL_SHORT_TERM	1.79	4.00	0	0	0	Enhanced
13324	REACTOME_RESPONSE_TO_METAL_IONS	1.79	4.00	0	0	0	Enhanced
13325	TENEDINI_MEGAKARYOCYTE_MARKERS	1.79	4.00	0	0	0	Enhanced
13326	GO_B_CELL_MEDIATED_IMMUNITY	1.79	2.78	0	0	0	Enhanced
13327	GO_SPHINGOSINE_1_PHOSPHATE_RECEPTOR_SIGNALING_PATHWAY	1.79	2.73	0	0	0	Enhanced
13328	HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_DN	1.79	2.43	0	0	0	Enhanced
13329	GO_PHOSPHATIDYLSERINE_METABOLIC_PROCESS	1.79	2.42	0	0	0	Enhanced
13330	GO_CHLORIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.80	4.00	0	0	0	Enhanced
13331	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_	1.80	4.00	0	0	0	Enhanced
13332	YAN_ESCAPE_FROM_ANOIKIS	1.80	2.73	0	0	0	Enhanced
13333	GO_SYNAPSIS	1.80	2.17	0	0	0	Enhanced
13334	GO_ANIMAL_ORGAN_MATURATION	1.81	4.00	0	0	0	Enhanced
13335	GO_SPHINGOSINE_1_PHOSPHATE_RECEPTOR_ACTIVITY	1.82	4.00	0	0	0	Enhanced
13336	GO_SPECIFICATION_OF_SYMMETRY	1.82	2.79	0	0	0	Enhanced
13337	REACTOME_LYSOSPHINGOLIPID_AND_LPA_RECEPTORS	1.83	4.00	0	0	0	Enhanced
13338	GO_GERMINAL_CENTER_FORMATION	1.83	2.71	0	0	0	Enhanced
13339	DUTERTRE_ESTRADIOL_RESPONSE_6HR_DN	1.84	4.00	0	0	0	Enhanced
13340	E2F3_UP.V1_UP	1.85	4.00	0	0	0	Enhanced
13341	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	1.85	2.75	0	0	0	Enhanced
13342	REACTOME_NEUREXINS_AND_NEUROLIGINS	1.86	4.00	0	0	0	Enhanced
13343	GO_CELLULAR_RESPONSE_TO_COPPER_ION	1.86	2.73	0	0	0	Enhanced
13344	GO_PROTEIN_TARGETING_TO_MEMBRANE	1.87	4.00	0	0	0	Enhanced
13345	REACTOME_NONSENSE_MEDIATED_DECAY_NMD	1.87	4.00	0	0	0	Enhanced
13346	CSR_EARLY_UP.V1_DN	1.88	4.00	0	0	0	Enhanced
13347	MARZEC_IL2_SIGNALING_DN	1.88	2.73	0	0	0	Enhanced
13348	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_	1.89	4.00	0	0	0	Enhanced
13349	MEISSNER_BRAIN_HCP_WITH_H3K27ME3	1.89	4.00	0	0	0	Enhanced
13350	NAKAJIMA_MAST_CELL	1.89	2.75	0	0	0	Enhanced
13351	SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_DN	1.89	2.44	0	0	0	Enhanced
13352	GO_CELLULAR_RESPONSE_TO_ZINC_ION	1.92	4.00	0	0	0	Enhanced
13353	HOLLEMAN_ASPARAGINASE_RESISTANCE_B_ALL_UP	1.92	4.00	0	0	0	Enhanced
13354	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION	1.92	4.00	0	0	0	Enhanced
13355	BILANGES_SERUM_RESPONSE_TRANSLATION	1.95	4.00	0	0	0	Enhanced
13356	GO_AXONEME_ASSEMBLY	1.95	4.00	0	0	0	Enhanced
13357	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP	1.96	4.00	0	0	0	Enhanced
13358	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	1.97	4.00	0	0	0	Enhanced
13359	GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUN	1.99	4.00	0	0	0	Enhanced
13360	GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERF	1.99	4.00	0	0	0	Enhanced
13361	GO_NEUROTRANSMITTER_RECEPTOR_COMPLEX	1.99	4.00	0	0	0	Enhanced
13362	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	2.04	4.00	0	0	0	Enhanced
13363	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_	2.04	4.00	0	0	0	Enhanced
13364	GO_BIOACTIVE_LIPID_RECEPTOR_ACTIVITY	2.05	4.00	0	0	0	Enhanced
13365	GO_CYTOSOLIC_RIBOSOME	2.06	4.00	0	0	0	Enhanced
13366	NAKAYAMA_FRA2_TARGETS	2.06	4.00	0	0	0	Enhanced
13367	CHR19P12	2.14	4.00	0	0	0	Enhanced
13368	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETI	2.14	4.00	0	0	0	Enhanced
13369	REACTOME_NONSENSE_MEDIATED_DECAY_NMD_INDEPENDENT_OF_TH	2.15	4.00	0	0	0	Enhanced
13370	KEGG_RIBOSOME	2.27	4.00	0	0	0	Enhanced
13371	MTOR_UP.N4.V1_DN	2.30	4.00	0	0	0	Enhanced
13372	BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES	2.31	4.00	0	0	0	Enhanced
13373	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	2.34	4.00	0	0	0	Enhanced

Supplementary Table 7B. Gene set enrichment for the transcriptional changes induced by RZ-2994 at Day 1 on KOPTK1 cells. MSigDB v7.0 collection, significance -log10(P-value+0.0001)>1. Effect of RZ-2994 on pathway based on Normalized Enrichment Score (NES): NES < -1.5 Repressed, NES > 1.5 Enhanced.

#	Gene set	Normalized Enrichment Score (NES) at Day 1	-log10 (P-value+0.0001) at Day 1	Amino Acid gene set signatures (1=yes, 0=no)	MYC gene set signatures (1=yes, 0=no)	Cell Cycle gene set signatures (1=yes, 0=no)	RZ-2994 vs. DMSO transcriptional effect on pathway at Day 1
1	GO_PRERIBOSOME	-2.59	4	0	0	0	Repressed
2	FISCHER_G2_M_CELL_CYCLE	-2.57	4	0	0	1	Repressed
3	GARY_CD5_TARGETS_DN	-2.50	4	0	0	0	Repressed
4	REACTOME_RRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL	-2.47	4	0	0	0	Repressed
5	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP	-2.46	4	0	0	0	Repressed
6	GO_RIBOSOME_BIOGENESIS	-2.45	4	0	0	0	Repressed
7	WHITFIELD_CELL_CYCLE_G2_M	-2.45	4	0	0	0	Repressed
8	PENG_GLUTAMINE_DEPRIVATION_DN	-2.44	4	1	0	0	Repressed
9	TANG_SENESCENCE_TP53_TARGETS_DN	-2.43	4	0	0	0	Repressed
10	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_11	-2.43	4	0	0	0	Repressed
11	PENG_LEUCINE_DEPRIVATION_DN	-2.41	4	1	0	0	Repressed
12	AMUNDSON_GAMMA_RADIATION_RESPONSE	-2.40	4	0	0	0	Repressed
13	REACTOME_APC_C:CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_AP	-2.40	4	0	0	0	Repressed
14	REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	-2.40	4	0	0	0	Repressed
15	ELVIDGE_HYPOXIA_DN	-2.38	4	0	0	0	Repressed
16	GO_RRNA_METABOLIC_PROCESS	-2.38	4	0	0	0	Repressed
17	HALLMARK_MYC_TARGETS_V2	-2.38	4	0	1	0	Repressed
18	GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	-2.37	4	0	0	0	Repressed
19	HALLMARK_MYC_TARGETS_V1	-2.37	4	0	1	0	Repressed
20	REACTOME_ACTIVATION_OF_APC_C_AND_APC_C:CDC20_MEDIATED_DEGRADATI	-2.37	4	0	0	0	Repressed
21	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_DN	-2.35	4	0	0	0	Repressed
22	GO_NCRNA_METABOLIC_PROCESS	-2.34	4	0	0	0	Repressed
23	KARLSSON_TGFB1_TARGETS_UP	-2.34	4	0	0	0	Repressed
24	REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	-2.33	4	0	0	0	Repressed
25	GO_NCRNA_PROCESSING	-2.31	4	0	0	0	Repressed
26	GO_SMALL_SUBUNIT_PROCESSOME	-2.31	4	0	0	0	Repressed
27	ODONNELL_TFRC_TARGETS_DN	-2.31	4	0	0	0	Repressed
28	MENSSEN_MYC_TARGETS	-2.30	4	0	1	0	Repressed
29	MALONEY_RESPONSE_TO_17AAG_DN	-2.29	4	0	0	0	Repressed
30	REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2_CHECKP	-2.29	4	0	0	0	Repressed
31	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	-2.29	4	0	0	0	Repressed
32	GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	-2.27	4	0	0	0	Repressed
33	GO_RNA_LOCALIZATION	-2.26	4	0	0	0	Repressed
34	REICHERT_MITOSIS_LIN9_TARGETS	-2.26	4	0	0	0	Repressed
35	RHODES_UNDIFFERENTIATED_CANCER	-2.26	4	0	0	0	Repressed
36	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN	-2.24	4	0	0	0	Repressed
37	CSR_EARLY_UP.V1_UP	-2.23	4	0	0	0	Repressed
38	REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION	-2.23	4	0	0	0	Repressed
39	FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	-2.22	4	0	0	0	Repressed
40	REACTOME_MITOTIC_SPINDLE_CHECKPOINT	-2.22	4	0	0	0	Repressed
41	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN	-2.21	4	0	0	0	Repressed
42	PENG_RAPAMYCIN_RESPONSE_DN	-2.21	4	0	0	0	Repressed
43	GO_MATURATION_OF_SSU_RRNA	-2.19	4	0	0	0	Repressed
44	LEE_BMP2_TARGETS_DN	-2.19	4	0	0	0	Repressed
45	PID_AURORA_B_PATHWAY	-2.19	4	0	0	0	Repressed
46	REACTOME_METABOLISM_OF_RNA	-2.19	4	0	0	0	Repressed
47	GO_PROTEASOME_ACCESSORY_COMPLEX	-2.18	4	0	0	0	Repressed
48	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	-2.18	4	0	0	0	Repressed
49	GO_90S_PRERIBOSOME	-2.17	4	0	0	0	Repressed
50	MANALO_HYPOXIA_DN	-2.17	4	0	0	0	Repressed
51	REACTOME_FBXL7_DOWN_REGULATES_AURKA_DURING_MITOTIC_ENTRY_AND_IN	-2.17	4	0	0	0	Repressed
52	FARMER_BREAST_CANCER_CLUSTER_2	-2.16	4	0	0	0	Repressed
53	GO_PRERIBOSOME_LARGE_SUBUNIT_PRECURSOR	-2.16	4	0	0	0	Repressed
54	GO_MITOTIC_SPINDLE_ORGANIZATION	-2.15	4	0	0	0	Repressed
55	GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	-2.15	4	0	0	0	Repressed
56	GO_SPINDLE_MIDZONE	-2.15	4	0	0	0	Repressed
57	REACTOME_DEGRADATION_OF_GLI1_BY_THE_PROTEASOME	-2.14	4	0	0	0	Repressed
58	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM	-2.14	4	0	0	0	Repressed
59	WEI_MYCN_TARGETS_WITH_E_BOX	-2.14	4	0	0	0	Repressed
60	BOYAULT_LIVER_CANCER_SUBCLASS_G3_UP	-2.13	4	0	0	0	Repressed
61	CAIRO_HEPATOBLASTOMA_CLASSES_UP	-2.13	4	0	0	0	Repressed
62	ELVIDGE_HIF1A_TARGETS_UP	-2.13	4	0	0	0	Repressed
63	GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU	-2.13	4	0	0	0	Repressed
64	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN	-2.13	4	0	0	0	Repressed
65	WHITFIELD_CELL_CYCLE_M_G1	-2.13	4	0	0	0	Repressed
66	GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	-2.12	4	0	0	0	Repressed
67	BIDUS_METASTASIS_UP	-2.11	4	0	0	0	Repressed
68	REACTOME_DEGRADATION_OF_BETA_CATENIN_BY_THE_DESTRUCTION_COMPLE	-2.11	4	0	0	0	Repressed
69	BURTON_ADIPOGENESIS_PEAK_AT_24HR	-2.10	4	0	0	0	Repressed
70	GO_SPINDLE_MICROTUBULE	-2.10	4	0	0	0	Repressed
71	PUJANA_CHEK2_PCC_NETWORK	-2.10	4	0	0	0	Repressed
72	REACTOME_REGULATION_OF_RUNX2_EXPRESSION_AND_ACTIVITY	-2.10	4	0	0	0	Repressed
73	REACTOME_RRNA_PROCESSING	-2.10	4	0	0	0	Repressed
74	GO_ESTABLISHMENT_OF_RNA_LOCALIZATION	-2.09	4	0	0	0	Repressed
75	GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS	-2.09	4	0	0	0	Repressed
76	REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	-2.09	4	0	0	0	Repressed
77	CHANG_CYCLING_GENES	-2.08	4	0	0	0	Repressed
78	MOHANKUMAR_HOXA1_TARGETS_UP	-2.08	4	0	0	0	Repressed
79	REACTOME_CELLULAR_RESPONSE_TO_HYPOXIA	-2.08	4	0	0	0	Repressed
80	REACTOME_RRNA_PROCESSING_IN_THE_NUCLEUS_AND_CYTOSOL	-2.08	4	0	0	0	Repressed
81	WONG_EMBRYONIC_STEM_CELL_CORE	-2.08	4	0	0	0	Repressed
82	GO_RNA_BINDING	-2.07	4	0	0	0	Repressed
83	RHODES_CANCER_META_SIGNATURE	-2.07	4	0	0	0	Repressed
84	GO_ENDOPEPTIDASE_COMPLEX	-2.06	4	0	0	0	Repressed
85	GO_RNA_METABOLIC_PROCESS	-2.06	4	0	0	0	Repressed
86	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN	-2.06	4	0	0	0	Repressed
87	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-2.06	4	0	0	0	Repressed
88	VEGF_A_UP.V1_DN	-2.06	4	0	0	0	Repressed
89	WONG_PROTEASOME_GENE_MODULE	-2.06	4	0	0	0	Repressed
90	CROONQUIST_IL6_DEPRIVATION_DN	-2.05	4	0	0	0	Repressed
91	CROONQUIST_NRAS_SIGNALING_DN	-2.05	4	0	0	0	Repressed
92	KANG_DOXORUBICIN_RESISTANCE_UP	-2.05	4	0	0	0	Repressed
93	KEGG_OOCYTE_MEIOSIS	-2.05	4	0	0	0	Repressed
94	REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDO	-2.05	4	0	0	0	Repressed
95	REACTOME_NEGATIVE_REGULATION_OF_NOTCH4_SIGNALING	-2.05	4	0	0	0	Repressed
96	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR	-2.05	4	0	0	0	Repressed
97	GO_MATURATION_OF_LSU_RRNA	-2.04	4	0	0	0	Repressed

98	HALLMARK_G2M_CHECKPOINT	-2.04	4	0	0	0	Repressed
99	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP	-2.04	4	0	0	0	Repressed
100	LY_AGING_MIDDLE_DN	-2.04	4	0	0	0	Repressed
101	LY_AGING_OLD_DN	-2.04	4	0	0	0	Repressed
102	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	-2.04	4	0	0	0	Repressed
103	REACTOME_REGULATION_OF_APOPTOSIS	-2.04	4	0	0	0	Repressed
104	YU_MYC_TARGETS_UP	-2.04	4	0	0	0	Repressed
105	BASAKI_YBX1_TARGETS_UP	-2.03	4	0	0	0	Repressed
106	GO_MOLECULAR_CARRIER_ACTIVITY	-2.03	4	0	0	0	Repressed
107	GO_SMALL_NUCLEOLAR_RIBONUCLEOPROTEIN_COMPLEX	-2.03	4	0	0	0	Repressed
108	MOHANKUMAR_TLX1_TARGETS_UP	-2.03	4	0	0	0	Repressed
109	PID_MYC_ACTIV_PATHWAY	-2.03	4	0	1	0	Repressed
110	GO_CATALYTIC_ACTIVITY_ACTING_ON_A_TRNA	-2.02	4	0	0	0	Repressed
111	GO_NUCLEAR_EXPORT	-2.02	4	0	0	0	Repressed
112	GO_NUCLEAR_PORE	-2.02	4	0	0	0	Repressed
113	MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP	-2.02	4	0	0	0	Repressed
114	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_UP	-2.02	4	0	0	0	Repressed
115	VECCHI_GASTRIC_CANCER_EARLY_UP	-2.02	4	0	0	0	Repressed
116	GO_NLS_BEARING_PROTEIN_IMPORT_INTO_NUCLEUS	-2.01	4	0	0	0	Repressed
117	GO_PROTEASOME_REGULATORY_PARTICLE_BASE_SUBCOMPLEX	-2.01	4	0	0	0	Repressed
118	GO_TRNA_METABOLIC_PROCESS	-2.01	4	1	0	0	Repressed
119	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP	-2.01	4	0	0	0	Repressed
120	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP	-2.01	4	0	0	0	Repressed
121	PID_AURORA_A_PATHWAY	-2.01	4	0	0	0	Repressed
122	REACTOME_HSP90_CHAPERONE_CYCLE_FOR_STEROID_HORMONE_RECEPTORS_	-2.01	4	0	0	0	Repressed
123	GO_POSITIVE_REGULATION_OF_TELOMERASE_RNA_LOCALIZATION_TO_CAJAL_BC	-2.00	4	0	0	0	Repressed
124	GO_RNA_EXPORT_FROM_NUCLEUS	-2.00	4	0	0	0	Repressed
125	REACTOME_AUF1_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA	-2.00	4	0	0	0	Repressed
126	SU_TESTIS	-2.00	4	0	0	0	Repressed
127	ZHAN_MULTIPLE_MYELOMA_PR_UP	-2.00	4	0	0	0	Repressed
128	GO_NUCLEAR_TRANSPORT	-1.99	4	0	0	0	Repressed
129	GO_NUCLEOCYTOPLASMIC_CARRIER_ACTIVITY	-1.99	4	0	0	0	Repressed
130	GO_PEPTIDASE_COMPLEX	-1.99	4	0	0	0	Repressed
131	KEGG_PROTEASOME	-1.98	4	0	0	0	Repressed
132	KIM_MYC_AMPLIFICATION_TARGETS_UP	-1.98	4	0	0	0	Repressed
133	REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	-1.98	4	0	0	0	Repressed
134	REACTOME_GLYCOLYSIS	-1.98	4	0	0	0	Repressed
135	REACTOME_RHO_GTPASES_ACTIVATE_FORMINS	-1.98	4	0	0	0	Repressed
136	REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	-1.98	4	0	0	0	Repressed
137	REACTOME_TRNA_AMINOACYLATION	-1.98	4	0	0	0	Repressed
138	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP	-1.98	4	0	0	0	Repressed
139	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP	-1.98	4	0	0	0	Repressed
140	GO_AMINO_ACID_ACTIVATION	-1.97	4	0	0	0	Repressed
141	GO_NUCLEOLAR_PART	-1.97	4	0	0	0	Repressed
142	GO_TELOMERASE_RNA_LOCALIZATION	-1.97	4	0	0	0	Repressed
143	HORIUCHI_WTAP_TARGETS_DN	-1.97	4	0	0	0	Repressed
144	REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	-1.97	4	0	0	0	Repressed
145	REACTOME_M_PHASE	-1.97	4	0	0	0	Repressed
146	REACTOME_REGULATION_OF_RAS_BY_GAPS	-1.97	4	0	0	0	Repressed
147	SCHUHMACHER_MYC_TARGETS_UP	-1.97	4	0	0	0	Repressed
148	SHEPARD_CRUSH_AND_BURN_MUTANT_DN	-1.97	4	0	0	0	Repressed
149	ANDERSEN_CHOLANGIOCARCINOMA_CLASS2	-1.96	4	0	0	0	Repressed
150	BURTON_ADIPOGENESIS_4	-1.96	4	0	0	0	Repressed
151	FOURNIER_ACINAR_DEVELOPMENT_LATE_2	-1.96	4	0	0	0	Repressed
152	REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	-1.96	4	0	0	0	Repressed
153	REACTOME_DEGRADATION_OF_AXIN	-1.96	4	0	0	0	Repressed
154	REACTOME_HEDGEHOG_ON_STATE	-1.96	4	0	0	0	Repressed
155	REACTOME_MRNA_SPLICING	-1.96	4	0	0	0	Repressed
156	DODD_NASOPHARYNGEAL_CARCINOMA_DN	-1.95	4	0	0	0	Repressed
157	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_UP	-1.95	4	0	0	0	Repressed
158	GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS	-1.95	4	0	0	0	Repressed
159	GO_MATURATION_OF_LSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_	-1.95	4	0	0	0	Repressed
160	KONG_E2F3_TARGETS	-1.95	4	0	0	0	Repressed
161	REACTOME_DEGRADATION_OF_DVL	-1.95	4	0	0	0	Repressed
162	REACTOME_HIV_INFECTION	-1.95	4	0	0	0	Repressed
163	REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	-1.95	4	0	0	0	Repressed
164	REACTOME_REGULATION_OF_PTEN_STABILITY_AND_ACTIVITY	-1.95	4	0	0	0	Repressed
165	BIOCARTA_RANMS_PATHWAY	-1.95	2.68	0	0	0	Repressed
166	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CHROMOSOME_TELOMERIC_R	-1.95	2.34	0	0	0	Repressed
167	GO_CATALYTIC_ACTIVITY_ACTING_ON_RNA	-1.94	4	0	0	0	Repressed
168	GO_SPINDLE_ORGANIZATION	-1.94	4	0	0	0	Repressed
169	WILLIAMS_ESR1_TARGETS_UP	-1.94	4	0	0	0	Repressed
170	WINNEPENNINCKX_MELANOMA_METASTASIS_UP	-1.94	4	0	0	0	Repressed
171	GAVIN_FOXP3_TARGETS_CLUSTER_P6	-1.93	4	0	0	0	Repressed
172	GO_OTHER_ORGANISM	-1.93	4	0	0	0	Repressed
173	GO_PROTEIN_IMPORT_INTO_MITOCHONDRIAL_MATRIX	-1.93	4	0	0	0	Repressed
174	GO_SPINDLE	-1.93	4	0	0	0	Repressed
175	GO_SPINDLE_POLE	-1.93	4	0	0	0	Repressed
176	REACTOME_HEDGEHOG_OFF_STATE	-1.93	4	0	0	0	Repressed
177	REACTOME_METABOLISM_OF_NON_CODING_RNA	-1.93	4	0	0	0	Repressed
178	REACTOME_REGULATION_OF_RUNX3_EXPRESSION_AND_ACTIVITY	-1.93	4	0	0	0	Repressed
179	REACTOME_PHOSPHORYLATION_OF_THE_APC_C	-1.93	2.62	0	0	0	Repressed
180	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP	-1.92	4	0	0	0	Repressed
181	GO_MRNA_TRANSPORT	-1.92	4	0	0	0	Repressed
182	GO_RAN_GTPASE_BINDING	-1.92	4	0	0	0	Repressed
183	GO_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.92	4	0	0	0	Repressed
184	GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	-1.92	4	0	0	0	Repressed
185	PUIFFE_INVASION_INHIBITED_BY_ASCITES_UP	-1.92	4	0	0	0	Repressed
186	REACTOME_NUCLEAR_PORE_COMPLEX_NPC_DISASSEMBLY	-1.92	4	0	0	0	Repressed
187	REACTOME_UCH_PROTEINASES	-1.92	4	0	0	0	Repressed
188	REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS	-1.92	4	0	0	0	Repressed
189	GO_PRERIBOSOME_SMALL_SUBUNIT_PRECURSOR	-1.92	2.64	0	0	0	Repressed
190	REACTOME_APC_C:CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	-1.92	2.59	0	0	0	Repressed
191	REACTOME_INTERACTIONS_OF_REV_WITH_HOST_CELLULAR_PROTEINS	-1.92	2.56	0	0	0	Repressed
192	BERENJENO_TRANSFORMED_BY_RHOA_UP	-1.91	4	0	0	0	Repressed
193	FERREIRA_EWINGS_SARCOMA_UNSTABLE_VS_STABLE_UP	-1.91	4	0	0	0	Repressed
194	FURUKAWA_DUSP6_TARGETS_PCI35_DN	-1.91	4	0	0	0	Repressed
195	GO_DOUBLE_STRANDED_RNA_BINDING	-1.91	4	0	0	0	Repressed
196	GO_REGULATION_OF_CHROMOSOME_SEPARATION	-1.91	4	0	0	0	Repressed
197	GO_REGULATION_OF_TRANSLATIONAL_ELONGATION	-1.91	4	0	0	0	Repressed
198	REACTOME_MAPK6_MAPK4_SIGNALING	-1.91	4	0	0	0	Repressed
199	REACTOME_STABILIZATION_OF_P53	-1.91	4	0	0	0	Repressed
200	REACTOME_SUMOYLATION_OF_DNA_REPLICATION_PROTEINS	-1.91	4	0	0	0	Repressed
201	GO_RIBONUCLEOPROTEIN_COMPLEX_BINDING	-1.90	4	0	0	0	Repressed
202	GO_SCF_DEPENDENT_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOL	-1.90	4	0	0	0	Repressed
203	LEE_EARLY_T_LYMPHOCYTE_UP	-1.90	4	0	0	0	Repressed
204	TARTE_PLASMA_CELL_VS_PLASMABLAST_DN	-1.90	4	0	0	0	Repressed
205	TIEN_INTESTINE_PROBIOTICS_24HR_UP	-1.90	4	0	0	0	Repressed
206	REACTOME_MITOTIC_TELOPHASE_CYTOKINESIS	-1.90	2.64	0	0	0	Repressed

207	BHAT_ESR1_TARGETS_NOT_VIA_AKT1_UP	-1.89	4	0	0	0	Repressed
208	CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_UP	-1.89	4	0	0	0	Repressed
209	GO_CHROMOSOME_CENTROMERIC_REGION	-1.89	4	0	0	0	Repressed
210	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP	-1.89	4	0	0	0	Repressed
211	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOT	-1.89	4	0	0	0	Repressed
212	REACTOME_TRNA_PROCESSING	-1.89	4	0	0	0	Repressed
213	GO_TRNA_TRANSPORT	-1.89	2.56	0	0	0	Repressed
214	GO_HEMATOPOIETIC_STEM_CELL_DIFFERENTIATION	-1.88	4	0	0	0	Repressed
215	GO_MITOTIC_SPINDLE_ASSEMBLY	-1.88	4	0	0	0	Repressed
216	GO_NCRNA_TRANSCRIPTION	-1.88	4	0	0	0	Repressed
217	MARTINEZ_RESPONSE_TO_TRABECTEDIN_DN	-1.88	4	0	0	0	Repressed
218	REACTOME_PCP_CE_PATHWAY	-1.88	4	0	0	0	Repressed
219	GO_PROTEIN_K11_LINKED_UBIQUITINATION	-1.88	2.59	0	0	0	Repressed
220	GO_TRNA_MODIFICATION	-1.88	2.51	0	0	0	Repressed
221	GENTILE_UV_RESPONSE_CLUSTER_D4	-1.87	4	0	0	0	Repressed
222	GENTILE_UV_RESPONSE_CLUSTER_D5	-1.87	4	0	0	0	Repressed
223	GO_CONDENSED_CHROMOSOME_OUTER_KINETOCHORE	-1.87	4	0	0	0	Repressed
224	GO_NUCLEOBASE_CONTAINING_COMPOUND_TRANSPORT	-1.87	4	0	0	0	Repressed
225	GO_REGULATION_OF_SISTER_CHROMATID_SEGREGATION	-1.87	4	0	0	0	Repressed
226	GREENBAUM_E2A_TARGETS_UP	-1.87	4	0	0	0	Repressed
227	REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	-1.87	4	0	0	0	Repressed
228	REACTOME_FCERI_MEDIATED_NF_KB_ACTIVATION	-1.87	4	0	0	0	Repressed
229	REACTOME_RNA_POLYMERASE_II_PRE_TRANSCRIPTION_EVENTS	-1.87	4	0	0	0	Repressed
230	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	-1.87	2.6	0	0	0	Repressed
231	GO_MITOCHONDRIAL_RNA_METABOLIC_PROCESS	-1.86	4	0	0	0	Repressed
232	GO_MITOTIC_NUCLEAR_ENVELOPE_DISASSEMBLY	-1.86	4	0	0	0	Repressed
233	GO_MITOTIC_SISTER_CHROMATID_SEGREGATION	-1.86	4	0	0	0	Repressed
234	GO_MITOTIC_SPINDLE	-1.86	4	0	0	0	Repressed
235	GRADE_METASTASIS_DN	-1.86	4	0	0	0	Repressed
236	KOBAYASHI_EGFR_SIGNALING_24HR_DN	-1.86	4	0	0	0	Repressed
237	REACTOME_RNA_POLYMERASE_II_TRANSCRIBES_SNRNA_GENES	-1.86	4	0	0	0	Repressed
238	SHEPARD_BMYB_TARGETS	-1.86	4	0	0	0	Repressed
239	CROMER_METASTASIS_DN	-1.86	2.54	0	0	0	Repressed
240	DASU_IL6_SIGNALING_SCAR_UP	-1.85	4	0	0	0	Repressed
241	GO_PROTEIN_IMPORT	-1.85	4	0	0	0	Repressed
242	GO_SISTER_CHROMATID_SEGREGATION	-1.85	4	0	0	0	Repressed
243	KEGG_SPLICEOSOME	-1.85	4	0	0	0	Repressed
244	MUELLER_PLURINET	-1.85	4	0	0	0	Repressed
245	REACTOME_DOWNSTREAM_TCR_SIGNALING	-1.85	4	0	0	0	Repressed
246	REACTOME_NUCLEAR_IMPORT_OF_REV_PROTEIN	-1.85	4	0	0	0	Repressed
247	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX2	-1.85	4	0	0	0	Repressed
248	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN	-1.85	4	0	0	0	Repressed
249	GO_CHAPERONE_COMPLEX	-1.85	2.63	0	0	0	Repressed
250	BURTON_ADIPOGENESIS_3	-1.85	2.5	0	0	0	Repressed
251	DAIRKEE_CANCER_PRONE_RESPONSE_BPA	-1.84	4	0	0	0	Repressed
252	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	-1.84	4	0	0	0	Repressed
253	GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	-1.84	4	0	0	0	Repressed
254	GO_TRANSLATIONAL_TERMINATION	-1.84	4	0	0	0	Repressed
255	PID_PLK1_PATHWAY	-1.84	4	0	0	0	Repressed
256	REACTOME_ASYMMETRIC_LOCALIZATION_OF_PCP_PROTEINS	-1.84	4	0	0	0	Repressed
257	REACTOME_CONVERSION_FROM_APC_C:CDC20_TO_APC_C:CDH1_IN_LATE_ANAPI	-1.84	4	0	0	0	Repressed
258	REACTOME_MRNA_SPLICING_MINOR_PATHWAY	-1.84	4	0	0	0	Repressed
259	LEE_INTRATHYMIC_T_PROGENITOR	-1.84	2.65	0	0	0	Repressed
260	NIKOLSKY_BREAST_CANCER_14Q22_AMPLICON	-1.84	2.65	0	0	0	Repressed
261	BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE	-1.84	2.64	0	0	0	Repressed
262	GO_REGULATION_OF_RIBOSOME_BIOGENESIS	-1.84	2.62	0	0	0	Repressed
263	GO_TRANSLATION_INITIATION_FACTOR_ACTIVITY	-1.84	2.56	0	0	0	Repressed
264	PID_ILK_PATHWAY	-1.84	2.56	0	0	0	Repressed
265	ELVIDGE_HYPOXIA_BY_DMOG_DN	-1.83	4	0	0	0	Repressed
266	GO_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE	-1.83	4	0	0	1	Repressed
267	JUBAN_TARGETS_OF_SPI1_AND_FLI1_DN	-1.83	4	0	0	0	Repressed
268	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	-1.83	4	1	0	0	Repressed
269	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN	-1.83	4	0	0	0	Repressed
270	PUJANA_BRCA1_PCC_NETWORK	-1.83	4	0	0	0	Repressed
271	REACTOME_CELL_CYCLE_CHECKPOINTS	-1.83	4	0	0	0	Repressed
272	REACTOME_COOPERATION_OF_PDCL_PHLP1_AND_TRIC_CCT_IN_G_PROTEIN_BET	-1.83	4	0	0	0	Repressed
273	REACTOME_SIGNALING_BY_HEDGEHOG	-1.83	4	0	0	0	Repressed
274	REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME	-1.83	4	0	0	0	Repressed
275	REACTOME_TRANSPORT_OF_THE_SLBP_DEPENDANT_MATURE_MRNA	-1.83	4	0	0	0	Repressed
276	SESTO_RESPONSE_TO_UV_C0	-1.83	4	0	0	0	Repressed
277	GO_PROTEIN_LOCALIZATION_TO_NUCLEOPLASM	-1.83	2.66	0	0	0	Repressed
278	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP	-1.83	2.66	0	0	0	Repressed
279	GO_POSITIVE_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLATION	-1.83	2.62	0	0	0	Repressed
280	REACTOME_TRANSCRIPTIONAL_ACTIVATION_OF_MITOCHONDRIAL_BIOGENESIS	-1.83	2.52	0	0	0	Repressed
281	GO_NUCLEOLUS	-1.82	4	0	0	0	Repressed
282	GO_RIBONUCLEOPROTEIN_COMPLEX	-1.82	4	0	0	0	Repressed
283	REACTOME_HOST_INTERACTIONS_WITH_INFLUENZA_FACTORS	-1.82	4	0	0	0	Repressed
284	REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_DIFFE	-1.82	4	0	0	0	Repressed
285	WHITEFORD_PEDIATRIC_CANCER_MARKERS	-1.82	4	0	0	0	Repressed
286	WHITFIELD_CELL_CYCLE_LITERATURE	-1.82	4	0	0	0	Repressed
287	FINETTI_BREAST_CANCER_KINOME_RED	-1.82	2.63	0	0	0	Repressed
288	GO_RNA_CAP_BINDING	-1.82	2.6	0	0	0	Repressed
289	KEGG_RNA_POLYMERASE	-1.82	2.6	0	0	0	Repressed
290	REACTOME_TRANSPORT_OF_MATURE_MRNAS_DERIVED_FROM_INTRONLESS_TRA	-1.82	2.58	0	0	0	Repressed
291	GO_NCRNA_EXPORT_FROM_NUCLEUS	-1.82	2.56	0	0	0	Repressed
292	GO_TBP_CLASS_PROTEIN_BINDING	-1.82	2.32	0	0	0	Repressed
293	BENPORATH_PROLIFERATION	-1.81	4	0	0	0	Repressed
294	BIOCARTA_EGFR_SMRTE_PATHWAY	-1.81	4	0	0	0	Repressed
295	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_DN	-1.81	4	0	0	0	Repressed
296	DANG_MYC_TARGETS_UP	-1.81	4	0	1	0	Repressed
297	GO_MITOCHONDRIAL_RNA_PROCESSING	-1.81	4	0	0	0	Repressed
298	GO_NUCLEOTIDYLTRANSFERASE_ACTIVITY	-1.81	4	0	0	0	Repressed
299	GO_REGULATION_OF_MRNA_CATABOLIC_PROCESS	-1.81	4	0	0	0	Repressed
300	GO_RNA_POLYMERASE_ACTIVITY	-1.81	4	0	0	0	Repressed
301	GO_SIGNAL_SEQUENCE_BINDING	-1.81	4	0	0	0	Repressed
302	GO_SISTER_CHROMATID_COHESION	-1.81	4	0	0	0	Repressed
303	LE_EGR2_TARGETS_UP	-1.81	4	0	0	0	Repressed
304	MILI_PSEUDOPODIA_HAPTOTAXIS_UP	-1.81	4	0	0	0	Repressed
305	ONDER_CDH1_TARGETS_1_DN	-1.81	4	0	0	0	Repressed
306	REACTOME_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING	-1.81	4	0	0	0	Repressed
307	REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	-1.81	4	0	0	0	Repressed
308	VISALA_RESPONSE_TO_HEAT_SHOCK_AND_AGING_DN	-1.81	4	0	0	0	Repressed
309	ZHANG_TLX_TARGETS_36HR_DN	-1.81	4	0	0	0	Repressed
310	GO_SNORNA_BINDING	-1.81	2.61	0	0	0	Repressed
311	GO_CATALYTIC_STEP_2_SPLICEOSOME	-1.80	4	0	0	0	Repressed
312	GO_CHROMOSOME_SEPARATION	-1.80	4	0	0	0	Repressed
313	GO_CYTOSOLIC_PROTEASOME_COMPLEX	-1.80	4	0	0	0	Repressed
314	GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	-1.80	4	0	0	0	Repressed
315	GO_REGULATION_OF_MEIOTIC_NUCLEAR_DIVISION	-1.80	4	0	0	0	Repressed

316	GO_TRNA_PROCESSING	-1.80	4	0	0	0	Repressed
317	HALLMARK_MITOTIC_SPINDLE	-1.80	4	0	0	0	Repressed
318	REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED	-1.80	4	0	0	0	Repressed
319	GO_REGULATION_OF_ATTACHMENT_OF_SPINDLE_MICROTUBULES_TO_KINETOCH	-1.80	2.63	0	0	0	Repressed
320	KARAKAS_TGFB1_SIGNALING	-1.80	2.63	0	0	0	Repressed
321	GO_REGULATION_OF_DNA_METHYLATION	-1.80	1.8	0	0	0	Repressed
322	GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	-1.79	4	0	0	0	Repressed
323	GO_KINETOCHORE	-1.79	4	0	0	0	Repressed
324	GO_POSITIVE_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	-1.79	4	0	0	0	Repressed
325	GO_PRE_SNORNP_COMPLEX	-1.79	4	0	0	0	Repressed
326	GO_REGULATION_OF_CYTOKINESIS	-1.79	4	0	0	0	Repressed
327	GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	-1.79	4	0	0	0	Repressed
328	GO_RIBOSOME_ASSEMBLY	-1.79	4	0	0	0	Repressed
329	GO_RNA_MODIFICATION	-1.79	4	0	0	0	Repressed
330	GO_SUBSTANTIA_NIGRA_DEVELOPMENT	-1.79	4	0	0	0	Repressed
331	GO_TRANSCRIPTION_BY_RNA_POLYMERASE_I	-1.79	4	0	0	0	Repressed
332	GO_NUCLEAR_LOCALIZATION_SEQUENCE_BINDING	-1.79	2.62	0	0	0	Repressed
333	GO_TELOMERASE_HOLOENZYME_COMPLEX	-1.79	2.62	0	0	0	Repressed
334	GO_POSITIVE_REGULATION_OF_CYTOKINESIS	-1.79	2.61	0	0	0	Repressed
335	GO_MEMBRANE_DISASSEMBLY	-1.79	2.31	0	0	0	Repressed
336	CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_UP	-1.78	4	0	0	0	Repressed
337	GO_IMPORT_INTO_NUCLEUS	-1.78	4	0	0	0	Repressed
338	GO_MORPHOGENESIS_OF_A_POLARIZED_EPITHELIUM	-1.78	4	0	0	0	Repressed
339	GO_MRNA_METABOLIC_PROCESS	-1.78	4	0	0	0	Repressed
340	GO_MULTI_ORGANISM_LOCALIZATION	-1.78	4	0	0	0	Repressed
341	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_UP	-1.78	4	0	0	0	Repressed
342	LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_DN	-1.78	4	0	0	0	Repressed
343	REACTOME_BMAL1:CLOCK_NPAS2_ACTIVATES_CIRCADIAN_GENE_EXPRESSION	-1.78	4	0	0	0	Repressed
344	REACTOME_CONDENSATION_OF_PROPHASE_CHROMOSOMES	-1.78	4	0	0	0	Repressed
345	REACTOME_NUCLEAR_ENVELOPE_BREAKDOWN	-1.78	4	0	0	0	Repressed
346	GO_RNA_5_END_PROCESSING	-1.78	2.62	0	0	0	Repressed
347	REACTOME_METABOLISM_OF_POLYAMINES	-1.78	2.54	0	0	0	Repressed
348	REACTOME_HEDGEHOG_LIGAND_BIOGENESIS	-1.78	2.23	0	0	0	Repressed
349	GO_CELL_DIVISION	-1.77	4	0	0	0	Repressed
350	GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_T	-1.77	4	0	0	0	Repressed
351	GO_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS	-1.77	4	0	0	0	Repressed
352	GO_RNA_POLYMERASE_COMPLEX	-1.77	4	0	0	0	Repressed
353	REACTOME_ACTIVATION_OF_NIMA_KINASES_NEK9_NEK6_NEK7	-1.77	4	0	0	0	Repressed
354	REACTOME_CIRCADIAN_CLOCK	-1.77	4	0	0	0	Repressed
355	REACTOME_MITOTIC_PROMETAPHASE	-1.77	4	0	0	0	Repressed
356	GO_CENTROSOME_SEPARATION	-1.77	2.64	0	0	0	Repressed
357	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN	-1.77	2.62	0	0	0	Repressed
358	DEN_INTERACT_WITH_LCA5	-1.77	2.61	0	0	0	Repressed
359	EGUCHI_CELL_CYCLE_RB1_TARGETS	-1.77	2.59	0	0	1	Repressed
360	GO_TRNA_METHYLTRANSFERASE_ACTIVITY	-1.77	2.59	0	0	0	Repressed
361	KEGG_BASAL_TRANSCRIPTION_FACTORS	-1.77	2.57	0	0	0	Repressed
362	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP	-1.77	2.57	0	0	0	Repressed
363	REACTOME_KINESINS	-1.77	2.56	0	0	0	Repressed
364	GO_SIRNA_BINDING	-1.77	2.34	0	0	0	Repressed
365	SIMBULAN_PARP1_TARGETS_DN	-1.77	2.34	0	0	0	Repressed
366	REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	-1.77	2.33	0	0	0	Repressed
367	REACTOME_SYNTHESIS_OF_ACTIVE_UBIQUITIN:_ROLES_OF_E1_AND_E2_ENZYMES	-1.77	2.16	0	0	0	Repressed
368	BHAT_ESR1_TARGETS_VIA_AKT1_UP	-1.76	4	0	0	0	Repressed
369	GO_INNATE_IMMUNE_RESPONSE_ACTIVATING_CELL_SURFACE_RECEPTOR_SIGNA	-1.76	4	0	0	0	Repressed
370	GO_REGULATION_OF_RNA_METABOLIC_PROCESS	-1.76	4	0	0	0	Repressed
371	GO_REGULATION_OF_STEM_CELL_DIFFERENTIATION	-1.76	4	0	0	0	Repressed
372	GO_SNRNA_TRANSCRIPTION	-1.76	4	0	0	0	Repressed
373	REACTOME_HIV_LIFE_CYCLE	-1.76	4	0	0	0	Repressed
374	REACTOME_PHOSPHORYLATION_OF_EMI1	-1.76	2.67	0	0	0	Repressed
375	COLLIS_PRKDC_REGULATORS	-1.76	2.6	0	0	0	Repressed
376	GO_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_BINDING	-1.76	2.59	0	0	0	Repressed
377	REACTOME_EXPORT_OF_VIRAL_RIBONUCLEOPROTEINS_FROM_NUCLEUS	-1.76	2.57	0	0	0	Repressed
378	SPIRA_SMOKERS_LUNG_CANCER_DN	-1.76	2.34	0	0	0	Repressed
379	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	-1.75	4	0	0	0	Repressed
380	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	-1.75	4	0	0	0	Repressed
381	GO_CONDENSED_CHROMOSOME_CENTROMERIC_REGION	-1.75	4	0	0	0	Repressed
382	GO_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	-1.75	4	0	0	0	Repressed
383	GO_MRNA_EXPORT_FROM_NUCLEUS	-1.75	4	0	0	0	Repressed
384	GO_SPINDLE_ASSEMBLY	-1.75	4	0	0	0	Repressed
385	HALLMARK_E2F_TARGETS	-1.75	4	0	0	0	Repressed
386	MARCHINI_TRABECTEDIN_RESISTANCE_DN	-1.75	4	0	0	0	Repressed
387	REACTOME_GOLGI_CISTERNAE_PERICENTRIOLAR_STACK_REORGANIZATION	-1.75	4	0	0	0	Repressed
388	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RI	-1.75	4	0	0	0	Repressed
389	REACTOME_TRNA_PROCESSING_IN_THE_NUCLEUS	-1.75	4	0	0	0	Repressed
390	VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_UP	-1.75	4	0	0	0	Repressed
391	FUNG_IL2_SIGNALING_1	-1.75	2.64	0	0	0	Repressed
392	GO_NEGATIVE_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	-1.75	2.63	0	0	0	Repressed
393	GO_CONDENSED_NUCLEAR_CHROMOSOME_CENTROMERIC_REGION	-1.75	2.62	0	0	0	Repressed
394	ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE	-1.75	2.62	0	0	0	Repressed
395	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_SMALL_RNAS	-1.75	2.51	0	0	0	Repressed
396	GO_TIM23_MITOCHONDRIAL_IMPORT_INNER_MEMBRANE_TRANSLOCASE_COMPLE	-1.75	2.34	0	0	0	Repressed
397	FU_INTERACT_WITH_ALKBH8	-1.75	2.18	0	0	0	Repressed
398	XU_HGF_SIGNALING_NOT_VIA_AKT1_48HR_DN	-1.75	2.04	0	0	0	Repressed
399	GO_BOX_H_ACA_RNP_COMPLEX	-1.74	4	0	0	0	Repressed
400	GO_PROTEIN_PHOSPHORYLATED_AMINO_ACID_BINDING	-1.74	4	0	0	0	Repressed
401	GO_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLATION	-1.74	4	0	0	0	Repressed
402	GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	-1.74	4	0	0	0	Repressed
403	GO_STRUCTURAL_CONSTITUENT_OF_NUCLEAR_PORE	-1.74	4	0	0	0	Repressed
404	REACTOME_SUMOYLATION_OF_UBIQUITINYLATION_PROTEINS	-1.74	4	0	0	0	Repressed
405	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX3	-1.74	4	0	0	0	Repressed
406	REACTOME_PHOSPHORYLATION_SITE_MUTANTS_OF_CTNNB1_ARE_NOT_TARGET	-1.74	2.63	0	0	0	Repressed
407	REACTOME_DEFECTIVE_TPR_MAY_CONFER_SUSCEPTIBILITY_TOWARDS_THYROI	-1.74	2.57	0	0	0	Repressed
408	GO_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	-1.74	2.54	0	0	0	Repressed
409	GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY	-1.74	2.47	0	0	0	Repressed
410	GO_CHAPERONIN_CONTAINING_T_COMPLEX	-1.74	2.2	0	0	0	Repressed
411	GO_TRNA_METHYLATION	-1.74	2.1	0	0	0	Repressed
412	EPPERT_PROGENITOR	-1.73	4	0	0	0	Repressed
413	GO_ALTERNATIVE_MRNA_SPLICING_VIA_SPLICEOSOME	-1.73	4	0	0	0	Repressed
414	GO_RESPONSE_TO_HEAT	-1.73	4	0	0	0	Repressed
415	GO_TRANSPORT_OF_VIRUS	-1.73	4	0	0	0	Repressed
416	GO_UNFOLDED_PROTEIN_BINDING	-1.73	4	0	0	0	Repressed
417	REACTOME_MITOTIC_G2_G2_M_PHASES	-1.73	4	0	0	0	Repressed
418	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP	-1.73	4	0	0	0	Repressed
419	GO_POSITIVE_REGULATION_OF_RIBOSOME_BIOGENESIS	-1.73	2.66	0	0	0	Repressed
420	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP	-1.73	2.66	0	0	0	Repressed
421	GO_MICROTUBULE_PLUS_END	-1.73	2.6	0	0	0	Repressed
422	GO_MICROTUBULE_MOTOR_ACTIVITY	-1.73	2.51	0	0	0	Repressed
423	GO_PROTEIN_LOCALIZATION_TO_CYTOPLASMIC_STRESS_GRANULE	-1.73	2.35	0	0	0	Repressed
424	GO_RNA_CAPPING	-1.73	2.31	0	0	0	Repressed

425	GO_KINESIN_COMPLEX	-1.73	2.25	0	0	0	Repressed
426	GO_SPINDLE_LOCALIZATION	-1.73	2.25	0	0	0	Repressed
427	GO_ATP_DEPENDENT_MICROTUBULE_MOTOR_ACTIVITY	-1.73	2.12	0	0	0	Repressed
428	GO_NEURAL_NUCLEUS_DEVELOPMENT	-1.73	1.98	0	0	0	Repressed
429	REACTOME_HSF1_DEPENDENT_TRANSACTIVATION	-1.73	1.96	0	0	0	Repressed
430	BILD_MYC_ONCOGENIC_SIGNATURE	-1.72	4	0	1	0	Repressed
431	BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP	-1.72	4	0	0	0	Repressed
432	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN	-1.72	4	0	0	0	Repressed
433	FISCHER_DREAM_TARGETS	-1.72	4	0	0	0	Repressed
434	GO_BOX_C_D_SNORNP_ASSEMBLY	-1.72	4	0	0	0	Repressed
435	GO_BOX_H_ACA_SNORNA_BINDING	-1.72	4	0	0	0	Repressed
436	GO_NUCLEAR_PERIPHERY	-1.72	4	0	0	0	Repressed
437	GO_REGULATION_OF_PROTEIN_DEPHOSPHORYLATION	-1.72	4	0	0	0	Repressed
438	GO_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	-1.72	4	0	0	0	Repressed
439	INAMURA_LUNG_CANCER_SCC_UP	-1.72	4	0	0	0	Repressed
440	PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_UP	-1.72	4	0	0	0	Repressed
441	REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	-1.72	4	0	0	0	Repressed
442	REACTOME_FOLDING_OF_ACTIN_BY_CCT_TRIC	-1.72	4	0	0	0	Repressed
443	REACTOME_REGULATION_OF_HSF1_MEDIATED_HEAT_SHOCK_RESPONSE	-1.72	4	0	0	0	Repressed
444	WINTER_HYPOXIA_UP	-1.72	4	0	0	0	Repressed
445	GO_SMALL_NUCLEOLAR_RIBONUCLEOPROTEIN_COMPLEX_ASSEMBLY	-1.72	2.66	0	0	0	Repressed
446	FUNG_IL2_TARGETS_WITH_STAT5_BINDING_SITES	-1.72	2.65	0	0	0	Repressed
447	GO_NEURON_PROJECTION_CYTOPLASM	-1.72	2.53	0	0	0	Repressed
448	HU_GENOTOXIC_DAMAGE_4HR	-1.72	2.3	0	0	0	Repressed
449	GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_CHROMO	-1.72	2.02	0	0	0	Repressed
450	REACTOME_ATTENUATION_PHASE	-1.72	2	0	0	0	Repressed
451	LIANG_SILENCED_BY_METHYLATION_UP	-1.72	1.87	0	0	0	Repressed
452	GO_CELLULAR_RESPONSE_TO_HEAT	-1.71	4	0	0	0	Repressed
453	GO_MITOTIC_NUCLEAR_DIVISION	-1.71	4	0	0	0	Repressed
454	GO_REGULATION_OF_MRNA_PROCESSING	-1.71	4	0	0	0	Repressed
455	GO_REGULATION_OF_TRANSLATIONAL_TERMINATION	-1.71	4	0	0	0	Repressed
456	REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SIGNALING	-1.71	4	0	0	0	Repressed
457	REACTOME_CELLULAR_RESPONSE_TO_HEAT_STRESS	-1.71	4	0	0	0	Repressed
458	TOYOTA_TARGETS_OF_MIR34B_AND_MIR34C	-1.71	4	0	0	0	Repressed
459	WHITFIELD_CELL_CYCLE_G2	-1.71	4	0	0	0	Repressed
460	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN	-1.71	4	0	0	0	Repressed
461	GO_HISTONE_SERINE_PHOSPHORYLATION	-1.71	2.67	0	0	0	Repressed
462	GO_RIBOSOMAL_PROTEIN_IMPORT_INTO_NUCLEUS	-1.71	2.65	0	0	0	Repressed
463	CHR17Q22	-1.71	2.59	0	0	0	Repressed
464	KENNY_CTNNB1_TARGETS_UP	-1.71	2.57	0	0	0	Repressed
465	KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	-1.71	2.55	0	0	0	Repressed
466	REACTOME_DEFECTIVE_CFTR_CAUSES_CYSTIC_FIBROSIS	-1.71	2.53	0	0	0	Repressed
467	REACTOME_FGFR2_ALTERNATIVE_SPLICING	-1.71	2.34	0	0	0	Repressed
468	REACTOME_RORA_ACTIVATES_GENE_EXPRESSION	-1.71	2.34	0	0	0	Repressed
469	GO_RNA_HELICASE_ACTIVITY	-1.71	2.26	0	0	0	Repressed
470	REACTOME_MRNA_CAPPING	-1.71	2.26	0	0	0	Repressed
471	REACTOME_COOPERATION_OF_PREFOLDIN_AND_TRIC_CCT_IN_ACTIN_AND_TUBU	-1.71	1.94	0	0	0	Repressed
472	BHATTACHARYA_EMBRYONIC_STEM_CELL	-1.70	4	0	0	0	Repressed
473	CHR1P34	-1.70	4	0	0	0	Repressed
474	GO_POSITIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	-1.70	4	0	0	0	Repressed
475	GO_RNA_SPLICING	-1.70	4	0	0	0	Repressed
476	GRADE_COLON_AND_RECTAL_CANCER_UP	-1.70	4	0	0	0	Repressed
477	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN	-1.70	4	0	0	0	Repressed
478	BIOCARTA_RARRXR_PATHWAY	-1.70	2.65	0	0	0	Repressed
479	CHENG_RESPONSE_TO_NICKEL_ACETATE	-1.70	2.56	0	0	0	Repressed
480	REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	-1.70	2.53	0	0	0	Repressed
481	GO_POSITIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	-1.70	2.5	0	0	0	Repressed
482	GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	-1.70	2.33	0	0	0	Repressed
483	REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	-1.70	2.3	0	0	0	Repressed
484	GO_NUCLEAR_EXPORT_SIGNAL_RECEPTOR_ACTIVITY	-1.70	2.2	0	0	0	Repressed
485	REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	-1.70	2.2	0	0	0	Repressed
486	LE_NEURONAL_DIFFERENTIATION_DN	-1.70	2.14	0	0	0	Repressed
487	WAESCH_ANAPHASE_PROMOTING_COMPLEX	-1.70	2.06	0	0	0	Repressed
488	GO_PROTEIN_PHOSPHATASE_TYPE_2A_COMPLEX	-1.70	2.05	0	0	0	Repressed
489	CHR5Q32	-1.70	2.04	0	0	0	Repressed
490	BIOCARTA_EIF2_PATHWAY	-1.69	4	0	0	0	Repressed
491	GO_BOX_H_ACA_SNORNP_COMPLEX	-1.69	4	0	0	0	Repressed
492	GO_CHROMOSOME_LOCALIZATION	-1.69	4	0	0	0	Repressed
493	GO_CHROMOSOME_PASSENGER_COMPLEX	-1.69	4	0	0	0	Repressed
494	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	-1.69	4	0	0	0	Repressed
495	GO_NEGATIVE_REGULATION_OF_NUCLEAR_DIVISION	-1.69	4	0	0	0	Repressed
496	GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME	-1.69	4	0	0	0	Repressed
497	GO_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	-1.69	4	0	0	0	Repressed
498	MITSIADES_RESPONSE_TO_APLIDIN_DN	-1.69	4	0	0	0	Repressed
499	REACTOME_TRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL	-1.69	4	0	0	0	Repressed
500	SESTO_RESPONSE_TO_UV_C5	-1.69	4	0	0	0	Repressed
501	GO_SAGA_COMPLEX	-1.69	2.63	0	0	0	Repressed
502	REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	-1.69	2.6	0	0	0	Repressed
503	GO_TOXIN_TRANSPORT	-1.69	2.58	0	0	0	Repressed
504	JIANG_HYPOXIA_CANCER	-1.69	2.57	0	0	0	Repressed
505	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_ELONGATION	-1.69	2.53	0	0	0	Repressed
506	GO_CHROMOSOME_MOVEMENT_TOWARDS_SPINDLE_POLE	-1.69	2.37	0	0	0	Repressed
507	GO_REGULATION_OF_WOUND_HEALING_SPREADING_OF_EPIDERMAL_CELLS	-1.69	2.37	0	0	0	Repressed
508	GO_ATP_DEPENDENT_MICROTUBULE_MOTOR_ACTIVITY_PLUS_END_DIRECTED	-1.69	2.32	0	0	0	Repressed
509	GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_ACTIVITY	-1.69	2.28	0	0	0	Repressed
510	GO_NUCLEAR_IMPORT_SIGNAL_RECEPTOR_ACTIVITY	-1.69	2.19	0	0	0	Repressed
511	GO_DE_NOVO_PROTEIN_FOLDING	-1.69	2.13	0	0	0	Repressed
512	GO_EXON_EXON_JUNCTION_COMPLEX	-1.69	2.04	0	0	0	Repressed
513	GO_RRNA_CONTAINING_RIBONUCLEOPROTEIN_COMPLEX_EXPORT_FROM_NUCLEU	-1.69	1.92	0	0	0	Repressed
514	GO_AXON_HILLOCK	-1.68	4	0	0	0	Repressed
515	GO_CHROMOSOME_SEGREGATION	-1.68	4	0	0	0	Repressed
516	GO_ENDONUCLEOLYTIC_CLEAVAGE_IN_5_ETS_OF_TRICISTRONIC_RRNA_TRANSC	-1.68	4	0	0	0	Repressed
517	GO_KINETOCHORE_BINDING	-1.68	4	0	0	0	Repressed
518	GO_NUCLEAR_ENVELOPE_ORGANIZATION	-1.68	4	0	0	0	Repressed
519	GO_NUCLEOLUS_ORGANIZATION	-1.68	4	0	0	0	Repressed
520	GO_PROTEIN_DEPHOSPHORYLATION	-1.68	4	0	0	0	Repressed
521	KIM_WT1_TARGETS_8HR_UP	-1.68	4	0	0	0	Repressed
522	REACTOME_GENE_SILENCING_BY_RNA	-1.68	4	0	0	0	Repressed
523	REACTOME_ORGANIC_CATION_TRANSPORT	-1.68	4	0	0	0	Repressed
524	REACTOME_RHO_GTPASE_EFFECTORS	-1.68	4	0	0	0	Repressed
525	REACTOME_TCF_DEPENDENT_SIGNALING_IN_RESPONSE_TO_WNT	-1.68	4	0	0	0	Repressed
526	GO_AXO_DENDRITIC_TRANSPORT	-1.68	2.56	0	0	0	Repressed
527	GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_II_PROMOTER	-1.68	2.4	0	0	0	Repressed
528	GO_UBIQUITIN_RECYCLING	-1.68	2.37	0	0	0	Repressed
529	GO_REGULATION_OF_CARDIAC_CONDUCTION	-1.68	2.29	0	0	0	Repressed
530	GO_ENDONUCLEOLYTIC_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	-1.68	2.18	0	0	0	Repressed
531	GO_NEGATIVE_REGULATION_OF_MRNA_PROCESSING	-1.68	2.12	0	0	0	Repressed
532	REACTOME_REGULATION_OF_GLYCOLYSIS_BY_FRUCTOSE_2_6_BISPHOSPHATE_	-1.68	1.87	0	0	0	Repressed
533	BORCZUK_MALIGNANT_MESOTHELIOMA_UP	-1.67	4	0	0	0	Repressed

534	DAZARD_RESPONSE_TO_UV_NHEK_DN	-1.67	4	0	0	0	Repressed
535	GO_NUCLEAR_CHROMOSOME_SEGREGATION	-1.67	4	0	0	0	Repressed
536	GO_RNA_METHYLTRANSFERASE_ACTIVITY	-1.67	4	0	0	0	Repressed
537	GROSS_HYPOXIA_VIA_ELK3_UP	-1.67	4	0	0	0	Repressed
538	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP	-1.67	4	0	0	0	Repressed
539	REACTOME_SIGNALING_BY_FGFR	-1.67	2.54	0	0	0	Repressed
540	MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_DN	-1.67	2.25	0	0	0	Repressed
541	GO_RIBOSOMAL_SMALL_SUBUNIT_BINDING	-1.67	2.05	0	0	0	Repressed
542	GO_3_5_RNA_HELICASE_ACTIVITY	-1.67	2.01	0	0	0	Repressed
543	GO_TRNA_THREONYLCARBAMOYLADENOSINE_METABOLIC_PROCESS	-1.67	1.94	1	0	0	Repressed
544	GO_FEMALE_MEIOTIC_NUCLEAR_DIVISION	-1.67	1.93	0	0	0	Repressed
545	BIOCARTA_VDR_PATHWAY	-1.67	1.85	0	0	0	Repressed
546	KORKOLA_TERATOMA	-1.67	1.84	0	0	0	Repressed
547	JAEGER_METASTASIS_UP	-1.67	1.8	0	0	0	Repressed
548	REACTOME_IMPORT_OF_PALMITOYL_COA_INTO_THE_MITOCHONDRIAL_MATRIX	-1.67	1.7	0	0	0	Repressed
549	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP	-1.66	4	0	0	0	Repressed
550	BROWNE_HCMV_INFECTION_20HR_UP	-1.66	4	0	0	0	Repressed
551	GO_MICROTUBULE_ASSOCIATED_COMPLEX	-1.66	4	0	0	0	Repressed
552	GO_MITOCHONDRIAL_GENE_EXPRESSION	-1.66	4	0	0	0	Repressed
553	GO_MRNA_BINDING	-1.66	4	0	0	0	Repressed
554	GO_PROTEIN_TRANSPORTER_ACTIVITY	-1.66	4	0	0	0	Repressed
555	GO_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENCING	-1.66	4	0	0	0	Repressed
556	GO_RNA_3_END_PROCESSING	-1.66	4	0	0	0	Repressed
557	REACTOME_FORMATION_OF_TC_NER_PRE_INCISION_COMPLEX	-1.66	4	0	0	0	Repressed
558	REACTOME_NEDDYLATION	-1.66	4	0	0	0	Repressed
559	GO_DNA_TOPOISOMERASE_ACTIVITY	-1.66	2.67	0	0	0	Repressed
560	LIU_CDX2_TARGETS_UP	-1.66	2.63	0	0	0	Repressed
561	GO_EPITHELIAL_STRUCTURE_MAINTENANCE	-1.66	2.6	0	0	0	Repressed
562	YANG_BREAST_CANCER_ESR1_LASER_DN	-1.66	2.56	0	0	0	Repressed
563	GO_DENDRITIC_TRANSPORT	-1.66	2.39	0	0	0	Repressed
564	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53	-1.66	2.25	0	0	0	Repressed
565	GO_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	-1.66	2.24	0	0	0	Repressed
566	GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	-1.66	2.23	0	0	0	Repressed
567	GO_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	-1.66	2.19	0	0	0	Repressed
568	GO_CHROMOCENTER	-1.66	2.17	0	0	0	Repressed
569	BILANGES_SERUM_SENSITIVE_VIA_TSC2	-1.66	2.15	0	0	0	Repressed
570	GO_ATTACHMENT_OF_SPINDLE_MICROTUBULES_TO_KINETOCHORE	-1.66	2.11	0	0	0	Repressed
571	REACTOME_SIGNALING_BY_FGFR2	-1.66	2.09	0	0	0	Repressed
572	REACTOME_CONDENSATION_OF_PROMETAPHASE_CHROMOSOMES	-1.66	2.05	0	0	0	Repressed
573	REACTOME_SIGNALING_BY_FGFR2_IIIA_TM	-1.66	1.94	0	0	0	Repressed
574	GO_WOUND_HEALING_SPREADING_OF_EPIDERMAL_CELLS	-1.66	1.93	0	0	0	Repressed
575	CHANDRAN_METASTASIS_TOP50_UP	-1.66	1.9	0	0	0	Repressed
576	REACTOME_PLATELET_SENSITIZATION_BY_LDL	-1.66	1.86	0	0	0	Repressed
577	GO_DYNEIN_INTERMEDIATE_CHAIN_BINDING	-1.66	1.85	0	0	0	Repressed
578	REACTOME_FGFR2_MUTANT_RECEPTOR_ACTIVATION	-1.66	1.85	0	0	0	Repressed
579	SMID_BREAST_CANCER_LUMINAL_A_DN	-1.66	1.66	0	0	0	Repressed
580	BASSO_B_LYMPHOCYTE_NETWORK	-1.65	4	0	0	0	Repressed
581	DING_LUNG_CANCER_EXPRESSION_BY_COPY_NUMBER	-1.65	4	0	0	0	Repressed
582	GO_AXON_CYTOPLASM	-1.65	4	0	0	0	Repressed
583	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP	-1.65	4	0	0	0	Repressed
584	JOHNSTONE_PARVB_TARGETS_3_DN	-1.65	4	0	0	0	Repressed
585	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN	-1.65	4	0	0	0	Repressed
586	YORDY_RECIPROCAL_REGULATION_BY_ETS1_AND_SP100_DN	-1.65	2.57	0	0	0	Repressed
587	GO_ANAPHASE_PROMOTING_COMPLEX_BINDING	-1.65	2.38	0	0	0	Repressed
588	GO_PROTEASOME_ACTIVATING_ATPASE_ACTIVITY	-1.65	2.22	0	0	0	Repressed
589	GO_MAINTENANCE_OF_GASTROINTESTINAL_EPITHELIUM	-1.65	2.07	0	0	0	Repressed
590	GO_CONDENSED_NUCLEAR_CHROMOSOME_KINETOCHORE	-1.65	1.97	0	0	0	Repressed
591	GO_CELLULAR_RESPONSE_TO_MANGANESE_ION	-1.65	1.92	0	0	0	Repressed
592	GO_NEURON_FATE_COMMITMENT	-1.65	1.78	0	0	0	Repressed
593	GO_CELL_CYCLE_G2_M_PHASE_TRANSITION	-1.64	4	0	0	1	Repressed
594	GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	-1.64	4	0	0	0	Repressed
595	GO_PHOSPHOPROTEIN_BINDING	-1.64	4	0	0	0	Repressed
596	GO_REGULATION_OF_CELL_DIVISION	-1.64	4	0	0	0	Repressed
597	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP	-1.64	4	0	0	0	Repressed
598	REACTOME_CELL_CYCLE_MITOTIC	-1.64	4	0	0	0	Repressed
599	REACTOME_MITOTIC_PROPHASE	-1.64	4	0	0	0	Repressed
600	REACTOME_ORGANIC_CATION_ANION_ZWITTERION_TRANSPORT	-1.64	4	0	0	0	Repressed
601	REACTOME_GOLGI_TO_ER_RETROGRADE_TRANSPORT	-1.64	2.44	0	0	0	Repressed
602	GO_BOX_H_ACA_TELOMERASE_RNP_COMPLEX	-1.64	2.36	0	0	0	Repressed
603	GO_RRNA_TRANSCRIPTION	-1.64	2.31	0	0	0	Repressed
604	GO_MITOCHONDRIAL_TRNA_PROCESSING	-1.64	2.16	0	0	0	Repressed
605	GO_MRNA_PSEUDOURIDINE_SYNTHESIS	-1.64	2.08	0	0	0	Repressed
606	GO_NEGATIVE_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYS	-1.64	2.05	0	0	0	Repressed
607	HO_LIVER_CANCER_VASCULAR_INVASION	-1.64	1.99	0	0	0	Repressed
608	GO_SPLICEOSOMAL_TRI_SNRNP_COMPLEX_ASSEMBLY	-1.64	1.96	0	0	0	Repressed
609	WANG_METASTASIS_OF_BREAST_CANCER_ESR1_UP	-1.64	1.85	0	0	0	Repressed
610	GO_MRNA_5_UTR_BINDING	-1.64	1.83	0	0	0	Repressed
611	GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME_TELOMERIC_REGION	-1.64	1.83	0	0	0	Repressed
612	GO_ANAPHASE_PROMOTING_COMPLEX	-1.64	1.8	0	0	0	Repressed
613	GO_U6_SNRNA_BINDING	-1.64	1.78	0	0	0	Repressed
614	GO_POSITIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	-1.64	1.73	0	0	0	Repressed
615	ABRAMSON_INTERACT_WITH_AIRE	-1.63	4	0	0	0	Repressed
616	GO_NUCLEUS_ORGANIZATION	-1.63	4	0	0	0	Repressed
617	GO_POSITIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	-1.63	4	0	0	0	Repressed
618	GO_PROTEIN_CONTAINING_COMPLEX_LOCALIZATION	-1.63	4	0	0	0	Repressed
619	REACTOME_MITOCHONDRIAL_BIOGENESIS	-1.63	4	0	0	0	Repressed
620	REACTOME_SIGNALING_BY_NOTCH4	-1.63	4	0	0	0	Repressed
621	GO_ENDOCYTIC_VESICLE_LUMEN	-1.63	2.67	0	0	0	Repressed
622	GO_REGULATION_OF_PROTEIN_EXPORT_FROM_NUCLEUS	-1.63	2.6	0	0	0	Repressed
623	DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2	-1.63	2.46	0	0	0	Repressed
624	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_I	-1.63	2.32	0	0	0	Repressed
625	GO_NEGATIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.63	2.25	0	0	0	Repressed
626	GO_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	-1.63	2.22	0	0	0	Repressed
627	REACTOME_ABC_TRANSPORTER_DISORDERS	-1.63	2.22	0	0	0	Repressed
628	ZHAN_VARIABLE_EARLY_DIFFERENTIATION_GENES_DN	-1.63	2.16	0	0	0	Repressed
629	REACTOME_SIGNALING_BY_FGFR2_IN_DISEASE	-1.63	2.13	0	0	0	Repressed
630	NAKAMURA_CANCER_MICROENVIRONMENT_DN	-1.63	2.07	0	0	0	Repressed
631	GO_ADENYLATE_CYCLASE_BINDING	-1.63	1.96	0	0	0	Repressed
632	GO_AMINOACYL_TRNA_SYNTHETASE_MULTIENZYME_COMPLEX	-1.63	1.93	0	0	0	Repressed
633	OHASHI_AURKA_TARGETS	-1.63	1.9	0	0	0	Repressed
634	HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_DN	-1.63	1.84	0	0	0	Repressed
635	REACTOME_ABORTIVE_ELONGATION_OF_HIV_1_TRANSCRIPT_IN_THE_ABSENCE_C	-1.63	1.84	0	0	0	Repressed
636	REACTOME_PIWI_INTERACTING_RNA_PIRNA_BIOGENESIS	-1.63	1.84	0	0	0	Repressed
637	GO_RNA_7_METHYLGUANOSINE_CAP_BINDING	-1.63	1.82	0	0	0	Repressed
638	GO_DICARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	-1.63	1.72	0	0	0	Repressed
639	GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU	-1.63	1.71	0	0	0	Repressed
640	GO_EMBRYO_IMPLANTATION	-1.63	1.69	0	0	0	Repressed
641	NAGY_TFTC_COMPONENTS_HUMAN	-1.63	1.63	0	0	0	Repressed
642	GO_MITOTIC_SPINDLE_MIDZONE	-1.63	1.59	0	0	0	Repressed

643	BLUM_RESPONSE_TO_SALIRASIB_DN	-1.62	4	0	0	0	Repressed
644	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN	-1.62	4	0	0	0	Repressed
645	LI_DCP2_BOUND_MRNA	-1.62	4	0	0	0	Repressed
646	REACTOME_ACTIVATION_OF_HOX_GENES_DURING_DIFFERENTIATION	-1.62	4	0	0	0	Repressed
647	REACTOME_COPI_DEPENDENT_GOLGI_TO_ER_RETROGRADE_TRAFFIC	-1.62	4	0	0	0	Repressed
648	REACTOME_INFECTIOUS_DISEASE	-1.62	4	0	0	0	Repressed
649	REACTOME_TCR_SIGNALING	-1.62	4	0	0	0	Repressed
650	REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_COMPLEX	-1.62	2.6	0	0	0	Repressed
651	HU_GENOTOXIN_ACTION_DIRECT_VS_INDIRECT_24HR	-1.62	2.59	0	0	0	Repressed
652	LIU_COMMON_CANCER_GENES	-1.62	2.55	0	0	0	Repressed
653	REACTOME_SUMOYLATION_OF_RNA_BINDING_PROTEINS	-1.62	2.24	0	0	0	Repressed
654	GO_ESTABLISHMENT_OF_MITOTIC_SPINDLE_LOCALIZATION	-1.62	2.01	0	0	0	Repressed
655	GO_MITOCHONDRIAL_RNA_MODIFICATION	-1.62	1.89	0	0	0	Repressed
656	REACTOME_SUMOYLATION_OF_SUMOYLATION_PROTEINS	-1.62	1.87	0	0	0	Repressed
657	GO_RNA_POLYMERASE_III_COMPLEX	-1.62	1.85	0	0	0	Repressed
658	YUAN_ZNF143_PARTNERS	-1.62	1.83	0	0	0	Repressed
659	GO_REGULATION_OF_MYELINATION	-1.62	1.81	0	0	0	Repressed
660	MULLIGAN_NTF3_SIGNALING_VIA_INSR_AND_IGF1R_UP	-1.62	1.8	0	0	0	Repressed
661	GO_REGULATION_OF_CELL_MATURATION	-1.62	1.59	0	0	0	Repressed
662	BENPORATH_CYCLING_GENES	-1.61	4	0	0	0	Repressed
663	CHANG_CORE_SERUM_RESPONSE_UP	-1.61	4	0	0	0	Repressed
664	GO_CONDENSED_CHROMOSOME	-1.61	4	0	0	0	Repressed
665	GO_FIBRILLAR_CENTER	-1.61	4	0	0	0	Repressed
666	GO_MICROTUBULE	-1.61	4	0	0	0	Repressed
667	GO_PLASMA_MEMBRANE_BOUNDED_CELL_PROJECTION_CYTOPLASM	-1.61	4	0	0	0	Repressed
668	GO_U4_SNRNA_BINDING	-1.61	4	0	0	0	Repressed
669	KIM_WT1_TARGETS_12HR_DN	-1.61	4	0	0	0	Repressed
670	LU_AGING_BRAIN_DN	-1.61	4	0	0	0	Repressed
671	MYC_UP.V1_UP	-1.61	4	0	1	0	Repressed
672	REACTOME_GLUCOSE_METABOLISM	-1.61	4	0	0	0	Repressed
673	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_7	-1.61	2.55	0	0	0	Repressed
674	SERVITJA_LIVER_HNF1A_TARGETS_UP	-1.61	2.51	0	0	0	Repressed
675	GO_NEGATIVE_REGULATION_OF_MEIOTIC_NUCLEAR_DIVISION	-1.61	2.37	0	0	0	Repressed
676	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_UP	-1.61	2.21	0	0	0	Repressed
677	GAJATE_RESPONSE_TO_TRABECTEDIN_DN	-1.61	2.13	0	0	0	Repressed
678	REACTOME_NOTCH3_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	-1.61	2.04	0	0	0	Repressed
679	REACTOME_DISEASES_ASSOCIATED_WITH_O_GLYCOSYLATION_OF_PROTEINS	-1.61	2	0	0	0	Repressed
680	GO_TFIID_CLASS_TRANSCRIPTION_FACTOR_COMPLEX_BINDING	-1.61	1.98	0	0	0	Repressed
681	KOMMAGANI_TP63_GAMMA_TARGETS	-1.61	1.9	0	0	0	Repressed
682	GO_PROTEIN_LOCALIZATION_TO_NUCLEOLUS	-1.61	1.88	0	0	0	Repressed
683	GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	-1.61	1.83	0	0	0	Repressed
684	OHASHI_AURKB_TARGETS	-1.61	1.82	0	0	0	Repressed
685	GO_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_TRANSPORT	-1.61	1.75	0	0	0	Repressed
686	CHR1Q43	-1.61	1.71	0	0	0	Repressed
687	GO_POSITIVE_REGULATION_OF_BEHAVIOR	-1.61	1.7	0	0	0	Repressed
688	BIOCARTA_NPC_PATHWAY	-1.61	1.68	0	0	0	Repressed
689	GO_CLATHRIN_COAT_ASSEMBLY	-1.61	1.67	0	0	0	Repressed
690	GO_SPINDLE_ELONGATION	-1.61	1.62	0	0	0	Repressed
691	BENPORATH_ES_1	-1.60	4	0	0	0	Repressed
692	GO_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	-1.60	4	0	0	0	Repressed
693	GO_POSTTRANSCRIPTIONAL_REGULATION_OF_GENE_EXPRESSION	-1.60	4	0	0	0	Repressed
694	GO_REGULATION_OF_REPRODUCTIVE_PROCESS	-1.60	4	0	0	0	Repressed
695	PAL_PRMT5_TARGETS_UP	-1.60	4	0	0	0	Repressed
696	REACTOME_ANTIGEN_PROCESSING:_UBIQUITINATION_PROTEASOME_DEGRADATIC	-1.60	4	0	0	0	Repressed
697	REACTOME_SIGNALING_BY_WNT	-1.60	4	0	0	0	Repressed
698	GO_BOX_C_D_SNORNP_COMPLEX	-1.60	2.67	0	0	0	Repressed
699	ITO_PTTG1_TARGETS_DN	-1.60	2.36	0	0	0	Repressed
700	REACTOME_MAPK_FAMILY_SIGNALING_CASCADES	-1.60	2.32	0	0	0	Repressed
701	CROSBY_E2F4_TARGETS	-1.60	2.19	0	0	0	Repressed
702	BYSTROEM_CORRELATED_WITH_IL5_DN	-1.60	2.08	0	0	0	Repressed
703	GO_EXTRINSIC_COMPONENT_OF_POSTSYNAPTIC_MEMBRANE	-1.60	2.06	0	0	0	Repressed
704	GO_MEIOTIC_CELL_CYCLE_CHECKPOINT	-1.60	2.06	0	0	1	Repressed
705	BIOCARTA_AKAP95_PATHWAY	-1.60	1.96	0	0	0	Repressed
706	GO_RNA_POLYMERASE_I_ACTIVITY	-1.60	1.89	0	0	0	Repressed
707	GO_MATURATION_OF_5_8S_RRNA	-1.60	1.82	0	0	0	Repressed
708	PID_RANBP2_PATHWAY	-1.60	1.78	0	0	0	Repressed
709	GO_PROTEIN_SERINE_THREONINE_KINASE_ACTIVATOR_ACTIVITY	-1.60	1.77	0	0	0	Repressed
710	BERENJENO_TRANSFORMED_BY_RHOA_REVERSIBLY_DN	-1.60	1.71	0	0	0	Repressed
711	GO_ANTERIOR_POSTERIOR_AXIS_SPECIFICATION	-1.60	1.7	0	0	0	Repressed
712	PID_RETINOIC_ACID_PATHWAY	-1.60	1.66	0	0	0	Repressed
713	GO_CHROMOSOMAL_REGION	-1.59	4	0	0	0	Repressed
817	GO_MITOTIC_CELL_CYCLE	-1.55	4	0	0	1	Repressed
818	GO_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	-1.55	4	0	0	1	Repressed
716	RAMALHO_STEMNESS_UP	-1.59	4	0	0	0	Repressed
717	SENESE_HDAC1_TARGETS_UP	-1.59	4	0	0	0	Repressed
718	GO_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	-1.59	2.49	0	0	0	Repressed
719	BERNARD_PPAPDC1B_TARGETS_DN	-1.59	2.06	0	0	0	Repressed
720	GO_T_CELL_EXTRAVASATION	-1.59	2.06	0	0	0	Repressed
721	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_DN	-1.59	2.03	0	0	0	Repressed
722	GO_POSITIVE_REGULATION_OF_CELL_DIVISION	-1.59	1.96	0	0	0	Repressed
723	GO_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	-1.59	1.91	0	0	0	Repressed
724	GO_MICROTUBULE_PLUS_END_BINDING	-1.59	1.86	0	0	0	Repressed
725	REACTOME_REGULATION_OF_SIGNALING_BY_CBL	-1.59	1.79	0	0	0	Repressed
726	GO_MITOTIC_SISTER_CHROMATID_COHESION	-1.59	1.74	0	0	0	Repressed
727	GO_REGULATION_OF_MRNA_3_END_PROCESSING	-1.59	1.7	0	0	0	Repressed
728	GO_POSITIVE_REGULATION_OF_UBIQUITIN_PROTEIN_TRANSFERASE_ACTIVITY	-1.59	1.68	0	0	0	Repressed
729	GO_CDP_DIACYLGLYCEROL_BIOSYNTHETIC_PROCESS	-1.59	1.66	0	0	0	Repressed
730	GO_RIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.59	1.64	0	0	0	Repressed
731	PID_TCR_JNK_PATHWAY	-1.59	1.6	0	0	0	Repressed
732	GO_POSITIVE_REGULATION_OF_MRNA_3_END_PROCESSING	-1.59	1.59	0	0	0	Repressed
733	GO_PEPTIDYL_SERINE_MODIFICATION	-1.58	4	0	0	0	Repressed
734	LEE_LIVER_CANCER_SURVIVAL_DN	-1.58	4	0	0	0	Repressed
735	REACTOME_CELLULAR_RESPONSES_TO_STRESS	-1.58	4	0	0	0	Repressed
736	WANG_TUMOR_INVASIVENESS_UP	-1.58	4	0	0	0	Repressed
737	REACTOME_DISORDERS_OF_TRANSMEMBRANE_TRANSPORTERS	-1.58	2.46	0	0	0	Repressed
738	THUM_SYSTOLIC_HEART_FAILURE_DN	-1.58	2.39	0	0	0	Repressed
741	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_UP	-1.58	2.21	0	1	0	Repressed
740	GO_POSITIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	-1.58	2.27	0	0	0	Repressed
739	ALFANO_MYC_TARGETS	-1.48	2.35	0	0	0	Repressed
742	KEGG_LONG_TERM_POTENTIATION	-1.58	2.09	0	0	0	Repressed
743	GO_PROTEIN_SERINE_THREONINE_PHOSPHATASE_COMPLEX	-1.58	2	0	0	0	Repressed
744	GENTILE_UV_LOW_DOSE_DN	-1.58	1.97	0	0	0	Repressed
745	GO_NEGATIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	-1.58	1.97	0	0	0	Repressed
746	REACTOME_RAF_ACTIVATION	-1.58	1.91	0	0	0	Repressed
747	GO_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_I	-1.58	1.89	0	0	0	Repressed
748	GO_POSITIVE_REGULATION_OF_MRNA_PROCESSING	-1.58	1.87	0	0	0	Repressed
749	GO_NEGATIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSP	-1.58	1.85	0	0	0	Repressed
750	GO_NEGATIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	-1.58	1.7	0	0	0	Repressed
751	GO_SPLICEOSOMAL_TRI_SNRNP_COMPLEX	-1.58	1.7	0	0	0	Repressed

996	GO_CELL_CYCLE_PHASE_TRANSITION	-1.50	4	0	0	1	Repressed
753	GO_RIBOSOME_BINDING	-1.58	1.69	0	0	0	Repressed
754	GO_EMBRYONIC_CLEAVAGE	-1.58	1.63	0	0	0	Repressed
755	GO_POSITIVE_REGULATION_OF_TELOMERASE_ACTIVITY	-1.58	1.55	0	0	0	Repressed
756	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_OF_NOTCH_RECEPTOR_TARGE	-1.58	1.53	0	0	0	Repressed
757	GO_SYNAPSE_MATURATION	-1.58	1.53	0	0	0	Repressed
758	BIOCARTA_LIS1_PATHWAY	-1.58	1.47	0	0	0	Repressed
759	GO_ALPHA_ACTININ_BINDING	-1.58	1.47	0	0	0	Repressed
760	GO_CELLULAR_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE	-1.58	1.45	0	0	0	Repressed
761	CSR_LATE_UP.V1_UP	-1.57	4	0	0	0	Repressed
762	GO_PURINE_NTP_DEPENDENT_HELICASE_ACTIVITY	-1.57	4	0	0	0	Repressed
763	GO_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.57	4	0	0	0	Repressed
764	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_OR_POLYSACCHA	-1.57	2.24	0	0	0	Repressed
765	GO_RNA_DEPENDENT_DNA_BIOSYNTHETIC_PROCESS	-1.57	2.24	0	0	0	Repressed
766	GO_REGULATION_OF_MICROTUBULE_MOTOR_ACTIVITY	-1.57	2.08	0	0	0	Repressed
767	GO_METAPHASE_PLATE_CONGRESSION	-1.57	2.05	0	0	0	Repressed
768	BIOCARTA_PPARG_PATHWAY	-1.57	1.9	0	0	0	Repressed
769	REACTOME_ACTIVATION_OF_RAC1_DOWNSTREAM_OF_NMDARS	-1.57	1.89	0	0	0	Repressed
770	JIANG_AGING_CEREBRAL_CORTEX_DN	-1.57	1.81	0	0	0	Repressed
771	GO_NONHOMOLOGOUS_END_JOINING_COMPLEX	-1.57	1.75	0	0	0	Repressed
772	WANG_TARGETS_OF_MLL_CBP_FUSION_DN	-1.57	1.75	0	0	0	Repressed
773	REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS	-1.57	1.68	0	0	0	Repressed
774	GO_RNA_CAP_BINDING_COMPLEX	-1.57	1.62	0	0	0	Repressed
775	GO_DNA_HELICASE_COMPLEX	-1.57	1.61	0	0	0	Repressed
776	REACTOME_RECYCLING_PATHWAY_OF_L1	-1.57	1.58	0	0	0	Repressed
777	GO_RESPONSE_TO_MORPHINE	-1.57	1.51	0	0	0	Repressed
778	GO_TRNA_5_END_PROCESSING	-1.57	1.45	0	0	0	Repressed
779	GO_IMP_BIOSYNTHETIC_PROCESS	-1.57	1.44	0	0	0	Repressed
780	MANN_RESPONSE_TO_AMIFOSTINE_DN	-1.57	1.35	0	0	0	Repressed
714	GO_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	-1.49	4	0	0	0	not significant
782	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP	-1.56	4	0	0	0	Repressed
783	GO_CADHERIN_BINDING	-1.56	4	0	0	0	Repressed
715	GO_REGULATION_OF_CELL_CYCLE_PROCESS	-1.49	4	0	0	0	not significant
785	GO_ORGANELLE_FISSION	-1.56	4	0	0	0	Repressed
786	GO_STEM_CELL_DIFFERENTIATION	-1.56	4	0	0	0	Repressed
787	MARKEY_RB1_ACUTE_LOF_UP	-1.56	4	0	0	0	Repressed
788	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN	-1.56	4	0	0	0	Repressed
789	REACTOME_CELL_CYCLE	-1.56	4	0	0	0	Repressed
790	ZHANG_BREAST_CANCER_PROGENITORS_UP	-1.56	4	0	0	0	Repressed
791	GO_PEPTIDYL_THREONINE_MODIFICATION	-1.56	2.5	0	0	0	Repressed
792	GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	-1.56	2.48	0	0	0	Repressed
793	GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	-1.56	2.46	0	0	0	Repressed
794	MCBRYAN_PUBERTAL_BREAST_6_7WK_DN	-1.56	2.06	0	0	0	Repressed
795	MORI_IMMATURE_B_LYMPHOCYTE_DN	-1.56	2.01	0	0	0	Repressed
796	NADERI_BREAST_CANCER_PROGNOSIS_UP	-1.56	1.99	0	0	0	Repressed
797	GO_AXONAL_TRANSPORT	-1.56	1.87	0	0	0	Repressed
798	GO_MAINTENANCE_OF_CENTROSOME_LOCATION	-1.56	1.84	0	0	0	Repressed
799	GO_REGULATION_OF_SPINDLE_ORGANIZATION	-1.56	1.81	0	0	0	Repressed
800	GO_POSITIVE_REGULATION_OF_INTERFERON_BETA_PRODUCTION	-1.56	1.75	0	0	0	Repressed
801	GO_PHOSPHOTYROSINE_RESIDUE_BINDING	-1.56	1.74	0	0	0	Repressed
802	GO_PROTEIN_LOCALIZATION_TO_NUCLEAR_ENVELOPE	-1.56	1.72	0	0	0	Repressed
803	REACTOME_ROLE_OF_ABL_IN_ROBO_SLIT_SIGNALING	-1.56	1.72	0	0	0	Repressed
804	GO_AP_2_ADAPTOR_COMPLEX_BINDING	-1.56	1.71	0	0	0	Repressed
805	GO_EXTRINSIC_COMPONENT_OF_SYNAPTIC_MEMBRANE	-1.56	1.67	0	0	0	Repressed
806	GO_NEGATIVE_REGULATION_OF_PRI_MIRNA_TRANSCRIPTION_BY_RNA_POLYMERA	-1.56	1.66	0	0	0	Repressed
807	GO_POSITIVE_REGULATION_OF_CHEMOKINE_C_X_C_MOTIF_LIGAND_2_PRODUCTI	-1.56	1.66	0	0	0	Repressed
808	SUH_COEXPRESSED_WITH_ID1_AND_ID2_UP	-1.56	1.62	0	0	0	Repressed
809	GO_CYTOPLASMIC_DYNEIN_COMPLEX	-1.56	1.6	0	0	0	Repressed
810	REACTOME_RECYCLING_OF_EIF2:GDP	-1.56	1.58	0	0	0	Repressed
811	GO_PSEUDOURIDINE_SYNTHESIS	-1.56	1.54	0	0	0	Repressed
812	CAFFAREL_RESPONSE_TO_THC_24HR_3_DN	-1.56	1.39	0	0	0	Repressed
813	CHR2Q36	-1.56	1.38	0	0	0	Repressed
814	GO_SERTOLI_CELL_DIFFERENTIATION	-1.56	1.27	0	0	0	Repressed
993	COLLER_MYC_TARGETS_UP	-1.41	1.14	0	0	0	Repressed
816	GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION	-1.55	4	0	0	0	Repressed
781	GO_REGULATION_OF_MEIOTIC_CELL_CYCLE	-1.37	1.05	0	0	0	not significant
784	GO_CELL_CYCLE_PROCESS	-1.36	4	0	0	0	not significant
819	GO_REGULATION_OF_NUCLEAR_DIVISION	-1.55	4	0	0	0	Repressed
820	OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_UP	-1.55	4	0	0	0	Repressed
821	REACTOME_MITOCHONDRIAL_TRANSLATION	-1.55	4	0	0	0	Repressed
822	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX1	-1.55	4	0	0	0	Repressed
823	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN	-1.55	4	0	0	0	Repressed
824	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE	-1.55	2.21	0	0	0	Repressed
825	VANTVEER_BREAST_CANCER_METASTASIS_DN	-1.55	2.19	0	0	0	Repressed
826	GO_NUCLEAR_RECEPTOR_TRANSCRIPTION_COACTIVATOR_ACTIVITY	-1.55	1.86	0	0	0	Repressed
827	GO_REGULATION_OF_DNA_DUPLEX_UNWINDING	-1.55	1.8	0	0	0	Repressed
828	GO_MEIOTIC_CELL_CYCLE_PROCESS	-1.35	1.76	0	0	0	not significant
829	GO_MITOTIC_SPINDLE_MIDZONE_ASSEMBLY	-1.55	1.63	0	0	0	Repressed
830	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQUOISE_DN	-1.55	1.6	0	0	0	Repressed
831	GO_POSITIVE_REGULATION_OF_ANOIKIS	-1.55	1.6	0	0	0	Repressed
832	GO_IRES_DEPENDENT_VIRAL_TRANSLATIONAL_INITIATION	-1.55	1.58	0	0	0	Repressed
833	BIOCARTA_EFP_PATHWAY	-1.55	1.57	0	0	0	Repressed
834	GO_NEGATIVE_REGULATION_OF_RNA_SPLICING	-1.55	1.54	0	0	0	Repressed
835	GO_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	-1.55	1.51	0	0	0	Repressed
836	SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY	-1.55	1.5	0	0	0	Repressed
837	KEGG_DORSO_VENTRAL_AXIS_FORMATION	-1.55	1.49	0	0	0	Repressed
838	GO_PSEUDOPODIUM	-1.55	1.45	0	0	0	Repressed
839	GO_RESPONSE_TO_MANGANESE_ION	-1.55	1.43	0	0	0	Repressed
840	CHEOK_RESPONSE_TO_MERCAPTOPURINE_UP	-1.55	1.4	0	0	0	Repressed
841	GO_CENTROMERIC_SISTER_CHROMATID_COHESION	-1.55	1.36	0	0	0	Repressed
842	GO_NEGATIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.54	4	0	0	0	Repressed
843	GO_REGULATION_OF_CELL_CYCLE	-1.34	4	0	0	0	not significant
844	REACTOME_INTERLEUKIN_1_SIGNALING	-1.54	4	0	0	0	Repressed
845	REACTOME_NEUROTRANSMITTER_RECEPTORS_AND_POSTSYNAPTIC_SIGNAL_TRA	-1.54	4	0	0	0	Repressed
846	KEGG_PURINE_METABOLISM	-1.50	2.45	1	0	0	Repressed
847	GO_BASAL_TRANSCRIPTION_MACHINERY_BINDING	-1.54	2.24	0	0	0	Repressed
848	GO_SNORNA_LOCALIZATION	-1.54	2.2	0	0	0	Repressed
849	GO_REGULATION_OF_TELOMERE_MAINTENANCE	-1.54	1.94	0	0	0	Repressed
850	GO_TRNA_BINDING	-1.54	1.94	0	0	0	Repressed
851	GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	-1.54	1.88	0	0	0	Repressed
852	GO_SNRNA_MODIFICATION	-1.54	1.85	0	0	0	Repressed
853	GO_ENDORIBONUCLEASE_ACTIVITY_PRODUCING_5_PHOSPHOMONOESTERS	-1.54	1.83	0	0	0	Repressed
854	REACTOME_MOLYBDENUM_COFACTOR_BIOSYNTHESIS	-1.54	1.83	0	0	0	Repressed
855	GO_ADENYLATE_CYCLASE_ACTIVATOR_ACTIVITY	-1.54	1.82	0	0	0	Repressed
856	PID_RAS_PATHWAY	-1.54	1.77	0	0	0	Repressed
857	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION	-1.54	1.77	0	0	0	Repressed
858	GO_REGULATION_OF_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_ELECTRON_T	-1.54	1.71	0	0	0	Repressed
859	GO_CORNIFIED_ENVELOPE	-1.54	1.66	0	0	0	Repressed
860	GO_TERMINATION_OF_RNA_POLYMERASE_I_TRANSCRIPTION	-1.54	1.62	0	0	0	Repressed

861	CHR9Q33	-1.54	1.61	0	0	0	Repressed
862	REACTOME_GLUTAMATE_AND_GLUTAMINE_METABOLISM	-1.54	1.61	0	0	0	Repressed
863	REACTOME_TRIGLYCERIDE_CATABOLISM	-1.54	1.6	0	0	0	Repressed
864	GO_RNA_POLYMERASE_III_ACTIVITY	-1.54	1.59	0	0	0	Repressed
865	GO_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	-1.54	1.58	0	0	0	Repressed
866	GO_NUCLEOSIDE_DIPHOSPHATE_KINASE_ACTIVITY	-1.54	1.53	0	0	0	Repressed
867	GO_RNA_STEM_LOOP_BINDING	-1.54	1.52	0	0	0	Repressed
868	GO_CELL_CORTEX_REGION	-1.54	1.49	0	0	0	Repressed
869	GO_REGULATION_OF_OOCYTE_MATURATION	-1.54	1.48	0	0	0	Repressed
870	GO_REGULATION_OF_SYNAPSE_MATURATION	-1.54	1.48	0	0	0	Repressed
871	GO_RIBONUCLEASE_P_COMPLEX	-1.54	1.48	0	0	0	Repressed
872	MOOTHA_GLYCOLYSIS	-1.54	1.44	0	0	0	Repressed
873	NIKOLSKY_BREAST_CANCER_10Q22_AMPLICON	-1.54	1.44	0	0	0	Repressed
874	TOMIDA_METASTASIS_UP	-1.54	1.42	0	0	0	Repressed
875	VALK_AML_CLUSTER_16	-1.54	1.39	0	0	0	Repressed
876	NAKAMURA_CANCER_MICROENVIRONMENT_UP	-1.54	1.38	0	0	0	Repressed
877	LIANG_SILENCED_BY_METHYLATION_DN	-1.54	1.37	0	0	0	Repressed
878	NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP	-1.54	1.37	0	0	0	Repressed
879	GLINSKY_CANCER_DEATH_UP	-1.54	1.35	0	0	0	Repressed
880	GO_POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_TRANSP	-1.54	1.35	0	0	0	Repressed
881	GEORGES_CELL_CYCLE_MIR192_TARGETS	-1.34	1.12	0	0	0	not significant
882	GO_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	-1.53	4	0	0	0	Repressed
883	GO_SPLICEOSOMAL_COMPLEX	-1.53	4	0	0	0	Repressed
884	REACTOME_SIGNALING_BY_RHO_GTPASES	-1.53	4	0	0	0	Repressed
885	RPS14_DN.V1_DN	-1.53	4	0	0	0	Repressed
886	DAZARD_UV_RESPONSE_CLUSTER_G6	-1.53	2.43	0	0	0	Repressed
887	GO_TRANSLATION_REGULATOR_ACTIVITY	-1.53	2.43	0	0	0	Repressed
888	GO_REGULATION_OF_DEPHOSPHORYLATION	-1.53	2.41	0	0	0	Repressed
889	SCIBETTA_KDM5B_TARGETS_DN	-1.53	2.22	0	0	0	Repressed
890	GO_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING	-1.53	2.19	0	0	0	Repressed
891	GO_PHOSPHATASE_REGULATOR_ACTIVITY	-1.53	2.05	0	0	0	Repressed
892	GO_RNA_POLYMERASE_II_HOLOENZYME	-1.53	2.03	0	0	0	Repressed
893	GO_PRECATALYTIC_SPLICEOSOME	-1.53	1.96	0	0	0	Repressed
894	REACTOME_PLATELET_HOMEOSTASIS	-1.53	1.88	0	0	0	Repressed
895	GO_REGULATION_OF_TELOMERASE_ACTIVITY	-1.53	1.87	0	0	0	Repressed
896	REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	-1.53	1.84	0	0	0	Repressed
897	REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS	-1.53	1.77	0	0	0	Repressed
898	REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21	-1.53	1.76	0	0	0	Repressed
899	GO_MIDBRAIN_DEVELOPMENT	-1.53	1.72	0	0	0	Repressed
900	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN	-1.53	1.58	0	0	0	Repressed
901	GO_U2_TYPE_CATALYTIC_STEP_2_SPLICEOSOME	-1.53	1.54	0	0	0	Repressed
902	SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_UP	-1.53	1.52	0	0	0	Repressed
903	SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_DN	-1.53	1.5	0	0	0	Repressed
904	GO_HISTONE_PHOSPHORYLATION	-1.53	1.48	0	0	0	Repressed
905	GO_MICROTUBULE_END	-1.53	1.48	0	0	0	Repressed
906	GO_PRONUCLEUS	-1.53	1.48	0	0	0	Repressed
907	JEON_SMAD6_TARGETS_DN	-1.53	1.47	0	0	0	Repressed
908	SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_UP	-1.53	1.44	0	0	0	Repressed
909	GO_ANATOMICAL_STRUCTURE_ARRANGEMENT	-1.53	1.42	0	0	0	Repressed
910	GO_SPINDLE_POLE_CENTROSOME	-1.53	1.4	0	0	0	Repressed
911	GO_BILE_ACID_AND_BILE_SALT_TRANSPORT	-1.53	1.36	0	0	0	Repressed
912	GO_CLATHRIN_COAT_OF_COATED_PIT	-1.53	1.34	0	0	0	Repressed
913	GO_MRNA_MODIFICATION	-1.53	1.31	0	0	0	Repressed
914	HAMAI_APOPTOSIS_VIA_TRAIL_UP	-1.52	4	0	0	0	Repressed
915	MARSON_BOUND_BY_E2F4_UNSTIMULATED	-1.52	4	0	0	0	Repressed
916	ROME_INSULIN_TARGETS_IN_MUSCLE_UP	-1.52	4	0	0	0	Repressed
917	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_TERMINATION	-1.52	2.53	0	0	0	Repressed
918	REACTOME_NEGATIVE_EPIGENETIC_REGULATION_OF_RRNA_EXPRESSION	-1.52	2.49	0	0	0	Repressed
919	RUIZ_TNC_TARGETS_DN	-1.52	2.48	0	0	0	Repressed
920	GRABARCZYK_BCL11B_TARGETS_UP	-1.52	2.23	0	0	0	Repressed
921	GO_MITOCHONDRIAL_TRANSLATIONAL_TERMINATION	-1.52	2.2	0	0	0	Repressed
922	GO_RNA_METHYLATION	-1.52	2.18	0	0	0	Repressed
923	REACTOME_SUMOYLATION_OF_CHROMATIN_ORGANIZATION_PROTEINS	-1.52	1.81	0	0	0	Repressed
924	GO_ZONA_PELLUCIDA_RECEPTOR_COMPLEX	-1.52	1.79	0	0	0	Repressed
925	REACTOME_CA_DEPENDENT_EVENTS	-1.52	1.69	0	0	0	Repressed
926	GO_PROTEIN_LOCALIZATION_TO_CHROMATIN	-1.52	1.67	0	0	0	Repressed
927	GO_CONDENSED_NUCLEAR_CHROMOSOME	-1.52	1.65	0	0	0	Repressed
928	AMIT_SERUM_RESPONSE_240_MCF10A	-1.52	1.6	0	0	0	Repressed
929	GO_REGULATION_OF_CHEMOKINE_C_X_C_MOTIF_LIGAND_2_PRODUCTION	-1.52	1.6	0	0	0	Repressed
930	GO_PTW_PP1_PHOSPHATASE_COMPLEX	-1.52	1.55	0	0	0	Repressed
931	GO_NCRNA_3_END_PROCESSING	-1.52	1.54	0	0	0	Repressed
932	GO_POSITIVE_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRINSIC_APOPTC	-1.52	1.53	0	0	0	Repressed
933	GO_POTASSIUM_ION_BINDING	-1.52	1.51	0	0	0	Repressed
934	GO_PWP2P_CONTAINING_SUBCOMPLEX_OF_90S_PRERIBOSOME	-1.52	1.47	0	0	0	Repressed
935	REACTOME_CHK1_CHK2_CDS1_MEDIATED_INACTIVATION_OF_CYCLIN_B:CDK1_CO	-1.52	1.46	0	0	0	Repressed
936	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_1_PR	-1.52	1.45	0	0	0	Repressed
937	GO_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	-1.52	1.44	0	0	0	Repressed
938	GO_AGGREPHAGY	-1.52	1.4	0	0	0	Repressed
939	GO_CHAPERONE_COFACTOR_DEPENDENT_PROTEIN_REFOLDING	-1.52	1.4	0	0	0	Repressed
940	BIOCARTA_PRION_PATHWAY	-1.52	1.39	0	0	0	Repressed
941	GO_ACTININ_BINDING	-1.52	1.38	0	0	0	Repressed
951	GO_CELL_CYCLE	-1.31	4	0	0	0	not significant
943	REACTOME_HUR_ELAVL1_BINDS_AND_STABILIZES_MRNA	-1.52	1.37	0	0	0	Repressed
944	GO_TRACHEA_DEVELOPMENT	-1.52	1.32	0	0	0	Repressed
945	REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	-1.52	1.32	0	0	0	Repressed
946	WANG_ADIPOGENIC_GENES_REPRESSED_BY_SIRT1	-1.52	1.29	0	0	0	Repressed
947	REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION	-1.52	1.27	0	0	0	Repressed
948	GO_RETROGRADE_AXONAL_TRANSPORT	-1.52	1.25	0	0	0	Repressed
815	DANG_REGULATED_BY_MYC_UP	-1.36	1.24	0	0	0	Repressed
950	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP	-1.51	4	0	0	0	Repressed
752	GO_POSITIVE_REGULATION_OF_CELL_CYCLE	-1.28	1.69	0	0	0	not significant
952	GO_MITOCHONDRIAL_PROTEIN_COMPLEX	-1.51	4	0	0	0	Repressed
953	GO_ORGANELLAR_RIBOSOME	-1.51	4	0	0	0	Repressed
954	GO_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS	-1.51	4	0	0	0	Repressed
955	ZHANG_TLX_TARGETS_60HR_DN	-1.51	4	0	0	0	Repressed
956	GROSS_HYPOXIA_VIA_ELK3_AND_HIF1A_DN	-1.51	2.5	0	0	0	Repressed
957	GO_ATP_DEPENDENT_CHROMATIN_REMODELING	-1.51	2.23	0	0	0	Repressed
958	GO_REGULATION_OF_CIRCADIAN_RHYTHM	-1.51	2.22	0	0	0	Repressed
959	BROWNE_HCMV_INFECTION_30MIN_DN	-1.51	2.16	0	0	0	Repressed
960	PID_P73PATHWAY	-1.51	2.03	0	0	0	Repressed
961	GO_MOTOR_ACTIVITY	-1.51	2.02	0	0	0	Repressed
962	BURTON_ADIPOGENESIS_2	-1.51	1.92	0	0	0	Repressed
963	PID_CDC42_PATHWAY	-1.51	1.92	0	0	0	Repressed
964	GO_NEGATIVE_REGULATION_OF_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_	-1.51	1.85	0	0	0	Repressed
965	GO_POSITIVE_REGULATION_OF_MICROTUBULE_BINDING	-1.51	1.74	0	0	0	Repressed
966	GO_ENDOPEPTIDASE_ACTIVATOR_ACTIVITY	-1.51	1.73	0	0	0	Repressed
967	GO_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	-1.51	1.73	0	0	0	Repressed
968	ISHIDA_E2F_TARGETS	-1.51	1.67	0	0	0	Repressed
969	GO_RRNA_BINDING	-1.51	1.65	0	0	0	Repressed

970	REACTOME_ACTIVATION_OF_NMDA_RECEPTORS_AND_POSTSYNAPTIC_EVENTS	-1.51	1.63	0	0	0	Repressed
971	MCCLUNG_COCAINE_REWARD_5D	-1.51	1.6	0	0	0	Repressed
972	GO_SNRNA_BINDING	-1.51	1.59	0	0	0	Repressed
973	GO_MEIOTIC_SPINDLE	-1.51	1.57	0	0	0	Repressed
974	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PR	-1.51	1.57	0	0	0	Repressed
975	REACTOME_FORMATION_OF_HIV_ELONGATION_COMPLEX_IN_THE_ABSENCE_OF_	-1.51	1.55	0	0	0	Repressed
976	GO_ATP_DEPENDENT_5_3_DNA_HELICASE_ACTIVITY	-1.51	1.52	0	0	0	Repressed
977	GO_IMPORTIN_ALPHA_FAMILY_PROTEIN_BINDING	-1.51	1.49	0	0	0	Repressed
978	GO_ISOPRENOID_BINDING	-1.51	1.48	0	0	0	Repressed
979	GO_DE_NOVO_IMP_BIOSYNTHETIC_PROCESS	-1.51	1.47	0	0	0	Repressed
980	GO_MODULATION_BY_SYMBIONT_OF_HOST_CELLULAR_PROCESS	-1.51	1.47	0	0	0	Repressed
981	GO_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_III	-1.51	1.42	0	0	0	Repressed
982	REACTOME_PROCESSING_OF_INTRONLESS_PRE_MRNAS	-1.51	1.41	0	0	0	Repressed
983	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	-1.48	1.39	1	0	0	Repressed
984	GO_CRD_MEDIATED_MRNA_STABILITY_COMPLEX	-1.51	1.38	0	0	0	Repressed
985	WIEMANN_TELOMERE_SHORTENING_AND_CHRONIC_LIVER_DAMAGE_UP	-1.51	1.33	0	0	0	Repressed
986	GO_REGULATION_OF_MICROTUBULE_BINDING	-1.51	1.32	0	0	0	Repressed
987	LI_WILMS_TUMOR_ANAPLASTIC_UP	-1.51	1.31	0	0	0	Repressed
988	BIOCARTA_CARM1_PATHWAY	-1.51	1.3	0	0	0	Repressed
989	HOUSTIS_ROS	-1.51	1.3	0	0	0	Repressed
990	CAFFAREL_RESPONSE_TO_THC_8HR_3_DN	-1.51	1.29	0	0	0	Repressed
991	GO_KERATINOCYTE_MIGRATION	-1.51	1.29	0	0	0	Repressed
992	GO_VIRAL_TRANSLATION	-1.51	1.25	0	0	0	Repressed
949	BENPORATH_MYC_MAX_TARGETS	-1.31	4	0	0	0	Repressed
994	GO_TRNA_CYTOSINE_METHYLTRANSFERASE_ACTIVITY	-1.41	1.06	1	0	0	Repressed
995	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN	-1.50	4	0	0	0	Repressed
942	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_PROCESS	-1.22	1.38	0	0	0	not significant
997	GO_CELLULAR_RESPONSE_TO_OXYGEN_LEVELS	-1.50	4	0	0	0	Repressed
998	GO_MICROTUBULE_BINDING	-1.50	4	0	0	0	Repressed
999	GO_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABOLIC_PROC	-1.50	4	0	0	0	Repressed
1000	GO_TUBULIN_BINDING	-1.50	4	0	0	0	Repressed
1001	REACTOME_INTRA_GOLGI_AND_RETROGRADE_GOLGI_TO_ER_TRAFFIC	-1.50	2.36	0	0	0	Repressed
1002	GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	-1.50	1.94	0	0	0	Repressed
1003	SANA_RESPONSE_TO_IFNG_DN	-1.50	1.9	0	0	0	Repressed
1004	GO_HIPPOCAMPUS_DEVELOPMENT	-1.50	1.77	0	0	0	Repressed
1005	GO_U2_TYPE_SPLICEOSOMAL_COMPLEX	-1.50	1.7	0	0	0	Repressed
1006	GO_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	-1.50	1.69	0	0	0	Repressed
1007	GO_REGULATION_OF_OOGENESIS	-1.50	1.65	0	0	0	Repressed
1008	GO_CAJAL_BODY	-1.50	1.63	0	0	0	Repressed
1009	GO_NUCLEAR_UBIQUITIN_LIGASE_COMPLEX	-1.50	1.62	0	0	0	Repressed
1010	GO_SCARNA_LOCALIZATION_TO_CAJAL_BODY	-1.50	1.61	0	0	0	Repressed
1011	GO_VESICLE_CYTOSKELETAL_TRAFFICKING	-1.50	1.61	0	0	0	Repressed
1012	REACTOME_PRE_NOTCH_PROCESSING_IN_THE_ENDOPLASMIC_RETICULUM	-1.50	1.59	0	0	0	Repressed
1013	GO_MITOTIC_METAPHASE_PLATE_CONGRESSION	-1.50	1.57	0	0	0	Repressed
1014	CHIN_BREAST_CANCER_COPY_NUMBER_UP	-1.50	1.53	0	0	0	Repressed
1015	REACTOME_TELOMERE_EXTENSION_BY_TELOMERASE	-1.50	1.52	0	0	0	Repressed
1016	GO_CELL_CELL_RECOGNITION	-1.50	1.51	0	0	0	Repressed
1017	BIOCARTA_G2_PATHWAY	-1.50	1.47	0	0	0	Repressed
1018	GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_DEPHOSPHORYLATION	-1.50	1.44	0	0	0	Repressed
1019	REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	-1.50	1.44	0	0	0	Repressed
1020	BIOCARTA_EIF_PATHWAY	-1.50	1.42	0	0	0	Repressed
1021	GO_MODIFICATION_BY_SYMBIONT_OF_HOST_MORPHOLOGY_OR_PHYSIOLOGY	-1.50	1.42	0	0	0	Repressed
1022	GO_PEBOW_COMPLEX	-1.50	1.37	0	0	0	Repressed
1023	GO_NITRIC_OXIDE_SYNTHASE_REGULATOR_ACTIVITY	-1.50	1.34	0	0	0	Repressed
1024	GO_NEURAL_CREST_FORMATION	-1.50	1.3	0	0	0	Repressed
1025	GO_C2H2_ZINC_FINGER_DOMAIN_BINDING	-1.50	1.29	0	0	0	Repressed
1026	GO_METHYLOSOME	-1.50	1.29	0	0	0	Repressed
1027	NAM_FXYD5_TARGETS_DN	-1.50	1.26	0	0	0	Repressed
1028	MA_PITUITARY_FETAL_VS_ADULT_DN	-1.50	1.25	0	0	0	Repressed
1029	GO_TRNA_CYTOSINE_5__METHYLTRANSFERASE_ACTIVITY	-1.39	1.06	1	0	0	Repressed
1030	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_BIOSYNTHESIS	-1.40	1.02	1	0	0	Repressed
1031	GO_MICROTUBULE_BASED_PROCESS	-1.49	4	0	0	0	not significant
1032	GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_C	-1.49	4	0	0	0	not significant
1033	GO_REGULATION_OF_MICROTUBULE_BASED_PROCESS	-1.49	4	0	0	0	not significant
1034	GO_REGULATION_OF_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS	-1.49	4	0	0	0	not significant
1035	REACTOME_CELLULAR_RESPONSES_TO_EXTERNAL_STIMULI	-1.49	4	0	0	0	not significant
1036	SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC	-1.49	2.48	0	0	0	not significant
1037	GO_MRNA_3_END_PROCESSING	-1.49	2.18	0	0	0	not significant
1038	REACTOME_REGULATION_OF_PLK1_ACTIVITY_AT_G2_M_TRANSITION	-1.49	1.88	0	0	0	not significant
1039	REACTOME_PROTEIN_FOLDING	-1.49	1.82	0	0	0	not significant
1040	KAMMINGA_EZH2_TARGETS	-1.49	1.74	0	0	0	not significant
1041	REACTOME_OPIOID_SIGNALLING	-1.49	1.69	0	0	0	not significant
1042	GO_PROTEIN_SERINE_THREONINE_TYROSINE_KINASE_ACTIVITY	-1.49	1.66	0	0	0	not significant
1043	GO_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE	-1.49	1.56	0	0	0	not significant
1044	BIOCARTA_SARS_PATHWAY	-1.49	1.54	0	0	0	not significant
1045	GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_I_PROMOTER	-1.49	1.51	0	0	0	not significant
1046	GO_PROTEIN_KINASE_A_BINDING	-1.49	1.5	0	0	0	not significant
1047	GO_OXIDATIVE_RNA_DEMETHYLATION	-1.49	1.44	0	0	0	not significant
1048	GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_2B_COMPLEX	-1.49	1.42	0	0	0	not significant
1049	GO_REGULATION_OF_TRANSLATION_AT_SYNAPSE_MODULATING_SYNAPTIC_TRAN	-1.49	1.4	0	0	0	not significant
1050	BURTON_ADIPOGENESIS_12	-1.49	1.38	0	0	0	not significant
1051	GO_VENTRICULAR_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	-1.49	1.35	0	0	0	not significant
1052	GO_OUTER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	-1.49	1.33	0	0	0	not significant
1053	REACTOME_BETA_CATENIN_PHOSPHORYLATION_CASCADE	-1.49	1.33	0	0	0	not significant
1054	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_UP	-1.49	1.33	0	0	0	not significant
1055	REACTOME_CRISTAE_FORMATION	-1.49	1.32	0	0	0	not significant
1056	GO_REGULATION_OF_SISTER_CHROMATID_COHESION	-1.49	1.3	0	0	0	not significant
1057	GO_FEMALE_MEIOSIS_I	-1.49	1.28	0	0	0	not significant
1058	YIH_RESPONSE_TO_ARSENITE_C4	-1.49	1.27	0	0	0	not significant
1059	GO_HISTONE_KINASE_ACTIVITY	-1.49	1.25	0	0	0	not significant
1060	GO_OXIDATIVE_RNA_DEMETHYLASE_ACTIVITY	-1.49	1.25	0	0	0	not significant
1061	GO_NEGATIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCH	-1.49	1.24	0	0	0	not significant
1062	GO_POSITIVE_REGULATION_OF_OXIDATIVE_PHOSPHORYLATION	-1.49	1.24	0	0	0	not significant
1063	GO_TRABECULA_FORMATION	-1.49	1.22	0	0	0	not significant
1064	NAGY_STAGA_COMPONENTS_HUMAN	-1.49	1.22	0	0	0	not significant
1065	REACTOME_BINDING_AND_UPTAKE_OF_LIGANDS_BY_SCAVENGER_RECEPTORS	-1.49	1.22	0	0	0	not significant
1066	REACTOME_FRS_MEDIATED_FGFR1_SIGNALING	-1.49	1.21	0	0	0	not significant
1067	REACTOME_NUCLEOBASE_BIOSYNTHESIS	-1.49	1.17	0	0	0	not significant
1068	GO_MRNA_CLEAVAGE_FACTOR_COMPLEX	-1.49	1.15	0	0	0	not significant
1069	GENTILE_UV_HIGH_DOSE_DN	-1.48	4	0	0	0	not significant
1070	GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	-1.48	4	0	0	0	not significant
1071	GO_CELLULAR_PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	-1.48	4	0	0	0	not significant
1072	GO_REGULATION_OF_MITOTIC_CELL_CYCLE	-1.48	4	0	0	0	not significant
1073	KEGG_CELL_CYCLE	-1.48	2.47	0	0	0	not significant
1074	BROWNE_HCMV_INFECTION_14HR_UP	-1.48	2.42	0	0	0	not significant
1075	GO_CYTOKINESIS	-1.48	2.12	0	0	0	not significant
1076	SASAKI_ADULT_T_CELL_LEUKEMIA	-1.48	2.12	0	0	0	not significant
1077	DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_DN	-1.48	2.04	0	0	0	not significant
1078	GO_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOL	-1.48	1.97	0	0	0	not significant

1079	REACTOME_POSITIVE_EPIGENETIC_REGULATION_OF_RRNA_EXPRESSION	-1.48	1.89	0	0	0	not significant
1080	REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS	-1.48	1.86	0	0	0	not significant
1081	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_10	-1.48	1.81	0	0	0	not significant
1082	GO_PERICHROMATIN_FIBRILS	-1.48	1.68	0	0	0	not significant
1083	GO_MATURE_RIBOSOME_ASSEMBLY	-1.48	1.64	0	0	0	not significant
1084	GO_TRANSCRIPTION_BY_RNA_POLYMERASE_III	-1.48	1.63	0	0	0	not significant
1085	REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	-1.48	1.49	0	0	0	not significant
1086	REACTOME_ION_HOMEOSTASIS	-1.48	1.48	0	0	0	not significant
1087	GO_REGULATION_OF_TRANSLATIONAL_FIDELITY	-1.48	1.46	0	0	0	not significant
1088	GO_REGULATORY_RNA_BINDING	-1.48	1.43	0	0	0	not significant
1089	GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.48	1.41	0	0	0	not significant
1090	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_CHROMOSOME	-1.48	1.39	0	0	0	not significant
1091	GO_MLL1_2_COMPLEX	-1.48	1.38	0	0	0	not significant
1092	GO_MITOTIC_SPINDLE_POLE	-1.48	1.37	0	0	0	not significant
1093	GO_TELOMERASE_RNA_BINDING	-1.48	1.36	0	0	0	not significant
1094	MIKKELSEN_PLURIPOTENT_STATE_UP	-1.48	1.36	0	0	0	not significant
1095	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_TELOMERE	-1.48	1.33	0	0	0	not significant
1096	GO_PORIN_ACTIVITY	-1.48	1.32	0	0	0	not significant
1097	GO_PROTEIN_DESUMOYLATION	-1.48	1.3	0	0	0	not significant
1098	REACTOME_RHO_GTPASES_ACTIVATE_PAKS	-1.48	1.28	0	0	0	not significant
1099	GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_I_PROMOTER	-1.48	1.27	0	0	0	not significant
1100	GO_NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIAT	-1.48	1.26	0	0	0	not significant
1101	GO_PROTEIN_LOCALIZATION_TO_CELL_CORTEX	-1.48	1.26	0	0	0	not significant
1102	GO_U5_SNRNP	-1.48	1.26	0	0	0	not significant
1103	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN	-1.48	1.24	0	0	0	not significant
1104	GO_CELLULAR_RESPONSE_TO_ESTRADIOL_STIMULUS	-1.48	1.23	0	0	0	not significant
1105	GO_SNRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_III	-1.48	1.2	0	0	0	not significant
1106	CAIRO_HEPATOBLASTOMA_POOR_SURVIVAL	-1.48	1.16	0	0	0	not significant
1107	GO_UBIQUITIN_PROTEIN_TRANSFERASE_ACTIVATOR_ACTIVITY	-1.48	1.16	0	0	0	not significant
1108	GO_CRISTAE_FORMATION	-1.48	1.14	0	0	0	not significant
1109	REACTOME_SUMOYLATION	-1.47	2.35	0	0	0	not significant
1110	GO_SINGLE_STRANDED_RNA_BINDING	-1.47	2.21	0	0	0	not significant
1111	GO_RETROGRADE_VESICLE_MEDIATED_TRANSPORT_GOLGI_TO_ENDOPLASMIC_	-1.47	2.19	0	0	0	not significant
1112	REACTOME_PROGRAMMED_CELL_DEATH	-1.47	2.11	0	0	0	not significant
1113	NIKOLSKY_BREAST_CANCER_17Q11_Q21_AMPLICON	-1.47	1.73	0	0	0	not significant
1114	GO_SM_LIKE_PROTEIN_FAMILY_COMPLEX	-1.47	1.6	0	0	0	not significant
1115	GO_REGULATION_OF_UBIQUITIN_PROTEIN_TRANSFERASE_ACTIVITY	-1.47	1.53	0	0	0	not significant
1116	GO_PROTEIN_TRANSMEMBRANE_IMPORT_INTO_INTRACELLULAR_ORGANELLE	-1.47	1.51	0	0	0	not significant
1117	CHR15Q22	-1.47	1.49	0	0	0	not significant
1118	LEE_AGING_NEOCORTEX_DN	-1.47	1.44	0	0	0	not significant
1119	REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	-1.47	1.44	0	0	0	not significant
1120	GO_RESPONSE_TO_ETHER	-1.47	1.42	0	0	0	not significant
1121	FARDIN_HYPOXIA_11	-1.47	1.41	0	0	0	not significant
1122	GO_POSITIVE_REGULATION_OF_CELL_MATURATION	-1.47	1.38	0	0	0	not significant
1123	GO_ATP_METABOLIC_PROCESS	-1.47	1.37	0	0	0	not significant
1124	GO_OXIDATIVE_DEMETHYLATION	-1.47	1.36	0	0	0	not significant
1125	REACTOME_SCAVENGING_BY_CLASS_F_RECEPTORS	-1.47	1.35	0	0	0	not significant
1126	CHR3Q22	-1.47	1.34	0	0	0	not significant
1127	GO_ESTABLISHMENT_OF_SPINDLE_ORIENTATION	-1.47	1.34	0	0	0	not significant
1128	NAGY_PCAF_COMPONENTS_HUMAN	-1.47	1.33	0	0	0	not significant
1129	GO_PROTEIN_DNA_COMPLEX_DISASSEMBLY	-1.47	1.32	0	0	0	not significant
1130	GO_WD40_REPEAT_DOMAIN_BINDING	-1.47	1.32	0	0	0	not significant
1131	GO_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_PROSTATE_GLAND_DEVEL	-1.47	1.3	0	0	0	not significant
1132	GO_HISTONE_SERINE_KINASE_ACTIVITY	-1.47	1.29	0	0	0	not significant
1133	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_ELONGATION_FROM_RNA_POLY	-1.47	1.29	0	0	0	not significant
1134	REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_7ALPHA_HYDROXY	-1.47	1.28	0	0	0	not significant
1135	GO_RNA_POLYMERASE_II_PREINITIATION_COMPLEX_ASSEMBLY	-1.47	1.27	0	0	0	not significant
1136	GO_TRNA_5_LEADER_REMOVAL	-1.47	1.27	0	0	0	not significant
1137	GO_HISTONE_ARGININE_N_METHYLTRANSFERASE_ACTIVITY	-1.47	1.26	0	0	0	not significant
1138	GO_MHC_CLASS_II_PROTEIN_COMPLEX_BINDING	-1.47	1.26	0	0	0	not significant
1139	REACTOME_LOSS_OF_MECP2_BINDING_ABILITY_TO_THE_NCOR_SMRT_COMPLEX	-1.47	1.23	0	0	0	not significant
1140	REACTOME_RETROGRADE_NEUROTROPHIN_SIGNALLING	-1.47	1.23	0	0	0	not significant
1141	GO_EYELID_DEVELOPMENT_IN_CAMERA_TYPE_EYE	-1.47	1.21	0	0	0	not significant
1142	GO_GLUTAMATE_CATABOLIC_PROCESS	-1.47	1.2	0	0	0	not significant
1143	REACTOME_APOPTOSIS_INDUCED_DNA_FRAGMENTATION	-1.47	1.2	0	0	0	not significant
1144	GO_OLFACTORY_LOBE_DEVELOPMENT	-1.47	1.18	0	0	0	not significant
1145	GO_PROTEASOME_ASSEMBLY	-1.47	1.17	0	0	0	not significant
1146	GO_REGULATION_OF_RNA_SPLICING	-1.46	2.42	0	0	0	not significant
1147	GO_NUCLEAR_MATRIX	-1.46	1.86	0	0	0	not significant
1148	GO_MITOCHONDRIAL_TRANSLATION	-1.46	1.84	0	0	0	not significant
1149	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN	-1.46	1.78	0	0	0	not significant
1150	GO_CHAPERONE_MEDIATED_PROTEIN_FOLDING	-1.46	1.69	0	0	0	not significant
1151	KEGG_RENAL_CELL_CARCINOMA	-1.46	1.62	0	0	0	not significant
1152	REACTOME_COPI_INDEPENDENT_GOLGI_TO_ER_RETROGRADE_TRAFFIC	-1.46	1.53	0	0	0	not significant
1153	REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_27_HYDROXYCHOL	-1.46	1.5	0	0	0	not significant
1154	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_TERMINATION	-1.46	1.44	0	0	0	not significant
1155	GO_ENDONUCLEASE_COMPLEX	-1.46	1.41	0	0	0	not significant
1156	RAHMAN_TP53_TARGETS_PHOSPHORYLATED	-1.46	1.34	0	0	0	not significant
1157	GO_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	-1.46	1.33	0	0	0	not significant
1158	REACTOME_SIGNALING_BY_WNT_IN_CANCER	-1.46	1.33	0	0	0	not significant
1159	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_UP	-1.46	1.33	0	0	0	not significant
1160	GO_SMN_SM_PROTEIN_COMPLEX	-1.46	1.32	0	0	0	not significant
1161	GO_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	-1.46	1.3	0	0	0	not significant
1162	GO_SNORNA_3_END_PROCESSING	-1.46	1.3	0	0	0	not significant
1163	KEGG_THYROID_CANCER	-1.46	1.3	0	0	0	not significant
1164	REACTOME_MICRORNA_MIRNA_BIOGENESIS	-1.46	1.28	0	0	0	not significant
1165	GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	-1.46	1.27	0	0	0	not significant
1166	REACTOME_SIGNALING_BY_RETINOIC_ACID	-1.46	1.27	0	0	0	not significant
1167	GO_MODULATION_BY_HOST_OF_VIRAL_PROCESS	-1.46	1.26	0	0	0	not significant
1168	GO_POSITIVE_REGULATION_OF_CAMP_MEDIATED_SIGNALING	-1.46	1.26	0	0	0	not significant
1169	GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY	-1.46	1.25	0	0	0	not significant
1170	GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCE	-1.46	1.25	0	0	0	not significant
1171	BIOCARTA_NDKDYNAMIN_PATHWAY	-1.46	1.24	0	0	0	not significant
1172	GO_RRNA_PSEUDOURIDINE_SYNTHESIS	-1.46	1.24	0	0	0	not significant
1173	GO_ADENYLATE_KINASE_ACTIVITY	-1.46	1.23	0	0	0	not significant
1174	GO_RAL_GTPASE_BINDING	-1.46	1.22	0	0	0	not significant
1175	GO_POSITIVE_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	-1.46	1.18	0	0	0	not significant
1176	GO_DNA_TOPOLOGICAL_CHANGE	-1.46	1.16	0	0	0	not significant
1177	REACTOME_TIE2_SIGNALING	-1.46	1.16	0	0	0	not significant
1178	GO_REGULATION_OF_INCLUSION_BODY_ASSEMBLY	-1.46	1.15	0	0	0	not significant
1179	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_INITIATION_FROM_RNA_POLYME	-1.46	1.13	0	0	0	not significant
1180	GO_QUINONE_BIOSYNTHETIC_PROCESS	-1.46	1.13	0	0	0	not significant
1181	GO_ENDONUCLEOLYTIC_CLEAVAGE_IN_ITS1_TO_SEPARATE_SSU_RRNA_FROM_5_	-1.46	1.11	0	0	0	not significant
1182	GO_TRANSCRIPTION_FACTOR_TFTC_COMPLEX	-1.46	1.06	0	0	0	not significant
1183	FEVR_CTNNB1_TARGETS_DN	-1.45	4	0	0	0	not significant
1184	GO_RNA_CATABOLIC_PROCESS	-1.45	4	0	0	0	not significant
1185	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	-1.45	4	0	0	0	not significant
1186	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	-1.45	4	0	0	0	not significant
1187	REACTOME_UB_SPECIFIC_PROCESSING_PROTEASES	-1.45	4	0	0	0	not significant

1188	SANSOM_APC_TARGETS_REQUIRE_MYC	-1.45	4	0	0	0	not significant
1189	WANG_LMO4_TARGETS_DN	-1.45	4	0	0	0	not significant
1190	WELCSH_BRCA1_TARGETS_DN	-1.45	2.46	0	0	0	not significant
1191	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT	-1.45	2	0	0	0	not significant
1192	GO_HELICASE_ACTIVITY	-1.45	1.84	0	0	0	not significant
1193	SESTO_RESPONSE_TO_UV_C1	-1.45	1.54	0	0	0	not significant
1194	GO_NEGATIVE_REGULATION_OF_GRANULOCYTE_DIFFERENTIATION	-1.45	1.43	0	0	0	not significant
1195	GO_KINASE_ACTIVATOR_ACTIVITY	-1.45	1.42	0	0	0	not significant
1196	GO_RESPONSE_TO_MAGNESIUM_ION	-1.45	1.4	0	0	0	not significant
1197	GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.45	1.33	0	0	0	not significant
1198	GO_ADENYLYLTRANSFERASE_ACTIVITY	-1.45	1.32	0	0	0	not significant
1199	GO_OXIDATIVE_DNA_DEMETHYLATION	-1.45	1.31	0	0	0	not significant
1200	GO_POSITIVE_REGULATION_OF_CELLULAR_RESPIRATION	-1.45	1.31	0	0	0	not significant
1201	GLI1_UP.V1_UP	-1.45	1.24	0	0	0	not significant
1202	GO_BHLH_TRANSCRIPTION_FACTOR_BINDING	-1.45	1.24	0	0	0	not significant
1203	GO_MOLYBDOPTERIN_COFACTOR_BIOSYNTHETIC_PROCESS	-1.45	1.24	0	0	0	not significant
1204	ZHAN_MULTIPLE_MYELOMA_LB_UP	-1.45	1.24	0	0	0	not significant
1205	GO_SAGA_TYPE_COMPLEX	-1.45	1.21	0	0	0	not significant
1206	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_8	-1.45	1.2	0	0	0	not significant
1207	GO_GLYCOLYTIC_PROCESS_THROUGH_FRUCTOSE_6_PHOSPHATE	-1.45	1.19	0	0	0	not significant
1208	GO_NEGATIVE_REGULATION_OF_METANEPHROS_DEVELOPMENT	-1.45	1.19	0	0	0	not significant
1209	GO_METHYL_CPG_BINDING	-1.45	1.18	0	0	0	not significant
1210	GO_SNORNA_PROCESSING	-1.45	1.18	0	0	0	not significant
1211	GO_POSITIVE_REGULATION_OF_PROTEIN_EXPORT_FROM_NUCLEUS	-1.45	1.14	0	0	0	not significant
1212	CHEN_LUNG_CANCER_SURVIVAL	-1.45	1.13	0	0	0	not significant
1213	LU_TUMOR_ENDOTHELIAL_MARKERS_UP	-1.45	1.13	0	0	0	not significant
1214	GO_REGULATION_OF_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING_INVOLV	-1.45	1.12	0	0	0	not significant
1215	GO_MULTIMERIC_RIBONUCLEASE_P_COMPLEX	-1.45	1.11	0	0	0	not significant
1216	LU_TUMOR_VASCULATURE_UP	-1.45	1.09	0	0	0	not significant
1217	CHUANG_OXIDATIVE_STRESS_RESPONSE_DN	-1.45	1.08	0	0	0	not significant
1218	GO_REGULATION_OF_KERATINOCYTE_MIGRATION	-1.45	1.07	0	0	0	not significant
1219	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PROCESS	-1.44	4	0	0	0	not significant
1220	GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_REMOVAL	-1.44	4	0	0	0	not significant
1221	OISHI_CHOLANGIOMA_STEM_CELL_LIKE_UP	-1.44	4	0	0	0	not significant
1222	GO_PALLIUM_DEVELOPMENT	-1.44	2.43	0	0	0	not significant
1223	GO_NON_CANONICAL_WNT_SIGNALING_PATHWAY	-1.44	2.02	0	0	0	not significant
1224	RASHI_RESPONSE_TO_IONIZING_RADIATION_5	-1.44	2	0	0	0	not significant
1225	REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY	-1.44	2	0	0	0	not significant
1226	MARZEC_IL2_SIGNALING_UP	-1.44	1.89	0	0	0	not significant
1227	REACTOME_CLEC7A_DECTIN_1_SIGNALING	-1.44	1.86	0	0	0	not significant
1228	REACTOME_HDACS_DEACETYLATE_HISTONES	-1.44	1.82	0	0	0	not significant
1229	GROSS_HYPOXIA_VIA_HIF1A_UP	-1.44	1.67	0	0	0	not significant
1230	REACTOME_CYCLIN_A:CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTRY	-1.44	1.55	0	0	0	not significant
1231	GO_TAU_PROTEIN_BINDING	-1.44	1.44	0	0	0	not significant
1232	LEE_CALORIE_RESTRICTION_NEOCORTEX_DN	-1.44	1.39	0	0	0	not significant
1233	GO_PROTEIN_O_LINKED_GLYCOSYLATION_VIA_SERINE	-1.44	1.33	0	0	0	not significant
1234	GO_REGULATION_OF_RNA_POLYMERASE_II_TRANSCRIPTIONAL_PREINITIATION_CC	-1.44	1.27	0	0	0	not significant
1235	GO_PSEUDOURIDINE_SYNTHASE_ACTIVITY	-1.44	1.23	0	0	0	not significant
1236	SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1B	-1.44	1.22	0	0	0	not significant
1237	GO_MHC_PROTEIN_COMPLEX_BINDING	-1.44	1.2	0	0	0	not significant
1238	GO_MODULATION_BY_HOST_OF_VIRAL_GENOME_REPLICATION	-1.44	1.2	0	0	0	not significant
1239	GO_NEURON_NEURON_SYNAPTIC_TRANSMISSION	-1.44	1.2	0	0	0	not significant
1240	GO_PROTEIN_INSERTION_INTO_MITOCHONDRIAL_OUTER_MEMBRANE	-1.44	1.17	0	0	0	not significant
1241	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREEN_DN	-1.44	1.16	0	0	0	not significant
1242	GO_MYELIN_SHEATH_ADAXONAL_REGION	-1.44	1.12	0	0	0	not significant
1243	STONER_ESOPHAGEAL_CARCINOGENESIS_DN	-1.44	1.12	0	0	0	not significant
1244	GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_DEVELOPMENT	-1.44	1.11	0	0	0	not significant
1245	REACTOME_FRS_MEDIATED_FGFR2_SIGNALING	-1.44	1.11	0	0	0	not significant
1246	GO_5_3_DNA_HELICASE_ACTIVITY	-1.44	1.1	0	0	0	not significant
1247	GO_MACROMOLECULE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.44	1.1	0	0	0	not significant
1248	GO_SEQUENCE_SPECIFIC_MRNA_BINDING	-1.44	1.1	0	0	0	not significant
1249	GO_REGULATION_OF_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING	-1.44	1.09	0	0	0	not significant
1250	REACTOME_FRS_MEDIATED_FGFR4_SIGNALING	-1.44	1.09	0	0	0	not significant
1251	RAMPON_ENRICHED_LEARNING_ENVIRONMENT_EARLY_UP	-1.44	1.08	0	0	0	not significant
1252	MATZUK_IMPLANTATION_AND_UTERINE	-1.44	1.04	0	0	0	not significant
1253	BLALOCK_ALZHEIMERS_DISEASE_DN	-1.43	4	0	0	0	not significant
1254	GO_PROTEIN_FOLDING	-1.43	4	0	0	0	not significant
1255	REACTOME_C_TYPE_LECTIN_RECEPTORS_CLRS	-1.43	2.15	0	0	0	not significant
1256	GO_INTERLEUKIN_1_MEDIATED_SIGNALING_PATHWAY	-1.43	2.01	0	0	0	not significant
1257	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	-1.43	1.92	0	0	0	not significant
1258	GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	-1.43	1.87	0	0	0	not significant
1259	GO_AMINE_METABOLIC_PROCESS	-1.43	1.79	0	0	0	not significant
1260	GO_LIMBIC_SYSTEM_DEVELOPMENT	-1.43	1.7	0	0	0	not significant
1261	MORI_PRE_BI_LYMPHOCYTE_UP	-1.43	1.68	0	0	0	not significant
1262	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP	-1.43	1.67	0	0	0	not significant
1263	SMITH_LIVER_CANCER	-1.43	1.38	0	0	0	not significant
1264	GO_CENTROMERE_COMPLEX_ASSEMBLY	-1.43	1.36	0	0	0	not significant
1265	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_INITIATION	-1.43	1.36	0	0	0	not significant
1266	REACTOME_INTRAFLAGELLAR_TRANSPORT	-1.43	1.33	0	0	0	not significant
1267	PID_HEDGEHOG_GLI_PATHWAY	-1.43	1.28	0	0	0	not significant
1268	GROSS_HYPOXIA_VIA_ELK3_ONLY_DN	-1.43	1.25	0	0	0	not significant
1269	GO_MEIOTIC_SPINDLE_ORGANIZATION	-1.43	1.2	0	0	0	not significant
1270	REACTOME_ACTIVATION_OF_AMPK_DOWNSTREAM_OF_NMDARS	-1.43	1.18	0	0	0	not significant
1271	GO_LATERAL_VENTRICLE_DEVELOPMENT	-1.43	1.15	0	0	0	not significant
1272	GO_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	-1.43	1.15	0	0	0	not significant
1273	GO_CATALYTIC_STEP_1_SPLICEOSOME	-1.43	1.14	0	0	0	not significant
1274	GO_NEGATIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_T	-1.43	1.14	0	0	0	not significant
1275	GO_PLASMINOGEN_ACTIVATION	-1.43	1.14	0	0	0	not significant
1276	GO_CYCLIN_DEPENDENT_PROTEIN_SERINE_THREONINE_KINASE_ACTIVATOR_ACTI	-1.43	1.13	0	0	0	not significant
1277	PID_IGF1_PATHWAY	-1.43	1.13	0	0	0	not significant
1278	DORN_ADENOVIRUS_INFECTION_24HR_UP	-1.43	1.12	0	0	0	not significant
1279	FIRESTEIN_CTNNB1_PATHWAY	-1.43	1.12	0	0	0	not significant
1280	GO_ARP2_3_PROTEIN_COMPLEX	-1.43	1.1	0	0	0	not significant
1281	GO_POSITIVE_REGULATION_OF_RYANODINE_SENSITIVE_CALCIUM_RELEASE_CHAN	-1.43	1.09	0	0	0	not significant
1282	VANDESLUIS_COMMD1_TARGETS_GROUP_2_UP	-1.43	1.09	0	0	0	not significant
1283	GO_HISTONE_PRE_MRNA_3_END_PROCESSING_COMPLEX	-1.43	1.07	0	0	0	not significant
1284	GO_CDC42_PROTEIN_SIGNAL_TRANSDUCTION	-1.43	1.06	0	0	0	not significant
1285	GO_PROTEASOME_REGULATORY_PARTICLE_LID_SUBCOMPLEX	-1.43	1.06	0	0	0	not significant
1286	GO_RNA_POLYMERASE_II_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_BINDIN	-1.43	1.06	0	0	0	not significant
1287	BIOCARTA_TEL_PATHWAY	-1.43	1.04	0	0	0	not significant
1288	GO_CULLIN_FAMILY_PROTEIN_BINDING	-1.43	1.04	0	0	0	not significant
1289	REACTOME_FRS_MEDIATED_FGFR3_SIGNALING	-1.43	1.03	0	0	0	not significant
1290	CHANDRAN_METASTASIS_UP	-1.42	4	0	0	0	not significant
1291	GO_CATALYTIC_COMPLEX	-1.42	4	0	0	0	not significant
1292	GO_NEGATIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	-1.42	4	0	0	0	not significant
1293	GO_POLYMERIC_CYTOSKELETAL_FIBER	-1.42	4	0	0	0	not significant
1294	REACTOME_GENE_EXPRESSION_TRANSCRIPTION	-1.42	4	0	0	0	not significant
1295	VILLANUEVA_LIVER_CANCER_KRT19_UP	-1.42	2.37	0	0	0	not significant
1296	GO_GENE_SILENCING_BY_RNA	-1.42	2.17	0	0	0	not significant

1297	GO_PROTEIN_LOCALIZATION_TO_NUCLEUS	-1.42	2.03	0	0	0	not significant
1298	REACTOME_COPI_MEDIATED_ANTEROGRADE_TRANSPORT	-1.42	1.87	0	0	0	not significant
1299	GO_GLYCOLYTIC_PROCESS	-1.42	1.68	0	0	0	not significant
1300	KEGG_GAP_JUNCTION	-1.42	1.53	0	0	0	not significant
1301	GO_INTERACTION_WITH_SYMBIONT	-1.42	1.49	0	0	0	not significant
1302	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTI	-1.42	1.47	0	0	0	not significant
1303	GO_RESPONSE_TO_ANESTHETIC	-1.42	1.42	0	0	0	not significant
1304	REACTOME_REGULATION_OF_ACTIN_DYNAMICS_FOR_PHAGOCYTIC_CUP_FORMAT	-1.42	1.4	0	0	0	not significant
1305	BROWNE_HCMV_INFECTION_10HR_DN	-1.42	1.33	0	0	0	not significant
1306	KORKOLA_SEMINOMA_UP	-1.42	1.33	0	0	0	not significant
1307	GO_BLASTOCYST_FORMATION	-1.42	1.23	0	0	0	not significant
1308	GO_DISORDERED_DOMAIN_SPECIFIC_BINDING	-1.42	1.22	0	0	0	not significant
1309	GO_U12_TYPE_SPLICEOSOMAL_COMPLEX	-1.42	1.2	0	0	0	not significant
1310	SHIN_B_CELL_LYMPHOMA_CLUSTER_7	-1.42	1.2	0	0	0	not significant
1311	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_HD_MTX_UP	-1.42	1.18	0	0	0	not significant
1312	YIH_RESPONSE_TO_ARSENITE_C1	-1.42	1.18	0	0	0	not significant
1313	GO_MICOS_COMPLEX	-1.42	1.16	0	0	0	not significant
1314	GO_REGULATION_OF_SMAD_PROTEIN_COMPLEX_ASSEMBLY	-1.42	1.14	0	0	0	not significant
1315	GO_RIBOSOMAL_SMALL_SUBUNIT_EXPORT_FROM_NUCLEUS	-1.42	1.14	0	0	0	not significant
1316	CHR17P12	-1.42	1.13	0	0	0	not significant
1317	GO_2_IRON_2_SULFUR_CLUSTER_BINDING	-1.42	1.13	0	0	0	not significant
1318	GO_HISTONE_H4_R3_METHYLATION	-1.42	1.13	0	0	0	not significant
1319	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_III	-1.42	1.12	0	0	0	not significant
1320	GO_MALE_MATING_BEHAVIOR	-1.42	1.11	0	0	0	not significant
1321	GO_MITOCHONDRION_DISTRIBUTION	-1.42	1.11	0	0	0	not significant
1322	GO_SPINDLE_MIDZONE_ASSEMBLY	-1.42	1.11	0	0	0	not significant
1323	GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK_BY_PHOTOPERIOD	-1.42	1.1	0	0	0	not significant
1324	BIOCARTA_PTC1_PATHWAY	-1.42	1.09	0	0	0	not significant
1325	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	-1.42	1.09	0	0	0	not significant
1326	GO_ENDOCYTIC_ADAPTOR_ACTIVITY	-1.42	1.08	0	0	0	not significant
1327	GO_RESPONSE_TO_VITAMIN_A	-1.42	1.07	0	0	0	not significant
1328	FARMER_BREAST_CANCER_CLUSTER_5	-1.42	1.06	0	0	0	not significant
1329	REACTOME_ACTIVATED_NTRK2_SIGNALS_THROUGH_FRS2_AND_FRS3	-1.42	1.06	0	0	0	not significant
1330	REACTOME_REGULATION_OF_PYRUVATE_DEHYDROGENASE_PDH_COMPLEX	-1.42	1.06	0	0	0	not significant
1331	CERIBELLI_PROMOTERS_INACTIVE_AND_BOUND_BY_NFY	-1.42	1.05	0	0	0	not significant
1332	GO_OUTFLOW_TRACT_SEPTUM_MORPHOGENESIS	-1.42	1.04	0	0	0	not significant
1333	GO_SARCOPLASMIC_RETICULUM_CALCIUM_ION_TRANSPORT	-1.42	1.03	0	0	0	not significant
1334	REACTOME_IL_6_TYPE_CYTOKINE_RECEPTOR_LIGAND_INTERACTIONS	-1.42	1.03	0	0	0	not significant
1335	REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHESIS	-1.42	1.03	0	0	0	not significant
1336	GO_RIBOSOMAL_LARGE_SUBUNIT_EXPORT_FROM_NUCLEUS	-1.42	1.01	0	0	0	not significant
1337	REACTOME_MASTL_FACILITATES_MITOTIC_PROGRESSION	-1.42	0.99	0	0	0	not significant
1338	GO_ADENYL_NUCLEOTIDE_BINDING	-1.41	4	0	0	0	not significant
1339	GO_DRUG_BINDING	-1.41	4	0	0	0	not significant
1340	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	-1.41	4	0	0	0	not significant
1341	GO_REGULATION_OF_PROTEIN_STABILITY	-1.41	4	0	0	0	not significant
1342	GO_SUPRAMOLECULAR_COMPLEX	-1.41	4	0	0	0	not significant
1343	JOHNSTONE_PARVB_TARGETS_2_DN	-1.41	4	0	0	0	not significant
1344	GO_TRANSFERASE_COMPLEX_TRANSFERRING_PHOSPHORUS_CONTAINING_GROU	-1.41	2.04	0	0	0	not significant
1345	WATANABE_RECTAL_CANCER_RADIOTHERAPY_RESPONSIVE_DN	-1.41	1.93	0	0	0	not significant
1346	DITTMER_PTHLH_TARGETS_UP	-1.41	1.85	0	0	0	not significant
1347	EIF4E_UP	-1.41	1.75	0	0	0	not significant
1348	BROWNE_HCMV_INFECTION_12HR_UP	-1.41	1.72	0	0	0	not significant
1349	REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	-1.41	1.67	0	0	0	not significant
1350	GCNP_SHH_UP_EARLY.V1_UP	-1.41	1.61	0	0	0	not significant
1351	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	-1.41	1.55	0	0	0	not significant
1352	REACTOME_RNA_POLYMERASE_I_PROMOTER_ESCAPE	-1.41	1.55	0	0	0	not significant
1353	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	-1.41	1.47	0	0	0	not significant
1354	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_DN	-1.41	1.3	0	0	0	not significant
1355	CHR5Q33	-1.41	1.28	0	0	0	not significant
1356	GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK	-1.41	1.27	0	0	0	not significant
1357	GO_CARTILAGE_DEVELOPMENT_INVOLVED_IN_ENDOCHONDRAL_BONE_MORPHOG	-1.41	1.21	0	0	0	not significant
1358	BIOCARTA_SALMONELLA_PATHWAY	-1.41	1.2	0	0	0	not significant
1359	REACTOME_DAG_AND_IP3_SIGNALING	-1.41	1.2	0	0	0	not significant
1360	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN	-1.41	1.2	0	0	0	not significant
1361	HWANG_PROSTATE_CANCER_MARKERS	-1.41	1.15	0	0	0	not significant
1362	BIOCARTA_SRCRPTP_PATHWAY	-1.41	1.14	0	0	0	not significant
1363	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MITOCHONDRIAL_MEMBRA	-1.41	1.14	0	0	0	not significant
1364	GO_RESPONSE_TO_COPPER_ION	-1.41	1.13	0	0	0	not significant
1365	REACTOME_ERKS_ARE_INACTIVATED	-1.41	1.12	0	0	0	not significant
1366	GO_IRON_SULFUR_CLUSTER_ASSEMBLY	-1.41	1.11	0	0	0	not significant
1367	GO_PROTEASOME_BINDING	-1.41	1.11	0	0	0	not significant
1368	GO_SMN_COMPLEX	-1.41	1.09	0	0	0	not significant
1369	YORDY_RECIPROCAL_REGULATION_BY_ETS1_AND_SP100_UP	-1.41	1.08	0	0	0	not significant
1370	GO_BINDING_OF_SPERM_TO_ZONA_PELLUCIDA	-1.41	1.07	0	0	0	not significant
1371	BIOCARTA_RAN_PATHWAY	-1.41	1.06	0	0	0	not significant
1372	GO_HEART_TRABECULA_FORMATION	-1.41	1.06	0	0	0	not significant
1373	GO_SUCCINATE_METABOLIC_PROCESS	-1.41	1.05	0	0	0	not significant
1374	GO_ADENYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	-1.41	1.02	0	0	0	not significant
1375	GO_POSITIVE_REGULATION_OF_AMYLOID_PRECURSOR_PROTEIN_CATABOLIC_PR	-1.41	1.01	0	0	0	not significant
1376	GAVIN_IL2_RESPONSIVE_FOXP3_TARGETS_UP	-1.41	0.96	0	0	0	not significant
1377	PUJANA_ATM_PCC_NETWORK	-1.40	4	0	0	0	not significant
1378	REACTOME_ADAPTIVE_IMMUNE_SYSTEM	-1.40	4	0	0	0	not significant
1379	HALLMARK_MTORC1_SIGNALING	-1.40	2.36	0	0	0	not significant
1380	GO_NUCLEOSOME_ORGANIZATION	-1.40	1.93	0	0	0	not significant
1381	GO_MICROTUBULE_BASED_MOVEMENT	-1.40	1.92	0	0	0	not significant
1382	MISSIAGLIA_REGULATED_BY_METHYLATION_DN	-1.40	1.87	0	0	0	not significant
1383	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN	-1.40	1.83	0	0	0	not significant
1384	SMIRNOV_RESPONSE_TO_IR_6HR_DN	-1.40	1.61	0	0	0	not significant
1385	GO_REGULATION_OF_VIRAL_TRANSCRIPTION	-1.40	1.51	0	0	0	not significant
1386	SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_UP	-1.40	1.46	0	0	0	not significant
1387	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_UP	-1.40	1.41	0	0	0	not significant
1388	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	-1.40	1.4	0	0	0	not significant
1389	GO_CHROMOSOME_CONDENSATION	-1.40	1.3	0	0	0	not significant
1390	REACTOME_SIGNALING_BY_NOTCH3	-1.40	1.23	0	0	0	not significant
1391	ZHU_CMV_8_HR_DN	-1.40	1.21	0	0	0	not significant
1392	REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	-1.40	1.2	0	0	0	not significant
1393	GO_SPERM_EGG_RECOGNITION	-1.40	1.17	0	0	0	not significant
1394	GO_PROSTATE_GLAND_DEVELOPMENT	-1.40	1.16	0	0	0	not significant
1395	GO_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	-1.40	1.15	0	0	0	not significant
1396	GO_REGULATION_OF_RYANODINE_SENSITIVE_CALCIUM_RELEASE_CHANNEL_ACTI	-1.40	1.11	0	0	0	not significant
1397	GO_POLYNUCLEOTIDE_ADENYLYLTRANSFERASE_ACTIVITY	-1.40	1.09	0	0	0	not significant
1398	BIOCARTA_AT1R_PATHWAY	-1.40	1.07	0	0	0	not significant
1399	GO_NEGATIVE_REGULATION_OF_NEURON_PROJECTION_REGENERATION	-1.40	1.07	0	0	0	not significant
1400	REACTOME_G_PROTEIN_MEDIATED_EVENTS	-1.40	1.07	0	0	0	not significant
1401	GO_DENSE_CORE_GRANULE_TRANSPORT	-1.40	1.06	0	0	0	not significant
1402	GO_RNA_POLYMERASE_II_CTD_HEPTAPEPTIDE_REPEAT_KINASE_ACTIVITY	-1.40	1.06	0	0	0	not significant
1403	GO_COMPACT_MYELIN	-1.40	1.04	0	0	0	not significant
1404	GO_KIDNEY_MESENCHYME_DEVELOPMENT	-1.40	1.04	0	0	0	not significant
1405	GO_MITOCHONDRIAL_RNA_3_END_PROCESSING	-1.40	1.04	0	0	0	not significant

1406	MINGUEZ_LIVER_CANCER_VASCULAR_INVASION_UP	-1.40	1.01	0	0	0	not significant
1407	GO_PRE_MIRNA_BINDING	-1.40	1	0	0	0	not significant
1408	GO_GLUCOSE_BINDING	-1.40	0.99	0	0	0	not significant
1409	GO_HEART_TRABECULA_MORPHOGENESIS	-1.40	0.99	0	0	0	not significant
1410	GO_NEGATIVE_REGULATION_OF_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	-1.40	0.99	0	0	0	not significant
1411	GO_CYCLOSPORIN_A_BINDING	-1.40	0.97	0	0	0	not significant
1412	GO_NEGATIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	-1.39	4	0	0	0	not significant
1413	GO_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	-1.39	2.42	0	0	0	not significant
1414	REACTOME_TRANSLATION	-1.39	2.31	0	0	0	not significant
1415	GO_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	-1.39	2.08	0	0	0	not significant
1416	GCNP_SHH_UP_LATE.V1_UP	-1.39	1.91	0	0	0	not significant
1417	GO_REGULATION_OF_TRANSLATIONAL_INITIATION	-1.39	1.75	0	0	0	not significant
1418	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION	-1.39	1.71	0	0	0	not significant
1419	GO_REGULATION_OF_GENE_SILENCING	-1.39	1.69	0	0	0	not significant
1420	HALLMARK_PI3K_AKT_MTOR_SIGNALING	-1.39	1.64	0	0	0	not significant
1421	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	-1.39	1.63	0	0	0	not significant
1422	REACTOME_ER_TO_GOLGI_ANTEROGRADE_TRANSPORT	-1.39	1.62	0	0	0	not significant
1423	GO_POSITIVE_REGULATION_OF_VIRAL_PROCESS	-1.39	1.59	0	0	0	not significant
1424	IKEDA_MIR30_TARGETS_UP	-1.39	1.56	0	0	0	not significant
1425	GO_MODIFICATION_OF_MORPHOLOGY_OR_PHYSIOLOGY_OF_OTHER_ORGANISM_	-1.39	1.3	0	0	0	not significant
1426	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_C	-1.39	1.27	0	0	0	not significant
1427	CHR14Q22	-1.39	1.25	0	0	0	not significant
1428	SWEET_KRAS_TARGETS_DN	-1.39	1.23	0	0	0	not significant
1429	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_CORTEX	-1.39	1.19	0	0	0	not significant
1430	VANTVEER_BREAST_CANCER_BRCA1_UP	-1.39	1.18	0	0	0	not significant
1431	BIOCARTA_PYK2_PATHWAY	-1.39	1.16	0	0	0	not significant
1432	GUTIERREZ_MULTIPLE_MYELOMA_UP	-1.39	1.16	0	0	0	not significant
1433	REACTOME_HIV_ELONGATION_ARREST_AND_RECOVERY	-1.39	1.16	0	0	0	not significant
1434	REACTOME_METABOLIC_DISORDERS_OF_BIOLOGICAL_OXIDATION_ENZYMES	-1.39	1.16	0	0	0	not significant
1435	REACTOME_VEGFR2_MEDIATED_VASCULAR_PERMEABILITY	-1.39	1.15	0	0	0	not significant
1436	GO_GLANDULAR_EPITHELIAL_CELL_DIFFERENTIATION	-1.39	1.14	0	0	0	not significant
1437	CHR2P22	-1.39	1.13	0	0	0	not significant
1438	KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	-1.39	1.11	0	0	0	not significant
1439	KEGG_TYPE_II_DIABETES_MELLITUS	-1.39	1.11	0	0	0	not significant
1440	REACTOME_HSF1_ACTIVATION	-1.39	1.1	0	0	0	not significant
1441	GO_AZOLE_TRANSPORT	-1.39	1.08	0	0	0	not significant
1442	GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY	-1.39	1.06	0	0	0	not significant
1443	GO_POSITIVE_REGULATION_OF_AMYLOID_BETA_FORMATION	-1.39	1.06	0	0	0	not significant
1444	GO_ELL_EAF_COMPLEX	-1.39	1.04	0	0	0	not significant
1445	REACTOME_CTLA4_INHIBITORY_SIGNALING	-1.39	1.04	0	0	0	not significant
1446	GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_CALCIUM_ION_SIGNA	-1.39	1.03	0	0	0	not significant
1447	BIOCARTA_IGF1MTOR_PATHWAY	-1.39	1.02	0	0	0	not significant
1448	FARDIN_HYPOXIA_9	-1.39	1.02	0	0	0	not significant
1449	GO_MAINTENANCE_OF_APICAL_BASAL_CELL_POLARITY	-1.39	1.02	0	0	0	not significant
1450	REACTOME_MET_ACTIVATES_RAP1_AND_RAC1	-1.39	1.01	0	0	0	not significant
1451	GO_LRR_DOMAIN_BINDING	-1.39	1	0	0	0	not significant
1452	KANG_CISPLATIN_RESISTANCE_DN	-1.39	1	0	0	0	not significant
1453	REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	-1.39	1	0	0	0	not significant
1454	GO_PHOTOPERIODISM	-1.39	0.99	0	0	0	not significant
1455	GO_TRNA_3_END_PROCESSING	-1.39	0.99	0	0	0	not significant
1456	KEGG_PHENYLALANINE_METABOLISM	-1.39	0.99	0	0	0	not significant
1457	GO_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	-1.39	0.98	0	0	0	not significant
1458	GO_UBIQUITIN_PROTEIN_TRANSFERASE_REGULATOR_ACTIVITY	-1.39	0.98	0	0	0	not significant
1459	REACTOME_ARMS_MEDIATED_ACTIVATION	-1.39	0.98	0	0	0	not significant
1460	GO_DE_NOVO_PYRIMIDINE_NUCLEOBASE_BIOSYNTHETIC_PROCESS	-1.39	0.97	0	0	0	not significant
1461	OLSSON_E2F3_TARGETS_UP	-1.39	0.97	0	0	0	not significant
1462	GO_RNA_POLYMERASE_I_COMPLEX	-1.39	0.93	0	0	0	not significant
1463	GO_DNA_PACKAGING	-1.38	4	0	0	0	not significant
1464	GO_NUCLEOPLASM_PART	-1.38	4	0	0	0	not significant
1465	GO_RIBONUCLEOTIDE_BINDING	-1.38	4	0	0	0	not significant
1466	LINDGREN_BLADDER_CANCER_CLUSTER_3_UP	-1.38	4	0	0	0	not significant
1467	WANG_SMARCE1_TARGETS_DN	-1.38	2.25	0	0	0	not significant
1468	REACTOME_FC_EPSILON_RECEPTOR_FCERI_SIGNALING	-1.38	2.15	0	0	0	not significant
1469	REACTOME_DEUBIQUITINATION	-1.38	2.01	0	0	0	not significant
1470	GO_ESTABLISHMENT_OF_CELL_POLARITY	-1.38	1.61	0	0	0	not significant
1471	TAKAO_RESPONSE_TO_UVB_RADIATION_DN	-1.38	1.6	0	0	0	not significant
1472	GO_DNA_REPLICATION_INDEPENDENT_NUCLEOSOME_ORGANIZATION	-1.38	1.35	0	0	0	not significant
1473	PID_FOXO_PATHWAY	-1.38	1.31	0	0	0	not significant
1474	GO_CELLULAR_SENESCENCE	-1.38	1.3	0	0	0	not significant
1475	REACTOME_TRANSLOCATION_OF_SLC2A4_GLUT4_TO_THE_PLASMA_MEMBRANE	-1.38	1.3	0	0	0	not significant
1476	KYNG_RESPONSE_TO_H2O2_VIA_ERCC6_UP	-1.38	1.12	0	0	0	not significant
1477	GO_REGULATION_OF_ACTION_POTENTIAL	-1.38	1.09	0	0	0	not significant
1478	CHR2Q32	-1.38	1.08	0	0	0	not significant
1479	GO_ALDITOL_CATABOLIC_PROCESS	-1.38	1.08	0	0	0	not significant
1480	REACTOME_GLUCAGON_LIKE_PEPTIDE_1_GLP1_REGULATES_INSULIN_SECRETION	-1.38	1.07	0	0	0	not significant
1481	GO_SNRNA_PROCESSING	-1.38	1.05	0	0	0	not significant
1482	REACTOME_PINK_PARKIN_MEDIATED_MITOPHAGY	-1.38	1.05	0	0	0	not significant
1483	FUKUSHIMA_TNFSF11_TARGETS	-1.38	1.04	0	0	0	not significant
1484	GO_POSITIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSP	-1.38	1.03	0	0	0	not significant
1485	REACTOME_SHC_RELATED_EVENTS_TRIGGERED_BY_IGF1R	-1.38	1.03	0	0	0	not significant
1486	BIOCARTA_NUCLEARRS_PATHWAY	-1.38	1.02	0	0	0	not significant
1487	GO_DNA_TOPOISOMERASE_BINDING	-1.38	1.02	0	0	0	not significant
1488	PHESSE_TARGETS_OF_APC_AND_MBD2_DN	-1.38	1	0	0	0	not significant
1489	GO_CALCIUM_ION_EXPORT	-1.38	0.99	0	0	0	not significant
1490	STEIN_ESTROGEN_RESPONSE_NOT_VIA_ESRRA	-1.38	0.99	0	0	0	not significant
1491	GO_ASYMMETRIC_CELL_DIVISION	-1.38	0.98	0	0	0	not significant
1492	GO_MAINTENANCE_OF_ORGANELLE_LOCATION	-1.38	0.97	0	0	0	not significant
1493	LOPEZ_MESOTHELIOMA_SURVIVAL_DN	-1.38	0.97	0	0	0	not significant
1494	REACTOME_FRS2_MEDIATED_ACTIVATION	-1.38	0.97	0	0	0	not significant
1495	TERAO_AOX4_TARGETS_SKIN_DN	-1.38	0.97	0	0	0	not significant
1496	GO_RESPONSE_TO_SALT	-1.38	0.96	0	0	0	not significant
1497	REACTOME_G_BETA:GAMMA_SIGNALLING_THROUGH_CDC42	-1.38	0.96	0	0	0	not significant
1498	GALLUZZI_PREVENT_MITOCHONDIAL_PERMEABILIZATION	-1.38	0.95	0	0	0	not significant
1499	REACTOME_RECEPTOR_TYPE_TYROSINE_PROTEIN_PHOSPHATASES	-1.38	0.94	0	0	0	not significant
1500	REACTOME_TRNA_MODIFICATION_IN_THE_MITOCHONDRION	-1.38	0.93	0	0	0	not significant
1501	GO_EPITHELIAL_CELL_FATE_COMMITMENT	-1.38	0.91	0	0	0	not significant
1502	GO_DEPYRIMIDINATION	-1.38	0.9	0	0	0	not significant
1503	GO_PROTEIN_POLYUBIQUITINATION	-1.37	4	0	0	0	not significant
1504	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN	-1.37	4	0	0	0	not significant
1505	BROWNE_HCMV_INFECTION_16HR_UP	-1.37	2.4	0	0	0	not significant
1506	REACTOME_SIGNALING_BY_NUCLEAR_RECEPTORS	-1.37	2.39	0	0	0	not significant
1507	WEST_ADRENOCORTICAL_TUMOR_UP	-1.37	2.24	0	0	0	not significant
1508	REACTOME_EPIGENETIC_REGULATION_OF_GENE_EXPRESSION	-1.37	2.15	0	0	0	not significant
1509	GO_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	-1.37	1.59	0	0	0	not significant
1510	PUJANA_BRCA_CENTERED_NETWORK	-1.37	1.43	0	0	0	not significant
1511	RAMASWAMY_METASTASIS_UP	-1.37	1.3	0	0	0	not significant
1512	GO_TRANSCRIPTION_ELONGATION_FACTOR_COMPLEX	-1.37	1.25	0	0	0	not significant
1513	REACTOME_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES	-1.37	1.24	0	0	0	not significant
1514	GO_HSP90_PROTEIN_BINDING	-1.37	1.21	0	0	0	not significant

1515	GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE	-1.37	1.21	0	0	0	not significant
1516	REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	-1.37	1.13	0	0	0	not significant
1517	REACTOME_NEGATIVE_REGULATION_OF_MAPK_PATHWAY	-1.37	1.1	0	0	0	not significant
1518	GO_CLATHRIN_COAT_OF_ENDOCYTIC_VESICLE	-1.37	1.03	0	0	0	not significant
1519	GO_DENDRITE_CYTOPLASM	-1.37	1.03	0	0	0	not significant
1520	GO_NUCLEAR_NUCLEOSOME	-1.37	1.03	0	0	0	not significant
1521	GO_NUCLEAR_STRESS_GRANULE	-1.37	1.03	0	0	0	not significant
1522	NIKOLSKY_BREAST_CANCER_19Q13.1_AMPLICON	-1.37	1.01	0	0	0	not significant
1523	REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	-1.37	1	0	0	0	not significant
1524	GO_VITAMIN_D_RECEPTOR_SIGNALING_PATHWAY	-1.37	0.99	0	0	0	not significant
1525	LIU_IL13_MEMORY_MODEL_UP	-1.37	0.98	0	0	0	not significant
1526	ONGUSAHA_BRCA1_TARGETS_DN	-1.37	0.98	0	0	0	not significant
1527	CAFFAREL_RESPONSE_TO_THC_8HR_5_DN	-1.37	0.97	0	0	0	not significant
1528	GO_BONE_GROWTH	-1.37	0.97	0	0	0	not significant
1529	GO_INTEGRATOR_COMPLEX	-1.37	0.97	0	0	0	not significant
1530	GO_MAP_KINASE_KINASE_ACTIVITY	-1.37	0.97	0	0	0	not significant
1531	GO_RESPONSE_TO_NITRIC_OXIDE	-1.37	0.97	0	0	0	not significant
1532	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_DN	-1.37	0.97	0	0	0	not significant
1533	GO_7S_RNA_BINDING	-1.37	0.96	0	0	0	not significant
1534	GO_RNA_DIRECTED_DNA_POLYMERASE_ACTIVITY	-1.37	0.96	0	0	0	not significant
1535	CONRAD_STEM_CELL	-1.37	0.95	0	0	0	not significant
1536	GO_NEGATIVE_REGULATION_OF_INCLUSION_BODY_ASSEMBLY	-1.37	0.95	0	0	0	not significant
1537	GO_RNA_POLYMERASE_II_ACTIVITY	-1.37	0.94	0	0	0	not significant
1538	NIELSEN_LEIOMYOSARCOMA_CNN1_UP	-1.37	0.94	0	0	0	not significant
1539	SEIDEN_MET_SIGNALING	-1.37	0.94	0	0	0	not significant
1540	CHR3P13	-1.37	0.93	0	0	0	not significant
1541	GO_POSITIVE_REGULATION_OF_ATTACHMENT_OF_SPINDLE_MICROTUBULES_TO_	-1.37	0.92	0	0	0	not significant
1542	GO_REGULATION_OF_T_HELPER_2_CELL_DIFFERENTIATION	-1.37	0.91	0	0	0	not significant
1543	GO_POLY_G_BINDING	-1.37	0.87	0	0	0	not significant
1544	GO_KINETOCHORE_ASSEMBLY	-1.37	0.86	0	0	0	not significant
1545	ENK_UV_RESPONSE_KERATINOCYTE_DN	-1.36	4	0	0	0	not significant
1546	GO_CHROMOSOME	-1.36	4	0	0	0	not significant
1547	GO_DEPHOSPHORYLATION	-1.36	4	0	0	0	not significant
1548	GO_ESTABLISHMENT_OF_ORGANELLE_LOCALIZATION	-1.36	4	0	0	0	not significant
1549	GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	-1.36	4	0	0	0	not significant
1550	GO_MODIFICATION_DEPENDENT_MACROMOLECULE_CATABOLIC_PROCESS	-1.36	4	0	0	0	not significant
1551	GO_NUCLEAR_BODY	-1.36	4	0	0	0	not significant
1552	REACTOME_ORGANELLE_BIOGENESIS_AND_MAINTENANCE	-1.36	4	0	0	0	not significant
1553	REACTOME_SIGNALING_BY_NOTCH	-1.36	2.37	0	0	0	not significant
1554	REACTOME_OTHER_INTERLEUKIN_SIGNALING	-1.36	2.32	0	0	0	not significant
1555	GO_PROTEIN_CONTAINING_COMPLEX_DISASSEMBLY	-1.36	1.93	0	0	0	not significant
1556	REACTOME_G2_M_CHECKPOINTS	-1.36	1.74	0	0	0	not significant
1557	PURBEY_TARGETS_OF_CTBP1_AND_SATB1_DN	-1.36	1.65	0	0	0	not significant
1558	GO_N_ACETYLTRANSFERASE_ACTIVITY	-1.36	1.51	0	0	0	not significant
1559	REACTOME_AURKA_ACTIVATION_BY_TPX2	-1.36	1.48	0	0	0	not significant
1560	SENESE_HDAC2_TARGETS_UP	-1.36	1.47	0	0	0	not significant
1561	GO_LAMELLIPODIUM_ORGANIZATION	-1.36	1.42	0	0	0	not significant
1562	GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	-1.36	1.38	0	0	0	not significant
1563	GO_P53_BINDING	-1.36	1.31	0	0	0	not significant
1564	GO_NEGATIVE_REGULATION_OF_RNA_CATABOLIC_PROCESS	-1.36	1.3	0	0	0	not significant
1565	ZHAN_MULTIPLE_MYELOMA_CD2_DN	-1.36	1.27	0	0	0	not significant
1566	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_MECP2	-1.36	1.26	0	0	0	not significant
1567	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_TERMINATION	-1.36	1.15	0	0	0	not significant
1568	PID_PI3KCI_AKT_PATHWAY	-1.36	1.13	0	0	0	not significant
1569	GO_POSITIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	-1.36	1.03	0	0	0	not significant
1570	GO_HETEROTRIMERIC_G_PROTEIN_COMPLEX	-1.36	1.02	0	0	0	not significant
1571	GO_CENTRAL_NERVOUS_SYSTEM_NEURON_AXONOGENESIS	-1.36	1.01	0	0	0	not significant
1572	REACTOME_ACTIVATION_OF_RAS_IN_B_CELLS	-1.36	1	0	0	0	not significant
1573	GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_3_COMPLEX_EIF3M	-1.36	0.99	0	0	0	not significant
1574	GO_TROPHECTODERMAL_CELL_DIFFERENTIATION	-1.36	0.99	0	0	0	not significant
1575	CAIRO_PML_TARGETS_BOUND_BY_MYC_UP	-1.36	0.98	0	0	0	not significant
1576	GO_SCHMIDT_LANTERMAN_INCISURE	-1.36	0.98	0	0	0	not significant
1577	REACTOME_EGFR_TRANSACTIVATION_BY_GASTRIN	-1.36	0.96	0	0	0	not significant
1578	GO_RNA_POLYMERASE_II_CORE_COMPLEX	-1.36	0.95	0	0	0	not significant
1579	LEE_METASTASIS_AND_RNA_PROCESSING_UP	-1.36	0.94	0	0	0	not significant
1580	REACTOME_PP2A_MEDIATED_DEPHOSPHORYLATION_OF_KEY_METABOLIC_FACTC	-1.36	0.94	0	0	0	not significant
1581	ZERBINI_RESPONSE_TO_SULINDAC_DN	-1.36	0.94	0	0	0	not significant
1582	HONRADO_BREAST_CANCER_BRCA1_VS_BRCA2	-1.36	0.93	0	0	0	not significant
1583	GO_MINUS_END_DIRECTED_ORGANELLE_TRANSPORT_ALONG_MICROTUBULE	-1.36	0.92	0	0	0	not significant
1584	GO_PYRIMIDINE_NUCLEOBASE_BIOSYNTHETIC_PROCESS	-1.36	0.92	0	0	0	not significant
1585	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN	-1.36	0.92	0	0	0	not significant
1586	GO_BETA_CATENIN_DESTRUCTION_COMPLEX_ASSEMBLY	-1.36	0.91	0	0	0	not significant
1587	GO_RESPONSE_TO_INSECTICIDE	-1.36	0.9	0	0	0	not significant
1588	REACTOME_JOSEPHIN_DOMAIN_DUBS	-1.36	0.9	0	0	0	not significant
1589	GO_REGULATION_OF_HIPPO_SIGNALING	-1.36	0.87	0	0	0	not significant
1590	GO_POSITIVE_REGULATION_OF_RNA_POLYMERASE_II_TRANSCRIPTIONAL_PREINIT	-1.36	0.84	0	0	0	not significant
1591	REACTOME_METHYLATION	-1.36	0.81	0	0	0	not significant
1592	GO_PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	-1.35	4	0	0	0	not significant
1593	GO_ANTIGEN_PROCESSING_AND_PRESENTATION	-1.35	1.88	0	0	0	not significant
1594	GO_POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABO	-1.35	1.75	0	0	0	not significant
1595	GO_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	-1.35	1.68	0	0	0	not significant
1596	GO_PROTEIN_STABILIZATION	-1.35	1.66	0	0	0	not significant
1597	YANG_BCL3_TARGETS_UP	-1.35	1.65	0	0	0	not significant
1598	ZHENG_GLIOBLASTOMA_PLASTICITY_UP	-1.35	1.61	0	0	0	not significant
1599	GO_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN	-1.35	1.57	0	0	0	not significant
1600	GO_ANTERIOR_POSTERIOR_PATTERN_SPECIFICATION	-1.35	1.46	0	0	0	not significant
1601	CHR22Q12	-1.35	1.41	0	0	0	not significant
1602	GO_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	-1.35	1.4	0	0	0	not significant
1603	MORI_MATURE_B_LYMPHOCYTE_DN	-1.35	1.33	0	0	0	not significant
1604	REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	-1.35	1.29	0	0	0	not significant
1605	GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_DN	-1.35	1.28	0	0	0	not significant
1606	GO_PEPTIDE_N_ACETYLTRANSFERASE_ACTIVITY	-1.35	1.24	0	0	0	not significant
1607	GO_REGULATION_OF_CARBOHYDRATE_CATABOLIC_PROCESS	-1.35	1.24	0	0	0	not significant
1608	GO_TRANSCRIPTION_FACTOR_TFIID_COMPLEX	-1.35	1.13	0	0	0	not significant
1609	THILLAINADESAN_ZNF217_TARGETS_UP	-1.35	1.08	0	0	0	not significant
1610	OLSSON_E2F3_TARGETS_DN	-1.35	1.07	0	0	0	not significant
1611	GO_POSITIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.35	1.06	0	0	0	not significant
1612	REACTOME_PYRUVATE_METABOLISM	-1.35	1.06	0	0	0	not significant
1613	CHR10Q21	-1.35	1.05	0	0	0	not significant
1614	GO_NUCLEAR_TRANSCRIPTIONAL_REPRESSOR_COMPLEX	-1.35	1.05	0	0	0	not significant
1615	GRADE_COLON_VS_RECTAL_CANCER_DN	-1.35	1.02	0	0	0	not significant
1616	GO_POSITIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	-1.35	1	0	0	0	not significant
1617	GO_ANNULATE_LAMELLAE	-1.35	0.97	0	0	0	not significant
1618	GO_REGULATION_OF_ANOIKIS	-1.35	0.97	0	0	0	not significant
1619	GO_POSITIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	-1.35	0.96	0	0	0	not significant
1620	PETRETTO_HEART_MASS_QTL_CIS_UP	-1.35	0.96	0	0	0	not significant
1621	GO_PROTEIN_FOLDING_IN_ENDOPLASMIC_RETICULUM	-1.35	0.95	0	0	0	not significant
1622	BIOCARTA_MPR_PATHWAY	-1.35	0.93	0	0	0	not significant
1623	GO_GEMINI_OF_COILED_BODIES	-1.35	0.93	0	0	0	not significant

1624	GO_MICROTUBULE_ORGANIZING_CENTER_LOCALIZATION	-1.35	0.93	0	0	0	not significant
1625	GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS	-1.35	0.93	0	0	0	not significant
1626	MARSON_FOXP3_TARGETS_STIMULATED_DN	-1.35	0.91	0	0	0	not significant
1627	REACTOME_REGULATION_OF_FOXO_TRANSCRIPTIONAL_ACTIVITY_BY_ACETYLATI	-1.35	0.91	0	0	0	not significant
1628	GO_PROTEIN_ARGININE_N_METHYLTRANSFERASE_ACTIVITY	-1.35	0.89	0	0	0	not significant
1629	GO_SYNAPTIC_VESICLE_BUDDING	-1.35	0.89	0	0	0	not significant
1630	GO_TRNA_WOBBLE_URIDINE_MODIFICATION	-1.35	0.89	0	0	0	not significant
1631	VALK_AML_CLUSTER_6	-1.35	0.89	0	0	0	not significant
1632	GO_CALCIUM_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-1.35	0.87	0	0	0	not significant
1633	GO_DEPHOSPHORYLATION_OF_RNA_POLYMERASE_II_C_TERMINAL_DOMAIN	-1.35	0.87	0	0	0	not significant
1634	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_SALMON_DN	-1.35	0.85	0	0	0	not significant
1635	REACTOME_TRANSPORT_OF_CONNEXONS_TO_THE_PLASMA_MEMBRANE	-1.35	0.84	0	0	0	not significant
1636	GO_NLRP3_INFLAMMASOME_COMPLEX_ASSEMBLY	-1.35	0.83	0	0	0	not significant
1637	GO_MORPHOGENESIS_OF_AN_EPITHELIUM	-1.34	4	0	0	0	not significant
1638	GO_DNA_CONFORMATION_CHANGE	-1.34	2.33	0	0	0	not significant
1639	GOLDRATH_ANTIGEN_RESPONSE	-1.34	2.26	0	0	0	not significant
1640	GO_ATPASE_ACTIVITY	-1.34	2.24	0	0	0	not significant
1641	REACTOME_PTEN_REGULATION	-1.34	1.67	0	0	0	not significant
1642	GO_REGULATION_OF_PHOSPHATASE_ACTIVITY	-1.34	1.6	0	0	0	not significant
1643	IWANAGA_CARCINOGENESIS_BY_KRAS_PTEN_UP	-1.34	1.41	0	0	0	not significant
1644	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC	-1.34	1.33	0	0	0	not significant
1645	GO_HISTONE_EXCHANGE	-1.34	1.23	0	0	0	not significant
1646	GO_CARDIOCYTE_DIFFERENTIATION	-1.34	1.22	0	0	0	not significant
1647	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER	-1.34	1.15	0	0	0	not significant
1648	HALLMARK_SPERMATOGENESIS	-1.34	1.12	0	0	0	not significant
1649	APRELIKOVA_BRCA1_TARGETS	-1.34	1.1	0	0	0	not significant
1650	GO_TORC2_SIGNALING	-1.34	1.06	0	0	0	not significant
1651	TONG_INTERACT_WITH_PTTG1	-1.34	1.02	0	0	0	not significant
1652	CHR5P15	-1.34	1	0	0	0	not significant
1653	GO_MOVEMENT_IN_ENVIRONMENT_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOT	-1.34	1	0	0	0	not significant
1654	GO_TRABECULA_MORPHOGENESIS	-1.34	0.97	0	0	0	not significant
1655	GO_GLOMERULUS_DEVELOPMENT	-1.34	0.96	0	0	0	not significant
1656	GO_NEGATIVE_REGULATION_OF_CELL_AGING	-1.34	0.95	0	0	0	not significant
1657	GO_REGULATION_OF_MALE_GONAD_DEVELOPMENT	-1.34	0.95	0	0	0	not significant
1658	REACTOME_SIGNALING_BY_EGFR_IN_CANCER	-1.34	0.95	0	0	0	not significant
1659	GO_REGULATION_OF_SPINDLE_ASSEMBLY	-1.34	0.94	0	0	0	not significant
1660	GO_PORE_COMPLEX	-1.34	0.93	0	0	0	not significant
1661	GO_POSITIVE_REGULATION_OF_BONE_RESORPTION	-1.34	0.93	0	0	0	not significant
1662	GO_SUMO_BINDING	-1.34	0.93	0	0	0	not significant
1663	GO_LEUCINE_CATABOLIC_PROCESS	-1.34	0.92	0	0	0	not significant
1664	REACTOME_ADP_SIGNALLING_THROUGH_P2Y_PURINOCEPTOR_12	-1.34	0.91	0	0	0	not significant
1665	GO_VITAMIN_TRANSPORT	-1.34	0.9	0	0	0	not significant
1666	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP	-1.34	0.87	0	0	0	not significant
1667	GO_AMP_METABOLIC_PROCESS	-1.34	0.86	0	0	0	not significant
1668	GO_RESPONSE_TO_OXYGEN_GLUCOSE_DEPRIVATION	-1.34	0.86	0	0	0	not significant
1669	BIOCARTA_AGPCR_PATHWAY	-1.34	0.85	0	0	0	not significant
1670	GO_NEGATIVE_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	-1.34	0.85	0	0	0	not significant
1671	GO_DENDRITE_TERMINUS	-1.34	0.84	0	0	0	not significant
1672	GO_STAGA_COMPLEX	-1.34	0.84	0	0	0	not significant
1673	GO_TRANSLATION_TERMINATION_FACTOR_ACTIVITY	-1.34	0.82	0	0	0	not significant
1674	GO_REGULATION_OF_INTRACELLULAR_LIPID_TRANSPORT	-1.34	0.81	0	0	0	not significant
1675	GO_CELLULAR_COMPONENT_DISASSEMBLY	-1.33	4	0	0	0	not significant
1676	GO_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	-1.33	4	0	0	0	not significant
1677	GO_POSITIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	-1.33	1.75	0	0	0	not significant
1678	ERBB2_UP.V1_DN	-1.33	1.71	0	0	0	not significant
1679	AFFAR_YY1_TARGETS_DN	-1.33	1.61	0	0	0	not significant
1680	GO_NEGATIVE_REGULATION_OF_NEURON_DIFFERENTIATION	-1.33	1.58	0	0	0	not significant
1681	REACTOME_INTERLEUKIN_1_FAMILY_SIGNALING	-1.33	1.38	0	0	0	not significant
1682	GO_FEMALE_GAMETE_GENERATION	-1.33	1.36	0	0	0	not significant
1683	DE_YY1_TARGETS_DN	-1.33	1.34	0	0	0	not significant
1684	KEGG_GLYCOLYSIS_GLUCONEOGENESIS	-1.33	1.11	0	0	0	not significant
1685	GO_RNA_STABILIZATION	-1.33	1.06	0	0	0	not significant
1686	GO_RNA_POLYMERASE_CORE_ENZYME_BINDING	-1.33	1.04	0	0	0	not significant
1687	BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_UP	-1.33	1.01	0	0	0	not significant
1688	GO_ACTIVATION_OF_MAPKK_ACTIVITY	-1.33	1.01	0	0	0	not significant
1689	REACTOME_SIGNALING_BY_MODERATE_KINASE_ACTIVITY_BRAF_MUTANTS	-1.33	1	0	0	0	not significant
1690	IIZUKA_LIVER_CANCER_PROGRESSION_G1_G2_DN	-1.33	0.97	0	0	0	not significant
1691	VARELA_ZMPSTE24_TARGETS_UP	-1.33	0.97	0	0	0	not significant
1692	GO_TELOMERASE_ACTIVITY	-1.33	0.96	0	0	0	not significant
1693	BARIS_THYROID_CANCER_UP	-1.33	0.95	0	0	0	not significant
1694	GO_REGULATION_OF_RESPIRATORY_GASEOUS_EXCHANGE_BY_NEUROLOGICAL_	-1.33	0.95	0	0	0	not significant
1695	GO_MODULATION_OF_TRANSCRIPTION_IN_OTHER_ORGANISM_INVOLVED_IN_SYM	-1.33	0.94	0	0	0	not significant
1696	GO_POTASSIUM_CHANNEL_REGULATOR_ACTIVITY	-1.33	0.94	0	0	0	not significant
1697	GO_TRNA_WOBBLE_BASE_MODIFICATION	-1.33	0.94	0	0	0	not significant
1698	GO_NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	-1.33	0.93	0	0	0	not significant
1699	GO_POSITIVE_REGULATION_OF_HEART_GROWTH	-1.33	0.93	0	0	0	not significant
1700	KIM_MYCL1_AMPLIFICATION_TARGETS_DN	-1.33	0.91	0	0	0	not significant
1701	GO_HOST_CELL_PART	-1.33	0.88	0	0	0	not significant
1702	GO_PEPTIDYL_ARGININE_N_METHYLATION	-1.33	0.87	0	0	0	not significant
1703	GO_TRANSCRIPTIONALLY_ACTIVE_CHROMATIN	-1.33	0.87	0	0	0	not significant
1704	GO_CHROMATIN_SILENCING_COMPLEX	-1.33	0.86	0	0	0	not significant
1705	GO_LARGE_RIBOSOMAL_SUBUNIT_RRNA_BINDING	-1.33	0.86	0	0	0	not significant
1706	GO_NEUROBLAST_DIVISION	-1.33	0.86	0	0	0	not significant
1707	GO_REGULATION_OF_PLASMINOGEN_ACTIVATION	-1.33	0.86	0	0	0	not significant
1708	GO_RNA_INTERFERENCE	-1.33	0.86	0	0	0	not significant
1709	REACTOME_MAP3K8_TPL2_DEPENDENT_MAPK1_3_ACTIVATION	-1.33	0.86	0	0	0	not significant
1710	REACTOME_RUNX1_REGULATES_ESTROGEN_RECEPTOR_MEDIATED_TRANSCRIPT	-1.33	0.86	0	0	0	not significant
1711	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_CYTOSKELETON_POLARITY	-1.33	0.85	0	0	0	not significant
1712	GO_CEREBELLAR_PURKINJE_CELL_LAYER_DEVELOPMENT	-1.33	0.84	0	0	0	not significant
1713	GO_NEGATIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	-1.33	0.84	0	0	0	not significant
1714	GO_SIGNAL_RECOGNITION_PARTICLE_ENDOPLASMIC_RETICULUM_TARGETING	-1.33	0.84	0	0	0	not significant
1715	REACTOME_SIGNALING_BY_LIGAND_RESPONSIVE_EGFR_VARIANTS_IN_CANCER	-1.33	0.84	0	0	0	not significant
1716	GO_GERM_CELL_NUCLEUS	-1.33	0.83	0	0	0	not significant
1717	GO_POSITIVE_REGULATION_OF_CIRCADIAN_RHYTHM	-1.33	0.83	0	0	0	not significant
1718	REACTOME_GAP_JUNCTION_ASSEMBLY	-1.33	0.82	0	0	0	not significant
1719	GO_DOUBLE_STRANDED_TELOMERIC_DNA_BINDING	-1.33	0.81	0	0	0	not significant
1720	GO_NERVE_GROWTH_FACTOR_SIGNALING_PATHWAY	-1.33	0.8	0	0	0	not significant
1721	REACTOME_SHC_MEDIATED_CASCADE:FGFR1	-1.33	0.79	0	0	0	not significant
1722	CHR13Q22	-1.33	0.78	0	0	0	not significant
1723	REACTOME_REGULATION_OF_CYTOSKELETAL_REMODELING_AND_CELL_SPREAD	-1.33	0.77	0	0	0	not significant
1724	GO_MORPHOGENESIS_OF_AN_EPITHELIAL_FOLD	-1.33	0.75	0	0	0	not significant
1725	REACTOME_MET_ACTIVATES_RAS_SIGNALING	-1.33	0.75	0	0	0	not significant
1726	GO_CELL_ADHESION_MOLECULE_BINDING	-1.32	4	0	0	0	not significant
1727	GO_MICROTUBULE_CYTOSKELETON	-1.32	4	0	0	0	not significant
1728	GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	-1.32	4	0	0	0	not significant
1729	LINSLEY_MIR16_TARGETS	-1.32	2.09	0	0	0	not significant
1730	REACTOME_SIGNALING_BY_ROBO_RECEPTORS	-1.32	1.98	0	0	0	not significant
1731	GO_GOLGI_VESICLE_TRANSPORT	-1.32	1.92	0	0	0	not significant
1732	GO_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	-1.32	1.89	0	0	0	not significant

1733	GO_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	-1.32	1.85	0	0	0	not significant
1734	MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_UP	-1.32	1.74	0	0	0	not significant
1735	PUJANA_BREAST_CANCER_LIT_INT_NETWORK	-1.32	1.4	0	0	0	not significant
1736	GO_NEGATIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	-1.32	1.36	0	0	0	not significant
1737	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	-1.32	1.36	0	0	0	not significant
1738	DARWICHE_PAPILLOMA_RISK_LOW_UP	-1.32	1.3	0	0	0	not significant
1739	GO_CEREBRAL_CORTEX_DEVELOPMENT	-1.32	1.22	0	0	0	not significant
1740	GO_PEPTIDYL_TYROSINE_DEPHOSPHORYLATION	-1.32	1.21	0	0	0	not significant
1741	BILD_CTNNB1_ONCOGENIC_SIGNATURE	-1.32	1.2	0	0	0	not significant
1742	GO_TRANSCRIPTIONAL_REPRESSOR_COMPLEX	-1.32	1.18	0	0	0	not significant
1743	PEART_HDAC_PROLIFERATION_CLUSTER_DN	-1.32	1.16	0	0	0	not significant
1744	DAIRKEE_TERT_TARGETS_DN	-1.32	1.14	0	0	0	not significant
1745	AMIT_SERUM_RESPONSE_120_MCF10A	-1.32	1.12	0	0	0	not significant
1746	CHR5Q13	-1.32	1.07	0	0	0	not significant
1747	GO_MULTI_ORGANISM_BEHAVIOR	-1.32	1.02	0	0	0	not significant
1748	REACTOME_NEGATIVE_REGULATION_OF_FGFR4_SIGNALING	-1.32	0.94	0	0	0	not significant
1749	CHR16Q21	-1.32	0.93	0	0	0	not significant
1750	REACTOME_NEGATIVE_REGULATION_OF_FGFR1_SIGNALING	-1.32	0.93	0	0	0	not significant
1751	CHR6P24	-1.32	0.92	0	0	0	not significant
1752	GO_RIBONUCLEOPROTEIN_COMPLEX_DISASSEMBLY	-1.32	0.91	0	0	0	not significant
1753	REACTOME_GAP_JUNCTION_TRAFFICKING_AND_REGULATION	-1.32	0.91	0	0	0	not significant
1754	GO_POSITIVE_REGULATION_OF_RNA_SPLICING	-1.32	0.9	0	0	0	not significant
1755	GO_GROWTH_PLATE_CARTILAGE_DEVELOPMENT	-1.32	0.89	0	0	0	not significant
1756	GO_MRNA_TRANSCRIPTION	-1.32	0.88	0	0	0	not significant
1757	REACTOME_RHO_GTPASES_ACTIVATE_IQGAPS	-1.32	0.88	0	0	0	not significant
1758	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_CHROMATIN	-1.32	0.87	0	0	0	not significant
1759	GO_MODULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	-1.32	0.87	0	0	0	not significant
1760	GO_POSITIVE_REGULATION_OF_DENDRITIC_CELL_CYTOKINE_PRODUCTION	-1.32	0.86	0	0	0	not significant
1761	GO_CATALYTIC_ACTIVITY_ACTING_ON_A_RRNA	-1.32	0.85	0	0	0	not significant
1762	GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_CYTOKINE_PRODUCTION_	-1.32	0.85	0	0	0	not significant
1763	GO_PROTEIN_K6_LINKED_UBIQUITINATION	-1.32	0.85	0	0	0	not significant
1764	REACTOME_NEGATIVE_REGULATION_OF_FGFR2_SIGNALING	-1.32	0.85	0	0	0	not significant
1765	GO_AT_DNA_BINDING	-1.32	0.84	0	0	0	not significant
1766	SEMENZA_HIF1_TARGETS	-1.32	0.84	0	0	0	not significant
1767	GO_MITOCHONDRIAL_TRNA_METHYLATION	-1.32	0.82	0	0	0	not significant
1768	GO_G_PROTEIN_COUPLED_GLUTAMATE_RECEPTOR_BINDING	-1.32	0.81	0	0	0	not significant
1769	SEMBA_FHIT_TARGETS_DN	-1.32	0.81	0	0	0	not significant
1770	GO_REGULATION_OF_MITOTIC_CENTROSOME_SEPARATION	-1.32	0.8	0	0	0	not significant
1771	GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_4F_COMPLEX	-1.32	0.78	0	0	0	not significant
1772	REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	-1.32	0.78	0	0	0	not significant
1773	GO_MUSCLE_ATROPHY	-1.32	0.76	0	0	0	not significant
1774	GO_NUCLEOLAR_RIBONUCLEASE_P_COMPLEX	-1.32	0.76	0	0	0	not significant
1775	GO_POSITIVE_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHWAY	-1.32	0.74	0	0	0	not significant
1776	GO_PROTEIN_CONTAINING_COMPLEX_BINDING	-1.31	4	0	0	0	not significant
1777	GO_PROTEIN_DOMAIN_SPECIFIC_BINDING	-1.31	4	0	0	0	not significant
1778	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING_GROU	-1.31	4	0	0	0	not significant
1779	GO_PROTEIN_AUTOPHOSPHORYLATION	-1.31	1.68	0	0	0	not significant
1780	GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE_TO_STR	-1.31	1.59	0	0	0	not significant
1781	GO_CYTOSKELETON_DEPENDENT_CYTOKINESIS	-1.31	1.3	0	0	0	not significant
1782	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN	-1.31	1.26	0	0	0	not significant
1783	GO_ION_CHANNEL_BINDING	-1.31	1.2	0	0	0	not significant
1784	GO_PROTEIN_SUMOYLATION	-1.31	1.17	0	0	0	not significant
1785	REACTOME_RMTS_METHYLATE_HISTONE_ARGININES	-1.31	1.1	0	0	0	not significant
1786	GO_TRANSCRIPTION_PREINITIATION_COMPLEX_ASSEMBLY	-1.31	1.02	0	0	0	not significant
1787	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN	-1.31	1	0	0	0	not significant
1788	PID_FOXM1_PATHWAY	-1.31	0.99	0	0	0	not significant
1789	GO_TELOMERIC_DNA_BINDING	-1.31	0.98	0	0	0	not significant
1790	REACTOME_MITOPHAGY	-1.31	0.98	0	0	0	not significant
1791	REACTOME_SIGNALING_BY_FGFR4	-1.31	0.98	0	0	0	not significant
1792	GO_2_OXOGLUTARATE_DEPENDENT_DIOXYGENASE_ACTIVITY	-1.31	0.97	0	0	0	not significant
1793	GO_AMIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.31	0.96	0	0	0	not significant
1794	KEGG_OLFACTORY_TRANSDUCTION	-1.31	0.91	0	0	0	not significant
1795	GO_PROTEIN_REFOLDING	-1.31	0.9	0	0	0	not significant
1796	REACTOME_INTERLEUKIN_6_FAMILY_SIGNALING	-1.31	0.9	0	0	0	not significant
1797	GO_RIBONUCLEASE_P_ACTIVITY	-1.31	0.85	0	0	0	not significant
1798	BIOCARTA_RNA_PATHWAY	-1.31	0.81	0	0	0	not significant
1799	GO_HISTONE_METHYLTRANSFERASE_BINDING	-1.31	0.81	0	0	0	not significant
1800	BIOCARTA_NOS1_PATHWAY	-1.31	0.8	0	0	0	not significant
1801	GO_ATP_DEPENDENT_PEPTIDASE_ACTIVITY	-1.31	0.8	0	0	0	not significant
1802	GO_REGULATION_OF_MRNA_POLYADENYLATION	-1.31	0.8	0	0	0	not significant
1803	GO_TYPE_I_INTERFERON_SECRETION	-1.31	0.8	0	0	0	not significant
1804	GO_ENDOPLASMIC_RETICULUM_EXIT_SITE	-1.31	0.79	0	0	0	not significant
1805	GO_RIBOSOMAL_LARGE_SUBUNIT_BINDING	-1.31	0.79	0	0	0	not significant
1806	WANG_IMMORTALIZED_BY_HOXA9_AND_MEIS1_UP	-1.31	0.78	0	0	0	not significant
1807	GO_FEMALE_PRONUCLEUS	-1.31	0.77	0	0	0	not significant
1808	GO_ALKALI_METAL_ION_BINDING	-1.31	0.75	0	0	0	not significant
1809	GO_RIBONUCLEASE_MRP_COMPLEX	-1.31	0.75	0	0	0	not significant
1810	GO_STAT_FAMILY_PROTEIN_BINDING	-1.31	0.73	0	0	0	not significant
1811	GO_CHROMOSOME_ORGANIZATION	-1.30	4	0	0	0	not significant
1812	GO_HYDROLASE_ACTIVITY_ACTING_ON_ACID_ANHYDRIDES	-1.30	4	0	0	0	not significant
1813	GO_NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION	-1.30	4	0	0	0	not significant
1814	GO_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	-1.30	1.56	0	0	0	not significant
1815	TGFB_UP.V1_UP	-1.30	1.3	0	0	0	not significant
1816	GO_HEAT_SHOCK_PROTEIN_BINDING	-1.30	1.28	0	0	0	not significant
1817	GO_PROTEIN_TARGETING_TO_MITOCHONDRION	-1.30	1.2	0	0	0	not significant
1818	CHR14Q32	-1.30	1.16	0	0	0	not significant
1819	FAELT_B_CLL_WITH_VH3_21_UP	-1.30	1.11	0	0	0	not significant
1820	GO_INTRACELLULAR_PROTEIN_TRANSMEMBRANE_TRANSPORT	-1.30	1.02	0	0	0	not significant
1821	GO_RNA_POLYADENYLATION	-1.30	1	0	0	0	not significant
1822	KORKOLA_EMBRYONAL_CARCINOMA_UP	-1.30	0.98	0	0	0	not significant
1823	REACTOME_SIGNALING_BY_FGFR3	-1.30	0.94	0	0	0	not significant
1824	REACTOME_SIGNALING_BY_FGFR1	-1.30	0.93	0	0	0	not significant
1825	STARK_HYPPOCAMPUS_22Q11_DELETION_UP	-1.30	0.93	0	0	0	not significant
1826	REACTOME_GENE_AND_PROTEIN_EXPRESSION_BY_JAK_STAT_SIGNALING_AFTER_	-1.30	0.91	0	0	0	not significant
1827	KEGG_HEDGEHOG_SIGNALING_PATHWAY	-1.30	0.9	0	0	0	not significant
1828	AMIT_EGF_RESPONSE_120_MCF10A	-1.30	0.88	0	0	0	not significant
1829	GO_DYNEIN_COMPLEX_BINDING	-1.30	0.87	0	0	0	not significant
1830	CHR1Q41	-1.30	0.85	0	0	0	not significant
1831	KIM_HYPOXIA	-1.30	0.85	0	0	0	not significant
1832	GO_NEGATIVE_REGULATION_OF_CALCINEURIN_MEDIATED_SIGNALING	-1.30	0.83	0	0	0	not significant
1833	GO_ENUCLEATE_ERYTHROCYTE_DIFFERENTIATION	-1.30	0.82	0	0	0	not significant
1834	GO_METANEPHRIC_EPITHELIUM_DEVELOPMENT	-1.30	0.82	0	0	0	not significant
1835	GO_SODIUM_CHANNEL_REGULATOR_ACTIVITY	-1.30	0.82	0	0	0	not significant
1836	GO_FEMALE_MEIOSIS_CHROMOSOME_SEGREGATION	-1.30	0.8	0	0	0	not significant
1837	GO_RESPONSE_TO_IRON_III_ION	-1.30	0.8	0	0	0	not significant
1838	GO_CARDIOLIPIN_METABOLIC_PROCESS	-1.30	0.79	0	0	0	not significant
1839	REACTOME_ASSEMBLY_AND_CELL_SURFACE_PRESENTATION_OF_NMDA_RECEPT	-1.30	0.79	0	0	0	not significant
1840	SUZUKI_RESPONSE_TO_TSA	-1.30	0.79	0	0	0	not significant
1841	GO_DYNACTIN_BINDING	-1.30	0.78	0	0	0	not significant

1842	GO_NUCLEAR_PORE_CENTRAL_TRANSPORT_CHANNEL	-1.30	0.78	0	0	0	not significant
1843	YAMANAKA_GLIOBLASTOMA_SURVIVAL_UP	-1.30	0.78	0	0	0	not significant
1844	GO_CHEMOKINE_C_X_C_MOTIF_LIGAND_2_PRODUCTION	-1.30	0.77	0	0	0	not significant
1845	GO_PERICARDIUM_DEVELOPMENT	-1.30	0.77	0	0	0	not significant
1846	GO_NADH_METABOLIC_PROCESS	-1.30	0.76	0	0	0	not significant
1847	REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR	-1.30	0.75	0	0	0	not significant
1848	GO_DENDRITIC_GROWTH_CONE	-1.30	0.74	0	0	0	not significant
1849	GO_HOST_INTRACELLULAR_PART	-1.30	0.73	0	0	0	not significant
1850	GO_MIRNA_CATABOLIC_PROCESS	-1.30	0.72	0	0	0	not significant
1851	REACTOME_BINDING_OF_TCF_LEF:CTNNB1_TO_TARGET_GENE_PROMOTERS	-1.30	0.72	0	0	0	not significant
1852	FARMER_BREAST_CANCER_BASAL_VS_LULMINAL	-1.29	1.83	0	0	0	not significant
1853	REACTOME_REGULATION_OF_EXPRESSION_OF_SLITS_AND_ROBOS	-1.29	1.74	0	0	0	not significant
1854	REACTOME_ESR_MEDIATED_SIGNALING	-1.29	1.61	0	0	0	not significant
1855	ALCALAY_AML_BY_NPM1_LOCALIZATION_DN	-1.29	1.53	0	0	0	not significant
1856	GO_MITOCHONDRIAL_MEMBRANE_PART	-1.29	1.45	0	0	0	not significant
1857	SMITH_TERT_TARGETS_UP	-1.29	1.32	0	0	0	not significant
1858	LI_AMPLIFIED_IN_LUNG_CANCER	-1.29	1.26	0	0	0	not significant
1859	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_UP	-1.29	1.17	0	0	0	not significant
1860	FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_DN	-1.29	1.17	0	0	0	not significant
1861	NIKOLSKY_MUTATED_AND_AMPLIFIED_IN_BREAST_CANCER	-1.29	1.02	0	0	0	not significant
1862	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP	-1.29	1.02	0	0	0	not significant
1863	CHR3Q29	-1.29	0.99	0	0	0	not significant
1864	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_UP	-1.29	0.95	0	0	0	not significant
1865	CHR1P31	-1.29	0.94	0	0	0	not significant
1866	JIANG_AGING_HYPOTHALAMUS_DN	-1.29	0.94	0	0	0	not significant
1867	GO_REGULATION_OF_LAMELLIPODIUM_ORGANIZATION	-1.29	0.9	0	0	0	not significant
1868	GO_POSITIVE_REGULATION_OF_PROTEIN_DEPHOSPHORYLATION	-1.29	0.87	0	0	0	not significant
1869	REACTOME_PERVASIVE_DEVELOPMENTAL_DISORDERS	-1.29	0.86	0	0	0	not significant
1870	GO_GLUTAMINE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	-1.29	0.84	0	0	0	not significant
1871	GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	-1.29	0.84	0	0	0	not significant
1872	GO_RRNA_MODIFICATION	-1.29	0.83	0	0	0	not significant
1873	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CENTROSOME	-1.29	0.82	0	0	0	not significant
1874	GO_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGNALING_PATHWAY	-1.29	0.81	0	0	0	not significant
1875	GO_NEGATIVE_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT_PROT	-1.29	0.8	0	0	0	not significant
1876	GO_PROTEIN_KINASE_A_REGULATORY_SUBUNIT_BINDING	-1.29	0.8	0	0	0	not significant
1877	REACTOME_CREB1_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_ADENYL	-1.29	0.78	0	0	0	not significant
1878	GO_DNA_APURINIC_OR_APYRIMIDINIC_SITE_ENDONUCLEASE_ACTIVITY	-1.29	0.77	0	0	0	not significant
1879	IVANOV_MUTATED_IN_COLON_CANCER	-1.29	0.77	0	0	0	not significant
1880	GO_CLASS_I_DNA_APURINIC_OR_APYRIMIDINIC_SITE_ENDONUCLEASE_ACTIVITY	-1.29	0.75	0	0	0	not significant
1881	GO_NEGATIVE_REGULATION_OF_NITRIC_OXIDE_BIOSYNTHETIC_PROCESS	-1.29	0.74	0	0	0	not significant
1882	GO_NEGATIVE_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	-1.29	0.72	0	0	0	not significant
1883	REACTOME_WAX_AND_PLASMALOGEN_BIOSYNTHESIS	-1.29	0.72	0	0	0	not significant
1884	SCHWAB_TARGETS_OF_BMYB_POLYMORPHIC_VARIANTS_UP	-1.29	0.72	0	0	0	not significant
1885	GO_RESPONSE_TO_INACTIVITY	-1.29	0.71	0	0	0	not significant
1886	SUZUKI_CTCFL_TARGETS_UP	-1.29	0.71	0	0	0	not significant
1887	GO_REGULATION_OF_VITAMIN_D_RECEPTOR_SIGNALING_PATHWAY	-1.29	0.68	0	0	0	not significant
1888	GO_CELLULAR_MACROMOLECULE_CATABOLIC_PROCESS	-1.28	4	0	0	0	not significant
1889	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR	-1.28	1.85	0	0	0	not significant
1890	HALLMARK_GLYCOLYSIS	-1.28	1.67	0	0	0	not significant
1891	GO_CANONICAL_WNT_SIGNALING_PATHWAY	-1.28	1.57	0	0	0	not significant
1892	PUJANA_XPRSS_INT_NETWORK	-1.28	1.4	0	0	0	not significant
1893	BOYLAN_MULTIPLE_MYELOMA_C_D_UP	-1.28	1.35	0	0	0	not significant
1894	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYLATION	-1.28	1.2	0	0	0	not significant
1895	GO_REGULATION_OF_SYNAPTIC_PLASTICITY	-1.28	1.18	0	0	0	not significant
1896	GO_PROTEIN_TRANSMEMBRANE_TRANSPORT	-1.28	1.08	0	0	0	not significant
1897	GO_MUSCLE_CELL_APOPTOTIC_PROCESS	-1.28	0.99	0	0	0	not significant
1898	GO_ADP_BINDING	-1.28	0.98	0	0	0	not significant
1899	GO_ANIMAL_ORGAN_REGENERATION	-1.28	0.95	0	0	0	not significant
1900	DORN_ADENOVIRUS_INFECTION_12HR_DN	-1.28	0.93	0	0	0	not significant
1901	GO_POSITIVE_REGULATION_OF_VIRAL_TRANSCRIPTION	-1.28	0.92	0	0	0	not significant
1902	GO_NEGATIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	-1.28	0.89	0	0	0	not significant
1903	DELPUECH_FOXO3_TARGETS_DN	-1.28	0.88	0	0	0	not significant
1904	YOKOE_CANCER_TESTIS_ANTIGENS	-1.28	0.87	0	0	0	not significant
1905	PID_EPHB_FWD_PATHWAY	-1.28	0.85	0	0	0	not significant
1906	REACTOME_NEGATIVE_REGULATION_OF_FGFR3_SIGNALING	-1.28	0.85	0	0	0	not significant
1907	GO_MRNA_CLEAVAGE	-1.28	0.84	0	0	0	not significant
1908	GO_PROTEIN_PEPTIDYL_PROLYL_ISOMERIZATION	-1.28	0.84	0	0	0	not significant
1909	GO_ATP_BIOSYNTHETIC_PROCESS	-1.28	0.83	0	0	0	not significant
1910	WEST_ADRENOCORTICAL_TUMOR_MARKERS_UP	-1.28	0.83	0	0	0	not significant
1911	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_8	-1.28	0.83	0	0	0	not significant
1912	GO_A_BAND	-1.28	0.82	0	0	0	not significant
1913	REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_BCR_LEADING_TO_GENER	-1.28	0.82	0	0	0	not significant
1914	GO_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING_INVOLVED_IN_CARDIAC_	-1.28	0.81	0	0	0	not significant
1915	GO_EUCHROMATIN	-1.28	0.81	0	0	0	not significant
1916	GO_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	-1.28	0.81	0	0	0	not significant
1917	BIOCARTA_WNT_PATHWAY	-1.28	0.8	0	0	0	not significant
1918	GO_NEGATIVE_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	-1.28	0.79	0	0	0	not significant
1919	REACTOME_SIGNALING_BY_FGFR3_FUSIONS_IN_CANCER	-1.28	0.78	0	0	0	not significant
1920	COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_DN	-1.28	0.77	0	0	0	not significant
1921	GO_COPPER_ION_HOMEOSTASIS	-1.28	0.76	0	0	0	not significant
1922	GO_E_BOX_BINDING	-1.28	0.76	0	0	0	not significant
1923	GO_PHOSPHORYLATION_OF_RNA_POLYMERASE_II_C_TERMINAL_DOMAIN	-1.28	0.76	0	0	0	not significant
1924	GO_BEHAVIORAL_RESPONSE_TO_COCAINE	-1.28	0.75	0	0	0	not significant
1925	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_APOPTOTIC_PROCESS	-1.28	0.75	0	0	0	not significant
1926	REACTOME_ATF6_ATF6_ALPHA_ACTIVATES_CHAPERONES	-1.28	0.75	0	0	0	not significant
1927	REACTOME_NOTCH3_ACTIVATION_AND_TRANSMISSION_OF_SIGNAL_TO_THE_NUC	-1.28	0.75	0	0	0	not significant
1928	REACTOME_TRAF3_DEPENDENT_IRF_ACTIVATION_PATHWAY	-1.28	0.75	0	0	0	not significant
1929	GO_POSITIVE_REGULATION_OF_T_HELPER_2_CELL_DIFFERENTIATION	-1.28	0.74	0	0	0	not significant
1930	GO_ARRESTIN_FAMILY_PROTEIN_BINDING	-1.28	0.73	0	0	0	not significant
1931	GO_CARDIOLIPIN_ACYL_CHAIN_REMODELING	-1.28	0.73	0	0	0	not significant
1932	GO_PROTEIN_COFACTOR_LINKAGE	-1.28	0.73	0	0	0	not significant
1933	REACTOME_G2_M_DNA_REPLICATION_CHECKPOINT	-1.28	0.73	0	0	0	not significant
1934	REACTOME_SHC_MEDIATED_CASCADE:FGFR4	-1.28	0.73	0	0	0	not significant
1935	GO_MULTI_ORGANISM_CELLULAR_LOCALIZATION	-1.28	0.72	0	0	0	not significant
1936	GO_NEGATIVE_REGULATION_OF_HIPPO_SIGNALING	-1.28	0.7	0	0	0	not significant
1937	GO_INSULIN_RECEPTOR_SUBSTRATE_BINDING	-1.28	0.69	0	0	0	not significant
1938	GO_NEGATIVE_REGULATION_OF_NUCLEASE_ACTIVITY	-1.28	0.69	0	0	0	not significant
1939	GO_RESPONSE_TO_MUSCLE_INACTIVITY	-1.28	0.69	0	0	0	not significant
1940	GO_REGULATION_OF_DNA_TOPOISOMERASE_ATP_HYDROLYZING_ACTIVITY	-1.28	0.68	0	0	0	not significant
1941	GO_HISTONE_METHYLTRANSFERASE_ACTIVITY_H3_K36_SPECIFIC_	-1.28	0.67	0	0	0	not significant
1942	GO_N_TERMINAL_PROTEIN_ACETYLTRANSFERASE_COMPLEX	-1.28	0.67	0	0	0	not significant
1943	GO_REGULATION_OF_PLATELET_AGGREGATION	-1.28	0.67	0	0	0	not significant
1944	BIOCARTA_CACAM_PATHWAY	-1.28	0.65	0	0	0	not significant
1945	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	-1.27	4	0	0	0	not significant
1946	GO_TISSUE_MORPHOGENESIS	-1.27	4	0	0	0	not significant
1947	KIM_WT1_TARGETS_DN	-1.27	2.16	0	0	0	not significant
1948	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP	-1.27	2.13	0	0	0	not significant
1949	GO_PEPTIDE_BIOSYNTHETIC_PROCESS	-1.27	1.94	0	0	0	not significant
1950	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP	-1.27	1.87	0	0	0	not significant

1951	GO_ORGANELLE_LOCALIZATION	-1.27	1.7	0	0	0	not significant
1952	GO_NEGATIVE_REGULATION_OF_CELLULAR_CATABOLIC_PROCESS	-1.27	1.57	0	0	0	not significant
1953	GO_ELECTRON_TRANSPORT_CHAIN	-1.27	1.21	0	0	0	not significant
1954	DAZARD_RESPONSE_TO_UV_SCC_DN	-1.27	1.11	0	0	0	not significant
1955	BROWN_MYELOID_CELL_DEVELOPMENT_DN	-1.27	1.07	0	0	0	not significant
1956	GO_PROTEIN_TYROSINE_PHOSPHATASE_ACTIVITY	-1.27	1.06	0	0	0	not significant
1957	GO_CHROMATIN_DNA_BINDING	-1.27	1.05	0	0	0	not significant
1958	GO_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	-1.27	1.05	0	0	0	not significant
1959	REACTOME_DNA_DOUBLE_STRAND_BREAK_RESPONSE	-1.27	1.04	0	0	0	not significant
1960	REACTOME_PROTEIN_UBIQUITINATION	-1.27	1.02	0	0	0	not significant
1961	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_DN	-1.27	1.01	0	0	0	not significant
1962	GO_CARBON_OXYGEN_LYASE_ACTIVITY	-1.27	0.95	0	0	0	not significant
1963	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN	-1.27	0.94	0	0	0	not significant
1964	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN	-1.27	0.94	0	0	0	not significant
1965	GO_POSITIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	-1.27	0.93	0	0	0	not significant
1966	GO_POSITIVE_REGULATION_OF_ATPASE_ACTIVITY	-1.27	0.92	0	0	0	not significant
1967	REACTOME_REGULATION_OF_INSULIN_SECRETION	-1.27	0.87	0	0	0	not significant
1968	BIOCARTA_ERK_PATHWAY	-1.27	0.85	0	0	0	not significant
1969	BIOCARTA_IGF1R_PATHWAY	-1.27	0.85	0	0	0	not significant
1970	GO_RESPONSE_TO_CATECHOLAMINE	-1.27	0.84	0	0	0	not significant
1971	GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LEN	-1.27	0.81	0	0	0	not significant
1972	MACLACHLAN_BRCA1_TARGETS_UP	-1.27	0.81	0	0	0	not significant
1973	CHR11P13	-1.27	0.79	0	0	0	not significant
1974	REACTOME_TRIGLYCERIDE_METABOLISM	-1.27	0.79	0	0	0	not significant
1975	STEIN_ESRRA_TARGETS_RESPONSIVE_TO_ESTROGEN_UP	-1.27	0.79	0	0	0	not significant
1976	SILIGAN_BOUND_BY_EWS_FLT1_FUSION	-1.27	0.78	0	0	0	not significant
1977	GO_AXONAL_GROWTH_CONE	-1.27	0.77	0	0	0	not significant
1978	GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_III_PROMOTER	-1.27	0.75	0	0	0	not significant
1979	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_DN	-1.27	0.75	0	0	0	not significant
1980	GO_1_PHOSPHATIDYLINOSITOL_3_KINASE_REGULATOR_ACTIVITY	-1.27	0.74	0	0	0	not significant
1981	GO_POSITIVE_REGULATION_OF_PROTEIN_MONOUBIQUITINATION	-1.27	0.74	0	0	0	not significant
1982	FINETTI_BREAST_CANCERS_KINOME_GRAY	-1.27	0.73	0	0	0	not significant
1983	GO_EMBRYONIC_HINDLIMB_MORPHOGENESIS	-1.27	0.73	0	0	0	not significant
1984	GO_RESPONSE_TO_IRON_ION	-1.27	0.73	0	0	0	not significant
1985	GO_RESPONSE_TO_PROSTAGLANDIN_E	-1.27	0.73	0	0	0	not significant
1986	MACLACHLAN_BRCA1_TARGETS_DN	-1.27	0.73	0	0	0	not significant
1987	GO_SMOOTH_MUSCLE_CELL_APOPTOTIC_PROCESS	-1.27	0.72	0	0	0	not significant
1988	GO_MITOCHONDRIAL_OUTER_MEMBRANE_TRANSLOCASE_COMPLEX	-1.27	0.71	0	0	0	not significant
1989	GO_REGULATION_OF_GLIAL_CELL_APOPTOTIC_PROCESS	-1.27	0.7	0	0	0	not significant
1990	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_4	-1.27	0.7	0	0	0	not significant
1991	GO_CELLULAR_RESPONSE_TO_INSULIN_LIKE_GROWTH_FACTOR_STIMULUS	-1.27	0.69	0	0	0	not significant
1992	GO_STRESS_RESPONSE_TO_METAL_ION	-1.27	0.69	0	0	0	not significant
1993	REACTOME_ACTIVATED_NTRK3_SIGNALS_THROUGH_RAS	-1.27	0.69	0	0	0	not significant
1994	REACTOME_SHC1_EVENTS_IN_EGFR_SIGNALING	-1.27	0.68	0	0	0	not significant
1995	GO_REGULATION_OF_CYTOSKELETON_ORGANIZATION	-1.26	2.18	0	0	0	not significant
1996	GO_REGULATION_OF_DNA_METABOLIC_PROCESS	-1.26	1.73	0	0	0	not significant
1997	GO_CYTOPLASMIC_REGION	-1.26	1.57	0	0	0	not significant
1998	GO_TRANSLATIONAL_INITIATION	-1.26	1.33	0	0	0	not significant
1999	GO_TRANSLATIONAL_ELONGATION	-1.26	1.26	0	0	0	not significant
2000	REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLA	-1.26	1.23	0	0	0	not significant
2001	GO_HISTONE_DEACETYLASE_BINDING	-1.26	1.21	0	0	0	not significant
2002	YAMAZAKI_TCEB3_TARGETS_DN	-1.26	1.21	0	0	0	not significant
2003	GO_MESENCHYMAL_CELL_DIFFERENTIATION	-1.26	1.17	0	0	0	not significant
2004	MILI_PSEUDOPODIA_CHEMOTAXIS_UP	-1.26	1.15	0	0	0	not significant
2005	CAIRO_LIVER_DEVELOPMENT_UP	-1.26	1.14	0	0	0	not significant
2006	LABBE_WNT3A_TARGETS_UP	-1.26	1.11	0	0	0	not significant
2007	CHR1Q42	-1.26	1.08	0	0	0	not significant
2008	GO_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	-1.26	1.07	0	0	0	not significant
2009	REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	-1.26	1	0	0	0	not significant
2010	REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3:SMAD4_HETEROTRI	-1.26	0.99	0	0	0	not significant
2011	PID_P53_REGULATION_PATHWAY	-1.26	0.96	0	0	0	not significant
2012	GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE	-1.26	0.95	0	0	0	not significant
2013	GO_LAMELLIPODIUM_ASSEMBLY	-1.26	0.91	0	0	0	not significant
2014	DUAN_PRDM5_TARGETS	-1.26	0.9	0	0	0	not significant
2015	GO_MEDIATOR_COMPLEX	-1.26	0.89	0	0	0	not significant
2016	GO_ATPASE_REGULATOR_ACTIVITY	-1.26	0.87	0	0	0	not significant
2017	PID_TRKR_PATHWAY	-1.26	0.86	0	0	0	not significant
2018	GO_POSITIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	-1.26	0.84	0	0	0	not significant
2019	GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.26	0.84	0	0	0	not significant
2020	GO_NEGATIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION	-1.26	0.82	0	0	0	not significant
2021	CORDENONSI_YAP_CONSERVED_SIGNATURE	-1.26	0.81	0	0	0	not significant
2022	REACTOME_DARPP_32_EVENTS	-1.26	0.81	0	0	0	not significant
2023	GO_PROTEIN_DESTABILIZATION	-1.26	0.8	0	0	0	not significant
2024	REACTOME_AQUAPORIN_MEDIATED_TRANSPORT	-1.26	0.8	0	0	0	not significant
2025	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CE	-1.26	0.8	0	0	0	not significant
2026	SCHLINGEMANN_SKIN_CARCINOGENESIS_TPA_UP	-1.26	0.79	0	0	0	not significant
2027	GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_INTERCONVERSION	-1.26	0.78	0	0	0	not significant
2028	GO_CELLULAR_RESPONSE_TO_COPPER_ION	-1.26	0.77	0	0	0	not significant
2029	GO_CHAPERONE_MEDIATED_PROTEIN_COMPLEX_ASSEMBLY	-1.26	0.75	0	0	0	not significant
2030	GO_COPII_VESICLE_COAT	-1.26	0.75	0	0	0	not significant
2031	LI_CYTIDINE_ANALOGS_CYCTOTOXICITY	-1.26	0.75	0	0	0	not significant
2032	STAMBOLSKY_RESPONSE_TO_VITAMIN_D3_DN	-1.26	0.75	0	0	0	not significant
2033	BIOCARTA_DNAFRAGMENT_PATHWAY	-1.26	0.73	0	0	0	not significant
2034	REACTOME_NEURODEGENERATIVE_DISEASES	-1.26	0.73	0	0	0	not significant
2035	GO_ER_OVERLOAD_RESPONSE	-1.26	0.72	0	0	0	not significant
2036	GO_SIN3_TYPE_COMPLEX	-1.26	0.72	0	0	0	not significant
2037	REACTOME_INWARDLY_RECTIFYING_KPLUS_CHANNELS	-1.26	0.72	0	0	0	not significant
2038	GO_PEPTIDYL_ARGININE_MODIFICATION	-1.26	0.71	0	0	0	not significant
2039	GO_LEWY_BODY	-1.26	0.7	0	0	0	not significant
2040	GO_NUCLEAR_PORE_OUTER_RING	-1.26	0.7	0	0	0	not significant
2041	GO_GLUCOSE_6_PHOSPHATE_METABOLIC_PROCESS	-1.26	0.69	0	0	0	not significant
2042	GO_REGULATION_OF_GOLGI_TO_PLASMA_MEMBRANE_PROTEIN_TRANSPORT	-1.26	0.69	0	0	0	not significant
2043	REACTOME_ATF6_ATF6_ALPHA_ACTIVATES_CHAPERONE_GENES	-1.26	0.69	0	0	0	not significant
2044	GO_ACROSOME_ASSEMBLY	-1.26	0.68	0	0	0	not significant
2045	GO_ACTIVATION_INDUCED_CELL_DEATH_OF_T_CELLS	-1.26	0.68	0	0	0	not significant
2046	GO_CELLULAR_RESPONSE_TO_IRON_ION	-1.26	0.67	0	0	0	not significant
2047	GO_MRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	-1.26	0.67	0	0	0	not significant
2048	GO_REGULATION_OF_TRIGLYCERIDE_METABOLIC_PROCESS	-1.26	0.67	0	0	0	not significant
2049	GO_TROPHOBLAST_CELL_MIGRATION	-1.26	0.67	0	0	0	not significant
2050	REACTOME_PI_3K_CASCADE:FGFR1	-1.26	0.66	0	0	0	not significant
2051	GO_POLYADENYLATION_DEPENDENT_SNORNA_3_END_PROCESSING	-1.26	0.64	0	0	0	not significant
2052	GO_CELLULAR_PROTEIN_CATABOLIC_PROCESS	-1.25	4	0	0	0	not significant
2053	GO_ENZYME_REGULATOR_ACTIVITY	-1.25	4	0	0	0	not significant
2054	GO_REGULATION_OF_ORGANELLE_ORGANIZATION	-1.25	4	0	0	0	not significant
2055	LINDGREN_BLADDER_CANCER_CLUSTER_1_DN	-1.25	2.24	0	0	0	not significant
2056	KIM_ALL_DISORDERS_CALB1_CORR_UP	-1.25	2.06	0	0	0	not significant
2057	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_1	-1.25	1.7	0	0	0	not significant
2058	GO_MITOCHONDRIAL_MATRIX	-1.25	1.64	0	0	0	not significant
2059	GO_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS	-1.25	1.56	0	0	0	not significant

2060	SHEPARD_CRUSH_AND_BURN_MUTANT_UP	-1.25	1.46	0	0	0	not significant
2061	GO_GTPASE_ACTIVITY	-1.25	1.45	0	0	0	not significant
2062	GO_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATIO	-1.25	1.39	0	0	0	not significant
2063	BROWNE_HCMV_INFECTION_18HR_UP	-1.25	1.35	0	0	0	not significant
2064	GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION	-1.25	1.27	0	0	0	not significant
2065	REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	-1.25	1.21	0	0	0	not significant
2066	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14	-1.25	1.2	0	0	0	not significant
2067	GO_REGULATION_OF_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERG	-1.25	1.18	0	0	0	not significant
2068	GO_OXIDATIVE_PHOSPHORYLATION	-1.25	1.17	0	0	0	not significant
2069	COLDREN_GEFITINIB_RESISTANCE_UP	-1.25	1.02	0	0	0	not significant
2070	GO_MODIFICATION_OF_MORPHOLOGY_OR_PHYSIOLOGY_OF_OTHER_ORGANISM	-1.25	1	0	0	0	not significant
2071	JI_RESPONSE_TO_FSH_DN	-1.25	0.92	0	0	0	not significant
2072	KEGG_GLIOMA	-1.25	0.92	0	0	0	not significant
2073	KEGG_TIGHT_JUNCTION	-1.25	0.92	0	0	0	not significant
2074	CERVERA_SDHB_TARGETS_2	-1.25	0.91	0	0	0	not significant
2075	GO_MUSCLE_ORGAN_MORPHOGENESIS	-1.25	0.89	0	0	0	not significant
2076	AMIT_EGF_RESPONSE_480_MCF10A	-1.25	0.88	0	0	0	not significant
2077	AUNG_GASTRIC_CANCER	-1.25	0.88	0	0	0	not significant
2078	REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOS	-1.25	0.85	0	0	0	not significant
2079	CAMPS_COLON_CANCER_COPY_NUMBER_DN	-1.25	0.84	0	0	0	not significant
2080	GO_TRANSLATION_INITIATION_FACTOR_BINDING	-1.25	0.84	0	0	0	not significant
2081	GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DEVELOPMENT	-1.25	0.83	0	0	0	not significant
2082	GO_FACE_DEVELOPMENT	-1.25	0.81	0	0	0	not significant
2083	GROSS_HIF1A_TARGETS_DN	-1.25	0.81	0	0	0	not significant
2084	WIERENGA_PML_INTERACTOME	-1.25	0.81	0	0	0	not significant
2085	GO_REGULATION_OF_CELL_AGING	-1.25	0.8	0	0	0	not significant
2086	CHR2Q21	-1.25	0.78	0	0	0	not significant
2087	PID_NEPHRIN_NEPH1_PATHWAY	-1.25	0.78	0	0	0	not significant
2088	GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT	-1.25	0.77	0	0	0	not significant
2089	PID_THROMBIN_PAR1_PATHWAY	-1.25	0.77	0	0	0	not significant
2090	KAPOSI_LIVER_CANCER_MET_UP	-1.25	0.76	0	0	0	not significant
2091	GO_NUCLEAR_EUCHROMATIN	-1.25	0.74	0	0	0	not significant
2092	GO_POSITIVE_REGULATION_OF_ORGAN_GROWTH	-1.25	0.74	0	0	0	not significant
2093	PID_AJDISS_2PATHWAY	-1.25	0.74	0	0	0	not significant
2094	GO_GLUTATHIONE_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	-1.25	0.72	0	0	0	not significant
2095	GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERASE	-1.25	0.72	0	0	0	not significant
2096	REACTOME_FORMATION_OF_SENESCENCE_ASSOCIATED_HETEROCHROMATIN_F	-1.25	0.72	0	0	0	not significant
2097	GO_POSITIVE_REGULATION_OF_EPIDERMAL_CELL_DIFFERENTIATION	-1.25	0.7	0	0	0	not significant
2098	GO_POSITIVE_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	-1.25	0.7	0	0	0	not significant
2099	GO_RESPONSE_TO_COCAINE	-1.25	0.7	0	0	0	not significant
2100	GO_U4_SNRNP	-1.25	0.7	0	0	0	not significant
2101	GO_REGULATION_OF_ISOMERASE_ACTIVITY	-1.25	0.69	0	0	0	not significant
2102	REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS	-1.25	0.69	0	0	0	not significant
2103	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_UP	-1.25	0.68	0	0	0	not significant
2104	REACTOME_G_PROTEIN_GATED_POTASSIUM_CHANNELS	-1.25	0.68	0	0	0	not significant
2105	REACTOME_SYNTHESIS_OF_PIPS_AT_THE_LATE_ENDOSOME_MEMBRANE	-1.25	0.68	0	0	0	not significant
2106	CHR2Q13	-1.25	0.67	0	0	0	not significant
2107	GO_U7_SNRNP	-1.25	0.67	0	0	0	not significant
2108	REACTOME_DNA_DAMAGE_REVERSAL	-1.25	0.67	0	0	0	not significant
2109	GO_5S_RRNA_BINDING	-1.25	0.66	0	0	0	not significant
2110	GO_FOREBRAIN_NEUROBLAST_DIVISION	-1.25	0.66	0	0	0	not significant
2111	GO_INTERLEUKIN_18_PRODUCTION	-1.25	0.66	0	0	0	not significant
2112	IVANOVA_HEMATOPOIESIS_STEM_CELL_SHORT_TERM	-1.25	0.66	0	0	0	not significant
2113	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS_N	-1.25	0.65	0	0	0	not significant
2114	REACTOME_PI_3K_CASCADE:FGFR4	-1.25	0.65	0	0	0	not significant
2115	REACTOME_SYNTHESIS_OF_PYROPHOSPHATES_IN_THE_CYTOSOL	-1.25	0.64	0	0	0	not significant
2116	GO_CHEMOKINE_C_C_MOTIF_LIGAND_2_SECRETION	-1.25	0.63	0	0	0	not significant
2117	GO_GLYCEROL_ETHER_BIOSYNTHETIC_PROCESS	-1.25	0.62	0	0	0	not significant
2118	GO_P_P_BOND_HYDROLYSIS_DRIVEN_PROTEIN_TRANSMEMBRANE_TRANSPORTE	-1.25	0.61	0	0	0	not significant
2119	GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION	-1.24	4	0	0	0	not significant
2120	GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	-1.24	4	0	0	0	not significant
2121	GO_NUCLEAR_SPECK	-1.24	2.22	0	0	0	not significant
2122	GO_REGULATION_OF_CELLULAR_CATABOLIC_PROCESS	-1.24	2	0	0	0	not significant
2123	GO_POSITIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	-1.24	1.8	0	0	0	not significant
2124	GO_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	-1.24	1.57	0	0	0	not significant
2125	GAL_LEUKEMIC_STEM_CELL_DN	-1.24	1.34	0	0	0	not significant
2126	GO_TELENCEPHALON_DEVELOPMENT	-1.24	1.25	0	0	0	not significant
2127	REACTOME_INFLUENZA_INFECTION	-1.24	1.24	0	0	0	not significant
2128	GO_CULLIN_RING_UBIQUITIN_LIGASE_COMPLEX	-1.24	1.14	0	0	0	not significant
2129	KEGG_INSULIN_SIGNALING_PATHWAY	-1.24	1.12	0	0	0	not significant
2130	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_DN	-1.24	1.01	0	0	0	not significant
2131	LINDGREN_BLADDER_CANCER_WITH_LOH_IN_CHR9Q	-1.24	1	0	0	0	not significant
2132	KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	-1.24	0.98	0	0	0	not significant
2133	KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_DN	-1.24	0.95	0	0	0	not significant
2134	GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	-1.24	0.88	0	0	0	not significant
2135	GO_MITOTIC_CYTOKINESIS	-1.24	0.87	0	0	0	not significant
2136	GO_AXIS_SPECIFICATION	-1.24	0.86	0	0	0	not significant
2137	ZHANG_RESPONSE_TO_CANTHARIDIN_DN	-1.24	0.85	0	0	0	not significant
2138	GO_ENDONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCL	-1.24	0.84	0	0	0	not significant
2139	REACTOME_CYTOSOLIC_SENSORS_OF_PATHOGEN_ASSOCIATED_DNA	-1.24	0.84	0	0	0	not significant
2140	GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENG	-1.24	0.82	0	0	0	not significant
2141	GO_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	-1.24	0.8	0	0	0	not significant
2142	TOMLINS_PROSTATE_CANCER_DN	-1.24	0.8	0	0	0	not significant
2143	GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	-1.24	0.78	0	0	0	not significant
2144	AMIT_SERUM_RESPONSE_480_MCF10A	-1.24	0.76	0	0	0	not significant
2145	REACTOME_VASOPRESSIN_REGULATES_RENAL_WATER_HOMEOSTASIS_VIA_AQU	-1.24	0.76	0	0	0	not significant
2146	GO_RIBOSOMAL_SMALL_SUBUNIT_ASSEMBLY	-1.24	0.75	0	0	0	not significant
2147	JAZAG_TGFB1_SIGNALING_DN	-1.24	0.75	0	0	0	not significant
2148	REACTOME_SUMOYLATION_OF_INTRACELLULAR_RECEPTORS	-1.24	0.73	0	0	0	not significant
2149	GO_POLARIZED_EPITHELIAL_CELL_DIFFERENTIATION	-1.24	0.72	0	0	0	not significant
2150	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN	-1.24	0.72	0	0	0	not significant
2151	GO_HINDLIMB_MORPHOGENESIS	-1.24	0.71	0	0	0	not significant
2152	GO_METANEPHROS_MORPHOGENESIS	-1.24	0.71	0	0	0	not significant
2153	AMIT_SERUM_RESPONSE_20_MCF10A	-1.24	0.69	0	0	0	not significant
2154	GO_MITOCHONDRION_MORPHOGENESIS	-1.24	0.69	0	0	0	not significant
2155	GO_REGULATION_OF_PSEUDOPODIUM_ASSEMBLY	-1.24	0.69	0	0	0	not significant
2156	GO_REPRODUCTIVE_BEHAVIOR	-1.24	0.69	0	0	0	not significant
2157	GO_RESPONSE_TO_PROSTAGLANDIN	-1.24	0.69	0	0	0	not significant
2158	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_DN	-1.24	0.69	0	0	0	not significant
2159	REACTOME_ESTROGEN_STIMULATED_SIGNALING_THROUGH_PRKCZ	-1.24	0.69	0	0	0	not significant
2160	REACTOME_G_PROTEIN_ACTIVATION	-1.24	0.69	0	0	0	not significant
2161	GO_PROTEIN_KINASE_B_BINDING	-1.24	0.68	0	0	0	not significant
2162	GO_AMINOACYL_TRNA_EDITING_ACTIVITY	-1.24	0.67	0	0	0	not significant
2163	GO_PEPTIDE_HORMONE_RECEPTOR_BINDING	-1.24	0.67	0	0	0	not significant
2164	GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_UBIQUINOL_TO_CYTOCHROME_C	-1.24	0.66	0	0	0	not significant
2165	GO_REGULATION_OF_PLASMA_MEMBRANE_ORGANIZATION	-1.24	0.66	0	0	0	not significant
2166	GO_FASCIA_ADHERENS	-1.24	0.65	0	0	0	not significant
2167	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_RECEPTOR_BINDING	-1.24	0.65	0	0	0	not significant
2168	GO_MITOCHONDRIAL_RNA_CATABOLIC_PROCESS	-1.24	0.65	0	0	0	not significant

2169	GO_NEGATIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	-1.24	0.65	0	0	0	not significant
2170	REACTOME_LRR_FLII_INTERACTING_PROTEIN_1_LRRFIP1_ACTIVATES_TYPE_I_IFN	-1.24	0.65	0	0	0	not significant
2171	REACTOME_RHO_GTPASES_ACTIVATE_KTN1	-1.24	0.65	0	0	0	not significant
2172	REACTOME_SHC_MEDIATED_CASCADE:FGFR2	-1.24	0.65	0	0	0	not significant
2173	REACTOME_SLBP_DEPENDENT_PROCESSING_OF_REPLICATION_DEPENDENT_HIST	-1.24	0.65	0	0	0	not significant
2174	GO_BENZENE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-1.24	0.64	0	0	0	not significant
2175	GO_SERINE_PHOSPHORYLATION_OF_STAT_PROTEIN	-1.24	0.64	0	0	0	not significant
2176	GO_NEGATIVE_REGULATION_OF_PLATELET_ACTIVATION	-1.24	0.63	0	0	0	not significant
2177	GO_NUCLEAR_PORE_NUCLEAR_BASKET	-1.24	0.63	0	0	0	not significant
2178	GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL	-1.24	0.63	0	0	0	not significant
2179	REACTOME_SHC_MEDIATED_CASCADE:FGFR3	-1.24	0.62	0	0	0	not significant
2180	SCHMAHL_PDGF_SIGNALING	-1.24	0.62	0	0	0	not significant
2181	GO_CELLULAR_RESPONSE_TO_NICOTINE	-1.24	0.6	0	0	0	not significant
2182	GO_POSITIVE_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIG	-1.24	0.6	0	0	0	not significant
2183	GO_CLATHRIN_LIGHT_CHAIN_BINDING	-1.24	0.58	0	0	0	not significant
2184	GO_CYTOSKELETAL_PROTEIN_BINDING	-1.23	4	0	0	0	not significant
2185	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN	-1.23	1.86	0	0	0	not significant
2186	GO_REGULATION_OF_CATABOLIC_PROCESS	-1.23	1.8	0	0	0	not significant
2187	GO_REGULATION_OF_WNT_SIGNALING_PATHWAY	-1.23	1.52	0	0	0	not significant
2188	GO_CELLULAR_KETONE_METABOLIC_PROCESS	-1.23	1.39	0	0	0	not significant
2189	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM1	-1.23	1.31	0	0	0	not significant
2190	MCBRYAN_PUBERTAL_BREAST_6_7WK_UP	-1.23	1.19	0	0	0	not significant
2191	GO_MESENCHYME_DEVELOPMENT	-1.23	1.14	0	0	0	not significant
2192	GO_OSTEOBLAST_DIFFERENTIATION	-1.23	1.08	0	0	0	not significant
2193	GO_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	-1.23	0.99	0	0	0	not significant
2194	GO_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	-1.23	0.94	0	0	0	not significant
2195	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	-1.23	0.9	0	0	0	not significant
2196	BROWNE_HCMV_INFECTION_4HR_UP	-1.23	0.88	0	0	0	not significant
2197	GO_CARDIAC_CONDUCTION	-1.23	0.88	0	0	0	not significant
2198	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	-1.23	0.85	0	0	0	not significant
2199	NAKAMURA_METASTASIS	-1.23	0.84	0	0	0	not significant
2200	HU_ANGIOGENESIS_DN	-1.23	0.81	0	0	0	not significant
2201	SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES	-1.23	0.81	0	0	0	not significant
2202	GO_ARTERY_MORPHOGENESIS	-1.23	0.79	0	0	0	not significant
2203	ZHAN_MULTIPLE_MYELOMA_SUBGROUPS	-1.23	0.78	0	0	0	not significant
2204	GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE	-1.23	0.77	0	0	0	not significant
2205	GO_CILIARY_BASE	-1.23	0.74	0	0	0	not significant
2206	GO_COP9_SIGNALOSOME	-1.23	0.74	0	0	0	not significant
2207	REACTOME_MITOCHONDRIAL_CALCIUM_ION_TRANSPORT	-1.23	0.73	0	0	0	not significant
2208	GO_MONOCARBOXYLIC_ACID_BINDING	-1.23	0.72	0	0	0	not significant
2209	BIOCARTA_GCR_PATHWAY	-1.23	0.7	0	0	0	not significant
2210	GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_OUTER_MEMBRANE	-1.23	0.7	0	0	0	not significant
2211	GO_MAINTENANCE_OF_CELL_POLARITY	-1.23	0.7	0	0	0	not significant
2212	GO_MEMBRANE_FISSION	-1.23	0.69	0	0	0	not significant
2213	GO_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATION	-1.23	0.69	0	0	0	not significant
2214	ROVERSI_GLIOMA_LOH_REGIONS	-1.23	0.69	0	0	0	not significant
2215	HALLMARK_NOTCH_SIGNALING	-1.23	0.68	0	0	0	not significant
2216	GO_AMINOACYL_TRNA_METABOLISM_INVOLVED_IN_TRANSLATIONAL_FIDELITY	-1.23	0.67	0	0	0	not significant
2217	GO_METANEPHRIC_NEPHRON_MORPHOGENESIS	-1.23	0.67	0	0	0	not significant
2218	GO_PLUS_END_DIRECTED_ORGANELLE_TRANSPORT_ALONG_MICROTUBULE	-1.23	0.67	0	0	0	not significant
2219	GO_RETINOIC_ACID_RECEPTOR_BINDING	-1.23	0.67	0	0	0	not significant
2220	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_THREONINE_PHOSPHORYLATION	-1.23	0.66	0	0	0	not significant
2221	GO_MITOCHONDRIAL_RIBOSOME_ASSEMBLY	-1.23	0.65	0	0	0	not significant
2222	GO_SULFUR_AMINO_ACID_METABOLIC_PROCESS	-1.23	0.65	0	0	0	not significant
2223	GO_TRNA_SPECIFIC_RIBONUCLEASE_ACTIVITY	-1.23	0.65	0	0	0	not significant
2224	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITORS_UP	-1.23	0.65	0	0	0	not significant
2225	REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	-1.23	0.65	0	0	0	not significant
2226	BRUNEAU_SEPTATION_VENTRICULAR	-1.23	0.64	0	0	0	not significant
2227	EHRLICH_ICF_SYNDROM_UP	-1.23	0.64	0	0	0	not significant
2228	GO_ASTER	-1.23	0.64	0	0	0	not significant
2229	GO_CYTOPLASM_ORGANIZATION	-1.23	0.64	0	0	0	not significant
2230	GO_POSITIVE_REGULATION_OF_MYELINATION	-1.23	0.64	0	0	0	not significant
2231	GO_5_3_EXODEOXYRIBONUCLEASE_ACTIVITY	-1.23	0.63	0	0	0	not significant
2232	GO_ENOYL_COA_HYDRATASE_ACTIVITY	-1.23	0.63	0	0	0	not significant
2233	GO_TPR_DOMAIN_BINDING	-1.23	0.63	0	0	0	not significant
2234	LUND_SILENCED_BY_METHYLATION	-1.23	0.63	0	0	0	not significant
2235	REACTOME_CREB1_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII_	-1.23	0.63	0	0	0	not significant
2236	GO_ACTOMYOSIN_CONTRACTILE_RING_ORGANIZATION	-1.23	0.62	0	0	0	not significant
2237	GO_POSITIVE_REGULATION_OF_HISTONE_UBIQUITINATION	-1.23	0.62	0	0	0	not significant
2238	REACTOME_ACTIVATED_NTRK2_SIGNALS_THROUGH_RAS	-1.23	0.61	0	0	0	not significant
2239	REACTOME_CAMK_IV_MEDIATED_PHOSPHORYLATION_OF_CREB	-1.23	0.61	0	0	0	not significant
2240	GALI_TP53_TARGETS_APOPTOTIC_DN	-1.23	0.6	0	0	0	not significant
2241	GO_RNA_POLYMERASE_III_TYPE_3_PROMOTER_DNA_BINDING	-1.23	0.6	0	0	0	not significant
2242	KEGG_LIMONENE_AND_PINENE_DEGRADATION	-1.23	0.6	0	0	0	not significant
2243	REACTOME_INACTIVATION_OF_CDC42_AND_RAC1	-1.23	0.59	0	0	0	not significant
2244	GO_PHOSPHATIDYLINOSITOL_3_KINASE_REGULATORY_SUBUNIT_BINDING	-1.23	0.58	0	0	0	not significant
2245	GO_PROTEIN_LOCALIZATION_TO_ORGANELLE	-1.22	4	0	0	0	not significant
2246	GO_CENTROSOME	-1.22	1.82	0	0	0	not significant
2247	SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_DN	-1.22	1.66	0	0	0	not significant
2248	MOOTHA_PGC	-1.22	1.57	0	0	0	not significant
2249	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP	-1.22	1.39	0	0	0	not significant
2250	KEGG_HUNTINGTONS_DISEASE	-1.22	1.16	0	0	0	not significant
2251	GO_S_ADENOSYLMETHIONINE_DEPENDENT_METHYLTRANSFERASE_ACTIVITY	-1.22	1.1	0	0	0	not significant
2252	GO_FC_RECEPTOR_SIGNALING_PATHWAY	-1.22	1.03	0	0	0	not significant
2253	GO_MAGNESIUM_ION_BINDING	-1.22	1.02	0	0	0	not significant
2254	GO_ORGAN_GROWTH	-1.22	0.96	0	0	0	not significant
2255	GO_REGENERATION	-1.22	0.95	0	0	0	not significant
2256	GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_ENDONUCLEOLYTIC	-1.22	0.91	0	0	0	not significant
2257	DURCHDEWALD_SKIN_CARCINOGENESIS_UP	-1.22	0.89	0	0	0	not significant
2258	JAIN_NFKB_SIGNALING	-1.22	0.84	0	0	0	not significant
2259	REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	-1.22	0.84	0	0	0	not significant
2260	REACTOME_SIGNALING_BY_RAS_MUTANTS	-1.22	0.84	0	0	0	not significant
2261	WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT	-1.22	0.82	0	0	0	not significant
2262	MODY_HIPPOCAMPUS_PRENATAL	-1.22	0.81	0	0	0	not significant
2263	REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	-1.22	0.79	0	0	0	not significant
2264	GO_NEGATIVE_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PF	-1.22	0.78	0	0	0	not significant
2265	CHR5Q23	-1.22	0.76	0	0	0	not significant
2266	APPIERTO_RESPONSE_TO_FENRETINIDE_UP	-1.22	0.75	0	0	0	not significant
2267	GO_RESPIRATORY_CHAIN_COMPLEX_IV_ASSEMBLY	-1.22	0.74	0	0	0	not significant
2268	REACTOME_SPRY_REGULATION_OF_FGF_SIGNALING	-1.22	0.72	0	0	0	not significant
2269	GO_POLY_PURINE_TRACT_BINDING	-1.22	0.71	0	0	0	not significant
2270	HOQUE_METHYLATED_IN_CANCER	-1.22	0.7	0	0	0	not significant
2271	STAMBOLSKY_TARGETS_OF_MUTATED_TP53_UP	-1.22	0.69	0	0	0	not significant
2272	BIOCARTA_LONGEVITY_PATHWAY	-1.22	0.68	0	0	0	not significant
2273	GO_LIPOPROTEIN_PARTICLE_RECEPTOR_BINDING	-1.22	0.68	0	0	0	not significant
2274	GO_REGULATION_OF_OXIDATIVE_PHOSPHORYLATION	-1.22	0.67	0	0	0	not significant
2275	ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_DN	-1.22	0.66	0	0	0	not significant
2276	GO_CHANNEL_INHIBITOR_ACTIVITY	-1.22	0.66	0	0	0	not significant
2277	GO_CYTOSKELETAL_ADAPTOR_ACTIVITY	-1.22	0.66	0	0	0	not significant

2278	GO_PROTEIN_DENEDDYLATION	-1.22	0.66	0	0	0	not significant
2279	GO_VENTRICULAR_TRABECULA_MYOCARDIUM_MORPHOGENESIS	-1.22	0.66	0	0	0	not significant
2280	REACTOME_DEFECTS_IN_BIOTIN_BTN_METABOLISM	-1.22	0.66	0	0	0	not significant
2281	GO_CELLULAR_RESPONSE_TO_NITRIC_OXIDE	-1.22	0.65	0	0	0	not significant
2282	WU_HBX_TARGETS_1_DN	-1.22	0.65	0	0	0	not significant
2283	REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	-1.22	0.64	0	0	0	not significant
2284	GO_GERM_CELL_PROLIFERATION	-1.22	0.63	0	0	0	not significant
2285	GO_LIGASE_ACTIVITY_FORMING_CARBON_CARBON_BONDS	-1.22	0.63	0	0	0	not significant
2286	GO_NUCLEOLAR_LARGE_RRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_I	-1.22	0.63	0	0	0	not significant
2287	GO_POSITIVE_REGULATION_OF_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	-1.22	0.63	0	0	0	not significant
2288	GO_CADHERIN_BINDING_INVOLVED_IN_CELL_CELL_ADHESION	-1.22	0.62	0	0	0	not significant
2289	GO_KINETOCHORE_MICROTUBULE	-1.22	0.62	0	0	0	not significant
2290	GO_MITOCHONDRIAL_DNA_REPLICATION	-1.22	0.62	0	0	0	not significant
2291	GO_PEPTIDYL_ARGININE_METHYLATION	-1.22	0.62	0	0	0	not significant
2292	GO_POSTSYNAPTIC_SIGNAL_TRANSDUCTION	-1.22	0.62	0	0	0	not significant
2293	REACTOME_RESPONSE_TO_METAL_IONS	-1.22	0.62	0	0	0	not significant
2294	GO_INOSITOL_TRISPHOSPHATE_KINASE_ACTIVITY	-1.22	0.61	0	0	0	not significant
2295	WAGNER_APO2_SENSITIVITY	-1.22	0.61	0	0	0	not significant
2296	GO_PRIMARY_AMINO_COMPOUND_METABOLIC_PROCESS	-1.22	0.6	0	0	0	not significant
2297	GO_MECHANOSENSORY_BEHAVIOR	-1.22	0.59	0	0	0	not significant
2298	GO_NEGATIVE_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS	-1.22	0.59	0	0	0	not significant
2299	GO_CORE_MEDIATOR_COMPLEX	-1.22	0.58	0	0	0	not significant
2300	VICENT_METASTASIS_UP	-1.22	0.58	0	0	0	not significant
2301	GO_PHOSPHATIDYLINOSITOL_3_5_BISPHOSPHATE_3_PHOSPHATASE_ACTIVITY	-1.22	0.57	0	0	0	not significant
2302	GO_LIPID_KINASE_ACTIVITY	-1.22	0.55	0	0	0	not significant
2303	GO_MITOCHONDRIAL_PART	-1.21	4	0	0	0	not significant
2304	GO_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	-1.21	4	0	0	0	not significant
2305	PILON_KLF1_TARGETS_DN	-1.21	4	0	0	0	not significant
2306	REACTOME_VESICLE_MEDIATED_TRANSPORT	-1.21	2.04	0	0	0	not significant
2307	GO_RESPONSE_TO_OXYGEN_LEVELS	-1.21	1.53	0	0	0	not significant
2308	MOOTHA_HUMAN_MITODB_6_2002	-1.21	1.53	0	0	0	not significant
2309	GO_RESPONSE_TO_TEMPERATURE_STIMULUS	-1.21	1.38	0	0	0	not significant
2310	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4	-1.21	1.26	0	0	0	not significant
2311	GO_CELLULAR_RESPIRATION	-1.21	1.22	0	0	0	not significant
2312	PGF_UP.V1_UP	-1.21	1.18	0	0	0	not significant
2313	GO_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	-1.21	1.17	0	0	0	not significant
2314	GO_ENDOPLASMIC_RETICULUM_TO_GOLGI_VESICLE_MEDIATED_TRANSPORT	-1.21	1.06	0	0	0	not significant
2315	GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS	-1.21	1.04	0	0	0	not significant
2316	XU_GH1_AUTOCRINE_TARGETS_DN	-1.21	0.96	0	0	0	not significant
2317	RIGGI_EWING_SARCOMA_PROGENITOR_DN	-1.21	0.95	0	0	0	not significant
2318	DOANE_RESPONSE_TO_ANDROGEN_UP	-1.21	0.94	0	0	0	not significant
2319	GO_REGULATION_OF_CELLULAR_KETONE_METABOLIC_PROCESS	-1.21	0.92	0	0	0	not significant
2320	KEGG_WNT_SIGNALING_PATHWAY	-1.21	0.91	0	0	0	not significant
2321	REACTOME_SIGNALING_BY_NTRK1_TRKA	-1.21	0.9	0	0	0	not significant
2322	GO_NUCLEOSOMAL_DNA_BINDING	-1.21	0.89	0	0	0	not significant
2323	GO_POLYSOME	-1.21	0.89	0	0	0	not significant
2324	GO_CIRCADIAN_REGULATION_OF_GENE_EXPRESSION	-1.21	0.82	0	0	0	not significant
2325	GO_ORGANELLE_TRANSPORT_ALONG_MICROTUBULE	-1.21	0.82	0	0	0	not significant
2326	GO_RESPONSE_TO_NERVE_GROWTH_FACTOR	-1.21	0.82	0	0	0	not significant
2327	GALE_APL_WITH_FLT3_MUTATED_UP	-1.21	0.81	0	0	0	not significant
2328	GO_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	-1.21	0.79	0	0	0	not significant
2329	GO_REGULATION_OF_HEART_RATE	-1.21	0.76	0	0	0	not significant
2330	GO_NUCLEOID	-1.21	0.75	0	0	0	not significant
2331	GO_ARTERY_DEVELOPMENT	-1.21	0.74	0	0	0	not significant
2332	GO_CARDIAC_MUSCLE_TISSUE_MORPHOGENESIS	-1.21	0.74	0	0	0	not significant
2333	CAFFAREL_RESPONSE_TO_THC_24HR_5_UP	-1.21	0.73	0	0	0	not significant
2334	REACTOME_DOWNREGULATION_OF_SMAD2_3:SMAD4_TRANSCRIPTIONAL_ACTIVIT	-1.21	0.73	0	0	0	not significant
2335	AMIT_EGF_RESPONSE_60_HELA	-1.21	0.72	0	0	0	not significant
2336	CHR9Q22	-1.21	0.72	0	0	0	not significant
2337	GO_MRNA_CIS_SPLICING_VIA_SPLICEOSOME	-1.21	0.72	0	0	0	not significant
2338	CHUANG_OXIDATIVE_STRESS_RESPONSE_UP	-1.21	0.69	0	0	0	not significant
2339	GO_MATING	-1.21	0.68	0	0	0	not significant
2340	GO_DOPAMINE_RECEPTOR_SIGNALING_PATHWAY	-1.21	0.66	0	0	0	not significant
2341	GO_POSITIVE_REGULATION_OF_VIRAL_RELEASE_FROM_HOST_CELL	-1.21	0.64	0	0	0	not significant
2342	GO_POSITIVE_REGULATION_OF_LAMELLIPODIUM_ORGANIZATION	-1.21	0.63	0	0	0	not significant
2343	REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	-1.21	0.63	0	0	0	not significant
2344	GO_MITOCHONDRIAL_TRANSCRIPTION	-1.21	0.62	0	0	0	not significant
2345	GO_PEROXISOME_PROLIFERATOR_ACTIVATED_RECEPTOR_SIGNALING_PATHWAY	-1.21	0.62	0	0	0	not significant
2346	GO_POSITIVE_REGULATION_BY_HOST_OF_VIRAL_PROCESS	-1.21	0.62	0	0	0	not significant
2347	GO_RNA_STRAND_ANNEALING_ACTIVITY	-1.21	0.62	0	0	0	not significant
2348	GO_SKELETAL_MUSCLE_ADAPTATION	-1.21	0.61	0	0	0	not significant
2349	GO_N6_METHYLADENOSINE_CONTAINING_RNA_BINDING	-1.21	0.6	0	0	0	not significant
2350	REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_DIFFE	-1.21	0.58	0	0	0	not significant
2351	GO_S_SHAPED_BODY_MORPHOGENESIS	-1.21	0.57	0	0	0	not significant
2352	GO_SENSORY_PERCEPTION_OF_TEMPERATURE_STIMULUS	-1.21	0.56	0	0	0	not significant
2353	GO_CYTOSKELETAL_PART	-1.20	4	0	0	0	not significant
2354	GO_CYTOSKELETON_ORGANIZATION	-1.20	4	0	0	0	not significant
2355	GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION	-1.20	4	0	0	0	not significant
2356	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN	-1.20	4	0	0	0	not significant
2357	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	-1.20	4	0	0	0	not significant
2358	GO_PROTEIN_KINASE_ACTIVITY	-1.20	1.6	0	0	0	not significant
2359	MOOTHA_MITOCHONDRIA	-1.20	1.55	0	0	0	not significant
2360	COLINA_TARGETS_OF_4EBP1_AND_4EBP2	-1.20	1.39	0	0	0	not significant
2361	GO_ATPASE_ACTIVITY_COUPLED	-1.20	1.27	0	0	0	not significant
2362	REACTOME_INTRACELLULAR_SIGNALING_BY_SECOND_MESSENGERS	-1.20	1.26	0	0	0	not significant
2363	GO_RIBOSOME	-1.20	1.16	0	0	0	not significant
2364	GO_NEGATIVE_REGULATION_OF_CATABOLIC_PROCESS	-1.20	1.15	0	0	0	not significant
2365	REACTOME_REGULATION_OF_TP53_ACTIVITY	-1.20	1.1	0	0	0	not significant
2366	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN	-1.20	1.06	0	0	0	not significant
2367	PRC2_EZH2_UP.V1_DN	-1.20	1	0	0	0	not significant
2368	GO_POSITIVE_REGULATION_OF_PROTEOLYSIS_INVOLVED_IN_CELLULAR_PROTEIN	-1.20	0.93	0	0	0	not significant
2369	ZHONG_SECRETOME_OF_LUNG_CANCER_AND_FIBROBLAST	-1.20	0.83	0	0	0	not significant
2370	GO_I_BAND	-1.20	0.82	0	0	0	not significant
2371	GO_PYRIMIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-1.20	0.81	0	0	0	not significant
2372	REACTOME_FCGAMMA_RECEPTOR_FCGR_DEPENDENT_PHAGOCYTOSIS	-1.20	0.8	0	0	0	not significant
2373	REACTOME_SLC_TRANSPORTER_DISORDERS	-1.20	0.8	0	0	0	not significant
2374	GO_POSITIVE_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	-1.20	0.75	0	0	0	not significant
2375	GO_SARCOPLASM	-1.20	0.75	0	0	0	not significant
2376	GO_MULTICELLULAR_ORGANISMAL_MOVEMENT	-1.20	0.71	0	0	0	not significant
2377	KIM_LIVER_CANCER_POOR_SURVIVAL_UP	-1.20	0.7	0	0	0	not significant
2378	PID_HIF1A_PATHWAY	-1.20	0.7	0	0	0	not significant
2379	WILCOX_RESPONSE_TO_PROGESTERONE_DN	-1.20	0.7	0	0	0	not significant
2380	CHR11Q14	-1.20	0.69	0	0	0	not significant
2381	GO_PHOSPHATASE_INHIBITOR_ACTIVITY	-1.20	0.69	0	0	0	not significant
2382	REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	-1.20	0.69	0	0	0	not significant
2383	GO_CHROMATIN_DISASSEMBLY	-1.20	0.68	0	0	0	not significant
2384	PID_NCADHERIN_PATHWAY	-1.20	0.68	0	0	0	not significant
2385	GO_CELL_COMMUNICATION_INVOLVED_IN_CARDIAC_CONDUCTION	-1.20	0.67	0	0	0	not significant
2386	GO_INCLUSION_BODY_ASSEMBLY	-1.20	0.67	0	0	0	not significant

2387	GO_NUCLEOTIDE_PHOSPHORYLATION	-1.20	0.66	0	0	0	not significant
2388	GO_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	-1.20	0.66	0	0	0	not significant
2389	PARENT_MTOR_SIGNALING_DN	-1.20	0.66	0	0	0	not significant
2390	ANASTASSIOU_MULTICANCER_INVASIVENESS_SIGNATURE	-1.20	0.65	0	0	0	not significant
2391	GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_REGULATION_OF_TH	-1.20	0.65	0	0	0	not significant
2392	GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME_CENTROMERIC_REGION	-1.20	0.64	0	0	0	not significant
2393	GO_REGULATION_OF_CELLULAR_RESPIRATION	-1.20	0.64	0	0	0	not significant
2394	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR4	-1.20	0.64	0	0	0	not significant
2395	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_OF_NUCLEOLAR_LARGE_RRNA_	-1.20	0.63	0	0	0	not significant
2396	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR3	-1.20	0.63	0	0	0	not significant
2397	ZHAN_V1_LATE_DIFFERENTIATION_GENES_DN	-1.20	0.63	0	0	0	not significant
2398	GO_MATERNAL_PLACENTA_DEVELOPMENT	-1.20	0.62	0	0	0	not significant
2399	GO_POSITIVE_REGULATION_BY_HOST_OF_VIRAL_TRANSCRIPTION	-1.20	0.62	0	0	0	not significant
2400	GO_SUCKLING_BEHAVIOR	-1.20	0.61	0	0	0	not significant
2401	PETRETTO_HEART_MASS_QTL_CIS_DN	-1.20	0.61	0	0	0	not significant
2402	GO_AXO_DENDRITIC_PROTEIN_TRANSPORT	-1.20	0.6	0	0	0	not significant
2403	HOEGERKORP_CD44_TARGETS_DIRECT_UP	-1.20	0.6	0	0	0	not significant
2404	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR1	-1.20	0.6	0	0	0	not significant
2405	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR2	-1.20	0.6	0	0	0	not significant
2406	GO_ACTIN_DEPENDENT_ATPASE_ACTIVITY	-1.20	0.59	0	0	0	not significant
2407	GO_HISTONE_H3_K36_METHYLATION	-1.20	0.59	0	0	0	not significant
2408	GO_NEGATIVE_REGULATION_OF_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTI	-1.20	0.59	0	0	0	not significant
2409	GO_SUMO_SPECIFIC_PROTEASE_ACTIVITY	-1.20	0.59	0	0	0	not significant
2410	REACTOME_PI_3K_CASCADE:FGFR3	-1.20	0.59	0	0	0	not significant
2411	GO_MEIOSIS_II_CELL_CYCLE_PROCESS	-1.20	0.58	0	0	0	not significant
2412	GO_MYOSIN_II_COMPLEX	-1.20	0.58	0	0	0	not significant
2413	GO_PURINE_NUCLEOBASE_BIOSYNTHETIC_PROCESS	-1.20	0.58	0	0	0	not significant
2414	REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	-1.20	0.58	0	0	0	not significant
2415	REACTOME_SURFACTANT_METABOLISM	-1.20	0.58	0	0	0	not significant
2416	GO_AXONAL_TRANSPORT_OF_MITOCHONDRION	-1.20	0.57	0	0	0	not significant
2417	GO_POSITIVE_REGULATION_OF_NEURON_MIGRATION	-1.20	0.57	0	0	0	not significant
2418	GO_RESPONSE_TO_TUMOR_CELL	-1.20	0.57	0	0	0	not significant
2419	WU_ALZHEIMER_DISEASE_UP	-1.20	0.57	0	0	0	not significant
2420	REACTOME_UBIQUINOL_BIOSYNTHESIS	-1.20	0.56	0	0	0	not significant
2421	GO_7SK_SNRNA_BINDING	-1.20	0.55	0	0	0	not significant
2422	GO_MALE_GENITALIA_DEVELOPMENT	-1.20	0.55	0	0	0	not significant
2423	GO_MOTOR_NEURON_APOPTOTIC_PROCESS	-1.20	0.54	0	0	0	not significant
2424	REACTOME_PI_3K_CASCADE:FGFR2	-1.20	0.54	0	0	0	not significant
2425	GO_HOST_INTRACELLULAR_ORGANELLE	-1.20	0.53	0	0	0	not significant
2426	GO_INTRACELLULAR_PROTEIN_TRANSPORT	-1.19	4	0	0	0	not significant
2427	GO_MACROMOLECULE_CATABOLIC_PROCESS	-1.19	4	0	0	0	not significant
2428	GO_ORGANELLE_ASSEMBLY	-1.19	4	0	0	0	not significant
2429	GO_TRANSFERASE_COMPLEX	-1.19	1.89	0	0	0	not significant
2430	GO_MITOCHONDRIAL_ENVELOPE	-1.19	1.54	0	0	0	not significant
2431	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE	-1.19	1.48	0	0	0	not significant
2432	GO_POSITIVE_REGULATION_OF_PROTEOLYSIS	-1.19	1.32	0	0	0	not significant
2433	YOSHIMURA_MAPK8_TARGETS_DN	-1.19	1.17	0	0	0	not significant
2434	GO_CYTOSKELETON_DEPENDENT_INTRACELLULAR_TRANSPORT	-1.19	1.12	0	0	0	not significant
2435	WANG_TUMOR_INVASIVENESS_DN	-1.19	1.11	0	0	0	not significant
2436	WONG_MITOCHONDRIA_GENE_MODULE	-1.19	1.04	0	0	0	not significant
2437	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	-1.19	0.96	0	0	0	not significant
2438	REACTOME_PROTEIN_LOCALIZATION	-1.19	0.95	0	0	0	not significant
2439	BURTON_ADIPOGENESIS_5	-1.19	0.92	0	0	0	not significant
2440	REACTOME_SIGNALING_BY_NTRKS	-1.19	0.89	0	0	0	not significant
2441	GO_HETEROCHROMATIN	-1.19	0.86	0	0	0	not significant
2442	GO_CYTOPLASMIC_STRESS_GRANULE	-1.19	0.85	0	0	0	not significant
2443	GO_DNA_GEOMETRIC_CHANGE	-1.19	0.79	0	0	0	not significant
2444	FIGUEROA_AML_METHYLATION_CLUSTER_1_UP	-1.19	0.78	0	0	0	not significant
2445	RODRIGUES_THYROID_CARCINOMA_DN	-1.19	0.78	0	0	0	not significant
2446	GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	-1.19	0.77	0	0	0	not significant
2447	GO_CYTOCHROME_COMPLEX_ASSEMBLY	-1.19	0.73	0	0	0	not significant
2448	REACTOME_RHO_GTPASES_ACTIVATE_WASPS_AND_WAVES	-1.19	0.73	0	0	0	not significant
2449	PID_LKB1_PATHWAY	-1.19	0.71	0	0	0	not significant
2450	GO_GROWTH_FACTOR_ACTIVITY	-1.19	0.7	0	0	0	not significant
2451	GO_NEURAL_CREST_CELL_DIFFERENTIATION	-1.19	0.7	0	0	0	not significant
2452	HASLINGER_B_CLL_WITH_17P13_DELETION	-1.19	0.69	0	0	0	not significant
2453	MOREIRA_RESPONSE_TO_TSA_UP	-1.19	0.69	0	0	0	not significant
2454	GO_THYMUS_DEVELOPMENT	-1.19	0.66	0	0	0	not significant
2455	GO_REGULATION_OF_CALCINEURIN_MEDIATED_SIGNALING	-1.19	0.65	0	0	0	not significant
2456	GO_T_TUBULE	-1.19	0.65	0	0	0	not significant
2457	REACTOME_SMAD2_SMAD3:SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTIO	-1.19	0.65	0	0	0	not significant
2458	TIEN_INTESTINE_PROBIOTICS_2HR_UP	-1.19	0.65	0	0	0	not significant
2459	GO_OOCYTE_DIFFERENTIATION	-1.19	0.63	0	0	0	not significant
2460	REACTOME_METABOLISM_OF_COFACTORS	-1.19	0.63	0	0	0	not significant
2461	GO_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	-1.19	0.61	0	0	0	not significant
2462	GO_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL_BY_ENDOPLASM	-1.19	0.61	0	0	0	not significant
2463	GO_CELLULAR_RESPONSE_TO_VITAMIN	-1.19	0.6	0	0	0	not significant
2464	GO_NEGATIVE_REGULATION_OF_CENTROSOME_CYCLE	-1.19	0.6	0	0	0	not significant
2465	GO_POSITIVE_REGULATION_OF_KERATINOCYTE_DIFFERENTIATION	-1.19	0.6	0	0	0	not significant
2466	REACTOME_GLUTAMATE_BINDING_ACTIVATION_OF_AMPA_RECEPTORS_AND_SYN	-1.19	0.6	0	0	0	not significant
2467	DISTECHE_ESCAPED_FROM_X_INACTIVATION	-1.19	0.59	0	0	0	not significant
2468	GO_FRUCTOSE_METABOLIC_PROCESS	-1.19	0.58	0	0	0	not significant
2469	GO_GENITALIA_DEVELOPMENT	-1.19	0.58	0	0	0	not significant
2470	GO_PSEUDOPODIUM_ORGANIZATION	-1.19	0.58	0	0	0	not significant
2471	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_17	-1.19	0.58	0	0	0	not significant
2472	RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POORLY_DN	-1.19	0.58	0	0	0	not significant
2473	GO_EXPLORATION_BEHAVIOR	-1.19	0.57	0	0	0	not significant
2474	GO_MYOSIN_FILAMENT	-1.19	0.57	0	0	0	not significant
2475	GO_NEGATIVE_REGULATION_OF_GLUCOSE_TRANSMEMBRANE_TRANSPORT	-1.19	0.57	0	0	0	not significant
2476	GO_PEPTIDYL_ARGININE_METHYLATION_TO_ASYMMETRICAL_DIMETHYL_ARGININE	-1.19	0.57	0	0	0	not significant
2477	GO_POSITIVE_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATION	-1.19	0.57	0	0	0	not significant
2478	GO_REGULATION_OF_LONG_TERM_NEURONAL_SYNAPTIC_PLASTICITY	-1.19	0.57	0	0	0	not significant
2479	GO_TRNA_GUANINE_METHYLTRANSFERASE_ACTIVITY	-1.19	0.57	0	0	0	not significant
2480	REACTOME_TRNA_PROCESSING_IN_THE_MITOCHONDRION	-1.19	0.56	0	0	0	not significant
2481	GO_ALDEHYDE_DEHYDROGENASE_NAD_ACTIVITY	-1.19	0.55	0	0	0	not significant
2482	GO_TRANSCRIPTION_FACTOR_TFIIIB_COMPLEX	-1.19	0.55	0	0	0	not significant
2483	GO_WASH_COMPLEX	-1.19	0.55	0	0	0	not significant
2484	REACTOME_REGULATION_OF_PTEN_LOCALIZATION	-1.19	0.55	0	0	0	not significant
2485	GO_CALCIUM_CHANNEL_INHIBITOR_ACTIVITY	-1.19	0.54	0	0	0	not significant
2486	REACTOME_SUMO_IS_PROTEOLYTICALLY_PROCESSED	-1.19	0.54	0	0	0	not significant
2487	GO_GROWTH_HORMONE_SECRETION	-1.19	0.53	0	0	0	not significant
2488	GO_NEGATIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	-1.19	0.53	0	0	0	not significant
2489	GO_OPSONIN_BINDING	-1.19	0.53	0	0	0	not significant
2490	GO_STRESS_GRANULE_DISASSEMBLY	-1.19	0.52	0	0	0	not significant
2491	GO_HYALURONIC_ACID_BINDING	-1.19	0.51	0	0	0	not significant
2492	GO_RESPONSE_TO_ISOLATION_STRESS	-1.19	0.51	0	0	0	not significant
2493	GO_PROTEIN_PHOSPHORYLATION	-1.18	4	0	0	0	not significant
2494	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	-1.18	4	0	0	0	not significant
2495	REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION	-1.18	1.65	0	0	0	not significant

2496	GO_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	-1.18	1.45	0	0	0	not significant
2497	STEIN_ESRRA_TARGETS_UP	-1.18	1.42	0	0	0	not significant
2498	GO_CELL_CYCLE_CHECKPOINT	-1.18	1.05	0	0	0	not significant
2499	GO_FICOLIN_1_RICH_GRANULE	-1.18	0.97	0	0	0	not significant
2500	GO_MIDBODY	-1.18	0.94	0	0	0	not significant
2501	GARCIA_TARGETS_OF_FLI1_AND_DAX1_DN	-1.18	0.9	0	0	0	not significant
2502	GO_MITOTIC_CELL_CYCLE_CHECKPOINT	-1.18	0.89	0	0	0	not significant
2503	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	-1.18	0.89	0	0	0	not significant
2504	GOLDRATH_HOMEOSTATIC_PROLIFERATION	-1.18	0.88	0	0	0	not significant
2505	FIRESTEIN_PROLIFERATION	-1.18	0.84	0	0	0	not significant
2506	GO_ACETYLTRANSFERASE_ACTIVITY	-1.18	0.84	0	0	0	not significant
2507	P53_DN.V2_DN	-1.18	0.81	0	0	0	not significant
2508	GO_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	-1.18	0.79	0	0	0	not significant
2509	TSENG_IRS1_TARGETS_UP	-1.18	0.78	0	0	0	not significant
2510	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN	-1.18	0.77	0	0	0	not significant
2511	GO_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	-1.18	0.77	0	0	0	not significant
2512	GO_ENDOPEPTIDASE_REGULATOR_ACTIVITY	-1.18	0.76	0	0	0	not significant
2513	SESTO_RESPONSE_TO_UV_C2	-1.18	0.74	0	0	0	not significant
2514	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	-1.18	0.72	0	0	0	not significant
2515	GO_ATP_DEPENDENT_DNA_HELICASE_ACTIVITY	-1.18	0.7	0	0	0	not significant
2516	BROWNE_HCMV_INFECTION_6HR_UP	-1.18	0.69	0	0	0	not significant
2517	CHOI_ATL_STAGE_PREDICTOR	-1.18	0.68	0	0	0	not significant
2518	PID_ECADHERIN_NASCENT_AJ_PATHWAY	-1.18	0.67	0	0	0	not significant
2519	BROWNE_HCMV_INFECTION_8HR_DN	-1.18	0.66	0	0	0	not significant
2520	GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_	-1.18	0.66	0	0	0	not significant
2521	GENTILE_UV_RESPONSE_CLUSTER_D6	-1.18	0.65	0	0	0	not significant
2522	WIEDERSCHAIN_TARGETS_OF_BMI1_AND_PCGF2	-1.18	0.65	0	0	0	not significant
2523	CHANGOLKAR_H2AFY_TARGETS_DN	-1.18	0.64	0	0	0	not significant
2524	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE	-1.18	0.62	0	0	0	not significant
2525	GO_INTRASPECIES_INTERACTION_BETWEEN_ORGANISMS	-1.18	0.62	0	0	0	not significant
2526	GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING	-1.18	0.62	0	0	0	not significant
2527	GO_NEGATIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	-1.18	0.61	0	0	0	not significant
2528	GO_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWAY	-1.18	0.61	0	0	0	not significant
2529	REACTOME_SIGNALING_BY_EGFRVIII_IN_CANCER	-1.18	0.6	0	0	0	not significant
2530	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH2_GROUP_OF_DONORS	-1.18	0.59	0	0	0	not significant
2531	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	-1.18	0.59	0	0	0	not significant
2532	GO_RESPIRATORY_CHAIN_COMPLEX_III	-1.18	0.59	0	0	0	not significant
2533	GO_GOLGI_TRANSPORT_COMPLEX	-1.18	0.58	0	0	0	not significant
2534	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS	-1.18	0.58	0	0	0	not significant
2535	SA_G2_AND_M_PHASES	-1.18	0.57	0	0	0	not significant
2536	GO_CELLULAR_RESPONSE_TO_EPINEPHRINE_STIMULUS	-1.18	0.56	0	0	0	not significant
2537	GO_N_TERMINAL_PEPTIDYL_METHIONINE_ACETYLATION	-1.18	0.56	0	0	0	not significant
2538	GO_NITRIC_OXIDE_SYNTHASE_BINDING	-1.18	0.56	0	0	0	not significant
2539	GO_POSITIVE_REGULATION_OF_MEMBRANE_POTENTIAL	-1.18	0.56	0	0	0	not significant
2540	GO_NEGATIVE_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	-1.18	0.55	0	0	0	not significant
2541	GO_NUCLEOSIDE_DIPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.18	0.55	0	0	0	not significant
2542	GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_	-1.18	0.55	0	0	0	not significant
2543	GO_SPONGIOTROPHOBLAST_LAYER_DEVELOPMENT	-1.18	0.55	0	0	0	not significant
2544	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHY_UP	-1.18	0.55	0	0	0	not significant
2545	GO_NEGATIVE_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY_INVOLVED_	-1.18	0.54	0	0	0	not significant
2546	GO_POSITIVE_REGULATION_OF_HISTONE_PHOSPHORYLATION	-1.18	0.54	0	0	0	not significant
2547	GO_REGULATION_BY_VIRUS_OF_VIRAL_PROTEIN_LEVELS_IN_HOST_CELL	-1.18	0.54	0	0	0	not significant
2548	REACTOME_PTK6_REGULATES_RHO_GTPASES_RAS_GTPASE_AND_MAP_KINASES	-1.18	0.54	0	0	0	not significant
2549	SUZUKI_AMPLIFIED_IN_ORAL_CANCER	-1.18	0.54	0	0	0	not significant
2550	GO_SCHWANN_CELL_PROLIFERATION	-1.18	0.53	0	0	0	not significant
2551	BIOCARTA_P35ALZHEIMERS_PATHWAY	-1.18	0.52	0	0	0	not significant
2552	GO_AMIDE_BIOSYNTHETIC_PROCESS	-1.17	4	0	0	0	not significant
2553	GO_INTRACELLULAR_TRANSPORT	-1.17	4	0	0	0	not significant
2554	SENESE_HDAC3_TARGETS_UP	-1.17	1.52	0	0	0	not significant
2555	GO_NUCLEAR_CHROMOSOME	-1.17	1.49	0	0	0	not significant
2556	GO_CHROMATIN	-1.17	1.4	0	0	0	not significant
2557	SMID_BREAST_CANCER_BASAL_UP	-1.17	1.28	0	0	0	not significant
2558	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP	-1.17	1.18	0	0	0	not significant
2559	PURBEY_TARGETS_OF_CTBP1_NOT_SATB1_UP	-1.17	1.12	0	0	0	not significant
2560	GO_DNA_BIOSYNTHETIC_PROCESS	-1.17	1.04	0	0	0	not significant
2561	FUJII_YBX1_TARGETS_DN	-1.17	1.01	0	0	0	not significant
2562	SANSOM_APC_MYC_TARGETS	-1.17	1	0	0	0	not significant
2563	SENESE_HDAC1_AND_HDAC2_TARGETS_UP	-1.17	0.95	0	0	0	not significant
2564	GO_CIRCADIAN_RHYTHM	-1.17	0.91	0	0	0	not significant
2565	KAAB_FAILED_HEART_ATRIUM_DN	-1.17	0.91	0	0	0	not significant
2566	GO_MICROTUBULE_ORGANIZING_CENTER_ORGANIZATION	-1.17	0.9	0	0	0	not significant
2567	GO_POSITIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.17	0.89	0	0	0	not significant
2568	GO_TELOMERE_ORGANIZATION	-1.17	0.89	0	0	0	not significant
2569	PENG_GLUCOSE_DEPRIVATION_DN	-1.17	0.89	0	0	0	not significant
2570	FIGUEROA_AML_METHYLATION_CLUSTER_3_UP	-1.17	0.84	0	0	0	not significant
2571	GO_RNA_POLYMERASE_II_DISTAL_ENHANCER_SEQUENCE_SPECIFIC_DNA_BINDING	-1.17	0.84	0	0	0	not significant
2572	SHEN_SMARCA2_TARGETS_DN	-1.17	0.83	0	0	0	not significant
2573	KAYO_AGING_MUSCLE_DN	-1.17	0.76	0	0	0	not significant
2574	GO_REGULATION_OF_MUSCLE_CONTRACTION	-1.17	0.75	0	0	0	not significant
2575	REACTOME_NONHOMOLOGOUS_END_JOINING_NHEJ	-1.17	0.73	0	0	0	not significant
2576	GO_CELLULAR_RESPONSE_TO_UV	-1.17	0.72	0	0	0	not significant
2577	PID_TAP63_PATHWAY	-1.17	0.71	0	0	0	not significant
2578	ZAMORA_NOS2_TARGETS_DN	-1.17	0.71	0	0	0	not significant
2579	REN_BOUND_BY_E2F	-1.17	0.7	0	0	0	not significant
2580	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_UP	-1.17	0.68	0	0	0	not significant
2581	GO_POSITIVE_REGULATION_OF_FIBROBLAST_PROLIFERATION	-1.17	0.67	0	0	0	not significant
2582	JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER	-1.17	0.66	0	0	0	not significant
2583	PID_ECADHERIN_STABILIZATION_PATHWAY	-1.17	0.66	0	0	0	not significant
2584	GO_NEUROTROPHIN_SIGNALING_PATHWAY	-1.17	0.65	0	0	0	not significant
2585	GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY_P53_CLAS	-1.17	0.65	0	0	0	not significant
2586	GO_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	-1.17	0.65	0	0	0	not significant
2587	GO_VESICLE_COAT	-1.17	0.65	0	0	0	not significant
2588	PID_WNT_CANONICAL_PATHWAY	-1.17	0.65	0	0	0	not significant
2589	GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	-1.17	0.64	0	0	0	not significant
2590	GO_POSITIVE_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENCING	-1.17	0.63	0	0	0	not significant
2591	GO_PROTEASOMAL_UBIQUITIN_INDEPENDENT_PROTEIN_CATABOLIC_PROCESS	-1.17	0.63	0	0	0	not significant
2592	CHESLER_BRAIN_HIGHEST_GENETIC_VARIANCE	-1.17	0.62	0	0	0	not significant
2593	GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	-1.17	0.62	0	0	0	not significant
2594	SIMBULAN_UV_RESPONSE_NORMAL_DN	-1.17	0.61	0	0	0	not significant
2595	GO_GLIAL_CELL_APOPTOTIC_PROCESS	-1.17	0.59	0	0	0	not significant
2596	GO_REGULATION_OF_GRANULOCYTE_CHEMOTAXIS	-1.17	0.59	0	0	0	not significant
2597	GRATIAS_RETINOBLASTOMA_16Q24	-1.17	0.59	0	0	0	not significant
2598	BIOCARTA_PML_PATHWAY	-1.17	0.58	0	0	0	not significant
2599	GO_EMBRYONIC_CAMERA_TYPE_EYE_DEVELOPMENT	-1.17	0.58	0	0	0	not significant
2600	GO_REGULATION_OF_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_II_P	-1.17	0.58	0	0	0	not significant
2601	WU_HBX_TARGETS_2_DN	-1.17	0.58	0	0	0	not significant
2602	GO_CELLULAR_RESPONSE_TO_REACTIVE_NITROGEN_SPECIES	-1.17	0.57	0	0	0	not significant
2603	GO_PLATELET_MORPHOGENESIS	-1.17	0.57	0	0	0	not significant
2604	GO_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY_INVOLVED_IN_DORSA	-1.17	0.57	0	0	0	not significant

2605	GO_SIGNAL_TRANSDUCTION_INVOLVED_IN_G2_DNA_DAMAGE_CHECKPOINT	-1.17	0.57	0	0	0	not significant
2606	GO_VITAMIN_D_RECEPTOR_BINDING	-1.17	0.57	0	0	0	not significant
2607	LY_AGING_PREMATURE_DN	-1.17	0.57	0	0	0	not significant
2608	GO_LACTATE_METABOLIC_PROCESS	-1.17	0.55	0	0	0	not significant
2609	GO_NEGATIVE_REGULATION_OF_CIRCADIAN_RHYTHM	-1.17	0.55	0	0	0	not significant
2610	GO_RESPONSE_TO_DOPAMINE	-1.17	0.55	0	0	0	not significant
2611	REACTOME_ACTIVATION_OF_BAD_AND_TRANSLOCATION_TO_MITOCHONDRIA	-1.17	0.55	0	0	0	not significant
2612	GO_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_BINDING	-1.17	0.54	0	0	0	not significant
2613	GO OXIDOREDUCTASE ACTIVITY ACTING ON THE CH CH GROUP OF DONORS	-1.17	0.54	0	0	0	not significant
2614	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	-1.17	0.54	0	0	0	not significant
2615	GO_NEGATIVE_REGULATION_OF_RYANODINE_SENSITIVE_CALCIUM_RELEASE_CHA	-1.17	0.53	0	0	0	not significant
2616	GO_RNA_POLYMERASE_III_TRANSCRIPTION_FACTOR_COMPLEX	-1.17	0.53	0	0	0	not significant
2617	GO POSTTRANSLATIONAL PROTEIN TARGETING TO ENDOPLASMIC RETICULUM	-1.17	0.52	0	0	0	not significant
2618	BIOCARTA_BARRESTIN_PATHWAY	-1.17	0.51	0	0	0	not significant
2619	GO_AMP_BIOSYNTHETIC_PROCESS	-1.17	0.51	0	0	0	not significant
2620	GO_TORC1_COMPLEX	-1.17	0.51	0	0	0	not significant
2621	GO_MODULATION_OF_SIGNAL_TRANSDUCTION_IN_OTHER_ORGANISM	-1.17	0.5	0	0	0	not significant
2622	PALOMERO_GSI_SENSITIVITY_UP	-1.17	0.49	0	0	0	not significant
2623	GO_PROTEIN_CATABOLIC_PROCESS	-1.16	1.82	0	0	0	not significant
2624	DANG_BOUND_BY_MYC	-1.16	1.72	0	0	0	not significant
2625	GO_MITOCHONDRION_ORGANIZATION	-1.16	1.58	0	0	0	not significant
2626	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN	-1.16	1.44	0	0	0	not significant
2627	SHEN_SMARCA2_TARGETS_UP	-1.16	1.43	0	0	0	not significant
2628	GO_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	-1.16	1.03	0	0	0	not significant
2629	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP	-1.16	1.01	0	0	0	not significant
2630	GO_INTERACTION_WITH_HOST	-1.16	0.93	0	0	0	not significant
2631	GO_MAINTENANCE_OF_CELL_NUMBER	-1.16	0.91	0	0	0	not significant
2632	REACTOME_ESTROGEN_DEPENDENT_GENE_EXPRESSION	-1.16	0.88	0	0	0	not significant
2633	GO_NEGATIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	-1.16	0.85	0	0	0	not significant
2634	GO_VESICLE_TARGETING_TO_FROM_OR_WITHIN_GOLGI	-1.16	0.79	0	0	0	not significant
2635	GO_POSITIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	-1.16	0.77	0	0	0	not significant
2636	KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	-1.16	0.76	0	0	0	not significant
2637	GO_REGULATION_OF_CENTROSOME_CYCLE	-1.16	0.72	0	0	0	not significant
2638	RB_P130_DN.V1_UP	-1.16	0.72	0	0	0	not significant
2639	GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	-1.16	0.69	0	0	0	not significant
2640	GO_MEIOTIC_CHROMOSOME_SEGREGATION	-1.16	0.68	0	0	0	not significant
2641	GO_MATERNAL_PROCESS_INVOLVED_IN_FEMALE_PREGNANCY	-1.16	0.67	0	0	0	not significant
2642	BIOCARTA_NFAT_PATHWAY	-1.16	0.64	0	0	0	not significant
2643	GO POSITIVE REGULATION OF TYROSINE PHOSPHORYLATION OF STAT PROTE	-1.16	0.64	0	0	0	not significant
2644	REACTOME_DNA_DAMAGE_RECOGNITION_IN_GG_NER	-1.16	0.64	0	0	0	not significant
2645	BIOCARTA_MTOR_PATHWAY	-1.16	0.63	0	0	0	not significant
2646	GO_ESTROGEN_RECEPTOR_BINDING	-1.16	0.63	0	0	0	not significant
2647	GO_CIS_TRANS_ISOMERASE_ACTIVITY	-1.16	0.62	0	0	0	not significant
2648	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX4_DN	-1.16	0.62	0	0	0	not significant
2649	REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK	-1.16	0.6	0	0	0	not significant
2650	BIOCARTA_STATHMIN_PATHWAY	-1.16	0.59	0	0	0	not significant
2651	GO_NEGATIVE_REGULATION_OF_CELL_MATRIX_ADHESION	-1.16	0.59	0	0	0	not significant
2652	GO_NUCLEAR_PORE_ORGANIZATION	-1.16	0.58	0	0	0	not significant
2653	GO_POSITIVE_REGULATION_OF_TRANSLATIONAL_INITIATION	-1.16	0.58	0	0	0	not significant
2654	GO_CALMODULIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-1.16	0.57	0	0	0	not significant
2655	GO_DENDRITE_EXTENSION	-1.16	0.57	0	0	0	not significant
2656	GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	-1.16	0.57	0	0	0	not significant
2657	PETROVA_PROX1_TARGETS_UP	-1.16	0.57	0	0	0	not significant
2658	GO_TRANSLATION_PREINITIATION_COMPLEX	-1.16	0.56	0	0	0	not significant
2659	GO_ENDOLYSOSOME_MEMBRANE	-1.16	0.55	0	0	0	not significant
2660	GO_MAMMARY_GLAND_DUCT_MORPHOGENESIS	-1.16	0.55	0	0	0	not significant
2661	REACTOME_ESTABLISHMENT_OF_SISTER_CHROMATID_COHESION	-1.16	0.55	0	0	0	not significant
2662	GO_DETECTION_OF_TEMPERATURE_STIMULUS	-1.16	0.54	0	0	0	not significant
2663	GO_REGULATION_OF_ATP_BIOSYNTHETIC_PROCESS	-1.16	0.54	0	0	0	not significant
2664	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP	-1.16	0.53	0	0	0	not significant
2665	GO_HISTONE_H2B_UBIQUITINATION	-1.16	0.53	0	0	0	not significant
2666	GO_VITAMIN_TRANSMEMBRANE_TRANSPORT	-1.16	0.53	0	0	0	not significant
2667	REACTOME_COHESIN_LOADING_ONTO_CHROMATIN	-1.16	0.53	0	0	0	not significant
2668	ZEMBUTSU_SENSITIVITY_TO_DOXORUBICIN	-1.16	0.53	0	0	0	not significant
2669	BIOCARTA_RNAPOL3_PATHWAY	-1.16	0.52	0	0	0	not significant
2670	GO_MATING_BEHAVIOR	-1.16	0.52	0	0	0	not significant
2671	BIOCARTA_CCR3_PATHWAY	-1.16	0.51	0	0	0	not significant
2672	GO_F_ACTIN_CAPPING_PROTEIN_COMPLEX	-1.16	0.51	0	0	0	not significant
2673	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_III_ASSEMBLY	-1.16	0.5	0	0	0	not significant
2674	GO_NEGATIVE_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	-1.16	0.5	0	0	0	not significant
2675	GO_NEGATIVE_REGULATION_OF_MYELINATION	-1.16	0.5	0	0	0	not significant
2676	GO_NOSE_DEVELOPMENT	-1.16	0.5	0	0	0	not significant
2677	GO_POSITIVE_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	-1.16	0.5	0	0	0	not significant
2678	GO_INTRACELLULAR_DISTRIBUTION_OF_MITOCHONDRIA	-1.16	0.49	0	0	0	not significant
2679	GO_STEREOCILIUM_TIP	-1.16	0.49	0	0	0	not significant
2680	GO_POSTTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE_TRANSLOCATIC	-1.16	0.48	0	0	0	not significant
2681	BENPORATH_NANOG_TARGETS	-1.15	4	0	0	0	not significant
2682	GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION	-1.15	4	0	0	0	not significant
2683	GO_POSITIVE_REGULATION_OF_PROTEIN_METABOLIC_PROCESS	-1.15	4	0	0	0	not significant
2684	GRYDER_PAX3FOXO1_ENHANCERS_IN_TADS	-1.15	1.83	0	0	0	not significant
2685	GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_II	-1.15	1.67	0	0	0	not significant
2686	GO_KINASE_ACTIVITY	-1.15	1.49	0	0	0	not significant
2687	GO_GUANYL_NUCLEOTIDE_BINDING	-1.15	1.12	0	0	0	not significant
2688	GO_UBIQUITIN_LIKE_PROTEIN_LIGASE_BINDING	-1.15	1.06	0	0	0	not significant
2689	HALLMARK_OXIDATIVE_PHOSPHORYLATION	-1.15	1.04	0	0	0	not significant
2690	GO_POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	-1.15	1.03	0	0	0	not significant
2691	GO_FOREBRAIN_DEVELOPMENT	-1.15	0.96	0	0	0	not significant
2692	TBK1.DF_DN	-1.15	0.95	0	0	0	not significant
2693	GO_RHYTHMIC_PROCESS	-1.15	0.91	0	0	0	not significant
2694	KUMAR_PATHOGEN_LOAD_BY_MACROPHAGES	-1.15	0.91	0	0	0	not significant
2695	GO_PHOSPHATASE_ACTIVITY	-1.15	0.89	0	0	0	not significant
2696	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ONE_CARBON_GROUPS	-1.15	0.89	0	0	0	not significant
2697	GO_PROTEIN_TETRAMERIZATION	-1.15	0.86	0	0	0	not significant
2698	GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	-1.15	0.82	0	0	0	not significant
2699	GO_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT	-1.15	0.74	0	0	0	not significant
2700	GO_CELL_AGING	-1.15	0.73	0	0	0	not significant
2701	GO_METAL_CLUSTER_BINDING	-1.15	0.73	0	0	0	not significant
2702	QUINTENS_EMBRYONIC_BRAIN_RESPONSE_TO_IR	-1.15	0.71	0	0	0	not significant
2703	GO_HEART_GROWTH	-1.15	0.7	0	0	0	not significant
2704	SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN	-1.15	0.7	0	0	0	not significant
2705	GO_SIGNAL_TRANSDUCTION_INVOLVED_IN_CELL_CYCLE_CHECKPOINT	-1.15	0.69	0	0	0	not significant
2706	CHR16P12	-1.15	0.67	0	0	0	not significant
2707	REACTOME TRANSCRIPTIONAL REGULATION OF WHITE ADIPOCYTE DIFFERENTI	-1.15	0.67	0	0	0	not significant
2708	REACTOME_REGULATION_OF_MECP2_EXPRESSION_AND_ACTIVITY	-1.15	0.63	0	0	0	not significant
2709	GO_NEGATIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	-1.15	0.62	0	0	0	not significant
2710	REACTOME_GLYCOGEN_METABOLISM	-1.15	0.62	0	0	0	not significant
2711	GO_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX	-1.15	0.6	0	0	0	not significant
2712	GO_INTRA_GOLGI_VESICLE_MEDIATED_TRANSPORT	-1.15	0.59	0	0	0	not significant
2713	BIOCARTA_INTEGRIN_PATHWAY	-1.15	0.58	0	0	0	not significant

2714	GO_SNRNA_3_END_PROCESSING	-1.15	0.58	0	0	0	not significant
2715	REACTOME_DISASSEMBLY_OF_THE_DESTRUCTION_COMPLEX_AND_RECRUITMENT	-1.15	0.58	0	0	0	not significant
2716	GO_POSITIVE_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	-1.15	0.57	0	0	0	not significant
2717	GO_ACTIVATION_OF_ADENYLATE_CYCLASE_ACTIVITY	-1.15	0.55	0	0	0	not significant
2718	GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMA	-1.15	0.54	0	0	0	not significant
2719	GU_PDEF_TARGETS_DN	-1.15	0.54	0	0	0	not significant
2720	MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_DN	-1.15	0.54	0	0	0	not significant
2721	REACTOME_MITOCHONDRIAL_IRON_SULFUR_CLUSTER_BIOGENESIS	-1.15	0.54	0	0	0	not significant
2722	GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE_MEMBRANE	-1.15	0.53	0	0	0	not significant
2723	GO_HAIR_FOLLICLE_MATURATION	-1.15	0.53	0	0	0	not significant
2724	GO_RENAL_SYSTEM_VASCULATURE_DEVELOPMENT	-1.15	0.53	0	0	0	not significant
2725	REACTOME_E2F_ENABLED_INHIBITION_OF_PRE_REPLICATION_COMPLEX_FORMAT	-1.15	0.53	0	0	0	not significant
2726	GO_DETECTION_OF_TEMPERATURE_STIMULUS_INVOLVED_IN_SENSORY_PERCEPT	-1.15	0.52	0	0	0	not significant
2727	GO_LEUCINE_ZIPPER_DOMAIN_BINDING	-1.15	0.52	0	0	0	not significant
2728	GO_NEGATIVE_REGULATION_OF_MRNA_3_END_PROCESSING	-1.15	0.52	0	0	0	not significant
2729	GO_RNA_POLYMERASE_I_CORE_BINDING	-1.15	0.52	0	0	0	not significant
2730	GO_EMBRYONIC_BODY_MORPHOGENESIS	-1.15	0.51	0	0	0	not significant
2731	GO_PEPTIDE_ALPHA_N_ACETYLTRANSFERASE_ACTIVITY	-1.15	0.51	0	0	0	not significant
2732	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX4_UP	-1.15	0.51	0	0	0	not significant
2733	GO_MONOUBIQUITINATED_PROTEIN_DEUBIQUITINATION	-1.15	0.5	0	0	0	not significant
2734	GO_OUTER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	-1.15	0.5	0	0	0	not significant
2735	BIOCARTA_RAB_PATHWAY	-1.15	0.49	0	0	0	not significant
2736	GO_MRNA_5_SPLICE_SITE_RECOGNITION	-1.15	0.49	0	0	0	not significant
2737	GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	-1.15	0.49	0	0	0	not significant
2738	GO_PROSTATE_GLAND_MORPHOGENESIS	-1.15	0.49	0	0	0	not significant
2739	GO_REGULATION_OF_MIRNA_METABOLIC_PROCESS	-1.15	0.49	0	0	0	not significant
2740	GO_TRNA_SPLICING_LIGASE_COMPLEX	-1.15	0.49	0	0	0	not significant
2741	LANDEMAINE_LUNG_METASTASIS	-1.15	0.49	0	0	0	not significant
2742	GO_CARBOHYDRATE_PHOSPHATASE_ACTIVITY	-1.15	0.48	0	0	0	not significant
2743	GO_CELLULAR_RESPONSE_TO_BRAIN_DERIVED_NEUROTROPHIC_FACTOR_STIMUL	-1.15	0.48	0	0	0	not significant
2744	GO_LIPASE_ACTIVATOR_ACTIVITY	-1.15	0.48	0	0	0	not significant
2745	GO_PHOSPHOLIPASE_ACTIVATOR_ACTIVITY	-1.15	0.48	0	0	0	not significant
2746	GO_REGULATION_OF_CALCIUM_TRANSPORTING_ATPASE_ACTIVITY	-1.15	0.48	0	0	0	not significant
2747	REACTOME_CASPASE_ACTIVATION_VIA_DEPENDENCE_RECEPTORS_IN_THE_ABSE	-1.15	0.48	0	0	0	not significant
2748	GO_BASEMENT_MEMBRANE_ASSEMBLY	-1.15	0.45	0	0	0	not significant
2749	GO_MITOCHONDRION	-1.14	4	0	0	0	not significant
2750	REACTOME_DISEASE	-1.14	1.76	0	0	0	not significant
2751	GO_POSITIVE_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	-1.14	1.73	0	0	0	not significant
2752	GO_POSITIVE_REGULATION_OF_CATALYTIC_ACTIVITY	-1.14	1.7	0	0	0	not significant
2753	GO_REGULATION_OF_PROTEOLYSIS	-1.14	1.26	0	0	0	not significant
2754	GO_REGULATION_OF_CELL_DEVELOPMENT	-1.14	1.18	0	0	0	not significant
2755	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN	-1.14	1.05	0	0	0	not significant
2756	GO_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	-1.14	0.91	0	0	0	not significant
2757	REACTOME_MITOTIC_G1_G1_S_PHASES	-1.14	0.83	0	0	0	not significant
2758	GO_NUCLEAR_TRANSCRIPTION_FACTOR_COMPLEX	-1.14	0.82	0	0	0	not significant
2759	GO_NEGATIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABO	-1.14	0.79	0	0	0	not significant
2760	REACTOME_DNA_REPLICATION_PRE_INITIATION	-1.14	0.75	0	0	0	not significant
2761	GO_MEIOTIC_CELL_CYCLE	-1.14	0.74	0	0	0	not significant
2762	CHR1P35	-1.14	0.68	0	0	0	not significant
2763	GO_POSITIVE_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PRO	-1.14	0.68	0	0	0	not significant
2764	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	-1.14	0.68	0	0	0	not significant
2765	GO_RESPONSE_TO_ALKALOID	-1.14	0.68	0	0	0	not significant
2766	REACTOME_PI_METABOLISM	-1.14	0.68	0	0	0	not significant
2767	SESTO_RESPONSE_TO_UV_C7	-1.14	0.68	0	0	0	not significant
2768	ZHAN_V2_LATE_DIFFERENTIATION_GENES	-1.14	0.67	0	0	0	not significant
2769	FONTAINE_FOLLICULAR_THYROID_ADENOMA_DN	-1.14	0.64	0	0	0	not significant
2770	GO_PROTEIN_TRANSPORT_ALONG_MICROTUBULE	-1.14	0.64	0	0	0	not significant
2771	GO_RESPONSE_TO_AMMONIUM_ION	-1.14	0.63	0	0	0	not significant
2772	BIOCARTA_TNFR1_PATHWAY	-1.14	0.6	0	0	0	not significant
2773	GO_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.14	0.6	0	0	0	not significant
2774	GO_POSITIVE_REGULATION_OF_VIRAL_LIFE_CYCLE	-1.14	0.6	0	0	0	not significant
2775	GO_ASTROCYTE_DIFFERENTIATION	-1.14	0.59	0	0	0	not significant
2776	LIN_MELANOMA_COPY_NUMBER_DN	-1.14	0.59	0	0	0	not significant
2777	GO_CEREBELLAR_CORTEX_DEVELOPMENT	-1.14	0.58	0	0	0	not significant
2778	GO_DYNEIN_COMPLEX	-1.14	0.58	0	0	0	not significant
2779	GO_ENDOCHONDRAL_BONE_MORPHOGENESIS	-1.14	0.58	0	0	0	not significant
2780	SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS	-1.14	0.57	0	0	0	not significant
2781	GO_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	-1.14	0.56	0	0	0	not significant
2782	WHITEHURST_PACLITAXEL_SENSITIVITY	-1.14	0.56	0	0	0	not significant
2783	YIH_RESPONSE_TO_ARSENITE_C3	-1.14	0.56	0	0	0	not significant
2784	GO_MITOCHONDRIAL_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	-1.14	0.55	0	0	0	not significant
2785	GO_NURD_COMPLEX	-1.14	0.55	0	0	0	not significant
2786	GO_PHOSPHATIDYLINOSITOL_3_KINASE_REGULATOR_ACTIVITY	-1.14	0.55	0	0	0	not significant
2787	GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_STIMULUS	-1.14	0.54	0	0	0	not significant
2788	PID_SYNDECAN_4_PATHWAY	-1.14	0.54	0	0	0	not significant
2789	REACTOME_VEGFR2_MEDIATED_CELL_PROLIFERATION	-1.14	0.54	0	0	0	not significant
2790	GO_REGULATION_OF_PLATELET_ACTIVATION	-1.14	0.53	0	0	0	not significant
2791	KEGG_BETA_ALANINE_METABOLISM	-1.14	0.53	0	0	0	not significant
2792	CHR14Q31	-1.14	0.52	0	0	0	not significant
2793	GO_GROWTH_CONE_PART	-1.14	0.52	0	0	0	not significant
2794	GO_NUCLEAR_CYCLIN_DEPENDENT_PROTEIN_KINASE_HOLOENZYME_COMPLEX	-1.14	0.52	0	0	0	not significant
2795	CHANG_POU5F1_TARGETS_DN	-1.14	0.51	0	0	0	not significant
2796	GO_CLATHRIN_COMPLEX	-1.14	0.51	0	0	0	not significant
2797	GO_EPITHELIAL_CELL_CELL_ADHESION	-1.14	0.51	0	0	0	not significant
2798	GO_NEUROTRANSMITTER_CATABOLIC_PROCESS	-1.14	0.51	0	0	0	not significant
2799	PARK_HSC_VS_MULTIPOTENT_PROGENITORS_DN	-1.14	0.51	0	0	0	not significant
2800	RAMPON_ENRICHED_LEARNING_ENVIRONMENT_EARLY_DN	-1.14	0.51	0	0	0	not significant
2801	REACTOME_SEMA3A_PAK_DEPENDENT_AXON_REPULSION	-1.14	0.51	0	0	0	not significant
2802	BIOCARTA_HIF_PATHWAY	-1.14	0.5	0	0	0	not significant
2803	REACTOME_MECP2_REGULATES_NEURONAL_RECEPTORS_AND_CHANNELS	-1.14	0.5	0	0	0	not significant
2804	SCHURINGA_STAT5A_TARGETS_UP	-1.14	0.5	0	0	0	not significant
2805	GO_FOREBRAIN_NEURON_DEVELOPMENT	-1.14	0.49	0	0	0	not significant
2806	GO_LAMELLIPODIUM_MORPHOGENESIS	-1.14	0.49	0	0	0	not significant
2807	GO_POSITIVE_REGULATION_OF_ATP_BIOSYNTHETIC_PROCESS	-1.14	0.49	0	0	0	not significant
2808	GO_RETINOID_X_RECEPTOR_BINDING	-1.14	0.49	0	0	0	not significant
2809	GO_CYTIDYLYLTRANSFERASE_ACTIVITY	-1.14	0.48	0	0	0	not significant
2810	GO_ECTODERMAL_PLACODE_DEVELOPMENT	-1.14	0.48	0	0	0	not significant
2811	GO_CENTRIOLAR_SUBDISTAL_APPENDAGE	-1.14	0.47	0	0	0	not significant
2812	GO_POSTSYNAPTIC_MODULATION_OF_CHEMICAL_SYNAPTIC_TRANSMISSION	-1.14	0.47	0	0	0	not significant
2813	GO_BLASTODERM_SEGMENTATION	-1.14	0.45	0	0	0	not significant
2814	GO_SATELLITE_DNA_BINDING	-1.14	0.44	0	0	0	not significant
2815	GO_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	-1.13	1.55	0	0	0	not significant
2816	DOUGLAS_BMI1_TARGETS_UP	-1.13	1.12	0	0	0	not significant
2817	GABRIELY_MIR21_TARGETS	-1.13	1.11	0	0	0	not significant
2818	GO_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	-1.13	1.05	0	0	0	not significant
2819	GO_REGULATION_OF_NEURON_DIFFERENTIATION	-1.13	1.03	0	0	0	not significant
2820	VANTVEER_BREAST_CANCER_ESR1_DN	-1.13	0.86	0	0	0	not significant
2821	REACTOME_S_PHASE	-1.13	0.81	0	0	0	not significant
2822	SHEPARD_BMYB_MORPHOLINO_DN	-1.13	0.77	0	0	0	not significant

2823	DARWICHE_SQUAMOUS_CELL_CARCINOMA_UP	-1.13	0.76	0	0	0	not significant
2824	HALLMARK_UNFOLDED_PROTEIN_RESPONSE	-1.13	0.76	0	0	0	not significant
2825	HOSHIDA_LIVER_CANCER_SUBCLASS_S2	-1.13	0.72	0	0	0	not significant
2826	GO_ISOMERASE_ACTIVITY	-1.13	0.71	0	0	0	not significant
2827	GO_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	-1.13	0.67	0	0	0	not significant
2828	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_TRANS	-1.13	0.66	0	0	0	not significant
2829	GO_COPII_COATED_VESICLE_BUDDING	-1.13	0.66	0	0	0	not significant
2830	NABA_SECRETED_FACTORS	-1.13	0.66	0	0	0	not significant
2831	WANG_ESOPHAGUS_CANCER_VS_NORMAL_DN	-1.13	0.65	0	0	0	not significant
2832	PID_ATR_PATHWAY	-1.13	0.64	0	0	0	not significant
2833	WNT_SIGNALING	-1.13	0.64	0	0	0	not significant
2834	PID_ERBB1_INTERNALIZATION_PATHWAY	-1.13	0.63	0	0	0	not significant
2835	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5	-1.13	0.63	0	0	0	not significant
2836	GO_MESODERM_DEVELOPMENT	-1.13	0.62	0	0	0	not significant
2837	GO_REGULATION_OF_PROTEIN_IMPORT	-1.13	0.62	0	0	0	not significant
2838	GO_RECEPTOR_INTERNALIZATION	-1.13	0.61	0	0	0	not significant
2839	GO_RNA_POLYMERASE_BINDING	-1.13	0.61	0	0	0	not significant
2840	GO_MYELIN_SHEATH	-1.13	0.6	0	0	0	not significant
2841	PID_SHP2_PATHWAY	-1.13	0.59	0	0	0	not significant
2842	GO_MIRNA_BINDING	-1.13	0.58	0	0	0	not significant
2843	BIOCARTA_MEF2D_PATHWAY	-1.13	0.55	0	0	0	not significant
2844	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_	-1.13	0.55	0	0	0	not significant
2845	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_UP	-1.13	0.54	0	0	0	not significant
2846	GO_NEGATIVE_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	-1.13	0.53	0	0	0	not significant
2847	GO_PRE_MRNA_BINDING	-1.13	0.53	0	0	0	not significant
2848	PID_CDC42_REG_PATHWAY	-1.13	0.53	0	0	0	not significant
2849	GO_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	-1.13	0.52	0	0	0	not significant
2850	MARCINIAK_ER_STRESS_RESPONSE_VIA_CHOP	-1.13	0.52	0	0	0	not significant
2851	GO_NEURONAL_STEM_CELL_POPULATION_MAINTENANCE	-1.13	0.51	0	0	0	not significant
2852	GO_REGULATION_OF_DIGESTIVE_SYSTEM_PROCESS	-1.13	0.51	0	0	0	not significant
2853	GO_REGULATION_OF_RIBONUCLEASE_ACTIVITY	-1.13	0.51	0	0	0	not significant
2854	GO_GOLGI_LOCALIZATION	-1.13	0.49	0	0	0	not significant
2855	MAINA_VHL_TARGETS_DN	-1.13	0.49	0	0	0	not significant
2856	KEGG_NON_HOMOLOGOUS_END_JOINING	-1.13	0.48	0	0	0	not significant
2857	CHRXQ11	-1.13	0.47	0	0	0	not significant
2858	GO_AXONEMAL_DYNEIN_COMPLEX_ASSEMBLY	-1.13	0.47	0	0	0	not significant
2859	GO_PURINE_NUCLEOSIDE_DIPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.13	0.47	0	0	0	not significant
2860	GO_REGULATION_OF_HISTONE_UBIQUITINATION	-1.13	0.47	0	0	0	not significant
2861	HAHTOLA_MYCOSIS_FUNGOIDES_UP	-1.13	0.47	0	0	0	not significant
2862	GO_ALDEHYDE_BIOSYNTHETIC_PROCESS	-1.13	0.46	0	0	0	not significant
2863	GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY_PHOSPHOTRANSFERASES	-1.13	0.46	0	0	0	not significant
2864	GO_POSITIVE_REGULATION_OF_GONAD_DEVELOPMENT	-1.13	0.46	0	0	0	not significant
2865	GO_REGULATION_OF_LOW_DENSITY_LIPOPROTEIN_PARTICLE_CLEARANCE	-1.13	0.46	0	0	0	not significant
2866	REACTOME_MET_RECEPTOR_RECYCLING	-1.13	0.46	0	0	0	not significant
2867	GO_REGULATION_OF_HIGH_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	-1.13	0.45	0	0	0	not significant
2868	GO_RIBOSOMAL_PROTEIN_S6_KINASE_ACTIVITY	-1.13	0.45	0	0	0	not significant
2869	GO_TRANSLATION_ACTIVATOR_ACTIVITY	-1.13	0.45	0	0	0	not significant
2870	GO_TRNA_PSEUDOURIDINE_SYNTHESIS	-1.13	0.45	0	0	0	not significant
2871	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CHROMATIN	-1.13	0.44	0	0	0	not significant
2872	MATZUK_EMBRYONIC_GERM_CELL	-1.13	0.44	0	0	0	not significant
2873	GO_REGULATION_OF_T_CIRCLE_FORMATION	-1.13	0.43	0	0	0	not significant
2874	REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_DIFFE	-1.13	0.43	0	0	0	not significant
2875	GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	-1.12	1.85	0	0	0	not significant
2876	GO_MOLECULAR_FUNCTION_REGULATOR	-1.12	1.73	0	0	0	not significant
2877	GO_REGULATION_OF_TRANSFERASE_ACTIVITY	-1.12	1.44	0	0	0	not significant
2878	REACTOME_SIGNALING_BY_INTERLEUKINS	-1.12	1.03	0	0	0	not significant
2879	GO_NEGATIVE_REGULATION_OF_PHOSPHORYLATION	-1.12	0.98	0	0	0	not significant
2880	GO_ENZYME_ACTIVATOR_ACTIVITY	-1.12	0.95	0	0	0	not significant
2881	GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	-1.12	0.9	0	0	0	not significant
2882	GO_CYTOSOLIC_PART	-1.12	0.89	0	0	0	not significant
2883	FARMER_BREAST_CANCER_APOCRINE_VS_BASAL	-1.12	0.78	0	0	0	not significant
2884	GO_POSITIVE_REGULATION_OF_GROWTH	-1.12	0.75	0	0	0	not significant
2885	GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY	-1.12	0.74	0	0	0	not significant
2886	ESC_J1_UP_LATE.V1_DN	-1.12	0.71	0	0	0	not significant
2887	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_UP	-1.12	0.69	0	0	0	not significant
2888	GO_NUCLEOSOME_BINDING	-1.12	0.68	0	0	0	not significant
2889	GO_MUSCLE_CELL_PROLIFERATION	-1.12	0.67	0	0	0	not significant
2890	GO_UBIQUITIN_LIKE_PROTEIN_SPECIFIC_PROTEASE_ACTIVITY	-1.12	0.67	0	0	0	not significant
2891	GO_STRIATED_MUSCLE_CONTRACTION	-1.12	0.64	0	0	0	not significant
2892	GO_CELLULAR_RESPONSE_TO_LIGHT_STIMULUS	-1.12	0.61	0	0	0	not significant
2893	GO_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	-1.12	0.6	0	0	0	not significant
2894	PID_AR_PATHWAY	-1.12	0.6	0	0	0	not significant
2895	GO_METENCEPHALON_DEVELOPMENT	-1.12	0.59	0	0	0	not significant
2896	GO_OOGENESIS	-1.12	0.59	0	0	0	not significant
2897	GO_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	-1.12	0.59	0	0	0	not significant
2898	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GROWTH_FAC	-1.12	0.59	0	0	0	not significant
2899	GO_ORGANIC_HYDROXY_COMPOUND_CATABOLIC_PROCESS	-1.12	0.58	0	0	0	not significant
2900	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_UP	-1.12	0.57	0	0	0	not significant
2901	GO_ADULT_LOCOMOTORY_BEHAVIOR	-1.12	0.56	0	0	0	not significant
2902	GO_MICROTUBULE_BUNDLE_FORMATION	-1.12	0.56	0	0	0	not significant
2903	GO_RESPONSE_TO_ESTROGEN	-1.12	0.56	0	0	0	not significant
2904	CHR19P12	-1.12	0.55	0	0	0	not significant
2905	GO_KINESIN_BINDING	-1.12	0.55	0	0	0	not significant
2906	GO_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPRE	-1.12	0.55	0	0	0	not significant
2907	BEIER_GLIOMA_STEM_CELL_UP	-1.12	0.54	0	0	0	not significant
2908	GO_ALCOHOL_CATABOLIC_PROCESS	-1.12	0.53	0	0	0	not significant
2909	GO_LIVER_REGENERATION	-1.12	0.53	0	0	0	not significant
2910	GO_POSITIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	-1.12	0.53	0	0	0	not significant
2911	GO_STEM_CELL_DIVISION	-1.12	0.53	0	0	0	not significant
2912	WU_HBX_TARGETS_3_UP	-1.12	0.53	0	0	0	not significant
2913	BIOCARTA_CREB_PATHWAY	-1.12	0.52	0	0	0	not significant
2914	CHR2P15	-1.12	0.52	0	0	0	not significant
2915	GO_CYTOKINETIC_PROCESS	-1.12	0.52	0	0	0	not significant
2916	GO_DNA_BINDING_BENDING	-1.12	0.51	0	0	0	not significant
2917	GO_SYNAPTONEMAL_COMPLEX_ORGANIZATION	-1.12	0.51	0	0	0	not significant
2918	GO_PYRIMIDINE_RIBONUCLEOTIDE_BIOSYNTHETIC_PROCESS	-1.12	0.5	0	0	0	not significant
2919	GO_TAU_PROTEIN_KINASE_ACTIVITY	-1.12	0.5	0	0	0	not significant
2920	WILLERT_WNT_SIGNALING	-1.12	0.5	0	0	0	not significant
2921	WHITE_NEUROBLASTOMA_WITH_1P36.3_DELETION	-1.12	0.49	0	0	0	not significant
2922	BIOCARTA_GSK3_PATHWAY	-1.12	0.48	0	0	0	not significant
2923	BOYERINAS_ONCOFETAL_TARGETS_OF_LET7A1	-1.12	0.48	0	0	0	not significant
2924	GO_TRNA_TRANSCRIPTION	-1.12	0.48	0	0	0	not significant
2925	BIOCARTA_IRES_PATHWAY	-1.12	0.47	0	0	0	not significant
2926	CHR5Q34	-1.12	0.47	0	0	0	not significant
2927	GO_CAMP_DEPENDENT_PROTEIN_KINASE_COMPLEX	-1.12	0.47	0	0	0	not significant
2928	GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_E_STIMULUS	-1.12	0.47	0	0	0	not significant
2929	GO_EXOCYST	-1.12	0.47	0	0	0	not significant
2930	GO_NEGATIVE_REGULATION_BY_HOST_OF_VIRAL_TRANSCRIPTION	-1.12	0.47	0	0	0	not significant
2931	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOSIS	-1.12	0.46	0	0	0	not significant

2932	GO_S100_PROTEIN_BINDING	-1.12	0.46	0	0	0	not significant
2933	REACTOME_NONCANONICAL_ACTIVATION_OF_NOTCH3	-1.12	0.46	0	0	0	not significant
2934	GO_EMBRYONIC_VISCEROCRANIUM_MORPHOGENESIS	-1.12	0.45	0	0	0	not significant
2935	GO_LONG_CHAIN_FATTY_ACID_TRANSPORTER_ACTIVITY	-1.12	0.45	0	0	0	not significant
2936	GO_MRE11_COMPLEX	-1.12	0.45	0	0	0	not significant
2937	GO_NEGATIVE_REGULATION_OF_MEGAKARYOCYTE_DIFFERENTIATION	-1.12	0.45	0	0	0	not significant
2938	WU_APOPTOSIS_BY_CDKN1A_NOT_VIA_TP53	-1.12	0.45	0	0	0	not significant
2939	GO_CDP_CHOLINE_PATHWAY	-1.12	0.44	0	0	0	not significant
2940	GO_GAS_HOMEOSTASIS	-1.12	0.44	0	0	0	not significant
2941	GO_REGULATION_OF_HISTONE_H3_K36_METHYLATION	-1.12	0.44	0	0	0	not significant
2942	REACTOME_OAS_ANTIVIRAL_RESPONSE	-1.12	0.44	0	0	0	not significant
2943	GO_TETRAHYDROFOLATE_BIOSYNTHETIC_PROCESS	-1.12	0.43	0	0	0	not significant
2944	REACTOME_RUNX3_REGULATES_P14_ARF	-1.12	0.43	0	0	0	not significant
2945	GO_POSITIVE_REGULATION_OF_MOLECULAR_FUNCTION	-1.11	4	0	0	0	not significant
2946	NUYTTEN_EZH2_TARGETS_DN	-1.11	1.73	0	0	0	not significant
2947	GO_PEPTIDYL_AMINO_ACID_MODIFICATION	-1.11	1.57	0	0	0	not significant
2948	GO_ENVELOPE	-1.11	1.32	0	0	0	not significant
2949	PUJANA_BRCA2_PCC_NETWORK	-1.11	1.19	0	0	0	not significant
2950	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN	-1.11	1.01	0	0	0	not significant
2951	GO_POSITIVE_REGULATION_OF_KINASE_ACTIVITY	-1.11	0.85	0	0	0	not significant
2952	REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES	-1.11	0.84	0	0	0	not significant
2953	KAAB_HEART_ATRIUM_VS_VENTRICLE_DN	-1.11	0.82	0	0	0	not significant
2954	GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	-1.11	0.79	0	0	0	not significant
2955	GO_PROTEIN_POLYMERIZATION	-1.11	0.79	0	0	0	not significant
2956	LEI_MYB_TARGETS	-1.11	0.78	0	0	0	not significant
2957	GO_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	-1.11	0.76	0	0	0	not significant
2958	GO_VIRAL_GENE_EXPRESSION	-1.11	0.76	0	0	0	not significant
2959	GO_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_COMPLEX	-1.11	0.73	0	0	0	not significant
2960	CYCLIN_D1_KE_.V1_UP	-1.11	0.68	0	0	0	not significant
2961	GO_VESICLE_TARGETING	-1.11	0.67	0	0	0	not significant
2962	GO_UROGENITAL_SYSTEM_DEVELOPMENT	-1.11	0.66	0	0	0	not significant
2963	MCBRYAN_PUBERTAL_BREAST_4_5WK_DN	-1.11	0.65	0	0	0	not significant
2964	DARWICHE_PAPILLOMA_RISK_HIGH_UP	-1.11	0.64	0	0	0	not significant
2965	GO_VESICLE_BUDDING_FROM_MEMBRANE	-1.11	0.63	0	0	0	not significant
2966	GO_ENSHEATHMENT_OF_NEURONS	-1.11	0.6	0	0	0	not significant
2967	GO_HISTONE_METHYLTRANSFERASE_ACTIVITY	-1.11	0.59	0	0	0	not significant
2968	GO_PROTEIN_LOCALIZATION_TO_CYTOSKELETON	-1.11	0.59	0	0	0	not significant
2969	REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	-1.11	0.59	0	0	0	not significant
2970	GO_GDP_BINDING	-1.11	0.57	0	0	0	not significant
2971	GO_MICROTUBULE_POLYMERIZATION	-1.11	0.57	0	0	0	not significant
2972	GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_	-1.11	0.57	0	0	0	not significant
2973	TCGA_GLIOBLASTOMA_COPY_NUMBER_UP	-1.11	0.57	0	0	0	not significant
2974	LIAO_HAVE_SOX4_BINDING_SITES	-1.11	0.56	0	0	0	not significant
2975	PARK_HSC_AND_MULTIPOTENT_PROGENITORS	-1.11	0.56	0	0	0	not significant
2976	REACTOME_COPII_MEDIATED_VESICLE_TRANSPORT	-1.11	0.55	0	0	0	not significant
2977	CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY	-1.11	0.54	0	0	0	not significant
2978	GO_MYD88_DEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	-1.11	0.53	0	0	0	not significant
2979	GO_POSITIVE_REGULATION_OF_PROTEIN_IMPORT	-1.11	0.53	0	0	0	not significant
2980	PID_ALPHA_SYNUCLEIN_PATHWAY	-1.11	0.53	0	0	0	not significant
2981	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	-1.11	0.52	0	0	0	not significant
2982	GO_NEGATIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	-1.11	0.52	0	0	0	not significant
2983	GO_PEPTIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.11	0.52	0	0	0	not significant
2984	REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	-1.11	0.52	0	0	0	not significant
2985	BIOCARTA_VEGF_PATHWAY	-1.11	0.51	0	0	0	not significant
2986	GO_POSITIVE_REGULATION_OF_INTERFERON_ALPHA_PRODUCTION	-1.11	0.51	0	0	0	not significant
2987	GO_POSITIVE_REGULATION_OF_TISSUE_REMODELING	-1.11	0.51	0	0	0	not significant
2988	PID_DELTA_NP63_PATHWAY	-1.11	0.51	0	0	0	not significant
2989	GO_MRNA_METHYLATION	-1.11	0.5	0	0	0	not significant
2990	GO_POSITIVE_REGULATION_OF_EPIDERMIS_DEVELOPMENT	-1.11	0.5	0	0	0	not significant
2991	GO_OOCYTE_MATURATION	-1.11	0.49	0	0	0	not significant
2992	GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE	-1.11	0.49	0	0	0	not significant
2993	GO_ANTIBIOTIC_CATABOLIC_PROCESS	-1.11	0.48	0	0	0	not significant
2994	GO_NEGATIVE_REGULATION_OF_COAGULATION	-1.11	0.48	0	0	0	not significant
2995	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	-1.11	0.48	0	0	0	not significant
2996	GO_BRANCHING_INVOLVED_IN_MAMMARY_GLAND_DUCT_MORPHOGENESIS	-1.11	0.47	0	0	0	not significant
2997	GO_DNA_INTEGRATION	-1.11	0.47	0	0	0	not significant
2998	GO_GLUCAN_CATABOLIC_PROCESS	-1.11	0.47	0	0	0	not significant
2999	GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	-1.11	0.47	0	0	0	not significant
3000	REACTOME_CHREBP_ACTIVATES_METABOLIC_GENE_EXPRESSION	-1.11	0.46	0	0	0	not significant
3001	GO_LONG_CHAIN_FATTY_ACID_COA_LIGASE_ACTIVITY	-1.11	0.45	0	0	0	not significant
3002	IRITANI_MAD1_TARGETS_UP	-1.11	0.45	0	0	0	not significant
3003	REACTOME_WNT5A_DEPENDENT_INTERNALIZATION_OF_FZD2_FZD5_AND_ROR2	-1.11	0.45	0	0	0	not significant
3004	GO_MOTILE_CILIUM_ASSEMBLY	-1.11	0.44	0	0	0	not significant
3005	GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGNALING_PAT	-1.11	0.44	0	0	0	not significant
3006	GO_RESPONSE_TO_EPINEPHRINE	-1.11	0.44	0	0	0	not significant
3007	KEGG_CIRCADIAN_RHYTHM_MAMMAL	-1.11	0.44	0	0	0	not significant
3008	ZEILSTRA_CD44_TARGETS_DN	-1.11	0.44	0	0	0	not significant
3009	GO_NSL_COMPLEX	-1.11	0.43	0	0	0	not significant
3010	GO_OXIDIZED_BASE_LESION_DNA_N_GLYCOSYLASE_ACTIVITY	-1.11	0.41	0	0	0	not significant
3011	GO_CELLULAR_MACROMOLECULE_LOCALIZATION	-1.10	4	0	0	0	not significant
3012	GO_MICROTUBULE_ORGANIZING_CENTER	-1.10	1.11	0	0	0	not significant
3013	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_TP53	-1.10	0.92	0	0	0	not significant
3014	GO_PROTEIN_HETERODIMERIZATION_ACTIVITY	-1.10	0.83	0	0	0	not significant
3015	REACTOME_CHROMATIN_ORGANIZATION	-1.10	0.75	0	0	0	not significant
3016	GO_CENTRIOLE	-1.10	0.65	0	0	0	not significant
3017	GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	-1.10	0.64	0	0	0	not significant
3018	GO_LARGE_RIBOSOMAL_SUBUNIT	-1.10	0.62	0	0	0	not significant
3019	GO_NEGATIVE_REGULATION_OF_PROTEIN_BINDING	-1.10	0.62	0	0	0	not significant
3020	MCBRYAN_PUBERTAL_BREAST_5_6WK_DN	-1.10	0.62	0	0	0	not significant
3021	GO_CELLULAR_COMPONENT_ASSEMBLY_INVOLVED_IN_MORPHOGENESIS	-1.10	0.61	0	0	0	not significant
3022	GO_MUSCLE_CELL_DEVELOPMENT	-1.10	0.61	0	0	0	not significant
3023	GO_NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	-1.10	0.59	0	0	0	not significant
3024	BRUECKNER_TARGETS_OF_MIRLET7A3_DN	-1.10	0.58	0	0	0	not significant
3025	GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	-1.10	0.58	0	0	0	not significant
3026	IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR	-1.10	0.57	0	0	0	not significant
3027	GO_NEPHRON_DEVELOPMENT	-1.10	0.56	0	0	0	not significant
3028	MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_DN	-1.10	0.56	0	0	0	not significant
3029	GO_MEIOSIS_I_CELL_CYCLE_PROCESS	-1.10	0.53	0	0	0	not significant
3030	GO_POSITIVE_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	-1.10	0.53	0	0	0	not significant
3031	GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	-1.10	0.52	0	0	0	not significant
3032	MARIADASON_REGULATED_BY_HISTONE_ACETYLATION_DN	-1.10	0.52	0	0	0	not significant
3033	MILI_PSEUDOPODIA	-1.10	0.52	0	0	0	not significant
3034	REACTOME_SIGNALING_BY_TYPE_1_INSULIN_LIKE_GROWTH_FACTOR_1_RECEPT	-1.10	0.52	0	0	0	not significant
3035	GUO_HEX_TARGETS_DN	-1.10	0.51	0	0	0	not significant
3036	HOELZEL_NF1_TARGETS_UP	-1.10	0.51	0	0	0	not significant
3037	SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN	-1.10	0.51	0	0	0	not significant
3038	GO_INO80_TYPE_COMPLEX	-1.10	0.5	0	0	0	not significant
3039	KEGG_MELANOMA	-1.10	0.5	0	0	0	not significant
3040	REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	-1.10	0.5	0	0	0	not significant

3041	AZARE_STAT3_TARGETS	-1.10	0.48	0	0	0	not significant
3042	GO_INOSITOL_PHOSPHATE_MEDIATED_SIGNALING	-1.10	0.48	0	0	0	not significant
3043	YAMASHITA_LIVER_CANCER_STEM_CELL_UP	-1.10	0.48	0	0	0	not significant
3044	GO_PHOSPHATIDYLINOSITOL_MONOPHOSPHATE_PHOSPHATASE_ACTIVITY	-1.10	0.47	0	0	0	not significant
3045	GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_TRANSLATION	-1.10	0.47	0	0	0	not significant
3046	PID_SMAD2_3PATHWAY	-1.10	0.47	0	0	0	not significant
3047	REACTOME_DEPOLYMERISATION_OF_THE_NUCLEAR_LAMINA	-1.10	0.47	0	0	0	not significant
3048	KORKOLA_YOLK_SAC_TUMOR_UP	-1.10	0.46	0	0	0	not significant
3049	GO_ACTIVIN_BINDING	-1.10	0.45	0	0	0	not significant
3050	GO_CYTOSKELETAL_ANCHORING_AT_PLASMA_MEMBRANE	-1.10	0.45	0	0	0	not significant
3051	GO_STARTLE_RESPONSE	-1.10	0.44	0	0	0	not significant
3052	PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN	-1.10	0.44	0	0	0	not significant
3053	REACTOME_PROTEIN_METHYLATION	-1.10	0.44	0	0	0	not significant
3054	GO_CELLULAR_HYPEROSMOTIC_RESPONSE	-1.10	0.43	0	0	0	not significant
3055	GO_INTERLEUKIN_5_PRODUCTION	-1.10	0.43	0	0	0	not significant
3056	GO_PHOSPHOSERINE_RESIDUE_BINDING	-1.10	0.43	0	0	0	not significant
3057	GO_SECRETORY_GRANULE_LOCALIZATION	-1.10	0.43	0	0	0	not significant
3058	GO_UMP_BIOSYNTHETIC_PROCESS	-1.10	0.43	0	0	0	not significant
3059	GO_XYLULOSE_5_PHOSPHATE_BIOSYNTHETIC_PROCESS	-1.10	0.43	0	0	0	not significant
3060	GO_ACTIN_CROSSLINK_FORMATION	-1.10	0.42	0	0	0	not significant
3061	GO_POSITIVE_REGULATION_OF_PROTEIN_HOMODIMERIZATION_ACTIVITY	-1.10	0.42	0	0	0	not significant
3062	GO_RESPONSE_TO_STIMULUS_INVOLVED_IN_REGULATION_OF_MUSCLE_ADAPTAT	-1.10	0.42	0	0	0	not significant
3063	GO_SPERM_CHROMATIN_CONDENSATION	-1.10	0.42	0	0	0	not significant
3064	GO_TRANSCRIPTION_FACTOR_TFIIH_CORE_COMPLEX	-1.10	0.42	0	0	0	not significant
3065	GO_TRANSCRIPTIONAL_PREINITIATION_COMPLEX	-1.10	0.42	0	0	0	not significant
3066	REACTOME_FORMATION_OF_XYLULOSE_5_PHOSPHATE	-1.10	0.42	0	0	0	not significant
3067	THUM_MIR21_TARGETS_HEART_DISEASE_DN	-1.10	0.42	0	0	0	not significant
3068	GO_REGULATION_OF_GLYCOGEN_CATABOLIC_PROCESS	-1.10	0.41	0	0	0	not significant
3069	GO_REGULATION_OF_LIPOPROTEIN_PARTICLE_CLEARANCE	-1.10	0.41	0	0	0	not significant
3070	GO_REGULATION_OF_MESODERM_DEVELOPMENT	-1.10	0.41	0	0	0	not significant
3071	GO_UBIQUINONE_BINDING	-1.10	0.41	0	0	0	not significant
3072	PETRETTO_BLOOD_PRESSURE_UP	-1.10	0.41	0	0	0	not significant
3073	GO_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS_BY_REGULATION_	-1.10	0.4	0	0	0	not significant
3074	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_MONOCYTE_DN	-1.10	0.4	0	0	0	not significant
3075	GO_CERAMIDE_1_PHOSPHATE_BINDING	-1.10	0.39	0	0	0	not significant
3076	GO_COVALENT_CHROMATIN_MODIFICATION	-1.09	1.01	0	0	0	not significant
3077	OSMAN_BLADDER_CANCER_UP	-1.09	0.89	0	0	0	not significant
3078	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF	-1.09	0.79	0	0	0	not significant
3079	GO_UBIQUITIN_LIGASE_COMPLEX	-1.09	0.75	0	0	0	not significant
3080	RAY_TUMORIGENESIS_BY_ERBB2_CDC25A_DN	-1.09	0.71	0	0	0	not significant
3081	REACTOME_NEURONAL_SYSTEM	-1.09	0.69	0	0	0	not significant
3082	GO_REGULATION_OF_PROTEIN_BINDING	-1.09	0.66	0	0	0	not significant
3083	GO_RIBONUCLEOPROTEIN_GRANULE	-1.09	0.66	0	0	0	not significant
3084	GO_CHROMATIN_ASSEMBLY	-1.09	0.63	0	0	0	not significant
3085	GO_PROTEIN_C_TERMINUS_BINDING	-1.09	0.63	0	0	0	not significant
3086	GO_STRIATED_MUSCLE_CELL_DIFFERENTIATION	-1.09	0.63	0	0	0	not significant
3087	CHR11P15	-1.09	0.62	0	0	0	not significant
3088	GO_PEPTIDE_BINDING	-1.09	0.59	0	0	0	not significant
3089	HALLMARK_PROTEIN_SECRETION	-1.09	0.59	0	0	0	not significant
3090	REACTOME_RECRUITMENT_OF_NUMA_TO_MITOTIC_CENTROSOMES	-1.09	0.59	0	0	0	not significant
3091	GO_RIBOSE_PHOSPHATE_BIOSYNTHETIC_PROCESS	-1.09	0.58	0	0	0	not significant
3092	GO_CHANNEL_REGULATOR_ACTIVITY	-1.09	0.56	0	0	0	not significant
3093	GO_CHROMATIN_REMODELING_AT_CENTROMERE	-1.09	0.55	0	0	0	not significant
3094	GO_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	-1.09	0.55	0	0	0	not significant
3095	HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	-1.09	0.55	0	0	0	not significant
3096	REACTOME_SIGNALING_BY_TGF_BETA_FAMILY_MEMBERS	-1.09	0.55	0	0	0	not significant
3097	GO_CYCLIN_DEPENDENT_PROTEIN_KINASE_HOLOENZYME_COMPLEX	-1.09	0.53	0	0	0	not significant
3098	YAGI_AML_WITH_T_9_11_TRANSLOCATION	-1.09	0.53	0	0	0	not significant
3099	GO_STEM_CELL_PROLIFERATION	-1.09	0.52	0	0	0	not significant
3100	GO_TISSUE_REGENERATION	-1.09	0.52	0	0	0	not significant
3101	GO_TIGHT_JUNCTION_ORGANIZATION	-1.09	0.51	0	0	0	not significant
3102	NADLER_HYPERGLYCEMIA_AT_OBESITY	-1.09	0.51	0	0	0	not significant
3103	PID_RET_PATHWAY	-1.09	0.51	0	0	0	not significant
3104	GO_POSITIVE_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-1.09	0.5	0	0	0	not significant
3105	GO_REGULATION_OF_GASTRULATION	-1.09	0.5	0	0	0	not significant
3106	GO_REGULATION_OF_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II	-1.09	0.5	0	0	0	not significant
3107	GO_NEUROBLAST_PROLIFERATION	-1.09	0.49	0	0	0	not significant
3108	HALMOS_CEBPA_TARGETS_DN	-1.09	0.49	0	0	0	not significant
3109	SIG_REGULATION_OF_THE_ACTIN_CYTOSKELETON_BY_RHO_GTPASES	-1.09	0.49	0	0	0	not significant
3110	KIM_TIAL1_TARGETS	-1.09	0.48	0	0	0	not significant
3111	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_YELLOW_DN	-1.09	0.47	0	0	0	not significant
3112	KEGG_DRUG_METABOLISM_OTHER_ENZYMES	-1.09	0.47	0	0	0	not significant
3113	BIOCARTA_CK1_PATHWAY	-1.09	0.46	0	0	0	not significant
3114	BIOCARTA_PITX2_PATHWAY	-1.09	0.46	0	0	0	not significant
3115	CHR12P12	-1.09	0.46	0	0	0	not significant
3116	GO_CELLULAR_RESPONSE_TO_VITAMIN_D	-1.09	0.46	0	0	0	not significant
3117	GO_NEGATIVE_REGULATION_OF_VIRAL_TRANSCRIPTION	-1.09	0.46	0	0	0	not significant
3118	GO_REGULATION_OF_MITOTIC_SPINDLE_ASSEMBLY	-1.09	0.46	0	0	0	not significant
3119	GO_TRANSLATION_REPRESSOR_ACTIVITY_MRNA_REGULATORY_ELEMENT_BINDIN	-1.09	0.46	0	0	0	not significant
3120	LIU_BREAST_CANCER	-1.09	0.46	0	0	0	not significant
3121	REACTOME_BIOTIN_TRANSPORT_AND_METABOLISM	-1.09	0.45	0	0	0	not significant
3122	GO_METANEPHRIC_MESENCHYME_DEVELOPMENT	-1.09	0.44	0	0	0	not significant
3123	REACTOME_SYNTHESIS_OF_PE	-1.09	0.44	0	0	0	not significant
3124	GO_DECIDUALIZATION	-1.09	0.43	0	0	0	not significant
3125	GO_MESENCHYMAL_TO_EPITHELIAL_TRANSITION	-1.09	0.43	0	0	0	not significant
3126	GO_POSITIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_P	-1.09	0.43	0	0	0	not significant
3127	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_5_PRODUCTION	-1.09	0.43	0	0	0	not significant
3128	REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB	-1.09	0.43	0	0	0	not significant
3129	GO_WIDE_PORE_CHANNEL_ACTIVITY	-1.09	0.42	0	0	0	not significant
3130	REACTOME_RUNX3_REGULATES_WNT_SIGNALING	-1.09	0.42	0	0	0	not significant
3131	BIOCARTA_TERC_PATHWAY	-1.09	0.41	0	0	0	not significant
3132	KRISHNAN_FURIN_TARGETS_DN	-1.09	0.41	0	0	0	not significant
3133	RAFFEL_VEGFA_TARGETS_UP	-1.09	0.41	0	0	0	not significant
3134	GO_METANEPHRIC_RENAL_VESICLE_MORPHOGENESIS	-1.09	0.4	0	0	0	not significant
3135	GO_NEURON_FATE_SPECIFICATION	-1.09	0.4	0	0	0	not significant
3136	GO_PARENTAL_BEHAVIOR	-1.09	0.4	0	0	0	not significant
3137	MUNSHI_MULTIPLE_MYELOMA_DN	-1.09	0.4	0	0	0	not significant
3138	GO_CARDIOBLAST_DIFFERENTIATION	-1.09	0.37	0	0	0	not significant
3139	GO_PROTEOLYSIS	-1.08	1.23	0	0	0	not significant
3140	GEORGES_TARGETS_OF_MIR192_AND_MIR215	-1.08	1	0	0	0	not significant
3141	GO_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	-1.08	0.92	0	0	0	not significant
3142	GO_ANATOMICAL_STRUCTURE_HOMEOSTASIS	-1.08	0.74	0	0	0	not significant
3143	GO_POSITIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	-1.08	0.74	0	0	0	not significant
3144	GO_CELL_CELL_SIGNALING_BY_WNT	-1.08	0.73	0	0	0	not significant
3145	GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	-1.08	0.73	0	0	0	not significant
3146	GO_REGULATION_OF_INNATE_IMMUNE_RESPONSE	-1.08	0.7	0	0	0	not significant
3147	REACTOME_CILIUM_ASSEMBLY	-1.08	0.63	0	0	0	not significant
3148	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN	-1.08	0.6	0	0	0	not significant
3149	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	-1.08	0.59	0	0	0	not significant

3150	GO_PROTEIN_ACETYLTRANSFERASE_COMPLEX	-1.08	0.58	0	0	0	not significant
3151	WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN	-1.08	0.58	0	0	0	not significant
3152	REACTOME_DNA_REPLICATION	-1.08	0.55	0	0	0	not significant
3153	REACTOME_SIGNALING_BY_ERBB2	-1.08	0.55	0	0	0	not significant
3154	LIU_NASOPHARYNGEAL_CARCINOMA	-1.08	0.53	0	0	0	not significant
3155	MOOTHA_VOXPHOS	-1.08	0.53	0	0	0	not significant
3156	RB_P107_DN.V1_DN	-1.08	0.53	0	0	0	not significant
3157	GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	-1.08	0.52	0	0	0	not significant
3158	GENTILE_RESPONSE_CLUSTER_D3	-1.08	0.51	0	0	0	not significant
3159	GO_NEURON_MIGRATION	-1.08	0.51	0	0	0	not significant
3160	GO_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	-1.08	0.51	0	0	0	not significant
3161	GO_SIGNAL_TRANSDUCTION_IN_ABSENCE_OF_LIGAND	-1.08	0.51	0	0	0	not significant
3162	REACTOME_NUCLEOSOME_ASSEMBLY	-1.08	0.51	0	0	0	not significant
3163	CHR2Q14	-1.08	0.5	0	0	0	not significant
3164	CHR8P21	-1.08	0.5	0	0	0	not significant
3165	GO_9PLUS2_MOTILE_CILIUM	-1.08	0.5	0	0	0	not significant
3166	GO_BLASTOCYST_DEVELOPMENT	-1.08	0.5	0	0	0	not significant
3167	GO_POSITIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	-1.08	0.5	0	0	0	not significant
3168	GO_PROTEIN_K63_LINKED_UBIQUITINATION	-1.08	0.5	0	0	0	not significant
3169	GO_UBIQUITIN_LIKE_PROTEIN_BINDING	-1.08	0.5	0	0	0	not significant
3170	GO_ENDOPLASMIC_RETICULUM_ORGANIZATION	-1.08	0.49	0	0	0	not significant
3171	GO_STRUCTURAL_CONSTITUENT_OF_CYTOSKELETON	-1.08	0.49	0	0	0	not significant
3172	TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA	-1.08	0.49	0	0	0	not significant
3173	GO_MAIN_AXON	-1.08	0.48	0	0	0	not significant
3174	GO_NEGATIVE_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEI	-1.08	0.48	0	0	0	not significant
3175	GO_REGULATION_OF_MICROTUBULE_POLYMERIZATION	-1.08	0.48	0	0	0	not significant
3176	MARTIN_INTERACT_WITH_HDAC	-1.08	0.47	0	0	0	not significant
3177	REACTOME_CARGO_CONCENTRATION_IN_THE_ER	-1.08	0.47	0	0	0	not significant
3178	GO_LUNG_MORPHOGENESIS	-1.08	0.46	0	0	0	not significant
3179	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_DN	-1.08	0.46	0	0	0	not significant
3180	GO_CUL4_RING_E3_UBIQUITIN_LIGASE_COMPLEX	-1.08	0.45	0	0	0	not significant
3181	GO_GLANDULAR_EPITHELIAL_CELL_DEVELOPMENT	-1.08	0.45	0	0	0	not significant
3182	GO_SYNAPTONEMAL_STRUCTURE	-1.08	0.45	0	0	0	not significant
3183	KEGG_STARCH_AND_SUCROSE_METABOLISM	-1.08	0.45	0	0	0	not significant
3184	GO_DOPAMINE_RECEPTOR_BINDING	-1.08	0.44	0	0	0	not significant
3185	GO_NEGATIVE_REGULATION_OF_MEIOTIC_CELL_CYCLE	-1.08	0.44	0	0	0	not significant
3186	GO_PHYSIOLOGICAL_CARDIAC_MUSCLE_HYPERTROPHY	-1.08	0.44	0	0	0	not significant
3187	GO_POLYOL_CATABOLIC_PROCESS	-1.08	0.44	0	0	0	not significant
3188	REACTOME_GLYCOGEN_SYNTHESIS	-1.08	0.44	0	0	0	not significant
3189	BIOCARTA_EIF4_PATHWAY	-1.08	0.43	0	0	0	not significant
3190	GO_POSITIVE_REGULATION_OF_MACROPHAGE_DIFFERENTIATION	-1.08	0.43	0	0	0	not significant
3191	REACTOME_REDUCTION_OF_CYTOSOLIC_CAPLUSPLUS_LEVELS	-1.08	0.43	0	0	0	not significant
3192	REACTOME_RRNA_PROCESSING_IN_THE_MITOCHONDRION	-1.08	0.43	0	0	0	not significant
3193	GO_ESTABLISHMENT_OF_EPITHELIAL_CELL_APICAL_BASAL_POLARITY	-1.08	0.42	0	0	0	not significant
3194	GO_POSITIVE_REGULATION_OF_HISTONE_H4_ACETYLATION	-1.08	0.42	0	0	0	not significant
3195	GO_CERAMIDE_1_PHOSPHATE_TRANSPORT	-1.08	0.41	0	0	0	not significant
3196	GO_EARLY_ENDOSOME_TO_GOLGI_TRANSPORT	-1.08	0.41	0	0	0	not significant
3197	GO_ENDOTHELIAL_CELL_ACTIVATION	-1.08	0.41	0	0	0	not significant
3198	GO_MYOBLAST_PROLIFERATION	-1.08	0.41	0	0	0	not significant
3199	GO_PHOSPHATIDYLETHANOLAMINE_BIOSYNTHETIC_PROCESS	-1.08	0.41	0	0	0	not significant
3200	GO_PRESYNAPTIC_CYTOSOL	-1.08	0.41	0	0	0	not significant
3201	GO_REGULATION_OF_TRANSLATIONAL_INITIATION_BY_EIF2_ALPHA_PHOSPHORYL	-1.08	0.41	0	0	0	not significant
3202	REACTOME_GAP_JUNCTION_DEGRADATION	-1.08	0.41	0	0	0	not significant
3203	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEOLUS	-1.08	0.4	0	0	0	not significant
3204	GO_RESPONSE_TO_SODIUM_ARSENITE	-1.08	0.4	0	0	0	not significant
3205	GO_RIBOSOME_DISASSEMBLY	-1.08	0.4	0	0	0	not significant
3206	GO_ANDROGEN_BIOSYNTHETIC_PROCESS	-1.08	0.39	0	0	0	not significant
3207	GO_PURINE_NUCLEOTIDE_SALVAGE	-1.08	0.39	0	0	0	not significant
3208	GO_REGULATION_OF_SKELETAL_MUSCLE_CONTRACTION	-1.08	0.39	0	0	0	not significant
3209	REACTOME_SYNTHESIS_OF_WYBUTOSINE_AT_G37_OF_TRNA_PHE	-1.08	0.39	0	0	0	not significant
3210	GO_REGULATION_OF_RECEPTOR_CATABOLIC_PROCESS	-1.08	0.38	0	0	0	not significant
3211	GO_NEGATIVE_REGULATION_OF_MEMBRANE_PERMEABILITY	-1.08	0.37	0	0	0	not significant
3212	GO_PRESYNAPTIC_ENDOCYTIC_ZONE	-1.08	0.35	0	0	0	not significant
3213	GO_EMBRYO_DEVELOPMENT	-1.07	0.96	0	0	0	not significant
3214	GO_SIGNAL_TRANSDUCTION_BY_PROTEIN_PHOSPHORYLATION	-1.07	0.8	0	0	0	not significant
3215	GO_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	-1.07	0.77	0	0	0	not significant
3216	GO_NEGATIVE_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS	-1.07	0.74	0	0	0	not significant
3217	GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	-1.07	0.66	0	0	0	not significant
3218	GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS	-1.07	0.62	0	0	0	not significant
3219	GO_AXON_PART	-1.07	0.6	0	0	0	not significant
3220	GO_NEGATIVE_REGULATION_OF_CELL_DEVELOPMENT	-1.07	0.6	0	0	0	not significant
3221	GO_CELLULAR_PROCESS_INVOLVED_IN_REPRODUCTION_IN_MULTICELLULAR_OR	-1.07	0.59	0	0	0	not significant
3222	GO_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONI	-1.07	0.56	0	0	0	not significant
3223	GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	-1.07	0.55	0	0	0	not significant
3224	KAYO_AGING_MUSCLE_UP	-1.07	0.54	0	0	0	not significant
3225	MASSARWEH_TAMOXIFEN_RESISTANCE_DN	-1.07	0.54	0	0	0	not significant
3226	GO_CONTRACTILE_FIBER	-1.07	0.53	0	0	0	not significant
3227	GO_EPIDERMAL_CELL_DIFFERENTIATION	-1.07	0.53	0	0	0	not significant
3228	GO_SMOOTH_MUSCLE_CELL_PROLIFERATION	-1.07	0.53	0	0	0	not significant
3229	GO_PRODUCTION_OF_SMALL_RNA_INVOLVED_IN_GENE_SILENCING_BY_RNA	-1.07	0.52	0	0	0	not significant
3230	GO_PROTEIN_SERINE_THREONINE_PHOSPHATASE_ACTIVITY	-1.07	0.52	0	0	0	not significant
3231	GO_SYNAPSE_ASSEMBLY	-1.07	0.52	0	0	0	not significant
3232	GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	-1.07	0.51	0	0	0	not significant
3233	FIGUEROA_AML_METHYLATION_CLUSTER_6_UP	-1.07	0.5	0	0	0	not significant
3234	GO_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	-1.07	0.5	0	0	0	not significant
3235	ESC_J1_UP_LATE.V1_UP	-1.07	0.49	0	0	0	not significant
3236	GO_MAP_KINASE_KINASE_KINASE_ACTIVITY	-1.07	0.49	0	0	0	not significant
3237	BONCI_TARGETS_OF_MIR15A_AND_MIR16_1	-1.07	0.48	0	0	0	not significant
3238	GO_HORMONE_BINDING	-1.07	0.48	0	0	0	not significant
3239	GO_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	-1.07	0.46	0	0	0	not significant
3240	HONMA_DOCETAXEL_RESISTANCE	-1.07	0.46	0	0	0	not significant
3241	REACTOME_CD28_CO_STIMULATION	-1.07	0.46	0	0	0	not significant
3242	GO_KINETOCHORE_ORGANIZATION	-1.07	0.45	0	0	0	not significant
3243	REACTOME_SIGNAL_AMPLIFICATION	-1.07	0.45	0	0	0	not significant
3244	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN	-1.07	0.45	0	0	0	not significant
3245	GO_POLY_A_BINDING	-1.07	0.44	0	0	0	not significant
3246	GO_RESPONSE_TO_PLATELET_DERIVED_GROWTH_FACTOR	-1.07	0.44	0	0	0	not significant
3247	ALONSO_METASTASIS_EMT_UP	-1.07	0.43	0	0	0	not significant
3248	BIOCARTA_NO1_PATHWAY	-1.07	0.43	0	0	0	not significant
3249	GO_MRNA_CLEAVAGE_INVOLVED_IN_MRNA_PROCESSING	-1.07	0.43	0	0	0	not significant
3250	GO_SKELETAL_MUSCLE_CONTRACTION	-1.07	0.43	0	0	0	not significant
3251	GO_MUSCLE_CELL_CELLULAR_HOMEOSTASIS	-1.07	0.42	0	0	0	not significant
3252	GO_POST_MRNA_RELEASE_SPLICEOSOMAL_COMPLEX	-1.07	0.42	0	0	0	not significant
3253	REACTOME_TGF_BETA_RECEPTOR_SIGNALING_IN_EMT_EPITHELIAL_TO_MESENC	-1.07	0.42	0	0	0	not significant
3254	GO_COSTAMERE	-1.07	0.41	0	0	0	not significant
3255	GO_NEGATIVE_REGULATION_OF_CELL_SIZE	-1.07	0.41	0	0	0	not significant
3256	GO_NEGATIVE_REGULATION_OF_VIRAL_RELEASE_FROM_HOST_CELL	-1.07	0.41	0	0	0	not significant
3257	MOOTHA_GLUCONEOGENESIS	-1.07	0.41	0	0	0	not significant
3258	REACTOME_ACTIVATION_OF_SMO	-1.07	0.41	0	0	0	not significant

3259	BIOCARTA_BARR_MAPK_PATHWAY	-1.07	0.4	0	0	0	not significant
3260	GO_CHOLESTEROL_CATABOLIC_PROCESS	-1.07	0.4	0	0	0	not significant
3261	GO_DEOXYRIBOSE_PHOSPHATE_CATABOLIC_PROCESS	-1.07	0.4	0	0	0	not significant
3262	GO_EUKARYOTIC_48S_PREINITIATION_COMPLEX	-1.07	0.4	0	0	0	not significant
3263	GO_GTP_BIOSYNTHETIC_PROCESS	-1.07	0.4	0	0	0	not significant
3264	GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_P	-1.07	0.4	0	0	0	not significant
3265	GO_PROTEIN_HEXAMERIZATION	-1.07	0.4	0	0	0	not significant
3266	HINATA_NFKB_TARGETS_KERATINOCYTE_DN	-1.07	0.4	0	0	0	not significant
3267	GO_INTRINSIC_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	-1.07	0.39	0	0	0	not significant
3268	GO_POSITIVE_REGULATION_OF_SISTER_CHROMATID_COHESION	-1.07	0.39	0	0	0	not significant
3269	GO_REGULATION_OF_PROTEIN_HETERODIMERIZATION_ACTIVITY	-1.07	0.39	0	0	0	not significant
3270	GO_RENAL_VESICLE_DEVELOPMENT	-1.07	0.39	0	0	0	not significant
3271	GO_SEX_DETERMINATION	-1.07	0.39	0	0	0	not significant
3272	MATZUK_MATERNAL_EFFECT	-1.07	0.39	0	0	0	not significant
3273	VALK_AML_WITH_11Q23_REARRANGED	-1.07	0.39	0	0	0	not significant
3274	GO_OXALOACETATE_METABOLIC_PROCESS	-1.07	0.38	0	0	0	not significant
3275	GO_TRANSCRIPTION_FACTOR_TFIIIC_COMPLEX	-1.07	0.38	0	0	0	not significant
3276	GO_BONE_TRABECULA_MORPHOGENESIS	-1.07	0.37	0	0	0	not significant
3277	GO_COMMITMENT_COMPLEX	-1.07	0.37	0	0	0	not significant
3278	GO_MSL_COMPLEX	-1.07	0.37	0	0	0	not significant
3279	GO_NEGATIVE_REGULATION_OF_PROTEIN_SUMOYLATION	-1.07	0.37	0	0	0	not significant
3280	INAMURA_LUNG_CANCER_SCC_SUBTYPES_DN	-1.07	0.37	0	0	0	not significant
3281	GO_REGULATION_OF_HYDROLASE_ACTIVITY	-1.06	0.99	0	0	0	not significant
3282	GO_CELLULAR_AMIDE_METABOLIC_PROCESS	-1.06	0.9	0	0	0	not significant
3283	GO_REGULATION_OF_INTRACELLULAR_TRANSPORT	-1.06	0.74	0	0	0	not significant
3284	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN	-1.06	0.64	0	0	0	not significant
3285	STEIN_ESRRA_TARGETS	-1.06	0.64	0	0	0	not significant
3286	GO_MACROMOLECULE_METHYLATION	-1.06	0.58	0	0	0	not significant
3287	GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	-1.06	0.55	0	0	0	not significant
3288	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	-1.06	0.55	0	0	0	not significant
3289	GO_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	-1.06	0.55	0	0	0	not significant
3290	AMIT_EGF_RESPONSE_480_HELA	-1.06	0.54	0	0	0	not significant
3291	E2F1_UP.V1_UP	-1.06	0.53	0	0	0	not significant
3292	GO_PROTEIN_N_TERMINUS_BINDING	-1.06	0.52	0	0	0	not significant
3293	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP	-1.06	0.52	0	0	0	not significant
3294	GO_ELECTRON_TRANSFER_ACTIVITY	-1.06	0.51	0	0	0	not significant
3295	GO_POSITIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	-1.06	0.51	0	0	0	not significant
3296	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN	-1.06	0.5	0	0	0	not significant
3297	REACTOME_REGULATION_OF_LIPID_METABOLISM_BY_PEROXISOME_PROLIFERAT	-1.06	0.5	0	0	0	not significant
3298	E2F3_UP.V1_DN	-1.06	0.49	0	0	0	not significant
3299	GO_PHOSPHATIDYLINOSITOL_METABOLIC_PROCESS	-1.06	0.49	0	0	0	not significant
3300	CHR20Q11	-1.06	0.48	0	0	0	not significant
3301	GO_MRNA_3_UTR_BINDING	-1.06	0.47	0	0	0	not significant
3302	GO_N_ACYLTRANSFERASE_ACTIVITY	-1.06	0.47	0	0	0	not significant
3303	GO_SCAFFOLD_PROTEIN_BINDING	-1.06	0.47	0	0	0	not significant
3304	GO_SOMITOGENESIS	-1.06	0.47	0	0	0	not significant
3305	KEGG_PYRIMIDINE_METABOLISM	-1.06	0.47	0	0	0	not significant
3306	SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_UP	-1.06	0.47	0	0	0	not significant
3307	GO_EMBRYONIC_CRANIAL_SKELETON_MORPHOGENESIS	-1.06	0.46	0	0	0	not significant
3308	JOHANSSON_GLIOMAGENESIS_BY_PDGFB_UP	-1.06	0.46	0	0	0	not significant
3309	PRAMOONJAGO_SOX4_TARGETS_DN	-1.06	0.46	0	0	0	not significant
3310	REACTOME_METABOLISM_OF_NUCLEOTIDES	-1.06	0.46	0	0	0	not significant
3311	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP	-1.06	0.46	0	0	0	not significant
3312	TERAO_AOX4_TARGETS_HG_UP	-1.06	0.45	0	0	0	not significant
3313	GO_HISTONE_MRNA_METABOLIC_PROCESS	-1.06	0.44	0	0	0	not significant
3314	MCCLUNG_DELTA_FOSB_TARGETS_8WK	-1.06	0.44	0	0	0	not significant
3315	REACTOME_MAP2K_AND_MAPK_ACTIVATION	-1.06	0.44	0	0	0	not significant
3316	GO_MIRNA_METABOLIC_PROCESS	-1.06	0.43	0	0	0	not significant
3317	LI_CISPLATIN_RESISTANCE_UP	-1.06	0.43	0	0	0	not significant
3318	MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3	-1.06	0.43	0	0	0	not significant
3319	CHEOK_RESPONSE_TO_HD_MTX_DN	-1.06	0.42	0	0	0	not significant
3320	GO_ATPASE_ACTIVATOR_ACTIVITY	-1.06	0.42	0	0	0	not significant
3321	GO_REGULATION_OF_RNA_POLYMERASE_II_REGULATORY_REGION_SEQUENCE_S	-1.06	0.42	0	0	0	not significant
3322	GO_ACYLGLYCEROL_O_ACYLTRANSFERASE_ACTIVITY	-1.06	0.41	0	0	0	not significant
3323	GO_RNA_POLYMERASE_II_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_ACTIVI	-1.06	0.41	0	0	0	not significant
3324	GO_SKELETAL_MUSCLE_CELL_PROLIFERATION	-1.06	0.41	0	0	0	not significant
3325	REACTOME_APOPTOTIC_FACTOR_MEDIATED_RESPONSE	-1.06	0.41	0	0	0	not significant
3326	REACTOME_INTERLEUKIN_12_SIGNALING	-1.06	0.41	0	0	0	not significant
3327	STAMBOLSKY_BOUND_BY_MUTATED_TP53	-1.06	0.41	0	0	0	not significant
3328	GO_RESPONSE_TO_ACETYLCHOLINE	-1.06	0.4	0	0	0	not significant
3329	REACTOME_SIGNALING_BY_FGFR4_IN_DISEASE	-1.06	0.4	0	0	0	not significant
3330	GO_REGULATION_OF_MACROPHAGE_DIFFERENTIATION	-1.06	0.39	0	0	0	not significant
3331	GO_REGULATION_OF_MAINTENANCE_OF_SISTER_CHROMATID_COHESION	-1.06	0.39	0	0	0	not significant
3332	GO_UDP_GLUCOSYLTRANSFERASE_ACTIVITY	-1.06	0.39	0	0	0	not significant
3333	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_OSMOTIC_S	-1.06	0.37	0	0	0	not significant
3334	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7	-1.06	0.37	0	0	0	not significant
3335	GO_CHROMATOID_BODY	-1.06	0.36	0	0	0	not significant
3336	GO_EMBRYONIC_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	-1.06	0.35	0	0	0	not significant
3337	GO_REGULATION_OF_SKELETAL_MUSCLE_ADAPTATION	-1.06	0.35	0	0	0	not significant
3338	GO_ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	-1.05	0.75	0	0	0	not significant
3339	GO_INTERSPECIES_INTERACTION_BETWEEN_ORGANISMS	-1.05	0.74	0	0	0	not significant
3340	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP	-1.05	0.72	0	0	0	not significant
3341	GO_CHROMATIN_ORGANIZATION	-1.05	0.69	0	0	0	not significant
3342	GO_HEAD_DEVELOPMENT	-1.05	0.64	0	0	0	not significant
3343	GO_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	-1.05	0.58	0	0	0	not significant
3344	MARTINEZ_RB1_TARGETS_UP	-1.05	0.58	0	0	0	not significant
3345	GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_CELL_CELL	-1.05	0.57	0	0	0	not significant
3346	PILON_KLF1_TARGETS_UP	-1.05	0.56	0	0	0	not significant
3347	GO_ENZYME_INHIBITOR_ACTIVITY	-1.05	0.55	0	0	0	not significant
3348	GO_STRUCTURAL_MOLECULE_ACTIVITY	-1.05	0.52	0	0	0	not significant
3349	GO_POSITIVE_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	-1.05	0.51	0	0	0	not significant
3350	WANG_CLIM2_TARGETS_DN	-1.05	0.49	0	0	0	not significant
3351	FIGUEROA_AML_METHYLATION_CLUSTER_7_UP	-1.05	0.48	0	0	0	not significant
3352	REACTOME_SIGNALING_BY_VEGF	-1.05	0.48	0	0	0	not significant
3353	GO_DNA_HELICASE_ACTIVITY	-1.05	0.47	0	0	0	not significant
3354	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP	-1.05	0.46	0	0	0	not significant
3355	PID_NFAT_3PATHWAY	-1.05	0.46	0	0	0	not significant
3356	GO_DNA_PACKAGING_COMPLEX	-1.05	0.45	0	0	0	not significant
3357	GO_NEGATIVE_REGULATION_OF_PROTEOLYSIS_INVOLVED_IN_CELLULAR_PROTEI	-1.05	0.45	0	0	0	not significant
3358	GO_REGULATION_OF_ORGAN_GROWTH	-1.05	0.45	0	0	0	not significant
3359	SHAFFER_IRF4_TARGETS_IN_ACTIVATED_B_LYMPHOCYTE	-1.05	0.45	0	0	0	not significant
3360	GO_POSITIVE_REGULATION_OF_GLIOGENESIS	-1.05	0.44	0	0	0	not significant
3361	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED	-1.05	0.43	0	0	0	not significant
3362	CHR3P14	-1.05	0.42	0	0	0	not significant
3363	GO_BONE_CELL_DEVELOPMENT	-1.05	0.42	0	0	0	not significant
3364	GO_MYELOID_LEUKOCYTE_CYTOKINE_PRODUCTION	-1.05	0.42	0	0	0	not significant
3365	GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE	-1.05	0.42	0	0	0	not significant
3366	GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	-1.05	0.42	0	0	0	not significant
3367	IKEDA_MIR133_TARGETS_UP	-1.05	0.42	0	0	0	not significant

3368	PID_LIS1_PATHWAY	-1.05	0.42	0	0	0	not significant
3369	CHR10P15	-1.05	0.41	0	0	0	not significant
3370	GO_CELLULAR_COPPER_ION_HOMEOSTASIS	-1.05	0.41	0	0	0	not significant
3371	GO_LYMPH_NODE_DEVELOPMENT	-1.05	0.41	0	0	0	not significant
3372	BIOCARTA_ACTINY_PATHWAY	-1.05	0.4	0	0	0	not significant
3373	CHR8P23	-1.05	0.4	0	0	0	not significant
3374	GO_HEMATOPOIETIC_STEM_CELL_PROLIFERATION	-1.05	0.4	0	0	0	not significant
3375	PID_NECTIN_PATHWAY	-1.05	0.4	0	0	0	not significant
3376	REACTOME_CREB1_PHOSPHORYLATION_THROUGH_NMDA_RECEPTOR_MEDIATED	-1.05	0.4	0	0	0	not significant
3377	REACTOME_SYNTHESIS_OF_IP2_IP_AND_INS_IN_THE_CYTOSOL	-1.05	0.4	0	0	0	not significant
3378	GO_MEGAKARYOCYTE_DEVELOPMENT	-1.05	0.39	0	0	0	not significant
3379	GO_NEGATIVE_REGULATION_OF_JNK_CASCADE	-1.05	0.39	0	0	0	not significant
3380	GO_NUCLEOSIDE_TRIPHOSPHATE_DIPHOSPHATASE_ACTIVITY	-1.05	0.39	0	0	0	not significant
3381	GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	-1.05	0.39	0	0	0	not significant
3382	GO_SKELETAL_MUSCLE_ACETYLCHOLINE_GATED_CHANNEL_CLUSTERING	-1.05	0.39	0	0	0	not significant
3383	BIOCARTA_CDC42RAC_PATHWAY	-1.05	0.38	0	0	0	not significant
3384	HAHTOLA_CTCL_PATHOGENESIS	-1.05	0.38	0	0	0	not significant
3385	GO_ASTRAL_MICROTUBULE_ORGANIZATION	-1.05	0.37	0	0	0	not significant
3386	GO_NEGATIVE_REGULATION_OF_PROTEIN_EXPORT_FROM_NUCLEUS	-1.05	0.37	0	0	0	not significant
3387	GO_TRANSLOCATION_OF_MOLECULES_INTO_HOST	-1.05	0.37	0	0	0	not significant
3388	GO_POSITIVE_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATION	-1.05	0.36	0	0	0	not significant
3389	GO_SNRNP_BINDING	-1.05	0.36	0	0	0	not significant
3390	REACTOME_SODIUM_CALCIUM_EXCHANGERS	-1.05	0.36	0	0	0	not significant
3391	SHIN_B_CELL_LYMPHOMA_CLUSTER_9	-1.05	0.36	0	0	0	not significant
3392	GO_CELL_DIFFERENTIATION_INVOLVED_IN_METANEPHROS_DEVELOPMENT	-1.05	0.35	0	0	0	not significant
3393	GO_POSITIVE_REGULATION_OF_SPINDLE_CHECKPOINT	-1.05	0.35	0	0	0	not significant
3394	GO_CELLULAR_RESPONSE_TO_SODIUM_ARSENITE	-1.05	0.34	0	0	0	not significant
3395	GO_PYRUVATE_DEHYDROGENASE_ACTIVITY	-1.05	0.34	0	0	0	not significant
3396	GO_REGULATION_OF_ALKALINE_PHOSPHATASE_ACTIVITY	-1.05	0.34	0	0	0	not significant
3397	GO_TRANSFERRIN_RECEPTOR_BINDING	-1.05	0.34	0	0	0	not significant
3398	REACTOME_FBXW7_MUTANTS_AND_NOTCH1_IN_CANCER	-1.05	0.34	0	0	0	not significant
3399	GO_DNA_METABOLIC_PROCESS	-1.04	0.84	0	0	0	not significant
3400	GO_POSITIVE_REGULATION_OF_HYDROLASE_ACTIVITY	-1.04	0.71	0	0	0	not significant
3401	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_TRANS	-1.04	0.61	0	0	0	not significant
3402	GO_CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT	-1.04	0.57	0	0	0	not significant
3403	GO_TRANSCRIPTION_COREGULATOR_ACTIVITY	-1.04	0.57	0	0	0	not significant
3404	GO_GTPASE_BINDING	-1.04	0.52	0	0	0	not significant
3405	GO_ACTIVATION_OF_PROTEIN_KINASE_ACTIVITY	-1.04	0.49	0	0	0	not significant
3406	GO_NEGATIVE_REGULATION_OF_BINDING	-1.04	0.48	0	0	0	not significant
3407	GO_CYTOPLASMIC_TRANSLATION	-1.04	0.47	0	0	0	not significant
3408	GO_CHROMATIN_REMODELING	-1.04	0.46	0	0	0	not significant
3409	GO_REGIONALIZATION	-1.04	0.46	0	0	0	not significant
3410	GO_REGULATION_OF_PROTEIN_POLYMERIZATION	-1.04	0.46	0	0	0	not significant
3411	KEGG_GNRH_SIGNALING_PATHWAY	-1.04	0.46	0	0	0	not significant
3412	REACTOME_L1CAM_INTERACTIONS	-1.04	0.46	0	0	0	not significant
3413	GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	-1.04	0.45	0	0	0	not significant
3414	GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-1.04	0.45	0	0	0	not significant
3415	GO_RIBOSOMAL_SUBUNIT	-1.04	0.45	0	0	0	not significant
3416	GO_SMOOTH_MUSCLE_CELL_MIGRATION	-1.04	0.45	0	0	0	not significant
3417	FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	-1.04	0.44	0	0	0	not significant
3418	LAIHO_COLORECTAL_CANCER_SERRATED_UP	-1.04	0.44	0	0	0	not significant
3419	BROWNE_HCMV_INFECTION_10HR_UP	-1.04	0.43	0	0	0	not significant
3420	REACTOME_REGULATION_OF_TP53_EXPRESSION_AND_DEGRADATION	-1.04	0.43	0	0	0	not significant
3421	REACTOME_RUNX1_INTERACTS_WITH_CO_FACTORS_WHOSE_PRECISE_EFFECT_	-1.04	0.43	0	0	0	not significant
3422	TIEN_INTESTINE_PROBIOTICS_6HR_DN	-1.04	0.43	0	0	0	not significant
3423	GO_PROTEIN_HETEROOLIGOMERIZATION	-1.04	0.42	0	0	0	not significant
3424	GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION	-1.04	0.42	0	0	0	not significant
3425	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2PLUS	-1.04	0.42	0	0	0	not significant
3426	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_UP	-1.04	0.41	0	0	0	not significant
3427	GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	-1.04	0.41	0	0	0	not significant
3428	GO_PROTEIN_TYROSINE_SERINE_THREONINE_PHOSPHATASE_ACTIVITY	-1.04	0.41	0	0	0	not significant
3429	GO_REGULATION_OF_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	-1.04	0.41	0	0	0	not significant
3430	REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	-1.04	0.41	0	0	0	not significant
3431	GO_LYSOPHOSPHOLIPID_ACYLTRANSFERASE_ACTIVITY	-1.04	0.4	0	0	0	not significant
3432	GO_SARCOPLASMIC_RETICULUM_MEMBRANE	-1.04	0.4	0	0	0	not significant
3433	GO_SYNAPTIC_TRANSMISSION_GABAERGIC	-1.04	0.4	0	0	0	not significant
3434	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_UP	-1.04	0.4	0	0	0	not significant
3435	BIOCARTA_P53HYPOXIA_PATHWAY	-1.04	0.39	0	0	0	not significant
3436	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_SEVERAL_ADDITIONAL_CELL_	-1.04	0.39	0	0	0	not significant
3437	ZUCCHI_METASTASIS_UP	-1.04	0.39	0	0	0	not significant
3438	GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	-1.04	0.38	0	0	0	not significant
3439	GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GABAERGIC	-1.04	0.38	0	0	0	not significant
3440	GO_U2_SNRNP	-1.04	0.38	0	0	0	not significant
3441	PID_CXCR3_PATHWAY	-1.04	0.38	0	0	0	not significant
3442	WANG_RECURRENT_LIVER_CANCER_DN	-1.04	0.38	0	0	0	not significant
3443	GO_ADA2_GCN5_ADA3_TRANSCRIPTION_ACTIVATOR_COMPLEX	-1.04	0.37	0	0	0	not significant
3444	GO_COENZYME_CATABOLIC_PROCESS	-1.04	0.37	0	0	0	not significant
3445	GO_NEGATIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION	-1.04	0.37	0	0	0	not significant
3446	GO_PROTEASOME_CORE_COMPLEX	-1.04	0.37	0	0	0	not significant
3447	REACTOME_CALCINEURIN_ACTIVATES_NFAT	-1.04	0.37	0	0	0	not significant
3448	GO_CELLULAR_RESPONSE_TO_SALT	-1.04	0.36	0	0	0	not significant
3449	GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_3_COMPLEX	-1.04	0.36	0	0	0	not significant
3450	GO_NUCLEAR_BODY_ORGANIZATION	-1.04	0.36	0	0	0	not significant
3451	GO_SMOOTHENED_SIGNALING_PATHWAY_INVOLVED_IN_DORSAL_VENTRAL_NEURA	-1.04	0.36	0	0	0	not significant
3452	GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE	-1.04	0.35	0	0	0	not significant
3453	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH2_GROUP_OF_DONORS	-1.04	0.35	0	0	0	not significant
3454	GO_TRNA_THIO_MODIFICATION	-1.04	0.35	0	0	0	not significant
3455	MIKKELSEN_MCV6_ICP_WITH_H3K4ME3_AND_H3K27ME3	-1.04	0.35	0	0	0	not significant
3456	GO_MESENCHYMAL_TO_EPITHELIAL_TRANSITION_INVOLVED_IN_METANEPHROS_M	-1.04	0.34	0	0	0	not significant
3457	REACTOME_CGMP_EFFECTS	-1.04	0.34	0	0	0	not significant
3458	REACTOME_NEGATIVE_REGULATION_OF_ACTIVITY_OF_TFAP2_AP_2_FAMILY_TRA	-1.04	0.34	0	0	0	not significant
3459	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_CHECKPOINT	-1.04	0.33	0	0	0	not significant
3460	REACTOME_SENSING_OF_DNA_DOUBLE_STRAND_BREAKS	-1.04	0.32	0	0	0	not significant
3461	FIGUEROA_AML_METHYLATION_CLUSTER_2_DN	-1.04	0.31	0	0	0	not significant
3462	REACTOME_DEVELOPMENTAL_BIOLOGY	-1.03	0.58	0	0	0	not significant
3463	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN	-1.03	0.56	0	0	0	not significant
3464	GO_PERINUCLEAR_REGION_OF_CYTOPLASM	-1.03	0.54	0	0	0	not significant
3465	GO_EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG_HATCHING	-1.03	0.5	0	0	0	not significant
3466	LU_EZH2_TARGETS_DN	-1.03	0.5	0	0	0	not significant
3467	GRADE_COLON_CANCER_UP	-1.03	0.47	0	0	0	not significant
3468	GO_CATALYTIC_ACTIVITY_ACTING_ON_DNA	-1.03	0.46	0	0	0	not significant
3469	GO_NUCLEAR_CHROMOSOME_TELOMERIC_REGION	-1.03	0.45	0	0	0	not significant
3470	GO_SINGLE_STRANDED_DNA_BINDING	-1.03	0.45	0	0	0	not significant
3471	MULLIGHAN_NPM1_SIGNATURE_3_UP	-1.03	0.45	0	0	0	not significant
3472	GO_REGULATION_OF_SYMBIOSIS_ENCOMPASSING_MUTUALISM_THROUGH_PARASI	-1.03	0.44	0	0	0	not significant
3473	GO_TYPE_I_INTERFERON_PRODUCTION	-1.03	0.44	0	0	0	not significant
3474	GO_HINDBRAIN_MORPHOGENESIS	-1.03	0.43	0	0	0	not significant
3475	GO_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	-1.03	0.43	0	0	0	not significant
3476	MCMURRAY_TP53_HRAS_COOPERATION_RESPONSE_DN	-1.03	0.43	0	0	0	not significant

3477	REACTOME_ONCOGENIC_MAPK_SIGNALING	-1.03	0.43	0	0	0	not significant
3478	GO_CELL_CORTEX_PART	-1.03	0.42	0	0	0	not significant
3479	GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	-1.03	0.42	0	0	0	not significant
3480	HESS_TARGETS_OF_HOXA9_AND_MEIS1_UP	-1.03	0.42	0	0	0	not significant
3481	REACTOME_ANCHORING_OF_THE_BASAL_BODY_TO_THE_PLASMA_MEMBRANE	-1.03	0.42	0	0	0	not significant
3482	ATF2_S_UP.V1_UP	-1.03	0.41	0	0	0	not significant
3483	GO_POSITIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	-1.03	0.41	0	0	0	not significant
3484	GO_POSITIVE_REGULATION_OF_PROTEIN_POLYMERIZATION	-1.03	0.41	0	0	0	not significant
3485	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	-1.03	0.41	0	0	0	not significant
3486	ZHANG_TLX_TARGETS_DN	-1.03	0.41	0	0	0	not significant
3487	GO_PEPTIDYL_PROLINE_MODIFICATION	-1.03	0.4	0	0	0	not significant
3488	GO_SOMATIC_STEM_CELL_POPULATION_MAINTENANCE	-1.03	0.4	0	0	0	not significant
3489	GO_SPLICEOSOMAL_COMPLEX_ASSEMBLY	-1.03	0.4	0	0	0	not significant
3490	GRADE_COLON_VS_RECTAL_CANCER_UP	-1.03	0.4	0	0	0	not significant
3491	PARK_HSC_MARKERS	-1.03	0.4	0	0	0	not significant
3492	PID_HIF1_TFPATHWAY	-1.03	0.4	0	0	0	not significant
3493	TERAO_AOX4_TARGETS_SKIN_UP	-1.03	0.4	0	0	0	not significant
3494	ZHU_CMV_ALL_DN	-1.03	0.4	0	0	0	not significant
3495	CHESLER_BRAIN_QTL_CIS	-1.03	0.39	0	0	0	not significant
3496	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_MAGENTA_DN	-1.03	0.39	0	0	0	not significant
3497	GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GR	-1.03	0.39	0	0	0	not significant
3498	GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GRO	-1.03	0.39	0	0	0	not significant
3499	HEIDENBLAD_AMPLICON_12P11_12_UP	-1.03	0.39	0	0	0	not significant
3500	KATSANOU_ELAVL1_TARGETS_DN	-1.03	0.39	0	0	0	not significant
3501	MCBRYAN_PUBERTAL_TGFB1_TARGETS_UP	-1.03	0.39	0	0	0	not significant
3502	REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	-1.03	0.39	0	0	0	not significant
3503	ABDELMOHSEN_ELAVL4_TARGETS	-1.03	0.38	0	0	0	not significant
3504	GO_HISTONE_H4_DEACETYLATION	-1.03	0.38	0	0	0	not significant
3505	GO_MEIOTIC_CHROMOSOME_SEPARATION	-1.03	0.38	0	0	0	not significant
3506	GO_MRNA_METHYLTRANSFERASE_ACTIVITY	-1.03	0.38	0	0	0	not significant
3507	GO_PHOSPHATIDYLINOSITOL_DEPHOSPHORYLATION	-1.03	0.38	0	0	0	not significant
3508	KEGG_TGF_BETA_SIGNALING_PATHWAY	-1.03	0.38	0	0	0	not significant
3509	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27	-1.03	0.38	0	0	0	not significant
3510	PID_IFNG_PATHWAY	-1.03	0.38	0	0	0	not significant
3511	WEIGEL_OXIDATIVE_STRESS_BY_HNE_AND_H2O2	-1.03	0.38	0	0	0	not significant
3512	GO_HISTONE_H4_K16_ACETYLATION	-1.03	0.37	0	0	0	not significant
3513	GO_NEGATIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	-1.03	0.37	0	0	0	not significant
3514	GO_PROTEIN_PHOSPHATASE_ACTIVATOR_ACTIVITY	-1.03	0.37	0	0	0	not significant
3515	GO_REGULATION_OF_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	-1.03	0.37	0	0	0	not significant
3516	PID_FRA_PATHWAY	-1.03	0.37	0	0	0	not significant
3517	REACTOME_FOXO_MEDIATED_TRANSCRIPTION_OF_CELL_DEATH_GENES	-1.03	0.37	0	0	0	not significant
3518	GO_APOPTOTIC_DNA_FRAGMENTATION	-1.03	0.36	0	0	0	not significant
3519	GO_ENDOPLASMIC_RETICULUM_SUBCOMPARTMENT	-1.03	0.36	0	0	0	not significant
3520	GO_GUANOSINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-1.03	0.36	0	0	0	not significant
3521	GO_MYELIN_ASSEMBLY	-1.03	0.36	0	0	0	not significant
3522	GO_POSITIVE_REGULATION_OF_HELICASE_ACTIVITY	-1.03	0.36	0	0	0	not significant
3523	REACTOME_INTEGRATION_OF_PROVIRUS	-1.03	0.36	0	0	0	not significant
3524	BERENJENO_TRANSFORMED_BY_RHOA_FOREVER_DN	-1.03	0.35	0	0	0	not significant
3525	GO_CERAMIDE_TRANSPORTER_ACTIVITY	-1.03	0.35	0	0	0	not significant
3526	GO_NUCLEOSIDE_MONOPHOSPHATE_KINASE_ACTIVITY	-1.03	0.35	0	0	0	not significant
3527	GO_POLYADENYLATION_DEPENDENT_RNA_CATABOLIC_PROCESS	-1.03	0.35	0	0	0	not significant
3528	GO_REGULATION_OF_HEXOKINASE_ACTIVITY	-1.03	0.35	0	0	0	not significant
3529	GO_REGULATION_OF_RESPIRATORY_SYSTEM_PROCESS	-1.03	0.35	0	0	0	not significant
3530	GO_DEADENYLATION_DEPENDENT_DECAPPING_OF_NUCLEAR_TRANSCRIBED_MRN	-1.03	0.34	0	0	0	not significant
3531	GO_SPERM_PRINCIPAL_PIECE	-1.03	0.34	0	0	0	not significant
3532	REACTOME_ACTIVATION_OF_CASPASES_THROUGH_APOPTOSOME_MEDIATED_CL	-1.03	0.34	0	0	0	not significant
3533	WEBER_METHYLATED_IN_COLON_CANCER	-1.03	0.34	0	0	0	not significant
3534	GO_NEGATIVE_REGULATION_OF_RNA_POLYMERASE_II_REGULATORY_REGION_SE	-1.03	0.33	0	0	0	not significant
3535	GO_NEGATIVE_REGULATION_OF_SYNAPTIC_VESICLE_TRANSPORT	-1.03	0.33	0	0	0	not significant
3536	REACTOME_EICOSANOIDS	-1.03	0.33	0	0	0	not significant
3537	REACTOME_SCAVENGING_BY_CLASS_A_RECEPTORS	-1.03	0.33	0	0	0	not significant
3538	GO_MEMBRANE_ORGANIZATION	-1.02	0.61	0	0	0	not significant
3539	REACTOME_AXON_GUIDANCE	-1.02	0.48	0	0	0	not significant
3540	FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP	-1.02	0.44	0	0	0	not significant
3541	PATIL_LIVER_CANCER	-1.02	0.44	0	0	0	not significant
3542	GO_ORGANELLE_INNER_MEMBRANE	-1.02	0.43	0	0	0	not significant
3543	GO_OSSIFICATION	-1.02	0.43	0	0	0	not significant
3544	GO_TRANSCRIPTION_COACTIVATOR_ACTIVITY	-1.02	0.43	0	0	0	not significant
3545	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY	-1.02	0.43	0	0	0	not significant
3546	REACTOME_HEMOSTASIS	-1.02	0.43	0	0	0	not significant
3547	GO_KINASE_REGULATOR_ACTIVITY	-1.02	0.42	0	0	0	not significant
3548	GO_CARBOHYDRATE_CATABOLIC_PROCESS	-1.02	0.41	0	0	0	not significant
3549	REACTOME_AUTOPHAGY	-1.02	0.41	0	0	0	not significant
3550	BIOCARTA_P38MAPK_PATHWAY	-1.02	0.4	0	0	0	not significant
3551	GO_CYTOPLASMIC_MICROTUBULE	-1.02	0.4	0	0	0	not significant
3552	QI_PLASMACYTOMA_DN	-1.02	0.4	0	0	0	not significant
3553	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_UP	-1.02	0.39	0	0	0	not significant
3554	GO_METHYLATION	-1.02	0.39	0	0	0	not significant
3555	GO_MITOCHONDRIAL_TRANSPORT	-1.02	0.39	0	0	0	not significant
3556	GO_NEURON_MATURATION	-1.02	0.39	0	0	0	not significant
3557	GO_POSITIVE_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION	-1.02	0.39	0	0	0	not significant
3558	REACTOME_SIGNALING_BY_MET	-1.02	0.39	0	0	0	not significant
3559	BROWNE_HCMV_INFECTION_24HR_UP	-1.02	0.38	0	0	0	not significant
3560	DARWICHE_SKIN_TUMOR_PROMOTER_DN	-1.02	0.38	0	0	0	not significant
3561	GO_CLATHRIN_VESICLE_COAT	-1.02	0.38	0	0	0	not significant
3562	GO_CYTOKINE_ACTIVITY	-1.02	0.38	0	0	0	not significant
3563	GO_PHOTORECEPTOR_OUTER_SEGMENT	-1.02	0.38	0	0	0	not significant
3564	GO_PROTEIN_HOMOTETRAMERIZATION	-1.02	0.38	0	0	0	not significant
3565	GO_REGULATION_OF_SYNAPSE_ASSEMBLY	-1.02	0.38	0	0	0	not significant
3566	GO_THYROID_HORMONE_RECEPTOR_BINDING	-1.02	0.38	0	0	0	not significant
3567	HOLLEMAN_PREDNISOLONE_RESISTANCE_B_ALL_UP	-1.02	0.38	0	0	0	not significant
3568	REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	-1.02	0.38	0	0	0	not significant
3569	BOYAULT_LIVER_CANCER_SUBCLASS_G12_UP	-1.02	0.37	0	0	0	not significant
3570	GO_NEGATIVE_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	-1.02	0.37	0	0	0	not significant
3571	GO_PERICENTRIC_HETEROCHROMATIN	-1.02	0.37	0	0	0	not significant
3572	GO_POSITIVE_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	-1.02	0.37	0	0	0	not significant
3573	GO_POSITIVE_REGULATION_OF_NUCLEAR_DIVISION	-1.02	0.37	0	0	0	not significant
3574	GO_PROTEIN_HETEROTETRAMERIZATION	-1.02	0.37	0	0	0	not significant
3575	GO_PROTEIN_LOCALIZATION_TO_KINETOCHORE	-1.02	0.37	0	0	0	not significant
3576	GO_REGULATION_OF_HEART_GROWTH	-1.02	0.37	0	0	0	not significant
3577	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_DN	-1.02	0.37	0	0	0	not significant
3578	ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_UP	-1.02	0.36	0	0	0	not significant
3579	GO_CARDIAC_CHAMBER_MORPHOGENESIS	-1.02	0.36	0	0	0	not significant
3580	GO_CELLULAR_ALDEHYDE_METABOLIC_PROCESS	-1.02	0.36	0	0	0	not significant
3581	GO_M_BAND	-1.02	0.36	0	0	0	not significant
3582	GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	-1.02	0.36	0	0	0	not significant
3583	GO_NUCLEOTIDE_SALVAGE	-1.02	0.36	0	0	0	not significant
3584	GO_POSITIVE_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION	-1.02	0.36	0	0	0	not significant
3585	GO_PRESYNAPSE_ORGANIZATION	-1.02	0.36	0	0	0	not significant

3586	ALONSO_METASTASIS_DN	-1.02	0.35	0	0	0	not significant
3587	GO_CAMP_RESPONSE_ELEMENT_BINDING_PROTEIN_BINDING	-1.02	0.35	0	0	0	not significant
3588	GO_CARBOXY_TERMINAL_DOMAIN_PROTEIN_KINASE_COMPLEX	-1.02	0.35	0	0	0	not significant
3589	GO_CORTICOSTEROID_RECEPTOR_SIGNALING_PATHWAY	-1.02	0.35	0	0	0	not significant
3590	GO_ESTABLISHMENT_OF_MITOCHONDRION_LOCALIZATION	-1.02	0.35	0	0	0	not significant
3591	GO_INTRONIC_TRANSCRIPTION_REGULATORY_REGION_DNA_BINDING	-1.02	0.35	0	0	0	not significant
3592	GO_LYS48_SPECIFIC_DEUBIQUITINASE_ACTIVITY	-1.02	0.35	0	0	0	not significant
3593	GO_PROTEIN_LOCALIZATION_TO_CELL_JUNCTION	-1.02	0.35	0	0	0	not significant
3594	GO_SKELETAL_MUSCLE_TISSUE_REGENERATION	-1.02	0.35	0	0	0	not significant
3595	MURATA_VIRULENCE_OF_H_PILORI	-1.02	0.35	0	0	0	not significant
3596	CHR10P14	-1.02	0.34	0	0	0	not significant
3597	GO_POSITIVE_REGULATION_OF_NUCLEAR_CELL_CYCLE_DNA_REPLICATION	-1.02	0.34	0	0	0	not significant
3598	GO_REGULATION_OF_RNA_BINDING	-1.02	0.34	0	0	0	not significant
3599	GO_RNA_POLYMERASE_II_INTRONIC_TRANSCRIPTION_REGULATORY_REGION_SEC	-1.02	0.34	0	0	0	not significant
3600	MARIADASON_RESPONSE_TO_BUTYRATE_CURCUMIN_SULINDAC_TSA_8	-1.02	0.34	0	0	0	not significant
3601	REACTOME_TETRAHYDROBIOPTERIN_BH4_SYNTHESIS_RECYCLING_SALVAGE_AND	-1.02	0.34	0	0	0	not significant
3602	SAGIV_CD24_TARGETS_UP	-1.02	0.34	0	0	0	not significant
3603	GO_CAMP_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-1.02	0.33	0	0	0	not significant
3604	GO_MITOTIC_SPINDLE_ASTRAL_MICROTUBULE	-1.02	0.33	0	0	0	not significant
3605	GO_NEGATIVE_REGULATION_OF_GLYCOLYTIC_PROCESS	-1.02	0.33	0	0	0	not significant
3606	REACTOME_WNT5A_DEPENDENT_INTERNALIZATION_OF_FZD4	-1.02	0.33	0	0	0	not significant
3607	XU_HGF_TARGETS_REPRESSED_BY_AKT1_UP	-1.02	0.33	0	0	0	not significant
3608	GO_CARBONYL_REDUCTASE_NADPH_ACTIVITY	-1.02	0.32	0	0	0	not significant
3609	GO_EGO_COMPLEX	-1.02	0.32	0	0	0	not significant
3610	GO_POSTSYNAPTIC_ENDOCYTIC_ZONE	-1.02	0.32	0	0	0	not significant
3611	GO_PYRAMIDAL_NEURON_DIFFERENTIATION	-1.02	0.32	0	0	0	not significant
3612	GO_REGULATION_OF_METAPHASE_PLATE_CONGRESSION	-1.02	0.32	0	0	0	not significant
3613	GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION_CELL_EXTENSION	-1.02	0.32	0	0	0	not significant
3614	GO_RRNA_TRANSPORT	-1.02	0.3	0	0	0	not significant
3615	LIU_SOX4_TARGETS_DN	-1.01	0.43	0	0	0	not significant
3616	CHR17P13	-1.01	0.41	0	0	0	not significant
3617	CHR10Q22	-1.01	0.4	0	0	0	not significant
3618	GO_ACTIN_FILAMENT_BUNDLE_ORGANIZATION	-1.01	0.4	0	0	0	not significant
3619	MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_UP	-1.01	0.4	0	0	0	not significant
3620	CHR3P25	-1.01	0.39	0	0	0	not significant
3621	GO_MULTICELLULAR_ORGANISMAL_SIGNALING	-1.01	0.39	0	0	0	not significant
3622	REACTOME_SYNTHESIS_OF_PA	-1.01	0.39	0	0	0	not significant
3623	REACTOME_TP53_REGULATES_METABOLIC_GENES	-1.01	0.39	0	0	0	not significant
3624	BROWNE_HCMV_INFECTION_1HR_DN	-1.01	0.38	0	0	0	not significant
3625	GO_REGULATION_OF_HISTONE_PHOSPHORYLATION	-1.01	0.38	0	0	0	not significant
3626	GO_RESPIRATORY_SYSTEM_PROCESS	-1.01	0.38	0	0	0	not significant
3627	GO_RESPONSE_TO_OSMOTIC_STRESS	-1.01	0.38	0	0	0	not significant
3628	IVANOVSKA_MIR106B_TARGETS	-1.01	0.38	0	0	0	not significant
3629	MCCLUNG_CREB1_TARGETS_DN	-1.01	0.38	0	0	0	not significant
3630	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM2	-1.01	0.38	0	0	0	not significant
3631	BROWNE_HCMV_INFECTION_6HR_DN	-1.01	0.37	0	0	0	not significant
3632	GO_INCLUSION_BODY	-1.01	0.37	0	0	0	not significant
3633	GO_LONG_TERM_MEMORY	-1.01	0.37	0	0	0	not significant
3634	GO_MUSCLE_CELL_MIGRATION	-1.01	0.37	0	0	0	not significant
3635	GO_NEGATIVE_REGULATION_OF_CELLULAR_SENESCENCE	-1.01	0.37	0	0	0	not significant
3636	GO_NEURAL_PRECURSOR_CELL_PROLIFERATION	-1.01	0.37	0	0	0	not significant
3637	GO_POSITIVE_REGULATION_OF_MRNA_CATABOLIC_PROCESS	-1.01	0.37	0	0	0	not significant
3638	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	-1.01	0.37	0	0	0	not significant
3639	MELLMAN_TUT1_TARGETS_UP	-1.01	0.37	0	0	0	not significant
3640	PID_CERAMIDE_PATHWAY	-1.01	0.37	0	0	0	not significant
3641	REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION_IN_TLR7_8_OR_9_SIGNALING	-1.01	0.37	0	0	0	not significant
3642	BIOCARTA_FAS_PATHWAY	-1.01	0.36	0	0	0	not significant
3643	GO_EMBRYONIC_AXIS_SPECIFICATION	-1.01	0.36	0	0	0	not significant
3644	GO_INTRACILIARY_RETROGRADE_TRANSPORT	-1.01	0.36	0	0	0	not significant
3645	GO_NON_RECOMBINATIONAL_REPAIR	-1.01	0.36	0	0	0	not significant
3646	GO_REGULATION_OF_HISTONE_H4_ACETYLATION	-1.01	0.36	0	0	0	not significant
3647	GO_RENAL_WATER_HOMEOSTASIS	-1.01	0.36	0	0	0	not significant
3648	GO_STRIATED_MUSCLE_ADAPTATION	-1.01	0.36	0	0	0	not significant
3649	GO_TRANSCRIPTION_COREPRESSOR_ACTIVITY	-1.01	0.36	0	0	0	not significant
3650	LOPEZ_TRANSLATION_VIA_FN1_SIGNALING	-1.01	0.36	0	0	0	not significant
3651	PID_P38_MK2_PATHWAY	-1.01	0.36	0	0	0	not significant
3652	REACTOME_INTEGRIN_SIGNALING	-1.01	0.36	0	0	0	not significant
3653	SWEET_KRAS_TARGETS_UP	-1.01	0.36	0	0	0	not significant
3654	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR	-1.01	0.36	0	0	0	not significant
3655	BERNARD_PPAPDC1B_TARGETS_UP	-1.01	0.35	0	0	0	not significant
3656	GO_AP_3_ADAPTOR_COMPLEX	-1.01	0.35	0	0	0	not significant
3657	GO_ENDORIBONUCLEASE_ACTIVITY	-1.01	0.35	0	0	0	not significant
3658	GO_MICROTUBULE_DEPOLYMERIZATION	-1.01	0.35	0	0	0	not significant
3659	GO_RESPONSE_TO_HYPEROXIA	-1.01	0.35	0	0	0	not significant
3660	GO_SEGMENTATION	-1.01	0.35	0	0	0	not significant
3661	KEGG_RNA_DEGRADATION	-1.01	0.35	0	0	0	not significant
3662	MASSARWEH_RESPONSE_TO_ESTRADIOL	-1.01	0.35	0	0	0	not significant
3663	BIOCARTA_MYOSIN_PATHWAY	-1.01	0.34	0	0	0	not significant
3664	BIOCARTA_SET_PATHWAY	-1.01	0.34	0	0	0	not significant
3665	GO_CERAMIDE_CATABOLIC_PROCESS	-1.01	0.34	0	0	0	not significant
3666	GO_DETECTION_OF_CALCIUM_ION	-1.01	0.34	0	0	0	not significant
3667	GO_FOLIC_ACID_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-1.01	0.34	0	0	0	not significant
3668	GO_NUCLEAR_LAMINA	-1.01	0.34	0	0	0	not significant
3669	GO_POST_EMBRYONIC_ANIMAL_ORGAN_DEVELOPMENT	-1.01	0.34	0	0	0	not significant
3670	KANG_DOXORUBICIN_RESISTANCE_DN	-1.01	0.34	0	0	0	not significant
3671	ZHENG_RESPONSE_TO_ARSENITE_UP	-1.01	0.34	0	0	0	not significant
3672	FIGUEROA_AML_METHYLATION_CLUSTER_4_DN	-1.01	0.33	0	0	0	not significant
3673	NGO_MALIGNANT_GLIOMA_1P_LOH	-1.01	0.33	0	0	0	not significant
3674	REACTOME_ADRENALINE_NORADRENALINE_INHIBITS_INSULIN_SECRETION	-1.01	0.33	0	0	0	not significant
3675	WU_HBX_TARGETS_3_DN	-1.01	0.33	0	0	0	not significant
3676	GO_CYCLIC_NUCLEOTIDE_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-1.01	0.32	0	0	0	not significant
3677	GO_MICRO_RIBONUCLEOPROTEIN_COMPLEX	-1.01	0.32	0	0	0	not significant
3678	GO_MUSCLE_MYOSIN_COMPLEX	-1.01	0.32	0	0	0	not significant
3679	GO_NADH_PYROPHOSPHATASE_ACTIVITY	-1.01	0.32	0	0	0	not significant
3680	GO_NEDD8_TRANSFERASE_ACTIVITY	-1.01	0.32	0	0	0	not significant
3681	GO_POSITIVE_REGULATION_OF_VASCULAR_ASSOCIATED_SMOOTH_MUSCLE_CELI	-1.01	0.32	0	0	0	not significant
3682	GO_FLOTILLIN_COMPLEX	-1.01	0.31	0	0	0	not significant
3683	GO_PLATELET_DENSE_TUBULAR_NETWORK_MEMBRANE	-1.01	0.31	0	0	0	not significant
3684	GO_POLY_A_PLUS_MRNA_EXPORT_FROM_NUCLEUS	-1.01	0.31	0	0	0	not significant
3685	GO_SPHINGOMYELIN_CATABOLIC_PROCESS	-1.01	0.31	0	0	0	not significant
3686	GO_SUMO_POLYMER_BINDING	-1.01	0.3	0	0	0	not significant
3687	REACTOME_UPTAKE_AND_FUNCTION_OF_DIPHTHERIA_TOXIN	-1.01	0.29	0	0	0	not significant
3688	HEDENFALK_BREAST_CANCER_BRCA1_VS_BRCA2	-1.00	0.4	0	0	0	not significant
3689	MACAEVA_PBMC_RESPONSE_TO_IR	-1.00	0.39	0	0	0	not significant
3690	CHR10Q23	-1.00	0.38	0	0	0	not significant
3691	GO_NEGATIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	-1.00	0.38	0	0	0	not significant
3692	GO_SWI_SNF_SUPERFAMILY_TYPE_COMPLEX	-1.00	0.38	0	0	0	not significant
3693	GO_INTERFERON_BETA_PRODUCTION	-1.00	0.37	0	0	0	not significant
3694	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_OXIDATIVE_S	-1.00	0.37	0	0	0	not significant

3695	GO_POSITIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	-1.00	0.37	0	0	0	not significant
3696	GO_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	-1.00	0.37	0	0	0	not significant
3697	GO_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	-1.00	0.37	0	0	0	not significant
3698	GO_RESPONSE_TO_INTERLEUKIN_12	-1.00	0.37	0	0	0	not significant
3699	YAUCH_HEDGEHOG_SIGNALING_PARACRINE_DN	-1.00	0.37	0	0	0	not significant
3700	DARWICHE_SKIN_TUMOR_PROMOTER_UP	-1.00	0.36	0	0	0	not significant
3701	GO_ACTIN_FILAMENT_BUNDLE	-1.00	0.36	0	0	0	not significant
3702	GO_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	-1.00	0.36	0	0	0	not significant
3703	GO_METHYLTRANSFERASE_COMPLEX	-1.00	0.36	0	0	0	not significant
3704	GO_MICROTUBULE_ORGANIZING_CENTER_PART	-1.00	0.36	0	0	0	not significant
3705	GO_POSITIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYME	-1.00	0.36	0	0	0	not significant
3706	GO_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE	-1.00	0.36	0	0	0	not significant
3707	GO_REGULATION_OF_ATPASE_ACTIVITY	-1.00	0.36	0	0	0	not significant
3708	GO_REGULATION_OF_CELL_SUBSTRATE_ADHESION	-1.00	0.36	0	0	0	not significant
3709	REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS	-1.00	0.36	0	0	0	not significant
3710	GO_CELL_FATE_COMMITMENT	-1.00	0.35	0	0	0	not significant
3711	GO_CHAPERONE_BINDING	-1.00	0.35	0	0	0	not significant
3712	GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	-1.00	0.35	0	0	0	not significant
3713	GO_GOLGI_TO_PLASMA_MEMBRANE_TRANSPORT	-1.00	0.35	0	0	0	not significant
3714	GO_POSITIVE_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	-1.00	0.35	0	0	0	not significant
3715	PID_FAK_PATHWAY	-1.00	0.35	0	0	0	not significant
3716	REACTOME_CYTOCHROME_C_MEDIATED_APOPTOTIC_RESPONSE	-1.00	0.35	0	0	0	not significant
3717	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRAN	-1.00	0.35	0	0	0	not significant
3718	DEMAGALHAES_AGING_DN	-1.00	0.34	0	0	0	not significant
3719	GO_ANOIKIS	-1.00	0.34	0	0	0	not significant
3720	GO_CYTOPLASMIC_MRNA_PROCESSING_BODY_ASSEMBLY	-1.00	0.34	0	0	0	not significant
3721	GO_FIBROBLAST_APOPTOTIC_PROCESS	-1.00	0.34	0	0	0	not significant
3722	GO_GLYCOLIPID_CATABOLIC_PROCESS	-1.00	0.34	0	0	0	not significant
3723	GO_NEGATIVE_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	-1.00	0.34	0	0	0	not significant
3724	GO_PHOSPHORIC_ESTER_HYDROLASE_ACTIVITY	-1.00	0.34	0	0	0	not significant
3725	GO_REGULATION_OF_EMBRYONIC_DEVELOPMENT	-1.00	0.34	0	0	0	not significant
3726	OZEN_MIR125B1_TARGETS	-1.00	0.34	0	0	0	not significant
3727	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP	-1.00	0.34	0	0	0	not significant
3728	UDAYAKUMAR_MED1_TARGETS_UP	-1.00	0.34	0	0	0	not significant
3729	BCAT.100_UP.V1_UP	-1.00	0.33	0	0	0	not significant
3730	CHR12Q15	-1.00	0.33	0	0	0	not significant
3731	CHR17Q24	-1.00	0.33	0	0	0	not significant
3732	GO_CARNITINE_SHUTTLE	-1.00	0.33	0	0	0	not significant
3733	GO_CYCLIN_CDK_POSITIVE_TRANSCRIPTION_ELONGATION_FACTOR_COMPLEX	-1.00	0.33	0	0	0	not significant
3734	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTO	-1.00	0.33	0	0	0	not significant
3735	GO_NUCLEAR_ENVELOPE_REASSEMBLY	-1.00	0.33	0	0	0	not significant
3736	GO_ORGANELLE_ENVELOPE_LUMEN	-1.00	0.33	0	0	0	not significant
3737	GO_PEPTIDYL_METHIONINE_MODIFICATION	-1.00	0.33	0	0	0	not significant
3738	GO_PHOSPHATASE_ACTIVATOR_ACTIVITY	-1.00	0.33	0	0	0	not significant
3739	GO_REGULATION_OF_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	-1.00	0.33	0	0	0	not significant
3740	GO_SYNAPTIC_VESICLE_CYTOSKELETAL_TRANSPORT	-1.00	0.33	0	0	0	not significant
3741	GO_T_CELL_HOMEOSTASIS	-1.00	0.33	0	0	0	not significant
3742	HOFMANN_CELL_LYMPHOMA_DN	-1.00	0.33	0	0	0	not significant
3743	PID_DNA_PK_PATHWAY	-1.00	0.33	0	0	0	not significant
3744	REACTOME_CENTROSOME_MATURATION	-1.00	0.33	0	0	0	not significant
3745	REACTOME_SYNTHESIS_OF_PROSTAGLANDINS_PG_AND_THROMBOXANES_TX	-1.00	0.33	0	0	0	not significant
3746	BIOCARTA_CPSF_PATHWAY	-1.00	0.32	0	0	0	not significant
3747	CHR20Q12	-1.00	0.32	0	0	0	not significant
3748	GO_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_BINDING	-1.00	0.32	0	0	0	not significant
3749	GO_FMN_BINDING	-1.00	0.32	0	0	0	not significant
3750	GO_FORMATION_OF_TRANSLATION_PREINITIATION_COMPLEX	-1.00	0.32	0	0	0	not significant
3751	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	-1.00	0.32	0	0	0	not significant
3752	GO_REGULATION_OF_AUTOPHAGOSOME_MATURATION	-1.00	0.32	0	0	0	not significant
3753	MARIADASON_RESPONSE_TO_CURCUMIN_SULINDAC_5	-1.00	0.32	0	0	0	not significant
3754	REACTOME_CLATHRIN_MEDIATED_ENDOCYTOSIS	-1.00	0.32	0	0	0	not significant
3755	BIOCARTA_PELP1_PATHWAY	-1.00	0.31	0	0	0	not significant
3756	GO_ESTABLISHMENT_OF_LYMPHOCYTE_POLARITY	-1.00	0.31	0	0	0	not significant
3757	GO_MUSCLE_CELL_DIFFERENTIATION	-1.00	0.31	0	0	0	not significant
3758	GO_THYROID_GLAND_DEVELOPMENT	-1.00	0.31	0	0	0	not significant
3759	GO_SHELTERIN_COMPLEX	-1.00	0.3	0	0	0	not significant
3760	GO_TRNA_AMINOACYLATION_FOR_MITOCHONDRIAL_PROTEIN_TRANSLATION	-1.00	0.3	0	0	0	not significant
3761	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	-1.00	0.29	0	0	0	not significant
3762	GO_PLATELET_DENSE_GRANULE_MEMBRANE	-1.00	0.29	0	0	0	not significant
3763	BIOCARTA_AKT_PATHWAY	-0.99	0.36	0	0	0	not significant
3764	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_ARREST	-0.99	0.35	0	0	0	not significant
3765	BURTON_ADIPOGENESIS_PEAK_AT_8HR	-0.99	0.34	0	0	0	not significant
3766	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_CIS	-0.99	0.34	0	0	0	not significant
3767	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_IV_ASSEMBLY	-0.99	0.34	0	0	0	not significant
3768	GO_PEPTIDASE_REGULATOR_ACTIVITY	-0.99	0.34	0	0	0	not significant
3769	GO_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	-0.99	0.34	0	0	0	not significant
3770	GO_SOMATIC_STEM_CELL_DIVISION	-0.99	0.34	0	0	0	not significant
3771	PID_MTOR_4PATHWAY	-0.99	0.34	0	0	0	not significant
3772	PID_TGFBR_PATHWAY	-0.99	0.34	0	0	0	not significant
3773	REACTOME_FORMATION_OF_THE_BETA_CATENIN:TCF_TRANSACTIVATING_COMPL	-0.99	0.34	0	0	0	not significant
3774	CHR10P13	-0.99	0.33	0	0	0	not significant
3775	CYCLIN_D1_UP.V1_UP	-0.99	0.33	0	0	0	not significant
3776	GO_CARDIAC_CHAMBER_DEVELOPMENT	-0.99	0.33	0	0	0	not significant
3777	GO_CILIARY_BASAL_BODY_PLASMA_MEMBRANE_DOCKING	-0.99	0.33	0	0	0	not significant
3778	GO_DEVELOPMENTAL_MATURATION	-0.99	0.33	0	0	0	not significant
3779	GO_FERROUS_IRON_BINDING	-0.99	0.33	0	0	0	not significant
3780	GO_P_BODY	-0.99	0.33	0	0	0	not significant
3781	GO_PROTEIN_KINASE_C_ACTIVITY	-0.99	0.33	0	0	0	not significant
3782	GO_REGULATION_OF_BROWN_FAT_CELL_DIFFERENTIATION	-0.99	0.33	0	0	0	not significant
3783	GO_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	-0.99	0.33	0	0	0	not significant
3784	GO_TRANS_GOLGI_NETWORK_MEMBRANE	-0.99	0.33	0	0	0	not significant
3785	HOEGERKORP_CD44_TARGETS_DIRECT_DN	-0.99	0.33	0	0	0	not significant
3786	MAGRANGEAS_MULTIPLE_MYELOMA_IGG_VS_IGA_DN	-0.99	0.33	0	0	0	not significant
3787	REACTOME_IRS_MEDIATED_SIGNALLING	-0.99	0.33	0	0	0	not significant
3788	GO_GOLGI_VESICLE_BUDDING	-0.99	0.32	0	0	0	not significant
3789	GO_HEART_PROCESS	-0.99	0.32	0	0	0	not significant
3790	GO_POSTSYNAPTIC_NEUROTRANSMITTER_RECEPTOR_INTERNALIZATION	-0.99	0.32	0	0	0	not significant
3791	GO_SUPEROXIDE_ANION_GENERATION	-0.99	0.32	0	0	0	not significant
3792	GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_BINDING	-0.99	0.32	0	0	0	not significant
3793	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP	-0.99	0.32	0	0	0	not significant
3794	REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	-0.99	0.32	0	0	0	not significant
3795	REACTOME_DOWNREGULATION_OF_ERBB4_SIGNALING	-0.99	0.32	0	0	0	not significant
3796	SU_LIVER	-0.99	0.32	0	0	0	not significant
3797	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP	-0.99	0.31	0	0	0	not significant
3798	GO_CARDIAC_MYOFIBRIL_ASSEMBLY	-0.99	0.31	0	0	0	not significant
3799	GO_REGULATION_OF_PEPTIDASE_ACTIVITY	-0.99	0.31	0	0	0	not significant
3800	GO_REGULATION_OF_PROTEIN_HOMODIMERIZATION_ACTIVITY	-0.99	0.31	0	0	0	not significant
3801	GO_RETINA_LAYER_FORMATION	-0.99	0.31	0	0	0	not significant
3802	GO_SMALL_GTPASE_BINDING	-0.99	0.31	0	0	0	not significant
3803	REACTOME_INOSITOL_PHOSPHATE_METABOLISM	-0.99	0.31	0	0	0	not significant

3804	GO_IRON_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.99	0.3	0	0	0	not significant
3805	GO_POSITIVE_REGULATION_OF_MONOOXYGENASE_ACTIVITY	-0.99	0.3	0	0	0	not significant
3806	GO_REGULATION_OF_KERATINOCYTE_DIFFERENTIATION	-0.99	0.3	0	0	0	not significant
3807	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CENTROSOME	-0.99	0.3	0	0	0	not significant
3808	GO_REGULATION_OF_VASCULOGENESIS	-0.99	0.3	0	0	0	not significant
3809	GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY_INTERCONVERTING_ALDOSE	-0.99	0.29	0	0	0	not significant
3810	GO_NEGATIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	-0.99	0.29	0	0	0	not significant
3811	GO_PEPTIDYL_LYSINE_MODIFICATION	-0.99	0.29	0	0	0	not significant
3812	GO_PHOTORECEPTOR_DISC_MEMBRANE	-0.99	0.29	0	0	0	not significant
3813	GO_UTP_BIOSYNTHETIC_PROCESS	-0.99	0.29	0	0	0	not significant
3814	GO_CYCLIC_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	-0.99	0.28	0	0	0	not significant
3815	GO_HISTONE_H2A_K63_LINKED_UBIQUITINATION	-0.99	0.28	0	0	0	not significant
3816	GO_REGULATION_OF_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	-0.99	0.28	0	0	0	not significant
3817	GO_LSM1_7_PAT1_COMPLEX	-0.99	0.27	0	0	0	not significant
3818	GO_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR	-0.98	0.34	0	0	0	not significant
3819	GO_REGULATION_OF_MUSCLE_SYSTEM_PROCESS	-0.98	0.34	0	0	0	not significant
3820	CHR16Q22	-0.98	0.33	0	0	0	not significant
3821	GO_CERAMIDE_BINDING	-0.98	0.33	0	0	0	not significant
3822	GO_N_METHYLTRANSFERASE_ACTIVITY	-0.98	0.33	0	0	0	not significant
3823	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	-0.98	0.33	0	0	0	not significant
3824	GO_REGULATION_OF_NUCLEASE_ACTIVITY	-0.98	0.33	0	0	0	not significant
3825	RIZKI_TUMOR_INVASIVENESS_3D_UP	-0.98	0.33	0	0	0	not significant
3826	SMIRNOV_RESPONSE_TO_IR_6HR_UP	-0.98	0.33	0	0	0	not significant
3827	BIOCARTA_AGR_PATHWAY	-0.98	0.32	0	0	0	not significant
3828	BIOCARTA_CALCINEURIN_PATHWAY	-0.98	0.32	0	0	0	not significant
3829	CHOI_ATL_CHRONIC_VS_ACUTE_DN	-0.98	0.32	0	0	0	not significant
3830	CHR9P21	-0.98	0.32	0	0	0	not significant
3831	FIGUEROA_AML_METHYLATION_CLUSTER_2_UP	-0.98	0.32	0	0	0	not significant
3832	GO_BASE_EXCISION_REPAIR_AP_SITE_FORMATION	-0.98	0.32	0	0	0	not significant
3833	GO_CARDIAC_CELL_DEVELOPMENT	-0.98	0.32	0	0	0	not significant
3834	GO_COATED_MEMBRANE	-0.98	0.32	0	0	0	not significant
3835	GO_PHOSPHATIDYLINOSITOL_3_5_BISPHOSPHATE_PHOSPHATASE_ACTIVITY	-0.98	0.32	0	0	0	not significant
3836	GO_PHOSPHATIDYLINOSITOL_3_KINASE_BINDING	-0.98	0.32	0	0	0	not significant
3837	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_	-0.98	0.32	0	0	0	not significant
3838	GO_PRE_MIRNA_PROCESSING	-0.98	0.32	0	0	0	not significant
3839	GO_REGULATION_OF_CELL_MATRIX_ADHESION	-0.98	0.32	0	0	0	not significant
3840	GO_REGULATION_OF_ER_TO_GOLGI_VESICLE_MEDIATED_TRANSPORT	-0.98	0.32	0	0	0	not significant
3841	GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	-0.98	0.32	0	0	0	not significant
3842	MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_UP	-0.98	0.32	0	0	0	not significant
3843	REACTOME_SHC1_EVENTS_IN_ERBB2_SIGNALING	-0.98	0.32	0	0	0	not significant
3844	WALLACE_PROSTATE_CANCER_UP	-0.98	0.32	0	0	0	not significant
3845	GO_PIGMENT_GRANULE_MATURATION	-0.98	0.31	0	0	0	not significant
3846	GO_POSITIVE_REGULATION_OF_VASCULOGENESIS	-0.98	0.31	0	0	0	not significant
3847	GO_REGULATION_OF_CELL_PROJECTION_ASSEMBLY	-0.98	0.31	0	0	0	not significant
3848	OUYANG_PROSTATE_CANCER_PROGRESSION_DN	-0.98	0.31	0	0	0	not significant
3849	REACTOME_SIGNALLING_TO_ERKS	-0.98	0.31	0	0	0	not significant
3850	GO_CORONARY_ARTERY_MORPHOGENESIS	-0.98	0.3	0	0	0	not significant
3851	GO_DEAMINASE_ACTIVITY	-0.98	0.3	0	0	0	not significant
3852	GO_IMMUNOLOGICAL_SYNAPSE_FORMATION	-0.98	0.3	0	0	0	not significant
3853	GO_LAYER_FORMATION_IN_CEREBRAL_CORTEX	-0.98	0.3	0	0	0	not significant
3854	GO_NEGATIVE_REGULATION_OF_PHAGOCYTOSIS	-0.98	0.3	0	0	0	not significant
3855	GO_PHOSPHATIDYLGLYCEROL_METABOLIC_PROCESS	-0.98	0.3	0	0	0	not significant
3856	GO_PYRIMIDINE_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-0.98	0.3	0	0	0	not significant
3857	GO_REGULATION_OF_MONOCYTE_DIFFERENTIATION	-0.98	0.3	0	0	0	not significant
3858	GO_REGULATION_OF_RUFFLE_ASSEMBLY	-0.98	0.3	0	0	0	not significant
3859	GO_RESPONSE_TO_NITROSATIVE_STRESS	-0.98	0.3	0	0	0	not significant
3860	MOOTHA_TCA	-0.98	0.3	0	0	0	not significant
3861	REACTOME_PLASMA_LIPOPROTEIN_ASSEMBLY	-0.98	0.3	0	0	0	not significant
3862	REACTOME_REPRESSION_OF_WNT_TARGET_GENES	-0.98	0.3	0	0	0	not significant
3863	REACTOME_SMAC_XIAP_REGULATED_APOPTOTIC_RESPONSE	-0.98	0.3	0	0	0	not significant
3864	CHR5Q31	-0.98	0.29	0	0	0	not significant
3865	GO_B_CELL_LINEAGE_COMMITMENT	-0.98	0.29	0	0	0	not significant
3866	GO_COHESIN_LOADING	-0.98	0.29	0	0	0	not significant
3867	GO_MODIFICATION_OF_POSTSYNAPTIC_ACTIN_CYTOSKELETON	-0.98	0.29	0	0	0	not significant
3868	GO_NK_T_CELL_ACTIVATION	-0.98	0.29	0	0	0	not significant
3869	GO_PROTEIN_SERINE_THREONINE_PHOSPHATASE_INHIBITOR_ACTIVITY	-0.98	0.29	0	0	0	not significant
3870	REACTOME_SIGNALING_BY_NTRK2_TRKB	-0.98	0.29	0	0	0	not significant
3871	CHR2P13	-0.98	0.28	0	0	0	not significant
3872	GO_CELLULAR_RESPONSE_TO_ESTROGEN_STIMULUS	-0.98	0.28	0	0	0	not significant
3873	GO_PEROXISOME_PROLIFERATOR_ACTIVATED_RECEPTOR_BINDING	-0.98	0.28	0	0	0	not significant
3874	GO_POSITIVE_REGULATION_BY_HOST_OF_VIRAL_GENOME_REPLICATION	-0.98	0.28	0	0	0	not significant
3875	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	-0.98	0.28	0	0	0	not significant
3876	GO_PROTEIN_LIPOYLATION	-0.98	0.28	0	0	0	not significant
3877	GO_PYRUVATE_DEHYDROGENASE_COMPLEX	-0.98	0.28	0	0	0	not significant
3878	GO_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	-0.98	0.28	0	0	0	not significant
3879	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CILIUM	-0.98	0.28	0	0	0	not significant
3880	GO_PARANODE_REGION_OF_AXON	-0.98	0.27	0	0	0	not significant
3881	BENPORATH_ES_2	-0.97	0.33	0	0	0	not significant
3882	GO_BLOOD_VESSEL_REMODELING	-0.97	0.33	0	0	0	not significant
3883	GO_ATPASE_BINDING	-0.97	0.32	0	0	0	not significant
3884	GO_MITOTIC_CYTOKINETIC_PROCESS	-0.97	0.32	0	0	0	not significant
3885	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_DRUG	-0.97	0.32	0	0	0	not significant
3886	GO_STRIATED_MUSCLE_CELL_PROLIFERATION	-0.97	0.32	0	0	0	not significant
3887	REACTOME_BASE_EXCISION_REPAIR_AP_SITE_FORMATION	-0.97	0.32	0	0	0	not significant
3888	AIGNER_ZEB1_TARGETS	-0.97	0.31	0	0	0	not significant
3889	GO_POSITIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	-0.97	0.31	0	0	0	not significant
3890	GO_REGION_OF_CYTOSOL	-0.97	0.31	0	0	0	not significant
3891	GO_SPERMATID_NUCLEUS_DIFFERENTIATION	-0.97	0.31	0	0	0	not significant
3892	JIANG_AGING_HYPOTHALAMUS_UP	-0.97	0.31	0	0	0	not significant
3893	KEGG_RIBOFLAVIN_METABOLISM	-0.97	0.31	0	0	0	not significant
3894	BAKER_HEMATOPOIESIS_STAT3_TARGETS	-0.97	0.3	0	0	0	not significant
3895	GO_CYTOPLASMIC_TRANSLATIONAL_INITIATION	-0.97	0.3	0	0	0	not significant
3896	GO_POSTSYNAPTIC_CYTOSOL	-0.97	0.3	0	0	0	not significant
3897	GO_PROTEIN_FOLDING_CHAPERONE	-0.97	0.3	0	0	0	not significant
3898	GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	-0.97	0.3	0	0	0	not significant
3899	GO_REGULATION_OF_TRANSLATIONAL_INITIATION_IN_RESPONSE_TO_STRESS	-0.97	0.3	0	0	0	not significant
3900	GO_RESPONSE_TO_VITAMIN_D	-0.97	0.3	0	0	0	not significant
3901	KYNG_WERNER_SYNDROM_DN	-0.97	0.3	0	0	0	not significant
3902	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_6	-0.97	0.3	0	0	0	not significant
3903	REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	-0.97	0.3	0	0	0	not significant
3904	REACTOME_CHAPERONE_MEDIATED_AUTOPHAGY	-0.97	0.3	0	0	0	not significant
3905	REACTOME_DUAL_INCISION_IN_TC_NER	-0.97	0.3	0	0	0	not significant
3906	REACTOME_MET_PROMOTES_CELL_MOTILITY	-0.97	0.3	0	0	0	not significant
3907	REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	-0.97	0.3	0	0	0	not significant
3908	REACTOME_UPTAKE_AND_FUNCTION_OF_ANTHRAX_TOXINS	-0.97	0.3	0	0	0	not significant
3909	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX1_UP	-0.97	0.3	0	0	0	not significant
3910	ALONSO_METASTASIS_UP	-0.97	0.29	0	0	0	not significant
3911	BIOCARTA_HIVNEF_PATHWAY	-0.97	0.29	0	0	0	not significant
3912	GO_EXIT_FROM_MITOSIS	-0.97	0.29	0	0	0	not significant

3913	GO_G_QUADRUPLEX_DNA_BINDING	-0.97	0.29	0	0	0	not significant
3914	GO_METHYLATION_DEPENDENT_CHROMATIN_SILENCING	-0.97	0.29	0	0	0	not significant
3915	GO_NEGATIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	-0.97	0.29	0	0	0	not significant
3916	GO_NEUROTROPHIN_TRK_RECEPTOR_SIGNALING_PATHWAY	-0.97	0.29	0	0	0	not significant
3917	GO_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOSIS	-0.97	0.29	0	0	0	not significant
3918	GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.97	0.29	0	0	0	not significant
3919	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	-0.97	0.29	0	0	0	not significant
3920	KOINUMA_COLON_CANCER_MSI_DN	-0.97	0.29	0	0	0	not significant
3921	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_24	-0.97	0.29	0	0	0	not significant
3922	GO_COLUMNAR_CUBOIDAL_EPITHELIAL_CELL_DIFFERENTIATION	-0.97	0.28	0	0	0	not significant
3923	GO_REGULATION_OF_RIBONUCLEOPROTEIN_COMPLEX_LOCALIZATION	-0.97	0.28	0	0	0	not significant
3924	GO_VASCULAR_ASSOCIATED_SMOOTH_MUSCLE_CELL_APOPTOTIC_PROCESS	-0.97	0.28	0	0	0	not significant
3925	GO_NEUROTRANSMITTER_RECEPTOR_INTERNALIZATION	-0.97	0.27	0	0	0	not significant
3926	GO_SCF_UBIQUITIN_LIGASE_COMPLEX	-0.97	0.27	0	0	0	not significant
3927	GO_VIRAL_TRANSLATIONAL_TERMINATION_REINITIATION	-0.97	0.27	0	0	0	not significant
3928	REACTOME_METHIONINE_SALVAGE_PATHWAY	-0.97	0.27	0	0	0	not significant
3929	SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_UP	-0.97	0.27	0	0	0	not significant
3930	SCHUHMACHER_MYC_TARGETS_DN	-0.97	0.27	0	0	0	not significant
3931	GO_CELL_CORTEX	-0.97	0.26	0	0	0	not significant
3932	GO_REGULATION_OF_GLUCOSE_TRANSMEMBRANE_TRANSPORT	-0.97	0.26	0	0	0	not significant
3933	GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	-0.97	0.26	0	0	0	not significant
3934	GO_VESICLE_TRANSPORT_ALONG_ACTIN_FILAMENT	-0.97	0.26	0	0	0	not significant
3935	GO_REGULATION_OF_ORGANELLE_ASSEMBLY	-0.97	0.25	0	0	0	not significant
3936	RICKMAN_METASTASIS_DN	-0.97	0.24	0	0	0	not significant
3937	VANOEVELEN_MYOGENESIS_SIN3A_TARGETS	-0.97	0.23	0	0	0	not significant
3938	GO_CELL_GROWTH	-0.97	0.2	0	0	0	not significant
3939	ASGHARZADEH_NEUROBLASTOMA_POOR_SURVIVAL_DN	-0.96	0.32	0	0	0	not significant
3940	GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	-0.96	0.31	0	0	0	not significant
3941	KYNG_RESPONSE_TO_H2O2_VIA_ERCC6	-0.96	0.31	0	0	0	not significant
3942	CHR2P23	-0.96	0.3	0	0	0	not significant
3943	GO_CORTICAL_CYTOSKELETON_ORGANIZATION	-0.96	0.3	0	0	0	not significant
3944	GO_GTP_METABOLIC_PROCESS	-0.96	0.3	0	0	0	not significant
3945	GO_LABYRINTHINE_LAYER_MORPHOGENESIS	-0.96	0.3	0	0	0	not significant
3946	GO_REGULATION_OF_PRESYNAPSE_ORGANIZATION	-0.96	0.3	0	0	0	not significant
3947	GO_S_ADENOSYL_L_METHIONINE_BINDING	-0.96	0.3	0	0	0	not significant
3948	HEIDENBLAD_AMPLIFIED_IN_PANCREATIC_CANCER	-0.96	0.3	0	0	0	not significant
3949	REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI	-0.96	0.3	0	0	0	not significant
3950	BIOCARTA_BAD_PATHWAY	-0.96	0.29	0	0	0	not significant
3951	GO_POSITIVE_REGULATION_OF_CELL_GROWTH	-0.96	0.29	0	0	0	not significant
3952	GO_POSITIVE_REGULATION_OF_MITOTIC_SISTER_CHROMATID_SEGREGATION	-0.96	0.29	0	0	0	not significant
3953	GO_POSITIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	-0.96	0.29	0	0	0	not significant
3954	GO_RETROMER_COMPLEX	-0.96	0.29	0	0	0	not significant
3955	GO_SOMITE_DEVELOPMENT	-0.96	0.29	0	0	0	not significant
3956	KERLEY_RESPONSE_TO_CISPLATIN_UP	-0.96	0.29	0	0	0	not significant
3957	PID_NOTCH_PATHWAY	-0.96	0.29	0	0	0	not significant
3958	REACTOME_NEF_MEDIATED_CD4_DOWN_REGULATION	-0.96	0.29	0	0	0	not significant
3959	REACTOME_RAP1_SIGNALLING	-0.96	0.29	0	0	0	not significant
3960	ZHENG_IL22_SIGNALING_DN	-0.96	0.29	0	0	0	not significant
3961	ZHONG_SECRETOME_OF_LUNG_CANCER_AND_ENDOTHELIUM	-0.96	0.29	0	0	0	not significant
3962	BIOCARTA_AKAP13_PATHWAY	-0.96	0.28	0	0	0	not significant
3963	CHR15Q13	-0.96	0.28	0	0	0	not significant
3964	CHR7Q33	-0.96	0.28	0	0	0	not significant
3965	GO_CELLULAR_RESPONSE_TO_NUTRIENT	-0.96	0.28	0	0	0	not significant
3966	GO_REGULATION_OF_GRANULOCYTE_DIFFERENTIATION	-0.96	0.28	0	0	0	not significant
3967	GO_REGULATION_OF_SUPEROXIDE_ANION_GENERATION	-0.96	0.28	0	0	0	not significant
3968	GO_RESPONSE_TO_HEPATOCYTE_GROWTH_FACTOR	-0.96	0.28	0	0	0	not significant
3969	PID_RAC1_PATHWAY	-0.96	0.28	0	0	0	not significant
3970	YE_METASTATIC_LIVER_CANCER	-0.96	0.28	0	0	0	not significant
3971	BIOCARTA_CBL_PATHWAY	-0.96	0.27	0	0	0	not significant
3972	DAZARD_UV_RESPONSE_CLUSTER_G1	-0.96	0.27	0	0	0	not significant
3973	FIRESTEIN_CTNNB1_PATHWAY_AND_PROLIFERATION	-0.96	0.27	0	0	0	not significant
3974	GO_ELONGATOR_HOLOENZYME_COMPLEX	-0.96	0.27	0	0	0	not significant
3975	GO_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	-0.96	0.27	0	0	0	not significant
3976	GO_NEGATIVE_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	-0.96	0.27	0	0	0	not significant
3977	GO_PANCREATIC_JUICE_SECRETION	-0.96	0.27	0	0	0	not significant
3978	GO_PIGMENT_ACCUMULATION	-0.96	0.27	0	0	0	not significant
3979	GO_UBIQUITIN_CONJUGATING_ENZYME_BINDING	-0.96	0.27	0	0	0	not significant
3980	GO_CYCLOOXYGENASE_PATHWAY	-0.96	0.26	0	0	0	not significant
3981	GO_H4_HISTONE_ACETYLTRANSFERASE_COMPLEX	-0.96	0.26	0	0	0	not significant
3982	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_HYPOXIA	-0.96	0.26	0	0	0	not significant
3983	GO_NEGATIVE_REGULATION_OF_CELL_DIVISION	-0.96	0.26	0	0	0	not significant
3984	MATTIOLI_MGUS_VS_PCL	-0.96	0.26	0	0	0	not significant
3985	MCBRYAN_TERMINAL_END_BUD_UP	-0.96	0.26	0	0	0	not significant
3986	GO_NEGATIVE_REGULATION_OF_MAPK_CASCADE	-0.96	0.24	0	0	0	not significant
3987	BENPORATH_OCT4_TARGETS	-0.96	0.23	0	0	0	not significant
3988	GO_POSITIVE_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	-0.96	0.23	0	0	0	not significant
3989	GRYDER_PAX3FOXO1_TOP_ENHANCERS	-0.96	0.18	0	0	0	not significant
3990	GO_CILIUM	-0.96	0.17	0	0	0	not significant
3991	GO_NUCLEAR_CHROMATIN	-0.96	0.17	0	0	0	not significant
3992	GO_ZINC_ION_BINDING	-0.96	0.14	0	0	0	not significant
3993	BIOCARTA_CTCF_PATHWAY	-0.95	0.31	0	0	0	not significant
3994	GO_BIOTIN_METABOLIC_PROCESS	-0.95	0.3	0	0	0	not significant
3995	GO_CATION_CATION_ANTIPORTER_ACTIVITY	-0.95	0.3	0	0	0	not significant
3996	GO_CALCINEURIN_MEDIATED_SIGNALING	-0.95	0.29	0	0	0	not significant
3997	GO_NEGATIVE_REGULATION_OF_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS	-0.95	0.29	0	0	0	not significant
3998	GO_POSITIVE_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_CELL_DEATH	-0.95	0.29	0	0	0	not significant
3999	CHR7Q32	-0.95	0.28	0	0	0	not significant
4000	GO_3_UTR_MEDIATED_MRNA_STABILIZATION	-0.95	0.28	0	0	0	not significant
4001	GO_MONONUCLEAR_CELL_DIFFERENTIATION	-0.95	0.28	0	0	0	not significant
4002	GO_MRNA_3_SPLICE_SITE_RECOGNITION	-0.95	0.28	0	0	0	not significant
4003	GO_NEGATIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	-0.95	0.28	0	0	0	not significant
4004	GO_NUCLEOSOME_POSITIONING	-0.95	0.28	0	0	0	not significant
4005	GO_POSITIVE_REGULATION_OF_RUFFLE_ASSEMBLY	-0.95	0.28	0	0	0	not significant
4006	GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE	-0.95	0.28	0	0	0	not significant
4007	GO_REGULATION_OF_MYOBLAST_DIFFERENTIATION	-0.95	0.28	0	0	0	not significant
4008	GO_SMALL_RNA_LOADING_ONTO_RISC	-0.95	0.28	0	0	0	not significant
4009	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_2_UP	-0.95	0.28	0	0	0	not significant
4010	PID_ERBB1_RECEPTOR_PROXIMAL_PATHWAY	-0.95	0.28	0	0	0	not significant
4011	REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	-0.95	0.28	0	0	0	not significant
4012	THEODOROU_MAMMARY_TUMORIGENESIS	-0.95	0.28	0	0	0	not significant
4013	CHR8Q21	-0.95	0.27	0	0	0	not significant
4014	CLIMENT_BREAST_CANCER_COPY_NUMBER_DN	-0.95	0.27	0	0	0	not significant
4015	GENTILE_UV_RESPONSE_CLUSTER_D2	-0.95	0.27	0	0	0	not significant
4016	GO_BRONCHUS_DEVELOPMENT	-0.95	0.27	0	0	0	not significant
4017	GO_ER_MEMBRANE_PROTEIN_COMPLEX	-0.95	0.27	0	0	0	not significant
4018	GO_FUCOSYLTRANSFERASE_ACTIVITY	-0.95	0.27	0	0	0	not significant
4019	GO_GLUTAMATE_RECEPTOR_BINDING	-0.95	0.27	0	0	0	not significant
4020	GO_NEURON_REMODELING	-0.95	0.27	0	0	0	not significant
4021	GO_PEPTIDYL_DIPHTHAMIDE_BIOSYNTHETIC_PROCESS_FROM_PEPTIDYL_HISTIDIN	-0.95	0.27	0	0	0	not significant

4022	GO_PEROXIREDOXIN_ACTIVITY	-0.95	0.27	0	0	0	not significant
4023	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	-0.95	0.27	0	0	0	not significant
4024	GO_REGULATION_OF_METANEPHROS_DEVELOPMENT	-0.95	0.27	0	0	0	not significant
4025	GO_RESPONSE_TO_BRONCHODILATOR	-0.95	0.27	0	0	0	not significant
4026	GO_SIN3_COMPLEX	-0.95	0.27	0	0	0	not significant
4027	GO_TELOMERASE_HOLOENZYME_COMPLEX_ASSEMBLY	-0.95	0.27	0	0	0	not significant
4028	CHR2Q35	-0.95	0.26	0	0	0	not significant
4029	GO_MACROLIDE_BINDING	-0.95	0.26	0	0	0	not significant
4030	GO_NEGATIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPRE	-0.95	0.26	0	0	0	not significant
4031	GO_PHOSPHOLIPID_DEPHOSPHORYLATION	-0.95	0.26	0	0	0	not significant
4032	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	-0.95	0.26	0	0	0	not significant
4033	GO_REGULATION_OF_NUCLEAR_TRANSCRIBED_MRNA_POLY_A_TAIL_SHORTENING	-0.95	0.26	0	0	0	not significant
4034	GO_RESPONSE_TO_THYROID_HORMONE	-0.95	0.26	0	0	0	not significant
4035	NIELSEN_SYNOVIAL_SARCOMA_UP	-0.95	0.26	0	0	0	not significant
4036	SIG_CHEMOTAXIS	-0.95	0.26	0	0	0	not significant
4037	TBK1.DN.48HRS_UP	-0.95	0.26	0	0	0	not significant
4038	CHR7Q34	-0.95	0.25	0	0	0	not significant
4039	GO_CDC73_PAF1_COMPLEX	-0.95	0.25	0	0	0	not significant
4040	GO_CYSTEINE_TYPE_PEPTIDASE_ACTIVITY	-0.95	0.25	0	0	0	not significant
4041	GO_D1_DOPAMINE_RECEPTOR_BINDING	-0.95	0.25	0	0	0	not significant
4042	GO_MONOVALENT_CATION_PROTON_ANTIPORTER_ACTIVITY	-0.95	0.25	0	0	0	not significant
4043	GO_PARASPECKLES	-0.95	0.25	0	0	0	not significant
4044	GO_STEROID_HORMONE_SECRETION	-0.95	0.25	0	0	0	not significant
4045	PRC2_EZH2_UP.V1_UP	-0.95	0.25	0	0	0	not significant
4046	GO_CAMERA_TYPE_EYE_PHOTORECEPTOR_CELL_DIFFERENTIATION	-0.95	0.24	0	0	0	not significant
4047	GO_NEGATIVE_REGULATION_OF_AUTOPHAGY	-0.95	0.24	0	0	0	not significant
4048	GO_POSITIVE_REGULATION_OF_BINDING	-0.95	0.24	0	0	0	not significant
4049	GO_POSITIVE_REGULATION_OF_LAMELLIPODIUM_MORPHOGENESIS	-0.95	0.24	0	0	0	not significant
4050	GO_REGULATION_OF_DENDRITE_DEVELOPMENT	-0.95	0.24	0	0	0	not significant
4051	GO_AMIDE_BINDING	-0.95	0.23	0	0	0	not significant
4052	GO_DEVELOPMENTAL_CELL_GROWTH	-0.95	0.22	0	0	0	not significant
4053	GO_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY	-0.95	0.22	0	0	0	not significant
4054	GO_PATTERN_SPECIFICATION_PROCESS	-0.95	0.21	0	0	0	not significant
4055	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3	-0.95	0.18	0	0	0	not significant
4056	GO_REGULATION_OF_SYSTEM_PROCESS	-0.95	0.17	0	0	0	not significant
4057	GO_EPITHELIUM_DEVELOPMENT	-0.95	0.12	0	0	0	not significant
4058	GO_TRANSITION_METAL_ION_BINDING	-0.95	0.12	0	0	0	not significant
4059	GO_CELL_CELL_SIGNALING	-0.95	0.1	0	0	0	not significant
4060	GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA	-0.94	0.29	0	0	0	not significant
4061	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_UP	-0.94	0.29	0	0	0	not significant
4062	BIOCARTA_BARRESTIN_SRC_PATHWAY	-0.94	0.28	0	0	0	not significant
4063	CHANG_IMMORTALIZED_BY_HPV31_UP	-0.94	0.28	0	0	0	not significant
4064	GO_CELLULAR_COMPONENT_DISASSEMBLY_INVOLVED_IN_EXECUTION_PHASE_OF	-0.94	0.28	0	0	0	not significant
4065	GO_COMPLEMENT_ACTIVATION	-0.94	0.28	0	0	0	not significant
4066	GO_CYTOCHROME_COMPLEX	-0.94	0.28	0	0	0	not significant
4067	GO_DETECTION_OF_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION	-0.94	0.28	0	0	0	not significant
4068	GO_GOLGI_TO_VACUOLE_TRANSPORT	-0.94	0.28	0	0	0	not significant
4069	GO_INHIBITORY_SYNAPSE	-0.94	0.28	0	0	0	not significant
4070	GO_MAMMARY_GLAND_MORPHOGENESIS	-0.94	0.28	0	0	0	not significant
4071	GO_MITOTIC_CHROMOSOME_CONDENSATION	-0.94	0.28	0	0	0	not significant
4072	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN	-0.94	0.28	0	0	0	not significant
4073	GO_9PLUS0_NON_MOTILE_CILIUM	-0.94	0.27	0	0	0	not significant
4074	GO_AXONEME_PART	-0.94	0.27	0	0	0	not significant
4075	GO_CELLULAR_RESPONSE_TO_OXYGEN_RADICAL	-0.94	0.27	0	0	0	not significant
4076	GO_NEGATIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	-0.94	0.27	0	0	0	not significant
4077	GO_REGULATION_OF_FILOPODIUM_ASSEMBLY	-0.94	0.27	0	0	0	not significant
4078	GO_TRACHEA_MORPHOGENESIS	-0.94	0.27	0	0	0	not significant
4079	GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION	-0.94	0.27	0	0	0	not significant
4080	KEGG_SELENOAMINO_ACID_METABOLISM	-0.94	0.27	0	0	0	not significant
4081	NADERI_BREAST_CANCER_PROGNOSIS_DN	-0.94	0.27	0	0	0	not significant
4082	REACTOME_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE	-0.94	0.27	0	0	0	not significant
4083	BIOCARTA_ARF_PATHWAY	-0.94	0.26	0	0	0	not significant
4084	CHR4Q12	-0.94	0.26	0	0	0	not significant
4085	GENTILE_UV_RESPONSE_CLUSTER_D8	-0.94	0.26	0	0	0	not significant
4086	GO_BETA_CATENIN_DESTRUCTION_COMPLEX	-0.94	0.26	0	0	0	not significant
4087	GO_CARDIAC_CONDUCTION_SYSTEM_DEVELOPMENT	-0.94	0.26	0	0	0	not significant
4088	GO_CORONARY_VASCULATURE_MORPHOGENESIS	-0.94	0.26	0	0	0	not significant
4089	GO_PEPTIDYL_HISTIDINE_MODIFICATION	-0.94	0.26	0	0	0	not significant
4090	GO_POSITIVE_REGULATION_OF_AMINO_ACID_TRANSPORT	-0.94	0.26	0	0	0	not significant
4091	GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	-0.94	0.26	0	0	0	not significant
4092	GO_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	-0.94	0.26	0	0	0	not significant
4093	KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	-0.94	0.26	0	0	0	not significant
4094	KEGG_PYRUVATE_METABOLISM	-0.94	0.26	0	0	0	not significant
4095	KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_DN	-0.94	0.26	0	0	0	not significant
4096	LABBE_TGFB1_TARGETS_DN	-0.94	0.26	0	0	0	not significant
4097	PID_IL2_PI3K_PATHWAY	-0.94	0.26	0	0	0	not significant
4098	REACTOME_RAS_ACTIVATION_UPON_CA2PLUS_INFLUX_THROUGH_NMDA_RECEPTO	-0.94	0.26	0	0	0	not significant
4099	XU_CREBBP_TARGETS_UP	-0.94	0.26	0	0	0	not significant
4100	FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_DN	-0.94	0.25	0	0	0	not significant
4101	GO_DNA_DEAMINATION	-0.94	0.25	0	0	0	not significant
4102	GO_MEMBRANE_DEPOLARIZATION_DURING_CARDIAC_MUSCLE_CELL_ACTION_POT	-0.94	0.25	0	0	0	not significant
4103	GO_OBSERVATIONAL_LEARNING	-0.94	0.25	0	0	0	not significant
4104	GO_POSTSYNAPTIC_DENSITY_ASSEMBLY	-0.94	0.25	0	0	0	not significant
4105	GO_SINGLE_STRANDED_VIRAL_RNA_REPLICATION_VIA_DOUBLE_STRANDED_DNA	-0.94	0.25	0	0	0	not significant
4106	GO_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	-0.94	0.25	0	0	0	not significant
4107	GO_SUCCINYL_COA_METABOLIC_PROCESS	-0.94	0.25	0	0	0	not significant
4108	LUI_THYROID_CANCER_CLUSTER_4	-0.94	0.25	0	0	0	not significant
4109	REACTOME_RSK_ACTIVATION	-0.94	0.25	0	0	0	not significant
4110	ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_UP	-0.94	0.25	0	0	0	not significant
4111	TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_DN	-0.94	0.25	0	0	0	not significant
4112	GO_INSULIN_BINDING	-0.94	0.24	0	0	0	not significant
4113	GO_MUSCLE_HYPERTROPHY	-0.94	0.24	0	0	0	not significant
4114	GO_PROTEIN_LOCALIZATION_TO_CILIUM	-0.94	0.24	0	0	0	not significant
4115	GO_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	-0.94	0.24	0	0	0	not significant
4116	GO_RESPONSE_TO_LEUKEMIA_INHIBITORY_FACTOR	-0.94	0.24	0	0	0	not significant
4117	PID_HIF2PATHWAY	-0.94	0.24	0	0	0	not significant
4118	REACTOME_SIGNALING_BY_BRAF_AND_RAF_FUSIONS	-0.94	0.24	0	0	0	not significant
4119	SEKI_INFLAMMATORY_RESPONSE_LPS_DN	-0.94	0.24	0	0	0	not significant
4120	GO_CONTRACTILE_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	-0.94	0.23	0	0	0	not significant
4121	GO_POSITIVE_REGULATION_OF_PLASMA_MEMBRANE_BOUNDED_CELL_PROJECTIO	-0.94	0.23	0	0	0	not significant
4122	GO_ENHANCER_BINDING	-0.94	0.22	0	0	0	not significant
4123	GO_EPIDERMIS_DEVELOPMENT	-0.94	0.22	0	0	0	not significant
4124	GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	-0.94	0.22	0	0	0	not significant
4125	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17	-0.94	0.22	0	0	0	not significant
4126	GO_RETROGRADE_TRANSPORT_ENDOSOME_TO_GOLGI	-0.94	0.21	0	0	0	not significant
4127	GO_ANIMAL_ORGAN_MORPHOGENESIS	-0.94	0.13	0	0	0	not significant
4128	GO_ACETYL_COA_BIOSYNTHETIC_PROCESS_FROM_PYRUVATE	-0.93	0.28	0	0	0	not significant
4129	GO_PEPTIDYL_LYSINE_DIMETHYLATION	-0.93	0.28	0	0	0	not significant
4130	GO_BODY_MORPHOGENESIS	-0.93	0.27	0	0	0	not significant

4131	ONGUSAHA_TP53_TARGETS	-0.93	0.27	0	0	0	not significant
4132	REACTOME_RECEPTOR_MEDIATED_MITOPHAGY	-0.93	0.27	0	0	0	not significant
4133	ROZANOV_MMP14_TARGETS_DN	-0.93	0.27	0	0	0	not significant
4134	BIOCARTA_VIP_PATHWAY	-0.93	0.26	0	0	0	not significant
4135	GO_CORONARY_VASCULATURE_DEVELOPMENT	-0.93	0.26	0	0	0	not significant
4136	GO_CYTOPLASMIC_TRANSLATIONAL_ELONGATION	-0.93	0.26	0	0	0	not significant
4137	GO_EXONUCLEOLYTIC_TRIMMING_INVOLVED_IN_RRNA_PROCESSING	-0.93	0.26	0	0	0	not significant
4138	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	-0.93	0.26	0	0	0	not significant
4139	GO_NEGATIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	-0.93	0.26	0	0	0	not significant
4140	GO_NEGATIVE_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATION	-0.93	0.26	0	0	0	not significant
4141	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	-0.93	0.26	0	0	0	not significant
4142	GO_REGULATION_OF_PROTON_TRANSPORT	-0.93	0.26	0	0	0	not significant
4143	GO_STRUCTURAL_CONSTITUENT_OF_MUSCLE	-0.93	0.26	0	0	0	not significant
4144	PID_IL1_PATHWAY	-0.93	0.26	0	0	0	not significant
4145	REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	-0.93	0.26	0	0	0	not significant
4146	SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_UP	-0.93	0.26	0	0	0	not significant
4147	CHR13Q12	-0.93	0.25	0	0	0	not significant
4148	CHR1P22	-0.93	0.25	0	0	0	not significant
4149	GO_DENDRITIC_SPINE_MAINTENANCE	-0.93	0.25	0	0	0	not significant
4150	GO_NEGATIVE_REGULATION_OF_TELOMERASE_ACTIVITY	-0.93	0.25	0	0	0	not significant
4151	GO_NUCLEOTIDE_SUGAR_BIOSYNTHETIC_PROCESS	-0.93	0.25	0	0	0	not significant
4152	GO_PEPTIDASE_ACTIVATOR_ACTIVITY	-0.93	0.25	0	0	0	not significant
4153	GO_POSITIVE_REGULATION_OF_GRANULOCYTE_CHEMOTAXIS	-0.93	0.25	0	0	0	not significant
4154	GO_POSITIVE_REGULATION_OF_HEXOKINASE_ACTIVITY	-0.93	0.25	0	0	0	not significant
4155	GO_PRESYNAPTIC_ACTIVE_ZONE	-0.93	0.25	0	0	0	not significant
4156	GO_REGULATION_OF_HISTONE_H4_K16_ACETYLATION	-0.93	0.25	0	0	0	not significant
4157	GO_REGULATION_OF_MITOCHONDRIAL_TRANSLATION	-0.93	0.25	0	0	0	not significant
4158	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN	-0.93	0.25	0	0	0	not significant
4159	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN	-0.93	0.25	0	0	0	not significant
4160	LEE_LIVER_CANCER_DENA_UP	-0.93	0.25	0	0	0	not significant
4161	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATIO	-0.93	0.25	0	0	0	not significant
4162	BARRIER_COLON_CANCER_RECURRENCE_UP	-0.93	0.24	0	0	0	not significant
4163	CHR2Q33	-0.93	0.24	0	0	0	not significant
4164	DAVIES_MULTIPLE_MYELOMA_VS_MGUS_UP	-0.93	0.24	0	0	0	not significant
4165	DORN_ADENOVIRUS_INFECTION_32HR_UP	-0.93	0.24	0	0	0	not significant
4166	GO_ADHERENS_JUNCTION_ASSEMBLY	-0.93	0.24	0	0	0	not significant
4167	GO_ANDROGEN_METABOLIC_PROCESS	-0.93	0.24	0	0	0	not significant
4168	GO_BETA_CATENIN_TCF_COMPLEX_ASSEMBLY	-0.93	0.24	0	0	0	not significant
4169	GO_CELLULAR_COMPONENT_MAINTENANCE	-0.93	0.24	0	0	0	not significant
4170	GO_CLATHRIN_DEPENDENT_ENDOCYTOSIS	-0.93	0.24	0	0	0	not significant
4171	GO_DNA_DEMETHYLATION	-0.93	0.24	0	0	0	not significant
4172	GO_NUCLEAR_EXOSOME_RNASE_COMPLEX_	-0.93	0.24	0	0	0	not significant
4173	GO_PRESYNAPTIC_MEMBRANE_ORGANIZATION	-0.93	0.24	0	0	0	not significant
4174	REACTOME_GABA_B_RECEPTOR_ACTIVATION	-0.93	0.24	0	0	0	not significant
4175	TURJANSKI_MAPK8_AND_MAPK9_TARGETS	-0.93	0.24	0	0	0	not significant
4176	HAHTOLA_SEZARY_SYNDROM_DN	-0.93	0.23	0	0	0	not significant
4177	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	-0.93	0.23	0	0	0	not significant
4178	REACTOME_LOSS_OF_FUNCTION_OF_TGFBR1_IN_CANCER	-0.93	0.23	0	0	0	not significant
4179	CHR10Q24	-0.93	0.22	0	0	0	not significant
4180	GNATENKO_PLATELET_SIGNATURE	-0.93	0.22	0	0	0	not significant
4181	GO_G_PROTEIN_COUPLED_SEROTONIN_RECEPTOR_BINDING	-0.93	0.22	0	0	0	not significant
4182	GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	-0.93	0.22	0	0	0	not significant
4183	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	-0.93	0.22	0	0	0	not significant
4184	GO_POSITIVE_REGULATION_OF_IRE1_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	-0.93	0.22	0	0	0	not significant
4185	KEGG_MTOR_SIGNALING_PATHWAY	-0.93	0.22	0	0	0	not significant
4186	PECE_MAMMARY_STEM_CELL_DN	-0.93	0.22	0	0	0	not significant
4187	GO_NEGATIVE_REGULATION_OF_PROTEIN_DEPHOSPHORYLATION	-0.93	0.21	0	0	0	not significant
4188	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_C	-0.93	0.21	0	0	0	not significant
4189	GO_U1_SNRNP_BINDING	-0.93	0.21	0	0	0	not significant
4190	REACTOME_NONSENSE_MEDIATED_DECAY_NMD	-0.93	0.21	0	0	0	not significant
4191	GO_POSITIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION	-0.93	0.2	0	0	0	not significant
4192	KEGG_CHEMOKINE_SIGNALING_PATHWAY	-0.93	0.2	0	0	0	not significant
4193	REACTOME_NUCLEOTIDE_EXCISION_REPAIR	-0.93	0.19	0	0	0	not significant
4194	GO_CAMERA_TYPE_EYE_DEVELOPMENT	-0.93	0.18	0	0	0	not significant
4195	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN	-0.93	0.18	0	0	0	not significant
4196	GO_NEGATIVE_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	-0.92	0.26	0	0	0	not significant
4197	GO_REGULATION_OF_NON_MOTILE_CILIUM_ASSEMBLY	-0.92	0.26	0	0	0	not significant
4198	GO_TRANSCRIPTION_FACTOR_TFIIH_HOLO_COMPLEX	-0.92	0.26	0	0	0	not significant
4199	REACTOME_ADP_SIGNALLING_THROUGH_P2Y_PURINOCEPTOR_1	-0.92	0.26	0	0	0	not significant
4200	WANG_TNF_TARGETS	-0.92	0.26	0	0	0	not significant
4201	BIOCARTA_MAL_PATHWAY	-0.92	0.25	0	0	0	not significant
4202	CHR18Q21	-0.92	0.25	0	0	0	not significant
4203	GO_ATTACHMENT_OF_MITOTIC_SPINDLE_MICROTUBULES_TO_KINETOCHORE	-0.92	0.25	0	0	0	not significant
4204	GO_CENTRAL_NERVOUS_SYSTEM_PROJECTION_NEURON_AXONOGENESIS	-0.92	0.25	0	0	0	not significant
4205	GO_PROTEIN_LOCALIZATION_TO_MICROTUBULE	-0.92	0.25	0	0	0	not significant
4206	MATZUK_SPERMATID_DIFFERENTIATION	-0.92	0.25	0	0	0	not significant
4207	REACTOME_IRAK2_MEDIATED_ACTIVATION_OF_TAK1_COMPLEX	-0.92	0.25	0	0	0	not significant
4208	CHR4Q27	-0.92	0.24	0	0	0	not significant
4209	GO_ATF6_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	-0.92	0.24	0	0	0	not significant
4210	GO_CORNIFICATION	-0.92	0.24	0	0	0	not significant
4211	GO_ENDODERMAL_CELL_FATE_COMMITMENT	-0.92	0.24	0	0	0	not significant
4212	GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS_WITHIN_A_TISSUE	-0.92	0.24	0	0	0	not significant
4213	GO_HYPOTONIC_RESPONSE	-0.92	0.24	0	0	0	not significant
4214	GO_PICLN_SM_PROTEIN_COMPLEX	-0.92	0.24	0	0	0	not significant
4215	GO_PRIMARY_MIRNA_PROCESSING	-0.92	0.24	0	0	0	not significant
4216	GO_SERTOLI_CELL_DEVELOPMENT	-0.92	0.24	0	0	0	not significant
4217	GO_SNAP_RECEPTOR_ACTIVITY	-0.92	0.24	0	0	0	not significant
4218	KUROKAWA_LIVER_CANCER_CHEMOTHERAPY_DN	-0.92	0.24	0	0	0	not significant
4219	LI_LUNG_CANCER	-0.92	0.24	0	0	0	not significant
4220	PID_TRAIL_PATHWAY	-0.92	0.24	0	0	0	not significant
4221	PID_VEGFR1_PATHWAY	-0.92	0.24	0	0	0	not significant
4222	REACTOME_SYNTHESIS_OF_PIPS_AT_THE_EARLY_ENDOSOME_MEMBRANE	-0.92	0.24	0	0	0	not significant
4223	SHIN_B_CELL_LYMPHOMA_CLUSTER_8	-0.92	0.24	0	0	0	not significant
4224	STONER_ESOPHAGEAL_CARCINOGENESIS_UP	-0.92	0.24	0	0	0	not significant
4225	SYED_ESTRADIOL_RESPONSE	-0.92	0.24	0	0	0	not significant
4226	TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_UP	-0.92	0.24	0	0	0	not significant
4227	BIOCARTA_CELL2CELL_PATHWAY	-0.92	0.23	0	0	0	not significant
4228	GO_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING	-0.92	0.23	0	0	0	not significant
4229	GO_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_ACTIVITY	-0.92	0.23	0	0	0	not significant
4230	GO_HISTONE_H3_K9_DIMETHYLATION	-0.92	0.23	0	0	0	not significant
4231	GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	-0.92	0.23	0	0	0	not significant
4232	GO_NEGATIVE_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION	-0.92	0.23	0	0	0	not significant
4233	GO_NEGATIVE_REGULATION_OF_PLATELET_DERIVED_GROWTH_FACTOR_RECEPT	-0.92	0.23	0	0	0	not significant
4234	GO_PML_BODY_ORGANIZATION	-0.92	0.23	0	0	0	not significant
4235	GO_POSITIVE_REGULATION_OF_VASCULAR_SMOOTH_MUSCLE_CELL_PROLIFERAT	-0.92	0.23	0	0	0	not significant
4236	GO_PROTEASOME_CORE_COMPLEX_ALPHA_SUBUNIT_COMPLEX	-0.92	0.23	0	0	0	not significant
4237	GO_REGULATION_OF_ACTIN_FILAMENT_BASED_MOVEMENT	-0.92	0.23	0	0	0	not significant
4238	GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_	-0.92	0.23	0	0	0	not significant
4239	GO_TRANSCRIPTION_DEPENDENT_TETHERING_OF_RNA_POLYMERASE_II_GENE_D	-0.92	0.23	0	0	0	not significant

4240	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQO_IN_WS	-0.92	0.23	0	0	0	not significant
4241	MATZUK_SPERMATOCYTE	-0.92	0.23	0	0	0	not significant
4242	REACTOME_KERATINIZATION	-0.92	0.23	0	0	0	not significant
4243	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP	-0.92	0.23	0	0	0	not significant
4244	WOTTON_RUNX_TARGETS_DN	-0.92	0.23	0	0	0	not significant
4245	YANG_BREAST_CANCER_ESR1_BULK_DN	-0.92	0.23	0	0	0	not significant
4246	AKL_HTLV1_INFECTION_UP	-0.92	0.22	0	0	0	not significant
4247	GO_DNA_POLYMERASE_ACTIVITY	-0.92	0.22	0	0	0	not significant
4248	GO_SMALL_PROTEIN_ACTIVATING_ENZYME_BINDING	-0.92	0.22	0	0	0	not significant
4249	KEGG_LONG_TERM_DEPRESSION	-0.92	0.22	0	0	0	not significant
4250	LUI_THYROID_CANCER_CLUSTER_5	-0.92	0.22	0	0	0	not significant
4251	REACTOME_PERK_REGULATES_GENE_EXPRESSION	-0.92	0.22	0	0	0	not significant
4252	REACTOME_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR_TC_NER	-0.92	0.2	0	0	0	not significant
4253	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_DEADENYLATION_DEF	-0.92	0.19	0	0	0	not significant
4254	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATE	-0.92	0.19	0	0	0	not significant
4255	REACTOME_HATS_ACETYLATE_HISTONES	-0.92	0.19	0	0	0	not significant
4256	TAYLOR_METHYLATED_IN_ACUTE_LYMPHOBLASTIC_LEUKEMIA	-0.92	0.19	0	0	0	not significant
4257	GO_CYTOSOLIC_TRANSPORT	-0.92	0.18	0	0	0	not significant
4258	REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	-0.92	0.18	0	0	0	not significant
4259	KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	-0.92	0.17	0	0	0	not significant
4260	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	-0.92	0.15	0	0	0	not significant
4261	GO_GLUTAMATERGIC_SYNAPSE	-0.92	0.13	0	0	0	not significant
4262	GO_MEMBRANE_DOCKING	-0.92	0.11	0	0	0	not significant
4263	BRUINS_UVC_RESPONSE_LATE	-0.92	0.04	0	0	0	not significant
4264	GO_POSITIVE_REGULATION_OF_PROTEIN_SUMOYLATION	-0.91	0.25	0	0	0	not significant
4265	GO_RESPIRATORY_GASEOUS_EXCHANGE	-0.91	0.25	0	0	0	not significant
4266	REACTOME_ERYTHROPOIETIN_ACTIVATES_RAS	-0.91	0.25	0	0	0	not significant
4267	REACTOME_FORMATION_OF_THE_CORNIFIED_ENVELOPE	-0.91	0.25	0	0	0	not significant
4268	GO_ACTIVATION_OF_NF_KAPPAB_INDUCING_KINASE_ACTIVITY	-0.91	0.24	0	0	0	not significant
4269	GO_AMYLOID_FIBRIL_FORMATION	-0.91	0.24	0	0	0	not significant
4270	GO_INTERLEUKIN_12_BIOSYNTHETIC_PROCESS	-0.91	0.24	0	0	0	not significant
4271	GO_NEDD8_SPECIFIC_PROTEASE_ACTIVITY	-0.91	0.24	0	0	0	not significant
4272	GO_POSITIVE_REGULATION_OF_NEUTROPHIL_MIGRATION	-0.91	0.24	0	0	0	not significant
4273	GO_PRESYNAPTIC_MEMBRANE_ASSEMBLY	-0.91	0.24	0	0	0	not significant
4274	PID_MYC_PATHWAY	-0.91	0.24	0	0	0	not significant
4275	URS_ADIPOCYTE_DIFFERENTIATION_DN	-0.91	0.24	0	0	0	not significant
4276	GO_JUN_KINASE_KINASE_KINASE_ACTIVITY	-0.91	0.23	0	0	0	not significant
4277	GO_MYOBLAST_DIFFERENTIATION	-0.91	0.23	0	0	0	not significant
4278	GO_REGULATION_OF_ENDOSOME_SIZE	-0.91	0.23	0	0	0	not significant
4279	GO_REGULATION_OF_PANCREATIC_JUICE_SECRETION	-0.91	0.23	0	0	0	not significant
4280	GO_V_D_J_RECOMBINATION	-0.91	0.23	0	0	0	not significant
4281	IKEDA_MIR1_TARGETS_UP	-0.91	0.23	0	0	0	not significant
4282	NIELSEN_LEIOMYOSARCOMA_UP	-0.91	0.23	0	0	0	not significant
4283	REACTOME_EGFR_DOWNREGULATION	-0.91	0.23	0	0	0	not significant
4284	REACTOME_GLUCONEOGENESIS	-0.91	0.23	0	0	0	not significant
4285	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN	-0.91	0.23	0	0	0	not significant
4286	GAUTSCHI_SRC_SIGNALING	-0.91	0.22	0	0	0	not significant
4287	GO_FORMATION_OF_CYTOPLASMIC_TRANSLATION_INITIATION_COMPLEX	-0.91	0.22	0	0	0	not significant
4288	GO_INTERLEUKIN_23_PRODUCTION	-0.91	0.22	0	0	0	not significant
4289	GO_LACTATION	-0.91	0.22	0	0	0	not significant
4290	GO_MACROPHAGE_DIFFERENTIATION	-0.91	0.22	0	0	0	not significant
4291	GO_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX_CLASS_III	-0.91	0.22	0	0	0	not significant
4292	GO_POSITIVE_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	-0.91	0.22	0	0	0	not significant
4293	GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-0.91	0.22	0	0	0	not significant
4294	GO_RRNA_ADENINE_METHYLTRANSFERASE_ACTIVITY	-0.91	0.22	0	0	0	not significant
4295	PID_EPHRINB_REV_PATHWAY	-0.91	0.22	0	0	0	not significant
4296	REACTOME_METALLOTHIONEINS_BIND_METALS	-0.91	0.22	0	0	0	not significant
4297	ROVERSI_GLIOMA_COPY_NUMBER_DN	-0.91	0.22	0	0	0	not significant
4298	WENDT_COHESIN_TARGETS_UP	-0.91	0.22	0	0	0	not significant
4299	GO_AP_TYPE_MEMBRANE_COAT_ADAPTOR_COMPLEX	-0.91	0.21	0	0	0	not significant
4300	TIEN_INTESTINE_PROBIOTICS_6HR_UP	-0.91	0.21	0	0	0	not significant
4301	CHR2Q37	-0.91	0.2	0	0	0	not significant
4302	FALVELLA_SMOKERS_WITH_LUNG_CANCER	-0.91	0.2	0	0	0	not significant
4303	GO_POSITIVE_REGULATION_OF_GLUCOKINASE_ACTIVITY	-0.91	0.2	0	0	0	not significant
4304	GO_RUFFLE_ORGANIZATION	-0.91	0.2	0	0	0	not significant
4305	BOYLAN_MULTIPLE_MYELOMA_D_UP	-0.91	0.19	0	0	0	not significant
4306	REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	-0.91	0.19	0	0	0	not significant
4307	CHR1Q32	-0.91	0.18	0	0	0	not significant
4308	GO_RESPONSE_TO_VITAMIN	-0.91	0.18	0	0	0	not significant
4309	BROWNE_HCMV_INFECTION_12HR_DN	-0.91	0.17	0	0	0	not significant
4310	GO_DNA_DEPENDENT_ATPASE_ACTIVITY	-0.91	0.17	0	0	0	not significant
4311	KIM_WT1_TARGETS_8HR_DN	-0.91	0.17	0	0	0	not significant
4312	LIN_NPAS4_TARGETS_UP	-0.91	0.17	0	0	0	not significant
4313	REACTOME_SUMOYLATION_OF_DNA_DAMAGE_RESPONSE_AND_REPAIR_PROTEIN	-0.91	0.17	0	0	0	not significant
4314	GO_CELLULAR_TRANSITION_METAL_ION_HOMEOSTASIS	-0.91	0.16	0	0	0	not significant
4315	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	-0.91	0.12	0	0	0	not significant
4316	RATTENBACHER_BOUND_BY_CELF1	-0.91	0.1	0	0	0	not significant
4317	GO_ACTIN_CYTOSKELETON	-0.91	0.09	0	0	0	not significant
4318	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN	-0.90	0.24	0	0	0	not significant
4319	GO_MAINTENANCE_OF_SISTER_CHROMATID_COHESION	-0.90	0.24	0	0	0	not significant
4320	GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_COMPLEX	-0.90	0.23	0	0	0	not significant
4321	GO_NEGATIVE_REGULATION_OF_CELL_GROWTH_INVOLVED_IN_CARDIAC_MUSCLE	-0.90	0.23	0	0	0	not significant
4322	GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSPORT	-0.90	0.23	0	0	0	not significant
4323	HEDENFALK_BREAST_CANCER_BRACX_DN	-0.90	0.23	0	0	0	not significant
4324	PID_INSULIN_GLUCOSE_PATHWAY	-0.90	0.23	0	0	0	not significant
4325	REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS	-0.90	0.23	0	0	0	not significant
4326	REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX_IN_CANCER	-0.90	0.23	0	0	0	not significant
4327	ZHAN_LATE_DIFFERENTIATION_GENES_DN	-0.90	0.23	0	0	0	not significant
4328	GO_EMBRYONIC_PLACENTA_MORPHOGENESIS	-0.90	0.22	0	0	0	not significant
4329	GO_METANEPHRIC_NEPHRON_EPITHELIUM_DEVELOPMENT	-0.90	0.22	0	0	0	not significant
4330	GO_MITOCHONDRION_LOCALIZATION	-0.90	0.22	0	0	0	not significant
4331	GO_NEGATIVE_REGULATION_OF_PRODUCTION_OF_MIRNAS_INVOLVED_IN_GENE_	-0.90	0.22	0	0	0	not significant
4332	GO_NEGATIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	-0.90	0.22	0	0	0	not significant
4333	GO_NEGATIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCES	-0.90	0.22	0	0	0	not significant
4334	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	-0.90	0.22	0	0	0	not significant
4335	GO_RDNA_BINDING	-0.90	0.22	0	0	0	not significant
4336	GO_REGULATION_OF_MRNA_BINDING	-0.90	0.22	0	0	0	not significant
4337	GO_REGULATION_OF_THE_FORCE_OF_HEART_CONTRACTION	-0.90	0.22	0	0	0	not significant
4338	GO_SUPERCOILED_DNA_BINDING	-0.90	0.22	0	0	0	not significant
4339	KEGG_TASTE_TRANSDUCTION	-0.90	0.22	0	0	0	not significant
4340	NIKOLSKY_BREAST_CANCER_12Q13_Q21_AMPLICON	-0.90	0.22	0	0	0	not significant
4341	NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON	-0.90	0.22	0	0	0	not significant
4342	POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN	-0.90	0.22	0	0	0	not significant
4343	CHR16Q23	-0.90	0.21	0	0	0	not significant
4344	GENTLES_LEUKEMIC_STEM_CELL_DN	-0.90	0.21	0	0	0	not significant
4345	GO_NEGATIVE_REGULATION_OF_HORMONE_SECRETION	-0.90	0.21	0	0	0	not significant
4346	GO_POSITIVE_REGULATION_OF_MITOTIC_SISTER_CHROMATID_SEPARATION	-0.90	0.21	0	0	0	not significant
4347	GO_POSITIVE_REGULATION_OF_RIG_I_SIGNALING_PATHWAY	-0.90	0.21	0	0	0	not significant
4348	GO_PROTEIN_K48_LINKED_UBIQUITINATION	-0.90	0.21	0	0	0	not significant

4349	HOFMANN_MYELODYSPLASTIC_SYNDROM_HIGH_RISK_UP	-0.90	0.21	0	0	0	not significant
4350	HOLLERN_SQUAMOUS_BREAST_TUMOR	-0.90	0.21	0	0	0	not significant
4351	KONDO_PROSTATE_CANCER_WITH_H3K27ME3	-0.90	0.21	0	0	0	not significant
4352	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_2	-0.90	0.21	0	0	0	not significant
4353	REACTOME_INTERLEUKIN_12_FAMILY_SIGNALING	-0.90	0.21	0	0	0	not significant
4354	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN	-0.90	0.21	0	0	0	not significant
4355	BIOCARTA_FMLP_PATHWAY	-0.90	0.2	0	0	0	not significant
4356	GO_ASYMMETRIC_STEM_CELL_DIVISION	-0.90	0.2	0	0	0	not significant
4357	GO_PANTOTHENATE_METABOLIC_PROCESS	-0.90	0.2	0	0	0	not significant
4358	GO_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	-0.90	0.2	0	0	0	not significant
4359	GO_TELOMERE_CAPPING	-0.90	0.2	0	0	0	not significant
4360	KANNAN_TP53_TARGETS_UP	-0.90	0.2	0	0	0	not significant
4361	KEGG_ACUTE_MYELOID_LEUKEMIA	-0.90	0.2	0	0	0	not significant
4362	OUILLETTE_CLL_13Q14_DELETION_DN	-0.90	0.2	0	0	0	not significant
4363	CHR12Q23	-0.90	0.19	0	0	0	not significant
4364	CHR17Q12	-0.90	0.19	0	0	0	not significant
4365	GO_CLATHRIN_COATED_PIT	-0.90	0.19	0	0	0	not significant
4366	GO_REGULATION_OF_SYNAPTIC_VESICLE_TRANSPORT	-0.90	0.19	0	0	0	not significant
4367	KEGG_ADHERENS_JUNCTION	-0.90	0.19	0	0	0	not significant
4368	REACTOME_BBSOME_MEDIATED_CARGO_TARGETING_TO_CILIUM	-0.90	0.19	0	0	0	not significant
4369	CHR7Q11	-0.90	0.18	0	0	0	not significant
4370	GO_NEGATIVE_REGULATION_OF_PROTEIN_POLYMERIZATION	-0.90	0.18	0	0	0	not significant
4371	GO_PROTEIN_INSERTION_INTO_MITOCHONDRIAL_MEMBRANE	-0.90	0.18	0	0	0	not significant
4372	GO_HINDBRAIN_DEVELOPMENT	-0.90	0.17	0	0	0	not significant
4373	GO_G_PROTEIN_COUPLED_RECEPTOR_BINDING	-0.90	0.16	0	0	0	not significant
4374	GO_PROTEIN_METHYLTRANSFERASE_ACTIVITY	-0.90	0.16	0	0	0	not significant
4375	PDGF_ERK_DN.V1_UP	-0.90	0.16	0	0	0	not significant
4376	LINDGREN_BLADDER_CANCER_CLUSTER_1_UP	-0.90	0.15	0	0	0	not significant
4377	KEGG_ALZHEIMERS_DISEASE	-0.90	0.13	0	0	0	not significant
4378	GO_VESICLE_LOCALIZATION	-0.90	0.11	0	0	0	not significant
4379	GO_CELL_SUBSTRATE_JUNCTION	-0.90	0.06	0	0	0	not significant
4380	GO_REGULATION_OF_MULTI_ORGANISM_PROCESS	-0.90	0.06	0	0	0	not significant
4381	GO_COPPER_ION_TRANSPORT	-0.89	0.23	0	0	0	not significant
4382	GO_ESTABLISHMENT_OF_SISTER_CHROMATID_COHESION	-0.89	0.23	0	0	0	not significant
4383	GO_OVULATION_CYCLE_PROCESS	-0.89	0.23	0	0	0	not significant
4384	DORMOY_ELAVL1_TARGETS	-0.89	0.22	0	0	0	not significant
4385	GO_EMBRYONIC_CAMERA_TYPE_EYE_FORMATION	-0.89	0.22	0	0	0	not significant
4386	GO_POSITIVE_REGULATION_OF_TELOMERE_CAPPING	-0.89	0.22	0	0	0	not significant
4387	GO_RECEPTOR_BIOSYNTHETIC_PROCESS	-0.89	0.22	0	0	0	not significant
4388	GO_VOLUNTARY_MUSCULOSKELETAL_MOVEMENT	-0.89	0.22	0	0	0	not significant
4389	REACTOME_CLEC7A_DECTIN_1_INDUCES_NFAT_ACTIVATION	-0.89	0.22	0	0	0	not significant
4390	WILLIAMS_ESR2_TARGETS_UP	-0.89	0.22	0	0	0	not significant
4391	GO_CELLULAR_RESPONSE_TO_ELECTRICAL_STIMULUS	-0.89	0.21	0	0	0	not significant
4392	GO_CENTRIOLAR_SATELLITE	-0.89	0.21	0	0	0	not significant
4393	GO_CHEMOKINE_C_C_MOTIF_LIGAND_5_PRODUCTION	-0.89	0.21	0	0	0	not significant
4394	GO_CILIARY_ROOTLET	-0.89	0.21	0	0	0	not significant
4395	GO_ER_MEMBRANE_INSERTION_COMPLEX	-0.89	0.21	0	0	0	not significant
4396	GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_KINASE_KINASE_BINDING	-0.89	0.21	0	0	0	not significant
4397	GO_N_TERMINAL_PROTEIN_AMINO_ACID_ACETYLATION	-0.89	0.21	0	0	0	not significant
4398	GO_POSITIVE_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	-0.89	0.21	0	0	0	not significant
4399	GO_POSITIVE_REGULATION_OF_SUPEROXIDE_ANION_GENERATION	-0.89	0.21	0	0	0	not significant
4400	GO_PREFOLDIN_COMPLEX	-0.89	0.21	0	0	0	not significant
4401	GO_REGULATION_OF_CYTOPLASMIC_TRANSLATION	-0.89	0.21	0	0	0	not significant
4402	GO_REGULATION_OF_RECEPTOR_BIOSYNTHETIC_PROCESS	-0.89	0.21	0	0	0	not significant
4403	HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_DN	-0.89	0.21	0	0	0	not significant
4404	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_UP	-0.89	0.21	0	0	0	not significant
4405	NIELSEN_SCHWANNOMA_UP	-0.89	0.21	0	0	0	not significant
4406	PID_ARF6_DOWNSTREAM_PATHWAY	-0.89	0.21	0	0	0	not significant
4407	PID_SYNDECAN_2_PATHWAY	-0.89	0.21	0	0	0	not significant
4408	REACTOME_PROCESSING_AND_ACTIVATION_OF_SUMO	-0.89	0.21	0	0	0	not significant
4409	GO_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	-0.89	0.2	0	0	0	not significant
4410	GO_NUCLEOSIDE_MONOPHOSPHATE_PHOSPHORYLATION	-0.89	0.2	0	0	0	not significant
4411	GO_PIGMENT_CELL_DIFFERENTIATION	-0.89	0.2	0	0	0	not significant
4412	GO_REGULATION_OF_AMINO_ACID_IMPORT_ACROSS_PLASMA_MEMBRANE	-0.89	0.2	0	0	0	not significant
4413	GO_REGULATION_OF_CD8_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	-0.89	0.2	0	0	0	not significant
4414	REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIUM_MOBILIZATION	-0.89	0.2	0	0	0	not significant
4415	TAVAZOIE_METASTASIS	-0.89	0.2	0	0	0	not significant
4416	TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP	-0.89	0.2	0	0	0	not significant
4417	YOSHIOKA_LIVER_CANCER_EARLY_RECURRENCE_UP	-0.89	0.2	0	0	0	not significant
4418	GO_CELLULAR_RESPONSE_TO_OSMOTIC_STRESS	-0.89	0.19	0	0	0	not significant
4419	GO_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNALING_PATHWAY	-0.89	0.19	0	0	0	not significant
4420	GO_NEGATIVE_REGULATION_OF_MACROAUTOPHAGY	-0.89	0.19	0	0	0	not significant
4421	GO_PHOTORECEPTOR_INNER_SEGMENT	-0.89	0.19	0	0	0	not significant
4422	MARTINEZ_RESPONSE_TO_TRABECTEDIN	-0.89	0.19	0	0	0	not significant
4423	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_ACETYLATION	-0.89	0.19	0	0	0	not significant
4424	TAVOR_CEBPA_TARGETS_UP	-0.89	0.19	0	0	0	not significant
4425	GO_INOSITOL_PHOSPHATE_METABOLIC_PROCESS	-0.89	0.18	0	0	0	not significant
4426	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	-0.89	0.18	0	0	0	not significant
4427	KUMAR_AUTOPHAGY_NETWORK	-0.89	0.18	0	0	0	not significant
4428	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_DN	-0.89	0.18	0	0	0	not significant
4429	WALLACE_PROSTATE_CANCER_RACE_DN	-0.89	0.18	0	0	0	not significant
4430	CHR20P13	-0.89	0.17	0	0	0	not significant
4431	GO_CARDIAC_MUSCLE_CONTRACTION	-0.89	0.17	0	0	0	not significant
4432	GO_CILIARY_PLASM	-0.89	0.17	0	0	0	not significant
4433	GO_POSITIVE_REGULATION_OF_ORGANELLE_ASSEMBLY	-0.89	0.17	0	0	0	not significant
4434	GO_REGULATION_OF_LIPID_KINASE_ACTIVITY	-0.89	0.17	0	0	0	not significant
4435	GO_CARDIAC_VENTRICLE_DEVELOPMENT	-0.89	0.16	0	0	0	not significant
4436	GO_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	-0.89	0.15	0	0	0	not significant
4437	GO_RESPIRATORY_CHAIN_COMPLEX	-0.89	0.15	0	0	0	not significant
4438	GO_TUBE_CLOSURE	-0.89	0.15	0	0	0	not significant
4439	KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	-0.89	0.15	0	0	0	not significant
4440	REACTOME_CARGO_RECOGNITION_FOR_CLATHRIN_MEDIATED_ENDOCYTOSIS	-0.89	0.15	0	0	0	not significant
4441	GO_POST_GOLGI_VESICLE_MEDIATED_TRANSPORT	-0.89	0.13	0	0	0	not significant
4442	GO_PEPTIDYL_LYSINE_ACETYLATION	-0.89	0.09	0	0	0	not significant
4443	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_22	-0.88	0.22	0	0	0	not significant
4444	GO_ESCRT_I_COMPLEX	-0.88	0.21	0	0	0	not significant
4445	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_MONOPOLAR_CELL_POLARITY	-0.88	0.21	0	0	0	not significant
4446	GO_FILAMENTOUS_ACTIN	-0.88	0.21	0	0	0	not significant
4447	GO_INTERLEUKIN_2_SECRETION	-0.88	0.21	0	0	0	not significant
4448	GO_NUCLEAR_PERICENTRIC_HETEROCHROMATIN	-0.88	0.21	0	0	0	not significant
4449	GO_POSITIVE_REGULATION_OF_AMINE_TRANSPORT	-0.88	0.21	0	0	0	not significant
4450	GO_RESPONSE_TO_LEAD_ION	-0.88	0.21	0	0	0	not significant
4451	GO_ZINC_ION_IMPORT_ACROSS_PLASMA_MEMBRANE	-0.88	0.21	0	0	0	not significant
4452	REACTOME_ENDOGENOUS_STEROLS	-0.88	0.21	0	0	0	not significant
4453	CHESLER_BRAIN_QTL_TRANS	-0.88	0.2	0	0	0	not significant
4454	CHR4Q24	-0.88	0.2	0	0	0	not significant
4455	GO_INSULIN_RECEPTOR_BINDING	-0.88	0.2	0	0	0	not significant
4456	GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_KINASE_BINDING	-0.88	0.2	0	0	0	not significant
4457	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_DEADENYLATION_INDI	-0.88	0.2	0	0	0	not significant

4458	GO_PHOSPHATIDYLINOSITOL_PHOSPHORYLATION	-0.88	0.2	0	0	0	not significant
4459	GO_REGULATION_OF_SYNAPTIC_VESICLE_CLUSTERING	-0.88	0.2	0	0	0	not significant
4460	GO_SINGLE_STRANDED_DNA_DEPENDENT_ATPASE_ACTIVITY	-0.88	0.2	0	0	0	not significant
4461	GO_TELOMERE_CAP_COMPLEX	-0.88	0.2	0	0	0	not significant
4462	GO_TRANSCRIPTION_EXPORT_COMPLEX	-0.88	0.2	0	0	0	not significant
4463	GO_VESICLE_CARGO_LOADING	-0.88	0.2	0	0	0	not significant
4464	MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_UP	-0.88	0.2	0	0	0	not significant
4465	REACTOME_INLB_MEDIATED_ENTRY_OF_LISTERIA_MONOCYTOGENES_INTO_HOST	-0.88	0.2	0	0	0	not significant
4466	VANDESLUIS_COMMD1_TARGETS_GROUP_4_UP	-0.88	0.2	0	0	0	not significant
4467	GO_ENDOPLASMIC_RETICULUM_TUBULAR_NETWORK	-0.88	0.19	0	0	0	not significant
4468	GO_NEURON_PROJECTION_MEMBRANE	-0.88	0.19	0	0	0	not significant
4469	GO_REGULATION_OF_CARTILAGE_DEVELOPMENT	-0.88	0.19	0	0	0	not significant
4470	GO_REGULATION_OF_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	-0.88	0.19	0	0	0	not significant
4471	GO_RRNA_METHYLATION	-0.88	0.19	0	0	0	not significant
4472	GO_WATER_HOMEOSTASIS	-0.88	0.19	0	0	0	not significant
4473	SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER	-0.88	0.19	0	0	0	not significant
4474	VANTVEER_BREAST_CANCER_BRCA1_DN	-0.88	0.19	0	0	0	not significant
4475	GO_CHROMATIN_SILENCING_AT_RDNA	-0.88	0.18	0	0	0	not significant
4476	GO_INSULIN_RESPONSIVE_COMPARTMENT	-0.88	0.18	0	0	0	not significant
4477	GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_ACTIVITY	-0.88	0.18	0	0	0	not significant
4478	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC	-0.88	0.18	0	0	0	not significant
4479	GO_SCHWANN_CELL_DIFFERENTIATION	-0.88	0.18	0	0	0	not significant
4480	XU_GH1_EXOGENOUS_TARGETS_DN	-0.88	0.18	0	0	0	not significant
4481	CHR2P11	-0.88	0.17	0	0	0	not significant
4482	CHR6Q21	-0.88	0.17	0	0	0	not significant
4483	GO_ACTIVATION_OF_PROTEIN_KINASE_B_ACTIVITY	-0.88	0.17	0	0	0	not significant
4484	GO_PROTEIN_INSERTION_INTO_MEMBRANE	-0.88	0.17	0	0	0	not significant
4485	GO_SUPEROXIDE_METABOLIC_PROCESS	-0.88	0.17	0	0	0	not significant
4486	REACTOME_PHASE_I_FUNCTIONALIZATION_OF_COMPOUNDS	-0.88	0.17	0	0	0	not significant
4487	STAMBOLSKY_RESPONSE_TO_VITAMIN_D3_UP	-0.88	0.17	0	0	0	not significant
4488	GO_DNA_REPAIR_COMPLEX	-0.88	0.16	0	0	0	not significant
4489	GO_NADH_DEHYDROGENASE_ACTIVITY	-0.88	0.16	0	0	0	not significant
4490	GO_FIBROBLAST_PROLIFERATION	-0.88	0.15	0	0	0	not significant
4491	GO_NON_MOTILE_CILIUM	-0.88	0.15	0	0	0	not significant
4492	GO_APPENDAGE_MORPHOGENESIS	-0.88	0.13	0	0	0	not significant
4493	RAO_BOUND_BY_SALL4_ISOFORM_A	-0.88	0.12	0	0	0	not significant
4494	WEI_MIR34A_TARGETS	-0.88	0.12	0	0	0	not significant
4495	LTE2_UP.V1_DN	-0.88	0.1	0	0	0	not significant
4496	GO_POSITIVE_REGULATION_OF_SUPRAMOLECULAR_FIBER_ORGANIZATION	-0.88	0.09	0	0	0	not significant
4497	GO_DENDRITE_DEVELOPMENT	-0.88	0.07	0	0	0	not significant
4498	GO_CELL_SUBSTRATE_ADHESION	-0.88	0.05	0	0	0	not significant
4499	RICKMAN_METASTASIS_UP	-0.88	0.04	0	0	0	not significant
4500	REACTOME_HYALURONAN_METABOLISM	-0.87	0.22	0	0	0	not significant
4501	GO_POSITIVE_REGULATION_OF_GLUCONEOGENESIS	-0.87	0.21	0	0	0	not significant
4502	GO_POSITIVE_REGULATION_OF_NON_MOTILE_CILIUM_ASSEMBLY	-0.87	0.21	0	0	0	not significant
4503	BIOCARTA_LEPTIN_PATHWAY	-0.87	0.2	0	0	0	not significant
4504	BIOCARTA_TALL1_PATHWAY	-0.87	0.2	0	0	0	not significant
4505	GO_CELL_PROLIFERATION_IN_FOREBRAIN	-0.87	0.2	0	0	0	not significant
4506	GO_CENTROMERIC_DNA_BINDING	-0.87	0.2	0	0	0	not significant
4507	GO_NAD_BIOSYNTHESIS_VIA_NICOTINAMIDE_RIBOSIDE_SALVAGE_PATHWAY	-0.87	0.2	0	0	0	not significant
4508	GO_POSITIVE_REGULATION_OF_CYTOPLASMIC_TRANSLATION	-0.87	0.2	0	0	0	not significant
4509	GO_POSITIVE_REGULATION_OF_MUSCLE_CONTRACTION	-0.87	0.2	0	0	0	not significant
4510	GO_POSITIVE_REGULATION_OF_RECEPTOR_INTERNALIZATION	-0.87	0.2	0	0	0	not significant
4511	GO_RESOLUTION_OF_MEIOTIC_RECOMBINATION_INTERMEDIATES	-0.87	0.2	0	0	0	not significant
4512	GO_VIRAL_LATENCY	-0.87	0.2	0	0	0	not significant
4513	REACTOME_SYNTHESIS_OF_GDP_MANNOSE	-0.87	0.2	0	0	0	not significant
4514	AMUNDSON_GAMMA_RADIATION_RESISTANCE	-0.87	0.19	0	0	0	not significant
4515	GO_ASPARTATE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	-0.87	0.19	0	0	0	not significant
4516	GO_CEREBELLAR_PURKINJE_CELL_LAYER_MORPHOGENESIS	-0.87	0.19	0	0	0	not significant
4517	GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_CLEARANCE	-0.87	0.19	0	0	0	not significant
4518	GO_NUCLEAR_INCLUSION_BODY	-0.87	0.19	0	0	0	not significant
4519	GO_PHOSPHATIDYLINOSITOL_TRANSPORTER_ACTIVITY	-0.87	0.19	0	0	0	not significant
4520	GO_POSITIVE_REGULATION_OF_PHOSPHOLIPID_TRANSPORT	-0.87	0.19	0	0	0	not significant
4521	GO_TUBULAR_ENDOSOME	-0.87	0.19	0	0	0	not significant
4522	NEBEN_AML_WITH_FLT3_OR_NRAS_UP	-0.87	0.19	0	0	0	not significant
4523	REACTOME_CREB_PHOSPHORYLATION	-0.87	0.19	0	0	0	not significant
4524	REACTOME_P75NTR_RECRUITS_SIGNALLING_COMPLEXES	-0.87	0.19	0	0	0	not significant
4525	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_METHYLATION	-0.87	0.19	0	0	0	not significant
4526	REACTOME_RUNX3_REGULATES_NOTCH_SIGNALING	-0.87	0.19	0	0	0	not significant
4527	BIOCARTA_RAC1_PATHWAY	-0.87	0.18	0	0	0	not significant
4528	CHEN_ETV5_TARGETS_SERTOLI	-0.87	0.18	0	0	0	not significant
4529	GO_CALCIUM_CHANNEL_COMPLEX	-0.87	0.18	0	0	0	not significant
4530	GO_COLUMNAR_CUBOIDAL_EPITHELIAL_CELL_DEVELOPMENT	-0.87	0.18	0	0	0	not significant
4531	GO_DENTATE_GYRUS_DEVELOPMENT	-0.87	0.18	0	0	0	not significant
4532	GO_INTERFERON_ALPHA_PRODUCTION	-0.87	0.18	0	0	0	not significant
4533	GO_POSITIVE_REGULATION_OF_CHROMOSOME_SEPARATION	-0.87	0.18	0	0	0	not significant
4534	GO_ROSTROCAUDAL_NEURAL_TUBE_PATTERNING	-0.87	0.18	0	0	0	not significant
4535	GO_TRNA_SPECIFIC_ADENOSINE_DEAMINASE_ACTIVITY	-0.87	0.18	0	0	0	not significant
4536	PID_ERB_GENOMIC_PATHWAY	-0.87	0.18	0	0	0	not significant
4537	REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPT	-0.87	0.18	0	0	0	not significant
4538	YAGI_AML_RELAPSE_PROGNOSIS	-0.87	0.18	0	0	0	not significant
4539	CERVERA_SDHB_TARGETS_1_UP	-0.87	0.17	0	0	0	not significant
4540	GO_PROTEIN_K63_LINKED_DEUBIQUITINATION	-0.87	0.17	0	0	0	not significant
4541	GO_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	-0.87	0.17	0	0	0	not significant
4542	MA_MYELOID_DIFFERENTIATION_UP	-0.87	0.17	0	0	0	not significant
4543	PID_ATM_PATHWAY	-0.87	0.17	0	0	0	not significant
4544	REACTOME_OVARIAN_TUMOR_DOMAIN_PROTEASES	-0.87	0.17	0	0	0	not significant
4545	ZHAN_MULTIPLE_MYELOMA_CD1_AND_CD2_DN	-0.87	0.17	0	0	0	not significant
4546	CHR17Q23	-0.87	0.16	0	0	0	not significant
4547	CHR2P25	-0.87	0.16	0	0	0	not significant
4548	GO_CLATHRIN_BINDING	-0.87	0.16	0	0	0	not significant
4549	REACTOME_APOPTOTIC_EXECUTION_PHASE	-0.87	0.16	0	0	0	not significant
4550	REACTOME_INTRA_GOLGI_TRAFFIC	-0.87	0.16	0	0	0	not significant
4551	KEGG_ENDOMETRIAL_CANCER	-0.87	0.15	0	0	0	not significant
4552	LANDIS_ERBB2_BREAST_PRENEOPLASTIC_DN	-0.87	0.15	0	0	0	not significant
4553	REACTOME_CARDIAC_CONDUCTION	-0.87	0.15	0	0	0	not significant
4554	REN_ALVEOLAR_RHABDOMYOSARCOMA_UP	-0.87	0.15	0	0	0	not significant
4555	OUILLETTE_CLL_13Q14_DELETION_UP	-0.87	0.14	0	0	0	not significant
4556	RIZ_ERYTHROID_DIFFERENTIATION	-0.87	0.14	0	0	0	not significant
4557	GO_EPHRIN_RECEPTOR_SIGNALING_PATHWAY	-0.87	0.13	0	0	0	not significant
4558	GO_PROTEIN_TYROSINE_KINASE_BINDING	-0.87	0.13	0	0	0	not significant
4559	GO_RIBONUCLEASE_ACTIVITY	-0.87	0.13	0	0	0	not significant
4560	GO_UBIQUITIN_BINDING	-0.87	0.13	0	0	0	not significant
4561	RAGHAVACHARI_PLATELET_SPECIFIC_GENES	-0.87	0.13	0	0	0	not significant
4562	REACTOME_MACROAUTOPHAGY	-0.87	0.13	0	0	0	not significant
4563	GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	-0.87	0.12	0	0	0	not significant
4564	REACTOME_NEGATIVE_REGULATION_OF_THE_PI3K_AKT_NETWORK	-0.87	0.12	0	0	0	not significant
4565	ROME_INSULIN_TARGETS_IN_MUSCLE_DN	-0.87	0.11	0	0	0	not significant
4566	CHR12Q24	-0.87	0.07	0	0	0	not significant

4567	GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	-0.87	0.05	0	0	0	not significant
4568	BRUINS_UVC_RESPONSE_EARLY_LATE	-0.87	0.04	0	0	0	not significant
4569	GO_REGULATION_OF_SUPRAMOLECULAR_FIBER_ORGANIZATION	-0.87	0.03	0	0	0	not significant
4570	GO_CARDIOBLAST_PROLIFERATION	-0.86	0.21	0	0	0	not significant
4571	GO_RESPONSE_TO_MUSCLE_ACTIVITY	-0.86	0.21	0	0	0	not significant
4572	GO_ALDITOL_METABOLIC_PROCESS	-0.86	0.2	0	0	0	not significant
4573	GO_NEUROTROPHIN_TRK_RECEPTOR_BINDING	-0.86	0.2	0	0	0	not significant
4574	GO_NUCLEAR_MEMBRANE_ORGANIZATION	-0.86	0.2	0	0	0	not significant
4575	GO_PEPTIDE_HORMONE_BINDING	-0.86	0.2	0	0	0	not significant
4576	GO_POSITIVE_REGULATION_OF_METANEPHROS_DEVELOPMENT	-0.86	0.2	0	0	0	not significant
4577	GO_PRE_MRNA_INTRONIC_BINDING	-0.86	0.2	0	0	0	not significant
4578	GO_REGULATION_OF_ENDODEOXYRIBONUCLEASE_ACTIVITY	-0.86	0.2	0	0	0	not significant
4579	GO_UBIQUITIN_SPECIFIC_PROTEASE_BINDING	-0.86	0.2	0	0	0	not significant
4580	ROZANOV_MMP14_CORRELATED	-0.86	0.2	0	0	0	not significant
4581	GENTILE_UV_LOW_DOSE_UP	-0.86	0.19	0	0	0	not significant
4582	GO_EMBRYONIC_NEUROCRANIUM_MORPHOGENESIS	-0.86	0.19	0	0	0	not significant
4583	GO_INOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	-0.86	0.19	0	0	0	not significant
4584	GO_INTEGRAL_COMPONENT_OF_PRESYNAPTIC_ACTIVE_ZONE_MEMBRANE	-0.86	0.19	0	0	0	not significant
4585	GO_MODIFICATION_OF_POSTSYNAPTIC_STRUCTURE	-0.86	0.19	0	0	0	not significant
4586	GO_POSITIVE_REGULATION_OF_CELL_AGING	-0.86	0.19	0	0	0	not significant
4587	GO_PRIMARY_MIRNA_BINDING	-0.86	0.19	0	0	0	not significant
4588	GO_REGULATION_OF_FEEDING_BEHAVIOR	-0.86	0.19	0	0	0	not significant
4589	GO_REGULATION_OF_NEUROTRANSMITTER_UPTAKE	-0.86	0.19	0	0	0	not significant
4590	GO_RISC_LOADING_COMPLEX	-0.86	0.19	0	0	0	not significant
4591	GO_VASCULAR_ASSOCIATED_SMOOTH_MUSCLE_CELL_MIGRATION	-0.86	0.19	0	0	0	not significant
4592	REACTOME_PKA_ACTIVATION_IN_GLUCAGON_SIGNALLING	-0.86	0.19	0	0	0	not significant
4593	REACTOME_ZINC_INFLUX_INTO_CELLS_BY_THE_SLC39_GENE_FAMILY	-0.86	0.19	0	0	0	not significant
4594	CHR3P26	-0.86	0.18	0	0	0	not significant
4595	GENTILE_UV_RESPONSE_CLUSTER_D9	-0.86	0.18	0	0	0	not significant
4596	GO_ACTIN_MONOMER_BINDING	-0.86	0.18	0	0	0	not significant
4597	GO_ACTIVATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_A	-0.86	0.18	0	0	0	not significant
4598	GO_DOUBLE_STRAND_BREAK_REPAIR_VIA_SINGLE_STRAND_ANNEALING	-0.86	0.18	0	0	0	not significant
4599	GO_MAINTENANCE_OF_DNA_REPEAT_ELEMENTS	-0.86	0.18	0	0	0	not significant
4600	GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	-0.86	0.18	0	0	0	not significant
4601	GO_PEPTIDYL_LYSINE_MONOMETHYLATION	-0.86	0.18	0	0	0	not significant
4602	GO_POSITIVE_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	-0.86	0.18	0	0	0	not significant
4603	GO_REGULATION_OF_SUPEROXIDE_METABOLIC_PROCESS	-0.86	0.18	0	0	0	not significant
4604	REACTOME_MAPK1_ERK2_ACTIVATION	-0.86	0.18	0	0	0	not significant
4605	REACTOME_REGULATION_OF_LOCALIZATION_OF_FOXO_TRANSCRIPTION_FACTOF	-0.86	0.18	0	0	0	not significant
4606	BIOCARTA_SM_PATHWAY	-0.86	0.17	0	0	0	not significant
4607	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	-0.86	0.17	0	0	0	not significant
4608	KORKOLA_EMBRYONAL_CARCINOMA	-0.86	0.17	0	0	0	not significant
4609	OKAWA_NEUROBLASTOMA_1P36_31_DELETION	-0.86	0.17	0	0	0	not significant
4610	TSENG_ADIPOGENIC_POTENTIAL_UP	-0.86	0.17	0	0	0	not significant
4611	GO_OLIGODENDROCYTE_DIFFERENTIATION	-0.86	0.16	0	0	0	not significant
4612	TOMLINS_PROSTATE_CANCER_UP	-0.86	0.16	0	0	0	not significant
4613	GO_NAD_BINDING	-0.86	0.15	0	0	0	not significant
4614	GO_PROTEIN_MONOUBIQUITINATION	-0.86	0.15	0	0	0	not significant
4615	GO_HISTONE_UBIQUITINATION	-0.86	0.14	0	0	0	not significant
4616	GO_REGULATION_OF_GLIOGENESIS	-0.86	0.14	0	0	0	not significant
4617	GO_TETHERING_COMPLEX	-0.86	0.14	0	0	0	not significant
4618	PID_RAC1_REG_PATHWAY	-0.86	0.14	0	0	0	not significant
4619	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	-0.86	0.12	0	0	0	not significant
4620	GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE	-0.86	0.12	0	0	0	not significant
4621	REACTOME_RHO_GTPASES_ACTIVATE_PKNS	-0.86	0.12	0	0	0	not significant
4622	GO_MONOCARBOXYLIC_ACID_TRANSPORT	-0.86	0.11	0	0	0	not significant
4623	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION	-0.86	0.1	0	0	0	not significant
4624	GO_SPERM_PART	-0.86	0.09	0	0	0	not significant
4625	PROVENZANI_METASTASIS_DN	-0.86	0.08	0	0	0	not significant
4626	GO_PYRIMIDINE_NUCLEOTIDE_CATABOLIC_PROCESS	-0.85	0.19	0	0	0	not significant
4627	MATZUK_SPERMATOGONIA	-0.85	0.19	0	0	0	not significant
4628	REACTOME_TYSND1_CLEAVES_PEROXISOMAL_PROTEINS	-0.85	0.19	0	0	0	not significant
4629	FINETTI_BREAST_CANCERS_KINOME_BLUE	-0.85	0.18	0	0	0	not significant
4630	GO_COPII_COATED_VESICLE_CARGO_LOADING	-0.85	0.18	0	0	0	not significant
4631	GO_DYNEIN_LIGHT_INTERMEDIATE_CHAIN_BINDING	-0.85	0.18	0	0	0	not significant
4632	GO_HISTONE_H4_K20_METHYLATION	-0.85	0.18	0	0	0	not significant
4633	GO_NEGATIVE_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	-0.85	0.18	0	0	0	not significant
4634	GO_NUCLEAR_PORE_COMPLEX_ASSEMBLY	-0.85	0.18	0	0	0	not significant
4635	GO_REGULATION_OF_INTEGRIN_ACTIVATION	-0.85	0.18	0	0	0	not significant
4636	GO_REGULATION_OF_RHODOPSIN_MEDIATED_SIGNALING_PATHWAY	-0.85	0.18	0	0	0	not significant
4637	GO_SKELETAL_MYOFIBRIL_ASSEMBLY	-0.85	0.18	0	0	0	not significant
4638	HEIDENBLAD_AMPLIFIED_IN_SOFT_TISSUE_CANCER	-0.85	0.18	0	0	0	not significant
4639	REACTOME_METABOLISM_OF_NITRIC_OXIDE:_ENOS_ACTIVATION_AND_REGULATIC	-0.85	0.18	0	0	0	not significant
4640	BIOCARTA_PLCE_PATHWAY	-0.85	0.17	0	0	0	not significant
4641	GO_CEREBELLAR_CORTEX_MORPHOGENESIS	-0.85	0.17	0	0	0	not significant
4642	GO_G_PROTEIN_BETA_SUBUNIT_BINDING	-0.85	0.17	0	0	0	not significant
4643	GO_IONOTROPIC_GLUTAMATE_RECEPTOR_BINDING	-0.85	0.17	0	0	0	not significant
4644	GO_NEGATIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	-0.85	0.17	0	0	0	not significant
4645	GO_NEGATIVE_REGULATION_OF_GENE_SILENCING	-0.85	0.17	0	0	0	not significant
4646	GO_NEGATIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMI	-0.85	0.17	0	0	0	not significant
4647	GO_NEGATIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	-0.85	0.17	0	0	0	not significant
4648	GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	-0.85	0.17	0	0	0	not significant
4649	GO_REGULATION_OF_GLUCOCORTICOID_RECEPTOR_SIGNALING_PATHWAY	-0.85	0.17	0	0	0	not significant
4650	NUMATA_CSF3_SIGNALING_VIA_STAT3	-0.85	0.17	0	0	0	not significant
4651	REACTOME_INTERLEUKIN_37_SIGNALING	-0.85	0.17	0	0	0	not significant
4652	REACTOME_TRISTETRAPROLIN_TTP_ZFP36_BINDS_AND_DESTABILIZES_MRNA	-0.85	0.17	0	0	0	not significant
4653	SESTO_RESPONSE_TO_UV_C3	-0.85	0.17	0	0	0	not significant
4654	WANG_RECURRENT_LIVER_CANCER_UP	-0.85	0.17	0	0	0	not significant
4655	ZHANG_ADIPOGENESIS_BY_BMP7	-0.85	0.17	0	0	0	not significant
4656	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP	-0.85	0.16	0	0	0	not significant
4657	GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_UP	-0.85	0.16	0	0	0	not significant
4658	REACTOME_NEF_AND_SIGNAL_TRANSDUCTION	-0.85	0.16	0	0	0	not significant
4659	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_YELLOW_UP	-0.85	0.15	0	0	0	not significant
4660	GO_DNA_DEALKYLATION	-0.85	0.15	0	0	0	not significant
4661	JOHANSSON_BRAIN_CANCER_EARLY_VS_LATE_DN	-0.85	0.15	0	0	0	not significant
4662	GO_RESPONSE_TO_AXON_INJURY	-0.85	0.14	0	0	0	not significant
4663	HENDRICKS_SMARCA4_TARGETS_UP	-0.85	0.14	0	0	0	not significant
4664	REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	-0.85	0.14	0	0	0	not significant
4665	GO_INTRACILIARY_TRANSPORT_INVOLVED_IN_CILIUM_ASSEMBLY	-0.85	0.13	0	0	0	not significant
4666	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_UP	-0.85	0.11	0	0	0	not significant
4667	GO_GLUCOSE_METABOLIC_PROCESS	-0.85	0.1	0	0	0	not significant
4668	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_CIS	-0.85	0.08	0	0	0	not significant
4669	GO_INSULIN_RECEPTOR_SIGNALING_PATHWAY	-0.85	0.07	0	0	0	not significant
4670	GRYDER_PAX3FOXO1_ENHANCERS_KO_DOWN	-0.85	0.02	0	0	0	not significant
4671	GO_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	-0.84	0.19	0	0	0	not significant
4672	GO_POSITIVE_REGULATION_OF_CALCINEURIN_MEDIATED_SIGNALING	-0.84	0.18	0	0	0	not significant
4673	GO_RESPONSE_TO_METHYLMERCURY	-0.84	0.18	0	0	0	not significant
4674	GO_RETINAL_METABOLIC_PROCESS	-0.84	0.18	0	0	0	not significant
4675	MARIADASON_RESPONSE_TO_CURCUMIN_SULINDAC_7	-0.84	0.18	0	0	0	not significant

4676	REACTOME_PROCESSING_OF_SMDT1	-0.84	0.18	0	0	0	not significant
4677	AMIT_DELAYED_EARLY_GENES	-0.84	0.17	0	0	0	not significant
4678	BIOCARTA_CHREBP_PATHWAY	-0.84	0.17	0	0	0	not significant
4679	GO_ADRENAL_GLAND_DEVELOPMENT	-0.84	0.17	0	0	0	not significant
4680	GO_CONTRACTILE_RING	-0.84	0.17	0	0	0	not significant
4681	GO_EXCITATORY_SYNAPSE_ASSEMBLY	-0.84	0.17	0	0	0	not significant
4682	GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING	-0.84	0.17	0	0	0	not significant
4683	GO_PROTEIN_NEDDYLATION	-0.84	0.17	0	0	0	not significant
4684	GO_REGULATION_OF_GTP_BINDING	-0.84	0.17	0	0	0	not significant
4685	GO_TRANSLOCON_COMPLEX	-0.84	0.17	0	0	0	not significant
4686	REACTOME_NEGATIVE_FEEDBACK_REGULATION_OF_MAPK_PATHWAY	-0.84	0.17	0	0	0	not significant
4687	REACTOME_REGULATION_OF_IFNG_SIGNALING	-0.84	0.17	0	0	0	not significant
4688	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN	-0.84	0.17	0	0	0	not significant
4689	XU_RESPONSE_TO_TRETINOIN_DN	-0.84	0.17	0	0	0	not significant
4690	BIOCARTA_AKAPCENTROSOME_PATHWAY	-0.84	0.16	0	0	0	not significant
4691	BIOCARTA_ETC_PATHWAY	-0.84	0.16	0	0	0	not significant
4692	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREEN_UP	-0.84	0.16	0	0	0	not significant
4693	GO_CELLULAR_RESPONSE_TO_GONADOTROPIN_STIMULUS	-0.84	0.16	0	0	0	not significant
4694	GO_FACE_MORPHOGENESIS	-0.84	0.16	0	0	0	not significant
4695	GO_MITOCHONDRIAL_ACETYL_COA_BIOSYNTHETIC_PROCESS_FROM_PYRUVATE	-0.84	0.16	0	0	0	not significant
4696	GO_MYOSIN_V_BINDING	-0.84	0.16	0	0	0	not significant
4697	GO_NEGATIVE_REGULATION_OF_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWA	-0.84	0.16	0	0	0	not significant
4698	GO_REGULATION_OF_FEMALE_GONAD_DEVELOPMENT	-0.84	0.16	0	0	0	not significant
4699	GO_SMAD_PROTEIN_COMPLEX_ASSEMBLY	-0.84	0.16	0	0	0	not significant
4700	GO_VENTRICULAR_SYSTEM_DEVELOPMENT	-0.84	0.16	0	0	0	not significant
4701	KEGG_PROPANOATE_METABOLISM	-0.84	0.16	0	0	0	not significant
4702	LANDIS_ERBB2_BREAST_TUMORS_65_UP	-0.84	0.16	0	0	0	not significant
4703	PID_THROMBIN_PAR4_PATHWAY	-0.84	0.16	0	0	0	not significant
4704	REACTOME_FOXO_MEDIATED_TRANSCRIPTION_OF_OXIDATIVE_STRESS_METABOL	-0.84	0.16	0	0	0	not significant
4705	ZEMBUTSU_SENSITIVITY_TO_VINBLASTINE	-0.84	0.16	0	0	0	not significant
4706	BIOCARTA_CXCR4_PATHWAY	-0.84	0.15	0	0	0	not significant
4707	GO_HISTONE_MONOUBIQUITINATION	-0.84	0.15	0	0	0	not significant
4708	GO_REGULATION_OF_IRE1_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	-0.84	0.15	0	0	0	not significant
4709	GO_REGULATION_OF_TELOMERE_CAPPING	-0.84	0.15	0	0	0	not significant
4710	GO_RESPONSE_TO_AUDITORY_STIMULUS	-0.84	0.15	0	0	0	not significant
4711	GO_SYNAPTIC_VESICLE_CLUSTERING	-0.84	0.15	0	0	0	not significant
4712	PID_ALK1_PATHWAY	-0.84	0.15	0	0	0	not significant
4713	PID_IL8_CXCR2_PATHWAY	-0.84	0.15	0	0	0	not significant
4714	REACTOME_INTERLEUKIN_RECEPTOR_SHC_SIGNALING	-0.84	0.15	0	0	0	not significant
4715	WEIGEL_OXIDATIVE_STRESS_BY_TBH_AND_H2O2	-0.84	0.15	0	0	0	not significant
4716	GO_DNA_DEALKYLATION_INVOLVED_IN_DNA_REPAIR	-0.84	0.14	0	0	0	not significant
4717	GO_FATTY_ACID_BINDING	-0.84	0.14	0	0	0	not significant
4718	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	-0.84	0.14	0	0	0	not significant
4719	GO_REGULATION_OF_STEM_CELL_PROLIFERATION	-0.84	0.14	0	0	0	not significant
4720	REACTOME_UPTAKE_AND_ACTIONS_OF_BACTERIAL_TOXINS	-0.84	0.14	0	0	0	not significant
4721	GO_CARDIAC_SEPTUM_MORPHOGENESIS	-0.84	0.13	0	0	0	not significant
4722	GO_RNA_DESTABILIZATION	-0.84	0.13	0	0	0	not significant
4723	LEE_CALORIE_RESTRICTION_MUSCLE_DN	-0.84	0.13	0	0	0	not significant
4724	REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	-0.84	0.12	0	0	0	not significant
4725	VANTVEER_BREAST_CANCER_POOR_PROGNOSIS	-0.84	0.12	0	0	0	not significant
4726	CHR1Q25	-0.84	0.11	0	0	0	not significant
4727	KEGG_MELANOGENESIS	-0.84	0.11	0	0	0	not significant
4728	PID_BETA_CATENIN_NUC_PATHWAY	-0.84	0.11	0	0	0	not significant
4729	REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	-0.84	0.11	0	0	0	not significant
4730	REACTOME_DEPURINATION	-0.84	0.11	0	0	0	not significant
4731	OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_UP	-0.84	0.09	0	0	0	not significant
4732	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN	-0.84	0.09	0	0	0	not significant
4733	GO_REGULATION_OF_BLOOD_CIRCULATION	-0.84	0.06	0	0	0	not significant
4734	GO_NEURON_APOPTOTIC_PROCESS	-0.84	0.04	0	0	0	not significant
4735	GO_PROTEIN_ACETYLATION	-0.84	0.04	0	0	0	not significant
4736	GO_SENSORY_SYSTEM_DEVELOPMENT	-0.84	0.03	0	0	0	not significant
4737	KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	-0.83	0.18	0	0	0	not significant
4738	CHRXQ21	-0.83	0.17	0	0	0	not significant
4739	GO_BERGMANN_GLIAL_CELL_DIFFERENTIATION	-0.83	0.17	0	0	0	not significant
4740	GO_DYNEIN_HEAVY_CHAIN_BINDING	-0.83	0.17	0	0	0	not significant
4741	GO_GLYCOSYLCERAMIDE_CATABOLIC_PROCESS	-0.83	0.17	0	0	0	not significant
4742	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_RECEPTOR_BIOSYNTHETIC_PROCES	-0.83	0.17	0	0	0	not significant
4743	GO_NEGATIVE_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENCING	-0.83	0.17	0	0	0	not significant
4744	GO_POSITIVE_REGULATION_OF_MACROPHAGE_MIGRATION	-0.83	0.17	0	0	0	not significant
4745	GO_REGULATION_OF_AEROBIC_RESPIRATION	-0.83	0.17	0	0	0	not significant
4746	GO_REGULATION_OF_WATER_LOSS_VIA_SKIN	-0.83	0.17	0	0	0	not significant
4747	GO_VESICLE_FUSION_WITH_GOLGI_APPARATUS	-0.83	0.17	0	0	0	not significant
4748	HEIDENBLAD_AMPLIFIED_IN_BONE_CANCER	-0.83	0.17	0	0	0	not significant
4749	BIOCARTA_TID_PATHWAY	-0.83	0.16	0	0	0	not significant
4750	GO_ERYTHROCYTE_DEVELOPMENT	-0.83	0.16	0	0	0	not significant
4751	GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	-0.83	0.16	0	0	0	not significant
4752	GO_NEGATIVE_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	-0.83	0.16	0	0	0	not significant
4753	GO_PRODUCTION_OF_SIRNA_INVOLVED_IN_RNA_INTERFERENCE	-0.83	0.16	0	0	0	not significant
4754	GO_REGULATION_OF_GLUCONEOGENESIS_BY_REGULATION_OF_TRANSCRIPTION_	-0.83	0.16	0	0	0	not significant
4755	GO_UBIQUITIN_CONJUGATING_ENZYME_COMPLEX	-0.83	0.16	0	0	0	not significant
4756	REACTOME_INSULIN_PROCESSING	-0.83	0.16	0	0	0	not significant
4757	VERNELL_RETINOBLASTOMA_PATHWAY_DN	-0.83	0.16	0	0	0	not significant
4758	GO_CORPUS_CALLOSUM_DEVELOPMENT	-0.83	0.15	0	0	0	not significant
4759	GO_GUANOSINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-0.83	0.15	0	0	0	not significant
4760	GO_INTRINSIC_COMPONENT_OF_PRESYNAPTIC_ACTIVE_ZONE_MEMBRANE	-0.83	0.15	0	0	0	not significant
4761	GO_POSITIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	-0.83	0.15	0	0	0	not significant
4762	GO_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRINSIC_APOPTOTIC_SIGNA	-0.83	0.15	0	0	0	not significant
4763	KEGG_TYROSINE_METABOLISM	-0.83	0.15	0	0	0	not significant
4764	REACTOME_ENOS_ACTIVATION	-0.83	0.15	0	0	0	not significant
4765	REACTOME_EPHB_MEDIATED_FORWARD_SIGNALING	-0.83	0.15	0	0	0	not significant
4766	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP	-0.83	0.15	0	0	0	not significant
4767	BIOCARTA_RAS_PATHWAY	-0.83	0.14	0	0	0	not significant
4768	GO_B_CELL_APOPTOTIC_PROCESS	-0.83	0.14	0	0	0	not significant
4769	GO_NEGATIVE_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-0.83	0.14	0	0	0	not significant
4770	GO_REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	-0.83	0.14	0	0	0	not significant
4771	REACTOME_ACTIVATION_OF_IRF3_IRF7_MEDIATED_BY_TBK1_IKK_EPSILON	-0.83	0.14	0	0	0	not significant
4772	CHR9Q31	-0.83	0.13	0	0	0	not significant
4773	GO_ACTIN_NUCLEATION	-0.83	0.13	0	0	0	not significant
4774	GO_HEAD_MORPHOGENESIS	-0.83	0.13	0	0	0	not significant
4775	REACTOME_BUDDING_AND_MATURATION_OF_HIV_VIRION	-0.83	0.13	0	0	0	not significant
4776	CHR3Q25	-0.83	0.12	0	0	0	not significant
4777	GO_RESPONSE_TO_TESTOSTERONE	-0.83	0.12	0	0	0	not significant
4778	GO_ION_CHANNEL_REGULATOR_ACTIVITY	-0.83	0.11	0	0	0	not significant
4779	GO_MANGANESE_ION_BINDING	-0.83	0.11	0	0	0	not significant
4780	ZHAN_MULTIPLE_MYELOMA_UP	-0.83	0.11	0	0	0	not significant
4781	GO_CHEMICAL_SYNAPTIC_TRANSMISSION_POSTSYNAPTIC	-0.83	0.1	0	0	0	not significant
4782	GO_MEGAKARYOCYTE_DIFFERENTIATION	-0.83	0.1	0	0	0	not significant
4783	RIZKI_TUMOR_INVASIVENESS_2D_DN	-0.83	0.1	0	0	0	not significant
4784	DITTMER_PTHLH_TARGETS_DN	-0.83	0.08	0	0	0	not significant

4785	GO_NEURAL_TUBE_FORMATION	-0.83	0.08	0	0	0	not significant
4786	GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	-0.83	0.08	0	0	0	not significant
4787	SIG_PIP3_SIGNALING_IN_CARDIAC_MYOCTES	-0.83	0.08	0	0	0	not significant
4788	GO_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	-0.83	0.07	0	0	0	not significant
4789	GO_REGULATION_OF_ENDOCYTOSIS	-0.83	0.05	0	0	0	not significant
4790	GO_NEGATIVE_REGULATION_OF_CARDIOCYTE_DIFFERENTIATION	-0.82	0.16	0	0	0	not significant
4791	GO_NEGATIVE_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIM	-0.82	0.16	0	0	0	not significant
4792	GO_NEGATIVE_REGULATION_OF_KERATINOCYTE_PROLIFERATION	-0.82	0.16	0	0	0	not significant
4793	GO_POSITIVE_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	-0.82	0.16	0	0	0	not significant
4794	GO_PROTON_TRANSPORTING_V_TYPE_ATPASE_V1_DOMAIN	-0.82	0.16	0	0	0	not significant
4795	IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_DN	-0.82	0.16	0	0	0	not significant
4796	ZHU_SKIL_TARGETS_DN	-0.82	0.16	0	0	0	not significant
4797	GO_ALDEHYDE_CATABOLIC_PROCESS	-0.82	0.15	0	0	0	not significant
4798	GO_MHC_CLASS_I_PEPTIDE_LOADING_COMPLEX	-0.82	0.15	0	0	0	not significant
4799	GO_NEGATIVE_REGULATION_OF_B_CELL_PROLIFERATION	-0.82	0.15	0	0	0	not significant
4800	GO_OXIDOREDUCTASE_ACTIVITY_OXIDIZING_METAL_IONS	-0.82	0.15	0	0	0	not significant
4801	GO_PHOSPHORYLATED_CARBOHYDRATE_DEPHOSPHORYLATION	-0.82	0.15	0	0	0	not significant
4802	GO_REGULATION_OF_HISTONE_H2B_UBIQUITINATION	-0.82	0.15	0	0	0	not significant
4803	GO_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	-0.82	0.15	0	0	0	not significant
4804	GO_SCHWANN_CELL_DEVELOPMENT	-0.82	0.15	0	0	0	not significant
4805	GO_SULFURTRANSFERASE_ACTIVITY	-0.82	0.15	0	0	0	not significant
4806	GO_SYMMETRIC_SYNAPSE	-0.82	0.15	0	0	0	not significant
4807	GO_VITAMIN_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.82	0.15	0	0	0	not significant
4808	REACTOME_PHOSPHATE_BOND_HYDROLYSIS_BY_NUDT_PROTEINS	-0.82	0.15	0	0	0	not significant
4809	REACTOME_PLATELET_CALCIUM_HOMEOSTASIS	-0.82	0.15	0	0	0	not significant
4810	BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_DN	-0.82	0.14	0	0	0	not significant
4811	CHR6Q14	-0.82	0.14	0	0	0	not significant
4812	GO_ACTIVATION_OF_PROTEIN_KINASE_A_ACTIVITY	-0.82	0.14	0	0	0	not significant
4813	GO_EMBRYONIC_PATTERN_SPECIFICATION	-0.82	0.14	0	0	0	not significant
4814	GO_ENDOLYSOSOME	-0.82	0.14	0	0	0	not significant
4815	GO_MICROFIBRIL	-0.82	0.14	0	0	0	not significant
4816	REACTOME_ASSEMBLY_OF_THE_HIV_VIRION	-0.82	0.14	0	0	0	not significant
4817	REACTOME_HYALURONAN_UPTAKE_AND_DEGRADATION	-0.82	0.14	0	0	0	not significant
4818	REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATE	-0.82	0.14	0	0	0	not significant
4819	RICKMAN_HEAD_AND_NECK_CANCER_A	-0.82	0.13	0	0	0	not significant
4820	GO_POLYSOMAL_RIBOSOME	-0.82	0.12	0	0	0	not significant
4821	REACTOME_DEADENYLATION_OF_MRNA	-0.82	0.12	0	0	0	not significant
4822	REACTOME_METALLOPROTEASE_DUBS	-0.82	0.12	0	0	0	not significant
4823	CHEN_NEUROBLASTOMA_COPY_NUMBER_GAINS	-0.82	0.11	0	0	0	not significant
4824	CHR1Q44	-0.82	0.11	0	0	0	not significant
4825	GO_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-0.82	0.11	0	0	0	not significant
4826	GO_NF_KAPPAB_BINDING	-0.82	0.11	0	0	0	not significant
4827	REACTOME_SIGNALING_BY_EGFR	-0.82	0.11	0	0	0	not significant
4828	GO_MORPHOGENESIS_OF_AN_EPITHELIAL_SHEET	-0.82	0.1	0	0	0	not significant
4829	PID_KIT_PATHWAY	-0.82	0.1	0	0	0	not significant
4830	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	-0.82	0.07	0	0	0	not significant
4831	CHR1P13	-0.82	0.06	0	0	0	not significant
4832	GO_NUCLEOTIDE_EXCISION_REPAIR	-0.82	0.06	0	0	0	not significant
4833	GO_NEGATIVE_REGULATION_OF_NEURON_DEATH	-0.82	0.04	0	0	0	not significant
4834	GO_ENDOSOMAL_TRANSPORT	-0.82	0.01	0	0	0	not significant
4835	GO_CELL_CELL_ADHESION_INVOLVED_IN_GASTRULATION	-0.81	0.17	0	0	0	not significant
4836	CHR4P12	-0.81	0.16	0	0	0	not significant
4837	GO_DORSAL_SPINAL_CORD_DEVELOPMENT	-0.81	0.16	0	0	0	not significant
4838	GO_POSITIVE_REGULATION_OF_NUCLEASE_ACTIVITY	-0.81	0.16	0	0	0	not significant
4839	GO_SPINAL_CORD_PATTERNING	-0.81	0.16	0	0	0	not significant
4840	MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA_VHL_UP	-0.81	0.16	0	0	0	not significant
4841	GO_AMINO_ACID_SALVAGE	-0.81	0.15	0	0	0	not significant
4842	GO_CERAMIDE_TRANSPORT	-0.81	0.15	0	0	0	not significant
4843	GO_EXTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE	-0.81	0.15	0	0	0	not significant
4844	GO_GATOR1_COMPLEX	-0.81	0.15	0	0	0	not significant
4845	GO_INTERMEDIATE_FILAMENT_BINDING	-0.81	0.15	0	0	0	not significant
4846	GO_POSITIVE_REGULATION_OF_PROTEIN_DEUBIQUITINATION	-0.81	0.15	0	0	0	not significant
4847	GO_PROTEIN_LOCALIZATION_TO_CILIARY_MEMBRANE	-0.81	0.15	0	0	0	not significant
4848	GO_PROTEIN_LOCALIZATION_TO_EARLY_ENDOSOME	-0.81	0.15	0	0	0	not significant
4849	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HYPOXIA	-0.81	0.15	0	0	0	not significant
4850	GO_REGULATION_OF_HELICASE_ACTIVITY	-0.81	0.15	0	0	0	not significant
4851	HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_UP	-0.81	0.15	0	0	0	not significant
4852	KIM_RESPONSE_TO_TSA_AND_DECITABINE_DN	-0.81	0.15	0	0	0	not significant
4853	BAKER_HEMATOPOESIS_STAT1_TARGETS	-0.81	0.14	0	0	0	not significant
4854	GO_ALPHA_TUBULIN_BINDING	-0.81	0.14	0	0	0	not significant
4855	GO_CELLULAR_RESPONSE_TO_NITROSATIVE_STRESS	-0.81	0.14	0	0	0	not significant
4856	GO_DENDRITIC_CELL_ANTIGEN_PROCESSING_AND_PRESENTATION	-0.81	0.14	0	0	0	not significant
4857	GO_GUANYLYLTRANSFERASE_ACTIVITY	-0.81	0.14	0	0	0	not significant
4858	GO_HYPEROSMOTIC_RESPONSE	-0.81	0.14	0	0	0	not significant
4859	GO_REGULATION_OF_DENDRITIC_SPINE_MAINTENANCE	-0.81	0.14	0	0	0	not significant
4860	GO_RESPONSE_TO_INTERLEUKIN_6	-0.81	0.14	0	0	0	not significant
4861	GO_SPLICEOSOMAL_CONFORMATIONAL_CHANGES_TO_GENERATE_CATALYTIC_C	-0.81	0.14	0	0	0	not significant
4862	GO_STRESS_GRANULE_ASSEMBLY	-0.81	0.14	0	0	0	not significant
4863	GO_SUMO_TRANSFERASE_ACTIVITY	-0.81	0.14	0	0	0	not significant
4864	REACTOME_2_LTR_CIRCLE_FORMATION	-0.81	0.14	0	0	0	not significant
4865	REACTOME_NF_KB_ACTIVATION_THROUGH_FADD_RIP_1_PATHWAY_MEDIATED_BY	-0.81	0.14	0	0	0	not significant
4866	CHR2Q12	-0.81	0.13	0	0	0	not significant
4867	GO_POSITIVE_REGULATION_OF_MUSCLE_HYPERTROPHY	-0.81	0.13	0	0	0	not significant
4868	REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE	-0.81	0.13	0	0	0	not significant
4869	GO_NEUROPEPTIDE_SIGNALING_PATHWAY	-0.81	0.12	0	0	0	not significant
4870	GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCE	-0.81	0.12	0	0	0	not significant
4871	REACTOME_FCERI_MEDIATED_CAPLUS2_MOBILIZATION	-0.81	0.12	0	0	0	not significant
4872	GO_CLATHRIN_ADAPTOR_COMPLEX	-0.81	0.11	0	0	0	not significant
4873	GO_CLATHRIN_COAT	-0.81	0.11	0	0	0	not significant
4874	CHR6Q25	-0.81	0.1	0	0	0	not significant
4875	CHRXP22	-0.81	0.1	0	0	0	not significant
4876	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_UP	-0.81	0.1	0	0	0	not significant
4877	GO_CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS	-0.81	0.1	0	0	0	not significant
4878	GO_O_ACYLTRANSFERASE_ACTIVITY	-0.81	0.1	0	0	0	not significant
4879	GO_EMBRYONIC_SKELETAL_SYSTEM_MORPHOGENESIS	-0.81	0.09	0	0	0	not significant
4880	GO_REGULATION_OF_MONOOXYGENASE_ACTIVITY	-0.81	0.09	0	0	0	not significant
4881	GO_REGULATION_OF_SODIUM_ION_TRANSPORT	-0.81	0.09	0	0	0	not significant
4882	JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_DN	-0.81	0.09	0	0	0	not significant
4883	GO_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	-0.81	0.08	0	0	0	not significant
4884	GO_INTRACILIARY_TRANSPORT	-0.81	0.07	0	0	0	not significant
4885	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP	-0.81	0.06	0	0	0	not significant
4886	GO_TRANSITION_METAL_ION_HOMEOSTASIS	-0.81	0.04	0	0	0	not significant
4887	GO_CHROMOSOME_TELOMERIC_REGION	-0.81	0.03	0	0	0	not significant
4888	GO_COENZYME_BIOSYNTHETIC_PROCESS	-0.81	0.03	0	0	0	not significant
4889	GO_REGULATION_OF_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	-0.80	0.16	0	0	0	not significant
4890	GO_GLUCOSAMINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-0.80	0.15	0	0	0	not significant
4891	GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	-0.80	0.15	0	0	0	not significant
4892	GO_NEPHRON_TUBULE_EPITHELIAL_CELL_DIFFERENTIATION	-0.80	0.15	0	0	0	not significant
4893	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_DIPHENOLS_AND_RELATED_SUBSTA	-0.80	0.15	0	0	0	not significant

4894	GO_PROTEIN_NITROSYLATION	-0.80	0.15	0	0	0	not significant
4895	REACTOME_IRAK4_DEFICIENCY_TLR2_4	-0.80	0.15	0	0	0	not significant
4896	GO_CELLULAR_RESPONSE_TO_SALT_STRESS	-0.80	0.14	0	0	0	not significant
4897	GO_CEREBELLAR_CORTEX_FORMATION	-0.80	0.14	0	0	0	not significant
4898	GO_CILIARY_TRANSITION_FIBER	-0.80	0.14	0	0	0	not significant
4899	GO_FOREBRAIN_MORPHOGENESIS	-0.80	0.14	0	0	0	not significant
4900	GO_NEGATIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	-0.80	0.14	0	0	0	not significant
4901	GO_NEUROTROPHIN_RECEPTOR_BINDING	-0.80	0.14	0	0	0	not significant
4902	GO_POSITIVE_REGULATION_OF_FIBROBLAST_MIGRATION	-0.80	0.14	0	0	0	not significant
4903	GO_PROTEIN_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	-0.80	0.14	0	0	0	not significant
4904	GO_REGULATION_OF_PROTEIN_MONOUBIQUITINATION	-0.80	0.14	0	0	0	not significant
4905	GO_RNA_SECONDARY_STRUCTURE_UNWINDING	-0.80	0.14	0	0	0	not significant
4906	GO_SOLUTE_PROTON_ANTIPORTER_ACTIVITY	-0.80	0.14	0	0	0	not significant
4907	GO_UDP_XYLOSYLTRANSFERASE_ACTIVITY	-0.80	0.14	0	0	0	not significant
4908	NIELSEN_LEIOMYOSARCOMA_CNN1_DN	-0.80	0.14	0	0	0	not significant
4909	REACTOME_PRESYNAPTIC_FUNCTION_OF_KAINATE_RECEPTORS	-0.80	0.14	0	0	0	not significant
4910	REACTOME_REGULATION_OF_FZD_BY_UBIQUITINATION	-0.80	0.14	0	0	0	not significant
4911	VERRECCHIA_RESPONSE_TO_TGFB1_C1	-0.80	0.14	0	0	0	not significant
4912	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_UP	-0.80	0.14	0	0	0	not significant
4913	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN	-0.80	0.13	0	0	0	not significant
4914	GO_CELLULAR_RESPONSE_TO_EXOGENOUS_DSRNA	-0.80	0.13	0	0	0	not significant
4915	GO_HYALURONAN_CATABOLIC_PROCESS	-0.80	0.13	0	0	0	not significant
4916	GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_CATALYTIC_DO	-0.80	0.13	0	0	0	not significant
4917	GO_REGULATION_OF_NEURON_MIGRATION	-0.80	0.13	0	0	0	not significant
4918	GO_REGULATION_OF_OSTEOCLAST_DEVELOPMENT	-0.80	0.13	0	0	0	not significant
4919	GO_UBIQUITIN_LIGASE_INHIBITOR_ACTIVITY	-0.80	0.13	0	0	0	not significant
4920	LEE_LIVER_CANCER	-0.80	0.13	0	0	0	not significant
4921	NIELSEN_LEIOMYOSARCOMA_DN	-0.80	0.13	0	0	0	not significant
4922	GO_DETECTION_OF_VISIBLE_LIGHT	-0.80	0.12	0	0	0	not significant
4923	GO_POSITIVE_REGULATION_OF_SYNAPSE_ASSEMBLY	-0.80	0.12	0	0	0	not significant
4924	GO_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STIMULUS	-0.80	0.12	0	0	0	not significant
4925	PID_CIRCADIAN_PATHWAY	-0.80	0.12	0	0	0	not significant
4926	BIOCARTA_CHEMICAL_PATHWAY	-0.80	0.11	0	0	0	not significant
4927	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_MAGENTA_UP	-0.80	0.11	0	0	0	not significant
4928	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_RED_DN	-0.80	0.11	0	0	0	not significant
4929	GO_DEVELOPMENTAL_PIGMENTATION	-0.80	0.11	0	0	0	not significant
4930	GO_HISTONE_METHYLTRANSFERASE_ACTIVITY_H3_K4_SPECIFIC_	-0.80	0.11	0	0	0	not significant
4931	GO_REGULATION_OF_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	-0.80	0.11	0	0	0	not significant
4932	GO_CELLULAR_IRON_ION_HOMEOSTASIS	-0.80	0.1	0	0	0	not significant
4933	REACTOME_IRON_UPTAKE_AND_TRANSPORT	-0.80	0.1	0	0	0	not significant
4934	ROY_WOUND_BLOOD_VESSEL_UP	-0.80	0.1	0	0	0	not significant
4935	BOYLAN_MULTIPLE_MYELOMA_C_CLUSTER_UP	-0.80	0.09	0	0	0	not significant
4936	GO_POSITIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	-0.80	0.09	0	0	0	not significant
4937	REACTOME_SUMOYLATION_OF_TRANSCRIPTION_COFACTORS	-0.80	0.09	0	0	0	not significant
4938	GO_CILIARY_TIP	-0.80	0.08	0	0	0	not significant
4939	GO_CRANIAL_SKELETAL_SYSTEM_DEVELOPMENT	-0.80	0.08	0	0	0	not significant
4940	KEGG_NON_SMALL_CELL_LUNG_CANCER	-0.80	0.08	0	0	0	not significant
4941	REACTOME_RET_SIGNALING	-0.80	0.08	0	0	0	not significant
4942	GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTENTIAL	-0.80	0.07	0	0	0	not significant
4943	KANG_IMMORTALIZED_BY_TERT_UP	-0.80	0.07	0	0	0	not significant
4944	REACTOME_RETROGRADE_TRANSPORT_AT_THE_TRANS_GOLGI_NETWORK	-0.80	0.07	0	0	0	not significant
4945	PID_TCR_PATHWAY	-0.80	0.06	0	0	0	not significant
4946	REACTOME_COMPLEX_I_BIOGENESIS	-0.80	0.06	0	0	0	not significant
4947	GO_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY	-0.80	0.05	0	0	0	not significant
4948	GO_REGULATION_OF_ACTIN_FILAMENT_ORGANIZATION	-0.80	0.01	0	0	0	not significant
4949	GO_CILIARY_PART	-0.80	0	0	0	0	not significant
4950	GO_NEGATIVE_REGULATION_OF_CENTRIOLE_REPLICATION	-0.79	0.15	0	0	0	not significant
4951	GO_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	-0.79	0.15	0	0	0	not significant
4952	GO_REGULATION_OF_NEURON_MATURATION	-0.79	0.15	0	0	0	not significant
4953	REACTOME_GP1B_IX_V_ACTIVATION_SIGNALLING	-0.79	0.15	0	0	0	not significant
4954	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN	-0.79	0.14	0	0	0	not significant
4955	CORRADETTI_MTOR_PATHWAY_REGULATORS_DN	-0.79	0.14	0	0	0	not significant
4956	GO_HEART_FIELD_SPECIFICATION	-0.79	0.14	0	0	0	not significant
4957	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNAI	-0.79	0.14	0	0	0	not significant
4958	KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	-0.79	0.14	0	0	0	not significant
4959	PETRETTO_LEFT_VENTRICLE_MASS_QTL_CIS_DN	-0.79	0.14	0	0	0	not significant
4960	BARRIER_CANCER_RELAPSE_TUMOR_SAMPLE_DN	-0.79	0.13	0	0	0	not significant
4961	CHR13Q21	-0.79	0.13	0	0	0	not significant
4962	DING_LUNG_CANCER_MUTATED_FREQUENTLY	-0.79	0.13	0	0	0	not significant
4963	GO_PHOSPHATIDYLGLYCEROL_BIOSYNTHETIC_PROCESS	-0.79	0.13	0	0	0	not significant
4964	GO_PHOSPHATIDYLINOSITOL_5_PHOSPHATE_BINDING	-0.79	0.13	0	0	0	not significant
4965	GO_POSITIVE_REGULATION_OF_MACROPHAGE_ACTIVATION	-0.79	0.13	0	0	0	not significant
4966	GO_POSITIVE_REGULATION_OF_PROTEIN_DEPOLYMERIZATION	-0.79	0.13	0	0	0	not significant
4967	GO_PROTEIN_LOCALIZATION_TO_MEMBRANE_RAFT	-0.79	0.13	0	0	0	not significant
4968	GO_U4_SNRNA_3_END_PROCESSING	-0.79	0.13	0	0	0	not significant
4969	LI_WILMS_TUMOR_ANAPLASTIC_DN	-0.79	0.13	0	0	0	not significant
4970	MARKS_ACETYLATED_NON_HISTONE_PROTEINS	-0.79	0.13	0	0	0	not significant
4971	MURAKAMI_UV_RESPONSE_1HR_UP	-0.79	0.13	0	0	0	not significant
4972	REACTOME_ACTIVATION_OF_THE_TFAP2_AP_2_FAMILY_OF_TRANSCRIPTION_FAC	-0.79	0.13	0	0	0	not significant
4973	REACTOME_GAB1_SIGNALOSOME	-0.79	0.13	0	0	0	not significant
4974	REACTOME_PD_1_SIGNALING	-0.79	0.13	0	0	0	not significant
4975	DAWSON_METHYLATED_IN_LYMPHOMA_TCL1	-0.79	0.12	0	0	0	not significant
4976	GO_BRANCHING_INVOLVED_IN_BLOOD_VESSEL_MORPHOGENESIS	-0.79	0.12	0	0	0	not significant
4977	GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE	-0.79	0.12	0	0	0	not significant
4978	GO_GRANULOCYTE_DIFFERENTIATION	-0.79	0.12	0	0	0	not significant
4979	GO_NATURAL_KILLER_CELL_DEGRANULATION	-0.79	0.12	0	0	0	not significant
4980	MOOTHA_GLYCOGEN_METABOLISM	-0.79	0.12	0	0	0	not significant
4981	PID_NETRIN_PATHWAY	-0.79	0.12	0	0	0	not significant
4982	REACTOME_INLA_MEDIATED_ENTRY_OF_LISTERIA_MONOCYTOGENES_INTO_HOST	-0.79	0.12	0	0	0	not significant
4983	REACTOME_LISTERIA_MONOCYTOGENES_ENTRY_INTO_HOST_CELLS	-0.79	0.12	0	0	0	not significant
4984	GO_REGULATION_OF_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTION_BY_P53	-0.79	0.11	0	0	0	not significant
4985	GO_REGULATION_OF_NEUTROPHIL_MIGRATION	-0.79	0.11	0	0	0	not significant
4986	GO_REGULATION_OF_TRIGLYCERIDE_BIOSYNTHETIC_PROCESS	-0.79	0.11	0	0	0	not significant
4987	GO_SH2_DOMAIN_BINDING	-0.79	0.11	0	0	0	not significant
4988	PID_IL8_CXCR1_PATHWAY	-0.79	0.11	0	0	0	not significant
4989	GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_UP	-0.79	0.1	0	0	0	not significant
4990	GO_N_TERMINAL_PROTEIN_AMINO_ACID_MODIFICATION	-0.79	0.09	0	0	0	not significant
4991	GO_POSITIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	-0.79	0.09	0	0	0	not significant
4992	GO_AMINOPEPTIDASE_ACTIVITY	-0.79	0.08	0	0	0	not significant
4993	ZHU_CMV_24_HR_DN	-0.79	0.08	0	0	0	not significant
4994	GO_CAMERA_TYPE_EYE_MORPHOGENESIS	-0.79	0.07	0	0	0	not significant
4995	GO_RESPONSE_TO_ACTIVITY	-0.79	0.07	0	0	0	not significant
4996	KONDO_PROSTATE_CANCER_HCP_WITH_H3K27ME3	-0.79	0.07	0	0	0	not significant
4997	PID_VEGFR1_2_PATHWAY	-0.79	0.07	0	0	0	not significant
4998	REACTOME_CA2PLUS_PATHWAY	-0.79	0.07	0	0	0	not significant
4999	REACTOME_CARGO_TRAFFICKING_TO_THE_PERICILIARY_MEMBRANE	-0.79	0.07	0	0	0	not significant
5000	REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRE	-0.79	0.07	0	0	0	not significant
5001	GO_BETA_CATENIN_BINDING	-0.79	0.06	0	0	0	not significant
5002	GO_POLYOL_METABOLIC_PROCESS	-0.79	0.06	0	0	0	not significant

5003	GO_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	-0.79	0.06	0	0	0	not significant
5004	GO_TIGHT_JUNCTION	-0.79	0.05	0	0	0	not significant
5005	GO_VESICLE_MEDIATED_TRANSPORT_TO_THE_PLASMA_MEMBRANE	-0.79	0.04	0	0	0	not significant
5006	GO_SKELETAL_SYSTEM_MORPHOGENESIS	-0.79	0.03	0	0	0	not significant
5007	GO_RESPONSE_TO_DEFENSES_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_	-0.78	0.15	0	0	0	not significant
5008	GO_NEGATIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	-0.78	0.14	0	0	0	not significant
5009	BERENJENO_TRANSFORMED_BY_RHOA_REVERSIBLY_UP	-0.78	0.13	0	0	0	not significant
5010	BIOCARTA_ECM_PATHWAY	-0.78	0.13	0	0	0	not significant
5011	BIOCARTA_UCALPAIN_PATHWAY	-0.78	0.13	0	0	0	not significant
5012	DING_LUNG_CANCER_MUTATED_RECURRENTLY	-0.78	0.13	0	0	0	not significant
5013	GO_DENDRITIC_CELL_CYTOKINE_PRODUCTION	-0.78	0.13	0	0	0	not significant
5014	GO_G_PROTEIN_COUPLED_RECEPTOR_INTERNALIZATION	-0.78	0.13	0	0	0	not significant
5015	GO_HYALURONAN_BIOSYNTHETIC_PROCESS	-0.78	0.13	0	0	0	not significant
5016	GO_L_METHIONINE_SALVAGE_FROM_METHYLTHIOADENOSINE	-0.78	0.13	0	0	0	not significant
5017	GO_MALE_GERM_CELL_NUCLEUS	-0.78	0.13	0	0	0	not significant
5018	GO_NATURAL_KILLER_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	-0.78	0.13	0	0	0	not significant
5019	GO_NEGATIVE_REGULATION_OF_SODIUM_ION_TRANSPORT	-0.78	0.13	0	0	0	not significant
5020	GO_PEPTIDYL_PROLINE_DIOXYGENASE_ACTIVITY	-0.78	0.13	0	0	0	not significant
5021	GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_	-0.78	0.13	0	0	0	not significant
5022	GO_RNAI_EFFECTOR_COMPLEX	-0.78	0.13	0	0	0	not significant
5023	GO_SECONDARY_HEART_FIELD_SPECIFICATION	-0.78	0.13	0	0	0	not significant
5024	KONDO_HYPOXIA	-0.78	0.13	0	0	0	not significant
5025	REACTOME_ALPHA_OXIDATION_OF_PHYTANATE	-0.78	0.13	0	0	0	not significant
5026	REACTOME_GLYCOGEN_STORAGE_DISEASES	-0.78	0.13	0	0	0	not significant
5027	REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTORS	-0.78	0.13	0	0	0	not significant
5028	GO_CYTIDINE_TO_URIDINE_EDITING	-0.78	0.12	0	0	0	not significant
5029	GO_EIF2ALPHA_PHOSPHORYLATION_IN_RESPONSE_TO_ENDOPLASMIC_RETICULU	-0.78	0.12	0	0	0	not significant
5030	GO_MITOCHONDRIAL_FRAGMENTATION_INVOLVED_IN_APOPTOTIC_PROCESS	-0.78	0.12	0	0	0	not significant
5031	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	-0.78	0.12	0	0	0	not significant
5032	GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC_3_	-0.78	0.12	0	0	0	not significant
5033	GO_REGULATION_OF_PROTEIN_DEUBIQUITINATION	-0.78	0.12	0	0	0	not significant
5034	GO_SEQUESTERING_OF_METAL_ION	-0.78	0.12	0	0	0	not significant
5035	GO_SMOOTH_MUSCLE_TISSUE_DEVELOPMENT	-0.78	0.12	0	0	0	not significant
5036	GO_UBIQUITINATION_LIKE_MODIFICATION_DEPENDENT_PROTEIN_BINDING	-0.78	0.12	0	0	0	not significant
5037	REACTOME_SUMOYLATION_OF_DNA_METHYLATION_PROTEINS	-0.78	0.12	0	0	0	not significant
5038	REACTOME_TRAF6_MEDIATED_INDUCTION_OF_TAK1_COMPLEX_WITHIN_TLR4_CO	-0.78	0.12	0	0	0	not significant
5039	GO_THREONINE_TYPE_PEPTIDASE_ACTIVITY	-0.78	0.11	0	0	0	not significant
5040	WINNEPENNINCKX_MELANOMA_METASTASIS_DN	-0.78	0.11	0	0	0	not significant
5041	GO_BLASTOCYST_GROWTH	-0.78	0.1	0	0	0	not significant
5042	PID_HDAC_CLASSIII_PATHWAY	-0.78	0.1	0	0	0	not significant
5043	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CANCER	-0.78	0.1	0	0	0	not significant
5044	GO_ANIMAL_ORGAN_FORMATION	-0.78	0.09	0	0	0	not significant
5045	GO_AORTA_DEVELOPMENT	-0.78	0.09	0	0	0	not significant
5046	GO_BETA_TUBULIN_BINDING	-0.78	0.09	0	0	0	not significant
5047	REACTOME_MTORC1_MEDIATED_SIGNALLING	-0.78	0.08	0	0	0	not significant
5048	GO_PDZ_DOMAIN_BINDING	-0.78	0.07	0	0	0	not significant
5049	GO_NEURON_SPINE	-0.78	0.05	0	0	0	not significant
5050	GO_REGULATION_OF_ACTOMYOSIN_STRUCTURE_ORGANIZATION	-0.78	0.05	0	0	0	not significant
5051	GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	-0.78	0.05	0	0	0	not significant
5052	BIOCARTA_GABA_PATHWAY	-0.77	0.13	0	0	0	not significant
5053	BIOCARTA_TRKA_PATHWAY	-0.77	0.12	0	0	0	not significant
5054	GO_CHEMICAL_HOMEOSTASIS_WITHIN_A_TISSUE	-0.77	0.12	0	0	0	not significant
5055	GO_MEMBRANE_DEPOLARIZATION_DURING_ACTION_POTENTIAL	-0.77	0.12	0	0	0	not significant
5056	GO_NEGATIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	-0.77	0.12	0	0	0	not significant
5057	GO_OSTEOCLAST_DEVELOPMENT	-0.77	0.12	0	0	0	not significant
5058	GO_POSITIVE_REGULATION_OF_CELL_PROLIFERATION_INVOLVED_IN_HEART_MO	-0.77	0.12	0	0	0	not significant
5059	GO_REGULATION_OF_CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS	-0.77	0.12	0	0	0	not significant
5060	GO_REGULATION_OF_LAMELLIPODIUM_MORPHOGENESIS	-0.77	0.12	0	0	0	not significant
5061	GO_REGULATION_OF_MEMBRANE_TUBULATION	-0.77	0.12	0	0	0	not significant
5062	GO_UBIQUITIN_PROTEIN_TRANSFERASE_INHIBITOR_ACTIVITY	-0.77	0.12	0	0	0	not significant
5063	REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	-0.77	0.12	0	0	0	not significant
5064	REACTOME_GLUCURONIDATION	-0.77	0.12	0	0	0	not significant
5065	REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS	-0.77	0.12	0	0	0	not significant
5066	REACTOME_REGULATION_OF_GENE_EXPRESSION_BY_HYPOXIA_INDUCIBLE_FACT	-0.77	0.12	0	0	0	not significant
5067	BIOCARTA_RELA_PATHWAY	-0.77	0.11	0	0	0	not significant
5068	BIOCARTA_TERT_PATHWAY	-0.77	0.11	0	0	0	not significant
5069	GO_CATECHOLAMINE_METABOLIC_PROCESS	-0.77	0.11	0	0	0	not significant
5070	GO_CYTOPLASMIC_UBIQUITIN_LIGASE_COMPLEX	-0.77	0.11	0	0	0	not significant
5071	GO_DNA_LIGATION	-0.77	0.11	0	0	0	not significant
5072	GO_ERROR_FREE_TRANSLESION_SYNTHESIS	-0.77	0.11	0	0	0	not significant
5073	GO_ISWI_TYPE_COMPLEX	-0.77	0.11	0	0	0	not significant
5074	GO_NEGATIVE_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHWAY	-0.77	0.11	0	0	0	not significant
5075	GO_PERIPHERAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	-0.77	0.11	0	0	0	not significant
5076	GO_POSITIVE_REGULATION_OF_VASCULAR_ASSOCIATED_SMOOTH_MUSCLE_CEL	-0.77	0.11	0	0	0	not significant
5077	GO_REGULATION_OF_GONAD_DEVELOPMENT	-0.77	0.11	0	0	0	not significant
5078	GO_STRUCTURAL_MOLECULE_ACTIVITY_CONFERRING_ELASTICITY	-0.77	0.11	0	0	0	not significant
5079	MIKKELSEN_PLURIPOTENT_STATE_DN	-0.77	0.11	0	0	0	not significant
5080	PID_ANTHRAX_PATHWAY	-0.77	0.11	0	0	0	not significant
5081	GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	-0.77	0.1	0	0	0	not significant
5082	GO_NEGATIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROC	-0.77	0.1	0	0	0	not significant
5083	GO_SOLUTE_CATION_ANTIPORTER_ACTIVITY	-0.77	0.1	0	0	0	not significant
5084	REACTOME_TRANSLESION_SYNTHESIS_BY_POLH	-0.77	0.1	0	0	0	not significant
5085	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_HD_MTX_DN	-0.77	0.09	0	0	0	not significant
5086	CHR9Q32	-0.77	0.09	0	0	0	not significant
5087	GO_MRNA_SPLICE_SITE_SELECTION	-0.77	0.09	0	0	0	not significant
5088	GO_POSITIVE_REGULATION_OF_CILIUM_ASSEMBLY	-0.77	0.09	0	0	0	not significant
5089	REACTOME_NEPHRIN_FAMILY_INTERACTIONS	-0.77	0.09	0	0	0	not significant
5090	BIOCARTA_STRESS_PATHWAY	-0.77	0.08	0	0	0	not significant
5091	GO_REGULATION_OF_CILIUM_ASSEMBLY	-0.77	0.07	0	0	0	not significant
5092	GO_INORGANIC_ION_IMPORT_ACROSS_PLASMA_MEMBRANE	-0.77	0.06	0	0	0	not significant
5093	GO_REGULATION_OF_RESPONSE_TO_DRUG	-0.77	0.06	0	0	0	not significant
5094	GO_MORPHOGENESIS_OF_EMBRYONIC_EPITHELIUM	-0.77	0.04	0	0	0	not significant
5095	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_UP	-0.77	0.04	0	0	0	not significant
5096	GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	-0.77	0.03	0	0	0	not significant
5097	SIRNA_EIF4GI_DN	-0.77	0.03	0	0	0	not significant
5098	GO_REGULATION_OF_HYALURONAN_BIOSYNTHETIC_PROCESS	-0.76	0.13	0	0	0	not significant
5099	INAMURA_LUNG_CANCER_SCC_SUBTYPES_UP	-0.76	0.13	0	0	0	not significant
5100	GO_CONDENSIN_COMPLEX	-0.76	0.12	0	0	0	not significant
5101	GO_MRNA_3_END_PROCESSING_BY_STEM_LOOP_BINDING_AND_CLEAVAGE	-0.76	0.12	0	0	0	not significant
5102	GO_NEGATIVE_REGULATION_OF_ATPASE_ACTIVITY	-0.76	0.12	0	0	0	not significant
5103	GO_NEGATIVE_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	-0.76	0.12	0	0	0	not significant
5104	GO_PHOSPHOFRUCTOKINASE_ACTIVITY	-0.76	0.12	0	0	0	not significant
5105	REACTOME_ACTIVATION_OF_RAC1	-0.76	0.12	0	0	0	not significant
5106	REACTOME_NEF_MEDIATED_CD8_DOWN_REGULATION	-0.76	0.12	0	0	0	not significant
5107	ZEMBUTSU_SENSITIVITY_TO_CISPLATIN	-0.76	0.12	0	0	0	not significant
5108	BIOCARTA_PCAF_PATHWAY	-0.76	0.11	0	0	0	not significant
5109	GO_HEPATOCYTE_APOPTOTIC_PROCESS	-0.76	0.11	0	0	0	not significant
5110	GO_NUCLEAR_RETENTION_OF_PRE_MRNA_AT_THE_SITE_OF_TRANSCRIPTION	-0.76	0.11	0	0	0	not significant
5111	GO_REFLEX	-0.76	0.11	0	0	0	not significant

5112	GO_SMALL_RIBOSOMAL_SUBUNIT_RRNA_BINDING	-0.76	0.11	0	0	0	not significant
5113	BIOCARTA_PKC_PATHWAY	-0.76	0.1	0	0	0	not significant
5114	GO_CYTOCHROME_B5_REDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	-0.76	0.1	0	0	0	not significant
5115	GO_EPIBOLY	-0.76	0.1	0	0	0	not significant
5116	GO_POSITIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	-0.76	0.1	0	0	0	not significant
5117	GO_POSTSYNAPTIC_SPECIALIZATION_ASSEMBLY	-0.76	0.1	0	0	0	not significant
5118	GO_REGULATION_OF_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_DE	-0.76	0.1	0	0	0	not significant
5119	GO_RRNA_BASE_METHYLATION	-0.76	0.1	0	0	0	not significant
5120	REACTOME_SYNTHESIS_OF_DIPHTHAMIDE_EEF2	-0.76	0.1	0	0	0	not significant
5121	WIKMAN_ASBESTOS_LUNG_CANCER_UP	-0.76	0.1	0	0	0	not significant
5122	GO_PLATELET_DENSE_GRANULE	-0.76	0.09	0	0	0	not significant
5123	REACTOME_GABA_RECEPTOR_ACTIVATION	-0.76	0.09	0	0	0	not significant
5124	GO_PHOTOTRANSDUCTION	-0.76	0.07	0	0	0	not significant
5125	GO_REGULATION_OF_RECEPTOR_INTERNALIZATION	-0.76	0.07	0	0	0	not significant
5126	EPPERT_LSC_R	-0.76	0.06	0	0	0	not significant
5127	GO_MICROBODY_LUMEN	-0.76	0.06	0	0	0	not significant
5128	GO_RESPONSE_TO_DSRNA	-0.76	0.06	0	0	0	not significant
5129	GO_VESICLE_DOCKING_INVOLVED_IN_EXOCYTOSIS	-0.76	0.06	0	0	0	not significant
5130	GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	-0.76	0.05	0	0	0	not significant
5131	GO_POSITIVE_REGULATION_OF_STRESS_FIBER_ASSEMBLY	-0.76	0.05	0	0	0	not significant
5132	GO_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	-0.76	0.05	0	0	0	not significant
5133	GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_NADH_TO_UBIQUINONE	-0.76	0.04	0	0	0	not significant
5134	GO_POSITIVE_REGULATION_OF_ENDOCYTOSIS	-0.76	0.04	0	0	0	not significant
5135	REACTOME_E3_UBIQUITIN_LIGASES_UBIQUITINATE_TARGET_PROTEINS	-0.76	0.04	0	0	0	not significant
5136	REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING	-0.76	0.03	0	0	0	not significant
5137	GO_RESPIRASOME	-0.76	0.02	0	0	0	not significant
5138	GO_SMALL_RIBOSOMAL_SUBUNIT	-0.76	0.02	0	0	0	not significant
5139	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIC	-0.76	0.02	0	0	0	not significant
5140	GO_GAMMA_AMINOBUTYRIC_ACID_TRANSPORT	-0.75	0.12	0	0	0	not significant
5141	GO_TUBULIN_COMPLEX_ASSEMBLY	-0.75	0.12	0	0	0	not significant
5142	GO_REGULATION_OF_ASPARTIC_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_	-0.75	0.11	0	0	0	not significant
5143	GO_REGULATION_OF_ER_ASSOCIATED_UBIQUITIN_DEPENDENT_PROTEIN_CATABC	-0.75	0.11	0	0	0	not significant
5144	GO_REGULATION_OF_PROTEIN_FOLDING	-0.75	0.11	0	0	0	not significant
5145	GO_REGULATION_OF_RESPIRATORY_GASEOUS_EXCHANGE	-0.75	0.11	0	0	0	not significant
5146	GO_SOMATIC_DIVERSIFICATION_OF_T_CELL_RECEPTOR_GENES	-0.75	0.11	0	0	0	not significant
5147	MIKKELSEN_IPS_ICP_WITH_H3K27ME3	-0.75	0.11	0	0	0	not significant
5148	WILLIAMS_ESR2_TARGETS_DN	-0.75	0.11	0	0	0	not significant
5149	BIOCARTA_PS1_PATHWAY	-0.75	0.1	0	0	0	not significant
5150	CHR4Q23	-0.75	0.1	0	0	0	not significant
5151	CHRXQ23	-0.75	0.1	0	0	0	not significant
5152	GO_AEROBIC_ELECTRON_TRANSPORT_CHAIN	-0.75	0.1	0	0	0	not significant
5153	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_ACTIN_CYTOSKELETON_POLARITY	-0.75	0.1	0	0	0	not significant
5154	GO_FOREBRAIN_NEURON_DIFFERENTIATION	-0.75	0.1	0	0	0	not significant
5155	GO_MITOTIC_NUCLEAR_ENVELOPE_REASSEMBLY	-0.75	0.1	0	0	0	not significant
5156	REACTOME_MYOCLONIC_EPILEPSY_OF_LAFORA	-0.75	0.1	0	0	0	not significant
5157	REACTOME_REGULATION_OF_KIT_SIGNALING	-0.75	0.1	0	0	0	not significant
5158	REACTOME_STING_MEDIATED_INDUCTION_OF_HOST_IMMUNE_RESPONSES	-0.75	0.1	0	0	0	not significant
5159	REACTOME_TRANSPORT_OF_NUCLEOTIDE_SUGARS	-0.75	0.1	0	0	0	not significant
5160	WEINMANN_ADAPTATION_TO_HYPOXIA_UP	-0.75	0.1	0	0	0	not significant
5161	GO_CELL_PROLIFERATION_INVOLVED_IN_HEART_MORPHOGENESIS	-0.75	0.09	0	0	0	not significant
5162	GO_ENDOPLASMIC_RETICULUM_TUBULAR_NETWORK_ORGANIZATION	-0.75	0.09	0	0	0	not significant
5163	GO_GASTRULATION_WITH_MOUTH_FORMING_SECOND	-0.75	0.09	0	0	0	not significant
5164	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP_OF_DONORS	-0.75	0.09	0	0	0	not significant
5165	GO_SECRETORY_GRANULE_ORGANIZATION	-0.75	0.09	0	0	0	not significant
5166	PARK_HSC_VS_MULTIPOTENT_PROGENITORS_UP	-0.75	0.09	0	0	0	not significant
5167	GO_POSITIVE_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	-0.75	0.08	0	0	0	not significant
5168	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_DN	-0.75	0.08	0	0	0	not significant
5169	GO_RAC_PROTEIN_SIGNAL_TRANSDUCTION	-0.75	0.07	0	0	0	not significant
5170	GO_DETERMINATION_OF_HEART_LEFT_RIGHT_ASYMMETRY	-0.75	0.06	0	0	0	not significant
5171	GO_METALLOENDOPEPTIDASE_ACTIVITY	-0.75	0.06	0	0	0	not significant
5172	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	-0.75	0.06	0	0	0	not significant
5173	GO_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_BINDING	-0.75	0.06	0	0	0	not significant
5174	REACTOME_MTOR_SIGNALLING	-0.75	0.06	0	0	0	not significant
5175	FAELT_B_CLL_WITH_VH_REARRANGEMENTS_DN	-0.75	0.05	0	0	0	not significant
5176	GO_APICAL_JUNCTION_ASSEMBLY	-0.75	0.05	0	0	0	not significant
5177	GO_EMBRYONIC_HEART_TUBE_DEVELOPMENT	-0.75	0.05	0	0	0	not significant
5178	REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESC	-0.75	0.05	0	0	0	not significant
5179	GO_ACTOMYOSIN	-0.75	0.03	0	0	0	not significant
5180	REACTOME_RAB_GEFS_EXCHANGE_GTP_FOR_GDP_ON_RABS	-0.75	0.03	0	0	0	not significant
5181	KEGG_PARKINSONS_DISEASE	-0.75	0.02	0	0	0	not significant
5182	GO_GAMMA_AMINOBUTYRIC_ACID_SECRETION	-0.74	0.12	0	0	0	not significant
5183	GO_NEGATIVE_REGULATION_OF_RECEPTOR_BINDING	-0.74	0.12	0	0	0	not significant
5184	BAFNA_MUC4_TARGETS_UP	-0.74	0.11	0	0	0	not significant
5185	BIOCARTA_HSWI_SNF_PATHWAY	-0.74	0.1	0	0	0	not significant
5186	FIGUEROA_AML_METHYLATION_CLUSTER_5_UP	-0.74	0.1	0	0	0	not significant
5187	GO_EOSINOPHIL_ACTIVATION	-0.74	0.1	0	0	0	not significant
5188	GO_KERATINIZATION	-0.74	0.1	0	0	0	not significant
5189	GO_MAINTENANCE_OF_SYNAPSE_STRUCTURE	-0.74	0.1	0	0	0	not significant
5190	GO_MEDIUM_CHAIN_FATTY_ACID_COA_LIGASE_ACTIVITY	-0.74	0.1	0	0	0	not significant
5191	GO_POSITIVE_REGULATION_OF_DEOXYRIBONUCLEASE_ACTIVITY	-0.74	0.1	0	0	0	not significant
5192	GO_PROTEIN_LOCALIZATION_TO_BASOLATERAL_PLASMA_MEMBRANE	-0.74	0.1	0	0	0	not significant
5193	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_ACTIVIT	-0.74	0.1	0	0	0	not significant
5194	HOLLERN_ADENOMYOEPITHELIAL_BREAST_TUMOR	-0.74	0.1	0	0	0	not significant
5195	MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA_VHL_DN	-0.74	0.1	0	0	0	not significant
5196	REACTOME_ARYL_HYDROCARBON_RECEPTOR_SIGNALLING	-0.74	0.1	0	0	0	not significant
5197	CHR14Q13	-0.74	0.09	0	0	0	not significant
5198	GO_REGULATION_OF_AMINO_ACID_TRANSPORT	-0.74	0.09	0	0	0	not significant
5199	GO_TITIN_BINDING	-0.74	0.09	0	0	0	not significant
5200	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_15	-0.74	0.09	0	0	0	not significant
5201	GO_COPI_VESICLE_COAT	-0.74	0.08	0	0	0	not significant
5202	GO_PHOTOTRANSDUCTION_VISIBLE_LIGHT	-0.74	0.08	0	0	0	not significant
5203	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	-0.74	0.08	0	0	0	not significant
5204	GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTC	-0.74	0.08	0	0	0	not significant
5205	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON	-0.74	0.08	0	0	0	not significant
5206	REACTOME_RAF_INDEPENDENT_MAPK1_3_ACTIVATION	-0.74	0.08	0	0	0	not significant
5207	REACTOME_SIGNALING_BY_NTRK3_TRKC	-0.74	0.08	0	0	0	not significant
5208	ZHAN_MULTIPLE_MYELOMA_MF_UP	-0.74	0.08	0	0	0	not significant
5209	CHR5P13	-0.74	0.07	0	0	0	not significant
5210	GO_INOSITOL_PHOSPHATE_CATABOLIC_PROCESS	-0.74	0.07	0	0	0	not significant
5211	GO_KERATINOCYTE_PROLIFERATION	-0.74	0.07	0	0	0	not significant
5212	GO_PODOSOME	-0.74	0.07	0	0	0	not significant
5213	GO_ARP2_3_COMPLEX_MEDIATED_ACTIN_NUCLEATION	-0.74	0.06	0	0	0	not significant
5214	GO_CARBOHYDRATE_PHOSPHORYLATION	-0.74	0.06	0	0	0	not significant
5215	NAKAMURA_METASTASIS_MODEL_UP	-0.74	0.06	0	0	0	not significant
5216	BURTON_ADIPOGENESIS_7	-0.74	0.05	0	0	0	not significant
5217	GO_CELL_CELL_CONTACT_ZONE	-0.74	0.04	0	0	0	not significant
5218	JOHNSTONE_PARVB_TARGETS_1_DN	-0.74	0.04	0	0	0	not significant
5219	GO_SITE_OF_DOUBLE_STRAND_BREAK	-0.74	0.03	0	0	0	not significant
5220	GO_ARYL_HYDROCARBON_RECEPTOR_BINDING	-0.73	0.11	0	0	0	not significant

5221	GO_ENDOCARDIUM_DEVELOPMENT	-0.73	0.11	0	0	0	not significant
5222	GO_RESPONSE_TO_MACROPHAGE_COLONY_STIMULATING_FACTOR	-0.73	0.11	0	0	0	not significant
5223	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_DN	-0.73	0.1	0	0	0	not significant
5224	GO_SODIUM_ION_IMPORT_ACROSS_PLASMA_MEMBRANE	-0.73	0.1	0	0	0	not significant
5225	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_25	-0.73	0.1	0	0	0	not significant
5226	REACTOME_IRF3_MEDIATED_INDUCTION_OF_TYPE_I_IFN	-0.73	0.1	0	0	0	not significant
5227	RIZ_ERYTHROID_DIFFERENTIATION_6HR	-0.73	0.1	0	0	0	not significant
5228	GO_ANATOMICAL_STRUCTURE_REGRESSION	-0.73	0.09	0	0	0	not significant
5229	GO_COMPLEMENT_BINDING	-0.73	0.09	0	0	0	not significant
5230	GO_CYTOPLASMIC_SEQUESTERING_OF_NF_KAPPAB	-0.73	0.09	0	0	0	not significant
5231	GO_DOPAMINERGIC_NEURON_DIFFERENTIATION	-0.73	0.09	0	0	0	not significant
5232	GO_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_INVOLVED_IN_ENDOCARDIAL_CU	-0.73	0.09	0	0	0	not significant
5233	GO_NEGATIVE_REGULATION_OF_GLUCOSE_IMPORT	-0.73	0.09	0	0	0	not significant
5234	GO_POSITIVE_REGULATION_OF_GRANULOCYTE_MACROPHAGE_COLONY_STIMULA	-0.73	0.09	0	0	0	not significant
5235	GO_REGULATION_OF_RAC_PROTEIN_SIGNAL_TRANSDUCTION	-0.73	0.09	0	0	0	not significant
5236	GO_UV_DAMAGE_EXCISION_REPAIR	-0.73	0.09	0	0	0	not significant
5237	NEBEN_AML_WITH_FLT3_OR_NRAS_DN	-0.73	0.09	0	0	0	not significant
5238	GO_AMINO_SUGAR_METABOLIC_PROCESS	-0.73	0.08	0	0	0	not significant
5239	GO_DEATH_RECEPTOR_BINDING	-0.73	0.08	0	0	0	not significant
5240	GO_VOLTAGE_GATED_CALCIUM_CHANNEL_COMPLEX	-0.73	0.08	0	0	0	not significant
5241	CHR21Q21	-0.73	0.07	0	0	0	not significant
5242	GO_H4_HISTONE_ACETYLTRANSFERASE_ACTIVITY	-0.73	0.07	0	0	0	not significant
5243	GO_WW_DOMAIN_BINDING	-0.73	0.07	0	0	0	not significant
5244	REACTOME_GLYOXYLATE_METABOLISM_AND_GLYCINE_DEGRADATION	-0.73	0.07	0	0	0	not significant
5245	REACTOME_METAL_ION_SLC_TRANSPORTERS	-0.73	0.07	0	0	0	not significant
5246	GO_EXOSOME_RNASE_COMPLEX_	-0.73	0.06	0	0	0	not significant
5247	GO_PROTEIN_TRANSPORT_WITHIN_LIPID_BILAYER	-0.73	0.06	0	0	0	not significant
5248	GO_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	-0.73	0.06	0	0	0	not significant
5249	GO_REGULATION_OF_COAGULATION	-0.73	0.05	0	0	0	not significant
5250	GO_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGION_DNA_BINDING	-0.73	0.05	0	0	0	not significant
5251	GO_RUFFLE_ASSEMBLY	-0.73	0.05	0	0	0	not significant
5252	CHR14Q23	-0.73	0.04	0	0	0	not significant
5253	NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON	-0.73	0.04	0	0	0	not significant
5254	REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	-0.73	0.04	0	0	0	not significant
5255	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_DN	-0.73	0.03	0	0	0	not significant
5256	GO_NEUROMUSCULAR_PROCESS	-0.73	0.03	0	0	0	not significant
5257	REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	-0.73	0.03	0	0	0	not significant
5258	REACTOME_PEROXISOMAL_PROTEIN_IMPORT	-0.73	0.02	0	0	0	not significant
5259	GO_APICAL_JUNCTION_COMPLEX	-0.73	0.01	0	0	0	not significant
5260	GO_RUFFLE	-0.73	0.01	0	0	0	not significant
5261	GO_SYNAPTIC_VESICLE_LOCALIZATION	-0.73	0.01	0	0	0	not significant
5262	GO_MODULATION_OF_AGE_RELATED_BEHAVIORAL_DECLINE	-0.72	0.1	0	0	0	not significant
5263	GO_NEGATIVE_REGULATION_OF_AMINE_TRANSPORT	-0.72	0.1	0	0	0	not significant
5264	GO_POSITIVE_REGULATION_OF_CELL_SIZE	-0.72	0.1	0	0	0	not significant
5265	GO_REGULATION_OF_CLATHRIN_DEPENDENT_ENDOCYTOSIS	-0.72	0.1	0	0	0	not significant
5266	ITO_PTTG1_TARGETS_UP	-0.72	0.1	0	0	0	not significant
5267	REACTOME_LIPOPHAGY	-0.72	0.1	0	0	0	not significant
5268	GO_ACTIVATION_OF_JNKK_ACTIVITY	-0.72	0.09	0	0	0	not significant
5269	GO_CELLULAR_ANION_HOMEOSTASIS	-0.72	0.09	0	0	0	not significant
5270	GO_CENTRIOLE_CENTRIOLE_COHESION	-0.72	0.09	0	0	0	not significant
5271	GO_EMBRYONIC_FORELIMB_MORPHOGENESIS	-0.72	0.09	0	0	0	not significant
5272	GO_ESTABLISHMENT_OF_VIRAL_LATENCY	-0.72	0.09	0	0	0	not significant
5273	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_IV	-0.72	0.09	0	0	0	not significant
5274	GO_PROTEIN_INSERTION_INTO_MITOCHONDRIAL_INNER_MEMBRANE	-0.72	0.09	0	0	0	not significant
5275	GO_TYPE_B_PANCREATIC_CELL_APOPTOTIC_PROCESS	-0.72	0.09	0	0	0	not significant
5276	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_UP	-0.72	0.09	0	0	0	not significant
5277	MOOTHA_PYR	-0.72	0.09	0	0	0	not significant
5278	RIZ_ERYTHROID_DIFFERENTIATION_APOBEC2	-0.72	0.09	0	0	0	not significant
5279	SHANK_TAL1_TARGETS_DN	-0.72	0.09	0	0	0	not significant
5280	BIOCARTA_41BB_PATHWAY	-0.72	0.08	0	0	0	not significant
5281	GO_ADAPTATION_OF_SIGNALING_PATHWAY	-0.72	0.08	0	0	0	not significant
5282	GO_CCR4_NOT_COMPLEX	-0.72	0.08	0	0	0	not significant
5283	GO_CELLULAR_RESPONSE_TO_LEPTIN_STIMULUS	-0.72	0.08	0	0	0	not significant
5284	GO_CORTICAL_ENDOPLASMIC_RETICULUM	-0.72	0.08	0	0	0	not significant
5285	GO_MUSCLE_HYPERTROPHY_IN_RESPONSE_TO_STRESS	-0.72	0.08	0	0	0	not significant
5286	GO_NEGATIVE_REGULATION_OF_CHROMATIN_SILENCING	-0.72	0.08	0	0	0	not significant
5287	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH_GROUP_OF_DONORS	-0.72	0.08	0	0	0	not significant
5288	ROZANOV_MMP14_TARGETS_SUBSET	-0.72	0.08	0	0	0	not significant
5289	GO_CARBOHYDRATE_KINASE_ACTIVITY	-0.72	0.07	0	0	0	not significant
5290	MATTIOLI_MGUS_VS_MULTIPLE_MYELOMA	-0.72	0.07	0	0	0	not significant
5291	REACTOME_SIGNAL_TRANSDUCTION_BY_L1	-0.72	0.07	0	0	0	not significant
5292	RUAN_RESPONSE_TO_TROGLITAZONE_UP	-0.72	0.07	0	0	0	not significant
5293	VIETOR_IFRD1_TARGETS	-0.72	0.07	0	0	0	not significant
5294	GO_MITOCHONDRIAL_FUSION	-0.72	0.06	0	0	0	not significant
5295	REACTOME_DOWNREGULATION_OF_ERBB2_SIGNALING	-0.72	0.06	0	0	0	not significant
5296	WATANABE_COLON_CANCER_MSI_VS_MSS_UP	-0.72	0.06	0	0	0	not significant
5297	GO_FEAR_RESPONSE	-0.72	0.05	0	0	0	not significant
5298	GO_RESPONSE_TO_AMYLOID_BETA	-0.72	0.05	0	0	0	not significant
5299	HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_UP	-0.72	0.05	0	0	0	not significant
5300	REACTOME_DAP12_SIGNALING	-0.72	0.05	0	0	0	not significant
5301	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_BIPOLAR_CELL_POLARITY	-0.72	0.04	0	0	0	not significant
5302	BURTON_ADIPOGENESIS_11	-0.72	0.03	0	0	0	not significant
5303	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13	-0.72	0	0	0	0	not significant
5304	GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_PHOSPHATASE_ACTIVITY	-0.71	0.09	0	0	0	not significant
5305	GO_POSITIVE_REGULATION_OF_RNA_BINDING	-0.71	0.09	0	0	0	not significant
5306	GO_POSITIVE_REGULATION_OF_TORC1_SIGNALING	-0.71	0.09	0	0	0	not significant
5307	GO_REGULATION_OF_MRNA_EXPORT_FROM_NUCLEUS	-0.71	0.09	0	0	0	not significant
5308	SABATES_COLORECTAL_ADENOMA_SIZE_DN	-0.71	0.09	0	0	0	not significant
5309	BIOCARTA_EPONFKB_PATHWAY	-0.71	0.08	0	0	0	not significant
5310	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_DN	-0.71	0.08	0	0	0	not significant
5311	GO_KERATINOCYTE_DEVELOPMENT	-0.71	0.08	0	0	0	not significant
5312	GO_MICROFILAMENT_MOTOR_ACTIVITY	-0.71	0.08	0	0	0	not significant
5313	GO_PROTEIN_KINASE_A_CATALYTIC_SUBUNIT_BINDING	-0.71	0.08	0	0	0	not significant
5314	GO_REGULATION_OF_UNSATURATED_FATTY_ACID_BIOSYNTHETIC_PROCESS	-0.71	0.08	0	0	0	not significant
5315	GO_CYTOKINE_SECRETION_INVOLVED_IN_IMMUNE_RESPONSE	-0.71	0.07	0	0	0	not significant
5316	GO_HYDROGEN_PEROXIDE_CATABOLIC_PROCESS	-0.71	0.07	0	0	0	not significant
5317	GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	-0.71	0.07	0	0	0	not significant
5318	GO_NEUROMUSCULAR_SYNAPTIC_TRANSMISSION	-0.71	0.07	0	0	0	not significant
5319	GO_NUCLEOTIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.71	0.07	0	0	0	not significant
5320	GO_RESPONSE_TO_LEPTIN	-0.71	0.07	0	0	0	not significant
5321	GO_SEQUENCE_SPECIFIC_SINGLE_STRANDED_DNA_BINDING	-0.71	0.07	0	0	0	not significant
5322	OXFORD_RALA_AND_RALB_TARGETS_UP	-0.71	0.07	0	0	0	not significant
5323	GO_FORMATION_OF_EXTRACHROMOSOMAL_CIRCULAR_DNA	-0.71	0.06	0	0	0	not significant
5324	GO_REGULATION_OF_PRODUCTION_OF_SMALL_RNA_INVOLVED_IN_GENE_SILENCI	-0.71	0.06	0	0	0	not significant
5325	REACTOME_G_PROTEIN_BETA:GAMMA_SIGNALLING	-0.71	0.05	0	0	0	not significant
5326	CHRXQ26	-0.71	0.04	0	0	0	not significant
5327	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP	-0.71	0.04	0	0	0	not significant
5328	GO_BASE_CONVERSION_OR_SUBSTITUTION_EDITING	-0.70	0.08	0	0	0	not significant
5329	GO_GAMMA_AMINOBUTYRIC_ACID_SIGNALING_PATHWAY	-0.70	0.08	0	0	0	not significant

5330	GO_INTERFERON_ALPHA_BIOSYNTHETIC_PROCESS	-0.70	0.08	0	0	0	not significant
5331	GO_LATE_ENDOSOME_TO_LYSOSOME_TRANSPORT	-0.70	0.08	0	0	0	not significant
5332	GO_METALLOCHAPERONE_ACTIVITY	-0.70	0.08	0	0	0	not significant
5333	GO_MYOBLAST_MIGRATION	-0.70	0.08	0	0	0	not significant
5334	HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_DN	-0.70	0.08	0	0	0	not significant
5335	REACTOME_GRB2:SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRIN	-0.70	0.08	0	0	0	not significant
5336	GO_EMBRYONIC_HEMOPOIESIS	-0.70	0.07	0	0	0	not significant
5337	GO_HISTONE_H3_K9_TRIMETHYLATION	-0.70	0.07	0	0	0	not significant
5338	GO_NEGATIVE_REGULATION_OF_CHOLESTEROL_BIOSYNTHETIC_PROCESS	-0.70	0.07	0	0	0	not significant
5339	GO_NEGATIVE_REGULATION_OF_GLUCONEOGENESIS	-0.70	0.07	0	0	0	not significant
5340	GO_REGULATION_OF_DEOXYRIBONUCLEASE_ACTIVITY	-0.70	0.07	0	0	0	not significant
5341	GO_RESPONSE_TO_SALT_STRESS	-0.70	0.07	0	0	0	not significant
5342	MANN_RESPONSE_TO_AMIFOSTINE_UP	-0.70	0.07	0	0	0	not significant
5343	SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_UP	-0.70	0.07	0	0	0	not significant
5344	ZEMBUTSU_SENSITIVITY_TO_CYCLOPHOSPHAMIDE	-0.70	0.07	0	0	0	not significant
5345	BIOCARTA_PTDINS_PATHWAY	-0.70	0.06	0	0	0	not significant
5346	CHR8Q13	-0.70	0.06	0	0	0	not significant
5347	GO_POSITIVE_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	-0.70	0.06	0	0	0	not significant
5348	GO_POSITIVE_REGULATION_OF_FOCAL_ADHESION_ASSEMBLY	-0.70	0.06	0	0	0	not significant
5349	GO_SET1C_COMPASS_COMPLEX	-0.70	0.06	0	0	0	not significant
5350	HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_UP	-0.70	0.06	0	0	0	not significant
5351	MARCHINI_TRABECTEDIN_RESISTANCE_UP	-0.70	0.06	0	0	0	not significant
5352	NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON	-0.70	0.06	0	0	0	not significant
5353	REACTOME_P75NTR_SIGNALS_VIA_NF_KB	-0.70	0.06	0	0	0	not significant
5354	WEINMANN_ADAPTATION_TO_HYPOXIA_DN	-0.70	0.06	0	0	0	not significant
5355	GO_DORSAL_VENTRAL_NEURAL_TUBE_PATTERNING	-0.70	0.05	0	0	0	not significant
5356	GO_NUCLEOTIDE_TRANSPORT	-0.70	0.05	0	0	0	not significant
5357	LEE_CALORIE_RESTRICTION_MUSCLE_UP	-0.70	0.05	0	0	0	not significant
5358	GO_FLEMMING_BODY	-0.70	0.04	0	0	0	not significant
5359	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	-0.70	0.04	0	0	0	not significant
5360	CHR8P11	-0.70	0.03	0	0	0	not significant
5361	GO_PROTEIN_CONTAINING_COMPLEX_SCAFFOLD_ACTIVITY	-0.70	0.02	0	0	0	not significant
5362	GO_NEGATIVE_REGULATION_OF_FIBROBLAST_APOPTOTIC_PROCESS	-0.69	0.09	0	0	0	not significant
5363	GO_UDP_N_ACETYLGLUCOSAMINE_METABOLIC_PROCESS	-0.69	0.09	0	0	0	not significant
5364	GO_MESSENGER_RIBONUCLEOPROTEIN_COMPLEX	-0.69	0.08	0	0	0	not significant
5365	GO_NEGATIVE_REGULATION_OF_CAMP_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-0.69	0.08	0	0	0	not significant
5366	GO_NEGATIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	-0.69	0.08	0	0	0	not significant
5367	GO_REGULATION_OF_MACROPHAGE_APOPTOTIC_PROCESS	-0.69	0.08	0	0	0	not significant
5368	GO_RS_DOMAIN_BINDING	-0.69	0.08	0	0	0	not significant
5369	GO_SEQUESTERING_OF_TRIGLYCERIDE	-0.69	0.08	0	0	0	not significant
5370	MATZUK_MALE_REPRODUCTION_SERTOLI	-0.69	0.08	0	0	0	not significant
5371	GO_AXON_ENSHEATHMENT_IN_CENTRAL_NERVOUS_SYSTEM	-0.69	0.07	0	0	0	not significant
5372	GO_FORELIMB_MORPHOGENESIS	-0.69	0.07	0	0	0	not significant
5373	GO_GOLGI_DISASSEMBLY	-0.69	0.07	0	0	0	not significant
5374	GO_PLATELET_DENSE_TUBULAR_NETWORK	-0.69	0.07	0	0	0	not significant
5375	GO_POSITIVE_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	-0.69	0.07	0	0	0	not significant
5376	REACTOME_TIGHT_JUNCTION_INTERACTIONS	-0.69	0.07	0	0	0	not significant
5377	REACTOME_WNT_LIGAND_BIOGENESIS_AND_TRAFFICKING	-0.69	0.07	0	0	0	not significant
5378	WACKER_HYPOXIA_TARGETS_OF_VHL	-0.69	0.07	0	0	0	not significant
5379	GO_NUCLEOTIDE_DIPHOSPHATASE_ACTIVITY	-0.69	0.06	0	0	0	not significant
5380	GO_REGULATION_OF_NEURON_PROJECTION_REGENERATION	-0.69	0.06	0	0	0	not significant
5381	GO_SINGLE_STRANDED_DNA_ENDODEOXYRIBONUCLEASE_ACTIVITY	-0.69	0.06	0	0	0	not significant
5382	NABA_BASEMENT_MEMBRANES	-0.69	0.06	0	0	0	not significant
5383	PID_SYNDECAN_1_PATHWAY	-0.69	0.06	0	0	0	not significant
5384	WU_HBX_TARGETS_2_UP	-0.69	0.06	0	0	0	not significant
5385	GO_CELLULAR_PROTEIN_CONTAINING_COMPLEX_LOCALIZATION	-0.69	0.05	0	0	0	not significant
5386	GO_CYTOPLASMIC_EXOSOME_RNASE_COMPLEX_	-0.69	0.05	0	0	0	not significant
5387	REACTOME_REGULATION_OF_INNATE_IMMUNE_RESPONSES_TO_CYTOSOLIC_DNA	-0.69	0.05	0	0	0	not significant
5388	FIGUEROA_AML_METHYLATION_CLUSTER_5_DN	-0.69	0.04	0	0	0	not significant
5389	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_CLEARANCE	-0.69	0.04	0	0	0	not significant
5390	GO_PROTEIN_TRANSPORT_WITHIN_PLASMA_MEMBRANE	-0.69	0.04	0	0	0	not significant
5391	KEGG_GALACTOSE_METABOLISM	-0.69	0.04	0	0	0	not significant
5392	GO_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	-0.69	0.03	0	0	0	not significant
5393	LEE_LIVER_CANCER_DENA_DN	-0.69	0.03	0	0	0	not significant
5394	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I	-0.69	0.02	0	0	0	not significant
5395	GO_PLATELET_DEGRANULATION	-0.69	0.01	0	0	0	not significant
5396	NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON	-0.69	0.01	0	0	0	not significant
5397	GO_FATTY_ACID_ALPHA_OXIDATION	-0.68	0.08	0	0	0	not significant
5398	GO_POLAR_MICROTUBULE	-0.68	0.08	0	0	0	not significant
5399	GO_CEREBRAL_CORTEX_NEURON_DIFFERENTIATION	-0.68	0.07	0	0	0	not significant
5400	GO_INOSITOL_METABOLIC_PROCESS	-0.68	0.07	0	0	0	not significant
5401	GO_MEMBRANOUS_SEPTUM_MORPHOGENESIS	-0.68	0.07	0	0	0	not significant
5402	GO_NUCLEAR_NCRNA_SURVEILLANCE	-0.68	0.07	0	0	0	not significant
5403	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	-0.68	0.07	0	0	0	not significant
5404	GO_REGULATION_OF_BICELLULAR_TIGHT_JUNCTION_ASSEMBLY	-0.68	0.07	0	0	0	not significant
5405	REACTOME_DCC_MEDIATED_ATTRACTIVE_SIGNALING	-0.68	0.07	0	0	0	not significant
5406	WANG_RESPONSE_TO_FORSKOLIN_DN	-0.68	0.07	0	0	0	not significant
5407	BIOCARTA_MALATEX_PATHWAY	-0.68	0.06	0	0	0	not significant
5408	CHR2P14	-0.68	0.06	0	0	0	not significant
5409	GO_INNER_CELL_MASS_CELL_PROLIFERATION	-0.68	0.06	0	0	0	not significant
5410	GO_NEGATIVE_REGULATION_OF_ACTIVATED_T_CELL_PROLIFERATION	-0.68	0.06	0	0	0	not significant
5411	GO_POSITIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_UNFOLDED_PROTEIN_	-0.68	0.06	0	0	0	not significant
5412	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_LATE_STAGE_BRANCHING_M	-0.68	0.06	0	0	0	not significant
5413	REACTOME_TICAM1_TRAF6_DEPENDENT_INDUCTION_OF_TAK1_COMPLEX	-0.68	0.06	0	0	0	not significant
5414	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_UP	-0.68	0.05	0	0	0	not significant
5415	GO_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZATION	-0.68	0.05	0	0	0	not significant
5416	GO_PRP19_COMPLEX	-0.68	0.05	0	0	0	not significant
5417	GO_QUINONE_BINDING	-0.68	0.05	0	0	0	not significant
5418	BIOCARTA_CERAMIDE_PATHWAY	-0.68	0.04	0	0	0	not significant
5419	GO_NEURAL_TUBE_PATTERNING	-0.68	0.04	0	0	0	not significant
5420	GO_PRC1_COMPLEX	-0.68	0.04	0	0	0	not significant
5421	GO_CALCIUM_ION_IMPORT	-0.68	0.03	0	0	0	not significant
5422	GO_HYDRO_LYASE_ACTIVITY	-0.68	0.03	0	0	0	not significant
5423	GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_	-0.68	0.03	0	0	0	not significant
5424	CHR1P32	-0.68	0.02	0	0	0	not significant
5425	PID_INSULIN_PATHWAY	-0.68	0.02	0	0	0	not significant
5426	REACTOME_G_ALPHA_12_13_SIGNALLING_EVENTS	-0.68	0.02	0	0	0	not significant
5427	GO_IRON_ION_HOMEOSTASIS	-0.68	0.01	0	0	0	not significant
5428	GO_BCL_2_FAMILY_PROTEIN_COMPLEX	-0.67	0.08	0	0	0	not significant
5429	GO_NEURON_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_OX	-0.67	0.08	0	0	0	not significant
5430	GO_DNA_METHYLTRANSFERASE_ACTIVITY	-0.67	0.07	0	0	0	not significant
5431	GO_EMBRYONIC_DIGESTIVE_TRACT_DEVELOPMENT	-0.67	0.07	0	0	0	not significant
5432	GO_MYOSIN_FILAMENT_ORGANIZATION	-0.67	0.07	0	0	0	not significant
5433	GO_REGULATION_OF_RESPONSE_TO_TUMOR_CELL	-0.67	0.07	0	0	0	not significant
5434	NOUSHMEHR_GBM_SOMATIC_MUTATED	-0.67	0.07	0	0	0	not significant
5435	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION_OF_UNSATURATED_	-0.67	0.07	0	0	0	not significant
5436	GO_ADENOSINE_DEAMINASE_ACTIVITY	-0.67	0.06	0	0	0	not significant
5437	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_EARLY_ENDOSOME	-0.67	0.06	0	0	0	not significant
5438	GO_RNA_POLYMERASE_I_PREINITIATION_COMPLEX_ASSEMBLY	-0.67	0.06	0	0	0	not significant

5439	NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON	-0.67	0.06	0	0	0	not significant
5440	PID_LPA4_PATHWAY	-0.67	0.06	0	0	0	not significant
5441	GO_ALDO_KETO_REDUCTASE_NADP_ACTIVITY	-0.67	0.05	0	0	0	not significant
5442	GO_PROTEIN_CONTAINING_COMPLEX_REMODELING	-0.67	0.05	0	0	0	not significant
5443	NIKOLSKY_OVERCONNECTED_IN_BREAST_CANCER	-0.67	0.05	0	0	0	not significant
5444	GO_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	-0.67	0.04	0	0	0	not significant
5445	GO_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS	-0.67	0.04	0	0	0	not significant
5446	GO_ACETYL_COA_BIOSYNTHETIC_PROCESS	-0.67	0.03	0	0	0	not significant
5447	GO_DETECTION_OF_LIGHT_STIMULUS	-0.67	0.03	0	0	0	not significant
5448	GO_POSITIVE_REGULATION_OF_CELL_MATRIX_ADHESION	-0.67	0.03	0	0	0	not significant
5449	GO_HISTONE_LYSINE_N_METHYLTRANSFERASE_ACTIVITY	-0.67	0.02	0	0	0	not significant
5450	GO_4_IRON_4_SULFUR_CLUSTER_BINDING	-0.67	0.01	0	0	0	not significant
5451	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	-0.67	0.01	0	0	0	not significant
5452	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	-0.67	0.01	0	0	0	not significant
5453	GO_ESTABLISHMENT_OF_GOLGI_LOCALIZATION	-0.66	0.07	0	0	0	not significant
5454	GO_HYPOTHALAMUS_DEVELOPMENT	-0.66	0.07	0	0	0	not significant
5455	PID_CONE_PATHWAY	-0.66	0.07	0	0	0	not significant
5456	BIOCARTA_CDC25_PATHWAY	-0.66	0.06	0	0	0	not significant
5457	GO_CALCIUM_IMPORT_INTO_THE_MITOCHONDRION	-0.66	0.06	0	0	0	not significant
5458	GO_HETEROCHROMATIN_ASSEMBLY	-0.66	0.06	0	0	0	not significant
5459	GO_INTERFERON_BETA_BIOSYNTHETIC_PROCESS	-0.66	0.06	0	0	0	not significant
5460	GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_DRUG	-0.66	0.06	0	0	0	not significant
5461	GO_NEGATIVE_REGULATION_OF_DIGESTIVE_SYSTEM_PROCESS	-0.66	0.06	0	0	0	not significant
5462	GO_POSITIVE_REGULATION_OF_PEROXISOME_PROLIFERATOR_ACTIVATED_RECE	-0.66	0.06	0	0	0	not significant
5463	GO_REGULATION_OF_SEQUESTERING_OF_TRIGLYCERIDE	-0.66	0.06	0	0	0	not significant
5464	GO_RNA_POLYMERASE_I_REGULATORY_REGION_DNA_BINDING	-0.66	0.06	0	0	0	not significant
5465	WATANABE_ULCERATIVE_COLITIS_WITH_CANCER_UP	-0.66	0.06	0	0	0	not significant
5466	GO_3_UTR_MEDIATED_MRNA_DESTABILIZATION	-0.66	0.05	0	0	0	not significant
5467	GO_PHOSPHOTRANSFERASE_ACTIVITY_FOR_OTHER_SUBSTITUTED_PHOSPHATE_	-0.66	0.05	0	0	0	not significant
5468	GO_REGULATION_OF_MEMBRANE_REPOLARIZATION	-0.66	0.05	0	0	0	not significant
5469	REACTOME_RHO_GTPASES_ACTIVATE_ROCKS	-0.66	0.05	0	0	0	not significant
5470	YIH_RESPONSE_TO_ARSENITE_C2	-0.66	0.05	0	0	0	not significant
5471	GO_DOSAGE_COMPENSATION	-0.66	0.04	0	0	0	not significant
5472	REACTOME_PURINE_SALVAGE	-0.66	0.04	0	0	0	not significant
5473	GO_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_COUPLED_RECEPTOR_SIGNAL	-0.66	0.03	0	0	0	not significant
5474	GO_EPHRIN_RECEPTOR_BINDING	-0.66	0.03	0	0	0	not significant
5475	GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	-0.66	0.03	0	0	0	not significant
5476	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	-0.66	0.03	0	0	0	not significant
5477	REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES	-0.66	0.03	0	0	0	not significant
5478	BIOCARTA_IL1R_PATHWAY	-0.66	0.02	0	0	0	not significant
5479	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_DN	-0.66	0.02	0	0	0	not significant
5480	GO_MYOFIBRIL_ASSEMBLY	-0.66	0.02	0	0	0	not significant
5481	GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_ASSEMBLY	-0.66	0.02	0	0	0	not significant
5482	GO_TRANSITION_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.66	0.02	0	0	0	not significant
5483	GO_POSITIVE_REGULATION_OF_TOR_SIGNALING	-0.66	0.01	0	0	0	not significant
5484	REACTOME_EPH_EPHRIN_SIGNALING	-0.66	0.01	0	0	0	not significant
5485	CHEBOTAEV_GR_TARGETS_DN	-0.66	0	0	0	0	not significant
5486	GO_CALCIUM_ION_REGULATED_EXOCYTOSIS	-0.66	0	0	0	0	not significant
5487	GO_DNA_CYTOSINE_DEAMINATION	-0.65	0.06	0	0	0	not significant
5488	GO_DOPAMINE_METABOLIC_PROCESS	-0.65	0.06	0	0	0	not significant
5489	GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_REMODELING	-0.65	0.06	0	0	0	not significant
5490	GO_MACROPHAGE_APOPTOTIC_PROCESS	-0.65	0.06	0	0	0	not significant
5491	GO_PROSTANOID_RECEPTOR_ACTIVITY	-0.65	0.06	0	0	0	not significant
5492	GO_SPERMATOPROTEASOME_COMPLEX	-0.65	0.06	0	0	0	not significant
5493	GO_VOCALIZATION_BEHAVIOR	-0.65	0.06	0	0	0	not significant
5494	GLI1_UP.V1_DN	-0.65	0.05	0	0	0	not significant
5495	GO_ESTABLISHMENT_OF_CENTROSOME_LOCALIZATION	-0.65	0.05	0	0	0	not significant
5496	GO_IRON_ION_TRANSMEMBRANE_TRANSPORT	-0.65	0.05	0	0	0	not significant
5497	GO_MEIOTIC_CHROMOSOME_CONDENSATION	-0.65	0.05	0	0	0	not significant
5498	GO_PHOTORECEPTOR_OUTER_SEGMENT_MEMBRANE	-0.65	0.05	0	0	0	not significant
5499	GO_PROTEIN_TAG	-0.65	0.05	0	0	0	not significant
5500	GO_REGULATION_OF_SECONDARY_HEART_FIELD_CARDIOBLAST_PROLIFERATION	-0.65	0.05	0	0	0	not significant
5501	REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	-0.65	0.05	0	0	0	not significant
5502	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	-0.65	0.05	0	0	0	not significant
5503	REACTOME_RUNX2_REGULATES_GENES_INVOLVED_IN_CELL_MIGRATION	-0.65	0.05	0	0	0	not significant
5504	PID_TOLL_ENDOGENOUS_PATHWAY	-0.65	0.04	0	0	0	not significant
5505	REACTOME_ZINC_TRANSPORTERS	-0.65	0.04	0	0	0	not significant
5506	GO_ACTIN_CORTICAL_PATCH	-0.65	0.03	0	0	0	not significant
5507	KANG_GIST_WITH_PDGFRA_UP	-0.65	0.03	0	0	0	not significant
5508	REACTOME_NUCLEOTIDE_SALVAGE	-0.65	0.03	0	0	0	not significant
5509	GO_PEPTIDYL_LYSINE_TRIMETHYLATION	-0.65	0.02	0	0	0	not significant
5510	GO_REGULATION_OF_CENTRIOLE_REPLICATION	-0.65	0.02	0	0	0	not significant
5511	GO_REGULATION_OF_EPIDERMAL_CELL_DIFFERENTIATION	-0.65	0.02	0	0	0	not significant
5512	REACTOME_MICROAUTOPHAGY	-0.65	0.02	0	0	0	not significant
5513	GO_CHONDROITIN_SULFATE_BINDING	-0.64	0.06	0	0	0	not significant
5514	GO_LATE_ENDOSOME_TO_VACUOLE_TRANSPORT_VIA_MULTIVESICULAR_BODY_S	-0.64	0.06	0	0	0	not significant
5515	GO_G_PROTEIN_BETA_GAMMA_SUBUNIT_COMPLEX_BINDING	-0.64	0.05	0	0	0	not significant
5516	GO_PALMITOYL_COA_HYDROLASE_ACTIVITY	-0.64	0.05	0	0	0	not significant
5517	GO_POSTSYNAPTIC_MEMBRANE_ASSEMBLY	-0.64	0.05	0	0	0	not significant
5518	GO_RESPONSE_TO_CAFFEINE	-0.64	0.05	0	0	0	not significant
5519	GO_SEQUESTERING_OF_ACTIN_MONOMERS	-0.64	0.05	0	0	0	not significant
5520	REACTOME_APOBEC3G_MEDIATED_RESISTANCE_TO_HIV_1_INFECTION	-0.64	0.05	0	0	0	not significant
5521	REACTOME_FREE_FATTY_ACIDS_REGULATE_INSULIN_SECRETION	-0.64	0.05	0	0	0	not significant
5522	FIGUEROA_AML_METHYLATION_CLUSTER_6_DN	-0.64	0.04	0	0	0	not significant
5523	GO_CHONDROCYTE_DIFFERENTIATION_INVOLVED_IN_ENDOCHONDRAL_BONE_MO	-0.64	0.04	0	0	0	not significant
5524	GO_NEUROMUSCULAR_PROCESS_CONTROLLING_POSTURE	-0.64	0.04	0	0	0	not significant
5525	GO_PIRNA_METABOLIC_PROCESS	-0.64	0.04	0	0	0	not significant
5526	GO_REGULATION_OF_URINE_VOLUME	-0.64	0.04	0	0	0	not significant
5527	MCMURRAY_TP53_HRAS_COOPERATION_RESPONSE_UP	-0.64	0.04	0	0	0	not significant
5528	BIOCARTA_TGFB_PATHWAY	-0.64	0.03	0	0	0	not significant
5529	GO_CELLULAR_RESPONSE_TO_DSRNA	-0.64	0.03	0	0	0	not significant
5530	GO_COPI_COATED_VESICLE	-0.64	0.03	0	0	0	not significant
5531	GO_CHONDROCYTE_DIFFERENTIATION	-0.64	0.01	0	0	0	not significant
5532	GO_REGULATION_OF_MUSCLE_HYPERTROPHY	-0.64	0.01	0	0	0	not significant
5533	HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_DN	-0.64	0.01	0	0	0	not significant
5534	LEE_LIVER_CANCER_E2F1_DN	-0.64	0.01	0	0	0	not significant
5535	GO_PIGMENTATION	-0.64	0	0	0	0	not significant
5536	GO_CORECEPTOR_ACTIVITY_INVOLVED_IN_WNT_SIGNALING_PATHWAY	-0.63	0.06	0	0	0	not significant
5537	GO_CYTIDINE_DEAMINASE_ACTIVITY	-0.63	0.05	0	0	0	not significant
5538	GO_HISTONE_THREONINE_KINASE_ACTIVITY	-0.63	0.05	0	0	0	not significant
5539	GO_POST_EMBRYONIC_EYE_MORPHOGENESIS	-0.63	0.05	0	0	0	not significant
5540	GO_THIOREDOXIN_PEROXIDASE_ACTIVITY	-0.63	0.05	0	0	0	not significant
5541	INAMURA_LUNG_CANCER_SCC_DN	-0.63	0.05	0	0	0	not significant
5542	CHR1P12	-0.63	0.04	0	0	0	not significant
5543	GO_CIRCADIAN_SLEEP_WAKE_CYCLE	-0.63	0.04	0	0	0	not significant
5544	GO_HISTONE_ACETYLTRANSFERASE_ACTIVITY_H4_K5_SPECIFIC_	-0.63	0.04	0	0	0	not significant
5545	GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_4_PHOSPHATASE_ACTIVITY	-0.63	0.04	0	0	0	not significant
5546	GO_POSITIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	-0.63	0.04	0	0	0	not significant
5547	GO_POSTSYNAPSE_ASSEMBLY	-0.63	0.04	0	0	0	not significant

5548	HALLMARK_PANCREAS_BETA_CELLS	-0.63	0.03	0	0	0	not significant
5549	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_DN	-0.63	0.03	0	0	0	not significant
5550	REACTOME_VXPX_CARGO_TARGETING_TO_CILIUM	-0.63	0.03	0	0	0	not significant
5551	TERAMOTO_OPN_TARGETS_CLUSTER_6	-0.63	0.03	0	0	0	not significant
5552	XU_GH1_EXOGENOUS_TARGETS_UP	-0.63	0.02	0	0	0	not significant
5553	KEGG_OXIDATIVE_PHOSPHORYLATION	-0.63	0	0	0	0	not significant
5554	REACTOME_BLOOD_GROUP_SYSTEMS_BIOSYNTHESIS	-0.62	0.06	0	0	0	not significant
5555	GO_ATP_DEPENDENT_MICROTUBULE_MOTOR_ACTIVITY_MINUS_END_DIRECTED	-0.62	0.05	0	0	0	not significant
5556	GO_CHROMO_SHADOW_DOMAIN_BINDING	-0.62	0.05	0	0	0	not significant
5557	GO_G_PROTEIN_COUPLED_ACETYLCHOLINE_RECEPTOR_SIGNALING_PATHWAY	-0.62	0.05	0	0	0	not significant
5558	GO_HEPATOCYTE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	-0.62	0.05	0	0	0	not significant
5559	GO_HISTONE_THREONINE_PHOSPHORYLATION	-0.62	0.05	0	0	0	not significant
5560	GO_MONOCYTE_ACTIVATION	-0.62	0.05	0	0	0	not significant
5561	GO_PROTEIN_INSERTION_INTO_ER_MEMBRANE	-0.62	0.05	0	0	0	not significant
5562	MOTAMED_RESPONSE_TO_ANDROGEN_DN	-0.62	0.05	0	0	0	not significant
5563	SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_DN	-0.62	0.05	0	0	0	not significant
5564	CERVERA_SDHB_TARGETS_1_DN	-0.62	0.04	0	0	0	not significant
5565	GO_MAMMARY_GLAND_ALVEOLUS_DEVELOPMENT	-0.62	0.04	0	0	0	not significant
5566	GO_NEURON_CELL_CELL_ADHESION	-0.62	0.04	0	0	0	not significant
5567	GO_POSITIVE_REGULATION_OF_AUTOPHAGOSOME_MATURATION	-0.62	0.04	0	0	0	not significant
5568	GO_POSITIVE_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	-0.62	0.04	0	0	0	not significant
5569	GO_REGULATION_OF_MYOSIN_LIGHT_CHAIN_PHOSPHATASE_ACTIVITY	-0.62	0.04	0	0	0	not significant
5570	GO_RESPONSE_TO_HERBICIDE	-0.62	0.04	0	0	0	not significant
5571	GO_REVERSE_CHOLESTEROL_TRANSPORT	-0.62	0.04	0	0	0	not significant
5572	GO_DEOXYRIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-0.62	0.03	0	0	0	not significant
5573	VALK_AML_CLUSTER_5	-0.62	0.03	0	0	0	not significant
5574	BIOCARTA_RHO_PATHWAY	-0.62	0.02	0	0	0	not significant
5575	GO_POSITIVE_REGULATION_OF_AXON_EXTENSION	-0.62	0.01	0	0	0	not significant
5576	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	-0.62	0	0	0	0	not significant
5577	GO_ACTIN_CORTICAL_PATCH_LOCALIZATION	-0.61	0.05	0	0	0	not significant
5578	GO_DETECTION_OF_MECHANICAL_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTIC	-0.61	0.05	0	0	0	not significant
5579	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPOR	-0.61	0.05	0	0	0	not significant
5580	GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	-0.61	0.05	0	0	0	not significant
5581	GO_PROGRAMMED_CELL_DEATH_INVOLVED_IN_CELL_DEVELOPMENT	-0.61	0.05	0	0	0	not significant
5582	GO_SPANNING_COMPONENT_OF_MEMBRANE	-0.61	0.05	0	0	0	not significant
5583	GO_CIRCADIAN_SLEEP_WAKE_CYCLE_SLEEP	-0.61	0.04	0	0	0	not significant
5584	GO_L_PHENYLALANINE_CATABOLIC_PROCESS	-0.61	0.04	0	0	0	not significant
5585	GO_LIPID_DROPLET_ORGANIZATION	-0.61	0.04	0	0	0	not significant
5586	GO_NEGATIVE_REGULATION_OF_SYNAPSE_ORGANIZATION	-0.61	0.04	0	0	0	not significant
5587	OXFORD_RALA_TARGETS_DN	-0.61	0.04	0	0	0	not significant
5588	GO_REGULATION_OF_CELL_GROWTH_INVOLVED_IN_CARDIAC_MUSCLE_CELL_DEV	-0.61	0.03	0	0	0	not significant
5589	GO_REGULATION_OF_RECEPTOR_BINDING	-0.61	0.03	0	0	0	not significant
5590	CHR2Q23	-0.61	0.02	0	0	0	not significant
5591	GO_CHONDROCYTE_DEVELOPMENT	-0.61	0.02	0	0	0	not significant
5592	GO_REGULATION_OF_RESPONSE_TO_INTERFERON_GAMMA	-0.61	0.01	0	0	0	not significant
5593	TBK1.DN.48HRS_DN	-0.61	0.01	0	0	0	not significant
5594	GO_AMINO_ACID_BETAINE_METABOLIC_PROCESS	-0.60	0.05	0	0	0	not significant
5595	GO_ADULT_HEART_DEVELOPMENT	-0.60	0.04	0	0	0	not significant
5596	GO_C4_DICARBOXYLATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.60	0.04	0	0	0	not significant
5597	GO_CALCIUM_ION_IMPORT_INTO_CYTOSOL	-0.60	0.04	0	0	0	not significant
5598	GO_FEMALE_GENITALIA_DEVELOPMENT	-0.60	0.04	0	0	0	not significant
5599	GO_POST_EMBRYONIC_ANIMAL_ORGAN_MORPHOGENESIS	-0.60	0.04	0	0	0	not significant
5600	KANG_GIST_WITH_PDGFRA_DN	-0.60	0.04	0	0	0	not significant
5601	REACTOME_PHENYLALANINE_AND_TYROSINE_METABOLISM	-0.60	0.04	0	0	0	not significant
5602	GO_POST_EMBRYONIC_ANIMAL_MORPHOGENESIS	-0.60	0.03	0	0	0	not significant
5603	GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_ASSEMBLY	-0.60	0.03	0	0	0	not significant
5604	SINGH_NFE2L2_TARGETS	-0.60	0.03	0	0	0	not significant
5605	GO_CRANIAL_NERVE_DEVELOPMENT	-0.60	0.02	0	0	0	not significant
5606	GO_NEGATIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	-0.60	0.02	0	0	0	not significant
5607	GO_RESPONSE_TO_INCREASED_OXYGEN_LEVELS	-0.60	0.02	0	0	0	not significant
5608	REACTOME_THE_PHOTOTRANSDUCTION_CASCADE	-0.60	0.02	0	0	0	not significant
5609	GO_NUCLEAR_HETEROCHROMATIN	-0.60	0.01	0	0	0	not significant
5610	GO_EYE_MORPHOGENESIS	-0.60	0	0	0	0	not significant
5611	GO_INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	-0.59	0.05	0	0	0	not significant
5612	GO_EXTRACELLULAR_MATRIX_CONSTITUENT_CONFERRING_ELASTICITY	-0.59	0.04	0	0	0	not significant
5613	GO_NEGATIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INV	-0.59	0.04	0	0	0	not significant
5614	GO_PROTEIN_PHOSPHATASE_2B_BINDING	-0.59	0.04	0	0	0	not significant
5615	GO_SPHINGOMYELIN_BIOSYNTHETIC_PROCESS	-0.59	0.04	0	0	0	not significant
5616	GO_SYNAPTIC_VESICLE_MATURATION	-0.59	0.04	0	0	0	not significant
5617	GO_CELLULAR_RESPONSE_TO_ATP	-0.59	0.03	0	0	0	not significant
5618	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH_GROUP_OF_DONORS	-0.59	0.03	0	0	0	not significant
5619	GO_PEPTIDE_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	-0.59	0.03	0	0	0	not significant
5620	GO_POSITIVE_REGULATION_OF_HEART_RATE	-0.59	0.03	0	0	0	not significant
5621	GO_REGULATION_OF_POSTSYNAPTIC_NEUROTRANSMITTER_RECEPTOR_INTERNA	-0.59	0.03	0	0	0	not significant
5622	MATZUK_POSTIMPLANTATION_AND_POSTPARTUM	-0.59	0.03	0	0	0	not significant
5623	SA_PROGRAMMED_CELL_DEATH	-0.59	0.03	0	0	0	not significant
5624	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_DN	-0.59	0.02	0	0	0	not significant
5625	MATZUK_POST-IMPLANTATION_AND_POST-PARTUM	-0.59	0.02	0	0	0	not significant
5626	GO_PRESYNAPTIC_ACTIVE_ZONE_MEMBRANE	-0.59	0.01	0	0	0	not significant
5627	GO_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	-0.59	0.01	0	0	0	not significant
5628	BENPORATH_ES_CORE_NINE	-0.58	0.03	0	0	0	not significant
5629	GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT_CONFERRING_COMPR	-0.58	0.03	0	0	0	not significant
5630	GO_FERRIC_IRON_BINDING	-0.58	0.03	0	0	0	not significant
5631	GO_POSITIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	-0.58	0.03	0	0	0	not significant
5632	GO_S_ADENOSYLMETHIONINE_CYCLE	-0.58	0.03	0	0	0	not significant
5633	YAO_HOXA10_TARGETS_VIA_PROGESTERONE_DN	-0.58	0.03	0	0	0	not significant
5634	BIOCARTA_MCALPAIN_PATHWAY	-0.58	0.02	0	0	0	not significant
5635	GO_DNA_UNWINDING_INVOLVED_IN_DNA_REPLICATION	-0.58	0.02	0	0	0	not significant
5636	GO_GRANULOCYTE_MACROPHAGE_COLONY_STIMULATING_FACTOR_PRODUCTION	-0.58	0.02	0	0	0	not significant
5637	GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	-0.58	0.02	0	0	0	not significant
5638	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	-0.58	0.02	0	0	0	not significant
5639	GO_REGULATION_OF_METHYLATION_DEPENDENT_CHROMATIN_SILENCING	-0.58	0.02	0	0	0	not significant
5640	GO_RESPONSE_TO_FOOD	-0.58	0.02	0	0	0	not significant
5641	GO_THO_COMPLEX	-0.58	0.02	0	0	0	not significant
5642	KYNG_NORMAL_AGING_DN	-0.58	0.02	0	0	0	not significant
5643	MIKKELSEN_MEF_LCP_WITH_H3K27ME3	-0.58	0.02	0	0	0	not significant
5644	GO_FOREBRAIN_GENERATION_OF_NEURONS	-0.58	0.01	0	0	0	not significant
5645	GO_REGULATION_OF_EPIDERMIS_DEVELOPMENT	-0.58	0.01	0	0	0	not significant
5646	REACTOME_G_BETA:GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	-0.58	0.01	0	0	0	not significant
5647	XU_CREBBP_TARGETS_DN	-0.58	0.01	0	0	0	not significant
5648	GO_PEROXISOMAL_TRANSPORT	-0.58	0	0	0	0	not significant
5649	BIOCARTA_FREE_PATHWAY	-0.57	0.03	0	0	0	not significant
5650	GO_1_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_3_KINASE_ACTIVITY	-0.57	0.03	0	0	0	not significant
5651	GO_HISTONE_H3_K36_DEMETHYLATION	-0.57	0.03	0	0	0	not significant
5652	GO_IMMUNE_RESPONSE_TO_TUMOR_CELL	-0.57	0.03	0	0	0	not significant
5653	GO_NEGATIVE_REGULATION_OF_HISTONE_H3_K4_METHYLATION	-0.57	0.03	0	0	0	not significant
5654	GO_POSITIVE_REGULATION_OF_HEAT_GENERATION	-0.57	0.03	0	0	0	not significant
5655	GO_PROTEIN_LOCALIZATION_TO_NON_MOTILE_CILIUM	-0.57	0.03	0	0	0	not significant
5656	GO_REGULATION_OF_MDA_5_SIGNALING_PATHWAY	-0.57	0.03	0	0	0	not significant

5657	GO_VITAMIN_D_METABOLIC_PROCESS	-0.57	0.03	0	0	0	not significant
5658	KUWANO_RNA_STABILIZED_BY_NO	-0.57	0.03	0	0	0	not significant
5659	GO_MELANOCYTE_DIFFERENTIATION	-0.57	0.02	0	0	0	not significant
5660	GO_NEGATIVE_REGULATION_OF_SINGLE_STRANDED_VIRAL_RNA_REPLICATION_VI	-0.57	0.02	0	0	0	not significant
5661	GO_ORGANELLE_INHERITANCE	-0.57	0.02	0	0	0	not significant
5662	GO_REGULATION_OF_TRANSPOSITION	-0.57	0.02	0	0	0	not significant
5663	GO_RESPONSE_TO_GRANULOCYTE_MACROPHAGE_COLONY_STIMULATING_FACT	-0.57	0.02	0	0	0	not significant
5664	GO_REGULATION_OF_CARDIOCYTE_DIFFERENTIATION	-0.57	0.01	0	0	0	not significant
5665	GO_RESPONSE_TO_ELECTRICAL_STIMULUS	-0.57	0.01	0	0	0	not significant
5666	KANG_CISPLATIN_RESISTANCE_UP	-0.57	0.01	0	0	0	not significant
5667	GO_REGULATION_OF_MEGAKARYOCYTE_DIFFERENTIATION	-0.57	0	0	0	0	not significant
5668	GO_NURF_COMPLEX	-0.56	0.04	0	0	0	not significant
5669	GO_POSITIVE_REGULATION_OF_KILLING_OF_CELLS_OF_OTHER_ORGANISM	-0.56	0.03	0	0	0	not significant
5670	GO_PYRIMIDINE_RIBONUCLEOSIDE_CATABOLIC_PROCESS	-0.56	0.03	0	0	0	not significant
5671	REACTOME_PI5P_REGULATES_TP53_ACETYLATION	-0.56	0.03	0	0	0	not significant
5672	BIOCARTA_CTBP1_PATHWAY	-0.56	0.02	0	0	0	not significant
5673	GO_CALCIUM_TRANSPORTING_ATPASE_ACTIVITY	-0.56	0.02	0	0	0	not significant
5674	GO_DEFINITIVE_HEMOPOIESIS	-0.56	0.02	0	0	0	not significant
5675	GO_HISTONE_DEMETHYLASE_ACTIVITY_H3_K36_SPECIFIC_	-0.56	0.02	0	0	0	not significant
5676	KOBAYASHI_EGFR_SIGNALING_6HR_DN	-0.56	0.02	0	0	0	not significant
5677	REACTOME_DECTIN_2_FAMILY	-0.56	0.02	0	0	0	not significant
5678	REACTOME_RNF_MUTANTS_SHOW_ENHANCED_WNT_SIGNALING_AND_PROLIFERA	-0.56	0.02	0	0	0	not significant
5679	GO_5_3_EXONUCLEASE_ACTIVITY	-0.56	0.01	0	0	0	not significant
5680	GO_GENETIC_IMPRINTING	-0.56	0.01	0	0	0	not significant
5681	GO_MITOCHONDRIAL_CALCIUM_ION_HOMEOSTASIS	-0.56	0.01	0	0	0	not significant
5682	GO_NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_IN_ABSENCE_OF_LIGAN	-0.56	0	0	0	0	not significant
5683	GO_ZINC_ION_HOMEOSTASIS	-0.56	0	0	0	0	not significant
5684	GO_FIBROBLAST_GROWTH_FACTOR_PRODUCTION	-0.55	0.03	0	0	0	not significant
5685	GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATION	-0.55	0.03	0	0	0	not significant
5686	GO_PURINE_RIBONUCLEOSIDE_SALVAGE	-0.55	0.03	0	0	0	not significant
5687	GO_UBIQUITIN_DEPENDENT_ENDOCYTOSIS	-0.55	0.03	0	0	0	not significant
5688	PLASARI_NFIC_TARGETS_BASAL_UP	-0.55	0.03	0	0	0	not significant
5689	ALONSO_METASTASIS_NEURAL_UP	-0.55	0.02	0	0	0	not significant
5690	BIOCARTA_SAM68_PATHWAY	-0.55	0.02	0	0	0	not significant
5691	GO_CELLULAR_RESPONSE_TO_COLD	-0.55	0.02	0	0	0	not significant
5692	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_CYSTEINE_S_NITROSYLATION	-0.55	0.02	0	0	0	not significant
5693	GO_NUCLEAR_POLYADENYLATION_DEPENDENT_TRNA_CATABOLIC_PROCESS	-0.55	0.02	0	0	0	not significant
5694	GO_PROTEASOME_CORE_COMPLEX_BETA_SUBUNIT_COMPLEX	-0.55	0.02	0	0	0	not significant
5695	ANDERSEN_CHOLANGIOCARCINOMA_CLASS1	-0.55	0.01	0	0	0	not significant
5696	FINETTI_BREAST_CANCER_KINOME_GREEN	-0.55	0.01	0	0	0	not significant
5697	GO_GABA_ERGIC_SYNAPSE	-0.55	0.01	0	0	0	not significant
5698	GO_REGULATION_OF_ACTIN_NUCLEATION	-0.55	0.01	0	0	0	not significant
5699	GO_CELLULAR_METABOLIC_COMPOUND_SALVAGE	-0.55	0	0	0	0	not significant
5700	GO_PHOSPHATIDYLINOSITOL_BISPHOSPHATE_PHOSPHATASE_ACTIVITY	-0.55	0	0	0	0	not significant
5701	GO_REGULATION_OF_PEPTIDYL_CYSTEINE_S_NITROSYLATION	-0.54	0.03	0	0	0	not significant
5702	REACTOME_SODIUM_PROTON_EXCHANGERS	-0.54	0.03	0	0	0	not significant
5703	GO_CAMP_DEPENDENT_PROTEIN_KINASE_INHIBITOR_ACTIVITY	-0.54	0.02	0	0	0	not significant
5704	GO_CRANIAL_NERVE_MORPHOGENESIS	-0.54	0.02	0	0	0	not significant
5705	GO_DNA_METHYLATION_INVOLVED_IN_GAMETE_GENERATION	-0.54	0.02	0	0	0	not significant
5706	GO_POSITIVE_REGULATION_OF_LYASE_ACTIVITY	-0.54	0.02	0	0	0	not significant
5707	GO_TOOTH_MINERALIZATION	-0.54	0.02	0	0	0	not significant
5708	SHI_SPARC_TARGETS_DN	-0.54	0.02	0	0	0	not significant
5709	TERAMOTO_OPN_TARGETS_CLUSTER_3	-0.54	0.02	0	0	0	not significant
5710	GO_EXTRACELLULAR_VESICLE_BIOGENESIS	-0.54	0.01	0	0	0	not significant
5711	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_8_SECRETION	-0.54	0.01	0	0	0	not significant
5712	REACTOME_BETA_OXIDATION_OF_DECANOYL_COA_TO_OCTANOYL_COA_COA	-0.54	0.01	0	0	0	not significant
5713	GO_PEROXISOME_ORGANIZATION	-0.54	0	0	0	0	not significant
5714	GO_XENOBIOTIC_CATABOLIC_PROCESS	-0.53	0.03	0	0	0	not significant
5715	CHR3Q24	-0.53	0.02	0	0	0	not significant
5716	GO_NEGATIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	-0.53	0.02	0	0	0	not significant
5717	GO_POSITIVE_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	-0.53	0.02	0	0	0	not significant
5718	GO_REGULATION_OF_EXOSOMAL_SECRETION	-0.53	0.02	0	0	0	not significant
5719	HUMMERICH_BENIGN_SKIN_TUMOR_UP	-0.53	0.02	0	0	0	not significant
5720	MEISSNER_BRAIN_HCP_WITH_H3K4ME2	-0.53	0.02	0	0	0	not significant
5721	REACTOME_EICOSANOID_LIGAND_BINDING_RECEPTORS	-0.53	0.02	0	0	0	not significant
5722	REACTOME_RUNX3_REGULATES_BCL2L11_BIM_TRANSCRIPTION	-0.53	0.02	0	0	0	not significant
5723	GO_HEART_FORMATION	-0.53	0.01	0	0	0	not significant
5724	GO_MEMBRANE_REPOLARIZATION	-0.53	0.01	0	0	0	not significant
5725	GO_METHIONINE_BIOSYNTHETIC_PROCESS	-0.52	0.02	0	0	0	not significant
5726	GO_POSITIVE_REGULATION_OF_PROTEIN_GLYCOSYLATION	-0.52	0.02	0	0	0	not significant
5727	HANSON_HRAS_SIGNALING_VIA_NFKB	-0.52	0.02	0	0	0	not significant
5728	WHITESIDE_CISPLATIN_RESISTANCE_UP	-0.52	0.02	0	0	0	not significant
5729	CHR8Q12	-0.52	0.01	0	0	0	not significant
5730	GO_CAMP_DEPENDENT_PROTEIN_KINASE_REGULATOR_ACTIVITY	-0.52	0.01	0	0	0	not significant
5731	GO_INHIBITORY_POSTSYNAPTIC_POTENTIAL	-0.52	0.01	0	0	0	not significant
5732	NABA_PROTEOGLYCANS	-0.52	0.01	0	0	0	not significant
5733	CHR2P21	-0.52	0	0	0	0	not significant
5734	GO_REGULATION_OF_COENZYME_METABOLIC_PROCESS	-0.52	0	0	0	0	not significant
5735	REACTOME_ACTIVATED_PKN1_STIMULATES_TRANSCRIPTION_OF_AR_ANDROGEN_	-0.52	0	0	0	0	not significant
5736	GO_1_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_5_KINASE_ACTIVITY	-0.51	0.01	0	0	0	not significant
5737	GO_CHAPERONE_MEDIATED_PROTEIN_TRANSPORT	-0.51	0.01	0	0	0	not significant
5738	GO_NEGATIVE_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	-0.51	0.01	0	0	0	not significant
5739	GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	-0.51	0.01	0	0	0	not significant
5740	GO_POSITIVE_REGULATION_OF_ACTIN_NUCLEATION	-0.51	0.01	0	0	0	not significant
5741	GO_PYRIMIDINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	-0.51	0.01	0	0	0	not significant
5742	GO_REGULATION_OF_ACYL_COA_BIOSYNTHETIC_PROCESS	-0.51	0.01	0	0	0	not significant
5743	GO_REGULATION_OF_MITOCHONDRIAL_FUSION	-0.51	0.01	0	0	0	not significant
5744	GO_RIBONUCLEOSIDE_CATABOLIC_PROCESS	-0.51	0.01	0	0	0	not significant
5745	PARK_TRETINOIN_RESPONSE	-0.51	0.01	0	0	0	not significant
5746	REACTOME_SEMA3A_PLEXIN_REPULSION_SIGNALING_BY_INHIBITING_INTEGRIN_AD	-0.51	0.01	0	0	0	not significant
5747	RODRIGUES_NTN1_TARGETS_UP	-0.51	0.01	0	0	0	not significant
5748	GO_POSITIVE_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	-0.51	0	0	0	0	not significant
5749	GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_ABSENCE_	-0.51	0	0	0	0	not significant
5750	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN	-0.51	0	0	0	0	not significant
5751	REACTOME_DNA_METHYLATION	-0.51	0	0	0	0	not significant
5752	GO_ADENOSINE_TO_INOSINE_EDITING	-0.50	0.01	0	0	0	not significant
5753	GO_RENAL_ABSORPTION	-0.50	0.01	0	0	0	not significant
5754	GO_VITAMIN_CATABOLIC_PROCESS	-0.50	0.01	0	0	0	not significant
5755	ZHAN_MULTIPLE_MYELOMA_DN	-0.50	0	0	0	0	not significant
5756	BIOCARTA_HES_PATHWAY	-0.49	0.01	0	0	0	not significant
5757	GO_BH_DOMAIN_BINDING	-0.49	0.01	0	0	0	not significant
5758	GO_HOMOCYSTEINE_METABOLIC_PROCESS	-0.49	0.01	0	0	0	not significant
5759	GO_PYRIMIDINE_NUCLEOTIDE_SALVAGE	-0.49	0.01	0	0	0	not significant
5760	GO_REGULATION_OF_KERATINOCYTE_PROLIFERATION	-0.49	0.01	0	0	0	not significant
5761	HALLMARK_COAGULATION	-0.49	0	0	0	0	not significant
5762	GO_VINCULIN_BINDING	-0.48	0.01	0	0	0	not significant
5763	GO_G_PROTEIN_COUPLED_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	-0.48	0	0	0	0	not significant
5764	GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_KINASE_ACTIVITY	-0.48	0	0	0	0	not significant
5765	GO_HISTAMINE_TRANSPORT	-0.47	0.01	0	0	0	not significant

5766	GO_STRESS_INDUCED_PREMATURE_SENESCENCE	-0.47	0.01	0	0	0	not significant
5767	BIOCARTA_CYTOKINE_PATHWAY	-0.47	0	0	0	0	not significant
5768	IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_UP	-0.47	0	0	0	0	not significant
5769	KEGG_STEROID_HORMONE_BIOSYNTHESIS	-0.47	0	0	0	0	not significant
5770	GO_ADP_RIBOSYLATION_FACTOR_BINDING	-0.46	0.01	0	0	0	not significant
5771	GO_NEUROPEPTIDE_RECEPTOR_ACTIVITY	-0.46	0.01	0	0	0	not significant
5772	GO_PRIMITIVE_HEMOPOIESIS	-0.46	0.01	0	0	0	not significant
5773	GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_DIFFERENTIATION	-0.46	0	0	0	0	not significant
5774	GO_CD4_RECEPTOR_BINDING	-0.46	0	0	0	0	not significant
5775	GO_DIGESTIVE_TRACT_MORPHOGENESIS	-0.46	0	0	0	0	not significant
5776	GO_INTRACILIARY_TRANSPORT_PARTICLE_B	-0.46	0	0	0	0	not significant
5777	GO_L_ASCORBIC_ACID_METABOLIC_PROCESS	-0.46	0	0	0	0	not significant
5778	BOYAULT_LIVER_CANCER_SUBCLASS_G12_DN	-0.45	0	0	0	0	not significant
5779	CHAN_INTERFERON_PRODUCING_DENDRITIC_CELL	-0.45	0	0	0	0	not significant
5780	GO_OXYGEN_BINDING	-0.45	0	0	0	0	not significant
5781	GO_PROTON_EXPORTING_ATPASE_ACTIVITY_PHOSPHORYLATIVE_MECHANISM	-0.45	0	0	0	0	not significant
5782	GO_RENAL_SODIUM_ION_TRANSPORT	-0.45	0	0	0	0	not significant
5783	GO_ADENOSINE_RECEPTOR_SIGNALING_PATHWAY	-0.44	0.01	0	0	0	not significant
5784	GO_DNA_PROTECTION	-0.44	0.01	0	0	0	not significant
5785	GO_VESICLE_FUSION_WITH_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_C	-0.44	0.01	0	0	0	not significant
5786	GO_NEGATIVE_REGULATION_OF_MITOCHONDRIAL_FUSION	-0.44	0	0	0	0	not significant
5787	GO_NEGATIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_R	-0.44	0	0	0	0	not significant
5788	GO_POSITIVE_REGULATION_OF_T_CELL_DIFFERENTIATION_IN_THYMUS	-0.44	0	0	0	0	not significant
5789	TUOMISTO_TUMOR_SUPPRESSION_BY_COL13A1_UP	-0.43	0.01	0	0	0	not significant
5790	GO_REGULATION_OF_CALCIUM_ION_IMPORT	-0.43	0	0	0	0	not significant
5791	GO_REGULATION_OF_REMOVAL_OF_SUPEROXIDE_RADICALS	-0.43	0	0	0	0	not significant
5792	GO_BETA_2_ADRENERGIC_RECEPTOR_BINDING	-0.42	0	0	0	0	not significant
5793	REACTOME_TICAM1_DEPENDENT_ACTIVATION_OF_IRF3_IRF7	-0.42	0	0	0	0	not significant
5794	GO_DYNEIN_LIGHT_CHAIN_BINDING	-0.41	0	0	0	0	not significant
5795	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP	-0.41	0	0	0	0	not significant
5796	GO_BLOC_1_COMPLEX	-0.40	0	0	0	0	not significant
5797	GO_MEMBRANE_RAFT_ASSEMBLY	-0.40	0	0	0	0	not significant
5798	GO_REGULATION_OF_LYASE_ACTIVITY	-0.40	0	0	0	0	not significant
5799	GO_MUCOPOLYSACCHARIDE_METABOLIC_PROCESS	-0.39	0	0	0	0	not significant
5800	GO_PARAXIAL_MESODERM_DEVELOPMENT	-0.39	0	0	0	0	not significant
5801	GO_ENDOPLASMIC_RETICULUM_LOCALIZATION	-0.37	0	0	0	0	not significant
5802	GO_CALCINEURIN_COMPLEX	-0.34	0	0	0	0	not significant
5803	GO_NEURAL_RETINA_DEVELOPMENT	0.33	0	0	0	0	not significant
5804	GO_CHEMOSENSORY_BEHAVIOR	0.37	0	0	0	0	not significant
5805	GO_COENZYME_A_BIOSYNTHETIC_PROCESS	0.37	0	0	0	0	not significant
5806	PID_RHODOPSIN_PATHWAY	0.37	0	0	0	0	not significant
5807	CHR11P14	0.38	0	0	0	0	not significant
5808	GO_FACIAL_NERVE_MORPHOGENESIS	0.38	0	0	0	0	not significant
5809	GO_N_ACETYLGLUCOSAMINE_METABOLIC_PROCESS	0.38	0	0	0	0	not significant
5810	GO_POSITIVE_REGULATION_OF_GLUTAMATE_SECRETION	0.38	0	0	0	0	not significant
5811	GO_REGULATION_OF_GLUTAMATE_SECRETION	0.38	0	0	0	0	not significant
5812	GO_GLYCINE_BINDING	0.39	0	0	0	0	not significant
5813	GO_REGULATION_OF_HISTONE_H3_K9_TRIMETHYLATION	0.39	0	0	0	0	not significant
5814	GO_S_ADENOSYLMETHIONINE_METABOLIC_PROCESS	0.39	0	0	0	0	not significant
5815	GO_UV_PROTECTION	0.39	0	0	0	0	not significant
5816	REACTOME_BETA_OXIDATION_OF_OCTANOYL_COA_TO_HEXANOYL_COA	0.39	0	0	0	0	not significant
5817	GO_LIPOPOLYSACCHARIDE_BINDING	0.40	0	0	0	0	not significant
5818	REACTOME_NOTCH4_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	0.40	0	0	0	0	not significant
5819	CHR4P11	0.41	0	0	0	0	not significant
5820	GO_DICHOTOMOUS_SUBDIVISION_OF_AN_EPITHELIAL_TERMINAL_UNIT	0.41	0	0	0	0	not significant
5821	GO_PARASYMPATHETIC_NERVOUS_SYSTEM_DEVELOPMENT	0.41	0	0	0	0	not significant
5822	REACTOME_NOTCH2_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	0.41	0	0	0	0	not significant
5823	GO_COA_HYDROLASE_ACTIVITY	0.42	0	0	0	0	not significant
5824	GO_H3_HISTONE_ACETYLTRANSFERASE_COMPLEX	0.42	0	0	0	0	not significant
5825	GO_MORPHOGENESIS_OF_AN_ENDOTHELIUM	0.42	0	0	0	0	not significant
5826	HASLINGER_B_CLL_WITH_6Q21_DELETION	0.42	0	0	0	0	not significant
5827	REACTOME_GLYCEROPHOSPHOLIPID_CATABOLISM	0.42	0	0	0	0	not significant
5828	GO_REGULATION_OF_KILLING_OF_CELLS_OF_OTHER_ORGANISM	0.43	0.01	0	0	0	not significant
5829	GO_REGULATION_OF_WNT_SIGNALING_PATHWAY_PLANAR_CELL_POLARITY_PAT	0.43	0.01	0	0	0	not significant
5830	GO_SPHINGOID_BIOSYNTHETIC_PROCESS	0.43	0.01	0	0	0	not significant
5831	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_HEME_PROTEIN_AS_ACC	0.43	0	0	0	0	not significant
5832	GO_PROTEIN_IMPORT_INTO_PEROXISOME_MEMBRANE	0.43	0	0	0	0	not significant
5833	KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	0.43	0	0	0	0	not significant
5834	SUMI_HNF4A_TARGETS	0.43	0	0	0	0	not significant
5835	GO_CARBONATE_DEHYDRATASE_ACTIVITY	0.44	0.01	0	0	0	not significant
5836	GO_NEURAL_PLATE_PATTERN_SPECIFICATION	0.44	0.01	0	0	0	not significant
5837	GO_OLIGOSACCHARIDE_BIOSYNTHETIC_PROCESS	0.44	0.01	0	0	0	not significant
5838	GO_ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_OF_IONS_P	0.44	0	0	0	0	not significant
5839	GO_MYELIN_MAINTENANCE	0.45	0.01	0	0	0	not significant
5840	HUMMERICH_MALIGNANT_SKIN_TUMOR_UP	0.45	0.01	0	0	0	not significant
5841	KRAS.50_UP.V1_UP	0.45	0.01	0	0	0	not significant
5842	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION	0.45	0	0	0	0	not significant
5843	GO_BETA_CATENIN_TCF_COMPLEX	0.45	0	0	0	0	not significant
5844	LI_PROSTATE_CANCER_EPIGENETIC	0.45	0	0	0	0	not significant
5845	REACTOME_VITAMIN_C_ASCORBATE_METABOLISM	0.45	0	0	0	0	not significant
5846	YANG_BREAST_CANCER_ESR1_DN	0.45	0	0	0	0	not significant
5847	GO_RAC_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	0.46	0.01	0	0	0	not significant
5848	GO_DETERMINATION_OF_DORSAL_VENTRAL_ASYMMETRY	0.46	0	0	0	0	not significant
5849	SA_TRKA_RECEPTOR	0.46	0	0	0	0	not significant
5850	BIOCARTA_SUMO_PATHWAY	0.47	0.01	0	0	0	not significant
5851	GO_BRANCHING_INVOLVED_IN_SALIVARY_GLAND_MORPHOGENESIS	0.47	0.01	0	0	0	not significant
5852	GO_ESTROGEN_METABOLIC_PROCESS	0.47	0.01	0	0	0	not significant
5853	GO_LIPOPROTEIN_METABOLIC_PROCESS	0.47	0.01	0	0	0	not significant
5854	GO_POLYPEPTIDE_N_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY	0.47	0.01	0	0	0	not significant
5855	GO_POTASSIUM_CHANNEL_INHIBITOR_ACTIVITY	0.47	0.01	0	0	0	not significant
5856	IGLESIAS_E2F_TARGETS_DN	0.47	0.01	0	0	0	not significant
5857	REACTOME_DISSOLUTION_OF_FIBRIN_CLOT	0.47	0.01	0	0	0	not significant
5858	VERNOCHET_ADIPOGENESIS	0.47	0.01	0	0	0	not significant
5859	CHR3Q12	0.47	0	0	0	0	not significant
5860	GO_EMBRYONIC_DIGIT_MORPHOGENESIS	0.47	0	0	0	0	not significant
5861	GO_EMBRYONIC_EYE_MORPHOGENESIS	0.47	0	0	0	0	not significant
5862	GO_REGULATION_OF_CYCLASE_ACTIVITY	0.47	0	0	0	0	not significant
5863	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_TOP20_UP	0.47	0	0	0	0	not significant
5864	GO_ACTIN_FILAMENT_BASED_TRANSPORT	0.48	0.01	0	0	0	not significant
5865	GO_CELLULAR_SODIUM_ION_HOMEOSTASIS	0.48	0.01	0	0	0	not significant
5866	GO_POSITIVE_REGULATION_OF_HEART_CONTRACTION	0.48	0.01	0	0	0	not significant
5867	GO_POTASSIUM_ION_ANTIPORTER_ACTIVITY	0.48	0.01	0	0	0	not significant
5868	GO_REGULATION_OF_HEART_MORPHOGENESIS	0.48	0.01	0	0	0	not significant
5869	GO_REGULATION_OF_LYMPHOID_PROGENITOR_CELL_DIFFERENTIATION	0.48	0.01	0	0	0	not significant
5870	GO_SODIUM_ION_EXPORT_ACROSS_PLASMA_MEMBRANE	0.48	0.01	0	0	0	not significant
5871	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_UP	0.49	0.01	0	0	0	not significant
5872	GO_DETECTION_OF_MECHANICAL_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTI	0.49	0.01	0	0	0	not significant
5873	GO_FILOPODIUM_MEMBRANE	0.49	0.01	0	0	0	not significant
5874	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PR	0.49	0.01	0	0	0	not significant

5875	KEGG_HISTIDINE_METABOLISM	0.49	0.01	0	0	0	not significant
5876	REACTOME_SUMO_IS_CONJUGATED_TO_E1_UBA2:SAE1	0.49	0.01	0	0	0	not significant
5877	BAUS_TFF2_TARGETS_UP	0.49	0	0	0	0	not significant
5878	GO_PIGMENT_GRANULE_ORGANIZATION	0.49	0	0	0	0	not significant
5879	GO_ZINC_ION_TRANSPORT	0.49	0	0	0	0	not significant
5880	GO_CELLULAR_RESPONSE_TO_ALDEHYDE	0.50	0.02	0	0	0	not significant
5881	GO_NUCLEOSIDE_TRIPHOSPHATE_CATABOLIC_PROCESS	0.50	0.02	0	0	0	not significant
5882	GO_PURINE_NUCLEOSIDE_CATABOLIC_PROCESS	0.50	0.02	0	0	0	not significant
5883	GO_CALMODULIN_DEPENDENT_PROTEIN_PHOSPHATASE_ACTIVITY	0.50	0.01	0	0	0	not significant
5884	GO_CELLULAR_RESPONSE_TO_ZINC_ION	0.50	0.01	0	0	0	not significant
5885	GO_POSITIVE_REGULATION_OF_CYCLASE_ACTIVITY	0.50	0.01	0	0	0	not significant
5886	GO_PROTEIN_BINDING_BRIDGING_INVOLVED_IN_SUBSTRATE_RECOGNITION_FOR_	0.50	0.01	0	0	0	not significant
5887	GO_INTRACILIARY_TRANSPORT_PARTICLE	0.50	0	0	0	0	not significant
5888	DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCOCORTICOIDS	0.51	0.02	0	0	0	not significant
5889	GO_CATION_TRANSPORTING_ATPASE_COMPLEX	0.51	0.02	0	0	0	not significant
5890	GO_MITOCHONDRIAL_DNA_REPAIR	0.51	0.02	0	0	0	not significant
5891	GO_PROTEIN_GERANYLGERANYLTRANSFERASE_ACTIVITY	0.51	0.02	0	0	0	not significant
5892	GO_REGULATION_OF_CELL_CELL_ADHESION_MEDIATED_BY_CADHERIN	0.51	0.02	0	0	0	not significant
5893	GO_REPLICATIVE_CELL_AGING	0.51	0.02	0	0	0	not significant
5894	GO_SODIUM_ION_BINDING	0.51	0.02	0	0	0	not significant
5895	PIEPOLI_LGI1_TARGETS_UP	0.51	0.02	0	0	0	not significant
5896	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN	0.51	0.01	0	0	0	not significant
5897	GO_CAMP_BINDING	0.51	0.01	0	0	0	not significant
5898	GO_NADPLUS_BINDING	0.51	0.01	0	0	0	not significant
5899	OZANNE_AP1_TARGETS_UP	0.51	0.01	0	0	0	not significant
5900	REACTOME_BH3_ONLY_PROTEINS_ASSOCIATE_WITH_AND_INACTIVATE_ANTI_APO	0.51	0.01	0	0	0	not significant
5901	REACTOME_CRMPS_IN_SEMA3A_SIGNALING	0.51	0.01	0	0	0	not significant
5902	REACTOME_PEROXISOMAL_LIPID_METABOLISM	0.51	0.01	0	0	0	not significant
5903	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_ASSOCIATION_WITH_CO_	0.51	0.01	0	0	0	not significant
5904	GO_PYRIMIDINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	0.51	0	0	0	0	not significant
5905	GRADE_COLON_CANCER_DN	0.51	0	0	0	0	not significant
5906	GO_LENS_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	0.52	0.02	0	0	0	not significant
5907	GO_PERIPHERAL_NERVOUS_SYSTEM_MYELIN_MAINTENANCE	0.52	0.02	0	0	0	not significant
5908	GO_POSITIVE_REGULATION_OF_VACUOLE_ORGANIZATION	0.52	0.02	0	0	0	not significant
5909	GO_PROTEIN_GERANYLGERANYLATION	0.52	0.02	0	0	0	not significant
5910	GO_RELAXATION_OF_SMOOTH_MUSCLE	0.52	0.02	0	0	0	not significant
5911	GO_POSITIVE_REGULATION_OF_HISTONE_H3_K4_METHYLATION	0.52	0.01	0	0	0	not significant
5912	GO_SERINE_TYPE_EXOPEPTIDASE_ACTIVITY	0.52	0.01	0	0	0	not significant
5913	REACTOME_MOLECULES_ASSOCIATED_WITH_ELASTIC_FIBRES	0.52	0.01	0	0	0	not significant
5914	REACTOME_PENTOSE_PHOSPHATE_PATHWAY	0.52	0.01	0	0	0	not significant
5915	GO_ESTABLISHMENT_OF_EPITHELIAL_CELL_POLARITY	0.52	0	0	0	0	not significant
5916	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP	0.52	0	0	0	0	not significant
5917	REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES	0.52	0	0	0	0	not significant
5918	GO_DEATH_DOMAIN_BINDING	0.53	0.03	0	0	0	not significant
5919	GO_GENITALIA_MORPHOGENESIS	0.53	0.03	0	0	0	not significant
5920	GO_REGULATION_OF_GROWTH_RATE	0.53	0.03	0	0	0	not significant
5921	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_UP	0.53	0.03	0	0	0	not significant
5922	GO_BLOC_COMPLEX	0.53	0.02	0	0	0	not significant
5923	GO_REGULATION_OF_BONE_DEVELOPMENT	0.53	0.02	0	0	0	not significant
5924	GO_RRNA_3_END_PROCESSING	0.53	0.02	0	0	0	not significant
5925	GO_SPHINGOLIPID_TRANSPORTER_ACTIVITY	0.53	0.02	0	0	0	not significant
5926	LEE_NAIVE_T_LYMPHOCYTE	0.53	0.02	0	0	0	not significant
5927	SANDERSON_PPARA_TARGETS	0.53	0.02	0	0	0	not significant
5928	CHR18Q12	0.53	0.01	0	0	0	not significant
5929	GO_GTP_DEPENDENT_PROTEIN_BINDING	0.53	0.01	0	0	0	not significant
5930	GO_REGULATION_OF_GENE_EXPRESSION_BY_GENETIC_IMPRINTING	0.53	0.01	0	0	0	not significant
5931	GO_RELAXATION_OF_MUSCLE	0.53	0.01	0	0	0	not significant
5932	REACTOME_SIGNALING_BY_NOTCH1_HD_DOMAIN_MUTANTS_IN_CANCER	0.53	0.01	0	0	0	not significant
5933	GO_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	0.53	0	0	0	0	not significant
5934	GO_LATERAL_PLASMA_MEMBRANE	0.53	0	0	0	0	not significant
5935	REACTOME_PROTEIN_PROTEIN_INTERACTIONS_AT_SYNAPSES	0.53	0	0	0	0	not significant
5936	REACTOME_RUNX1_REGULATES_GENES_INVOLVED_IN_MEGAKARYOCYTE_DIFFER	0.53	0	0	0	0	not significant
5937	GO_HISTONE_METHYLTRANSFERASE_ACTIVITY_H3_K27_SPECIFIC_	0.54	0.03	0	0	0	not significant
5938	GO_REGULATION_OF_CATECHOLAMINE_METABOLIC_PROCESS	0.54	0.03	0	0	0	not significant
5939	GO_MRNA_EDITING_COMPLEX	0.54	0.02	0	0	0	not significant
5940	GO_NEGATIVE_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	0.54	0.02	0	0	0	not significant
5941	GO_NEGATIVE_REGULATION_OF_LYASE_ACTIVITY	0.54	0.02	0	0	0	not significant
5942	GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	0.54	0.02	0	0	0	not significant
5943	GO_PROTEIN_PRENYLTRANSFERASE_ACTIVITY	0.54	0.02	0	0	0	not significant
5944	GO_PULMONARY_VALVE_DEVELOPMENT	0.54	0.02	0	0	0	not significant
5945	OXFORD_RALB_TARGETS_DN	0.54	0.02	0	0	0	not significant
5946	REACTOME_OLFACTORY_SIGNALING_PATHWAY	0.54	0.02	0	0	0	not significant
5947	GO_EMBRYONIC_CAMERA_TYPE_EYE_MORPHOGENESIS	0.54	0.01	0	0	0	not significant
5948	GO_PHENOL_CONTAINING_COMPOUND_METABOLIC_PROCESS	0.54	0.01	0	0	0	not significant
5949	GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	0.55	0.04	0	0	0	not significant
5950	CHR4P13	0.55	0.03	0	0	0	not significant
5951	GO_COPPER_CHAPERONE_ACTIVITY	0.55	0.03	0	0	0	not significant
5952	GO_PULMONARY_VALVE_MORPHOGENESIS	0.55	0.03	0	0	0	not significant
5953	REACTOME_BETA_OXIDATION_OF_PRISTANOYL_COA	0.55	0.03	0	0	0	not significant
5954	BIOCARTA_EPHA4_PATHWAY	0.55	0.02	0	0	0	not significant
5955	GO_ACTIVATION_OF_MAPKKK_ACTIVITY	0.55	0.02	0	0	0	not significant
5956	GO_CELLULAR_RESPONSE_TO_OXIDISED_LOW_DENSITY_LIPOPROTEIN_PARTICLE	0.55	0.02	0	0	0	not significant
5957	GO_FATTY_ACID_DERIVATIVE_CATABOLIC_PROCESS	0.55	0.02	0	0	0	not significant
5958	GO_INTRACELLULAR_MRNA_LOCALIZATION	0.55	0.02	0	0	0	not significant
5959	GO_LONG_CHAIN_FATTY_ACID_BINDING	0.55	0.02	0	0	0	not significant
5960	GO_NUCLEOTIDE_TRANSMEMBRANE_TRANSPORT	0.55	0.02	0	0	0	not significant
5961	GO_POSITIVE_REGULATION_OF_CARDIOCYTE_DIFFERENTIATION	0.55	0.02	0	0	0	not significant
5962	GO_REGULATION_OF_DEVELOPMENTAL_PIGMENTATION	0.55	0.02	0	0	0	not significant
5963	GO_FAT_SOLUBLE_VITAMIN_METABOLIC_PROCESS	0.55	0.01	0	0	0	not significant
5964	GO_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	0.55	0	0	0	0	not significant
5965	GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_NEUROTRANSMITTER_RECEPT	0.55	0	0	0	0	not significant
5966	PID_AMB2_NEUTROPHILS_PATHWAY	0.55	0	0	0	0	not significant
5967	GO_EXTRACELLULAR_MATRIX_COMPONENT	0.56	0.03	0	0	0	not significant
5968	GO_FATTY_ACID_DERIVATIVE_METABOLIC_PROCESS	0.56	0.03	0	0	0	not significant
5969	GO_MITOCHONDRIAL_INTERMEMBRANE_SPACE_PROTEIN_TRANSPORTER_COMPL	0.56	0.03	0	0	0	not significant
5970	GO_PENTOSE_PHOSPHATE_SHUNT_NON_OXIDATIVE_BRANCH	0.56	0.03	0	0	0	not significant
5971	GO_PRENYLATION	0.56	0.03	0	0	0	not significant
5972	MIKKELSEN_IPS_LCP_WITH_H3K27ME3	0.56	0.03	0	0	0	not significant
5973	BIOCARTA_HCMV_PATHWAY	0.56	0.02	0	0	0	not significant
5974	GO_ER_ASSOCIATED_MISFOLDED_PROTEIN_CATABOLIC_PROCESS	0.56	0.02	0	0	0	not significant
5975	GO_HETEROCHROMATIN_ORGANIZATION	0.56	0.02	0	0	0	not significant
5976	GO_INNATE_IMMUNE_RESPONSE_IN_MUCOSA	0.56	0.02	0	0	0	not significant
5977	GO_PROTEIN_MATURATION_BY_PROTEIN_FOLDING	0.56	0.02	0	0	0	not significant
5978	GO_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFERENTIATION	0.56	0.02	0	0	0	not significant
5979	GO_RNA_POLYMERASE_III_REGULATORY_REGION_DNA_BINDING	0.56	0.02	0	0	0	not significant
5980	GO_TYPE_B_PANCREATIC_CELL_DEVELOPMENT	0.56	0.02	0	0	0	not significant
5981	GO_TYPE_I_INTERFERON_BIOSYNTHETIC_PROCESS	0.56	0.02	0	0	0	not significant
5982	GO_ZINC_ION_TRANSMEMBRANE_TRANSPORT	0.56	0.02	0	0	0	not significant
5983	LIM_MAMMARY_LUMINAL_PROGENITOR_DN	0.56	0.02	0	0	0	not significant

5984	GO_FOREBRAIN_CELL_MIGRATION	0.56	0.01	0	0	0	not significant
5985	MIKKELSEN_NPC_LCP_WITH_H3K4ME3	0.56	0.01	0	0	0	not significant
5986	REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK	0.56	0.01	0	0	0	not significant
5987	REACTOME_IKK_COMPLEX_RECRUITMENT_MEDIATED_BY_RIP1	0.56	0.01	0	0	0	not significant
5988	REACTOME_NEUREXINS_AND_NEUROLIGINS	0.56	0.01	0	0	0	not significant
5989	WANG_RESPONSE_TO_BEXAROTENE_DN	0.56	0.01	0	0	0	not significant
5990	GO_PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	0.56	0	0	0	0	not significant
5991	GO_PURINE_NUCLEOSIDE_TRIPHOSPHATE_CATABOLIC_PROCESS	0.57	0.04	0	0	0	not significant
5992	KIM_ALL_DISORDERS_DURATION_CORR_UP	0.57	0.04	0	0	0	not significant
5993	BIOCARTA_CFTR_PATHWAY	0.57	0.03	0	0	0	not significant
5994	GO_ATP_TRANSPORT	0.57	0.03	0	0	0	not significant
5995	GO_EKC_KEOPS_COMPLEX	0.57	0.03	0	0	0	not significant
5996	GO_ESTABLISHMENT_OR_MAINTENANCE_OF_TRANSMEMBRANE_ELECTROCHEMIC	0.57	0.03	0	0	0	not significant
5997	GO_RAGE_RECEPTOR_BINDING	0.57	0.03	0	0	0	not significant
5998	REACTOME_BETA_OXIDATION_OF_VERY_LONG_CHAIN_FATTY_ACIDS	0.57	0.03	0	0	0	not significant
5999	REACTOME_TRP_CHANNELS	0.57	0.03	0	0	0	not significant
6000	REACTOME_VITAMIN_D_CALCIFEROL_METABOLISM	0.57	0.03	0	0	0	not significant
6001	GO_APOPTOTIC_PROCESS_INVOLVED_IN_MORPHOGENESIS	0.57	0.02	0	0	0	not significant
6002	GO_EPITHELIAL_CELL_MORPHOGENESIS	0.57	0.02	0	0	0	not significant
6003	GO_GLUCOSE_CATABOLIC_PROCESS	0.57	0.02	0	0	0	not significant
6004	GO_MDA_5_SIGNALING_PATHWAY	0.57	0.02	0	0	0	not significant
6005	GO_MLL3_4_COMPLEX	0.57	0.02	0	0	0	not significant
6006	GO_OSTEOBLAST_DEVELOPMENT	0.57	0.02	0	0	0	not significant
6007	GO_RESPIRATORY_CHAIN_COMPLEX_IV	0.57	0.02	0	0	0	not significant
6008	GO_SPHINGOLIPID_BINDING	0.57	0.02	0	0	0	not significant
6009	GO_TRACHEA_FORMATION	0.57	0.02	0	0	0	not significant
6010	KEGG_FATTY_ACID_METABOLISM	0.57	0.01	0	0	0	not significant
6011	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM	0.57	0.01	0	0	0	not significant
6012	GO_LYSINE_N_METHYLTRANSFERASE_ACTIVITY	0.57	0	0	0	0	not significant
6013	GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	0.57	0	0	0	0	not significant
6014	GO_REGULATION_OF_NEUROTRANSMITTER_SECRETION	0.57	0	0	0	0	not significant
6015	GO_COENZYME_TRANSPORT	0.58	0.05	0	0	0	not significant
6016	GO_REGULATION_OF_MICROVILLUS_ORGANIZATION	0.58	0.05	0	0	0	not significant
6017	GO_PEPTIDYL_SERINE_AUTOPHOSPHORYLATION	0.58	0.04	0	0	0	not significant
6018	GO_POSITIVE_REGULATION_OF_METHYLATION_DEPENDENT_CHROMATIN_SILENCI	0.58	0.04	0	0	0	not significant
6019	GO_POSTSYNAPTIC_ACTIN_CYTOSKELETON_ORGANIZATION	0.58	0.04	0	0	0	not significant
6020	GO_POSTSYNAPTIC_CYTOSKELETON_ORGANIZATION	0.58	0.04	0	0	0	not significant
6021	GO_ELASTIC_FIBER_ASSEMBLY	0.58	0.03	0	0	0	not significant
6022	GO_METHIONINE_METABOLIC_PROCESS	0.58	0.03	0	0	0	not significant
6023	GO_MRNA_3_UTR_AU_RICH_REGION_BINDING	0.58	0.03	0	0	0	not significant
6024	GO_PONS_DEVELOPMENT	0.58	0.03	0	0	0	not significant
6025	GO_PROTEIN_OXIDATION	0.58	0.03	0	0	0	not significant
6026	GO_REGULATION_OF_ENDOTHELIAL_CELL_DEVELOPMENT	0.58	0.03	0	0	0	not significant
6027	GO_REGULATION_OF_RESPONSE_TO_FOOD	0.58	0.03	0	0	0	not significant
6028	GO_THIOESTERASE_BINDING	0.58	0.03	0	0	0	not significant
6029	GO_ZINC_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.58	0.03	0	0	0	not significant
6030	REACTOME_NF_KB_IS_ACTIVATED_AND_SIGNALS_SURVIVAL	0.58	0.03	0	0	0	not significant
6031	GO_GTPASE_ACTIVATING_PROTEIN_BINDING	0.58	0.02	0	0	0	not significant
6032	GO_NEURON_CELLULAR_HOMEOSTASIS	0.58	0.02	0	0	0	not significant
6033	NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_DN	0.58	0.02	0	0	0	not significant
6034	GO_FIBROBLAST_MIGRATION	0.58	0.01	0	0	0	not significant
6035	GO_REGULATION_OF_MUSCLE_ADAPTATION	0.58	0.01	0	0	0	not significant
6036	GO_LAMELLIPODIUM	0.58	0	0	0	0	not significant
6037	REACTOME_SIRT1_NEGATIVELY_REGULATES_RRNA_EXPRESSION	0.58	0	0	0	0	not significant
6038	CHR13Q33	0.59	0.04	0	0	0	not significant
6039	CHR8P22	0.59	0.04	0	0	0	not significant
6040	GO_ATP_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.59	0.04	0	0	0	not significant
6041	GO_CALCIUM_CATION_ANTIPORTER_ACTIVITY	0.59	0.04	0	0	0	not significant
6042	GO_CARDIAC_LEFT_VENTRICLE_MORPHOGENESIS	0.59	0.04	0	0	0	not significant
6043	GO_NEGATIVE_REGULATION_OF_ACTIN_NUCLEATION	0.59	0.04	0	0	0	not significant
6044	GO_OLIGOPEPTIDE_BINDING	0.59	0.04	0	0	0	not significant
6045	BIOCARTA_INFLAM_PATHWAY	0.59	0.03	0	0	0	not significant
6046	GO_EXCRETION	0.59	0.03	0	0	0	not significant
6047	GO_G_RICH_STRAND_TELOMERIC_DNA_BINDING	0.59	0.03	0	0	0	not significant
6048	GO_POSITIVE_REGULATION_OF_BLOOD_PRESSURE	0.59	0.03	0	0	0	not significant
6049	RUAN_RESPONSE_TO_TNF_TROGLITAZONE_UP	0.59	0.03	0	0	0	not significant
6050	GO_BARBED_END_ACTIN_FILAMENT_CAPPING	0.59	0.02	0	0	0	not significant
6051	GO_CYCLIC_NUCLEOTIDE_BINDING	0.59	0.02	0	0	0	not significant
6052	GO_GLYCOPROTEIN_COMPLEX	0.59	0.02	0	0	0	not significant
6053	GO_HISTONE_H3_K4_TRIMETHYLATION	0.59	0.02	0	0	0	not significant
6054	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	0.59	0.02	0	0	0	not significant
6055	GO_SARCOMERE_ORGANIZATION	0.59	0.02	0	0	0	not significant
6056	GO_TELOMERE_MAINTENANCE_VIA_RECOMBINATION	0.59	0.02	0	0	0	not significant
6057	GO_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS_VIA_THE_MULTIVESI	0.59	0.02	0	0	0	not significant
6058	HUANG_FOXA2_TARGETS_DN	0.59	0.02	0	0	0	not significant
6059	REACTOME_EPHRIN_SIGNALING	0.59	0.02	0	0	0	not significant
6060	VALK_AML_WITH_FLT3_ITD	0.59	0.02	0	0	0	not significant
6061	KEEN_RESPONSE_TO_ROSIGLITAZONE_UP	0.59	0.01	0	0	0	not significant
6062	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_UP	0.59	0.01	0	0	0	not significant
6063	GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT_CONFERRING_TENSIL	0.60	0.05	0	0	0	not significant
6064	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_HYDROGEN_	0.60	0.05	0	0	0	not significant
6065	GO_REGULATION_OF_TYPE_B_PANCREATIC_CELL_DEVELOPMENT	0.60	0.05	0	0	0	not significant
6066	GO_HISTONE_DEMETHYLASE_ACTIVITY_H3_K4_SPECIFIC_	0.60	0.04	0	0	0	not significant
6067	GO_REGULATION_OF_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	0.60	0.04	0	0	0	not significant
6068	REACTOME_MAPK3_ERK1_ACTIVATION	0.60	0.04	0	0	0	not significant
6069	GO_CELL_CELL_SIGNALING_INVOLVED_IN_CARDIAC_CONDUCTION	0.60	0.03	0	0	0	not significant
6070	GO_HAIR_CELL_DIFFERENTIATION	0.60	0.03	0	0	0	not significant
6071	GO_INTRINSIC_COMPONENT_OF_POSTSYNAPTIC_DENSITY_MEMBRANE	0.60	0.03	0	0	0	not significant
6072	GO_POSITIVE_REGULATION_OF_ARP2_3_COMPLEX_MEDIATED_ACTIN_NUCLEATIO	0.60	0.03	0	0	0	not significant
6073	GO_PROTECTION_FROM_NON_HOMOLOGOUS_END_JOINING_AT_TELOMERE	0.60	0.03	0	0	0	not significant
6074	GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_	0.60	0.03	0	0	0	not significant
6075	LU_TUMOR_VASCULATURE_DN	0.60	0.03	0	0	0	not significant
6076	VERRECCHIA_RESPONSE_TO_TGFB1_C3	0.60	0.03	0	0	0	not significant
6077	DING_LUNG_CANCER_MUTATED_SIGNIFICANTLY	0.60	0.02	0	0	0	not significant
6078	GO_DIVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.60	0.02	0	0	0	not significant
6079	GO_INTRINSIC_COMPONENT_OF_PEROXISOMAL_MEMBRANE	0.60	0.02	0	0	0	not significant
6080	GO_POSITIVE_REGULATION_OF_AUTOPHAGY_OF_MITOCHONDRION	0.60	0.02	0	0	0	not significant
6081	GO_REGULATION_OF_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNA	0.60	0.02	0	0	0	not significant
6082	GO_DIENCEPHALON_DEVELOPMENT	0.60	0.01	0	0	0	not significant
6083	GO_NON_MOTILE_CILIUM_ASSEMBLY	0.60	0.01	0	0	0	not significant
6084	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_DRUG	0.60	0.01	0	0	0	not significant
6085	REACTOME_DEACTIVATION_OF_THE_BETA_CATENIN_TRANSACTIVATING_COMPLE	0.60	0.01	0	0	0	not significant
6086	GO_ACTIN_FILAMENT_BINDING	0.60	0	0	0	0	not significant
6087	GO_POSITIVE_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT	0.60	0	0	0	0	not significant
6088	GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_LOCALIZATION_TO_POST	0.61	0.06	0	0	0	not significant
6089	GO_APICAL_DENDRITE	0.61	0.05	0	0	0	not significant
6090	GO_FATTY_ACYL_COA_METABOLIC_PROCESS	0.61	0.05	0	0	0	not significant
6091	GO_LENS_FIBER_CELL_DEVELOPMENT	0.61	0.05	0	0	0	not significant
6092	GO_NEGATIVE_REGULATION_OF_DNA_ENDOREDUPLICATION	0.61	0.05	0	0	0	not significant

6093	DASU_IL6_SIGNALING_SCAR_DN	0.61	0.04	0	0	0	not significant
6094	DAZARD_UV_RESPONSE_CLUSTER_G5	0.61	0.04	0	0	0	not significant
6095	GO_CELLULAR_RESPONSE_TO_NITROGEN_STARVATION	0.61	0.04	0	0	0	not significant
6096	GO_NEGATIVE_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRINSIC_APOPT	0.61	0.04	0	0	0	not significant
6097	GO_POSITIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	0.61	0.04	0	0	0	not significant
6098	GO_POSITIVE_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_NONHOMC	0.61	0.04	0	0	0	not significant
6099	GO_PROTEIN_ACTIVATION_CASCADE	0.61	0.04	0	0	0	not significant
6100	GO_REGULATION_OF_PHOSPHOLIPID_BIOSYNTHETIC_PROCESS	0.61	0.04	0	0	0	not significant
6101	IIZUKA_LIVER_CANCER_PROGRESSION_L0_L1_UP	0.61	0.04	0	0	0	not significant
6102	REACTOME_COLLAGEN_CHAIN_TRIMERIZATION	0.61	0.04	0	0	0	not significant
6103	GO_DEOXYRIBONUCLEOSIDE_TRIPHOSPHATE_CATABOLIC_PROCESS	0.61	0.03	0	0	0	not significant
6104	GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALI	0.61	0.03	0	0	0	not significant
6105	GO_POSITIVE_REGULATION_OF_CHROMATIN_SILENCING	0.61	0.03	0	0	0	not significant
6106	GO_REGULATION_OF_DNA_DAMAGE_CHECKPOINT	0.61	0.03	0	0	0	not significant
6107	NABA_COLLAGENS	0.61	0.03	0	0	0	not significant
6108	REACTOME_TRANSLOCATION_OF_ZAP_70_TO_IMMUNOLOGICAL_SYNAPSE	0.61	0.03	0	0	0	not significant
6109	CHR2Q24	0.61	0.02	0	0	0	not significant
6110	GO_LYSINE_ACETYLATED_HISTONE_BINDING	0.61	0.02	0	0	0	not significant
6111	GO_POSITIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	0.61	0.02	0	0	0	not significant
6112	GO_PROTEIN_QUALITY_CONTROL_FOR_MISFOLDED_OR_INCOMPLETELY_SYNTHE	0.61	0.02	0	0	0	not significant
6113	GO_POSITIVE_REGULATION_OF_DNA_BINDING	0.61	0.01	0	0	0	not significant
6114	GO_PRIMARY_ALCOHOL_METABOLIC_PROCESS	0.61	0.01	0	0	0	not significant
6115	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_DN	0.61	0.01	0	0	0	not significant
6116	GO_CHANGES_TO_DNA_METHYLATION_INVOLVED_IN_EMBRYO_DEVELOPMENT	0.62	0.06	0	0	0	not significant
6117	GO_ICOSANOID_RECEPTOR_ACTIVITY	0.62	0.06	0	0	0	not significant
6118	REACTOME_BETA_OXIDATION_OF_HEXANOYL_COA_TO_BUTANOYL_COA	0.62	0.06	0	0	0	not significant
6119	REACTOME_CROSSLINKING_OF_COLLAGEN_FIBRILS	0.62	0.06	0	0	0	not significant
6120	REACTOME_INTRINSIC_PATHWAY_OF_FIBRIN_CLOT_FORMATION	0.62	0.06	0	0	0	not significant
6121	CASTELLANO_HRAS_AND_NRAS_TARGETS_DN	0.62	0.05	0	0	0	not significant
6122	GO_EATING_BEHAVIOR	0.62	0.05	0	0	0	not significant
6123	GO_HISTONE_H2A_K119_MONOUBIQUITINATION	0.62	0.05	0	0	0	not significant
6124	GO_ENDOSOME_TO_LYSOSOME_TRANSPORT_VIA_MULTIVESICULAR_BODY_SORT	0.62	0.04	0	0	0	not significant
6125	GO_MALE_MEIOSIS_I	0.62	0.04	0	0	0	not significant
6126	GO_NEGATIVE_REGULATION_OF_HISTONE_H3_K9_METHYLATION	0.62	0.04	0	0	0	not significant
6127	GO_RNA_SPLICING_VIA_ENDONUCLEOLYTIC_CLEAVAGE_AND_LIGATION	0.62	0.04	0	0	0	not significant
6128	CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_DN	0.62	0.03	0	0	0	not significant
6129	GO_MAST_CELL_GRANULE	0.62	0.03	0	0	0	not significant
6130	GO_PURINE_CONTAINING_COMPOUND_SALVAGE	0.62	0.03	0	0	0	not significant
6131	CHR3P24	0.62	0.02	0	0	0	not significant
6132	GO_ENDOPLASMIC_RETICULUM_CALCIUM_ION_HOMEOSTASIS	0.62	0.02	0	0	0	not significant
6133	GO_NUCLEAR_MIGRATION	0.62	0.02	0	0	0	not significant
6134	GO_PEPTIDYL_CYSTEINE_MODIFICATION	0.62	0.02	0	0	0	not significant
6135	YU_BAP1_TARGETS	0.62	0.02	0	0	0	not significant
6136	GO_RHO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	0.62	0.01	0	0	0	not significant
6137	GO_METALLOPEPTIDASE_ACTIVITY	0.62	0	0	0	0	not significant
6138	GO_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	0.62	0	0	0	0	not significant
6139	GO_C_TERMINAL_PROTEIN_LIPIDATION	0.63	0.06	0	0	0	not significant
6140	GO_CARNITINE_O_ACYLTRANSFERASE_ACTIVITY	0.63	0.06	0	0	0	not significant
6141	GO_COENZYME_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.63	0.06	0	0	0	not significant
6142	GO_FIBROBLAST_ACTIVATION	0.63	0.06	0	0	0	not significant
6143	GO_NEGATIVE_REGULATION_OF_HELICASE_ACTIVITY	0.63	0.06	0	0	0	not significant
6144	GO_THALAMUS_DEVELOPMENT	0.63	0.06	0	0	0	not significant
6145	IIZUKA_LIVER_CANCER_PROGRESSION_G1_G2_UP	0.63	0.06	0	0	0	not significant
6146	REACTOME_FCGR_ACTIVATION	0.63	0.06	0	0	0	not significant
6147	GO_BLOOD_COAGULATION_INTRINSIC_PATHWAY	0.63	0.05	0	0	0	not significant
6148	GO_BRANCHING_INVOLVED_IN_LABYRINTHINE_LAYER_MORPHOGENESIS	0.63	0.05	0	0	0	not significant
6149	GO_DIPHOSPHOTRANSFERASE_ACTIVITY	0.63	0.05	0	0	0	not significant
6150	GO_NK_T_CELL_DIFFERENTIATION	0.63	0.05	0	0	0	not significant
6151	GO_REGULATION_OF_POTASSIUM_ION_IMPORT	0.63	0.05	0	0	0	not significant
6152	GO_REGULATION_OF_SKELETAL_MUSCLE_CELL_DIFFERENTIATION	0.63	0.05	0	0	0	not significant
6153	GO_REGULATION_OF_T_CELL_CHEMOTAXIS	0.63	0.05	0	0	0	not significant
6154	GO_SULFUR_AMINO_ACID_CATABOLIC_PROCESS	0.63	0.05	0	0	0	not significant
6155	REACTOME_ACETYLCHOLINE_REGULATES_INSULIN_SECRETION	0.63	0.05	0	0	0	not significant
6156	STEGER_ADIPOGENESIS_DN	0.63	0.05	0	0	0	not significant
6157	STEGMEIER_PRE-MITOTIC_CELL_CYCLE_REGULATORS	0.63	0.05	0	0	0	not significant
6158	GO_CHEMOKINE_RECEPTOR_BINDING	0.63	0.04	0	0	0	not significant
6159	GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_OXIDASE	0.63	0.04	0	0	0	not significant
6160	GO_NEGATIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	0.63	0.04	0	0	0	not significant
6161	GO_TUMOR_NECROSIS_FACTOR_SECRETION	0.63	0.04	0	0	0	not significant
6162	KYNG_NORMAL_AGING_UP	0.63	0.04	0	0	0	not significant
6163	CHR12Q12	0.63	0.03	0	0	0	not significant
6164	GO_DNA_REPLICATION_ORIGIN_BINDING	0.63	0.03	0	0	0	not significant
6165	GO_NEGATIVE_REGULATION_OF_MUSCLE_HYPERTROPHY	0.63	0.03	0	0	0	not significant
6166	GO_POSITIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	0.63	0.03	0	0	0	not significant
6167	GO_PROTEIN_LOCALIZATION_TO_GOLGI_APPARATUS	0.63	0.03	0	0	0	not significant
6168	MEISSNER_BRAIN_ICP_WITH_H3K4ME3	0.63	0.03	0	0	0	not significant
6169	REACTOME_HDMS_DEMETHYLATE_HISTONES	0.63	0.03	0	0	0	not significant
6170	REACTOME_NEGATIVE_REGULATION_OF_MET_ACTIVITY	0.63	0.03	0	0	0	not significant
6171	REACTOME_SYNTHESIS_OF_PIPS_AT_THE_GOLGI_MEMBRANE	0.63	0.03	0	0	0	not significant
6172	GO_BRAIN_MORPHOGENESIS	0.63	0.02	0	0	0	not significant
6173	GO_CELLULAR_RESPONSE_TO_RETINOIC_ACID	0.63	0.02	0	0	0	not significant
6174	GO_EMBRYONIC_SKELETAL_SYSTEM_DEVELOPMENT	0.63	0.01	0	0	0	not significant
6175	GO_VESICLE_MEDIATED_TRANSPORT_IN_SYNAPSE	0.63	0	0	0	0	not significant
6176	GO_NEGATIVE_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	0.64	0.07	0	0	0	not significant
6177	GO_CALYX_OF_HELD	0.64	0.06	0	0	0	not significant
6178	GO_MYELIN_SHEATH_ABAXONAL_REGION	0.64	0.06	0	0	0	not significant
6179	GO_POSITIVE_REGULATION_OF_MONOCYTE_DIFFERENTIATION	0.64	0.06	0	0	0	not significant
6180	GO_POSITIVE_REGULATION_OF_NON_CANONICAL_WNT_SIGNALING_PATHWAY	0.64	0.06	0	0	0	not significant
6181	GO_SCAR_COMPLEX	0.64	0.06	0	0	0	not significant
6182	GO_VCP_NPL4_UFD1_AAA_ATPASE_COMPLEX	0.64	0.06	0	0	0	not significant
6183	REACTOME_SYNTHESIS_OF_PG	0.64	0.06	0	0	0	not significant
6184	GO_MITOTIC_DNA_REPLICATION_CHECKPOINT	0.64	0.05	0	0	0	not significant
6185	GO_POSITIVE_REGULATION_OF_FIBROBLAST_APOPTOTIC_PROCESS	0.64	0.05	0	0	0	not significant
6186	GO_REGULATION_OF_PODOSOME_ASSEMBLY	0.64	0.05	0	0	0	not significant
6187	GO_WNT_SIGNALING_PATHWAY_INVOLVED_IN_MIDBRAIN_DOPAMINERGIC_NEURON	0.64	0.05	0	0	0	not significant
6188	LEIN_LOCALIZED_TO_DISTAL_AND_PROXIMAL_DENDRITES	0.64	0.05	0	0	0	not significant
6189	REACTOME_EPHA_MEDIATED_GROWTH_CONE_COLLAPSE	0.64	0.05	0	0	0	not significant
6190	REACTOME_THE_CANONICAL_RETINOID_CYCLE_IN_RODS_TWILIGHT_VISION	0.64	0.05	0	0	0	not significant
6191	STEGMEIER_PREMITOTIC_CELL_CYCLE_REGULATORS	0.64	0.05	0	0	0	not significant
6192	GO_CHAPERONE_MEDIATED_AUTOPHAGY	0.64	0.04	0	0	0	not significant
6193	GO_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	0.64	0.04	0	0	0	not significant
6194	POS_RESPONSE_TO_HISTAMINE_UP	0.64	0.04	0	0	0	not significant
6195	REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE	0.64	0.04	0	0	0	not significant
6196	REACTOME_O_GLYCOSYLATION_OF_TSR_DOMAIN_CONTAINING_PROTEINS	0.64	0.04	0	0	0	not significant
6197	MCCABE_HOXC6_TARGETS_CANCER_DN	0.64	0.03	0	0	0	not significant
6198	PID_EPHA_FWDPATHWAY	0.64	0.03	0	0	0	not significant
6199	GO_REGULATION_OF_BMP_SIGNALING_PATHWAY	0.64	0.02	0	0	0	not significant
6200	GO_REGULATION_OF_CENTROSOME_DUPLICATION	0.64	0.02	0	0	0	not significant
6201	CHR3Q13	0.64	0.01	0	0	0	not significant

6202	CHR7P22	0.64	0.01	0	0	0	not significant
6203	GO_ANDROGEN_RECEPTOR_BINDING	0.64	0.01	0	0	0	not significant
6204	MIKKELSEN_ES_ICP_WITH_H3K27ME3	0.65	0.07	0	0	0	not significant
6205	REACTOME_UNBLOCKING_OF_NMDA_RECEPTORS_GLUTAMATE_BINDING_AND_AC	0.65	0.07	0	0	0	not significant
6206	GO_ACETYLCHOLINE_GATED_CHANNEL_COMPLEX	0.65	0.06	0	0	0	not significant
6207	GO_CEREBELLAR_PURKINJE_CELL_LAYER_FORMATION	0.65	0.06	0	0	0	not significant
6208	GO_FIBRINOLYSIS	0.65	0.06	0	0	0	not significant
6209	GO_GAMMA_CATENIN_BINDING	0.65	0.06	0	0	0	not significant
6210	GO_NEGATIVE_REGULATION_OF_OSTEOBLAST_PROLIFERATION	0.65	0.06	0	0	0	not significant
6211	GO_POSITIVE_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS	0.65	0.06	0	0	0	not significant
6212	GO_REGULATION_OF_MITOTIC_RECOMBINATION	0.65	0.06	0	0	0	not significant
6213	GO_REGULATION_OF_NEUTROPHIL_DEGRANULATION	0.65	0.06	0	0	0	not significant
6214	HASINA_NOL7_TARGETS_DN	0.65	0.06	0	0	0	not significant
6215	CHR16Q13	0.65	0.05	0	0	0	not significant
6216	GO_POSITIVE_REGULATION_OF_RECEPTOR_BIOSYNTHETIC_PROCESS	0.65	0.05	0	0	0	not significant
6217	GO_REGULATION_OF_APOPTOTIC_DNA_FRAGMENTATION	0.65	0.05	0	0	0	not significant
6218	GO_SEMINIFEROUS_TUBULE_DEVELOPMENT	0.65	0.05	0	0	0	not significant
6219	NAKAJIMA_EOSINOPHIL	0.65	0.05	0	0	0	not significant
6220	GO_REGULATION_OF_FIBROBLAST_MIGRATION	0.65	0.04	0	0	0	not significant
6221	PID_BETA_CATENIN_DEG_PATHWAY	0.65	0.04	0	0	0	not significant
6222	REACTOME_BUTYRATE_RESPONSE_FACTOR_1_BRF1_BINDS_AND_DESTABILIZES_	0.65	0.04	0	0	0	not significant
6223	REACTOME_ROLE_OF_PHOSPHOLIPIDS_IN_PHAGOCYTOSIS	0.65	0.04	0	0	0	not significant
6224	WALLACE_JAK2_TARGETS_UP	0.65	0.04	0	0	0	not significant
6225	CHANGOLKAR_H2AFY_TARGETS_UP	0.65	0.03	0	0	0	not significant
6226	GO_H4_H2A_HISTONE_ACETYLTRANSFERASE_COMPLEX	0.65	0.03	0	0	0	not significant
6227	GO_HISTONE_DEMETHYLASE_ACTIVITY	0.65	0.03	0	0	0	not significant
6228	GO_LONG_TERM_SYNAPTIC_POTENTIATION	0.65	0.03	0	0	0	not significant
6229	GO_NEGATIVE_REGULATION_OF_ORGANELLE_ASSEMBLY	0.65	0.03	0	0	0	not significant
6230	GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABIL	0.65	0.03	0	0	0	not significant
6231	KEGG_REGULATION_OF_AUTOPHAGY	0.65	0.03	0	0	0	not significant
6232	CHR8Q22	0.65	0.02	0	0	0	not significant
6233	GO_CELL_REDOX_HOMEOSTASIS	0.65	0.02	0	0	0	not significant
6234	GO_EXTRINSIC_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_PLASMA_MEMBRANE	0.65	0.01	0	0	0	not significant
6235	GO_SPECIFICATION_OF_SYMMETRY	0.65	0.01	0	0	0	not significant
6236	GO_SYNAPTIC_VESICLE_EXOCYTOSIS	0.65	0.01	0	0	0	not significant
6237	GO_MELANOSOME_MEMBRANE	0.66	0.08	0	0	0	not significant
6238	GO_GROWTH_PLATE_CARTILAGE_CHONDROCYTE_DIFFERENTIATION	0.66	0.07	0	0	0	not significant
6239	GO_POSITIVE_REGULATION_OF_GLIAL_CELL_MIGRATION	0.66	0.07	0	0	0	not significant
6240	GO_SYNAPTIC_VESICLE_DOCKING	0.66	0.07	0	0	0	not significant
6241	DE_YY1_TARGETS_UP	0.66	0.06	0	0	0	not significant
6242	GO_AUTOPHAGY_OF_PEROXISOME	0.66	0.06	0	0	0	not significant
6243	GO_MIDBRAIN_DOPAMINERGIC_NEURON_DIFFERENTIATION	0.66	0.06	0	0	0	not significant
6244	GO_NEGATIVE_REGULATION_OF_RIG_I_SIGNALING_PATHWAY	0.66	0.06	0	0	0	not significant
6245	GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGION_DNA_BI	0.66	0.06	0	0	0	not significant
6246	GO_NEGATIVE_REGULATION_OF_VIRAL_INDUCED_CYTOPLASMIC_PATTERN_RECO	0.66	0.06	0	0	0	not significant
6247	GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_CALCIUM_ION_CONCENTRATION	0.66	0.06	0	0	0	not significant
6248	KAMIKUBO_MYELOID_MN1_NETWORK	0.66	0.06	0	0	0	not significant
6249	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13	0.66	0.06	0	0	0	not significant
6250	REACTOME_PROTON_COUPLED_MONOCARBOXYLATE_TRANSPORT	0.66	0.06	0	0	0	not significant
6251	CHR20P12	0.66	0.05	0	0	0	not significant
6252	CHR2P24	0.66	0.05	0	0	0	not significant
6253	CHR6Q16	0.66	0.05	0	0	0	not significant
6254	GO_CELL_FATE_COMMITMENT_INVOLVED_IN_FORMATION_OF_PRIMARY_GERM_L	0.66	0.05	0	0	0	not significant
6255	GO_MITOCHONDRIA_ASSOCIATED_ENDOPLASMIC_RETICULUM_MEMBRANE	0.66	0.05	0	0	0	not significant
6256	GO_NUCLEOSIDE_KINASE_ACTIVITY	0.66	0.05	0	0	0	not significant
6257	MADAN_DPPA4_TARGETS	0.66	0.05	0	0	0	not significant
6258	ZHANG_RESPONSE_TO_CANTHARIDIN_UP	0.66	0.05	0	0	0	not significant
6259	CHR12P11	0.66	0.04	0	0	0	not significant
6260	GO_AU_RICH_ELEMENT_BINDING	0.66	0.04	0	0	0	not significant
6261	GO_ERBB2_SIGNALING_PATHWAY	0.66	0.04	0	0	0	not significant
6262	GO_GAMMA_TUBULIN_BINDING	0.66	0.04	0	0	0	not significant
6263	GO_POLYSACCHARIDE_CATABOLIC_PROCESS	0.66	0.04	0	0	0	not significant
6264	GO_SWR1_COMPLEX	0.66	0.04	0	0	0	not significant
6265	KEGG_PROTEIN_EXPORT	0.66	0.04	0	0	0	not significant
6266	REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	0.66	0.04	0	0	0	not significant
6267	GO_GOLGI_TO_PLASMA_MEMBRANE_PROTEIN_TRANSPORT	0.66	0.03	0	0	0	not significant
6268	GO_NEURON_PROJECTION_REGENERATION	0.66	0.03	0	0	0	not significant
6269	GO_CELLULAR_PIGMENTATION	0.66	0.02	0	0	0	not significant
6270	GO_NEGATIVE_REGULATION_OF_TOR_SIGNALING	0.66	0.02	0	0	0	not significant
6271	GO_RNA_POLYMERASE_II_REPRESSING_TRANSCRIPTION_FACTOR_BINDING	0.66	0.02	0	0	0	not significant
6272	GO_SNARE_COMPLEX	0.66	0.02	0	0	0	not significant
6273	GO_ATPASE_COMPLEX	0.66	0.01	0	0	0	not significant
6274	GO_TUBE_FORMATION	0.66	0.01	0	0	0	not significant
6275	BENPORATH_NOS_TARGETS	0.66	0	0	0	0	not significant
6276	GO_ADHERENS_JUNCTION_ORGANIZATION	0.66	0	0	0	0	not significant
6277	CHANG_POU5F1_TARGETS_UP	0.67	0.08	0	0	0	not significant
6278	GO_HISTONE_H3_K4_DEMETHYLATION	0.67	0.08	0	0	0	not significant
6279	GO_3_HYDROXYACYL_COA_DEHYDROGENASE_ACTIVITY	0.67	0.07	0	0	0	not significant
6280	GO_CORPUS_CALLOSUM_MORPHOGENESIS	0.67	0.07	0	0	0	not significant
6281	GO_LOCOMOTORY_EXPLORATION_BEHAVIOR	0.67	0.07	0	0	0	not significant
6282	GO_NEGATIVE_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFEREN	0.67	0.07	0	0	0	not significant
6283	GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PRO	0.67	0.07	0	0	0	not significant
6284	GO_RAP_PROTEIN_SIGNAL_TRANSDUCTION	0.67	0.07	0	0	0	not significant
6285	GO_RELAXATION_OF_CARDIAC_MUSCLE	0.67	0.07	0	0	0	not significant
6286	REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	0.67	0.07	0	0	0	not significant
6287	GO_3_5_CYCLIC_GMP_PHOSPHODIESTERASE_ACTIVITY	0.67	0.06	0	0	0	not significant
6288	GO_CELLULAR_RESPONSE_TO_THYROID_HORMONE_STIMULUS	0.67	0.06	0	0	0	not significant
6289	GO_NEGATIVE_REGULATION_OF_HEART_CONTRACTION	0.67	0.06	0	0	0	not significant
6290	GO_POSITIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	0.67	0.06	0	0	0	not significant
6291	GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_FISSION	0.67	0.06	0	0	0	not significant
6292	GO_POSITIVE_REGULATION_OF_PODOSOME_ASSEMBLY	0.67	0.06	0	0	0	not significant
6293	GO_POSITIVE_REGULATION_OF_TRIGLYCERIDE_BIOSYNTHETIC_PROCESS	0.67	0.06	0	0	0	not significant
6294	GO_REGULATION_OF_TOLERANCE_INDUCTION	0.67	0.06	0	0	0	not significant
6295	BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN	0.67	0.05	0	0	0	not significant
6296	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_UP	0.67	0.05	0	0	0	not significant
6297	GO_COPI_COATED_VESICLE_MEMBRANE	0.67	0.05	0	0	0	not significant
6298	GO_NEGATIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_STRESS_INDUCED_I	0.67	0.05	0	0	0	not significant
6299	GO_PENTOSE_PHOSPHATE_SHUNT	0.67	0.05	0	0	0	not significant
6300	NIELSEN_LIPOSARCOMA_DN	0.67	0.05	0	0	0	not significant
6301	REACTOME_TICAM1_RIP1_MEDIATED_IKK_COMPLEX_RECRUITMENT	0.67	0.05	0	0	0	not significant
6302	CHR14Q21	0.67	0.04	0	0	0	not significant
6303	GO_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY	0.67	0.04	0	0	0	not significant
6304	GO_INTRACELLULAR_LIPID_TRANSPORT	0.67	0.04	0	0	0	not significant
6305	GO_POSITIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	0.67	0.04	0	0	0	not significant
6306	GO_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY	0.67	0.04	0	0	0	not significant
6307	GO_DORSAL_VENTRAL_PATTERN_FORMATION	0.67	0.03	0	0	0	not significant
6308	GO_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	0.67	0.03	0	0	0	not significant
6309	GO_MUSCLE_ADAPTATION	0.67	0.02	0	0	0	not significant
6310	GO_NEGATIVE_REGULATION_OF_DNA_REPLICATION	0.67	0.02	0	0	0	not significant

6311	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	0.67	0.02	0	0	0	not significant
6312	BOUDOUKHA_BOUND_BY_IGF2BP2	0.67	0.01	0	0	0	not significant
6313	GO_REGULATION_OF_CILIUM_MOVEMENT	0.68	0.09	0	0	0	not significant
6314	KANG_GLIS3_TARGETS	0.68	0.09	0	0	0	not significant
6315	GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SECRETION	0.68	0.08	0	0	0	not significant
6316	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZATION	0.68	0.08	0	0	0	not significant
6317	GO_SYNAPTIC_TRANSMISSION_CHOLINERGIC	0.68	0.08	0	0	0	not significant
6318	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_FLI1	0.68	0.07	0	0	0	not significant
6319	CHR7P21	0.68	0.07	0	0	0	not significant
6320	GO_ASPARTATE_TRANSMEMBRANE_TRANSPORT	0.68	0.07	0	0	0	not significant
6321	GO_ENTRY_OF_BACTERIUM_INTO_HOST_CELL	0.68	0.07	0	0	0	not significant
6322	GO_POSITIVE_REGULATION_OF_HETEROTYPIC_CELL_CELL_ADHESION	0.68	0.07	0	0	0	not significant
6323	GO_REGULATION_OF_CILIUM_BEAT_FREQUENCY	0.68	0.07	0	0	0	not significant
6324	BIOCARTA_SPPA_PATHWAY	0.68	0.06	0	0	0	not significant
6325	GO_INNER_EAR_AUDITORY_RECEPTOR_CELL_DIFFERENTIATION	0.68	0.06	0	0	0	not significant
6326	GO_SYNTAXIN_1_BINDING	0.68	0.06	0	0	0	not significant
6327	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_DN	0.68	0.06	0	0	0	not significant
6328	REACTOME_PECAM1_INTERACTIONS	0.68	0.06	0	0	0	not significant
6329	DARWICHE_PAPILLOMA_RISK_HIGH_VS_LOW_DN	0.68	0.05	0	0	0	not significant
6330	GO_INTERCALATED_DISC	0.68	0.05	0	0	0	not significant
6331	MEISSNER_NPC_ICP_WITH_H3K4ME3	0.68	0.05	0	0	0	not significant
6332	CHR4Q35	0.68	0.04	0	0	0	not significant
6333	GO_POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	0.68	0.04	0	0	0	not significant
6334	PETRETTO_CARDIAC_HYPERTROPHY	0.68	0.04	0	0	0	not significant
6335	BALDWIN_PRKCI_TARGETS_UP	0.68	0.03	0	0	0	not significant
6336	CHRXQ22	0.68	0.03	0	0	0	not significant
6337	GO_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	0.68	0.03	0	0	0	not significant
6338	GO_HOMOTYPIC_CELL_CELL_ADHESION	0.68	0.03	0	0	0	not significant
6339	PID_PI3KCI_PATHWAY	0.68	0.03	0	0	0	not significant
6340	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	0.68	0.02	0	0	0	not significant
6341	GO_SITE_OF_DNA_DAMAGE	0.68	0.02	0	0	0	not significant
6342	IWANAGA_CARCINOGENESIS_BY_KRAS_UP	0.68	0.01	0	0	0	not significant
6343	NOTCH_DN.V1_UP	0.68	0.01	0	0	0	not significant
6344	CHR8Q23	0.69	0.09	0	0	0	not significant
6345	GO_MACROPHAGE_CYTOKINE_PRODUCTION	0.69	0.09	0	0	0	not significant
6346	GO_NEGATIVE_REGULATION_OF_AUTOPHAGY_OF_MITOCHONDRION	0.69	0.09	0	0	0	not significant
6347	GO_NOTOCHORD_DEVELOPMENT	0.69	0.09	0	0	0	not significant
6348	GO_PLATELET_DENSE_GRANULE_LUMEN	0.69	0.09	0	0	0	not significant
6349	GO_ANTEROGRADE_AXONAL_PROTEIN_TRANSPORT	0.69	0.08	0	0	0	not significant
6350	GO_EARLY_PHAGOSOME	0.69	0.08	0	0	0	not significant
6351	GO_EMBRYONIC_BRAIN_DEVELOPMENT	0.69	0.08	0	0	0	not significant
6352	GO_NEGATIVE_REGULATION_OF_PROTEIN_K63_LINKED_UBIQUITINATION	0.69	0.08	0	0	0	not significant
6353	GO_POSITIVE_REGULATION_OF_NEUROBLAST_PROLIFERATION	0.69	0.08	0	0	0	not significant
6354	GO_REGULATION_OF_ARP2_3_COMPLEX_MEDIATED_ACTIN_NUCLEATION	0.69	0.08	0	0	0	not significant
6355	HESSON_TUMOR_SUPPRESSOR_CLUSTER_3P21_3	0.69	0.08	0	0	0	not significant
6356	MATZUK_EARLY_ANTRAL_FOLLICLE	0.69	0.08	0	0	0	not significant
6357	REACTOME_SYNTHESIS_OF_PIPS_AT_THE_ER_MEMBRANE	0.69	0.08	0	0	0	not significant
6358	ELLWOOD_MYC_TARGETS_UP	0.69	0.07	0	0	0	not significant
6359	GO_3_PHOSPHOADENOSINE_5_PHOSPHOSULFATE_METABOLIC_PROCESS	0.69	0.07	0	0	0	not significant
6360	GO_CUL2_RING_UBIQUITIN_LIGASE_COMPLEX	0.69	0.07	0	0	0	not significant
6361	GO_HISTONE_MRNA_CATABOLIC_PROCESS	0.69	0.07	0	0	0	not significant
6362	GO_NEGATIVE_REGULATION_OF_GLIOGENESIS	0.69	0.07	0	0	0	not significant
6363	GO_NEGATIVE_REGULATION_OF_PROTEIN_ACETYLATION	0.69	0.07	0	0	0	not significant
6364	GO_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	0.69	0.07	0	0	0	not significant
6365	GO_POSITIVE_REGULATION_OF_CENTROSOME_CYCLE	0.69	0.07	0	0	0	not significant
6366	GO_RNA_DNA_HYBRID_RIBONUCLEASE_ACTIVITY	0.69	0.07	0	0	0	not significant
6367	REACTOME_RA_BIOSYNTHESIS_PATHWAY	0.69	0.07	0	0	0	not significant
6368	WANG_NFKB_TARGETS	0.69	0.07	0	0	0	not significant
6369	CHR11Q22	0.69	0.06	0	0	0	not significant
6370	GO_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	0.69	0.06	0	0	0	not significant
6371	GO_FOAM_CELL_DIFFERENTIATION	0.69	0.06	0	0	0	not significant
6372	GO_GLUCOSYLTRANSFERASE_ACTIVITY	0.69	0.06	0	0	0	not significant
6373	GO_MITOCHONDRIAL_PROTEIN_PROCESSING	0.69	0.06	0	0	0	not significant
6374	GO_NECROPTOTIC_SIGNALING_PATHWAY	0.69	0.06	0	0	0	not significant
6375	GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	0.69	0.06	0	0	0	not significant
6376	GO_PHOSPHATIDYLCHOLINE_BIOSYNTHETIC_PROCESS	0.69	0.06	0	0	0	not significant
6377	GO_PTERIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	0.69	0.06	0	0	0	not significant
6378	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN	0.69	0.06	0	0	0	not significant
6379	REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS	0.69	0.06	0	0	0	not significant
6380	REACTOME_METABOLISM_OF_PORPHYRINS	0.69	0.06	0	0	0	not significant
6381	REACTOME_REGULATION_OF_IFNA_SIGNALING	0.69	0.06	0	0	0	not significant
6382	GO_MULTICELLULAR_ORGANISM_AGING	0.69	0.05	0	0	0	not significant
6383	GO_POSITIVE_REGULATION_OF_G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	0.69	0.05	0	0	0	not significant
6384	GO_PROTEIN_LOCALIZATION_TO_MICROTUBULE_ORGANIZING_CENTER	0.69	0.05	0	0	0	not significant
6385	MARTIN_NFKB_TARGETS_UP	0.69	0.05	0	0	0	not significant
6386	LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_SMALL_VS_HUGE_UP	0.69	0.04	0	0	0	not significant
6387	ULE_SPLICING_VIA_NOVA2	0.69	0.04	0	0	0	not significant
6388	GO_CELLULAR_RESPONSE_TO_MECHANICAL_STIMULUS	0.69	0.03	0	0	0	not significant
6389	REACTOME_PKMTS_METHYLATE_HISTONE_LYSINES	0.69	0.03	0	0	0	not significant
6390	GO_CELL_SUBSTRATE_JUNCTION_ASSEMBLY	0.69	0.02	0	0	0	not significant
6391	GO_NUCLEOSIDE_PHOSPHATE_CATABOLIC_PROCESS	0.69	0.02	0	0	0	not significant
6392	GO_PML_BODY	0.69	0.02	0	0	0	not significant
6393	GO_SH3_DOMAIN_BINDING	0.69	0.02	0	0	0	not significant
6394	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN	0.69	0.01	0	0	0	not significant
6395	GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	0.69	0	0	0	0	not significant
6396	GO_AXON_INITIAL_SEGMENT	0.70	0.1	0	0	0	not significant
6397	GO_FACIAL_NERVE_STRUCTURAL_ORGANIZATION	0.70	0.1	0	0	0	not significant
6398	GO_PURINE_DEOXYRIBONUCLEOTIDE_CATABOLIC_PROCESS	0.70	0.1	0	0	0	not significant
6399	GO_EUKARYOTIC_INITIATION_FACTOR_4E_BINDING	0.70	0.09	0	0	0	not significant
6400	GO_FRUCTOSE_1_6_BISPHOSPHATE_METABOLIC_PROCESS	0.70	0.09	0	0	0	not significant
6401	GO_MIRNA_LOADING_ONTO_RISC_INVOLVED_IN_GENE_SILENCING_BY_MIRNA	0.70	0.09	0	0	0	not significant
6402	GO_NEGATIVE_REGULATION_OF_MITOPHAGY	0.70	0.09	0	0	0	not significant
6403	GO_WHITE_FAT_CELL_DIFFERENTIATION	0.70	0.09	0	0	0	not significant
6404	KOINUMA_COLON_CANCER_MSI_UP	0.70	0.09	0	0	0	not significant
6405	PID_S1P_S1P4_PATHWAY	0.70	0.09	0	0	0	not significant
6406	GO_CELLULAR_RESPONSE_TO_TESTOSTERONE_STIMULUS	0.70	0.08	0	0	0	not significant
6407	GO_DENDRITIC_SHAFT	0.70	0.08	0	0	0	not significant
6408	GO_POSITIVE_REGULATION_OF_GLYCOLYTIC_PROCESS	0.70	0.08	0	0	0	not significant
6409	GO_REGULATION_OF_EXIT_FROM_MITOSIS	0.70	0.08	0	0	0	not significant
6410	GO_RETINOL_DEHYDROGENASE_ACTIVITY	0.70	0.08	0	0	0	not significant
6411	REACTOME_ETHANOL_OXIDATION	0.70	0.08	0	0	0	not significant
6412	GO_APICAL_PROTEIN_LOCALIZATION	0.70	0.07	0	0	0	not significant
6413	GO_CYCLIC_NUCLEOTIDE_CATABOLIC_PROCESS	0.70	0.07	0	0	0	not significant
6414	GO_GABA_RECEPTOR_BINDING	0.70	0.07	0	0	0	not significant
6415	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_DRUG	0.70	0.07	0	0	0	not significant
6416	GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PR	0.70	0.07	0	0	0	not significant
6417	GO_REGULATION_OF_BILE_ACID_METABOLIC_PROCESS	0.70	0.07	0	0	0	not significant
6418	GO_REGULATION_OF_ENDOCRINE_PROCESS	0.70	0.07	0	0	0	not significant
6419	GO_TELOMERE_MAINTENANCE_IN_RESPONSE_TO_DNA_DAMAGE	0.70	0.07	0	0	0	not significant

6420	HE_PTEN_TARGETS_UP	0.70	0.07	0	0	0	not significant
6421	MIKKELSEN_ES_HCP_WITH_H3_UNMETHYLATED	0.70	0.07	0	0	0	not significant
6422	REACTOME_NEF_MEDIATED_DOWNREGULATION_OF_MHC_CLASS_I_COMPLEX_CE	0.70	0.07	0	0	0	not significant
6423	REACTOME_RUNX2_REGULATES_OSTEOBLAST_DIFFERENTIATION	0.70	0.07	0	0	0	not significant
6424	REACTOME_SMALL_INTERFERING_RNA_SIRNA_BIOGENESIS	0.70	0.07	0	0	0	not significant
6425	VALK_AML_CLUSTER_1	0.70	0.07	0	0	0	not significant
6426	CHR7P13	0.70	0.06	0	0	0	not significant
6427	GO_CARDIAC_MUSCLE_CELL_CONTRACTION	0.70	0.06	0	0	0	not significant
6428	GO_HISTONE_H2A_UBIQUITINATION	0.70	0.06	0	0	0	not significant
6429	GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_STABILIZATION	0.70	0.06	0	0	0	not significant
6430	GO_TRANSPOSITION	0.70	0.06	0	0	0	not significant
6431	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_ADDITIONAL_CELL_CYCLE_G	0.70	0.06	0	0	0	not significant
6432	YAP1_DN	0.70	0.06	0	0	0	not significant
6433	BRIDEAU_IMPRINTED_GENES	0.70	0.05	0	0	0	not significant
6434	GO_NUCLEAR_TRANSCRIBED_MRNA_POLY_A_TAIL_SHORTENING	0.70	0.05	0	0	0	not significant
6435	GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	0.70	0.05	0	0	0	not significant
6436	GO_SCHAFFER_COLLATERAL__CA1_SYNAPSE	0.70	0.05	0	0	0	not significant
6437	KRAS.AMP.LUNG_UP.V1_UP	0.70	0.05	0	0	0	not significant
6438	BOYLAN_MULTIPLE_MYELOMA_C_UP	0.70	0.04	0	0	0	not significant
6439	GO_POSITIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	0.70	0.04	0	0	0	not significant
6440	GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN	0.70	0.03	0	0	0	not significant
6441	GO_ACTION_POTENTIAL	0.70	0.03	0	0	0	not significant
6442	GO_HISTONE_H4_ACETYLATION	0.70	0.03	0	0	0	not significant
6443	GO_RETINA_DEVELOPMENT_IN_CAMERA_TYPE_EYE	0.70	0.02	0	0	0	not significant
6444	TAKAO_RESPONSE_TO_UVB_RADIATION_UP	0.70	0.01	0	0	0	not significant
6445	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	0.70	0	0	0	0	not significant
6446	GO_CELL_LEADING_EDGE	0.70	0	0	0	0	not significant
6447	GO_CRANIAL_NERVE_STRUCTURAL_ORGANIZATION	0.71	0.1	0	0	0	not significant
6448	GO_NADP_METABOLIC_PROCESS	0.71	0.1	0	0	0	not significant
6449	GO_NEGATIVE_REGULATION_OF_PROTEIN_POLYUBIQUITINATION	0.71	0.1	0	0	0	not significant
6450	GO_PINOSOME	0.71	0.1	0	0	0	not significant
6451	GO_POTASSIUM_TRANSPORTING_ATPASE_ACTIVITY	0.71	0.1	0	0	0	not significant
6452	GO_RNA_POLYMERASE_III_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_ACTIVI	0.71	0.1	0	0	0	not significant
6453	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_DN	0.71	0.09	0	0	0	not significant
6454	DELACROIX_RAR_TARGETS_DN	0.71	0.09	0	0	0	not significant
6455	GO_ALCOHOL_DEHYDROGENASE_NADPPLUS_ACTIVITY	0.71	0.09	0	0	0	not significant
6456	GO_CALCIUM_DEPENDENT_PROTEIN_SERINE_THREONINE_PHOSPHATASE_ACTIVIT	0.71	0.09	0	0	0	not significant
6457	GO_POSITIVE_REGULATION_OF_ER_ASSOCIATED_UBIQUITIN_DEPENDENT_PROTEI	0.71	0.09	0	0	0	not significant
6458	GO_PROTEIN_HORMONE_RECEPTOR_ACTIVITY	0.71	0.09	0	0	0	not significant
6459	GO_SODIUM_POTASSIUM_EXCHANGING_ATPASE_COMPLEX	0.71	0.09	0	0	0	not significant
6460	PID_ALK2_PATHWAY	0.71	0.09	0	0	0	not significant
6461	REACTOME_SEMA4D_MEDIATED_INHIBITION_OF_CELL_ATTACHMENT_AND_MIGRAT	0.71	0.09	0	0	0	not significant
6462	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP	0.71	0.09	0	0	0	not significant
6463	BIOCARTA_PLC_PATHWAY	0.71	0.08	0	0	0	not significant
6464	GO_CELLULAR_RESPONSE_TO_ETHANOL	0.71	0.08	0	0	0	not significant
6465	GO_FATTY_ACID_LIGASE_ACTIVITY	0.71	0.08	0	0	0	not significant
6466	GO_I_SMAD_BINDING	0.71	0.08	0	0	0	not significant
6467	GO_POSITIVE_REGULATION_OF_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	0.71	0.08	0	0	0	not significant
6468	GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_	0.71	0.08	0	0	0	not significant
6469	GO_PROTEIN_LOCALIZATION_TO_PRESYNAPSE	0.71	0.08	0	0	0	not significant
6470	GO_SINGLE_STRAND_BREAK_REPAIR	0.71	0.08	0	0	0	not significant
6471	HAN_JNK_SINGALING_DN	0.71	0.08	0	0	0	not significant
6472	PID_ECADHERIN_KERATINOCYTE_PATHWAY	0.71	0.08	0	0	0	not significant
6473	REACTOME_TRANSCRIPTION_OF_E2F_TARGETS_UNDER_NEGATIVE_CONTROL_BY	0.71	0.08	0	0	0	not significant
6474	SA_PTEN_PATHWAY	0.71	0.08	0	0	0	not significant
6475	ZEMBUTSU_SENSITIVITY_TO_METHOTREXATE	0.71	0.08	0	0	0	not significant
6476	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_CYAN_UP	0.71	0.07	0	0	0	not significant
6477	GO_MICROTUBULE_ANCHORING_AT_MICROTUBULE_ORGANIZING_CENTER	0.71	0.07	0	0	0	not significant
6478	GO_RECEPTOR_SIGNALING_COMPLEX_SCAFFOLD_ACTIVITY	0.71	0.07	0	0	0	not significant
6479	KEGG_PENTOSE_PHOSPHATE_PATHWAY	0.71	0.07	0	0	0	not significant
6480	VALK_AML_CLUSTER_8	0.71	0.07	0	0	0	not significant
6481	GO_INTRINSIC_COMPONENT_OF_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE	0.71	0.06	0	0	0	not significant
6482	GO_NUCLEAR_OUTER_MEMBRANE	0.71	0.06	0	0	0	not significant
6483	BIOCARTA_EDG1_PATHWAY	0.71	0.05	0	0	0	not significant
6484	CHR15Q21	0.71	0.05	0	0	0	not significant
6485	EHLERS_ANEUPLOIDY_UP	0.71	0.05	0	0	0	not significant
6486	GO_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	0.71	0.05	0	0	0	not significant
6487	GO_POSITIVE_REGULATION_OF_WOUND_HEALING	0.71	0.05	0	0	0	not significant
6488	GO_RENAL_SYSTEM_PROCESS	0.71	0.05	0	0	0	not significant
6489	NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	0.71	0.05	0	0	0	not significant
6490	GO_DENDRITIC_SPINE_DEVELOPMENT	0.71	0.04	0	0	0	not significant
6491	GO_MOLTING_CYCLE	0.71	0.04	0	0	0	not significant
6492	GO_PCG_PROTEIN_COMPLEX	0.71	0.04	0	0	0	not significant
6493	GO_ROOF_OF_MOUTH_DEVELOPMENT	0.71	0.04	0	0	0	not significant
6494	GO_SENSORY_PERCEPTION_OF_PAIN	0.71	0.04	0	0	0	not significant
6495	GO_VESICLE_DOCKING	0.71	0.04	0	0	0	not significant
6496	HUTTMANN_B_CLL_POOR_SURVIVAL_DN	0.71	0.04	0	0	0	not significant
6497	GO_ACTIVATION_OF_GTPASE_ACTIVITY	0.71	0.03	0	0	0	not significant
6498	GO_OXIDOREDUCTASE_COMPLEX	0.71	0.03	0	0	0	not significant
6499	GO_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALI	0.71	0.03	0	0	0	not significant
6500	GO_RUFFLE_MEMBRANE	0.71	0.03	0	0	0	not significant
6501	GO_HISTONE_METHYLATION	0.71	0.02	0	0	0	not significant
6502	GO_REGULATION_OF_CELL_SHAPE	0.71	0.02	0	0	0	not significant
6503	GO_REGULATION_OF_MEMBRANE_POTENTIAL	0.71	0	0	0	0	not significant
6504	GO_ACETYLCHOLINE_GATED_CATION_SELECTIVE_CHANNEL_ACTIVITY	0.72	0.11	0	0	0	not significant
6505	GO_DIPEPTIDYL_PEPTIDASE_ACTIVITY	0.72	0.1	0	0	0	not significant
6506	GO_ETHANOL_OXIDATION	0.72	0.1	0	0	0	not significant
6507	GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_ELONGATION_FROM_RNA_POL	0.72	0.1	0	0	0	not significant
6508	GO_PEPTIDYL_LYSINE_HYDROXYLATION	0.72	0.1	0	0	0	not significant
6509	GO_POSITIVE_REGULATION_OF_METALLOPEPTIDASE_ACTIVITY	0.72	0.1	0	0	0	not significant
6510	TAGHAVI_NEOPLASTIC_TRANSFORMATION	0.72	0.1	0	0	0	not significant
6511	GO_CELLULAR_RESPONSE_TO_INTERFERON_BETA	0.72	0.09	0	0	0	not significant
6512	GO_PRENYLTRANSFERASE_ACTIVITY	0.72	0.09	0	0	0	not significant
6513	GO_REGULATION_OF_ISOTYPE_SWITCHING_TO_IGE_ISOTYPES	0.72	0.09	0	0	0	not significant
6514	GO_REGULATION_OF_MICROTUBULE_DEPOLYMERIZATION	0.72	0.09	0	0	0	not significant
6515	GO_REGULATION_OF_PEROXISOME_PROLIFERATOR_ACTIVATED_RECEPTOR_SIG	0.72	0.09	0	0	0	not significant
6516	GO_WNT_SIGNALOSOME	0.72	0.09	0	0	0	not significant
6517	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_2HR	0.72	0.09	0	0	0	not significant
6518	GO_ANTIMICROBIAL_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_ANTIMICROBIA	0.72	0.08	0	0	0	not significant
6519	GO_PYRUVATE_METABOLIC_PROCESS	0.72	0.08	0	0	0	not significant
6520	GO_REGULATION_OF_HETEROTYPIC_CELL_CELL_ADHESION	0.72	0.08	0	0	0	not significant
6521	GO_TRANSFORMING_GROWTH_FACTOR_BETA_BINDING	0.72	0.08	0	0	0	not significant
6522	HASLINGER_B_CLL_WITH_11Q23_DELETION	0.72	0.08	0	0	0	not significant
6523	REACTOME_DISEASES_ASSOCIATED_WITH_N_GLYCOSYLATION_OF_PROTEINS	0.72	0.08	0	0	0	not significant
6524	REACTOME_NUCLEAR_ENVELOPE_REASSEMBLY	0.72	0.08	0	0	0	not significant
6525	CHR6Q22	0.72	0.07	0	0	0	not significant
6526	GO_AXON_REGENERATION	0.72	0.07	0	0	0	not significant
6527	GO_DNA_REPLICATION_DEPENDENT_NUCLEOSOME_ORGANIZATION	0.72	0.07	0	0	0	not significant
6528	GO_POSITIVE_REGULATION_OF_GLYCOPROTEIN_BIOSYNTHETIC_PROCESS	0.72	0.07	0	0	0	not significant

6529	GO_PROTEIN_LOCALIZATION_TO_POSTSYNAPTIC_MEMBRANE	0.72	0.07	0	0	0	not significant
6530	KORKOLA_YOLK_SAC_TUMOR	0.72	0.07	0	0	0	not significant
6531	GO_HISTONE_H3_K9_METHYLATION	0.72	0.06	0	0	0	not significant
6532	GO_LYSOSOME_LOCALIZATION	0.72	0.06	0	0	0	not significant
6533	GO_OUTFLOW_TRACT_MORPHOGENESIS	0.72	0.06	0	0	0	not significant
6534	KYNG_DNA_DAMAGE_BY_4NQO_OR_UV	0.72	0.06	0	0	0	not significant
6535	PID_HIV_NEF_PATHWAY	0.72	0.06	0	0	0	not significant
6536	COATES_MACROPHAGE_M1_VS_M2_UP	0.72	0.05	0	0	0	not significant
6537	GO_VIRION_ASSEMBLY	0.72	0.05	0	0	0	not significant
6538	SIG_BCR_SIGNALING_PATHWAY	0.72	0.05	0	0	0	not significant
6539	CHR2Q11	0.72	0.04	0	0	0	not significant
6540	GO_BONE_MORPHOGENESIS	0.72	0.04	0	0	0	not significant
6541	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	0.72	0.04	0	0	0	not significant
6542	GO_AEROBIC_RESPIRATION	0.72	0.03	0	0	0	not significant
6543	GO_INDOLE_CONTAINING_COMPOUND_METABOLIC_PROCESS	0.73	0.12	0	0	0	not significant
6544	GO_ALPHA_CATENIN_BINDING	0.73	0.11	0	0	0	not significant
6545	GO_FOREBRAIN_REGIONALIZATION	0.73	0.11	0	0	0	not significant
6546	GO_NEGATIVE_REGULATION_OF_MEMBRANE_POTENTIAL	0.73	0.11	0	0	0	not significant
6547	GO_REGULATION_OF_DEVELOPMENT_HETEROCHRONIC	0.73	0.11	0	0	0	not significant
6548	GO_TYPE_I_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING	0.73	0.11	0	0	0	not significant
6549	BIOCARTA_HBX_PATHWAY	0.73	0.1	0	0	0	not significant
6550	CHRXQ25	0.73	0.1	0	0	0	not significant
6551	GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_DEHYDROGENASE	0.73	0.1	0	0	0	not significant
6552	GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	0.73	0.1	0	0	0	not significant
6553	GO_POSITIVE_REGULATION_OF_CYTOPLASMIC_MRNA_PROCESSING_BODY_ASSEM	0.73	0.1	0	0	0	not significant
6554	GO_POSITIVE_REGULATION_OF_RECEPTOR_BINDING	0.73	0.1	0	0	0	not significant
6555	GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_NONHOMOLOGOUS_	0.73	0.1	0	0	0	not significant
6556	GO_REGULATION_OF_SENSORY_PERCEPTION	0.73	0.1	0	0	0	not significant
6557	GO_SYNAPTIC_CLEFT	0.73	0.1	0	0	0	not significant
6558	GO_CUL4A_RING_E3_UBIQUITIN_LIGASE_COMPLEX	0.73	0.09	0	0	0	not significant
6559	GO_MICROTUBULE_MINUS_END	0.73	0.09	0	0	0	not significant
6560	GO_NEGATIVE_REGULATION_OF_HISTONE_H3_K9_TRIMETHYLATION	0.73	0.09	0	0	0	not significant
6561	GO_NUCLEOTIDE_EXCISION_REPAIR_COMPLEX	0.73	0.09	0	0	0	not significant
6562	GO_PROTEIN_KINASE_A_SIGNALING	0.73	0.09	0	0	0	not significant
6563	GO_PROTEIN_LOCALIZATION_TO_ENDOSOME	0.73	0.09	0	0	0	not significant
6564	GO_REGULATION_OF_PROTEIN_K63_LINKED_UBIQUITINATION	0.73	0.09	0	0	0	not significant
6565	GO_REGULATION_OF_VITAMIN_METABOLIC_PROCESS	0.73	0.09	0	0	0	not significant
6566	GO_UBIQUITIN_LIKE_MODIFIER_ACTIVATING_ENZYME_ACTIVITY	0.73	0.09	0	0	0	not significant
6567	CHR12Q14	0.73	0.08	0	0	0	not significant
6568	GO_BETA_CATENIN_DESTRUCTION_COMPLEX_DISASSEMBLY	0.73	0.08	0	0	0	not significant
6569	GO_DETERMINATION_OF_ADULT_LIFESPAN	0.73	0.08	0	0	0	not significant
6570	GO_PHOTORECEPTOR_CONNECTING_CILIUM	0.73	0.08	0	0	0	not significant
6571	GO_POSITIVE_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	0.73	0.08	0	0	0	not significant
6572	GO_PROTEIN_SERINE_THREONINE_KINASE_INHIBITOR_ACTIVITY	0.73	0.08	0	0	0	not significant
6573	GO_QUATERNARY_AMMONIUM_GROUP_BINDING	0.73	0.08	0	0	0	not significant
6574	JIANG_AGING_CEREBRAL_CORTEX_UP	0.73	0.08	0	0	0	not significant
6575	PID_EPHA2_FWD_PATHWAY	0.73	0.08	0	0	0	not significant
6576	REACTOME_ADVANCED_GLYCOSYLATION_ENDPRODUCT_RECEPTOR_SIGNALING	0.73	0.08	0	0	0	not significant
6577	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	0.73	0.08	0	0	0	not significant
6578	REACTOME_SYNTHESIS_OF_IP3_AND_IP4_IN_THE_CYTOSOL	0.73	0.08	0	0	0	not significant
6579	REACTOME_TRANSCRIPTION_OF_E2F_TARGETS_UNDER_NEGATIVE_CONTROL_BY	0.73	0.08	0	0	0	not significant
6580	DIRMEIER_LMP1_RESPONSE_LATE_DN	0.73	0.07	0	0	0	not significant
6581	GO_CEREBRAL_CORTEX_CELL_MIGRATION	0.73	0.07	0	0	0	not significant
6582	GO_POSTSYNAPTIC_DENSITY_MEMBRANE	0.73	0.07	0	0	0	not significant
6583	GO_REGULATION_OF_VACUOLE_ORGANIZATION	0.73	0.07	0	0	0	not significant
6584	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	0.73	0.07	0	0	0	not significant
6585	GO_VENTRICULAR_SEPTUM_DEVELOPMENT	0.73	0.07	0	0	0	not significant
6586	GO_VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	0.73	0.07	0	0	0	not significant
6587	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION	0.73	0.07	0	0	0	not significant
6588	RIGGINS_TAMOXIFEN_RESISTANCE_UP	0.73	0.07	0	0	0	not significant
6589	CHR18P11	0.73	0.06	0	0	0	not significant
6590	GO_MITOCHONDRIAL_FISSION	0.73	0.06	0	0	0	not significant
6591	GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	0.73	0.06	0	0	0	not significant
6592	GO_TRICARBOXYLIC_ACID_CYCLE	0.73	0.06	0	0	0	not significant
6593	BROWNE_HCMV_INFECTION_20HR_DN	0.73	0.05	0	0	0	not significant
6594	GO_MYELOID_CELL_DEVELOPMENT	0.73	0.05	0	0	0	not significant
6595	GO_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	0.73	0.05	0	0	0	not significant
6596	GO_SEQUESTERING_OF_CALCIUM_ION	0.73	0.04	0	0	0	not significant
6597	PID_MET_PATHWAY	0.73	0.04	0	0	0	not significant
6598	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_UP	0.73	0.03	0	0	0	not significant
6599	GO_CARDIAC_SEPTUM_DEVELOPMENT	0.73	0.03	0	0	0	not significant
6600	GO_CARTILAGE_DEVELOPMENT	0.73	0.03	0	0	0	not significant
6601	GO_TRANSITION_METAL_ION_TRANSPORT	0.73	0.03	0	0	0	not significant
6602	REACTOME_MUSCLE_CONTRACTION	0.73	0.03	0	0	0	not significant
6603	GO_RAS_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	0.73	0.02	0	0	0	not significant
6604	GO_ACTIN_FILAMENT_POLYMERIZATION	0.73	0.01	0	0	0	not significant
6605	GO_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	0.73	0.01	0	0	0	not significant
6606	GO_INOSITOL_TRISPHOSPHATE_PHOSPHATASE_ACTIVITY	0.74	0.12	0	0	0	not significant
6607	GO_VESICLE_UNCOATING	0.74	0.12	0	0	0	not significant
6608	GO_FILOPODIUM_TIP	0.74	0.11	0	0	0	not significant
6609	GO_HISTONE_METHYLTRANSFERASE_ACTIVITY_H3_K9_SPECIFIC_	0.74	0.11	0	0	0	not significant
6610	GO_NADP_RETINOL_DEHYDROGENASE_ACTIVITY	0.74	0.11	0	0	0	not significant
6611	GO_NODAL_SIGNALING_PATHWAY	0.74	0.11	0	0	0	not significant
6612	GO_REGULATION_OF_CYTOPLASMIC_TRANSLATIONAL_INITIATION	0.74	0.11	0	0	0	not significant
6613	GO_REGULATION_OF_PROTEIN_GLYCOSYLATION	0.74	0.11	0	0	0	not significant
6614	BIOCARTA_CTLA4_PATHWAY	0.74	0.1	0	0	0	not significant
6615	CHR19Q12	0.74	0.1	0	0	0	not significant
6616	GO_CATECHOLAMINE_SECRETION	0.74	0.1	0	0	0	not significant
6617	GO_DEATH_INDUCING_SIGNALING_COMPLEX_ASSEMBLY	0.74	0.1	0	0	0	not significant
6618	GO_HISTONE_DEMETHYLASE_ACTIVITY_H3_K9_SPECIFIC_	0.74	0.1	0	0	0	not significant
6619	GO_NEURONAL_ION_CHANNEL_CLUSTERING	0.74	0.1	0	0	0	not significant
6620	GO_NPBAF_COMPLEX	0.74	0.1	0	0	0	not significant
6621	GO_REGULATION_OF_METALLOENDOPEPTIDASE_ACTIVITY	0.74	0.1	0	0	0	not significant
6622	REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	0.74	0.1	0	0	0	not significant
6623	GO_COLLECTING_DUCT_DEVELOPMENT	0.74	0.09	0	0	0	not significant
6624	GO_ENERGY_HOMEOSTASIS	0.74	0.09	0	0	0	not significant
6625	GO_ENTEROENDOCRINE_CELL_DIFFERENTIATION	0.74	0.09	0	0	0	not significant
6626	GO_INACTIVATION_OF_MAPK_ACTIVITY	0.74	0.09	0	0	0	not significant
6627	GO_METALLOAMINOPEPTIDASE_ACTIVITY	0.74	0.09	0	0	0	not significant
6628	GO_MICROTUBULE_SEVERING	0.74	0.09	0	0	0	not significant
6629	GO_NAD_METABOLIC_PROCESS	0.74	0.09	0	0	0	not significant
6630	GO_NEGATIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFEREN	0.74	0.09	0	0	0	not significant
6631	GO_ORGANOPHOSPHATE_ESTER_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.74	0.09	0	0	0	not significant
6632	GO_REGULATION_OF_EARLY_ENDOSOME_TO_LATE_ENDOSOME_TRANSPORT	0.74	0.09	0	0	0	not significant
6633	HAHTOLA_MYCOSIS_FUNGOIDES_DN	0.74	0.09	0	0	0	not significant
6634	REACTOME_SUMOYLATION_OF_TRANSCRIPTION_FACTORS	0.74	0.09	0	0	0	not significant
6635	GO_NEGATIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS	0.74	0.08	0	0	0	not significant
6636	GO_RESPONSE_TO_X_RAY	0.74	0.08	0	0	0	not significant
6637	LEIN_LOCALIZED_TO_PROXIMAL_DENDRITES	0.74	0.08	0	0	0	not significant

6638	PID_ER_NONGENOMIC_PATHWAY	0.74	0.08	0	0	0	not significant
6639	REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM	0.74	0.08	0	0	0	not significant
6640	REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_O	0.74	0.08	0	0	0	not significant
6641	HEIDENBLAD_AMPLICON_8Q24_DN	0.74	0.07	0	0	0	not significant
6642	REACTOME_ECM_PROTEOGLYCANS	0.74	0.07	0	0	0	not significant
6643	WOOD_EBV_EBNA1_TARGETS_DN	0.74	0.07	0	0	0	not significant
6644	GO_KINASE_INHIBITOR_ACTIVITY	0.74	0.06	0	0	0	not significant
6645	GO_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	0.74	0.06	0	0	0	not significant
6646	GO_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	0.74	0.06	0	0	0	not significant
6647	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_PENTOSYL_GROUPS	0.74	0.06	0	0	0	not significant
6648	HEIDENBLAD_AMPLICON_8Q24_UP	0.74	0.06	0	0	0	not significant
6649	GO_POSITIVE_REGULATION_OF_PROTEIN_BINDING	0.74	0.05	0	0	0	not significant
6650	GO_MOTILE_CILIUM	0.74	0.04	0	0	0	not significant
6651	GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	0.74	0.04	0	0	0	not significant
6652	GO_NEGATIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION	0.74	0.03	0	0	0	not significant
6653	GO_UBIQUITIN_LIKE_PROTEIN_LIGASE_ACTIVITY	0.74	0.02	0	0	0	not significant
6654	GO_PROTEIN_TARGETING	0.74	0	0	0	0	not significant
6655	GO_AUDITORY_RECEPTOR_CELL_MORPHOGENESIS	0.75	0.13	0	0	0	not significant
6656	GO_ACTIN_POLYMERIZATION_DEPENDENT_CELL_MOTILITY	0.75	0.12	0	0	0	not significant
6657	GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_HEART_DEV	0.75	0.12	0	0	0	not significant
6658	GO_CLATHRIN_HEAVY_CHAIN_BINDING	0.75	0.12	0	0	0	not significant
6659	GO_REGULATION_OF_MICROTUBULE_NUCLEATION	0.75	0.12	0	0	0	not significant
6660	GO_RNA_POLYMERASE_III_TYPE_1_PROMOTER_DNA_BINDING	0.75	0.12	0	0	0	not significant
6661	IKEDA_MIR30_TARGETS_DN	0.75	0.12	0	0	0	not significant
6662	BUDHU_LIVER_CANCER_METASTASIS_UP	0.75	0.11	0	0	0	not significant
6663	FARMER_BREAST_CANCER_CLUSTER_4	0.75	0.11	0	0	0	not significant
6664	GO_CELL_DIFFERENTIATION_IN_HINDBRAIN	0.75	0.11	0	0	0	not significant
6665	GO_CHLORIDE_ION_BINDING	0.75	0.11	0	0	0	not significant
6666	GO_ENDOCARDIAL_CUSHION_MORPHOGENESIS	0.75	0.11	0	0	0	not significant
6667	GO_INTRACILIARY_TRANSPORT_PARTICLE_A	0.75	0.11	0	0	0	not significant
6668	GO_NEGATIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_CALCIUM_ION_CONC	0.75	0.11	0	0	0	not significant
6669	GO_NEGATIVE_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	0.75	0.11	0	0	0	not significant
6670	GO_REGULATION_OF_ANIMAL_ORGAN_FORMATION	0.75	0.11	0	0	0	not significant
6671	GO_REGULATION_OF_STEM_CELL_POPULATION_MAINTENANCE	0.75	0.11	0	0	0	not significant
6672	GO_TRANSLATIONAL_READTHROUGH	0.75	0.11	0	0	0	not significant
6673	GO_VESICLE_TETHERING	0.75	0.11	0	0	0	not significant
6674	REACTOME_CD209_DC_SIGN_SIGNALING	0.75	0.11	0	0	0	not significant
6675	REACTOME_CELLULAR_HEXOSE_TRANSPORT	0.75	0.11	0	0	0	not significant
6676	REACTOME_DOWNREGULATION_OF_ERBB2:ERBB3_SIGNALING	0.75	0.11	0	0	0	not significant
6677	REACTOME_TRIF_MEDIATED_PROGRAMMED_CELL_DEATH	0.75	0.11	0	0	0	not significant
6678	BIOCARTA_PRC2_PATHWAY	0.75	0.1	0	0	0	not significant
6679	BIOCARTA_PTEN_PATHWAY	0.75	0.1	0	0	0	not significant
6680	GO_AMINO_SUGAR_BIOSYNTHETIC_PROCESS	0.75	0.1	0	0	0	not significant
6681	GO_COLLAGEN_FIBRIL_ORGANIZATION	0.75	0.1	0	0	0	not significant
6682	GO_DEOXYRIBOSE_PHOSPHATE_BIOSYNTHETIC_PROCESS	0.75	0.1	0	0	0	not significant
6683	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_POSTSYNAPTIC_MEMBRAN	0.75	0.1	0	0	0	not significant
6684	GO_MESENCHYME_MORPHOGENESIS	0.75	0.1	0	0	0	not significant
6685	GO_MITOTIC_DNA_REPLICATION	0.75	0.1	0	0	0	not significant
6686	GO_RESPONSE_TO_ATP	0.75	0.1	0	0	0	not significant
6687	REACTOME_PHASE_0_RAPID_DEPOLARISATION	0.75	0.1	0	0	0	not significant
6688	CHR4P14	0.75	0.09	0	0	0	not significant
6689	GO_NCRNA_CATABOLIC_PROCESS	0.75	0.09	0	0	0	not significant
6690	GO_NUCLEOSIDE_SALVAGE	0.75	0.09	0	0	0	not significant
6691	GO_PHOSPHATIDIC_ACID_BIOSYNTHETIC_PROCESS	0.75	0.09	0	0	0	not significant
6692	GO_REGULATION_OF_NEUROBLAST_PROLIFERATION	0.75	0.09	0	0	0	not significant
6693	REACTOME_ELASTIC_FIBRE_FORMATION	0.75	0.09	0	0	0	not significant
6694	GO_G2_DNA_DAMAGE_CHECKPOINT	0.75	0.08	0	0	0	not significant
6695	GO_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.75	0.08	0	0	0	not significant
6696	GO_REGULATION_OF_LIPID_CATABOLIC_PROCESS	0.75	0.08	0	0	0	not significant
6697	GO_RESPONSE_TO_EPIDERMAL_GROWTH_FACTOR	0.75	0.08	0	0	0	not significant
6698	HUMMEL_BURKITTS_LYMPHOMA_UP	0.75	0.08	0	0	0	not significant
6699	MARTIN_VIRAL_GPCR_SIGNALING_DN	0.75	0.08	0	0	0	not significant
6700	REACTOME_REGULATION_OF_RUNX1_EXPRESSION_AND_ACTIVITY	0.75	0.08	0	0	0	not significant
6701	GO_MESODERM_MORPHOGENESIS	0.75	0.07	0	0	0	not significant
6702	GO_POSITIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	0.75	0.07	0	0	0	not significant
6703	GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSO	0.75	0.07	0	0	0	not significant
6704	CHR3P22	0.75	0.06	0	0	0	not significant
6705	PKCA_DN.V1_UP	0.75	0.06	0	0	0	not significant
6706	GO_HISTONE_METHYLTRANSFERASE_COMPLEX	0.75	0.04	0	0	0	not significant
6707	GO_MEMBRANE_FUSION	0.75	0.03	0	0	0	not significant
6708	REACTOME_G2_M_DNA_DAMAGE_CHECKPOINT	0.75	0.03	0	0	0	not significant
6709	CHR3P21	0.75	0.02	0	0	0	not significant
6710	GO_UBIQUITIN_LIKE_PROTEIN_TRANSFERASE_ACTIVITY	0.75	0.01	0	0	0	not significant
6711	GO_ANCHORING_JUNCTION	0.75	0	0	0	0	not significant
6712	GO_NEUROTRANSMITTER_RECEPTOR_LOCALIZATION_TO_POSTSYNAPTIC_SPECIA	0.76	0.14	0	0	0	not significant
6713	GO_CELLULAR_RESPONSE_TO_INCREASED_OXYGEN_LEVELS	0.76	0.13	0	0	0	not significant
6714	GO_REGULATION_OF_CILIUM_BEAT_FREQUENCY_INVOLVED_IN_CILIARY_MOTILITY	0.76	0.13	0	0	0	not significant
6715	GO_REGULATION_OF_PROTEIN_COMPLEX_STABILITY	0.76	0.13	0	0	0	not significant
6716	GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZATION	0.76	0.13	0	0	0	not significant
6717	PIEPOLI_LGI1_TARGETS_DN	0.76	0.13	0	0	0	not significant
6718	GO_C4_DICARBOXYLATE_TRANSPORT	0.76	0.12	0	0	0	not significant
6719	GO_CALCIUM_ION_REGULATED_EXOCYTOSIS_OF_NEUROTRANSMITTER	0.76	0.12	0	0	0	not significant
6720	GO_MULTI_ORGANISM_MEMBRANE_ORGANIZATION	0.76	0.12	0	0	0	not significant
6721	GO_POSITIVE_REGULATION_OF_STEROID_BIOSYNTHETIC_PROCESS	0.76	0.12	0	0	0	not significant
6722	GO_PRO_B_CELL_DIFFERENTIATION	0.76	0.12	0	0	0	not significant
6723	GO_REGULATION_OF_CARDIAC_MUSCLE_ADAPTATION	0.76	0.12	0	0	0	not significant
6724	GO_TELOMERE_LOCALIZATION	0.76	0.12	0	0	0	not significant
6725	MCGARVEY_SILENCED_BY_METHYLATION_IN_COLON_CANCER	0.76	0.12	0	0	0	not significant
6726	SHIRAISHI_PLZF_TARGETS_DN	0.76	0.12	0	0	0	not significant
6727	VANDESLUIS_COMMD1_TARGETS_GROUP_3_DN	0.76	0.12	0	0	0	not significant
6728	GO_C_TERMINAL_PROTEIN_AMINO_ACID_MODIFICATION	0.76	0.11	0	0	0	not significant
6729	GO_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX_CLASS_I	0.76	0.11	0	0	0	not significant
6730	GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTE	0.76	0.11	0	0	0	not significant
6731	GO_POSITIVE_REGULATION_OF_STEROID_METABOLIC_PROCESS	0.76	0.11	0	0	0	not significant
6732	GO_TRANSCRIPTION_COACTIVATOR_BINDING	0.76	0.11	0	0	0	not significant
6733	LI_ADIPOGENESIS_BY_ACTIVATED_PPARG	0.76	0.11	0	0	0	not significant
6734	MOOTHA_ROS	0.76	0.11	0	0	0	not significant
6735	REACTOME_DISEASES_OF_MISMATCH_REPAIR_MMR	0.76	0.11	0	0	0	not significant
6736	WONG_ENDMETRIUM_CANCER_DN	0.76	0.11	0	0	0	not significant
6737	BIOCARTA_ATM_PATHWAY	0.76	0.1	0	0	0	not significant
6738	GO_BRANCHED_CHAIN_AMINO_ACID_CATABOLIC_PROCESS	0.76	0.1	0	0	0	not significant
6739	GO_MICROTUBULE_ANCHORING	0.76	0.1	0	0	0	not significant
6740	GO_MODIFICATION_OF_SYNAPTIC_STRUCTURE	0.76	0.1	0	0	0	not significant
6741	GO_POSITIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	0.76	0.1	0	0	0	not significant
6742	KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	0.76	0.1	0	0	0	not significant
6743	PID_ARF_3PATHWAY	0.76	0.1	0	0	0	not significant
6744	REACTOME_AKT_PHOSPHORYLATES_TARGETS_IN_THE_CYTOSOL	0.76	0.1	0	0	0	not significant
6745	REACTOME_CD28_DEPENDENT_VAV1_PATHWAY	0.76	0.1	0	0	0	not significant
6746	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_THE_AP_2_TFAP2_FAMILY_OF_T	0.76	0.1	0	0	0	not significant

6747	DELASERNA_MYOD_TARGETS_DN	0.76	0.09	0	0	0	not significant
6748	GO_ENDOSOME_TRANSPORT_VIA_MULTIVESICULAR_BODY_SORTING_PATHWAY	0.76	0.09	0	0	0	not significant
6749	HASLINGER_B_CLL_WITH_CHROMOSOME_12_TRISOMY	0.76	0.09	0	0	0	not significant
6750	MATTIOLI_MULTIPLE_MYELOMA_WITH_14Q32_TRANSLOCATIONS	0.76	0.09	0	0	0	not significant
6751	REACTOME_INTERLEUKIN_10_SIGNALING	0.76	0.09	0	0	0	not significant
6752	GO_CENTRIOLE_ASSEMBLY	0.76	0.08	0	0	0	not significant
6753	GO_DEMETHYLASE_ACTIVITY	0.76	0.08	0	0	0	not significant
6754	GO_ENDODERM_FORMATION	0.76	0.08	0	0	0	not significant
6755	GO_SEX_CHROMOSOME	0.76	0.08	0	0	0	not significant
6756	CHR11P11	0.76	0.07	0	0	0	not significant
6757	GO_ACTIVATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_A	0.76	0.07	0	0	0	not significant
6758	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	0.76	0.07	0	0	0	not significant
6759	PID_TXA2PATHWAY	0.76	0.07	0	0	0	not significant
6760	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_UP	0.76	0.06	0	0	0	not significant
6761	GO_ACTIN_FILAMENT	0.76	0.06	0	0	0	not significant
6762	GO_SNARE_BINDING	0.76	0.05	0	0	0	not significant
6763	GO_CYTOSOLIC_CALCIUM_ION_TRANSPORT	0.76	0.04	0	0	0	not significant
6764	GO_SKIN_DEVELOPMENT	0.76	0.04	0	0	0	not significant
6765	KEGG_FOCAL_ADHESION	0.76	0.04	0	0	0	not significant
6766	GO_TISSUE_HOMEOSTASIS	0.76	0.03	0	0	0	not significant
6767	GO_PROTEIN_METHYLATION	0.76	0.02	0	0	0	not significant
6768	HOLLMANN_APOPTOSIS_VIA_CD40_UP	0.76	0.02	0	0	0	not significant
6769	ABBUD_LIF_SIGNALING_2_UP	0.77	0.13	0	0	0	not significant
6770	EHRLICH_ICF_SYNDROM_DN	0.77	0.13	0	0	0	not significant
6771	GO_AUDITORY_RECEPTOR_CELL_DEVELOPMENT	0.77	0.13	0	0	0	not significant
6772	GO_MULTI_ORGANISM_MEMBRANE_FUSION	0.77	0.13	0	0	0	not significant
6773	GO_REGULATION_OF_DENDRITIC_CELL_CHEMOTAXIS	0.77	0.13	0	0	0	not significant
6774	GO_REGULATION_OF_FATTY_ACID_BETA_OXIDATION	0.77	0.13	0	0	0	not significant
6775	GO_REGULATION_OF_HEART_RATE_BY_CHEMICAL_SIGNAL	0.77	0.13	0	0	0	not significant
6776	GO_REGULATION_OF_SYNAPTIC_VESICLE_ENDOCYTOSIS	0.77	0.13	0	0	0	not significant
6777	GO_SPHINGOSINE_N_ACYLTRANSFERASE_ACTIVITY	0.77	0.13	0	0	0	not significant
6778	GO_SURFACTANT_HOMEOSTASIS	0.77	0.13	0	0	0	not significant
6779	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_2_BINDING	0.77	0.13	0	0	0	not significant
6780	REACTOME_INTERLEUKIN_6_SIGNALING	0.77	0.13	0	0	0	not significant
6781	GO_AUDITORY_RECEPTOR_CELL_STEREOCILIUM_ORGANIZATION	0.77	0.12	0	0	0	not significant
6782	GO_DNA_N_GLYCOSYLASE_ACTIVITY	0.77	0.12	0	0	0	not significant
6783	GO_PEPTIDYL_PROLINE_4_DIOXYGENASE_ACTIVITY	0.77	0.12	0	0	0	not significant
6784	GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION_INVOLVED_IN_IMMUNE_RE	0.77	0.12	0	0	0	not significant
6785	GO_POSITIVE_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PA	0.77	0.12	0	0	0	not significant
6786	GO_REGULATION_OF_BILE_ACID_BIOSYNTHETIC_PROCESS	0.77	0.12	0	0	0	not significant
6787	GO_REGULATION_OF_CYTOPLASMIC_TRANSPORT	0.77	0.12	0	0	0	not significant
6788	GO_REPLACEMENT_OSSIFICATION	0.77	0.12	0	0	0	not significant
6789	GO_RNA_SURVEILLANCE	0.77	0.12	0	0	0	not significant
6790	KEGG_RETINOL_METABOLISM	0.77	0.12	0	0	0	not significant
6791	MAEKAWA_ATF2_TARGETS	0.77	0.12	0	0	0	not significant
6792	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_9	0.77	0.12	0	0	0	not significant
6793	STARK_BRAIN_22Q11_DELETION	0.77	0.12	0	0	0	not significant
6794	BIOCARTA_HER2_PATHWAY	0.77	0.11	0	0	0	not significant
6795	GO_LATE_ENDOSOME_TO_VACUOLE_TRANSPORT	0.77	0.11	0	0	0	not significant
6796	GO_LUNG_ALVEOLUS_DEVELOPMENT	0.77	0.11	0	0	0	not significant
6797	GO_MICROVILLUS_ORGANIZATION	0.77	0.11	0	0	0	not significant
6798	GO_OLIGODENDROCYTE_DEVELOPMENT	0.77	0.11	0	0	0	not significant
6799	GO_OLIGOSACCHARIDE_LIPID_INTERMEDIATE_BIOSYNTHETIC_PROCESS	0.77	0.11	0	0	0	not significant
6800	GO_PEROXISOME_FISSION	0.77	0.11	0	0	0	not significant
6801	GO_PHOSPHATIDYLGLYCEROL_ACYL_CHAIN_REMODELING	0.77	0.11	0	0	0	not significant
6802	GO_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	0.77	0.11	0	0	0	not significant
6803	GO_REGULATION_OF_HISTONE_H3_K9_METHYLATION	0.77	0.11	0	0	0	not significant
6804	GO_VASODILATION	0.77	0.11	0	0	0	not significant
6805	WANG_BARRETTS_ESOPHAGUS_DN	0.77	0.11	0	0	0	not significant
6806	BIOCARTA_CSK_PATHWAY	0.77	0.1	0	0	0	not significant
6807	GO_FAD_BINDING	0.77	0.1	0	0	0	not significant
6808	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	0.77	0.1	0	0	0	not significant
6809	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_LYSINE_ACETYLATION	0.77	0.1	0	0	0	not significant
6810	GO_POSITIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	0.77	0.1	0	0	0	not significant
6811	GO_PROLINE_RICH_REGION_BINDING	0.77	0.1	0	0	0	not significant
6812	GO_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATION	0.77	0.1	0	0	0	not significant
6813	GO_TRANS_GOLGI_NETWORK_TRANSPORT_VESICLE	0.77	0.1	0	0	0	not significant
6814	REACTOME_INSERTION_OF_TAIL_ANCHORED_PROTEINS_INTO_THE_ENDOPLASMIC	0.77	0.1	0	0	0	not significant
6815	REACTOME_THE_ROLE_OF_NEF_IN_HIV_1_REPLICATION_AND_DISEASE_PATHOGE	0.77	0.1	0	0	0	not significant
6816	SIG_IL4RECEPTOR_IN_B_LYPHOCYTES	0.77	0.1	0	0	0	not significant
6817	CHR9Q21	0.77	0.09	0	0	0	not significant
6818	GO_TERTIARY_GRANULE_MEMBRANE	0.77	0.09	0	0	0	not significant
6819	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.77	0.09	0	0	0	not significant
6820	CHRXQ28	0.77	0.08	0	0	0	not significant
6821	GO_NEGATIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFEREN	0.77	0.08	0	0	0	not significant
6822	GO_PROTEIN_TARGETING_TO_VACUOLE	0.77	0.08	0	0	0	not significant
6823	GO_RAC_GTPASE_BINDING	0.77	0.08	0	0	0	not significant
6824	GO_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	0.77	0.08	0	0	0	not significant
6825	KEGG_PPAR_SIGNALING_PATHWAY	0.77	0.08	0	0	0	not significant
6826	LIN_APC_TARGETS	0.77	0.08	0	0	0	not significant
6827	GO_CORTICAL_ACTIN_CYTOSKELETON	0.77	0.07	0	0	0	not significant
6828	KEGG_APOPTOSIS	0.77	0.07	0	0	0	not significant
6829	GO_CALCIUM_ION_TRANSMEMBRANE_IMPORT_INTO_CYTOSOL	0.77	0.06	0	0	0	not significant
6830	GO_CORTICAL_CYTOSKELETON	0.77	0.06	0	0	0	not significant
6831	GO_EPITHELIAL_CELL_DEVELOPMENT	0.77	0.06	0	0	0	not significant
6832	KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	0.77	0.06	0	0	0	not significant
6833	XU_GH1_AUTOCRINE_TARGETS_UP	0.77	0.05	0	0	0	not significant
6834	LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN	0.77	0.04	0	0	0	not significant
6835	GO_HEART_DEVELOPMENT	0.77	0.02	0	0	0	not significant
6836	GO_NUCLEOSIDE_TRIPHOSPHATASE_REGULATOR_ACTIVITY	0.77	0.01	0	0	0	not significant
6837	IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR	0.77	0.01	0	0	0	not significant
6838	GO_COENZYME_A_METABOLIC_PROCESS	0.78	0.14	0	0	0	not significant
6839	GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_BINDING	0.78	0.14	0	0	0	not significant
6840	GO_RNA_POLYMERASE_III_PREINITIATION_COMPLEX_ASSEMBLY	0.78	0.14	0	0	0	not significant
6841	GO_SUGAR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.78	0.14	0	0	0	not significant
6842	BIOCARTA_HSP27_PATHWAY	0.78	0.13	0	0	0	not significant
6843	GO_ATP_DEPENDENT_3_5_DNA_HELICASE_ACTIVITY	0.78	0.13	0	0	0	not significant
6844	GO_DENDRITE_MEMBRANE	0.78	0.13	0	0	0	not significant
6845	GO_MALE_SEX_DETERMINATION	0.78	0.13	0	0	0	not significant
6846	GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_P38_BINDING	0.78	0.13	0	0	0	not significant
6847	GO_POSITIVE_REGULATION_OF_MAMMARY_GLAND_EPITHELIAL_CELL_PROLIFERA	0.78	0.13	0	0	0	not significant
6848	GO_PYRIMIDINE_DIMER_REPAIR	0.78	0.13	0	0	0	not significant
6849	GO_REGULATION_OF_AMYLOID_PRECURSOR_PROTEIN_CATABOLIC_PROCESS	0.78	0.13	0	0	0	not significant
6850	GO_REGULATION_OF_NEUTROPHIL_ACTIVATION	0.78	0.13	0	0	0	not significant
6851	GO_RESPONSE_TO_DIETARY_EXCESS	0.78	0.13	0	0	0	not significant
6852	HAHTOLA_CTCL_CUTANEOUS	0.78	0.13	0	0	0	not significant
6853	REACTOME_FATTY_ACIDS_BOUND_TO_GPR40_FFAR1_REGULATE_INSULIN_SECRE	0.78	0.13	0	0	0	not significant
6854	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION_OF_SATURATED_FA	0.78	0.13	0	0	0	not significant
6855	WU_HBX_TARGETS_1_UP	0.78	0.13	0	0	0	not significant

6856	BIOCARTA_IL12_PATHWAY	0.78	0.12	0	0	0	not significant
6857	BIOCARTA_SHH_PATHWAY	0.78	0.12	0	0	0	not significant
6858	CORRE_MULTIPLE_MYELOMA_UP	0.78	0.12	0	0	0	not significant
6859	GO_DYNACTIN_COMPLEX	0.78	0.12	0	0	0	not significant
6860	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNAL	0.78	0.12	0	0	0	not significant
6861	GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	0.78	0.12	0	0	0	not significant
6862	GO_PROSTANOID_BIOSYNTHETIC_PROCESS	0.78	0.12	0	0	0	not significant
6863	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_IN_WS	0.78	0.12	0	0	0	not significant
6864	PARK_TRETINOIN_RESPONSE_AND_RARA_PLZF_FUSION	0.78	0.12	0	0	0	not significant
6865	REACTOME_ELEVATION_OF_CYTOSOLIC_CA2PLUS_LEVELS	0.78	0.12	0	0	0	not significant
6866	CHR7P15	0.78	0.11	0	0	0	not significant
6867	DAZARD_UV_RESPONSE_CLUSTER_G2	0.78	0.11	0	0	0	not significant
6868	FERRANDO_LYL1_NEIGHBORS	0.78	0.11	0	0	0	not significant
6869	GO_CELLULAR_RESPONSE_TO_ALKALOID	0.78	0.11	0	0	0	not significant
6870	GO_COPPER_ION_BINDING	0.78	0.11	0	0	0	not significant
6871	GO_PEROXISOMAL_MEMBRANE_TRANSPORT	0.78	0.11	0	0	0	not significant
6872	GO_PITUITARY_GLAND_DEVELOPMENT	0.78	0.11	0	0	0	not significant
6873	GO_PROTEIN_K48_LINKED_DEUBIQUITINATION	0.78	0.11	0	0	0	not significant
6874	GO_PYRIMIDINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	0.78	0.11	0	0	0	not significant
6875	MARIADASON_RESPONSE_TO_BUTYRATE_SULINDAC_4	0.78	0.11	0	0	0	not significant
6876	YANG_BREAST_CANCER_ESR1_BULK_UP	0.78	0.11	0	0	0	not significant
6877	CHR1Q31	0.78	0.1	0	0	0	not significant
6878	GO_ANTIBIOTIC_METABOLIC_PROCESS	0.78	0.1	0	0	0	not significant
6879	GO_PIGMENT_METABOLIC_PROCESS	0.78	0.1	0	0	0	not significant
6880	GO_PYRIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	0.78	0.1	0	0	0	not significant
6881	KUNINGER_IGF1_VS_PDGFB_TARGETS_DN	0.78	0.1	0	0	0	not significant
6882	CHR11Q23	0.78	0.09	0	0	0	not significant
6883	GO_PIGMENT_BIOSYNTHETIC_PROCESS	0.78	0.09	0	0	0	not significant
6884	GO_PLATELET_AGGREGATION	0.78	0.09	0	0	0	not significant
6885	GO_VESICLE_MEDIATED_TRANSPORT_BETWEEN_ENDOSOMAL_COMPARTMENTS	0.78	0.09	0	0	0	not significant
6886	LEE_CALORIE_RESTRICTION_NEOCORTEX_UP	0.78	0.09	0	0	0	not significant
6887	LINDSTEDT_DENDRITIC_CELL_MATURATION_D	0.78	0.09	0	0	0	not significant
6888	PETROVA_PROX1_TARGETS_DN	0.78	0.09	0	0	0	not significant
6889	REACTOME_ONCOGENE_INDUCED_SENESCENCE	0.78	0.09	0	0	0	not significant
6890	GO_FORMATION_OF_PRIMARY_GERM_LAYER	0.78	0.08	0	0	0	not significant
6891	GO_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	0.78	0.08	0	0	0	not significant
6892	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_C	0.78	0.08	0	0	0	not significant
6893	SASSON_RESPONSE_TO_GONADOTROPHINS_DN	0.78	0.08	0	0	0	not significant
6894	GO_LIPID_PHOSPHORYLATION	0.78	0.07	0	0	0	not significant
6895	GO_PROTEIN_DEPOLYMERIZATION	0.78	0.07	0	0	0	not significant
6896	GO_REGULATION_OF_SYNAPTIC_VESICLE_CYCLE	0.78	0.07	0	0	0	not significant
6897	GO_CYTOSOLIC_RIBOSOME	0.78	0.06	0	0	0	not significant
6898	GO_REGULATION_OF_VIRAL_LIFE_CYCLE	0.78	0.06	0	0	0	not significant
6899	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_DN	0.78	0.06	0	0	0	not significant
6900	GO_ACTIN_FILAMENT_ORGANIZATION	0.78	0.02	0	0	0	not significant
6901	YAGI_AML_WITH_INV_16_TRANSLOCATION	0.78	0.02	0	0	0	not significant
6902	GO_4_HYDROXYPROLINE_METABOLIC_PROCESS	0.79	0.15	0	0	0	not significant
6903	GO_ALPHA_BETA_T_CELL_RECEPTOR_COMPLEX	0.79	0.15	0	0	0	not significant
6904	GO_EPHRIN_RECEPTOR_ACTIVITY	0.79	0.15	0	0	0	not significant
6905	GO_NEGATIVE_REGULATION_OF_PROTEIN_KINASE_ACTIVITY_BY_REGULATION_OF	0.79	0.15	0	0	0	not significant
6906	GO_PEPTIDYL_PROLINE_HYDROXYLATION_TO_4_HYDROXY_L_PROLINE	0.79	0.15	0	0	0	not significant
6907	ISHIKAWA_STING_SIGNALING	0.79	0.15	0	0	0	not significant
6908	BIOCARTA_MTA3_PATHWAY	0.79	0.14	0	0	0	not significant
6909	FRIDMAN_SENESCENCE_DN	0.79	0.14	0	0	0	not significant
6910	GO_AORTA_MORPHOGENESIS	0.79	0.14	0	0	0	not significant
6911	GO_G1_TO_G0_TRANSITION	0.79	0.14	0	0	0	not significant
6912	GO_METANEPHRIC_COLLECTING_DUCT_DEVELOPMENT	0.79	0.14	0	0	0	not significant
6913	GO_MOTOR_BEHAVIOR	0.79	0.14	0	0	0	not significant
6914	GO_MUTLALPHA_COMPLEX	0.79	0.14	0	0	0	not significant
6915	GO_NEGATIVE_REGULATION_OF_PROTEIN_HOMOOLIGOMERIZATION	0.79	0.14	0	0	0	not significant
6916	GO_PHOSPHOLIPASE_BINDING	0.79	0.14	0	0	0	not significant
6917	GO_REGULATION_OF_CYTOLYSIS	0.79	0.14	0	0	0	not significant
6918	GO_REGULATION_OF_OVARIAN_FOLLICLE_DEVELOPMENT	0.79	0.14	0	0	0	not significant
6919	REACTOME_NEGATIVE_REGULATION_OF_NMDA_RECEPTOR_MEDIATED_NEURONA	0.79	0.14	0	0	0	not significant
6920	RICKMAN_HEAD_AND_NECK_CANCER_C	0.79	0.14	0	0	0	not significant
6921	RUNNE_GENDER_EFFECT_UP	0.79	0.14	0	0	0	not significant
6922	XU_AKT1_TARGETS_48HR	0.79	0.14	0	0	0	not significant
6923	BIOCARTA_RANBP2_PATHWAY	0.79	0.13	0	0	0	not significant
6924	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_DN	0.79	0.13	0	0	0	not significant
6925	CHR8P12	0.79	0.13	0	0	0	not significant
6926	GHO_ATF5_TARGETS_UP	0.79	0.13	0	0	0	not significant
6927	GO_C3HC4_TYPE_RING_FINGER_DOMAIN_BINDING	0.79	0.13	0	0	0	not significant
6928	GO_DIACYLGLYCEROL_BINDING	0.79	0.13	0	0	0	not significant
6929	GO_GOLGI_RIBBON_FORMATION	0.79	0.13	0	0	0	not significant
6930	GO_INTEGRIN_ACTIVATION	0.79	0.13	0	0	0	not significant
6931	GO_NEUROPEPTIDE_RECEPTOR_BINDING	0.79	0.13	0	0	0	not significant
6932	GO_PODOSOME_ASSEMBLY	0.79	0.13	0	0	0	not significant
6933	GO_SEX_CHROMATIN	0.79	0.13	0	0	0	not significant
6934	GO_U6_SNRNP	0.79	0.13	0	0	0	not significant
6935	GREENBAUM_E2A_TARGETS_DN	0.79	0.13	0	0	0	not significant
6936	KEGG_PRION_DISEASES	0.79	0.13	0	0	0	not significant
6937	LI_CISPLATIN_RESISTANCE_DN	0.79	0.13	0	0	0	not significant
6938	MANTOVANI_NFKB_TARGETS_UP	0.79	0.13	0	0	0	not significant
6939	MARKS_HDAC_TARGETS_DN	0.79	0.13	0	0	0	not significant
6940	REACTOME_NICOTINAMIDE_SALVAGING	0.79	0.13	0	0	0	not significant
6941	VALK_AML_CLUSTER_15	0.79	0.13	0	0	0	not significant
6942	WANG_NEOPLASTIC_TRANSFORMATION_BY_CCND1_MYC	0.79	0.13	0	0	0	not significant
6943	WELCH_GATA1_TARGETS	0.79	0.13	0	0	0	not significant
6944	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_24HR_UP	0.79	0.12	0	0	0	not significant
6945	BIOCARTA_ERK5_PATHWAY	0.79	0.12	0	0	0	not significant
6946	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_SCP2_QTL_TRANS	0.79	0.12	0	0	0	not significant
6947	GO_L_ASCORBIC_ACID_BINDING	0.79	0.12	0	0	0	not significant
6948	GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	0.79	0.12	0	0	0	not significant
6949	GO_POLYAMINE_METABOLIC_PROCESS	0.79	0.12	0	0	0	not significant
6950	GO_REGULATION_OF_CHROMATIN_SILENCING	0.79	0.12	0	0	0	not significant
6951	GO_REGULATION_OF_NON_CANONICAL_WNT_SIGNALING_PATHWAY	0.79	0.12	0	0	0	not significant
6952	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_DN	0.79	0.12	0	0	0	not significant
6953	KORKOLA_CORRELATED_WITH_POU5F1	0.79	0.12	0	0	0	not significant
6954	LIU_LIVER_CANCER	0.79	0.12	0	0	0	not significant
6955	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_CYTOC	0.79	0.12	0	0	0	not significant
6956	GO_FATTY_ACID_TRANSMEMBRANE_TRANSPORT	0.79	0.11	0	0	0	not significant
6957	GO_POSITIVE_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	0.79	0.11	0	0	0	not significant
6958	GO_REGULATION_OF_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABILIZATION_IN	0.79	0.11	0	0	0	not significant
6959	KAAB_FAILED_HEART_ATRIUM_UP	0.79	0.11	0	0	0	not significant
6960	KYNG_RESPONSE_TO_H2O2_VIA_ERCC6_DN	0.79	0.11	0	0	0	not significant
6961	GO_CYTOPLASMIC_MICROTUBULE_ORGANIZATION	0.79	0.1	0	0	0	not significant
6962	GO_MEMBRANE_DEPOLARIZATION	0.79	0.1	0	0	0	not significant
6963	GO_MULTI_ORGANISM_CELLULAR_PROCESS	0.79	0.1	0	0	0	not significant
6964	GO_POLY_PYRIMIDINE_TRACT_BINDING	0.79	0.1	0	0	0	not significant

6965	XU_HGF_TARGETS_REPRESSED_BY_AKT1_DN	0.79	0.1	0	0	0	not significant
6966	GUO_HEX_TARGETS_UP	0.79	0.09	0	0	0	not significant
6967	GO_DETECTION_OF_ABIOTIC_STIMULUS	0.79	0.08	0	0	0	not significant
6968	GO_DNA_MODIFICATION	0.79	0.08	0	0	0	not significant
6969	ROESSLER_LIVER_CANCER_METASTASIS_UP	0.79	0.08	0	0	0	not significant
6970	REACTOME_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR_GG_NER	0.79	0.07	0	0	0	not significant
6971	IVANOVA_HEMATOPOIESIS_STEM_CELL_LONG_TERM	0.79	0.06	0	0	0	not significant
6972	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	0.79	0.05	0	0	0	not significant
6973	GO_EPITHELIAL_TUBE_MORPHOGENESIS	0.79	0.04	0	0	0	not significant
6974	GO_REGULATION_OF_TRANS_SYNAPTIC_SIGNALING	0.79	0.04	0	0	0	not significant
6975	GO_MUSCLE_SYSTEM_PROCESS	0.79	0.03	0	0	0	not significant
6976	GO_PROTEIN_ACYLATION	0.79	0.03	0	0	0	not significant
6977	GO_EMBRYONIC_MORPHOGENESIS	0.79	0.02	0	0	0	not significant
6978	GO_VESICLE_ORGANIZATION	0.79	0.02	0	0	0	not significant
6979	GO_PROTEIN_LOCALIZATION_TO_MEMBRANE	0.79	0.01	0	0	0	not significant
6980	CHR2Q34	0.80	0.16	0	0	0	not significant
6981	GO_COPPER_ION_TRANSMEMBRANE_TRANSPORT	0.80	0.16	0	0	0	not significant
6982	GO_LIPOXYGENASE_PATHWAY	0.80	0.16	0	0	0	not significant
6983	REACTOME_SYNTHESIS_OF_DOLICHYL_PHOSPHATE	0.80	0.16	0	0	0	not significant
6984	CHR7P11	0.80	0.15	0	0	0	not significant
6985	GHANDHI_BYSTANDER_IRRADIATION_DN	0.80	0.15	0	0	0	not significant
6986	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTOF	0.80	0.15	0	0	0	not significant
6987	GO_POSITIVE_REGULATION_OF_PROTEIN_POLYUBIQUITINATION	0.80	0.15	0	0	0	not significant
6988	GO_PROTEIN_PHOSPHATASE_TYPE_1_COMPLEX	0.80	0.15	0	0	0	not significant
6989	GO_REGULATION_OF_NUCLEAR_CELL_CYCLE_DNA_REPLICATION	0.80	0.15	0	0	0	not significant
6990	GO_SORTING_ENDOSOME	0.80	0.15	0	0	0	not significant
6991	GO_TRIGLYCERIDE_CATABOLIC_PROCESS	0.80	0.15	0	0	0	not significant
6992	GO_VERY_LONG_CHAIN_FATTY_ACID_COA_LIGASE_ACTIVITY	0.80	0.15	0	0	0	not significant
6993	HOLLEMAN_DAUNORUBICIN_ALL_UP	0.80	0.15	0	0	0	not significant
6994	LE_SKI_TARGETS_UP	0.80	0.15	0	0	0	not significant
6995	NIKOLSKY_BREAST_CANCER_6P24_P22_AMPLICON	0.80	0.15	0	0	0	not significant
6996	REACTOME_HEME_BIOSYNTHESIS	0.80	0.15	0	0	0	not significant
6997	YANG_MUC2_TARGETS_DUODENUM_3MO_DN	0.80	0.15	0	0	0	not significant
6998	GO_CHONDROCYTE_DEVELOPMENT_INVOLVED_IN_ENDOCHONDRAL_BONE_MORP	0.80	0.14	0	0	0	not significant
6999	GO_DIAPEDESIS	0.80	0.14	0	0	0	not significant
7000	GO_EQUATORIAL_MICROTUBULE_ORGANIZING_CENTER	0.80	0.14	0	0	0	not significant
7001	GO_NEGATIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PR	0.80	0.14	0	0	0	not significant
7002	GO_PALMITOYLTRANSFERASE_COMPLEX	0.80	0.14	0	0	0	not significant
7003	GO_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	0.80	0.14	0	0	0	not significant
7004	GO_RETINAL_ROD_CELL_DEVELOPMENT	0.80	0.14	0	0	0	not significant
7005	GO_T_CELL_RECEPTOR_COMPLEX	0.80	0.14	0	0	0	not significant
7006	REACTOME_POST_TRANSCRIPTIONAL_SILENCING_BY_SMALL_RNAS	0.80	0.14	0	0	0	not significant
7007	REACTOME_SIGNALING_BY_BMP	0.80	0.14	0	0	0	not significant
7008	WORSCHECH_TUMOR_REJECTION_DN	0.80	0.14	0	0	0	not significant
7009	ZHENG_FOXP3_TARGETS_DN	0.80	0.14	0	0	0	not significant
7010	BREDEMEYER_RAG_SIGNALING_VIA_ATM_NOT_VIA_NFKB_DN	0.80	0.13	0	0	0	not significant
7011	GO_FUCOSE_METABOLIC_PROCESS	0.80	0.13	0	0	0	not significant
7012	GO_INNER_EAR_RECEPTOR_CELL_STEREOCILIUM_ORGANIZATION	0.80	0.13	0	0	0	not significant
7013	GO_INTERMEMBRANE_LIPID_TRANSFER	0.80	0.13	0	0	0	not significant
7014	GO_LONG_TERM_SYNAPTIC_DEPRESSION	0.80	0.13	0	0	0	not significant
7015	GO_MISMATCH_REPAIR_COMPLEX	0.80	0.13	0	0	0	not significant
7016	GO_NEGATIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	0.80	0.13	0	0	0	not significant
7017	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_	0.80	0.13	0	0	0	not significant
7018	GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BIOSYNTHETIC_PROCESS	0.80	0.13	0	0	0	not significant
7019	GO_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNALING_PATHW	0.80	0.13	0	0	0	not significant
7020	GO_REGULATION_OF_T_CELL_TOLERANCE_INDUCTION	0.80	0.13	0	0	0	not significant
7021	GO_U1_SNRNP	0.80	0.13	0	0	0	not significant
7022	GO_ZYMOGEN_ACTIVATION	0.80	0.13	0	0	0	not significant
7023	PID_A6B1_A6B4_INTEGRIN_PATHWAY	0.80	0.13	0	0	0	not significant
7024	REACTOME_RUNX2_REGULATES_BONE_DEVELOPMENT	0.80	0.13	0	0	0	not significant
7025	REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	0.80	0.13	0	0	0	not significant
7026	REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING	0.80	0.13	0	0	0	not significant
7027	ZWANG_CLASS_2_TRANSIENTLY_INDUCED_BY_EGF	0.80	0.13	0	0	0	not significant
7028	BECKER_TAMOXIFEN_RESISTANCE_DN	0.80	0.12	0	0	0	not significant
7029	CHEN_HOXA5_TARGETS_9HR_DN	0.80	0.12	0	0	0	not significant
7030	GO_MITOCHONDRIAL_GENOME_MAINTENANCE	0.80	0.12	0	0	0	not significant
7031	HU_GENOTOXIC_DAMAGE_24HR	0.80	0.12	0	0	0	not significant
7032	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN	0.80	0.12	0	0	0	not significant
7033	SU_PANCREAS	0.80	0.12	0	0	0	not significant
7034	YAMASHITA_LIVER_CANCER_STEM_CELL_DN	0.80	0.12	0	0	0	not significant
7035	BIOCARTA_ALK_PATHWAY	0.80	0.11	0	0	0	not significant
7036	GO_FILOPODIUM_ASSEMBLY	0.80	0.11	0	0	0	not significant
7037	REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	0.80	0.11	0	0	0	not significant
7038	REACTOME_PRC2_METHYLATES_HISTONES_AND_DNA	0.80	0.11	0	0	0	not significant
7039	REACTOME_TRANSPORT_OF_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_IONS_AN	0.80	0.11	0	0	0	not significant
7040	GO_NEGATIVE_REGULATION_OF_ION_TRANSPORT	0.80	0.1	0	0	0	not significant
7041	JAZAG_TGFB1_SIGNALING_UP	0.80	0.1	0	0	0	not significant
7042	LEE_LIVER_CANCER_MYC_TGFA_UP	0.80	0.1	0	0	0	not significant
7043	REACTOME_DISEASES_OF_METABOLISM	0.80	0.09	0	0	0	not significant
7044	GO_NEGATIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	0.80	0.08	0	0	0	not significant
7045	PKCA_DN.V1_DN	0.80	0.08	0	0	0	not significant
7046	PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_DN	0.80	0.08	0	0	0	not significant
7047	REACTOME_CHROMOSOME_MAINTENANCE	0.80	0.08	0	0	0	not significant
7048	SMID_BREAST_CANCER_LUMINAL_B_UP	0.80	0.08	0	0	0	not significant
7049	TIEN_INTESTINE_PROBIOTICS_2HR_DN	0.80	0.08	0	0	0	not significant
7050	MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_DN	0.80	0.07	0	0	0	not significant
7051	MULLIGHAN_NPM1_SIGNATURE_3_DN	0.80	0.07	0	0	0	not significant
7052	GAUSSMANN_MLL_AF4_FUSION_TARGETS_A_UP	0.80	0.06	0	0	0	not significant
7053	GO_APPENDAGE_DEVELOPMENT	0.80	0.06	0	0	0	not significant
7054	GO_REGULATION_OF_EXOCYTOSIS	0.80	0.06	0	0	0	not significant
7055	GO_RHO_GTPASE_BINDING	0.80	0.06	0	0	0	not significant
7056	NOUZOVA_TRETINOIN_AND_H4_ACETYLATION	0.80	0.06	0	0	0	not significant
7057	GO_REGULATION_OF_MACROAUTOPHAGY	0.80	0.05	0	0	0	not significant
7058	GO_SYNAPSE	0.80	0.01	0	0	0	not significant
7059	GO_POSITIVE_REGULATION_OF_VESICLE_FUSION	0.81	0.17	0	0	0	not significant
7060	FRASOR_TAMOXIFEN_RESPONSE_DN	0.81	0.16	0	0	0	not significant
7061	GO_AXIS_ELONGATION	0.81	0.16	0	0	0	not significant
7062	GO_LYSOSOMAL_PROTEIN_CATABOLIC_PROCESS	0.81	0.16	0	0	0	not significant
7063	GO_MAINTENANCE_OF_DNA_METHYLATION	0.81	0.16	0	0	0	not significant
7064	GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALIN	0.81	0.16	0	0	0	not significant
7065	GO_REGULATION_OF_EXTRACELLULAR_MATRIX_DISASSEMBLY	0.81	0.16	0	0	0	not significant
7066	MAGRANGEAS_MULTIPLE_MYELOMA_IGG_VS_IGA_UP	0.81	0.16	0	0	0	not significant
7067	SHIRAISHI_PLZF_TARGETS_UP	0.81	0.16	0	0	0	not significant
7068	TSUDA_ALVEOLAR_SOFT_PART_SARCOMA	0.81	0.16	0	0	0	not significant
7069	GO_AMYLOID_BETA_CLEARANCE_BY_TRANSCYTOSIS	0.81	0.15	0	0	0	not significant
7070	GO_CENTRIOLE_ELONGATION	0.81	0.15	0	0	0	not significant
7071	GO_CROSSOVER_JUNCTION_ENDODEOXYRIBONUCLEASE_ACTIVITY	0.81	0.15	0	0	0	not significant
7072	GO_DOLICHYL_DIPHOSPHATE_BIOSYNTHETIC_PROCESS	0.81	0.15	0	0	0	not significant
7073	GO_FRUCTOSE_6_PHOSPHATE_METABOLIC_PROCESS	0.81	0.15	0	0	0	not significant

7074	GO_GLUTAMATE_SECRETION	0.81	0.15	0	0	0	not significant
7075	GO_HINDBRAIN_RADIAL_GLIA_GUIDED_CELL_MIGRATION	0.81	0.15	0	0	0	not significant
7076	GO_JUN_KINASE_BINDING	0.81	0.15	0	0	0	not significant
7077	GO_MICROTUBULE_ANCHORING_AT_CENTROSOME	0.81	0.15	0	0	0	not significant
7078	GO_NUCLEOTIDASE_ACTIVITY	0.81	0.15	0	0	0	not significant
7079	REACTOME_SOS_MEDIATED_SIGNALLING	0.81	0.15	0	0	0	not significant
7080	REACTOME_SUMO_IS_TRANSFERRED_FROM_E1_TO_E2_UBE2I_UBC9	0.81	0.15	0	0	0	not significant
7081	REACTOME_SYNTHESIS_OF_5_EICOSATETRAENOIC_ACIDS	0.81	0.15	0	0	0	not significant
7082	SESTO_RESPONSE_TO_UV_C4	0.81	0.15	0	0	0	not significant
7083	TCGA_GLIOBLASTOMA_MUTATED	0.81	0.15	0	0	0	not significant
7084	CHR2P16	0.81	0.14	0	0	0	not significant
7085	GO_EYE_PHOTORECEPTOR_CELL_DEVELOPMENT	0.81	0.14	0	0	0	not significant
7086	GO_MISMATCHED_DNA_BINDING	0.81	0.14	0	0	0	not significant
7087	GO_NEGATIVE_REGULATION_OF_MYOSIN_LIGHT_CHAIN_PHOSPHATASE_ACTIVITY	0.81	0.14	0	0	0	not significant
7088	GO_POSITIVE_REGULATION_OF_FILOPODIUM_ASSEMBLY	0.81	0.14	0	0	0	not significant
7089	GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RE	0.81	0.14	0	0	0	not significant
7090	GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	0.81	0.14	0	0	0	not significant
7091	GO_REGULATION_OF_MAST_CELL_ACTIVATION	0.81	0.14	0	0	0	not significant
7092	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS	0.81	0.14	0	0	0	not significant
7093	HALLMARK_ANGIOGENESIS	0.81	0.14	0	0	0	not significant
7094	HENDRICKS_SMARCA4_TARGETS_DN	0.81	0.14	0	0	0	not significant
7095	MIZUSHIMA_AUTOPHAGOSOME_FORMATION	0.81	0.14	0	0	0	not significant
7096	ONGUSAHA_BRCA1_TARGETS_UP	0.81	0.14	0	0	0	not significant
7097	REACTOME_GDP_FUCOSE_BIOSYNTHESIS	0.81	0.14	0	0	0	not significant
7098	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_3	0.81	0.14	0	0	0	not significant
7099	BOYLAN_MULTIPLE_MYELOMA_D_CLUSTER_UP	0.81	0.13	0	0	0	not significant
7100	CHR1Q24	0.81	0.13	0	0	0	not significant
7101	GO_CELL_MIGRATION_IN_HINDBRAIN	0.81	0.13	0	0	0	not significant
7102	GO_ENDOCRINE_HORMONE_SECRETION	0.81	0.13	0	0	0	not significant
7103	GO_O_GLYCAN_PROCESSING	0.81	0.13	0	0	0	not significant
7104	GO_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	0.81	0.13	0	0	0	not significant
7105	STEARMAN_LUNG_CANCER_EARLY_VS_LATE_DN	0.81	0.13	0	0	0	not significant
7106	GO_MULTIVESICULAR_BODY_SORTING_PATHWAY	0.81	0.12	0	0	0	not significant
7107	GO_NEGATIVE_REGULATION_OF_HISTONE_MODIFICATION	0.81	0.12	0	0	0	not significant
7108	GO_SH3_SH2_ADAPTOR_ACTIVITY	0.81	0.12	0	0	0	not significant
7109	KENNY_CTNNB1_TARGETS_DN	0.81	0.12	0	0	0	not significant
7110	REACTOME_LYSOSOME_VESICLE_BIOGENESIS	0.81	0.12	0	0	0	not significant
7111	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM5	0.81	0.12	0	0	0	not significant
7112	WOO_LIVER_CANCER_RECURRENCE_DN	0.81	0.12	0	0	0	not significant
7113	GO_IRON_ION_TRANSPORT	0.81	0.11	0	0	0	not significant
7114	GO_RECEPTOR_TYROSINE_KINASE_BINDING	0.81	0.11	0	0	0	not significant
7115	GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL	0.81	0.11	0	0	0	not significant
7116	GO_SYNTAXIN_BINDING	0.81	0.11	0	0	0	not significant
7117	HEDENFALK_BREAST_CANCER_HEREDITARY_VS_SPORADIC	0.81	0.11	0	0	0	not significant
7118	KEGG_CARDIAC_MUSCLE_CONTRACTION	0.81	0.11	0	0	0	not significant
7119	KEGG_PANCREATIC_CANCER	0.81	0.11	0	0	0	not significant
7120	CHR10Q26	0.81	0.1	0	0	0	not significant
7121	GO_EXONUCLEASE_ACTIVITY	0.81	0.1	0	0	0	not significant
7122	KAYO_CALORIE_RESTRICTION_MUSCLE_DN	0.81	0.1	0	0	0	not significant
7123	KEGG_PEROXISOME	0.81	0.1	0	0	0	not significant
7124	GO_CILIARY_BASAL_BODY	0.81	0.09	0	0	0	not significant
7125	GO_NEGATIVE_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	0.81	0.09	0	0	0	not significant
7126	GO_POSITIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	0.81	0.09	0	0	0	not significant
7127	MORI_SMALL_PRE_BII_LYMPHOCYTE_DN	0.81	0.09	0	0	0	not significant
7128	GO_PIGMENT_GRANULE	0.81	0.08	0	0	0	not significant
7129	GO_ACTOMYOSIN_STRUCTURE_ORGANIZATION	0.81	0.07	0	0	0	not significant
7130	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP	0.81	0.07	0	0	0	not significant
7131	BONOME_OVARIAN_CANCER_SURVIVAL_OPTIMAL_DEBULKING	0.81	0.06	0	0	0	not significant
7132	RIGGINS_TAMOXIFEN_RESISTANCE_DN	0.81	0.06	0	0	0	not significant
7133	GO_SKELETAL_SYSTEM_DEVELOPMENT	0.81	0.05	0	0	0	not significant
7134	GO_POSITIVE_REGULATION_OF_CATABOLIC_PROCESS	0.81	0.03	0	0	0	not significant
7135	GO_POSTSYNAPSE	0.81	0.03	0	0	0	not significant
7136	GO_SENSORY_PERCEPTION_OF_SMELL	0.82	0.18	0	0	0	not significant
7137	CUI_TCF21_TARGETS_UP	0.82	0.17	0	0	0	not significant
7138	GO_CELLULAR_POTASSIUM_ION_HOMEOSTASIS	0.82	0.17	0	0	0	not significant
7139	GO_REGULATION_OF_DENDRITE_EXTENSION	0.82	0.17	0	0	0	not significant
7140	GO_SEMAPHORIN_RECEPTOR_ACTIVITY	0.82	0.17	0	0	0	not significant
7141	GO_UDP_N_ACETYLGLUCOSAMINE_BIOSYNTHETIC_PROCESS	0.82	0.17	0	0	0	not significant
7142	GO_CHEMOATTRACTANT_ACTIVITY	0.82	0.16	0	0	0	not significant
7143	GO_DOPAMINE_SECRETION	0.82	0.16	0	0	0	not significant
7144	GO_EXTRACELLULAR_MATRIX_ASSEMBLY	0.82	0.16	0	0	0	not significant
7145	GO_FAT_SOLUBLE_VITAMIN_BIOSYNTHETIC_PROCESS	0.82	0.16	0	0	0	not significant
7146	GO_INTERMEMBRANE_LIPID_TRANSFER_ACTIVITY	0.82	0.16	0	0	0	not significant
7147	GO_KERATAN_SULFATE_BIOSYNTHETIC_PROCESS	0.82	0.16	0	0	0	not significant
7148	GO_POSITIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	0.82	0.16	0	0	0	not significant
7149	GO_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY_INVOLVED_IN_NEURON_PROJECT	0.82	0.16	0	0	0	not significant
7150	GO_SWI_SNF_COMPLEX	0.82	0.16	0	0	0	not significant
7151	RICKMAN_HEAD_AND_NECK_CANCER_E	0.82	0.16	0	0	0	not significant
7152	YANG_MUC2_TARGETS_DUODENUM_6MO_DN	0.82	0.16	0	0	0	not significant
7153	BIOCARTA_BIOPEPTIDES_PATHWAY	0.82	0.15	0	0	0	not significant
7154	BIOCARTA_DICER_PATHWAY	0.82	0.15	0	0	0	not significant
7155	CHR18Q11	0.82	0.15	0	0	0	not significant
7156	CHR5Q21	0.82	0.15	0	0	0	not significant
7157	CROMER_TUMORIGENESIS_UP	0.82	0.15	0	0	0	not significant
7158	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_DN	0.82	0.15	0	0	0	not significant
7159	GO_HISTONE_H2A_MONOUBIQUITINATION	0.82	0.15	0	0	0	not significant
7160	GO_MIDBODY_ABSCISSION	0.82	0.15	0	0	0	not significant
7161	GO_RIG_I_SIGNALING_PATHWAY	0.82	0.15	0	0	0	not significant
7162	GO_WNT_SIGNALING_PATHWAY_CALCIUM_MODULATING_PATHWAY	0.82	0.15	0	0	0	not significant
7163	MEISSNER_ES_ICP_WITH_H3K4ME3	0.82	0.15	0	0	0	not significant
7164	OXFORD_RALA_OR_RALB_TARGETS_DN	0.82	0.15	0	0	0	not significant
7165	PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION	0.82	0.15	0	0	0	not significant
7166	REACTOME_P75NTR_REGULATES_AXONOGENESIS	0.82	0.15	0	0	0	not significant
7167	REACTOME_SYNTHESIS_OF_UDP_N_ACETYL_GLUCOSAMINE	0.82	0.15	0	0	0	not significant
7168	REACTOME_TRAF6_MEDIATED_NF_KB_ACTIVATION	0.82	0.15	0	0	0	not significant
7169	BIOCARTA_PPARA_PATHWAY	0.82	0.14	0	0	0	not significant
7170	BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN	0.82	0.14	0	0	0	not significant
7171	GO_HSP70_PROTEIN_BINDING	0.82	0.14	0	0	0	not significant
7172	GO_INTERLEUKIN_6_MEDIATED_SIGNALING_PATHWAY	0.82	0.14	0	0	0	not significant
7173	GO_MIRNA_MEDIATED_INHIBITION_OF_TRANSLATION	0.82	0.14	0	0	0	not significant
7174	GO_NUCLEOSIDE_METABOLIC_PROCESS	0.82	0.14	0	0	0	not significant
7175	GO_PROTON_EXPORTING_ATPASE_ACTIVITY	0.82	0.14	0	0	0	not significant
7176	GO_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	0.82	0.14	0	0	0	not significant
7177	KEGG_INOSITOL_PHOSPHATE_METABOLISM	0.82	0.14	0	0	0	not significant
7178	NIKOLSKY_BREAST_CANCER_20Q11_AMPLICON	0.82	0.14	0	0	0	not significant
7179	REACTOME_POTASSIUM_CHANNELS	0.82	0.14	0	0	0	not significant
7180	ENGELMANN_CANCER_PROGENITORS_DN	0.82	0.13	0	0	0	not significant
7181	GO_HISTONE_H3_ACETYLATION	0.82	0.13	0	0	0	not significant
7182	GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_INCISION	0.82	0.13	0	0	0	not significant

7183	GO_PRESYNAPTIC_ENDOCYTOSIS	0.82	0.13	0	0	0	not significant
7184	GO_TRANSCRIPTION_COFACTOR_BINDING	0.82	0.13	0	0	0	not significant
7185	SCIAN_INVERSED_TARGETS_OF_TP53_AND_TP73_DN	0.82	0.13	0	0	0	not significant
7186	BCAT_BILD_ET_AL_DN	0.82	0.12	0	0	0	not significant
7187	FONTAINE_PAPILLARY_THYROID_CARCINOMA_UP	0.82	0.12	0	0	0	not significant
7188	GOLUB_ALL_VS_AML_UP	0.82	0.12	0	0	0	not significant
7189	HOLLERN_EMT_BREAST_TUMOR_DN	0.82	0.12	0	0	0	not significant
7190	GO_CELL_DEATH_IN_RESPONSE_TO_OXIDATIVE_STRESS	0.82	0.11	0	0	0	not significant
7191	GO_ENDOCRINE_SYSTEM_DEVELOPMENT	0.82	0.11	0	0	0	not significant
7192	GO_EXECUTION_PHASE_OF_APOPTOSIS	0.82	0.11	0	0	0	not significant
7193	GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	0.82	0.11	0	0	0	not significant
7194	KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	0.82	0.11	0	0	0	not significant
7195	RB_P130_DN.V1_DN	0.82	0.1	0	0	0	not significant
7196	ZHANG_BREAST_CANCER_PROGENITORS_DN	0.82	0.1	0	0	0	not significant
7197	GO_NEURON_PROJECTION_EXTENSION	0.82	0.09	0	0	0	not significant
7198	GO_POSITIVE_REGULATION_OF_ION_TRANSPORT	0.82	0.09	0	0	0	not significant
7199	GO_TOR_SIGNALING	0.82	0.09	0	0	0	not significant
7200	HALLMARK_DNA_REPAIR	0.82	0.09	0	0	0	not significant
7201	GO_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	0.82	0.08	0	0	0	not significant
7202	PROVENZANI_METASTASIS_UP	0.82	0.08	0	0	0	not significant
7203	GO_POSITIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	0.82	0.05	0	0	0	not significant
7204	CONRAD_GERMLINE_STEM_CELL	0.83	0.18	0	0	0	not significant
7205	GO_REGULATION_OF_T_HELPER_17_TYPE_IMMUNE_RESPONSE	0.83	0.18	0	0	0	not significant
7206	REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	0.83	0.18	0	0	0	not significant
7207	GO_CAVEOLIN_MEDIATED_ENDOCYTOSIS	0.83	0.17	0	0	0	not significant
7208	GO_COLLAGEN_TRIMER	0.83	0.17	0	0	0	not significant
7209	GO_I_KAPPAB_PHOSPHORYLATION	0.83	0.17	0	0	0	not significant
7210	GO_LONG_CHAIN_FATTY_ACID_IMPORT_INTO_CELL	0.83	0.17	0	0	0	not significant
7211	GO_NEGATIVE_REGULATION_OF_HISTONE_ACETYLATION	0.83	0.17	0	0	0	not significant
7212	GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_BETA_SIGNALING_PATHW	0.83	0.17	0	0	0	not significant
7213	GO_PROTEIN_LIPID_COMPLEX_SUBUNIT_ORGANIZATION	0.83	0.17	0	0	0	not significant
7214	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM_EXIT_SITE	0.83	0.17	0	0	0	not significant
7215	GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	0.83	0.17	0	0	0	not significant
7216	GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	0.83	0.17	0	0	0	not significant
7217	PIONTEK_PKD1_TARGETS_UP	0.83	0.17	0	0	0	not significant
7218	REACTOME_FERTILIZATION	0.83	0.17	0	0	0	not significant
7219	REACTOME_KERATAN_SULFATE_BIOSYNTHESIS	0.83	0.17	0	0	0	not significant
7220	STEINER_ERYTHROCYTE_MEMBRANE_GENES	0.83	0.17	0	0	0	not significant
7221	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_24HR_DN	0.83	0.16	0	0	0	not significant
7222	BIOCARTA_CARM_ER_PATHWAY	0.83	0.16	0	0	0	not significant
7223	BIOCARTA_MITOCHONDRIA_PATHWAY	0.83	0.16	0	0	0	not significant
7224	BIOCARTA_RB_PATHWAY	0.83	0.16	0	0	0	not significant
7225	GO_COHESIN_COMPLEX	0.83	0.16	0	0	0	not significant
7226	GO_FIBROBLAST_GROWTH_FACTOR_BINDING	0.83	0.16	0	0	0	not significant
7227	GO_HEME_BIOSYNTHETIC_PROCESS	0.83	0.16	0	0	0	not significant
7228	GO_LSM2_8_COMPLEX	0.83	0.16	0	0	0	not significant
7229	GO_LYS63_SPECIFIC_DEUBIQUITINASE_ACTIVITY	0.83	0.16	0	0	0	not significant
7230	GO_NEGATIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	0.83	0.16	0	0	0	not significant
7231	GO_RECEPTOR_SERINE_THREONINE_KINASE_BINDING	0.83	0.16	0	0	0	not significant
7232	GO_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.83	0.16	0	0	0	not significant
7233	GO_REGULATION_OF_GOLGI_ORGANIZATION	0.83	0.16	0	0	0	not significant
7234	GO_SEMAPHORIN_RECEPTOR_COMPLEX	0.83	0.16	0	0	0	not significant
7235	GO_SMC5_SMC6_COMPLEX	0.83	0.16	0	0	0	not significant
7236	GO_VENOUS_BLOOD_VESSEL_MORPHOGENESIS	0.83	0.16	0	0	0	not significant
7237	GOLUB_ALL_VS_AML_DN	0.83	0.16	0	0	0	not significant
7238	KANG_AR_TARGETS_UP	0.83	0.16	0	0	0	not significant
7239	PARK_APL_PATHOGENESIS_UP	0.83	0.16	0	0	0	not significant
7240	REACTOME_PURINE_CATABOLISM	0.83	0.16	0	0	0	not significant
7241	BIOCARTA_PAR1_PATHWAY	0.83	0.15	0	0	0	not significant
7242	GO_CELL_FATE_SPECIFICATION	0.83	0.15	0	0	0	not significant
7243	GO_DNA_CATABOLIC_PROCESS_ENDONUCLEOLYTIC	0.83	0.15	0	0	0	not significant
7244	GO_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	0.83	0.15	0	0	0	not significant
7245	GO_RESPONSE_TO_INTERFERON_BETA	0.83	0.15	0	0	0	not significant
7246	GO_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	0.83	0.15	0	0	0	not significant
7247	KAAB_FAILED_HEART_VENTRICLE_DN	0.83	0.15	0	0	0	not significant
7248	KEGG_NOTCH_SIGNALING_PATHWAY	0.83	0.15	0	0	0	not significant
7249	REACTOME_SIGNALING_BY_HIPPO	0.83	0.15	0	0	0	not significant
7250	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM6	0.83	0.15	0	0	0	not significant
7251	XU_HGF_SIGNALING_NOT_VIA_AKT1_6HR	0.83	0.15	0	0	0	not significant
7252	ANDERSEN_LIVER_CANCER_KRT19_UP	0.83	0.14	0	0	0	not significant
7253	BREDEMEYER_RAG_SIGNALING_NOT_VIA_ATM_UP	0.83	0.14	0	0	0	not significant
7254	GO_CELL_CELL_ADHESION_MEDIATOR_ACTIVITY	0.83	0.14	0	0	0	not significant
7255	GO_NEGATIVE_REGULATION_OF_CHROMATIN_ORGANIZATION	0.83	0.14	0	0	0	not significant
7256	GO_NUCLEOBASE_CONTAINING_COMPOUND_KINASE_ACTIVITY	0.83	0.14	0	0	0	not significant
7257	GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	0.83	0.14	0	0	0	not significant
7258	GO_RESPONSE_TO_NICOTINE	0.83	0.14	0	0	0	not significant
7259	PID_CASPASE_PATHWAY	0.83	0.14	0	0	0	not significant
7260	REACTOME_G1_PHASE	0.83	0.14	0	0	0	not significant
7261	GO_ENERGY_RESERVE_METABOLIC_PROCESS	0.83	0.13	0	0	0	not significant
7262	GO_EXOCYTIC_PROCESS	0.83	0.13	0	0	0	not significant
7263	GO_GLYCOSYL_COMPOUND_METABOLIC_PROCESS	0.83	0.13	0	0	0	not significant
7264	GO_GRANULOCYTE_MIGRATION	0.83	0.13	0	0	0	not significant
7265	ZHONG_SECRETOME_OF_LUNG_CANCER_AND_MACROPHAGE	0.83	0.13	0	0	0	not significant
7266	GO_ACTIN_FILAMENT_BASED_MOVEMENT	0.83	0.12	0	0	0	not significant
7267	GO_MICROBODY_PART	0.83	0.12	0	0	0	not significant
7268	GO_NEGATIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	0.83	0.12	0	0	0	not significant
7269	PID_CMYB_PATHWAY	0.83	0.12	0	0	0	not significant
7270	CHR13Q14	0.83	0.11	0	0	0	not significant
7271	GO_CHROMATIN_ORGANIZATION_INVOLVED_IN_REGULATION_OF_TRANSCRIPTION	0.83	0.1	0	0	0	not significant
7272	KEGG_CALCIUM_SIGNALING_PATHWAY	0.83	0.1	0	0	0	not significant
7273	WATANABE_RECTAL_CANCER_RADIOTHERAPY_RESPONSIVE_UP	0.83	0.1	0	0	0	not significant
7274	ESC_V6.5_UP_EARLY.V1_UP	0.83	0.09	0	0	0	not significant
7275	GO_CELL_MATRIX_ADHESION	0.83	0.09	0	0	0	not significant
7276	GO_HISTONE_BINDING	0.83	0.08	0	0	0	not significant
7277	MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_UP	0.83	0.08	0	0	0	not significant
7278	GO_POSITIVE_REGULATION_OF_NEURON_DIFFERENTIATION	0.83	0.06	0	0	0	not significant
7279	GO_IN_UTERO_EMBRYONIC_DEVELOPMENT	0.83	0.05	0	0	0	not significant
7280	GO_SYNAPTIC_SIGNALING	0.83	0.05	0	0	0	not significant
7281	GO_CELL_PROJECTION_ASSEMBLY	0.83	0.04	0	0	0	not significant
7282	BIOCARTA_PGC1A_PATHWAY	0.84	0.19	0	0	0	not significant
7283	FERRARI_RESPONSE_TO_FENRETINIDE_UP	0.84	0.18	0	0	0	not significant
7284	GO_NADPH_BINDING	0.84	0.18	0	0	0	not significant
7285	GO_NEGATIVE_REGULATION_OF_MONOOXYGENASE_ACTIVITY	0.84	0.18	0	0	0	not significant
7286	GO_PHOSPHATIDYLGLYCEROL_BINDING	0.84	0.18	0	0	0	not significant
7287	GO_POSITIVE_REGULATION_OF_STEM_CELL_PROLIFERATION	0.84	0.18	0	0	0	not significant
7288	GO_REGULATION_OF_CYTOPLASMIC_MRNA_PROCESSING_BODY_ASSEMBLY	0.84	0.18	0	0	0	not significant
7289	GO_REGULATION_OF_TUBULIN_DEACETYLATION	0.84	0.18	0	0	0	not significant
7290	KALMA_E2F1_TARGETS	0.84	0.18	0	0	0	not significant
7291	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_DN	0.84	0.17	0	0	0	not significant

7292	GO_DNA_REPLICATION_FACTOR_A_COMPLEX	0.84	0.17	0	0	0	not significant
7293	GO_KERATAN_SULFATE_CATABOLIC_PROCESS	0.84	0.17	0	0	0	not significant
7294	GO_MHC_CLASS_II_BIOSYNTHETIC_PROCESS	0.84	0.17	0	0	0	not significant
7295	GO_NEGATIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	0.84	0.17	0	0	0	not significant
7296	GO_NEGATIVE_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATION	0.84	0.17	0	0	0	not significant
7297	GO_OMEGA_PEPTIDASE_ACTIVITY	0.84	0.17	0	0	0	not significant
7298	GO_POSITIVE_REGULATION_OF_MEIOTIC_CELL_CYCLE	0.84	0.17	0	0	0	not significant
7299	GO_POSITIVE_REGULATION_OF_NAD_P_H_OXIDASE_ACTIVITY	0.84	0.17	0	0	0	not significant
7300	GO_PRESYNAPTIC_ACTIVE_ZONE_CYTOPLASMIC_COMPONENT	0.84	0.17	0	0	0	not significant
7301	GO_REGULATION_OF_AMYLOID_BETA_FORMATION	0.84	0.17	0	0	0	not significant
7302	GO_RESPONSE_TO_ANGIOTENSIN	0.84	0.17	0	0	0	not significant
7303	GO_WNT_ACTIVATED_RECEPTOR_ACTIVITY	0.84	0.17	0	0	0	not significant
7304	NELSON_RESPONSE_TO_ANDROGEN_DN	0.84	0.17	0	0	0	not significant
7305	REACTOME_ATF4_ACTIVATES_GENES_IN_RESPONSE_TO_ENDOPLASMIC_RETICUL	0.84	0.17	0	0	0	not significant
7306	REACTOME_IRAK1_RECRUITS_IKK_COMPLEX	0.84	0.17	0	0	0	not significant
7307	BALLIF_DEVELOPMENTAL_DISABILITY_P16_P12_DELETION	0.84	0.16	0	0	0	not significant
7308	BIOCARTA_RACC_PATHWAY	0.84	0.16	0	0	0	not significant
7309	CHR11Q21	0.84	0.16	0	0	0	not significant
7310	GO_CALCIUM_DEPENDENT_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	0.84	0.16	0	0	0	not significant
7311	GO_CEREBRAL_CORTEX_RADIALLY_ORIENTED_CELL_MIGRATION	0.84	0.16	0	0	0	not significant
7312	GO_COLLAGEN_BIOSYNTHETIC_PROCESS	0.84	0.16	0	0	0	not significant
7313	GO_GALACTOSYLTRANSFERASE_ACTIVITY	0.84	0.16	0	0	0	not significant
7314	GO_POSITIVE_REGULATION_OF_LIGASE_ACTIVITY	0.84	0.16	0	0	0	not significant
7315	GO_PROTEIN_LIPID_COMPLEX_ASSEMBLY	0.84	0.16	0	0	0	not significant
7316	GO_REGULATION_OF_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	0.84	0.16	0	0	0	not significant
7317	GO_REGULATION_OF_NAD_P_H_OXIDASE_ACTIVITY	0.84	0.16	0	0	0	not significant
7318	GO_T_CELL_TOLERANCE_INDUCTION	0.84	0.16	0	0	0	not significant
7319	HOWLIN_CITED1_TARGETS_1_DN	0.84	0.16	0	0	0	not significant
7320	LUI_TARGETS_OF_PAX8_PPARG_FUSION	0.84	0.16	0	0	0	not significant
7321	REACTOME_REGULATION_OF_PTEN_MRNA_TRANSLATION	0.84	0.16	0	0	0	not significant
7322	REACTOME_TLR3_MEDIATED_TICAM1_DEPENDENT_PROGRAMMED_CELL_DEATH	0.84	0.16	0	0	0	not significant
7323	REICHERT_G1S_REGULATORS_AS_PI3K_TARGETS	0.84	0.16	0	0	0	not significant
7324	STANELLE_E2F1_TARGETS	0.84	0.16	0	0	0	not significant
7325	WANG_METASTASIS_OF_BREAST_CANCER_ESR1_DN	0.84	0.16	0	0	0	not significant
7326	CASTELLANO_NRAS_TARGETS_UP	0.84	0.15	0	0	0	not significant
7327	CHR11P12	0.84	0.15	0	0	0	not significant
7328	CHR3Q26	0.84	0.15	0	0	0	not significant
7329	FIGUEROA_AML_METHYLATION_CLUSTER_3_DN	0.84	0.15	0	0	0	not significant
7330	GO_CUL3_RING_UBIQUITIN_LIGASE_COMPLEX	0.84	0.15	0	0	0	not significant
7331	GO_METALLOEXOPEPTIDASE_ACTIVITY	0.84	0.15	0	0	0	not significant
7332	GO_MYOSIN_BINDING	0.84	0.15	0	0	0	not significant
7333	GO_PURINE_NUCLEOSIDE_METABOLIC_PROCESS	0.84	0.15	0	0	0	not significant
7334	GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	0.84	0.15	0	0	0	not significant
7335	GO_REGULATION_OF_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	0.84	0.15	0	0	0	not significant
7336	GO_REGULATION_OF_VIRAL_INDUCED_CYTOPLASMIC_PATTERN_RECOGNITION_RI	0.84	0.15	0	0	0	not significant
7337	LEE_AGING_CEREBELLUM_DN	0.84	0.15	0	0	0	not significant
7338	RASHI_RESPONSE_TO_IONIZING_RADIATION_3	0.84	0.15	0	0	0	not significant
7339	RIZ_ERYTHROID_DIFFERENTIATION_CCNE1	0.84	0.15	0	0	0	not significant
7340	RUAN_RESPONSE_TO_TNF_TROGLITAZONE_DN	0.84	0.15	0	0	0	not significant
7341	BHAT_ESR1_TARGETS_NOT_VIA_AKT1_DN	0.84	0.14	0	0	0	not significant
7342	GO_MOLTING_CYCLE_PROCESS	0.84	0.14	0	0	0	not significant
7343	GO_NEGATIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCT	0.84	0.14	0	0	0	not significant
7344	GO_NEUROMUSCULAR_PROCESS_CONTROLLING_BALANCE	0.84	0.14	0	0	0	not significant
7345	GO_NEURON_PROJECTION_ORGANIZATION	0.84	0.14	0	0	0	not significant
7346	REACTOME_DEFECTS_IN_VITAMIN_AND_COFACTOR_METABOLISM	0.84	0.14	0	0	0	not significant
7347	SONG_TARGETS_OF_IE86_CMV_PROTEIN	0.84	0.14	0	0	0	not significant
7348	GO_CELL_ADHESION_MEDIATED_BY_INTEGRIN	0.84	0.13	0	0	0	not significant
7349	GO_CELL_RECOGNITION	0.84	0.13	0	0	0	not significant
7350	QI_HYPOXIA_TARGETS_OF_HIF1A_AND_FOXA2	0.84	0.13	0	0	0	not significant
7351	GO_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNALING_PATHWAY	0.84	0.12	0	0	0	not significant
7352	GO_REGULATION_OF_VIRAL_GENOME_REPLICATION	0.84	0.12	0	0	0	not significant
7353	ASTON_MAJOR_DEPRESSIVE_DISORDER_DN	0.84	0.11	0	0	0	not significant
7354	GO_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	0.84	0.11	0	0	0	not significant
7355	GO_GASTRULATION	0.84	0.1	0	0	0	not significant
7356	GO_POSTSYNAPTIC_MEMBRANE	0.84	0.1	0	0	0	not significant
7357	GO_CELL_JUNCTION_ORGANIZATION	0.84	0.09	0	0	0	not significant
7358	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	0.84	0.09	0	0	0	not significant
7359	GO_REGULATION_OF_METAL_ION_TRANSPORT	0.84	0.09	0	0	0	not significant
7360	CHR1P36	0.84	0.07	0	0	0	not significant
7361	GO_VIRAL_LIFE_CYCLE	0.84	0.07	0	0	0	not significant
7362	TBK1.DF_UP	0.84	0.07	0	0	0	not significant
7363	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	0.84	0.06	0	0	0	not significant
7364	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP	0.84	0.03	0	0	0	not significant
7365	CHR13Q13	0.85	0.2	0	0	0	not significant
7366	REACTOME_KERATAN_SULFATE_DEGRADATION	0.85	0.2	0	0	0	not significant
7367	GO_NEGATIVE_REGULATION_OF_PROTEIN_FOLDING	0.85	0.19	0	0	0	not significant
7368	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS_D	0.85	0.19	0	0	0	not significant
7369	GO_POST_EMBRYONIC_CAMERA_TYPE_EYE_DEVELOPMENT	0.85	0.19	0	0	0	not significant
7370	GO_REGULATION_OF_PERK_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	0.85	0.19	0	0	0	not significant
7371	GO_RETINOL_METABOLIC_PROCESS	0.85	0.19	0	0	0	not significant
7372	CHR15Q23	0.85	0.18	0	0	0	not significant
7373	CHR16Q12	0.85	0.18	0	0	0	not significant
7374	CHR18Q22	0.85	0.18	0	0	0	not significant
7375	GO_APOPTOTIC_PROCESS_INVOLVED_IN_DEVELOPMENT	0.85	0.18	0	0	0	not significant
7376	GO_CYCLIN_DEPENDENT_PROTEIN_SERINE_THREONINE_KINASE_INHIBITOR_ACTIVI	0.85	0.18	0	0	0	not significant
7377	GO_HISTONE_H2A_ACETYLATION	0.85	0.18	0	0	0	not significant
7378	GO_NEGATIVE_REGULATION_OF_MICROTUBULE_DEPOLYMERIZATION	0.85	0.18	0	0	0	not significant
7379	GO_POSITIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_STRESS_INDUCED_INT	0.85	0.18	0	0	0	not significant
7380	GO_PROTEIN_INSERTION_INTO_MITOCHONDRIAL_MEMBRANE_INVOLVED_IN_APOPT	0.85	0.18	0	0	0	not significant
7381	GO_REGULATION_OF_EXTRACELLULAR_MATRIX_ASSEMBLY	0.85	0.18	0	0	0	not significant
7382	GO_RESPONSE_TO_COBALT_ION	0.85	0.18	0	0	0	not significant
7383	GO_SPERM_MIDPIECE	0.85	0.18	0	0	0	not significant
7384	GO_T_CELL_CHEMOTAXIS	0.85	0.18	0	0	0	not significant
7385	IWANAGA_E2F1_TARGETS_NOT_INDUCED_BY_SERUM	0.85	0.18	0	0	0	not significant
7386	JACKSON_DNMT1_TARGETS_DN	0.85	0.18	0	0	0	not significant
7387	REACTOME_DISPLACEMENT_OF_DNA_GLYCOSYLASE_BY_APEX1	0.85	0.18	0	0	0	not significant
7388	BIOCARTA_TOB1_PATHWAY	0.85	0.17	0	0	0	not significant
7389	GO_CALCIUM_CHANNEL_REGULATOR_ACTIVITY	0.85	0.17	0	0	0	not significant
7390	GO_CALCIUM_RELEASE_CHANNEL_ACTIVITY	0.85	0.17	0	0	0	not significant
7391	GO_DNA_POLYMERASE_BINDING	0.85	0.17	0	0	0	not significant
7392	GO_ENDOPLASMIC_RETICULUM_CHAPERONE_COMPLEX	0.85	0.17	0	0	0	not significant
7393	GO_HEPARAN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	0.85	0.17	0	0	0	not significant
7394	GO_K63_LINKED_POLYUBIQUITIN_MODIFICATION_DEPENDENT_PROTEIN_BINDING	0.85	0.17	0	0	0	not significant
7395	GO_MICROTUBULE_SEVERING_ATPASE_ACTIVITY	0.85	0.17	0	0	0	not significant
7396	GO_MITOCHONDRIAL_DEPOLARIZATION	0.85	0.17	0	0	0	not significant
7397	GO_NEGATIVE_REGULATION_OF_GLIAL_CELL_PROLIFERATION	0.85	0.17	0	0	0	not significant
7398	GO_NEGATIVE_REGULATION_OF_HISTONE_METHYLATION	0.85	0.17	0	0	0	not significant
7399	GO_NUCLEOTIDE_SUGAR_METABOLIC_PROCESS	0.85	0.17	0	0	0	not significant
7400	GO_REGULATION_OF_COLLAGEN_BIOSYNTHETIC_PROCESS	0.85	0.17	0	0	0	not significant

7401	GO_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	0.85	0.17	0	0	0	not significant
7402	GO_U1_SNRNA_BINDING	0.85	0.17	0	0	0	not significant
7403	HOLLERN_PAPILLARY_BREAST_TUMOR	0.85	0.17	0	0	0	not significant
7404	LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_SMALL_VS_HUGE_DN	0.85	0.17	0	0	0	not significant
7405	MA_PITUITARY_FETAL_VS_ADULT_UP	0.85	0.17	0	0	0	not significant
7406	MANTOVANI_VIRAL_GPCR_SIGNALING_DN	0.85	0.17	0	0	0	not significant
7407	GO_ACTIVE_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.85	0.16	0	0	0	not significant
7408	GO_G_PROTEIN_ALPHA_SUBUNIT_BINDING	0.85	0.16	0	0	0	not significant
7409	GO_LOW_DENSITY_LIPOPROTEIN_RECEPTOR_PARTICLE_METABOLIC_PROCESS	0.85	0.16	0	0	0	not significant
7410	GO_POLYAMINE_BIOSYNTHETIC_PROCESS	0.85	0.16	0	0	0	not significant
7411	GO_POSITIVE_REGULATION_OF_GLUCOSE_TRANSMEMBRANE_TRANSPORT	0.85	0.16	0	0	0	not significant
7412	GO_REGULATION_OF_VASCULAR_SMOOTH_MUSCLE_CELL_PROLIFERATION	0.85	0.16	0	0	0	not significant
7413	JIANG_HYPOXIA_VIA_VHL	0.85	0.16	0	0	0	not significant
7414	REACTOME_DAP12_INTERACTIONS	0.85	0.16	0	0	0	not significant
7415	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	0.85	0.16	0	0	0	not significant
7416	REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECULE	0.85	0.16	0	0	0	not significant
7417	YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP	0.85	0.16	0	0	0	not significant
7418	CHENG_IMPRINTED_BY_ESTRADIOL	0.85	0.15	0	0	0	not significant
7419	DELASERNA_MYOD_TARGETS_UP	0.85	0.15	0	0	0	not significant
7420	GO_CARDIAC_VENTRICLE_MORPHOGENESIS	0.85	0.15	0	0	0	not significant
7421	GO_GLAND_MORPHOGENESIS	0.85	0.15	0	0	0	not significant
7422	GO_POTASSIUM_CHANNEL_COMPLEX	0.85	0.15	0	0	0	not significant
7423	JIANG_TIP30_TARGETS_UP	0.85	0.15	0	0	0	not significant
7424	REACTOME_INTERLEUKIN_3_INTERLEUKIN_5_AND_GM_CSF_SIGNALING	0.85	0.15	0	0	0	not significant
7425	CHR4P16	0.85	0.14	0	0	0	not significant
7426	GO_MICROBODY_MEMBRANE	0.85	0.14	0	0	0	not significant
7427	GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	0.85	0.14	0	0	0	not significant
7428	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.85	0.14	0	0	0	not significant
7429	PRC2_SUZ12_UP.V1_DN	0.85	0.14	0	0	0	not significant
7430	GO_ERYTHROCYTE_HOMEOSTASIS	0.85	0.13	0	0	0	not significant
7431	GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MITOCH	0.85	0.13	0	0	0	not significant
7432	GO_NOTCH_SIGNALING_PATHWAY	0.85	0.12	0	0	0	not significant
7433	GO_ORGANELLE_FUSION	0.85	0.12	0	0	0	not significant
7434	GO_PROTEIN_KINASE_B_SIGNALING	0.85	0.11	0	0	0	not significant
7435	REACTOME_SELENOAMINO_ACID_METABOLISM	0.85	0.11	0	0	0	not significant
7436	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP	0.85	0.11	0	0	0	not significant
7437	GO_OUTER_MEMBRANE	0.85	0.1	0	0	0	not significant
7438	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP	0.85	0.09	0	0	0	not significant
7439	BROWNE_HCMV_INFECTION_4HR_DN	0.85	0.09	0	0	0	not significant
7440	IWANAGA_CARCINOGENESIS_BY_KRAS_PTEN_DN	0.85	0.09	0	0	0	not significant
7441	GO_NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	0.85	0.08	0	0	0	not significant
7442	UDAYAKUMAR_MED1_TARGETS_DN	0.85	0.08	0	0	0	not significant
7443	BAELDE_DIABETIC_NEPHROPATHY_DN	0.85	0.07	0	0	0	not significant
7444	GO_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	0.85	0.06	0	0	0	not significant
7445	HSIAO_HOUSEKEEPING_GENES	0.85	0.06	0	0	0	not significant
7446	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN	0.85	0.04	0	0	0	not significant
7447	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP	0.85	0.04	0	0	0	not significant
7448	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN	0.86	0.2	0	0	0	not significant
7449	COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_UP	0.86	0.2	0	0	0	not significant
7450	GO_POSITIVE_REGULATION_OF_MONOCYTE_CHEMOTAXIS	0.86	0.2	0	0	0	not significant
7451	GO_REGULATION_OF_LYSOSOMAL_PROTEIN_CATABOLIC_PROCESS	0.86	0.2	0	0	0	not significant
7452	BOYAULT_LIVER_CANCER_SUBCLASS_G2	0.86	0.19	0	0	0	not significant
7453	CHR1P21	0.86	0.19	0	0	0	not significant
7454	CLIMENT_BREAST_CANCER_COPY_NUMBER_UP	0.86	0.19	0	0	0	not significant
7455	GHANDHI_DIRECT_IRRADIATION_DN	0.86	0.19	0	0	0	not significant
7456	GO_CELLULAR_LIPID_BIOSYNTHETIC_PROCESS	0.86	0.19	0	0	0	not significant
7457	GO_CGMP_MEDIATED_SIGNALING	0.86	0.19	0	0	0	not significant
7458	GO_CHLORIDE_CHANNEL_REGULATOR_ACTIVITY	0.86	0.19	0	0	0	not significant
7459	GO_INWARD_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	0.86	0.19	0	0	0	not significant
7460	GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_MICROTUBULE	0.86	0.19	0	0	0	not significant
7461	GO_PHOSPHODIESTERASE_I_ACTIVITY	0.86	0.19	0	0	0	not significant
7462	GO_POTASSIUM_ION_IMPORT_ACROSS_PLASMA_MEMBRANE	0.86	0.19	0	0	0	not significant
7463	GO_PROTEIN_PHOSPHATASE_1_BINDING	0.86	0.19	0	0	0	not significant
7464	GO_PROTOPORPHYRINOGEN_IX_BIOSYNTHETIC_PROCESS	0.86	0.19	0	0	0	not significant
7465	GO_TROPHOBLAST_GIANT_CELL_DIFFERENTIATION	0.86	0.19	0	0	0	not significant
7466	KIM_LIVER_CANCER_POOR_SURVIVAL_DN	0.86	0.19	0	0	0	not significant
7467	LUI_THYROID_CANCER_CLUSTER_2	0.86	0.19	0	0	0	not significant
7468	PID_IL2_STAT5_PATHWAY	0.86	0.19	0	0	0	not significant
7469	WATANABE_COLON_CANCER_MSI_VS_MSS_DN	0.86	0.19	0	0	0	not significant
7470	ZIRN_TRETINOIN_RESPONSE_WT1_DN	0.86	0.19	0	0	0	not significant
7471	BYSTROEM_CORRELATED_WITH_IL5_UP	0.86	0.18	0	0	0	not significant
7472	CHEN_ETV5_TARGETS_TESTIS	0.86	0.18	0	0	0	not significant
7473	CROONQUIST_NRAS_SIGNALING_UP	0.86	0.18	0	0	0	not significant
7474	EINAV_INTERFERON_SIGNATURE_IN_CANCER	0.86	0.18	0	0	0	not significant
7475	ENGELMANN_CANCER_PROGENITORS_UP	0.86	0.18	0	0	0	not significant
7476	GO_ACTIVATION_OF_JANUS_KINASE_ACTIVITY	0.86	0.18	0	0	0	not significant
7477	GO_CERAMIDE_METABOLIC_PROCESS	0.86	0.18	0	0	0	not significant
7478	GO_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	0.86	0.18	0	0	0	not significant
7479	GO_L_GLUTAMATE_TRANSMEMBRANE_TRANSPORT	0.86	0.18	0	0	0	not significant
7480	GO_NEGATIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	0.86	0.18	0	0	0	not significant
7481	GO_NEGATIVE_REGULATION_OF_PLASMA_MEMBRANE_BOUNDED_CELL_PROJECT	0.86	0.18	0	0	0	not significant
7482	GO_PEPTIDYL_TYROSINE_AUTOPHOSPHORYLATION	0.86	0.18	0	0	0	not significant
7483	GO_POSITIVE_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	0.86	0.18	0	0	0	not significant
7484	GO_REGULATION_OF_B_CELL_APOPTOTIC_PROCESS	0.86	0.18	0	0	0	not significant
7485	GO_REGULATION_OF_POSTSYNAPTIC_SPECIALIZATION_ASSEMBLY	0.86	0.18	0	0	0	not significant
7486	GO_RESPONSE_TO_MISFOLDED_PROTEIN	0.86	0.18	0	0	0	not significant
7487	GO_TELOMERIC_LOOP_DISASSEMBLY	0.86	0.18	0	0	0	not significant
7488	GO_TRANSFERRIN_TRANSPORT	0.86	0.18	0	0	0	not significant
7489	KYNG_DNA_DAMAGE_BY_GAMMA_RADIATION	0.86	0.18	0	0	0	not significant
7490	PID_REELIN_PATHWAY	0.86	0.18	0	0	0	not significant
7491	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTYELLOW_UP	0.86	0.17	0	0	0	not significant
7492	GO_3_PHOSPHOADENOSINE_5_PHOSPHOSULFATE_BIOSYNTHETIC_PROCESS	0.86	0.17	0	0	0	not significant
7493	GO_ADIPONECTIN_ACTIVATED_SIGNALING_PATHWAY	0.86	0.17	0	0	0	not significant
7494	GO_AGGRESOME	0.86	0.17	0	0	0	not significant
7495	GO_MUCUS_SECRETION	0.86	0.17	0	0	0	not significant
7496	GO_REGULATION_OF_CAMP_MEDIATED_SIGNALING	0.86	0.17	0	0	0	not significant
7497	GO_REGULATION_OF_PROTEIN_TARGETING_TO_MITOCHONDRION	0.86	0.17	0	0	0	not significant
7498	ROESSLER_LIVER_CANCER_METASTASIS_DN	0.86	0.17	0	0	0	not significant
7499	GO_AMINE_TRANSPORT	0.86	0.16	0	0	0	not significant
7500	GO_CELLULAR_RESPONSE_TO_GLUCOSE_STARVATION	0.86	0.16	0	0	0	not significant
7501	GO_ENDOSOME_TO_LYSOSOME_TRANSPORT	0.86	0.16	0	0	0	not significant
7502	GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	0.86	0.16	0	0	0	not significant
7503	GO_REGULATION_OF_PROTEIN_ACETYLATION	0.86	0.16	0	0	0	not significant
7504	GO_SENSORY_PERCEPTION_OF_LIGHT_STIMULUS	0.86	0.16	0	0	0	not significant
7505	GO_SIGNALING_ADAPTOR_ACTIVITY	0.86	0.16	0	0	0	not significant
7506	GO_VOLTAGE_GATED_CATION_CHANNEL_ACTIVITY	0.86	0.16	0	0	0	not significant
7507	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT	0.86	0.16	0	0	0	not significant
7508	CHR4Q31	0.86	0.15	0	0	0	not significant
7509	GO_ORGANELLE_DISASSEMBLY	0.86	0.15	0	0	0	not significant

7510	GO_PROTEIN_LOCALIZATION_TO_SYNAPSE	0.86	0.15	0	0	0	not significant
7511	FIGUEROA_AML_METHYLATION_CLUSTER_4_UP	0.86	0.14	0	0	0	not significant
7512	GO_EXTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	0.86	0.14	0	0	0	not significant
7513	GO_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	0.86	0.14	0	0	0	not significant
7514	GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	0.86	0.13	0	0	0	not significant
7515	KIM_ALL_DISORDERS_DURATION_CORR_DN	0.86	0.13	0	0	0	not significant
7516	STEARMAN_LUNG_CANCER_EARLY_VS_LATE_UP	0.86	0.13	0	0	0	not significant
7517	GO_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	0.86	0.12	0	0	0	not significant
7518	GO_REGULATION_OF_CHROMATIN_ORGANIZATION	0.86	0.12	0	0	0	not significant
7519	GO_SEX_DIFFERENTIATION	0.86	0.12	0	0	0	not significant
7520	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_UP	0.86	0.11	0	0	0	not significant
7521	GO_NEURON_TO_NEURON_SYNAPSE	0.86	0.11	0	0	0	not significant
7522	GO_POSITIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	0.86	0.11	0	0	0	not significant
7523	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ACYL_GROUPS	0.86	0.11	0	0	0	not significant
7524	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER	0.86	0.11	0	0	0	not significant
7525	GO_POSITIVE_REGULATION_OF_GTPASE_ACTIVITY	0.86	0.1	0	0	0	not significant
7526	GRUETZMANN_PANCREATIC_CANCER_UP	0.86	0.1	0	0	0	not significant
7527	NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON	0.86	0.1	0	0	0	not significant
7528	GO_ENDOMEMBRANE_SYSTEM_ORGANIZATION	0.86	0.09	0	0	0	not significant
7529	RAO_BOUND_BY_SALL4_ISOFORM_B	0.86	0.09	0	0	0	not significant
7530	GO_NEGATIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS	0.86	0.08	0	0	0	not significant
7531	GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	0.86	0.08	0	0	0	not significant
7532	REACTOME_DNA_REPAIR	0.86	0.08	0	0	0	not significant
7533	GO_SYNAPSE_PART	0.86	0.07	0	0	0	not significant
7534	GO_DNA_REPAIR	0.86	0.06	0	0	0	not significant
7535	GO_CELL_PROJECTION_PART	0.86	0.04	0	0	0	not significant
7536	GO_CONNECTIVE_TISSUE_REPLACEMENT	0.87	0.21	0	0	0	not significant
7537	GO_G_QUADRUPLEX_DNA_UNWINDING	0.87	0.21	0	0	0	not significant
7538	GO_REGULATION_OF_LIGASE_ACTIVITY	0.87	0.21	0	0	0	not significant
7539	KUROKAWA_LIVER_CANCER_CHEMOTHERAPY_UP	0.87	0.21	0	0	0	not significant
7540	GO_AMINE_BIOSYNTHETIC_PROCESS	0.87	0.2	0	0	0	not significant
7541	GO_BLEB_ASSEMBLY	0.87	0.2	0	0	0	not significant
7542	GO_NAD_BIOSYNTHETIC_PROCESS	0.87	0.2	0	0	0	not significant
7543	GO_POSITIVE_REGULATION_OF_MESONEPHROS_DEVELOPMENT	0.87	0.2	0	0	0	not significant
7544	GO_POSITIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIAT	0.87	0.2	0	0	0	not significant
7545	GO_PYRIMIDINE_CONTAINING_COMPOUND_SALVAGE	0.87	0.2	0	0	0	not significant
7546	GO_REGULATION_OF_POSTSYNAPTIC_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	0.87	0.2	0	0	0	not significant
7547	GO_TRANS_GOLGI_NETWORK_TRANSPORT_VESICLE_MEMBRANE	0.87	0.2	0	0	0	not significant
7548	REACTOME_ACYL_CHAIN_REMODELLING_OF_PG	0.87	0.2	0	0	0	not significant
7549	REACTOME_APEX1_INDEPENDENT_RESOLUTION_OF_AP_SITES_VIA_THE_SINGLE_	0.87	0.2	0	0	0	not significant
7550	RIZ_ERYTHROID_DIFFERENTIATION_HEMGN	0.87	0.2	0	0	0	not significant
7551	SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_UP	0.87	0.2	0	0	0	not significant
7552	TOMLINS_METASTASIS_UP	0.87	0.2	0	0	0	not significant
7553	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN	0.87	0.2	0	0	0	not significant
7554	CLAUS_PGR_POSITIVE_MENINGIOMA_DN	0.87	0.19	0	0	0	not significant
7555	GO_BRCA1_A_COMPLEX	0.87	0.19	0	0	0	not significant
7556	GO_CYTOPLASMIC_SIDE_OF_ROUGH_ENDOPLASMIC_RETICULUM_MEMBRANE	0.87	0.19	0	0	0	not significant
7557	GO_LAGGING_STRAND_ELONGATION	0.87	0.19	0	0	0	not significant
7558	GO_PHARYNGEAL_SYSTEM_DEVELOPMENT	0.87	0.19	0	0	0	not significant
7559	GO_PIGMENT_GRANULE_LOCALIZATION	0.87	0.19	0	0	0	not significant
7560	GO_POSITIVE_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	0.87	0.19	0	0	0	not significant
7561	GO_PURINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	0.87	0.19	0	0	0	not significant
7562	GO_REGULATION_OF_BONE_REMODELING	0.87	0.19	0	0	0	not significant
7563	GO_REGULATION_OF_PROTEIN_POLYUBIQUITINATION	0.87	0.19	0	0	0	not significant
7564	GO_TOR_COMPLEX	0.87	0.19	0	0	0	not significant
7565	KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	0.87	0.19	0	0	0	not significant
7566	LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_DN	0.87	0.19	0	0	0	not significant
7567	PAL_PRMT5_TARGETS_DN	0.87	0.19	0	0	0	not significant
7568	RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_SMAD4_DN	0.87	0.19	0	0	0	not significant
7569	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	0.87	0.19	0	0	0	not significant
7570	ZHAN_MULTIPLE_MYELOMA_MS_DN	0.87	0.19	0	0	0	not significant
7571	ZHOU_TNF_SIGNALING_4HR	0.87	0.19	0	0	0	not significant
7572	GILDEA_METASTASIS	0.87	0.18	0	0	0	not significant
7573	GO_DRUG_CATABOLIC_PROCESS	0.87	0.18	0	0	0	not significant
7574	GO_ENDOCYTIC_RECYCLING	0.87	0.18	0	0	0	not significant
7575	GO_HEPARAN_SULFATE_SULFOTRANSFERASE_ACTIVITY	0.87	0.18	0	0	0	not significant
7576	GO_NEGATIVE_REGULATION_OF_UBIQUITIN_PROTEIN_TRANSFERASE_ACTIVITY	0.87	0.18	0	0	0	not significant
7577	GO_RESPONSE_TO_OXYGEN_RADICAL	0.87	0.18	0	0	0	not significant
7578	GO_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	0.87	0.18	0	0	0	not significant
7579	GO_X_CHROMOSOME	0.87	0.18	0	0	0	not significant
7580	KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	0.87	0.18	0	0	0	not significant
7581	KYNG_DNA_DAMAGE_BY_GAMMA_AND_UV_RADIATION	0.87	0.18	0	0	0	not significant
7582	LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_QTL	0.87	0.18	0	0	0	not significant
7583	PID_AR_TF_PATHWAY	0.87	0.18	0	0	0	not significant
7584	REACTOME_TRANSPORT_AND_SYNTHESIS_OF_PAPS	0.87	0.18	0	0	0	not significant
7585	GO_NEGATIVE_REGULATION_OF_METALLOPEPTIDASE_ACTIVITY	0.87	0.17	0	0	0	not significant
7586	GO_REGULATION_OF_VESICLE_FUSION	0.87	0.17	0	0	0	not significant
7587	HUMMERICH_SKIN_CANCER_PROGRESSION_DN	0.87	0.17	0	0	0	not significant
7588	ROSS_AML_OF_FAB_M7_TYPE	0.87	0.17	0	0	0	not significant
7589	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP	0.87	0.17	0	0	0	not significant
7590	WU_CELL_MIGRATION	0.87	0.17	0	0	0	not significant
7591	CHR15Q15	0.87	0.16	0	0	0	not significant
7592	GO_ENDONUCLEASE_ACTIVITY	0.87	0.16	0	0	0	not significant
7593	GO_FILOPODIUM	0.87	0.16	0	0	0	not significant
7594	GO_REGULATION_OF_MUSCLE_ORGAN_DEVELOPMENT	0.87	0.16	0	0	0	not significant
7595	PID_CD8_TCR_PATHWAY	0.87	0.16	0	0	0	not significant
7596	REACTOME_BIOLOGICAL_OXIDATIONS	0.87	0.16	0	0	0	not significant
7597	BENPORATH_ES_CORE_NINE_CORRELATED	0.87	0.15	0	0	0	not significant
7598	GO_NEGATIVE_REGULATION_OF_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVIT	0.87	0.15	0	0	0	not significant
7599	GO_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	0.87	0.15	0	0	0	not significant
7600	CHR21Q22	0.87	0.14	0	0	0	not significant
7601	GO_CALCIUM_MEDIATED_SIGNALING	0.87	0.14	0	0	0	not significant
7602	GO_CYTOPLASMIC_SIDE_OF_MEMBRANE	0.87	0.14	0	0	0	not significant
7603	GO_NEURAL_TUBE_DEVELOPMENT	0.87	0.14	0	0	0	not significant
7604	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	0.87	0.14	0	0	0	not significant
7605	GO_REGULATION_OF_HISTONE_MODIFICATION	0.87	0.14	0	0	0	not significant
7606	BROWNE_HCMV_INFECTION_48HR_UP	0.87	0.13	0	0	0	not significant
7607	GO_PLATELET_ACTIVATION	0.87	0.13	0	0	0	not significant
7608	GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	0.87	0.13	0	0	0	not significant
7609	GO_ACTIN_BINDING	0.87	0.12	0	0	0	not significant
7610	GO_REGULATION_OF_DEVELOPMENTAL_GROWTH	0.87	0.12	0	0	0	not significant
7611	GO_GTPASE_REGULATOR_ACTIVITY	0.87	0.11	0	0	0	not significant
7612	GO_SENSORY_ORGAN_DEVELOPMENT	0.87	0.11	0	0	0	not significant
7613	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	0.87	0.1	0	0	0	not significant
7614	GO_REGULATION_OF_HEMOPOIESIS	0.87	0.09	0	0	0	not significant
7615	GO_CHROMATIN_BINDING	0.87	0.08	0	0	0	not significant
7616	BENPORATH_SOX2_TARGETS	0.87	0.07	0	0	0	not significant
7617	GO_SUPRAMOLECULAR_FIBER_ORGANIZATION	0.87	0.07	0	0	0	not significant
7618	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOSIS	0.88	0.22	0	0	0	not significant

7619	GO_REGULATION_OF_NECROTIC_CELL_DEATH	0.88	0.22	0	0	0	not significant
7620	BIOCARTA_PLK3_PATHWAY	0.88	0.21	0	0	0	not significant
7621	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN	0.88	0.21	0	0	0	not significant
7622	GO_3_5_DNA_HELICASE_ACTIVITY	0.88	0.21	0	0	0	not significant
7623	GO_GLYOXYLATE_METABOLIC_PROCESS	0.88	0.21	0	0	0	not significant
7624	GO_NEGATIVE_REGULATION_OF_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABI	0.88	0.21	0	0	0	not significant
7625	GO_POSITIVE_REGULATION_OF_RECEPTOR_RECYCLING	0.88	0.21	0	0	0	not significant
7626	GO_PURINE_NUCLEOTIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.88	0.21	0	0	0	not significant
7627	GO_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	0.88	0.21	0	0	0	not significant
7628	GO_REGULATION_OF_MESONEPHROS_DEVELOPMENT	0.88	0.21	0	0	0	not significant
7629	GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.88	0.21	0	0	0	not significant
7630	GO_TRNA_CATABOLIC_PROCESS	0.88	0.21	0	0	0	not significant
7631	GO_ZYMOGEN_GRANULE	0.88	0.21	0	0	0	not significant
7632	PID_HEDGEHOG_2PATHWAY	0.88	0.21	0	0	0	not significant
7633	REACTOME_CASPASE_ACTIVATION_VIA_EXTRINSIC_APOPTOTIC_SIGNALLING_PATH	0.88	0.21	0	0	0	not significant
7634	ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_DN	0.88	0.21	0	0	0	not significant
7635	SA_FAS_SIGNALING	0.88	0.21	0	0	0	not significant
7636	YOSHIOKA_LIVER_CANCER_EARLY_RECURRENCE_DN	0.88	0.21	0	0	0	not significant
7637	CHOW_RASSF1_TARGETS_UP	0.88	0.2	0	0	0	not significant
7638	GENTILE_UV_RESPONSE_CLUSTER_D7	0.88	0.2	0	0	0	not significant
7639	GO_DNA_DOUBLE_STRAND_BREAK_PROCESSING	0.88	0.2	0	0	0	not significant
7640	GO_ENDOCARDIAL_CUSHION_DEVELOPMENT	0.88	0.2	0	0	0	not significant
7641	GO_ENDOSOME_TO_PLASMA_MEMBRANE_PROTEIN_TRANSPORT	0.88	0.2	0	0	0	not significant
7642	GO_INOSITOL_PHOSPHATE_BIOSYNTHETIC_PROCESS	0.88	0.2	0	0	0	not significant
7643	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	0.88	0.2	0	0	0	not significant
7644	GO_POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	0.88	0.2	0	0	0	not significant
7645	GO_REGULATION_OF_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	0.88	0.2	0	0	0	not significant
7646	GO_REGULATION_OF_METALLOPEPTIDASE_ACTIVITY	0.88	0.2	0	0	0	not significant
7647	GO_REGULATION_OF_VASCULAR_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	0.88	0.2	0	0	0	not significant
7648	GO_RESPONSE_TO_POTASSIUM_ION	0.88	0.2	0	0	0	not significant
7649	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_BINDING	0.88	0.2	0	0	0	not significant
7650	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_PLURIPOTENT_STEM_CELLS	0.88	0.2	0	0	0	not significant
7651	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_DN	0.88	0.2	0	0	0	not significant
7652	GO_ATP_HYDROLYSIS_COUPLED_CATION_TRANSMEMBRANE_TRANSPORT	0.88	0.19	0	0	0	not significant
7653	GO_BONE_MINERALIZATION	0.88	0.19	0	0	0	not significant
7654	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY_INVOLVED_IN_APOPT	0.88	0.19	0	0	0	not significant
7655	GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	0.88	0.19	0	0	0	not significant
7656	GO_DNA_RECOMBINASE_MEDIATOR_COMPLEX	0.88	0.19	0	0	0	not significant
7657	GO_FATTY_ACID_TRANSPORT	0.88	0.19	0	0	0	not significant
7658	GO_MULTIVESICULAR_BODY_ORGANIZATION	0.88	0.19	0	0	0	not significant
7659	GO_PROTEIN_SELF_ASSOCIATION	0.88	0.19	0	0	0	not significant
7660	GO_VASCULAR_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	0.88	0.19	0	0	0	not significant
7661	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_1_DN	0.88	0.19	0	0	0	not significant
7662	HOWLIN_CITED1_TARGETS_1_UP	0.88	0.19	0	0	0	not significant
7663	LABBE_TARGETS_OF_TGFB1_AND_WNT3A_DN	0.88	0.19	0	0	0	not significant
7664	LANDIS_ERBB2_BREAST_TUMORS_65_DN	0.88	0.19	0	0	0	not significant
7665	REACTOME_DISEASES_OF_CARBOHYDRATE_METABOLISM	0.88	0.19	0	0	0	not significant
7666	REACTOME_PREGNENOLONE_BIOSYNTHESIS	0.88	0.19	0	0	0	not significant
7667	ATM_DN.V1_DN	0.88	0.18	0	0	0	not significant
7668	BURTON_ADIPOGENESIS_8	0.88	0.18	0	0	0	not significant
7669	CHR15Q24	0.88	0.18	0	0	0	not significant
7670	GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.88	0.18	0	0	0	not significant
7671	GO_FEMALE_SEX_DIFFERENTIATION	0.88	0.18	0	0	0	not significant
7672	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	0.88	0.18	0	0	0	not significant
7673	GO_PROTEIN_TYROSINE_KINASE_ACTIVITY	0.88	0.18	0	0	0	not significant
7674	GO_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_CELL_DEATH	0.88	0.18	0	0	0	not significant
7675	KEGG_COLORECTAL_CANCER	0.88	0.18	0	0	0	not significant
7676	PID_ANGIOPOIETIN_RECEPTOR_PATHWAY	0.88	0.18	0	0	0	not significant
7677	PID_HDAC_CLASSI_PATHWAY	0.88	0.18	0	0	0	not significant
7678	VANDESLUIS_COMMD1_TARGETS_GROUP_3_UP	0.88	0.18	0	0	0	not significant
7679	CHUNG_BLISTER_CYTOTOXICITY_UP	0.88	0.17	0	0	0	not significant
7680	FONTAINE_PAPILLARY_THYROID_CARCINOMA_DN	0.88	0.17	0	0	0	not significant
7681	GO_ADAPTIVE_THERMOGENESIS	0.88	0.17	0	0	0	not significant
7682	GO_DEMETHYLATION	0.88	0.17	0	0	0	not significant
7683	GO_DIOXYGENASE_ACTIVITY	0.88	0.17	0	0	0	not significant
7684	GO_HISTONE_H3_K4_METHYLATION	0.88	0.17	0	0	0	not significant
7685	GO_REGULATION_OF_EXTENT_OF_CELL_GROWTH	0.88	0.17	0	0	0	not significant
7686	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	0.88	0.17	0	0	0	not significant
7687	REACTOME_MEIOTIC_SYNAPSIS	0.88	0.17	0	0	0	not significant
7688	BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE	0.88	0.16	0	0	0	not significant
7689	GO_HISTONE_DEACETYLASE_COMPLEX	0.88	0.16	0	0	0	not significant
7690	GO_NEGATIVE_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	0.88	0.16	0	0	0	not significant
7691	REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	0.88	0.16	0	0	0	not significant
7692	GO_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	0.88	0.15	0	0	0	not significant
7693	GO_MUSCLE_CONTRACTION	0.88	0.14	0	0	0	not significant
7694	GO_REGULATION_OF_CELLULAR_COMPONENT_SIZE	0.88	0.12	0	0	0	not significant
7695	GO_REPRODUCTIVE_SYSTEM_DEVELOPMENT	0.88	0.11	0	0	0	not significant
7696	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_UP	0.88	0.1	0	0	0	not significant
7697	GO_REGULATION_OF_GROWTH	0.88	0.1	0	0	0	not significant
7698	GO_RESPONSE_TO_WOUNDING	0.88	0.09	0	0	0	not significant
7699	GO_NEURON_DIFFERENTIATION	0.88	0.06	0	0	0	not significant
7700	GO_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	0.89	0.23	0	0	0	not significant
7701	GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	0.89	0.23	0	0	0	not significant
7702	CAFFAREL_RESPONSE_TO_THC_24HR_3_UP	0.89	0.22	0	0	0	not significant
7703	GO_DNA_INSERTION_OR_DELETION_BINDING	0.89	0.22	0	0	0	not significant
7704	GO_ENDOCARDIAL_CUSHION_FORMATION	0.89	0.22	0	0	0	not significant
7705	GO_MONOCARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.89	0.22	0	0	0	not significant
7706	GO_NEGATIVE_REGULATION_OF_EPIDERMAL_GROWTH_FACTOR_ACTIVATED_RE	0.89	0.22	0	0	0	not significant
7707	GO_PINOCYTOSIS	0.89	0.22	0	0	0	not significant
7708	GO_PRESYNAPTIC_MODULATION_OF_CHEMICAL_SYNAPTIC_TRANSMISSION	0.89	0.22	0	0	0	not significant
7709	GO_PURINE_NUCLEOTIDE_TRANSPORT	0.89	0.22	0	0	0	not significant
7710	GO_SYNAPTIC_MEMBRANE_ADHESION	0.89	0.22	0	0	0	not significant
7711	KORKOLA_TERATOMA_UP	0.89	0.22	0	0	0	not significant
7712	LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_UP	0.89	0.22	0	0	0	not significant
7713	PID_S1P_S1P3_PATHWAY	0.89	0.22	0	0	0	not significant
7714	REACTOME_NRIF_SIGNALS_CELL_DEATH_FROM_THE_NUCLEUS	0.89	0.22	0	0	0	not significant
7715	SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1A	0.89	0.22	0	0	0	not significant
7716	CERIBELLI_GENES_INACTIVE_AND_BOUND_BY_NFY	0.89	0.21	0	0	0	not significant
7717	GO_BASEMENT_MEMBRANE_ORGANIZATION	0.89	0.21	0	0	0	not significant
7718	GO_DNA_REPLICATION_SYNTHESIS_OF_RNA_PRIMER	0.89	0.21	0	0	0	not significant
7719	GO_MAST_CELL_MEDIATED_IMMUNITY	0.89	0.21	0	0	0	not significant
7720	GO_NEPHRON_EPITHELIUM_DEVELOPMENT	0.89	0.21	0	0	0	not significant
7721	GO_NEURON_PROJECTION_MAINTENANCE	0.89	0.21	0	0	0	not significant
7722	GO_PYRIMIDINE_DEOXYRIBONUCLEOTIDE_BIOSYNTHETIC_PROCESS	0.89	0.21	0	0	0	not significant
7723	GO_RECEPTOR_CATABOLIC_PROCESS	0.89	0.21	0	0	0	not significant
7724	GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION	0.89	0.21	0	0	0	not significant
7725	GO_VITAMIN_B6_BINDING	0.89	0.21	0	0	0	not significant
7726	RIZ_ERYTHROID_DIFFERENTIATION_HBZ	0.89	0.21	0	0	0	not significant
7727	WATTEL_AUTONOMOUS_THYROID_ADENOMA_UP	0.89	0.21	0	0	0	not significant

7728	CEBALLOS_TARGETS_OF_TP53_AND_MYC_DN	0.89	0.2	0	0	0	not significant
7729	GO_ACROSOMAL_VESICLE	0.89	0.2	0	0	0	not significant
7730	GO_BODY_FLUID_SECRETION	0.89	0.2	0	0	0	not significant
7731	GO_CENTROSOME_DUPLICATION	0.89	0.2	0	0	0	not significant
7732	GO_ER_TO_GOLGI_TRANSPORT_VESICLE_MEMBRANE	0.89	0.2	0	0	0	not significant
7733	GO_MECHANORECEPTOR_DIFFERENTIATION	0.89	0.2	0	0	0	not significant
7734	GO_NEGATIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PAT	0.89	0.2	0	0	0	not significant
7735	GO_POSITIVE_REGULATION_OF_DNA_CATABOLIC_PROCESS	0.89	0.2	0	0	0	not significant
7736	GO_REGULATION_OF_DNA_CATABOLIC_PROCESS	0.89	0.2	0	0	0	not significant
7737	GO_REGULATION_OF_TISSUE_REMODELING	0.89	0.2	0	0	0	not significant
7738	GO_SMAD_PROTEIN_COMPLEX	0.89	0.2	0	0	0	not significant
7739	GO_TETRAPYRROLE_BINDING	0.89	0.2	0	0	0	not significant
7740	GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	0.89	0.2	0	0	0	not significant
7741	GO_TRAIL_ACTIVATED_APOPTOTIC_SIGNALING_PATHWAY	0.89	0.2	0	0	0	not significant
7742	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_DN	0.89	0.2	0	0	0	not significant
7743	REACTOME_SIGNALING_BY_ERBB4	0.89	0.2	0	0	0	not significant
7744	TCGA_GLIOBLASTOMA_COPY_NUMBER_DN	0.89	0.2	0	0	0	not significant
7745	WESTON_VEGFA_TARGETS_12HR	0.89	0.2	0	0	0	not significant
7746	ZHAN_MULTIPLE_MYELOMA_MF_DN	0.89	0.2	0	0	0	not significant
7747	BIOCARTA_CIRCADIAN_PATHWAY	0.89	0.19	0	0	0	not significant
7748	GO_CARBOHYDRATE_TRANSMEMBRANE_TRANSPORT	0.89	0.19	0	0	0	not significant
7749	GO_FLAVIN_ADENINE_DINUCLEOTIDE_BINDING	0.89	0.19	0	0	0	not significant
7750	GO_GLUCOSIDASE_ACTIVITY	0.89	0.19	0	0	0	not significant
7751	GO_LEADING_EDGE_MEMBRANE	0.89	0.19	0	0	0	not significant
7752	GO_LEUKOCYTE_APOPTOTIC_PROCESS	0.89	0.19	0	0	0	not significant
7753	GO_NEGATIVE_REGULATION_OF_DEPHOSPHORYLATION	0.89	0.19	0	0	0	not significant
7754	GO_NEGATIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	0.89	0.19	0	0	0	not significant
7755	GO_POSITIVE_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	0.89	0.19	0	0	0	not significant
7756	REACTOME_LONG_TERM_POTENTIATION	0.89	0.19	0	0	0	not significant
7757	REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	0.89	0.19	0	0	0	not significant
7758	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_DNA_REPAIR_GENES	0.89	0.19	0	0	0	not significant
7759	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_DN	0.89	0.19	0	0	0	not significant
7760	GO_ACTIN_CYTOSKELETON_REORGANIZATION	0.89	0.18	0	0	0	not significant
7761	GO_APOPTOTIC_MITOCHONDRIAL_CHANGES	0.89	0.18	0	0	0	not significant
7762	GO_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN_RECEPTO	0.89	0.18	0	0	0	not significant
7763	GO_NEGATIVE_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT	0.89	0.18	0	0	0	not significant
7764	DARWICHE_SQUAMOUS_CELL_CARCINOMA_DN	0.89	0.17	0	0	0	not significant
7765	GO_BONE_DEVELOPMENT	0.89	0.17	0	0	0	not significant
7766	GO_EMBRYONIC_ORGAN_MORPHOGENESIS	0.89	0.17	0	0	0	not significant
7767	GO_NUCLEASE_ACTIVITY	0.89	0.17	0	0	0	not significant
7768	GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	0.89	0.17	0	0	0	not significant
7769	GO_TISSUE_REMODELING	0.89	0.17	0	0	0	not significant
7770	GO_POSITIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	0.89	0.16	0	0	0	not significant
7771	KYNG_DNA_DAMAGE_UP	0.89	0.16	0	0	0	not significant
7772	GO_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	0.89	0.15	0	0	0	not significant
7773	GO_EMBRYONIC_ORGAN_DEVELOPMENT	0.89	0.14	0	0	0	not significant
7774	GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_P	0.89	0.14	0	0	0	not significant
7775	GO_PRESYNAPSE	0.89	0.14	0	0	0	not significant
7776	GO_CELL_CYCLE_G1_S_PHASE_TRANSITION	0.89	0.13	0	0	0	not significant
7777	GO_MYELOID_CELL_DIFFERENTIATION	0.89	0.13	0	0	0	not significant
7778	SWEET_LUNG_CANCER_KRAS_UP	0.89	0.12	0	0	0	not significant
7779	GO_REGULATION_OF_KINASE_ACTIVITY	0.89	0.1	0	0	0	not significant
7780	GO_NEGATIVE_REGULATION_OF_RNA_BIOSYNTHETIC_PROCESS	0.89	0.08	0	0	0	not significant
7781	GO_REGULATION_OF_CELLULAR_LOCALIZATION	0.89	0.08	0	0	0	not significant
7782	ACEVEDO_LIVER_CANCER_UP	0.89	0.07	0	0	0	not significant
7783	GO_IDENTICAL_PROTEIN_BINDING	0.89	0.06	0	0	0	not significant
7784	CHR13Q31	0.90	0.24	0	0	0	not significant
7785	GO_NEGATIVE_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	0.90	0.24	0	0	0	not significant
7786	GO_POSITIVE_REGULATION_OF_CYTOPLASMIC_TRANSPORT	0.90	0.24	0	0	0	not significant
7787	GO_PROGESTERONE_RECEPTOR_SIGNALING_PATHWAY	0.90	0.24	0	0	0	not significant
7788	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ADAPTOR_ACTIV	0.90	0.24	0	0	0	not significant
7789	PID_GLYPICAN_1PATHWAY	0.90	0.24	0	0	0	not significant
7790	CHR10P11	0.90	0.23	0	0	0	not significant
7791	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN	0.90	0.23	0	0	0	not significant
7792	GO_AROMATIC_AMINO_ACID_FAMILY_METABOLIC_PROCESS	0.90	0.23	0	0	0	not significant
7793	GO_ESTABLISHMENT_OF_PIGMENT_GRANULE_LOCALIZATION	0.90	0.23	0	0	0	not significant
7794	GO_NEGATIVE_REGULATION_OF_NECROTIC_CELL_DEATH	0.90	0.23	0	0	0	not significant
7795	GO_NEGATIVE_REGULATION_OF_TELOMERE_CAPPING	0.90	0.23	0	0	0	not significant
7796	GO_RAB_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	0.90	0.23	0	0	0	not significant
7797	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_48HR_UP	0.90	0.22	0	0	0	not significant
7798	CHR5Q15	0.90	0.22	0	0	0	not significant
7799	CROMER_TUMORIGENESIS_DN	0.90	0.22	0	0	0	not significant
7800	DANG_MYC_TARGETS_DN	0.90	0.22	0	0	0	not significant
7801	GAUSSMANN_MLL_AF4_FUSION_TARGETS_A_DN	0.90	0.22	0	0	0	not significant
7802	GO_AMMONIUM_TRANSMEMBRANE_TRANSPORT	0.90	0.22	0	0	0	not significant
7803	GO_CELLULAR_BIOGENIC_AMINE_METABOLIC_PROCESS	0.90	0.22	0	0	0	not significant
7804	GO_DNA_METHYLATION_OR_DEMETHYLATION	0.90	0.22	0	0	0	not significant
7805	GO_ISOCITRATE_DEHYDROGENASE_ACTIVITY	0.90	0.22	0	0	0	not significant
7806	GO_MEMBRANE_REPOLARIZATION_DURING_ACTION_POTENTIAL	0.90	0.22	0	0	0	not significant
7807	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	0.90	0.22	0	0	0	not significant
7808	GO_NEGATIVE_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	0.90	0.22	0	0	0	not significant
7809	GO_PHOSPHOTRANSFERASE_ACTIVITY_PHOSPHATE_GROUP_AS_ACCEPTOR	0.90	0.22	0	0	0	not significant
7810	GO_POSITIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	0.90	0.22	0	0	0	not significant
7811	GO_POSITIVE_REGULATION_OF_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	0.90	0.22	0	0	0	not significant
7812	GO_PROTEIN_AUTOUBIQUITINATION	0.90	0.22	0	0	0	not significant
7813	GO_PROTEIN_IMPORT_INTO_PEROXISOME_MATRIX	0.90	0.22	0	0	0	not significant
7814	GO_REGULATION_OF_BEHAVIOR	0.90	0.22	0	0	0	not significant
7815	GO_TRAPP_COMPLEX	0.90	0.22	0	0	0	not significant
7816	GO_UDP_GALACTOSYLTRANSFERASE_ACTIVITY	0.90	0.22	0	0	0	not significant
7817	GO_VIRAL_RNA_GENOME_REPLICATION	0.90	0.22	0	0	0	not significant
7818	HEIDENBLAD_AMPLICON_12P11_12_DN	0.90	0.22	0	0	0	not significant
7819	KIM_GLIS2_TARGETS_UP	0.90	0.22	0	0	0	not significant
7820	REACTOME_PRESYNAPTIC_DEPOLARIZATION_AND_CALCIUM_CHANNEL_OPENING	0.90	0.22	0	0	0	not significant
7821	REACTOME_RHO_GTPASES_ACTIVATE_CIT	0.90	0.22	0	0	0	not significant
7822	VETTER_TARGETS_OF_PRKCA_AND_ETS1_UP	0.90	0.22	0	0	0	not significant
7823	CHR14Q12	0.90	0.21	0	0	0	not significant
7824	DOANE_BREAST_CANCER_CLASSES_DN	0.90	0.21	0	0	0	not significant
7825	GO_CELL_DIVISION_SITE	0.90	0.21	0	0	0	not significant
7826	GO_ETHER_METABOLIC_PROCESS	0.90	0.21	0	0	0	not significant
7827	GO_GROWTH_FACTOR_RECEPTOR_BINDING	0.90	0.21	0	0	0	not significant
7828	GO_LIPID_GLYCOSYLATION	0.90	0.21	0	0	0	not significant
7829	GO_NEGATIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	0.90	0.21	0	0	0	not significant
7830	GO_NEGATIVE_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	0.90	0.21	0	0	0	not significant
7831	GO_NEURAL_CREST_CELL_MIGRATION	0.90	0.21	0	0	0	not significant
7832	GO_PERICENTRIOLAR_MATERIAL	0.90	0.21	0	0	0	not significant
7833	GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	0.90	0.21	0	0	0	not significant
7834	GO_POSTREPLICATION_REPAIR	0.90	0.21	0	0	0	not significant
7835	GO_REGULATION_OF_MITOCHONDRIAL_FISSION	0.90	0.21	0	0	0	not significant
7836	GO_REGULATION_OF_PROTEIN_DEACETYLATION	0.90	0.21	0	0	0	not significant

7837	GO_REPLICATION_FORK_PROTECTION_COMPLEX	0.90	0.21	0	0	0	not significant
7838	GO_TAT_PROTEIN_BINDING	0.90	0.21	0	0	0	not significant
7839	LANDIS_BREAST_CANCER_PROGRESSION_DN	0.90	0.21	0	0	0	not significant
7840	LASTOWSKA_COAMPLIFIED_WITH_MYCN	0.90	0.21	0	0	0	not significant
7841	LUI_THYROID_CANCER_PAX8_PPARG_DN	0.90	0.21	0	0	0	not significant
7842	MARIADASON_RESPONSE_TO_BUTYRATE_SULINDAC_6	0.90	0.21	0	0	0	not significant
7843	SCIBETTA_KDM5B_TARGETS_UP	0.90	0.21	0	0	0	not significant
7844	CAFFAREL_RESPONSE_TO_THC_24HR_5_DN	0.90	0.2	0	0	0	not significant
7845	GO_ASTROCYTE_CELL_MIGRATION	0.90	0.2	0	0	0	not significant
7846	GO_GLYCOSPHINGOLIPID_BIOSYNTHETIC_PROCESS	0.90	0.2	0	0	0	not significant
7847	GO_NEGATIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_C	0.90	0.2	0	0	0	not significant
7848	GO_NUCLEOBASE_CONTAINING_COMPOUND_TRANSMEMBRANE_TRANSPORTER_A	0.90	0.2	0	0	0	not significant
7849	GO_POSITIVE_REGULATION_OF_MEMBRANE_PERMEABILITY	0.90	0.2	0	0	0	not significant
7850	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	0.90	0.2	0	0	0	not significant
7851	KAUFFMANN_MELANOMA_RELAPSE_DN	0.90	0.2	0	0	0	not significant
7852	KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	0.90	0.2	0	0	0	not significant
7853	KEGG_CHRONIC_MYELOID_LEUKEMIA	0.90	0.2	0	0	0	not significant
7854	KIM_WT1_TARGETS_12HR_UP	0.90	0.2	0	0	0	not significant
7855	MIKKELSEN_MEF_LCP_WITH_H3K4ME3	0.90	0.2	0	0	0	not significant
7856	VARELA_ZMPSTE24_TARGETS_DN	0.90	0.2	0	0	0	not significant
7857	GO_CHORION_DEVELOPMENT	0.90	0.19	0	0	0	not significant
7858	GO_GLUCAN_METABOLIC_PROCESS	0.90	0.19	0	0	0	not significant
7859	GO_POSITIVE_REGULATION_OF_AUTOPHAGY	0.90	0.19	0	0	0	not significant
7860	GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	0.90	0.19	0	0	0	not significant
7861	GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	0.90	0.19	0	0	0	not significant
7862	GO_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	0.90	0.19	0	0	0	not significant
7863	GO_RENAL_TUBULE_DEVELOPMENT	0.90	0.19	0	0	0	not significant
7864	GO_SITE_OF_POLARIZED_GROWTH	0.90	0.19	0	0	0	not significant
7865	GO_VITAMIN_METABOLIC_PROCESS	0.90	0.19	0	0	0	not significant
7866	KRAS.DF.V1_DN	0.90	0.19	0	0	0	not significant
7867	MIKKELSEN_MEF_HCP_WITH_H3K27ME3	0.90	0.19	0	0	0	not significant
7868	GO_NEGATIVE_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS	0.90	0.18	0	0	0	not significant
7869	PECE_MAMMARY_STEM_CELL_UP	0.90	0.18	0	0	0	not significant
7870	GO_RECEPTOR_METABOLIC_PROCESS	0.90	0.17	0	0	0	not significant
7871	GREGORY_SYNTHETIC_LETHAL_WITH_IMATINIB	0.90	0.17	0	0	0	not significant
7872	MARKEY_RB1_ACUTE_LOF_DN	0.90	0.17	0	0	0	not significant
7873	RAF_UP.V1_DN	0.90	0.17	0	0	0	not significant
7874	GO_JNK_CASCADE	0.90	0.16	0	0	0	not significant
7875	GO_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	0.90	0.15	0	0	0	not significant
7876	GO_REGULATION_OF_GTPASE_ACTIVITY	0.90	0.14	0	0	0	not significant
7877	GO_CILIUM_ORGANIZATION	0.90	0.13	0	0	0	not significant
7878	GO_ACTIN_FILAMENT_BASED_PROCESS	0.90	0.11	0	0	0	not significant
7879	GO_NEURON_DEVELOPMENT	0.90	0.1	0	0	0	not significant
7880	GO_CELLULAR_COMPONENT_MORPHOGENESIS	0.90	0.09	0	0	0	not significant
7881	GO_RETINAL_GANGLION_CELL_AXON_GUIDANCE	0.91	0.25	0	0	0	not significant
7882	WONG_IFNA2_RESISTANCE_DN	0.91	0.25	0	0	0	not significant
7883	BIOCARTA_D4GDI_PATHWAY	0.91	0.24	0	0	0	not significant
7884	DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_UP	0.91	0.24	0	0	0	not significant
7885	GO_ATRIAL_CARDIAC_MUSCLE_CELL_TO_AV_NODE_CELL_SIGNALING	0.91	0.24	0	0	0	not significant
7886	GO_CARDIAC_ATRIUM_DEVELOPMENT	0.91	0.24	0	0	0	not significant
7887	GO_CELL_DIFFERENTIATION_INVOLVED_IN_EMBRYONIC_PLACENTA_DEVELOPMEN	0.91	0.24	0	0	0	not significant
7888	GO_CLEAVAGE_FURROW	0.91	0.24	0	0	0	not significant
7889	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	0.91	0.24	0	0	0	not significant
7890	GO_POSTSYNAPTIC_DENSITY_INTRACELLULAR_COMPONENT	0.91	0.24	0	0	0	not significant
7891	GO_POSTSYNAPTIC_SPECIALIZATION_ORGANIZATION	0.91	0.24	0	0	0	not significant
7892	GO_RECEPTOR_LOCALIZATION_TO_SYNAPSE	0.91	0.24	0	0	0	not significant
7893	KYNG_WERNER_SYNDROM_UP	0.91	0.24	0	0	0	not significant
7894	OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN	0.91	0.24	0	0	0	not significant
7895	REACTOME_CARBOXYTERMINAL_POST_TRANSLATIONAL_MODIFICATIONS_OF_TUB	0.91	0.24	0	0	0	not significant
7896	SASSON_RESPONSE_TO_FORSKOLIN_UP	0.91	0.24	0	0	0	not significant
7897	BIOCARTA_ACH_PATHWAY	0.91	0.23	0	0	0	not significant
7898	CASTELLANO_NRAS_TARGETS_DN	0.91	0.23	0	0	0	not significant
7899	CHRXQ24	0.91	0.23	0	0	0	not significant
7900	GO_ANGIOTENSIN_RECEPTOR_BINDING	0.91	0.23	0	0	0	not significant
7901	GO_CHONDROITIN_SULFATE_BIOSYNTHETIC_PROCESS	0.91	0.23	0	0	0	not significant
7902	GO_CONVERGENT_EXTENSION	0.91	0.23	0	0	0	not significant
7903	GO_ESCRT_COMPLEX	0.91	0.23	0	0	0	not significant
7904	GO_N_TERMINAL_PROTEIN_LIPIDATION	0.91	0.23	0	0	0	not significant
7905	GO_ORGAN_OR_TISSUE_SPECIFIC_IMMUNE_RESPONSE	0.91	0.23	0	0	0	not significant
7906	GO_POSITIVE_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYS	0.91	0.23	0	0	0	not significant
7907	GO_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	0.91	0.23	0	0	0	not significant
7908	GO_REGULATION_OF_PROTEIN_DEPOLYMERIZATION	0.91	0.23	0	0	0	not significant
7909	GO_SERINE_TYPE_CARBOXYPEPTIDASE_ACTIVITY	0.91	0.23	0	0	0	not significant
7910	GO_SPECIFIC_GRANULE_LUMEN	0.91	0.23	0	0	0	not significant
7911	GO_TELOMERIC_D_LOOP_DISASSEMBLY	0.91	0.23	0	0	0	not significant
7912	KEGG_RENIN_ANGIOTENSIN_SYSTEM	0.91	0.23	0	0	0	not significant
7913	ONDER_CDH1_TARGETS_3_DN	0.91	0.23	0	0	0	not significant
7914	REACTOME_DISEASES_ASSOCIATED_WITH_GLYCOSYLATION_PRECURSOR_BIOSY	0.91	0.23	0	0	0	not significant
7915	REACTOME_DNA_REPLICATION_INITIATION	0.91	0.23	0	0	0	not significant
7916	REACTOME_PI3K_AKT_ACTIVATION	0.91	0.23	0	0	0	not significant
7917	RUAN_RESPONSE_TO_TROGLITAZONE_DN	0.91	0.23	0	0	0	not significant
7918	TSENG_ADIPOGENIC_POTENTIAL_DN	0.91	0.23	0	0	0	not significant
7919	UEDA_CENTRAL_CLOCK	0.91	0.23	0	0	0	not significant
7920	ZHENG_RESPONSE_TO_ARSENITE_DN	0.91	0.23	0	0	0	not significant
7921	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN	0.91	0.22	0	0	0	not significant
7922	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TAN_DN	0.91	0.22	0	0	0	not significant
7923	GO_CARD_DOMAIN_BINDING	0.91	0.22	0	0	0	not significant
7924	GO_CERAMIDE_BIOSYNTHETIC_PROCESS	0.91	0.22	0	0	0	not significant
7925	GO_EXTRAEMBRYONIC_MEMBRANE_DEVELOPMENT	0.91	0.22	0	0	0	not significant
7926	GO_IRE1_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	0.91	0.22	0	0	0	not significant
7927	GO_MEMBRANE_LIPID_CATABOLIC_PROCESS	0.91	0.22	0	0	0	not significant
7928	GO_NEGATIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	0.91	0.22	0	0	0	not significant
7929	GO_NEURON_DEATH_IN_RESPONSE_TO_OXIDATIVE_STRESS	0.91	0.22	0	0	0	not significant
7930	GO_PHOSPHATIDYLINOSITOL_3_5_BISPHOSPHATE_BINDING	0.91	0.22	0	0	0	not significant
7931	GO_PHOSPHOLIPASE_INHIBITOR_ACTIVITY	0.91	0.22	0	0	0	not significant
7932	GO_REGULATION_OF_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	0.91	0.22	0	0	0	not significant
7933	GO_REGULATION_OF_INTERLEUKIN_2_SECRETION	0.91	0.22	0	0	0	not significant
7934	GO_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS_IN_THE_VACUOLE	0.91	0.22	0	0	0	not significant
7935	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_UP	0.91	0.22	0	0	0	not significant
7936	HAHTOLA_SEZARY_SYNDROM_UP	0.91	0.22	0	0	0	not significant
7937	KAYO_CALORIE_RESTRICTION_MUSCLE_UP	0.91	0.22	0	0	0	not significant
7938	KIM_GERMINAL_CENTER_T_HELPER_UP	0.91	0.22	0	0	0	not significant
7939	MARTINEZ_RESPONSE_TO_TRABECTEDIN_UP	0.91	0.22	0	0	0	not significant
7940	MIKKELSEN_MEF_ICP_WITH_H3K27ME3	0.91	0.22	0	0	0	not significant
7941	PARK_APL_PATHOGENESIS_DN	0.91	0.22	0	0	0	not significant
7942	REACTOME_NEGATIVE_REGULATORS_OF_DDX58_IFIH1_SIGNALING	0.91	0.22	0	0	0	not significant
7943	SCHEIDEREIT_IKK_INTERACTING_PROTEINS	0.91	0.22	0	0	0	not significant
7944	BIOCARTA_EICOSANOID_PATHWAY	0.91	0.21	0	0	0	not significant
7945	COATES_MACROPHAGE_M1_VS_M2_DN	0.91	0.21	0	0	0	not significant

7946	GO_AP_1_ADAPTOR_COMPLEX_BINDING	0.91	0.21	0	0	0	not significant
7947	GO_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	0.91	0.21	0	0	0	not significant
7948	GO_SYNAPTIC_VESICLE_RECYCLING	0.91	0.21	0	0	0	not significant
7949	HOLLERN_MICROACINAR_BREAST_TUMOR_DN	0.91	0.21	0	0	0	not significant
7950	HUI_MAPK14_TARGETS_UP	0.91	0.21	0	0	0	not significant
7951	PID_ERBB1_DOWNSTREAM_PATHWAY	0.91	0.21	0	0	0	not significant
7952	GO_GLIAL_CELL_DIFFERENTIATION	0.91	0.19	0	0	0	not significant
7953	GO_GOLGI_ORGANIZATION	0.91	0.19	0	0	0	not significant
7954	GO_HORMONE_RECEPTOR_BINDING	0.91	0.19	0	0	0	not significant
7955	GO_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	0.91	0.19	0	0	0	not significant
7956	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_UP	0.91	0.19	0	0	0	not significant
7957	REACTOME_RHO_GTPASE_CYCLE	0.91	0.19	0	0	0	not significant
7958	RODWELL_AGING_KIDNEY_DN	0.91	0.19	0	0	0	not significant
7959	GO_LIPID_MODIFICATION	0.91	0.18	0	0	0	not significant
7960	KEGG_ENDOCYTOSIS	0.91	0.18	0	0	0	not significant
7961	QI_PLASMACYTOMA_UP	0.91	0.18	0	0	0	not significant
7962	GO_NUCLEOSIDE_PHOSPHATE_METABOLIC_PROCESS	0.91	0.17	0	0	0	not significant
7963	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP	0.91	0.16	0	0	0	not significant
7964	GO_DENDRITIC_TREE	0.91	0.16	0	0	0	not significant
7965	GO_REGULATION_OF_AUTOPHAGY	0.91	0.16	0	0	0	not significant
7966	GO_REGULATION_OF_BINDING	0.91	0.16	0	0	0	not significant
7967	GO_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	0.91	0.16	0	0	0	not significant
7968	KOYAMA_SEMA3B_TARGETS_DN	0.91	0.16	0	0	0	not significant
7969	LOPEZ_MBD_TARGETS	0.91	0.12	0	0	0	not significant
7970	GO_CELL_PROJECTION_ORGANIZATION	0.91	0.1	0	0	0	not significant
7971	GO_NEGATIVE_REGULATION_OF_MOLECULAR_FUNCTION	0.91	0.1	0	0	0	not significant
7972	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP	0.92	0.26	0	0	0	not significant
7973	GO_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	0.92	0.26	0	0	0	not significant
7974	REACTOME_ZBP1_DAI_MEDIATED_INDUCTION_OF_TYPE_I_IFNS	0.92	0.26	0	0	0	not significant
7975	STARK_HYPPOCAMPUS_22Q11_DELETION_DN	0.92	0.26	0	0	0	not significant
7976	GO_ACYL_COA_DEHYDROGENASE_ACTIVITY	0.92	0.25	0	0	0	not significant
7977	GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_ASSEMBLY	0.92	0.25	0	0	0	not significant
7978	GO_MAST_CELL_ACTIVATION	0.92	0.25	0	0	0	not significant
7979	GO_NEGATIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATIO	0.92	0.25	0	0	0	not significant
7980	GO_NUCLEOTIDE_SUGAR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.92	0.25	0	0	0	not significant
7981	GO_OLIGOSACCHARIDE_BINDING	0.92	0.25	0	0	0	not significant
7982	GO_POLY_A_SPECIFIC_RIBONUCLEASE_ACTIVITY	0.92	0.25	0	0	0	not significant
7983	MOOTHA_FFA_OXYDATION	0.92	0.25	0	0	0	not significant
7984	NICK_RESPONSE_TO_PROC_TREATMENT_DN	0.92	0.25	0	0	0	not significant
7985	NOUSHMEHR_GBM_SILENCED_BY_METHYLATION	0.92	0.25	0	0	0	not significant
7986	STREICHER_LSM1_TARGETS_DN	0.92	0.25	0	0	0	not significant
7987	VALK_AML_CLUSTER_9	0.92	0.25	0	0	0	not significant
7988	CHR10Q25	0.92	0.24	0	0	0	not significant
7989	CHR8Q11	0.92	0.24	0	0	0	not significant
7990	GO_CARDIAC_MUSCLE_CELL_PROLIFERATION	0.92	0.24	0	0	0	not significant
7991	GO_CELLULAR_RESPONSE_TO_GAMMA_RADIATION	0.92	0.24	0	0	0	not significant
7992	GO_INNER_EAR_RECEPTOR_CELL_DEVELOPMENT	0.92	0.24	0	0	0	not significant
7993	GO_LAMELLAR_BODY	0.92	0.24	0	0	0	not significant
7994	GO_NEGATIVE_REGULATION_OF_ERAD_PATHWAY	0.92	0.24	0	0	0	not significant
7995	GO_NEGATIVE_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_STRESS	0.92	0.24	0	0	0	not significant
7996	GO_NEGATIVE_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	0.92	0.24	0	0	0	not significant
7997	GO_NEPHRON_MORPHOGENESIS	0.92	0.24	0	0	0	not significant
7998	GO_PORE_COMPLEX_ASSEMBLY	0.92	0.24	0	0	0	not significant
7999	GO_POSITIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PAT	0.92	0.24	0	0	0	not significant
8000	GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	0.92	0.24	0	0	0	not significant
8001	GO_POSITIVE_REGULATION_OF_PROTEIN_MATURATION	0.92	0.24	0	0	0	not significant
8002	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PR	0.92	0.24	0	0	0	not significant
8003	GO_PURINERGIC_RECEPTOR_ACTIVITY	0.92	0.24	0	0	0	not significant
8004	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES	0.92	0.24	0	0	0	not significant
8005	IRITANI_MAD1_TARGETS_DN	0.92	0.24	0	0	0	not significant
8006	NGUYEN_NOTCH1_TARGETS_UP	0.92	0.24	0	0	0	not significant
8007	REACTOME_CLASS_I_PEROXISOMAL_MEMBRANE_PROTEIN_IMPORT	0.92	0.24	0	0	0	not significant
8008	REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTOR	0.92	0.24	0	0	0	not significant
8009	REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_ZBP1	0.92	0.24	0	0	0	not significant
8010	WIKMAN_ASBESTOS_LUNG_CANCER_DN	0.92	0.24	0	0	0	not significant
8011	ALCALAY_AML_BY_NPM1_LOCALIZATION_UP	0.92	0.23	0	0	0	not significant
8012	GO_BRANCHING_MORPHOGENESIS_OF_AN_EPITHELIAL_TUBE	0.92	0.23	0	0	0	not significant
8013	GO_DYSTROGLYCAN_BINDING	0.92	0.23	0	0	0	not significant
8014	GO_LEUKOCYTE_AGGREGATION	0.92	0.23	0	0	0	not significant
8015	GO_LYMPHOCYTE_APOPTOTIC_PROCESS	0.92	0.23	0	0	0	not significant
8016	GO_NECROTIC_CELL_DEATH	0.92	0.23	0	0	0	not significant
8017	GO_NEGATIVE_REGULATION_OF_EPIDERMIS_DEVELOPMENT	0.92	0.23	0	0	0	not significant
8018	GO_NEGATIVE_REGULATION_OF_HEART_RATE	0.92	0.23	0	0	0	not significant
8019	GO_NEGATIVE_REGULATION_OF_PROTEIN_IMPORT_INTO_NUCLEUS	0.92	0.23	0	0	0	not significant
8020	GO_NEGATIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALIN	0.92	0.23	0	0	0	not significant
8021	GO_ORGANELLE_MEMBRANE_FUSION	0.92	0.23	0	0	0	not significant
8022	GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BINDING	0.92	0.23	0	0	0	not significant
8023	GO_POSITIVE_REGULATION_OF_DEACETYLASE_ACTIVITY	0.92	0.23	0	0	0	not significant
8024	GO_POSITIVE_REGULATION_OF_DNA_REPAIR	0.92	0.23	0	0	0	not significant
8025	GO_PROTEIN_LOCALIZATION_TO_VACUOLE	0.92	0.23	0	0	0	not significant
8026	GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_EXONUCLEOLYTIC	0.92	0.23	0	0	0	not significant
8027	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHW	0.92	0.23	0	0	0	not significant
8028	GO_WNT_PROTEIN_BINDING	0.92	0.23	0	0	0	not significant
8029	HEDVAT_ELF4_TARGETS_UP	0.92	0.23	0	0	0	not significant
8030	HOOI_ST7_TARGETS_UP	0.92	0.23	0	0	0	not significant
8031	MAYBURD_RESPONSE_TO_L663536_DN	0.92	0.23	0	0	0	not significant
8032	REACTOME_RAB_GERANYLGERANYLATION	0.92	0.23	0	0	0	not significant
8033	WARTERS_IR_RESPONSE_5GY	0.92	0.23	0	0	0	not significant
8034	GO_CELL_CELL_ADHERENS_JUNCTION	0.92	0.22	0	0	0	not significant
8035	GO_DEVELOPMENT_OF_PRIMARY_FEMALE_SEXUAL_CHARACTERISTICS	0.92	0.22	0	0	0	not significant
8036	GO_LIPASE_INHIBITOR_ACTIVITY	0.92	0.22	0	0	0	not significant
8037	GO_MEMBRANE_BIOGENESIS	0.92	0.22	0	0	0	not significant
8038	GO_MYELOID_CELL_HOMEOSTASIS	0.92	0.22	0	0	0	not significant
8039	GO_POSITIVE_REGULATION_OF_CHROMATIN_ORGANIZATION	0.92	0.22	0	0	0	not significant
8040	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	0.92	0.22	0	0	0	not significant
8041	GO_SARCOLEMMA	0.92	0.22	0	0	0	not significant
8042	CHR20Q13	0.92	0.21	0	0	0	not significant
8043	GO_CELL_JUNCTION_ASSEMBLY	0.92	0.21	0	0	0	not significant
8044	GO_CONNECTIVE_TISSUE_DEVELOPMENT	0.92	0.21	0	0	0	not significant
8045	GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENT	0.92	0.21	0	0	0	not significant
8046	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	0.92	0.21	0	0	0	not significant
8047	GO_NEURON_DEATH	0.92	0.2	0	0	0	not significant
8048	GO_REGULATION_OF_HORMONE_SECRETION	0.92	0.2	0	0	0	not significant
8049	GO_VIRAL_GENOME_REPLICATION	0.92	0.2	0	0	0	not significant
8050	GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	0.92	0.19	0	0	0	not significant
8051	MARTINEZ_RB1_AND_TP53_TARGETS_DN	0.92	0.16	0	0	0	not significant
8052	GO_GROWTH	0.92	0.14	0	0	0	not significant
8053	GO_NEGATIVE_REGULATION_OF_CATALYTIC_ACTIVITY	0.92	0.14	0	0	0	not significant
8054	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN	0.92	0.08	0	0	0	not significant

8055	GO_GLUTAMATE_METABOLIC_PROCESS	0.93	0.27	0	0	0	not significant
8056	GO_NEGATIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	0.93	0.27	0	0	0	not significant
8057	GO_REGULATION_OF_SPHINGOLIPID_BIOSYNTHETIC_PROCESS	0.93	0.27	0	0	0	not significant
8058	GO_RESPONSE_TO_HYDROPEROXIDE	0.93	0.27	0	0	0	not significant
8059	GO_T_CELL_APOPTOTIC_PROCESS	0.93	0.27	0	0	0	not significant
8060	PID_WNT_SIGNALING_PATHWAY	0.93	0.27	0	0	0	not significant
8061	REACTOME_LDL_CLEARANCE	0.93	0.27	0	0	0	not significant
8062	BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_UP	0.93	0.26	0	0	0	not significant
8063	CAFFAREL_RESPONSE_TO_THC_DN	0.93	0.26	0	0	0	not significant
8064	CHR12Q22	0.93	0.26	0	0	0	not significant
8065	GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	0.93	0.26	0	0	0	not significant
8066	GO_POSITIVE_REGULATION_OF_EARLY_ENDOSOME_TO_LATE_ENDOSOME_TRANS	0.93	0.26	0	0	0	not significant
8067	GO_RESPONSE_TO_FUNGUS	0.93	0.26	0	0	0	not significant
8068	HATADA_METHYLATED_IN_LUNG_CANCER_DN	0.93	0.26	0	0	0	not significant
8069	REACTOME_NCAM1_INTERACTIONS	0.93	0.26	0	0	0	not significant
8070	REACTOME_NONSENSE_MEDIATED_DECAY_NMD_INDEPENDENT_OF_THE_EXON_JU	0.93	0.26	0	0	0	not significant
8071	REACTOME_SIGNALING_BY_NOTCH1	0.93	0.26	0	0	0	not significant
8072	BIOCARTA_NFKB_PATHWAY	0.93	0.25	0	0	0	not significant
8073	BIOCARTA_SPRY_PATHWAY	0.93	0.25	0	0	0	not significant
8074	FIGUEROA_AML_METHYLATION_CLUSTER_1_DN	0.93	0.25	0	0	0	not significant
8075	GO_CALCIUM_DEPENDENT_PROTEIN_BINDING	0.93	0.25	0	0	0	not significant
8076	GO_EXORIBONUCLEASE_ACTIVITY	0.93	0.25	0	0	0	not significant
8077	GO_LYMPHANGIOGENESIS	0.93	0.25	0	0	0	not significant
8078	GO_MYOTUBE_CELL_DEVELOPMENT	0.93	0.25	0	0	0	not significant
8079	GO_NEGATIVE_REGULATION_OF_DNA_BINDING	0.93	0.25	0	0	0	not significant
8080	GO_NEGATIVE_REGULATION_OF_ENDOCYTOSIS	0.93	0.25	0	0	0	not significant
8081	GO_NEGATIVE_REGULATION_OF_MUSCLE_CONTRACTION	0.93	0.25	0	0	0	not significant
8082	GO_NEGATIVE_REGULATION_OF_PROGRAMMED_NECROTIC_CELL_DEATH	0.93	0.25	0	0	0	not significant
8083	GO_OVARIAN_FOLLICLE_DEVELOPMENT	0.93	0.25	0	0	0	not significant
8084	GO_PEPTIDYL_THREONINE_DEPHOSPHORYLATION	0.93	0.25	0	0	0	not significant
8085	GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	0.93	0.25	0	0	0	not significant
8086	GO_PLASMA_MEMBRANE_TUBULATION	0.93	0.25	0	0	0	not significant
8087	GO_POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	0.93	0.25	0	0	0	not significant
8088	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	0.93	0.25	0	0	0	not significant
8089	GO_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	0.93	0.25	0	0	0	not significant
8090	GO_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	0.93	0.25	0	0	0	not significant
8091	KEGG_SULFUR_METABOLISM	0.93	0.25	0	0	0	not significant
8092	LIU_TOPBP1_TARGETS	0.93	0.25	0	0	0	not significant
8093	REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	0.93	0.25	0	0	0	not significant
8094	REACTOME_LYSINE_CATABOLISM	0.93	0.25	0	0	0	not significant
8095	REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING	0.93	0.25	0	0	0	not significant
8096	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CELL_DEATH_GENES	0.93	0.25	0	0	0	not significant
8097	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN	0.93	0.24	0	0	0	not significant
8098	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREY_DN	0.93	0.24	0	0	0	not significant
8099	GO_KIDNEY_EPITHELIUM_DEVELOPMENT	0.93	0.24	0	0	0	not significant
8100	GO_LYMPHOCYTE_HOMEOSTASIS	0.93	0.24	0	0	0	not significant
8101	GO_MICROTUBULE_NUCLEATION_BY_INTERPHASE_MICROTUBULE_ORGANIZING_CE	0.93	0.24	0	0	0	not significant
8102	GO_MUSCLE_ALPHA_ACTININ_BINDING	0.93	0.24	0	0	0	not significant
8103	GO_ORGANOPHOSPHATE_CATABOLIC_PROCESS	0.93	0.24	0	0	0	not significant
8104	GO_PLACENTA_DEVELOPMENT	0.93	0.24	0	0	0	not significant
8105	GO_POLYUBIQUITIN_MODIFICATION_DEPENDENT_PROTEIN_BINDING	0.93	0.24	0	0	0	not significant
8106	GO_POSITIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	0.93	0.24	0	0	0	not significant
8107	GO_REGULATION_OF_AUTOPHAGY_OF_MITOCHONDRION	0.93	0.24	0	0	0	not significant
8108	GO_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	0.93	0.24	0	0	0	not significant
8109	GO_SIGNAL_TRANSDUCTION_INVOLVED_IN_REGULATION_OF_GENE_EXPRESSION	0.93	0.24	0	0	0	not significant
8110	GO_TRANSLATION_ELONGATION_FACTOR_ACTIVITY	0.93	0.24	0	0	0	not significant
8111	KEGG_ONE_CARBON_POOL_BY_FOLATE	0.93	0.24	0	0	0	not significant
8112	REACTOME_METABOLISM_OF_WATER_SOLUBLE_VITAMINS_AND_COFACTORS	0.93	0.24	0	0	0	not significant
8113	SEMBA_FHIT_TARGETS_UP	0.93	0.24	0	0	0	not significant
8114	DASU_IL6_SIGNALING_UP	0.93	0.23	0	0	0	not significant
8115	GO_GLYCOLIPID_TRANSPORT	0.93	0.23	0	0	0	not significant
8116	GO_HYDROXYMETHYL__FORMYL_AND_RELATED_TRANSFERASE_ACTIVITY	0.93	0.23	0	0	0	not significant
8117	GO_MYELOID_LEUKOCYTE_DIFFERENTIATION	0.93	0.23	0	0	0	not significant
8118	GO_REGULATION_OF_MEMBRANE_PERMEABILITY	0.93	0.23	0	0	0	not significant
8119	GO_SEMI_LUNAR_VALVE_DEVELOPMENT	0.93	0.23	0	0	0	not significant
8120	GO_SMOOTH_MUSCLE_CONTRACTION	0.93	0.23	0	0	0	not significant
8121	GO_SMOOTHENED_SIGNALING_PATHWAY	0.93	0.23	0	0	0	not significant
8122	GO_SYNAPTIC_VESICLE_CYCLE	0.93	0.23	0	0	0	not significant
8123	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER_THAN_ME	0.93	0.23	0	0	0	not significant
8124	ONDER_CDH1_TARGETS_2_UP	0.93	0.23	0	0	0	not significant
8125	REACTOME_PYRIMIDINE_SALVAGE	0.93	0.23	0	0	0	not significant
8126	YAN_ESCAPE_FROM_ANOIKIS	0.93	0.23	0	0	0	not significant
8127	BOQUEST_STEM_CELL_UP	0.93	0.22	0	0	0	not significant
8128	GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	0.93	0.22	0	0	0	not significant
8129	GO_EPSILON_DNA_POLYMERASE_COMPLEX	0.93	0.22	0	0	0	not significant
8130	GO_GERM_CELL_DEVELOPMENT	0.93	0.22	0	0	0	not significant
8131	GO_POSITIVE_REGULATION_OF_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	0.93	0.22	0	0	0	not significant
8132	GO_REGULATION_OF_TRANSPORTER_ACTIVITY	0.93	0.22	0	0	0	not significant
8133	GO_SENSORY_ORGAN_MORPHOGENESIS	0.93	0.22	0	0	0	not significant
8134	GO_SIGNAL_RELEASE_FROM_SYNAPSE	0.93	0.22	0	0	0	not significant
8135	HALLMARK_FATTY_ACID_METABOLISM	0.93	0.22	0	0	0	not significant
8136	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_UP	0.93	0.22	0	0	0	not significant
8137	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_DN	0.93	0.21	0	0	0	not significant
8138	DARWICHE_PAPILLOMA_RISK_HIGH_DN	0.93	0.21	0	0	0	not significant
8139	GO_COENZYME_METABOLIC_PROCESS	0.93	0.21	0	0	0	not significant
8140	GO_VESICLE_LUMEN	0.93	0.21	0	0	0	not significant
8141	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_UP	0.93	0.21	0	0	0	not significant
8142	GO_CELL_CELL_JUNCTION	0.93	0.2	0	0	0	not significant
8143	GO_DEVELOPMENT_OF_PRIMARY_SEXUAL_CHARACTERISTICS	0.93	0.2	0	0	0	not significant
8144	REACTOME_INTERFERON_SIGNALING	0.93	0.2	0	0	0	not significant
8145	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	0.93	0.17	0	0	0	not significant
8146	GO_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	0.93	0.17	0	0	0	not significant
8147	GO_ACTIVATION_OF_IMMUNE_RESPONSE	0.93	0.16	0	0	0	not significant
8148	WAKABAYASHI_ADIPOGENESIS_PPARG_BOUND_8D	0.93	0.16	0	0	0	not significant
8149	GO_FATTY_ACYL_COA_BINDING	0.94	0.28	0	0	0	not significant
8150	GO_FOUR_WAY_JUNCTION_DNA_BINDING	0.94	0.28	0	0	0	not significant
8151	GO_MICROVILLUS_MEMBRANE	0.94	0.28	0	0	0	not significant
8152	GO_NEGATIVE_REGULATION_OF_B_CELL_ACTIVATION	0.94	0.28	0	0	0	not significant
8153	GO_POSITIVE_REGULATION_OF_PROTEIN_DEACETYLATION	0.94	0.28	0	0	0	not significant
8154	GO_TRANSFORMING_GROWTH_FACTOR_BETA_ACTIVATION	0.94	0.28	0	0	0	not significant
8155	BIOCARTA_AHSP_PATHWAY	0.94	0.27	0	0	0	not significant
8156	GO_CILIARY_TRANSITION_ZONE	0.94	0.27	0	0	0	not significant
8157	GO_FATTY_ACID_HOMEOSTASIS	0.94	0.27	0	0	0	not significant
8158	GO_GALACTOSE_CATABOLIC_PROCESS	0.94	0.27	0	0	0	not significant
8159	GO_HOMOLOGOUS_CHROMOSOME_SEGREGATION	0.94	0.27	0	0	0	not significant
8160	GO_MYOSIN_COMPLEX	0.94	0.27	0	0	0	not significant
8161	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	0.94	0.27	0	0	0	not significant
8162	GO_NEGATIVE_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_NEURON_DEATH	0.94	0.27	0	0	0	not significant
8163	GO_NERVE_DEVELOPMENT	0.94	0.27	0	0	0	not significant

8164	GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TC	0.94	0.27	0	0	0	not significant
8165	GO_POSITIVE_REGULATION_OF_LIPID_STORAGE	0.94	0.27	0	0	0	not significant
8166	GO_POSITIVE_REGULATION_OF_P38MAPK_CASCADE	0.94	0.27	0	0	0	not significant
8167	GO_POSITIVE_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	0.94	0.27	0	0	0	not significant
8168	GO_PROTEIN_PHOSPHATASE_2A_BINDING	0.94	0.27	0	0	0	not significant
8169	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_DN	0.94	0.27	0	0	0	not significant
8170	PID_WNT_NONCANONICAL_PATHWAY	0.94	0.27	0	0	0	not significant
8171	REACTOME_NETRIN_1_SIGNALING	0.94	0.27	0	0	0	not significant
8172	BILANGES_SERUM_SENSITIVE_VIA_TSC1	0.94	0.26	0	0	0	not significant
8173	GO_CUL4B_RING_E3_UBIQUITIN_LIGASE_COMPLEX	0.94	0.26	0	0	0	not significant
8174	GO_HISTONE_DEUBIQUITINATION	0.94	0.26	0	0	0	not significant
8175	GO_INTERCELLULAR_BRIDGE	0.94	0.26	0	0	0	not significant
8176	GO_INVADOPODIUM	0.94	0.26	0	0	0	not significant
8177	GO_LYMPHOCYTE_COSTIMULATION	0.94	0.26	0	0	0	not significant
8178	GO_MESONEPHRIC_TUBULE_MORPHOGENESIS	0.94	0.26	0	0	0	not significant
8179	GO_METHYLATED_HISTONE_BINDING	0.94	0.26	0	0	0	not significant
8180	GO_MITOTIC_RECOMBINATION	0.94	0.26	0	0	0	not significant
8181	GO_NEGATIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.94	0.26	0	0	0	not significant
8182	GO_PARTURITION	0.94	0.26	0	0	0	not significant
8183	GO_POSITIVE_REGULATION_OF_PROTEIN_TARGETING_TO_MITOCHONDRION	0.94	0.26	0	0	0	not significant
8184	GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	0.94	0.26	0	0	0	not significant
8185	GO_REGULATION_OF_HEART_RATE_BY_CARDIAC_CONDUCTION	0.94	0.26	0	0	0	not significant
8186	GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_PERMEABILITY_INVOLVED_IN_	0.94	0.26	0	0	0	not significant
8187	GO_REGULATION_OF_PROTEIN_SUMOYLATION	0.94	0.26	0	0	0	not significant
8188	GO_REGULATION_OF_WOUND_HEALING	0.94	0.26	0	0	0	not significant
8189	GO_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	0.94	0.26	0	0	0	not significant
8190	JACKSON_DNMT1_TARGETS_UP	0.94	0.26	0	0	0	not significant
8191	KAMMINGA_SENESCENCE	0.94	0.26	0	0	0	not significant
8192	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAMMA_IN_WS	0.94	0.26	0	0	0	not significant
8193	LEE_LIVER_CANCER_MYC_UP	0.94	0.26	0	0	0	not significant
8194	MEISSNER_BRAIN_HCP_WITH_H3_UNMETHYLATED	0.94	0.26	0	0	0	not significant
8195	NOUZOVA_METHYLATED_IN_APL	0.94	0.26	0	0	0	not significant
8196	PID_INTEGRIN_A4B1_PATHWAY	0.94	0.26	0	0	0	not significant
8197	PID_INTEGRIN5_PATHWAY	0.94	0.26	0	0	0	not significant
8198	REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	0.94	0.26	0	0	0	not significant
8199	RODRIGUES_THYROID_CARCINOMA_UP	0.94	0.26	0	0	0	not significant
8200	YAP1_UP	0.94	0.26	0	0	0	not significant
8201	BIOCARTA_SODD_PATHWAY	0.94	0.25	0	0	0	not significant
8202	CHR11Q25	0.94	0.25	0	0	0	not significant
8203	CHR17P11	0.94	0.25	0	0	0	not significant
8204	CROONQUIST_STROMAL_STIMULATION_DN	0.94	0.25	0	0	0	not significant
8205	GO_ALDEHYDE_LYASE_ACTIVITY	0.94	0.25	0	0	0	not significant
8206	GO_LAMELLIPODIUM_MEMBRANE	0.94	0.25	0	0	0	not significant
8207	GO_MALE_SEX_DIFFERENTIATION	0.94	0.25	0	0	0	not significant
8208	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	0.94	0.25	0	0	0	not significant
8209	GO_NEGATIVE_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	0.94	0.25	0	0	0	not significant
8210	GO_NOTCH_BINDING	0.94	0.25	0	0	0	not significant
8211	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	0.94	0.25	0	0	0	not significant
8212	GO_REGULATION_OF_SECONDARY_METABOLIC_PROCESS	0.94	0.25	0	0	0	not significant
8213	GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	0.94	0.25	0	0	0	not significant
8214	KAUFFMANN_MELANOMA_RELAPSE_UP	0.94	0.25	0	0	0	not significant
8215	RAY_TUMORIGENESIS_BY_ERBB2_CDC25A_UP	0.94	0.25	0	0	0	not significant
8216	ROSS_AML_WITH_PML_RARA_FUSION	0.94	0.25	0	0	0	not significant
8217	SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES	0.94	0.25	0	0	0	not significant
8218	GO_HIGH_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	0.94	0.24	0	0	0	not significant
8219	GO_NEGATIVE_REGULATION_OF_SUPRAMOLECULAR_FIBER_ORGANIZATION	0.94	0.24	0	0	0	not significant
8220	GO_REGULATION_OF_EPIDERMAL_GROWTH_FACTOR_ACTIVATED_RECEPTOR_AC	0.94	0.24	0	0	0	not significant
8221	GO_REGULATION_OF_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWAY	0.94	0.24	0	0	0	not significant
8222	GO_TORC2_COMPLEX	0.94	0.24	0	0	0	not significant
8223	KEGG_ERBB_SIGNALING_PATHWAY	0.94	0.24	0	0	0	not significant
8224	REACTOME_DEX_H_BOX_HELICASES_ACTIVATE_TYPE_I_IFN_AND_INFLAMMATORY_	0.94	0.24	0	0	0	not significant
8225	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G	0.94	0.23	0	0	0	not significant
8226	GO_HORMONE_TRANSPORT	0.94	0.23	0	0	0	not significant
8227	GO_LIGASE_ACTIVITY_FORMING_PHOSPHORIC_ESTER_BONDS	0.94	0.23	0	0	0	not significant
8228	GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	0.94	0.23	0	0	0	not significant
8229	POOLA_INVASIVE_BREAST_CANCER_DN	0.94	0.23	0	0	0	not significant
8230	PUIFFE_INVASION_INHIBITED_BY_ASCITES_DN	0.94	0.23	0	0	0	not significant
8231	GO_NUCLEAR_MEMBRANE	0.94	0.21	0	0	0	not significant
8232	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP	0.94	0.2	0	0	0	not significant
8233	GO_DEVELOPMENTAL_PROCESS_INVOLVED_IN_REPRODUCTION	0.94	0.2	0	0	0	not significant
8234	GO_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	0.94	0.2	0	0	0	not significant
8235	GO_DEVELOPMENTAL_GROWTH	0.94	0.19	0	0	0	not significant
8236	NUYTTEN_EZH2_TARGETS_UP	0.94	0.16	0	0	0	not significant
8237	GO_CELLULAR_RESPONSE_TO_DNA_DAMAGE_STIMULUS	0.94	0.15	0	0	0	not significant
8238	GO_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	0.94	0.14	0	0	0	not significant
8239	GO_NEGATIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	0.94	0.13	0	0	0	not significant
8240	GO_DIGESTIVE_SYSTEM_PROCESS	0.95	0.3	0	0	0	not significant
8241	AMIT_EGF_RESPONSE_20_MCF10A	0.95	0.29	0	0	0	not significant
8242	GO_PROGRAMMED_NECROTIC_CELL_DEATH	0.95	0.29	0	0	0	not significant
8243	BIOCARTA_MAPK_PATHWAY	0.95	0.28	0	0	0	not significant
8244	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_UP	0.95	0.28	0	0	0	not significant
8245	CHR6Q27	0.95	0.28	0	0	0	not significant
8246	DER_IFN_GAMMA_RESPONSE_DN	0.95	0.28	0	0	0	not significant
8247	GO_BONE_RESORPTION	0.95	0.28	0	0	0	not significant
8248	GO_CILIARY_MEMBRANE	0.95	0.28	0	0	0	not significant
8249	GO_COFACTOR_CATABOLIC_PROCESS	0.95	0.28	0	0	0	not significant
8250	GO_ENDOCRINE_PANCREAS_DEVELOPMENT	0.95	0.28	0	0	0	not significant
8251	GO_MYELOID_CELL_APOPTOTIC_PROCESS	0.95	0.28	0	0	0	not significant
8252	GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	0.95	0.28	0	0	0	not significant
8253	GO_POSITIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	0.95	0.28	0	0	0	not significant
8254	GO_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	0.95	0.28	0	0	0	not significant
8255	GO_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	0.95	0.28	0	0	0	not significant
8256	GO_RESPONSE_TO_ISCHEMIA	0.95	0.28	0	0	0	not significant
8257	KYNG_DNA_DAMAGE_BY_UV	0.95	0.28	0	0	0	not significant
8258	PID_ARF6_PATHWAY	0.95	0.28	0	0	0	not significant
8259	REACTOME_O_LINKED_GLYCOSYLATION	0.95	0.28	0	0	0	not significant
8260	REACTOME_SULFUR_AMINO_ACID_METABOLISM	0.95	0.28	0	0	0	not significant
8261	SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_DN	0.95	0.28	0	0	0	not significant
8262	BCAT_GDS748_UP	0.95	0.27	0	0	0	not significant
8263	CHR18Q23	0.95	0.27	0	0	0	not significant
8264	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_UP	0.95	0.27	0	0	0	not significant
8265	GO_ACTIN_FILAMENT_SEVERING	0.95	0.27	0	0	0	not significant
8266	GO_AXON_EXTENSION	0.95	0.27	0	0	0	not significant
8267	GO_BRANCH_ELONGATION_OF_AN_EPITHELIUM	0.95	0.27	0	0	0	not significant
8268	GO_HIPPO_SIGNALING	0.95	0.27	0	0	0	not significant
8269	GO_MAP_KINASE_SCAFFOLD_ACTIVITY	0.95	0.27	0	0	0	not significant
8270	GO_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABILIZATION	0.95	0.27	0	0	0	not significant
8271	GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_S	0.95	0.27	0	0	0	not significant
8272	GO_NEGATIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	0.95	0.27	0	0	0	not significant

8273	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTRACELLULAR_STIMULUS	0.95	0.27	0	0	0	not significant
8274	GO_OVULATION	0.95	0.27	0	0	0	not significant
8275	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS_C	0.95	0.27	0	0	0	not significant
8276	GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RE	0.95	0.27	0	0	0	not significant
8277	GO_REGULATION_OF_PEPTIDYL_LYSINE_ACETYLATION	0.95	0.27	0	0	0	not significant
8278	GO_TOXIN_METABOLIC_PROCESS	0.95	0.27	0	0	0	not significant
8279	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_NITROGENOUS_GROUPS	0.95	0.27	0	0	0	not significant
8280	HOEGERKORP_CD44_TARGETS_TEMPORAL_DN	0.95	0.27	0	0	0	not significant
8281	IL15_UP.V1_UP	0.95	0.27	0	0	0	not significant
8282	PID_P53_DOWNSTREAM_PATHWAY	0.95	0.27	0	0	0	not significant
8283	REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS	0.95	0.27	0	0	0	not significant
8284	SESTO_RESPONSE_TO_UV_C8	0.95	0.27	0	0	0	not significant
8285	GO_ANKYRIN_BINDING	0.95	0.26	0	0	0	not significant
8286	GO_AUTOLYSOSOME	0.95	0.26	0	0	0	not significant
8287	GO_CARBOHYDRATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.95	0.26	0	0	0	not significant
8288	GO_CARBOHYDRATE_TRANSPORT	0.95	0.26	0	0	0	not significant
8289	GO_CELL_MATURATION	0.95	0.26	0	0	0	not significant
8290	GO_CELLULAR_RESPONSE_TO_X_RAY	0.95	0.26	0	0	0	not significant
8291	GO_DISTAL_AXON	0.95	0.26	0	0	0	not significant
8292	GO_G_QUADRUPLEX_RNA_BINDING	0.95	0.26	0	0	0	not significant
8293	GO_GLYCEROLIPID_BIOSYNTHETIC_PROCESS	0.95	0.26	0	0	0	not significant
8294	GO_INTRA_S_DNA_DAMAGE_CHECKPOINT	0.95	0.26	0	0	0	not significant
8295	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	0.95	0.26	0	0	0	not significant
8296	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	0.95	0.26	0	0	0	not significant
8297	GO_PERK_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	0.95	0.26	0	0	0	not significant
8298	GO_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS	0.95	0.26	0	0	0	not significant
8299	GO_POSITIVE_REGULATION_OF_PROTEIN_ACETYLATION	0.95	0.26	0	0	0	not significant
8300	GO_PROTEIN_AUTOPROCESSING	0.95	0.26	0	0	0	not significant
8301	GO_PROTON_TRANSMEMBRANE_TRANSPORT	0.95	0.26	0	0	0	not significant
8302	GO_PROTON_TRANSPORTING_V_TYPE_ATPASE_COMPLEX	0.95	0.26	0	0	0	not significant
8303	GO_REGULATION_OF_DENDRITE_MORPHOGENESIS	0.95	0.26	0	0	0	not significant
8304	GO_RNA_POLYMERASE_II_C_TERMINAL_DOMAIN_BINDING	0.95	0.26	0	0	0	not significant
8305	GO_SMOOTH_ENDOPLASMIC_RETICULUM	0.95	0.26	0	0	0	not significant
8306	GO_VERY_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	0.95	0.26	0	0	0	not significant
8307	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_UP	0.95	0.26	0	0	0	not significant
8308	MELLMAN_TUT1_TARGETS_DN	0.95	0.26	0	0	0	not significant
8309	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_DN	0.95	0.26	0	0	0	not significant
8310	NIKOLSKY_BREAST_CANCER_11Q12_Q14_AMPLICON	0.95	0.26	0	0	0	not significant
8311	PID_PDGFRB_PATHWAY	0.95	0.26	0	0	0	not significant
8312	REACTOME_ASPARTATE_AND_ASPARAGINE_METABOLISM	0.95	0.26	0	0	0	not significant
8313	WOOD_EBV_EBNA1_TARGETS_UP	0.95	0.26	0	0	0	not significant
8314	ZHANG_GATA6_TARGETS_UP	0.95	0.26	0	0	0	not significant
8315	GAL_LEUKEMIC_STEM_CELL_UP	0.95	0.25	0	0	0	not significant
8316	GAUSSMANN_MLL_AF4_FUSION_TARGETS_C_UP	0.95	0.25	0	0	0	not significant
8317	GO_CELLULAR_RESPONSE_TO_RADIATION	0.95	0.25	0	0	0	not significant
8318	GO_CYTOKINE_RECEPTOR_BINDING	0.95	0.25	0	0	0	not significant
8319	GO_DEVELOPMENTAL_GROWTH_INVOLVED_IN_MORPHOGENESIS	0.95	0.25	0	0	0	not significant
8320	GO_GPI_ANCHOR_TRANSAMIDASE_ACTIVITY	0.95	0.25	0	0	0	not significant
8321	GO_HEART_MORPHOGENESIS	0.95	0.25	0	0	0	not significant
8322	GO_LYSINE_CATABOLIC_PROCESS	0.95	0.25	0	0	0	not significant
8323	GO_NEGATIVE_REGULATION_OF_VASOCONSTRICTION	0.95	0.25	0	0	0	not significant
8324	GO_RECEPTOR_ANTAGONIST_ACTIVITY	0.95	0.25	0	0	0	not significant
8325	GO_TRIGLYCERIDE_LIPASE_ACTIVITY	0.95	0.25	0	0	0	not significant
8326	HALLMARK_COMPLEMENT	0.95	0.25	0	0	0	not significant
8327	LIM_MAMMARY_STEM_CELL_UP	0.95	0.25	0	0	0	not significant
8328	PETRETTO_BLOOD_PRESSURE_DN	0.95	0.25	0	0	0	not significant
8329	REACTOME_SIGNALING_BY_NOTCH2	0.95	0.25	0	0	0	not significant
8330	GO_PEPTIDYL_LYSINE_METHYLATION	0.95	0.24	0	0	0	not significant
8331	GO_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	0.95	0.24	0	0	0	not significant
8332	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN	0.95	0.24	0	0	0	not significant
8333	SWEET_LUNG_CANCER_KRAS_DN	0.95	0.24	0	0	0	not significant
8334	GO_REGULATION_OF_CELL_MORPHOGENESIS	0.95	0.23	0	0	0	not significant
8335	BONOME_OVARIAN_CANCER_SURVIVAL_SUBOPTIMAL_DEBULKING	0.95	0.21	0	0	0	not significant
8336	GO_HYDROLASE_ACTIVITY_ACTING_ON_ESTER_BONDS	0.95	0.2	0	0	0	not significant
8337	GO_TRANSCRIPTION_FACTOR_BINDING	0.95	0.2	0	0	0	not significant
8338	GO_CELL_JUNCTION	0.95	0.19	0	0	0	not significant
8339	BOYLAN_MULTIPLE_MYELOMA_PCA3_DN	0.96	0.31	0	0	0	not significant
8340	GO_CYTOPLASMIC_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY_IN	0.96	0.31	0	0	0	not significant
8341	GO_PEPTIDYL_L_CYSTEINE_S_PALMITOYLATION	0.96	0.3	0	0	0	not significant
8342	GO_POSITIVE_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	0.96	0.3	0	0	0	not significant
8343	GO_TRANSCRIPTION_COREPRESSOR_BINDING	0.96	0.3	0	0	0	not significant
8344	GO_TRANSLATION_REPRESSOR_ACTIVITY	0.96	0.3	0	0	0	not significant
8345	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	0.96	0.3	0	0	0	not significant
8346	PID_PI3K_PLC_TRK_PATHWAY	0.96	0.3	0	0	0	not significant
8347	ZHENG_GLIOBLASTOMA_PLASTICITY_DN	0.96	0.3	0	0	0	not significant
8348	DER_IFN_BETA_RESPONSE_UP	0.96	0.29	0	0	0	not significant
8349	GO_ARMADILLO_REPEAT_DOMAIN_BINDING	0.96	0.29	0	0	0	not significant
8350	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_VACUOLE	0.96	0.29	0	0	0	not significant
8351	GO_G1_DNA_DAMAGE_CHECKPOINT	0.96	0.29	0	0	0	not significant
8352	GO_GOLGI_TO_ENDOSOME_TRANSPORT	0.96	0.29	0	0	0	not significant
8353	GO_KETONE_BIOSYNTHETIC_PROCESS	0.96	0.29	0	0	0	not significant
8354	GO_MICROVILLUS	0.96	0.29	0	0	0	not significant
8355	GO_NEGATIVE_REGULATION_OF_GTPASE_ACTIVITY	0.96	0.29	0	0	0	not significant
8356	GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGNALING_PAT	0.96	0.29	0	0	0	not significant
8357	GO_REGULATION_OF_CELLULAR_EXTRAVASATION	0.96	0.29	0	0	0	not significant
8358	GO_REGULATION_OF_DNA_REPLICATION	0.96	0.29	0	0	0	not significant
8359	KEGG_AXON_GUIDANCE	0.96	0.29	0	0	0	not significant
8360	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_2_DN	0.96	0.29	0	0	0	not significant
8361	RUAN_RESPONSE_TO_TNF_DN	0.96	0.29	0	0	0	not significant
8362	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_DN	0.96	0.29	0	0	0	not significant
8363	ZHAN_MULTIPLE_MYELOMA_CD1_DN	0.96	0.29	0	0	0	not significant
8364	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_48HR_DN	0.96	0.28	0	0	0	not significant
8365	BROWNE_HCMV_INFECTION_2HR_DN	0.96	0.28	0	0	0	not significant
8366	CHEOK_RESPONSE_TO_MERCAPTOPURINE_DN	0.96	0.28	0	0	0	not significant
8367	GAVIN_FOXP3_TARGETS_CLUSTER_P4	0.96	0.28	0	0	0	not significant
8368	GO_ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_OF_IONS_R	0.96	0.28	0	0	0	not significant
8369	GO_EPIDERMIS_MORPHOGENESIS	0.96	0.28	0	0	0	not significant
8370	GO_HOPS_COMPLEX	0.96	0.28	0	0	0	not significant
8371	GO_INFLAMMATORY_CELL_APOPTOTIC_PROCESS	0.96	0.28	0	0	0	not significant
8372	GO_INTRACELLULAR_STEROL_TRANSPORT	0.96	0.28	0	0	0	not significant
8373	GO_MAGNESIUM_DEPENDENT_PROTEIN_SERINE_THREONINE_PHOSPHATASE_ACTI	0.96	0.28	0	0	0	not significant
8374	GO_MONOSACCHARIDE_BINDING	0.96	0.28	0	0	0	not significant
8375	GO_NEGATIVE_REGULATION_OF_AXONOGENESIS	0.96	0.28	0	0	0	not significant
8376	GO_NEGATIVE_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	0.96	0.28	0	0	0	not significant
8377	GO_NEGATIVE_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	0.96	0.28	0	0	0	not significant
8378	GO_NUCLEOSIDE_CATABOLIC_PROCESS	0.96	0.28	0	0	0	not significant
8379	GO_PHAGOSOME_ACIDIFICATION	0.96	0.28	0	0	0	not significant
8380	GO_PHOSPHATIDYLINOSITOL_BIOSYNTHETIC_PROCESS	0.96	0.28	0	0	0	not significant
8381	GO_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	0.96	0.28	0	0	0	not significant

8382	GO_REGULATION_OF_AUTOPHAGY_OF_MITOCHONDRION_IN_RESPONSE_TO_MITC	0.96	0.28	0	0	0	not significant
8383	GO_REGULATION_OF_RESPONSE_TO_WOUNDING	0.96	0.28	0	0	0	not significant
8384	HOFMANN_MYELODYSPLASTIC_SYNDROM_HIGH_RISK_DN	0.96	0.28	0	0	0	not significant
8385	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.96	0.28	0	0	0	not significant
8386	KESHELAVA_MULTIPLE_DRUG_RESISTANCE	0.96	0.28	0	0	0	not significant
8387	MARSON_FOXP3_TARGETS_STIMULATED_UP	0.96	0.28	0	0	0	not significant
8388	REACTOME_COMPETING_ENDOGENOUS_RNAS_CERNAS_REGULATE_PTEN_TRANS	0.96	0.28	0	0	0	not significant
8389	REACTOME_PROCESSING_OF_DNA_DOUBLE_STRAND_BREAK_ENDS	0.96	0.28	0	0	0	not significant
8390	STAEGE_EWING_FAMILY_TUMOR	0.96	0.28	0	0	0	not significant
8391	WENG_POR_TARGETS_LIVER_DN	0.96	0.28	0	0	0	not significant
8392	CHRYQ11	0.96	0.27	0	0	0	not significant
8393	GO_ALPHA_DNA_POLYMERASE_PRIMASE_COMPLEX	0.96	0.27	0	0	0	not significant
8394	GO_APICOLATERAL_PLASMA_MEMBRANE	0.96	0.27	0	0	0	not significant
8395	GO_ASTROCYTE_DEVELOPMENT	0.96	0.27	0	0	0	not significant
8396	GO_ESTABLISHMENT_OF_ENDOTHELIAL_BARRIER	0.96	0.27	0	0	0	not significant
8397	GO_NEUROTRANSMITTER_TRANSPORT	0.96	0.27	0	0	0	not significant
8398	GO_OXIDIZED_DNA_BINDING	0.96	0.27	0	0	0	not significant
8399	GO_POSITIVE_REGULATION_OF_SYNAPTIC_VESICLE_RECYCLING	0.96	0.27	0	0	0	not significant
8400	GO_POSITIVE_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	0.96	0.27	0	0	0	not significant
8401	GO_PROTEIN_HYDROXYLATION	0.96	0.27	0	0	0	not significant
8402	GO_REGULATION_OF_APPETITE	0.96	0.27	0	0	0	not significant
8403	GO_REGULATION_OF_DEACETYLASE_ACTIVITY	0.96	0.27	0	0	0	not significant
8404	GO_RESPONSE_TO_FOLIC_ACID	0.96	0.27	0	0	0	not significant
8405	GO_SECONDARY_LYSOSOME	0.96	0.27	0	0	0	not significant
8406	KEGG_PROSTATE_CANCER	0.96	0.27	0	0	0	not significant
8407	LIEN_BREAST_CARCINOMA_METAPLASTIC	0.96	0.27	0	0	0	not significant
8408	REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	0.96	0.27	0	0	0	not significant
8409	STEGER_ADIPOGENESIS_UP	0.96	0.27	0	0	0	not significant
8410	VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_DN	0.96	0.27	0	0	0	not significant
8411	BASSO_HAIRY_CELL_LEUKEMIA_UP	0.96	0.26	0	0	0	not significant
8412	GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_HEAR	0.96	0.26	0	0	0	not significant
8413	GO_HEPARIN_BIOSYNTHETIC_PROCESS	0.96	0.26	0	0	0	not significant
8414	GO_MAP_KINASE_PHOSPHATASE_ACTIVITY	0.96	0.26	0	0	0	not significant
8415	GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS	0.96	0.26	0	0	0	not significant
8416	GO_NEGATIVE_REGULATION_OF_MAST_CELL_ACTIVATION	0.96	0.26	0	0	0	not significant
8417	GO_NEGATIVE_REGULATION_OF_PROTEOLYSIS	0.96	0.26	0	0	0	not significant
8418	GO_NUCLEAR_HORMONE_RECEPTOR_BINDING	0.96	0.26	0	0	0	not significant
8419	GO_PHOSPHORYLASE_KINASE_COMPLEX	0.96	0.26	0	0	0	not significant
8420	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	0.96	0.26	0	0	0	not significant
8421	GO_POSITIVE_THYMIC_T_CELL_SELECTION	0.96	0.26	0	0	0	not significant
8422	GO_REGULATION_OF_FERTILIZATION	0.96	0.26	0	0	0	not significant
8423	OKUMURA_INFLAMMATORY_RESPONSE_LPS	0.96	0.26	0	0	0	not significant
8424	GO_GPI_ANCHOR_TRANSAMIDASE_COMPLEX	0.96	0.25	0	0	0	not significant
8425	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN	0.96	0.25	0	0	0	not significant
8426	GO_NUCLEAR_ENVELOPE	0.96	0.24	0	0	0	not significant
8427	GO_POSITIVE_REGULATION_OF_MUSCLE_ADAPTATION	0.96	0.24	0	0	0	not significant
8428	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	0.96	0.22	0	0	0	not significant
8429	GO_KINASE_BINDING	0.96	0.21	0	0	0	not significant
8430	GO_POSITIVE_REGULATION_OF_RNA_BIOSYNTHETIC_PROCESS	0.96	0.19	0	0	0	not significant
8431	GO_VISUAL_BEHAVIOR	0.97	0.32	0	0	0	not significant
8432	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN	0.97	0.31	0	0	0	not significant
8433	CHR10P12	0.97	0.31	0	0	0	not significant
8434	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_REGULATOR_ACTIVITY_INVOLVED_IN_APOI	0.97	0.31	0	0	0	not significant
8435	GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY	0.97	0.31	0	0	0	not significant
8436	GO_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	0.97	0.31	0	0	0	not significant
8437	GO_REGULATION_OF_POTASSIUM_ION_TRANSPORT	0.97	0.31	0	0	0	not significant
8438	GO_RESPONSE_TO_MITOCHONDRIAL_DEPOLARISATION	0.97	0.31	0	0	0	not significant
8439	REACTOME_RAB_REGULATION_OF_TRAFFICKING	0.97	0.31	0	0	0	not significant
8440	REACTOME_SIGNALING_BY_SCF_KIT	0.97	0.31	0	0	0	not significant
8441	BAE_BRCA1_TARGETS_DN	0.97	0.3	0	0	0	not significant
8442	CHR13Q34	0.97	0.3	0	0	0	not significant
8443	CHR5Q12	0.97	0.3	0	0	0	not significant
8444	GO_1_PHOSPHATIDYLINOSITOL_BINDING	0.97	0.3	0	0	0	not significant
8445	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVATOR_ACTIVITY_INVOLVED_IN_APOP	0.97	0.3	0	0	0	not significant
8446	GO_LABYRINTHINE_LAYER_DEVELOPMENT	0.97	0.3	0	0	0	not significant
8447	GO_NEGATIVE_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	0.97	0.3	0	0	0	not significant
8448	GO_POSITIVE_REGULATION_OF_LIPID_KINASE_ACTIVITY	0.97	0.3	0	0	0	not significant
8449	GO_POSITIVE_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	0.97	0.3	0	0	0	not significant
8450	GO_RECEPTOR_MEDIATED_ENDOCYTOSIS	0.97	0.3	0	0	0	not significant
8451	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_DN	0.97	0.3	0	0	0	not significant
8452	RAMPON_ENRICHED_LEARNING_ENVIRONMENT_LATE_UP	0.97	0.3	0	0	0	not significant
8453	REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES	0.97	0.3	0	0	0	not significant
8454	WANG_CLASSIC_ADIPOGENIC_TARGETS_OF_PPARG	0.97	0.3	0	0	0	not significant
8455	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_UP	0.97	0.29	0	0	0	not significant
8456	BENPORATH_MYC_TARGETS_WITH_EBOX	0.97	0.29	0	0	0	not significant
8457	CHR2Q31	0.97	0.29	0	0	0	not significant
8458	GO_DNA_INTEGRITY_CHECKPOINT	0.97	0.29	0	0	0	not significant
8459	GO_DNA_SECONDARY_STRUCTURE_BINDING	0.97	0.29	0	0	0	not significant
8460	GO_IKAPPAB_KINASE_COMPLEX	0.97	0.29	0	0	0	not significant
8461	GO_LONG_CHAIN_FATTY_ACID_BIOSYNTHETIC_PROCESS	0.97	0.29	0	0	0	not significant
8462	GO_MAMMARY_GLAND_EPITHELIAL_CELL_PROLIFERATION	0.97	0.29	0	0	0	not significant
8463	GO_NEGATIVE_REGULATION_OF_PROTEIN_OLIGOMERIZATION	0.97	0.29	0	0	0	not significant
8464	GO_PHOSPHATIDYLINOSITOL_KINASE_ACTIVITY	0.97	0.29	0	0	0	not significant
8465	GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_5_PHOSPHATASE_ACTIVITY	0.97	0.29	0	0	0	not significant
8466	GO_POSITIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	0.97	0.29	0	0	0	not significant
8467	GO_REGULATION_OF_CELL_CYCLE_ARREST	0.97	0.29	0	0	0	not significant
8468	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	0.97	0.29	0	0	0	not significant
8469	GO_RIPOPTOSOME	0.97	0.29	0	0	0	not significant
8470	GO_SIGNAL_RECOGNITION_PARTICLE	0.97	0.29	0	0	0	not significant
8471	GROSS_ELK3_TARGETS_DN	0.97	0.29	0	0	0	not significant
8472	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP	0.97	0.29	0	0	0	not significant
8473	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	0.97	0.29	0	0	0	not significant
8474	REACTOME_INHIBITION_OF_REPLICATION_INITIATION_OF_DAMAGED_DNA_BY_RB1	0.97	0.29	0	0	0	not significant
8475	REACTOME_RUNX3_REGULATES_CDKN1A_TRANSCRIPTION	0.97	0.29	0	0	0	not significant
8476	REACTOME_SIALIC_ACID_METABOLISM	0.97	0.29	0	0	0	not significant
8477	RODWELL_AGING_KIDNEY_NO_BLOOD_DN	0.97	0.29	0	0	0	not significant
8478	SASSON_RESPONSE_TO_FORSKOLIN_DN	0.97	0.29	0	0	0	not significant
8479	VETTER_TARGETS_OF_PRKCA_AND_ETS1_DN	0.97	0.29	0	0	0	not significant
8480	ZHANG_PROLIFERATING_VS_QUIESCENT	0.97	0.29	0	0	0	not significant
8481	CHR6P23	0.97	0.28	0	0	0	not significant
8482	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_UP	0.97	0.28	0	0	0	not significant
8483	GO_ATTACHMENT_OF_GPI_ANCHOR_TO_PROTEIN	0.97	0.28	0	0	0	not significant
8484	GO_GDP_DISSOCIATION_INHIBITOR_ACTIVITY	0.97	0.28	0	0	0	not significant
8485	GO_GLYCOSPHINGOLIPID_BINDING	0.97	0.28	0	0	0	not significant
8486	GO_MODIFICATION_DEPENDENT_PROTEIN_BINDING	0.97	0.28	0	0	0	not significant
8487	GO_NEGATIVE_REGULATION_OF_B_CELL_APOPTOTIC_PROCESS	0.97	0.28	0	0	0	not significant
8488	GO_NEGATIVE_REGULATION_OF_ERBB_SIGNALING_PATHWAY	0.97	0.28	0	0	0	not significant
8489	GO_NEGATIVE_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	0.97	0.28	0	0	0	not significant
8490	GO_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	0.97	0.28	0	0	0	not significant

8491	IIZUKA_LIVER_CANCER_PROGRESSION_L0_L1_DN	0.97	0.28	0	0	0	not significant
8492	REACTOME_CYTOSOLIC_IRON_SULFUR_CLUSTER_ASSEMBLY	0.97	0.28	0	0	0	not significant
8493	VALK_AML_WITH_CEBPA	0.97	0.28	0	0	0	not significant
8494	WOTTON_RUNX_TARGETS_UP	0.97	0.28	0	0	0	not significant
8495	ZHAN_EARLY_DIFFERENTIATION_GENES_DN	0.97	0.28	0	0	0	not significant
8496	BIOCARTA_STAT3_PATHWAY	0.97	0.27	0	0	0	not significant
8497	GO_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	0.97	0.27	0	0	0	not significant
8498	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DEGRANULATION	0.97	0.27	0	0	0	not significant
8499	GO_NEGATIVE_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_	0.97	0.27	0	0	0	not significant
8500	GO_PARAXIAL_MESODERM_MORPHOGENESIS	0.97	0.27	0	0	0	not significant
8501	GO_PHAGOLYSOSOME_ASSEMBLY	0.97	0.27	0	0	0	not significant
8502	GO_PHOSPHORYLASE_KINASE_ACTIVITY	0.97	0.27	0	0	0	not significant
8503	GO_POSITIVE_REGULATION_OF_CELL_CYCLE_ARREST	0.97	0.27	0	0	0	not significant
8504	GO_PROTEIN_O_LINKED_FUCOSYLATION	0.97	0.27	0	0	0	not significant
8505	GO_SUMO_LIGASE_ACTIVITY	0.97	0.27	0	0	0	not significant
8506	MARTINEZ_TP53_TARGETS_DN	0.97	0.27	0	0	0	not significant
8507	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_16	0.97	0.27	0	0	0	not significant
8508	BROWNE_HCMV_INFECTION_14HR_DN	0.97	0.26	0	0	0	not significant
8509	GO_AXON	0.97	0.26	0	0	0	not significant
8510	GO_PHOSPHATIDYLINOSITOL_BINDING	0.97	0.26	0	0	0	not significant
8511	GO_PHOSPHATIDYLINOSITOL_BISPHOSPHATE_KINASE_ACTIVITY	0.97	0.26	0	0	0	not significant
8512	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP	0.97	0.25	0	0	0	not significant
8513	GO_NEGATIVE_REGULATION_OF_SIGNALING	0.97	0.22	0	0	0	not significant
8514	GO_APOPTOTIC_PROCESS	0.97	0.21	0	0	0	not significant
8515	GO_NEUROGENESIS	0.97	0.21	0	0	0	not significant
8516	GO_NEURON_PART	0.97	0.21	0	0	0	not significant
8517	GO_REGULATION_OF_CELL_DIFFERENTIATION	0.97	0.2	0	0	0	not significant
8518	GO_PROTEIN_LOCALIZATION_TO_LYSOSOME	0.98	0.34	0	0	0	not significant
8519	NOTCH_DN.V1_DN	0.98	0.34	0	0	0	not significant
8520	GO_ENDODERM_DEVELOPMENT	0.98	0.33	0	0	0	not significant
8521	GO_PROTON_TRANSPORTING_ATPASE_ACTIVITY_ROTATIONAL_MECHANISM	0.98	0.33	0	0	0	not significant
8522	GO_RESPONSE_TO_ETHANOL	0.98	0.33	0	0	0	not significant
8523	PDGF_UP.V1_UP	0.98	0.33	0	0	0	not significant
8524	BIOCARTA_HDAC_PATHWAY	0.98	0.32	0	0	0	not significant
8525	CHR22Q11	0.98	0.32	0	0	0	not significant
8526	GO_CELL_CELL_JUNCTION_ORGANIZATION	0.98	0.32	0	0	0	not significant
8527	GO_CELLULAR_RESPONSE_TO_AMMONIUM_ION	0.98	0.32	0	0	0	not significant
8528	GO_HETEROPHILIC_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHES	0.98	0.32	0	0	0	not significant
8529	GO_NEGATIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	0.98	0.32	0	0	0	not significant
8530	GO_PHOSPHATIDYLINOSITOL_4_5_BISPHOSPHATE_BINDING	0.98	0.32	0	0	0	not significant
8531	GO_POSITIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	0.98	0.32	0	0	0	not significant
8532	GO_PROTON_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.98	0.32	0	0	0	not significant
8533	GO_REGULATION_OF_CD8_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	0.98	0.32	0	0	0	not significant
8534	KEGG_LYSINE_DEGRADATION	0.98	0.32	0	0	0	not significant
8535	REACTOME_NOTCH_HLH_TRANSCRIPTION_PATHWAY	0.98	0.32	0	0	0	not significant
8536	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_48HR_UP	0.98	0.31	0	0	0	not significant
8537	BCAT_GDS748_DN	0.98	0.31	0	0	0	not significant
8538	DORSAM_HOXA9_TARGETS_UP	0.98	0.31	0	0	0	not significant
8539	GO_ACTIN_FILAMENT_DEPOLYMERIZATION	0.98	0.31	0	0	0	not significant
8540	GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	0.98	0.31	0	0	0	not significant
8541	GO_CELL_ADHESION_MEDIATOR_ACTIVITY	0.98	0.31	0	0	0	not significant
8542	GO_CELL_DEATH_IN_RESPONSE_TO_HYDROGEN_PEROXIDE	0.98	0.31	0	0	0	not significant
8543	GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY_COUPLED_TO_CYC	0.98	0.31	0	0	0	not significant
8544	GO_MONOSACCHARIDE_METABOLIC_PROCESS	0.98	0.31	0	0	0	not significant
8545	GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	0.98	0.31	0	0	0	not significant
8546	GO_NEUROTRANSMITTER_BINDING	0.98	0.31	0	0	0	not significant
8547	GO_NEUTRAL_LIPID_BIOSYNTHETIC_PROCESS	0.98	0.31	0	0	0	not significant
8548	GO_POSITIVE_REGULATION_OF_MACROAUTOPHAGY	0.98	0.31	0	0	0	not significant
8549	GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	0.98	0.31	0	0	0	not significant
8550	GO_POSITIVE_REGULATION_OF_PEPTIDYL_LYSINE_ACETYLATION	0.98	0.31	0	0	0	not significant
8551	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	0.98	0.31	0	0	0	not significant
8552	GO_PTERIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	0.98	0.31	0	0	0	not significant
8553	GO_REGULATION_OF_AXONOGENESIS	0.98	0.31	0	0	0	not significant
8554	GO_REGULATION_OF_OSSIFICATION	0.98	0.31	0	0	0	not significant
8555	GO_RHO_PROTEIN_SIGNAL_TRANSDUCTION	0.98	0.31	0	0	0	not significant
8556	GO_TRANSLESION_SYNTHESIS	0.98	0.31	0	0	0	not significant
8557	GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_SUPERFAMILY_BINDING	0.98	0.31	0	0	0	not significant
8558	GRABARCZYK_BCL11B_TARGETS_DN	0.98	0.31	0	0	0	not significant
8559	MARSON_FOXP3_TARGETS_UP	0.98	0.31	0	0	0	not significant
8560	REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR	0.98	0.31	0	0	0	not significant
8561	REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	0.98	0.31	0	0	0	not significant
8562	REACTOME_ROBO_RECEPTORS_BIND_AKAP5	0.98	0.31	0	0	0	not significant
8563	SMITH_TERT_TARGETS_DN	0.98	0.31	0	0	0	not significant
8564	CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70	0.98	0.3	0	0	0	not significant
8565	CHR3Q21	0.98	0.3	0	0	0	not significant
8566	CHR6P25	0.98	0.3	0	0	0	not significant
8567	CHR6Q13	0.98	0.3	0	0	0	not significant
8568	GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	0.98	0.3	0	0	0	not significant
8569	GO_ERK1_AND_ERK2_CASCADE	0.98	0.3	0	0	0	not significant
8570	GO_EXTRINSIC_COMPONENT_OF_ORGANELLE_MEMBRANE	0.98	0.3	0	0	0	not significant
8571	GO_REGULATION_OF_KIDNEY_DEVELOPMENT	0.98	0.3	0	0	0	not significant
8572	GO_RETROGRADE_TRANSPORT_ENDOSOME_TO_PLASMA_MEMBRANE	0.98	0.3	0	0	0	not significant
8573	GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	0.98	0.3	0	0	0	not significant
8574	GO_WOUND_HEALING	0.98	0.3	0	0	0	not significant
8575	IVANOVA_HEMATOPOIESIS_STEM_CELL_AND_PROGENITOR	0.98	0.3	0	0	0	not significant
8576	KONDO_COLON_CANCER_HCP_WITH_H3K27ME1	0.98	0.3	0	0	0	not significant
8577	LEF1_UP.V1_UP	0.98	0.3	0	0	0	not significant
8578	PASTURAL_RIZ1_TARGETS_UP	0.98	0.3	0	0	0	not significant
8579	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_DN	0.98	0.3	0	0	0	not significant
8580	REACTOME_PTK6_REGULATES_RTKS_AND_THEIR_EFFECTORS_AKT1_AND_DOK1	0.98	0.3	0	0	0	not significant
8581	REACTOME_SMOOTH_MUSCLE_CONTRACTION	0.98	0.3	0	0	0	not significant
8582	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX1_DN	0.98	0.3	0	0	0	not significant
8583	SCHAVOLT_TARGETS_OF_TP53_AND_TP63	0.98	0.3	0	0	0	not significant
8584	YANAGISAWA_LUNG_CANCER_RECURRENCE	0.98	0.3	0	0	0	not significant
8585	BIOCARTA_IL4_PATHWAY	0.98	0.29	0	0	0	not significant
8586	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_D	0.98	0.29	0	0	0	not significant
8587	GO_METAL_ION_HOMEOSTASIS	0.98	0.29	0	0	0	not significant
8588	GO_NEGATIVE_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	0.98	0.29	0	0	0	not significant
8589	GO_NEGATIVE_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	0.98	0.29	0	0	0	not significant
8590	GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	0.98	0.29	0	0	0	not significant
8591	GO_SOMATODENDRITIC_COMPARTMENT	0.98	0.29	0	0	0	not significant
8592	GO_SYNAPSE_ORGANIZATION	0.98	0.29	0	0	0	not significant
8593	GO_VESICLE_FUSION_TO_PLASMA_MEMBRANE	0.98	0.29	0	0	0	not significant
8594	KEGG_VEGF_SIGNALING_PATHWAY	0.98	0.29	0	0	0	not significant
8595	REACTOME_METABOLISM_OF_CARBOHYDRATES	0.98	0.29	0	0	0	not significant
8596	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP	0.98	0.29	0	0	0	not significant
8597	ZIRN_TRETINOIN_RESPONSE_WT1_UP	0.98	0.29	0	0	0	not significant
8598	GO_EXTRINSIC_COMPONENT_OF_MEMBRANE	0.98	0.28	0	0	0	not significant
8599	GO_FOREGUT_MORPHOGENESIS	0.98	0.28	0	0	0	not significant

8600	GO_NEGATIVE_REGULATION_OF_CYTOPLASMIC_TRANSLATION	0.98	0.28	0	0	0	not significant
8601	GO_POSITIVE_REGULATION_OF_CENTROSOME_DUPLICATION	0.98	0.28	0	0	0	not significant
8602	GO_PROTEIN_RETENTION_IN_ER_LUMEN	0.98	0.28	0	0	0	not significant
8603	GO_RESPONSE_TO_METAL_ION	0.98	0.28	0	0	0	not significant
8604	SCHLOSSER_SERUM_RESPONSE_DN	0.98	0.27	0	0	0	not significant
8605	GO_AUTOPHAGOSOME_MATURATION	0.99	0.35	0	0	0	not significant
8606	GO_PEPTIDE_HORMONE_SECRETION	0.99	0.35	0	0	0	not significant
8607	GO_14_3_3_PROTEIN_BINDING	0.99	0.34	0	0	0	not significant
8608	GO_DOUBLE_STRAND_BREAK_REPAIR	0.99	0.34	0	0	0	not significant
8609	GO_HISTONE_DEACETYLATION	0.99	0.34	0	0	0	not significant
8610	GO_MICROTUBULE_NUCLEATION	0.99	0.34	0	0	0	not significant
8611	GO_POSITIVE_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	0.99	0.34	0	0	0	not significant
8612	KEGG_NUCLEOTIDE_EXCISION_REPAIR	0.99	0.34	0	0	0	not significant
8613	NEMETH_INFLAMMATORY_RESPONSE_LPS_DN	0.99	0.34	0	0	0	not significant
8614	NUTT_GBM_VS_AO_GLIOMA_UP	0.99	0.34	0	0	0	not significant
8615	AIYAR_COBRA1_TARGETS_DN	0.99	0.33	0	0	0	not significant
8616	GO_CELLULAR_RESPONSE_TO_ABIOTIC_STIMULUS	0.99	0.33	0	0	0	not significant
8617	GO_COPII_COATED_ER_TO_GOLGI_TRANSPORT_VESICLE	0.99	0.33	0	0	0	not significant
8618	GO_GLUTAMINE_METABOLIC_PROCESS	0.99	0.33	0	0	0	not significant
8619	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	0.99	0.33	0	0	0	not significant
8620	GO_RESPONSE_TO_HYDROGEN_PEROXIDE	0.99	0.33	0	0	0	not significant
8621	GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_GERMLINE_RECOM	0.99	0.33	0	0	0	not significant
8622	KRIEG_KDM3A_TARGETS_NOT_HYPOXIA	0.99	0.33	0	0	0	not significant
8623	NUTT_GBM_VS_AO_GLIOMA_DN	0.99	0.33	0	0	0	not significant
8624	REACTOME_EPH_EPHRIN_MEDIATED_REPULSION_OF_CELLS	0.99	0.33	0	0	0	not significant
8625	REACTOME_G0_AND_EARLY_G1	0.99	0.33	0	0	0	not significant
8626	REACTOME_PHOSPHOLIPID_METABOLISM	0.99	0.33	0	0	0	not significant
8627	FARMER_BREAST_CANCER_CLUSTER_7	0.99	0.32	0	0	0	not significant
8628	FERRANDO_TAL1_NEIGHBORS	0.99	0.32	0	0	0	not significant
8629	GO_ASPARTATE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	0.99	0.32	0	0	0	not significant
8630	GO_CARBON_NITROGEN_LIGASE_ACTIVITY_WITH_GLUTAMINE_AS_AMIDO_N_DONC	0.99	0.32	0	0	0	not significant
8631	GO_CELL_CYCLE_ARREST	0.99	0.32	0	0	0	not significant
8632	GO_DNA_METHYLATION	0.99	0.32	0	0	0	not significant
8633	GO_MITOTIC_DNA_INTEGRITY_CHECKPOINT	0.99	0.32	0	0	0	not significant
8634	GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	0.99	0.32	0	0	0	not significant
8635	GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	0.99	0.32	0	0	0	not significant
8636	GO_NEGATIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_F	0.99	0.32	0	0	0	not significant
8637	GO_NEGATIVE_REGULATION_OF_PEPTIDE_HORMONE_SECRETION	0.99	0.32	0	0	0	not significant
8638	GO_NUCLEOSIDE_BISPHOSPHATE_BIOSYNTHETIC_PROCESS	0.99	0.32	0	0	0	not significant
8639	GO_ODONTOGENESIS	0.99	0.32	0	0	0	not significant
8640	GO_POSITIVE_REGULATION_OF_SMOOTHENED_SIGNALING_PATHWAY	0.99	0.32	0	0	0	not significant
8641	GO_PROTEIN_KINASE_COMPLEX	0.99	0.32	0	0	0	not significant
8642	GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	0.99	0.32	0	0	0	not significant
8643	GO_SIGNAL_RELEASE	0.99	0.32	0	0	0	not significant
8644	GO_SODIUM_ION_HOMEOSTASIS	0.99	0.32	0	0	0	not significant
8645	LEE_LIVER_CANCER_CIPROFIBRATE_DN	0.99	0.32	0	0	0	not significant
8646	LENAOUR_DENDRITIC_CELL_MATURATION_DN	0.99	0.32	0	0	0	not significant
8647	PID_HES_HEY_PATHWAY	0.99	0.32	0	0	0	not significant
8648	REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS	0.99	0.32	0	0	0	not significant
8649	SHI_SPARC_TARGETS_UP	0.99	0.32	0	0	0	not significant
8650	DELACROIX_RAR_BOUND_ES	0.99	0.31	0	0	0	not significant
8651	GO_CALMODULIN_BINDING	0.99	0.31	0	0	0	not significant
8652	GO_DEOXYRIBONUCLEOTIDE_BIOSYNTHETIC_PROCESS	0.99	0.31	0	0	0	not significant
8653	GO_LIGASE_ACTIVITY	0.99	0.31	0	0	0	not significant
8654	GO_NEGATIVE_REGULATION_OF_INSULIN_SECRETION	0.99	0.31	0	0	0	not significant
8655	GO_ONE_CARBON_METABOLIC_PROCESS	0.99	0.31	0	0	0	not significant
8656	GO_PHOTORECEPTOR_CELL_DEVELOPMENT	0.99	0.31	0	0	0	not significant
8657	GO_POSITIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	0.99	0.31	0	0	0	not significant
8658	GO_REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHOGENESIS	0.99	0.31	0	0	0	not significant
8659	GO_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	0.99	0.31	0	0	0	not significant
8660	GO_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	0.99	0.31	0	0	0	not significant
8661	GO_REGULATION_OF_DEFENSE_RESPONSE	0.99	0.31	0	0	0	not significant
8662	GO_REGULATION_OF_MITOCHONDRION_ORGANIZATION	0.99	0.31	0	0	0	not significant
8663	GO_SULFURIC_ESTER_HYDROLASE_ACTIVITY	0.99	0.31	0	0	0	not significant
8664	NUYTTEN_NIPP1_TARGETS_DN	0.99	0.31	0	0	0	not significant
8665	ONDER_CDH1_TARGETS_3_UP	0.99	0.31	0	0	0	not significant
8666	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_UP	0.99	0.3	0	0	0	not significant
8667	BIOCARTA_CELLCYCLE_PATHWAY	0.99	0.3	0	0	0	not significant
8668	DAZARD_UV_RESPONSE_CLUSTER_G4	0.99	0.3	0	0	0	not significant
8669	GO_LEFT_RIGHT_PATTERN_FORMATION	0.99	0.3	0	0	0	not significant
8670	GO_MODIFIED_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0.99	0.3	0	0	0	not significant
8671	GO_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	0.99	0.3	0	0	0	not significant
8672	GO_PEPTIDYL_TYROSINE_MODIFICATION	0.99	0.3	0	0	0	not significant
8673	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_II	0.99	0.3	0	0	0	not significant
8674	GO_POSITIVE_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	0.99	0.3	0	0	0	not significant
8675	SASAKI_TARGETS_OF_TP73_AND_TP63	0.99	0.3	0	0	0	not significant
8676	WEBER_METHYLATED_HCP_IN_FIBROBLAST_DN	0.99	0.3	0	0	0	not significant
8677	ZEMBUTSU_SENSITIVITY_TO_FLUOROURACIL	0.99	0.3	0	0	0	not significant
8678	GO_DEVELOPMENT_OF_SECONDARY_FEMALE_SEXUAL_CHARACTERISTICS	0.99	0.29	0	0	0	not significant
8679	GO_PHOTORECEPTOR_CELL_OUTER_SEGMENT_ORGANIZATION	0.99	0.29	0	0	0	not significant
8680	GO_POSITIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_4_SIGNALING_PATHWAY	0.99	0.29	0	0	0	not significant
8681	GO_RESPONSE_TO_ABIOTIC_STIMULUS	0.99	0.29	0	0	0	not significant
8682	REACTOME_GALACTOSE_CATABOLISM	0.99	0.29	0	0	0	not significant
8683	REACTOME_PHASE_2_PLATEAU_PHASE	0.99	0.29	0	0	0	not significant
8684	BIOCARTA_NOTCH_PATHWAY	0.99	0.28	0	0	0	not significant
8685	GO_CDP_ALCOHOL_PHOSPHATIDYLTRANSFERASE_ACTIVITY	0.99	0.28	0	0	0	not significant
8686	GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MIRNAS_INVOLVED_IN_GENE_S	0.99	0.28	0	0	0	not significant
8687	GO_PROTEIN_GLYCOSYLATION_IN_GOLGI	0.99	0.28	0	0	0	not significant
8688	KONG_E2F1_TARGETS	0.99	0.28	0	0	0	not significant
8689	GO_DOUBLE_STRANDED_METHYLATED_DNA_BINDING	0.99	0.27	0	0	0	not significant
8690	GO_PLATELET_ALPHA_GRANULE_LUMEN	1.00	0.37	0	0	0	not significant
8691	ZHAN_LATE_DIFFERENTIATION_GENES_UP	1.00	0.37	0	0	0	not significant
8692	GO_ENDOCYTIC_VESICLE	1.00	0.36	0	0	0	not significant
8693	GO_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	1.00	0.36	0	0	0	not significant
8694	GO_SPHINGOLIPID_BIOSYNTHETIC_PROCESS	1.00	0.36	0	0	0	not significant
8695	REACTOME_N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CALRETICULIN_CYC	1.00	0.36	0	0	0	not significant
8696	WORSCHECH_TUMOR_REJECTION_UP	1.00	0.36	0	0	0	not significant
8697	BIOCARTA_TCR_PATHWAY	1.00	0.35	0	0	0	not significant
8698	CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_DN	1.00	0.35	0	0	0	not significant
8699	DARWICHE_PAPILLOMA_RISK_LOW_DN	1.00	0.35	0	0	0	not significant
8700	GO_ANATOMICAL_STRUCTURE_MATURATION	1.00	0.35	0	0	0	not significant
8701	GO_APICAL_PLASMA_MEMBRANE	1.00	0.35	0	0	0	not significant
8702	GO_DETOXIFICATION	1.00	0.35	0	0	0	not significant
8703	GO_ENERGY_COUPLED_PROTON_TRANSMEMBRANE_TRANSPORT_AGAINST_ELEC	1.00	0.35	0	0	0	not significant
8704	GO_PANCREAS_DEVELOPMENT	1.00	0.35	0	0	0	not significant
8705	GO_PROTEIN_TARGETING_TO_MEMBRANE	1.00	0.35	0	0	0	not significant
8706	GO_RENAL_SYSTEM_DEVELOPMENT	1.00	0.35	0	0	0	not significant
8707	GO_REPLICATION_FORK	1.00	0.35	0	0	0	not significant
8708	GO_RESPONSE_TO_RETINOIC_ACID	1.00	0.35	0	0	0	not significant

8709	GO_SECONDARY_METABOLIC_PROCESS	1.00	0.35	0	0	0	not significant
8710	GO_THIOESTER_BIOSYNTHETIC_PROCESS	1.00	0.35	0	0	0	not significant
8711	GO_THIOLESTER_HYDROLASE_ACTIVITY	1.00	0.35	0	0	0	not significant
8712	GRUETZMANN_PANCREATIC_CANCER_DN	1.00	0.35	0	0	0	not significant
8713	HALLMARK_UV_RESPONSE_DN	1.00	0.35	0	0	0	not significant
8714	JIANG_VHL_TARGETS	1.00	0.35	0	0	0	not significant
8715	PEDRIOLI_MIR31_TARGETS_UP	1.00	0.35	0	0	0	not significant
8716	PEREZ_TP53_AND_TP63_TARGETS	1.00	0.35	0	0	0	not significant
8717	REACTOME_CONSTITUTIVE_SIGNALING_BY_ABERRANT_PI3K_IN_CANCER	1.00	0.35	0	0	0	not significant
8718	REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDUCED_SENESCENCE	1.00	0.35	0	0	0	not significant
8719	REACTOME_EXTRA_NUCLEAR_ESTROGEN_SIGNALING	1.00	0.35	0	0	0	not significant
8720	GO_ATP_HYDROLYSIS_COUPLED_TRANSMEMBRANE_TRANSPORT	1.00	0.34	0	0	0	not significant
8721	GO_BONE_REMODELING	1.00	0.34	0	0	0	not significant
8722	GO_DRUG_METABOLIC_PROCESS	1.00	0.34	0	0	0	not significant
8723	GO_GAMETE_GENERATION	1.00	0.34	0	0	0	not significant
8724	GO_NEGATIVE_REGULATION_OF_PROTEIN_METABOLIC_PROCESS	1.00	0.34	0	0	0	not significant
8725	GO_OXIDATION_REDUCTION_PROCESS	1.00	0.34	0	0	0	not significant
8726	GO_POSITIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	1.00	0.34	0	0	0	not significant
8727	GO_RESPONSE_TO_ESTRADIOL	1.00	0.34	0	0	0	not significant
8728	GO_SERINE_THREONINE_PROTEIN_KINASE_COMPLEX	1.00	0.34	0	0	0	not significant
8729	GO_TOLL_LIKE_RECEPTOR_9_SIGNALING_PATHWAY	1.00	0.34	0	0	0	not significant
8730	LEE_LIVER_CANCER_MYC_DN	1.00	0.34	0	0	0	not significant
8731	ZHAN_MULTIPLE_MYELOMA_PR_DN	1.00	0.34	0	0	0	not significant
8732	BILANGES_SERUM_RESPONSE_TRANSLATION	1.00	0.33	0	0	0	not significant
8733	GO_ADIPOSE_TISSUE_DEVELOPMENT	1.00	0.33	0	0	0	not significant
8734	GO_FOLIC_ACID_METABOLIC_PROCESS	1.00	0.33	0	0	0	not significant
8735	GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	1.00	0.33	0	0	0	not significant
8736	GO_NUCLEOBASE_METABOLIC_PROCESS	1.00	0.33	0	0	0	not significant
8737	GO_POSITIVE_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR	1.00	0.33	0	0	0	not significant
8738	GO_REGULATION_OF_AMPA_RECEPTOR_ACTIVITY	1.00	0.33	0	0	0	not significant
8739	GO_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVIT	1.00	0.33	0	0	0	not significant
8740	GO_REGULATION_OF_PROTEIN_TARGETING	1.00	0.33	0	0	0	not significant
8741	GO_STORE_OPERATED_CALCIUM_ENTRY	1.00	0.33	0	0	0	not significant
8742	GO_SYNAPTIC_VESICLE_ENDOSOMAL_PROCESSING	1.00	0.33	0	0	0	not significant
8743	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_UP	1.00	0.33	0	0	0	not significant
8744	RASHI_RESPONSE_TO_IONIZING_RADIATION_4	1.00	0.33	0	0	0	not significant
8745	REACTOME_INTERFERON_GAMMA_SIGNALING	1.00	0.33	0	0	0	not significant
8746	REACTOME_METABOLISM_OF_FOLATE_AND_PTERINES	1.00	0.33	0	0	0	not significant
8747	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_DN	1.00	0.33	0	0	0	not significant
8748	GO_COBALAMIN_BINDING	1.00	0.32	0	0	0	not significant
8749	GO_NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	1.00	0.32	0	0	0	not significant
8750	GO_ORGANOPHOSPHATE_METABOLIC_PROCESS	1.00	0.32	0	0	0	not significant
8751	GO_POSITIVE_REGULATION_OF_CD8_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	1.00	0.32	0	0	0	not significant
8752	GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_F	1.00	0.32	0	0	0	not significant
8753	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	1.00	0.32	0	0	0	not significant
8754	GO_PROTEIN_HOMODIMERIZATION_ACTIVITY	1.00	0.32	0	0	0	not significant
8755	GO_REGULATION_OF_BODY_FLUID_LEVELS	1.00	0.32	0	0	0	not significant
8756	GO_SEQUENCE_SPECIFIC_DNA_BINDING	1.00	0.32	0	0	0	not significant
8757	HALLMARK_APICAL_SURFACE	1.00	0.32	0	0	0	not significant
8758	HALLMARK_XENOBIOTIC_METABOLISM	1.00	0.32	0	0	0	not significant
8759	KIM_MYC_AMPLIFICATION_TARGETS_DN	1.00	0.32	0	0	0	not significant
8760	LUI_THYROID_CANCER_PAX8_PPARG_UP	1.00	0.32	0	0	0	not significant
8761	NATSUME_RESPONSE_TO_INTERFERON_BETA_DN	1.00	0.32	0	0	0	not significant
8762	TERAMOTO_OPN_TARGETS_CLUSTER_4	1.00	0.32	0	0	0	not significant
8763	GO_DEATH_INDUCING_SIGNALING_COMPLEX	1.00	0.31	0	0	0	not significant
8764	GO_IMMUNOLOGICAL_SYNAPSE	1.00	0.31	0	0	0	not significant
8765	GO_MACROPINOCYTOSIS	1.00	0.31	0	0	0	not significant
8766	GO_MODULATION_OF_MOLECULAR_FUNCTION_IN_OTHER_ORGANISM	1.00	0.31	0	0	0	not significant
8767	GO_MULTIVESICULAR_BODY_MEMBRANE	1.00	0.31	0	0	0	not significant
8768	GO_NEGATIVE_REGULATION_OF_CYTOKINESIS	1.00	0.31	0	0	0	not significant
8769	GO_NUCLEOBASE_TRANSPORT	1.00	0.31	0	0	0	not significant
8770	GO_PROSTAGLANDIN_TRANSPORT	1.00	0.31	0	0	0	not significant
8771	GO_PYRIMIDINE_NUCLEOSIDE_CATABOLIC_PROCESS	1.00	0.31	0	0	0	not significant
8772	GO_REGULATION_OF_PROTEIN_KINASE_A_SIGNALING	1.00	0.31	0	0	0	not significant
8773	GO_REGULATION_OF_STORE_OPERATED_CALCIUM_ENTRY	1.00	0.31	0	0	0	not significant
8774	GO_WATER_SOLUBLE_VITAMIN_BIOSYNTHETIC_PROCESS	1.00	0.31	0	0	0	not significant
8775	REACTOME_CASPASE_MEDIATED_CLEAVAGE_OF_CYTOSKELETAL_PROTEINS	1.00	0.31	0	0	0	not significant
8776	REACTOME_ERYTHROPOIETIN_ACTIVATES_PHOSPHOINOSITIDE_3_KINASE_PI3K	1.00	0.31	0	0	0	not significant
8777	SENESE_HDAC3_TARGETS_DN	1.00	0.31	0	0	0	not significant
8778	GO_DORSAL_VENTRAL_AXIS_SPECIFICATION	1.00	0.3	0	0	0	not significant
8779	GO_L_GLUTAMATE_IMPORT	1.00	0.3	0	0	0	not significant
8780	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS_	1.00	0.3	0	0	0	not significant
8781	GO_PRESPLICEOSOME	1.00	0.3	0	0	0	not significant
8782	GO_VERY_LOW_DENSITY_LIPOPROTEIN_PARTICLE_ASSEMBLY	1.00	0.3	0	0	0	not significant
8783	GO_C_X_C_CHEMOKINE_RECEPTOR_ACTIVITY	1.00	0.29	0	0	0	not significant
8784	GO_CELL_MIGRATION_INVOLVED_IN_GASTRULATION	1.00	0.29	0	0	0	not significant
8785	GO_CELLULAR_TRIGLYCERIDE_HOMEOSTASIS	1.00	0.29	0	0	0	not significant
8786	GO_VASCULAR_SMOOTH_MUSCLE_CELL_DEVELOPMENT	1.00	0.29	0	0	0	not significant
8787	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_UP	1.01	0.38	0	0	0	not significant
8788	CHR17Q21	1.01	0.38	0	0	0	not significant
8789	CHRXP11	1.01	0.38	0	0	0	not significant
8790	GO_COAGULATION	1.01	0.38	0	0	0	not significant
8791	GO_NEURON_PROJECTION_TERMINUS	1.01	0.38	0	0	0	not significant
8792	GO_PROTEIN_DEMETHYLATION	1.01	0.38	0	0	0	not significant
8793	PASINI_SUZ12_TARGETS_DN	1.01	0.38	0	0	0	not significant
8794	RADMACHER_AML_PROGNOSIS	1.01	0.38	0	0	0	not significant
8795	GO_CELLULAR_RESPONSE_TO_INORGANIC_SUBSTANCE	1.01	0.37	0	0	0	not significant
8796	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS	1.01	0.37	0	0	0	not significant
8797	GO_PHOSPHOLIPID_BINDING	1.01	0.37	0	0	0	not significant
8798	GO_PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY	1.01	0.37	0	0	0	not significant
8799	HOEBEKE_LYMPHOID_STEM_CELL_UP	1.01	0.37	0	0	0	not significant
8800	JNK_DN.V1_UP	1.01	0.37	0	0	0	not significant
8801	LI_INDUCED_T_TO_NATURAL_KILLER_DN	1.01	0.37	0	0	0	not significant
8802	OXFORD_RALA_OR_RALB_TARGETS_UP	1.01	0.37	0	0	0	not significant
8803	RB_DN.V1_DN	1.01	0.37	0	0	0	not significant
8804	REACTOME_TRANSLESION_SYNTHESIS_BY_Y_FAMILY_DNA_POLYMERASES_BYPAS	1.01	0.37	0	0	0	not significant
8805	CHR9Q34	1.01	0.36	0	0	0	not significant
8806	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN	1.01	0.36	0	0	0	not significant
8807	GO_FATTY_ACID_BETA_OXIDATION	1.01	0.36	0	0	0	not significant
8808	GO_MESONEPHROS_DEVELOPMENT	1.01	0.36	0	0	0	not significant
8809	GO_RAB_GTPASE_BINDING	1.01	0.36	0	0	0	not significant
8810	GO_REGULATION_OF_B_CELL_PROLIFERATION	1.01	0.36	0	0	0	not significant
8811	GO_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	1.01	0.36	0	0	0	not significant
8812	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP	1.01	0.36	0	0	0	not significant
8813	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN	1.01	0.36	0	0	0	not significant
8814	PID_TELOMERASE_PATHWAY	1.01	0.36	0	0	0	not significant
8815	PRC1_BMI_UP.V1_DN	1.01	0.36	0	0	0	not significant
8816	PURBEY_TARGETS_OF_CTBP1_NOT_SATB1_DN	1.01	0.36	0	0	0	not significant
8817	REACTOME_IRE1ALPHA_ACTIVATES_CHAPERONES	1.01	0.36	0	0	0	not significant

8818	ROSS_ACUTE_MYELOID_LEUKEMIA_CBF	1.01	0.36	0	0	0	not significant
8819	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS	1.01	0.35	0	0	0	not significant
8820	GO_EXONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCLEI	1.01	0.35	0	0	0	not significant
8821	GO_MHC_PROTEIN_BINDING	1.01	0.35	0	0	0	not significant
8822	GO_NEGATIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	1.01	0.35	0	0	0	not significant
8823	GO_POSITIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	1.01	0.35	0	0	0	not significant
8824	GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	1.01	0.35	0	0	0	not significant
8825	GO_POSITIVE_REGULATION_OF_HISTONE_METHYLATION	1.01	0.35	0	0	0	not significant
8826	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_STRESS	1.01	0.35	0	0	0	not significant
8827	GO_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	1.01	0.35	0	0	0	not significant
8828	GO_REPLICATION_FORK_PROCESSING	1.01	0.35	0	0	0	not significant
8829	GO_VITAMIN_BIOSYNTHETIC_PROCESS	1.01	0.35	0	0	0	not significant
8830	GO_XY_BODY	1.01	0.35	0	0	0	not significant
8831	HOLLEMAN_VINCRISTINE_RESISTANCE_B_ALL_UP	1.01	0.35	0	0	0	not significant
8832	LANDIS_ERBB2_BREAST_PRENEOPLASTIC_UP	1.01	0.35	0	0	0	not significant
8833	NAKAMURA_ADIPOGENESIS_EARLY_UP	1.01	0.35	0	0	0	not significant
8834	REACTOME_DNA_DAMAGE_BYPASS	1.01	0.35	0	0	0	not significant
8835	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_6	1.01	0.35	0	0	0	not significant
8836	AMIT_EGF_RESPONSE_240_MCF10A	1.01	0.34	0	0	0	not significant
8837	BCAT.100_UP.V1_DN	1.01	0.34	0	0	0	not significant
8838	BRUECKNER_TARGETS_OF_MIRLET7A3_UP	1.01	0.34	0	0	0	not significant
8839	CEBALLOS_TARGETS_OF_TP53_AND_MYC_UP	1.01	0.34	0	0	0	not significant
8840	GO_ENGULFMENT_OF_APOPTOTIC_CELL	1.01	0.34	0	0	0	not significant
8841	GO_GOLGI_TO_LYSOSOME_TRANSPORT	1.01	0.34	0	0	0	not significant
8842	GO_MANNOSYLATION	1.01	0.34	0	0	0	not significant
8843	GO_MONOVALENT_INORGANIC_ANION_HOMEOSTASIS	1.01	0.34	0	0	0	not significant
8844	GO_MULTICELLULAR_ORGANISMAL_HOMEOSTASIS	1.01	0.34	0	0	0	not significant
8845	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	1.01	0.34	0	0	0	not significant
8846	GO_NEURON_PROJECTION	1.01	0.34	0	0	0	not significant
8847	GO_POSITIVE_REGULATION_OF_GLIAL_CELL_PROLIFERATION	1.01	0.34	0	0	0	not significant
8848	GO_POSITIVE_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	1.01	0.34	0	0	0	not significant
8849	GO_REGULATION_OF_HISTONE_DEACETYLATION	1.01	0.34	0	0	0	not significant
8850	PIONTEK_PKD1_TARGETS_DN	1.01	0.34	0	0	0	not significant
8851	REACTOME_SIGNALLING_TO_RAS	1.01	0.34	0	0	0	not significant
8852	XU_AKT1_TARGETS_6HR	1.01	0.34	0	0	0	not significant
8853	BIOCARTA_TFF_PATHWAY	1.01	0.33	0	0	0	not significant
8854	GO_AXONAL_FASCICULATION	1.01	0.33	0	0	0	not significant
8855	GO_GAMMA_TUBULIN_COMPLEX	1.01	0.33	0	0	0	not significant
8856	GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	1.01	0.33	0	0	0	not significant
8857	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	1.01	0.33	0	0	0	not significant
8858	GO_QUINONE_METABOLIC_PROCESS	1.01	0.33	0	0	0	not significant
8859	KAMIKUBO_MYELOID_CEBPA_NETWORK	1.01	0.33	0	0	0	not significant
8860	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREY_UP	1.01	0.32	0	0	0	not significant
8861	GO_AP_1_ADAPTOR_COMPLEX	1.01	0.32	0	0	0	not significant
8862	GO_GLYCOGEN_GRANULE	1.01	0.32	0	0	0	not significant
8863	GO_MACROPHAGE_CHEMOTAXIS	1.01	0.32	0	0	0	not significant
8864	MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_DN	1.01	0.32	0	0	0	not significant
8865	GO_ARGININE_CATABOLIC_PROCESS	1.01	0.31	0	0	0	not significant
8866	GO_CELLULAR_RESPONSE_TO_LEUCINE_STARVATION	1.01	0.31	0	0	0	not significant
8867	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	1.01	0.31	0	0	0	not significant
8868	GO_DETECTION_OF_EXTERNAL_BIOTIC_STIMULUS	1.01	0.3	0	0	0	not significant
8869	GO_GLYCINE_METABOLIC_PROCESS	1.01	0.3	0	0	0	not significant
8870	GO_REGULATION_OF_NEUROTROPHIN_TRK_RECEPTOR_SIGNALING_PATHWAY	1.01	0.3	0	0	0	not significant
8871	MCGOWAN_RSP6_TARGETS_UP	1.01	0.3	0	0	0	not significant
8872	REACTOME_ERBB2_REGULATES_CELL_MOTILITY	1.01	0.3	0	0	0	not significant
8873	BLALOCK_ALZHEIMERS_DISEASE_UP	1.02	0.41	0	0	0	not significant
8874	FORTSCHEGGER_PHF8_TARGETS_DN	1.02	0.41	0	0	0	not significant
8875	GO_ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	1.02	0.4	0	0	0	not significant
8876	GO_REGULATION_OF_CELL_DEATH	1.02	0.4	0	0	0	not significant
8877	GO_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	1.02	0.4	0	0	0	not significant
8878	GRESHOCK_CANCER_COPY_NUMBER_UP	1.02	0.4	0	0	0	not significant
8879	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN	1.02	0.4	0	0	0	not significant
8880	GO_ACTIN_BASED_CELL_PROJECTION	1.02	0.39	0	0	0	not significant
8881	GO_GLYCOSAMINOGLYCAN_BINDING	1.02	0.39	0	0	0	not significant
8882	GO_MACROMOLECULE_DEACYLATION	1.02	0.39	0	0	0	not significant
8883	GO_MULTICELLULAR_ORGANISM_REPRODUCTION	1.02	0.39	0	0	0	not significant
8884	GO_NEGATIVE_REGULATION_OF_CELL_DEATH	1.02	0.39	0	0	0	not significant
8885	GO_NEGATIVE_REGULATION_OF_SMALL_MOLECULE_METABOLIC_PROCESS	1.02	0.39	0	0	0	not significant
8886	GO_REGULATION_OF_INSULIN_SECRETION	1.02	0.39	0	0	0	not significant
8887	KEGG_JAK_STAT_SIGNALING_PATHWAY	1.02	0.39	0	0	0	not significant
8888	SASSON_RESPONSE_TO_GONADOTROPHINS_UP	1.02	0.39	0	0	0	not significant
8889	SEIDEN_ONCOGENESIS_BY_MET	1.02	0.39	0	0	0	not significant
8890	ALCALA_APOPTOSIS	1.02	0.38	0	0	0	not significant
8891	BAKKER_FOXO3_TARGETS_DN	1.02	0.38	0	0	0	not significant
8892	BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AND_TSC2	1.02	0.38	0	0	0	not significant
8893	BRACHAT_RESPONSE_TO_CISPLATIN	1.02	0.38	0	0	0	not significant
8894	EGFR_UP.V1_DN	1.02	0.38	0	0	0	not significant
8895	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN	1.02	0.38	0	0	0	not significant
8896	GO_CLATHRIN_COATED_VESICLE	1.02	0.38	0	0	0	not significant
8897	GO_INSULIN_SECRETION	1.02	0.38	0	0	0	not significant
8898	GO_LYSOSOMAL_TRANSPORT	1.02	0.38	0	0	0	not significant
8899	GO_POSITIVE_REGULATION_OF_AXONOGENESIS	1.02	0.38	0	0	0	not significant
8900	GO_PROTEIN_PHOSPHATASE_BINDING	1.02	0.38	0	0	0	not significant
8901	GO_REGULATION_OF_MAPK_CASCADE	1.02	0.38	0	0	0	not significant
8902	GO_RESPONSE_TO_CADMIUM_ION	1.02	0.38	0	0	0	not significant
8903	GO_VACUOLAR_TRANSPORT	1.02	0.38	0	0	0	not significant
8904	KEGG_BLADDER_CANCER	1.02	0.38	0	0	0	not significant
8905	LABBE_TARGETS_OF_TGFB1_AND_WNT3A_UP	1.02	0.38	0	0	0	not significant
8906	LANDIS_ERBB2_BREAST_TUMORS_324_DN	1.02	0.38	0	0	0	not significant
8907	AMIT_EGF_RESPONSE_120_HELA	1.02	0.37	0	0	0	not significant
8908	AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP	1.02	0.37	0	0	0	not significant
8909	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_48HR_DN	1.02	0.37	0	0	0	not significant
8910	BIOCARTA_KERATINOCYTE_PATHWAY	1.02	0.37	0	0	0	not significant
8911	GO_ACIDIC_AMINO_ACID_TRANSPORT	1.02	0.37	0	0	0	not significant
8912	GO_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	1.02	0.37	0	0	0	not significant
8913	GO_NEGATIVE_REGULATION_OF_DNA_REPAIR	1.02	0.37	0	0	0	not significant
8914	GO_POSITIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	1.02	0.37	0	0	0	not significant
8915	GO_RAS_PROTEIN_SIGNAL_TRANSDUCTION	1.02	0.37	0	0	0	not significant
8916	GO_REGULATION_OF_PEPTIDE_HORMONE_SECRETION	1.02	0.37	0	0	0	not significant
8917	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAMMA_IN_OLD	1.02	0.37	0	0	0	not significant
8918	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM3	1.02	0.37	0	0	0	not significant
8919	SMIRNOV_RESPONSE_TO_IR_2HR_UP	1.02	0.37	0	0	0	not significant
8920	VANHARANTA_UTERINE_FIBROID_UP	1.02	0.37	0	0	0	not significant
8921	WANG_CLIM2_TARGETS_UP	1.02	0.37	0	0	0	not significant
8922	GO_AMYLOID_BETA_METABOLIC_PROCESS	1.02	0.36	0	0	0	not significant
8923	GO_EYE_PHOTORECEPTOR_CELL_DIFFERENTIATION	1.02	0.36	0	0	0	not significant
8924	GO_METANEPHRIC_NEPHRON_DEVELOPMENT	1.02	0.36	0	0	0	not significant
8925	GO_MHC_CLASS_I_PROTEIN_BINDING	1.02	0.36	0	0	0	not significant
8926	GO_MYOFILAMENT	1.02	0.36	0	0	0	not significant

8927	GO_NEGATIVE_REGULATION_OF_AXON_GUIDANCE	1.02	0.36	0	0	0	not significant
8928	GO_NEGATIVE_REGULATION_OF_BLOOD_PRESSURE	1.02	0.36	0	0	0	not significant
8929	GO_POSTSYNAPSE_ORGANIZATION	1.02	0.36	0	0	0	not significant
8930	GO_REGULATION_OF_PROGRAMMED_NECROTIC_CELL_DEATH	1.02	0.36	0	0	0	not significant
8931	GO_SINGLE_FERTILIZATION	1.02	0.36	0	0	0	not significant
8932	GO_STEREOCILIUM_BUNDLE	1.02	0.36	0	0	0	not significant
8933	GO_TORC1_SIGNALING	1.02	0.36	0	0	0	not significant
8934	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	1.02	0.36	0	0	0	not significant
8935	PEART_HDAC_PROLIFERATION_CLUSTER_UP	1.02	0.36	0	0	0	not significant
8936	PRC1_BMI_UP.V1_UP	1.02	0.36	0	0	0	not significant
8937	REACTOME_SIGNALING_BY_FGFR1_IN_DISEASE	1.02	0.36	0	0	0	not significant
8938	REACTOME_SIGNALING_BY_PDGF	1.02	0.36	0	0	0	not significant
8939	CAMP_UP.V1_DN	1.02	0.35	0	0	0	not significant
8940	GO_APOPTOTIC_CELL_CLEARANCE	1.02	0.35	0	0	0	not significant
8941	GO_NEGATIVE_REGULATION_OF_OSSIFICATION	1.02	0.35	0	0	0	not significant
8942	GO_NEUTROPHIL_DIFFERENTIATION	1.02	0.35	0	0	0	not significant
8943	GO_NUCLEOTIDE_RECEPTOR_ACTIVITY	1.02	0.35	0	0	0	not significant
8944	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_SYNAPSE	1.02	0.35	0	0	0	not significant
8945	DAIRKEE_CANCER_PRONE_RESPONSE_E2	1.02	0.34	0	0	0	not significant
8946	GENTILE_UV_RESPONSE_CLUSTER_D1	1.02	0.34	0	0	0	not significant
8947	GO_DNA_ENDOREDUPLICATION	1.02	0.34	0	0	0	not significant
8948	GO_ENDOSOME_LUMEN	1.02	0.34	0	0	0	not significant
8949	GO_EPITHELIAL_TUBE_BRANCHING_INVOLVED_IN_LUNG_MORPHOGENESIS	1.02	0.34	0	0	0	not significant
8950	GO_FLAP_ENDONUCLEASE_ACTIVITY	1.02	0.34	0	0	0	not significant
8951	GO_LEFT_RIGHT_AXIS_SPECIFICATION	1.02	0.34	0	0	0	not significant
8952	GO_POSITIVE_REGULATION_OF_SPHINGOLIPID_BIOSYNTHETIC_PROCESS	1.02	0.34	0	0	0	not significant
8953	GO_REGULATION_OF_MITOPHAGY	1.02	0.34	0	0	0	not significant
8954	GO_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	1.02	0.34	0	0	0	not significant
8955	GO_ZYMOGEN_GRANULE_MEMBRANE	1.02	0.34	0	0	0	not significant
8956	KEGG_ETHER_LIPID_METABOLISM	1.02	0.34	0	0	0	not significant
8957	GO_CELL_PROLIFERATION_INVOLVED_IN_METANEPHROS_DEVELOPMENT	1.02	0.33	0	0	0	not significant
8958	GO_DERLIN_1_RETROTRANSLOCATION_COMPLEX	1.02	0.33	0	0	0	not significant
8959	GO_HMG_BOX_DOMAIN_BINDING	1.02	0.33	0	0	0	not significant
8960	GO_MEIOTIC_TELOMERE_CLUSTERING	1.02	0.33	0	0	0	not significant
8961	GO_NEGATIVE_REGULATION_OF_NEUROTRANSMITTER_SECRETION	1.02	0.33	0	0	0	not significant
8962	GO_REGULATION_OF_GASTRIC_ACID_SECRETION	1.02	0.33	0	0	0	not significant
8963	GO_COPI_COATED_VESICLE_BUDDING	1.02	0.32	0	0	0	not significant
8964	GO_PLASMA_MEMBRANE_TO_ENDOSOME_TRANSPORT	1.02	0.32	0	0	0	not significant
8965	GO_RNA_POLYMERASE_II_CTD_HEPTAPEPTIDE_REPEAT_PHOSPHATASE_ACTIVITY	1.02	0.32	0	0	0	not significant
8966	MIKKELSEN_MCV6_LCP_WITH_H3K27ME3	1.02	0.32	0	0	0	not significant
8967	ROY_WOUND_BLOOD_VESSEL_DN	1.02	0.32	0	0	0	not significant
8968	GO_PROTEIN_MATURATION_BY_IRON_SULFUR_CLUSTER_TRANSFER	1.02	0.31	0	0	0	not significant
8969	GO_REGULATION_OF_CHAPERONE_MEDIATED_AUTOPHAGY	1.02	0.31	0	0	0	not significant
8970	GO_REGULATION_OF_DNA_DEMETHYLATION	1.02	0.31	0	0	0	not significant
8971	GO_REGULATION_OF_TAU_PROTEIN_KINASE_ACTIVITY	1.02	0.31	0	0	0	not significant
8972	GO_THYROID_HORMONE_METABOLIC_PROCESS	1.02	0.31	0	0	0	not significant
8973	MINGUEZ_LIVER_CANCER_VASCULAR_INVASION_DN	1.02	0.31	0	0	0	not significant
8974	GO_POSITIVE_REGULATION_OF_PINOCYTOSIS	1.02	0.29	0	0	0	not significant
8975	LIN_MELANOMA_COPY_NUMBER_UP	1.03	0.43	0	0	0	not significant
8976	ONKEN_UVEAL_MELANOMA_UP	1.03	0.43	0	0	0	not significant
8977	GO_SENSORY_PERCEPTION	1.03	0.42	0	0	0	not significant
8978	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATH	1.03	0.42	0	0	0	not significant
8979	YOSHIMURA_MAPK8_TARGETS_UP	1.03	0.42	0	0	0	not significant
8980	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_2G	1.03	0.41	0	0	0	not significant
8981	GO_B_CELL_PROLIFERATION	1.03	0.41	0	0	0	not significant
8982	GO_CELL_PART_MORPHOGENESIS	1.03	0.41	0	0	0	not significant
8983	GO_REGULATION_OF_HISTONE_METHYLATION	1.03	0.41	0	0	0	not significant
8984	GO_TRANSCRIPTION_FACTOR_COMPLEX	1.03	0.41	0	0	0	not significant
8985	BIDUS_METASTASIS_DN	1.03	0.4	0	0	0	not significant
8986	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP	1.03	0.4	0	0	0	not significant
8987	FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN	1.03	0.4	0	0	0	not significant
8988	GO_3_5_EXONUCLEASE_ACTIVITY	1.03	0.4	0	0	0	not significant
8989	GO_APICAL_PART_OF_CELL	1.03	0.4	0	0	0	not significant
8990	GO_REGULATION_OF_CELL_SIZE	1.03	0.4	0	0	0	not significant
8991	GO_TRANSPORT_VESICLE_MEMBRANE	1.03	0.4	0	0	0	not significant
8992	GO_WATER_SOLUBLE_VITAMIN_METABOLIC_PROCESS	1.03	0.4	0	0	0	not significant
8993	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON	1.03	0.4	0	0	0	not significant
8994	TOOKER_GEMCITABINE_RESISTANCE_DN	1.03	0.4	0	0	0	not significant
8995	WELCSH_BRCA1_TARGETS_UP	1.03	0.4	0	0	0	not significant
8996	GO_DICARBOXYLIC_ACID_TRANSPORT	1.03	0.39	0	0	0	not significant
8997	GO_GLIAL_CELL_DEVELOPMENT	1.03	0.39	0	0	0	not significant
8998	GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	1.03	0.39	0	0	0	not significant
8999	GO_RECEPTOR_REGULATOR_ACTIVITY	1.03	0.39	0	0	0	not significant
9000	GO_REGULATION_OF_DNA_REPAIR	1.03	0.39	0	0	0	not significant
9001	GO_RESPONSE_TO_IONIZING_RADIATION	1.03	0.39	0	0	0	not significant
9002	GO_SULFUR_COMPOUND_TRANSPORT	1.03	0.39	0	0	0	not significant
9003	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS	1.03	0.39	0	0	0	not significant
9004	LEIN_MEDULLA_MARKERS	1.03	0.39	0	0	0	not significant
9005	PID_AVB3_INTEGRIN_PATHWAY	1.03	0.39	0	0	0	not significant
9006	BROWNE_HCMV_INFECTION_16HR_DN	1.03	0.38	0	0	0	not significant
9007	GO_ACTIN_MEDIATED_CELL_CONTRACTION	1.03	0.38	0	0	0	not significant
9008	GO_BIOMINERAL_TISSUE_DEVELOPMENT	1.03	0.38	0	0	0	not significant
9009	GO_CELL_CELL_JUNCTION_ASSEMBLY	1.03	0.38	0	0	0	not significant
9010	GO_NEGATIVE_CHEMOTAXIS	1.03	0.38	0	0	0	not significant
9011	GO_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	1.03	0.38	0	0	0	not significant
9012	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGION_DNA_BIN	1.03	0.38	0	0	0	not significant
9013	GO_POSTSYNAPTIC_MEMBRANE_ORGANIZATION	1.03	0.38	0	0	0	not significant
9014	GO_REGULATION_OF_FATTY_ACID_OXIDATION	1.03	0.38	0	0	0	not significant
9015	GO_REGULATION_OF_HISTONE_H3_K4_METHYLATION	1.03	0.38	0	0	0	not significant
9016	GO_VENTRICULAR_SEPTUM_MORPHOGENESIS	1.03	0.38	0	0	0	not significant
9017	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_DN	1.03	0.38	0	0	0	not significant
9018	LABBE_TGFB1_TARGETS_UP	1.03	0.38	0	0	0	not significant
9019	PRC2_EED_UP.V1_UP	1.03	0.38	0	0	0	not significant
9020	STEIN_ESRRA_TARGETS_RESPONSIVE_TO_ESTROGEN_DN	1.03	0.38	0	0	0	not significant
9021	WNT_UP.V1_DN	1.03	0.38	0	0	0	not significant
9022	GHO_ATF5_TARGETS_DN	1.03	0.37	0	0	0	not significant
9023	GO_AORTIC_VALVE_DEVELOPMENT	1.03	0.37	0	0	0	not significant
9024	GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	1.03	0.37	0	0	0	not significant
9025	GO_COCHLEA_DEVELOPMENT	1.03	0.37	0	0	0	not significant
9026	GO_KIDNEY_MORPHOGENESIS	1.03	0.37	0	0	0	not significant
9027	GO_PROTEIN_PALMITOYLATION	1.03	0.37	0	0	0	not significant
9028	GO_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_STRESS	1.03	0.37	0	0	0	not significant
9029	GYORFFY_MITOXANTRONE_RESISTANCE	1.03	0.37	0	0	0	not significant
9030	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_DN	1.03	0.37	0	0	0	not significant
9031	LIANG_SILENCED_BY_METHYLATION_2	1.03	0.37	0	0	0	not significant
9032	REACTOME_RHO_GTPASES_ACTIVATE_NADPH_OXIDASES	1.03	0.37	0	0	0	not significant
9033	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1	1.03	0.37	0	0	0	not significant
9034	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_15	1.03	0.37	0	0	0	not significant
9035	DAZARD_UV_RESPONSE_CLUSTER_G28	1.03	0.36	0	0	0	not significant

9036	DING_LUNG_CANCER_BY_MUTATION_RATE	1.03	0.36	0	0	0	not significant
9037	DOANE_BREAST_CANCER_ESR1_UP	1.03	0.36	0	0	0	not significant
9038	GO_FICOLIN_1_RICH_GRANULE_MEMBRANE	1.03	0.36	0	0	0	not significant
9039	GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATION	1.03	0.36	0	0	0	not significant
9040	GO_NEGATIVE_REGULATION_OF_JUN_KINASE_ACTIVITY	1.03	0.36	0	0	0	not significant
9041	GO_POSITIVE_REGULATION_OF_CELLULAR_EXTRAVASATION	1.03	0.36	0	0	0	not significant
9042	GO_PROTEIN_K11_LINKED_DEUBIQUITINATION	1.03	0.36	0	0	0	not significant
9043	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_ENDOSOME	1.03	0.36	0	0	0	not significant
9044	GO_TRICARBOXYLIC_ACID_METABOLIC_PROCESS	1.03	0.36	0	0	0	not significant
9045	WONG_IFNA2_RESISTANCE_UP	1.03	0.36	0	0	0	not significant
9046	DORN_ADENOVIRUS_INFECTION_48HR_UP	1.03	0.35	0	0	0	not significant
9047	GO_ACTIVATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	1.03	0.35	0	0	0	not significant
9048	GO_MICROTUBULE_MINUS_END_BINDING	1.03	0.35	0	0	0	not significant
9049	GO_NEGATIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	1.03	0.35	0	0	0	not significant
9050	LIN_TUMOR_ESCAPE_FROM_IMMUNE_ATTACK	1.03	0.35	0	0	0	not significant
9051	FARMER_BREAST_CANCER_CLUSTER_6	1.03	0.34	0	0	0	not significant
9052	GO_GOLGI_MEDIAL_CISTERNA	1.03	0.34	0	0	0	not significant
9053	GO_NEURAL_PLATE_DEVELOPMENT	1.03	0.34	0	0	0	not significant
9054	GO_ORIGIN_RECOGNITION_COMPLEX	1.03	0.34	0	0	0	not significant
9055	GO_PHAGOPHORE_ASSEMBLY_SITE_MEMBRANE	1.03	0.34	0	0	0	not significant
9056	GO_POSITIVE_REGULATION_OF_VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVIT	1.03	0.34	0	0	0	not significant
9057	GO_REGULATION_OF_POSTSYNAPTIC_DENSITY_ORGANIZATION	1.03	0.34	0	0	0	not significant
9058	REACTOME_TRAFFICKING_AND_PROCESSING_OF_ENDOSOMAL_TLR	1.03	0.34	0	0	0	not significant
9059	GO_HISTONE_H3_K27_DEMETHYLATION	1.03	0.33	0	0	0	not significant
9060	GO_HYDROGEN_PEROXIDE_METABOLIC_PROCESS	1.03	0.33	0	0	0	not significant
9061	GO_ORGANIC_HYDROXY_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.03	0.33	0	0	0	not significant
9062	GO_PEPTIDYL_PROLINE_HYDROXYLATION	1.03	0.33	0	0	0	not significant
9063	GO_POSITIVE_REGULATION_OF_MITOPHAGY	1.03	0.33	0	0	0	not significant
9064	GO_POSITIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_3_SIGNALING_PATHWAY	1.03	0.33	0	0	0	not significant
9065	GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_PROLIFERATION_INVOLVED_IN_SPROUT	1.03	0.32	0	0	0	not significant
9066	GO_LIPOPROTEIN_LOCALIZATION	1.03	0.32	0	0	0	not significant
9067	GO_NAD_P_H_OXIDASE_ACTIVITY	1.03	0.32	0	0	0	not significant
9068	GO_VITAMIN_D_BIOSYNTHETIC_PROCESS	1.03	0.32	0	0	0	not significant
9069	CHR16Q11	1.03	0.31	0	0	0	not significant
9070	GO_REGULATION_OF_PINOCYTOSIS	1.03	0.31	0	0	0	not significant
9071	GO_POSITIVE_REGULATION_OF_SIGNALING	1.04	0.48	0	0	0	not significant
9072	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_STIMULUS	1.04	0.47	0	0	0	not significant
9073	MASSARWEH_TAMOXIFEN_RESISTANCE_UP	1.04	0.47	0	0	0	not significant
9074	GO_ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	1.04	0.46	0	0	0	not significant
9075	GO_PROTEIN_DIMERIZATION_ACTIVITY	1.04	0.45	0	0	0	not significant
9076	GO_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	1.04	0.45	0	0	0	not significant
9077	GO_NEGATIVE_REGULATION_OF_CELL_POPULATION_PROLIFERATION	1.04	0.44	0	0	0	not significant
9078	BIOCARTA_GPCR_PATHWAY	1.04	0.43	0	0	0	not significant
9079	GO_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	1.04	0.43	0	0	0	not significant
9080	GO_MICROBODY	1.04	0.43	0	0	0	not significant
9081	GO_NEGATIVE_REGULATION_OF_CELL_DIFFERENTIATION	1.04	0.43	0	0	0	not significant
9082	HOSHIDA_LIVER_CANCER_SUBCLASS_S1	1.04	0.43	0	0	0	not significant
9083	ZWANG_DOWN_BY_2ND_EGF_PULSE	1.04	0.43	0	0	0	not significant
9084	GO_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	1.04	0.42	0	0	0	not significant
9085	GO_EARLY_ENDOSOME_MEMBRANE	1.04	0.42	0	0	0	not significant
9086	GO_ENDOPEPTIDASE_ACTIVITY	1.04	0.42	0	0	0	not significant
9087	GO_LIPID_OXIDATION	1.04	0.42	0	0	0	not significant
9088	GO_MACROAUTOPHAGY	1.04	0.42	0	0	0	not significant
9089	GO_MUSCLE_TISSUE_DEVELOPMENT	1.04	0.42	0	0	0	not significant
9090	GO_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	1.04	0.42	0	0	0	not significant
9091	GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS	1.04	0.42	0	0	0	not significant
9092	GROSS_HYPOXIA_VIA_HIF1A_DN	1.04	0.42	0	0	0	not significant
9093	HALLMARK_P53_PATHWAY	1.04	0.42	0	0	0	not significant
9094	HOFMANN_CELL_LYMPHOMA_UP	1.04	0.42	0	0	0	not significant
9095	IWANAGA_CARCINOGENESIS_BY_KRAS_DN	1.04	0.42	0	0	0	not significant
9096	MEK_UP.V1_DN	1.04	0.42	0	0	0	not significant
9097	NAKAMURA_ADIPOGENESIS_LATE_UP	1.04	0.42	0	0	0	not significant
9098	BIOCARTA_FCER1_PATHWAY	1.04	0.41	0	0	0	not significant
9099	GO_DIVALENT_INORGANIC_CATION_TRANSPORT	1.04	0.41	0	0	0	not significant
9100	GO_POSITIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	1.04	0.41	0	0	0	not significant
9101	GO_PROMOTER_SPECIFIC_CHROMATIN_BINDING	1.04	0.41	0	0	0	not significant
9102	HALLMARK_INFLAMMATORY_RESPONSE	1.04	0.41	0	0	0	not significant
9103	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP	1.04	0.41	0	0	0	not significant
9104	ABBUD_LIF_SIGNALING_1_DN	1.04	0.4	0	0	0	not significant
9105	CAVARD_LIVER_CANCER_MALIGNANT_VS_BENIGN	1.04	0.4	0	0	0	not significant
9106	GO_COATED_VESICLE_MEMBRANE	1.04	0.4	0	0	0	not significant
9107	GO_ENDODEOXYRIBONUCLEASE_ACTIVITY_PRODUCING_5_PHOSPHOMONOESTERS	1.04	0.4	0	0	0	not significant
9108	GO_ENTRY_INTO_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	1.04	0.4	0	0	0	not significant
9109	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	1.04	0.4	0	0	0	not significant
9110	HALLMARK_HEDGEHOG_SIGNALING	1.04	0.4	0	0	0	not significant
9111	HALLMARK_TGF_BETA_SIGNALING	1.04	0.4	0	0	0	not significant
9112	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP	1.04	0.4	0	0	0	not significant
9113	MODY_HIPPOCAMPUS_POSTNATAL	1.04	0.4	0	0	0	not significant
9114	MUNSHI_MULTIPLE_MYELOMA_UP	1.04	0.4	0	0	0	not significant
9115	BRACHAT_RESPONSE_TO_METHOTREXATE_DN	1.04	0.39	0	0	0	not significant
9116	DARWICHE_PAPILLOMA_PROGRESSION_RISK	1.04	0.39	0	0	0	not significant
9117	GO_ACTIVATION_OF_MAPK_ACTIVITY	1.04	0.39	0	0	0	not significant
9118	GO_DIOL_BIOSYNTHETIC_PROCESS	1.04	0.39	0	0	0	not significant
9119	GO_ESC_E_Z_COMPLEX	1.04	0.39	0	0	0	not significant
9120	GO_NEGATIVE_REGULATION_OF_FIBROBLAST_PROLIFERATION	1.04	0.39	0	0	0	not significant
9121	GO_POSITIVE_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	1.04	0.39	0	0	0	not significant
9122	GO_REGULATION_OF_CELL_CYCLE_CHECKPOINT	1.04	0.39	0	0	0	not significant
9123	GO_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	1.04	0.39	0	0	0	not significant
9124	GO_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	1.04	0.39	0	0	0	not significant
9125	PID_IL3_PATHWAY	1.04	0.39	0	0	0	not significant
9126	SCHRAMM_INHBA_TARGETS_DN	1.04	0.39	0	0	0	not significant
9127	SUBTIL_PROGESTIN_TARGETS	1.04	0.39	0	0	0	not significant
9128	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_DN	1.04	0.38	0	0	0	not significant
9129	CHR4Q25	1.04	0.38	0	0	0	not significant
9130	GO_CARBOXY_LYASE_ACTIVITY	1.04	0.38	0	0	0	not significant
9131	GO_DICARBOXYLIC_ACID_CATABOLIC_PROCESS	1.04	0.38	0	0	0	not significant
9132	GO_ENDOTHELIAL_CELL_DEVELOPMENT	1.04	0.38	0	0	0	not significant
9133	GO_EXOPEPTIDASE_ACTIVITY	1.04	0.38	0	0	0	not significant
9134	GO_NEGATIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	1.04	0.38	0	0	0	not significant
9135	GO_PLATELET_ALPHA_GRANULE	1.04	0.38	0	0	0	not significant
9136	GO_VIRAL_BUDDING	1.04	0.38	0	0	0	not significant
9137	MOREIRA_RESPONSE_TO_TSA_DN	1.04	0.38	0	0	0	not significant
9138	POS_HISTAMINE_RESPONSE_NETWORK	1.04	0.38	0	0	0	not significant
9139	YANG_BREAST_CANCER_ESR1_LASER_UP	1.04	0.38	0	0	0	not significant
9140	GO_LIGAND_GATED_CALCIUM_CHANNEL_ACTIVITY	1.04	0.37	0	0	0	not significant
9141	GO_NEGATIVE_REGULATION_OF_RECEPTOR_INTERNALIZATION	1.04	0.37	0	0	0	not significant
9142	MALONEY_RESPONSE_TO_17AAG_UP	1.04	0.37	0	0	0	not significant
9143	REACTOME_COENZYME_A_BIOSYNTHESIS	1.04	0.37	0	0	0	not significant
9144	SINGH_KRAS_DEPENDENCY_SIGNATURE_	1.04	0.37	0	0	0	not significant

9145	GO_NEGATIVE_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFEREN	1.04	0.36	0	0	0	not significant
9146	GO_SYNAPTIC_VESICLE_PRIMING	1.04	0.36	0	0	0	not significant
9147	GO_UNCONVENTIONAL_MYOSIN_COMPLEX	1.04	0.36	0	0	0	not significant
9148	MCBRYAN_PUBERTAL_BREAST_3_4WK_DN	1.04	0.36	0	0	0	not significant
9149	REACTOME_CASPASE_ACTIVATION_VIA_DEATH_RECEPTORS_IN_THE_PRESENCE_	1.04	0.36	0	0	0	not significant
9150	GO_CD95_DEATH_INDUCING_SIGNALING_COMPLEX	1.04	0.35	0	0	0	not significant
9151	GO_INOSITOL_1_4_5_TRISPHOSPHATE_BINDING	1.04	0.35	0	0	0	not significant
9152	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION_INVOLVED_IN	1.04	0.35	0	0	0	not significant
9153	GO_SENSORY_PERCEPTION_OF_BITTER_TASTE	1.04	0.35	0	0	0	not significant
9154	GO_REGULATION_OF_SKELETAL_MUSCLE_FIBER_DEVELOPMENT	1.04	0.33	0	0	0	not significant
9155	REACTOME_ACYL_CHAIN_REMODELING_OF_CL	1.04	0.33	0	0	0	not significant
9156	GO_HOLLIDAY_JUNCTION_RESOLVASE_COMPLEX	1.04	0.32	0	0	0	not significant
9157	GO_HOMEOSTATIC_PROCESS	1.05	0.53	0	0	0	not significant
9158	MARTINEZ_TP53_TARGETS_UP	1.05	0.5	0	0	0	not significant
9159	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP	1.05	0.5	0	0	0	not significant
9160	GO_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE	1.05	0.49	0	0	0	not significant
9161	GO_COFACTOR_BINDING	1.05	0.48	0	0	0	not significant
9162	GO_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	1.05	0.47	0	0	0	not significant
9163	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_UP	1.05	0.46	0	0	0	not significant
9164	GO_SEXUAL_REPRODUCTION	1.05	0.46	0	0	0	not significant
9165	LU_AGING_BRAIN_UP	1.05	0.46	0	0	0	not significant
9166	RIZKI_TUMOR_INVASIVENESS_3D_DN	1.05	0.46	0	0	0	not significant
9167	GO_CELL_PROJECTION_MEMBRANE	1.05	0.45	0	0	0	not significant
9168	GO_PHOSPHATIDYLINOSITOL_BISPHOSPHATE_BINDING	1.05	0.45	0	0	0	not significant
9169	GO_RESPONSE_TO_OXIDATIVE_STRESS	1.05	0.45	0	0	0	not significant
9170	GO_RESPONSE_TO_TUMOR_NECROSIS_FACTOR	1.05	0.45	0	0	0	not significant
9171	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNAL	1.05	0.45	0	0	0	not significant
9172	JAATINEN_HEMATOPOIETIC_STEM_CELL_UP	1.05	0.45	0	0	0	not significant
9173	REACTOME_INTERLEUKIN_17_SIGNALING	1.05	0.45	0	0	0	not significant
9174	BURTON_ADIPOGENESIS_6	1.05	0.44	0	0	0	not significant
9175	EIF4E_DN	1.05	0.44	0	0	0	not significant
9176	GO_CIRCULATORY_SYSTEM_PROCESS	1.05	0.44	0	0	0	not significant
9177	GO_DAMAGED_DNA_BINDING	1.05	0.44	0	0	0	not significant
9178	GO_LOCOMOTORY_BEHAVIOR	1.05	0.44	0	0	0	not significant
9179	GO_MUSCLE_STRUCTURE_DEVELOPMENT	1.05	0.44	0	0	0	not significant
9180	GO_PHAGOCYTOSIS	1.05	0.44	0	0	0	not significant
9181	GO_TRANSPORT_VESICLE	1.05	0.44	0	0	0	not significant
9182	IL2_UP.V1_UP	1.05	0.44	0	0	0	not significant
9183	PID_RB_1PATHWAY	1.05	0.44	0	0	0	not significant
9184	POOLA_INVASIVE_BREAST_CANCER_UP	1.05	0.44	0	0	0	not significant
9185	REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LI	1.05	0.44	0	0	0	not significant
9186	BILANGES_SERUM_SENSITIVE_GENES	1.05	0.43	0	0	0	not significant
9187	CHR12Q21	1.05	0.43	0	0	0	not significant
9188	GHANDHI_DIRECT_IRRADIATION_UP	1.05	0.43	0	0	0	not significant
9189	GO_POSITIVE_REGULATION_OF_HORMONE_SECRETION	1.05	0.43	0	0	0	not significant
9190	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP	1.05	0.43	0	0	0	not significant
9191	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3	1.05	0.43	0	0	0	not significant
9192	REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	1.05	0.43	0	0	0	not significant
9193	DCA_UP.V1_UP	1.05	0.42	0	0	0	not significant
9194	GO_ACTIVATION_OF_JUN_KINASE_ACTIVITY	1.05	0.42	0	0	0	not significant
9195	GO_CLATHRIN_COATED_VESICLE_MEMBRANE	1.05	0.42	0	0	0	not significant
9196	GO_POSITIVE_REGULATION_OF_ANION_TRANSPORT	1.05	0.42	0	0	0	not significant
9197	NAKAMURA_METASTASIS_MODEL_DN	1.05	0.42	0	0	0	not significant
9198	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_UP	1.05	0.41	0	0	0	not significant
9199	FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN	1.05	0.41	0	0	0	not significant
9200	GO_REGULATION_OF_SYNAPTIC_VESICLE_RECYCLING	1.05	0.41	0	0	0	not significant
9201	LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_UP	1.05	0.41	0	0	0	not significant
9202	MARTIN_VIRAL_GPCR_SIGNALING_UP	1.05	0.41	0	0	0	not significant
9203	WANG_RESPONSE_TO_ANDROGEN_UP	1.05	0.41	0	0	0	not significant
9204	WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLESTEROL_UP	1.05	0.41	0	0	0	not significant
9205	AMUNDSON_DNA_DAMAGE_RESPONSE_TP53	1.05	0.4	0	0	0	not significant
9206	GO_REGULATION_OF_GLIAL_CELL_PROLIFERATION	1.05	0.4	0	0	0	not significant
9207	SHIPP_DLBCL_CURED_VS_FATAL_DN	1.05	0.4	0	0	0	not significant
9208	GO_ARF_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	1.05	0.39	0	0	0	not significant
9209	GO_FLUID_TRANSPORT	1.05	0.39	0	0	0	not significant
9210	GO_LYMPHOID_PROGENITOR_CELL_DIFFERENTIATION	1.05	0.39	0	0	0	not significant
9211	GO_NEGATIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	1.05	0.39	0	0	0	not significant
9212	GO_NUCLEOSIDE_DIPHOSPHATASE_ACTIVITY	1.05	0.39	0	0	0	not significant
9213	GO_NUCLEOTIDE_ACTIVATED_PROTEIN_KINASE_COMPLEX	1.05	0.39	0	0	0	not significant
9214	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN	1.05	0.39	0	0	0	not significant
9215	GO_S_ACYLTRANSFERASE_ACTIVITY	1.05	0.38	0	0	0	not significant
9216	GO_TRANSCYTOSIS	1.05	0.38	0	0	0	not significant
9217	HOWLIN_CITED1_TARGETS_2_DN	1.05	0.38	0	0	0	not significant
9218	GO_CCR_CHEMOKINE_RECEPTOR_BINDING	1.05	0.37	0	0	0	not significant
9219	JEON_SMAD6_TARGETS_UP	1.05	0.37	0	0	0	not significant
9220	JI_METASTASIS_REPRESSED_BY_STK11	1.05	0.37	0	0	0	not significant
9221	REACTOME_HDR_THROUGH_MMEJ_ALT_NHEJ	1.05	0.37	0	0	0	not significant
9222	YANG_BREAST_CANCER_ESR1_UP	1.05	0.37	0	0	0	not significant
9223	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_IL3RA	1.05	0.36	0	0	0	not significant
9224	GO_AUTOPHAGY_OF_NUCLEUS	1.05	0.36	0	0	0	not significant
9225	GO_SULFATE_TRANSPORT	1.05	0.36	0	0	0	not significant
9226	BIOCARTA_BTG2_PATHWAY	1.05	0.35	0	0	0	not significant
9227	BIOCARTA_VITCB_PATHWAY	1.05	0.35	0	0	0	not significant
9228	GO_CELLULAR_RESPONSE_TO_LITHIUM_ION	1.05	0.35	0	0	0	not significant
9229	GO_EPITHELIAL_CELL_PROLIFERATION_INVOLVED_IN_PROSTATE_GLAND_DEVEL	1.05	0.35	0	0	0	not significant
9230	GO_NEGATIVE_REGULATION_OF_VASCULAR_SMOOTH_MUSCLE_CELL_DIFFERENT	1.05	0.35	0	0	0	not significant
9231	GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_SYNAPSE	1.05	0.35	0	0	0	not significant
9232	GO_DENDRITE_SELF_AVOIDANCE	1.05	0.34	0	0	0	not significant
9233	GO_HISTONE_DEMETHYLASE_ACTIVITY_H3_K27_SPECIFIC_	1.05	0.34	0	0	0	not significant
9234	GO_REGULATION_OF_APOPTOTIC_PROCESS_INVOLVED_IN_MORPHOGENESIS	1.05	0.34	0	0	0	not significant
9235	GO_REGULATION_OF_HYDROGEN_PEROXIDE_METABOLIC_PROCESS	1.05	0.34	0	0	0	not significant
9236	ABDULRAHMAN_KIDNEY_CANCER_VHL_UP	1.05	0.33	0	0	0	not significant
9237	GO_INTERFERON_RECEPTOR_ACTIVITY	1.05	0.33	0	0	0	not significant
9238	NUYTTEN_NIPP1_TARGETS_UP	1.06	0.55	0	0	0	not significant
9239	MARTENS_TRETINOIN_RESPONSE_DN	1.06	0.53	0	0	0	not significant
9240	REACTOME_SIGNALING_BY_GPCR	1.06	0.53	0	0	0	not significant
9241	GO_CELLULAR_CHEMICAL_HOMEOSTASIS	1.06	0.52	0	0	0	not significant
9242	GO_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	1.06	0.52	0	0	0	not significant
9243	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_8D	1.06	0.52	0	0	0	not significant
9244	GO_PROTEIN_COMPLEX_OLIGOMERIZATION	1.06	0.51	0	0	0	not significant
9245	GO_REGULATORY_REGION_NUCLEIC_ACID_BINDING	1.06	0.51	0	0	0	not significant
9246	DAIRKEE_TERT_TARGETS_UP	1.06	0.5	0	0	0	not significant
9247	GO_CELLULAR_ION_HOMEOSTASIS	1.06	0.5	0	0	0	not significant
9248	GO_DNA_BINDING_TRANSCRIPTION_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_	1.06	0.5	0	0	0	not significant
9249	GO_ENDOCYTOSIS	1.06	0.5	0	0	0	not significant
9250	GO_IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY	1.06	0.49	0	0	0	not significant
9251	GO_PEPTIDASE_ACTIVITY	1.06	0.49	0	0	0	not significant
9252	LU_EZH2_TARGETS_UP	1.06	0.49	0	0	0	not significant
9253	GO_LOCALIZATION_WITHIN_MEMBRANE	1.06	0.48	0	0	0	not significant

9254	FISCHER_DIRECT_P53_TARGETS_META_ANALYSIS	1.06	0.47	0	0	0	not significant
9255	GO_GLYCEROPHOSPHOLIPID_METABOLIC_PROCESS	1.06	0.47	0	0	0	not significant
9256	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS	1.06	0.47	0	0	0	not significant
9257	GO_POLYSACCHARIDE_METABOLIC_PROCESS	1.06	0.47	0	0	0	not significant
9258	KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	1.06	0.47	0	0	0	not significant
9259	REACTOME_DDX58_IFIH1_MEDIATED_INDUCTION_OF_INTERFERON_ALPHA_BETA	1.06	0.47	0	0	0	not significant
9260	REACTOME_FATTY_ACID_METABOLISM	1.06	0.47	0	0	0	not significant
9261	DEMAGALHAES_AGING_UP	1.06	0.46	0	0	0	not significant
9262	DURCHDEWALD_SKIN_CARCINOGENESIS_DN	1.06	0.46	0	0	0	not significant
9263	GO_DNA_RECOMBINATION	1.06	0.46	0	0	0	not significant
9264	GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR	1.06	0.46	0	0	0	not significant
9265	GO_REGULATION_OF_POSTSYNAPSE_ORGANIZATION	1.06	0.46	0	0	0	not significant
9266	GO_RESPONSE_TO_INTERLEUKIN_1	1.06	0.46	0	0	0	not significant
9267	HALLMARK_PEROXISOME	1.06	0.46	0	0	0	not significant
9268	REACTOME_TELOMERE_MAINTENANCE	1.06	0.46	0	0	0	not significant
9269	GO_AUTOPHAGOSOME_ORGANIZATION	1.06	0.45	0	0	0	not significant
9270	GO_NEGATIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	1.06	0.45	0	0	0	not significant
9271	GO_PROTEASE_BINDING	1.06	0.45	0	0	0	not significant
9272	WIERENGA_STAT5A_TARGETS_GROUP1	1.06	0.45	0	0	0	not significant
9273	GO_IRON_ION_BINDING	1.06	0.44	0	0	0	not significant
9274	GO_POSITIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION	1.06	0.44	0	0	0	not significant
9275	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_UP	1.06	0.44	0	0	0	not significant
9276	REACTOME_SIGNALING_BY_NOTCH1_IN_CANCER	1.06	0.44	0	0	0	not significant
9277	SANSOM_APC_TARGETS_UP	1.06	0.44	0	0	0	not significant
9278	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_DN	1.06	0.44	0	0	0	not significant
9279	WARTERS_RESPONSE_TO_IR_SKIN	1.06	0.44	0	0	0	not significant
9280	GO_CARBON_CARBON_LYASE_ACTIVITY	1.06	0.43	0	0	0	not significant
9281	GO_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	1.06	0.43	0	0	0	not significant
9282	GO_POSITIVE_REGULATION_OF_PEPTIDE_HORMONE_SECRETION	1.06	0.43	0	0	0	not significant
9283	REACTOME_TOLL_LIKE_RECEPTOR_9_TLR9_CASCADE	1.06	0.43	0	0	0	not significant
9284	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN	1.06	0.42	0	0	0	not significant
9285	CHR6Q23	1.06	0.42	0	0	0	not significant
9286	GO_AMMONIUM_ION_BINDING	1.06	0.42	0	0	0	not significant
9287	GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	1.06	0.42	0	0	0	not significant
9288	GO_DICARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.06	0.42	0	0	0	not significant
9289	GO_FATTY_ACID_DERIVATIVE_BINDING	1.06	0.42	0	0	0	not significant
9290	GO_PEPTIDASE_ACTIVATOR_ACTIVITY_INVOLVED_IN_APOPTOTIC_PROCESS	1.06	0.42	0	0	0	not significant
9291	GO_POLYSACCHARIDE_BIOSYNTHETIC_PROCESS	1.06	0.42	0	0	0	not significant
9292	LEE_LIVER_CANCER_ACOX1_UP	1.06	0.42	0	0	0	not significant
9293	PID_ERBB2_ERBB3_PATHWAY	1.06	0.42	0	0	0	not significant
9294	PID_TCPTP_PATHWAY	1.06	0.42	0	0	0	not significant
9295	BRACHAT_RESPONSE_TO_METHOTREXATE_UP	1.06	0.41	0	0	0	not significant
9296	GO_B_CELL_RECEPTOR_SIGNALING_PATHWAY	1.06	0.41	0	0	0	not significant
9297	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	1.06	0.41	0	0	0	not significant
9298	GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS	1.06	0.41	0	0	0	not significant
9299	REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	1.06	0.41	0	0	0	not significant
9300	FERRANDO_HOX11_NEIGHBORS	1.06	0.4	0	0	0	not significant
9301	GO_CHLORIDE_CHANNEL_INHIBITOR_ACTIVITY	1.06	0.4	0	0	0	not significant
9302	GO_GTPASE_INHIBITOR_ACTIVITY	1.06	0.4	0	0	0	not significant
9303	GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	1.06	0.4	0	0	0	not significant
9304	GO_POSITIVE_REGULATION_OF_NEUROTRANSMITTER_SECRETION	1.06	0.4	0	0	0	not significant
9305	GO_PROTEIN_PROCESSING_INVOLVED_IN_PROTEIN_TARGETING_TO_MITOCHOND	1.06	0.4	0	0	0	not significant
9306	GROSS_ELK3_TARGETS_UP	1.06	0.4	0	0	0	not significant
9307	HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_UP	1.06	0.4	0	0	0	not significant
9308	KEGG_O_GLYCAN_BIOSYNTHESIS	1.06	0.4	0	0	0	not significant
9309	BERENJENO_ROCK_SIGNALING_NOT_VIA_RHOA_UP	1.06	0.39	0	0	0	not significant
9310	GO_REGULATION_OF_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	1.06	0.39	0	0	0	not significant
9311	GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_SOMATIC_MUTATI	1.06	0.39	0	0	0	not significant
9312	GO_COFACTOR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.06	0.38	0	0	0	not significant
9313	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP	1.06	0.38	0	0	0	not significant
9314	GO_BBSOME	1.06	0.37	0	0	0	not significant
9315	GO_GLOMERULAR_MESANGIUM_DEVELOPMENT	1.06	0.37	0	0	0	not significant
9316	GO_HISTONE_H3_K27_TRIMETHYLATION	1.06	0.37	0	0	0	not significant
9317	GO_NEGATIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	1.06	0.37	0	0	0	not significant
9318	GO_REGULATION_OF_CHROMATIN_BINDING	1.06	0.37	0	0	0	not significant
9319	GO_RESPONSE_TO_UV_B	1.06	0.37	0	0	0	not significant
9320	GO_POSITIVE_REGULATION_OF_CELL_MIGRATION_BY_VASCULAR_ENDOTHELIAL_	1.06	0.36	0	0	0	not significant
9321	GO_Y_FORM_DNA_BINDING	1.06	0.36	0	0	0	not significant
9322	CLAUS_PGR_POSITIVE_MENINGIOMA_UP	1.06	0.35	0	0	0	not significant
9323	GO_MODULATION_OF_PROGRAMMED_CELL_DEATH_IN_OTHER_ORGANISM	1.06	0.35	0	0	0	not significant
9324	GO_NEGATIVE_REGULATION_OF_HORMONE_METABOLIC_PROCESS	1.06	0.35	0	0	0	not significant
9325	GO_REGULATION_OF_APOPTOTIC_PROCESS_INVOLVED_IN_DEVELOPMENT	1.06	0.35	0	0	0	not significant
9326	GO_REGULATION_OF_HISTONE_DEACETYLASE_ACTIVITY	1.06	0.35	0	0	0	not significant
9327	GO_REGULATION_OF_RESPONSE_TO_STRESS	1.07	0.62	0	0	0	not significant
9328	GO_RESPONSE_TO_GROWTH_FACTOR	1.07	0.55	0	0	0	not significant
9329	WANG_LMO4_TARGETS_UP	1.07	0.53	0	0	0	not significant
9330	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN	1.07	0.51	0	0	0	not significant
9331	GO_COENZYME_BINDING	1.07	0.5	0	0	0	not significant
9332	PLASARI_TGFB1_TARGETS_10HR_DN	1.07	0.5	0	0	0	not significant
9333	GO_SYNAPTIC_MEMBRANE	1.07	0.49	0	0	0	not significant
9334	LIM_MAMMARY_LUMINAL_MATURE_UP	1.07	0.49	0	0	0	not significant
9335	KEGG_MAPK_SIGNALING_PATHWAY	1.07	0.48	0	0	0	not significant
9336	LEE_LIVER_CANCER_SURVIVAL_UP	1.07	0.48	0	0	0	not significant
9337	CADWELL_ATG16L1_TARGETS_DN	1.07	0.47	0	0	0	not significant
9338	GO_DENDRITE_MORPHOGENESIS	1.07	0.47	0	0	0	not significant
9339	GO_MULTICELLULAR_ORGANISM_GROWTH	1.07	0.47	0	0	0	not significant
9340	GO_SMAD_BINDING	1.07	0.47	0	0	0	not significant
9341	KAUFFMANN_DNA_REPLICATION_GENES	1.07	0.47	0	0	0	not significant
9342	BARIS_THYROID_CANCER_DN	1.07	0.46	0	0	0	not significant
9343	CHR3Q23	1.07	0.46	0	0	0	not significant
9344	GO_CYCLIN_DEPENDENT_PROTEIN_SERINE_THREONINE_KINASE_REGULATOR_ACT	1.07	0.46	0	0	0	not significant
9345	GO_ENDOTHELIUM_DEVELOPMENT	1.07	0.46	0	0	0	not significant
9346	GO_NEGATIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	1.07	0.46	0	0	0	not significant
9347	MANTOVANI_VIRAL_GPCR_SIGNALING_UP	1.07	0.46	0	0	0	not significant
9348	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP	1.07	0.46	0	0	0	not significant
9349	GO_CELLULAR_RESPONSE_TO_FATTY_ACID	1.07	0.45	0	0	0	not significant
9350	GO_EMBRYONIC_PLACENTA_DEVELOPMENT	1.07	0.45	0	0	0	not significant
9351	GO_LEUKOCYTE_HOMEOSTASIS	1.07	0.45	0	0	0	not significant
9352	GO_POSITIVE_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS	1.07	0.45	0	0	0	not significant
9353	GO_REGULATION_OF_ORGANIC_ACID_TRANSPORT	1.07	0.45	0	0	0	not significant
9354	HUANG_GATA2_TARGETS_DN	1.07	0.45	0	0	0	not significant
9355	SANSOM_WNT_PATHWAY_REQUIRE_MYC	1.07	0.45	0	0	0	not significant
9356	GO_ARF_PROTEIN_SIGNAL_TRANSDUCTION	1.07	0.44	0	0	0	not significant
9357	GO_GLYCOGEN_BIOSYNTHETIC_PROCESS	1.07	0.44	0	0	0	not significant
9358	LANG_MYB_FAMILY_TARGETS	1.07	0.44	0	0	0	not significant
9359	LEONARD_HYPOXIA	1.07	0.44	0	0	0	not significant
9360	GO_HISTONE_H3_K9_MODIFICATION	1.07	0.43	0	0	0	not significant
9361	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	1.07	0.43	0	0	0	not significant
9362	GO_TELENCEPHALON_GLIAL_CELL_MIGRATION	1.07	0.43	0	0	0	not significant

9363	HASINA_NOL7_TARGETS_UP	1.07	0.43	0	0	0	not significant
9364	KEGG_CITRATE_CYCLE_TCA_CYCLE	1.07	0.43	0	0	0	not significant
9365	VANDESLUIS_NORMAL_EMBRYOS_DN	1.07	0.43	0	0	0	not significant
9366	GO_ODONTOGENESIS_OF_DENTIN_CONTAINING_TOOTH	1.07	0.42	0	0	0	not significant
9367	PID_S1P_META_PATHWAY	1.07	0.42	0	0	0	not significant
9368	REACTOME_REGULATED_NECROSIS	1.07	0.42	0	0	0	not significant
9369	GO_CD40_RECEPTOR_COMPLEX	1.07	0.41	0	0	0	not significant
9370	GO_DITERPENOID_METABOLIC_PROCESS	1.07	0.41	0	0	0	not significant
9371	GO_ERROR_PRONE_TRANSLESION_SYNTHESIS	1.07	0.41	0	0	0	not significant
9372	GO_MANNOSE_BINDING	1.07	0.41	0	0	0	not significant
9373	GO_O_METHYLTRANSFERASE_ACTIVITY	1.07	0.41	0	0	0	not significant
9374	GO_POSITIVE_REGULATION_OF_ACTIVATED_T_CELL_PROLIFERATION	1.07	0.41	0	0	0	not significant
9375	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	1.07	0.41	0	0	0	not significant
9376	REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYCLE	1.07	0.41	0	0	0	not significant
9377	GO_CYCLOHYDROLASE_ACTIVITY	1.07	0.4	0	0	0	not significant
9378	GO_ESCRT_COMPLEX_DISASSEMBLY	1.07	0.4	0	0	0	not significant
9379	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_RECEPTOR_CATABOLIC_PROCESS	1.07	0.4	0	0	0	not significant
9380	GO_PHOSPHATIDYLCHOLINE_TRANSPORTER_ACTIVITY	1.07	0.4	0	0	0	not significant
9381	GO_RESPONSE_TO_WATER	1.07	0.4	0	0	0	not significant
9382	LIM_MAMMARY_LUMINAL_PROGENITOR_UP	1.07	0.4	0	0	0	not significant
9383	REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE	1.07	0.4	0	0	0	not significant
9384	REACTOME_NOTCH2_ACTIVATION_AND_TRANSMISSION_OF_SIGNAL_TO_THE_NUC	1.07	0.4	0	0	0	not significant
9385	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_PURPLE_DN	1.07	0.39	0	0	0	not significant
9386	GO_NEUROTRANSMITTER_REUPTAKE	1.07	0.39	0	0	0	not significant
9387	GO_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	1.07	0.39	0	0	0	not significant
9388	REACTOME_P38MAPK_EVENTS	1.07	0.39	0	0	0	not significant
9389	GO_DEAD_H_BOX_RNA_HELICASE_BINDING	1.07	0.38	0	0	0	not significant
9390	REACTOME_ASSEMBLY_OF_THE_ORC_COMPLEX_AT_THE_ORIGIN_OF_REPLICATI	1.07	0.38	0	0	0	not significant
9391	REACTOME_SIGNAL_REGULATORY_PROTEIN_FAMILY_INTERACTIONS	1.07	0.38	0	0	0	not significant
9392	CHIN_BREAST_CANCER_COPY_NUMBER_DN	1.07	0.37	0	0	0	not significant
9393	GO_NEGATIVE_REGULATION_OF_ARP2_3_COMPLEX_MEDIATED_ACTIN_NUCLEATI	1.07	0.37	0	0	0	not significant
9394	GO_PLATELET_DENSE_GRANULE_ORGANIZATION	1.07	0.37	0	0	0	not significant
9395	GO_POSITIVE_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_STRESS	1.07	0.37	0	0	0	not significant
9396	LIU_CMYB_TARGETS_DN	1.07	0.37	0	0	0	not significant
9397	MCCABE_HOXC6_TARGETS_DN	1.07	0.37	0	0	0	not significant
9398	PHONG_TNF_TARGETS_DN	1.07	0.37	0	0	0	not significant
9399	GO_SUSCEPTIBILITY_TO_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	1.07	0.36	0	0	0	not significant
9400	GO_CELLULAR_HOMEOSTASIS	1.08	0.59	0	0	0	not significant
9401	GO_MALE_GAMETE_GENERATION	1.08	0.58	0	0	0	not significant
9402	GO_EPITHELIAL_CELL_DIFFERENTIATION	1.08	0.56	0	0	0	not significant
9403	GO_CARBOHYDRATE_METABOLIC_PROCESS	1.08	0.55	0	0	0	not significant
9404	ZHU_CMV_ALL_UP	1.08	0.53	0	0	0	not significant
9405	CHEN_HOXA5_TARGETS_9HR_UP	1.08	0.52	0	0	0	not significant
9406	GO_PHOSPHATIDYLINOSITOL_PHOSPHATE_BINDING	1.08	0.52	0	0	0	not significant
9407	NABA_MATRISOME_ASSOCIATED	1.08	0.52	0	0	0	not significant
9408	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN	1.08	0.51	0	0	0	not significant
9409	GO_GLIOGENESIS	1.08	0.51	0	0	0	not significant
9410	GO_CELLULAR_GLUCOSE_HOMEOSTASIS	1.08	0.5	0	0	0	not significant
9411	REACTOME_TOLL_LIKE_RECEPTOR_TLR1:TLR2_CASCADE	1.08	0.5	0	0	0	not significant
9412	UEDA_PERIFERAL_CLOCK	1.08	0.5	0	0	0	not significant
9413	ZHU_CMV_24_HR_UP	1.08	0.5	0	0	0	not significant
9414	EPPERT_HSC_R	1.08	0.49	0	0	0	not significant
9415	GO_REPRESSING_TRANSCRIPTION_FACTOR_BINDING	1.08	0.49	0	0	0	not significant
9416	KOYAMA_SEMA3B_TARGETS_UP	1.08	0.49	0	0	0	not significant
9417	GO_AUTOPHAGY_OF_MITOCHONDRION	1.08	0.48	0	0	0	not significant
9418	GO_CELLULAR_RESPONSE_TO_STARVATION	1.08	0.48	0	0	0	not significant
9419	GO_PHOSPHOLIPID_TRANSPORTER_ACTIVITY	1.08	0.48	0	0	0	not significant
9420	GO_RAB_PROTEIN_SIGNAL_TRANSDUCTION	1.08	0.48	0	0	0	not significant
9421	HUANG_DASATINIB_RESISTANCE_DN	1.08	0.48	0	0	0	not significant
9422	REACTOME_SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE_SASP	1.08	0.48	0	0	0	not significant
9423	REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYTHESIS	1.08	0.48	0	0	0	not significant
9424	BILBAN_B_CLL_LPL_UP	1.08	0.47	0	0	0	not significant
9425	GOLDRATH_IMMUNE_MEMORY	1.08	0.47	0	0	0	not significant
9426	GO_DNA_DIRECTED_DNA_POLYMERASE_ACTIVITY	1.08	0.46	0	0	0	not significant
9427	GO_NEGATIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_V	1.08	0.46	0	0	0	not significant
9428	PID_PS1_PATHWAY	1.08	0.46	0	0	0	not significant
9429	REACTOME_REGULATION_OF_PTEN_GENE_TRANSCRIPTION	1.08	0.46	0	0	0	not significant
9430	WAKABAYASHI_ADIPOGENESIS_PPARG_BOUND_36HR	1.08	0.46	0	0	0	not significant
9431	GO_CELLULAR_DETOXIFICATION	1.08	0.45	0	0	0	not significant
9432	GO_MITOPHAGY	1.08	0.45	0	0	0	not significant
9433	GO_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	1.08	0.45	0	0	0	not significant
9434	GO_REGULATION_OF_HAIR_CYCLE	1.08	0.45	0	0	0	not significant
9435	KEGG_TRYPTOPHAN_METABOLISM	1.08	0.45	0	0	0	not significant
9436	REACTOME_DUAL_INCISION_IN_GG_NER	1.08	0.45	0	0	0	not significant
9437	GO_NUCLEUS_LOCALIZATION	1.08	0.44	0	0	0	not significant
9438	GO_POSITIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	1.08	0.44	0	0	0	not significant
9439	GO_REGULATION_OF_RECEPTOR_RECYCLING	1.08	0.44	0	0	0	not significant
9440	GO_RIBONUCLEOTIDE_CATABOLIC_PROCESS	1.08	0.44	0	0	0	not significant
9441	LEE_LIVER_CANCER_MYC_E2F1_UP	1.08	0.44	0	0	0	not significant
9442	MCDOWELL_ACUTE_LUNG_INJURY_DN	1.08	0.44	0	0	0	not significant
9443	REACTOME_SYNTHESIS_OF_PC	1.08	0.44	0	0	0	not significant
9444	SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_UP	1.08	0.44	0	0	0	not significant
9445	GO_LYMPH_VESSEL_DEVELOPMENT	1.08	0.43	0	0	0	not significant
9446	NOJIMA_SFRP2_TARGETS_UP	1.08	0.43	0	0	0	not significant
9447	SA_G1_AND_S_PHASES	1.08	0.43	0	0	0	not significant
9448	GO_INTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	1.08	0.42	0	0	0	not significant
9449	GO_PROTEIN_TARGETING_TO_LYSOSOME	1.08	0.42	0	0	0	not significant
9450	GO_RESPONSE_TO_L_GLUTAMATE	1.08	0.41	0	0	0	not significant
9451	CARDOSO_RESPONSE_TO_GAMMA_RADIATION_AND_3AB	1.08	0.4	0	0	0	not significant
9452	GO_GAMMA_TUBULIN_LARGE_COMPLEX	1.08	0.4	0	0	0	not significant
9453	GO_POSITIVE_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_HOMOLO	1.08	0.4	0	0	0	not significant
9454	GO_QUATERNARY_AMMONIUM_GROUP_TRANSMEMBRANE_TRANSPORTER_ACTIVI	1.08	0.4	0	0	0	not significant
9455	GO_CELL_PROLIFERATION_IN_HINDBRAIN	1.08	0.39	0	0	0	not significant
9456	GO_FATTY_ACID_SYNTHASE_ACTIVITY	1.08	0.39	0	0	0	not significant
9457	GO_REGULATION_OF_INOSITOL_PHOSPHATE_BIOSYNTHETIC_PROCESS	1.08	0.39	0	0	0	not significant
9458	GO_RESPONSE_TO_CELL_CYCLE_CHECKPOINT_SIGNALING	1.08	0.39	0	0	0	not significant
9459	REACTOME_ACTIVATION_OF_NOXA_AND_TRANSLOCATION_TO_MITOCHONDRIA	1.08	0.39	0	0	0	not significant
9460	GO_1_ACYLGLYCEROPHOSPHOCHOLINE_O_ACYLTRANSFERASE_ACTIVITY	1.08	0.38	0	0	0	not significant
9461	GO_ACETYL_COA_C_ACYLTRANSFERASE_ACTIVITY	1.08	0.38	0	0	0	not significant
9462	GO_FOREBRAIN_RADIAL_GLIAL_CELL_DIFFERENTIATION	1.08	0.38	0	0	0	not significant
9463	GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_DRUG	1.08	0.38	0	0	0	not significant
9464	GO_CAMP_CATABOLIC_PROCESS	1.08	0.37	0	0	0	not significant
9465	MEISSNER_NPC_ICP_WITH_H3_UNMETHYLATED	1.08	0.37	0	0	0	not significant
9466	GO_DOUBLE_STRANDED_DNA_BINDING	1.09	0.68	0	0	0	not significant
9467	GO_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	1.09	0.63	0	0	0	not significant
9468	GO_PROCESS_UTILIZING_AUTOPHAGIC_MECHANISM	1.09	0.6	0	0	0	not significant
9469	MCCABE_BOUND_BY_HOXC6	1.09	0.58	0	0	0	not significant
9470	GO_RESPONSE_TO_INORGANIC_SUBSTANCE	1.09	0.57	0	0	0	not significant
9471	MATSUDA_NATURAL_KILLER_DIFFERENTIATION	1.09	0.57	0	0	0	not significant

9472	GCNP_SHH_UP_LATE.V1_DN	1.09	0.56	0	0	0	not significant
9473	GO_GLAND_DEVELOPMENT	1.09	0.56	0	0	0	not significant
9474	REACTOME_CELLULAR_SENESCENCE	1.09	0.56	0	0	0	not significant
9475	YAGI_AML_WITH_11Q23_REARRANGED	1.09	0.56	0	0	0	not significant
9476	CHICAS_RB1_TARGETS_GROWING	1.09	0.55	0	0	0	not significant
9477	GO_INTRACELLULAR_RECEPTOR_SIGNALING_PATHWAY	1.09	0.55	0	0	0	not significant
9478	REACTOME_UNFOLDED_PROTEIN_RESPONSE_UPR	1.09	0.54	0	0	0	not significant
9479	JISON_SICKLE_CELL_DISEASE_UP	1.09	0.53	0	0	0	not significant
9480	GO_EXOCYTIC_VESICLE	1.09	0.52	0	0	0	not significant
9481	GO_G0_TO_G1_TRANSITION	1.09	0.52	0	0	0	not significant
9482	KAAB_HEART_ATRIUM_VS_VENTRICLE_UP	1.09	0.52	0	0	0	not significant
9483	PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_DN	1.09	0.52	0	0	0	not significant
9484	CAMPS_COLON_CANCER_COPY_NUMBER_UP	1.09	0.51	0	0	0	not significant
9485	GO_BRUSH_BORDER	1.09	0.51	0	0	0	not significant
9486	BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP	1.09	0.5	0	0	0	not significant
9487	GO_DENDRITIC_SPINE_MORPHOGENESIS	1.09	0.5	0	0	0	not significant
9488	GO_ENDODEOXYRIBONUCLEASE_ACTIVITY	1.09	0.5	0	0	0	not significant
9489	GO_RESPONSE_TO_AMINO_ACID_STARVATION	1.09	0.5	0	0	0	not significant
9490	GO_VITAMIN_BINDING	1.09	0.5	0	0	0	not significant
9491	KIM_MYCN_AMPLIFICATION_TARGETS_UP	1.09	0.5	0	0	0	not significant
9492	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CELL_CYCLE_GENES	1.09	0.5	0	0	0	not significant
9493	SANA_TNF_SIGNALING_DN	1.09	0.5	0	0	0	not significant
9494	SUNG_METASTASIS_STROMA_DN	1.09	0.5	0	0	0	not significant
9495	CAHOY_ASTROGLIAL	1.09	0.49	0	0	0	not significant
9496	GO_RESPONSE_TO_GAMMA_RADIATION	1.09	0.49	0	0	0	not significant
9497	GO_SPINAL_CORD_DEVELOPMENT	1.09	0.49	0	0	0	not significant
9498	KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	1.09	0.49	0	0	0	not significant
9499	LEIN_MIDBRAIN_MARKERS	1.09	0.49	0	0	0	not significant
9500	PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP	1.09	0.49	0	0	0	not significant
9501	PID_ENDOTHELIN_PATHWAY	1.09	0.49	0	0	0	not significant
9502	REACTOME_TRIF_TICAM1_MEDIATED_TLR4_SIGNALING	1.09	0.49	0	0	0	not significant
9503	STEIN_ESR1_TARGETS	1.09	0.49	0	0	0	not significant
9504	GO_NUCLEAR_REPLICATION_FORK	1.09	0.48	0	0	0	not significant
9505	GO_SOMATIC_RECOMBINATION_OF_IMMUNOGLOBULIN_GENE_SEGMENTS	1.09	0.48	0	0	0	not significant
9506	REACTOME_ANTIGEN_PRESENTATION:_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADI	1.09	0.48	0	0	0	not significant
9507	GO_HOMOLOGOUS_RECOMBINATION	1.09	0.47	0	0	0	not significant
9508	GO_PHAGOPHORE_ASSEMBLY_SITE	1.09	0.47	0	0	0	not significant
9509	GO_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	1.09	0.47	0	0	0	not significant
9510	GO_REGULATION_OF_SPINDLE_CHECKPOINT	1.09	0.47	0	0	0	not significant
9511	PID_NFKAPPAB_CANONICAL_PATHWAY	1.09	0.47	0	0	0	not significant
9512	PID_SMAD2_3NUCLEAR_PATHWAY	1.09	0.47	0	0	0	not significant
9513	BIOCARTA_NKCELLS_PATHWAY	1.09	0.46	0	0	0	not significant
9514	BRACHAT_RESPONSE_TO_CAMPTOTHECIN_DN	1.09	0.46	0	0	0	not significant
9515	GO_NEGATIVE_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	1.09	0.46	0	0	0	not significant
9516	GO_POSITIVE_REGULATION_OF_BLOOD_VESSEL_DIAMETER	1.09	0.46	0	0	0	not significant
9517	KEGG_NITROGEN_METABOLISM	1.09	0.46	0	0	0	not significant
9518	REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	1.09	0.46	0	0	0	not significant
9519	GO_CYTOPLASMIC_SEQUESTERING_OF_PROTEIN	1.09	0.45	0	0	0	not significant
9520	GO_MISFOLDED_PROTEIN_BINDING	1.09	0.45	0	0	0	not significant
9521	GO_NEGATIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	1.09	0.45	0	0	0	not significant
9522	GO_STEROID_CATABOLIC_PROCESS	1.09	0.45	0	0	0	not significant
9523	GO_GLYCOLIPID_BINDING	1.09	0.44	0	0	0	not significant
9524	GO_NEGATIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	1.09	0.44	0	0	0	not significant
9525	GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	1.09	0.44	0	0	0	not significant
9526	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12	1.09	0.44	0	0	0	not significant
9527	REACTOME_ACTIVATION_OF_PUMA_AND_TRANSLOCATION_TO_MITOCHONDRIA	1.09	0.44	0	0	0	not significant
9528	GO_POSITIVE_REGULATION_OF_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTIC	1.09	0.43	0	0	0	not significant
9529	GO_POSTSYNAPTIC_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	1.09	0.43	0	0	0	not significant
9530	GO_SEMAPHORIN_RECEPTOR_BINDING	1.09	0.43	0	0	0	not significant
9531	REACTOME_STRIATED_MUSCLE_CONTRACTION	1.09	0.43	0	0	0	not significant
9532	GO_CYTOPLASMIC_SIDE_OF_ENDOPLASMIC_RETICULUM_MEMBRANE	1.09	0.42	0	0	0	not significant
9533	GO_NEUROPILIN_BINDING	1.09	0.42	0	0	0	not significant
9534	GO_VENOUS_BLOOD_VESSEL_DEVELOPMENT	1.09	0.42	0	0	0	not significant
9535	SHIPP_DLBCL_CURED_VS_FATAL_UP	1.09	0.42	0	0	0	not significant
9536	ZHENG_FOXP3_TARGETS_IN_T_LYMPHOCYTE_UP	1.09	0.42	0	0	0	not significant
9537	BAKER_HEMATOPOESIS_STAT5_TARGETS	1.09	0.41	0	0	0	not significant
9538	LIU_TARGETS_OF_VMYB_VS_CMYB_UP	1.09	0.41	0	0	0	not significant
9539	GO_GRANZYME_MEDIATED_APOPTOTIC_SIGNALING_PATHWAY	1.09	0.4	0	0	0	not significant
9540	GO_L_GLUTAMATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.09	0.4	0	0	0	not significant
9541	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	1.09	0.4	0	0	0	not significant
9542	GO_PROTEIN_MEMBRANE_ANCHOR	1.09	0.4	0	0	0	not significant
9543	GO_SEGMENT_SPECIFICATION	1.09	0.4	0	0	0	not significant
9544	REACTOME_TRYPTOPHAN_CATABOLISM	1.09	0.4	0	0	0	not significant
9545	GO_CHROMATIN_SILENCING_AT_TELOMERE	1.09	0.39	0	0	0	not significant
9546	GO_FAT_CELL_PROLIFERATION	1.09	0.39	0	0	0	not significant
9547	GO_INTERLEUKIN_1_RECEPTOR_BINDING	1.09	0.39	0	0	0	not significant
9548	GO_POLYOL_TRANSPORT	1.09	0.39	0	0	0	not significant
9549	GO_TOLL_LIKE_RECEPTOR_BINDING	1.09	0.39	0	0	0	not significant
9550	GO_HEME_TRANSPORTER_ACTIVITY	1.09	0.38	0	0	0	not significant
9551	GO_NODE_OF_RANVIER	1.09	0.38	0	0	0	not significant
9552	REACTOME_INNATE_IMMUNE_SYSTEM	1.10	0.72	0	0	0	not significant
9553	GO_LIPID_BINDING	1.10	0.71	0	0	0	not significant
9554	GO_ORGANIC_ACID_METABOLIC_PROCESS	1.10	0.7	0	0	0	not significant
9555	GO_AGING	1.10	0.62	0	0	0	not significant
9556	MULLIGHAN_MLL_SIGNATURE_2_UP	1.10	0.62	0	0	0	not significant
9557	GO_PROTEIN_HOMOOLIGOMERIZATION	1.10	0.61	0	0	0	not significant
9558	KAUFFMANN_DNA_REPAIR_GENES	1.10	0.61	0	0	0	not significant
9559	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_DN	1.10	0.61	0	0	0	not significant
9560	IVANOVA_HEMATOPOIESIS_MATURE_CELL	1.10	0.6	0	0	0	not significant
9561	KEGG_PATHWAYS_IN_CANCER	1.10	0.59	0	0	0	not significant
9562	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM4	1.10	0.58	0	0	0	not significant
9563	BROWNE_HCMV_INFECTION_8HR_UP	1.10	0.56	0	0	0	not significant
9564	LTE2_UP.V1_UP	1.10	0.56	0	0	0	not significant
9565	REACTOME_TOLL_LIKE_RECEPTOR_4_TLR4_CASCADE	1.10	0.56	0	0	0	not significant
9566	GO_BASOLATERAL_PLASMA_MEMBRANE	1.10	0.55	0	0	0	not significant
9567	IGARASHI_ATF4_TARGETS_DN	1.10	0.55	0	0	0	not significant
9568	GO_POLYOL_BIOSYNTHETIC_PROCESS	1.10	0.54	0	0	0	not significant
9569	REACTOME_MYD88_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	1.10	0.54	0	0	0	not significant
9570	STEIN_ESRRA_TARGETS_DN	1.10	0.54	0	0	0	not significant
9571	GO_CARBOXYLIC_ESTER_HYDROLASE_ACTIVITY	1.10	0.53	0	0	0	not significant
9572	REACTOME_DISEASES_OF_GLYCOSYLATION	1.10	0.53	0	0	0	not significant
9573	TOOKER_GEMCITABINE_RESISTANCE_UP	1.10	0.52	0	0	0	not significant
9574	BIOCARTA_MET_PATHWAY	1.10	0.51	0	0	0	not significant
9575	GO_FERTILIZATION	1.10	0.51	0	0	0	not significant
9576	NAGASHIMA_NRG1_SIGNALING_DN	1.10	0.51	0	0	0	not significant
9577	REACTOME_FOXO_MEDIATED_TRANSCRIPTION	1.10	0.51	0	0	0	not significant
9578	ZHOU_TNF_SIGNALING_30MIN	1.10	0.51	0	0	0	not significant
9579	BIOCARTA_RACCYCD_PATHWAY	1.10	0.5	0	0	0	not significant
9580	KEGG_ARGININE_AND_PROLINE_METABOLISM	1.10	0.5	0	0	0	not significant

9581	BIOCARTA_CASPASE_PATHWAY	1.10	0.49	0	0	0	not significant
9582	FRASOR_TAMOXIFEN_RESPONSE_UP	1.10	0.49	0	0	0	not significant
9583	GO_INTRINSIC_COMPONENT_OF_POSTSYNAPTIC_MEMBRANE	1.10	0.49	0	0	0	not significant
9584	GO_NEGATIVE_REGULATION_OF_T_CELL_DIFFERENTIATION	1.10	0.49	0	0	0	not significant
9585	GO_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	1.10	0.49	0	0	0	not significant
9586	PID_HDAC_CLASSII_PATHWAY	1.10	0.49	0	0	0	not significant
9587	CHR10Q11	1.10	0.48	0	0	0	not significant
9588	GO_B_CELL_HOMEOSTASIS	1.10	0.48	0	0	0	not significant
9589	GO_CYTOPLASMIC_SEQUESTERING_OF_TRANSCRIPTION_FACTOR	1.10	0.48	0	0	0	not significant
9590	GO_DNA_STRAND_ELONGATION	1.10	0.48	0	0	0	not significant
9591	KEGG_VIBRIO_CHOLERAE_INFECTION	1.10	0.48	0	0	0	not significant
9592	REACTOME_FATTY_ACYL_COA_BIOSYNTHESIS	1.10	0.48	0	0	0	not significant
9593	ZHAN_MULTIPLE_MYELOMA_CD2_UP	1.10	0.48	0	0	0	not significant
9594	BREUHAHN_GROWTH_FACTOR_SIGNALING_IN_LIVER_CANCER	1.10	0.47	0	0	0	not significant
9595	CHIBA_RESPONSE_TO_TSA	1.10	0.47	0	0	0	not significant
9596	GO_MUSCLE_FIBER_DEVELOPMENT	1.10	0.47	0	0	0	not significant
9597	GO_REGULATION_OF_ISOTYPE_SWITCHING	1.10	0.47	0	0	0	not significant
9598	GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	1.10	0.47	0	0	0	not significant
9599	GO_REGULATION_OF_T_CELL_MIGRATION	1.10	0.47	0	0	0	not significant
9600	LIN_NPAS4_TARGETS_DN	1.10	0.47	0	0	0	not significant
9601	REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	1.10	0.47	0	0	0	not significant
9602	REACTOME_INFLAMMASOMES	1.10	0.47	0	0	0	not significant
9603	DELLA_RESPONSE_TO_TSA_AND_BUTYRATE	1.10	0.46	0	0	0	not significant
9604	GO_ADRENERGIC_RECEPTOR_BINDING	1.10	0.46	0	0	0	not significant
9605	GO_NEGATIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_UNFOLDED_PROTEIN	1.10	0.46	0	0	0	not significant
9606	GO_NEGATIVE_REGULATION_OF_ORGAN_GROWTH	1.10	0.46	0	0	0	not significant
9607	GO_NEUTROPHIL_MIGRATION	1.10	0.46	0	0	0	not significant
9608	GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	1.10	0.46	0	0	0	not significant
9609	GO_UBIQUITIN_UBIQUITIN_LIGASE_ACTIVITY	1.10	0.46	0	0	0	not significant
9610	CHR4Q13	1.10	0.45	0	0	0	not significant
9611	GO_DNA_POLYMERASE_COMPLEX	1.10	0.45	0	0	0	not significant
9612	GO_PROTEIN_DISULFIDE_ISOMERASE_ACTIVITY	1.10	0.45	0	0	0	not significant
9613	HASLINGER_B_CLL_WITH_13Q14_DELETION	1.10	0.45	0	0	0	not significant
9614	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_UP	1.10	0.44	0	0	0	not significant
9615	GO_RESPONSE_TO_LEUCINE	1.10	0.44	0	0	0	not significant
9616	GO_TUBULIN_DEACETYLATION	1.10	0.44	0	0	0	not significant
9617	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3	1.10	0.44	0	0	0	not significant
9618	HOLLEMAN_VINCRISTINE_RESISTANCE_B_ALL_DN	1.10	0.44	0	0	0	not significant
9619	REACTOME_KSRP_KHSRP_BINDS_AND_DESTABILIZES_MRNA	1.10	0.44	0	0	0	not significant
9620	REACTOME_REGULATION_BY_C_FLIP	1.10	0.44	0	0	0	not significant
9621	YEMELYANOV_GR_TARGETS_DN	1.10	0.44	0	0	0	not significant
9622	ZEMBUTSU_SENSITIVITY_TO_MITOMYCIN	1.10	0.44	0	0	0	not significant
9623	BIOCARTA_MHC_PATHWAY	1.10	0.43	0	0	0	not significant
9624	GO_ATRIAL_SEPTUM_DEVELOPMENT	1.10	0.43	0	0	0	not significant
9625	GO_ENDODEOXYRIBONUCLEASE_ACTIVITY_PRODUCING_3_PHOSPHOMONOESTERS	1.10	0.43	0	0	0	not significant
9626	GO_NEGATIVE_REGULATION_OF_AMYLOID_PRECURSOR_PROTEIN_CATABOLIC_P	1.10	0.43	0	0	0	not significant
9627	GO_PHOSPHATIDYLETHANOLAMINE_BINDING	1.10	0.43	0	0	0	not significant
9628	GO_REGULATION_OF_GERMINAL_CENTER_FORMATION	1.10	0.43	0	0	0	not significant
9629	WILSON_PROTEASES_AT_TUMOR_BONE_INTERFACE_UP	1.10	0.43	0	0	0	not significant
9630	GO_ANCHORED_COMPONENT_OF_SYNAPTIC_VESICLE_MEMBRANE	1.10	0.42	0	0	0	not significant
9631	GO_PARKIN_MEDIATED_STIMULATION_OF_MITOPHAGY_IN_RESPONSE_TO_MITOCH	1.10	0.42	0	0	0	not significant
9632	GO_SPERM_CAPACITATION	1.10	0.42	0	0	0	not significant
9633	GO_WALKING_BEHAVIOR	1.10	0.42	0	0	0	not significant
9634	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_UP	1.10	0.42	0	0	0	not significant
9635	GO_DEVELOPMENT_OF_SECONDARY_SEXUAL_CHARACTERISTICS	1.10	0.41	0	0	0	not significant
9636	GO_MUCOSAL_ASSOCIATED_LYMPHOID_TISSUE_DEVELOPMENT	1.10	0.41	0	0	0	not significant
9637	GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_CHECKPOINT	1.10	0.41	0	0	0	not significant
9638	WEBER_METHYLATED_HCP_IN_SPERM_DN	1.10	0.41	0	0	0	not significant
9639	GO_CELLULAR_RESPONSE_TO_UV_B	1.10	0.4	0	0	0	not significant
9640	GO_HEME_TRANSPORT	1.10	0.4	0	0	0	not significant
9641	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_OXYGEN_AS_ACCEPTOR	1.10	0.39	0	0	0	not significant
9642	GO_POSITIVE_REGULATION_OF_TRANSPORT	1.11	0.73	0	0	0	not significant
9643	GO_AXON_DEVELOPMENT	1.11	0.67	0	0	0	not significant
9644	GO_CELL_BODY	1.11	0.67	0	0	0	not significant
9645	CUI_TCF21_TARGETS_2_UP	1.11	0.64	0	0	0	not significant
9646	GO_DNA_BINDING_TRANSCRIPTION_FACTOR_BINDING	1.11	0.64	0	0	0	not significant
9647	GO_RNA_POLYMERASE_II_SPECIFIC_DNA_BINDING_TRANSCRIPTION_FACTOR_BIND	1.11	0.64	0	0	0	not significant
9648	HELLER_HDAC_TARGETS_DN	1.11	0.64	0	0	0	not significant
9649	GO_POSITIVE_REGULATION_OF_MAPK_CASCADE	1.11	0.63	0	0	0	not significant
9650	GO_SECOND_MESSENGER_MEDIATED_SIGNALING	1.11	0.63	0	0	0	not significant
9651	FOSTER_KDM1A_TARGETS_DN	1.11	0.62	0	0	0	not significant
9652	GO_COATED_VESICLE	1.11	0.61	0	0	0	not significant
9653	GO_POSITIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	1.11	0.61	0	0	0	not significant
9654	ROZANOV_MMP14_TARGETS_UP	1.11	0.61	0	0	0	not significant
9655	HALLMARK_IL2_STAT5_SIGNALING	1.11	0.6	0	0	0	not significant
9656	COLDREN_GEFITINIB_RESISTANCE_DN	1.11	0.59	0	0	0	not significant
9657	GO_PHAGOCYTIC_VESICLE	1.11	0.59	0	0	0	not significant
9658	GO_NUCLEAR_RECEPTOR_BINDING	1.11	0.58	0	0	0	not significant
9659	GO_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	1.11	0.58	0	0	0	not significant
9660	GO_TEMPERATURE_HOMEOSTASIS	1.11	0.58	0	0	0	not significant
9661	GO_REGULATION_OF_RAS_PROTEIN_SIGNAL_TRANSDUCTION	1.11	0.57	0	0	0	not significant
9662	CHR12P13	1.11	0.56	0	0	0	not significant
9663	DAZARD_RESPONSE_TO_UV_SCC_UP	1.11	0.55	0	0	0	not significant
9664	MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3	1.11	0.55	0	0	0	not significant
9665	CHR14Q24	1.11	0.54	0	0	0	not significant
9666	GO_POST_EMBRYONIC_DEVELOPMENT	1.11	0.54	0	0	0	not significant
9667	NEMETH_INFLAMMATORY_RESPONSE_LPS_UP	1.11	0.54	0	0	0	not significant
9668	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_GRANULOPOIESIS	1.11	0.54	0	0	0	not significant
9669	GO_POSITIVE_REGULATION_OF_JUN_KINASE_ACTIVITY	1.11	0.53	0	0	0	not significant
9670	GO_NEGATIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	1.11	0.52	0	0	0	not significant
9671	GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	1.11	0.52	0	0	0	not significant
9672	LEE_TARGETS_OF_PTCH1_AND_SUFU_UP	1.11	0.52	0	0	0	not significant
9673	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_DN	1.11	0.51	0	0	0	not significant
9674	CHR20P11	1.11	0.51	0	0	0	not significant
9675	MUELLER_METHYLATED_IN_GLIOBLASTOMA	1.11	0.51	0	0	0	not significant
9676	PURBEY_TARGETS_OF_CTBP1_AND_SATB1_UP	1.11	0.51	0	0	0	not significant
9677	ASTON_MAJOR_DEPRESSIVE_DISORDER_UP	1.11	0.5	0	0	0	not significant
9678	GO_ER_NUCLEUS_SIGNALING_PATHWAY	1.11	0.5	0	0	0	not significant
9679	GO_NEGATIVE_REGULATION_OF_BLOOD_CIRCULATION	1.11	0.5	0	0	0	not significant
9680	GO_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_BINDING	1.11	0.5	0	0	0	not significant
9681	GO_RESPONSE_TO_AMPHETAMINE	1.11	0.5	0	0	0	not significant
9682	MARKS_HDAC_TARGETS_UP	1.11	0.5	0	0	0	not significant
9683	PID_EPO_PATHWAY	1.11	0.5	0	0	0	not significant
9684	ZAMORA_NOS2_TARGETS_UP	1.11	0.5	0	0	0	not significant
9685	REACTOME_TRANSLESION_SYNTHESIS_BY_POLK	1.11	0.49	0	0	0	not significant
9686	BORLAK_LIVER_CANCER_EGF_UP	1.11	0.48	0	0	0	not significant
9687	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_DN	1.11	0.48	0	0	0	not significant
9688	GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_CATABOLIC_PROCESS	1.11	0.48	0	0	0	not significant
9689	GO_POSTSYNAPTIC_SPECIALIZATION_INTRACELLULAR_COMPONENT	1.11	0.48	0	0	0	not significant

9690	HEDENFALK_BREAST_CANCER_BRACX_UP	1.11	0.48	0	0	0	not significant
9691	NAKAMURA_ADIPOGENESIS_LATE_DN	1.11	0.48	0	0	0	not significant
9692	REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	1.11	0.48	0	0	0	not significant
9693	FINAK_BREAST_CANCER_SDPP_SIGNATURE	1.11	0.47	0	0	0	not significant
9694	GO_CELLULAR_RESPONSE_TO_LEUCINE	1.11	0.47	0	0	0	not significant
9695	LAMB_CCND1_TARGETS	1.11	0.47	0	0	0	not significant
9696	ZUCCHI_METASTASIS_DN	1.11	0.47	0	0	0	not significant
9697	GO_2_OXOGLUTARATE_METABOLIC_PROCESS	1.11	0.46	0	0	0	not significant
9698	GO_ENDOSOMAL_VESICLE_FUSION	1.11	0.46	0	0	0	not significant
9699	GO_MOTOR_NEURON_AXON_GUIDANCE	1.11	0.46	0	0	0	not significant
9700	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_ADHESION_TO_VASCULAR_ENDOTHE	1.11	0.46	0	0	0	not significant
9701	GO_REGULATION_OF_ENDOPLASMIC_RETICULUM_UNFOLDED_PROTEIN_RESPONS	1.11	0.46	0	0	0	not significant
9702	HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_DN	1.11	0.46	0	0	0	not significant
9703	PID_S1P_S1P1_PATHWAY	1.11	0.46	0	0	0	not significant
9704	PLASARI_NFIC_TARGETS_BASAL_DN	1.11	0.46	0	0	0	not significant
9705	HOLLEMAN_DAUNORUBICIN_ALL_DN	1.11	0.45	0	0	0	not significant
9706	REACTOME_ATTACHMENT_OF_GPI_ANCHOR_TO_UPAR	1.11	0.45	0	0	0	not significant
9707	GO_GLYCOSYLPHOSPHATIDYLINOSITOL_N_ACETYLGLUCOSAMINYLTRANSFERASE_	1.11	0.43	0	0	0	not significant
9708	GO_REGULATION_OF_MAMMARY_GLAND_EPITHELIAL_CELL_PROLIFERATION	1.11	0.43	0	0	0	not significant
9709	GO_SPHINGOSINE_1_PHOSPHATE_RECEPTOR_SIGNALING_PATHWAY	1.11	0.43	0	0	0	not significant
9710	GO_STEROID_ESTERIFICATION	1.11	0.43	0	0	0	not significant
9711	GO_REGULATION_OF_PRESYNAPTIC_CYTOSOLIC_CALCIUM_ION_CONCENTRATION	1.11	0.42	0	0	0	not significant
9712	REACTOME_WNT_MEDIATED_ACTIVATION_OF_DVL	1.11	0.42	0	0	0	not significant
9713	GO_PHOSPHATIDYLINOSITOL_N_ACETYLGLUCOSAMINYLTRANSFERASE_ACTIVITY	1.11	0.41	0	0	0	not significant
9714	REACTOME_TRAIL_SIGNALING	1.11	0.41	0	0	0	not significant
9715	GO_POSITIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	1.12	0.85	0	0	0	not significant
9716	MARSON_BOUND_BY_FOXP3_STIMULATED	1.12	0.84	0	0	0	not significant
9717	GO_METAL_ION_TRANSPORT	1.12	0.77	0	0	0	not significant
9718	MARTINEZ_RB1_AND_TP53_TARGETS_UP	1.12	0.71	0	0	0	not significant
9719	GO_REGULATION_OF_MAP_KINASE_ACTIVITY	1.12	0.7	0	0	0	not significant
9720	GO_REGULATION_OF_ION_TRANSPORT	1.12	0.69	0	0	0	not significant
9721	MULLIGHAN_MLL_SIGNATURE_1_UP	1.12	0.68	0	0	0	not significant
9722	GO_NEGATIVE_REGULATION_OF_TRANSPORT	1.12	0.67	0	0	0	not significant
9723	GO_MUSCLE_ORGAN_DEVELOPMENT	1.12	0.66	0	0	0	not significant
9724	CYCLIN_D1_KE_.V1_DN	1.12	0.62	0	0	0	not significant
9725	GO_RESPONSE_TO_NUTRIENT	1.12	0.62	0	0	0	not significant
9726	KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_UP	1.12	0.59	0	0	0	not significant
9727	BRUINS_UVC_RESPONSE_MIDDLE	1.12	0.58	0	0	0	not significant
9728	CHR11Q12	1.12	0.57	0	0	0	not significant
9729	CHR9P13	1.12	0.57	0	0	0	not significant
9730	GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	1.12	0.57	0	0	0	not significant
9731	GO_MAMMARY_GLAND_DEVELOPMENT	1.12	0.56	0	0	0	not significant
9732	GO_POSITIVE_REGULATION_OF_SMALL_MOLECULE_METABOLIC_PROCESS	1.12	0.56	0	0	0	not significant
9733	MENSE_HYPOXIA_UP	1.12	0.56	0	0	0	not significant
9734	NELSON_RESPONSE_TO_ANDROGEN_UP	1.12	0.55	0	0	0	not significant
9735	BEIER_GLIOMA_STEM_CELL_DN	1.12	0.54	0	0	0	not significant
9736	BRUNO_HEMATOPOIESIS	1.12	0.54	0	0	0	not significant
9737	CHR15Q25	1.12	0.54	0	0	0	not significant
9738	CHR6Q24	1.12	0.54	0	0	0	not significant
9739	GO_BLOOD_MICROPARTICLE	1.12	0.53	0	0	0	not significant
9740	GO_PHAGOSOME_MATURATION	1.12	0.53	0	0	0	not significant
9741	GO_POSITIVE_REGULATION_OF_B_CELL_PROLIFERATION	1.12	0.52	0	0	0	not significant
9742	GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION	1.12	0.52	0	0	0	not significant
9743	GO_CILIUM_MOVEMENT	1.12	0.51	0	0	0	not significant
9744	GO_MONOAMINE_TRANSPORT	1.12	0.51	0	0	0	not significant
9745	GO_REGULATION_OF_JUN_KINASE_ACTIVITY	1.12	0.51	0	0	0	not significant
9746	GUILLAUMOND_KLF10_TARGETS_DN	1.12	0.51	0	0	0	not significant
9747	LUI_THYROID_CANCER_CLUSTER_3	1.12	0.51	0	0	0	not significant
9748	MURAKAMI_UV_RESPONSE_6HR_UP	1.12	0.51	0	0	0	not significant
9749	PID_FAS_PATHWAY	1.12	0.51	0	0	0	not significant
9750	REACTOME_FGFR1_MUTANT_RECEPTOR_ACTIVATION	1.12	0.51	0	0	0	not significant
9751	BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES	1.12	0.5	0	0	0	not significant
9752	BIOCARTA_BCR_PATHWAY	1.12	0.5	0	0	0	not significant
9753	GO_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL_INVOLVED_IN_CONTRACTION	1.12	0.5	0	0	0	not significant
9754	GO_ORGANELLE_MEMBRANE_CONTACT_SITE	1.12	0.5	0	0	0	not significant
9755	GO_REGULATION_OF_RECEPTOR_LOCALIZATION_TO_SYNAPSE	1.12	0.5	0	0	0	not significant
9756	GO_THYMOCYTE_APOPTOTIC_PROCESS	1.12	0.5	0	0	0	not significant
9757	GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_DN	1.12	0.5	0	0	0	not significant
9758	KEGG_BUTANOATE_METABOLISM	1.12	0.5	0	0	0	not significant
9759	CHR4Q32	1.12	0.49	0	0	0	not significant
9760	GAVIN_PDE3B_TARGETS	1.12	0.49	0	0	0	not significant
9761	GO_SENSORY_PERCEPTION_OF_CHEMICAL_STIMULUS	1.12	0.49	0	0	0	not significant
9762	GO_TRANSMISSION_OF_NERVE_IMPULSE	1.12	0.49	0	0	0	not significant
9763	KANNAN_TP53_TARGETS_DN	1.12	0.49	0	0	0	not significant
9764	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP	1.12	0.49	0	0	0	not significant
9765	GO_FRIZZLED_BINDING	1.12	0.48	0	0	0	not significant
9766	GO_NUCLEOTIDE_SUGAR_TRANSMEMBRANE_TRANSPORT	1.12	0.48	0	0	0	not significant
9767	GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_	1.12	0.48	0	0	0	not significant
9768	WU_ALZHEIMER_DISEASE_DN	1.12	0.48	0	0	0	not significant
9769	GO_CALCIUM_MEDIATED_SIGNALING_USING_INTRACELLULAR_CALCIUM_SOURCE	1.12	0.47	0	0	0	not significant
9770	GO_CILIUM_OR_FLAGELLUM_DEPENDENT_CELL_MOTILITY	1.12	0.47	0	0	0	not significant
9771	GO_PROFILIN_BINDING	1.12	0.47	0	0	0	not significant
9772	GO_REGULATION_OF_LEUKOCYTE_ADHESION_TO_VASCULAR_ENDOTHELIAL_CEL	1.12	0.47	0	0	0	not significant
9773	GO_RESPONSE_TO_REDOX_STATE	1.12	0.47	0	0	0	not significant
9774	GO_SPHINGOLIPID_MEDIATED_SIGNALING_PATHWAY	1.12	0.47	0	0	0	not significant
9775	GO_TRICARBOXYLIC_ACID_CYCLE_ENZYME_COMPLEX	1.12	0.47	0	0	0	not significant
9776	WANG_IMMORTALIZED_BY_HOXA9_AND_MEIS1_DN	1.12	0.47	0	0	0	not significant
9777	GO_POSITIVE_REGULATION_OF_HISTONE_H3_K9_METHYLATION	1.12	0.46	0	0	0	not significant
9778	GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_9_SIGNALING_PATHWAY	1.12	0.46	0	0	0	not significant
9779	GO_SECONDARY_METABOLITE_BIOSYNTHETIC_PROCESS	1.12	0.46	0	0	0	not significant
9780	LIU_VAV3_PROSTATE_CARCINOGENESIS_DN	1.12	0.46	0	0	0	not significant
9781	REACTOME_DISEASES_OF_IMMUNE_SYSTEM	1.12	0.46	0	0	0	not significant
9782	GO_EPOXIDE_HYDROLASE_ACTIVITY	1.12	0.45	0	0	0	not significant
9783	GO_LYMPH_VESSEL_MORPHOGENESIS	1.12	0.45	0	0	0	not significant
9784	GO_POSITIVE_REGULATION_OF_CREB_TRANSCRIPTION_FACTOR_ACTIVITY	1.12	0.45	0	0	0	not significant
9785	GO_REGULATION_OF_GLIAL_CELL_MIGRATION	1.12	0.45	0	0	0	not significant
9786	REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS	1.12	0.45	0	0	0	not significant
9787	GO_CYCLASE_ACTIVITY	1.12	0.44	0	0	0	not significant
9788	GO_ENDORIBONUCLEASE_ACTIVITY_PRODUCING_3_PHOSPHOMONOESTERS	1.12	0.44	0	0	0	not significant
9789	GO_MELANOSOME_ASSEMBLY	1.12	0.44	0	0	0	not significant
9790	GO_HORMONE_CATABOLIC_PROCESS	1.12	0.43	0	0	0	not significant
9791	GO_POSITIVE_REGULATION_OF_CHEMOKINE_SECRETION	1.12	0.43	0	0	0	not significant
9792	MCCABE_HOXC6_TARGETS_UP	1.12	0.43	0	0	0	not significant
9793	GO_CELL_AGGREGATION	1.12	0.41	0	0	0	not significant
9794	GO_IRON_COORDINATION_ENTITY_TRANSPORT	1.12	0.41	0	0	0	not significant
9795	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	1.12	0.41	0	0	0	not significant
9796	GO_MEIOTIC_COHESIN_COMPLEX	1.12	0.39	0	0	0	not significant
9797	GO_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	1.13	1.04	0	0	0	not significant
9798	GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	1.13	0.91	0	0	0	not significant

9799	GO_MEMBRANE_PROTEIN_COMPLEX	1.13	0.9	0	0	0	not significant
9800	GO_ION_HOMEOSTASIS	1.13	0.81	0	0	0	not significant
9801	GO_POSITIVE_REGULATION_OF_CELL_DEATH	1.13	0.81	0	0	0	not significant
9802	GO_SEQUENCE_SPECIFIC_DOUBLE_STRANDED_DNA_BINDING	1.13	0.8	0	0	0	not significant
9803	GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	1.13	0.76	0	0	0	not significant
9804	GO_SMALL_MOLECULE_CATABOLIC_PROCESS	1.13	0.72	0	0	0	not significant
9805	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP	1.13	0.7	0	0	0	not significant
9806	MEISSNER_NPC_HCP_WITH_H3K4ME2	1.13	0.69	0	0	0	not significant
9807	GO_RECYCLING_ENDOSOME	1.13	0.68	0	0	0	not significant
9808	HALLMARK_ADIPOGENESIS	1.13	0.67	0	0	0	not significant
9809	GO_TRANS_GOLGI_NETWORK	1.13	0.66	0	0	0	not significant
9810	GO_PROTEIN_DNA_COMPLEX	1.13	0.65	0	0	0	not significant
9811	OISHI_CHOLANGIOMA_STEM_CELL_LIKE_DN	1.13	0.65	0	0	0	not significant
9812	SANSOM_APC_TARGETS	1.13	0.64	0	0	0	not significant
9813	REACTOME_DEATH_RECEPTOR_SIGNALLING	1.13	0.63	0	0	0	not significant
9814	GO_SODIUM_ION_TRANSPORT	1.13	0.62	0	0	0	not significant
9815	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN	1.13	0.62	0	0	0	not significant
9816	TSAI_RESPONSE_TO_IONIZING_RADIATION	1.13	0.62	0	0	0	not significant
9817	VERHAAK_GLIOBLASTOMA_NEURAL	1.13	0.62	0	0	0	not significant
9818	REACTOME_CELL_CELL_COMMUNICATION	1.13	0.61	0	0	0	not significant
9819	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_36HR	1.13	0.61	0	0	0	not significant
9820	GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	1.13	0.6	0	0	0	not significant
9821	WEIGEL_OXIDATIVE_STRESS_BY_HNE_AND_TBH	1.13	0.6	0	0	0	not significant
9822	GO_INOSITOL_LIPID_MEDIATED_SIGNALING	1.13	0.59	0	0	0	not significant
9823	LINDVALL_IMMORTALIZED_BY_TERT_DN	1.13	0.58	0	0	0	not significant
9824	GO_POSITIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	1.13	0.57	0	0	0	not significant
9825	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_9	1.13	0.57	0	0	0	not significant
9826	GO_POSITIVE_REGULATION_OF_EXOCYTOSIS	1.13	0.56	0	0	0	not significant
9827	GO_REGULATION_OF_PLASMA_LIPOPROTEIN_PARTICLE_LEVELS	1.13	0.56	0	0	0	not significant
9828	GO_REGULATION_OF_TUBE_SIZE	1.13	0.56	0	0	0	not significant
9829	KYNG_RESPONSE_TO_H2O2	1.13	0.56	0	0	0	not significant
9830	PID_LYSOPHOSPHOLIPID_PATHWAY	1.13	0.56	0	0	0	not significant
9831	ROSS_AML_WITH_AML1_ETO_FUSION	1.13	0.56	0	0	0	not significant
9832	REACTOME_PHASE_II_CONJUGATION_OF_COMPOUNDS	1.13	0.55	0	0	0	not significant
9833	REACTOME_SIGNALING_BY_NON_RECEPTOR_TYROSINE_KINASES	1.13	0.55	0	0	0	not significant
9834	RIZKI_TUMOR_INVASIVENESS_2D_UP	1.13	0.55	0	0	0	not significant
9835	GO_GLUCOSE_IMPORT	1.13	0.54	0	0	0	not significant
9836	JAK2_DN.V1_UP	1.13	0.54	0	0	0	not significant
9837	KOHOUTEK_CCNT1_TARGETS	1.13	0.54	0	0	0	not significant
9838	ONO_AML1_TARGETS_DN	1.13	0.54	0	0	0	not significant
9839	GO_LONG_CHAIN_FATTY_ACID_TRANSPORT	1.13	0.53	0	0	0	not significant
9840	GO_NEGATIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	1.13	0.53	0	0	0	not significant
9841	GO_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	1.13	0.53	0	0	0	not significant
9842	REACTOME_ROS_AND_RNS_PRODUCTION_IN_PHAGOCYTES	1.13	0.53	0	0	0	not significant
9843	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR	1.13	0.53	0	0	0	not significant
9844	GO_INTERLEUKIN_12_PRODUCTION	1.13	0.52	0	0	0	not significant
9845	GO_REGULATION_OF_ENDOPLASMIC_RETICULUM_STRESS_INDUCED_INTRINSIC_A	1.13	0.52	0	0	0	not significant
9846	CHIARETTI_T_ALL_RELAPSE_PROGNOSIS	1.13	0.51	0	0	0	not significant
9847	GO_AMYLOID_PRECURSOR_PROTEIN_CATABOLIC_PROCESS	1.13	0.51	0	0	0	not significant
9848	GO_BRUSH_BORDER_MEMBRANE	1.13	0.51	0	0	0	not significant
9849	WANG_RESPONSE_TO_FORSKOLIN_UP	1.13	0.51	0	0	0	not significant
9850	GO_MANNOSYLTRANSFERASE_ACTIVITY	1.13	0.5	0	0	0	not significant
9851	GO_NEURON_RECOGNITION	1.13	0.5	0	0	0	not significant
9852	GO_SENSORY_PERCEPTION_OF_TASTE	1.13	0.5	0	0	0	not significant
9853	HUNSBERGER_EXERCISE_REGULATED_GENES	1.13	0.5	0	0	0	not significant
9854	GO_BROWN_FAT_CELL_DIFFERENTIATION	1.13	0.49	0	0	0	not significant
9855	GO_NEUROTRANSMITTER_UPTAKE	1.13	0.49	0	0	0	not significant
9856	REACTOME_THE_NLRP3_INFLAMMASOME	1.13	0.49	0	0	0	not significant
9857	GEISS_RESPONSE_TO_DSRNA_DN	1.13	0.48	0	0	0	not significant
9858	CHR15Q11	1.13	0.47	0	0	0	not significant
9859	GO_1_PHOSPHATIDYLINOSITOL_4_KINASE_ACTIVITY	1.13	0.47	0	0	0	not significant
9860	GO_NEGATIVE_REGULATION_OF_LIPASE_ACTIVITY	1.13	0.47	0	0	0	not significant
9861	GO_SPECIFICATION_OF_ANIMAL_ORGAN_IDENTITY	1.13	0.47	0	0	0	not significant
9862	SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_DN	1.13	0.47	0	0	0	not significant
9863	ZHAN_VARIABLE_EARLY_DIFFERENTIATION_GENES_UP	1.13	0.46	0	0	0	not significant
9864	GO_LATERAL_ELEMENT	1.13	0.45	0	0	0	not significant
9865	GO_POSITIVE_REGULATION_OF_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	1.13	0.45	0	0	0	not significant
9866	GO_POST_ANAL_TAIL_MORPHOGENESIS	1.13	0.43	0	0	0	not significant
9867	GO_WATER_TRANSPORT	1.13	0.43	0	0	0	not significant
9868	GO_PLASMA_MEMBRANE_REGION	1.14	0.85	0	0	0	not significant
9869	ENK_UV_RESPONSE_EPIDERMIS_UP	1.14	0.73	0	0	0	not significant
9870	ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP	1.14	0.73	0	0	0	not significant
9871	GO_RESPONSE_TO_ANTIBIOTIC	1.14	0.71	0	0	0	not significant
9872	CHR6P21	1.14	0.7	0	0	0	not significant
9873	GO_NIK_NF_KAPPAB_SIGNALING	1.14	0.7	0	0	0	not significant
9874	GO_DEFENSE_RESPONSE_TO_VIRUS	1.14	0.69	0	0	0	not significant
9875	GO_COFACTOR_BIOSYNTHETIC_PROCESS	1.14	0.68	0	0	0	not significant
9876	GO_PHOSPHATASE_BINDING	1.14	0.68	0	0	0	not significant
9877	GO_LYASE_ACTIVITY	1.14	0.67	0	0	0	not significant
9878	GO_PHOSPHOLIPID_BIOSYNTHETIC_PROCESS	1.14	0.67	0	0	0	not significant
9879	GO_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	1.14	0.67	0	0	0	not significant
9880	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_UP	1.14	0.66	0	0	0	not significant
9881	GO_NEGATIVE_REGULATION_OF_CELL_GROWTH	1.14	0.65	0	0	0	not significant
9882	JUBAN_TARGETS_OF_SPI1_AND_FLI1_UP	1.14	0.65	0	0	0	not significant
9883	HALLMARK_UV_RESPONSE_UP	1.14	0.64	0	0	0	not significant
9884	GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_	1.14	0.61	0	0	0	not significant
9885	SENESE_HDAC2_TARGETS_DN	1.14	0.61	0	0	0	not significant
9886	BRCA1_DN.V1_DN	1.14	0.6	0	0	0	not significant
9887	FRIDMAN_SENESCENCE_UP	1.14	0.6	0	0	0	not significant
9888	GO_REGULATION_OF_LIPID_LOCALIZATION	1.14	0.6	0	0	0	not significant
9889	GO_SENSORY_PERCEPTION_OF_MECHANICAL_STIMULUS	1.14	0.6	0	0	0	not significant
9890	GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	1.14	0.59	0	0	0	not significant
9891	GO_OSTEOCLAST_DIFFERENTIATION	1.14	0.59	0	0	0	not significant
9892	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP	1.14	0.59	0	0	0	not significant
9893	CHR3Q27	1.14	0.58	0	0	0	not significant
9894	GO_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLUCOSE_STI	1.14	0.58	0	0	0	not significant
9895	GO_PLASMA_LIPOPROTEIN_PARTICLE_CLEARANCE	1.14	0.58	0	0	0	not significant
9896	PID_BCR_5PATHWAY	1.14	0.58	0	0	0	not significant
9897	PTEN_DN.V1_DN	1.14	0.58	0	0	0	not significant
9898	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY	1.14	0.57	0	0	0	not significant
9899	REACTOME_EXTENSION_OF_TELOMERES	1.14	0.57	0	0	0	not significant
9900	BIOCARTA_NTHI_PATHWAY	1.14	0.56	0	0	0	not significant
9901	GO_ENDOCRINE_PROCESS	1.14	0.56	0	0	0	not significant
9902	GO_POSITIVE_REGULATION_OF_COAGULATION	1.14	0.56	0	0	0	not significant
9903	GO_POSITIVE_REGULATION_OF_LIPID_LOCALIZATION	1.14	0.56	0	0	0	not significant
9904	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	1.14	0.56	0	0	0	not significant
9905	MATZUK_SPERMATOZOA	1.14	0.56	0	0	0	not significant
9906	KEGG_GLUTATHIONE_METABOLISM	1.14	0.55	0	0	0	not significant
9907	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP	1.14	0.55	0	0	0	not significant

9908	MCLACHLAN_DENTAL_CARIES_DN	1.14	0.55	0	0	0	not significant
9909	REACTOME_TBC_RABGAPS	1.14	0.55	0	0	0	not significant
9910	GO_POSITIVE_REGULATION_OF_LIPID_TRANSPORT	1.14	0.54	0	0	0	not significant
9911	GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	1.14	0.54	0	0	0	not significant
9912	GO_REPLISOME	1.14	0.54	0	0	0	not significant
9913	DUTTA_APOPTOSIS_VIA_NFKB	1.14	0.53	0	0	0	not significant
9914	KANG_FLUOROURACIL_RESISTANCE_UP	1.14	0.53	0	0	0	not significant
9915	MIKKELSEN_IPS_ICP_WITH_H3K4ME3_AND_H327ME3	1.14	0.53	0	0	0	not significant
9916	GO_EXODEOXYRIBONUCLEASE_ACTIVITY	1.14	0.52	0	0	0	not significant
9917	GO_NBAF_COMPLEX	1.14	0.52	0	0	0	not significant
9918	GO_NEUROMUSCULAR_JUNCTION_DEVELOPMENT	1.14	0.52	0	0	0	not significant
9919	GO_OSTEOBLAST_PROLIFERATION	1.14	0.52	0	0	0	not significant
9920	GO_POSITIVE_REGULATION_OF_BLOOD_CIRCULATION	1.14	0.52	0	0	0	not significant
9921	GO_RACEMASE_AND_EPIMERASE_ACTIVITY_ACTING_ON_CARBOHYDRATES_AND_	1.14	0.52	0	0	0	not significant
9922	MARSHALL_VIRAL_INFECTION_RESPONSE_DN	1.14	0.52	0	0	0	not significant
9923	SIMBULAN_PARP1_TARGETS_UP	1.14	0.52	0	0	0	not significant
9924	GO_ARACHIDONIC_ACID_METABOLIC_PROCESS	1.14	0.51	0	0	0	not significant
9925	GO_LABYRINTHINE_LAYER_BLOOD_VESSEL_DEVELOPMENT	1.14	0.51	0	0	0	not significant
9926	GO_PEPTIDYL_SERINE_DEPHOSPHORYLATION	1.14	0.51	0	0	0	not significant
9927	GO_SALIVARY_GLAND_DEVELOPMENT	1.14	0.51	0	0	0	not significant
9928	KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS	1.14	0.5	0	0	0	not significant
9929	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_3	1.14	0.5	0	0	0	not significant
9930	GO_INTERLEUKIN_35_MEDIATED_SIGNALING_PATHWAY	1.14	0.49	0	0	0	not significant
9931	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	1.14	0.49	0	0	0	not significant
9932	GO_NEUTRAL_LIPID_CATABOLIC_PROCESS	1.14	0.49	0	0	0	not significant
9933	MATTHEWS_SKIN_CARCINOGENESIS_VIA_JUN	1.14	0.49	0	0	0	not significant
9934	ZHAN_MULTIPLE_MYELOMA_MS_UP	1.14	0.49	0	0	0	not significant
9935	GO_EXCITATORY_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	1.14	0.48	0	0	0	not significant
9936	GO_NEGATIVE_REGULATION_OF_ANOIKIS	1.14	0.48	0	0	0	not significant
9937	GO_PLATELET_ALPHA_GRANULE_MEMBRANE	1.14	0.48	0	0	0	not significant
9938	SCHRAETS_MLL_TARGETS_DN	1.14	0.48	0	0	0	not significant
9939	TANG_SENESCENCE_TP53_TARGETS_UP	1.14	0.48	0	0	0	not significant
9940	GO_FAT_PAD_DEVELOPMENT	1.14	0.47	0	0	0	not significant
9941	GO_REGULATION_OF_BLOOD_VESSEL_REMODELING	1.14	0.47	0	0	0	not significant
9942	GO_ASTROCYTE_PROJECTION	1.14	0.46	0	0	0	not significant
9943	GO_DEOXYRIBONUCLEOTIDE_BINDING	1.14	0.46	0	0	0	not significant
9944	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_DIFFERENTIATION	1.14	0.46	0	0	0	not significant
9945	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQO_IN_OLD	1.14	0.46	0	0	0	not significant
9946	GO_POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_SECRETION	1.14	0.45	0	0	0	not significant
9947	GO_STORE_OPERATED_CALCIUM_CHANNEL_ACTIVITY	1.14	0.45	0	0	0	not significant
9948	GO_MELANIN_BIOSYNTHETIC_PROCESS	1.14	0.44	0	0	0	not significant
9949	GO_APOPTOTIC_SIGNALING_PATHWAY	1.15	0.9	0	0	0	not significant
9950	GO_CELL_MORPHOGENESIS_INVOLVED_IN_NEURON_DIFFERENTIATION	1.15	0.82	0	0	0	not significant
9951	BOCHKIS_FOXA2_TARGETS	1.15	0.8	0	0	0	not significant
9952	YAGI_AML_WITH_T_8_21_TRANSLOCATION	1.15	0.76	0	0	0	not significant
9953	GO_HORMONE_MEDIATED_SIGNALING_PATHWAY	1.15	0.7	0	0	0	not significant
9954	GO_SULFUR_COMPOUND_BINDING	1.15	0.68	0	0	0	not significant
9955	WIERENGA_STAT5A_TARGETS_DN	1.15	0.67	0	0	0	not significant
9956	TGFB_UP.V1_DN	1.15	0.66	0	0	0	not significant
9957	GO_CELLULAR_RESPONSE_TO_CARBOHYDRATE_STIMULUS	1.15	0.65	0	0	0	not significant
9958	GO_MULTI_MULTICELLULAR_ORGANISM_PROCESS	1.15	0.65	0	0	0	not significant
9959	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	1.15	0.65	0	0	0	not significant
9960	GO_ERBB_SIGNALING_PATHWAY	1.15	0.64	0	0	0	not significant
9961	GO_NEGATIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	1.15	0.64	0	0	0	not significant
9962	GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_DN	1.15	0.64	0	0	0	not significant
9963	GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	1.15	0.63	0	0	0	not significant
9964	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	1.15	0.63	0	0	0	not significant
9965	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP	1.15	0.63	0	0	0	not significant
9966	GO_PROTEOGLYCAN_METABOLIC_PROCESS	1.15	0.62	0	0	0	not significant
9967	REACTOME_TOLL_LIKE_RECEPTOR_CASCADES	1.15	0.62	0	0	0	not significant
9968	KEEN_RESPONSE_TO_ROSIGLITAZONE_DN	1.15	0.61	0	0	0	not significant
9969	BIOCARTA_DEATH_PATHWAY	1.15	0.6	0	0	0	not significant
9970	CUI_GLUCOSE_DEPRIVATION	1.15	0.6	0	0	0	not significant
9971	GO_NEUROMUSCULAR_JUNCTION	1.15	0.6	0	0	0	not significant
9972	GO_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	1.15	0.6	0	0	0	not significant
9973	GO_THIOESTER_METABOLIC_PROCESS	1.15	0.6	0	0	0	not significant
9974	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN	1.15	0.6	0	0	0	not significant
9975	MAHAJAN_RESPONSE_TO_IL1A_DN	1.15	0.6	0	0	0	not significant
9976	MARIADASON_REGULATED_BY_HISTONE_ACETYLATION_UP	1.15	0.6	0	0	0	not significant
9977	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_E2F6	1.15	0.6	0	0	0	not significant
9978	GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	1.15	0.59	0	0	0	not significant
9979	GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR	1.15	0.59	0	0	0	not significant
9980	GO_REGULATION_OF_MACROPHAGE_MIGRATION	1.15	0.59	0	0	0	not significant
9981	APPIERTO_RESPONSE_TO_FENRETINIDE_DN	1.15	0.58	0	0	0	not significant
9982	GO_MEMBRANE_PROTEIN_PROTEOLYSIS	1.15	0.58	0	0	0	not significant
9983	KEGG_BASAL_CELL_CARCINOMA	1.15	0.58	0	0	0	not significant
9984	ANDERSEN_LIVER_CANCER_KRT19_DN	1.15	0.57	0	0	0	not significant
9985	CHR11Q24	1.15	0.57	0	0	0	not significant
9986	GO_INTERMEDIATE_FILAMENT_BASED_PROCESS	1.15	0.57	0	0	0	not significant
9987	HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_UP	1.15	0.57	0	0	0	not significant
9988	HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_UP	1.15	0.56	0	0	0	not significant
9989	LEE_LIVER_CANCER_MYC_E2F1_DN	1.15	0.56	0	0	0	not significant
9990	GO_CALCIUM_DEPENDENT_PHOSPHOLIPID_BINDING	1.15	0.55	0	0	0	not significant
9991	GO_LAMININ_BINDING	1.15	0.55	0	0	0	not significant
9992	GO_PHOTORECEPTOR_CELL_DIFFERENTIATION	1.15	0.55	0	0	0	not significant
9993	GO_REGULATION_OF_POLYSACCHARIDE_METABOLIC_PROCESS	1.15	0.55	0	0	0	not significant
9994	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_MEDIATED_BY_A	1.15	0.55	0	0	0	not significant
9995	PID_BMP_PATHWAY	1.15	0.55	0	0	0	not significant
9996	PID_ERBB4_PATHWAY	1.15	0.55	0	0	0	not significant
9997	BIOCARTA_IGF1_PATHWAY	1.15	0.54	0	0	0	not significant
9998	GO_DENDRITIC_CELL_MIGRATION	1.15	0.54	0	0	0	not significant
9999	GO_NEGATIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	1.15	0.54	0	0	0	not significant
10000	GO_POSITIVE_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	1.15	0.54	0	0	0	not significant
10001	GO_PALMITOYLTRANSFERASE_ACTIVITY	1.15	0.53	0	0	0	not significant
10002	GO_POSITIVE_REGULATION_OF_CHROMATIN_BINDING	1.15	0.53	0	0	0	not significant
10003	BIOCARTA_CDK5_PATHWAY	1.15	0.52	0	0	0	not significant
10004	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_6_SECRETION	1.15	0.52	0	0	0	not significant
10005	GO_REGULATION_OF_NATURAL_KILLER_CELL_DIFFERENTIATION	1.15	0.52	0	0	0	not significant
10006	LEIN_ASTROCYTE_MARKERS	1.15	0.52	0	0	0	not significant
10007	SA_MMP_CYTOKINE_CONNECTION	1.15	0.52	0	0	0	not significant
10008	GO_PROXIMAL_DISTAL_PATTERN_FORMATION	1.15	0.5	0	0	0	not significant
10009	REACTOME_VLDLR_INTERNALISATION_AND_DEGRADATION	1.15	0.5	0	0	0	not significant
10010	BIOCARTA_IFNG_PATHWAY	1.15	0.49	0	0	0	not significant
10011	GO_REGULATION_OF_CELL_PROLIFERATION_INVOLVED_IN_KIDNEY_DEVELOPMEN	1.15	0.49	0	0	0	not significant
10012	GO_ERYTHROCYTE_MATURATION	1.15	0.48	0	0	0	not significant
10013	GO_MITOCHONDRIAL_ALPHA_KETOGLUTARATE_DEHYDROGENASE_COMPLEX	1.15	0.48	0	0	0	not significant
10014	GO_POSITIVE_REGULATION_OF_DNA_LIGATION	1.15	0.48	0	0	0	not significant
10015	GO_POSITIVE_REGULATION_OF_T_HELPER_17_TYPE_IMMUNE_RESPONSE	1.15	0.48	0	0	0	not significant
10016	GO_T_CELL_RECEPTOR_BINDING	1.15	0.48	0	0	0	not significant

10017	SAENZ_DETOX_PATHWAY_AND_CARCINOGENESIS_DN	1.15	0.48	0	0	0	not significant
10018	CHR3Q11	1.15	0.47	0	0	0	not significant
10019	GO_BUBBLE_DNA_BINDING	1.15	0.47	0	0	0	not significant
10020	GO_CHEMOKINE_SECRETION	1.15	0.47	0	0	0	not significant
10021	GO_HYDROLASE_ACTIVITY_ACTING_ON_ETHER_BONDS	1.15	0.47	0	0	0	not significant
10022	GO_MITOCHONDRIAL_TRICARBOXYLIC_ACID_CYCLE_ENZYME_COMPLEX	1.15	0.47	0	0	0	not significant
10023	GO_SECRETION_OF_LYSOSOMAL_ENZYMES	1.15	0.47	0	0	0	not significant
10024	JOHANSSON_BRAIN_CANCER_EARLY_VS_LATE_UP	1.15	0.47	0	0	0	not significant
10025	REACTOME_PHASE_4_RESTING_MEMBRANE_POTENTIAL	1.15	0.47	0	0	0	not significant
10026	GO_CELL_CELL_JUNCTION_MAINTENANCE	1.15	0.46	0	0	0	not significant
10027	GO_MACROMOLECULE_DEPALMITOYLATION	1.15	0.46	0	0	0	not significant
10028	GO_RESPONSE_TO_SORBITOL	1.15	0.46	0	0	0	not significant
10029	GO_PROTEIN_POLYUFMYLATION	1.15	0.45	0	0	0	not significant
10030	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN	1.15	0.45	0	0	0	not significant
10031	GO_SPECTRIN_ASSOCIATED_CYTOSKELETON	1.15	0.44	0	0	0	not significant
10032	MARSON_BOUND_BY_FOXP3_UNSTIMULATED	1.16	1.17	0	0	0	not significant
10033	GO_SIGNALING_RECEPTOR_BINDING	1.16	1.15	0	0	0	not significant
10034	GO_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	1.16	1.13	0	0	0	not significant
10035	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP	1.16	1.08	0	0	0	not significant
10036	GO_CIRCULATORY_SYSTEM_DEVELOPMENT	1.16	1.07	0	0	0	not significant
10037	GO_REGULATION_OF_PROTEIN_LOCALIZATION	1.16	1.02	0	0	0	not significant
10038	LIAO_METASTASIS	1.16	0.95	0	0	0	not significant
10039	GO_OXIDOREDUCTASE_ACTIVITY	1.16	0.91	0	0	0	not significant
10040	ONKEN_UVEAL_MELANOMA_DN	1.16	0.88	0	0	0	not significant
10041	GO_POSITIVE_REGULATION_OF_LOCOMOTION	1.16	0.84	0	0	0	not significant
10042	GO_CELLULAR_RESPONSE_TO_OXIDATIVE_STRESS	1.16	0.83	0	0	0	not significant
10043	DELYS_THYROID_CANCER_UP	1.16	0.82	0	0	0	not significant
10044	GO_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	1.16	0.82	0	0	0	not significant
10045	GO_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT	1.16	0.81	0	0	0	not significant
10046	GO_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	1.16	0.8	0	0	0	not significant
10047	GO_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCAD	1.16	0.76	0	0	0	not significant
10048	LEE_RECENT_THYMIC_EMIGRANT	1.16	0.76	0	0	0	not significant
10049	GO_CARBOHYDRATE_HOMEOSTASIS	1.16	0.73	0	0	0	not significant
10050	GO_SULFUR_COMPOUND_METABOLIC_PROCESS	1.16	0.72	0	0	0	not significant
10051	DER_IFN_GAMMA_RESPONSE_UP	1.16	0.66	0	0	0	not significant
10052	GO_REGULATION_OF_DNA_RECOMBINATION	1.16	0.66	0	0	0	not significant
10053	GO_PLASMA_MEMBRANE_RAFT	1.16	0.65	0	0	0	not significant
10054	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED	1.16	0.65	0	0	0	not significant
10055	SWEET_KRAS_ONCOGENIC_SIGNATURE	1.16	0.65	0	0	0	not significant
10056	GO_CLUSTER_OF_ACTIN_BASED_CELL_PROJECTIONS	1.16	0.64	0	0	0	not significant
10057	GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	1.16	0.64	0	0	0	not significant
10058	GO_REGULATION_OF_CATION_CHANNEL_ACTIVITY	1.16	0.64	0	0	0	not significant
10059	GO_XENOBIOTIC_METABOLIC_PROCESS	1.16	0.64	0	0	0	not significant
10060	HUANG_DASATINIB_RESISTANCE_UP	1.16	0.63	0	0	0	not significant
10061	PTEN_DN.V2_UP	1.16	0.63	0	0	0	not significant
10062	CHR1Q22	1.16	0.62	0	0	0	not significant
10063	GO_CELLULAR_RESPONSE_TO_IONIZING_RADIATION	1.16	0.62	0	0	0	not significant
10064	HALLMARK_ANDROGEN_RESPONSE	1.16	0.62	0	0	0	not significant
10065	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON	1.16	0.62	0	0	0	not significant
10066	PID_TNF_PATHWAY	1.16	0.62	0	0	0	not significant
10067	GO_MEMBRANE_INVAGINATION	1.16	0.61	0	0	0	not significant
10068	GO_SYNAPTIC_VESICLE_MEMBRANE	1.16	0.6	0	0	0	not significant
10069	SESTO_RESPONSE_TO_UV_C6	1.16	0.6	0	0	0	not significant
10070	VILLANUEVA_LIVER_CANCER_KRT19_DN	1.16	0.6	0	0	0	not significant
10071	WANG_TARGETS_OF_MLL_CBP_FUSION_UP	1.16	0.6	0	0	0	not significant
10072	GO_METANEPHROS_DEVELOPMENT	1.16	0.59	0	0	0	not significant
10073	REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS	1.16	0.59	0	0	0	not significant
10074	CHR7P14	1.16	0.58	0	0	0	not significant
10075	GALLUZZI_PERMEABILIZE_MITOCHONDRIA	1.16	0.58	0	0	0	not significant
10076	GO_POSITIVE_REGULATION_OF_DNA_REPLICATION	1.16	0.58	0	0	0	not significant
10077	KUUSELO_PANCREATIC_CANCER_19Q13_AMPLIFICATION	1.16	0.58	0	0	0	not significant
10078	GO_AMYLOID_BETA_FORMATION	1.16	0.57	0	0	0	not significant
10079	GO_PROTEIN_MANNOSYLATION	1.16	0.57	0	0	0	not significant
10080	SHIN_B_CELL_LYMPHOMA_CLUSTER_3	1.16	0.57	0	0	0	not significant
10081	ZWANG_EGF_PERSISTENTLY_UP	1.16	0.57	0	0	0	not significant
10082	BRACHAT_RESPONSE_TO_CAMPTOTHECIN_UP	1.16	0.56	0	0	0	not significant
10083	MODY_HIPPOCAMPUS_NEONATAL	1.16	0.56	0	0	0	not significant
10084	TRAYNOR_RETT_SYNDROM_UP	1.16	0.56	0	0	0	not significant
10085	COLLIS_PRKDC_SUBSTRATES	1.16	0.55	0	0	0	not significant
10086	GO_POSITIVE_REGULATION_OF_COLLAGEN_BIOSYNTHETIC_PROCESS	1.16	0.55	0	0	0	not significant
10087	GO_RACEMASE_AND_EPIMERASE_ACTIVITY	1.16	0.55	0	0	0	not significant
10088	GO_POSITIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	1.16	0.54	0	0	0	not significant
10089	BOYAULT_LIVER_CANCER_SUBCLASS_G6_DN	1.16	0.53	0	0	0	not significant
10090	GO_MCM_COMPLEX	1.16	0.53	0	0	0	not significant
10091	GO_REGULATION_OF_PROTEIN_HOMOOLIGOMERIZATION	1.16	0.53	0	0	0	not significant
10092	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_23	1.16	0.53	0	0	0	not significant
10093	GO_PERINUCLEAR_ENDOPLASMIC_RETICULUM	1.16	0.52	0	0	0	not significant
10094	GO_POSITIVE_REGULATION_OF_HISTONE_DEACETYLATION	1.16	0.52	0	0	0	not significant
10095	REACTOME_NUCLEOBASE_CATABOLISM	1.16	0.52	0	0	0	not significant
10096	REACTOME_PROLACTIN_RECEPTOR_SIGNALING	1.16	0.52	0	0	0	not significant
10097	BIOCARTA_PDZS_PATHWAY	1.16	0.51	0	0	0	not significant
10098	FLORIO_HUMAN_NEOCORTEX	1.16	0.51	0	0	0	not significant
10099	GO_SPECTRIN	1.16	0.51	0	0	0	not significant
10100	GO_3_5_CYCLIC_AMP_PHOSPHODIESTERASE_ACTIVITY	1.16	0.5	0	0	0	not significant
10101	GO_NEGATIVE_REGULATION_OF_CILIUM_ASSEMBLY	1.16	0.5	0	0	0	not significant
10102	MIKKELSEN_IPS_HCP_WITH_H3_UNMETHYLATED	1.16	0.5	0	0	0	not significant
10103	REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS	1.16	0.5	0	0	0	not significant
10104	BIOCARTA_TCRA_PATHWAY	1.16	0.49	0	0	0	not significant
10105	GO_MICROTUBULE_NUCLEATION_BY_MICROTUBULE_ORGANIZING_CENTER	1.16	0.49	0	0	0	not significant
10106	GO_REGULATION_OF_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_BETA_	1.16	0.49	0	0	0	not significant
10107	GO_LEPTIN_MEDIATED_SIGNALING_PATHWAY	1.16	0.48	0	0	0	not significant
10108	GO_POSITIVE_REGULATION_OF_SYNAPTIC_VESICLE_TRANSPORT	1.16	0.48	0	0	0	not significant
10109	GO_CO_SMAD_BINDING	1.16	0.47	0	0	0	not significant
10110	GO_RAGULATOR_COMPLEX	1.16	0.47	0	0	0	not significant
10111	GO_REPLICATION_FORK_ARREST	1.16	0.47	0	0	0	not significant
10112	LEE_SP4_THYMOCYTE	1.16	0.47	0	0	0	not significant
10113	GO_REGULATION_OF_TRANSPORT	1.17	1.4	0	0	0	not significant
10114	GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	1.17	1.23	0	0	0	not significant
10115	GO_CHEMICAL_HOMEOSTASIS	1.17	1.18	0	0	0	not significant
10116	CUI_TCF21_TARGETS_2_DN	1.17	1.02	0	0	0	not significant
10117	GO_INNATE_IMMUNE_RESPONSE	1.17	1.02	0	0	0	not significant
10118	GO_MULTI_ORGANISM_REPRODUCTIVE_PROCESS	1.17	0.99	0	0	0	not significant
10119	DELACROIX_RARG_BOUND_MEF	1.17	0.89	0	0	0	not significant
10120	GO_EARLY_ENDOSOME	1.17	0.87	0	0	0	not significant
10121	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	1.17	0.87	0	0	0	not significant
10122	GO_RESPONSE_TO_INSULIN	1.17	0.83	0	0	0	not significant
10123	CAIRO_HEPATOBLASTOMA_UP	1.17	0.77	0	0	0	not significant
10124	GO_RESPONSE_TO_STARVATION	1.17	0.77	0	0	0	not significant
10125	GO_STEROID_HORMONE_MEDIATED_SIGNALING_PATHWAY	1.17	0.77	0	0	0	not significant

10126	GO_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	1.17	0.75	0	0	0	not significant
10127	HALLMARK_ESTROGEN_RESPONSE_EARLY	1.17	0.75	0	0	0	not significant
10128	GO_RESPONSE_TO_UV	1.17	0.74	0	0	0	not significant
10129	GO_CELLULAR_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	1.17	0.72	0	0	0	not significant
10130	P53_DN.V1_UP	1.17	0.72	0	0	0	not significant
10131	REACTOME_ION_CHANNEL_TRANSPORT	1.17	0.72	0	0	0	not significant
10132	RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POORLY_UP	1.17	0.72	0	0	0	not significant
10133	GO_DETECTION_OF_STIMULUS	1.17	0.7	0	0	0	not significant
10134	ESC_V6.5_UP_LATE.V1_UP	1.17	0.69	0	0	0	not significant
10135	GO_AZUROPHIL_GRANULE_LUMEN	1.17	0.69	0	0	0	not significant
10136	GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS	1.17	0.69	0	0	0	not significant
10137	IL21_UP.V1_UP	1.17	0.68	0	0	0	not significant
10138	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE	1.17	0.68	0	0	0	not significant
10139	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP	1.17	0.67	0	0	0	not significant
10140	GO_SPERMATID_DIFFERENTIATION	1.17	0.66	0	0	0	not significant
10141	KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	1.17	0.66	0	0	0	not significant
10142	MARKEY_RB1_CHRONIC_LOF_DN	1.17	0.66	0	0	0	not significant
10143	MORI_PLASMA_CELL_UP	1.17	0.65	0	0	0	not significant
10144	GO_DIGESTION	1.17	0.64	0	0	0	not significant
10145	GO_REGULATION_OF_ERAD_PATHWAY	1.17	0.64	0	0	0	not significant
10146	LEE_TARGETS_OF_PTCH1_AND_SUFU_DN	1.17	0.64	0	0	0	not significant
10147	LIM_MAMMARY_LUMINAL_MATURE_DN	1.17	0.64	0	0	0	not significant
10148	GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT_MEMBRAN	1.17	0.62	0	0	0	not significant
10149	GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_BINDING	1.17	0.62	0	0	0	not significant
10150	ZWANG_EGF_INTERVAL_UP	1.17	0.62	0	0	0	not significant
10151	BOYLAN_MULTIPLE_MYELOMA_D_CLUSTER_DN	1.17	0.61	0	0	0	not significant
10152	GO_GLIAL_CELL_MIGRATION	1.17	0.61	0	0	0	not significant
10153	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_UP	1.17	0.61	0	0	0	not significant
10154	REACTOME_NON_INTEGRIN_MEMBRANE_ECM_INTERACTIONS	1.17	0.61	0	0	0	not significant
10155	SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_DN	1.17	0.61	0	0	0	not significant
10156	GO_POSITIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	1.17	0.6	0	0	0	not significant
10157	GO_RESPONSE_TO_INTERLEUKIN_4	1.17	0.6	0	0	0	not significant
10158	HU_GENOTOXIN_ACTION_DIRECT_VS_INDIRECT_4HR	1.17	0.6	0	0	0	not significant
10159	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	1.17	0.6	0	0	0	not significant
10160	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	1.17	0.6	0	0	0	not significant
10161	GO_ACTIVATED_T_CELL_PROLIFERATION	1.17	0.59	0	0	0	not significant
10162	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	1.17	0.59	0	0	0	not significant
10163	GO_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	1.17	0.59	0	0	0	not significant
10164	REACTOME_ER_QUALITY_CONTROL_COMPARTMENT_ERQC	1.17	0.59	0	0	0	not significant
10165	OUYANG_PROSTATE_CANCER_MARKERS	1.17	0.58	0	0	0	not significant
10166	REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI	1.17	0.58	0	0	0	not significant
10167	BIOCARTA_GATA3_PATHWAY	1.17	0.57	0	0	0	not significant
10168	GO_PEPTIDE_CATABOLIC_PROCESS	1.17	0.57	0	0	0	not significant
10169	PID_RHOA_REG_PATHWAY	1.17	0.57	0	0	0	not significant
10170	GO_RESPONSE_TO_GLUCAGON	1.17	0.56	0	0	0	not significant
10171	GO_SPECTRIN_BINDING	1.17	0.56	0	0	0	not significant
10172	REACTOME_INSULIN_RECEPTOR_RECYCLING	1.17	0.56	0	0	0	not significant
10173	VISALA_AGING_LYMPHOCYTE_DN	1.17	0.56	0	0	0	not significant
10174	GO_REGULATION_OF_CELL_CELL_ADHESION_MEDIATED_BY_INTEGRIN	1.17	0.55	0	0	0	not significant
10175	GO_C_ACYLTRANSFERASE_ACTIVITY	1.17	0.54	0	0	0	not significant
10176	GO_ECTODERM_DEVELOPMENT	1.17	0.54	0	0	0	not significant
10177	REACTOME_METABOLISM_OF_STEROID_HORMONES	1.17	0.54	0	0	0	not significant
10178	REACTOME_MUCOPOLYSACCHARIDOSES	1.17	0.54	0	0	0	not significant
10179	GO_CELL_BODY_MEMBRANE	1.17	0.53	0	0	0	not significant
10180	GO_MAINTENANCE_OF_PROTEIN_LOCALIZATION_IN_ENDOPLASMIC_RETICULUM	1.17	0.53	0	0	0	not significant
10181	GO_PALMITOYL_PROTEIN_HYDROLASE_ACTIVITY	1.17	0.53	0	0	0	not significant
10182	GO_PHOSPHATIDYLINOSITOL_4_5_BISPHOSPHATE_PHOSPHATASE_ACTIVITY	1.17	0.53	0	0	0	not significant
10183	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	1.17	0.53	0	0	0	not significant
10184	GO_VIRAL_BUDDING_VIA_HOST_ESCRT_COMPLEX	1.17	0.53	0	0	0	not significant
10185	GO_GASTRIC_ACID_SECRETION	1.17	0.52	0	0	0	not significant
10186	GO_SECRETION_BY_TISSUE	1.17	0.52	0	0	0	not significant
10187	GO_TETRAHYDROFOLATE_INTERCONVERSION	1.17	0.52	0	0	0	not significant
10188	GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	1.17	0.52	0	0	0	not significant
10189	REACTOME_POLB_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR	1.17	0.52	0	0	0	not significant
10190	GO_CARDIAC_MUSCLE_FIBER_DEVELOPMENT	1.17	0.51	0	0	0	not significant
10191	GO_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	1.17	0.51	0	0	0	not significant
10192	GO_GALACTOSIDASE_ACTIVITY	1.17	0.51	0	0	0	not significant
10193	GO_POSITIVE_REGULATION_OF_T_HELPER_17_CELL_DIFFERENTIATION	1.17	0.51	0	0	0	not significant
10194	BIOCARTA_RECK_PATHWAY	1.17	0.5	0	0	0	not significant
10195	GO_GLYCINE_TRANSPORT	1.17	0.5	0	0	0	not significant
10196	GO_ZYMOGEN_INHIBITION	1.17	0.5	0	0	0	not significant
10197	GO_PYROPTOSIS	1.17	0.49	0	0	0	not significant
10198	GO_NEGATIVE_REGULATION_OF_PERK_MEDIATED_UNFOLDED_PROTEIN_RESPON	1.17	0.48	0	0	0	not significant
10199	GO_SPHINGOSINE_1_PHOSPHATE_RECEPTOR_ACTIVITY	1.17	0.48	0	0	0	not significant
10200	GO_RESPONSE_TO_ENDOGENOUS_STIMULUS	1.18	1.38	0	0	0	not significant
10201	PEREZ_TP53_TARGETS	1.18	1.2	0	0	0	not significant
10202	REACTOME_TRANSPORT_OF_SMALL_MOLECULES	1.18	1.02	0	0	0	not significant
10203	GO_NERVOUS_SYSTEM_PROCESS	1.18	0.96	0	0	0	not significant
10204	GO_REGULATION_OF_CELL_ADHESION	1.18	0.96	0	0	0	not significant
10205	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP	1.18	0.88	0	0	0	not significant
10206	GO_PHOSPHOLIPID_METABOLIC_PROCESS	1.18	0.86	0	0	0	not significant
10207	GO_ENDOCYTIC_VESICLE_MEMBRANE	1.18	0.79	0	0	0	not significant
10208	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN	1.18	0.79	0	0	0	not significant
10209	GO_NEGATIVE_REGULATION_OF_CELL_ADHESION	1.18	0.78	0	0	0	not significant
10210	GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	1.18	0.76	0	0	0	not significant
10211	GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	1.18	0.75	0	0	0	not significant
10212	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN	1.18	0.75	0	0	0	not significant
10213	YAGI_AML_SURVIVAL	1.18	0.74	0	0	0	not significant
10214	GO_POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	1.18	0.73	0	0	0	not significant
10215	GO_ENDOSOME_ORGANIZATION	1.18	0.71	0	0	0	not significant
10216	GO_POSITIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	1.18	0.71	0	0	0	not significant
10217	GO_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	1.18	0.7	0	0	0	not significant
10218	PID_MYC_REPRESS_PATHWAY	1.18	0.7	0	0	0	not significant
10219	SCHLOSSER_SERUM_RESPONSE_UP	1.18	0.69	0	0	0	not significant
10220	GO_ADULT_BEHAVIOR	1.18	0.68	0	0	0	not significant
10221	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	1.18	0.68	0	0	0	not significant
10222	GO_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	1.18	0.67	0	0	0	not significant
10223	PID_P75_NTR_PATHWAY	1.18	0.67	0	0	0	not significant
10224	SNF5_DN.V1_DN	1.18	0.67	0	0	0	not significant
10225	GO_CHROMOSOME_ORGANIZATION_INVOLVED_IN_MEIOTIC_CELL_CYCLE	1.18	0.66	0	0	0	not significant
10226	GO_MAMMARY_GLAND_EPITHELIUM_DEVELOPMENT	1.18	0.66	0	0	0	not significant
10227	SMIRNOV_RESPONSE_TO_IR_2HR_DN	1.18	0.66	0	0	0	not significant
10228	REACTOME_SEMAPHORIN_INTERACTIONS	1.18	0.65	0	0	0	not significant
10229	GO_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPT	1.18	0.64	0	0	0	not significant
10230	HOSHIDA_LIVER_CANCER_SURVIVAL_UP	1.18	0.64	0	0	0	not significant
10231	MEISSNER_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3	1.18	0.64	0	0	0	not significant
10232	GO_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	1.18	0.63	0	0	0	not significant
10233	GO_MONOSACCHARIDE_CATABOLIC_PROCESS	1.18	0.63	0	0	0	not significant
10234	GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	1.18	0.63	0	0	0	not significant

10235	LUCAS_HNF4A_TARGETS_UP	1.18	0.63	0	0	0	not significant
10236	BREDEMEYER_RAG_SIGNALING_NOT_VIA_ATM_DN	1.18	0.62	0	0	0	not significant
10237	GO_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	1.18	0.62	0	0	0	not significant
10238	DELACROIX_RAR_TARGETS_UP	1.18	0.61	0	0	0	not significant
10239	GAZIN_EPIGENETIC_SILENCING_BY_KRAS	1.18	0.61	0	0	0	not significant
10240	GO_OVULATION_CYCLE	1.18	0.61	0	0	0	not significant
10241	GO_POSITIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHO	1.18	0.61	0	0	0	not significant
10242	GO_ROUGH_ENDOPLASMIC_RETICULUM_MEMBRANE	1.18	0.61	0	0	0	not significant
10243	GO_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	1.18	0.6	0	0	0	not significant
10244	GO_RRNA_CATABOLIC_PROCESS	1.18	0.6	0	0	0	not significant
10245	PID_LYMPH_ANGIOGENESIS_PATHWAY	1.18	0.6	0	0	0	not significant
10246	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_RED_UP	1.18	0.59	0	0	0	not significant
10247	GO_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMATORY_RESPONSE	1.18	0.59	0	0	0	not significant
10248	GO_REGULATION_OF_B_CELL_DIFFERENTIATION	1.18	0.59	0	0	0	not significant
10249	GO_TRIGLYCERIDE_METABOLIC_PROCESS	1.18	0.59	0	0	0	not significant
10250	GO_NEGATIVE_REGULATION_OF_TRANSLATIONAL_INITIATION	1.18	0.58	0	0	0	not significant
10251	GO_AMINE_CATABOLIC_PROCESS	1.18	0.57	0	0	0	not significant
10252	GO_BONE_MARROW_DEVELOPMENT	1.18	0.57	0	0	0	not significant
10253	GO_CELL_TRAILING_EDGE	1.18	0.57	0	0	0	not significant
10254	GO_NEGATIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_I	1.18	0.57	0	0	0	not significant
10255	GO_PREASSEMBLY_OF_GPI_ANCHOR_IN_ER_MEMBRANE	1.18	0.57	0	0	0	not significant
10256	GO_PROTEIN_LOCALIZATION_TO_PHAGOPHORE_ASSEMBLY_SITE	1.18	0.57	0	0	0	not significant
10257	GO_REGULATION_OF_SNARE_COMPLEX_ASSEMBLY	1.18	0.57	0	0	0	not significant
10258	KOHOUTEK_CCNT2_TARGETS	1.18	0.57	0	0	0	not significant
10259	GO_CILIUM_MOVEMENT_INVOLVED_IN_CELL_MOTILITY	1.18	0.56	0	0	0	not significant
10260	GO_G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_ACTIVITY	1.18	0.56	0	0	0	not significant
10261	GO_NEURON_PROJECTION_ARBORIZATION	1.18	0.56	0	0	0	not significant
10262	GRANDVAUX_IRF3_TARGETS_UP	1.18	0.56	0	0	0	not significant
10263	BARRIER_CANCER_RELAPSE_TUMOR_SAMPLE_UP	1.18	0.55	0	0	0	not significant
10264	GO_ANTIBIOTIC_BIOSYNTHETIC_PROCESS	1.18	0.54	0	0	0	not significant
10265	GO_CELL_JUNCTION_MAINTENANCE	1.18	0.54	0	0	0	not significant
10266	NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_DN	1.18	0.54	0	0	0	not significant
10267	GO_REGULATION_OF_ANTIGEN_PROCESSING_AND_PRESENTATION	1.18	0.53	0	0	0	not significant
10268	GO_SINGLE_STRANDED_DNA_3_5_EXODEOXYRIBONUCLEASE_ACTIVITY	1.18	0.53	0	0	0	not significant
10269	GO_TETRAHYDROFOLATE_METABOLIC_PROCESS	1.18	0.53	0	0	0	not significant
10270	KEGG_FOLATE_BIOSYNTHESIS	1.18	0.53	0	0	0	not significant
10271	REACTOME_IKBA_VARIANT_LEADS_TO_EDA_ID	1.18	0.53	0	0	0	not significant
10272	SASAI_TARGETS_OF_CXCR6_AND_PTCH1_UP	1.18	0.53	0	0	0	not significant
10273	GO_CARDIOLIPIN_BINDING	1.18	0.52	0	0	0	not significant
10274	GO_REGULATION_OF_COLLATERAL_SPROUTING	1.18	0.52	0	0	0	not significant
10275	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_CIRCULATOR	1.18	0.52	0	0	0	not significant
10276	GO_REGULATION_OF_XENOPHAGY	1.18	0.52	0	0	0	not significant
10277	GO_N_ACETYLNEURAMINATE_CATABOLIC_PROCESS	1.18	0.51	0	0	0	not significant
10278	GO_POSTSYNAPTIC_DENSITY_PROTEIN_95_CLUSTERING	1.18	0.51	0	0	0	not significant
10279	GO_SERINE_TRANSPORT	1.18	0.5	0	0	0	not significant
10280	REACTOME_TNFR1_MEDIATED_CERAMIDE_PRODUCTION	1.18	0.49	0	0	0	not significant
10281	GO_REGULATION_OF_CELL_POPULATION_PROLIFERATION	1.19	1.32	0	0	0	not significant
10282	GO_EXOCYTOSIS	1.19	1.19	0	0	0	not significant
10283	GO_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	1.19	1.17	0	0	0	not significant
10284	GO_REGULATION_OF_IMMUNE_RESPONSE	1.19	1.15	0	0	0	not significant
10285	GO_IMPORT_INTO_CELL	1.19	1.09	0	0	0	not significant
10286	GO_CARBOHYDRATE_DERIVATIVE_BIOSYNTHETIC_PROCESS	1.19	1.04	0	0	0	not significant
10287	MARTINEZ_RB1_TARGETS_DN	1.19	0.97	0	0	0	not significant
10288	GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	1.19	0.93	0	0	0	not significant
10289	GO_MEMBRANE_REGION	1.19	0.88	0	0	0	not significant
10290	CHR17Q25	1.19	0.84	0	0	0	not significant
10291	JIANG_HYPOXIA_NORMAL	1.19	0.83	0	0	0	not significant
10292	CHR22Q13	1.19	0.81	0	0	0	not significant
10293	WANG_CISPLATIN_RESPONSE_AND_XPC_UP	1.19	0.81	0	0	0	not significant
10294	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN	1.19	0.79	0	0	0	not significant
10295	CAIRO_HEPATOBLASTOMA_CLASSES_DN	1.19	0.78	0	0	0	not significant
10296	WANG_MLL_TARGETS	1.19	0.78	0	0	0	not significant
10297	GO_HEPATICOBILIARY_SYSTEM_DEVELOPMENT	1.19	0.77	0	0	0	not significant
10298	GO_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	1.19	0.77	0	0	0	not significant
10299	AKT_UP_MTOR_DN.V1_UP	1.19	0.76	0	0	0	not significant
10300	GO_ORGANIC_ACID_BINDING	1.19	0.76	0	0	0	not significant
10301	GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_	1.19	0.73	0	0	0	not significant
10302	GO_CORE_PROMOTER_BINDING	1.19	0.71	0	0	0	not significant
10303	GO_RESPONSE_TO_CALCIUM_ION	1.19	0.71	0	0	0	not significant
10304	RELA_DN.V1_DN	1.19	0.71	0	0	0	not significant
10305	GO_BASE_EXCISION_REPAIR	1.19	0.7	0	0	0	not significant
10306	GO_PLASMA_MEMBRANE_ORGANIZATION	1.19	0.7	0	0	0	not significant
10307	GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	1.19	0.7	0	0	0	not significant
10308	GO_MITOTIC_G2_M_TRANSITION_CHECKPOINT	1.19	0.68	0	0	0	not significant
10309	GO_CELLULAR_RESPONSE_TO_VIRUS	1.19	0.67	0	0	0	not significant
10310	GO_CORE_PROMOTER_SEQUENCE_SPECIFIC_DNA_BINDING	1.19	0.67	0	0	0	not significant
10311	GO_RETINA_HOMEOSTASIS	1.19	0.67	0	0	0	not significant
10312	ONO_FOXP3_TARGETS_DN	1.19	0.67	0	0	0	not significant
10313	REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	1.19	0.67	0	0	0	not significant
10314	REACTOME_FANCONI_ANEMIA_PATHWAY	1.19	0.67	0	0	0	not significant
10315	GO_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	1.19	0.66	0	0	0	not significant
10316	GO_CELLULAR_MODIFIED_AMINO_ACID_METABOLIC_PROCESS	1.19	0.65	0	0	0	not significant
10317	GO_REGULATION_OF_ERBB_SIGNALING_PATHWAY	1.19	0.65	0	0	0	not significant
10318	GO_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	1.19	0.64	0	0	0	not significant
10319	GO_MALE_MEIOTIC_NUCLEAR_DIVISION	1.19	0.64	0	0	0	not significant
10320	PID_P38_MKK3_6PATHWAY	1.19	0.63	0	0	0	not significant
10321	PID_PTP1B_PATHWAY	1.19	0.63	0	0	0	not significant
10322	GO_CYCLIN_BINDING	1.19	0.62	0	0	0	not significant
10323	GO_HYDROLASE_ACTIVITY_HYDROLYZING_N_GLYCOSYL_COMPOUNDS	1.19	0.62	0	0	0	not significant
10324	GO_LYMPHOCYTE_CHEMOTAXIS	1.19	0.62	0	0	0	not significant
10325	GO_NEUROEPITHELIAL_CELL_DIFFERENTIATION	1.19	0.62	0	0	0	not significant
10326	REACTOME_CELL_JUNCTION_ORGANIZATION	1.19	0.62	0	0	0	not significant
10327	WANG_RESPONSE_TO_BEXAROTENE_UP	1.19	0.62	0	0	0	not significant
10328	GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	1.19	0.61	0	0	0	not significant
10329	GO_NEGATIVE_REGULATION_OF_LIPID_STORAGE	1.19	0.61	0	0	0	not significant
10330	GO_GLUTATHIONE_METABOLIC_PROCESS	1.19	0.6	0	0	0	not significant
10331	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_BIOSYNTHETIC_PROCESS	1.19	0.6	0	0	0	not significant
10332	HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_DN	1.19	0.6	0	0	0	not significant
10333	KEGG_GLYCEROLIPID_METABOLISM	1.19	0.6	0	0	0	not significant
10334	KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	1.19	0.6	0	0	0	not significant
10335	YANAGIHARA_ESX1_TARGETS	1.19	0.6	0	0	0	not significant
10336	GO_GLUTAMINE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	1.19	0.59	0	0	0	not significant
10337	GO_NEGATIVE_REGULATION_OF_INTERFERON_BETA_PRODUCTION	1.19	0.59	0	0	0	not significant
10338	RICKMAN_HEAD_AND_NECK_CANCER_F	1.19	0.59	0	0	0	not significant
10339	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_TOP20_DN	1.19	0.59	0	0	0	not significant
10340	GO_PEPTIDE_HORMONE_PROCESSING	1.19	0.58	0	0	0	not significant
10341	GO_REGULATION_OF_LIPOPROTEIN_LIPASE_ACTIVITY	1.19	0.58	0	0	0	not significant
10342	GO_SEH1_ASSOCIATED_COMPLEX	1.19	0.58	0	0	0	not significant
10343	GO_DOPAMINE_TRANSPORT	1.19	0.56	0	0	0	not significant

10344	GO_PROGRAMMED_CELL_DEATH_IN_RESPONSE_TO_REACTIVE_OXYGEN_SPECIE	1.19	0.56	0	0	0	not significant
10345	PID_IL5_PATHWAY	1.19	0.56	0	0	0	not significant
10346	VANASSE_BCL2_TARGETS_UP	1.19	0.56	0	0	0	not significant
10347	GO_POSITIVE_REGULATION_OF_CENTRIOLE_REPLICATION	1.19	0.55	0	0	0	not significant
10348	GO_PYRIMIDINE_DEOXYRIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PRO	1.19	0.55	0	0	0	not significant
10349	GO_RESPONSE_TO_LITHIUM_ION	1.19	0.55	0	0	0	not significant
10350	GO_TROPOMYOSIN_BINDING	1.19	0.55	0	0	0	not significant
10351	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_DEATH_RECEPTORS_AND_LI	1.19	0.55	0	0	0	not significant
10352	GO_PURINERGIC_NUCLEOTIDE_RECEPTOR_SIGNALING_PATHWAY	1.19	0.54	0	0	0	not significant
10353	THILLAINADESAN_ZNF217_TARGETS_DN	1.19	0.54	0	0	0	not significant
10354	GO_MYOSIN_II_BINDING	1.19	0.53	0	0	0	not significant
10355	GO_REGULATION_OF_DNA_LIGATION	1.19	0.53	0	0	0	not significant
10356	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_TRANS	1.19	0.53	0	0	0	not significant
10357	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX5_UP	1.19	0.53	0	0	0	not significant
10358	GO_ISOCITRATE_METABOLIC_PROCESS	1.19	0.52	0	0	0	not significant
10359	GO_NEGATIVE_REGULATION_OF_FIBROBLAST_MIGRATION	1.19	0.52	0	0	0	not significant
10360	GO_NEGATIVE_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	1.19	0.52	0	0	0	not significant
10361	GO_SINGLE_STRANDED_DNA_EXODEOXYRIBONUCLEASE_ACTIVITY	1.19	0.52	0	0	0	not significant
10362	REACTOME_CS_DS_DEGRADATION	1.19	0.52	0	0	0	not significant
10363	GO_CELLULAR_RESPONSE_TO_PURINE_CONTAINING_COMPOUND	1.19	0.51	0	0	0	not significant
10364	GO_PROTEIN_RETENTION_IN_GOLGI_APPARATUS	1.19	0.51	0	0	0	not significant
10365	GO_URETER_DEVELOPMENT	1.19	0.51	0	0	0	not significant
10366	GO_REPRODUCTION	1.20	1.4	0	0	0	not significant
10367	GO_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	1.20	1.39	0	0	0	not significant
10368	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3	1.20	1.14	0	0	0	not significant
10369	GO_COFACTOR_METABOLIC_PROCESS	1.20	1	0	0	0	not significant
10370	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5	1.20	0.99	0	0	0	not significant
10371	GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	1.20	0.97	0	0	0	not significant
10372	ZHOU_INFLAMMATORY_RESPONSE_LPS_UP	1.20	0.89	0	0	0	not significant
10373	GO_ORGANIC_ACID_CATABOLIC_PROCESS	1.20	0.88	0	0	0	not significant
10374	VANTVEER_BREAST_CANCER_ESR1_UP	1.20	0.88	0	0	0	not significant
10375	HATADA_METHYLATED_IN_LUNG_CANCER_UP	1.20	0.87	0	0	0	not significant
10376	RAO_BOUND_BY_SALL4	1.20	0.84	0	0	0	not significant
10377	GO_NEGATIVE_REGULATION_OF_SECRETION	1.20	0.83	0	0	0	not significant
10378	REACTOME_OXIDATIVE_STRESS_INDUCED_SENESCENCE	1.20	0.8	0	0	0	not significant
10379	GO_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	1.20	0.79	0	0	0	not significant
10380	GO_SERINE_HYDROLASE_ACTIVITY	1.20	0.79	0	0	0	not significant
10381	GROSS_HYPOXIA_VIA_ELK3_AND_HIF1A_UP	1.20	0.78	0	0	0	not significant
10382	GO_EAR_DEVELOPMENT	1.20	0.77	0	0	0	not significant
10383	GO_CATION_CHANNEL_COMPLEX	1.20	0.75	0	0	0	not significant
10384	GO_CYCLIC_NUCLEOTIDE_MEDIATED_SIGNALING	1.20	0.73	0	0	0	not significant
10385	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STR	1.20	0.72	0	0	0	not significant
10386	BERENJENO_ROCK_SIGNALING_NOT_VIA_RHOA_DN	1.20	0.71	0	0	0	not significant
10387	MORI_MATURE_B_LYMPHOCYTE_UP	1.20	0.71	0	0	0	not significant
10388	MCCLUNG_CREB1_TARGETS_UP	1.20	0.7	0	0	0	not significant
10389	GO_IMMUNOGLOBULIN_PRODUCTION_INVOLVED_IN_IMMUNOGLOBULIN_MEDIATED_	1.20	0.69	0	0	0	not significant
10390	GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	1.20	0.69	0	0	0	not significant
10391	GO_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	1.20	0.68	0	0	0	not significant
10392	REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	1.20	0.68	0	0	0	not significant
10393	BIOCARTA_GH_PATHWAY	1.20	0.67	0	0	0	not significant
10394	GO_HEART_VALVE_DEVELOPMENT	1.20	0.67	0	0	0	not significant
10395	GO_REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	1.20	0.66	0	0	0	not significant
10396	GERHOLD_ADIPOGENESIS_DN	1.20	0.65	0	0	0	not significant
10397	GO_REGULATION_OF_GLUCONEOGENESIS	1.20	0.65	0	0	0	not significant
10398	HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_DN	1.20	0.65	0	0	0	not significant
10399	REACTOME_PEPTIDE_HORMONE_METABOLISM	1.20	0.65	0	0	0	not significant
10400	CHR9P24	1.20	0.64	0	0	0	not significant
10401	DORSAM_HOXA9_TARGETS_DN	1.20	0.64	0	0	0	not significant
10402	GO_REGULATION_OF_PROTEIN_MATURATION	1.20	0.64	0	0	0	not significant
10403	GO_SNARE_COMPLEX_ASSEMBLY	1.20	0.64	0	0	0	not significant
10404	REACTOME_TNFR1_INDUCED_NFKAPPAB_SIGNALING_PATHWAY	1.20	0.64	0	0	0	not significant
10405	GO_CORECEPTOR_ACTIVITY	1.20	0.63	0	0	0	not significant
10406	GO_MAGNESIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.20	0.63	0	0	0	not significant
10407	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DEGRANULATION	1.20	0.63	0	0	0	not significant
10408	HALLMARK_WNT_BETA_CATENIN_SIGNALING	1.20	0.63	0	0	0	not significant
10409	REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE_COLLAPS	1.20	0.63	0	0	0	not significant
10410	GO_ESTABLISHMENT_OF_PLANAR_POLARITY_OF_EMBRYONIC_EPITHELIUM	1.20	0.62	0	0	0	not significant
10411	GO_GLYCOSYL_COMPOUND_CATABOLIC_PROCESS	1.20	0.62	0	0	0	not significant
10412	GO_MAGNESIUM_ION_TRANSPORT	1.20	0.62	0	0	0	not significant
10413	GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATIO	1.20	0.62	0	0	0	not significant
10414	PID_PDGFRA_PATHWAY	1.20	0.62	0	0	0	not significant
10415	VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1	1.20	0.62	0	0	0	not significant
10416	GO_MODIFIED_AMINO_ACID_TRANSPORT	1.20	0.61	0	0	0	not significant
10417	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	1.20	0.61	0	0	0	not significant
10418	GO_DETECTION_OF_MECHANICAL_STIMULUS	1.20	0.59	0	0	0	not significant
10419	GO_BLEB	1.20	0.58	0	0	0	not significant
10420	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGN	1.20	0.58	0	0	0	not significant
10421	GO_MEMBRANE_HYPERPOLARIZATION	1.20	0.58	0	0	0	not significant
10422	GO_RADIAL_GLIAL_CELL_DIFFERENTIATION	1.20	0.58	0	0	0	not significant
10423	COURTOIS_SENESCENCE_TRIGGERS	1.20	0.57	0	0	0	not significant
10424	GO_BIOACTIVE_LIPID_RECEPTOR_ACTIVITY	1.20	0.57	0	0	0	not significant
10425	MATZUK_OVULATION	1.20	0.57	0	0	0	not significant
10426	GO_ISG15_PROTEIN_CONJUGATION	1.20	0.56	0	0	0	not significant
10427	GO_LOCOMOTOR_RHYTHM	1.20	0.56	0	0	0	not significant
10428	GO_MICROVILLUS_ASSEMBLY	1.20	0.56	0	0	0	not significant
10429	GO_POLYNUCLEOTIDE_DEPHOSPHORYLATION	1.20	0.56	0	0	0	not significant
10430	SASSON_FSH_RESPONSE	1.20	0.56	0	0	0	not significant
10431	GO_CELL_PROLIFERATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	1.20	0.55	0	0	0	not significant
10432	GO_NEUREXIN_FAMILY_PROTEIN_BINDING	1.20	0.55	0	0	0	not significant
10433	GO_PHOSPHORUS_OXYGEN_LYASE_ACTIVITY	1.20	0.55	0	0	0	not significant
10434	CHR4Q26	1.20	0.54	0	0	0	not significant
10435	GO_EPITHELIAL_FLUID_TRANSPORT	1.20	0.54	0	0	0	not significant
10436	REACTOME_ACYL_CHAIN_REMODELLING_OF_PS	1.20	0.54	0	0	0	not significant
10437	BAUS_TFF2_TARGETS_DN	1.20	0.53	0	0	0	not significant
10438	GO_LIPOPHAGY	1.20	0.53	0	0	0	not significant
10439	YAMANAKA_GLIOBLASTOMA_SURVIVAL_DN	1.20	0.52	0	0	0	not significant
10440	GO_REGULATION_OF_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_	1.20	0.51	0	0	0	not significant
10441	GO_CELLULAR_RESPONSE_TO_ENDOGENOUS_STIMULUS	1.21	1.57	0	0	0	not significant
10442	GO_RESPONSE_TO_CYTOKINE	1.21	1.4	0	0	0	not significant
10443	GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_UP	1.21	1.21	0	0	0	not significant
10444	GO_DNA_REPLICATION	1.21	1.05	0	0	0	not significant
10445	GO_REGULATION_OF_HORMONE_LEVELS	1.21	1.05	0	0	0	not significant
10446	NABA_MATRISOME	1.21	1.01	0	0	0	not significant
10447	DAZARD_RESPONSE_TO_UV_NHEK_UP	1.21	0.99	0	0	0	not significant
10448	FERNANDEZ_BOUND_BY_MYC	1.21	0.87	0	0	0	not significant
10449	CHR7Q22	1.21	0.85	0	0	0	not significant
10450	CYCLIN_D1_UP.V1_DN	1.21	0.85	0	0	0	not significant
10451	GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT	1.21	0.82	0	0	0	not significant
10452	LU_IL4_SIGNALING	1.21	0.82	0	0	0	not significant

10453	GO_RESPIRATORY_SYSTEM_DEVELOPMENT	1.21	0.81	0	0	0	not significant
10454	GO_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR	1.21	0.78	0	0	0	not significant
10455	GO_STEROID_HORMONE_RECEPTOR_BINDING	1.21	0.78	0	0	0	not significant
10456	CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_UP	1.21	0.77	0	0	0	not significant
10457	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY_P53_CLASS_MEDIATOR	1.21	0.77	0	0	0	not significant
10458	GO_ORGANOPHOSPHATE_ESTER_TRANSPORT	1.21	0.77	0	0	0	not significant
10459	NGUYEN_NOTCH1_TARGETS_DN	1.21	0.75	0	0	0	not significant
10460	REACTOME_FCERI_MEDIATED_MAPK_ACTIVATION	1.21	0.74	0	0	0	not significant
10461	REACTOME_SPHINGOLIPID_METABOLISM	1.21	0.73	0	0	0	not significant
10462	GO_LIPID_DROPLET	1.21	0.72	0	0	0	not significant
10463	GO_CIS_GOLGI_NETWORK	1.21	0.71	0	0	0	not significant
10464	GO_RECEPTOR_CLUSTERING	1.21	0.71	0	0	0	not significant
10465	CHEBOTAEV_GR_TARGETS_UP	1.21	0.7	0	0	0	not significant
10466	GO_POSITIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	1.21	0.7	0	0	0	not significant
10467	GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	1.21	0.7	0	0	0	not significant
10468	GO_T_CELL_MIGRATION	1.21	0.7	0	0	0	not significant
10469	KRAS.KIDNEY_UP.V1_UP	1.21	0.7	0	0	0	not significant
10470	GO_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	1.21	0.69	0	0	0	not significant
10471	GO_PHOSPHOLIPID_TRANSPORT	1.21	0.69	0	0	0	not significant
10472	GO_DNA_CATABOLIC_PROCESS	1.21	0.68	0	0	0	not significant
10473	LIAN_LIPA_TARGETS_6M	1.21	0.68	0	0	0	not significant
10474	LEIN_NEURON_MARKERS	1.21	0.67	0	0	0	not significant
10475	STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN	1.21	0.67	0	0	0	not significant
10476	CHR4Q22	1.21	0.66	0	0	0	not significant
10477	GO_INTERLEUKIN_6_SECRETION	1.21	0.66	0	0	0	not significant
10478	GO_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	1.21	0.66	0	0	0	not significant
10479	GO_REGULATION_OF_BONE_MINERALIZATION	1.21	0.66	0	0	0	not significant
10480	GO_EXTRACELLULAR_MATRIX_BINDING	1.21	0.65	0	0	0	not significant
10481	GO_PROTEIN_KINASE_C_BINDING	1.21	0.65	0	0	0	not significant
10482	GO_MYELOID_DENDRITIC_CELL_DIFFERENTIATION	1.21	0.64	0	0	0	not significant
10483	GO_POSITIVE_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	1.21	0.64	0	0	0	not significant
10484	GO_INTESTINAL_EPITHELIAL_CELL_DIFFERENTIATION	1.21	0.63	0	0	0	not significant
10485	GO_PHOSPHOLIPASE_C_ACTIVITY	1.21	0.63	0	0	0	not significant
10486	GO_POSITIVE_REGULATION_OF_B_CELL_DIFFERENTIATION	1.21	0.63	0	0	0	not significant
10487	GO_ATRIOVENTRICULAR_VALVE_DEVELOPMENT	1.21	0.62	0	0	0	not significant
10488	KASLER_HDAC7_TARGETS_1_DN	1.21	0.62	0	0	0	not significant
10489	VALK_AML_CLUSTER_7	1.21	0.62	0	0	0	not significant
10490	GO_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	1.21	0.61	0	0	0	not significant
10491	GO_CHONDROITIN_SULFATE_CATABOLIC_PROCESS	1.21	0.61	0	0	0	not significant
10492	GO_CYTOLYSIS	1.21	0.61	0	0	0	not significant
10493	REACTOME_SIGNALING_BY_CYTOSOLIC_FGFR1_FUSION_MUTANTS	1.21	0.61	0	0	0	not significant
10494	GO_GDP_METABOLIC_PROCESS	1.21	0.6	0	0	0	not significant
10495	GO_HISTONE_H3_K9_DEMETHYLATION	1.21	0.6	0	0	0	not significant
10496	GO_POSITIVE_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	1.21	0.6	0	0	0	not significant
10497	GO_RESPONSE_TO_GONADOTROPIN	1.21	0.6	0	0	0	not significant
10498	HOLLERN_SOLID_NODULAR_BREAST_TUMOR_DN	1.21	0.6	0	0	0	not significant
10499	JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN	1.21	0.6	0	0	0	not significant
10500	GO_CHEMOREPELLENT_ACTIVITY	1.21	0.59	0	0	0	not significant
10501	GO_DIACYLGLYCEROL_KINASE_ACTIVITY	1.21	0.59	0	0	0	not significant
10502	GO_ENDOPLASMIC_RETICULUM_PALMITOYLTRANSFERASE_COMPLEX	1.21	0.59	0	0	0	not significant
10503	GO_FUCOSYLATION	1.21	0.59	0	0	0	not significant
10504	GO_OTIC_VESICLE_DEVELOPMENT	1.21	0.59	0	0	0	not significant
10505	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_13_PRODUCTION	1.21	0.59	0	0	0	not significant
10506	GO_EXTRACELLULAR_MATRIX_CONSTITUENT_SECRETION	1.21	0.58	0	0	0	not significant
10507	NEWMAN_ERCC6_TARGETS_DN	1.21	0.58	0	0	0	not significant
10508	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	1.21	0.58	0	0	0	not significant
10509	GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT_VIA_HIGH_VOLTAGE_GATED_C	1.21	0.57	0	0	0	not significant
10510	GO_STEROL_IMPORT	1.21	0.57	0	0	0	not significant
10511	GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_CYTOPLASMIC_MEDIA	1.21	0.57	0	0	0	not significant
10512	MALIK_REPRESSED_BY_ESTROGEN	1.21	0.57	0	0	0	not significant
10513	MIZUKAMI_HYPOXIA_UP	1.21	0.57	0	0	0	not significant
10514	PHESSE_TARGETS_OF_APC_AND_MBD2_UP	1.21	0.57	0	0	0	not significant
10515	GO_POLYAMINE_TRANSPORT	1.21	0.56	0	0	0	not significant
10516	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP	1.21	0.56	0	0	0	not significant
10517	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	1.21	0.55	0	0	0	not significant
10518	GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS	1.21	0.54	0	0	0	not significant
10519	GO_ENDOTHELIAL_CELL_MORPHOGENESIS	1.21	0.54	0	0	0	not significant
10520	GO_COMMON_MYELOID_PROGENITOR_CELL_PROLIFERATION	1.21	0.52	0	0	0	not significant
10521	GO_SMALL_MOLECULE_METABOLIC_PROCESS	1.22	2.07	0	0	0	not significant
10522	GO_IMMUNE_SYSTEM_DEVELOPMENT	1.22	1.53	0	0	0	not significant
10523	RUTELLA_RESPONSE_TO_HGF_UP	1.22	1.21	0	0	0	not significant
10524	CHR19P13	1.22	1.18	0	0	0	not significant
10525	GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	1.22	1.06	0	0	0	not significant
10526	GO_REGULATION_OF_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	1.22	1.06	0	0	0	not significant
10527	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN	1.22	1.05	0	0	0	not significant
10528	PEREZ_TP63_TARGETS	1.22	0.96	0	0	0	not significant
10529	GO_NEGATIVE_REGULATION_OF_CELL_MOTILITY	1.22	0.9	0	0	0	not significant
10530	GO_CELLULAR_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN	1.22	0.89	0	0	0	not significant
10531	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	1.22	0.89	0	0	0	not significant
10532	GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	1.22	0.86	0	0	0	not significant
10533	VERHAAK_GLIOBLASTOMA_CLASSICAL	1.22	0.86	0	0	0	not significant
10534	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	1.22	0.84	0	0	0	not significant
10535	GO_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	1.22	0.84	0	0	0	not significant
10536	GO_POSITIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	1.22	0.83	0	0	0	not significant
10537	REACTOME_REPRODUCTION	1.22	0.83	0	0	0	not significant
10538	AMUNDSON_GENOTOXIC_SIGNATURE	1.22	0.82	0	0	0	not significant
10539	BROWNE_HCMV_INFECTION_18HR_DN	1.22	0.82	0	0	0	not significant
10540	GO_CYTOKINE_BINDING	1.22	0.8	0	0	0	not significant
10541	GO_CYTOKINE_RECEPTOR_ACTIVITY	1.22	0.76	0	0	0	not significant
10542	GO_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.22	0.76	0	0	0	not significant
10543	HALLMARK_IL6_JAK_STAT3_SIGNALING	1.22	0.76	0	0	0	not significant
10544	GO_RESPONSE_TO_FATTY_ACID	1.22	0.75	0	0	0	not significant
10545	MARSON_FOXP3_TARGETS_DN	1.22	0.75	0	0	0	not significant
10546	GO_DEOXYRIBONUCLEASE_ACTIVITY	1.22	0.74	0	0	0	not significant
10547	GO_LIGAND_GATED_CATION_CHANNEL_ACTIVITY	1.22	0.74	0	0	0	not significant
10548	GO_INTERSTRAND_CROSS_LINK_REPAIR	1.22	0.73	0	0	0	not significant
10549	REACTOME_TERMINATION_OF_TRANSLESION_DNA_SYNTHESIS	1.22	0.73	0	0	0	not significant
10550	GO_LENS_DEVELOPMENT_IN_CAMERA_TYPE_EYE	1.22	0.72	0	0	0	not significant
10551	GO_POSITIVE_REGULATION_OF_OSSIFICATION	1.22	0.72	0	0	0	not significant
10552	GO_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	1.22	0.72	0	0	0	not significant
10553	LINDSTEDT_DENDRITIC_CELL_MATURATION_C	1.22	0.71	0	0	0	not significant
10554	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN	1.22	0.7	0	0	0	not significant
10555	GOTTWEIN_TARGETS_OF_KSHV_MIR_K12_11	1.22	0.7	0	0	0	not significant
10556	REACTOME_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_ARYLSULFAT	1.22	0.7	0	0	0	not significant
10557	CHR5Q11	1.22	0.69	0	0	0	not significant
10558	ELLWOOD_MYC_TARGETS_DN	1.22	0.69	0	0	0	not significant
10559	GO_AMINOGLYCAN_CATABOLIC_PROCESS	1.22	0.69	0	0	0	not significant
10560	LEIN_CEREBELLUM_MARKERS	1.22	0.69	0	0	0	not significant
10561	LINDGREN_BLADDER_CANCER_HIGH_RECURRENCE	1.22	0.69	0	0	0	not significant

10562	BURTON_ADIPOGENESIS_1	1.22	0.67	0	0	0	not significant
10563	GO_CELLULAR_DEFENSE_RESPONSE	1.22	0.67	0	0	0	not significant
10564	GO_NEGATIVE_REGULATION_OF_AXON_EXTENSION	1.22	0.67	0	0	0	not significant
10565	CHIBA_RESPONSE_TO_TSA_DN	1.22	0.66	0	0	0	not significant
10566	GO_POTASSIUM_CHANNEL_ACTIVITY	1.22	0.66	0	0	0	not significant
10567	LANDIS_BREAST_CANCER_PROGRESSION_UP	1.22	0.66	0	0	0	not significant
10568	GO_CELL_DIFFERENTIATION_IN_SPINAL_CORD	1.22	0.65	0	0	0	not significant
10569	GO_POSITIVE_REGULATION_OF_ERAD_PATHWAY	1.22	0.65	0	0	0	not significant
10570	LIAN_LIPA_TARGETS_3M	1.22	0.64	0	0	0	not significant
10571	REACTOME_ARACHIDONIC_ACID_METABOLISM	1.22	0.64	0	0	0	not significant
10572	REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	1.22	0.64	0	0	0	not significant
10573	REACTOME_SYNDECAN_INTERACTIONS	1.22	0.64	0	0	0	not significant
10574	GO_DEFENSE_RESPONSE_TO_FUNGUS	1.22	0.63	0	0	0	not significant
10575	GO_NADPLUS_KINASE_ACTIVITY	1.22	0.63	0	0	0	not significant
10576	FARMER_BREAST_CANCER_CLUSTER_3	1.22	0.62	0	0	0	not significant
10577	GO_ANGIOGENESIS_INVOLVED_IN_WOUND_HEALING	1.22	0.62	0	0	0	not significant
10578	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_	1.22	0.62	0	0	0	not significant
10579	GO_PHOSPHATIDYLINOSITOL_4_5_BISPHOSPHATE_5_PHOSPHATASE_ACTIVITY	1.22	0.62	0	0	0	not significant
10580	WENG_POR_DOSAGE	1.22	0.62	0	0	0	not significant
10581	BIOCARTA_DSP_PATHWAY	1.22	0.61	0	0	0	not significant
10582	BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_UP	1.22	0.61	0	0	0	not significant
10583	GO_POSITIVE_REGULATION_OF_GRANULOCYTE_DIFFERENTIATION	1.22	0.61	0	0	0	not significant
10584	GO_TRANSFORMING_GROWTH_FACTOR_BETA1_PRODUCTION	1.22	0.61	0	0	0	not significant
10585	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY	1.22	0.61	0	0	0	not significant
10586	IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_DN	1.22	0.61	0	0	0	not significant
10587	REACTOME_INTERLEUKIN_35_SIGNALLING	1.22	0.61	0	0	0	not significant
10588	ZHAN_MULTIPLE_MYELOMA_SPIKED	1.22	0.61	0	0	0	not significant
10589	GO_CUL7_RING_UBIQUITIN_LIGASE_COMPLEX	1.22	0.6	0	0	0	not significant
10590	MULLIGAN_NTF3_SIGNALING_VIA_INSR_AND_IGF1R_DN	1.22	0.6	0	0	0	not significant
10591	GO_DNA_REPLICATION_PREINITIATION_COMPLEX	1.22	0.59	0	0	0	not significant
10592	REACTOME_SIGNAL_ATTENUATION	1.22	0.59	0	0	0	not significant
10593	EHLERS_ANEUPLOIDY_DN	1.22	0.58	0	0	0	not significant
10594	GO_GPI_ANCHOR_BINDING	1.22	0.58	0	0	0	not significant
10595	GO_FATTY_ACID_ELONGATION	1.22	0.57	0	0	0	not significant
10596	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON	1.22	0.57	0	0	0	not significant
10597	ZHENG_FOXP3_TARGETS_IN_THYMUS_DN	1.22	0.56	0	0	0	not significant
10598	BIOCARTA_NEUTROPHIL_PATHWAY	1.22	0.54	0	0	0	not significant
10599	GO_SECRETORY_VESICLE	1.23	1.61	0	0	0	not significant
10600	GO_RESPONSE_TO_HORMONE	1.23	1.52	0	0	0	not significant
10601	GO_POSITIVE_REGULATION_OF_CELL_POPULATION_PROLIFERATION	1.23	1.34	0	0	0	not significant
10602	GO_CALCIUM_ION_BINDING	1.23	1.13	0	0	0	not significant
10603	GO_MONOVALENT_INORGANIC_CATION_TRANSPORT	1.23	1.1	0	0	0	not significant
10604	MIKKELSEN_NPC_ICP_WITH_H3K4ME3	1.23	1.09	0	0	0	not significant
10605	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN	1.23	1.09	0	0	0	not significant
10606	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP	1.23	1.01	0	0	0	not significant
10607	GO_RESPONSE_TO_CARBOHYDRATE	1.23	0.96	0	0	0	not significant
10608	GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	1.23	0.92	0	0	0	not significant
10609	HALLMARK_APICAL_JUNCTION	1.23	0.91	0	0	0	not significant
10610	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_UP	1.23	0.89	0	0	0	not significant
10611	SRC_UP.V1_DN	1.23	0.89	0	0	0	not significant
10612	ATF2_UP.V1_DN	1.23	0.87	0	0	0	not significant
10613	REACTOME_MEIOSIS	1.23	0.87	0	0	0	not significant
10614	PID_FCER1_PATHWAY	1.23	0.86	0	0	0	not significant
10615	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DNA_DAMAG	1.23	0.84	0	0	0	not significant
10616	TSENG_IRS1_TARGETS_DN	1.23	0.82	0	0	0	not significant
10617	GO_HEPARIN_BINDING	1.23	0.81	0	0	0	not significant
10618	GO_PROTEIN_N_LINKED_GLYCOSYLATION	1.23	0.81	0	0	0	not significant
10619	PID_ERA_GENOMIC_PATHWAY	1.23	0.81	0	0	0	not significant
10620	GO_PROTEIN_O_LINKED_GLYCOSYLATION	1.23	0.79	0	0	0	not significant
10621	GO_REGULATION_OF_PHAGOCYTOSIS	1.23	0.79	0	0	0	not significant
10622	REACTOME_MEIOTIC_RECOMBINATION	1.23	0.79	0	0	0	not significant
10623	BOYLAN_MULTIPLE_MYELOMA_PCA3_UP	1.23	0.78	0	0	0	not significant
10624	GO_CELLULAR_RESPONSE_TO_CAMP	1.23	0.77	0	0	0	not significant
10625	KEGG_VIRAL_MYOCARDITIS	1.23	0.77	0	0	0	not significant
10626	CHR5Q14	1.23	0.75	0	0	0	not significant
10627	MAGRANGEAS_MULTIPLE_MYELOMA_IGLL_VS_IGLK_UP	1.23	0.74	0	0	0	not significant
10628	GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYT	1.23	0.73	0	0	0	not significant
10629	GO_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	1.23	0.73	0	0	0	not significant
10630	GO_ORGANISM_EMERGENCE_FROM_PROTECTIVE_STRUCTURE	1.23	0.72	0	0	0	not significant
10631	GOBERT_CORE_OLIGODENDROCYTE_DIFFERENTIATION	1.23	0.71	0	0	0	not significant
10632	BOWIE_RESPONSE_TO_TAMOXIFEN	1.23	0.69	0	0	0	not significant
10633	GO_LAMIN_BINDING	1.23	0.69	0	0	0	not significant
10634	CHR4P15	1.23	0.68	0	0	0	not significant
10635	GO_TERTIARY_GRANULE_LUMEN	1.23	0.68	0	0	0	not significant
10636	PID_RXR_VDR_PATHWAY	1.23	0.68	0	0	0	not significant
10637	CHR5Q22	1.23	0.67	0	0	0	not significant
10638	GO_CELLULAR_RESPONSE_TO_CADMIUM_ION	1.23	0.67	0	0	0	not significant
10639	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	1.23	0.67	0	0	0	not significant
10640	GO_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	1.23	0.67	0	0	0	not significant
10641	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	1.23	0.67	0	0	0	not significant
10642	GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	1.23	0.66	0	0	0	not significant
10643	SANCHEZ_MDM2_TARGETS	1.23	0.66	0	0	0	not significant
10644	GO_HISTONE_H4_K5_ACETYLATION	1.23	0.65	0	0	0	not significant
10645	GO_SIALYLATION	1.23	0.65	0	0	0	not significant
10646	GO_PURINE_NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	1.23	0.64	0	0	0	not significant
10647	BIOCARTA_CTL_PATHWAY	1.23	0.63	0	0	0	not significant
10648	GO_NEGATIVE_REGULATION_OF_VASCULAR_SMOOTH_MUSCLE_CELL_PROLIFERA	1.23	0.63	0	0	0	not significant
10649	GO_REGULATION_OF_T_CELL_DIFFERENTIATION_IN_THYMUS	1.23	0.63	0	0	0	not significant
10650	GO_VOLTAGE_GATED_ANION_CHANNEL_ACTIVITY	1.23	0.63	0	0	0	not significant
10651	GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_CELL_PROLIFERATION	1.23	0.62	0	0	0	not significant
10652	GO_ESCRT_III_COMPLEX	1.23	0.61	0	0	0	not significant
10653	GO_POSTSYNAPTIC_RECYCLING_ENDOSOME	1.23	0.61	0	0	0	not significant
10654	GO_REGULATION_OF_ENDOCYTIC_RECYCLING	1.23	0.61	0	0	0	not significant
10655	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	1.23	0.61	0	0	0	not significant
10656	REACTOME_SYNTHESIS_OF_KETONE_BODIES	1.23	0.61	0	0	0	not significant
10657	GO_OXOGLUTARATE_DEHYDROGENASE_COMPLEX	1.23	0.6	0	0	0	not significant
10658	REACTOME_INTERLEUKIN_27_SIGNALING	1.23	0.59	0	0	0	not significant
10659	GO_REGULATION_OF_ODONTOGENESIS	1.23	0.58	0	0	0	not significant
10660	GO_SERINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.23	0.58	0	0	0	not significant
10661	HINATA_NFKB_IMMU_INF	1.23	0.58	0	0	0	not significant
10662	GO_INDUCTION_OF_POSITIVE_CHEMOTAXIS	1.23	0.57	0	0	0	not significant
10663	GO_POSITIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_	1.23	0.53	0	0	0	not significant
10664	GO_BIOLOGICAL_ADHESION	1.24	1.67	0	0	0	not significant
10665	GO_ANATOMICAL_STRUCTURE_FORMATION_INVOLVED_IN_MORPHOGENESIS	1.24	1.55	0	0	0	not significant
10666	GO_REGULATION_OF_CELLULAR_COMPONENT_MOVEMENT	1.24	1.49	0	0	0	not significant
10667	GO_SECRETORY_GRANULE	1.24	1.44	0	0	0	not significant
10668	MARTENS_BOUND_BY_PML_RARA_FUSION	1.24	1.31	0	0	0	not significant
10669	ZHOU_INFLAMMATORY_RESPONSE_LIVE_DN	1.24	1.18	0	0	0	not significant
10670	JISON_SICKLE_CELL_DISEASE_DN	1.24	1.05	0	0	0	not significant

10671	ZHOU_INFLAMMATORY_RESPONSE_FIMA_DN	1.24	1.03	0	0	0	not significant
10672	GO_NEGATIVE_REGULATION_OF_LOCOMOTION	1.24	1.01	0	0	0	not significant
10673	GO_GOLGI_ASSOCIATED_VESICLE	1.24	0.94	0	0	0	not significant
10674	HALLMARK_MYOGENESIS	1.24	0.94	0	0	0	not significant
10675	GO_MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS	1.24	0.92	0	0	0	not significant
10676	GAVIN_FOXP3_TARGETS_CLUSTER_T7	1.24	0.9	0	0	0	not significant
10677	MTOR_UP.V1_UP	1.24	0.9	0	0	0	not significant
10678	RASHI_RESPONSE_TO_IONIZING_RADIATION_2	1.24	0.89	0	0	0	not significant
10679	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_DN	1.24	0.84	0	0	0	not significant
10680	CARD_MIR302A_TARGETS	1.24	0.83	0	0	0	not significant
10681	GO_INTERMEDIATE_FILAMENT_CYTOSKELETON	1.24	0.83	0	0	0	not significant
10682	GO_PEPTIDE_METABOLIC_PROCESS	1.24	0.83	0	0	0	not significant
10683	GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	1.24	0.83	0	0	0	not significant
10684	GO_CELLULAR_RESPONSE_TO_HYDROGEN_PEROXIDE	1.24	0.82	0	0	0	not significant
10685	GO_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	1.24	0.82	0	0	0	not significant
10686	PTEN_DN.V1_UP	1.24	0.82	0	0	0	not significant
10687	KRAS.AMP.LUNG_UP.V1_DN	1.24	0.81	0	0	0	not significant
10688	GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IM	1.24	0.79	0	0	0	not significant
10689	OHGUCHI_LIVER_HNF4A_TARGETS_DN	1.24	0.79	0	0	0	not significant
10690	GO_DNA_DAMAGE_RESPONSE_DETECTION_OF_DNA_DAMAGE	1.24	0.76	0	0	0	not significant
10691	KEGG_MISMATCH_REPAIR	1.24	0.76	0	0	0	not significant
10692	GO_REGULATION_OF_MEMBRANE_LIPID_DISTRIBUTION	1.24	0.75	0	0	0	not significant
10693	CASORELLI_APL_SECONDARY_VS_DE_NOVO_DN	1.24	0.74	0	0	0	not significant
10694	GO_NEGATIVE_REGULATION_OF_DNA_RECOMBINATION	1.24	0.74	0	0	0	not significant
10695	GO_PRI_MIRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	1.24	0.74	0	0	0	not significant
10696	GO_REGULATION_OF_LIPID_STORAGE	1.24	0.74	0	0	0	not significant
10697	KRAS.KIDNEY_UP.V1_DN	1.24	0.74	0	0	0	not significant
10698	MORI_PLASMA_CELL_DN	1.24	0.74	0	0	0	not significant
10699	NADLER_OBESITY_DN	1.24	0.74	0	0	0	not significant
10700	REACTOME_NICOTINATE_METABOLISM	1.24	0.74	0	0	0	not significant
10701	REACTOME_SIGNALING_BY_ERYTHROPOIETIN	1.24	0.74	0	0	0	not significant
10702	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN	1.24	0.74	0	0	0	not significant
10703	GO_MYELOID_DENDRITIC_CELL_ACTIVATION	1.24	0.73	0	0	0	not significant
10704	GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	1.24	0.73	0	0	0	not significant
10705	GO_HEXOSE_CATABOLIC_PROCESS	1.24	0.72	0	0	0	not significant
10706	REACTOME_MISCELLANEOUS_TRANSPORT_AND_BINDING_EVENTS	1.24	0.72	0	0	0	not significant
10707	GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_BINDING	1.24	0.7	0	0	0	not significant
10708	GO_NATURAL_KILLER_CELL_DIFFERENTIATION	1.24	0.7	0	0	0	not significant
10709	GO_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	1.24	0.7	0	0	0	not significant
10710	GO_C_C_CHEMOKINE_BINDING	1.24	0.69	0	0	0	not significant
10711	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_SECRETION	1.24	0.69	0	0	0	not significant
10712	GO_PHOTORECEPTOR_CELL_MAINTENANCE	1.24	0.68	0	0	0	not significant
10713	GO_POSITIVE_REGULATION_OF_MYOTUBE_DIFFERENTIATION	1.24	0.68	0	0	0	not significant
10714	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVITY	1.24	0.68	0	0	0	not significant
10715	GO_INTERLEUKIN_13_PRODUCTION	1.24	0.67	0	0	0	not significant
10716	GO_POSITIVE_REGULATION_OF_ISOTYPE_SWITCHING	1.24	0.67	0	0	0	not significant
10717	GO_POSITIVE_REGULATION_OF_T_CELL_CYTOKINE_PRODUCTION	1.24	0.67	0	0	0	not significant
10718	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_BACTERIUM	1.24	0.67	0	0	0	not significant
10719	WESTON_VEGFA_TARGETS_6HR	1.24	0.67	0	0	0	not significant
10720	GO_PROTEIN_CATABOLIC_PROCESS_IN_THE_VACUOLE	1.24	0.66	0	0	0	not significant
10721	REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES	1.24	0.66	0	0	0	not significant
10722	GO_ORNITHINE_DECARBOXYLASE_REGULATOR_ACTIVITY	1.24	0.65	0	0	0	not significant
10723	DONATO_CELL_CYCLE_TRETINOIN	1.24	0.64	0	0	0	not significant
10724	GO_REPLICATION_FORK_PROTECTION	1.24	0.64	0	0	0	not significant
10725	GO_SPINAL_CORD_MOTOR_NEURON_DIFFERENTIATION	1.24	0.64	0	0	0	not significant
10726	REACTOME_DEGRADATION_OF_CYSTEINE_AND_HOMOCYSTEINE	1.24	0.64	0	0	0	not significant
10727	GO_REGULATION_OF_STEROID_HORMONE_BIOSYNTHETIC_PROCESS	1.24	0.63	0	0	0	not significant
10728	MARSHALL_VIRAL_INFECTION_RESPONSE_UP	1.24	0.63	0	0	0	not significant
10729	REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS	1.24	0.63	0	0	0	not significant
10730	REACTOME_KETONE_BODY_METABOLISM	1.24	0.63	0	0	0	not significant
10731	GO_PHOSPHATE_ION_BINDING	1.24	0.62	0	0	0	not significant
10732	GO_REGULATION_OF_HEPATOCYTE_PROLIFERATION	1.24	0.62	0	0	0	not significant
10733	YAGUE_PRETUMOR_DRUG_RESISTANCE_DN	1.24	0.62	0	0	0	not significant
10734	GO_INTESTINAL_EPITHELIAL_CELL_DEVELOPMENT	1.24	0.61	0	0	0	not significant
10735	GO_PHOSPHATIDYLSERINE_ACYL_CHAIN_REMODELING	1.24	0.61	0	0	0	not significant
10736	GO_INTERLEUKIN_27_MEDIATED_SIGNALING_PATHWAY	1.24	0.6	0	0	0	not significant
10737	GO_MANNOSYL_OLIGOSACCHARIDE_1_2_ALPHA_MANNOSIDASE_ACTIVITY	1.24	0.6	0	0	0	not significant
10738	GO_SIALYLTRANSFERASE_ACTIVITY	1.24	0.6	0	0	0	not significant
10739	GO_REGULATION_OF_POLYAMINE_TRANSMEMBRANE_TRANSPORT	1.24	0.59	0	0	0	not significant
10740	GO_CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	1.25	1.68	0	0	0	not significant
10741	KRIEG_HYPOXIA_NOT_VIA_KDM3A	1.25	1.56	0	0	0	not significant
10742	REACTOME_METABOLISM_OF_LIPIDS	1.25	1.55	0	0	0	not significant
10743	GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	1.25	1.53	0	0	0	not significant
10744	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN	1.25	1.3	0	0	0	not significant
10745	GO_GLYCEROLIPID_METABOLIC_PROCESS	1.25	1.1	0	0	0	not significant
10746	GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	1.25	1.08	0	0	0	not significant
10747	GO_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	1.25	1.05	0	0	0	not significant
10748	SHEPARD_BMYB_MORPHOLINO_UP	1.25	1.05	0	0	0	not significant
10749	GO_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN	1.25	1.01	0	0	0	not significant
10750	CHR1Q21	1.25	0.94	0	0	0	not significant
10751	BROWN_MYELOID_CELL_DEVELOPMENT_UP	1.25	0.91	0	0	0	not significant
10752	GO_RESPONSE_TO_MECHANICAL_STIMULUS	1.25	0.91	0	0	0	not significant
10753	KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_UP	1.25	0.87	0	0	0	not significant
10754	WAKASUGI_HAVE_ZNF143_BINDING_SITES	1.25	0.86	0	0	0	not significant
10755	GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_	1.25	0.83	0	0	0	not significant
10756	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRE	1.25	0.81	0	0	0	not significant
10757	GO_REGULATION_OF_LIPASE_ACTIVITY	1.25	0.8	0	0	0	not significant
10758	WESTON_VEGFA_TARGETS	1.25	0.8	0	0	0	not significant
10759	BURTON_ADIPOGENESIS_PEAK_AT_16HR	1.25	0.79	0	0	0	not significant
10760	DELPUECH_FOXO3_TARGETS_UP	1.25	0.78	0	0	0	not significant
10761	GO_MACROPHAGE_MIGRATION	1.25	0.78	0	0	0	not significant
10762	GO_FATTY_ACYL_COA_BIOSYNTHETIC_PROCESS	1.25	0.76	0	0	0	not significant
10763	KEGG_SPHINGOLIPID_METABOLISM	1.25	0.76	0	0	0	not significant
10764	REACTOME_RECOGNITION_OF_DNA_DAMAGE_BY_PCNA_CONTAINING_REPLICATIO	1.25	0.76	0	0	0	not significant
10765	LEE_AGING_MUSCLE_DN	1.25	0.75	0	0	0	not significant
10766	VALK_AML_CLUSTER_2	1.25	0.75	0	0	0	not significant
10767	GO_CHOLESTEROL_STORAGE	1.25	0.74	0	0	0	not significant
10768	GO_HISTONE_H3_DEACETYLATION	1.25	0.74	0	0	0	not significant
10769	GO_POSITIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	1.25	0.74	0	0	0	not significant
10770	GO_ANION_HOMEOSTASIS	1.25	0.73	0	0	0	not significant
10771	REACTOME_CALNEXIN_CALRETICULIN_CYCLE	1.25	0.73	0	0	0	not significant
10772	GO_ACETYL_COA_METABOLIC_PROCESS	1.25	0.71	0	0	0	not significant
10773	ZEMBUTSU_SENSITIVITY_TO_VINCRISTINE	1.25	0.7	0	0	0	not significant
10774	GO_DESMOSOME	1.25	0.69	0	0	0	not significant
10775	GO_DETECTION_OF_VIRUS	1.25	0.69	0	0	0	not significant
10776	GO_NEGATIVE_REGULATION_OF_LIPID_TRANSPORT	1.25	0.69	0	0	0	not significant
10777	REACTOME_COLLAGEN_DEGRADATION	1.25	0.69	0	0	0	not significant
10778	GO_MAMMARY_GLAND_EPITHELIAL_CELL_DIFFERENTIATION	1.25	0.68	0	0	0	not significant
10779	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_PROLIFERATION	1.25	0.68	0	0	0	not significant

10780	BIOCARTA_BLYMPHOCYTE_PATHWAY	1.25	0.67	0	0	0	not significant
10781	GO_MAP_KINASE_ACTIVITY	1.25	0.67	0	0	0	not significant
10782	NAKAMURA_ADIPOGENESIS_EARLY_DN	1.25	0.67	0	0	0	not significant
10783	BIOCARTA_BCELLSURVIVAL_PATHWAY	1.25	0.66	0	0	0	not significant
10784	GO_NEGATIVE_REGULATION_OF_RESPIRATORY_BURST	1.25	0.66	0	0	0	not significant
10785	KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	1.25	0.66	0	0	0	not significant
10786	SAKAI_TUMOR_INFILTRATING_MONOCYTES_UP	1.25	0.66	0	0	0	not significant
10787	GO_CALCIUM_ACTIVATED_CATION_CHANNEL_ACTIVITY	1.25	0.65	0	0	0	not significant
10788	GO_COLLAGEN_METABOLIC_PROCESS	1.25	0.65	0	0	0	not significant
10789	GO_INNERVATION	1.25	0.65	0	0	0	not significant
10790	GO_PROTEIN_TYROSINE_KINASE_ACTIVATOR_ACTIVITY	1.25	0.65	0	0	0	not significant
10791	HOLLEMAN_DAUNORUBICIN_B_ALL_DN	1.25	0.65	0	0	0	not significant
10792	TSUNODA_CISPLATIN_RESISTANCE_UP	1.25	0.65	0	0	0	not significant
10793	VALK_AML_CLUSTER_13	1.25	0.65	0	0	0	not significant
10794	GO_REGULATION_OF_MODIFICATION_OF_SYNAPTIC_STRUCTURE	1.25	0.64	0	0	0	not significant
10795	GO_RETINA_VASCULATURE_DEVELOPMENT_IN_CAMERA_TYPE_EYE	1.25	0.64	0	0	0	not significant
10796	GO_ATG1_ULK1_KINASE_COMPLEX	1.25	0.63	0	0	0	not significant
10797	GO_C_ACETYLTRANSFERASE_ACTIVITY	1.25	0.63	0	0	0	not significant
10798	MARTIN_NFKB_TARGETS_DN	1.25	0.63	0	0	0	not significant
10799	GO_LEUCINE_BINDING	1.25	0.62	0	0	0	not significant
10800	GO_GLYCOSIDE_CATABOLIC_PROCESS	1.25	0.61	0	0	0	not significant
10801	GO_CONVERGENT_EXTENSION_INVOLVED_IN_GASTRULATION	1.25	0.59	0	0	0	not significant
10802	GO_POSITIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	1.26	1.8	0	0	0	not significant
10803	GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	1.26	1.46	0	0	0	not significant
10804	REACTOME_NEUTROPHIL_DEGRANULATION	1.26	1.43	0	0	0	not significant
10805	GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	1.26	1.41	0	0	0	not significant
10806	GO_PROXIMAL_PROMOTER_SEQUENCE_SPECIFIC_DNA_BINDING	1.26	1.28	0	0	0	not significant
10807	GO_RESPONSE_TO_LIGHT_STIMULUS	1.26	1.06	0	0	0	not significant
10808	GO_FATTY_ACID_CATABOLIC_PROCESS	1.26	0.97	0	0	0	not significant
10809	GO_DRUG_TRANSPORT	1.26	0.95	0	0	0	not significant
10810	GO_TERTIARY_GRANULE	1.26	0.94	0	0	0	not significant
10811	KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	1.26	0.94	0	0	0	not significant
10812	LAIHO_COLORECTAL_CANCER_SERRATED_DN	1.26	0.93	0	0	0	not significant
10813	REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS	1.26	0.93	0	0	0	not significant
10814	GO_RECYCLING_ENDOSOME_MEMBRANE	1.26	0.9	0	0	0	not significant
10815	PID_CD8_TCR_DOWNSTREAM_PATHWAY	1.26	0.9	0	0	0	not significant
10816	KEGG_P53_SIGNALING_PATHWAY	1.26	0.87	0	0	0	not significant
10817	MIKKELSEN_ES_LCP_WITH_H3K4ME3	1.26	0.87	0	0	0	not significant
10818	GO_CARBOHYDRATE_DERIVATIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.26	0.85	0	0	0	not significant
10819	PRAMOONJAGO_SOX4_TARGETS_UP	1.26	0.85	0	0	0	not significant
10820	HOOI_ST7_TARGETS_DN	1.26	0.84	0	0	0	not significant
10821	REACTOME_STIMULI_SENSING_CHANNELS	1.26	0.84	0	0	0	not significant
10822	REACTOME_VISUAL_PHOTOTRANSDUCTION	1.26	0.83	0	0	0	not significant
10823	GO_NEGATIVE_REGULATION_OF_BLOOD_VESSEL_DIAMETER	1.26	0.82	0	0	0	not significant
10824	HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_DN	1.26	0.82	0	0	0	not significant
10825	GO_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	1.26	0.81	0	0	0	not significant
10826	MOHANKUMAR_HOXA1_TARGETS_DN	1.26	0.81	0	0	0	not significant
10827	BCAT_BILD_ET_AL_UP	1.26	0.8	0	0	0	not significant
10828	PID_AVB3_OPN_PATHWAY	1.26	0.8	0	0	0	not significant
10829	GO_PHOSPHOLIPID_CATABOLIC_PROCESS	1.26	0.77	0	0	0	not significant
10830	GO_REGULATION_OF_TORC1_SIGNALING	1.26	0.77	0	0	0	not significant
10831	GO_PEPTIDYL_ASPARAGINE_MODIFICATION	1.26	0.75	0	0	0	not significant
10832	GO_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTION_RESULTING_IN_TRANSCRI	1.26	0.74	0	0	0	not significant
10833	GO_MESODERMAL_CELL_DIFFERENTIATION	1.26	0.73	0	0	0	not significant
10834	GO_REGULATION_OF_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	1.26	0.73	0	0	0	not significant
10835	JOHANSSON_GLIOMAGENESIS_BY_PDGFB_DN	1.26	0.73	0	0	0	not significant
10836	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	1.26	0.72	0	0	0	not significant
10837	REACTOME_BASIGIN_INTERACTIONS	1.26	0.72	0	0	0	not significant
10838	GO_CARBOXYPEPTIDASE_ACTIVITY	1.26	0.71	0	0	0	not significant
10839	GO_REGULATION_OF_CAMP_DEPENDENT_PROTEIN_KINASE_ACTIVITY	1.26	0.71	0	0	0	not significant
10840	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_HORMONE	1.26	0.71	0	0	0	not significant
10841	GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_GROWTH	1.26	0.7	0	0	0	not significant
10842	GO_NEGATIVE_REGULATION_OF_MYOTUBE_DIFFERENTIATION	1.26	0.7	0	0	0	not significant
10843	GO_XENOPHAGY	1.26	0.7	0	0	0	not significant
10844	GO_ESTABLISHMENT_OF_ENDOTHELIAL_INTESTINAL_BARRIER	1.26	0.69	0	0	0	not significant
10845	GO_T_HELPER_1_CELL_DIFFERENTIATION	1.26	0.69	0	0	0	not significant
10846	REACTOME_LYSOSPHINGOLIPID_AND_LPA_RECEPTORS	1.26	0.69	0	0	0	not significant
10847	GO_CLATHRIN_SCULPTED_GAMMA_AMINOBUTYRIC_ACID_TRANSPORT_VESICLE_M	1.26	0.68	0	0	0	not significant
10848	GO_POSITIVE_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	1.26	0.68	0	0	0	not significant
10849	GO_PRE_MRNA_3_SPLICE_SITE_BINDING	1.26	0.68	0	0	0	not significant
10850	GO_REGULATION_OF_CELL_FATE_COMMITMENT	1.26	0.68	0	0	0	not significant
10851	GO_REGULATION_OF_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNALING_PATH	1.26	0.68	0	0	0	not significant
10852	GO_RESPIRATORY_BURST_INVOLVED_IN_INFLAMMATORY_RESPONSE	1.26	0.68	0	0	0	not significant
10853	LE_NEURONAL_DIFFERENTIATION_UP	1.26	0.68	0	0	0	not significant
10854	GO_ARP2_3_COMPLEX_BINDING	1.26	0.67	0	0	0	not significant
10855	GO_DISTAL_TUBULE_DEVELOPMENT	1.26	0.67	0	0	0	not significant
10856	HOLLEMAN_DAUNORUBICIN_B_ALL_UP	1.26	0.67	0	0	0	not significant
10857	GO_HEPARAN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS_POLYSACCH	1.26	0.66	0	0	0	not significant
10858	GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	1.26	0.65	0	0	0	not significant
10859	GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_ORGANIZATION	1.26	0.65	0	0	0	not significant
10860	GO_TRANSEPITHELIAL_TRANSPORT	1.26	0.65	0	0	0	not significant
10861	REACTOME_STAT5_ACTIVATION	1.26	0.64	0	0	0	not significant
10862	GO_BETA_GALACTOSIDASE_ACTIVITY	1.26	0.63	0	0	0	not significant
10863	GO_HAUS_COMPLEX	1.26	0.63	0	0	0	not significant
10864	GO_POSITIVE_REGULATION_OF_COLLATERAL_SPROUTING	1.26	0.61	0	0	0	not significant
10865	GO_SECRETION	1.27	2.66	0	0	0	not significant
10866	GO_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	1.27	1.77	0	0	0	not significant
10867	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN	1.27	1.5	0	0	0	not significant
10868	GO_REGULATION_OF_SECRETION	1.27	1.47	0	0	0	not significant
10869	OSMAN_BLADDER_CANCER_DN	1.27	1.43	0	0	0	not significant
10870	GO_REGULATION_OF_CELL_ACTIVATION	1.27	1.42	0	0	0	not significant
10871	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN	1.27	1.32	0	0	0	not significant
10872	FOSTER_TOLERANT_MACROPHAGE_DN	1.27	1.3	0	0	0	not significant
10873	LI_INDUCED_T_TO_NATURAL_KILLER_UP	1.27	1.26	0	0	0	not significant
10874	CAMP_UP.V1_UP	1.27	1.23	0	0	0	not significant
10875	FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL	1.27	1.16	0	0	0	not significant
10876	GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	1.27	1.06	0	0	0	not significant
10877	CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_DN	1.27	1.03	0	0	0	not significant
10878	KYNG_DNA_DAMAGE_DN	1.27	1.03	0	0	0	not significant
10879	CHR6P22	1.27	1.02	0	0	0	not significant
10880	GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	1.27	1.02	0	0	0	not significant
10881	GO_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	1.27	1.01	0	0	0	not significant
10882	SENGUPTA_EBNA1_ANTICORRELATED	1.27	0.99	0	0	0	not significant
10883	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQUOISE_UP	1.27	0.98	0	0	0	not significant
10884	RAPA_EARLY_UP.V1_DN	1.27	0.98	0	0	0	not significant
10885	DER_IFN_ALPHA_RESPONSE_UP	1.27	0.96	0	0	0	not significant
10886	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPOR	1.27	0.96	0	0	0	not significant
10887	HOEBEKE_LYMPHOID_STEM_CELL_DN	1.27	0.96	0	0	0	not significant
10888	CAHOY_ASTROCYTIC	1.27	0.93	0	0	0	not significant

10889	CAHOY_OLIGODENDROCUTIC	1.27	0.91	0	0	0	not significant
10890	GO_NUCLEAR_INNER_MEMBRANE	1.27	0.91	0	0	0	not significant
10891	GO_ROUGH_ENDOPLASMIC_RETICULUM	1.27	0.91	0	0	0	not significant
10892	GO_REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	1.27	0.9	0	0	0	not significant
10893	CHR17Q11	1.27	0.88	0	0	0	not significant
10894	GO_COFACTOR_TRANSPORT	1.27	0.88	0	0	0	not significant
10895	CTIP_DN.V1_DN	1.27	0.87	0	0	0	not significant
10896	NATSUME_RESPONSE_TO_INTERFERON_BETA_UP	1.27	0.87	0	0	0	not significant
10897	CADWELL_ATG16L1_TARGETS_UP	1.27	0.86	0	0	0	not significant
10898	GO_DRUG_TRANSMEMBRANE_TRANSPORT	1.27	0.83	0	0	0	not significant
10899	TAVOR_CEBPA_TARGETS_DN	1.27	0.83	0	0	0	not significant
10900	GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	1.27	0.82	0	0	0	not significant
10901	GO_PH_REDUCTION	1.27	0.82	0	0	0	not significant
10902	GO_T_CELL_DIFFERENTIATION_IN_THYMUS	1.27	0.82	0	0	0	not significant
10903	ABE_INNER_EAR	1.27	0.81	0	0	0	not significant
10904	BILANGES_RAPAMYCIN_SENSITIVE_GENES	1.27	0.81	0	0	0	not significant
10905	SATO_SILENCED_EPIGENETICALLY_IN_PANCREATIC_CANCER	1.27	0.79	0	0	0	not significant
10906	BREDEMEYER_RAG_SIGNALING_VIA_ATM_NOT_VIA_NFKB_UP	1.27	0.78	0	0	0	not significant
10907	GO_SPERM_MOTILITY	1.27	0.78	0	0	0	not significant
10908	LOPES_METHYLATED_IN_COLON_CANCER_DN	1.27	0.78	0	0	0	not significant
10909	BIOCARTA_TOLL_PATHWAY	1.27	0.77	0	0	0	not significant
10910	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PR	1.27	0.77	0	0	0	not significant
10911	REACTOME_GLYCOSPHINGOLIPID_METABOLISM	1.27	0.77	0	0	0	not significant
10912	CHR15Q14	1.27	0.76	0	0	0	not significant
10913	SHAFFER_IRF4_MULTIPLE_MYELOMA_PROGRAM	1.27	0.76	0	0	0	not significant
10914	FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_UP	1.27	0.75	0	0	0	not significant
10915	GO_DENDRITIC_CELL_DIFFERENTIATION	1.27	0.75	0	0	0	not significant
10916	GO_REGULATION_OF_ANION_TRANSMEMBRANE_TRANSPORT	1.27	0.75	0	0	0	not significant
10917	GO_REGULATION_OF_MYOBLAST_FUSION	1.27	0.75	0	0	0	not significant
10918	MANTOVANI_NFKB_TARGETS_DN	1.27	0.75	0	0	0	not significant
10919	GO_AMYLOID_BETA_CLEARANCE	1.27	0.74	0	0	0	not significant
10920	GO_NITRIC_OXIDE_MEDIATED_SIGNAL_TRANSDUCTION	1.27	0.74	0	0	0	not significant
10921	GO_THYMIC_T_CELL_SELECTION	1.27	0.74	0	0	0	not significant
10922	GO_INTERLEUKIN_17_PRODUCTION	1.27	0.72	0	0	0	not significant
10923	GO_INTESTINAL_ABSORPTION	1.27	0.72	0	0	0	not significant
10924	GO_MITOTIC_G2_DNA_DAMAGE_CHECKPOINT	1.27	0.72	0	0	0	not significant
10925	GO_MUSCLE_FILAMENT_SLIDING	1.27	0.72	0	0	0	not significant
10926	GO_NUCLEAR_RECEPTOR_ACTIVITY	1.27	0.72	0	0	0	not significant
10927	BIOCARTA_NO2IL12_PATHWAY	1.27	0.71	0	0	0	not significant
10928	GO_CELLULAR_KETONE_BODY_METABOLIC_PROCESS	1.27	0.71	0	0	0	not significant
10929	GO_INTERMEDIATE_FILAMENT_ORGANIZATION	1.27	0.71	0	0	0	not significant
10930	PID_HNF3B_PATHWAY	1.27	0.71	0	0	0	not significant
10931	REACTOME_N_GLYCAN_ANTENNAE_ELONGATION	1.27	0.71	0	0	0	not significant
10932	VANLOO_SP3_TARGETS_UP	1.27	0.71	0	0	0	not significant
10933	ZERBINI_RESPONSE_TO_SULINDAC_UP	1.27	0.71	0	0	0	not significant
10934	GO_NUCLEAR_MEMBRANE_PROTEIN_COMPLEX	1.27	0.7	0	0	0	not significant
10935	GO_T_CELL_ACTIVATION_VIA_T_CELL_RECEPTOR_CONTACT_WITH_ANTIGEN_BOU	1.27	0.7	0	0	0	not significant
10936	MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN	1.27	0.7	0	0	0	not significant
10937	GO_DENSE_CORE_GRANULE	1.27	0.69	0	0	0	not significant
10938	GO_GLUCURONOSYLTRANSFERASE_ACTIVITY	1.27	0.69	0	0	0	not significant
10939	GO_GLUCOCORTICOID_METABOLIC_PROCESS	1.27	0.68	0	0	0	not significant
10940	GO_INTERLEUKIN_6_BIOSYNTHETIC_PROCESS	1.27	0.68	0	0	0	not significant
10941	GO_SERINE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	1.27	0.68	0	0	0	not significant
10942	REACTOME_CHL1_INTERACTIONS	1.27	0.68	0	0	0	not significant
10943	REACTOME_CLEC7A_INFLAMMASOME_PATHWAY	1.27	0.66	0	0	0	not significant
10944	GO_REGULATION_OF_STORE_OPERATED_CALCIUM_CHANNEL_ACTIVITY	1.27	0.65	0	0	0	not significant
10945	MATZUK_PREOVULATORY_FOLLICLE	1.27	0.65	0	0	0	not significant
10946	GO_LOCOMOTION_INVOLVED_IN_LOCOMOTORY_BEHAVIOR	1.27	0.64	0	0	0	not significant
10947	GO_CYTOPLASMIC_VESICLE_PART	1.28	2.27	0	0	0	not significant
10948	GO_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	1.28	2.27	0	0	0	not significant
10949	GO_MYELOID_LEUKOCYTE_ACTIVATION	1.28	1.65	0	0	0	not significant
10950	CHR19Q13	1.28	1.62	0	0	0	not significant
10951	GO_ENDOSOMAL_PART	1.28	1.56	0	0	0	not significant
10952	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN	1.28	1.55	0	0	0	not significant
10953	BLUM_RESPONSE_TO_SALIRASIB_UP	1.28	1.32	0	0	0	not significant
10954	GO_POSITIVE_REGULATION_OF_CELL_ADHESION	1.28	1.3	0	0	0	not significant
10955	GO_MAINTENANCE_OF_LOCATION	1.28	1.23	0	0	0	not significant
10956	HELLER_SILENCED_BY_METHYLATION_UP	1.28	1.23	0	0	0	not significant
10957	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	1.28	1.15	0	0	0	not significant
10958	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN	1.28	1.13	0	0	0	not significant
10959	KARLSSON_TGFB1_TARGETS_DN	1.28	1.08	0	0	0	not significant
10960	COULOUARN_TEMPORAL_TGFB1_SIGNATURE_DN	1.28	1.06	0	0	0	not significant
10961	CRX_DN.V1_UP	1.28	1.02	0	0	0	not significant
10962	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP	1.28	1.02	0	0	0	not significant
10963	GO_RESPONSE_TO_ORGANOPHOSPHORUS	1.28	1	0	0	0	not significant
10964	GO_ENDOPLASMIC_RETICULUM_UNFOLDED_PROTEIN_RESPONSE	1.28	0.97	0	0	0	not significant
10965	GO_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	1.28	0.97	0	0	0	not significant
10966	GO_POSITIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALIN	1.28	0.96	0	0	0	not significant
10967	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN	1.28	0.94	0	0	0	not significant
10968	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN	1.28	0.94	0	0	0	not significant
10969	BOSCO_TH1_CYTOTOXIC_MODULE	1.28	0.93	0	0	0	not significant
10970	GO_CELLULAR_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	1.28	0.93	0	0	0	not significant
10971	GOZGIT_ESR1_TARGETS_UP	1.28	0.93	0	0	0	not significant
10972	HINATA_NFKB_TARGETS_FIBROBLAST_UP	1.28	0.91	0	0	0	not significant
10973	GO_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	1.28	0.89	0	0	0	not significant
10974	KEGG_BASE_EXCISION_REPAIR	1.28	0.87	0	0	0	not significant
10975	MATZUK_MEIOTIC_AND_DNA_REPAIR	1.28	0.86	0	0	0	not significant
10976	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_UP	1.28	0.85	0	0	0	not significant
10977	GO_CAVEOLA	1.28	0.85	0	0	0	not significant
10978	WESTON_VEGFA_TARGETS_3HR	1.28	0.84	0	0	0	not significant
10979	GO_CELLULAR_EXTRAVASATION	1.28	0.83	0	0	0	not significant
10980	LEE_LIVER_CANCER_MYC_TGFA_DN	1.28	0.8	0	0	0	not significant
10981	BIOCARTA_INSULIN_PATHWAY	1.28	0.79	0	0	0	not significant
10982	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DNA_DAMAG	1.28	0.79	0	0	0	not significant
10983	GO_PHENOL_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	1.28	0.79	0	0	0	not significant
10984	GO_PYRIMIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	1.28	0.79	0	0	0	not significant
10985	GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	1.28	0.78	0	0	0	not significant
10986	GO_T_CELL_LINEAGE_COMMITMENT	1.28	0.78	0	0	0	not significant
10987	CHR4Q28	1.28	0.77	0	0	0	not significant
10988	GO_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	1.28	0.77	0	0	0	not significant
10989	GALE_APL_WITH_FLT3_MUTATED_DN	1.28	0.76	0	0	0	not significant
10990	GO_CELL_CELL_ADHESION_MEDIATED_BY_CADHERIN	1.28	0.76	0	0	0	not significant
10991	PATTERSON_DOCETAXEL_RESISTANCE	1.28	0.76	0	0	0	not significant
10992	REACTOME_SYNTHESIS_OF_VERY_LONG_CHAIN_FATTY_ACYL_COAS	1.28	0.76	0	0	0	not significant
10993	GO_ENDONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCL	1.28	0.75	0	0	0	not significant
10994	GO_MONONUCLEAR_CELL_MIGRATION	1.28	0.75	0	0	0	not significant
10995	GO_DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATION	1.28	0.74	0	0	0	not significant
10996	GO_HORMONE_ACTIVITY	1.28	0.74	0	0	0	not significant
10997	GO_INTERLEUKIN_21_MEDIATED_SIGNALING_PATHWAY	1.28	0.74	0	0	0	not significant

10998	GO_LATERAL_MESODERM_DEVELOPMENT	1.28	0.74	0	0	0	not significant
10999	GO_LONG_CHAIN_FATTY_ACYL_COA_BIOSYNTHETIC_PROCESS	1.28	0.74	0	0	0	not significant
11000	GO_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMUL	1.28	0.74	0	0	0	not significant
11001	OSADA_ASCL1_TARGETS_UP	1.28	0.74	0	0	0	not significant
11002	GO_GATOR2_COMPLEX	1.28	0.73	0	0	0	not significant
11003	GO_KETONE_CATABOLIC_PROCESS	1.28	0.73	0	0	0	not significant
11004	GO_PHOSPHATE_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.28	0.73	0	0	0	not significant
11005	GO_PLACENTA_BLOOD_VESSEL_DEVELOPMENT	1.28	0.73	0	0	0	not significant
11006	KANG_FLUOROURACIL_RESISTANCE_DN	1.28	0.73	0	0	0	not significant
11007	GO_DIAPHRAGM_DEVELOPMENT	1.28	0.72	0	0	0	not significant
11008	BIOCARTA_IFNA_PATHWAY	1.28	0.71	0	0	0	not significant
11009	GO_AMINO_ACID_BETAINE_BIOSYNTHETIC_PROCESS	1.28	0.71	0	0	0	not significant
11010	GO_CYTOSKELETAL_ANCHORING_AT_NUCLEAR_MEMBRANE	1.28	0.71	0	0	0	not significant
11011	GO_UTERUS_DEVELOPMENT	1.28	0.71	0	0	0	not significant
11012	PID_INTEGRIN3_PATHWAY	1.28	0.71	0	0	0	not significant
11013	REACTOME_NOTCH4_ACTIVATION_AND_TRANSMISSION_OF_SIGNAL_TO_THE_NUC	1.28	0.71	0	0	0	not significant
11014	SHIN_B_CELL_LYMPHOMA_CLUSTER_1	1.28	0.71	0	0	0	not significant
11015	GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATIN	1.28	0.7	0	0	0	not significant
11016	CROONQUIST_IL6_DEPRIVATION_UP	1.28	0.69	0	0	0	not significant
11017	GO_KETONE_BODY_BIOSYNTHETIC_PROCESS	1.28	0.69	0	0	0	not significant
11018	GO_PEPTIDYL_LYSINE_DEACETYLATION	1.28	0.69	0	0	0	not significant
11019	GO_PROTEIN_C_LINKED_GLYCOSYLATION	1.28	0.69	0	0	0	not significant
11020	GO_TOLL_LIKE_RECEPTOR_7_SIGNALING_PATHWAY	1.28	0.69	0	0	0	not significant
11021	PID_P38_GAMMA_DELTA_PATHWAY	1.28	0.69	0	0	0	not significant
11022	WANG_LSD1_TARGETS_UP	1.28	0.69	0	0	0	not significant
11023	GO_ANNEALING_ACTIVITY	1.28	0.68	0	0	0	not significant
11024	GO_SIGNAL_PEPTIDASE_COMPLEX	1.28	0.68	0	0	0	not significant
11025	HUMMERICH_MALIGNANT_SKIN_TUMOR_DN	1.28	0.68	0	0	0	not significant
11026	GO_ENDOSOME	1.29	2.36	0	0	0	not significant
11027	GO_TRANSMEMBRANE_TRANSPORT	1.29	2.12	0	0	0	not significant
11028	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_B	1.29	1.51	0	0	0	not significant
11029	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP	1.29	1.49	0	0	0	not significant
11030	GO_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	1.29	1.43	0	0	0	not significant
11031	HAN_SATB1_TARGETS_DN	1.29	1.38	0	0	0	not significant
11032	GO_NEGATIVE_REGULATION_OF_GROWTH	1.29	1.18	0	0	0	not significant
11033	GO_ORGANIC_ACID_TRANSPORT	1.29	1.18	0	0	0	not significant
11034	PDGF_ERK_DN.V1_DN	1.29	1.18	0	0	0	not significant
11035	PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_DN	1.29	1.15	0	0	0	not significant
11036	GO_SPECIFIC_GRANULE	1.29	1.12	0	0	0	not significant
11037	MANALO_HYPOXIA_UP	1.29	1.11	0	0	0	not significant
11038	GO_PRIMARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.29	1.08	0	0	0	not significant
11039	REACTOME_HOMOLOGY_DIRECTED_REPAIR	1.29	1.08	0	0	0	not significant
11040	GO_POTASSIUM_ION_TRANSPORT	1.29	1.05	0	0	0	not significant
11041	GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	1.29	1.03	0	0	0	not significant
11042	GAVIN_FOXP3_TARGETS_CLUSTER_T4	1.29	0.99	0	0	0	not significant
11043	GO_UBIQUITIN_DEPENDENT_ERAD_PATHWAY	1.29	0.97	0	0	0	not significant
11044	KRAS.PROSTATE_UP.V1_UP	1.29	0.97	0	0	0	not significant
11045	WNT_UP.V1_UP	1.29	0.95	0	0	0	not significant
11046	GO_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	1.29	0.94	0	0	0	not significant
11047	GO_REGULATION_OF_LIPID_TRANSPORT	1.29	0.94	0	0	0	not significant
11048	GO_REGULATION_OF_ANION_TRANSPORT	1.29	0.92	0	0	0	not significant
11049	NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON	1.29	0.92	0	0	0	not significant
11050	YEGNASUBRAMANIAN_PROSTATE_CANCER	1.29	0.92	0	0	0	not significant
11051	GO_CYTOPLASMIC_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	1.29	0.91	0	0	0	not significant
11052	GO_INTRINSIC_COMPONENT_OF_GOLGI_MEMBRANE	1.29	0.91	0	0	0	not significant
11053	CHRXQ13	1.29	0.9	0	0	0	not significant
11054	DIRMEIER_LMP1_RESPONSE_LATE_UP	1.29	0.9	0	0	0	not significant
11055	DOANE_BREAST_CANCER_CLASSES_UP	1.29	0.87	0	0	0	not significant
11056	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	1.29	0.87	0	0	0	not significant
11057	PID_GMCSF_PATHWAY	1.29	0.86	0	0	0	not significant
11058	GO_BASEMENT_MEMBRANE	1.29	0.85	0	0	0	not significant
11059	PID_P38_ALPHA_BETA_PATHWAY	1.29	0.85	0	0	0	not significant
11060	GO_RHYTHMIC_BEHAVIOR	1.29	0.83	0	0	0	not significant
11061	GO_REGULATION_OF_PROTEIN_OLIGOMERIZATION	1.29	0.82	0	0	0	not significant
11062	GO_REGULATION_OF_VASOCONSTRICTION	1.29	0.82	0	0	0	not significant
11063	GO_ACID_AMINO_ACID_LIGASE_ACTIVITY	1.29	0.81	0	0	0	not significant
11064	KEGG_HOMOLOGOUS_RECOMBINATION	1.29	0.81	0	0	0	not significant
11065	GO_VASCULAR_ENDOTHELIAL_CELL_PROLIFERATION	1.29	0.8	0	0	0	not significant
11066	REACTOME_THE_ACTIVATION_OF_ARYLSULFATASES	1.29	0.8	0	0	0	not significant
11067	GO_RESPIRATORY_BURST	1.29	0.79	0	0	0	not significant
11068	WATANABE_ULCERATIVE_COLITIS_WITH_CANCER_DN	1.29	0.79	0	0	0	not significant
11069	GO_DEOXYRIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	1.29	0.78	0	0	0	not significant
11070	GO_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	1.29	0.78	0	0	0	not significant
11071	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_IN_OLD	1.29	0.78	0	0	0	not significant
11072	GO_PROTON_TRANSPORTING_V_TYPE_ATPASE_V0_DOMAIN	1.29	0.77	0	0	0	not significant
11073	GO_TERMINAL_BOUTON	1.29	0.77	0	0	0	not significant
11074	GO_WOUND_HEALING_INVOLVED_IN_INFLAMMATORY_RESPONSE	1.29	0.77	0	0	0	not significant
11075	BIOCARTA_DC_PATHWAY	1.29	0.76	0	0	0	not significant
11076	GO_NATURAL_KILLER_CELL_PROLIFERATION	1.29	0.76	0	0	0	not significant
11077	GO_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	1.29	0.76	0	0	0	not significant
11078	GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_MEMBRANE_FUSION	1.29	0.76	0	0	0	not significant
11079	TRAYNOR_RETT_SYNDROM_DN	1.29	0.76	0	0	0	not significant
11080	BIOCARTA_CCR5_PATHWAY	1.29	0.75	0	0	0	not significant
11081	GO_EPITHELIAL_CILIUM_MOVEMENT	1.29	0.75	0	0	0	not significant
11082	GO_POSITIVE_REGULATION_OF_PROTEIN_OLIGOMERIZATION	1.29	0.75	0	0	0	not significant
11083	LA_MEN1_TARGETS	1.29	0.75	0	0	0	not significant
11084	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	1.29	0.74	0	0	0	not significant
11085	GO_REGULATION_OF_RESPIRATORY_BURST	1.29	0.74	0	0	0	not significant
11086	GO_AROMATIC_AMINO_ACID_TRANSPORT	1.29	0.72	0	0	0	not significant
11087	GO_CARBOHYDRATE_CATION_SYMPORTER_ACTIVITY	1.29	0.72	0	0	0	not significant
11088	GO_NEGATIVE_REGULATION_OF_TISSUE_REMODELING	1.29	0.72	0	0	0	not significant
11089	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GLOBO_SERIES	1.29	0.72	0	0	0	not significant
11090	GO_DNA_REPAIR_COMPLEX_ASSEMBLY	1.29	0.71	0	0	0	not significant
11091	GO_MUTLALPHA_COMPLEX_BINDING	1.29	0.71	0	0	0	not significant
11092	REACTOME_REACTIONS_SPECIFIC_TO_THE_COMPLEX_N_GLYCAN_SYNTHESIS_PA	1.29	0.71	0	0	0	not significant
11093	GO_INTERLEUKIN_5_SECRETION	1.29	0.7	0	0	0	not significant
11094	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP	1.29	0.7	0	0	0	not significant
11095	GO_INSULIN_LIKE_GROWTH_FACTOR_BINDING	1.29	0.69	0	0	0	not significant
11096	GO_RESPONSE_TO_DRUG	1.30	2.05	0	0	0	not significant
11097	GO_VESICLE_MEMBRANE	1.30	1.99	0	0	0	not significant
11098	ENK_UV_RESPONSE_KERATINOCYTE_UP	1.30	1.82	0	0	0	not significant
11099	GO_TUBE_MORPHOGENESIS	1.30	1.73	0	0	0	not significant
11100	GO_CATION_TRANSMEMBRANE_TRANSPORT	1.30	1.7	0	0	0	not significant
11101	ACEVEDO_LIVER_CANCER_DN	1.30	1.55	0	0	0	not significant
11102	SMID_BREAST_CANCER_BASAL_DN	1.30	1.49	0	0	0	not significant
11103	NFE2L2.V2	1.30	1.35	0	0	0	not significant
11104	GO_LIPID_CATABOLIC_PROCESS	1.30	1.34	0	0	0	not significant
11105	GO_CELLULAR_RESPONSE_TO_DRUG	1.30	1.33	0	0	0	not significant
11106	GO_CELLULAR_RESPONSE_TO_STEROID_HORMONE_STIMULUS	1.30	1.29	0	0	0	not significant

11107	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_UP	1.30	1.26	0	0	0	not significant
11108	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12	1.30	1.22	0	0	0	not significant
11109	BENPORATH_PRC2_TARGETS	1.30	1.21	0	0	0	not significant
11110	GO_NEGATIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	1.30	1.21	0	0	0	not significant
11111	GO_FATTY_ACID_METABOLIC_PROCESS	1.30	1.18	0	0	0	not significant
11112	PRC2_EED_UP.V1_DN	1.30	1.18	0	0	0	not significant
11113	SNF5_DN.V1_UP	1.30	1.17	0	0	0	not significant
11114	GO_CARBOHYDRATE_DERIVATIVE_CATABOLIC_PROCESS	1.30	1.11	0	0	0	not significant
11115	ATF2_UP.V1_UP	1.30	1.09	0	0	0	not significant
11116	CHR5Q35	1.30	1.09	0	0	0	not significant
11117	GO_LIPID_TRANSPORTER_ACTIVITY	1.30	1.02	0	0	0	not significant
11118	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP	1.30	1.01	0	0	0	not significant
11119	KEGG_RIBOSOME	1.30	1.01	0	0	0	not significant
11120	GO_GOLGI_ASSOCIATED_VESICLE_MEMBRANE	1.30	1	0	0	0	not significant
11121	KEGG_SMALL_CELL_LUNG_CANCER	1.30	0.97	0	0	0	not significant
11122	PID_E2F_PATHWAY	1.30	0.96	0	0	0	not significant
11123	BAELDE_DIABETIC_NEPHROPATHY_UP	1.30	0.93	0	0	0	not significant
11124	NABA_ECM_REGULATORS	1.30	0.92	0	0	0	not significant
11125	GO_MACROPHAGE_ACTIVATION	1.30	0.91	0	0	0	not significant
11126	KEGG_DILATED_CARDIOMYOPATHY	1.30	0.91	0	0	0	not significant
11127	PID_RHOA_PATHWAY	1.30	0.9	0	0	0	not significant
11128	GO_GLIAL_CELL_PROLIFERATION	1.30	0.89	0	0	0	not significant
11129	GO_RNA_POLYMERASE_II_CORE_PROMOTER_SEQUENCE_SPECIFIC_DNA_BINDING	1.30	0.87	0	0	0	not significant
11130	GO_PYRIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	1.30	0.85	0	0	0	not significant
11131	CHR7Q21	1.30	0.83	0	0	0	not significant
11132	GO_INTERLEUKIN_4_MEDIATED_SIGNALING_PATHWAY	1.30	0.83	0	0	0	not significant
11133	GO_LENS_FIBER_CELL_DIFFERENTIATION	1.30	0.83	0	0	0	not significant
11134	PID_TCR_RAS_PATHWAY	1.30	0.83	0	0	0	not significant
11135	GO_CAP_INDEPENDENT_TRANSLATIONAL_INITIATION	1.30	0.82	0	0	0	not significant
11136	GO_REGULATION_OF_GLYCOPROTEIN_BIOSYNTHETIC_PROCESS	1.30	0.81	0	0	0	not significant
11137	REACTOME_TRANSPORT_OF_NUCLEOSIDES_AND_FREE_PURINE_AND_PYRIMIDINE	1.30	0.81	0	0	0	not significant
11138	FRIDMAN_IMMORTALIZATION_DN	1.30	0.8	0	0	0	not significant
11139	GO_NEGATIVE_REGULATION_OF_ANION_TRANSPORT	1.30	0.8	0	0	0	not significant
11140	GO_NEGATIVE_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	1.30	0.8	0	0	0	not significant
11141	MIKKELSEN_MEF_ICP_WITH_H3K4ME3_AND_H3K27ME3	1.30	0.8	0	0	0	not significant
11142	REACTOME_DOPAMINE_NEUROTRANSMITTER_RELEASE_CYCLE	1.30	0.8	0	0	0	not significant
11143	GO_BILE_ACID_BIOSYNTHETIC_PROCESS	1.30	0.79	0	0	0	not significant
11144	GO_NEGATIVE_REGULATION_OF_MACROPHAGE_MIGRATION	1.30	0.79	0	0	0	not significant
11145	DORSEY_GAB2_TARGETS	1.30	0.78	0	0	0	not significant
11146	GO_ACTIN_FILAMENT_REORGANIZATION	1.30	0.78	0	0	0	not significant
11147	GO_NADPLUS_ADP_RIBOSYLTRANSFERASE_ACTIVITY	1.30	0.78	0	0	0	not significant
11148	REACTOME_CELL_CELL_JUNCTION_ORGANIZATION	1.30	0.78	0	0	0	not significant
11149	BIOCARTA_LAIR_PATHWAY	1.30	0.77	0	0	0	not significant
11150	GO_CYSTEINE_METABOLIC_PROCESS	1.30	0.77	0	0	0	not significant
11151	GO_DIHYDROLIPOYL_DEHYDROGENASE_COMPLEX	1.30	0.77	0	0	0	not significant
11152	GO_MACROPHAGE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	1.30	0.77	0	0	0	not significant
11153	GO_RECEPTOR_INHIBITOR_ACTIVITY	1.30	0.77	0	0	0	not significant
11154	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_RENIN_ANGIO	1.30	0.77	0	0	0	not significant
11155	GO_CRANIAL_SUTURE_MORPHOGENESIS	1.30	0.76	0	0	0	not significant
11156	GO_POSITIVE_REGULATION_OF_FC_RECEPTOR_MEDIATED_STIMULATORY_SIGNA	1.30	0.76	0	0	0	not significant
11157	GO_RESPONSE_TO_INTERFERON_ALPHA	1.30	0.76	0	0	0	not significant
11158	KREPPEL_CD99_TARGETS_DN	1.30	0.76	0	0	0	not significant
11159	REACTOME_PLATELET_ADHESION_TO_EXPOSED_COLLAGEN	1.30	0.76	0	0	0	not significant
11160	VERRECCHIA_RESPONSE_TO_TGFB1_C2	1.30	0.76	0	0	0	not significant
11161	ABE_VEGFA_TARGETS	1.30	0.75	0	0	0	not significant
11162	REACTOME_BIOSYNTHESIS_OF_SPECIALIZED_PRORESOLVING_MEDIATORS_SPMS	1.30	0.74	0	0	0	not significant
11163	REACTOME_PYRIMIDINE_CATABOLISM	1.30	0.74	0	0	0	not significant
11164	SCIAN_INVERSED_TARGETS_OF_TP53_AND_TP73_UP	1.30	0.74	0	0	0	not significant
11165	BOYAULT_LIVER_CANCER_SUBCLASS_G56_UP	1.30	0.73	0	0	0	not significant
11166	CHEN_PDGF_TARGETS	1.30	0.73	0	0	0	not significant
11167	GO_FOLIC_ACID_BINDING	1.30	0.73	0	0	0	not significant
11168	GO_INSULIN_LIKE_GROWTH_FACTOR_I_BINDING	1.30	0.73	0	0	0	not significant
11169	REACTOME_SEROTONIN_NEUROTRANSMITTER_RELEASE_CYCLE	1.30	0.73	0	0	0	not significant
11170	GO_REGULATION_OF_FC_GAMMA_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_I	1.30	0.72	0	0	0	not significant
11171	MAHADEVAN_IMATINIB_RESISTANCE_DN	1.30	0.72	0	0	0	not significant
11172	OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_DN	1.30	0.72	0	0	0	not significant
11173	GO_REGULATION_OF_PROTEIN_ADP_RIBOSYLATION	1.30	0.7	0	0	0	not significant
11174	GO_SECONDARY_PALATE_DEVELOPMENT	1.30	0.7	0	0	0	not significant
11175	GO_CELL_MOTILITY	1.31	2.65	0	0	0	not significant
11176	GO_CELLULAR_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	1.31	2.26	0	0	0	not significant
11177	GO_CELLULAR_RESPONSE_TO_HORMONE_STIMULUS	1.31	1.9	0	0	0	not significant
11178	GO_MOLECULAR_ADAPTOR_ACTIVITY	1.31	1.33	0	0	0	not significant
11179	GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	1.31	1.29	0	0	0	not significant
11180	GO_CELLULAR_RESPONSE_TO_TOXIC_SUBSTANCE	1.31	1.27	0	0	0	not significant
11181	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN	1.31	1.26	0	0	0	not significant
11182	PHONG_TNF_RESPONSE_VIA_P38_PARTIAL	1.31	1.2	0	0	0	not significant
11183	ESC_V6.5_UP_LATE.V1_DN	1.31	1.19	0	0	0	not significant
11184	GO_SIGNAL_TRANSDUCTION_IN_RESPONSE_TO_DNA_DAMAGE	1.31	1.14	0	0	0	not significant
11185	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN	1.31	1.14	0	0	0	not significant
11186	JAK2_DN.V1_DN	1.31	1.1	0	0	0	not significant
11187	GO_REGULATION_OF_DNA_BINDING	1.31	1.08	0	0	0	not significant
11188	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN	1.31	1.06	0	0	0	not significant
11189	GO_VASCULOGENESIS	1.31	0.97	0	0	0	not significant
11190	GRADE_COLON_AND_RECTAL_CANCER_DN	1.31	0.97	0	0	0	not significant
11191	CHR16Q24	1.31	0.96	0	0	0	not significant
11192	GO_DNA_DEPENDENT_DNA_REPLICATION_MAINTENANCE_OF_FIDELITY	1.31	0.96	0	0	0	not significant
11193	GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	1.31	0.96	0	0	0	not significant
11194	WOO_LIVER_CANCER_RECURRENCE_UP	1.31	0.96	0	0	0	not significant
11195	GO_ISOPRENOID_METABOLIC_PROCESS	1.31	0.94	0	0	0	not significant
11196	ROSS_LEUKEMIA_WITH_MLL_FUSIONS	1.31	0.94	0	0	0	not significant
11197	REACTOME_TNF_SIGNALING	1.31	0.93	0	0	0	not significant
11198	PID_IL6_7_PATHWAY	1.31	0.92	0	0	0	not significant
11199	ZHAN_MULTIPLE_MYELOMA_LB_DN	1.31	0.91	0	0	0	not significant
11200	BIOCARTA_EGF_PATHWAY	1.31	0.9	0	0	0	not significant
11201	GO_NEGATIVE_REGULATION_OF_CYTOKINE_SECRETION	1.31	0.89	0	0	0	not significant
11202	GO_POSITIVE_REGULATION_OF_DNA_RECOMBINATION	1.31	0.88	0	0	0	not significant
11203	TRACEY_RESISTANCE_TO_IFNA2_DN	1.31	0.88	0	0	0	not significant
11204	GO_POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	1.31	0.87	0	0	0	not significant
11205	JIANG_TIP30_TARGETS_DN	1.31	0.87	0	0	0	not significant
11206	BIOCARTA_NGF_PATHWAY	1.31	0.86	0	0	0	not significant
11207	GO_SODIUM_CHANNEL_COMPLEX	1.31	0.86	0	0	0	not significant
11208	GO_POSITIVE_REGULATION_OF_CELLULAR_CARBOHYDRATE_METABOLIC_PROCE	1.31	0.85	0	0	0	not significant
11209	IWANAGA_E2F1_TARGETS_INDUCED_BY_SERUM	1.31	0.85	0	0	0	not significant
11210	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CASPASE_ACTIVATORS_AND	1.31	0.85	0	0	0	not significant
11211	PID_AR_NONGENOMIC_PATHWAY	1.31	0.84	0	0	0	not significant
11212	PID_TCR_CALCIUM_PATHWAY	1.31	0.83	0	0	0	not significant
11213	PODAR_RESPONSE_TO_ADAPHOSTIN_DN	1.31	0.83	0	0	0	not significant
11214	TSUNODA_CISPLATIN_RESISTANCE_DN	1.31	0.83	0	0	0	not significant
11215	GO_ANTIBIOTIC_TRANSPORT	1.31	0.82	0	0	0	not significant

11216	GO_ATP_DEPENDENT_PROTEIN_BINDING	1.31	0.82	0	0	0	not significant
11217	GO_GLUTATHIONE_DERIVATIVE_BIOSYNTHETIC_PROCESS	1.31	0.82	0	0	0	not significant
11218	GO_OLIGOSACCHARIDE_CATABOLIC_PROCESS	1.31	0.82	0	0	0	not significant
11219	GO_POSITIVE_REGULATION_OF_MAST_CELL_ACTIVATION	1.31	0.82	0	0	0	not significant
11220	GO_POSITIVE_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	1.31	0.82	0	0	0	not significant
11221	GO_REGULATION_OF_DNA_DIRECTED_DNA_POLYMERASE_ACTIVITY	1.31	0.82	0	0	0	not significant
11222	FUJII_YBX1_TARGETS_UP	1.31	0.81	0	0	0	not significant
11223	GO_LIVER_MORPHOGENESIS	1.31	0.81	0	0	0	not significant
11224	SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_DN	1.31	0.81	0	0	0	not significant
11225	GO_CELLULAR_RESPONSE_TO_PH	1.31	0.8	0	0	0	not significant
11226	GO_HEART_VALVE_FORMATION	1.31	0.8	0	0	0	not significant
11227	VALK_AML_CLUSTER_3	1.31	0.8	0	0	0	not significant
11228	GO_AMP_BINDING	1.31	0.79	0	0	0	not significant
11229	GO_CARBON_NITROGEN_LYASE_ACTIVITY	1.31	0.79	0	0	0	not significant
11230	GO_CRANIOFACIAL_SUTURE_MORPHOGENESIS	1.31	0.79	0	0	0	not significant
11231	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_UP	1.31	0.79	0	0	0	not significant
11232	GO_CALCIUM_ACTIVATED_POTASSIUM_CHANNEL_ACTIVITY	1.31	0.78	0	0	0	not significant
11233	GO_LIPOPROTEIN_CATABOLIC_PROCESS	1.31	0.78	0	0	0	not significant
11234	GO_METALLOCARBOXYPEPTIDASE_ACTIVITY	1.31	0.77	0	0	0	not significant
11235	GO_NEGATIVE_REGULATION_OF_AMYLOID_PRECURSOR_PROTEIN_BIOSYNTHETIC_	1.31	0.77	0	0	0	not significant
11236	GO_REGULATION_OF_MEMBRANE_INVAGINATION	1.31	0.77	0	0	0	not significant
11237	GO_ESTROGEN_BIOSYNTHETIC_PROCESS	1.31	0.76	0	0	0	not significant
11238	GO_MITOTIC_CELL_CYCLE_ARREST	1.31	0.74	0	0	0	not significant
11239	GO_DOLICHYL_PHOSPHATE_MANNOSE_PROTEIN_MANNOSYLTRANSFERASE_ACTIV	1.31	0.73	0	0	0	not significant
11240	GO_REGULATION_OF_HEAT_GENERATION	1.31	0.73	0	0	0	not significant
11241	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY	1.32	4	0	0	0	not significant
11242	GO_TUBE_DEVELOPMENT	1.32	2.33	0	0	0	not significant
11243	GO_REGULATION_OF_LIPID_METABOLIC_PROCESS	1.32	1.58	0	0	0	not significant
11244	AMUNDSON_RESPONSE_TO_ARSENITE	1.32	1.42	0	0	0	not significant
11245	GO_REGULATION_OF_SMALL_MOLECULE_METABOLIC_PROCESS	1.32	1.35	0	0	0	not significant
11246	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP	1.32	1.35	0	0	0	not significant
11247	CHR12Q13	1.32	1.33	0	0	0	not significant
11248	PGF_UP.V1_DN	1.32	1.26	0	0	0	not significant
11249	GO_POSITIVE_REGULATION_OF_JNK_CASCADE	1.32	1.22	0	0	0	not significant
11250	RAF_UP.V1_UP	1.32	1.19	0	0	0	not significant
11251	GO_MAINTENANCE_OF_LOCATION_IN_CELL	1.32	1.17	0	0	0	not significant
11252	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	1.32	1.14	0	0	0	not significant
11253	GO_GROWTH_FACTOR_BINDING	1.32	1.1	0	0	0	not significant
11254	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_DN	1.32	1.07	0	0	0	not significant
11255	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	1.32	1.06	0	0	0	not significant
11256	MOHANKUMAR_TLX1_TARGETS_DN	1.32	1.05	0	0	0	not significant
11257	RAMALHO_STEMNESS_DN	1.32	1.01	0	0	0	not significant
11258	FAELT_B_CLL_WITH_VH3_21_DN	1.32	1	0	0	0	not significant
11259	GO_CHEMOKINE_PRODUCTION	1.32	0.97	0	0	0	not significant
11260	LEIN_PONS_MARKERS	1.32	0.97	0	0	0	not significant
11261	GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_ENDOPLASM	1.32	0.95	0	0	0	not significant
11262	GO_LIGAND_GATED_ION_CHANNEL_ACTIVITY	1.32	0.94	0	0	0	not significant
11263	GO_TETRAPYRROLE_METABOLIC_PROCESS	1.32	0.94	0	0	0	not significant
11264	GO_AMYLOID_PRECURSOR_PROTEIN_METABOLIC_PROCESS	1.32	0.92	0	0	0	not significant
11265	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	1.32	0.92	0	0	0	not significant
11266	GO_POSITIVE_CHEMOTAXIS	1.32	0.92	0	0	0	not significant
11267	GO_PROTEIN_DEACETYLASE_ACTIVITY	1.32	0.91	0	0	0	not significant
11268	LEE_LIVER_CANCER_CIPROFIBRATE_UP	1.32	0.9	0	0	0	not significant
11269	GO_ENDOPLASMIC_RETICULUM_TO_CYTOSOL_TRANSPORT	1.32	0.89	0	0	0	not significant
11270	TING_SILENCED_BY_DICER	1.32	0.89	0	0	0	not significant
11271	GO_POSITIVE_REGULATION_OF_CHEMOKINE_PRODUCTION	1.32	0.88	0	0	0	not significant
11272	GO_CELL_MOTILITY_INVOLVED_IN_CEREBRAL_CORTEX_RADIAL_GLIA_GUIDED_MI	1.32	0.87	0	0	0	not significant
11273	GO_CHROMAFFIN_GRANULE	1.32	0.87	0	0	0	not significant
11274	SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN	1.32	0.87	0	0	0	not significant
11275	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_SIGNALING_PATHWAY	1.32	0.86	0	0	0	not significant
11276	HAN_JNK_SINGALING_UP	1.32	0.86	0	0	0	not significant
11277	SPIRA_SMOKERS_LUNG_CANCER_UP	1.32	0.86	0	0	0	not significant
11278	GO_CELL_FATE_DETERMINATION	1.32	0.85	0	0	0	not significant
11279	GO_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	1.32	0.85	0	0	0	not significant
11280	GO_PROSTANOID_METABOLIC_PROCESS	1.32	0.84	0	0	0	not significant
11281	GO_MITOCHONDRIAL_DNA_METABOLIC_PROCESS	1.32	0.83	0	0	0	not significant
11282	GO_NEGATIVE_REGULATION_OF_FATTY_ACID_OXIDATION	1.32	0.83	0	0	0	not significant
11283	MCCLUNG_DELTA_FOSB_TARGETS_2WK	1.32	0.83	0	0	0	not significant
11284	GO_CELLULAR_RESPONSE_TO_FOLLICLE_STIMULATING_HORMONE_STIMULUS	1.32	0.82	0	0	0	not significant
11285	GO_XENOBIOTIC_TRANSPORT	1.32	0.82	0	0	0	not significant
11286	GO_PROTEIN_CARBOXYL_O_METHYLTRANSFERASE_ACTIVITY	1.32	0.81	0	0	0	not significant
11287	GO_ESTRADIOL_17_BETA_DEHYDROGENASE_ACTIVITY	1.32	0.8	0	0	0	not significant
11288	GO_VOLTAGE_GATED_SODIUM_CHANNEL_COMPLEX	1.32	0.8	0	0	0	not significant
11289	GO_GUANYLATE_KINASE_ACTIVITY	1.32	0.79	0	0	0	not significant
11290	GO_DNA_LIGATION_INVOLVED_IN_DNA_REPAIR	1.32	0.78	0	0	0	not significant
11291	GO_CELLULAR_RESPONSE_TO_GLUCAGON_STIMULUS	1.32	0.77	0	0	0	not significant
11292	GO_ESTROUS_CYCLE	1.32	0.77	0	0	0	not significant
11293	GO_GTP_RHO_BINDING	1.32	0.77	0	0	0	not significant
11294	GO_PROTEIN_AUTO_ADP_RIBOSYLATION	1.32	0.77	0	0	0	not significant
11295	GO_STABILIZATION_OF_MEMBRANE_POTENTIAL	1.32	0.77	0	0	0	not significant
11296	CHR1P33	1.32	0.76	0	0	0	not significant
11297	GO_NEGATIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	1.32	0.76	0	0	0	not significant
11298	GO_POSITIVE_REGULATION_OF_INTEGRIN_ACTIVATION	1.32	0.74	0	0	0	not significant
11299	GO_LOCOMOTION	1.33	2.94	0	0	0	not significant
11300	GO_WHOLE_MEMBRANE	1.33	2.94	0	0	0	not significant
11301	GO_ION_TRANSPORT	1.33	2.93	0	0	0	not significant
11302	GO_CATION_TRANSPORT	1.33	2.91	0	0	0	not significant
11303	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY	1.33	2.33	0	0	0	not significant
11304	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_7	1.33	1.77	0	0	0	not significant
11305	GO_ORGANELLE_SUBCOMPARTMENT	1.33	1.67	0	0	0	not significant
11306	GO_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	1.33	1.53	0	0	0	not significant
11307	GO_PROTEIN_MATURATION	1.33	1.46	0	0	0	not significant
11308	GO_AMEBOIDAL_TYPE_CELL_MIGRATION	1.33	1.44	0	0	0	not significant
11309	GO_REGULATION_OF_T_CELL_ACTIVATION	1.33	1.43	0	0	0	not significant
11310	GO_DNA_DEPENDENT_DNA_REPLICATION	1.33	1.38	0	0	0	not significant
11311	GO_VACUOLE_ORGANIZATION	1.33	1.32	0	0	0	not significant
11312	HALLMARK_APOPTOSIS	1.33	1.28	0	0	0	not significant
11313	FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_UP	1.33	1.25	0	0	0	not significant
11314	ELVIDGE_HIF1A_TARGETS_DN	1.33	1.17	0	0	0	not significant
11315	DURAND_STROMA_NS_UP	1.33	1.16	0	0	0	not significant
11316	GO_PRESYNAPTIC_MEMBRANE	1.33	1.16	0	0	0	not significant
11317	GO_REGULATION_OF_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS	1.33	1.14	0	0	0	not significant
11318	MCBRYAN_PUBERTAL_BREAST_3_4WK_UP	1.33	1.14	0	0	0	not significant
11319	GO_SPECIFIC_GRANULE_MEMBRANE	1.33	1.09	0	0	0	not significant
11320	GO_IMMUNOGLOBULIN_PRODUCTION	1.33	1.07	0	0	0	not significant
11321	SHAFFER_IRF4_TARGETS_IN_ACTIVATED_DENDRITIC_CELL	1.33	1.07	0	0	0	not significant
11322	ROSS_AML_WITH_MLL_FUSIONS	1.33	1.06	0	0	0	not significant
11323	CRX_NRL_DN.V1_UP	1.33	1.05	0	0	0	not significant
11324	AKL_HTLV1_INFECTION_DN	1.33	1.04	0	0	0	not significant

11325	VANASSE_BCL2_TARGETS_DN	1.33	1.04	0	0	0	not significant
11326	WIELAND_UP_BY_HBV_INFECTION	1.33	1.04	0	0	0	not significant
11327	GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	1.33	1.02	0	0	0	not significant
11328	ZHAN_MULTIPLE_MYELOMA_HP_DN	1.33	1.01	0	0	0	not significant
11329	BOYAULT_LIVER_CANCER_SUBCLASS_G6_UP	1.33	0.98	0	0	0	not significant
11330	GO_SELECTIVE_AUTOPHAGY	1.33	0.98	0	0	0	not significant
11331	GERHOLD_ADIPOGENESIS_UP	1.33	0.97	0	0	0	not significant
11332	KRAS.LUNG_UP.V1_DN	1.33	0.96	0	0	0	not significant
11333	GO_REGULATION_OF_MYOTUBE_DIFFERENTIATION	1.33	0.95	0	0	0	not significant
11334	GO_LYTIC_VACUOLE_ORGANIZATION	1.33	0.94	0	0	0	not significant
11335	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	1.33	0.94	0	0	0	not significant
11336	PID_BARD1_PATHWAY	1.33	0.93	0	0	0	not significant
11337	GO_MONOCYTE_CHEMOTACTIC_PROTEIN_1_PRODUCTION	1.33	0.89	0	0	0	not significant
11338	GO_POSITIVE_REGULATION_OF_ERBB_SIGNALING_PATHWAY	1.33	0.87	0	0	0	not significant
11339	REACTOME_TNF_RECEPTOR_SUPERFAMILY_TNFSF_MEMBERS_MEDIATING_NON_	1.33	0.87	0	0	0	not significant
11340	GO_GALACTOSE_METABOLIC_PROCESS	1.33	0.86	0	0	0	not significant
11341	GO_ALPHA_BETA_T_CELL_LINEAGE_COMMITMENT	1.33	0.85	0	0	0	not significant
11342	GO_DEVELOPMENTAL_INDUCTION	1.33	0.85	0	0	0	not significant
11343	GO_PROTEIN_UFMYLATION	1.33	0.85	0	0	0	not significant
11344	GO_REGULATION_OF_THYMOCYTE_APOPTOTIC_PROCESS	1.33	0.85	0	0	0	not significant
11345	GO_DNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC	1.33	0.84	0	0	0	not significant
11346	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_BINDING	1.33	0.84	0	0	0	not significant
11347	GO_STRIATUM_DEVELOPMENT	1.33	0.84	0	0	0	not significant
11348	GO_CHLORIDE_ION_HOMEOSTASIS	1.33	0.83	0	0	0	not significant
11349	GO_POSITIVE_REGULATION_OF_SPROUTING_ANGIOGENESIS	1.33	0.83	0	0	0	not significant
11350	KEGG_OTHER_GLYCAN_DEGRADATION	1.33	0.83	0	0	0	not significant
11351	GO_INOSITOL_TRISPHOSPHATE_BIOSYNTHETIC_PROCESS	1.33	0.82	0	0	0	not significant
11352	GO_NEGATIVE_REGULATION_OF_FATTY_ACID_TRANSPORT	1.33	0.82	0	0	0	not significant
11353	GO_NEGATIVE_REGULATION_OF_T_CELL_DIFFERENTIATION_IN_THYMUS	1.33	0.82	0	0	0	not significant
11354	GO_POSITIVE_REGULATION_OF_STEROL_TRANSPORT	1.33	0.82	0	0	0	not significant
11355	GO_THIAMINE_PYROPHOSPHATE_BINDING	1.33	0.82	0	0	0	not significant
11356	GO_POLYSACCHARIDE_BINDING	1.33	0.81	0	0	0	not significant
11357	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	1.33	0.81	0	0	0	not significant
11358	KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS_AND_CYCLIC_RGD	1.33	0.81	0	0	0	not significant
11359	CHR4Q34	1.33	0.8	0	0	0	not significant
11360	GO_REGULATION_OF_CGMP_MEDIATED_SIGNALING	1.33	0.8	0	0	0	not significant
11361	GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	1.33	0.8	0	0	0	not significant
11362	GO_STRUCTURAL_CONSTITUENT_OF_SYNAPSE	1.33	0.8	0	0	0	not significant
11363	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_UP	1.33	0.8	0	0	0	not significant
11364	GO_AMPA_GLUTAMATE_RECEPTOR_COMPLEX	1.33	0.79	0	0	0	not significant
11365	GO_ANGIOTENSIN_ACTIVATED_SIGNALING_PATHWAY	1.33	0.78	0	0	0	not significant
11366	GO_CELL_MATRIX_ADHESION_MEDIATOR_ACTIVITY	1.33	0.76	0	0	0	not significant
11367	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP	1.34	1.67	0	0	0	not significant
11368	GO_RESPONSE_TO_RADIATION	1.34	1.66	0	0	0	not significant
11369	GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	1.34	1.61	0	0	0	not significant
11370	KUMAR_TARGETS_OF_MLL_AF9_FUSION	1.34	1.61	0	0	0	not significant
11371	GO_REGULATION_OF_NEUROTRANSMITTER_LEVELS	1.34	1.48	0	0	0	not significant
11372	GO_CELLULAR_LIPID_CATABOLIC_PROCESS	1.34	1.4	0	0	0	not significant
11373	NAGASHIMA_NRG1_SIGNALING_UP	1.34	1.34	0	0	0	not significant
11374	GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	1.34	1.31	0	0	0	not significant
11375	GO_PLASMA_MEMBRANE_RECEPTOR_COMPLEX	1.34	1.24	0	0	0	not significant
11376	VERHAAK_AML_WITH_NPM1_MUTATED_UP	1.34	1.23	0	0	0	not significant
11377	GO_ATPASE_ACTIVITY_COUPLED_TO_MOVEMENT_OF_SUBSTANCES	1.34	1.22	0	0	0	not significant
11378	RODWELL_AGING_KIDNEY_NO_BLOOD_UP	1.34	1.21	0	0	0	not significant
11379	REACTOME_AMYLOID_FIBER_FORMATION	1.34	1.19	0	0	0	not significant
11380	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	1.34	1.16	0	0	0	not significant
11381	REACTOME_PLASMA_LIPOPROTEIN_ASSEMBLY_REMODELING_AND_CLEARANCE	1.34	1.12	0	0	0	not significant
11382	RHEIN_ALL_GLUCOCORTICOID_THERAPY_UP	1.34	1.1	0	0	0	not significant
11383	ASTIER_INTEGRIN_SIGNALING	1.34	1.07	0	0	0	not significant
11384	GO_ANTIOXIDANT_ACTIVITY	1.34	1.02	0	0	0	not significant
11385	KRAS.PROSTATE_UP.V1_DN	1.34	1	0	0	0	not significant
11386	GO_NATURAL_KILLER_CELL_ACTIVATION	1.34	0.99	0	0	0	not significant
11387	GO_GPI_ANCHOR_BIOSYNTHETIC_PROCESS	1.34	0.98	0	0	0	not significant
11388	BOYLAN_MULTIPLE_MYELOMA_C_DN	1.34	0.96	0	0	0	not significant
11389	GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	1.34	0.96	0	0	0	not significant
11390	PID_ARF6_TRAFFICKING_PATHWAY	1.34	0.96	0	0	0	not significant
11391	GO_RESPONSE_TO_LIGHT_INTENSITY	1.34	0.95	0	0	0	not significant
11392	GO_PHOSPHOLIPID_TRANSLOCATING_ATPASE_ACTIVITY	1.34	0.93	0	0	0	not significant
11393	GO_AUTONOMIC_NERVOUS_SYSTEM_DEVELOPMENT	1.34	0.92	0	0	0	not significant
11394	GO_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_P	1.34	0.92	0	0	0	not significant
11395	GO_RESPONSE_TO_PROGESTERONE	1.34	0.92	0	0	0	not significant
11396	EPPERT_CE_HSC_LSC	1.34	0.91	0	0	0	not significant
11397	GO_POSTSYNAPTIC_ENDOSOME	1.34	0.91	0	0	0	not significant
11398	GO_KILLING_OF_CELLS_OF_OTHER_ORGANISM	1.34	0.9	0	0	0	not significant
11399	GO_NLRP3_INFLAMMASOME_COMPLEX	1.34	0.9	0	0	0	not significant
11400	KEGG_DRUG_METABOLISM_CYTOCHROME_P450	1.34	0.9	0	0	0	not significant
11401	BIOCARTA_TCAPOPTOSIS_PATHWAY	1.34	0.89	0	0	0	not significant
11402	GO_SUBPALLIUM_DEVELOPMENT	1.34	0.89	0	0	0	not significant
11403	KEGG_ARACHIDONIC_ACID_METABOLISM	1.34	0.89	0	0	0	not significant
11404	REACTOME_HS_GAG_BIOSYNTHESIS	1.34	0.88	0	0	0	not significant
11405	WENG_POR_TARGETS_GLOBAL_DN	1.34	0.88	0	0	0	not significant
11406	GO_CHROMAFFIN_GRANULE_MEMBRANE	1.34	0.87	0	0	0	not significant
11407	GO_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_PROC	1.34	0.87	0	0	0	not significant
11408	GO_POSITIVE_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_	1.34	0.87	0	0	0	not significant
11409	GO_RESPONSE_TO_STEROL_DEPLETION	1.34	0.87	0	0	0	not significant
11410	REACTOME_ABC_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	1.34	0.87	0	0	0	not significant
11411	TERAMOTO_OPN_TARGETS_CLUSTER_5	1.34	0.87	0	0	0	not significant
11412	GO_MANNOSE_METABOLIC_PROCESS	1.34	0.86	0	0	0	not significant
11413	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	1.34	0.86	0	0	0	not significant
11414	GO_POSITIVE_REGULATION_OF_NEURON_PROJECTION_REGENERATION	1.34	0.86	0	0	0	not significant
11415	GO_PROTEIN_ADP_RIBOSYLASE_ACTIVITY	1.34	0.86	0	0	0	not significant
11416	GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRAN	1.34	0.86	0	0	0	not significant
11417	REACTOME_MYOGENESIS	1.34	0.86	0	0	0	not significant
11418	GO_ACYLGLYCEROL_HOMEOSTASIS	1.34	0.85	0	0	0	not significant
11419	GO_SREBP_SIGNALING_PATHWAY	1.34	0.85	0	0	0	not significant
11420	HOWLIN_CITED1_TARGETS_2_UP	1.34	0.85	0	0	0	not significant
11421	GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_LINEAGE_COMMITMENT	1.34	0.84	0	0	0	not significant
11422	GO_LYSOPHOSPHOLIPASE_ACTIVITY	1.34	0.84	0	0	0	not significant
11423	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	1.34	0.84	0	0	0	not significant
11424	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	1.34	0.84	0	0	0	not significant
11425	REACTOME_SIGNALING_BY_ACTIVIN	1.34	0.83	0	0	0	not significant
11426	GO_CHROMATIN_MEDIATED_MAINTENANCE_OF_TRANSCRIPTION	1.34	0.82	0	0	0	not significant
11427	GO_HEAT_GENERATION	1.34	0.82	0	0	0	not significant
11428	GO_NEGATIVE_REGULATION_OF_TORC1_SIGNALING	1.34	0.82	0	0	0	not significant
11429	HE_PTEN_TARGETS_DN	1.34	0.81	0	0	0	not significant
11430	SU_PLACENTA	1.34	0.81	0	0	0	not significant
11431	GO_POSITIVE_REGULATION_OF_PROTEIN_HOMOOLIGOMERIZATION	1.34	0.8	0	0	0	not significant
11432	GO_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION_INITIATION	1.34	0.8	0	0	0	not significant
11433	REACTOME_UNWINDING_OF_DNA	1.34	0.77	0	0	0	not significant

11434	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_A	1.35	2.15	0	0	0	not significant
11435	GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	1.35	2.07	0	0	0	not significant
11436	BENPORATH_ES_WITH_H3K27ME3	1.35	1.91	0	0	0	not significant
11437	GO_RESPONSE_TO_PEPTIDE_HORMONE	1.35	1.76	0	0	0	not significant
11438	LIU_PROSTATE_CANCER_DN	1.35	1.67	0	0	0	not significant
11439	GO_REGULATION_OF_LYMPHOCYTE_ACTIVATION	1.35	1.65	0	0	0	not significant
11440	MULLIGHAN_MLL_SIGNATURE_2_DN	1.35	1.57	0	0	0	not significant
11441	FORTSCHEGGER_PHF8_TARGETS_UP	1.35	1.51	0	0	0	not significant
11442	GO_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION	1.35	1.45	0	0	0	not significant
11443	CHR16P13	1.35	1.35	0	0	0	not significant
11444	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP	1.35	1.28	0	0	0	not significant
11445	GO_LATE_ENDOSOME_MEMBRANE	1.35	1.27	0	0	0	not significant
11446	GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RE	1.35	1.25	0	0	0	not significant
11447	GO_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	1.35	1.24	0	0	0	not significant
11448	BROWNE_HCMV_INFECTION_24HR_DN	1.35	1.21	0	0	0	not significant
11449	GO_VASCULAR_PROCESS_IN_CIRCULATORY_SYSTEM	1.35	1.21	0	0	0	not significant
11450	GO_REGULATION_OF_BLOOD_PRESSURE	1.35	1.19	0	0	0	not significant
11451	CHEN_LIVER_METABOLISM_QTL_CIS	1.35	1.17	0	0	0	not significant
11452	GO_POSITIVE_REGULATION_OF_NEURON_DEATH	1.35	1.17	0	0	0	not significant
11453	LABBE_WNT3A_TARGETS_DN	1.35	1.17	0	0	0	not significant
11454	MIKKELSEN_NPC_HCP_WITH_H3K27ME3	1.35	1.16	0	0	0	not significant
11455	GO_ERAD_PATHWAY	1.35	1.14	0	0	0	not significant
11456	NABA_CORE_MATRISOME	1.35	1.13	0	0	0	not significant
11457	GO_GLUTAMINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	1.35	1.12	0	0	0	not significant
11458	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_12	1.35	1.12	0	0	0	not significant
11459	NABA_ECM_AFFILIATED	1.35	1.09	0	0	0	not significant
11460	GO_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	1.35	1.07	0	0	0	not significant
11461	REACTOME_INTERLEUKIN_2_FAMILY_SIGNALING	1.35	1.06	0	0	0	not significant
11462	GO_EXOGENOUS_PROTEIN_BINDING	1.35	1.05	0	0	0	not significant
11463	GAVIN_FOXP3_TARGETS_CLUSTER_P2	1.35	1.04	0	0	0	not significant
11464	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP	1.35	1.04	0	0	0	not significant
11465	REACTOME_PLASMA_LIPOPROTEIN_CLEARANCE	1.35	1.04	0	0	0	not significant
11466	GO_AMINOGLYCAN_BIOSYNTHETIC_PROCESS	1.35	1.03	0	0	0	not significant
11467	BASSO_CD40_SIGNALING_DN	1.35	1.01	0	0	0	not significant
11468	GUILLAUMOND_KLF10_TARGETS_UP	1.35	1	0	0	0	not significant
11469	GO_LIGASE_ACTIVITY_FORMING_CARBON_SULFUR_BONDS	1.35	0.97	0	0	0	not significant
11470	OHM_METHYLATED_IN_ADULT_CANCERS	1.35	0.97	0	0	0	not significant
11471	CHR9P22	1.35	0.96	0	0	0	not significant
11472	GO_NEGATIVE_REGULATION_OF_LIPID_LOCALIZATION	1.35	0.96	0	0	0	not significant
11473	GO_BEHAVIORAL_RESPONSE_TO_PAIN	1.35	0.94	0	0	0	not significant
11474	REACTOME_METABOLISM_OF_INGESTED_SEMET_SEC_MESEC_INTO_H2SE	1.35	0.94	0	0	0	not significant
11475	GO_POSITIVE_REGULATION_OF_PRI_MIRNA_TRANSCRIPTION_BY_RNA_POLYMERA	1.35	0.93	0	0	0	not significant
11476	GO_REGULATION_OF_HAIR_FOLLICLE_DEVELOPMENT	1.35	0.93	0	0	0	not significant
11477	HARRIS_BRAIN_CANCER_PROGENITORS	1.35	0.93	0	0	0	not significant
11478	MAGRANGEAS_MULTIPLE_MYELOMA_IGLL_VS_IGLK_DN	1.35	0.92	0	0	0	not significant
11479	GO_TRANSMITTER_GATED_CHANNEL_ACTIVITY	1.35	0.91	0	0	0	not significant
11480	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_1_UP	1.35	0.91	0	0	0	not significant
11481	GO_NEGATIVE_REGULATION_OF_BONE_REMODELING	1.35	0.9	0	0	0	not significant
11482	GO_REGULATION_OF_MAST_CELL_CHEMOTAXIS	1.35	0.9	0	0	0	not significant
11483	LOPEZ_MESOTHELIOMA_SURVIVAL_UP	1.35	0.9	0	0	0	not significant
11484	REACTOME_TNFR1_INDUCED_PROAPOPTOTIC_SIGNALING	1.35	0.9	0	0	0	not significant
11485	GO_NEGATIVE_T_CELL_SELECTION	1.35	0.89	0	0	0	not significant
11486	BIOCARTA_CDMAC_PATHWAY	1.35	0.88	0	0	0	not significant
11487	GO_COMMON_PARTNER_SMAD_PROTEIN_PHOSPHORYLATION	1.35	0.88	0	0	0	not significant
11488	GO_MIDDLE_EAR_MORPHOGENESIS	1.35	0.88	0	0	0	not significant
11489	REACTOME_DEFECTIVE_B4GALT7_CAUSES_EDS_PROGEROID_TYPE	1.35	0.88	0	0	0	not significant
11490	REACTOME_GLUTATHIONE_SYNTHESIS_AND_RECYCLING	1.35	0.88	0	0	0	not significant
11491	REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLUCOSE_DEPENDE	1.35	0.88	0	0	0	not significant
11492	GO_COCHLEA_MORPHOGENESIS	1.35	0.87	0	0	0	not significant
11493	GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	1.35	0.87	0	0	0	not significant
11494	LI_CYTIDINE_ANALOG_PATHWAY	1.35	0.86	0	0	0	not significant
11495	REACTOME_NOREPINEPHRINE_NEUROTRANSMITTER_RELEASE_CYCLE	1.35	0.86	0	0	0	not significant
11496	REACTOME_TFAP2_AP_2_FAMILY_REGULATES_TRANSCRIPTION_OF_GROWTH_FA	1.35	0.86	0	0	0	not significant
11497	GO_REGULATION_OF_SYNAPTIC_VESICLE_FUSION_TO_PRESYNAPTIC_ACTIVE_ZO	1.35	0.85	0	0	0	not significant
11498	GO_PHOSPHOLIPASE_A2_ACTIVITY_CONSUMING_1_2_DIPALMITOYLPHOSPHATIDYL	1.35	0.84	0	0	0	not significant
11499	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_5	1.35	0.84	0	0	0	not significant
11500	NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON	1.35	0.83	0	0	0	not significant
11501	GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_PROLIFERATION	1.35	0.81	0	0	0	not significant
11502	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3	1.36	2.32	0	0	0	not significant
11503	GO_CARDIOVASCULAR_SYSTEM_DEVELOPMENT	1.36	2.08	0	0	0	not significant
11504	GO_RESPONSE_TO_EXTRACELLULAR_STIMULUS	1.36	2.01	0	0	0	not significant
11505	GO_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.36	1.68	0	0	0	not significant
11506	HELLER_HDAC_TARGETS_UP	1.36	1.68	0	0	0	not significant
11507	HOLLMANN_APOPTOSIS_VIA_CD40_DN	1.36	1.57	0	0	0	not significant
11508	GO_CELLULAR_RESPONSE_TO_PEPTIDE_HORMONE_STIMULUS	1.36	1.56	0	0	0	not significant
11509	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_ACTIVATION	1.36	1.47	0	0	0	not significant
11510	GO_RESPONSE_TO_XENOBIOTIC_STIMULUS	1.36	1.47	0	0	0	not significant
11511	WINTER_HYPOXIA_METAGENE	1.36	1.47	0	0	0	not significant
11512	GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE	1.36	1.43	0	0	0	not significant
11513	GAVIN_FOXP3_TARGETS_CLUSTER_P3	1.36	1.4	0	0	0	not significant
11514	PLASARI_TGFB1_TARGETS_10HR_UP	1.36	1.3	0	0	0	not significant
11515	JNK_DN.V1_DN	1.36	1.24	0	0	0	not significant
11516	BMI1_DN.V1_DN	1.36	1.21	0	0	0	not significant
11517	DAUER_STAT3_TARGETS_DN	1.36	1.19	0	0	0	not significant
11518	CHR7Q36	1.36	1.16	0	0	0	not significant
11519	GO_REGULATION_OF_B_CELL_ACTIVATION	1.36	1.16	0	0	0	not significant
11520	INGRAM_SHH_TARGETS_UP	1.36	1.15	0	0	0	not significant
11521	GO_LYMPHOCYTE_MIGRATION	1.36	1.13	0	0	0	not significant
11522	SAFFORD_T_LYMPHOCYTE_ANERGY	1.36	1.13	0	0	0	not significant
11523	FONTAINE_FOLLICULAR_THYROID_ADENOMA_UP	1.36	1.08	0	0	0	not significant
11524	GO_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	1.36	1.08	0	0	0	not significant
11525	PID_P38_ALPHA_BETA_DOWNSTREAM_PATHWAY	1.36	1.08	0	0	0	not significant
11526	GO_LEARNING	1.36	1.07	0	0	0	not significant
11527	GO_DNA_REPLICATION_INITIATION	1.36	1.06	0	0	0	not significant
11528	GO_LYSOSOMAL_LUMEN_ACIDIFICATION	1.36	1.05	0	0	0	not significant
11529	KEGG_DNA_REPLICATION	1.36	1.05	0	0	0	not significant
11530	GO_INTRINSIC_COMPONENT_OF_SYNAPTIC_MEMBRANE	1.36	1.04	0	0	0	not significant
11531	HARRIS_HYPOXIA	1.36	1.04	0	0	0	not significant
11532	PID_MAPK_TRK_PATHWAY	1.36	1.03	0	0	0	not significant
11533	POMEROY_MEDULLOBLASTOMA_PROGNOSIS_UP	1.36	1.02	0	0	0	not significant
11534	YAMASHITA_METHYLATED_IN_PROSTATE_CANCER	1.36	1.01	0	0	0	not significant
11535	GO_RESPONSE_TO_CHEMOKINE	1.36	1	0	0	0	not significant
11536	GO_AXONEME_ASSEMBLY	1.36	0.99	0	0	0	not significant
11537	LINDSTEDT_DENDRITIC_CELL_MATURATION_A	1.36	0.99	0	0	0	not significant
11538	GO_GLIAL_CELL_PROJECTION	1.36	0.98	0	0	0	not significant
11539	GO_PROTEIN_HOMOTRIMERIZATION	1.36	0.98	0	0	0	not significant
11540	HOLLEMAN_ASPARAGINASE_RESISTANCE_B_ALL_UP	1.36	0.98	0	0	0	not significant
11541	BIOCARTA_G1_PATHWAY	1.36	0.97	0	0	0	not significant
11542	VERRECCHIA_RESPONSE_TO_TGFB1_C5	1.36	0.97	0	0	0	not significant

11543	GO_IMMUNOGLOBULIN_SECRETION	1.36	0.96	0	0	0	not significant
11544	GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_INVOLVED_IN_INFLAMMATORY_RE	1.36	0.95	0	0	0	not significant
11545	GO_T_CELL_CYTOKINE_PRODUCTION	1.36	0.95	0	0	0	not significant
11546	GO_HISTONE_H3_K14_ACETYLATION	1.36	0.94	0	0	0	not significant
11547	GO_NEGATIVE_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_HOMOLO	1.36	0.93	0	0	0	not significant
11548	GO_ACROSOMAL_MEMBRANE	1.36	0.92	0	0	0	not significant
11549	GO_INFLAMMASOME_COMPLEX	1.36	0.92	0	0	0	not significant
11550	GO_NEGATIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATIO	1.36	0.92	0	0	0	not significant
11551	GO_NEGATIVE_REGULATION_OF_BONE_MINERALIZATION	1.36	0.92	0	0	0	not significant
11552	REACTOME_CATION_COUPLED_CHLORIDE_COTRANSPORTERS	1.36	0.92	0	0	0	not significant
11553	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX	1.36	0.91	0	0	0	not significant
11554	GO_APOLIPOPROTEIN_BINDING	1.36	0.91	0	0	0	not significant
11555	GO_PROTEIN_O_LINKED_MANNOSYLATION	1.36	0.91	0	0	0	not significant
11556	GO_GMP_METABOLIC_PROCESS	1.36	0.9	0	0	0	not significant
11557	GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVATING_G_PROTEIN_COUPLED_	1.36	0.9	0	0	0	not significant
11558	BIOCARTA_IL7_PATHWAY	1.36	0.89	0	0	0	not significant
11559	GO_ATRIAL_SEPTUM_MORPHOGENESIS	1.36	0.89	0	0	0	not significant
11560	GO_CATALYTIC_ACTIVITY_ACTING_ON_A_GLYCOPROTEIN	1.36	0.89	0	0	0	not significant
11561	GO_PROTEIN_LIPID_COMPLEX	1.36	0.89	0	0	0	not significant
11562	GO_REPLICATIVE_SENESCENCE	1.36	0.89	0	0	0	not significant
11563	KYNG_DNA_DAMAGE_BY_4NQO_OR_GAMMA_RADIATION	1.36	0.89	0	0	0	not significant
11564	MARIADASON_RESPONSE_TO_BUTYRATE_CURCUMIN_SULINDAC_TSA_2	1.36	0.89	0	0	0	not significant
11565	TERAMOTO_OPN_TARGETS_CLUSTER_1	1.36	0.89	0	0	0	not significant
11566	FRASOR_RESPONSE_TO_ESTRADIOL_UP	1.36	0.88	0	0	0	not significant
11567	GO_EXTRACELLULAR_REGULATION_OF_SIGNAL_TRANSDUCTION	1.36	0.88	0	0	0	not significant
11568	GO_L_SERINE_METABOLIC_PROCESS	1.36	0.88	0	0	0	not significant
11569	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_MONOCYTE_UP	1.36	0.88	0	0	0	not significant
11570	GO_NEGATIVE_REGULATION_OF_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULU	1.36	0.87	0	0	0	not significant
11571	GO_REGULATION_OF_STEM_CELL_DIVISION	1.36	0.87	0	0	0	not significant
11572	GO_QUATERNARY_AMMONIUM_GROUP_TRANSPORT	1.36	0.86	0	0	0	not significant
11573	GO_NEGATIVE_REGULATION_OF_CHOLESTEROL_STORAGE	1.36	0.84	0	0	0	not significant
11574	GO_RESPONSE_TO_NITROGEN_COMPOUND	1.37	2.92	0	0	0	not significant
11575	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP	1.37	1.75	0	0	0	not significant
11576	GO_RECEPTOR_COMPLEX	1.37	1.71	0	0	0	not significant
11577	DOANE_RESPONSE_TO_ANDROGEN_DN	1.37	1.62	0	0	0	not significant
11578	KASLER_HDAC7_TARGETS_1_UP	1.37	1.59	0	0	0	not significant
11579	GO_GLYCOSYLATION	1.37	1.56	0	0	0	not significant
11580	LINDGREN_BLADDER_CANCER_CLUSTER_3_DN	1.37	1.52	0	0	0	not significant
11581	FOSTER_KDM1A_TARGETS_UP	1.37	1.37	0	0	0	not significant
11582	PID_CXCR4_PATHWAY	1.37	1.36	0	0	0	not significant
11583	GO_INTERLEUKIN_6_PRODUCTION	1.37	1.3	0	0	0	not significant
11584	GO_LIPID_STORAGE	1.37	1.26	0	0	0	not significant
11585	GO_CELLULAR_RESPONSE_TO_ANTIBIOTIC	1.37	1.24	0	0	0	not significant
11586	GO_LIPOPROTEIN_BIOSYNTHETIC_PROCESS	1.37	1.23	0	0	0	not significant
11587	GO_PHAGOCYTIC_VESICLE_MEMBRANE	1.37	1.21	0	0	0	not significant
11588	GO_RESPONSE_TO_CAMP	1.37	1.21	0	0	0	not significant
11589	NIELSEN_GIST	1.37	1.2	0	0	0	not significant
11590	ZHAN_MULTIPLE_MYELOMA_CD1_AND_CD2_UP	1.37	1.2	0	0	0	not significant
11591	GO_AMINOGLYCAN_METABOLIC_PROCESS	1.37	1.19	0	0	0	not significant
11592	HOSHIDA_LIVER_CANCER_SURVIVAL_DN	1.37	1.19	0	0	0	not significant
11593	ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION	1.37	1.19	0	0	0	not significant
11594	MCBRYAN_PUBERTAL_BREAST_5_6WK_UP	1.37	1.18	0	0	0	not significant
11595	SERVITJA_LIVER_HNF1A_TARGETS_DN	1.37	1.18	0	0	0	not significant
11596	RASHI_RESPONSE_TO_IONIZING_RADIATION_6	1.37	1.17	0	0	0	not significant
11597	GO_RESPONSE_TO_BMP	1.37	1.15	0	0	0	not significant
11598	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	1.37	1.14	0	0	0	not significant
11599	LAU_APOPTOSIS_CDKN2A_UP	1.37	1.13	0	0	0	not significant
11600	GO_POSITIVE_REGULATION_OF_B_CELL_ACTIVATION	1.37	1.09	0	0	0	not significant
11601	KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	1.37	1.09	0	0	0	not significant
11602	VANTVEER_BREAST_CANCER_METASTASIS_UP	1.37	1.07	0	0	0	not significant
11603	GO_FATTY_ACID_DERIVATIVE_BIOSYNTHETIC_PROCESS	1.37	1.04	0	0	0	not significant
11604	GO_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCTION	1.37	1.04	0	0	0	not significant
11605	WANG_METHYLATED_IN_BREAST_CANCER	1.37	1.02	0	0	0	not significant
11606	LIU_SMARCA4_TARGETS	1.37	1.01	0	0	0	not significant
11607	BIOCARTA_PDGF_PATHWAY	1.37	1	0	0	0	not significant
11608	REACTOME_COMPLEMENT_CASCADE	1.37	1	0	0	0	not significant
11609	REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	1.37	1	0	0	0	not significant
11610	BIOCARTA_IL6_PATHWAY	1.37	0.99	0	0	0	not significant
11611	LEE_AGING_MUSCLE_UP	1.37	0.99	0	0	0	not significant
11612	BIOCARTA_ARENRF2_PATHWAY	1.37	0.98	0	0	0	not significant
11613	GO_GOLGI_LUMEN	1.37	0.98	0	0	0	not significant
11614	REACTOME_NAPLUS_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPORTERS	1.37	0.98	0	0	0	not significant
11615	GO_CELLULAR_MODIFIED_AMINO_ACID_CATABOLIC_PROCESS	1.37	0.97	0	0	0	not significant
11616	GO_IMMATURE_B_CELL_DIFFERENTIATION	1.37	0.97	0	0	0	not significant
11617	GO_PROTEIN_DEMANNOSYLATION	1.37	0.97	0	0	0	not significant
11618	GO_EXOCRINE_SYSTEM_DEVELOPMENT	1.37	0.95	0	0	0	not significant
11619	GO_EXPORT_ACROSS_PLASMA_MEMBRANE	1.37	0.95	0	0	0	not significant
11620	GO_NEGATIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_PROLIFER	1.37	0.95	0	0	0	not significant
11621	GO_POSITIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	1.37	0.94	0	0	0	not significant
11622	SCHEIDEREIT_IKK_TARGETS	1.37	0.94	0	0	0	not significant
11623	GO_INHIBITORY_SYNAPSE_ASSEMBLY	1.37	0.93	0	0	0	not significant
11624	GO_DNA_DAMAGE_INDUCED_PROTEIN_PHOSPHORYLATION	1.37	0.92	0	0	0	not significant
11625	GO_MISMATCH_REPAIR_COMPLEX_BINDING	1.37	0.92	0	0	0	not significant
11626	GO_SULFOTRANSFERASE_ACTIVITY	1.37	0.92	0	0	0	not significant
11627	GO_CD8_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	1.37	0.91	0	0	0	not significant
11628	GO_GAMMA_SECRETASE_COMPLEX	1.37	0.91	0	0	0	not significant
11629	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5	1.37	0.91	0	0	0	not significant
11630	RICKMAN_HEAD_AND_NECK_CANCER_B	1.37	0.91	0	0	0	not significant
11631	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_GRANULOCYTE_U	1.37	0.91	0	0	0	not significant
11632	GO_MESODERMAL_CELL_FATE_COMMITMENT	1.37	0.9	0	0	0	not significant
11633	GO_MUTSALPHA_COMPLEX_BINDING	1.37	0.9	0	0	0	not significant
11634	SA_REG_CASCADE_OF_CYCLIN_EXPR	1.37	0.89	0	0	0	not significant
11635	GO_VOLTAGE_GATED_SODIUM_CHANNEL_ACTIVITY	1.37	0.88	0	0	0	not significant
11636	GO_PROTEIN_POLY_ADP_RIBOSYLATION	1.37	0.87	0	0	0	not significant
11637	REACTOME_REGULATED_PROTEOLYSIS_OF_P75NTR	1.37	0.87	0	0	0	not significant
11638	GO_NEGATIVE_REGULATION_OF_ANION_TRANSMEMBRANE_TRANSPORT	1.37	0.86	0	0	0	not significant
11639	GO_RESPONSE_TO_FUNGICIDE	1.37	0.84	0	0	0	not significant
11640	GO_INORGANIC_ION_TRANSMEMBRANE_TRANSPORT	1.38	2.31	0	0	0	not significant
11641	BENPORATH_SUZ12_TARGETS	1.38	2.07	0	0	0	not significant
11642	BROWNE_HCMV_INFECTION_48HR_DN	1.38	1.95	0	0	0	not significant
11643	BILD_HRAS_ONCOGENIC_SIGNATURE	1.38	1.65	0	0	0	not significant
11644	WANG_SMARCE1_TARGETS_UP	1.38	1.57	0	0	0	not significant
11645	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	1.38	1.56	0	0	0	not significant
11646	GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	1.38	1.53	0	0	0	not significant
11647	LANDIS_ERBB2_BREAST_TUMORS_324_UP	1.38	1.51	0	0	0	not significant
11648	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_WITH_H4K20ME1_MARK	1.38	1.51	0	0	0	not significant
11649	ATF2_S_UP.V1_DN	1.38	1.46	0	0	0	not significant
11650	STK33_SKM_DN	1.38	1.46	0	0	0	not significant
11651	GO_CARBOHYDRATE_BINDING	1.38	1.45	0	0	0	not significant

11652	GO_SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS	1.38	1.43	0	0	0	not significant
11653	AFFAR_YY1_TARGETS_UP	1.38	1.32	0	0	0	not significant
11654	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN	1.38	1.29	0	0	0	not significant
11655	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP	1.38	1.28	0	0	0	not significant
11656	BECKER_TAMOXIFEN_RESISTANCE_UP	1.38	1.17	0	0	0	not significant
11657	KRAS.LUNG.BREAST_UP.V1_UP	1.38	1.17	0	0	0	not significant
11658	LIU_TARGETS_OF_VMYB_VS_CMYB_DN	1.38	1.14	0	0	0	not significant
11659	GHANDHI_BYSTANDER_IRRADIATION_UP	1.38	1.13	0	0	0	not significant
11660	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP	1.38	1.13	0	0	0	not significant
11661	KRASNOSELSKAYA_ILF3_TARGETS_DN	1.38	1.12	0	0	0	not significant
11662	SMID_BREAST_CANCER_RELAPSE_IN_BONE_UP	1.38	1.1	0	0	0	not significant
11663	SERVITJA_ISLET_HNF1A_TARGETS_DN	1.38	1.09	0	0	0	not significant
11664	GO_MESENCHYMAL_CELL_PROLIFERATION	1.38	1.07	0	0	0	not significant
11665	URS_ADIPOCYTE_DIFFERENTIATION_UP	1.38	1.07	0	0	0	not significant
11666	GO_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	1.38	1.05	0	0	0	not significant
11667	GO_POSITIVE_REGULATION_OF_BONE_MINERALIZATION	1.38	1.03	0	0	0	not significant
11668	GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	1.38	1.02	0	0	0	not significant
11669	GO_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	1.38	1.01	0	0	0	not significant
11670	GO_SOLUTE_PROTON_SYMPORTER_ACTIVITY	1.38	1	0	0	0	not significant
11671	REACTOME_NOD1_2_SIGNALING_PATHWAY	1.38	1	0	0	0	not significant
11672	BIOCARTA_CARDIACEGF_PATHWAY	1.38	0.99	0	0	0	not significant
11673	DORN_ADENOVIRUS_INFECTION_48HR_DN	1.38	0.99	0	0	0	not significant
11674	GO_LEUKOCYTE_ACTIVATION_INVOLVED_IN_INFLAMMATORY_RESPONSE	1.38	0.99	0	0	0	not significant
11675	GO_SHORT_CHAIN_FATTY_ACID_CATABOLIC_PROCESS	1.38	0.99	0	0	0	not significant
11676	GO_VACUOLAR_PROTON_TRANSPORTING_V_TYPE_ATPASE_COMPLEX	1.38	0.99	0	0	0	not significant
11677	GO_BILE_ACID_METABOLIC_PROCESS	1.38	0.98	0	0	0	not significant
11678	GO_RENAL_SYSTEM_PROCESS_INVOLVED_IN_REGULATION_OF_SYSTEMIC_ARTE	1.38	0.98	0	0	0	not significant
11679	GO_RESPONSE_TO_INTERLEUKIN_15	1.38	0.98	0	0	0	not significant
11680	HUPER_BREAST_BASAL_VS_LUMINAL_UP	1.38	0.98	0	0	0	not significant
11681	NAKAJIMA_MAST_CELL	1.38	0.98	0	0	0	not significant
11682	PID_INTEGRIN_A9B1_PATHWAY	1.38	0.98	0	0	0	not significant
11683	BIOCARTA_TNFR2_PATHWAY	1.38	0.97	0	0	0	not significant
11684	GO_NEUTROPHIL_HOMEOSTASIS	1.38	0.97	0	0	0	not significant
11685	GO_POSITIVE_REGULATION_OF_T_CELL_MIGRATION	1.38	0.97	0	0	0	not significant
11686	GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	1.38	0.97	0	0	0	not significant
11687	GO_SODIUM_BICARBONATE_SYMPORTER_ACTIVITY	1.38	0.97	0	0	0	not significant
11688	GO_TOLL_LIKE_RECEPTOR_3_SIGNALING_PATHWAY	1.38	0.97	0	0	0	not significant
11689	REACTOME_DEFECTS_IN_COBALAMIN_B12_METABOLISM	1.38	0.97	0	0	0	not significant
11690	MEISSNER_NPC_HCP_WITH_H3K27ME3	1.38	0.96	0	0	0	not significant
11691	BIOCARTA_GRANULOCYTES_PATHWAY	1.38	0.95	0	0	0	not significant
11692	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN	1.38	0.95	0	0	0	not significant
11693	GO_NEGATIVE_REGULATION_OF_BEHAVIOR	1.38	0.95	0	0	0	not significant
11694	GO_NOTCH_RECEPTOR_PROCESSING_LIGAND_DEPENDENT	1.38	0.95	0	0	0	not significant
11695	GO_ORGAN_INDUCTION	1.38	0.95	0	0	0	not significant
11696	GO_POSITIVE_REGULATION_OF_HISTONE_H3_K9_ACETYLATION	1.38	0.95	0	0	0	not significant
11697	CHEMELLO_SOLEUS_VS_EDL_MYOFIBERS_UP	1.38	0.92	0	0	0	not significant
11698	GO_HIPPOCAMPAL_MOSSY_FIBER_TO_CA3_SYNAPSE	1.38	0.89	0	0	0	not significant
11699	GO_MAST_CELL_MIGRATION	1.38	0.89	0	0	0	not significant
11700	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_UP	1.38	0.88	0	0	0	not significant
11701	GO_GOLGI_MEMBRANE	1.39	4	0	0	0	not significant
11702	MTOR_UP.N4.V1_UP	1.39	2.02	0	0	0	not significant
11703	GO_RESPONSE_TO_TOXIC_SUBSTANCE	1.39	1.99	0	0	0	not significant
11704	GO_PLASMA_MEMBRANE_PROTEIN_COMPLEX	1.39	1.95	0	0	0	not significant
11705	GO_POSITIVE_REGULATION_OF_SECRETION	1.39	1.77	0	0	0	not significant
11706	GO_LIPID_LOCALIZATION	1.39	1.73	0	0	0	not significant
11707	RIGGI_EWING_SARCOMA_PROGENITOR_UP	1.39	1.71	0	0	0	not significant
11708	GO_TISSUE_MIGRATION	1.39	1.52	0	0	0	not significant
11709	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_UP	1.39	1.52	0	0	0	not significant
11710	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A4	1.39	1.52	0	0	0	not significant
11711	GO_CATION_CHANNEL_ACTIVITY	1.39	1.51	0	0	0	not significant
11712	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_ME	1.39	1.51	0	0	0	not significant
11713	RB_DN.V1_UP	1.39	1.46	0	0	0	not significant
11714	GO_RECOMBINATIONAL_REPAIR	1.39	1.44	0	0	0	not significant
11715	PTEN_DN.V2_DN	1.39	1.41	0	0	0	not significant
11716	HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_UP	1.39	1.33	0	0	0	not significant
11717	GO_UDP_GLYCOSYLTRANSFERASE_ACTIVITY	1.39	1.3	0	0	0	not significant
11718	GO_RESPONSE_TO_TYPE_I_INTERFERON	1.39	1.27	0	0	0	not significant
11719	GO_MYOTUBE_DIFFERENTIATION	1.39	1.26	0	0	0	not significant
11720	FERREIRA_EWINGS_SARCOMA_UNSTABLE_VS_STABLE_DN	1.39	1.24	0	0	0	not significant
11721	ROPERO_HDAC2_TARGETS	1.39	1.22	0	0	0	not significant
11722	GO_EAR_MORPHOGENESIS	1.39	1.21	0	0	0	not significant
11723	BROWNE_INTERFERON_RESPONSIVE_GENES	1.39	1.19	0	0	0	not significant
11724	CROMER_METASTASIS_UP	1.39	1.19	0	0	0	not significant
11725	GO_GLYCOLIPID_BIOSYNTHETIC_PROCESS	1.39	1.17	0	0	0	not significant
11726	GO_NUCLEAR_DNA_REPLICATION	1.39	1.17	0	0	0	not significant
11727	LEE_NEURAL_CREST_STEM_CELL_UP	1.39	1.15	0	0	0	not significant
11728	PEDERSEN_TARGETS_OF_611CTF_ISOFORM_OF_ERBB2	1.39	1.13	0	0	0	not significant
11729	GO_PEPTIDE_RECEPTOR_ACTIVITY	1.39	1.12	0	0	0	not significant
11730	GO_TELOMERE_MAINTENANCE_VIA_SEMI_CONSERVATIVE_REPLICATION	1.39	1.12	0	0	0	not significant
11731	REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	1.39	1.12	0	0	0	not significant
11732	GO_GLYCEROLIPID_CATABOLIC_PROCESS	1.39	1.11	0	0	0	not significant
11733	GEISS_RESPONSE_TO_DSRNA_UP	1.39	1.09	0	0	0	not significant
11734	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_TRANSPORT_	1.39	1.09	0	0	0	not significant
11735	GO_SULFUR_COMPOUND_CATABOLIC_PROCESS	1.39	1.07	0	0	0	not significant
11736	GO_NEGATIVE_REGULATION_OF_CHEMOKINE_PRODUCTION	1.39	1.05	0	0	0	not significant
11737	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTGREEN_DN	1.39	1.04	0	0	0	not significant
11738	REACTOME_ASSEMBLY_OF_ACTIVE_LPL_AND_LIPC_LIPASE_COMPLEXES	1.39	1.04	0	0	0	not significant
11739	REACTOME_DEFECTIVE_EXT2_CAUSES_EXOSTOSES_2	1.39	1.04	0	0	0	not significant
11740	GO_REELIN_MEDIATED_SIGNALING_PATHWAY	1.39	1.03	0	0	0	not significant
11741	GO_CD4_POSITIVE_OR_CD8_POSITIVE_ALPHA_BETA_T_CELL_LINEAGE_COMMITM	1.39	1.02	0	0	0	not significant
11742	GO_PHAGOCYTIC_CUP	1.39	1.02	0	0	0	not significant
11743	REACTOME_PLASMA_LIPOPROTEIN_REMODELING	1.39	1.02	0	0	0	not significant
11744	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN	1.39	1.01	0	0	0	not significant
11745	GO_INFLAMMATORY_RESPONSE_TO_WOUNDING	1.39	1.01	0	0	0	not significant
11746	GO_PRE_B_CELL_DIFFERENTIATION	1.39	1.01	0	0	0	not significant
11747	GO_POTASSIUM_CHLORIDE_SYMPORTER_ACTIVITY	1.39	1	0	0	0	not significant
11748	PID_UPA_UPAR_PATHWAY	1.39	1	0	0	0	not significant
11749	FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_DN	1.39	0.99	0	0	0	not significant
11750	GO_DNA_CLAMP_LOADER_ACTIVITY	1.39	0.99	0	0	0	not significant
11751	REACTOME_SIGNALING_BY_NODAL	1.39	0.99	0	0	0	not significant
11752	GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_	1.39	0.98	0	0	0	not significant
11753	GO_ORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.39	0.98	0	0	0	not significant
11754	GO_IMMUNOLOGICAL_MEMORY_FORMATION_PROCESS	1.39	0.97	0	0	0	not significant
11755	GO_NEGATIVE_REGULATION_OF_THYMOCYTE_APOPTOTIC_PROCESS	1.39	0.97	0	0	0	not significant
11756	GO_NEURON_PROJECTION_EXTENSION_INVOLVED_IN_NEURON_PROJECTION_GUID	1.39	0.97	0	0	0	not significant
11757	GO_PLASMA_MEMBRANE_PHOSPHOLIPID_SCRAMBLING	1.39	0.97	0	0	0	not significant
11758	GO_REGULATION_OF_INORGANIC_ANION_TRANSMEMBRANE_TRANSPORT	1.39	0.97	0	0	0	not significant
11759	GO_TETRAHYDROBIOPTERIN_BIOSYNTHETIC_PROCESS	1.39	0.95	0	0	0	not significant
11760	MAHADEVAN_RESPONSE_TO_MP470_DN	1.39	0.95	0	0	0	not significant

11761	DARWICHE_PAPILLOMA_RISK_HIGH_VS_LOW_UP	1.39	0.93	0	0	0	not significant
11762	GO_COBALAMIN_TRANSPORT	1.39	0.93	0	0	0	not significant
11763	GO_CARDIAC_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	1.39	0.92	0	0	0	not significant
11764	GO_POSITIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	1.39	0.92	0	0	0	not significant
11765	GO_LUNG_CELL_DIFFERENTIATION	1.39	0.91	0	0	0	not significant
11766	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_LIPID_ANTIGEN_VIA_MHC_CL	1.39	0.89	0	0	0	not significant
11767	GO_POLE_PLASM	1.39	0.85	0	0	0	not significant
11768	LEI_HOXC8_TARGETS_UP	1.39	0.84	0	0	0	not significant
11769	GO_CELLULAR_RESPONSE_TO_LIPID	1.40	2.21	0	0	0	not significant
11770	GOZGIT_ESR1_TARGETS_DN	1.40	2.03	0	0	0	not significant
11771	HALLMARK_ALLOGRAFT_REJECTION	1.40	1.7	0	0	0	not significant
11772	KIM_WT1_TARGETS_UP	1.40	1.7	0	0	0	not significant
11773	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP	1.40	1.7	0	0	0	not significant
11774	HALLMARK_HEME_METABOLISM	1.40	1.64	0	0	0	not significant
11775	HOXA9_DN.V1_UP	1.40	1.64	0	0	0	not significant
11776	HALLMARK_INTERFERON_GAMMA_RESPONSE	1.40	1.62	0	0	0	not significant
11777	GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	1.40	1.58	0	0	0	not significant
11778	GO_AZUROPHIL_GRANULE	1.40	1.53	0	0	0	not significant
11779	GO_RESPONSE_TO_ALCOHOL	1.40	1.5	0	0	0	not significant
11780	GO_PROTEIN_PROCESSING	1.40	1.48	0	0	0	not significant
11781	CHR16P11	1.40	1.44	0	0	0	not significant
11782	REACTOME_PI3K_AKT_SIGNALING_IN_CANCER	1.40	1.41	0	0	0	not significant
11783	JOHNSTONE_PARVB_TARGETS_2_UP	1.40	1.38	0	0	0	not significant
11784	HECKER_IFNB1_TARGETS	1.40	1.28	0	0	0	not significant
11785	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_UP	1.40	1.25	0	0	0	not significant
11786	FAELT_B_CLL_WITH_VH_REARRANGEMENTS_UP	1.40	1.24	0	0	0	not significant
11787	GO_CELLULAR_RESPONSE_TO_CORTICOSTEROID_STIMULUS	1.40	1.22	0	0	0	not significant
11788	GO_INTEGRIN_BINDING	1.40	1.22	0	0	0	not significant
11789	PENG_GLUTAMINE_DEPRIVATION_UP	1.40	1.22	0	0	0	not significant
11790	REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	1.40	1.22	0	0	0	not significant
11791	GO_ICOSANOID_METABOLIC_PROCESS	1.40	1.19	0	0	0	not significant
11792	FRASOR_RESPONSE_TO_ESTRADIOL_DN	1.40	1.18	0	0	0	not significant
11793	MAYBURD_RESPONSE_TO_L663536_UP	1.40	1.18	0	0	0	not significant
11794	GO_PROTEIN_ADP_RIBOSYLATION	1.40	1.15	0	0	0	not significant
11795	GO_UNSATURATED_FATTY_ACID_BIOSYNTHETIC_PROCESS	1.40	1.15	0	0	0	not significant
11796	GO_P38MAPK_CASCADE	1.40	1.11	0	0	0	not significant
11797	GO_ATP_GATED_ION_CHANNEL_ACTIVITY	1.40	1.1	0	0	0	not significant
11798	GO_CELL_VOLUME_HOMEOSTASIS	1.40	1.09	0	0	0	not significant
11799	GO_DOUBLE_STRAND_BREAK_REPAIR_VIA_SYNTHESIS_DEPENDENT_STRAND_ANN	1.40	1.09	0	0	0	not significant
11800	MIKKELSEN_MCV6_ICP_WITH_H3K27ME3	1.40	1.09	0	0	0	not significant
11801	GO_INTRINSIC_COMPONENT_OF_PRESYNAPTIC_MEMBRANE	1.40	1.08	0	0	0	not significant
11802	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	1.40	1.08	0	0	0	not significant
11803	REACTOME_HDR_THROUGH_SINGLE_STRAND_ANNEALING_SSA	1.40	1.08	0	0	0	not significant
11804	SHIN_B_CELL_LYMPHOMA_CLUSTER_2	1.40	1.07	0	0	0	not significant
11805	CHR6Q15	1.40	1.06	0	0	0	not significant
11806	GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	1.40	1.06	0	0	0	not significant
11807	GO_NOTCH_RECEPTOR_PROCESSING	1.40	1.06	0	0	0	not significant
11808	BERENJENO_TRANSFORMED_BY_RHOA_FOREVER_UP	1.40	1.04	0	0	0	not significant
11809	GO_ALANINE_TRANSPORT	1.40	1.04	0	0	0	not significant
11810	GO_POSITIVE_REGULATION_OF_FATTY_ACID_BETA_OXIDATION	1.40	1.04	0	0	0	not significant
11811	GO_TUMOR_NECROSIS_FACTOR_ACTIVATED_RECEPTOR_ACTIVITY	1.40	1.04	0	0	0	not significant
11812	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_DN	1.40	1.03	0	0	0	not significant
11813	GO_STRAND_INVASION	1.40	1.02	0	0	0	not significant
11814	REACTOME_SUMOYLATION_OF_IMMUNE_RESPONSE_PROTEINS	1.40	1.02	0	0	0	not significant
11815	GO_RESPONSE_TO_MUSCLE_STRETCH	1.40	1.01	0	0	0	not significant
11816	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_AMINO_ACYL_GROUPS	1.40	1.01	0	0	0	not significant
11817	GROSS_HYPOXIA_VIA_HIF1A_ONLY	1.40	1.01	0	0	0	not significant
11818	KIM_ALL_DISORDERS_CALB1_CORR_DN	1.40	1.01	0	0	0	not significant
11819	GO_MKS_COMPLEX	1.40	1	0	0	0	not significant
11820	GO_CELLULAR_RESPONSE_TO_MURAMYL_DIPEPTIDE	1.40	0.99	0	0	0	not significant
11821	GO_GALACTOSE_CATABOLIC_PROCESS_VIA_UDP_GALACTOSE	1.40	0.99	0	0	0	not significant
11822	NEWMAN_ERCC6_TARGETS_UP	1.40	0.99	0	0	0	not significant
11823	GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	1.40	0.98	0	0	0	not significant
11824	GO_DEATH_RECEPTOR_ACTIVITY	1.40	0.98	0	0	0	not significant
11825	GO_REGULATION_OF_EXCITATORY_SYNAPSE_ASSEMBLY	1.40	0.98	0	0	0	not significant
11826	GO_NEGATIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	1.40	0.96	0	0	0	not significant
11827	KIM_GLIS2_TARGETS_DN	1.40	0.94	0	0	0	not significant
11828	GO_SIGNAL_COMPLEX_ASSEMBLY	1.40	0.89	0	0	0	not significant
11829	GO_GOLGI_APPARATUS_PART	1.41	4	0	0	0	not significant
11830	GO_BLOOD_VESSEL_MORPHOGENESIS	1.41	2.42	0	0	0	not significant
11831	GO_CELLULAR_RESPONSE_TO_PEPTIDE	1.41	2.41	0	0	0	not significant
11832	GO_RESPONSE_TO_PEPTIDE	1.41	2.21	0	0	0	not significant
11833	GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	1.41	2.19	0	0	0	not significant
11834	BENPORATH_EED_TARGETS	1.41	2.02	0	0	0	not significant
11835	HADDAD_B_LYMPHOCYTE_PROGENITOR	1.41	1.86	0	0	0	not significant
11836	GO_REGULATION_OF_CELL_CELL_ADHESION	1.41	1.85	0	0	0	not significant
11837	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN	1.41	1.82	0	0	0	not significant
11838	IVANOVA_HEMATOPOIESIS_STEM_CELL	1.41	1.59	0	0	0	not significant
11839	GO_ALPHA_AMINO_ACID_METABOLIC_PROCESS	1.41	1.58	0	0	0	not significant
11840	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_DN	1.41	1.47	0	0	0	not significant
11841	GO_COLLAGEN_CONTAINING_EXTRACELLULAR_MATRIX	1.41	1.45	0	0	0	not significant
11842	GO_CELLULAR_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	1.41	1.39	0	0	0	not significant
11843	REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	1.41	1.37	0	0	0	not significant
11844	REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_	1.41	1.36	0	0	0	not significant
11845	BIOCARTA_IL2RB_PATHWAY	1.41	1.28	0	0	0	not significant
11846	GO_NEUTRAL_LIPID_METABOLIC_PROCESS	1.41	1.28	0	0	0	not significant
11847	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN	1.41	1.27	0	0	0	not significant
11848	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_UP	1.41	1.21	0	0	0	not significant
11849	REACTOME_REGULATION_OF_CHOLESTEROL_BIOSYNTHESIS_BY_SREBP_SREBF	1.41	1.2	0	0	0	not significant
11850	GO_ION_ANTIPORTER_ACTIVITY	1.41	1.15	0	0	0	not significant
11851	GO_POSITIVE_T_CELL_SELECTION	1.41	1.14	0	0	0	not significant
11852	GO_ADENYLATE_CYCLASE_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNA	1.41	1.13	0	0	0	not significant
11853	GO_EXTRACELLULAR_MATRIX_DISASSEMBLY	1.41	1.11	0	0	0	not significant
11854	GO_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	1.41	1.11	0	0	0	not significant
11855	GO_NEGATIVE_REGULATION_OF_T_CELL_PROLIFERATION	1.41	1.11	0	0	0	not significant
11856	GO_REGULATION_OF_CD40_SIGNALING_PATHWAY	1.41	1.11	0	0	0	not significant
11857	GO_RESPONSE_TO_ZINC_ION	1.41	1.11	0	0	0	not significant
11858	PID_IL23_PATHWAY	1.41	1.11	0	0	0	not significant
11859	REACTOME_INTERLEUKIN_15_SIGNALING	1.41	1.11	0	0	0	not significant
11860	VALK_AML_CLUSTER_12	1.41	1.1	0	0	0	not significant
11861	GO_NEUROTRANSMITTER_SODIUM_SYMPORTER_ACTIVITY	1.41	1.09	0	0	0	not significant
11862	GO_RECEPTOR_RECYCLING	1.41	1.09	0	0	0	not significant
11863	GO_3_5_EXODEOXYRIBONUCLEASE_ACTIVITY	1.41	1.08	0	0	0	not significant
11864	GO_REGULATION_OF_NEURON_PROJECTION_ARBORIZATION	1.41	1.08	0	0	0	not significant
11865	REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GOLGI	1.41	1.07	0	0	0	not significant
11866	REACTOME_SYNTHESIS_SECRETION_AND_DEACYLATION_OF_GHRELIN	1.41	1.07	0	0	0	not significant
11867	GO_INTERLEUKIN_12_SECRETION	1.41	1.06	0	0	0	not significant
11868	GO_NUCLEOTIDE_BINDING_OLIGOMERIZATION_DOMAIN_CONTAINING_2_SIGNALING_	1.41	1.06	0	0	0	not significant
11869	REACTOME_INTERLEUKIN_2_SIGNALING	1.41	1.06	0	0	0	not significant

11870	GO_NEGATIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	1.41	1.05	0	0	0	not significant
11871	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_SECRETION	1.41	1.05	0	0	0	not significant
11872	GO_POSITIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_2_SIGNALING_PATHWAY	1.41	1.05	0	0	0	not significant
11873	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GRO	1.41	1.05	0	0	0	not significant
11874	GO_SIGNAL_PEPTIDE_PROCESSING	1.41	1.04	0	0	0	not significant
11875	OUYANG_PROSTATE_CANCER_PROGRESSION_UP	1.41	1.04	0	0	0	not significant
11876	GO_RESPONSE_TO_IMMOBILIZATION_STRESS	1.41	1.03	0	0	0	not significant
11877	BIOCARTA_FBW7_PATHWAY	1.41	1.02	0	0	0	not significant
11878	GO_POSITIVE_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	1.41	1.02	0	0	0	not significant
11879	GO_REGULATION_OF_RENAL_SYSTEM_PROCESS	1.41	1.02	0	0	0	not significant
11880	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE	1.41	1.01	0	0	0	not significant
11881	GO_POSITIVE_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	1.41	1.01	0	0	0	not significant
11882	GO_NEGATIVE_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_R	1.41	1	0	0	0	not significant
11883	ZIRN_TRETINOIN_RESPONSE_UP	1.41	0.99	0	0	0	not significant
11884	GO_REGULATION_OF_T_HELPER_1_CELL_DIFFERENTIATION	1.41	0.98	0	0	0	not significant
11885	GO_DNA_REPLICATION_FACTOR_C_COMPLEX	1.41	0.97	0	0	0	not significant
11886	GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIM	1.41	0.97	0	0	0	not significant
11887	GO_POSITIVE_REGULATION_OF_VASOCONSTRICTION	1.41	0.97	0	0	0	not significant
11888	GO_INTRINSIC_COMPONENT_OF_VACUOLAR_MEMBRANE	1.41	0.96	0	0	0	not significant
11889	GO_NEURONAL_ACTION_POTENTIAL	1.41	0.96	0	0	0	not significant
11890	CAFFAREL_RESPONSE_TO_THC_8HR_5_UP	1.41	0.95	0	0	0	not significant
11891	DODD_NASOPHARYNGEAL_CARCINOMA_UP	1.42	4	0	0	0	not significant
11892	GO_TRANSPORTER_ACTIVITY	1.42	4	0	0	0	not significant
11893	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP	1.42	2.2	0	0	0	not significant
11894	GO_PEPTIDE_SECRETION	1.42	2.13	0	0	0	not significant
11895	GO_ORGANIC_ANION_TRANSPORT	1.42	2	0	0	0	not significant
11896	WANG_CISPLATIN_RESPONSE_AND_XPC_DN	1.42	1.97	0	0	0	not significant
11897	GO_EPITHELIAL_CELL_PROLIFERATION	1.42	1.77	0	0	0	not significant
11898	GO_CELLULAR_RESPONSE_TO_ACID_CHEMICAL	1.42	1.64	0	0	0	not significant
11899	CHR8Q24	1.42	1.59	0	0	0	not significant
11900	NRL_DN.V1_UP	1.42	1.57	0	0	0	not significant
11901	GO_RESPONSE_TO_KETONE	1.42	1.54	0	0	0	not significant
11902	ESC_J1_UP_EARLY.V1_DN	1.42	1.5	0	0	0	not significant
11903	GO_ORGANIC_HYDROXY_COMPOUND_TRANSPORT	1.42	1.48	0	0	0	not significant
11904	BASSO_CD40_SIGNALING_UP	1.42	1.33	0	0	0	not significant
11905	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP	1.42	1.33	0	0	0	not significant
11906	MEL18_DN.V1_DN	1.42	1.31	0	0	0	not significant
11907	GO_LIPOSACCHARIDE_METABOLIC_PROCESS	1.42	1.26	0	0	0	not significant
11908	HOELZEL_NF1_TARGETS_DN	1.42	1.26	0	0	0	not significant
11909	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP	1.42	1.22	0	0	0	not significant
11910	GO_POSITIVE_REGULATION_OF_FATTY_ACID_TRANSPORT	1.42	1.21	0	0	0	not significant
11911	OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_UP	1.42	1.21	0	0	0	not significant
11912	GO_POSITIVE_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	1.42	1.19	0	0	0	not significant
11913	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_CHEMOTAXIS	1.42	1.18	0	0	0	not significant
11914	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_DN	1.42	1.18	0	0	0	not significant
11915	GO_MODIFIED_AMINO_ACID_BINDING	1.42	1.17	0	0	0	not significant
11916	GO_DETECTION_OF_BIOTIC_STIMULUS	1.42	1.16	0	0	0	not significant
11917	GO_HISTONE_ACETYLTRANSFERASE_BINDING	1.42	1.16	0	0	0	not significant
11918	GO_NEUROTRANSMITTER_RECEPTOR_COMPLEX	1.42	1.16	0	0	0	not significant
11919	KASLER_HDAC7_TARGETS_2_DN	1.42	1.14	0	0	0	not significant
11920	GO_LONG_CHAIN_FATTY_ACID_IMPORT_ACROSS_PLASMA_MEMBRANE	1.42	1.13	0	0	0	not significant
11921	GO_PEPTIDYL_GLUTAMIC_ACID_MODIFICATION	1.42	1.13	0	0	0	not significant
11922	RAMASWAMY_METASTASIS_DN	1.42	1.13	0	0	0	not significant
11923	GO_CELL_CELL_ADHESION_MEDIATED_BY_INTEGRIN	1.42	1.12	0	0	0	not significant
11924	GO_CHEMOKINE_BINDING	1.42	1.12	0	0	0	not significant
11925	GO_RESPIRATORY_BURST_INVOLVED_IN_DEFENSE_RESPONSE	1.42	1.12	0	0	0	not significant
11926	GO_GLIAL_CELL_ACTIVATION	1.42	1.11	0	0	0	not significant
11927	GO_TOLL_LIKE_RECEPTOR_4_SIGNALING_PATHWAY	1.42	1.11	0	0	0	not significant
11928	GO_DOPAMINERGIC_SYNAPSE	1.42	1.1	0	0	0	not significant
11929	GO_INTEGRAL_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_ENDOPLASMIC_RETICU	1.42	1.1	0	0	0	not significant
11930	BIOCARTA_GLEEVEC_PATHWAY	1.42	1.09	0	0	0	not significant
11931	BIOCARTA_IL17_PATHWAY	1.42	1.08	0	0	0	not significant
11932	GO_AMIDINE_LYASE_ACTIVITY	1.42	1.08	0	0	0	not significant
11933	GO_T_HELPER_17_TYPE_IMMUNE_RESPONSE	1.42	1.08	0	0	0	not significant
11934	GO_PEPTIDE_ANTIGEN_BINDING	1.42	1.07	0	0	0	not significant
11935	GO_CTF18_RFC_LIKE_COMPLEX	1.42	1.06	0	0	0	not significant
11936	SABATES_COLORECTAL_ADENOMA_SIZE_UP	1.42	1.06	0	0	0	not significant
11937	GO_CELLULAR_RESPONSE_TO_INTERFERON_ALPHA	1.42	1.05	0	0	0	not significant
11938	GO_NEGATIVE_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_P	1.42	1.05	0	0	0	not significant
11939	GO_NEUTROPHIL_APOPTOTIC_PROCESS	1.42	1.05	0	0	0	not significant
11940	GO_ASPARTATE_METABOLIC_PROCESS	1.42	1.04	0	0	0	not significant
11941	KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	1.42	1.04	0	0	0	not significant
11942	GO_REGULATION_OF_PROTEIN_KINASE_C_SIGNALING	1.42	1.02	0	0	0	not significant
11943	GO_POSITIVE_REGULATION_OF_REGULATORY_T_CELL_DIFFERENTIATION	1.42	1	0	0	0	not significant
11944	PID_VEGF_VEGFR_PATHWAY	1.42	0.99	0	0	0	not significant
11945	GO_LUTEINIZATION	1.42	0.96	0	0	0	not significant
11946	GO_RESPONSE_TO_HYDROXYUREA	1.42	0.96	0	0	0	not significant
11947	REACTOME_UREA_CYCLE	1.42	0.95	0	0	0	not significant
11948	GO_NEGATIVE_REGULATION_OF_CAMP_MEDIATED_SIGNALING	1.42	0.94	0	0	0	not significant
11949	GO_CELL_CELL_ADHESION	1.43	4	0	0	0	not significant
11950	GO_CELLULAR_LIPID_METABOLIC_PROCESS	1.43	4	0	0	0	not significant
11951	GO_DEFENSE_RESPONSE	1.43	4	0	0	0	not significant
11952	GO_DNA_BINDING_TRANSCRIPTION_ACTIVATOR_ACTIVITY	1.43	4	0	0	0	not significant
11953	GO_GOLGI_APPARATUS	1.43	4	0	0	0	not significant
11954	GO_IMMUNE_EFFECTOR_PROCESS	1.43	4	0	0	0	not significant
11955	MITSIADES_RESPONSE_TO_APLIDIN_UP	1.43	2.9	0	0	0	not significant
11956	GO_RESPONSE_TO_STEROID_HORMONE	1.43	2.41	0	0	0	not significant
11957	GO_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	1.43	2.23	0	0	0	not significant
11958	HAN_SATB1_TARGETS_UP	1.43	2.12	0	0	0	not significant
11959	GO_LATE_ENDOSOME	1.43	2.04	0	0	0	not significant
11960	RUTELLA_RESPONSE_TO_HGF_DN	1.43	1.98	0	0	0	not significant
11961	GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	1.43	1.79	0	0	0	not significant
11962	NIKOLSKY_BREAST_CANCER_8Q23_Q24_AMPLICON	1.43	1.66	0	0	0	not significant
11963	GO_RESPONSE_TO_INTERFERON_GAMMA	1.43	1.65	0	0	0	not significant
11964	CHICAS_RB1_TARGETS_LOW_SERUM	1.43	1.55	0	0	0	not significant
11965	GO_FATTY_ACID_BIOSYNTHETIC_PROCESS	1.43	1.54	0	0	0	not significant
11966	HALLMARK_KRAS_SIGNALING_UP	1.43	1.52	0	0	0	not significant
11967	GO_RESPONSE_TO_PURINE_CONTAINING_COMPOUND	1.43	1.49	0	0	0	not significant
11968	RODRIGUES_DCC_TARGETS_DN	1.43	1.49	0	0	0	not significant
11969	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	1.43	1.47	0	0	0	not significant
11970	P53_DN.V1_DN	1.43	1.42	0	0	0	not significant
11971	GO_CELL_CYCLE_DNA_REPLICATION	1.43	1.41	0	0	0	not significant
11972	REACTOME_BASE_EXCISION_REPAIR	1.43	1.4	0	0	0	not significant
11973	GO_IMPORT_ACROSS_PLASMA_MEMBRANE	1.43	1.34	0	0	0	not significant
11974	NABA_ECM_GLYCOPROTEINS	1.43	1.34	0	0	0	not significant
11975	REACTOME_ACTIVATION_OF_GENE_EXPRESSION_BY_SREBF_SREBP	1.43	1.34	0	0	0	not significant
11976	GO_DEACETYLASE_ACTIVITY	1.43	1.32	0	0	0	not significant
11977	GO_ASPARTIC_ENDOPEPTIDASE_ACTIVITY_INTRAMEMBRANE_CLEAVING	1.43	1.27	0	0	0	not significant
11978	HOWLIN_PUBERTAL_MAMMARY_GLAND	1.43	1.26	0	0	0	not significant

11979	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN	1.43	1.26	0	0	0	not significant
11980	XU_RESPONSE_TO_TRETINOIN_UP	1.43	1.25	0	0	0	not significant
11981	GO_ALPHA_AMINO_ACID_BIOSYNTHETIC_PROCESS	1.43	1.22	0	0	0	not significant
11982	GO_REGULATION_OF_RETROGRADE_PROTEIN_TRANSPORT_ER_TO_CYTOSOL	1.43	1.21	0	0	0	not significant
11983	GO_TRANSCRIPTION_FACTOR_AP_1_COMPLEX	1.43	1.2	0	0	0	not significant
11984	GO_NARROW_PORE_CHANNEL_ACTIVITY	1.43	1.19	0	0	0	not significant
11985	GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	1.43	1.18	0	0	0	not significant
11986	PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP	1.43	1.18	0	0	0	not significant
11987	PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_UP	1.43	1.18	0	0	0	not significant
11988	FOURNIER_ACINAR_DEVELOPMENT_EARLY_DN	1.43	1.16	0	0	0	not significant
11989	GO_REGULATORY_T_CELL_DIFFERENTIATION	1.43	1.16	0	0	0	not significant
11990	GO_UREA_CYCLE	1.43	1.16	0	0	0	not significant
11991	BIOCARTA_SKP2E2F_PATHWAY	1.43	1.14	0	0	0	not significant
11992	GO_MYOBLAST_FUSION	1.43	1.12	0	0	0	not significant
11993	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_1	1.43	1.12	0	0	0	not significant
11994	REACTOME_CDC6_ASSOCIATION_WITH_THE_ORC:ORIGIN_COMPLEX	1.43	1.12	0	0	0	not significant
11995	GO_REGULATION_OF_ENDOTHELIAL_CELL_CHEMOTAXIS	1.43	1.11	0	0	0	not significant
11996	GO_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_ENDOPLASMIC_RETICULU	1.43	1.1	0	0	0	not significant
11997	GERHOLD_RESPONSE_TO_TZD_DN	1.43	1.09	0	0	0	not significant
11998	GO_MANNOSYL_OLIGOSACCHARIDE_MANNOSIDASE_ACTIVITY	1.43	1.09	0	0	0	not significant
11999	GO_RESPONSE_TO_VITAMIN_E	1.43	1.09	0	0	0	not significant
12000	SA_B_CELL_RECEPTOR_COMPLEXES	1.43	1.08	0	0	0	not significant
12001	LU_TUMOR_ANGIOGENESIS_UP	1.43	1.07	0	0	0	not significant
12002	GO_C21_STEROID_HORMONE_BIOSYNTHETIC_PROCESS	1.43	1.06	0	0	0	not significant
12003	REACTOME_MET_ACTIVATES_PTK2_SIGNALING	1.43	1.06	0	0	0	not significant
12004	UROSEVIC_RESPONSE_TO_IMIQUIMOD	1.43	1.06	0	0	0	not significant
12005	RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_SMAD4_UP	1.43	1.05	0	0	0	not significant
12006	GO_NEGATIVE_REGULATION_OF_STEROID_METABOLIC_PROCESS	1.43	1.03	0	0	0	not significant
12007	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_DN	1.43	1.01	0	0	0	not significant
12008	GO_MEMBRANE_RAFT_LOCALIZATION	1.43	0.99	0	0	0	not significant
12009	GO_REGULATION_OF_ICOSANOID_SECRETION	1.43	0.99	0	0	0	not significant
12010	GO_BEHAVIOR	1.44	2.88	0	0	0	not significant
12011	MIKKELSEN_ES_ICP_WITH_H3K4ME3	1.44	2.43	0	0	0	not significant
12012	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP	1.44	2.29	0	0	0	not significant
12013	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	1.44	2.09	0	0	0	not significant
12014	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP	1.44	1.92	0	0	0	not significant
12015	GO_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	1.44	1.82	0	0	0	not significant
12016	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_DN	1.44	1.74	0	0	0	not significant
12017	GO_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATO	1.44	1.66	0	0	0	not significant
12018	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP	1.44	1.59	0	0	0	not significant
12019	GO_LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	1.44	1.49	0	0	0	not significant
12020	MORI_SMALL_PRE_BII_LYMPHOCYTE_UP	1.44	1.42	0	0	0	not significant
12021	KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	1.44	1.4	0	0	0	not significant
12022	AMIT_EGF_RESPONSE_240_HELA	1.44	1.37	0	0	0	not significant
12023	GO_CELLULAR_RESPONSE_TO_KETONE	1.44	1.35	0	0	0	not significant
12024	HILLION_HMGA1B_TARGETS	1.44	1.31	0	0	0	not significant
12025	KLEIN_TARGETS_OF_BCR_ABL1_FUSION	1.44	1.26	0	0	0	not significant
12026	GO_PROTEIN_TRIMERIZATION	1.44	1.25	0	0	0	not significant
12027	BIOCARTA_ERAD_PATHWAY	1.44	1.24	0	0	0	not significant
12028	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PR	1.44	1.23	0	0	0	not significant
12029	KEGG_PRIMARY_IMMUNODEFICIENCY	1.44	1.22	0	0	0	not significant
12030	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	1.44	1.21	0	0	0	not significant
12031	GO_COMMISSURAL_NEURON_AXON_GUIDANCE	1.44	1.19	0	0	0	not significant
12032	GO_MULTIVESICULAR_BODY	1.44	1.19	0	0	0	not significant
12033	HOEGERKORP_CD44_TARGETS_TEMPORAL_UP	1.44	1.19	0	0	0	not significant
12034	GO_LEUKOCYTE_ADHESION_TO_VASCULAR_ENDOTHELIAL_CELL	1.44	1.18	0	0	0	not significant
12035	GO_MISMATCH_REPAIR	1.44	1.18	0	0	0	not significant
12036	GO_ORGANIC_CATION_TRANSPORT	1.44	1.18	0	0	0	not significant
12037	GO_REGULATION_OF_AXON_GUIDANCE	1.44	1.17	0	0	0	not significant
12038	GO_TERPENOID_BIOSYNTHETIC_PROCESS	1.44	1.16	0	0	0	not significant
12039	GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_UP	1.44	1.16	0	0	0	not significant
12040	REACTOME_DSCAM_INTERACTIONS	1.44	1.16	0	0	0	not significant
12041	GO_POTASSIUM_ION_EXPORT_ACROSS_PLASMA_MEMBRANE	1.44	1.15	0	0	0	not significant
12042	PID_PRL_SIGNALING_EVENTS_PATHWAY	1.44	1.15	0	0	0	not significant
12043	GO_BONE_MATURATION	1.44	1.14	0	0	0	not significant
12044	GO_GLYCEROPHOSPHOLIPID_CATABOLIC_PROCESS	1.44	1.14	0	0	0	not significant
12045	GO_PHOSPHATIDIC_ACID_BINDING	1.44	1.14	0	0	0	not significant
12046	TURJANSKI_MAPK7_TARGETS	1.44	1.14	0	0	0	not significant
12047	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BROWN_UP	1.44	1.13	0	0	0	not significant
12048	KRAS.50_UP.V1_DN	1.44	1.13	0	0	0	not significant
12049	GO_ACROSOME_REACTION	1.44	1.12	0	0	0	not significant
12050	NAKAYAMA_FGF2_TARGETS	1.44	1.12	0	0	0	not significant
12051	REACTOME_NEUROTOXICITY_OF_CLOSTRIDIUM_TOXINS	1.44	1.12	0	0	0	not significant
12052	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_DN	1.44	1.12	0	0	0	not significant
12053	NIELSEN_SYNOVIAL_SARCOMA_DN	1.44	1.11	0	0	0	not significant
12054	GO_REGULATION_OF_HISTONE_H3_K9_ACETYLATION	1.44	1.1	0	0	0	not significant
12055	GO_REGULATION_OF_FATTY_ACID_TRANSPORT	1.44	1.09	0	0	0	not significant
12056	GO_SERINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	1.44	1.09	0	0	0	not significant
12057	KYNG_DNA_DAMAGE_BY_4NQO	1.44	1.09	0	0	0	not significant
12058	REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	1.44	1.09	0	0	0	not significant
12059	GO_GOLGI_TRANS_CISTERNA	1.44	1.08	0	0	0	not significant
12060	GO_GLUTATHIONE_PEROXIDASE_ACTIVITY	1.44	1.06	0	0	0	not significant
12061	GO_HISTONE_H3_K9_ACETYLATION	1.44	1.06	0	0	0	not significant
12062	GO_POSITIVE_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANG	1.44	1.05	0	0	0	not significant
12063	GO_AMYLOID_PRECURSOR_PROTEIN_BIOSYNTHETIC_PROCESS	1.44	1.03	0	0	0	not significant
12064	GO_LEUKOTRIENE_METABOLIC_PROCESS	1.44	0.99	0	0	0	not significant
12065	GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	1.45	4	0	0	0	not significant
12066	GO_RESPONSE_TO_LIPID	1.45	4	0	0	0	not significant
12067	HOXA9_DN.V1_DN	1.45	2.17	0	0	0	not significant
12068	DANG_REGULATED_BY_MYC_DN	1.45	2.02	0	0	0	not significant
12069	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP	1.45	1.91	0	0	0	not significant
12070	LIU_VMYB_TARGETS_UP	1.45	1.71	0	0	0	not significant
12071	MIKKELSEN_IPS_LCP_WITH_H3K4ME3	1.45	1.66	0	0	0	not significant
12072	HOSHIDA_LIVER_CANCER_SUBCLASS_S3	1.45	1.65	0	0	0	not significant
12073	GO_MONOCARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	1.45	1.64	0	0	0	not significant
12074	GO_REGULATION_OF_PH	1.45	1.53	0	0	0	not significant
12075	CHR1Q23	1.45	1.49	0	0	0	not significant
12076	GO_ACETYLGLUCOSAMINYLTRANSFERASE_ACTIVITY	1.45	1.42	0	0	0	not significant
12077	REACTOME_HOMOLOGOUS_DNA_PAIRING_AND_STRAND_EXCHANGE	1.45	1.41	0	0	0	not significant
12078	PID_FANCONI_PATHWAY	1.45	1.36	0	0	0	not significant
12079	GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_G1_S_TRANSITION_OF_MITO	1.45	1.35	0	0	0	not significant
12080	GO_NADP_BINDING	1.45	1.34	0	0	0	not significant
12081	GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTI	1.45	1.3	0	0	0	not significant
12082	GO_CELLULAR_RESPONSE_TO_CALCIUM_ION	1.45	1.29	0	0	0	not significant
12083	GO_ORGANIC_ACID_SODIUM_SYMPORTER_ACTIVITY	1.45	1.29	0	0	0	not significant
12084	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP	1.45	1.28	0	0	0	not significant
12085	GO_PHOSPHOLIPASE_ACTIVITY	1.45	1.28	0	0	0	not significant
12086	GO_POSITIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	1.45	1.27	0	0	0	not significant
12087	GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_HOMOLOGOUS_REC	1.45	1.27	0	0	0	not significant

12088	GO_PHOSPHOLIPASE_A2_ACTIVITY	1.45	1.25	0	0	0	not significant
12089	MEISSNER_BRAIN_HCP_WITH_H3K4ME2_AND_H3K27ME3	1.45	1.24	0	0	0	not significant
12090	GO_FOUR_WAY_JUNCTION_HELICASE_ACTIVITY	1.45	1.23	0	0	0	not significant
12091	GO_FEEDING_BEHAVIOR	1.45	1.22	0	0	0	not significant
12092	GO_EPITHELIAL_CELL_MATURATION	1.45	1.21	0	0	0	not significant
12093	GO_INTRINSIC_COMPONENT_OF_SYNAPTIC_VESICLE_MEMBRANE	1.45	1.21	0	0	0	not significant
12094	JEPSEN_SMRT_TARGETS	1.45	1.21	0	0	0	not significant
12095	KRIEG_HYPOXIA_VIA_KDM3A	1.45	1.21	0	0	0	not significant
12096	ZAIDI_OSTEOBLAST_TRANSCRIPTION_FACTORS	1.45	1.2	0	0	0	not significant
12097	GO_NEPHRIC_DUCT_MORPHOGENESIS	1.45	1.19	0	0	0	not significant
12098	TAKADA_GASTRIC_CANCER_COPY_NUMBER_DN	1.45	1.19	0	0	0	not significant
12099	GO_COBALAMIN_METABOLIC_PROCESS	1.45	1.17	0	0	0	not significant
12100	GO_RESPONSE_TO_AMINE	1.45	1.17	0	0	0	not significant
12101	GO_CAMP_RESPONSE_ELEMENT_BINDING	1.45	1.16	0	0	0	not significant
12102	GO_CELLULAR_RESPONSE_TO_GROWTH_HORMONE_STIMULUS	1.45	1.16	0	0	0	not significant
12103	GO_ENDOPLASMIC_RETICULUM_MANNOSE_TRIMMING	1.45	1.16	0	0	0	not significant
12104	GO_POTASSIUM_ION_HOMEOSTASIS	1.45	1.16	0	0	0	not significant
12105	NOJIMA_SFRP2_TARGETS_DN	1.45	1.15	0	0	0	not significant
12106	REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG_	1.45	1.15	0	0	0	not significant
12107	MAHADEVAN_RESPONSE_TO_MP470_UP	1.45	1.14	0	0	0	not significant
12108	GO_N_GLYCAN_PROCESSING	1.45	1.13	0	0	0	not significant
12109	ODONNELL_METASTASIS_DN	1.45	1.13	0	0	0	not significant
12110	BIOCARTA_DREAM_PATHWAY	1.45	1.12	0	0	0	not significant
12111	GO_REGULATION_OF_MICROTUBULE_BASED_MOVEMENT	1.45	1.12	0	0	0	not significant
12112	MATHEW_FANCONI_ANEMIA_GENES	1.45	1.12	0	0	0	not significant
12113	MATZUK_CENTRAL_FOR_FEMALE_FERTILITY	1.45	1.12	0	0	0	not significant
12114	GO_SULFUR_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.45	1.11	0	0	0	not significant
12115	GO_NEGATIVE_REGULATION_OF_PROTEIN_MATURATION	1.45	1.08	0	0	0	not significant
12116	GO_ION_TRANSMEMBRANE_TRANSPORT	1.46	4	0	0	0	not significant
12117	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP	1.46	4	0	0	0	not significant
12118	MILI_PSEUDOPODIA_CHEMOTAXIS_DN	1.46	4	0	0	0	not significant
12119	THUM_SYSTOLIC_HEART_FAILURE_UP	1.46	2.6	0	0	0	not significant
12120	GO_MONOVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVI	1.46	2.25	0	0	0	not significant
12121	GO_COGNITION	1.46	2.16	0	0	0	not significant
12122	GO_LEUKOCYTE_CELL_CELL_ADHESION	1.46	2.11	0	0	0	not significant
12123	BOQUEST_STEM_CELL_DN	1.46	1.81	0	0	0	not significant
12124	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN	1.46	1.74	0	0	0	not significant
12125	RELA_DN.V1_UP	1.46	1.74	0	0	0	not significant
12126	GO_REGULATION_OF_T_CELL_DIFFERENTIATION	1.46	1.72	0	0	0	not significant
12127	PYEON_HPV_POSITIVE_TUMORS_UP	1.46	1.68	0	0	0	not significant
12128	AMBROSINI_FLAVOPIRIDOL_TREATMENT_TP53	1.46	1.55	0	0	0	not significant
12129	REACTOME_HDR_THROUGH_HOMOLOGOUS_RECOMBINATION_HRR	1.46	1.54	0	0	0	not significant
12130	REACTOME_POST_TRANSLATIONAL_MODIFICATION:_SYNTHESIS_OF_GPI_ANCHOR	1.46	1.51	0	0	0	not significant
12131	GO_ASSOCIATIVE_LEARNING	1.46	1.49	0	0	0	not significant
12132	GO_CELLULAR_RESPONSE_TO_ALCOHOL	1.46	1.45	0	0	0	not significant
12133	GO_MEMORY	1.46	1.44	0	0	0	not significant
12134	GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	1.46	1.44	0	0	0	not significant
12135	GO_CARBOHYDRATE_DERIVATIVE_TRANSPORT	1.46	1.38	0	0	0	not significant
12136	GO_AMYLOID_BETA_BINDING	1.46	1.35	0	0	0	not significant
12137	KEGG_ECM_RECEPTOR_INTERACTION	1.46	1.35	0	0	0	not significant
12138	GO_POSITIVE_REGULATION_OF_CHEMOKINE_BIOSYNTHETIC_PROCESS	1.46	1.34	0	0	0	not significant
12139	GO_PROTEIN_KINASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALI	1.46	1.34	0	0	0	not significant
12140	CHR6P12	1.46	1.32	0	0	0	not significant
12141	HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_UP	1.46	1.32	0	0	0	not significant
12142	REACTOME_P2Y_RECEPTORS	1.46	1.32	0	0	0	not significant
12143	AMIT_EGF_RESPONSE_60_MCF10A	1.46	1.31	0	0	0	not significant
12144	GO_POSITIVE_REGULATION_OF_AMYLOID_BETA_CLEARANCE	1.46	1.3	0	0	0	not significant
12145	MCCLUNG_COCAIN_REWARD_4WK	1.46	1.3	0	0	0	not significant
12146	GO_INTERLEUKIN_13_SECRETION	1.46	1.29	0	0	0	not significant
12147	GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_GAP_FILLING	1.46	1.29	0	0	0	not significant
12148	GO_CELL_MIGRATION_INVOLVED_IN_HEART_DEVELOPMENT	1.46	1.27	0	0	0	not significant
12149	CHESLER_BRAIN_HIGHEST_EXPRESSION	1.46	1.26	0	0	0	not significant
12150	GO_OLIGOPEPTIDE_TRANSPORT	1.46	1.26	0	0	0	not significant
12151	PID_FGF_PATHWAY	1.46	1.26	0	0	0	not significant
12152	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	1.46	1.25	0	0	0	not significant
12153	MMS_MOUSE_LYMPH_HIGH_4HRS_UP	1.46	1.24	0	0	0	not significant
12154	GO_NEGATIVE_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPROUTING_AN	1.46	1.23	0	0	0	not significant
12155	GO_NUCLEAR_MEMBRANE_PART	1.46	1.23	0	0	0	not significant
12156	GO_POTASSIUM_ION_LEAK_CHANNEL_ACTIVITY	1.46	1.22	0	0	0	not significant
12157	GO_HISTONE_DEACETYLASE_ACTIVITY_H3_K14_SPECIFIC_	1.46	1.21	0	0	0	not significant
12158	GO_MODULATION_OF_GROWTH_OF_SYMBIONT_INVOLVED_IN_INTERACTION_WITH	1.46	1.21	0	0	0	not significant
12159	REACTOME_CONSTITUTIVE_SIGNALING_BY_AKT1_E17K_IN_CANCER	1.46	1.21	0	0	0	not significant
12160	GO_DNA_REPLICATION_CHECKPOINT	1.46	1.2	0	0	0	not significant
12161	GO_IONOTROPIC_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	1.46	1.2	0	0	0	not significant
12162	KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	1.46	1.2	0	0	0	not significant
12163	CHR7P12	1.46	1.18	0	0	0	not significant
12164	GO_CARBON_SULFUR_LYASE_ACTIVITY	1.46	1.18	0	0	0	not significant
12165	GO_CLATHRIN_SCULPTED_VESICLE	1.46	1.18	0	0	0	not significant
12166	GO_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_	1.46	1.18	0	0	0	not significant
12167	GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	1.46	1.16	0	0	0	not significant
12168	GO_VENTRAL_SPINAL_CORD_DEVELOPMENT	1.46	1.16	0	0	0	not significant
12169	REACTOME_SYNTHESIS_OF_LEUKOTRIENES_LT_AND_EOXINS_EX	1.46	1.16	0	0	0	not significant
12170	DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN	1.46	1.15	0	0	0	not significant
12171	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	1.46	1.15	0	0	0	not significant
12172	GO_ISOTYPE_SWITCHING_TO_IGG_ISOTYPES	1.46	1.14	0	0	0	not significant
12173	RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP	1.46	1.14	0	0	0	not significant
12174	POS_RESPONSE_TO_HISTAMINE_DN	1.46	1.08	0	0	0	not significant
12175	GO_CELL_ACTIVATION	1.47	4	0	0	0	not significant
12176	GO_LIPID_METABOLIC_PROCESS	1.47	4	0	0	0	not significant
12177	GO_LIPID_BIOSYNTHETIC_PROCESS	1.47	2.9	0	0	0	not significant
12178	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_DN	1.47	2.86	0	0	0	not significant
12179	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN	1.47	2.31	0	0	0	not significant
12180	STK33_NOMO_DN	1.47	2.28	0	0	0	not significant
12181	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_UP	1.47	2.16	0	0	0	not significant
12182	MULLIGHAN_MLL_SIGNATURE_1_DN	1.47	2.02	0	0	0	not significant
12183	GO_POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	1.47	1.83	0	0	0	not significant
12184	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	1.47	1.83	0	0	0	not significant
12185	CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_DN	1.47	1.73	0	0	0	not significant
12186	GO_REGULATION_OF_LEUKOCYTE_MIGRATION	1.47	1.72	0	0	0	not significant
12187	HOLLERN_EMT_BREAST_TUMOR_UP	1.47	1.71	0	0	0	not significant
12188	GO_MAINTENANCE_OF_PROTEIN_LOCATION	1.47	1.69	0	0	0	not significant
12189	GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	1.47	1.65	0	0	0	not significant
12190	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	1.47	1.62	0	0	0	not significant
12191	GO_ARGININE_TRANSMEMBRANE_TRANSPORT	1.47	1.6	0	0	0	not significant
12192	GO_VOLTAGE_GATED_ION_CHANNEL_ACTIVITY	1.47	1.57	0	0	0	not significant
12193	CHR15Q26	1.47	1.52	0	0	0	not significant
12194	GO_MIDGUT_DEVELOPMENT	1.47	1.48	0	0	0	not significant
12195	GO_FATTY_ACID_DERIVATIVE_TRANSPORT	1.47	1.41	0	0	0	not significant
12196	MAHAJAN_RESPONSE_TO_IL1A_UP	1.47	1.39	0	0	0	not significant

12197	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_UP	1.47	1.39	0	0	0	not significant
12198	LEE_LIVER_CANCER_E2F1_UP	1.47	1.36	0	0	0	not significant
12199	GO_HEXOSAMINIDASE_ACTIVITY	1.47	1.35	0	0	0	not significant
12200	GO_AMINO_ACID_BINDING	1.47	1.34	0	0	0	not significant
12201	GO_L_ALPHA_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	1.47	1.34	0	0	0	not significant
12202	PID_S1P_S1P2_PATHWAY	1.47	1.34	0	0	0	not significant
12203	REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND	1.47	1.33	0	0	0	not significant
12204	GO_RESPONSE_TO_INTERLEUKIN_7	1.47	1.32	0	0	0	not significant
12205	GO_NUCLEAR_ENVELOPE_LUMEN	1.47	1.31	0	0	0	not significant
12206	MEDINA_SMARCA4_TARGETS	1.47	1.31	0	0	0	not significant
12207	GO_O_ACETYLTRANSFERASE_ACTIVITY	1.47	1.3	0	0	0	not significant
12208	MURAKAMI_UV_RESPONSE_24HR	1.47	1.3	0	0	0	not significant
12209	GO_ISOPRENOID_BIOSYNTHETIC_PROCESS	1.47	1.29	0	0	0	not significant
12210	BIOCARTA_ATRBRCA_PATHWAY	1.47	1.28	0	0	0	not significant
12211	LEIN_CHOROID_PLEXUS_MARKERS	1.47	1.28	0	0	0	not significant
12212	HUPER_BREAST_BASAL_VS_LUMINAL_DN	1.47	1.27	0	0	0	not significant
12213	REACTOME_BICARBONATE_TRANSPORTERS	1.47	1.26	0	0	0	not significant
12214	GO_FANCONI_ANAEMIA_NUCLEAR_COMPLEX	1.47	1.25	0	0	0	not significant
12215	GO_EXTRINSIC_COMPONENT_OF_ENDOSOME_MEMBRANE	1.47	1.24	0	0	0	not significant
12216	GO_PEPTIDE_CROSS_LINKING	1.47	1.24	0	0	0	not significant
12217	GO_VOLTAGE_GATED_CHLORIDE_CHANNEL_ACTIVITY	1.47	1.23	0	0	0	not significant
12218	REACTOME_METABOLISM_OF_FAT_SOLUBLE_VITAMINS	1.47	1.23	0	0	0	not significant
12219	GO_CATION_CHLORIDE_SYMPORTER_ACTIVITY	1.47	1.22	0	0	0	not significant
12220	GESERICK_TERT_TARGETS_DN	1.47	1.21	0	0	0	not significant
12221	GO_NEGATIVE_REGULATION_OF_GLYCOPROTEIN_BIOSYNTHETIC_PROCESS	1.47	1.21	0	0	0	not significant
12222	GO_R_SMAD_BINDING	1.47	1.21	0	0	0	not significant
12223	KIM_PTEN_TARGETS_UP	1.47	1.19	0	0	0	not significant
12224	MURAKAMI_UV_RESPONSE_6HR_DN	1.47	1.19	0	0	0	not significant
12225	GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_3_SIGNALING_PATHWAY	1.47	1.17	0	0	0	not significant
12226	PLASARI_TGFB1_TARGETS_1HR_UP	1.47	1.17	0	0	0	not significant
12227	GO_REGULATION_OF_LYSOSOMAL_LUMEN_PH	1.47	1.15	0	0	0	not significant
12228	REACTOME_COBALAMIN_CBL_VITAMIN_B12_TRANSPORT_AND_METABOLISM	1.47	1.11	0	0	0	not significant
12229	MILI_PSEUDOPODIA_HAPTOTAXIS_DN	1.48	4	0	0	0	not significant
12230	GO_EXTRACELLULAR_MATRIX	1.48	2.83	0	0	0	not significant
12231	STK33_DN	1.48	2.57	0	0	0	not significant
12232	TIEN_INTESTINE_PROBIOTICS_24HR_DN	1.48	2.57	0	0	0	not significant
12233	PEDRIOLI_MIR31_TARGETS_DN	1.48	2.42	0	0	0	not significant
12234	GO_GLYCOPROTEIN_BIOSYNTHETIC_PROCESS	1.48	2.41	0	0	0	not significant
12235	GO_LEUKOCYTE_PROLIFERATION	1.48	2.17	0	0	0	not significant
12236	GO_NEURON_PROJECTION_GUIDANCE	1.48	2.15	0	0	0	not significant
12237	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP	1.48	2	0	0	0	not significant
12238	WIERENGA_STAT5A_TARGETS_UP	1.48	1.96	0	0	0	not significant
12239	GO_GLYCOPROTEIN_METABOLIC_PROCESS	1.48	1.74	0	0	0	not significant
12240	HALLMARK_BILE_ACID_METABOLISM	1.48	1.71	0	0	0	not significant
12241	MIKKELSEN_MCV6_LCP_WITH_H3K4ME3	1.48	1.71	0	0	0	not significant
12242	WANG_HCP_PROSTATE_CANCER	1.48	1.66	0	0	0	not significant
12243	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	1.48	1.61	0	0	0	not significant
12244	GO_NEUROTRANSMITTER_METABOLIC_PROCESS	1.48	1.58	0	0	0	not significant
12245	GO_AMPA_GLUTAMATE_RECEPTOR_CLUSTERING	1.48	1.56	0	0	0	not significant
12246	GO_MAINTENANCE_OF_PROTEIN_LOCATION_IN_CELL	1.48	1.53	0	0	0	not significant
12247	MYC_UP.V1_DN	1.48	1.53	0	0	0	not significant
12248	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_ENDOGENOUS_LIPID_ANTIGEN_\	1.48	1.49	0	0	0	not significant
12249	KRAS.300_UP.V1_UP	1.48	1.49	0	0	0	not significant
12250	MA_MYELOID_DIFFERENTIATION_DN	1.48	1.48	0	0	0	not significant
12251	GO_URIDYLYLTRANSFERASE_ACTIVITY	1.48	1.47	0	0	0	not significant
12252	VILIMAS_NOTCH1_TARGETS_UP	1.48	1.46	0	0	0	not significant
12253	GO_ARGININE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.48	1.44	0	0	0	not significant
12254	MEISSNER_BRAIN_HCP_WITH_H3K27ME3	1.48	1.43	0	0	0	not significant
12255	KEGG_N_GLYCAN_BIOSYNTHESIS	1.48	1.4	0	0	0	not significant
12256	KRASNOSELSKAYA_ILF3_TARGETS_UP	1.48	1.4	0	0	0	not significant
12257	CAFFAREL_RESPONSE_TO_THC_UP	1.48	1.39	0	0	0	not significant
12258	GO_ACYLGLYCEROL_LIPASE_ACTIVITY	1.48	1.39	0	0	0	not significant
12259	GO_HISTONE_H4_K12_ACETYLATION	1.48	1.38	0	0	0	not significant
12260	GO_OLIGOSACCHARIDE_METABOLIC_PROCESS	1.48	1.38	0	0	0	not significant
12261	GO_RESPONSE_TO_CISPLATIN	1.48	1.37	0	0	0	not significant
12262	REACTOME_VEGF_LIGAND_RECEPTOR_INTERACTIONS	1.48	1.36	0	0	0	not significant
12263	REACTOME_GAP_FILLING_DNA_REPAIR_SYNTHESIS_AND_LIGATION_IN_GG_NER	1.48	1.32	0	0	0	not significant
12264	GO_RESPONSE_TO_PAIN	1.48	1.31	0	0	0	not significant
12265	BIOCARTA_P53_PATHWAY	1.48	1.3	0	0	0	not significant
12266	GO_DOUBLE_STRAND_BREAK_REPAIR_VIA_BREAK_INDUCED_REPLICATION	1.48	1.3	0	0	0	not significant
12267	GO_T_HELPER_17_CELL_LINEAGE_COMMITMENT	1.48	1.3	0	0	0	not significant
12268	GO_CELLULAR_RESPONSE_TO_LIPOPROTEIN_PARTICLE_STIMULUS	1.48	1.28	0	0	0	not significant
12269	GO_CATENIN_COMPLEX	1.48	1.25	0	0	0	not significant
12270	ROETH_TERT_TARGETS_UP	1.48	1.24	0	0	0	not significant
12271	GO_RESPONSE_TO_PH	1.48	1.23	0	0	0	not significant
12272	REACTOME_MISMATCH_REPAIR	1.48	1.23	0	0	0	not significant
12273	REACTOME_ERYTHROPOIETIN_ACTIVATES_PHOSPHOLIPASE_C_GAMMA_PLCG	1.48	1.22	0	0	0	not significant
12274	VALK_AML_CLUSTER_10	1.48	1.2	0	0	0	not significant
12275	GO_GROWTH_INVOLVED_IN_SYMBIOTIC_INTERACTION	1.48	1.16	0	0	0	not significant
12276	GO_ANIMAL_ORGAN_MATURATION	1.48	1.15	0	0	0	not significant
12277	ZHENG_BOUND_BY_FOXP3	1.49	4	0	0	0	not significant
12278	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN	1.49	2.89	0	0	0	not significant
12279	GO_REGULATION_OF_PEPTIDE_SECRETION	1.49	2.6	0	0	0	not significant
12280	GO_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS	1.49	2.59	0	0	0	not significant
12281	HORIUCHI_WTAP_TARGETS_UP	1.49	2.28	0	0	0	not significant
12282	BROCKE_APOPTOSIS_REVERSED_BY_IL6	1.49	2.15	0	0	0	not significant
12283	SHAFFER_IRF4_TARGETS_IN_MYELOMA_VS_MATURE_B_LYMPHOCYTE	1.49	1.98	0	0	0	not significant
12284	GO_POSITIVE_REGULATION_OF_PEPTIDE_SECRETION	1.49	1.97	0	0	0	not significant
12285	GO_ALCOHOL_METABOLIC_PROCESS	1.49	1.87	0	0	0	not significant
12286	QI_HYPOXIA	1.49	1.71	0	0	0	not significant
12287	GO_B_CELL_MEDIATED_IMMUNITY	1.49	1.64	0	0	0	not significant
12288	GO_NATURAL_KILLER_CELL_LECTIN_LIKE_RECEPTOR_BINDING	1.49	1.6	0	0	0	not significant
12289	GO_SPHINGOLIPID_METABOLIC_PROCESS	1.49	1.6	0	0	0	not significant
12290	REACTOME_RESOLUTION_OF_ABASIC_SITES_AP_SITES	1.49	1.6	0	0	0	not significant
12291	LENAOUR_DENDRITIC_CELL_MATURATION_UP	1.49	1.59	0	0	0	not significant
12292	DORN_ADENOVIRUS_INFECTION_24HR_DN	1.49	1.53	0	0	0	not significant
12293	BILD_SRC_ONCOGENIC_SIGNATURE	1.49	1.52	0	0	0	not significant
12294	BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE	1.49	1.52	0	0	0	not significant
12295	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP	1.49	1.47	0	0	0	not significant
12296	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS	1.49	1.47	0	0	0	not significant
12297	GO_RESPONSE_TO_GRAVITY	1.49	1.45	0	0	0	not significant
12298	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	1.49	1.44	0	0	0	not significant
12299	GO_INNER_EAR_MORPHOGENESIS	1.49	1.43	0	0	0	not significant
12300	GO_CELLULAR_RESPONSE_TO_DEXAMETHASONE_STIMULUS	1.49	1.42	0	0	0	not significant
12301	WILLIAMS_ESR1_TARGETS_DN	1.49	1.42	0	0	0	not significant
12302	GO_UNSATURATED_FATTY_ACID_METABOLIC_PROCESS	1.49	1.4	0	0	0	not significant
12303	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN	1.49	1.4	0	0	0	not significant
12304	GO_POSITIVE_REGULATION_OF_ISOTYPE_SWITCHING_TO_IGG_ISOTYPES	1.49	1.38	0	0	0	not significant
12305	GO_RESPONSE_TO_CAMPTOTHECIN	1.49	1.38	0	0	0	not significant

12306	REACTOME_GLUTATHIONE_CONJUGATION	1.49	1.36	0	0	0	not significant
12307	SU_THYMUS	1.49	1.35	0	0	0	not significant
12308	GO_RESPONSE_TO_MINERALOCORTICOID	1.49	1.34	0	0	0	not significant
12309	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_UP	1.49	1.34	0	0	0	not significant
12310	GO ANTIGEN PROCESSING AND PRESENTATION OF ENDOGENOUS PEPTIDE AN	1.49	1.33	0	0	0	not significant
12311	RASHI_NFKB1_TARGETS	1.49	1.33	0	0	0	not significant
12312	REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	1.49	1.33	0	0	0	not significant
12313	GO_HYPERSENSITIVITY	1.49	1.32	0	0	0	not significant
12314	GO_SIGNAL_RECOGNITION_PARTICLE_RECEPTOR_COMPLEX	1.49	1.32	0	0	0	not significant
12315	CHO_NR4A1_TARGETS	1.49	1.31	0	0	0	not significant
12316	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_RECEPTOR_ACTIVITY	1.49	1.31	0	0	0	not significant
12317	SA_CASPASE_CASCADE	1.49	1.31	0	0	0	not significant
12318	ZHENG_FOXP3_TARGETS_UP	1.49	1.31	0	0	0	not significant
12319	GO_IMMUNOLOGICAL_MEMORY_PROCESS	1.49	1.3	0	0	0	not significant
12320	GO_REGULATION_OF_STEROL_TRANSPORT	1.49	1.3	0	0	0	not significant
12321	GO_MITRAL_VALVE_DEVELOPMENT	1.49	1.29	0	0	0	not significant
12322	GO_NAD_DEPENDENT_PROTEIN_DEACETYLASE_ACTIVITY	1.49	1.29	0	0	0	not significant
12323	VANDESLUIS_COMMD1_TARGETS_GROUP_4_DN	1.49	1.28	0	0	0	not significant
12324	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_DN	1.49	1.24	0	0	0	not significant
12325	GO_ENDOPLASMIC_RETICULUM_QUALITY_CONTROL_COMPARTMENT	1.49	1.22	0	0	0	not significant
12326	GO NUCLEAR OUTER MEMBRANE ENDOPLASMIC RETICULUM MEMBRANE NETW	1.50	4	0	0	0	Enhanced
12327	PHONG_TNF_RESPONSE_NOT_VIA_P38	1.50	2.88	0	0	0	Enhanced
12328	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP	1.50	2.24	0	0	0	Enhanced
12329	HALLMARK_ESTROGEN_RESPONSE_LATE	1.50	1.93	0	0	0	Enhanced
12330	ROVERSI_GLIOMA_COPY_NUMBER_UP	1.50	1.83	0	0	0	Enhanced
12331	GO_NEGATIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	1.50	1.76	0	0	0	Enhanced
12332	REACTOME_ACTIVATION_OF_PPARGC1A_PGC_1ALPHA_BY_PHOSPHORYLATION	1.50	1.71	0	0	0	Enhanced
12333	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP	1.50	1.7	0	0	0	Enhanced
12334	GO_COLLAGEN_BINDING	1.50	1.64	0	0	0	Enhanced
12335	GO_ATP_BINDING_CASSETTE_ABC_TRANSPORTER_COMPLEX	1.50	1.61	0	0	0	Enhanced
12336	GERY_CEBP_TARGETS	1.50	1.6	0	0	0	Enhanced
12337	GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	1.50	1.59	0	0	0	Enhanced
12338	NADLER_OBESITY_UP	1.50	1.54	0	0	0	Enhanced
12339	HILLION_HMGA1_TARGETS	1.50	1.51	0	0	0	Enhanced
12340	GO_REGULATION_OF_CHRONIC_INFLAMMATORY_RESPONSE	1.50	1.49	0	0	0	Enhanced
12341	LEE_LIVER_CANCER_ACOX1_DN	1.50	1.49	0	0	0	Enhanced
12342	GO_NEGATIVE_REGULATION_OF_P38MAPK_CASCADE	1.50	1.47	0	0	0	Enhanced
12343	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP	1.50	1.46	0	0	0	Enhanced
12344	CHR4Q21	1.50	1.46	0	0	0	Enhanced
12345	DAZARD_UV_RESPONSE_CLUSTER_G24	1.50	1.46	0	0	0	Enhanced
12346	GO_SYMPATHETIC_NERVOUS_SYSTEM_DEVELOPMENT	1.50	1.46	0	0	0	Enhanced
12347	GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_CELL_FATE_COMMITMENT	1.50	1.44	0	0	0	Enhanced
12348	GROSS_HYPOXIA_VIA_ELK3_ONLY_UP	1.50	1.44	0	0	0	Enhanced
12349	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP	1.50	1.42	0	0	0	Enhanced
12350	STREICHER_LSM1_TARGETS_UP	1.50	1.42	0	0	0	Enhanced
12351	GO_CELLULAR_MODIFIED_AMINO_ACID_BIOSYNTHETIC_PROCESS	1.50	1.41	0	0	0	Enhanced
12352	GO_DIACYLGLYCEROL_METABOLIC_PROCESS	1.50	1.41	0	0	0	Enhanced
12353	GO_ATPASE_DEPENDENT_TRANSMEMBRANE_TRANSPORT_COMPLEX	1.50	1.38	0	0	0	Enhanced
12354	WANG_METASTASIS_OF_BREAST_CANCER	1.50	1.38	0	0	0	Enhanced
12355	GO_ACID_THIOL_LIGASE_ACTIVITY	1.50	1.37	0	0	0	Enhanced
12356	GO_FIBRONECTIN_BINDING	1.50	1.37	0	0	0	Enhanced
12357	GO_REGULATION_OF_POSITIVE_CHEMOTAXIS	1.50	1.37	0	0	0	Enhanced
12358	AIYAR_COBRA1_TARGETS_UP	1.50	1.36	0	0	0	Enhanced
12359	GO_ANION_CATION_SYMPORTER_ACTIVITY	1.50	1.36	0	0	0	Enhanced
12360	GO_LIPID_ANTIGEN_BINDING	1.50	1.36	0	0	0	Enhanced
12361	BIOCARTA_LYMPHOCYTE_PATHWAY	1.50	1.35	0	0	0	Enhanced
12362	GALI_TP53_TARGETS_APOPTOTIC_UP	1.50	1.35	0	0	0	Enhanced
12363	GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	1.50	1.34	0	0	0	Enhanced
12364	GO_T_CELL_SELECTION	1.50	1.34	0	0	0	Enhanced
12365	GO_PHOSPHATIDYLCHOLINE_CATABOLIC_PROCESS	1.50	1.32	0	0	0	Enhanced
12366	GO_LUNG_EPITHELIUM_DEVELOPMENT	1.50	1.31	0	0	0	Enhanced
12367	GO_RESPONSE_TO_INTERLEUKIN_2	1.50	1.3	0	0	0	Enhanced
12368	GO_SYNCYTIUM_FORMATION	1.50	1.3	0	0	0	Enhanced
12369	GO_HEPATOCYTE_DIFFERENTIATION	1.50	1.28	0	0	0	Enhanced
12370	GO_SYNAPSIS	1.50	1.27	0	0	0	Enhanced
12371	REACTOME_LEADING_STRAND_SYNTHESIS	1.50	1.27	0	0	0	Enhanced
12372	TURJANSKI_MAPK1_AND_MAPK2_TARGETS	1.50	1.27	0	0	0	Enhanced
12373	GO_AMINO_SUGAR_CATABOLIC_PROCESS	1.50	1.25	0	0	0	Enhanced
12374	GO_CHRONIC_INFLAMMATORY_RESPONSE	1.50	1.24	0	0	0	Enhanced
12375	ENK_UV_RESPONSE_EPIDERMIS_DN	1.51	4	0	0	0	Enhanced
12376	GO_CYTOKINE_PRODUCTION	1.51	4	0	0	0	Enhanced
12377	GO_RESPONSE_TO_VIRUS	1.51	2.87	0	0	0	Enhanced
12378	GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	1.51	2.6	0	0	0	Enhanced
12379	GO_DEFENSE_RESPONSE_TO_OTHER_ORGANISM	1.51	2.59	0	0	0	Enhanced
12380	CHR11Q13	1.51	2.56	0	0	0	Enhanced
12381	GO_SECRETORY_GRANULE_MEMBRANE	1.51	2.39	0	0	0	Enhanced
12382	GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_DN	1.51	2.38	0	0	0	Enhanced
12383	GO_MEMBRANE_LIPID_METABOLIC_PROCESS	1.51	2.24	0	0	0	Enhanced
12384	GO_VACUOLAR_LUMEN	1.51	1.94	0	0	0	Enhanced
12385	KRAS.600_UP.V1_DN	1.51	1.87	0	0	0	Enhanced
12386	MEL18_DN.V1_UP	1.51	1.83	0	0	0	Enhanced
12387	GO_HORMONE_METABOLIC_PROCESS	1.51	1.82	0	0	0	Enhanced
12388	BMI1_DN.V1_UP	1.51	1.8	0	0	0	Enhanced
12389	GO_RESPONSE_TO_AMINO_ACID	1.51	1.77	0	0	0	Enhanced
12390	PID_IL2_1PATHWAY	1.51	1.69	0	0	0	Enhanced
12391	GO_DIGESTIVE_SYSTEM_DEVELOPMENT	1.51	1.67	0	0	0	Enhanced
12392	CRX_NRL_DN.V1_DN	1.51	1.64	0	0	0	Enhanced
12393	REACTOME_REGULATION_OF_TNFR1_SIGNALING	1.51	1.58	0	0	0	Enhanced
12394	BIOCARTA_NKT_PATHWAY	1.51	1.52	0	0	0	Enhanced
12395	GO_ARGININE_TRANSPORT	1.51	1.52	0	0	0	Enhanced
12396	GO_METALLOENDOPEPTIDASE_INHIBITOR_ACTIVITY	1.51	1.52	0	0	0	Enhanced
12397	GO_RESPONSE_TO_OLEIC_ACID	1.51	1.5	0	0	0	Enhanced
12398	GO_CELLULAR_HORMONE_METABOLIC_PROCESS	1.51	1.49	0	0	0	Enhanced
12399	HINATA_NFKB_TARGETS_KERATINOCYTE_UP	1.51	1.49	0	0	0	Enhanced
12400	MCBRYAN_PUBERTAL_TGFB1_TARGETS_DN	1.51	1.47	0	0	0	Enhanced
12401	DORN_ADENOVIRUS_INFECTION_32HR_DN	1.51	1.46	0	0	0	Enhanced
12402	GO_RESPONSE_TO_DEXAMETHASONE	1.51	1.44	0	0	0	Enhanced
12403	BIOCARTA_MONOCYTE_PATHWAY	1.51	1.43	0	0	0	Enhanced
12404	GAURNIER_PSMD4_TARGETS	1.51	1.42	0	0	0	Enhanced
12405	GO_ICOSANOID_BIOSYNTHETIC_PROCESS	1.51	1.4	0	0	0	Enhanced
12406	WHITESIDE_CISPLATIN_RESISTANCE_DN	1.51	1.4	0	0	0	Enhanced
12407	GO_GLUTATHIONE_TRANSFERASE_ACTIVITY	1.51	1.39	0	0	0	Enhanced
12408	GO_REGULATION_OF_AMYLOID_BETA_CLEARANCE	1.51	1.38	0	0	0	Enhanced
12409	GO_PHOSPHATIDYLSERINE_METABOLIC_PROCESS	1.51	1.37	0	0	0	Enhanced
12410	GO_SULFATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.51	1.37	0	0	0	Enhanced
12411	SASAI_RESISTANCE_TO_NEOPLASTIC_TRANSFROMATION	1.51	1.37	0	0	0	Enhanced
12412	GO_RESPONSE_TO_CORTICOSTERONE	1.51	1.36	0	0	0	Enhanced
12413	MIKKELSEN_IPS_WITH_HCP_H3K27ME3	1.51	1.35	0	0	0	Enhanced
12414	GYORFFY_DOXORUBICIN_RESISTANCE	1.51	1.33	0	0	0	Enhanced

12415	GO_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	1.51	1.31	0	0	0	Enhanced
12416	GO_THROMBIN_ACTIVATED_RECEPTOR_SIGNALING_PATHWAY	1.51	1.31	0	0	0	Enhanced
12417	ISSAEVA_MLL2_TARGETS	1.51	1.31	0	0	0	Enhanced
12418	GO_ADRENERGIC_RECEPTOR_SIGNALING_PATHWAY	1.51	1.3	0	0	0	Enhanced
12419	GO_INTEGRAL_COMPONENT_OF_SYNAPTIC_VESICLE_MEMBRANE	1.51	1.28	0	0	0	Enhanced
12420	GO_STEROID_DEHYDROGENASE_ACTIVITY	1.51	1.24	0	0	0	Enhanced
12421	GO_REGULATION_OF_HISTONE_H3_K27_METHYLATION	1.51	1.19	0	0	0	Enhanced
12422	GO_INTRINSIC_COMPONENT_OF_ORGANELLE_MEMBRANE	1.52	4	0	0	0	Enhanced
12423	GO_LEUKOCYTE_MEDIATED_IMMUNITY	1.52	4	0	0	0	Enhanced
12424	PHONG_TNF_RESPONSE_VIA_P38_COMPLETE	1.52	4	0	0	0	Enhanced
12425	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP	1.52	2.86	0	0	0	Enhanced
12426	GO_RESPONSE_TO_ACID_CHEMICAL	1.52	2.84	0	0	0	Enhanced
12427	DOUGLAS_BMI1_TARGETS_DN	1.52	2.42	0	0	0	Enhanced
12428	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_GLYCOSYL_GROUPS	1.52	2.09	0	0	0	Enhanced
12429	PRC2_SUZ12_UP.V1_UP	1.52	2.05	0	0	0	Enhanced
12430	HSIAO_LIVER_SPECIFIC_GENES	1.52	1.98	0	0	0	Enhanced
12431	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	1.52	1.8	0	0	0	Enhanced
12432	GO_AMINO_ACID_TRANSPORT	1.52	1.79	0	0	0	Enhanced
12433	BMI1_DN_MEL18_DN.V1_DN	1.52	1.74	0	0	0	Enhanced
12434	SMID_BREAST_CANCER_ERBB2_UP	1.52	1.74	0	0	0	Enhanced
12435	GO_MAINTENANCE_OF_PROTEIN_LOCALIZATION_IN_ORGANELLE	1.52	1.72	0	0	0	Enhanced
12436	GO_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	1.52	1.67	0	0	0	Enhanced
12437	GO_EPITHELIAL_CELL_APOPTOTIC_PROCESS	1.52	1.65	0	0	0	Enhanced
12438	GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS	1.52	1.63	0	0	0	Enhanced
12439	GO_AMMONIUM_ION_METABOLIC_PROCESS	1.52	1.62	0	0	0	Enhanced
12440	LUI_THYROID_CANCER_CLUSTER_1	1.52	1.62	0	0	0	Enhanced
12441	GO_SERINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	1.52	1.61	0	0	0	Enhanced
12442	NIKOLSKY_BREAST_CANCER_22Q13_AMPLICON	1.52	1.59	0	0	0	Enhanced
12443	GO_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	1.52	1.58	0	0	0	Enhanced
12444	GO_POSITIVE_REGULATION_OF_HISTONE_H3_K27_METHYLATION	1.52	1.55	0	0	0	Enhanced
12445	HALMOS_CEBPA_TARGETS_UP	1.52	1.55	0	0	0	Enhanced
12446	REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS	1.52	1.54	0	0	0	Enhanced
12447	MOSERLE_IFNA_RESPONSE	1.52	1.51	0	0	0	Enhanced
12448	GO_ACYLGLYCEROL_METABOLIC_PROCESS	1.52	1.5	0	0	0	Enhanced
12449	GO_ARACHIDONIC_ACID_SECRETION	1.52	1.5	0	0	0	Enhanced
12450	GO_DNA_STRAND_RENATURATION	1.52	1.5	0	0	0	Enhanced
12451	GO_CD40_SIGNALING_PATHWAY	1.52	1.47	0	0	0	Enhanced
12452	GO_INORGANIC_ANION_EXCHANGER_ACTIVITY	1.52	1.47	0	0	0	Enhanced
12453	KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	1.52	1.47	0	0	0	Enhanced
12454	KRAS.BREAST_UP.V1_UP	1.52	1.47	0	0	0	Enhanced
12455	GO_INTERLEUKIN_23_MEDIATED_SIGNALING_PATHWAY	1.52	1.46	0	0	0	Enhanced
12456	GO_NEGATIVE_REGULATION_OF_CELL_KILLING	1.52	1.46	0	0	0	Enhanced
12457	GO_STEROID_DEHYDROGENASE_ACTIVITY_ACTING_ON_THE_CH_OH_GROUP_OF_	1.52	1.46	0	0	0	Enhanced
12458	REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	1.52	1.45	0	0	0	Enhanced
12459	GO_OLIGOSACCHARYL_TRANSFERASE_ACTIVITY	1.52	1.44	0	0	0	Enhanced
12460	BROWNE_HCMV_INFECTION_30MIN_UP	1.52	1.43	0	0	0	Enhanced
12461	GO_DERMATAN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	1.52	1.42	0	0	0	Enhanced
12462	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	1.52	1.42	0	0	0	Enhanced
12463	BIOCARTA_ARAP_PATHWAY	1.52	1.41	0	0	0	Enhanced
12464	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_PINK_DN	1.52	1.4	0	0	0	Enhanced
12465	REACTOME_COLLAGEN_BIOSYNTHESIS_AND_MODIFYING_ENZYMES	1.52	1.4	0	0	0	Enhanced
12466	REACTOME_ESTROGEN_DEPENDENT_NUCLEAR_EVENTS_DOWNSTREAM_OF_ESR	1.52	1.4	0	0	0	Enhanced
12467	GO_PROTEIN_POLYGLUTAMYLATION	1.52	1.38	0	0	0	Enhanced
12468	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_DN	1.52	1.38	0	0	0	Enhanced
12469	GO_REGULATION_OF_VASCULAR_PERMEABILITY	1.52	1.32	0	0	0	Enhanced
12470	BIOCARTA_REELIN_PATHWAY	1.52	1.31	0	0	0	Enhanced
12471	GO_ACUTE_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	1.52	1.27	0	0	0	Enhanced
12472	MEK_UP.V1_UP	1.53	2.54	0	0	0	Enhanced
12473	RODRIGUES_NTN1_TARGETS_DN	1.53	2.53	0	0	0	Enhanced
12474	GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	1.53	2.12	0	0	0	Enhanced
12475	GO_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	1.53	2	0	0	0	Enhanced
12476	DELYS_THYROID_CANCER_DN	1.53	1.99	0	0	0	Enhanced
12477	GO_LEUKOCYTE_CHEMOTAXIS	1.53	1.98	0	0	0	Enhanced
12478	GO_ANNEALING_HELICASE_ACTIVITY	1.53	1.87	0	0	0	Enhanced
12479	GO_MYELOID_LEUKOCYTE_MIGRATION	1.53	1.87	0	0	0	Enhanced
12480	KATSANOU_ELAVL1_TARGETS_UP	1.53	1.86	0	0	0	Enhanced
12481	SRC_UP.V1_UP	1.53	1.85	0	0	0	Enhanced
12482	SIRNA_EIF4GI_UP	1.53	1.83	0	0	0	Enhanced
12483	GO_REGULATION_OF_FAT_CELL_DIFFERENTIATION	1.53	1.8	0	0	0	Enhanced
12484	GO_PERIKARYON	1.53	1.78	0	0	0	Enhanced
12485	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP	1.53	1.76	0	0	0	Enhanced
12486	GO_AUTOPHAGOSOME	1.53	1.75	0	0	0	Enhanced
12487	REACTOME_INTERLEUKIN_1_PROCESSING	1.53	1.67	0	0	0	Enhanced
12488	GO_NEPHRIC_DUCT_DEVELOPMENT	1.53	1.66	0	0	0	Enhanced
12489	BILBAN_B_CLL_LPL_DN	1.53	1.64	0	0	0	Enhanced
12490	BIOCARTA_LYM_PATHWAY	1.53	1.6	0	0	0	Enhanced
12491	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC	1.53	1.56	0	0	0	Enhanced
12492	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN	1.53	1.55	0	0	0	Enhanced
12493	GO_NEUROINFLAMMATORY_RESPONSE	1.53	1.54	0	0	0	Enhanced
12494	GO_SPERM_AXONEME_ASSEMBLY	1.53	1.54	0	0	0	Enhanced
12495	LEE_EARLY_T_LYMPHOCYTE_DN	1.53	1.54	0	0	0	Enhanced
12496	GO_SKELETAL_MUSCLE_CELL_DIFFERENTIATION	1.53	1.5	0	0	0	Enhanced
12497	GO_BETA_2_MICROGLOBULIN_BINDING	1.53	1.47	0	0	0	Enhanced
12498	REACTOME_RESOLUTION_OF_D_LOOP_STRUCTURES_THROUGH_SYNTHESIS_DEP	1.53	1.47	0	0	0	Enhanced
12499	LEE_DOUBLE_POLAR_THYMOCYTE	1.53	1.46	0	0	0	Enhanced
12500	OXFORD_RALA_TARGETS_UP	1.53	1.46	0	0	0	Enhanced
12501	REACTOME_INTERLEUKIN_23_SIGNALING	1.53	1.46	0	0	0	Enhanced
12502	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPOR	1.53	1.45	0	0	0	Enhanced
12503	REACTOME_ALPHA_LINOLENIC_OMEGA3_AND_LINOLEIC_OMEGA6_ACID_METABOL	1.53	1.45	0	0	0	Enhanced
12504	GO_MONOCYTE_CHEMOTAXIS	1.53	1.44	0	0	0	Enhanced
12505	GO_REGULATION_OF_NMDA_RECEPTOR_ACTIVITY	1.53	1.44	0	0	0	Enhanced
12506	AMIT_EGF_RESPONSE_20_HELA	1.53	1.41	0	0	0	Enhanced
12507	KEGG_TYPE_I_DIABETES_MELLITUS	1.53	1.41	0	0	0	Enhanced
12508	OSADA_ASCL1_TARGETS_DN	1.53	1.41	0	0	0	Enhanced
12509	BIOCARTA_BARD1_PATHWAY	1.53	1.39	0	0	0	Enhanced
12510	BIOCARTA_IL2_PATHWAY	1.53	1.37	0	0	0	Enhanced
12511	SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_DN	1.53	1.33	0	0	0	Enhanced
12512	GO_ESTABLISHMENT_OF_PLANAR_POLARITY_INVOLVED_IN_NEURAL_TUBE_CLOSU	1.53	1.27	0	0	0	Enhanced
12513	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP	1.54	4	0	0	0	Enhanced
12514	GO_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.54	4	0	0	0	Enhanced
12515	GO_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	1.54	4	0	0	0	Enhanced
12516	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN	1.54	4	0	0	0	Enhanced
12517	PARENT_MTOR_SIGNALING_UP	1.54	4	0	0	0	Enhanced
12518	LEF1_UP.V1_DN	1.54	2.82	0	0	0	Enhanced
12519	WILCOX_RESPONSE_TO_PROGESTERONE_UP	1.54	2.24	0	0	0	Enhanced
12520	CHYLA_CBFA2T3_TARGETS_DN	1.54	2.15	0	0	0	Enhanced
12521	GO_REGULATION_OF_CHEMOTAXIS	1.54	2.12	0	0	0	Enhanced
12522	GO_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	1.54	1.97	0	0	0	Enhanced
12523	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS	1.54	1.72	0	0	0	Enhanced

12524	GO_SCAVENGER_RECEPTOR_ACTIVITY	1.54	1.69	0	0	0	Enhanced
12525	REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS	1.54	1.66	0	0	0	Enhanced
12526	GO_ACID_SECRETION	1.54	1.65	0	0	0	Enhanced
12527	KEGG_LEISHMANIA_INFECTION	1.54	1.65	0	0	0	Enhanced
12528	GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STIMULUS	1.54	1.61	0	0	0	Enhanced
12529	WANG_BARRETTS_ESOPHAGUS_UP	1.54	1.61	0	0	0	Enhanced
12530	RADAEVA_RESPONSE_TO_IFNA1_UP	1.54	1.59	0	0	0	Enhanced
12531	GO_AMELOGENESIS	1.54	1.57	0	0	0	Enhanced
12532	GO_GROWTH_HORMONE_RECEPTOR_SIGNALING_PATHWAY_VIA_JAK_STAT	1.54	1.57	0	0	0	Enhanced
12533	GO_BASIC_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	1.54	1.54	0	0	0	Enhanced
12534	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	1.54	1.52	0	0	0	Enhanced
12535	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	1.54	1.5	0	0	0	Enhanced
12536	REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	1.54	1.5	0	0	0	Enhanced
12537	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	1.54	1.49	0	0	0	Enhanced
12538	GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS_ENGULFMENT	1.54	1.47	0	0	0	Enhanced
12539	APPEL_IMATINIB_RESPONSE	1.54	1.45	0	0	0	Enhanced
12540	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	1.54	1.45	0	0	0	Enhanced
12541	GO_REGULATION_OF_EPITHELIAL_TUBE_FORMATION	1.54	1.45	0	0	0	Enhanced
12542	CHR7Q31	1.54	1.44	0	0	0	Enhanced
12543	GO_NEUROTRANSMITTER_TRANSPORTER_ACTIVITY	1.54	1.44	0	0	0	Enhanced
12544	GO_ALPHA_LINOLENIC_ACID_METABOLIC_PROCESS	1.54	1.43	0	0	0	Enhanced
12545	GO_RESPONSE_TO_GROWTH_HORMONE	1.54	1.43	0	0	0	Enhanced
12546	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_SINGLE_DONORS_WITH_INCORPORA	1.54	1.42	0	0	0	Enhanced
12547	NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	1.54	1.42	0	0	0	Enhanced
12548	BIOCARTA_CD40_PATHWAY	1.54	1.38	0	0	0	Enhanced
12549	BIOCARTA_TCYTOTOXIC_PATHWAY	1.54	1.37	0	0	0	Enhanced
12550	REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_C_STRAND_OF_THE_TELOMERE	1.54	1.3	0	0	0	Enhanced
12551	LEE_DIFFERENTIATING_T_LYMPHOCYTE	1.55	4	0	0	0	Enhanced
12552	RODWELL_AGING_KIDNEY_UP	1.55	4	0	0	0	Enhanced
12553	MARTENS_TRETINOIN_RESPONSE_UP	1.55	2.86	0	0	0	Enhanced
12554	STK33_NOMO_UP	1.55	2.86	0	0	0	Enhanced
12555	CHYLA_CBFA2T3_TARGETS_UP	1.55	2.85	0	0	0	Enhanced
12556	GO_REGULATION_OF_INFLAMMATORY_RESPONSE	1.55	2.84	0	0	0	Enhanced
12557	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	1.55	2.83	0	0	0	Enhanced
12558	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_HEXOSYL_GROUPS	1.55	2.55	0	0	0	Enhanced
12559	REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	1.55	2.54	0	0	0	Enhanced
12560	AKT_UP.V1_UP	1.55	2.35	0	0	0	Enhanced
12561	DURAND_STROMA_S_UP	1.55	2.17	0	0	0	Enhanced
12562	GO_CYTOKINE_SECRETION	1.55	2.01	0	0	0	Enhanced
12563	MATZUK_LUTEAL_GENES	1.55	1.94	0	0	0	Enhanced
12564	GO_ANTIPORTER_ACTIVITY	1.55	1.86	0	0	0	Enhanced
12565	GO_RESPONSE_TO_ANTIMETABOLITE	1.55	1.83	0	0	0	Enhanced
12566	GO_AUTOPHAGIC_CELL_DEATH	1.55	1.74	0	0	0	Enhanced
12567	GO_L_AMINO_ACID_TRANSPORT	1.55	1.74	0	0	0	Enhanced
12568	BIOCARTA_TSP1_PATHWAY	1.55	1.71	0	0	0	Enhanced
12569	GO_PROTEIN_KINASE_C_SIGNALING	1.55	1.69	0	0	0	Enhanced
12570	GO_VOLUME_SENSITIVE_ANION_CHANNEL_ACTIVITY	1.55	1.69	0	0	0	Enhanced
12571	GO_AMINO_ACID_IMPORT	1.55	1.67	0	0	0	Enhanced
12572	REACTOME_RESOLUTION_OF_D_LOOP_STRUCTURES	1.55	1.65	0	0	0	Enhanced
12573	GO_DISRUPTION_OF_CELLS_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INT	1.55	1.63	0	0	0	Enhanced
12574	GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	1.55	1.62	0	0	0	Enhanced
12575	GO_MEMBRANE_RAFT_ORGANIZATION	1.55	1.58	0	0	0	Enhanced
12576	BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_DN	1.55	1.55	0	0	0	Enhanced
12577	GO_EXCITATORY_SYNAPSE	1.55	1.55	0	0	0	Enhanced
12578	HOLLEMAN_PREDNISOLONE_RESISTANCE_B_ALL_DN	1.55	1.55	0	0	0	Enhanced
12579	PID_ATF2_PATHWAY	1.55	1.55	0	0	0	Enhanced
12580	KIM_LRRC3B_TARGETS	1.55	1.54	0	0	0	Enhanced
12581	GO_MONOOXYGENASE_ACTIVITY	1.55	1.52	0	0	0	Enhanced
12582	SANA_RESPONSE_TO_IFNG_UP	1.55	1.52	0	0	0	Enhanced
12583	SCHURINGA_STAT5A_TARGETS_DN	1.55	1.51	0	0	0	Enhanced
12584	BIOCARTA_S1P_PATHWAY	1.55	1.48	0	0	0	Enhanced
12585	GO_POSITIVE_REGULATION_OF_CHOLESTEROL_EFFLUX	1.55	1.48	0	0	0	Enhanced
12586	TERAMOTO_OPN_TARGETS_CLUSTER_7	1.55	1.48	0	0	0	Enhanced
12587	GO_STEROL_TRANSPORTER_ACTIVITY	1.55	1.46	0	0	0	Enhanced
12588	PID_IL12_STAT4_PATHWAY	1.55	1.46	0	0	0	Enhanced
12589	GO_LEUKOCYTE_TETHERING_OR_ROLLING	1.55	1.43	0	0	0	Enhanced
12590	GO_MEMBRANE_PROTEIN_INTRACELLULAR_DOMAIN_PROTEOLYSIS	1.55	1.42	0	0	0	Enhanced
12591	GO_FAT_CELL_DIFFERENTIATION	1.56	2.53	0	0	0	Enhanced
12592	GO_ORGANIC_ACID_BIOSYNTHETIC_PROCESS	1.56	2.39	0	0	0	Enhanced
12593	LIU_CMYB_TARGETS_UP	1.56	2.37	0	0	0	Enhanced
12594	KONDO_EZH2_TARGETS	1.56	2.25	0	0	0	Enhanced
12595	IL21_UP.V1_DN	1.56	2.09	0	0	0	Enhanced
12596	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP	1.56	2	0	0	0	Enhanced
12597	BHAT_ESR1_TARGETS_VIA_AKT1_DN	1.56	1.95	0	0	0	Enhanced
12598	GALINDO_IMMUNE_RESPONSE_TO_ENTEROTOXIN	1.56	1.95	0	0	0	Enhanced
12599	GO_HEPARAN_SULFATE_PROTEOGLYCAN_BINDING	1.56	1.94	0	0	0	Enhanced
12600	PARK_OSTEOBLAST_DIFFERENTIATION_BY_PHENYLAMIL_UP	1.56	1.94	0	0	0	Enhanced
12601	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	1.56	1.87	0	0	0	Enhanced
12602	GO_CELLULAR_AMINO_ACID_BIOSYNTHETIC_PROCESS	1.56	1.83	0	0	0	Enhanced
12603	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_1	1.56	1.82	0	0	0	Enhanced
12604	BIOCARTA_IL22BP_PATHWAY	1.56	1.79	0	0	0	Enhanced
12605	MCCABE_HOXC6_TARGETS_CANCER_UP	1.56	1.79	0	0	0	Enhanced
12606	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_16	1.56	1.77	0	0	0	Enhanced
12607	BIOCARTA_ETS_PATHWAY	1.56	1.76	0	0	0	Enhanced
12608	GO_LIPOPROTEIN_PARTICLE_RECEPTOR_ACTIVITY	1.56	1.76	0	0	0	Enhanced
12609	GO_LIPOPEPTIDE_BINDING	1.56	1.75	0	0	0	Enhanced
12610	HOLLEMAN_ASPARAGINASE_RESISTANCE_B_ALL_DN	1.56	1.74	0	0	0	Enhanced
12611	GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	1.56	1.72	0	0	0	Enhanced
12612	GO_NEGATIVE_REGULATION_OF_NEUROINFLAMMATORY_RESPONSE	1.56	1.71	0	0	0	Enhanced
12613	GO_CELLULAR_RESPONSE_TO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_STIMULUS	1.56	1.63	0	0	0	Enhanced
12614	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN	1.56	1.63	0	0	0	Enhanced
12615	GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY_TRANSPOSING_C_C_BONDS	1.56	1.57	0	0	0	Enhanced
12616	GO_RESPONSE_TO_UV_C	1.56	1.57	0	0	0	Enhanced
12617	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP	1.56	1.57	0	0	0	Enhanced
12618	GO_BICARBONATE_TRANSPORT	1.56	1.56	0	0	0	Enhanced
12619	GO_COLLATERAL_SPROUTING	1.56	1.56	0	0	0	Enhanced
12620	GO_POSITIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVO	1.56	1.54	0	0	0	Enhanced
12621	CROONQUIST_STROMAL_STIMULATION_UP	1.56	1.5	0	0	0	Enhanced
12622	GO_PHOSPHATIDYLCHOLINE_ACYL_CHAIN_REMODELING	1.56	1.49	0	0	0	Enhanced
12623	LEIN_OLIGODENDROCYTE_MARKERS	1.56	1.49	0	0	0	Enhanced
12624	SIG_CD40PATHWAYMAP	1.56	1.48	0	0	0	Enhanced
12625	VALK_AML_WITH_EVI1	1.56	1.42	0	0	0	Enhanced
12626	PID_SYNDECAN_3_PATHWAY	1.56	1.39	0	0	0	Enhanced
12627	GO_C21_STEROID_HORMONE_METABOLIC_PROCESS	1.56	1.36	0	0	0	Enhanced
12628	GO_PROTEIN_LIPID_COMPLEX_BINDING	1.56	1.33	0	0	0	Enhanced
12629	CHEN_METABOLIC_SYNDROM_NETWORK	1.57	4	0	0	0	Enhanced
12630	GO_RESPONSE_TO_BIOTIC_STIMULUS	1.57	4	0	0	0	Enhanced
12631	GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	1.57	2.84	0	0	0	Enhanced
12632	GO_REGULATION_OF_NUCLEOTIDE_BINDING_OLIGOMERIZATION_DOMAIN_CONTAIN	1.57	2.69	0	0	0	Enhanced

12633	HUMMERICH_SKIN_CANCER_PROGRESSION_UP	1.57	2.34	0	0	0	Enhanced
12634	JAEGER_METASTASIS_DN	1.57	2.34	0	0	0	Enhanced
12635	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN	1.57	2.13	0	0	0	Enhanced
12636	IGLESIAS_E2F_TARGETS_UP	1.57	2.13	0	0	0	Enhanced
12637	GO_NEGATIVE_REGULATION_OF_PEPTIDE_SECRETION	1.57	2.11	0	0	0	Enhanced
12638	GO_GAP_JUNCTION	1.57	2.02	0	0	0	Enhanced
12639	GO_NEGATIVE_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	1.57	1.88	0	0	0	Enhanced
12640	GAVIN_FOXP3_TARGETS_CLUSTER_P7	1.57	1.86	0	0	0	Enhanced
12641	REACTOME_RHO_GTPASES_ACTIVATE_RHOTEKIN_AND_RHOPHILINS	1.57	1.86	0	0	0	Enhanced
12642	GO_NEGATIVE_REGULATION_OF_CHEMOTAXIS	1.57	1.82	0	0	0	Enhanced
12643	GO_STEROID_BINDING	1.57	1.8	0	0	0	Enhanced
12644	GO_ALCOHOL_BINDING	1.57	1.79	0	0	0	Enhanced
12645	REACTOME_LINOLEIC_ACID_LA_METABOLISM	1.57	1.79	0	0	0	Enhanced
12646	BIOCARTA_P27_PATHWAY	1.57	1.78	0	0	0	Enhanced
12647	GO_CHEMOKINE_BIOSYNTHETIC_PROCESS	1.57	1.75	0	0	0	Enhanced
12648	GO_HORMONE_BIOSYNTHETIC_PROCESS	1.57	1.75	0	0	0	Enhanced
12649	GO_NEUROTRANSMITTER_GATED_ION_CHANNEL_CLUSTERING	1.57	1.73	0	0	0	Enhanced
12650	DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_UP	1.57	1.68	0	0	0	Enhanced
12651	GO_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	1.57	1.68	0	0	0	Enhanced
12652	REACTOME_LAGGING_STRAND_SYNTHESIS	1.57	1.67	0	0	0	Enhanced
12653	WEIGEL_OXIDATIVE_STRESS_RESPONSE	1.57	1.67	0	0	0	Enhanced
12654	WINZEN_DEGRADED_VIA_KHSRP	1.57	1.66	0	0	0	Enhanced
12655	KIM_GERMINAL_CENTER_T_HELPER_DN	1.57	1.65	0	0	0	Enhanced
12656	BOYLAN_MULTIPLE_MYELOMA_C_CLUSTER_DN	1.57	1.63	0	0	0	Enhanced
12657	GO_CD8_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	1.57	1.62	0	0	0	Enhanced
12658	PENG_GLUCOSE_DEPRIVATION_UP	1.57	1.62	0	0	0	Enhanced
12659	GO_GLYCOPROTEIN_CATABOLIC_PROCESS	1.57	1.6	0	0	0	Enhanced
12660	GU_PDEF_TARGETS_UP	1.57	1.58	0	0	0	Enhanced
12661	GO_STEROID_HORMONE_RECEPTOR_ACTIVITY	1.57	1.57	0	0	0	Enhanced
12662	GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMM	1.57	1.54	0	0	0	Enhanced
12663	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP	1.57	1.53	0	0	0	Enhanced
12664	BIOCARTA_THELPER_PATHWAY	1.57	1.52	0	0	0	Enhanced
12665	RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_MAPK1_DN	1.57	1.52	0	0	0	Enhanced
12666	GO_BASIC_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.57	1.45	0	0	0	Enhanced
12667	GO_INTERLEUKIN_1_SECRETION	1.57	1.45	0	0	0	Enhanced
12668	ABE_VEGFA_TARGETS_2HR	1.57	1.44	0	0	0	Enhanced
12669	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTI	1.57	1.4	0	0	0	Enhanced
12670	GO_ANION_TRANSPORT	1.58	4	0	0	0	Enhanced
12671	GO_ENDOPLASMIC_RETICULUM	1.58	4	0	0	0	Enhanced
12672	GO_ENDOPLASMIC_RETICULUM_PART	1.58	4	0	0	0	Enhanced
12673	GO_TAXIS	1.58	2.88	0	0	0	Enhanced
12674	ZHANG_TLX_TARGETS_36HR_UP	1.58	2.85	0	0	0	Enhanced
12675	GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	1.58	2.83	0	0	0	Enhanced
12676	HALLMARK_INTERFERON_ALPHA_RESPONSE	1.58	2.35	0	0	0	Enhanced
12677	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN	1.58	2.21	0	0	0	Enhanced
12678	YAUCH_HEDGEHOG_SIGNALING_PARACRINE_UP	1.58	2.21	0	0	0	Enhanced
12679	GO_REGULATION_OF_ANION_CHANNEL_ACTIVITY	1.58	2.09	0	0	0	Enhanced
12680	GO_CELL_KILLING	1.58	2.04	0	0	0	Enhanced
12681	BORCZUK_MALIGNANT_MESOTHELIOMA_DN	1.58	1.97	0	0	0	Enhanced
12682	GO_MHC_CLASS_I_PROTEIN_COMPLEX	1.58	1.96	0	0	0	Enhanced
12683	GO_NEGATIVE_REGULATION_OF_MACROPHAGE_ACTIVATION	1.58	1.95	0	0	0	Enhanced
12684	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN	1.58	1.9	0	0	0	Enhanced
12685	GO_NITRIC_OXIDE_BIOSYNTHETIC_PROCESS	1.58	1.88	0	0	0	Enhanced
12686	KUNINGER_IGF1_VS_PDGFB_TARGETS_UP	1.58	1.88	0	0	0	Enhanced
12687	GO_BASIC_AMINO_ACID_TRANSPORT	1.58	1.87	0	0	0	Enhanced
12688	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_OXIDATION	1.58	1.85	0	0	0	Enhanced
12689	REACTOME_ACYL_CHAIN_REMODELLING_OF_PC	1.58	1.84	0	0	0	Enhanced
12690	GO_INTERLEUKIN_1_BETA_SECRETION	1.58	1.81	0	0	0	Enhanced
12691	GO_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	1.58	1.81	0	0	0	Enhanced
12692	GO_RESPONSE_TO_STEROL	1.58	1.8	0	0	0	Enhanced
12693	GO_NEUROTRANSMITTER_BIOSYNTHETIC_PROCESS	1.58	1.77	0	0	0	Enhanced
12694	GO_REGULATION_OF_KETONE_BIOSYNTHETIC_PROCESS	1.58	1.77	0	0	0	Enhanced
12695	GO_RESPONSE_TO_INTERLEUKIN_9	1.58	1.76	0	0	0	Enhanced
12696	GO_AZUROPHIL_GRANULE_MEMBRANE	1.58	1.75	0	0	0	Enhanced
12697	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_PEPTIDE_AN	1.58	1.7	0	0	0	Enhanced
12698	BIOCARTA_TPO_PATHWAY	1.58	1.69	0	0	0	Enhanced
12699	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTYELLOW_DN	1.58	1.68	0	0	0	Enhanced
12700	GO_POSITIVE_REGULATION_OF_HORMONE_BIOSYNTHETIC_PROCESS	1.58	1.67	0	0	0	Enhanced
12701	GO_SODIUM_CHANNEL_ACTIVITY	1.58	1.66	0	0	0	Enhanced
12702	GO_TRIGLYCERIDE_RICH_PLASMA_LIPOPROTEIN_PARTICLE	1.58	1.65	0	0	0	Enhanced
12703	GO_POSITIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_PROD	1.58	1.62	0	0	0	Enhanced
12704	BIOCARTA_RANKL_PATHWAY	1.58	1.6	0	0	0	Enhanced
12705	DOANE_BREAST_CANCER_ESR1_DN	1.58	1.59	0	0	0	Enhanced
12706	MARSON_FOXP3_CORE_DIRECT_TARGETS	1.58	1.57	0	0	0	Enhanced
12707	CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_UP	1.58	1.55	0	0	0	Enhanced
12708	REACTOME_CREB3_FACTORS_ACTIVATE_GENES	1.58	1.54	0	0	0	Enhanced
12709	GO_RESPONSE_TO_MURAMYL_DIPEPTIDE	1.58	1.52	0	0	0	Enhanced
12710	TURJANSKI_MAPK14_TARGETS	1.58	1.48	0	0	0	Enhanced
12711	ZHAN_V1_LATE_DIFFERENTIATION_GENES_UP	1.58	1.48	0	0	0	Enhanced
12712	GO_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	1.58	1.47	0	0	0	Enhanced
12713	STOSSI_RESPONSE_TO_ESTRADIOL	1.58	1.47	0	0	0	Enhanced
12714	GO_NEGATIVE_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SI	1.58	1.46	0	0	0	Enhanced
12715	GO_HISTONE_H3_K27_METHYLATION	1.58	1.44	0	0	0	Enhanced
12716	RODRIGUES_NTN1_AND_DCC_TARGETS	1.58	1.42	0	0	0	Enhanced
12717	TOMLINS_METASTASIS_DN	1.58	1.4	0	0	0	Enhanced
12718	DCA_UP.V1_DN	1.59	4	0	0	0	Enhanced
12719	WONG_ADULT_TISSUE_STEM_MODULE	1.59	4	0	0	0	Enhanced
12720	GO_REGULATION_OF_T_HELPER_2_CELL_CYTOKINE_PRODUCTION	1.59	2.69	0	0	0	Enhanced
12721	AKT_UP_MTOR_DN.V1_DN	1.59	2.55	0	0	0	Enhanced
12722	LIU_SOX4_TARGETS_UP	1.59	2.55	0	0	0	Enhanced
12723	GROSS_HYPOXIA_VIA_ELK3_DN	1.59	2.52	0	0	0	Enhanced
12724	GO_SKELETAL_MUSCLE_ORGAN_DEVELOPMENT	1.59	2.51	0	0	0	Enhanced
12725	GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORT	1.59	2.33	0	0	0	Enhanced
12726	MORI_IMMATURE_B_LYMPHOCYTE_UP	1.59	2.3	0	0	0	Enhanced
12727	KANG_AR_TARGETS_DN	1.59	2.14	0	0	0	Enhanced
12728	BIOCARTA_AMAN_PATHWAY	1.59	2.12	0	0	0	Enhanced
12729	GO_REGULATION_OF_TYPE_B_PANCREATIC_CELL_PROLIFERATION	1.59	2.12	0	0	0	Enhanced
12730	GO_DRUG_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.59	1.95	0	0	0	Enhanced
12731	REACTOME_BUTYROPHILIN_BTN_FAMILY_INTERACTIONS	1.59	1.95	0	0	0	Enhanced
12732	GO_L_SERINE_BIOSYNTHETIC_PROCESS	1.59	1.93	0	0	0	Enhanced
12733	GO_MAINTENANCE_OF_PROTEIN_LOCATION_IN_NUCLEUS	1.59	1.88	0	0	0	Enhanced
12734	NAGASHIMA_EGF_SIGNALING_UP	1.59	1.85	0	0	0	Enhanced
12735	GO_PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	1.59	1.79	0	0	0	Enhanced
12736	CAHOY_NEURONAL	1.59	1.75	0	0	0	Enhanced
12737	GO_DICARBOXYLIC_ACID_METABOLIC_PROCESS	1.59	1.74	0	0	0	Enhanced
12738	CAIRO_PML_TARGETS_BOUND_BY_MYC_DN	1.59	1.72	0	0	0	Enhanced
12739	WANG_LSD1_TARGETS_DN	1.59	1.71	0	0	0	Enhanced
12740	REACTOME_SERINE_BIOSYNTHESIS	1.59	1.7	0	0	0	Enhanced
12741	GO_PHOSPHATIDYLCHOLINE_METABOLIC_PROCESS	1.59	1.64	0	0	0	Enhanced

12742	GO_POSITIVE_REGULATION_OF_HORMONE_METABOLIC_PROCESS	1.59	1.61	0	0	0	Enhanced
12743	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	1.59	1.57	0	0	0	Enhanced
12744	GO_GOLGI_CIS_CISTERNA	1.59	1.55	0	0	0	Enhanced
12745	IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_UP	1.59	1.54	0	0	0	Enhanced
12746	OHGUCHI_LIVER_HNF4A_TARGETS_UP	1.59	1.41	0	0	0	Enhanced
12747	GO_TOLL_LIKE_RECEPTOR_2_SIGNALING_PATHWAY	1.59	1.39	0	0	0	Enhanced
12748	WEST_ADRENOCORTICAL_TUMOR_DN	1.60	4	0	0	0	Enhanced
12749	GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	1.60	2.84	0	0	0	Enhanced
12750	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP	1.60	2.83	0	0	0	Enhanced
12751	COULOUARN_TEMPORAL_TGFB1_SIGNATURE_UP	1.60	2.51	0	0	0	Enhanced
12752	YAMAZAKI_TCEB3_TARGETS_UP	1.60	2.35	0	0	0	Enhanced
12753	REACTOME_METABOLISM_OF_STEROIDS	1.60	2.24	0	0	0	Enhanced
12754	GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	1.60	2.11	0	0	0	Enhanced
12755	GO_LIPASE_ACTIVITY	1.60	2.1	0	0	0	Enhanced
12756	CHEN_HOXA5_TARGETS_6HR_UP	1.60	1.95	0	0	0	Enhanced
12757	GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_2_SIGNALING_PATHWAY	1.60	1.93	0	0	0	Enhanced
12758	GO_STEROL_BINDING	1.60	1.93	0	0	0	Enhanced
12759	GO_STEROL_HOMEOSTASIS	1.60	1.9	0	0	0	Enhanced
12760	LEE_NEURAL_CREST_STEM_CELL_DN	1.60	1.9	0	0	0	Enhanced
12761	GO_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECUL	1.60	1.89	0	0	0	Enhanced
12762	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	1.60	1.89	0	0	0	Enhanced
12763	GO_T_CELL_MEDIATED_CYTOTOXICITY	1.60	1.88	0	0	0	Enhanced
12764	REACTOME_INTERLEUKIN_7_SIGNALING	1.60	1.88	0	0	0	Enhanced
12765	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_2	1.60	1.87	0	0	0	Enhanced
12766	INGA_TP53_TARGETS	1.60	1.85	0	0	0	Enhanced
12767	GO_INTERLEUKIN_10_SECRETION	1.60	1.82	0	0	0	Enhanced
12768	GO_CARGO_RECEPTOR_ACTIVITY	1.60	1.81	0	0	0	Enhanced
12769	BROWNE_HCMV_INFECTION_1HR_UP	1.60	1.8	0	0	0	Enhanced
12770	COWLING_MYCN_TARGETS	1.60	1.8	0	0	0	Enhanced
12771	GO_PHOSPHATIDYLETHANOLAMINE_ACYL_CHAIN_REMODELING	1.60	1.8	0	0	0	Enhanced
12772	ZHAN_MULTIPLE_MYELOMA_HP_UP	1.60	1.8	0	0	0	Enhanced
12773	GO_OLIGOSACCHARYLTRANSFERASE_COMPLEX	1.60	1.79	0	0	0	Enhanced
12774	GO_NEGATIVE_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	1.60	1.75	0	0	0	Enhanced
12775	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN	1.60	1.74	0	0	0	Enhanced
12776	GO_REGULATION_OF_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHW	1.60	1.74	0	0	0	Enhanced
12777	BIOCARTA_TH1TH2_PATHWAY	1.60	1.73	0	0	0	Enhanced
12778	REACTOME_PCNA_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR	1.60	1.72	0	0	0	Enhanced
12779	PID_CD40_PATHWAY	1.60	1.69	0	0	0	Enhanced
12780	REACTOME_ENDOSOMAL_VACUOLAR_PATHWAY	1.60	1.69	0	0	0	Enhanced
12781	GO_PROTEIN_DEGLYCOSYLATION	1.60	1.66	0	0	0	Enhanced
12782	GO_GLUCOCORTICOID_RECEPTOR_BINDING	1.60	1.65	0	0	0	Enhanced
12783	SCHLINGEMANN_SKIN_CARCINOGENESIS_TPA_DN	1.60	1.64	0	0	0	Enhanced
12784	GO_T_HELPER_2_CELL_DIFFERENTIATION	1.60	1.61	0	0	0	Enhanced
12785	GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_4_SIGNALING_PATHWAY	1.60	1.57	0	0	0	Enhanced
12786	CHICAS_RB1_TARGETS_CONFLUENT	1.61	4	0	0	0	Enhanced
12787	GO_LYMPHOCYTE_ACTIVATION	1.61	4	0	0	0	Enhanced
12788	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP	1.61	4	0	0	0	Enhanced
12789	MONNIER_POSTRADIATION_TUMOR_ESCAPE_DN	1.61	4	0	0	0	Enhanced
12790	SANSOM_APC_TARGETS_DN	1.61	2.58	0	0	0	Enhanced
12791	CAIRO_HEPATOBLASTOMA_DN	1.61	2.55	0	0	0	Enhanced
12792	GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	1.61	2.5	0	0	0	Enhanced
12793	GO_POSITIVE_REGULATION_OF_T_HELPER_2_CELL_CYTOKINE_PRODUCTION	1.61	2.41	0	0	0	Enhanced
12794	MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_DN	1.61	2.34	0	0	0	Enhanced
12795	GO_SLEEP	1.61	2.25	0	0	0	Enhanced
12796	VILIMAS_NOTCH1_TARGETS_DN	1.61	2.23	0	0	0	Enhanced
12797	GO_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	1.61	2.08	0	0	0	Enhanced
12798	GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_SECRETION	1.61	2.01	0	0	0	Enhanced
12799	RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_DN	1.61	2.01	0	0	0	Enhanced
12800	GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	1.61	1.95	0	0	0	Enhanced
12801	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_UP	1.61	1.93	0	0	0	Enhanced
12802	CUI_TCF21_TARGETS_DN	1.61	1.9	0	0	0	Enhanced
12803	GO_CARDIAC_RIGHT_VENTRICLE_MORPHOGENESIS	1.61	1.88	0	0	0	Enhanced
12804	GO_RESPONSE_TO_COLD	1.61	1.88	0	0	0	Enhanced
12805	GO_RESPONSE_TO_FOLLICLE_STIMULATING_HORMONE	1.61	1.88	0	0	0	Enhanced
12806	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	1.61	1.87	0	0	0	Enhanced
12807	REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH	1.61	1.87	0	0	0	Enhanced
12808	GO_PHOSPHATIDYLSERINE_BINDING	1.61	1.72	0	0	0	Enhanced
12809	GO_REGULATION_OF_MACROPHAGE_ACTIVATION	1.61	1.72	0	0	0	Enhanced
12810	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	1.61	1.71	0	0	0	Enhanced
12811	GO_REGULATION_OF_MICROGLIAL_CELL_ACTIVATION	1.61	1.71	0	0	0	Enhanced
12812	GO_ASTROCYTE_ACTIVATION	1.61	1.7	0	0	0	Enhanced
12813	GO_REGULATION_OF_HORMONE_METABOLIC_PROCESS	1.61	1.69	0	0	0	Enhanced
12814	BIOCARTA_MCM_PATHWAY	1.61	1.68	0	0	0	Enhanced
12815	JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_UP	1.61	1.65	0	0	0	Enhanced
12816	REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIMERIC_STRU	1.61	1.6	0	0	0	Enhanced
12817	BILD_E2F3_ONCOGENIC_SIGNATURE	1.62	4	0	0	0	Enhanced
12818	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP	1.62	4	0	0	0	Enhanced
12819	GO_B_CELL_ACTIVATION	1.62	4	0	0	0	Enhanced
12820	GO_GOLGI_STACK	1.62	4	0	0	0	Enhanced
12821	GO_VACUOLAR_MEMBRANE	1.62	4	0	0	0	Enhanced
12822	GO_VACUOLAR_PART	1.62	4	0	0	0	Enhanced
12823	ODONNELL_TFRC_TARGETS_UP	1.62	4	0	0	0	Enhanced
12824	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP	1.62	2.84	0	0	0	Enhanced
12825	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	1.62	2.81	0	0	0	Enhanced
12826	GO_T_CELL_PROLIFERATION	1.62	2.54	0	0	0	Enhanced
12827	GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	1.62	2.5	0	0	0	Enhanced
12828	BMI1_DN_MEL18_DN.V1_UP	1.62	2.35	0	0	0	Enhanced
12829	VERHAAK_GLIOBLASTOMA_PRONEURAL	1.62	2.35	0	0	0	Enhanced
12830	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN	1.62	2.32	0	0	0	Enhanced
12831	BURTON_ADIPOGENESIS_PEAK_AT_0HR	1.62	2.29	0	0	0	Enhanced
12832	GO_INTRACELLULAR_CALCIUM_ACTIVATED_CHLORIDE_CHANNEL_ACTIVITY	1.62	2.25	0	0	0	Enhanced
12833	ESC_J1_UP_EARLY.V1_UP	1.62	2.23	0	0	0	Enhanced
12834	GO_REGULATION_OF_INTERFERON_GAMMA_SECRETION	1.62	2.23	0	0	0	Enhanced
12835	SANA_TNF_SIGNALING_UP	1.62	2.2	0	0	0	Enhanced
12836	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_DN	1.62	2.16	0	0	0	Enhanced
12837	MORI_PRE_BI_LYMPHOCYTE_DN	1.62	2.12	0	0	0	Enhanced
12838	BAKKER_FOXO3_TARGETS_UP	1.62	2.08	0	0	0	Enhanced
12839	ONO_FOXP3_TARGETS_UP	1.62	2.05	0	0	0	Enhanced
12840	GO_ENDOTHELIAL_CELL_PROLIFERATION	1.62	2.03	0	0	0	Enhanced
12841	KRAS.BREAST_UP.V1_DN	1.62	2.03	0	0	0	Enhanced
12842	BIOCARTA_ASBCELL_PATHWAY	1.62	2.02	0	0	0	Enhanced
12843	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP	1.62	2.02	0	0	0	Enhanced
12844	GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_CYTOKINE_PRODUCTION	1.62	1.96	0	0	0	Enhanced
12845	REACTOME_ACYL_CHAIN_REMODELLING_OF_PE	1.62	1.95	0	0	0	Enhanced
12846	NRL_DN.V1_DN	1.62	1.94	0	0	0	Enhanced
12847	SMID_BREAST_CANCER_LUMINAL_A_UP	1.62	1.89	0	0	0	Enhanced
12848	GO_MHC_PROTEIN_COMPLEX	1.62	1.88	0	0	0	Enhanced
12849	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN	1.62	1.86	0	0	0	Enhanced
12850	GO_REGULATION_OF_SPROUTING_ANGIOGENESIS	1.62	1.85	0	0	0	Enhanced

12851	CHR5P12	1.62	1.84	0	0	0	Enhanced
12852	VALK_AML_CLUSTER_4	1.62	1.78	0	0	0	Enhanced
12853	GO_SERINE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	1.62	1.77	0	0	0	Enhanced
12854	REACTOME_AFLATOXIN_ACTIVATION_AND_DETOXIFICATION	1.62	1.77	0	0	0	Enhanced
12855	BIOCARTA_EPO_PATHWAY	1.62	1.75	0	0	0	Enhanced
12856	REACTOME_INTERLEUKIN_9_SIGNALING	1.62	1.75	0	0	0	Enhanced
12857	GO_REGULATION_OF_CHOLESTEROL_METABOLIC_PROCESS	1.62	1.73	0	0	0	Enhanced
12858	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_SECRETION	1.62	1.69	0	0	0	Enhanced
12859	ZHENG_IL22_SIGNALING_UP	1.62	1.55	0	0	0	Enhanced
12860	AKT_UP.V1_DN	1.63	4	0	0	0	Enhanced
12861	FEVR_CTNNB1_TARGETS_UP	1.63	4	0	0	0	Enhanced
12862	GO_CELL_CHEMOTAXIS	1.63	2.84	0	0	0	Enhanced
12863	HALLMARK_HYPOXIA	1.63	2.83	0	0	0	Enhanced
12864	GCNP_SHH_UP_EARLY.V1_DN	1.63	2.81	0	0	0	Enhanced
12865	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP	1.63	2.8	0	0	0	Enhanced
12866	SERVITJA_ISLET_HNF1A_TARGETS_UP	1.63	2.8	0	0	0	Enhanced
12867	SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B_LYMPHOCYTE	1.63	2.5	0	0	0	Enhanced
12868	GO_TRANSPORTER_COMPLEX	1.63	2.38	0	0	0	Enhanced
12869	ZHAN_EARLY_DIFFERENTIATION_GENES_UP	1.63	2.37	0	0	0	Enhanced
12870	MTOR_UP.V1_DN	1.63	2.35	0	0	0	Enhanced
12871	GO_B_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	1.63	2.32	0	0	0	Enhanced
12872	GO_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	1.63	2.18	0	0	0	Enhanced
12873	ZHANG_TLX_TARGETS_UP	1.63	2.13	0	0	0	Enhanced
12874	BOYLAN_MULTIPLE_MYELOMA_PCA1_UP	1.63	2.02	0	0	0	Enhanced
12875	GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	1.63	2	0	0	0	Enhanced
12876	REACTOME_SIGNALING_BY_LEPTIN	1.63	1.96	0	0	0	Enhanced
12877	GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	1.63	1.92	0	0	0	Enhanced
12878	GO_TOLERANCE_INDUCTION	1.63	1.91	0	0	0	Enhanced
12879	GO_AMMONIUM_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.63	1.9	0	0	0	Enhanced
12880	GO_INTERLEUKIN_4_PRODUCTION	1.63	1.9	0	0	0	Enhanced
12881	PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_DN	1.63	1.89	0	0	0	Enhanced
12882	GO_ANCHORED_COMPONENT_OF_PLASMA_MEMBRANE	1.63	1.86	0	0	0	Enhanced
12883	GO_NONRIBOSOMAL_PEPTIDE_BIOSYNTHETIC_PROCESS	1.63	1.8	0	0	0	Enhanced
12884	REACTOME_DISEASES_ASSOCIATED_WITH_GLYCOSAMINOGLYCAN_METABOLISM	1.63	1.8	0	0	0	Enhanced
12885	CHEOK_RESPONSE_TO_HD_MTX_UP	1.63	1.79	0	0	0	Enhanced
12886	PID_IL4_2PATHWAY	1.63	1.79	0	0	0	Enhanced
12887	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	1.63	1.78	0	0	0	Enhanced
12888	TSAI_DNAJB4_TARGETS_UP	1.63	1.78	0	0	0	Enhanced
12889	YU_MYC_TARGETS_DN	1.63	1.74	0	0	0	Enhanced
12890	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	1.63	1.65	0	0	0	Enhanced
12891	GO_SIDE_OF_MEMBRANE	1.64	4	0	0	0	Enhanced
12892	HUTTMANN_B_CLL_POOR_SURVIVAL_UP	1.64	4	0	0	0	Enhanced
12893	SENESE_HDAC1_AND_HDAC2_TARGETS_DN	1.64	4	0	0	0	Enhanced
12894	GO_GATED_CHANNEL_ACTIVITY	1.64	2.83	0	0	0	Enhanced
12895	CAIRO_LIVER_DEVELOPMENT_DN	1.64	2.81	0	0	0	Enhanced
12896	EGFR_UP.V1_UP	1.64	2.81	0	0	0	Enhanced
12897	GO_RESPONSE_TO_CORTICOSTEROID	1.64	2.81	0	0	0	Enhanced
12898	MARKEY_RB1_CHRONIC_LOF_UP	1.64	2.79	0	0	0	Enhanced
12899	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHY_DN	1.64	2.68	0	0	0	Enhanced
12900	GO_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	1.64	2.51	0	0	0	Enhanced
12901	GO_ENDOTHELIAL_CELL_MIGRATION	1.64	2.36	0	0	0	Enhanced
12902	GO_POSITIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	1.64	2.24	0	0	0	Enhanced
12903	MURAKAMI_UV_RESPONSE_1HR_DN	1.64	2.22	0	0	0	Enhanced
12904	GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	1.64	2.21	0	0	0	Enhanced
12905	BURTON_ADIPOGENESIS_9	1.64	2.2	0	0	0	Enhanced
12906	REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM	1.64	2.16	0	0	0	Enhanced
12907	KRAS.300_UP.V1_DN	1.64	2.12	0	0	0	Enhanced
12908	REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G1_CE	1.64	2.12	0	0	0	Enhanced
12909	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN	1.64	2.05	0	0	0	Enhanced
12910	GO_HYDROLASE_ACTIVITY_ACTING_ON_GLYCOSYL_BONDS	1.64	2.04	0	0	0	Enhanced
12911	CHUNG_BLISTER_CYTOTOXICITY_DN	1.64	2.01	0	0	0	Enhanced
12912	ZHANG_GATA6_TARGETS_DN	1.64	1.99	0	0	0	Enhanced
12913	PID_HNF3A_PATHWAY	1.64	1.92	0	0	0	Enhanced
12914	GO_PROTEOGLYCAN_BINDING	1.64	1.89	0	0	0	Enhanced
12915	AMIT_EGF_RESPONSE_40_MCF10A	1.64	1.85	0	0	0	Enhanced
12916	GO_BASAL_PART_OF_CELL	1.64	1.82	0	0	0	Enhanced
12917	REACTOME_HS_GAG_DEGRADATION	1.64	1.79	0	0	0	Enhanced
12918	ZHU_SKIL_TARGETS_UP	1.64	1.79	0	0	0	Enhanced
12919	GO_RESPONSE_TO_LAMINAR_FLUID_SHEAR_STRESS	1.64	1.74	0	0	0	Enhanced
12920	WATTEL_AUTONOMOUS_THYROID_ADENOMA_DN	1.64	1.69	0	0	0	Enhanced
12921	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_VIA_MHC_CLASS_IB	1.64	1.55	0	0	0	Enhanced
12922	BASAKI_YBX1_TARGETS_DN	1.65	4	0	0	0	Enhanced
12923	GO_LEUKOCYTE_MIGRATION	1.65	4	0	0	0	Enhanced
12924	GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	1.65	4	0	0	0	Enhanced
12925	REACTOME_ERYTHROPOIETIN_ACTIVATES_STAT5	1.65	4	0	0	0	Enhanced
12926	GO_CELLULAR_RESPONSE_TO_XENOBIOTIC_STIMULUS	1.65	2.79	0	0	0	Enhanced
12927	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	1.65	2.78	0	0	0	Enhanced
12928	KRAS.600_UP.V1_UP	1.65	2.54	0	0	0	Enhanced
12929	REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	1.65	2.5	0	0	0	Enhanced
12930	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	1.65	2.31	0	0	0	Enhanced
12931	GO_STEROL_TRANSPORT	1.65	2.3	0	0	0	Enhanced
12932	KEGG_GRAFT_VERSUS_HOST_DISEASE	1.65	2.25	0	0	0	Enhanced
12933	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	1.65	2.2	0	0	0	Enhanced
12934	TOMIDA_METASTASIS_DN	1.65	2.05	0	0	0	Enhanced
12935	SCHWAB_TARGETS_OF_BMYB_POLYMORPHIC_VARIANTS_DN	1.65	1.97	0	0	0	Enhanced
12936	REACTOME_ANTIMICROBIAL_PEPTIDES	1.65	1.96	0	0	0	Enhanced
12937	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_BETA_PRODUCTION	1.65	1.95	0	0	0	Enhanced
12938	CTIP_DN.V1_UP	1.65	1.94	0	0	0	Enhanced
12939	REACTOME_DNA_STRAND_ELONGATION	1.65	1.93	0	0	0	Enhanced
12940	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	1.65	1.92	0	0	0	Enhanced
12941	GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PR	1.65	1.88	0	0	0	Enhanced
12942	GO_CELLULAR_RESPONSE_TO_LAMINAR_FLUID_SHEAR_STRESS	1.65	1.82	0	0	0	Enhanced
12943	GO_NEGATIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	1.65	1.74	0	0	0	Enhanced
12944	PID_IL27_PATHWAY	1.65	1.66	0	0	0	Enhanced
12945	GRANDVAUX_IRF3_TARGETS_DN	1.65	1.64	0	0	0	Enhanced
12946	GO_ENDOPLASMIC_RETICULUM_LUMEN	1.66	4	0	0	0	Enhanced
12947	GO_REGULATION_OF_VASCULATURE_DEVELOPMENT	1.66	4	0	0	0	Enhanced
12948	GO_T_CELL_ACTIVATION	1.66	4	0	0	0	Enhanced
12949	GO_VACUOLE	1.66	4	0	0	0	Enhanced
12950	KRAS.DF.V1_UP	1.66	2.84	0	0	0	Enhanced
12951	FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_UP	1.66	2.77	0	0	0	Enhanced
12952	GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.66	2.5	0	0	0	Enhanced
12953	VANLOO_SP3_TARGETS_DN	1.66	2.49	0	0	0	Enhanced
12954	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	1.66	2.42	0	0	0	Enhanced
12955	TIAN_BHLHA15_TARGETS	1.66	2.42	0	0	0	Enhanced
12956	REACTOME_ACTIVATION_OF_THE_AP_1_FAMILY_OF_TRANSCRIPTION_FACTORS	1.66	2.41	0	0	0	Enhanced
12957	GO_LIPID_HOMEOSTASIS	1.66	2.36	0	0	0	Enhanced
12958	HU_ANGIOGENESIS_UP	1.66	2.16	0	0	0	Enhanced
12959	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS_	1.66	2.15	0	0	0	Enhanced

12960	GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	1.66	2.15	0	0	0	Enhanced
12961	GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	1.66	2.14	0	0	0	Enhanced
12962	GO_TYPE_B_PANCREATIC_CELL_PROLIFERATION	1.66	2.12	0	0	0	Enhanced
12963	INGRAM_SHH_TARGETS_DN	1.66	2.07	0	0	0	Enhanced
12964	DACOSTA_ERCC3_ALLELE_XPCS_VS_TTD_DN	1.66	2.06	0	0	0	Enhanced
12965	GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_BIOSYNTHETIC_PROCESS	1.66	2.06	0	0	0	Enhanced
12966	MARIADASON_RESPONSE_TO_BUTYRATE_CURCUMIN_SULINDAC_TSA_1	1.66	2.03	0	0	0	Enhanced
12967	KEGG_ASTHMA	1.66	2.02	0	0	0	Enhanced
12968	DAZARD_UV_RESPONSE_CLUSTER_G3	1.66	1.96	0	0	0	Enhanced
12969	GO_COLLAGEN_CATABOLIC_PROCESS	1.66	1.96	0	0	0	Enhanced
12970	GO_ACUTE_INFLAMMATORY_RESPONSE	1.66	1.95	0	0	0	Enhanced
12971	GO_REGULATION_OF_NEUROINFLAMMATORY_RESPONSE	1.66	1.94	0	0	0	Enhanced
12972	ALK_DN.V1_DN	1.66	1.92	0	0	0	Enhanced
12973	BIOCARTA_IL10_PATHWAY	1.66	1.89	0	0	0	Enhanced
12974	GO_BASAL_PLASMA_MEMBRANE	1.66	1.89	0	0	0	Enhanced
12975	XU_HGF_SIGNALING_NOT_VIA_AKT1_48HR_UP	1.66	1.87	0	0	0	Enhanced
12976	ROSS_AML_WITH_CBFB_MYH11_FUSION	1.66	1.86	0	0	0	Enhanced
12977	GO_CELLULAR_RESPONSE_TO_CHOLESTEROL	1.66	1.79	0	0	0	Enhanced
12978	GO_INTERLEUKIN_8_BIOSYNTHETIC_PROCESS	1.67	4	0	0	0	Enhanced
12979	GO_LEUKOCYTE_DIFFERENTIATION	1.67	4	0	0	0	Enhanced
12980	HAMAI_APOPTOSIS_VIA_TRAIL_DN	1.67	4	0	0	0	Enhanced
12981	REACTOME_TYPE_I_HEMIDESMOSOME_ASSEMBLY	1.67	4	0	0	0	Enhanced
12982	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP	1.67	4	0	0	0	Enhanced
12983	GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	1.67	2.8	0	0	0	Enhanced
12984	GO_ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.67	2.53	0	0	0	Enhanced
12985	GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.67	2.5	0	0	0	Enhanced
12986	GO_RESPONSE_TO_ANTINEOPLASTIC_AGENT	1.67	2.34	0	0	0	Enhanced
12987	ONO_AML1_TARGETS_UP	1.67	2.27	0	0	0	Enhanced
12988	HUMMEL_BURKITTS_LYMPHOMA_DN	1.67	2.26	0	0	0	Enhanced
12989	DUTERTRE_ESTRADIOL_RESPONSE_6HR_DN	1.67	2.19	0	0	0	Enhanced
12990	NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_UP	1.67	2.12	0	0	0	Enhanced
12991	LEI_HOXC8_TARGETS_DN	1.67	2.1	0	0	0	Enhanced
12992	GO_SPLEEN_DEVELOPMENT	1.67	2.05	0	0	0	Enhanced
12993	ZHANG_INTERFERON_RESPONSE	1.67	2.04	0	0	0	Enhanced
12994	GO_RESPONSE_TO_PROTOZOAN	1.67	2.02	0	0	0	Enhanced
12995	SABATES_COLORECTAL_ADENOMA_UP	1.67	2.01	0	0	0	Enhanced
12996	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	1.67	1.98	0	0	0	Enhanced
12997	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_BETA_SECRETION	1.67	1.94	0	0	0	Enhanced
12998	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN	1.67	1.9	0	0	0	Enhanced
12999	PID_NFKAPPAB_ATYPICAL_PATHWAY	1.67	1.9	0	0	0	Enhanced
13000	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER	1.67	1.86	0	0	0	Enhanced
13001	GO_RESPONSE_TO_ACIDIC_PH	1.67	1.82	0	0	0	Enhanced
13002	PID_INTEGRIN2_PATHWAY	1.67	1.78	0	0	0	Enhanced
13003	GO_POSITIVE_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	1.67	1.74	0	0	0	Enhanced
13004	BUSA_SAM68_TARGETS_UP	1.68	4	0	0	0	Enhanced
13005	ELVIDGE_HYPOXIA_UP	1.68	4	0	0	0	Enhanced
13006	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP	1.68	4	0	0	0	Enhanced
13007	VERHAAK_GLIOBLASTOMA_MESENCHYMAL	1.68	4	0	0	0	Enhanced
13008	CHANDRAN_METASTASIS_DN	1.68	2.84	0	0	0	Enhanced
13009	GO_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	1.68	2.52	0	0	0	Enhanced
13010	GO_GAMMA_DELTA_T_CELL_DIFFERENTIATION	1.68	2.41	0	0	0	Enhanced
13011	KANG_IMMORTALIZED_BY_TERT_DN	1.68	2.34	0	0	0	Enhanced
13012	GO_BICARBONATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.68	2.24	0	0	0	Enhanced
13013	SAGIV_CD24_TARGETS_DN	1.68	2.19	0	0	0	Enhanced
13014	NAKAYAMA_FRA2_TARGETS	1.68	2.17	0	0	0	Enhanced
13015	GO_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	1.68	2.16	0	0	0	Enhanced
13016	GO_CHOLESTEROL_TRANSPORTER_ACTIVITY	1.68	2.1	0	0	0	Enhanced
13017	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_UP	1.68	2.08	0	0	0	Enhanced
13018	GO_AMMONIUM_TRANSPORT	1.68	2.08	0	0	0	Enhanced
13019	GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBUL	1.68	2.07	0	0	0	Enhanced
13020	SCHOEN_NFKB_SIGNALING	1.68	2.05	0	0	0	Enhanced
13021	STEARMAN_TUMOR_FIELD_EFFECT_UP	1.68	2.04	0	0	0	Enhanced
13022	REACTOME_AKT_PHOSPHORYLATES_TARGETS_IN_THE_NUCLEUS	1.68	2.02	0	0	0	Enhanced
13023	GO_CHLORIDE_CHANNEL_COMPLEX	1.68	1.97	0	0	0	Enhanced
13024	GO_MATURE_B_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	1.68	1.97	0	0	0	Enhanced
13025	LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS	1.68	1.96	0	0	0	Enhanced
13026	REACTOME_INTERLEUKIN_21_SIGNALING	1.68	1.94	0	0	0	Enhanced
13027	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP	1.68	1.9	0	0	0	Enhanced
13028	REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM	1.68	1.77	0	0	0	Enhanced
13029	GO_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.69	4	0	0	0	Enhanced
13030	GO_ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS	1.69	4	0	0	0	Enhanced
13031	GO_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	1.69	4	0	0	0	Enhanced
13032	GO_T_HELPER_2_CELL_CYTOKINE_PRODUCTION	1.69	4	0	0	0	Enhanced
13033	GO_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.69	4	0	0	0	Enhanced
13034	HELLER_SILENCED_BY_METHYLATION_DN	1.69	4	0	0	0	Enhanced
13035	HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN	1.69	4	0	0	0	Enhanced
13036	REACTOME_GPCR_LIGAND_BINDING	1.69	4	0	0	0	Enhanced
13037	YAGI_AML_FAB_MARKERS	1.69	4	0	0	0	Enhanced
13038	ZHANG_TLX_TARGETS_60HR_UP	1.69	2.86	0	0	0	Enhanced
13039	VEGF_A_UP.V1_UP	1.69	2.82	0	0	0	Enhanced
13040	ZWANG_EGF_INTERVAL_DN	1.69	2.82	0	0	0	Enhanced
13041	GO_MARGINAL_ZONE_B_CELL_DIFFERENTIATION	1.69	2.7	0	0	0	Enhanced
13042	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	1.69	2.5	0	0	0	Enhanced
13043	BAE_BRCA1_TARGETS_UP	1.69	2.49	0	0	0	Enhanced
13044	SCHRAETS_MLL_TARGETS_UP	1.69	2.42	0	0	0	Enhanced
13045	VANHARANTA_UTERINE_FIBROID_DN	1.69	2.32	0	0	0	Enhanced
13046	GO_NEUTRAL_AMINO_ACID_TRANSPORT	1.69	2.29	0	0	0	Enhanced
13047	BOYLAN_MULTIPLE_MYELOMA_D_DN	1.69	2.2	0	0	0	Enhanced
13048	GO_HYDROLASE_ACTIVITY_HYDROLYZING_O_GLYCOSYL_COMPOUNDS	1.69	2.2	0	0	0	Enhanced
13049	GO_INTERLEUKIN_2_PRODUCTION	1.69	2.2	0	0	0	Enhanced
13050	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP	1.69	2.17	0	0	0	Enhanced
13051	GO_ALPHA_BETA_T_CELL_PROLIFERATION	1.69	2.16	0	0	0	Enhanced
13052	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	1.69	2.16	0	0	0	Enhanced
13053	GO_MATURE_B_CELL_DIFFERENTIATION	1.69	2.15	0	0	0	Enhanced
13054	GO_NEGATIVE_REGULATION_OF_SPROUTING_ANGIOGENESIS	1.69	2.14	0	0	0	Enhanced
13055	TIAN_TNF_SIGNALING_VIA_NFKB	1.69	2.14	0	0	0	Enhanced
13056	REACTOME_ACTIVATION_OF_MATRIX_METALLOPROTEINASES	1.69	2.13	0	0	0	Enhanced
13057	HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGENESIS	1.69	2.1	0	0	0	Enhanced
13058	LOPES_METHYLATED_IN_COLON_CANCER_UP	1.69	1.97	0	0	0	Enhanced
13059	GO_CELLULAR_RESPONSE_TO_FLUID_SHEAR_STRESS	1.69	1.96	0	0	0	Enhanced
13060	GO_NEGATIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	1.69	1.94	0	0	0	Enhanced
13061	GO_CALCIUM_DEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL	1.69	1.88	0	0	0	Enhanced
13062	GO_REGULATION_OF_HORMONE_BIOSYNTHETIC_PROCESS	1.69	1.75	0	0	0	Enhanced
13063	ELVIDGE_HYPOXIA_BY_DMOG_UP	1.70	4	0	0	0	Enhanced
13064	GO_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.70	4	0	0	0	Enhanced
13065	GO_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	1.70	4	0	0	0	Enhanced
13066	GO_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALIN	1.70	4	0	0	0	Enhanced
13067	GOUYER_TATI_TARGETS_DN	1.70	4	0	0	0	Enhanced
13068	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN	1.70	4	0	0	0	Enhanced

13069	RB_P107_DN.V1_UP	1.70	4	0	0	0	Enhanced
13070	SENESE_HDAC1_TARGETS_DN	1.70	2.83	0	0	0	Enhanced
13071	FOSTER_TOLERANT_MACROPHAGE_UP	1.70	2.82	0	0	0	Enhanced
13072	KIM_MYCN_AMPLIFICATION_TARGETS_DN	1.70	2.81	0	0	0	Enhanced
13073	GO_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	1.70	2.8	0	0	0	Enhanced
13074	SUNG_METASTASIS_STROMA_UP	1.70	2.51	0	0	0	Enhanced
13075	PID_IL12_2PATHWAY	1.70	2.32	0	0	0	Enhanced
13076	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	1.70	2.22	0	0	0	Enhanced
13077	GO_GOLGI_CISTERNA_MEMBRANE	1.70	2.19	0	0	0	Enhanced
13078	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN	1.70	2.15	0	0	0	Enhanced
13079	GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	1.70	2.1	0	0	0	Enhanced
13080	ATM_DN.V1_UP	1.71	4	0	0	0	Enhanced
13081	GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	1.71	4	0	0	0	Enhanced
13082	RADAEVA_RESPONSE_TO_IFNA1_DN	1.71	4	0	0	0	Enhanced
13083	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1	1.71	4	0	0	0	Enhanced
13084	STK33_SKM_UP	1.71	4	0	0	0	Enhanced
13085	STK33_UP	1.71	4	0	0	0	Enhanced
13086	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	1.71	2.79	0	0	0	Enhanced
13087	GO_INTERLEUKIN_1_PRODUCTION	1.71	2.78	0	0	0	Enhanced
13088	LIU_IL13_PRIMING_MODEL	1.71	2.74	0	0	0	Enhanced
13089	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_DN	1.71	2.44	0	0	0	Enhanced
13090	GO_DIPEPTIDASE_ACTIVITY	1.71	2.42	0	0	0	Enhanced
13091	TENEDINI_MEGAKARYOCYTE_MARKERS	1.71	2.31	0	0	0	Enhanced
13092	ZHENG_FOXP3_TARGETS_IN_T_LYMPHOCYTE_DN	1.71	2.3	0	0	0	Enhanced
13093	YAO_HOXA10_TARGETS_VIA_PROGESTERONE_UP	1.71	2.28	0	0	0	Enhanced
13094	DALESSIO_TSA_RESPONSE	1.71	2.27	0	0	0	Enhanced
13095	REACTOME_INTERLEUKIN_20_FAMILY_SIGNALING	1.71	2.16	0	0	0	Enhanced
13096	DORN_ADENOVIRUS_INFECTION_12HR_UP	1.71	2.14	0	0	0	Enhanced
13097	GO_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_STI	1.71	2.08	0	0	0	Enhanced
13098	GO_ANCHORED_COMPONENT_OF_MEMBRANE	1.71	2	0	0	0	Enhanced
13099	BERENJENO_TRANSFORMED_BY_RHOA_DN	1.72	4	0	0	0	Enhanced
13100	GO_HEMIDESMOSOME_ASSEMBLY	1.72	4	0	0	0	Enhanced
13101	GO_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	1.72	4	0	0	0	Enhanced
13102	GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	1.72	4	0	0	0	Enhanced
13103	GO_PASSIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.72	4	0	0	0	Enhanced
13104	GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	1.72	4	0	0	0	Enhanced
13105	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN	1.72	4	0	0	0	Enhanced
13106	KRAS.LUNG_UP.V1_UP	1.72	4	0	0	0	Enhanced
13107	LIM_MAMMARY_STEM_CELL_DN	1.72	4	0	0	0	Enhanced
13108	LINDGREN_BLADDER_CANCER_CLUSTER_2B	1.72	4	0	0	0	Enhanced
13109	GO_INTERLEUKIN_1_BETA_PRODUCTION	1.72	2.77	0	0	0	Enhanced
13110	GO_MANNOSIDASE_ACTIVITY	1.72	2.73	0	0	0	Enhanced
13111	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP	1.72	2.5	0	0	0	Enhanced
13112	GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	1.72	2.49	0	0	0	Enhanced
13113	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINDED_IN_ERYTHROCYTE_	1.72	2.29	0	0	0	Enhanced
13114	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_DN	1.72	2.27	0	0	0	Enhanced
13115	FURUKAWA_DUSP6_TARGETS_PCI35_UP	1.72	2.18	0	0	0	Enhanced
13116	GILMORE_CORE_NFKB_PATHWAY	1.72	2.15	0	0	0	Enhanced
13117	ABBUD_LIF_SIGNALING_1_UP	1.72	2.07	0	0	0	Enhanced
13118	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_2	1.72	1.85	0	0	0	Enhanced
13119	GO_B_CELL_DIFFERENTIATION	1.73	4	0	0	0	Enhanced
13120	GO_RESPONSE_TO_BACTERIUM	1.73	4	0	0	0	Enhanced
13121	GO_TYPE_2_IMMUNE_RESPONSE	1.73	4	0	0	0	Enhanced
13122	ONDER_CDH1_TARGETS_2_DN	1.73	4	0	0	0	Enhanced
13123	ESC_V6.5_UP_EARLY.V1_DN	1.73	2.8	0	0	0	Enhanced
13124	KEGG_ALLOGRAFT_REJECTION	1.73	2.72	0	0	0	Enhanced
13125	IIZUKA_LIVER_CANCER_EARLY_RECURRENCE	1.73	2.71	0	0	0	Enhanced
13126	GO_PHOSPHATE_ION_TRANSPORT	1.73	2.44	0	0	0	Enhanced
13127	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_4	1.73	2.32	0	0	0	Enhanced
13128	CORRE_MULTIPLE_MYELOMA_DN	1.73	2.3	0	0	0	Enhanced
13129	GO_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.73	2.3	0	0	0	Enhanced
13130	GO_AUTOPHAGOSOME_MEMBRANE	1.73	1.88	0	0	0	Enhanced
13131	CSR_EARLY_UP.V1_DN	1.74	4	0	0	0	Enhanced
13132	JOHNSTONE_PARVB_TARGETS_3_UP	1.74	4	0	0	0	Enhanced
13133	PENG_LEUCINE_DEPRIVATION_UP	1.74	4	0	0	0	Enhanced
13134	REACTOME_LAMININ_INTERACTIONS	1.74	4	0	0	0	Enhanced
13135	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	1.74	2.73	0	0	0	Enhanced
13136	GO_LINOLEIC_ACID_METABOLIC_PROCESS	1.74	2.7	0	0	0	Enhanced
13137	GO_GERMINAL_CENTER_FORMATION	1.74	2.42	0	0	0	Enhanced
13138	GO_GOLGI_CISTERNA	1.74	2.34	0	0	0	Enhanced
13139	GO_HETEROTYPIC_CELL_CELL_ADHESION	1.74	2.3	0	0	0	Enhanced
13140	KEGG_HEMATOPOIETIC_CELL_LINEAGE	1.74	2.3	0	0	0	Enhanced
13141	ODONNELL_METASTASIS_UP	1.74	2.29	0	0	0	Enhanced
13142	GO_TUMOR_NECROSIS_FACTOR_BIOSYNTHETIC_PROCESS	1.74	2.23	0	0	0	Enhanced
13143	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	1.74	2.16	0	0	0	Enhanced
13144	GO_DEFENSE_RESPONSE_TO_GRAM_NEGATIVE_BACTERIUM	1.74	2.15	0	0	0	Enhanced
13145	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_DN	1.74	2.14	0	0	0	Enhanced
13146	GO_VACUOLAR_ACIDIFICATION	1.74	1.84	0	0	0	Enhanced
13147	CHASSOT_SKIN_WOUND	1.75	4	0	0	0	Enhanced
13148	KOBAYASHI_EGFR_SIGNALING_6HR_UP	1.75	4	0	0	0	Enhanced
13149	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN	1.75	4	0	0	0	Enhanced
13150	PASINI_SUZ12_TARGETS_UP	1.75	4	0	0	0	Enhanced
13151	FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP	1.75	2.8	0	0	0	Enhanced
13152	GO_REGULATION_OF_CHOLESTEROL_BIOSYNTHETIC_PROCESS	1.75	2.76	0	0	0	Enhanced
13153	GO_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	1.75	2.48	0	0	0	Enhanced
13154	PID_NFAT_TFPATHWAY	1.75	2.47	0	0	0	Enhanced
13155	PID_INTEGRIN_CS_PATHWAY	1.75	2.46	0	0	0	Enhanced
13156	GO_SOLUTE_SODIUM_SYMPORTER_ACTIVITY	1.75	2.43	0	0	0	Enhanced
13157	WIERENGA_STAT5A_TARGETS_GROUP2	1.75	2.3	0	0	0	Enhanced
13158	WILENSKY_RESPONSE_TO_DARAPLADIB	1.75	2.29	0	0	0	Enhanced
13159	CHR13Q32	1.75	2.28	0	0	0	Enhanced
13160	LINDVALL_IMMORTALIZED_BY_TERT_UP	1.75	2.28	0	0	0	Enhanced
13161	PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_UP	1.75	2.26	0	0	0	Enhanced
13162	GAUSSMANN_MLL_AF4_FUSION_TARGETS_C_DN	1.76	4	0	0	0	Enhanced
13163	GO_GAMMA_DELTA_T_CELL_ACTIVATION	1.76	4	0	0	0	Enhanced
13164	GO_INFLAMMATORY_RESPONSE	1.76	4	0	0	0	Enhanced
13165	GO_LYMPHOCYTE_MEDIATED_IMMUNITY	1.76	4	0	0	0	Enhanced
13166	KRAS.600.LUNG.BREAST_UP.V1_UP	1.76	4	0	0	0	Enhanced
13167	PENG_RAPAMYCIN_RESPONSE_UP	1.76	4	0	0	0	Enhanced
13168	RPS14_DN.V1_UP	1.76	4	0	0	0	Enhanced
13169	VECCHI_GASTRIC_CANCER_EARLY_DN	1.76	2.83	0	0	0	Enhanced
13170	GO_INTERFERON_GAMMA_PRODUCTION	1.76	2.79	0	0	0	Enhanced
13171	GO_SYMPORTER_ACTIVITY	1.76	2.77	0	0	0	Enhanced
13172	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_SECRETION	1.76	2.72	0	0	0	Enhanced
13173	GO_PHOSPHATE_ION_TRANSMEMBRANE_TRANSPORT	1.76	2.7	0	0	0	Enhanced
13174	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_UP	1.76	2.48	0	0	0	Enhanced
13175	DACOSTA_ERCC3_ALLELE_XPCS_VS_TTD_UP	1.76	2.43	0	0	0	Enhanced
13176	REACTOME_COLLAGEN_FORMATION	1.76	2.31	0	0	0	Enhanced
13177	CHIBA_RESPONSE_TO_TSA_UP	1.76	2.17	0	0	0	Enhanced

13178	CHICAS_RB1_TARGETS_SENESCENT	1.77	4	0	0	0	Enhanced
13179	GO_ANION_ANION_ANTIPORTER_ACTIVITY	1.77	4	0	0	0	Enhanced
13180	GO_INTRINSIC_COMPONENT_OF_ENDOPLASMIC_RETICULUM_MEMBRANE	1.77	4	0	0	0	Enhanced
13181	GO_MOLECULAR_TRANSDUCER_ACTIVITY	1.77	4	0	0	0	Enhanced
13182	GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	1.77	4	0	0	0	Enhanced
13183	GO_POSITIVE_REGULATION_OF_CELL_KILLING	1.77	4	0	0	0	Enhanced
13184	GO_RESPONSE_TO_FLUID_SHEAR_STRESS	1.77	4	0	0	0	Enhanced
13185	MATTHEWS_AP1_TARGETS	1.77	4	0	0	0	Enhanced
13186	ZHU_CMV_8_HR_UP	1.77	4	0	0	0	Enhanced
13187	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF	1.77	4	0	0	0	Enhanced
13188	E2F1_UP.V1_DN	1.77	2.82	0	0	0	Enhanced
13189	GUO_TARGETS_OF_IRS1_AND_IRS2	1.77	2.8	0	0	0	Enhanced
13190	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN	1.77	2.77	0	0	0	Enhanced
13191	ONDER_CDH1_SIGNALING_VIA_CTNNB1	1.77	2.77	0	0	0	Enhanced
13192	GO_PROTEIN_COMPLEX_INVOLVED_IN_CELL_ADHESION	1.77	2.75	0	0	0	Enhanced
13193	LEE_LIVER_CANCER_HEPATOBLAST	1.77	2.7	0	0	0	Enhanced
13194	RASHI_RESPONSE_TO_IONIZING_RADIATION_1	1.77	2.48	0	0	0	Enhanced
13195	DAUER_STAT3_TARGETS_UP	1.77	2.47	0	0	0	Enhanced
13196	BARRIER_COLON_CANCER_RECURRENCE_DN	1.77	2.45	0	0	0	Enhanced
13197	BIOCARTA_IL3_PATHWAY	1.77	2.44	0	0	0	Enhanced
13198	KEGG_ABC_TRANSPORTERS	1.77	2.44	0	0	0	Enhanced
13199	REACTOME_FOXO_MEDIATED_TRANSCRIPTION_OF_CELL_CYCLE_GENES	1.77	2.43	0	0	0	Enhanced
13200	TSAI_RESPONSE_TO_RADIATION_THERAPY	1.77	2.26	0	0	0	Enhanced
13201	BOYLAN_MULTIPLE_MYELOMA_C_D_DN	1.78	4	0	0	0	Enhanced
13202	CHR14Q11	1.78	4	0	0	0	Enhanced
13203	GO_G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	1.78	4	0	0	0	Enhanced
13204	LINDSTEDT_DENDRITIC_CELL_MATURATION_B	1.78	4	0	0	0	Enhanced
13205	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP	1.78	2.76	0	0	0	Enhanced
13206	AMIT_SERUM_RESPONSE_60_MCF10A	1.78	2.74	0	0	0	Enhanced
13207	GO_LUMENAL_SIDE_OF_MEMBRANE	1.78	2.74	0	0	0	Enhanced
13208	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN	1.78	2.73	0	0	0	Enhanced
13209	GO_CELLULAR_RESPONSE_TO_STEROL	1.78	2.72	0	0	0	Enhanced
13210	GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	1.78	2.72	0	0	0	Enhanced
13211	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN	1.78	2.5	0	0	0	Enhanced
13212	GO_SPROUTING_ANGIOGENESIS	1.78	2.49	0	0	0	Enhanced
13213	HOLLERN_MICROACINAR_BREAST_TUMOR_UP	1.78	2.46	0	0	0	Enhanced
13214	FOURNIER_ACINAR_DEVELOPMENT_EARLY_UP	1.78	2.44	0	0	0	Enhanced
13215	GO_ACUTE_PHASE_RESPONSE	1.78	2.44	0	0	0	Enhanced
13216	GO_L_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.78	2.3	0	0	0	Enhanced
13217	GO_LYMPHOCYTE_DIFFERENTIATION	1.79	4	0	0	0	Enhanced
13218	GO_REGULATION_OF_CELL_KILLING	1.79	4	0	0	0	Enhanced
13219	GO_REGULATION_OF_CHOLESTEROL_EFFLUX	1.79	4	0	0	0	Enhanced
13220	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP	1.79	4	0	0	0	Enhanced
13221	RAPA_EARLY_UP.V1_UP	1.79	4	0	0	0	Enhanced
13222	REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	1.79	4	0	0	0	Enhanced
13223	PDGF_UP.V1_DN	1.79	2.78	0	0	0	Enhanced
13224	VISALA_RESPONSE_TO_HEAT_SHOCK_AND_AGING_UP	1.79	2.74	0	0	0	Enhanced
13225	GO_NEGATIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	1.79	2.73	0	0	0	Enhanced
13226	GO_NEUTRAL_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.79	2.73	0	0	0	Enhanced
13227	GO_REGULATION_OF_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	1.79	2.45	0	0	0	Enhanced
13228	GENTLES_LEUKEMIC_STEM_CELL_UP	1.79	2.27	0	0	0	Enhanced
13229	GENTILE_UV_HIGH_DOSE_UP	1.80	4	0	0	0	Enhanced
13230	GO_ENDOTHELIAL_CELL_CHEMOTAXIS	1.80	4	0	0	0	Enhanced
13231	HUANG_GATA2_TARGETS_UP	1.80	4	0	0	0	Enhanced
13232	KEGG_AUTOIMMUNE_THYROID_DISEASE	1.80	4	0	0	0	Enhanced
13233	PID_AP1_PATHWAY	1.80	4	0	0	0	Enhanced
13234	GO_SECONDARY_ALCOHOL_METABOLIC_PROCESS	1.80	2.78	0	0	0	Enhanced
13235	GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	1.80	2.75	0	0	0	Enhanced
13236	GO_POSITIVE_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION_INV	1.80	2.71	0	0	0	Enhanced
13237	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_DN	1.80	2.51	0	0	0	Enhanced
13238	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	1.80	2.28	0	0	0	Enhanced
13239	GEORGANTAS_HSC_MARKERS	1.81	4	0	0	0	Enhanced
13240	GO_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	1.81	4	0	0	0	Enhanced
13241	GO_LYSOSOMAL_LUMEN	1.81	4	0	0	0	Enhanced
13242	GO_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	1.81	4	0	0	0	Enhanced
13243	GO_SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.81	4	0	0	0	Enhanced
13244	LIU_PROSTATE_CANCER_UP	1.81	4	0	0	0	Enhanced
13245	MISSIAGLIA_REGULATED_BY_METHYLATION_UP	1.81	4	0	0	0	Enhanced
13246	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_5	1.81	4	0	0	0	Enhanced
13247	SABATES_COLORECTAL_ADENOMA_DN	1.81	4	0	0	0	Enhanced
13248	VERNELL_RETINOBLASTOMA_PATHWAY_UP	1.81	4	0	0	0	Enhanced
13249	WHITFIELD_CELL_CYCLE_S	1.81	4	0	0	0	Enhanced
13250	LEE_AGING_NEOCORTEX_UP	1.81	2.79	0	0	0	Enhanced
13251	GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	1.81	2.76	0	0	0	Enhanced
13252	GO_CELL_SURFACE	1.82	4	0	0	0	Enhanced
13253	GO_STEROL_METABOLIC_PROCESS	1.82	4	0	0	0	Enhanced
13254	GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	1.82	4	0	0	0	Enhanced
13255	KOBAYASHI_RESPONSE_TO_ROMIDEPSIN	1.82	4	0	0	0	Enhanced
13256	MEISSNER_NPC_HCP_WITH_H3_UNMETHYLATED	1.82	4	0	0	0	Enhanced
13257	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP	1.82	4	0	0	0	Enhanced
13258	PID_REG_GR_PATHWAY	1.82	4	0	0	0	Enhanced
13259	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN	1.82	4	0	0	0	Enhanced
13260	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP	1.82	4	0	0	0	Enhanced
13261	VALK_AML_CLUSTER_11	1.82	2.74	0	0	0	Enhanced
13262	REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	1.82	2.44	0	0	0	Enhanced
13263	GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYT	1.82	2.16	0	0	0	Enhanced
13264	GO_ANTIGEN_BINDING	1.82	2.09	0	0	0	Enhanced
13265	GO_ALPHA_BETA_T_CELL_ACTIVATION	1.83	4	0	0	0	Enhanced
13266	GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	1.83	4	0	0	0	Enhanced
13267	GO_T_CELL_DIFFERENTIATION	1.83	4	0	0	0	Enhanced
13268	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_DN	1.83	4	0	0	0	Enhanced
13269	RIZ_ERYTHROID_DIFFERENTIATION_12HR	1.83	4	0	0	0	Enhanced
13270	GO_CHOLESTEROL_EFFLUX	1.83	2.74	0	0	0	Enhanced
13271	WENG_POR_TARGETS_LIVER_UP	1.83	2.74	0	0	0	Enhanced
13272	CASORELLI_APL_SECONDARY_VS_DE_NOVO_UP	1.83	2.46	0	0	0	Enhanced
13273	KHETCHOUMIAN_TRIM24_TARGETS_UP	1.83	2.28	0	0	0	Enhanced
13274	CHANG_IMMORTALIZED_BY_HPV31_DN	1.84	4	0	0	0	Enhanced
13275	GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	1.84	4	0	0	0	Enhanced
13276	KEGG_LYSOSOME	1.84	4	0	0	0	Enhanced
13277	KRAS.600.LUNG.BREAST_UP.V1_DN	1.84	4	0	0	0	Enhanced
13278	PHONG_TNF_TARGETS_UP	1.84	4	0	0	0	Enhanced
13279	PID_INTEGRIN1_PATHWAY	1.84	4	0	0	0	Enhanced
13280	SHIN_B_CELL_LYMPHOMA_CLUSTER_5	1.84	4	0	0	0	Enhanced
13281	ZWANG_EGF_PERSISTENTLY_DN	1.84	4	0	0	0	Enhanced
13282	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	1.84	2.8	0	0	0	Enhanced
13283	CHOW_RASSF1_TARGETS_DN	1.84	2.76	0	0	0	Enhanced
13284	GO_NEGATIVE_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	1.84	2.74	0	0	0	Enhanced
13285	GO_INTERLEUKIN_8_SECRETION	1.84	2.72	0	0	0	Enhanced
13286	ERBB2_UP.V1_UP	1.85	4	0	0	0	Enhanced

13287	GO_ALCOHOL_BIOSYNTHETIC_PROCESS	1.85	4	0	0	0	Enhanced
13288	GO_INTERFERON_GAMMA_SECRETION	1.85	4	0	0	0	Enhanced
13289	GO_INTERLEUKIN_8_PRODUCTION	1.85	4	0	0	0	Enhanced
13290	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	1.85	4	0	0	0	Enhanced
13291	ALK_DN.V1_UP	1.86	4	0	0	0	Enhanced
13292	BRCA1_DN.V1_UP	1.86	4	0	0	0	Enhanced
13293	GAJATE_RESPONSE_TO_TRABECTEDIN_UP	1.86	4	0	0	0	Enhanced
13294	GO_HUMORAL_IMMUNE_RESPONSE	1.86	4	0	0	0	Enhanced
13295	MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_UP	1.86	4	0	0	0	Enhanced
13296	REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	1.86	4	0	0	0	Enhanced
13297	SEKI_INFLAMMATORY_RESPONSE_LPS_UP	1.86	4	0	0	0	Enhanced
13298	WHITFIELD_CELL_CYCLE_G1_S	1.86	4	0	0	0	Enhanced
13299	BURTON_ADIPOGENESIS_10	1.87	4	0	0	0	Enhanced
13300	GO_INTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	1.87	4	0	0	0	Enhanced
13301	GO_ORGANIC_HYDROXY_COMPOUND_BIOSYNTHETIC_PROCESS	1.87	4	0	0	0	Enhanced
13302	GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	1.87	4	0	0	0	Enhanced
13303	HALLMARK_KRAS_SIGNALING_DN	1.87	4	0	0	0	Enhanced
13304	LE_EGR2_TARGETS_DN	1.87	4	0	0	0	Enhanced
13305	ONDER_CDH1_TARGETS_1_UP	1.87	4	0	0	0	Enhanced
13306	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_	1.87	4	0	0	0	Enhanced
13307	SMID_BREAST_CANCER_NORMAL_LIKE_UP	1.87	4	0	0	0	Enhanced
13308	GO_INTERLEUKIN_7_MEDIATED_SIGNALING_PATHWAY	1.87	2.74	0	0	0	Enhanced
13309	GO_TRANSMEMBRANE_SIGNALING_RECEPTOR_ACTIVITY	1.88	4	0	0	0	Enhanced
13310	HORTON_SREBF_TARGETS	1.88	4	0	0	0	Enhanced
13311	WINTER_HYPOXIA_DN	1.88	2.78	0	0	0	Enhanced
13312	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN	1.88	2.76	0	0	0	Enhanced
13313	AMIT_SERUM_RESPONSE_40_MCF10A	1.89	4	0	0	0	Enhanced
13314	FARMER_BREAST_CANCER_CLUSTER_1	1.89	4	0	0	0	Enhanced
13315	GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IM	1.89	4	0	0	0	Enhanced
13316	GO_POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	1.89	4	0	0	0	Enhanced
13317	GO_REGULATION_OF_STEROID_BIOSYNTHETIC_PROCESS	1.89	4	0	0	0	Enhanced
13318	GO_SOLUTE_CATION_SYMPORTER_ACTIVITY	1.89	4	0	0	0	Enhanced
13319	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION	1.90	4	0	0	0	Enhanced
13320	GO_ADAPTIVE_IMMUNE_RESPONSE	1.90	4	0	0	0	Enhanced
13321	GO_ANION_TRANSMEMBRANE_TRANSPORT	1.90	4	0	0	0	Enhanced
13322	GO_STEROID_METABOLIC_PROCESS	1.90	4	0	0	0	Enhanced
13323	VERHAAK_AML_WITH_NPM1_MUTATED_DN	1.90	4	0	0	0	Enhanced
13324	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP	1.90	4	0	0	0	Enhanced
13325	ZHAN_MULTIPLE_MYELOMA_CD1_UP	1.90	2.77	0	0	0	Enhanced
13326	TIAN_TNF_SIGNALING_NOT_VIA_NFKB	1.90	2.71	0	0	0	Enhanced
13327	E2F3_UP.V1_UP	1.91	4	0	0	0	Enhanced
13328	GO_DEFENSE_RESPONSE_TO_BACTERIUM	1.91	4	0	0	0	Enhanced
13329	GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	1.91	4	0	0	0	Enhanced
13330	GO_T_CELL_MEDIATED_IMMUNITY	1.91	4	0	0	0	Enhanced
13331	LEE_AGING_CEREBELLUM_UP	1.91	4	0	0	0	Enhanced
13332	REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_O	1.91	4	0	0	0	Enhanced
13333	CRX_DN.V1_DN	1.92	4	0	0	0	Enhanced
13334	GO_CHLORIDE_CHANNEL_ACTIVITY	1.92	4	0	0	0	Enhanced
13335	JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_DN	1.92	4	0	0	0	Enhanced
13336	KRAS.LUNG.BREAST_UP.V1_DN	1.92	4	0	0	0	Enhanced
13337	MARZEC_IL2_SIGNALING_DN	1.92	4	0	0	0	Enhanced
13338	WENG_POR_TARGETS_GLOBAL_UP	1.92	4	0	0	0	Enhanced
13339	GO_ANION_CHANNEL_ACTIVITY	1.92	2.77	0	0	0	Enhanced
13340	P53_DN.V2_UP	1.92	2.76	0	0	0	Enhanced
13341	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN	1.93	4	0	0	0	Enhanced
13342	BOYAULT_LIVER_CANCER_SUBCLASS_G5_DN	1.93	4	0	0	0	Enhanced
13343	GO_STEROID_BIOSYNTHETIC_PROCESS	1.93	4	0	0	0	Enhanced
13344	GO_STEROL_BIOSYNTHETIC_PROCESS	1.93	4	0	0	0	Enhanced
13345	KEGG_STEROID_BIOSYNTHESIS	1.93	4	0	0	0	Enhanced
13346	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN	1.93	4	0	0	0	Enhanced
13347	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_0	1.93	2.77	0	0	0	Enhanced
13348	BROWNE_HCMV_INFECTION_2HR_UP	1.94	4	0	0	0	Enhanced
13349	GO_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.94	4	0	0	0	Enhanced
13350	GO_REGULATION_OF_STEROID_METABOLIC_PROCESS	1.94	4	0	0	0	Enhanced
13351	KOBAYASHI_EGFR_SIGNALING_24HR_UP	1.94	4	0	0	0	Enhanced
13352	LEE_BMP2_TARGETS_UP	1.94	4	0	0	0	Enhanced
13353	WALLACE_PROSTATE_CANCER_RACE_UP	1.94	4	0	0	0	Enhanced
13354	GO_CHLORIDE_TRANSMEMBRANE_TRANSPORT	1.95	4	0	0	0	Enhanced
13355	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP	1.95	4	0	0	0	Enhanced
13356	SMID_BREAST_CANCER_LUMINAL_B_DN	1.95	4	0	0	0	Enhanced
13357	GO_CYTOKINE_METABOLIC_PROCESS	1.96	4	0	0	0	Enhanced
13358	GO_INTERLEUKIN_10_PRODUCTION	1.97	4	0	0	0	Enhanced
13359	MCDOWELL_ACUTE_LUNG_INJURY_UP	1.97	4	0	0	0	Enhanced
13360	RUIZ_TNC_TARGETS_UP	1.97	4	0	0	0	Enhanced
13361	BURTON_ADIPOGENESIS_PEAK_AT_2HR	1.98	4	0	0	0	Enhanced
13362	DIRMEIER_LMP1_RESPONSE_EARLY	1.98	4	0	0	0	Enhanced
13363	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN	1.98	4	0	0	0	Enhanced
13364	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP	1.98	4	0	0	0	Enhanced
13365	GO_CHLORIDE_TRANSPORT	1.98	2.76	0	0	0	Enhanced
13366	CHANDRAN_METASTASIS_TOP50_DN	1.99	4	0	0	0	Enhanced
13367	GO_ANTIBACTERIAL_HUMORAL_RESPONSE	1.99	4	0	0	0	Enhanced
13368	HALLMARK_TNFA_SIGNALING_VIA_NFKB	1.99	4	0	0	0	Enhanced
13369	MCLACHLAN_DENTAL_CARIES_UP	1.99	4	0	0	0	Enhanced
13370	ABE_VEGFA_TARGETS_30MIN	2.00	4	0	0	0	Enhanced
13371	GO_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	2.00	4	0	0	0	Enhanced
13372	PODAR_RESPONSE_TO_ADAPHOSTIN_UP	2.01	4	0	0	0	Enhanced
13373	GO_CHLORIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	2.02	4	0	0	0	Enhanced
13374	GO_INORGANIC_ANION_TRANSPORT	2.02	4	0	0	0	Enhanced
13375	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	2.02	4	0	0	0	Enhanced
13376	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP	2.02	4	0	0	0	Enhanced
13377	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP	2.03	4	0	0	0	Enhanced
13378	FISCHER_G1_S_CELL_CYCLE	2.04	4	0	0	0	Enhanced
13379	KEGG_CELL_ADHESION_MOLECULES_CAMS	2.05	4	0	0	0	Enhanced
13380	IL2_UP.V1_DN	2.06	4	0	0	0	Enhanced
13381	JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	2.06	4	0	0	0	Enhanced
13382	GO_INORGANIC_ANION_TRANSMEMBRANE_TRANSPORT	2.07	4	0	0	0	Enhanced
13383	JI_RESPONSE_TO_FSH_UP	2.07	4	0	0	0	Enhanced
13384	MTOR_UP.N4.V1_DN	2.07	4	0	0	0	Enhanced
13385	HUANG_FOXA2_TARGETS_UP	2.08	4	0	0	0	Enhanced
13386	KRIGE_AMINO_ACID_DEPRIVATION	2.08	4	0	0	0	Enhanced
13387	CHANG_CORE_SERUM_RESPONSE_DN	2.09	4	0	0	0	Enhanced
13388	IL15_UP.V1_DN	2.09	4	0	0	0	Enhanced
13389	REACTOME_CHOLESTEROL_BIOSYNTHESIS	2.09	4	0	0	0	Enhanced
13390	AMIT_EGF_RESPONSE_40_HELA	2.12	4	0	0	0	Enhanced
13391	GO_INORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	2.12	4	0	0	0	Enhanced
13392	SCHMIDT_POR_TARGETS_IN_LIMB_BUD_UP	2.12	4	0	0	0	Enhanced
13393	GARY_CD5_TARGETS_UP	2.14	4	0	0	0	Enhanced
13394	TARTE_PLASMA_CELL_VS_PLASMABLAST_UP	2.14	4	0	0	0	Enhanced
13395	GO_ANTIMICROBIAL_HUMORAL_RESPONSE	2.15	4	0	0	0	Enhanced

13396	CSR_LATE_UP.V1_DN	2.19	4	0	0	0	Enhanced
13397	HALLMARK_CHOLESTEROL_HOMEOSTASIS	2.19	4	0	0	0	Enhanced

Supplementary Table 7C: Gene expression changes induced by RZ-2994 vs. DMSO at Day 3 on KOPTK1 cells.
Significance estimated based on DESeq2 (apeglm shrunken fold change) padj < 0.10. Effect of RZ-2994 on gene expression: decreased if log2FoldChange < -1.5, Increased if log2FoldChange > 1.5. Base mean is the average DESeq2 normalized reads in DMSO replicates. Expressed genes have at least 10 reads in at least three replicate samples. Shown are the expressed genes at Day 3 ranked by RZ-2994 vs. DMSO log2FoldChange expression.

#	Gene symbol (hg19)	log2FoldChange RZ-2994 vs. DMSO Day3 DESeq2 apeglm	pvalue RZ-2994 vs. DMSO Day3 DESeq2	padj RZ-2994 vs. DMSO Day3 DESeq2	baseMean RZ-2994 vs. DMSO Day3 DESeq2	RZ-2994 effect on gene expression at Day 3
1	DEFA6	-4.63	4.43E-05	1.35E-04	11.35	Decreased
2	CCR5	-4.49	5.61E-07	2.19E-06	17.95	Decreased
3	ELK3	-4.01	7.78E-06	2.62E-05	16.29	Decreased
4	USH1C	-3.78	5.28E-04	1.33E-03	8.45	Decreased
5	TMPRSS13	-3.74	4.93E-05	1.48E-04	13.04	Decreased
6	ABCC8	-3.53	1.27E-09	6.63E-09	36.37	Decreased
7	STRA6	-3.36	2.83E-19	3.46E-18	87.54	Decreased
8	MTSS1	-3.33	2.75E-20	3.57E-19	91.97	Decreased
9	GBP5	-3.31	1.81E-49	1.10E-47	260.44	Decreased
10	CXCR3	-3.17	1.90E-03	4.30E-03	7.30	Decreased
11	MYT1	-3.11	1.68E-05	5.42E-05	18.30	Decreased
12	MKLN1-AS	-3.01	4.12E-09	2.05E-08	41.28	Decreased
13	ANXA1	-3.00	6.33E-33	1.86E-31	189.57	Decreased
14	H19	-2.85	3.55E-34	1.14E-32	214.95	Decreased
15	METTL7A	-2.75	6.84E-22	9.85E-21	154.42	Decreased
16	IRF8	-2.75	5.69E-10	3.10E-09	52.61	Decreased
17	ASS1	-2.61	2.19E-14	1.79E-13	106.55	Decreased
18	COL5A2	-2.60	1.50E-07	6.29E-07	199.90	Decreased
19	IFIT1	-2.59	1.78E-13	1.34E-12	84.39	Decreased
20	PTMS	-2.56	1.74E-86	3.27E-84	755.58	Decreased
21	PFKFB4	-2.55	8.08E-25	1.41E-23	188.15	Decreased
22	CLEC12A	-2.53	3.25E-11	2.00E-10	74.51	Decreased
23	PAPSS2	-2.52	3.28E-13	2.41E-12	91.55	Decreased
24	RNF43	-2.44	2.04E-04	5.56E-04	19.29	Decreased
25	KCNJ11	-2.39	4.60E-109	1.56E-106	1206.59	Decreased
26	APOBEC3H	-2.38	1.52E-16	1.49E-15	130.65	Decreased
27	NDUFA4L2	-2.33	4.43E-04	1.13E-03	17.63	Decreased
28	CD4	-2.30	2.23E-09	1.14E-08	82.35	Decreased
29	ANXA2	-2.25	1.35E-26	2.65E-25	265.14	Decreased
30	PTPN3	-2.25	8.14E-48	4.65E-46	493.88	Decreased
31	CCR2	-2.24	1.76E-03	4.03E-03	12.96	Decreased
32	LOC101927482	-2.23	7.99E-17	8.02E-16	173.01	Decreased
33	TLR9	-2.23	2.11E-29	4.94E-28	297.69	Decreased
34	ACSL6	-2.22	4.21E-09	2.09E-08	69.41	Decreased
35	CDC20	-2.21	3.10E-229	9.48E-226	5647.42	Decreased
36	BMP10	-2.20	4.74E-06	1.65E-05	38.94	Decreased
37	TRAF3IP2	-2.19	8.92E-24	1.47E-22	244.76	Decreased
38	TBKBP1	-2.18	1.71E-07	7.09E-07	57.21	Decreased
39	IFFO2	-2.18	2.01E-10	1.15E-09	91.80	Decreased
40	HIST1H2BH	-2.18	1.82E-10	1.05E-09	88.95	Decreased
41	HMMR	-2.17	1.09E-192	1.67E-189	3572.61	Decreased
42	ZNF385A	-2.17	1.08E-08	5.16E-08	85.82	Decreased
43	GPR114	-2.16	7.20E-06	2.44E-05	40.23	Decreased
44	SPR	-2.14	6.05E-05	1.80E-04	31.78	Decreased
45	RASSF4	-2.13	1.52E-21	2.14E-20	233.29	Decreased
46	DHRS2	-2.12	4.30E-04	1.10E-03	24.00	Decreased
47	TREML2	-2.12	4.45E-52	3.00E-50	727.89	Decreased
48	SLC35F3	-2.11	1.17E-15	1.07E-14	164.69	Decreased
49	HMGN5	-2.10	1.23E-62	1.18E-60	880.03	Decreased
50	RHBDF2	-2.10	3.67E-11	2.25E-10	108.21	Decreased
51	PDE9A	-2.08	1.43E-13	1.08E-12	145.24	Decreased
52	KCNH3	-2.08	3.38E-03	7.34E-03	11.92	Decreased
53	GPC3	-2.07	1.94E-06	7.08E-06	55.80	Decreased
54	THEMIS2	-2.07	3.98E-04	1.03E-03	23.57	Decreased
55	NINJ2	-2.05	2.73E-08	1.25E-07	74.48	Decreased
56	PPFIA4	-2.04	1.00E-10	5.89E-10	120.27	Decreased
57	EHD3	-2.04	4.17E-10	2.31E-09	100.25	Decreased
58	HSD3B7	-2.04	7.10E-05	2.09E-04	32.85	Decreased
59	ROPN1L	-2.00	6.69E-04	1.65E-03	22.67	Decreased
60	RTN4RL2	-2.00	2.98E-06	1.06E-05	60.01	Decreased
61	TUBA4A	-1.99	4.67E-13	3.39E-12	148.84	Decreased
62	KCTD21	-1.98	9.52E-19	1.12E-17	252.18	Decreased
63	DOK2	-1.97	5.16E-04	1.30E-03	26.13	Decreased
64	PIF1	-1.97	8.89E-31	2.25E-29	486.76	Decreased
65	ANGPTL2	-1.97	6.99E-09	3.41E-08	94.80	Decreased
66	SH3PXD2B	-1.97	2.75E-05	8.59E-05	49.47	Decreased
67	ANXA3	-1.96	1.01E-05	3.36E-05	54.19	Decreased
68	SLC14A2	-1.95	1.18E-04	3.33E-04	34.61	Decreased
69	PLAC8	-1.94	1.58E-25	2.91E-24	377.44	Decreased
70	RASGRP3	-1.94	1.71E-13	1.29E-12	172.99	Decreased
71	TMEM229B	-1.94	7.76E-38	3.14E-36	650.69	Decreased
72	RTN4IP1	-1.93	2.22E-14	1.81E-13	208.70	Decreased
73	FBLN5	-1.93	8.65E-18	9.41E-17	260.15	Decreased
74	WASF1	-1.92	1.84E-80	2.96E-78	1581.94	Decreased
75	IL2RB	-1.91	5.65E-51	3.67E-49	1074.83	Decreased
76	PSTPIP2	-1.91	4.00E-27	8.11E-26	440.56	Decreased

77	PLK1	-1.91	4.02E-156	3.50E-153	5164.08	Decreased
78	MIR22HG	-1.90	1.79E-03	4.07E-03	20.63	Decreased
79	PLXNA4	-1.89	5.04E-04	1.28E-03	31.57	Decreased
80	HIST1H3C	-1.89	3.59E-04	9.33E-04	32.06	Decreased
81	CTSG	-1.88	6.89E-08	2.99E-07	89.51	Decreased
82	LFNG	-1.88	1.74E-06	6.40E-06	74.49	Decreased
83	TNNT1	-1.88	5.74E-07	2.23E-06	80.34	Decreased
84	SUSD2	-1.88	5.46E-03	1.13E-02	12.36	Decreased
85	CD27	-1.88	8.47E-09	4.10E-08	106.34	Decreased
86	ID2	-1.87	9.43E-04	2.27E-03	25.73	Decreased
87	TLR7	-1.87	4.17E-03	8.88E-03	14.86	Decreased
88	NEIL2	-1.85	1.86E-33	5.65E-32	574.96	Decreased
89	KLF9	-1.85	5.03E-04	1.27E-03	33.55	Decreased
90	WNK4	-1.84	2.61E-07	1.06E-06	92.64	Decreased
91	IL18R1	-1.84	5.27E-06	1.81E-05	65.02	Decreased
92	KLHL13	-1.84	2.21E-11	1.38E-10	164.78	Decreased
93	TM6SF1	-1.84	3.35E-07	1.35E-06	83.58	Decreased
94	CST7	-1.83	1.87E-07	7.74E-07	91.66	Decreased
95	NR6A1	-1.83	8.67E-05	2.52E-04	46.63	Decreased
96	CHCHD10	-1.81	6.48E-30	1.56E-28	565.98	Decreased
97	IL10RA	-1.81	6.98E-04	1.72E-03	29.88	Decreased
98	RARG	-1.81	2.18E-07	8.94E-07	103.33	Decreased
99	TOR4A	-1.81	1.98E-03	4.47E-03	22.23	Decreased
100	GABARAPL1	-1.81	1.12E-13	8.56E-13	210.46	Decreased
101	OAS1	-1.80	5.15E-11	3.11E-10	164.03	Decreased
102	PKIG	-1.80	3.87E-07	1.54E-06	91.11	Decreased
103	ALDOC	-1.79	3.24E-36	1.18E-34	735.11	Decreased
104	EPHX4	-1.79	2.59E-07	1.06E-06	96.41	Decreased
105	KPNA2	-1.78	2.18E-138	1.56E-135	5359.10	Decreased
106	TPMT	-1.78	1.50E-27	3.14E-26	566.91	Decreased
107	C6orf52	-1.78	3.23E-04	8.46E-04	38.98	Decreased
108	CDKN1A	-1.77	2.66E-20	3.46E-19	369.80	Decreased
109	SH3BP5	-1.77	5.52E-10	3.02E-09	164.37	Decreased
110	DOK4	-1.77	5.15E-11	3.11E-10	186.93	Decreased
111	NR1H3	-1.77	6.02E-10	3.27E-09	157.45	Decreased
112	LINC00263	-1.77	7.07E-15	6.07E-14	268.03	Decreased
113	ENPEP	-1.76	2.28E-41	1.06E-39	1355.07	Decreased
114	MICAL2	-1.75	1.48E-13	1.13E-12	232.89	Decreased
115	KIAA0513	-1.75	1.01E-04	2.91E-04	52.83	Decreased
116	ARHGAP5-AS1	-1.75	5.93E-03	1.22E-02	15.13	Decreased
117	PTPRU	-1.74	1.58E-30	3.92E-29	675.82	Decreased
118	FAM64A	-1.74	1.13E-34	3.71E-33	1039.70	Decreased
119	UBE2S	-1.73	7.12E-74	9.26E-72	5186.02	Decreased
120	TFEB	-1.73	6.39E-14	5.02E-13	270.47	Decreased
121	CPNE2	-1.72	3.56E-16	3.38E-15	306.27	Decreased
122	CYTH3	-1.72	4.91E-08	2.18E-07	122.37	Decreased
123	HIST1H2AH	-1.72	3.76E-03	8.10E-03	21.01	Decreased
124	AXIN2	-1.72	2.78E-07	1.13E-06	117.73	Decreased
125	PPFIBP1	-1.72	2.13E-39	9.14E-38	976.70	Decreased
126	FBLN2	-1.72	1.24E-13	9.48E-13	263.21	Decreased
127	LDHA	-1.71	1.94E-128	1.13E-125	35219.09	Decreased
128	UBTD1	-1.71	3.20E-03	6.96E-03	22.95	Decreased
129	SMTN	-1.71	7.49E-29	1.69E-27	707.56	Decreased
130	HSPA5	-1.71	1.15E-133	7.40E-131	7932.55	Decreased
131	GARS	-1.71	5.83E-125	2.96E-122	7937.44	Decreased
132	SFXN3	-1.70	7.62E-05	2.23E-04	57.63	Decreased
133	RDH10	-1.70	5.21E-56	4.13E-54	1650.61	Decreased
134	LINC01132	-1.70	2.17E-13	1.63E-12	255.06	Decreased
135	RAP1GAP2	-1.70	1.15E-03	2.72E-03	34.83	Decreased
136	FAM72B	-1.69	1.77E-11	1.11E-10	219.32	Decreased
137	DARS2	-1.69	2.40E-69	2.79E-67	2083.42	Decreased
138	HDHD1	-1.69	1.11E-39	4.83E-38	1036.10	Decreased
139	EGR1	-1.69	1.11E-73	1.41E-71	2407.65	Decreased
140	SSR4P1	-1.69	5.25E-05	1.57E-04	66.95	Decreased
141	DGUOK-AS1	-1.68	3.68E-04	9.55E-04	47.33	Decreased
142	BCL9L	-1.68	1.17E-28	2.59E-27	679.54	Decreased
143	ZDHHC11	-1.68	3.79E-05	1.16E-04	67.87	Decreased
144	CREB3L1	-1.68	1.01E-04	2.91E-04	59.52	Decreased
145	C4orf32	-1.68	2.23E-07	9.12E-07	136.93	Decreased
146	MYL4	-1.67	8.02E-03	1.61E-02	14.30	Decreased
147	GEMIN8P4	-1.67	3.37E-05	1.04E-04	78.33	Decreased
148	SCD	-1.67	1.08E-129	6.58E-127	39556.57	Decreased
149	EFNA1	-1.67	1.31E-04	3.68E-04	66.54	Decreased
150	LOC728084	-1.67	6.55E-55	4.97E-53	2054.60	Decreased
151	TUBB4B	-1.67	2.83E-109	1.02E-106	6577.42	Decreased
152	IFI30	-1.66	8.79E-23	1.34E-21	539.72	Decreased
153	SH3BGR	-1.66	1.58E-06	5.84E-06	104.48	Decreased
154	DAB1	-1.66	5.86E-04	1.46E-03	43.22	Decreased
155	EBNA1BP2	-1.66	4.90E-49	2.95E-47	2825.73	Decreased
156	CBWD1	-1.66	8.94E-16	8.21E-15	361.32	Decreased
157	TFRC	-1.66	8.07E-168	1.10E-164	28882.49	Decreased
158	FAH	-1.66	2.70E-26	5.17E-25	713.08	Decreased
159	PHPT1	-1.65	6.83E-25	1.21E-23	712.00	Decreased
160	ICAM4	-1.65	1.46E-04	4.08E-04	61.46	Decreased
161	FARSB	-1.65	1.77E-77	2.48E-75	2767.05	Decreased
162	MAP1A	-1.65	1.03E-19	1.29E-18	4232.10	Decreased
163	ARHGAP18	-1.64	1.55E-20	2.04E-19	520.83	Decreased
164	SLC50A1	-1.64	1.89E-30	4.67E-29	932.74	Decreased

165	PGK1	-1.64	6.44E-104	1.87E-101	12665.70	Decreased
166	PRF1	-1.63	4.64E-08	2.07E-07	166.51	Decreased
167	GREB1	-1.63	4.74E-11	2.88E-10	269.62	Decreased
168	ATP6V1E2	-1.63	3.48E-09	1.75E-08	188.61	Decreased
169	DHRS4L2	-1.62	5.66E-26	1.06E-24	757.45	Decreased
170	RRAS	-1.62	8.78E-06	2.94E-05	98.20	Decreased
171	PLCD3	-1.62	3.14E-09	1.59E-08	205.19	Decreased
172	SH3BGRL3	-1.62	7.69E-73	9.59E-71	4557.55	Decreased
173	ZBED5-AS1	-1.62	2.48E-06	8.93E-06	113.99	Decreased
174	CEP112	-1.61	3.35E-13	2.46E-12	316.31	Decreased
175	KATNAL2	-1.61	2.15E-06	7.82E-06	116.17	Decreased
176	PKM	-1.61	1.23E-137	8.36E-135	14069.68	Decreased
177	CCNB1	-1.61	1.02E-108	3.37E-106	5771.94	Decreased
178	PTTG1	-1.61	4.08E-66	4.19E-64	2969.87	Decreased
179	SLC7A11	-1.61	3.04E-14	2.46E-13	413.57	Decreased
180	RYR2	-1.61	3.81E-05	1.17E-04	83.98	Decreased
181	LYAR	-1.61	6.74E-58	5.53E-56	2335.05	Decreased
182	KBTBD8	-1.61	5.50E-17	5.62E-16	435.27	Decreased
183	MRPL24	-1.61	9.27E-28	1.97E-26	888.31	Decreased
184	CCR7	-1.60	4.46E-10	2.46E-09	237.16	Decreased
185	KLF10	-1.60	2.34E-22	3.47E-21	712.80	Decreased
186	ARHGEF11	-1.60	2.75E-05	8.59E-05	90.89	Decreased
187	RGS9	-1.60	6.79E-08	2.96E-07	169.48	Decreased
188	SPEF1	-1.60	1.12E-02	2.19E-02	12.04	Decreased
189	FAM86C2P	-1.60	2.08E-05	6.61E-05	90.95	Decreased
190	ADORA3	-1.59	4.47E-03	9.48E-03	27.77	Decreased
191	LIMA1	-1.59	1.51E-31	3.99E-30	1069.94	Decreased
192	ADM2	-1.59	1.31E-09	6.83E-09	241.96	Decreased
193	IQCK	-1.59	2.69E-04	7.16E-04	62.28	Decreased
194	CBR4	-1.59	6.32E-27	1.27E-25	860.09	Decreased
195	MARS	-1.59	3.11E-107	9.99E-105	7043.72	Decreased
196	GPRIN3	-1.59	1.17E-11	7.51E-11	320.47	Decreased
197	STAT4	-1.59	6.61E-25	1.17E-23	847.34	Decreased
198	CNN2	-1.59	3.56E-76	4.89E-74	3854.05	Decreased
199	PLBD2	-1.58	1.09E-08	5.19E-08	207.11	Decreased
200	CCDC107	-1.58	5.22E-08	2.31E-07	200.07	Decreased
201	DAB2IP	-1.58	2.18E-03	4.89E-03	39.53	Decreased
202	CCT5	-1.58	1.81E-78	2.73E-76	14785.46	Decreased
203	43526_22646	-1.58	2.15E-06	7.80E-06	126.25	Decreased
204	MRM1	-1.58	1.19E-03	2.82E-03	51.85	Decreased
205	ATP5EP2	-1.57	1.74E-04	4.81E-04	73.50	Decreased
206	HSP90B1	-1.57	1.32E-96	3.05E-94	21377.88	Decreased
207	PLXNC1	-1.57	1.38E-04	3.86E-04	74.35	Decreased
208	DLGAP5	-1.57	3.65E-60	3.21E-58	4978.12	Decreased
209	CREM	-1.57	4.53E-22	6.60E-21	660.85	Decreased
210	SGSH	-1.57	5.74E-03	1.19E-02	28.22	Decreased
211	CKS2	-1.57	2.49E-57	2.03E-55	3313.35	Decreased
212	RHOU	-1.57	3.86E-27	7.84E-26	880.30	Decreased
213	THSD1	-1.57	4.69E-03	9.91E-03	29.87	Decreased
214	DLEU1	-1.57	3.65E-19	4.42E-18	677.92	Decreased
215	PINX1	-1.57	2.55E-22	3.76E-21	806.55	Decreased
216	ETFB	-1.57	1.11E-24	1.93E-23	1298.26	Decreased
217	MUC4	-1.57	4.26E-05	1.30E-04	113.44	Decreased
218	NKG7	-1.57	4.20E-17	4.31E-16	652.97	Decreased
219	CFH	-1.57	1.69E-14	1.39E-13	429.82	Decreased
220	EIF5AL1	-1.57	1.37E-05	4.46E-05	107.91	Decreased
221	CENPE	-1.56	8.02E-74	1.03E-71	5369.87	Decreased
222	ANKRD6	-1.56	9.59E-03	1.89E-02	17.10	Decreased
223	HES1	-1.56	1.53E-06	5.68E-06	142.26	Decreased
224	RARA	-1.56	1.75E-24	3.00E-23	857.05	Decreased
225	PTGDR2	-1.56	1.40E-05	4.55E-05	123.37	Decreased
226	PPAP2B	-1.56	8.94E-05	2.59E-04	86.87	Decreased
227	CDKN3	-1.56	1.13E-40	5.09E-39	1542.45	Decreased
228	GPR126	-1.55	6.12E-03	1.26E-02	28.95	Decreased
229	TMPRSS3	-1.55	1.08E-04	3.06E-04	93.22	Decreased
230	SSH3	-1.55	1.65E-04	4.56E-04	78.44	Decreased
231	STIP1	-1.55	6.42E-110	2.38E-107	12157.97	Decreased
232	RETN	-1.55	4.10E-06	1.43E-05	137.18	Decreased
233	TNFSF4	-1.55	1.51E-07	6.34E-07	194.83	Decreased
234	CCDC86	-1.55	5.34E-49	3.18E-47	2177.12	Decreased
235	PSAT1	-1.55	4.62E-76	6.28E-74	4456.23	Decreased
236	TMEM71	-1.55	6.95E-10	3.74E-09	278.63	Decreased
237	EIF4EBP1	-1.55	1.80E-43	8.82E-42	1939.03	Decreased
238	RAET1E	-1.55	1.42E-03	3.30E-03	46.92	Decreased
239	DLEU2	-1.55	2.05E-21	2.88E-20	694.65	Decreased
240	EDARADD	-1.55	1.46E-10	8.41E-10	333.21	Decreased
241	CORO1C	-1.55	4.98E-82	8.33E-80	5132.48	Decreased
242	CHAC1	-1.55	9.75E-05	2.81E-04	85.93	Decreased
243	ATP6V0E2	-1.55	3.05E-19	3.70E-18	651.62	Decreased
244	STX11	-1.54	7.57E-04	1.85E-03	58.11	Decreased
245	COX20	-1.54	3.49E-26	6.63E-25	992.39	Decreased
246	BAG3	-1.54	2.04E-25	3.72E-24	858.35	Decreased
247	HLF	-1.54	2.02E-03	4.56E-03	42.52	Decreased
248	FN3K	-1.54	5.72E-03	1.18E-02	29.24	Decreased
249	MLKL	-1.54	1.51E-18	1.75E-17	607.77	Decreased
250	LUCAT1	-1.54	1.93E-03	4.36E-03	45.58	Decreased
251	FAM98A	-1.53	1.59E-35	5.52E-34	1635.95	Decreased
252	COX17	-1.53	1.03E-23	1.69E-22	981.80	Decreased

253	BHLHE40	-1.53	2.05E-17	2.16E-16	580.41	Decreased
254	WDR18	-1.53	3.27E-37	1.26E-35	1507.15	Decreased
255	DUSP6	-1.53	3.06E-89	6.12E-87	6969.10	Decreased
256	LOC101927045	-1.53	3.22E-04	8.46E-04	76.55	Decreased
257	NME1	-1.53	1.19E-32	3.43E-31	1368.11	Decreased
258	NDUFB8	-1.53	1.44E-54	1.06E-52	4299.50	Decreased
259	ALPK1	-1.53	1.18E-09	6.18E-09	290.12	Decreased
260	PACSIN3	-1.53	2.25E-06	8.16E-06	159.40	Decreased
261	MRPL13	-1.53	5.05E-43	2.44E-41	2019.50	Decreased
262	SPNS3	-1.53	1.74E-21	2.45E-20	801.64	Decreased
263	TAMM41	-1.53	8.56E-08	3.68E-07	210.46	Decreased
264	COQ3	-1.53	2.71E-13	2.01E-12	403.67	Decreased
265	CCNB2	-1.53	2.63E-61	2.35E-59	3283.86	Decreased
266	DANCR	-1.53	2.88E-40	1.28E-38	1821.07	Decreased
267	AIF1	-1.53	1.34E-34	4.41E-33	1867.43	Decreased
268	AAK1	-1.52	4.68E-29	1.07E-27	1687.37	Decreased
269	SRP14-AS1	-1.52	3.58E-03	7.73E-03	40.27	Decreased
270	CD79B	-1.52	1.85E-13	1.39E-12	420.09	Decreased
271	CDK2AP2	-1.52	9.76E-46	5.23E-44	4029.04	Decreased
272	CEP19	-1.52	1.03E-14	8.69E-14	456.28	Decreased
273	BST1	-1.52	1.56E-04	4.34E-04	84.77	Decreased
274	WT1	-1.52	2.88E-19	3.51E-18	701.91	Decreased
275	RNASE6	-1.52	2.09E-03	4.71E-03	45.18	Decreased
276	IKBKE	-1.52	8.04E-11	4.76E-10	367.54	Decreased
277	GPAM	-1.52	2.35E-31	6.17E-30	1227.66	Decreased
278	DHRS4	-1.52	4.09E-17	4.21E-16	654.35	Decreased
279	PAK1IP1	-1.52	8.79E-31	2.23E-29	1362.33	Decreased
280	SLC25A23	-1.52	6.15E-32	1.67E-30	1310.86	Decreased
281	ABCG1	-1.52	1.89E-12	1.30E-11	408.38	Decreased
282	S100A10	-1.52	2.27E-13	1.69E-12	532.49	Decreased
283	TUBA1C	-1.51	1.40E-68	1.57E-66	6158.95	Decreased
284	FAM86A	-1.51	4.35E-08	1.94E-07	242.57	Decreased
285	MORN2	-1.51	1.28E-03	3.00E-03	57.03	Decreased
286	XBP1	-1.51	1.31E-39	5.63E-38	2334.72	Decreased
287	LGALS1	-1.51	3.21E-07	1.29E-06	205.16	Decreased
288	FRMD4B	-1.51	1.88E-04	5.16E-04	88.06	Decreased
289	CTSH	-1.51	1.67E-20	2.20E-19	952.18	Decreased
290	FAM83F	-1.51	1.08E-04	3.08E-04	95.32	Decreased
291	ARPC5L	-1.51	2.65E-27	5.45E-26	1581.10	Decreased
292	NDRG2	-1.51	6.64E-03	1.36E-02	28.70	Decreased
293	SREBF1	-1.51	1.72E-62	1.60E-60	6205.87	Decreased
294	EHD4	-1.51	7.26E-11	4.32E-10	334.21	Decreased
295	RRAS2	-1.51	2.87E-14	2.32E-13	510.86	Decreased
296	KLRG1	-1.51	3.52E-04	9.17E-04	78.04	Decreased
297	HCST	-1.51	1.07E-08	5.10E-08	271.50	Decreased
298	DDIT4	-1.50	1.71E-16	1.66E-15	721.05	Decreased
299	SERPINF1	-1.50	3.62E-10	2.01E-09	325.96	Decreased
300	AURKA	-1.50	5.53E-50	3.48E-48	2793.06	Decreased
301	PLS1	-1.50	3.28E-30	8.04E-29	1281.06	Decreased
302	S100Z	-1.50	4.87E-04	1.24E-03	75.31	Decreased
303	PAPLN	-1.50	5.84E-04	1.46E-03	85.65	Decreased
304	LTV1	-1.50	1.85E-38	7.62E-37	1847.73	Decreased
305	RPF2	-1.50	3.30E-34	1.06E-32	1566.52	Decreased
306	SEPN1	-1.50	8.38E-04	2.03E-03	71.02	not significant
307	NCR3LG1	-1.50	5.11E-19	6.08E-18	704.09	not significant
308	ASUN	-1.49	5.68E-44	2.89E-42	2677.44	not significant
309	PIK3AP1	-1.49	2.32E-05	7.31E-05	138.85	not significant
310	SIRPG	-1.49	4.22E-05	1.29E-04	115.54	not significant
311	FAM171A1	-1.49	2.64E-05	8.27E-05	129.46	not significant
312	DUSP3	-1.49	4.93E-15	4.28E-14	569.13	not significant
313	CD8B	-1.49	1.12E-03	2.66E-03	62.17	not significant
314	CERCAM	-1.49	9.33E-03	1.84E-02	25.46	not significant
315	SIGLEC12	-1.49	5.84E-08	2.57E-07	236.70	not significant
316	CDCA2	-1.49	1.29E-49	7.91E-48	2844.69	not significant
317	CHORDC1	-1.49	6.27E-51	4.05E-49	2716.75	not significant
318	GPATCH4	-1.49	8.13E-23	1.24E-21	1654.30	not significant
319	ITGA2	-1.49	3.00E-08	1.37E-07	288.27	not significant
320	PACSIN1	-1.49	1.26E-09	6.60E-09	327.19	not significant
321	SESN2	-1.49	3.79E-12	2.54E-11	413.30	not significant
322	C3orf18	-1.49	1.71E-17	1.81E-16	655.49	not significant
323	CD52	-1.48	9.76E-20	1.23E-18	908.94	not significant
324	FLNB	-1.48	2.52E-10	1.43E-09	3461.10	not significant
325	ELOVL6	-1.48	1.50E-16	1.48E-15	713.61	not significant
326	RARS	-1.48	1.92E-38	7.85E-37	2017.01	not significant
327	FOCAD	-1.48	1.47E-27	3.06E-26	1219.72	not significant
328	RIMS3	-1.48	1.02E-32	2.95E-31	1810.70	not significant
329	IARS	-1.48	5.24E-62	4.82E-60	6372.41	not significant
330	PRDX1	-1.48	3.61E-39	1.52E-37	9672.36	not significant
331	HIST1H2BC	-1.48	5.26E-03	1.10E-02	40.19	not significant
332	LINC01061	-1.48	1.50E-05	4.86E-05	145.81	not significant
333	PPIL1	-1.48	9.66E-31	2.43E-29	1923.03	not significant
334	LOC90784	-1.48	4.09E-09	2.04E-08	358.29	not significant
335	RIMBP2	-1.48	3.95E-04	1.02E-03	81.58	not significant
336	AUH	-1.48	9.80E-07	3.71E-06	195.32	not significant
337	KRT10	-1.48	1.06E-18	1.24E-17	913.46	not significant
338	CPT2	-1.48	6.48E-15	5.58E-14	723.96	not significant
339	PCED1B	-1.47	1.11E-04	3.16E-04	112.17	not significant
340	SNRPG	-1.47	2.53E-35	8.60E-34	2060.18	not significant

341	PPP1R14B	-1.47	3.44E-34	1.10E-32	2214.37	not significant
342	GGACT	-1.47	4.29E-03	9.13E-03	42.21	not significant
343	CHAC2	-1.47	1.47E-15	1.33E-14	598.97	not significant
344	CDCA3	-1.47	3.96E-11	2.42E-10	442.20	not significant
345	ST3GAL4-AS1	-1.47	8.94E-06	2.99E-05	161.75	not significant
346	ITGB1BP1	-1.47	7.27E-34	2.30E-32	2665.33	not significant
347	CORO1A	-1.47	4.09E-67	4.30E-65	15044.88	not significant
348	DBI	-1.47	4.73E-41	2.17E-39	4695.11	not significant
349	ENO1	-1.47	8.05E-77	1.12E-74	82924.86	not significant
350	PPA2	-1.47	1.27E-22	1.93E-21	1035.27	not significant
351	FADS2	-1.47	1.99E-63	1.94E-61	14574.54	not significant
352	PNPT1	-1.46	1.41E-30	3.50E-29	1979.02	not significant
353	GTPBP4	-1.46	6.24E-46	3.36E-44	4160.87	not significant
354	PRMT5	-1.46	2.42E-52	1.66E-50	3316.99	not significant
355	RFTN1	-1.46	2.29E-37	8.90E-36	1942.70	not significant
356	TRMT10C	-1.46	2.92E-30	7.16E-29	1740.58	not significant
357	AHDC1	-1.46	1.22E-26	2.42E-25	1242.29	not significant
358	LRRC59	-1.46	9.28E-75	1.23E-72	8408.64	not significant
359	SLC45A3	-1.46	7.89E-03	1.59E-02	31.95	not significant
360	ARHGDIA	-1.46	2.23E-87	4.40E-85	23959.58	not significant
361	WDR43	-1.46	4.72E-52	3.17E-50	3507.55	not significant
362	UCHL3	-1.46	2.52E-21	3.51E-20	975.66	not significant
363	BUB1	-1.46	1.83E-68	2.02E-66	7327.03	not significant
364	NDUFAF2	-1.46	3.95E-10	2.19E-09	364.11	not significant
365	TAF12	-1.46	2.47E-25	4.48E-24	1232.88	not significant
366	TIMM44	-1.46	2.65E-29	6.12E-28	1514.43	not significant
367	TAP2	-1.46	1.63E-16	1.59E-15	773.01	not significant
368	PSMD1	-1.45	3.77E-59	3.15E-57	4377.79	not significant
369	SGOL2	-1.45	9.55E-45	5.01E-43	4911.29	not significant
370	FAM162A	-1.45	4.61E-23	7.19E-22	1392.36	not significant
371	TUBB4A	-1.45	6.85E-08	2.98E-07	282.65	not significant
372	FSIP1	-1.45	1.49E-02	2.82E-02	15.72	not significant
373	PFN1	-1.45	1.43E-62	1.34E-60	44545.74	not significant
374	COMMD1	-1.45	2.01E-10	1.15E-09	380.74	not significant
375	NANS	-1.45	1.09E-11	7.03E-11	554.92	not significant
376	TIMM23	-1.45	1.99E-05	6.34E-05	152.35	not significant
377	MANF	-1.45	6.50E-15	5.60E-14	802.49	not significant
378	BNIPL	-1.45	1.22E-02	2.35E-02	23.24	not significant
379	PYCR1	-1.45	7.93E-24	1.31E-22	1275.18	not significant
380	LCP1	-1.45	2.50E-78	3.67E-76	40712.84	not significant
381	IZUMO4	-1.45	2.89E-03	6.34E-03	58.02	not significant
382	SNHG4	-1.45	1.75E-06	6.42E-06	221.27	not significant
383	NFS1	-1.45	4.56E-22	6.64E-21	1025.61	not significant
384	VPREB1	-1.45	1.49E-02	2.81E-02	17.38	not significant
385	S100A11	-1.45	3.16E-17	3.28E-16	782.51	not significant
386	PSPH	-1.45	2.22E-24	3.78E-23	1350.33	not significant
387	ACTB	-1.45	2.77E-69	3.16E-67	168054.54	not significant
388	POLR3G	-1.44	5.57E-22	8.07E-21	1025.15	not significant
389	TCTN1	-1.44	8.65E-05	2.51E-04	127.25	not significant
390	CAMKMT	-1.44	9.11E-07	3.46E-06	217.66	not significant
391	IGFBP2	-1.44	1.07E-33	3.33E-32	5621.81	not significant
392	EIF5A	-1.44	3.78E-50	2.39E-48	14357.89	not significant
393	HIST1H4I	-1.44	1.56E-02	2.92E-02	16.30	not significant
394	ARL6IP5	-1.44	3.66E-42	1.73E-40	2508.45	not significant
395	MRPS28	-1.44	1.04E-20	1.39E-19	1146.00	not significant
396	PSMD12	-1.44	9.70E-41	4.37E-39	2533.25	not significant
397	NOL10	-1.44	1.21E-31	3.23E-30	1807.64	not significant
398	CCDC53	-1.44	2.48E-17	2.59E-16	783.78	not significant
399	ILK	-1.44	1.69E-32	4.80E-31	1740.04	not significant
400	FRRS1	-1.44	4.66E-06	1.62E-05	189.85	not significant
401	HEXIM1	-1.44	2.34E-32	6.60E-31	1912.68	not significant
402	FOXO6	-1.44	5.48E-11	3.29E-10	444.03	not significant
403	ATP5J2	-1.44	6.65E-33	1.95E-31	2154.30	not significant
404	ACTR3	-1.43	1.46E-66	1.53E-64	11488.49	not significant
405	SLC4A10	-1.43	7.35E-05	2.15E-04	140.21	not significant
406	TPM3	-1.43	5.35E-79	8.17E-77	27202.04	not significant
407	ACSL3	-1.43	1.35E-37	5.36E-36	3411.74	not significant
408	ADARB1	-1.43	4.80E-20	6.15E-19	1125.14	not significant
409	SH3BP1	-1.43	1.93E-20	2.53E-19	1053.42	not significant
410	CHD3	-1.43	7.65E-51	4.92E-49	6105.40	not significant
411	SWI5	-1.43	3.15E-07	1.27E-06	317.16	not significant
412	PRELID1	-1.43	9.09E-36	3.21E-34	3626.46	not significant
413	MAGOH	-1.43	4.57E-29	1.05E-27	2301.34	not significant
414	TMEM156	-1.43	1.29E-06	4.82E-06	253.70	not significant
415	SNRNP40	-1.43	6.28E-36	2.26E-34	2813.67	not significant
416	SFPQ	-1.43	1.23E-54	9.13E-53	20747.65	not significant
417	PXN	-1.43	2.88E-13	2.13E-12	575.82	not significant
418	PSME2	-1.43	1.01E-38	4.22E-37	6686.59	not significant
419	KCNJ14	-1.43	4.04E-03	8.64E-03	60.68	not significant
420	ALG8	-1.43	3.01E-27	6.15E-26	1586.29	not significant
421	ZCCHC14	-1.43	8.63E-09	4.18E-08	374.30	not significant
422	TIMM21	-1.43	1.10E-18	1.28E-17	978.35	not significant
423	KIAA0040	-1.42	1.07E-19	1.34E-18	980.42	not significant
424	MRPL17	-1.42	1.32E-27	2.77E-26	1587.49	not significant
425	HNRNPA2B1	-1.42	7.51E-50	4.66E-48	73955.95	not significant
426	FKBP1A	-1.42	2.68E-69	3.09E-67	12379.38	not significant
427	ALDH1B1	-1.42	1.45E-04	4.05E-04	131.60	not significant
428	C12orf5	-1.42	2.70E-08	1.24E-07	346.76	not significant

429	LONRF2	-1.42	4.49E-13	3.26E-12	689.39	not significant
430	AGTRAP	-1.42	5.24E-09	2.58E-08	366.66	not significant
431	XPOT	-1.42	9.96E-70	1.17E-67	8549.18	not significant
432	SLC25A19	-1.42	3.64E-24	6.14E-23	1355.47	not significant
433	IDH3A	-1.42	6.21E-39	2.61E-37	2637.35	not significant
434	GAR1	-1.42	8.70E-27	1.73E-25	1982.21	not significant
435	UCHL5	-1.42	2.36E-35	8.09E-34	3768.68	not significant
436	IDE	-1.42	4.28E-28	9.25E-27	1877.46	not significant
437	GIPC1	-1.42	1.18E-20	1.57E-19	1235.95	not significant
438	C10orf54	-1.42	6.43E-24	1.06E-22	1456.07	not significant
439	RUVBL1	-1.42	1.83E-37	7.19E-36	3652.01	not significant
440	TC2N	-1.42	5.84E-17	5.96E-16	875.63	not significant
441	TTC1	-1.42	2.22E-23	3.54E-22	1972.12	not significant
442	CALM3	-1.42	1.92E-68	2.08E-66	19914.38	not significant
443	ANAPC1	-1.42	8.23E-37	3.10E-35	2597.13	not significant
444	PRMT3	-1.42	4.57E-21	6.25E-20	1384.77	not significant
445	POLR3B	-1.42	2.91E-17	3.02E-16	939.68	not significant
446	CCDC124	-1.42	4.01E-35	1.35E-33	2908.30	not significant
447	SLC9A9	-1.42	2.18E-03	4.88E-03	69.25	not significant
448	AMZ2	-1.42	3.41E-14	2.75E-13	778.02	not significant
449	CBS	-1.42	3.13E-17	3.25E-16	935.75	not significant
450	CMC1	-1.41	2.28E-16	2.21E-15	851.16	not significant
451	CRADD	-1.41	1.05E-06	3.96E-06	264.78	not significant
452	PPAP2A	-1.41	2.81E-09	1.43E-08	411.11	not significant
453	CCDC51	-1.41	2.06E-08	9.55E-08	411.46	not significant
454	TMPO-AS1	-1.41	6.69E-18	7.35E-17	1062.83	not significant
455	NOP16	-1.41	4.96E-26	9.34E-25	1497.35	not significant
456	HELZ2	-1.41	7.73E-07	2.96E-06	252.14	not significant
457	GSTM4	-1.41	2.83E-03	6.23E-03	73.15	not significant
458	C12orf60	-1.41	1.19E-02	2.30E-02	32.29	not significant
459	YARS	-1.41	1.93E-62	1.79E-60	7661.66	not significant
460	PSMB3	-1.41	3.51E-31	9.06E-30	3290.90	not significant
461	NANP	-1.41	5.41E-18	5.97E-17	987.61	not significant
462	YBX1	-1.41	6.81E-55	5.14E-53	45359.57	not significant
463	ARPP21	-1.41	1.63E-14	1.35E-13	785.20	not significant
464	PFDN6	-1.41	1.24E-13	9.47E-13	742.33	not significant
465	AMIGO3	-1.41	3.39E-10	1.89E-09	494.28	not significant
466	GGA2	-1.41	1.41E-17	1.52E-16	909.05	not significant
467	DNTTIP2	-1.41	9.10E-31	2.29E-29	2807.82	not significant
468	GSPT1	-1.41	1.69E-68	1.87E-66	8746.93	not significant
469	UQCR10	-1.41	2.77E-31	7.20E-30	2663.05	not significant
470	HSP90AA1	-1.41	2.51E-39	1.07E-37	87590.95	not significant
471	NT5DC2	-1.41	7.66E-29	1.73E-27	1810.54	not significant
472	FAS	-1.41	6.71E-18	7.36E-17	1033.48	not significant
473	TRERF1	-1.41	7.12E-17	7.19E-16	903.61	not significant
474	GLDC	-1.41	2.20E-09	1.12E-08	426.90	not significant
475	PSMC4	-1.41	2.12E-43	1.03E-41	3497.51	not significant
476	MPP6	-1.41	7.91E-10	4.23E-09	440.41	not significant
477	IFT27	-1.41	1.26E-07	5.31E-07	313.21	not significant
478	TNFSF9	-1.40	3.27E-03	7.11E-03	65.51	not significant
479	SPDL1	-1.40	2.58E-32	7.23E-31	2663.87	not significant
480	AHSA1	-1.40	1.64E-32	4.67E-31	7058.32	not significant
481	SH3TC1	-1.40	2.48E-11	1.54E-10	580.18	not significant
482	TAF15	-1.40	2.26E-35	7.77E-34	4814.76	not significant
483	FLT3LG	-1.40	1.39E-07	5.83E-07	347.87	not significant
484	FKBP2	-1.40	3.12E-14	2.52E-13	820.53	not significant
485	FBXO6	-1.40	4.71E-05	1.42E-04	171.92	not significant
486	BRIX1	-1.40	1.23E-28	2.72E-27	2018.68	not significant
487	INTS8	-1.40	1.10E-25	2.05E-24	1858.87	not significant
488	MZB1	-1.40	8.92E-51	5.71E-49	5088.33	not significant
489	ETFA	-1.40	1.46E-33	4.48E-32	2969.07	not significant
490	PHB	-1.40	1.23E-43	6.09E-42	5184.77	not significant
491	ODC1	-1.40	1.01E-53	7.25E-52	13559.24	not significant
492	FASTKD5	-1.40	6.87E-17	6.94E-16	1084.59	not significant
493	XPR1	-1.40	6.32E-30	1.52E-28	1993.95	not significant
494	GNAO1	-1.40	7.57E-05	2.22E-04	153.29	not significant
495	NUS1	-1.40	2.07E-29	4.85E-28	2051.53	not significant
496	COX7B	-1.40	3.28E-06	1.16E-05	1538.22	not significant
497	LOC257396	-1.40	6.08E-03	1.25E-02	52.18	not significant
498	RXRA	-1.40	2.22E-06	8.04E-06	274.78	not significant
499	MIF	-1.40	4.03E-36	1.45E-34	15165.36	not significant
500	VARS	-1.40	1.01E-19	1.27E-18	2038.32	not significant
501	ABCB9	-1.40	3.64E-03	7.84E-03	63.42	not significant
502	MED27	-1.40	1.82E-11	1.14E-10	567.27	not significant
503	CISH	-1.40	2.95E-63	2.86E-61	9216.87	not significant
504	KIAA1804	-1.40	1.58E-04	4.38E-04	138.75	not significant
505	NDUFC1	-1.40	4.28E-16	4.03E-15	1020.01	not significant
506	G6PD	-1.39	1.46E-17	1.56E-16	1096.61	not significant
507	RANBP1	-1.39	6.26E-50	3.92E-48	7792.69	not significant
508	BID	-1.39	1.22E-33	3.78E-32	3542.47	not significant
509	RANGAP1	-1.39	9.19E-50	5.67E-48	7742.34	not significant
510	MTHFD1L	-1.39	3.39E-27	6.90E-26	2128.62	not significant
511	PDE6G	-1.39	1.04E-02	2.04E-02	39.25	not significant
512	TOMM40	-1.39	2.29E-27	4.72E-26	4094.36	not significant
513	PSMA4	-1.39	2.96E-46	1.60E-44	4766.46	not significant
514	SPIB	-1.39	1.75E-02	3.26E-02	21.58	not significant
515	ITPR2	-1.39	9.50E-29	2.12E-27	3501.32	not significant
516	PTPN7	-1.39	5.39E-60	4.71E-58	8523.95	not significant

517	ISOC2	-1.39	6.20E-17	6.31E-16	1101.62	not significant
518	MRPL47	-1.39	2.55E-21	3.54E-20	1413.84	not significant
519	SLC38A3	-1.39	1.89E-02	3.48E-02	18.41	not significant
520	CAMKK1	-1.39	3.25E-05	1.01E-04	180.39	not significant
521	CIB1	-1.39	4.86E-30	1.18E-28	2351.02	not significant
522	COQ2	-1.39	1.91E-05	6.11E-05	200.62	not significant
523	GAS2L1	-1.39	3.73E-07	1.49E-06	295.81	not significant
524	LSS	-1.39	6.03E-29	1.37E-27	2104.48	not significant
525	VEGFA	-1.39	1.64E-11	1.03E-10	645.33	not significant
526	PSME3	-1.39	2.42E-51	1.58E-49	7171.88	not significant
527	THNSL1	-1.39	8.04E-11	4.76E-10	666.85	not significant
528	SRXN1	-1.39	1.11E-04	3.16E-04	170.66	not significant
529	EIF2B3	-1.39	5.63E-17	5.75E-16	1214.49	not significant
530	PAPOLA	-1.39	7.22E-49	4.24E-47	10952.26	not significant
531	LACTB2	-1.39	1.26E-07	5.31E-07	359.49	not significant
532	TAGLN2	-1.39	5.11E-49	3.06E-47	8726.62	not significant
533	GTSF1	-1.39	3.17E-06	1.13E-05	246.35	not significant
534	GLS	-1.39	2.28E-48	1.32E-46	7168.08	not significant
535	CSE1L	-1.39	3.68E-55	2.81E-53	9829.02	not significant
536	PGAM1	-1.39	3.26E-35	1.10E-33	2666.93	not significant
537	HMBS	-1.38	5.45E-14	4.31E-13	1090.64	not significant
538	MYLK2	-1.38	1.08E-02	2.10E-02	43.09	not significant
539	KLHL29	-1.38	8.18E-04	1.99E-03	114.86	not significant
540	DEPDC1B	-1.38	1.25E-31	3.32E-30	2474.49	not significant
541	NDUFAF1	-1.38	3.50E-07	1.40E-06	351.85	not significant
542	METAP1D	-1.38	1.15E-04	3.25E-04	166.63	not significant
543	NUBPL	-1.38	1.42E-06	5.30E-06	275.36	not significant
544	CSRNP1	-1.38	3.61E-05	1.11E-04	190.76	not significant
545	EFHD2	-1.38	6.34E-29	1.43E-27	3071.38	not significant
546	ITPRIPL1	-1.38	2.86E-15	2.53E-14	959.68	not significant
547	NINJ1	-1.38	7.19E-07	2.77E-06	302.62	not significant
548	ETF1	-1.38	4.41E-37	1.70E-35	6062.58	not significant
549	POP4	-1.38	3.76E-22	5.50E-21	1530.09	not significant
550	SLC36A1	-1.38	1.62E-07	6.73E-07	385.13	not significant
551	CDH23	-1.38	2.34E-04	6.31E-04	141.71	not significant
552	MAMDC4	-1.38	2.07E-03	4.67E-03	114.18	not significant
553	PKI55	-1.38	4.90E-08	2.18E-07	406.39	not significant
554	DDX21	-1.38	1.34E-58	1.12E-56	12922.85	not significant
555	SLC7A5	-1.38	1.09E-36	4.09E-35	14615.13	not significant
556	ATP10D	-1.38	3.61E-07	1.45E-06	330.76	not significant
557	HSD17B10	-1.38	3.07E-12	2.07E-11	728.75	not significant
558	RND2	-1.38	5.79E-03	1.20E-02	58.24	not significant
559	SDHB	-1.38	1.37E-29	3.25E-28	2690.53	not significant
560	DBF4	-1.38	2.02E-33	6.11E-32	3498.23	not significant
561	TMEM173	-1.38	1.75E-19	2.16E-18	1352.55	not significant
562	LOC440600	-1.38	1.84E-02	3.40E-02	23.62	not significant
563	DPH6	-1.38	1.28E-05	4.20E-05	223.69	not significant
564	ARHGEF3	-1.38	1.71E-25	3.14E-24	1849.23	not significant
565	UBE2V2	-1.38	1.18E-30	2.96E-29	4979.01	not significant
566	ADM5	-1.38	8.09E-05	2.36E-04	194.91	not significant
567	PDIA5	-1.37	6.90E-13	4.94E-12	727.53	not significant
568	TCEB3-AS1	-1.37	1.63E-03	3.75E-03	93.80	not significant
569	BOLA3	-1.37	3.38E-13	2.48E-12	882.09	not significant
570	CACYBP	-1.37	7.86E-40	3.42E-38	4819.25	not significant
571	NDUFA3	-1.37	2.18E-13	1.63E-12	778.04	not significant
572	SCPEP1	-1.37	7.66E-09	3.72E-08	520.65	not significant
573	CYCS	-1.37	7.29E-30	1.75E-28	7221.64	not significant
574	PNO1	-1.37	3.43E-19	4.16E-18	1315.43	not significant
575	PRADC1	-1.37	1.47E-12	1.03E-11	763.86	not significant
576	SBDS	-1.37	3.12E-13	2.30E-12	926.44	not significant
577	NMB	-1.37	3.70E-04	9.60E-04	141.21	not significant
578	ACSS2	-1.37	6.99E-07	2.70E-06	321.54	not significant
579	MPC1	-1.37	1.88E-18	2.16E-17	1166.24	not significant
580	USP5	-1.37	3.64E-30	8.90E-29	2369.31	not significant
581	PPP1R7	-1.37	8.71E-22	1.25E-20	2249.57	not significant
582	POR	-1.37	1.03E-08	4.93E-08	523.89	not significant
583	UBE3C	-1.37	4.93E-32	1.35E-30	3630.70	not significant
584	THRA	-1.37	1.66E-12	1.15E-11	780.40	not significant
585	GMPPA	-1.37	6.13E-12	4.04E-11	683.10	not significant
586	HLA-F	-1.37	1.44E-02	2.73E-02	34.55	not significant
587	NFE2L2	-1.37	1.11E-24	1.93E-23	1792.73	not significant
588	MRPL2	-1.37	6.63E-14	5.19E-13	813.48	not significant
589	RPP38	-1.37	1.49E-07	6.26E-07	370.02	not significant
590	LGALS8	-1.37	2.24E-26	4.32E-25	2020.22	not significant
591	ENDOG	-1.37	1.82E-05	5.82E-05	244.63	not significant
592	MAML2	-1.37	1.66E-02	3.11E-02	29.74	not significant
593	HLA-B	-1.37	4.36E-27	8.78E-26	7754.05	not significant
594	NOC2L	-1.37	7.37E-36	2.63E-34	3634.94	not significant
595	NARS2	-1.37	2.40E-15	2.13E-14	1288.32	not significant
596	C1GALT1C1	-1.37	2.08E-07	8.54E-07	407.70	not significant
597	CD3EAP	-1.37	6.79E-11	4.05E-10	714.25	not significant
598	AIFM1	-1.37	9.40E-21	1.26E-19	2145.24	not significant
599	MECR	-1.37	2.85E-11	1.76E-10	624.52	not significant
600	IL15RA	-1.37	7.03E-05	2.07E-04	208.65	not significant
601	RPS27L	-1.37	1.06E-13	8.15E-13	860.72	not significant
602	SAT2	-1.36	2.92E-03	6.40E-03	90.20	not significant
603	GOT1	-1.36	8.88E-20	1.12E-18	1481.98	not significant
604	ANXA6	-1.36	3.19E-47	1.78E-45	7708.91	not significant

605	METTL5	-1.36	4.53E-13	3.29E-12	879.46	not significant
606	TAF13	-1.36	1.76E-05	5.66E-05	241.70	not significant
607	CCNA2	-1.36	7.23E-57	5.85E-55	8397.48	not significant
608	GALK2	-1.36	4.16E-08	1.86E-07	458.78	not significant
609	IKZF4	-1.36	1.73E-11	1.09E-10	650.19	not significant
610	KANK2	-1.36	4.85E-04	1.23E-03	134.15	not significant
611	GALK1	-1.36	1.65E-21	2.32E-20	1739.03	not significant
612	TUBG1	-1.36	1.02E-22	1.55E-21	1855.07	not significant
613	ETNK1	-1.36	3.46E-33	1.02E-31	4047.32	not significant
614	WARS	-1.36	2.72E-26	5.20E-25	2030.13	not significant
615	C1orf74	-1.36	5.38E-04	1.35E-03	132.21	not significant
616	TIMMDC1	-1.36	2.04E-22	3.04E-21	1708.53	not significant
617	DKC1	-1.36	3.91E-31	1.01E-29	3215.27	not significant
618	SCOC-AS1	-1.36	1.27E-02	2.44E-02	46.40	not significant
619	HIST1H2AJ	-1.36	2.04E-02	3.74E-02	23.09	not significant
620	CHTF8	-1.36	6.85E-33	2.00E-31	5408.16	not significant
621	MRPL36	-1.36	1.29E-09	6.72E-09	533.74	not significant
622	RPL26L1	-1.36	5.73E-08	2.52E-07	550.50	not significant
623	PRMT1	-1.36	8.15E-34	2.55E-32	7952.65	not significant
624	LINC00852	-1.36	1.15E-02	2.23E-02	44.90	not significant
625	SNRPC	-1.36	1.13E-29	2.68E-28	3664.05	not significant
626	TBC1D16	-1.36	1.13E-06	4.25E-06	338.29	not significant
627	HMGCL	-1.36	3.99E-08	1.79E-07	454.11	not significant
628	CDC123	-1.36	5.55E-31	1.42E-29	4139.88	not significant
629	ANXA4	-1.36	8.83E-10	4.68E-09	592.02	not significant
630	ARHGDIB	-1.36	6.14E-44	3.10E-42	39419.17	not significant
631	ABCE1	-1.36	3.22E-45	1.70E-43	6673.27	not significant
632	DPF3	-1.36	2.25E-09	1.15E-08	566.52	not significant
633	SBF2-AS1	-1.36	3.40E-06	1.20E-05	317.10	not significant
634	CFL1	-1.36	4.93E-34	1.57E-32	33634.19	not significant
635	GNAI2	-1.36	7.95E-33	2.30E-31	4533.02	not significant
636	ATP5G1	-1.36	4.72E-22	6.85E-21	2055.01	not significant
637	HSPA4L	-1.36	5.56E-16	5.20E-15	1052.73	not significant
638	C2orf74	-1.36	5.18E-04	1.31E-03	147.33	not significant
639	HLA-A	-1.36	6.57E-25	1.17E-23	3276.23	not significant
640	CDC27	-1.36	5.02E-40	2.20E-38	4773.38	not significant
641	STEAP1B	-1.36	3.06E-03	6.68E-03	83.09	not significant
642	TBRG4	-1.35	2.44E-32	6.86E-31	3647.65	not significant
643	HOXB7	-1.35	1.69E-03	3.86E-03	102.58	not significant
644	NUGGC	-1.35	3.02E-05	9.37E-05	233.43	not significant
645	TMEM163	-1.35	1.69E-05	5.43E-05	235.82	not significant
646	MDH2	-1.35	1.55E-28	3.42E-27	4614.53	not significant
647	GTF3A	-1.35	5.86E-44	2.97E-42	10407.62	not significant
648	LAMTOR2	-1.35	1.26E-13	9.60E-13	890.74	not significant
649	MRPL4	-1.35	2.98E-28	6.47E-27	3237.66	not significant
650	PRKCD	-1.35	2.86E-05	8.92E-05	247.83	not significant
651	LSM10	-1.35	8.56E-11	5.06E-10	833.86	not significant
652	MRPL51	-1.35	4.29E-24	7.20E-23	3543.97	not significant
653	MPP5	-1.35	5.79E-12	3.83E-11	756.79	not significant
654	KAZALD1	-1.35	2.04E-02	3.74E-02	15.01	not significant
655	SHC1	-1.35	9.93E-27	1.98E-25	2553.44	not significant
656	DUSP2	-1.35	2.32E-10	1.32E-09	611.80	not significant
657	CYP4F3	-1.35	1.85E-02	3.42E-02	11.50	not significant
658	MCU	-1.35	8.86E-14	6.85E-13	963.95	not significant
659	GPD1L	-1.35	8.25E-10	4.39E-09	577.53	not significant
660	PALD1	-1.35	6.53E-08	2.85E-07	434.80	not significant
661	AKAP6	-1.35	6.25E-03	1.28E-02	73.78	not significant
662	TRDMT1	-1.35	2.67E-11	1.65E-10	751.72	not significant
663	BCCIP	-1.35	1.66E-29	3.92E-28	3537.03	not significant
664	MMAA	-1.35	3.52E-08	1.59E-07	469.79	not significant
665	EMP3	-1.35	4.08E-10	2.26E-09	594.81	not significant
666	PLGRKT	-1.35	2.51E-08	1.15E-07	483.16	not significant
667	UQCRQ	-1.35	1.35E-22	2.04E-21	2442.54	not significant
668	PELI3	-1.35	6.88E-03	1.40E-02	71.56	not significant
669	TUBE1	-1.35	3.39E-04	8.86E-04	163.62	not significant
670	LOC100506100	-1.35	2.28E-05	7.19E-05	255.28	not significant
671	USP40	-1.35	2.28E-11	1.42E-10	690.46	not significant
672	IL22RA1	-1.35	2.32E-03	5.17E-03	95.37	not significant
673	BATF	-1.35	1.33E-10	7.74E-10	741.12	not significant
674	CCDC28B	-1.35	1.47E-11	9.36E-11	829.71	not significant
675	MEMO1	-1.35	1.42E-09	7.36E-09	669.40	not significant
676	DAZAP1	-1.35	5.05E-38	2.06E-36	8657.65	not significant
677	MRTO4	-1.35	2.94E-33	8.78E-32	3515.74	not significant
678	ACOT11	-1.35	1.22E-02	2.35E-02	46.73	not significant
679	C1orf131	-1.35	1.53E-13	1.16E-12	976.55	not significant
680	AGRN	-1.35	5.63E-03	1.17E-02	73.32	not significant
681	HEATR3	-1.34	4.33E-14	3.44E-13	1010.45	not significant
682	BCS1L	-1.34	1.83E-09	9.43E-09	558.67	not significant
683	SNHG3	-1.34	3.77E-05	1.16E-04	1516.82	not significant
684	MRPL23	-1.34	5.63E-23	8.74E-22	2058.45	not significant
685	ZNF788	-1.34	7.40E-08	3.21E-07	464.13	not significant
686	ASPH	-1.34	1.52E-06	5.63E-06	332.08	not significant
687	RNF6	-1.34	8.76E-28	1.86E-26	2674.81	not significant
688	PPP1CA	-1.34	1.99E-34	6.47E-33	10455.64	not significant
689	NETO1	-1.34	2.32E-03	5.19E-03	104.35	not significant
690	FPGT	-1.34	2.71E-05	8.46E-05	238.88	not significant
691	STX8	-1.34	1.39E-08	6.53E-08	650.35	not significant
692	PIWIL3	-1.34	1.46E-03	3.40E-03	118.60	not significant

693	PSRC1	-1.34	1.71E-12	1.18E-11	1083.90	not significant
694	AMPD3	-1.34	3.82E-15	3.35E-14	1157.14	not significant
695	PPID	-1.34	6.96E-25	1.23E-23	2141.26	not significant
696	MKNK2	-1.34	2.92E-28	6.36E-27	5719.57	not significant
697	AVIL	-1.34	1.46E-02	2.77E-02	42.08	not significant
698	PCGF2	-1.34	4.53E-06	1.57E-05	308.29	not significant
699	MCEE	-1.34	1.21E-03	2.85E-03	120.76	not significant
700	BCL2L14	-1.34	1.85E-02	3.42E-02	34.58	not significant
701	OXNAD1	-1.34	3.03E-11	1.87E-10	756.93	not significant
702	HEATR1	-1.34	1.53E-21	2.15E-20	4089.98	not significant
703	AP1S1	-1.34	4.57E-17	4.69E-16	1295.59	not significant
704	NAT1	-1.34	3.74E-06	1.31E-05	316.54	not significant
705	ARPC2	-1.34	1.87E-34	6.08E-33	12148.01	not significant
706	COMMD10	-1.34	1.12E-11	7.22E-11	843.13	not significant
707	GALNS	-1.34	4.92E-06	1.70E-05	308.32	not significant
708	PSMC2	-1.34	1.43E-34	4.70E-33	3615.71	not significant
709	MRPL20	-1.34	5.13E-18	5.69E-17	2258.07	not significant
710	ZHX1	-1.34	2.65E-33	7.95E-32	3814.84	not significant
711	BMS1	-1.34	5.03E-26	9.45E-25	3440.68	not significant
712	CTU2	-1.34	5.45E-11	3.28E-10	816.67	not significant
713	NAA15	-1.34	3.31E-36	1.21E-34	5599.84	not significant
714	ITPR1	-1.34	6.16E-10	3.34E-09	752.23	not significant
715	COASY	-1.34	1.61E-27	3.36E-26	2617.93	not significant
716	IMPDH1	-1.34	1.63E-12	1.13E-11	929.95	not significant
717	MRPL22	-1.34	1.29E-14	1.08E-13	1184.13	not significant
718	NLN	-1.34	1.66E-16	1.62E-15	1455.34	not significant
719	ALDH2	-1.34	1.84E-02	3.40E-02	35.50	not significant
720	EIF3J	-1.34	6.31E-24	1.05E-22	3127.59	not significant
721	CISD3	-1.34	6.39E-16	5.96E-15	1335.93	not significant
722	PAPD5	-1.34	5.62E-15	4.85E-14	1081.63	not significant
723	BATF3	-1.34	3.24E-10	1.81E-09	652.43	not significant
724	RITA1	-1.34	9.37E-17	9.40E-16	1683.05	not significant
725	ACN9	-1.34	2.37E-11	1.47E-10	842.97	not significant
726	ATP5G3	-1.33	1.37E-32	3.92E-31	7112.47	not significant
727	NOLC1	-1.33	2.35E-47	1.32E-45	12557.61	not significant
728	ECHDC1	-1.33	2.01E-26	3.89E-25	3149.71	not significant
729	TPCN1	-1.33	2.93E-12	1.98E-11	852.78	not significant
730	PPIP5K1	-1.33	2.16E-04	5.86E-04	185.90	not significant
731	TUBB2A	-1.33	7.20E-03	1.46E-02	73.05	not significant
732	NDUFA12	-1.33	4.08E-20	5.24E-19	2642.27	not significant
733	RRP36	-1.33	1.21E-17	1.30E-16	1942.46	not significant
734	SNAPC5	-1.33	1.58E-04	4.39E-04	200.84	not significant
735	ANAPC15	-1.33	1.07E-22	1.63E-21	1976.67	not significant
736	RSU1	-1.33	2.09E-21	2.92E-20	1975.46	not significant
737	KIF20A	-1.33	6.91E-25	1.22E-23	2484.41	not significant
738	ATG3	-1.33	2.94E-32	8.16E-31	3541.83	not significant
739	CDKN2AIPNL	-1.33	8.90E-14	6.87E-13	1273.67	not significant
740	CHMP2A	-1.33	1.15E-14	9.66E-14	1298.21	not significant
741	ARF3	-1.33	5.08E-28	1.09E-26	8448.76	not significant
742	UACA	-1.33	1.81E-02	3.36E-02	11.58	not significant
743	NDUFS6	-1.33	6.81E-06	2.31E-05	2736.09	not significant
744	LTB	-1.33	1.09E-08	5.21E-08	637.87	not significant
745	SSB	-1.33	1.52E-21	2.15E-20	5162.48	not significant
746	C20orf24	-1.33	9.16E-12	5.95E-11	1072.73	not significant
747	ERH	-1.33	1.26E-35	4.40E-34	8310.23	not significant
748	INPP4B	-1.33	2.74E-07	1.11E-06	447.04	not significant
749	PPARGC1B	-1.33	2.27E-07	9.30E-07	617.45	not significant
750	FTH1	-1.33	1.06E-27	2.23E-26	22079.61	not significant
751	ZNF480	-1.33	8.52E-21	1.15E-19	1814.83	not significant
752	PPP2R2A	-1.33	5.00E-24	8.33E-23	2779.13	not significant
753	SLC2A3	-1.33	1.67E-07	6.95E-07	457.84	not significant
754	STRAP	-1.33	2.20E-32	6.23E-31	5446.08	not significant
755	EIF4E	-1.33	3.94E-19	4.74E-18	1596.39	not significant
756	EHBP1	-1.33	2.79E-13	2.07E-12	965.12	not significant
757	ADCY7	-1.33	5.79E-22	8.38E-21	2322.29	not significant
758	SKP1	-1.33	7.93E-34	2.49E-32	9368.87	not significant
759	GPSM2	-1.33	9.52E-17	9.53E-16	1696.86	not significant
760	BRE	-1.33	1.17E-11	7.48E-11	841.69	not significant
761	ANKRD52	-1.33	1.81E-08	8.43E-08	5853.23	not significant
762	RPL39L	-1.33	9.64E-17	9.63E-16	1377.00	not significant
763	SNX33	-1.32	1.07E-02	2.08E-02	61.66	not significant
764	KNOP1	-1.32	4.14E-13	3.03E-12	1107.42	not significant
765	AIMP2	-1.32	8.15E-15	6.94E-14	1232.55	not significant
766	TXNIP	-1.32	8.56E-10	4.55E-09	717.45	not significant
767	ACAT1	-1.32	2.26E-18	2.57E-17	1785.15	not significant
768	MRPS34	-1.32	2.69E-21	3.73E-20	3019.48	not significant
769	POLR2L	-1.32	3.10E-20	3.99E-19	2179.11	not significant
770	DCLRE1A	-1.32	7.51E-15	6.41E-14	1260.49	not significant
771	TCP10L	-1.32	7.54E-03	1.52E-02	74.39	not significant
772	APOBEC3D	-1.32	5.65E-08	2.49E-07	594.42	not significant
773	CA6	-1.32	5.19E-03	1.08E-02	94.76	not significant
774	TRAPPC1	-1.32	1.70E-23	2.74E-22	3524.05	not significant
775	TANK	-1.32	2.82E-20	3.66E-19	1787.26	not significant
776	KIAA0196	-1.32	3.86E-26	7.33E-25	3215.36	not significant
777	HSPA4	-1.32	1.14E-36	4.24E-35	6659.79	not significant
778	RUVBL2	-1.32	2.45E-31	6.42E-30	4877.08	not significant
779	UTP15	-1.32	9.87E-13	6.99E-12	983.49	not significant
780	CRYZ	-1.32	1.62E-10	9.35E-10	907.32	not significant

781	PUS7	-1.32	3.88E-18	4.36E-17	1801.75	not significant
782	OASL	-1.32	1.16E-03	2.75E-03	141.76	not significant
783	MRPL39	-1.32	4.25E-13	3.10E-12	1052.43	not significant
784	KCND1	-1.32	1.96E-02	3.60E-02	11.02	not significant
785	COA7	-1.32	6.21E-09	3.03E-08	634.15	not significant
786	DYNLL1	-1.32	1.34E-32	3.84E-31	4705.95	not significant
787	TIMM8B	-1.32	1.63E-10	9.38E-10	936.02	not significant
788	SLC19A2	-1.32	3.14E-07	1.27E-06	449.76	not significant
789	HAT1	-1.32	2.75E-25	4.99E-24	3802.87	not significant
790	GPI	-1.32	1.27E-46	6.91E-45	15519.86	not significant
791	MRPS12	-1.32	2.84E-13	2.10E-12	1237.64	not significant
792	CAP1	-1.32	7.70E-40	3.36E-38	10122.83	not significant
793	DHX15	-1.32	6.02E-45	3.17E-43	11677.79	not significant
794	DIMT1	-1.32	1.33E-15	1.21E-14	1398.49	not significant
795	ALDOA	-1.32	7.43E-47	4.11E-45	24525.86	not significant
796	NSUN2	-1.32	4.64E-35	1.56E-33	5017.99	not significant
797	VCL	-1.32	1.50E-02	2.83E-02	49.99	not significant
798	TOMM5	-1.32	1.26E-27	2.66E-26	3672.01	not significant
799	LST1	-1.32	2.44E-03	5.42E-03	120.98	not significant
800	BIRC5	-1.32	5.67E-34	1.80E-32	11055.48	not significant
801	DYNLRB1	-1.32	1.64E-24	2.82E-23	3266.93	not significant
802	RBM26-AS1	-1.32	7.44E-04	1.82E-03	158.18	not significant
803	NCEH1	-1.32	5.43E-06	1.87E-05	346.12	not significant
804	SORD	-1.32	3.58E-12	2.40E-11	967.48	not significant
805	HIGD1A	-1.32	1.42E-19	1.76E-18	3162.82	not significant
806	MCTS2P	-1.32	1.24E-04	3.49E-04	224.81	not significant
807	EIF3B	-1.32	6.82E-39	2.85E-37	11534.78	not significant
808	AK6	-1.32	1.61E-05	5.21E-05	335.98	not significant
809	USB1	-1.32	1.21E-22	1.83E-21	3065.05	not significant
810	CCZ1B	-1.32	1.07E-09	5.66E-09	768.83	not significant
811	TPI1	-1.32	3.21E-24	5.42E-23	5655.48	not significant
812	TMEM241	-1.32	1.58E-05	5.11E-05	319.72	not significant
813	ZMAT5	-1.32	1.29E-08	6.11E-08	731.84	not significant
814	SCN2A	-1.31	2.69E-02	4.78E-02	23.32	not significant
815	ITGB2	-1.31	8.82E-29	1.98E-27	3458.77	not significant
816	DOC2A	-1.31	8.46E-03	1.69E-02	80.81	not significant
817	RNF145	-1.31	7.91E-31	2.01E-29	4724.45	not significant
818	PMAIP1	-1.31	1.44E-27	3.01E-26	3305.51	not significant
819	SRA1	-1.31	4.93E-09	2.44E-08	711.25	not significant
820	TARS	-1.31	2.28E-30	5.62E-29	6273.41	not significant
821	ZMPSTE24	-1.31	1.76E-23	2.83E-22	2395.15	not significant
822	UBAP2L	-1.31	1.15E-33	3.54E-32	8228.82	not significant
823	ERC1	-1.31	1.48E-10	8.58E-10	835.64	not significant
824	IGSF3	-1.31	8.08E-08	3.49E-07	523.12	not significant
825	MRPS15	-1.31	1.24E-18	1.45E-17	2746.67	not significant
826	FADD	-1.31	5.03E-11	3.04E-10	1029.52	not significant
827	DCAF13	-1.31	3.72E-20	4.78E-19	2676.54	not significant
828	CIRH1A	-1.31	1.68E-21	2.36E-20	2112.52	not significant
829	ADAT3	-1.31	1.16E-03	2.75E-03	148.52	not significant
830	GRWD1	-1.31	1.47E-16	1.45E-15	2226.32	not significant
831	ZNF593	-1.31	3.95E-05	1.21E-04	285.11	not significant
832	TOB1	-1.31	8.44E-08	3.63E-07	513.77	not significant
833	ARL15	-1.31	2.99E-04	7.88E-04	209.20	not significant
834	KIF14	-1.31	1.13E-26	2.23E-25	4359.81	not significant
835	LOC440028	-1.31	2.73E-02	4.85E-02	23.33	not significant
836	FXYD2	-1.31	8.19E-03	1.64E-02	92.97	not significant
837	TAP1	-1.31	2.46E-12	1.68E-11	1020.07	not significant
838	HRSP12	-1.31	1.33E-07	5.58E-07	521.74	not significant
839	LIN28B	-1.31	1.52E-24	2.61E-23	3247.11	not significant
840	SUPT4H1	-1.31	1.48E-33	4.51E-32	5024.29	not significant
841	C12orf66	-1.31	6.10E-07	2.37E-06	445.26	not significant
842	GPR75	-1.31	2.08E-02	3.80E-02	46.19	not significant
843	XRCC6	-1.31	5.67E-32	1.54E-30	20979.61	not significant
844	FARP2	-1.31	2.16E-05	6.83E-05	316.75	not significant
845	CRELD2	-1.31	5.59E-09	2.74E-08	885.65	not significant
846	HSD17B4	-1.31	1.13E-23	1.85E-22	2993.46	not significant
847	PDP2	-1.31	1.17E-13	8.94E-13	1477.35	not significant
848	SLFN12L	-1.31	1.16E-03	2.74E-03	166.93	not significant
849	USP7	-1.31	1.24E-37	4.92E-36	10918.55	not significant
850	RRP9	-1.31	6.68E-16	6.21E-15	1454.96	not significant
851	PHGDH	-1.31	1.28E-35	4.45E-34	7663.96	not significant
852	DPM1	-1.31	4.35E-18	4.87E-17	2030.98	not significant
853	DNAJB6	-1.31	1.62E-27	3.36E-26	6381.68	not significant
854	ICT1	-1.31	5.88E-12	3.88E-11	1199.48	not significant
855	ETFDH	-1.31	3.80E-09	1.90E-08	720.23	not significant
856	AARS	-1.31	2.29E-35	7.86E-34	7257.28	not significant
857	POLR2F	-1.31	2.92E-16	2.79E-15	1672.33	not significant
858	CLN8	-1.31	7.51E-06	2.54E-05	350.26	not significant
859	CINP	-1.31	2.19E-11	1.37E-10	867.77	not significant
860	WDR75	-1.31	1.97E-17	2.08E-16	1986.45	not significant
861	CALM1	-1.31	1.14E-33	3.54E-32	6609.44	not significant
862	HABP4	-1.31	3.84E-03	8.26E-03	105.95	not significant
863	MRPL52	-1.31	2.15E-13	1.62E-12	1229.48	not significant
864	TOP1	-1.31	5.30E-37	2.02E-35	9945.39	not significant
865	SLC25A32	-1.31	3.26E-16	3.10E-15	2867.19	not significant
866	N6AMT2	-1.31	1.38E-05	4.48E-05	336.20	not significant
867	TPX2	-1.31	2.49E-44	1.29E-42	17237.85	not significant
868	WDR4	-1.31	1.35E-08	6.37E-08	597.63	not significant

869	ZFP69	-1.31	6.90E-04	1.70E-03	178.96	not significant
870	NQO2	-1.31	2.34E-09	1.20E-08	731.28	not significant
871	ATPIF1	-1.31	1.58E-22	2.37E-21	2520.82	not significant
872	GMNN	-1.31	1.01E-28	2.24E-27	4268.97	not significant
873	CTSK	-1.31	9.94E-03	1.95E-02	73.30	not significant
874	SCFD2	-1.31	3.16E-10	1.77E-09	775.99	not significant
875	MPHOSPH6	-1.31	9.20E-19	1.08E-17	1877.51	not significant
876	MALSU1	-1.31	5.38E-12	3.56E-11	1026.32	not significant
877	DEPDC1	-1.31	1.90E-19	2.35E-18	2109.59	not significant
878	CD63	-1.31	7.32E-15	6.27E-14	2070.46	not significant
879	MSN	-1.31	6.29E-49	3.71E-47	35436.73	not significant
880	TMEM99	-1.31	1.27E-03	2.99E-03	152.18	not significant
881	SGTB	-1.30	7.89E-08	3.41E-07	596.67	not significant
882	SRRT	-1.30	1.42E-25	2.62E-24	8964.32	not significant
883	GHRLOS	-1.30	1.96E-02	3.60E-02	48.91	not significant
884	C2orf43	-1.30	2.12E-19	2.60E-18	1996.70	not significant
885	KIAA2022	-1.30	2.72E-02	4.85E-02	28.17	not significant
886	BMS1P20	-1.30	3.74E-10	2.07E-09	771.43	not significant
887	CCDC92	-1.30	2.17E-14	1.78E-13	1400.31	not significant
888	NOP58	-1.30	2.38E-28	5.21E-27	5628.08	not significant
889	GTF2A2	-1.30	3.26E-15	2.87E-14	1458.18	not significant
890	CLYBL	-1.30	3.60E-04	9.36E-04	196.16	not significant
891	MIEN1	-1.30	1.54E-17	1.64E-16	1729.38	not significant
892	EIF2S2	-1.30	1.19E-24	2.06E-23	5921.81	not significant
893	ACAD10	-1.30	1.05E-10	6.16E-10	1002.83	not significant
894	MAGOHB	-1.30	1.85E-15	1.66E-14	1731.71	not significant
895	EXOSC8	-1.30	2.48E-17	2.59E-16	1662.21	not significant
896	PSMD2	-1.30	2.07E-31	5.45E-30	7637.05	not significant
897	FERMT3	-1.30	3.16E-26	6.03E-25	5941.30	not significant
898	HNRNPC	-1.30	1.24E-26	2.45E-25	22491.60	not significant
899	C7orf61	-1.30	2.89E-02	5.11E-02	25.57	not significant
900	IMP4	-1.30	2.50E-16	2.41E-15	1628.87	not significant
901	NTMT1	-1.30	6.30E-09	3.08E-08	684.86	not significant
902	SLC29A1	-1.30	1.62E-34	5.28E-33	7840.58	not significant
903	SPATA24	-1.30	2.36E-02	4.25E-02	38.48	not significant
904	SESN1	-1.30	1.55E-08	7.22E-08	659.83	not significant
905	GRN	-1.30	1.81E-07	7.48E-07	606.36	not significant
906	BCAT1	-1.30	7.51E-23	1.15E-21	2867.81	not significant
907	COQ5	-1.30	7.64E-09	3.71E-08	783.10	not significant
908	SNTA1	-1.30	6.71E-08	2.93E-07	557.58	not significant
909	MRPL35	-1.30	1.08E-16	1.08E-15	1848.48	not significant
910	DMD	-1.30	2.15E-03	4.84E-03	159.27	not significant
911	HN1	-1.30	2.20E-26	4.24E-25	8233.98	not significant
912	SETD7	-1.30	3.89E-14	3.11E-13	1311.70	not significant
913	PSME4	-1.30	4.06E-17	4.18E-16	3291.63	not significant
914	SCARB1	-1.30	6.46E-14	5.07E-13	1369.50	not significant
915	UMPS	-1.30	1.68E-13	1.27E-12	1751.41	not significant
916	MAPKAP1	-1.30	1.41E-22	2.13E-21	3171.42	not significant
917	CENPW	-1.30	3.12E-04	8.20E-04	1096.46	not significant
918	HNRNPM	-1.30	4.70E-23	7.32E-22	16864.17	not significant
919	MAK16	-1.30	1.06E-21	1.50E-20	2483.45	not significant
920	FAHD2B	-1.30	3.45E-04	9.00E-04	220.27	not significant
921	DNAJA1	-1.30	6.26E-25	1.11E-23	12028.33	not significant
922	HSD17B7	-1.30	5.97E-06	2.04E-05	379.20	not significant
923	PRIMPOL	-1.30	1.22E-07	5.15E-07	561.76	not significant
924	KPNA1	-1.30	1.88E-25	3.44E-24	3433.63	not significant
925	ATP5H	-1.30	5.84E-19	6.92E-18	3800.59	not significant
926	HSPBP1	-1.30	2.85E-12	1.93E-11	1405.44	not significant
927	RNFT1	-1.30	8.11E-06	2.73E-05	366.87	not significant
928	WDR1	-1.30	1.39E-33	4.28E-32	13760.90	not significant
929	MROH6	-1.30	1.03E-05	3.40E-05	448.91	not significant
930	UBE2N	-1.30	9.44E-32	2.53E-30	8048.72	not significant
931	GTF2E2	-1.30	1.49E-15	1.35E-14	2175.41	not significant
932	PPP6R1	-1.30	7.26E-41	3.28E-39	17177.78	not significant
933	PRR13	-1.30	5.70E-23	8.82E-22	3216.58	not significant
934	MRPL3	-1.30	3.62E-26	6.87E-25	4362.67	not significant
935	C3orf67	-1.30	2.94E-02	5.18E-02	24.25	not significant
936	MYO1B	-1.30	1.90E-20	2.50E-19	2217.20	not significant
937	TOP1MT	-1.30	5.65E-19	6.71E-18	2113.34	not significant
938	PUF60	-1.30	1.19E-15	1.08E-14	1940.68	not significant
939	TCAP	-1.29	2.99E-02	5.26E-02	30.36	not significant
940	JDP2	-1.29	7.36E-04	1.80E-03	185.10	not significant
941	ALOX5AP	-1.29	2.46E-17	2.58E-16	1755.27	not significant
942	ZBTB11-AS1	-1.29	8.79E-03	1.75E-02	84.76	not significant
943	UQCR11	-1.29	3.99E-18	4.48E-17	3064.73	not significant
944	DDC	-1.29	2.69E-02	4.79E-02	14.45	not significant
945	METTL8	-1.29	3.57E-11	2.19E-10	978.19	not significant
946	SSBP1	-1.29	1.61E-16	1.58E-15	2627.16	not significant
947	FAM118B	-1.29	2.40E-09	1.22E-08	738.63	not significant
948	PREB	-1.29	3.08E-18	3.49E-17	2023.13	not significant
949	CHRNA5	-1.29	2.13E-07	8.76E-07	566.26	not significant
950	PMM2	-1.29	8.50E-20	1.08E-18	2586.29	not significant
951	NUP37	-1.29	1.94E-15	1.73E-14	2073.64	not significant
952	TRMT1L	-1.29	3.61E-11	2.22E-10	967.39	not significant
953	PSMA6	-1.29	4.12E-26	7.80E-25	7207.23	not significant
954	NOP56	-1.29	3.90E-29	8.97E-28	12144.70	not significant
955	NDUFAB1	-1.29	1.39E-18	1.61E-17	2527.49	not significant
956	SPC25	-1.29	2.96E-10	1.67E-09	899.87	not significant

957	PRKACA	-1.29	9.01E-24	1.48E-22	3704.50	not significant
958	PSMB8	-1.29	6.58E-16	6.12E-15	1963.17	not significant
959	RAB30	-1.29	1.32E-03	3.09E-03	162.55	not significant
960	TAF2	-1.29	1.33E-19	1.65E-18	2709.74	not significant
961	PDIA4	-1.29	6.92E-28	1.48E-26	6603.64	not significant
962	DAD1	-1.29	1.32E-16	1.31E-15	2184.26	not significant
963	WDR12	-1.29	5.06E-17	5.18E-16	2028.12	not significant
964	ECI2	-1.29	1.35E-16	1.33E-15	1752.24	not significant
965	MRPL41	-1.29	1.76E-06	6.45E-06	468.49	not significant
966	NUDT5	-1.29	6.14E-17	6.25E-16	2744.36	not significant
967	POLR1C	-1.29	2.72E-08	1.24E-07	666.53	not significant
968	RGL1	-1.29	4.82E-03	1.01E-02	117.20	not significant
969	RFT1	-1.29	7.39E-15	6.32E-14	1530.47	not significant
970	MAFG-AS1	-1.29	1.13E-02	2.19E-02	78.44	not significant
971	ADORA2B	-1.29	1.79E-04	4.93E-04	286.67	not significant
972	CHAT	-1.29	7.47E-03	1.51E-02	104.57	not significant
973	SRP54	-1.29	2.48E-22	3.66E-21	3112.21	not significant
974	NOP10	-1.29	1.81E-18	2.09E-17	2097.99	not significant
975	ZNF878	-1.29	2.77E-02	4.91E-02	35.59	not significant
976	HNRNPD	-1.29	1.17E-23	1.90E-22	22672.99	not significant
977	AMMECR1	-1.29	1.47E-06	5.48E-06	462.06	not significant
978	RIOK1	-1.29	9.53E-21	1.27E-19	2449.26	not significant
979	LINC00176	-1.29	2.42E-02	4.36E-02	44.02	not significant
980	RPF1	-1.29	1.09E-15	9.98E-15	2135.29	not significant
981	CSTF3	-1.29	9.62E-15	8.14E-14	1862.25	not significant
982	RGS6	-1.29	4.76E-03	1.00E-02	115.64	not significant
983	WDR77	-1.29	1.18E-23	1.92E-22	3577.08	not significant
984	BCL7C	-1.29	4.23E-08	1.89E-07	905.18	not significant
985	CCNF	-1.29	6.99E-25	1.23E-23	4088.46	not significant
986	CBWD2	-1.29	5.02E-06	1.73E-05	499.39	not significant
987	FDPS	-1.29	5.44E-26	1.02E-24	5869.99	not significant
988	PCK2	-1.29	1.55E-07	6.49E-07	706.05	not significant
989	RAP1A	-1.29	4.76E-15	4.13E-14	2189.35	not significant
990	PNP	-1.29	8.79E-21	1.18E-19	3589.76	not significant
991	POLR2B	-1.29	8.43E-34	2.63E-32	7693.61	not significant
992	TIMM17A	-1.29	5.97E-05	1.78E-04	2029.79	not significant
993	EPB41L2	-1.29	1.19E-30	2.96E-29	5056.30	not significant
994	PSMD7	-1.29	1.80E-23	2.89E-22	4261.17	not significant
995	RNH1	-1.29	7.28E-19	8.56E-18	2355.31	not significant
996	DDI2	-1.29	5.92E-06	2.03E-05	459.63	not significant
997	ZNHIT1	-1.29	1.59E-12	1.10E-11	1602.72	not significant
998	TIMM22	-1.29	3.78E-09	1.89E-08	808.55	not significant
999	NCL	-1.29	1.33E-23	2.15E-22	53082.53	not significant
1000	COX7A2	-1.29	6.83E-20	8.67E-19	4092.39	not significant
1001	LEPR	-1.29	1.64E-02	3.07E-02	63.91	not significant
1002	TMEM14A	-1.29	4.96E-08	2.20E-07	704.86	not significant
1003	PTP4A2	-1.28	1.15E-37	4.62E-36	46473.95	not significant
1004	AQP3	-1.28	3.01E-23	4.76E-22	3784.29	not significant
1005	NUP35	-1.28	2.04E-09	1.05E-08	844.90	not significant
1006	CYBA	-1.28	1.92E-14	1.57E-13	2145.04	not significant
1007	DZIP3	-1.28	3.60E-09	1.80E-08	766.47	not significant
1008	FASTKD3	-1.28	4.64E-07	1.83E-06	579.41	not significant
1009	FGD2	-1.28	1.92E-02	3.53E-02	59.53	not significant
1010	ERCC4	-1.28	8.95E-08	3.84E-07	682.24	not significant
1011	MORF4L2	-1.28	9.54E-28	2.02E-26	4856.17	not significant
1012	MPV17L2	-1.28	1.03E-08	4.95E-08	832.28	not significant
1013	NDUFA7	-1.28	2.35E-12	1.60E-11	1433.54	not significant
1014	E2F5	-1.28	5.44E-09	2.67E-08	752.85	not significant
1015	TCEB2	-1.28	8.93E-15	7.57E-14	2262.06	not significant
1016	TAGAP	-1.28	1.78E-07	7.39E-07	632.13	not significant
1017	CNOT1	-1.28	2.62E-27	5.40E-26	16598.82	not significant
1018	CARS2	-1.28	3.04E-12	2.06E-11	1458.55	not significant
1019	ROGDI	-1.28	7.43E-03	1.50E-02	100.51	not significant
1020	CDCA8	-1.28	9.67E-29	2.16E-27	5048.43	not significant
1021	EGLN3	-1.28	1.90E-04	5.20E-04	284.19	not significant
1022	ATP5I	-1.28	5.35E-15	4.62E-14	1691.49	not significant
1023	TMEM205	-1.28	1.25E-07	5.26E-07	642.86	not significant
1024	TTC4	-1.28	3.01E-02	5.29E-02	18.14	not significant
1025	POLR2E	-1.28	8.24E-25	1.44E-23	6571.59	not significant
1026	AP1B1	-1.28	5.06E-30	1.22E-28	5654.90	not significant
1027	PSMC1	-1.28	1.17E-08	5.58E-08	758.22	not significant
1028	CDC42	-1.28	1.79E-27	3.72E-26	7378.22	not significant
1029	SRR	-1.28	4.60E-07	1.82E-06	587.34	not significant
1030	RAB29	-1.28	3.80E-09	1.90E-08	846.71	not significant
1031	CENPA	-1.28	5.17E-16	4.86E-15	2044.02	not significant
1032	EIF4G1	-1.28	1.86E-28	4.08E-27	17443.74	not significant
1033	C12orf75	-1.28	2.01E-18	2.30E-17	4069.23	not significant
1034	KIF21B	-1.28	1.94E-23	3.09E-22	6347.72	not significant
1035	DDX1	-1.28	5.67E-23	8.78E-22	4102.39	not significant
1036	PER1	-1.28	3.20E-08	1.45E-07	692.74	not significant
1037	ARG2	-1.28	2.30E-02	4.17E-02	50.43	not significant
1038	AP1S3	-1.28	3.14E-02	5.51E-02	17.76	not significant
1039	CLPP	-1.28	6.18E-19	7.32E-18	2499.57	not significant
1040	WWP1	-1.28	1.50E-15	1.36E-14	1737.14	not significant
1041	DNMT3B	-1.28	3.39E-16	3.21E-15	2427.47	not significant
1042	MMAB	-1.28	1.05E-14	8.86E-14	1534.42	not significant
1043	DPP9	-1.28	4.37E-22	6.38E-21	3111.13	not significant
1044	DENND4A	-1.28	2.58E-07	1.05E-06	615.30	not significant

1045	CUL3	-1.28	3.25E-25	5.90E-24	3742.86	not significant
1046	OGDH	-1.28	2.62E-29	6.08E-28	4681.02	not significant
1047	IFI6	-1.28	8.15E-12	5.32E-11	1472.92	not significant
1048	LSM4	-1.28	1.61E-22	2.40E-21	9210.83	not significant
1049	KIF4A	-1.28	7.84E-22	1.12E-20	3280.57	not significant
1050	SEPHS2	-1.28	3.80E-18	4.28E-17	2991.29	not significant
1051	SSBP4	-1.28	1.27E-19	1.58E-18	3822.07	not significant
1052	API5	-1.28	7.21E-32	1.94E-30	6753.53	not significant
1053	HOXB2	-1.28	1.02E-02	2.00E-02	87.16	not significant
1054	RAG1	-1.28	8.22E-03	1.64E-02	99.47	not significant
1055	AK2	-1.28	7.60E-36	2.71E-34	9043.96	not significant
1056	MICAL3	-1.28	6.26E-08	2.74E-07	751.65	not significant
1057	SLC6A20	-1.28	6.94E-04	1.71E-03	234.96	not significant
1058	CETN3	-1.28	3.81E-08	1.71E-07	862.71	not significant
1059	ATP1A1	-1.28	1.35E-38	5.61E-37	18979.43	not significant
1060	DUS2	-1.28	5.77E-06	1.98E-05	450.69	not significant
1061	PGAM5	-1.28	1.77E-26	3.44E-25	4415.95	not significant
1062	ATP5L	-1.28	5.83E-16	5.45E-15	1936.02	not significant
1063	TFB1M	-1.28	3.67E-05	1.13E-04	365.02	not significant
1064	AMICA1	-1.28	3.34E-02	5.82E-02	28.11	not significant
1065	LSAMP	-1.28	3.08E-04	8.10E-04	271.47	not significant
1066	FITM2	-1.28	3.40E-02	5.89E-02	23.86	not significant
1067	PSMD14	-1.28	1.57E-20	2.07E-19	3847.78	not significant
1068	TOP1P1	-1.28	2.24E-02	4.06E-02	55.89	not significant
1069	LDLR	-1.28	1.21E-18	1.42E-17	2495.32	not significant
1070	FSD1	-1.28	2.69E-04	7.17E-04	262.65	not significant
1071	LPHN1	-1.28	5.76E-06	1.98E-05	439.47	not significant
1072	PCDH12	-1.28	3.39E-02	5.88E-02	23.77	not significant
1073	ACKR3	-1.28	8.26E-03	1.65E-02	99.53	not significant
1074	SPRED1	-1.28	7.13E-04	1.75E-03	247.79	not significant
1075	ATP5J	-1.28	4.87E-14	3.86E-13	3235.31	not significant
1076	NIFK	-1.28	9.98E-15	8.43E-14	2311.12	not significant
1077	GEMIN7	-1.28	5.22E-06	1.80E-05	442.63	not significant
1078	NUP88	-1.28	1.73E-17	1.84E-16	2267.68	not significant
1079	PDSS1	-1.28	2.96E-09	1.50E-08	815.88	not significant
1080	NUDC	-1.28	6.27E-21	8.53E-20	6564.04	not significant
1081	ZBTB8OS	-1.28	1.73E-06	6.38E-06	492.62	not significant
1082	ADCK1	-1.28	1.60E-04	4.44E-04	285.42	not significant
1083	CCDC58	-1.28	8.04E-08	3.47E-07	691.62	not significant
1084	BTN2A3P	-1.28	1.81E-02	3.36E-02	67.38	not significant
1085	LOC101928766	-1.28	1.15E-02	2.23E-02	89.50	not significant
1086	TNS4	-1.28	9.56E-03	1.88E-02	96.57	not significant
1087	FAR2	-1.28	1.36E-16	1.34E-15	1963.99	not significant
1088	SKIV2L2	-1.28	6.37E-22	9.21E-21	3351.21	not significant
1089	KBTBD3	-1.28	1.81E-02	3.36E-02	71.38	not significant
1090	CGN	-1.28	9.95E-06	3.30E-05	413.09	not significant
1091	POP1	-1.28	2.30E-09	1.17E-08	1084.57	not significant
1092	PRPF19	-1.28	1.33E-31	3.52E-30	9674.84	not significant
1093	EBAG9	-1.28	2.57E-11	1.59E-10	1442.03	not significant
1094	GNG5	-1.28	4.81E-22	6.98E-21	4921.06	not significant
1095	TRA2B	-1.28	1.34E-29	3.19E-28	13489.24	not significant
1096	TIMM10	-1.28	1.13E-09	5.93E-09	872.24	not significant
1097	PSMD6	-1.28	1.65E-17	1.75E-16	2445.44	not significant
1098	CXorf40A	-1.28	2.99E-02	5.26E-02	41.65	not significant
1099	LRRFIP1	-1.28	1.05E-21	1.50E-20	6249.30	not significant
1100	C21orf59	-1.27	1.07E-13	8.26E-13	1933.87	not significant
1101	DOK1	-1.27	1.71E-05	5.49E-05	383.30	not significant
1102	USP44	-1.27	1.07E-10	6.25E-10	1171.47	not significant
1103	SMC4	-1.27	3.62E-21	4.99E-20	14740.86	not significant
1104	GLRX2	-1.27	2.06E-04	5.61E-04	276.83	not significant
1105	BPGM	-1.27	1.14E-07	4.85E-07	688.94	not significant
1106	MAGI3	-1.27	2.50E-04	6.71E-04	262.89	not significant
1107	VDAC1	-1.27	2.18E-33	6.56E-32	8911.44	not significant
1108	PKP4	-1.27	4.56E-18	5.09E-17	2205.20	not significant
1109	DYRK2	-1.27	4.09E-15	3.57E-14	1819.56	not significant
1110	C6orf203	-1.27	8.95E-03	1.77E-02	102.48	not significant
1111	KIF18A	-1.27	3.55E-13	2.60E-12	1522.78	not significant
1112	C7orf50	-1.27	3.84E-09	1.92E-08	919.94	not significant
1113	DPP3	-1.27	1.02E-21	1.44E-20	3220.30	not significant
1114	SIK1	-1.27	2.07E-03	4.66E-03	172.90	not significant
1115	C9orf3	-1.27	6.67E-03	1.36E-02	109.73	not significant
1116	LYPLA2	-1.27	1.32E-14	1.10E-13	1799.85	not significant
1117	DCAF6	-1.27	6.82E-14	5.33E-13	1634.77	not significant
1118	INTS9	-1.27	6.78E-13	4.85E-12	1555.11	not significant
1119	METTL2B	-1.27	1.05E-08	5.02E-08	860.80	not significant
1120	IFI44L	-1.27	2.08E-02	3.79E-02	10.32	not significant
1121	WDR3	-1.27	2.73E-21	3.77E-20	3183.94	not significant
1122	TIMM50	-1.27	1.20E-14	1.00E-13	1934.31	not significant
1123	ACACA	-1.27	2.09E-15	1.86E-14	4643.95	not significant
1124	MPHOSPH10	-1.27	2.37E-13	1.77E-12	1939.60	not significant
1125	TTLL11	-1.27	9.27E-03	1.83E-02	99.29	not significant
1126	TSPAN17	-1.27	5.66E-10	3.09E-09	1003.53	not significant
1127	CLUH	-1.27	2.47E-22	3.66E-21	4318.78	not significant
1128	FTSJ3	-1.27	3.68E-25	6.64E-24	4850.04	not significant
1129	HK1	-1.27	5.88E-24	9.78E-23	3707.59	not significant
1130	PDCD5	-1.27	8.95E-11	5.28E-10	1376.69	not significant
1131	NDUFA8	-1.27	5.65E-09	2.77E-08	971.75	not significant
1132	LOC399815	-1.27	2.93E-03	6.41E-03	162.09	not significant

1133	PLEKHB2	-1.27	2.79E-29	6.45E-28	5970.55	not significant
1134	BIRC3	-1.27	3.78E-08	1.70E-07	819.69	not significant
1135	TIPIN	-1.27	3.21E-07	1.29E-06	698.01	not significant
1136	DNAJB5	-1.27	5.61E-05	1.68E-04	356.00	not significant
1137	AGER	-1.27	1.30E-02	2.48E-02	86.31	not significant
1138	INPP5D	-1.27	3.39E-33	1.00E-31	8158.17	not significant
1139	MPV17	-1.27	1.44E-09	7.49E-09	1026.93	not significant
1140	B3GNTL1	-1.27	2.48E-05	7.79E-05	419.54	not significant
1141	ALG2	-1.27	2.05E-06	7.46E-06	520.04	not significant
1142	HIBCH	-1.27	1.13E-08	5.37E-08	882.02	not significant
1143	NGFRAP1	-1.27	4.15E-06	1.45E-05	493.51	not significant
1144	AK4	-1.27	5.05E-04	1.28E-03	251.84	not significant
1145	TACC3	-1.27	9.83E-33	2.84E-31	8692.41	not significant
1146	NDRG1	-1.27	1.88E-18	2.16E-17	2635.12	not significant
1147	JMJD6	-1.27	1.30E-11	8.31E-11	1254.59	not significant
1148	NAA10	-1.27	8.27E-13	5.88E-12	1388.58	not significant
1149	METTL1	-1.27	4.44E-06	1.55E-05	585.04	not significant
1150	POLR1B	-1.27	8.83E-16	8.13E-15	2141.91	not significant
1151	ONECUT2	-1.27	8.95E-03	1.77E-02	106.31	not significant
1152	GBP1	-1.27	2.28E-15	2.03E-14	1868.95	not significant
1153	GLRX5	-1.27	2.80E-16	2.68E-15	2513.96	not significant
1154	OAS3	-1.27	1.27E-22	1.92E-21	5390.85	not significant
1155	LIPT2	-1.27	1.71E-02	3.19E-02	74.60	not significant
1156	CCDC59	-1.27	4.29E-14	3.42E-13	1642.33	not significant
1157	ACTR2	-1.27	7.71E-21	1.04E-19	20047.30	not significant
1158	TRMT61A	-1.27	4.28E-09	2.13E-08	933.00	not significant
1159	IL17RE	-1.27	6.98E-03	1.42E-02	114.13	not significant
1160	PTRH2	-1.27	4.45E-09	2.21E-08	898.38	not significant
1161	SH2D2A	-1.27	5.77E-04	1.44E-03	234.25	not significant
1162	STOM	-1.27	6.02E-08	2.64E-07	788.92	not significant
1163	WDR46	-1.27	7.53E-09	3.66E-08	868.93	not significant
1164	HSPH1	-1.27	3.10E-32	8.58E-31	16077.66	not significant
1165	DDX18	-1.27	4.56E-26	8.59E-25	5248.36	not significant
1166	COG2	-1.27	9.94E-12	6.43E-11	1297.43	not significant
1167	UQCRFS1	-1.27	3.46E-15	3.05E-14	2707.65	not significant
1168	SRP14	-1.27	2.47E-22	3.66E-21	5512.55	not significant
1169	SLC41A2	-1.27	3.27E-03	7.11E-03	169.76	not significant
1170	PSMG1	-1.27	6.65E-14	5.20E-13	1690.95	not significant
1171	ZDHHC3	-1.27	8.66E-18	9.41E-17	2494.21	not significant
1172	MST4	-1.27	1.78E-29	4.18E-28	5908.19	not significant
1173	DDX27	-1.27	2.89E-15	2.55E-14	3397.61	not significant
1174	MBD2	-1.27	2.65E-22	3.89E-21	3466.04	not significant
1175	C12orf4	-1.26	4.94E-08	2.20E-07	757.14	not significant
1176	C1orf216	-1.26	6.54E-07	2.53E-06	670.41	not significant
1177	LRIG1	-1.26	5.65E-09	2.77E-08	859.73	not significant
1178	HDAC3	-1.26	9.99E-20	1.25E-18	2747.95	not significant
1179	FAM136A	-1.26	1.49E-16	1.47E-15	3572.63	not significant
1180	BAK1	-1.26	7.36E-10	3.95E-09	1276.90	not significant
1181	RAE1	-1.26	1.03E-16	1.03E-15	2646.73	not significant
1182	SLC39A14	-1.26	1.84E-19	2.28E-18	3362.88	not significant
1183	HNRNPK	-1.26	8.28E-35	2.75E-33	35571.09	not significant
1184	GART	-1.26	1.42E-26	2.78E-25	5394.59	not significant
1185	SLC25A20	-1.26	1.34E-08	6.34E-08	1137.39	not significant
1186	PAG1	-1.26	3.88E-24	6.53E-23	5133.60	not significant
1187	ADRM1	-1.26	1.25E-14	1.04E-13	2626.57	not significant
1188	POLD2	-1.26	4.38E-28	9.45E-27	6807.16	not significant
1189	COPB2	-1.26	3.91E-22	5.70E-21	4883.49	not significant
1190	ABCD1	-1.26	8.05E-03	1.61E-02	114.97	not significant
1191	KIAA0020	-1.26	2.83E-16	2.70E-15	2363.88	not significant
1192	CCT7	-1.26	8.84E-21	1.19E-19	15504.90	not significant
1193	KIF20B	-1.26	1.34E-19	1.66E-18	3996.88	not significant
1194	PDLIM7	-1.26	2.44E-04	6.54E-04	299.15	not significant
1195	C11orf45	-1.26	1.28E-04	3.60E-04	326.46	not significant
1196	S100P	-1.26	3.64E-02	6.27E-02	32.50	not significant
1197	DCUN1D5	-1.26	6.06E-14	4.77E-13	1718.50	not significant
1198	MRPL12	-1.26	7.63E-16	7.07E-15	3500.29	not significant
1199	FAM96B	-1.26	8.67E-13	6.16E-12	2039.81	not significant
1200	HUWE1	-1.26	1.59E-04	4.40E-04	4911.94	not significant
1201	TNKS1BP1	-1.26	3.98E-06	1.40E-05	592.91	not significant
1202	CSTF2	-1.26	1.35E-09	7.04E-09	1043.35	not significant
1203	FABP5	-1.26	5.08E-07	1.99E-06	807.10	not significant
1204	MTIF3	-1.26	8.33E-08	3.59E-07	764.20	not significant
1205	GALNT6	-1.26	1.57E-12	1.09E-11	1641.37	not significant
1206	YBX3	-1.26	8.20E-17	8.22E-16	2781.12	not significant
1207	MAPKAPK3	-1.26	1.01E-28	2.25E-27	6867.80	not significant
1208	NDUFB3	-1.26	4.94E-12	3.29E-11	1527.16	not significant
1209	NOP2	-1.26	1.49E-15	1.34E-14	2868.89	not significant
1210	PROSC	-1.26	2.70E-21	3.74E-20	5253.16	not significant
1211	TNFAIP8L1	-1.26	1.22E-07	5.16E-07	702.48	not significant
1212	PDAP1	-1.26	6.60E-18	7.25E-17	5212.59	not significant
1213	GNL2	-1.26	7.07E-14	5.52E-13	2402.18	not significant
1214	HOMER1	-1.26	1.42E-12	9.89E-12	1455.47	not significant
1215	TRAP1	-1.26	6.03E-15	5.20E-14	2532.61	not significant
1216	SCO1	-1.26	4.95E-11	2.99E-10	1271.75	not significant
1217	DHRS4-AS1	-1.26	9.47E-09	4.56E-08	856.96	not significant
1218	EPHA1	-1.26	2.75E-02	4.89E-02	12.42	not significant
1219	KPNB1	-1.26	1.13E-37	4.55E-36	22819.78	not significant
1220	NUP93	-1.26	9.68E-22	1.38E-20	3688.29	not significant

1221	PSMB6	-1.26	1.36E-15	1.24E-14	2674.27	not significant
1222	LOC100996324	-1.26	1.39E-03	3.25E-03	211.34	not significant
1223	MLLT3	-1.26	3.12E-15	2.75E-14	2117.74	not significant
1224	MTFMT	-1.26	4.84E-05	1.46E-04	455.40	not significant
1225	HIST1H1D	-1.26	3.85E-02	6.58E-02	34.19	not significant
1226	RAB1B	-1.26	5.67E-20	7.23E-19	6615.22	not significant
1227	EIF5B	-1.26	6.89E-23	1.06E-21	6252.46	not significant
1228	MINOS1	-1.26	9.63E-08	4.12E-07	856.03	not significant
1229	ATPAF1	-1.26	1.47E-16	1.45E-15	2241.99	not significant
1230	KPNA3	-1.26	2.87E-23	4.54E-22	4072.69	not significant
1231	FOXRED1	-1.26	1.42E-11	9.01E-11	1309.60	not significant
1232	SERF2	-1.26	3.73E-23	5.85E-22	4688.30	not significant
1233	USP54	-1.26	4.64E-05	1.40E-04	431.88	not significant
1234	CHRNA9	-1.26	3.39E-03	7.36E-03	193.45	not significant
1235	IQSEC1	-1.26	2.20E-16	2.13E-15	2298.99	not significant
1236	PMPCA	-1.26	5.01E-13	3.62E-12	1596.19	not significant
1237	TWF1	-1.26	3.16E-07	1.27E-06	687.85	not significant
1238	RABEPK	-1.26	9.98E-08	4.27E-07	814.60	not significant
1239	LOC100130899	-1.26	3.77E-02	6.46E-02	34.55	not significant
1240	VCP	-1.26	3.72E-32	1.02E-30	12978.57	not significant
1241	HEATR2	-1.26	4.24E-15	3.70E-14	1991.99	not significant
1242	LINC00260	-1.26	3.74E-02	6.42E-02	19.06	not significant
1243	DDX10	-1.26	7.29E-13	5.20E-12	1662.30	not significant
1244	LSM3	-1.26	1.33E-12	9.30E-12	2493.87	not significant
1245	SERTAD1	-1.26	1.46E-02	2.76E-02	92.90	not significant
1246	MTRF1L	-1.26	1.45E-03	3.37E-03	207.91	not significant
1247	STAT6	-1.26	6.81E-21	9.22E-20	5037.43	not significant
1248	SLCO3A1	-1.26	7.81E-03	1.57E-02	123.48	not significant
1249	SIL1	-1.26	6.38E-05	1.89E-04	391.80	not significant
1250	UTP3	-1.26	4.49E-11	2.73E-10	2273.71	not significant
1251	DNAJC2	-1.26	3.78E-15	3.32E-14	2175.62	not significant
1252	ZCRB1	-1.26	2.24E-17	2.37E-16	3448.02	not significant
1253	AEN	-1.26	1.86E-11	1.16E-10	1358.99	not significant
1254	CMSS1	-1.25	2.85E-13	2.11E-12	1796.11	not significant
1255	UBAC2-AS1	-1.25	3.88E-02	6.62E-02	34.47	not significant
1256	EXT1	-1.25	2.51E-05	7.87E-05	430.72	not significant
1257	ABCD3	-1.25	1.32E-16	1.31E-15	3672.70	not significant
1258	TACO1	-1.25	3.51E-10	1.95E-09	1173.84	not significant
1259	SLC1A5	-1.25	4.40E-25	7.89E-24	6399.25	not significant
1260	FAM173B	-1.25	7.61E-05	2.23E-04	400.88	not significant
1261	TRMT5	-1.25	1.99E-07	8.21E-07	741.55	not significant
1262	DHX29	-1.25	6.09E-11	3.65E-10	1325.55	not significant
1263	DHX57	-1.25	3.10E-10	1.74E-09	1121.29	not significant
1264	REEP4	-1.25	8.34E-13	5.92E-12	1619.05	not significant
1265	KIF1B	-1.25	1.76E-09	9.10E-09	1268.20	not significant
1266	GUK1	-1.25	1.84E-20	2.42E-19	5803.01	not significant
1267	NUTF2	-1.25	1.44E-23	2.33E-22	5043.96	not significant
1268	CCT6A	-1.25	1.82E-23	2.91E-22	15381.27	not significant
1269	SARS	-1.25	4.86E-19	5.80E-18	3998.25	not significant
1270	FCF1	-1.25	2.50E-13	1.86E-12	2425.28	not significant
1271	DCAF4	-1.25	4.55E-07	1.80E-06	690.50	not significant
1272	SOCS2	-1.25	2.01E-14	1.65E-13	2259.45	not significant
1273	MRPS17	-1.25	2.29E-06	8.30E-06	725.55	not significant
1274	SRGAP2	-1.25	8.29E-04	2.01E-03	260.34	not significant
1275	EIF1AY	-1.25	2.76E-13	2.04E-12	3685.37	not significant
1276	PALLD	-1.25	1.07E-11	6.90E-11	1464.16	not significant
1277	INTS12	-1.25	5.55E-07	2.16E-06	847.80	not significant
1278	COPS6	-1.25	4.67E-15	4.06E-14	2859.86	not significant
1279	NCBP1	-1.25	1.14E-19	1.42E-18	3354.80	not significant
1280	EIF5	-1.25	2.29E-25	4.18E-24	12789.79	not significant
1281	KLLN	-1.25	3.37E-04	8.82E-04	298.39	not significant
1282	HIST1H3F	-1.25	3.70E-02	6.35E-02	20.21	not significant
1283	LOC643733	-1.25	3.82E-02	6.55E-02	20.96	not significant
1284	NDUFAF4	-1.25	8.83E-08	3.80E-07	1063.70	not significant
1285	IFT46	-1.25	5.53E-04	1.39E-03	297.65	not significant
1286	GNGT2	-1.25	5.54E-04	1.39E-03	317.52	not significant
1287	STC2	-1.25	2.98E-02	5.25E-02	12.89	not significant
1288	STX4	-1.25	2.11E-06	7.65E-06	676.38	not significant
1289	POP5	-1.25	4.95E-08	2.20E-07	868.86	not significant
1290	G2E3	-1.25	3.43E-10	1.91E-09	1504.32	not significant
1291	MOCS2	-1.25	1.58E-13	1.19E-12	1876.20	not significant
1292	AHCTF1	-1.25	1.90E-17	2.01E-16	2950.88	not significant
1293	FHL2	-1.25	2.63E-04	7.03E-04	327.47	not significant
1294	CAPZB	-1.25	5.61E-21	7.66E-20	7473.49	not significant
1295	ACTN1	-1.25	1.20E-05	3.94E-05	501.25	not significant
1296	XRCC4	-1.25	2.12E-05	6.72E-05	502.78	not significant
1297	UBA1	-1.25	5.52E-26	1.03E-24	6064.19	not significant
1298	DDX31	-1.25	2.81E-07	1.14E-06	705.65	not significant
1299	NUDCD2	-1.25	1.22E-10	7.10E-10	1357.35	not significant
1300	TSPAN13	-1.25	4.78E-05	1.44E-04	437.85	not significant
1301	CAB39L	-1.25	1.10E-02	2.14E-02	120.58	not significant
1302	RHOBTB3	-1.25	2.80E-03	6.17E-03	279.56	not significant
1303	CTDP1	-1.25	1.42E-10	8.23E-10	1745.86	not significant
1304	HMOX2	-1.25	1.83E-10	1.05E-09	1378.99	not significant
1305	GNPNAT1	-1.25	6.70E-17	6.79E-16	2734.42	not significant
1306	SDF2L1	-1.25	4.42E-03	9.38E-03	788.62	not significant
1307	NDUFB7	-1.25	3.21E-12	2.17E-11	1701.62	not significant
1308	HCCS	-1.25	6.01E-05	1.79E-04	480.29	not significant

1309	C5orf55	-1.25	3.67E-02	6.30E-02	51.27	not significant
1310	RFESD	-1.25	1.29E-03	3.02E-03	227.95	not significant
1311	CMC2	-1.25	9.61E-11	5.66E-10	1576.22	not significant
1312	IL32	-1.25	2.60E-17	2.72E-16	4100.22	not significant
1313	CNOT11	-1.25	2.72E-20	3.53E-19	3682.02	not significant
1314	PARPBP	-1.25	4.39E-12	2.93E-11	1745.28	not significant
1315	LARP4	-1.25	2.43E-21	3.39E-20	5990.89	not significant
1316	TPD52	-1.25	8.44E-16	7.79E-15	3201.26	not significant
1317	PLD2	-1.25	3.62E-02	6.22E-02	54.49	not significant
1318	WBP11	-1.25	3.97E-26	7.52E-25	6548.49	not significant
1319	GYG2	-1.25	5.91E-05	1.76E-04	411.74	not significant
1320	PPP2R5A	-1.25	1.15E-14	9.63E-14	2585.29	not significant
1321	DNHD1	-1.25	1.82E-04	4.99E-04	466.88	not significant
1322	ADK	-1.25	3.20E-10	1.79E-09	1314.39	not significant
1323	ATG101	-1.25	1.39E-06	5.17E-06	849.30	not significant
1324	NEK2	-1.25	1.99E-14	1.64E-13	2350.88	not significant
1325	COQ9	-1.25	1.41E-06	5.24E-06	705.52	not significant
1326	SUSD1	-1.25	1.07E-03	2.53E-03	271.50	not significant
1327	TSR1	-1.25	2.61E-20	3.41E-19	3506.91	not significant
1328	MTCH2	-1.25	7.44E-17	7.49E-16	3573.11	not significant
1329	PRKCB	-1.25	1.14E-21	1.62E-20	8247.19	not significant
1330	PDCD6IPP2	-1.25	2.92E-02	5.15E-02	62.16	not significant
1331	HNRNPAB	-1.25	4.01E-16	3.78E-15	14352.22	not significant
1332	TPK1	-1.25	2.65E-02	4.73E-02	71.22	not significant
1333	RHPN1-AS1	-1.25	1.37E-02	2.62E-02	106.15	not significant
1334	GNL3	-1.25	5.88E-23	9.07E-22	4635.58	not significant
1335	FDX1L	-1.25	5.51E-05	1.65E-04	465.55	not significant
1336	NDUFA6	-1.25	2.34E-05	7.38E-05	682.77	not significant
1337	APRT	-1.25	6.23E-17	6.33E-16	3600.56	not significant
1338	HSPA14	-1.25	8.41E-18	9.16E-17	2883.46	not significant
1339	LMLN	-1.25	6.72E-03	1.37E-02	144.64	not significant
1340	NCBP2	-1.25	3.49E-19	4.23E-18	5908.93	not significant
1341	SEC13	-1.25	4.31E-15	3.76E-14	3199.38	not significant
1342	PRR7	-1.24	1.09E-02	2.13E-02	119.31	not significant
1343	USP35	-1.24	1.49E-03	3.46E-03	246.24	not significant
1344	BCAT2	-1.24	5.57E-09	2.74E-08	1031.87	not significant
1345	GPX1	-1.24	8.83E-13	6.26E-12	2202.60	not significant
1346	SAFB2	-1.24	1.10E-17	1.19E-16	2994.52	not significant
1347	DDX60L	-1.24	3.52E-11	2.16E-10	1804.50	not significant
1348	C8orf33	-1.24	6.75E-24	1.12E-22	5378.15	not significant
1349	GALE	-1.24	3.66E-06	1.29E-05	595.12	not significant
1350	TRIT1	-1.24	3.43E-08	1.55E-07	981.34	not significant
1351	DCTN3	-1.24	1.67E-12	1.15E-11	1772.46	not significant
1352	TREX1	-1.24	6.53E-05	1.93E-04	400.73	not significant
1353	DNAJB1	-1.24	5.91E-20	7.52E-19	4101.61	not significant
1354	TMEM165	-1.24	1.06E-14	8.87E-14	2142.00	not significant
1355	CORO1B	-1.24	1.29E-10	7.51E-10	1495.84	not significant
1356	PPP3CB	-1.24	3.28E-12	2.21E-11	1891.72	not significant
1357	SCO2	-1.24	7.55E-04	1.84E-03	272.18	not significant
1358	CBR1	-1.24	1.59E-05	5.14E-05	525.82	not significant
1359	RBM8A	-1.24	7.86E-12	5.14E-11	1863.07	not significant
1360	CARS	-1.24	2.53E-12	1.73E-11	1743.64	not significant
1361	KIF3B	-1.24	6.92E-08	3.01E-07	1037.38	not significant
1362	BOP1	-1.24	2.38E-05	7.48E-05	477.94	not significant
1363	ACOT13	-1.24	3.13E-07	1.26E-06	801.59	not significant
1364	MTDH	-1.24	1.45E-26	2.83E-25	16027.26	not significant
1365	NAA50	-1.24	2.12E-27	4.38E-26	10993.91	not significant
1366	MRPS23	-1.24	1.48E-11	9.41E-11	2281.15	not significant
1367	ARPC1B	-1.24	2.55E-16	2.45E-15	7244.58	not significant
1368	NUDT1	-1.24	5.75E-10	3.13E-09	2375.78	not significant
1369	COG8	-1.24	1.54E-05	4.98E-05	532.27	not significant
1370	NTPCR	-1.24	3.56E-07	1.43E-06	858.77	not significant
1371	MBNL1	-1.24	7.79E-25	1.36E-23	28005.65	not significant
1372	MRPS6	-1.24	7.68E-15	6.55E-14	2507.67	not significant
1373	MRPS10	-1.24	1.09E-13	8.35E-13	2051.31	not significant
1374	GTF3C6	-1.24	3.57E-10	1.99E-09	2013.35	not significant
1375	PITPNB	-1.24	7.59E-10	4.06E-09	1330.64	not significant
1376	TRMT10A	-1.24	2.71E-04	7.21E-04	336.59	not significant
1377	XPO5	-1.24	9.25E-21	1.24E-19	4896.76	not significant
1378	SEC14L2	-1.24	1.60E-04	4.44E-04	389.37	not significant
1379	MRPS14	-1.24	1.11E-07	4.70E-07	971.57	not significant
1380	H2AFZ	-1.24	2.59E-06	9.29E-06	17632.62	not significant
1381	POLR2J	-1.24	1.24E-07	5.24E-07	1212.93	not significant
1382	ARHGEF6	-1.24	1.17E-24	2.03E-23	10226.58	not significant
1383	PSMD8	-1.24	1.03E-16	1.03E-15	4925.94	not significant
1384	FAM126A	-1.24	3.25E-12	2.19E-11	1783.53	not significant
1385	LRRC8D	-1.24	4.39E-11	2.67E-10	1597.25	not significant
1386	NAT10	-1.24	2.59E-17	2.71E-16	5784.88	not significant
1387	WDR89	-1.24	5.42E-09	2.66E-08	1337.26	not significant
1388	ZNF143	-1.24	2.98E-07	1.20E-06	770.71	not significant
1389	FAM49B	-1.24	7.89E-29	1.77E-27	10604.79	not significant
1390	BCAR3	-1.24	3.92E-02	6.69E-02	17.74	not significant
1391	ODF2	-1.24	3.82E-18	4.30E-17	4243.23	not significant
1392	FAM114A2	-1.24	3.59E-08	1.62E-07	931.06	not significant
1393	CLPB	-1.24	4.86E-08	2.17E-07	972.42	not significant
1394	SAR1B	-1.24	1.25E-08	5.92E-08	1237.01	not significant
1395	R3HDM1	-1.24	5.43E-20	6.93E-19	5560.65	not significant
1396	NDUFV3	-1.24	4.02E-04	1.04E-03	326.33	not significant

1397	UBE2E2	-1.24	5.04E-07	1.98E-06	754.15	not significant
1398	RWDD2B	-1.24	5.30E-06	1.82E-05	619.23	not significant
1399	MTFR2	-1.24	7.52E-07	2.88E-06	849.90	not significant
1400	COX5B	-1.24	3.71E-15	3.26E-14	3020.58	not significant
1401	TRIP13	-1.24	2.46E-17	2.58E-16	2945.38	not significant
1402	EIF2AK4	-1.24	7.72E-14	6.00E-13	2468.31	not significant
1403	HYOU1	-1.24	1.24E-18	1.44E-17	3334.07	not significant
1404	CTSB	-1.24	2.07E-19	2.54E-18	5192.26	not significant
1405	DOLK	-1.24	5.36E-03	1.12E-02	170.76	not significant
1406	APOO	-1.24	4.03E-06	1.41E-05	616.43	not significant
1407	BCL9	-1.24	7.27E-03	1.47E-02	163.10	not significant
1408	DGUOK	-1.24	1.11E-12	7.86E-12	2031.62	not significant
1409	NEDD8	-1.24	1.45E-12	1.01E-11	1804.92	not significant
1410	ABHD6	-1.24	1.96E-03	4.44E-03	222.53	not significant
1411	GOSR2	-1.24	1.77E-11	1.11E-10	1588.71	not significant
1412	NUDT6	-1.24	1.06E-03	2.53E-03	280.00	not significant
1413	PSMA3	-1.24	3.15E-17	3.27E-16	4139.80	not significant
1414	INPP1	-1.24	7.69E-03	1.55E-02	153.64	not significant
1415	EXOSC7	-1.24	6.29E-08	2.75E-07	997.43	not significant
1416	ANP32E	-1.24	3.14E-10	1.76E-09	2262.43	not significant
1417	SPATA5L1	-1.24	1.94E-04	5.31E-04	365.80	not significant
1418	C1QBP	-1.24	7.52E-19	8.84E-18	12039.65	not significant
1419	LSP1	-1.24	1.58E-17	1.68E-16	3525.37	not significant
1420	TRAK2	-1.24	1.50E-10	8.68E-10	1467.71	not significant
1421	EIF2B5	-1.24	2.23E-13	1.67E-12	1992.04	not significant
1422	ATG5	-1.24	7.32E-09	3.56E-08	1465.78	not significant
1423	TLDC1	-1.24	9.38E-04	2.25E-03	285.39	not significant
1424	TOP2A	-1.24	7.75E-22	1.11E-20	42048.63	not significant
1425	MYBBP1A	-1.24	5.78E-13	4.16E-12	4188.09	not significant
1426	GOT2	-1.24	3.15E-24	5.33E-23	7452.10	not significant
1427	PTCD2	-1.24	9.56E-04	2.29E-03	295.19	not significant
1428	IPO11	-1.24	8.78E-08	3.77E-07	902.05	not significant
1429	C20orf27	-1.24	3.92E-12	2.62E-11	2454.72	not significant
1430	COA4	-1.24	5.60E-09	2.75E-08	1227.57	not significant
1431	LSM1	-1.24	2.01E-12	1.38E-11	1853.44	not significant
1432	FAM216A	-1.24	1.08E-08	5.16E-08	1099.01	not significant
1433	METTL4	-1.24	4.77E-07	1.88E-06	943.43	not significant
1434	UBE2L3	-1.23	9.94E-23	1.51E-21	5166.89	not significant
1435	GLIPR2	-1.23	1.55E-04	4.32E-04	432.81	not significant
1436	YWHAE	-1.23	1.22E-26	2.42E-25	18311.71	not significant
1437	DNAJC11	-1.23	3.22E-13	2.37E-12	2182.37	not significant
1438	SFXN1	-1.23	3.64E-22	5.33E-21	4770.54	not significant
1439	SGTA	-1.23	7.17E-15	6.14E-14	4036.40	not significant
1440	RRS1	-1.23	4.02E-11	2.46E-10	1824.44	not significant
1441	CAPN14	-1.23	4.12E-02	6.98E-02	49.40	not significant
1442	CSTF1	-1.23	2.11E-11	1.32E-10	1612.54	not significant
1443	SEC23IP	-1.23	4.41E-14	3.51E-13	2331.21	not significant
1444	PRDX3	-1.23	9.97E-22	1.42E-20	9374.00	not significant
1445	PLEKHO2	-1.23	6.26E-06	2.14E-05	713.37	not significant
1446	NOL6	-1.23	8.29E-16	7.67E-15	2811.77	not significant
1447	SHQ1	-1.23	2.97E-20	3.85E-19	4449.53	not significant
1448	BMP4	-1.23	4.55E-03	9.63E-03	184.78	not significant
1449	CYB5D2	-1.23	2.30E-03	5.14E-03	236.90	not significant
1450	MRPL1	-1.23	1.40E-07	5.89E-07	936.50	not significant
1451	NRF1	-1.23	1.52E-09	7.86E-09	1525.35	not significant
1452	EWSR1	-1.23	2.38E-28	5.21E-27	11723.16	not significant
1453	USMG5	-1.23	4.99E-15	4.32E-14	2821.20	not significant
1454	PRICKLE4	-1.23	2.24E-02	4.07E-02	94.26	not significant
1455	SMARCA5	-1.23	4.87E-19	5.81E-18	11462.03	not significant
1456	NIF3L1	-1.23	6.76E-10	3.65E-09	1547.30	not significant
1457	MRPL49	-1.23	3.47E-14	2.79E-13	2902.21	not significant
1458	CENPF	-1.23	5.32E-15	4.61E-14	17045.98	not significant
1459	TDG	-1.23	5.06E-17	5.18E-16	3728.71	not significant
1460	CRLS1	-1.23	8.71E-11	5.14E-10	1760.40	not significant
1461	RQCD1	-1.23	3.05E-20	3.94E-19	5444.36	not significant
1462	SYNGR2	-1.23	1.28E-10	7.44E-10	2242.07	not significant
1463	MRPL28	-1.23	2.18E-13	1.63E-12	2442.16	not significant
1464	MKNK1	-1.23	8.37E-06	2.81E-05	590.52	not significant
1465	VRK1	-1.23	2.11E-13	1.58E-12	3628.32	not significant
1466	PREPL	-1.23	1.81E-13	1.37E-12	2319.54	not significant
1467	POLR3E	-1.23	1.54E-11	9.78E-11	1865.40	not significant
1468	LOXL1	-1.23	4.95E-02	8.24E-02	28.66	not significant
1469	TRIM66	-1.23	2.81E-04	7.44E-04	501.13	not significant
1470	NIPA2	-1.23	6.15E-14	4.84E-13	3064.51	not significant
1471	USP14	-1.23	2.62E-21	3.64E-20	5602.82	not significant
1472	PDIA3	-1.23	2.88E-19	3.51E-18	7269.35	not significant
1473	ID3	-1.23	1.34E-05	4.38E-05	606.35	not significant
1474	PPIH	-1.23	1.68E-10	9.67E-10	2092.95	not significant
1475	ELP4	-1.23	3.95E-07	1.57E-06	880.01	not significant
1476	CARM1	-1.23	2.29E-16	2.21E-15	3684.36	not significant
1477	LOC103611081	-1.23	2.81E-03	6.18E-03	300.04	not significant
1478	NDUFB4	-1.23	6.52E-13	4.68E-12	2982.85	not significant
1479	LOC100507250	-1.23	5.04E-02	8.38E-02	28.43	not significant
1480	NFU1	-1.23	3.53E-06	1.25E-05	746.00	not significant
1481	RPUSD2	-1.23	2.81E-04	7.43E-04	426.37	not significant
1482	HIBADH	-1.23	1.58E-06	5.84E-06	827.20	not significant
1483	ZFP36	-1.23	8.06E-05	2.35E-04	462.91	not significant
1484	THUMPD3	-1.23	2.71E-13	2.01E-12	2908.32	not significant

1485	SNRPA1	-1.23	2.09E-11	1.30E-10	2089.59	not significant
1486	PSMD3	-1.23	1.11E-20	1.48E-19	6493.40	not significant
1487	PPIB	-1.23	2.40E-16	2.31E-15	6965.68	not significant
1488	WDR61	-1.23	1.06E-08	5.07E-08	1357.41	not significant
1489	UTP20	-1.23	2.78E-04	7.37E-04	3224.90	not significant
1490	FAM69A	-1.23	4.38E-06	1.53E-05	734.62	not significant
1491	C4orf27	-1.23	2.19E-09	1.12E-08	1480.16	not significant
1492	TRMU	-1.23	3.66E-06	1.29E-05	836.10	not significant
1493	UBL5	-1.23	2.70E-04	7.18E-04	3070.59	not significant
1494	ATP5B	-1.23	3.86E-17	3.99E-16	34682.85	not significant
1495	PRDM1	-1.23	3.34E-02	5.81E-02	71.44	not significant
1496	RNASEH1-AS1	-1.23	6.64E-04	1.64E-03	321.57	not significant
1497	MYO1C	-1.23	1.54E-06	5.70E-06	838.16	not significant
1498	CHP1	-1.23	3.34E-09	1.68E-08	2079.65	not significant
1499	POMP	-1.23	4.50E-12	3.00E-11	3747.48	not significant
1500	TRUB1	-1.23	1.41E-08	6.61E-08	1200.41	not significant
1501	DNAJC25	-1.23	5.46E-03	1.13E-02	202.02	not significant
1502	POLR2D	-1.23	2.52E-17	2.64E-16	4060.02	not significant
1503	SUSD3	-1.23	9.44E-03	1.86E-02	155.30	not significant
1504	KRTCAP2	-1.23	8.87E-09	4.29E-08	1324.63	not significant
1505	MAP4K1	-1.23	1.16E-14	9.74E-14	2695.07	not significant
1506	CPVL	-1.23	9.18E-12	5.96E-11	2437.97	not significant
1507	TCOF1	-1.23	6.40E-21	8.69E-20	5967.69	not significant
1508	IFRD2	-1.23	2.20E-06	7.98E-06	761.68	not significant
1509	TANGO6	-1.23	5.06E-07	1.99E-06	888.49	not significant
1510	KLHL18	-1.23	3.64E-07	1.46E-06	903.70	not significant
1511	PES1	-1.22	8.26E-15	7.03E-14	3129.73	not significant
1512	TNFRSF8	-1.22	1.81E-06	6.63E-06	750.96	not significant
1513	NPRL2	-1.22	5.44E-06	1.87E-05	758.30	not significant
1514	VAMP8	-1.22	2.64E-04	7.03E-04	414.14	not significant
1515	HN1L	-1.22	2.71E-21	3.75E-20	4955.31	not significant
1516	SRSF1	-1.22	4.22E-25	7.58E-24	26568.82	not significant
1517	SPATA2L	-1.22	5.94E-03	1.22E-02	186.91	not significant
1518	FKBP3	-1.22	3.63E-14	2.91E-13	3089.56	not significant
1519	POLR3GL	-1.22	3.40E-04	8.89E-04	418.29	not significant
1520	SLC16A1	-1.22	2.30E-23	3.65E-22	7820.61	not significant
1521	EI24	-1.22	1.54E-10	8.88E-10	2401.29	not significant
1522	NDUFB6	-1.22	5.11E-07	2.00E-06	1536.88	not significant
1523	EIF2S1	-1.22	1.38E-18	1.61E-17	5409.02	not significant
1524	NOTCH2	-1.22	2.79E-10	1.57E-09	3024.99	not significant
1525	ZNF652	-1.22	6.64E-04	1.64E-03	414.20	not significant
1526	TTLL12	-1.22	4.82E-20	6.15E-19	6349.88	not significant
1527	TMEM5	-1.22	5.74E-05	1.71E-04	645.65	not significant
1528	CPSF2	-1.22	9.54E-20	1.20E-18	5740.87	not significant
1529	UTP11L	-1.22	5.33E-11	3.21E-10	1952.67	not significant
1530	43533_16638	-1.22	6.61E-10	3.57E-09	1767.08	not significant
1531	SMPD4	-1.22	1.82E-14	1.50E-13	3665.64	not significant
1532	TCEAL4	-1.22	1.92E-02	3.53E-02	111.93	not significant
1533	FTSJ1	-1.22	1.35E-05	4.41E-05	612.89	not significant
1534	CEP55	-1.22	4.62E-15	4.02E-14	5548.03	not significant
1535	RANGRF	-1.22	2.25E-10	1.28E-09	1920.78	not significant
1536	SLC6A9	-1.22	1.11E-02	2.16E-02	150.43	not significant
1537	ACTN4	-1.22	7.47E-15	6.39E-14	4866.19	not significant
1538	NSRP1	-1.22	3.57E-06	1.26E-05	1084.59	not significant
1539	C14orf64	-1.22	3.21E-04	8.43E-04	469.83	not significant
1540	EARS2	-1.22	4.02E-08	1.80E-07	1347.24	not significant
1541	MTFP1	-1.22	3.89E-10	2.16E-09	2011.43	not significant
1542	AGPS	-1.22	2.06E-15	1.84E-14	3510.66	not significant
1543	CAB39	-1.22	4.85E-15	4.20E-14	5636.75	not significant
1544	KIAA0226L	-1.22	2.33E-06	8.44E-06	780.91	not significant
1545	IDH1	-1.22	2.51E-07	1.02E-06	1121.16	not significant
1546	RALB	-1.22	6.47E-06	2.21E-05	694.10	not significant
1547	C1orf52	-1.22	1.08E-06	4.07E-06	881.89	not significant
1548	SAR1A	-1.22	8.22E-18	8.96E-17	4032.03	not significant
1549	PPP6R3	-1.22	2.28E-17	2.40E-16	5982.31	not significant
1550	C10orf2	-1.22	4.60E-10	2.53E-09	1676.06	not significant
1551	LZTS2	-1.22	2.68E-04	7.13E-04	428.06	not significant
1552	NAB2	-1.22	1.13E-06	4.25E-06	863.97	not significant
1553	MYO7B	-1.22	3.28E-16	3.11E-15	46730.36	not significant
1554	BORA	-1.22	2.00E-10	1.14E-09	1822.10	not significant
1555	LYPLAL1	-1.22	2.88E-03	6.31E-03	239.68	not significant
1556	TOMM6	-1.22	1.63E-13	1.23E-12	4269.55	not significant
1557	CAPNS1	-1.22	1.43E-22	2.15E-21	6596.09	not significant
1558	SLC7A6	-1.22	1.89E-14	1.55E-13	2750.01	not significant
1559	SLC38A10	-1.22	2.15E-15	1.92E-14	3682.49	not significant
1560	SPRTN	-1.22	2.51E-05	7.87E-05	675.47	not significant
1561	DOHH	-1.22	2.24E-06	8.11E-06	1102.08	not significant
1562	FYCO1	-1.22	8.77E-10	4.65E-09	1630.71	not significant
1563	ZNF518B	-1.22	1.18E-09	6.20E-09	1471.66	not significant
1564	PPP2R1B	-1.22	7.83E-15	6.68E-14	2786.92	not significant
1565	MIR4697HG	-1.22	1.67E-03	3.83E-03	350.11	not significant
1566	SUMO1	-1.22	6.73E-12	4.42E-11	4365.30	not significant
1567	BRCC3	-1.22	5.97E-03	1.23E-02	256.86	not significant
1568	MRPL48	-1.22	3.17E-09	1.60E-08	1571.73	not significant
1569	NDUFC2	-1.22	1.65E-06	6.10E-06	941.34	not significant
1570	PDCL3	-1.22	1.37E-06	5.13E-06	1032.13	not significant
1571	MRPL46	-1.22	8.79E-05	2.55E-04	507.02	not significant
1572	ULBP1	-1.22	2.83E-05	8.83E-05	573.13	not significant

1573	HDDC3	-1.22	3.87E-03	8.32E-03	265.84	not significant
1574	DENR	-1.22	1.02E-22	1.55E-21	8347.83	not significant
1575	FKBP1B	-1.22	5.54E-02	9.10E-02	32.73	not significant
1576	PSMC5	-1.22	2.45E-14	1.99E-13	6686.62	not significant
1577	NDUFB9	-1.22	3.39E-14	2.73E-13	3772.19	not significant
1578	RFK	-1.22	7.13E-10	3.84E-09	1592.47	not significant
1579	SLC35C1	-1.22	1.20E-06	4.51E-06	955.54	not significant
1580	RBM14	-1.22	1.51E-17	1.62E-16	4486.47	not significant
1581	HDAC8	-1.22	1.32E-02	2.53E-02	152.56	not significant
1582	LINC00998	-1.22	3.84E-07	1.53E-06	996.98	not significant
1583	GEMIN6	-1.22	2.83E-05	8.82E-05	647.42	not significant
1584	B9D2	-1.22	1.82E-02	3.37E-02	138.62	not significant
1585	NUDT7	-1.22	2.98E-02	5.25E-02	91.09	not significant
1586	TMEM86B	-1.22	2.15E-03	4.84E-03	283.73	not significant
1587	PARL	-1.22	1.17E-08	5.55E-08	1473.41	not significant
1588	ARHGAP19	-1.22	6.42E-11	3.84E-10	3182.83	not significant
1589	ALG3	-1.22	1.59E-07	6.61E-07	1335.46	not significant
1590	ITGA5	-1.22	1.52E-12	1.05E-11	2340.20	not significant
1591	SEH1L	-1.22	4.48E-14	3.56E-13	4123.51	not significant
1592	ZNF684	-1.22	4.30E-03	9.14E-03	218.24	not significant
1593	MED10	-1.22	6.91E-10	3.72E-09	1696.91	not significant
1594	PPP2CA	-1.22	2.12E-21	2.96E-20	11068.59	not significant
1595	DHFRL1	-1.22	1.66E-06	6.13E-06	825.98	not significant
1596	RRP12	-1.22	1.45E-08	6.81E-08	1737.11	not significant
1597	VPS45	-1.22	4.87E-06	1.68E-05	732.39	not significant
1598	EIF2B1	-1.22	1.10E-15	1.01E-14	4114.03	not significant
1599	DCXR	-1.22	6.58E-10	3.55E-09	1589.68	not significant
1600	SUCLG1	-1.22	8.37E-14	6.49E-13	3041.80	not significant
1601	MRPL16	-1.22	1.50E-10	8.64E-10	2390.19	not significant
1602	FOXO4	-1.22	2.92E-04	7.72E-04	460.23	not significant
1603	COX6B1	-1.22	8.75E-15	7.43E-14	3893.76	not significant
1604	USP10	-1.22	6.25E-17	6.34E-16	4183.88	not significant
1605	TRUB2	-1.22	2.20E-06	7.98E-06	963.16	not significant
1606	SMC6	-1.22	2.30E-12	1.57E-11	2922.77	not significant
1607	PIGK	-1.22	8.14E-08	3.51E-07	1346.67	not significant
1608	WT1-AS	-1.22	5.57E-02	9.15E-02	37.94	not significant
1609	PSMA7	-1.22	1.93E-11	1.21E-10	5036.15	not significant
1610	CYP27B1	-1.22	2.96E-02	5.21E-02	105.26	not significant
1611	SRGN	-1.21	4.28E-05	1.30E-04	595.95	not significant
1612	FKBP5	-1.21	3.87E-19	4.66E-18	6631.92	not significant
1613	KPNA4	-1.21	1.89E-18	2.16E-17	5476.34	not significant
1614	IFT57	-1.21	5.45E-05	1.63E-04	549.04	not significant
1615	C17orf89	-1.21	3.02E-03	6.60E-03	1840.05	not significant
1616	C1D	-1.21	6.94E-05	2.04E-04	555.98	not significant
1617	ZNF41	-1.21	7.37E-05	2.16E-04	543.65	not significant
1618	PPRC1	-1.21	2.12E-09	1.09E-08	2757.19	not significant
1619	ERVFRD-1	-1.21	3.90E-02	6.66E-02	14.28	not significant
1620	TNF	-1.21	5.80E-02	9.46E-02	36.30	not significant
1621	HNRNPL	-1.21	3.23E-27	6.59E-26	16396.45	not significant
1622	RNF213	-1.21	1.16E-02	2.25E-02	22960.26	not significant
1623	PDHA1	-1.21	2.99E-11	1.84E-10	3386.03	not significant
1624	ARF1	-1.21	1.15E-16	1.14E-15	12748.21	not significant
1625	LOC100862671	-1.21	4.22E-03	8.98E-03	230.08	not significant
1626	MFNG	-1.21	1.20E-10	7.03E-10	2063.09	not significant
1627	ITIH4	-1.21	1.23E-02	2.36E-02	207.52	not significant
1628	DNAJA3	-1.21	2.47E-16	2.37E-15	3778.50	not significant
1629	MIPEP	-1.21	3.32E-04	8.70E-04	428.82	not significant
1630	GADD45GIP1	-1.21	1.41E-08	6.61E-08	1786.13	not significant
1631	ZFYVE9	-1.21	2.14E-02	3.89E-02	124.03	not significant
1632	ELAC2	-1.21	3.58E-14	2.88E-13	3947.57	not significant
1633	C6orf89	-1.21	2.73E-19	3.34E-18	5419.95	not significant
1634	C8orf37	-1.21	5.32E-03	1.11E-02	239.06	not significant
1635	UBE2MP1	-1.21	5.65E-02	9.24E-02	43.53	not significant
1636	PCED1B-AS1	-1.21	6.25E-04	1.55E-03	378.43	not significant
1637	SRM	-1.21	4.63E-17	4.75E-16	4211.71	not significant
1638	PPP2R5D	-1.21	2.26E-17	2.38E-16	4518.17	not significant
1639	TSTA3	-1.21	4.74E-07	1.87E-06	1401.97	not significant
1640	ROMO1	-1.21	5.71E-06	1.96E-05	965.67	not significant
1641	MMACHC	-1.21	2.37E-04	6.38E-04	482.29	not significant
1642	PPP4R2	-1.21	3.26E-09	1.64E-08	2028.98	not significant
1643	SNRNP70	-1.21	1.16E-17	1.25E-16	8458.80	not significant
1644	CHKA	-1.21	9.92E-06	3.29E-05	880.98	not significant
1645	AMIGO2	-1.21	2.50E-03	5.55E-03	276.15	not significant
1646	RAB8A	-1.21	3.29E-14	2.65E-13	5000.15	not significant
1647	LACTB	-1.21	9.58E-03	1.89E-02	180.52	not significant
1648	C4orf33	-1.21	9.34E-05	2.70E-04	592.44	not significant
1649	HLA-C	-1.21	3.47E-18	3.92E-17	7653.29	not significant
1650	ZC3H15	-1.21	9.88E-15	8.36E-14	3364.61	not significant
1651	CACUL1	-1.21	1.78E-09	9.18E-09	1532.54	not significant
1652	GNG4	-1.21	1.91E-05	6.12E-05	761.87	not significant
1653	IFITM2	-1.21	5.29E-02	8.73E-02	19.69	not significant
1654	CARD16	-1.21	5.83E-03	1.20E-02	253.70	not significant
1655	TUBA1B	-1.21	3.96E-19	4.76E-18	69042.21	not significant
1656	C2orf27A	-1.21	3.61E-02	6.21E-02	83.59	not significant
1657	LY6E	-1.21	9.67E-09	4.65E-08	1584.70	not significant
1658	CCNC	-1.21	5.47E-14	4.32E-13	3575.06	not significant
1659	ORC5	-1.21	8.03E-07	3.07E-06	1063.84	not significant
1660	MKI67	-1.21	1.53E-03	3.54E-03	29381.06	not significant

1661	CLTC	-1.21	9.89E-11	5.81E-10	14161.06	not significant
1662	ACOT7	-1.21	3.11E-15	2.74E-14	5971.84	not significant
1663	CDK2AP1	-1.21	1.98E-12	1.36E-11	4098.09	not significant
1664	NDUFV2	-1.21	6.56E-13	4.70E-12	2860.46	not significant
1665	RREB1	-1.21	1.22E-07	5.15E-07	1244.30	not significant
1666	NDUFS5	-1.21	6.13E-10	3.32E-09	2512.01	not significant
1667	DIAPH3	-1.21	1.27E-10	7.42E-10	2247.81	not significant
1668	C10orf12	-1.21	2.14E-04	5.80E-04	526.64	not significant
1669	AKAP1	-1.21	1.45E-14	1.21E-13	3797.90	not significant
1670	MXRA7	-1.21	1.45E-04	4.05E-04	524.46	not significant
1671	GBE1	-1.21	4.83E-07	1.90E-06	1369.20	not significant
1672	OTUD6B	-1.21	1.74E-09	8.97E-09	1707.16	not significant
1673	CD248	-1.21	3.13E-04	8.23E-04	433.10	not significant
1674	CHST2	-1.21	1.25E-12	8.77E-12	3896.85	not significant
1675	NUDCD1	-1.21	4.94E-12	3.29E-11	2856.63	not significant
1676	XPNPEP3	-1.21	5.31E-04	1.34E-03	415.42	not significant
1677	CAPZA1	-1.21	3.85E-23	6.04E-22	11609.19	not significant
1678	ARCN1	-1.21	4.04E-08	1.81E-07	1367.07	not significant
1679	TNFRSF10A	-1.21	1.41E-02	2.68E-02	6.64	not significant
1680	VPS33A	-1.21	3.96E-09	1.98E-08	2009.43	not significant
1681	ACSL1	-1.21	4.24E-04	1.09E-03	463.53	not significant
1682	PYGM	-1.21	4.78E-02	7.99E-02	66.10	not significant
1683	TSNAX	-1.21	5.30E-09	2.61E-08	1540.72	not significant
1684	STAG1	-1.21	1.19E-12	8.38E-12	3245.76	not significant
1685	LINC00999	-1.21	3.30E-02	5.76E-02	101.04	not significant
1686	ASCC3	-1.21	1.69E-16	1.64E-15	5235.98	not significant
1687	NDUFA4	-1.21	6.28E-12	4.14E-11	4536.40	not significant
1688	FAM120A	-1.21	9.96E-19	1.17E-17	7970.64	not significant
1689	LCT	-1.21	1.36E-03	3.17E-03	356.62	not significant
1690	ANAPC7	-1.21	6.26E-14	4.92E-13	4027.53	not significant
1691	PSMB2	-1.21	1.29E-16	1.28E-15	9135.17	not significant
1692	ZCCHC17	-1.21	1.09E-07	4.63E-07	1377.70	not significant
1693	TCEB3	-1.21	8.91E-10	4.72E-09	2149.54	not significant
1694	HEBP2	-1.21	2.00E-03	4.51E-03	338.94	not significant
1695	MYBL2	-1.21	7.05E-18	7.72E-17	14119.97	not significant
1696	POLE3	-1.21	6.06E-18	6.68E-17	6829.98	not significant
1697	STK40	-1.21	4.22E-12	2.82E-11	2706.96	not significant
1698	MTERF3	-1.21	6.36E-08	2.78E-07	1208.68	not significant
1699	APBB1IP	-1.21	1.98E-11	1.24E-10	2443.33	not significant
1700	LNP1	-1.21	2.33E-02	4.22E-02	130.21	not significant
1701	DTYMK	-1.21	1.50E-12	1.04E-11	2875.20	not significant
1702	EEF1E1	-1.21	8.89E-04	2.15E-03	432.53	not significant
1703	ALKBH8	-1.21	4.12E-05	1.26E-04	657.70	not significant
1704	TXNL4A	-1.21	4.04E-12	2.70E-11	3584.68	not significant
1705	CWC27	-1.21	1.98E-09	1.02E-08	2217.58	not significant
1706	HIST1H2AM	-1.21	6.39E-02	1.03E-01	35.85	not significant
1707	DNAJC17	-1.21	2.36E-03	5.27E-03	326.56	not significant
1708	HMGN3	-1.21	3.30E-12	2.22E-11	3903.85	not significant
1709	GEMIN2	-1.21	1.89E-04	5.18E-04	522.04	not significant
1710	ZHX3	-1.21	2.37E-08	1.09E-07	1360.76	not significant
1711	FARSA	-1.21	8.97E-16	8.23E-15	5037.71	not significant
1712	RPS19BP1	-1.21	6.29E-08	2.75E-07	2735.64	not significant
1713	EPHB1	-1.21	7.54E-03	1.52E-02	205.62	not significant
1714	PA2G4	-1.21	4.15E-19	4.98E-18	18758.86	not significant
1715	FASTKD1	-1.21	1.67E-09	8.64E-09	1656.35	not significant
1716	TSFM	-1.21	5.65E-08	2.49E-07	1351.47	not significant
1717	RHOQ	-1.21	1.30E-03	3.04E-03	336.98	not significant
1718	EMC8	-1.21	1.09E-09	5.76E-09	1681.88	not significant
1719	MON1A	-1.21	1.35E-04	3.78E-04	552.64	not significant
1720	PRDX5	-1.20	6.24E-11	3.73E-10	4725.16	not significant
1721	FTH1P3	-1.20	6.42E-02	1.03E-01	35.07	not significant
1722	SMIM24	-1.20	2.52E-10	1.43E-09	2042.45	not significant
1723	FAM63B	-1.20	2.40E-03	5.34E-03	320.38	not significant
1724	SMIM15	-1.20	6.12E-03	1.26E-02	256.67	not significant
1725	PDZD11	-1.20	2.30E-07	9.42E-07	1143.42	not significant
1726	SNRPB	-1.20	1.30E-13	9.91E-13	12741.77	not significant
1727	DDX28	-1.20	8.77E-06	2.94E-05	841.38	not significant
1728	FGD6	-1.20	1.22E-03	2.88E-03	384.37	not significant
1729	PLEKHB1	-1.20	3.27E-03	7.11E-03	275.54	not significant
1730	LARS2	-1.20	3.69E-11	2.26E-10	2506.95	not significant
1731	MOSPD1	-1.20	1.28E-04	3.60E-04	565.22	not significant
1732	PRDX4	-1.20	5.57E-07	2.17E-06	1329.08	not significant
1733	USP24	-1.20	1.96E-15	1.75E-14	5972.36	not significant
1734	CCT2	-1.20	2.62E-17	2.73E-16	14780.04	not significant
1735	RSC1A1	-1.20	2.79E-03	6.14E-03	291.07	not significant
1736	ACTR1A	-1.20	5.40E-17	5.52E-16	5130.19	not significant
1737	GSTP1	-1.20	2.82E-16	2.70E-15	9485.45	not significant
1738	MEA1	-1.20	1.51E-11	9.59E-11	3407.62	not significant
1739	FOXN2	-1.20	8.41E-12	5.47E-11	2487.32	not significant
1740	IARS2	-1.20	2.38E-14	1.94E-13	4746.83	not significant
1741	RAD54B	-1.20	2.46E-08	1.13E-07	1470.69	not significant
1742	CCDC137	-1.20	8.01E-10	4.27E-09	1892.09	not significant
1743	C2orf47	-1.20	4.50E-04	1.15E-03	505.59	not significant
1744	SCFD1	-1.20	4.06E-07	1.61E-06	1274.57	not significant
1745	PSMC3	-1.20	1.44E-16	1.42E-15	6222.67	not significant
1746	NQO1	-1.20	2.10E-02	3.83E-02	139.03	not significant
1747	GTF3C2	-1.20	5.21E-13	3.76E-12	3344.03	not significant
1748	GP5	-1.20	4.05E-02	6.88E-02	13.54	not significant

1749	SMG7	-1.20	5.28E-18	5.84E-17	6622.62	not significant
1750	SPOP	-1.20	6.02E-10	3.27E-09	2042.22	not significant
1751	IMMT	-1.20	6.24E-18	6.87E-17	5777.39	not significant
1752	OXSM	-1.20	4.45E-03	9.45E-03	265.09	not significant
1753	COX18	-1.20	1.08E-04	3.06E-04	592.43	not significant
1754	DHX34	-1.20	4.44E-07	1.76E-06	1151.93	not significant
1755	SEC61B	-1.20	4.97E-03	1.04E-02	2034.49	not significant
1756	LUZP1	-1.20	8.22E-12	5.36E-11	2851.40	not significant
1757	SF3B6	-1.20	1.67E-09	8.64E-09	2874.50	not significant
1758	PSMD11	-1.20	9.97E-15	8.43E-14	3814.66	not significant
1759	GRPEL1	-1.20	1.06E-06	4.02E-06	1392.53	not significant
1760	PEPD	-1.20	2.69E-07	1.10E-06	1261.42	not significant
1761	DLAT	-1.20	7.36E-07	2.82E-06	1050.01	not significant
1762	C19orf53	-1.20	1.67E-11	1.05E-10	2655.66	not significant
1763	NOMO1	-1.20	4.16E-05	1.27E-04	730.26	not significant
1764	F2RL2	-1.20	1.71E-02	3.19E-02	154.87	not significant
1765	PFKM	-1.20	7.85E-10	4.19E-09	1998.43	not significant
1766	EPT1	-1.20	4.61E-16	4.33E-15	4121.44	not significant
1767	FKBP4	-1.20	1.77E-18	2.04E-17	8237.49	not significant
1768	ARHGAP5	-1.20	1.92E-10	1.10E-09	2663.16	not significant
1769	APOBEC3G	-1.20	3.60E-06	1.27E-05	1096.74	not significant
1770	INSIG1	-1.20	2.99E-19	3.64E-18	20943.62	not significant
1771	EMG1	-1.20	5.35E-04	1.35E-03	439.99	not significant
1772	MAP3K7CL	-1.20	6.83E-03	1.39E-02	261.18	not significant
1773	POLE2	-1.20	6.11E-06	2.09E-05	1055.01	not significant
1774	MRPS18C	-1.20	4.65E-05	1.41E-04	739.77	not significant
1775	SWAP70	-1.20	3.12E-10	1.75E-09	2815.49	not significant
1776	HINT2	-1.20	1.23E-05	4.05E-05	815.18	not significant
1777	USPL1	-1.20	7.40E-09	3.60E-08	2022.28	not significant
1778	ATP6V1E1	-1.20	1.73E-12	1.19E-11	3252.43	not significant
1779	ISOC1	-1.20	2.92E-08	1.33E-07	1565.40	not significant
1780	CHUK	-1.20	1.29E-11	8.26E-11	2477.35	not significant
1781	RNF219	-1.20	2.43E-08	1.12E-07	1890.99	not significant
1782	WBP5	-1.20	8.90E-03	1.76E-02	216.92	not significant
1783	SERBP1	-1.20	1.18E-16	1.17E-15	17146.80	not significant
1784	PUS1	-1.20	1.12E-08	5.32E-08	1941.05	not significant
1785	SGK223	-1.20	6.69E-02	1.07E-01	32.95	not significant
1786	PDCD10	-1.20	1.53E-09	7.94E-09	2099.83	not significant
1787	CYC1	-1.20	6.26E-14	4.92E-13	4866.71	not significant
1788	ASNSD1	-1.20	2.46E-10	1.39E-09	2173.87	not significant
1789	MOSPD3	-1.20	1.44E-03	3.36E-03	459.90	not significant
1790	PRKDC	-1.20	2.75E-02	4.88E-02	27958.39	not significant
1791	AURKB	-1.20	3.34E-12	2.24E-11	4588.59	not significant
1792	NOL11	-1.20	1.03E-14	8.66E-14	5342.59	not significant
1793	POLR3K	-1.20	4.77E-06	1.65E-05	1015.74	not significant
1794	PPP2R4	-1.20	1.07E-09	5.66E-09	3771.79	not significant
1795	MKX	-1.20	6.86E-02	1.10E-01	33.50	not significant
1796	ABCF2	-1.20	4.48E-15	3.90E-14	4571.56	not significant
1797	SURF6	-1.20	1.50E-02	2.82E-02	172.69	not significant
1798	APOA1BP	-1.20	5.60E-09	2.75E-08	2083.18	not significant
1799	SLC25A46	-1.20	7.36E-13	5.25E-12	2914.28	not significant
1800	DDX24	-1.20	6.84E-15	5.88E-14	5786.16	not significant
1801	HNRNPU	-1.20	1.84E-21	2.58E-20	40631.85	not significant
1802	LARS	-1.20	1.69E-17	1.80E-16	7147.49	not significant
1803	SLC27A4	-1.20	1.36E-05	4.44E-05	874.17	not significant
1804	NCOA5	-1.20	3.18E-13	2.34E-12	3969.75	not significant
1805	CISD1	-1.20	2.80E-06	1.00E-05	955.36	not significant
1806	RPUSD3	-1.20	1.80E-05	5.76E-05	855.19	not significant
1807	CHMP2B	-1.20	1.73E-08	8.07E-08	1664.95	not significant
1808	HK2	-1.20	2.16E-08	9.99E-08	1578.98	not significant
1809	PIK3C2B	-1.20	7.00E-08	3.04E-07	1780.47	not significant
1810	SSNA1	-1.20	2.96E-07	1.20E-06	1996.49	not significant
1811	LPCAT2	-1.20	7.04E-02	1.12E-01	35.35	not significant
1812	MAP2K3	-1.20	2.03E-07	8.33E-07	1364.12	not significant
1813	TWISTNB	-1.20	8.03E-10	4.28E-09	2177.56	not significant
1814	YWHAG	-1.20	1.90E-19	2.35E-18	19546.74	not significant
1815	GRHL1	-1.20	6.74E-02	1.08E-01	24.75	not significant
1816	FAM65A	-1.20	5.23E-06	1.80E-05	911.30	not significant
1817	KRAS	-1.20	1.34E-10	7.78E-10	3825.66	not significant
1818	RPAP3	-1.20	3.33E-12	2.24E-11	2993.70	not significant
1819	LONP2	-1.20	1.64E-10	9.42E-10	2877.36	not significant
1820	PIH1D1	-1.20	6.39E-09	3.12E-08	1764.71	not significant
1821	TBCCD1	-1.20	4.69E-05	1.42E-04	693.13	not significant
1822	WDR25	-1.19	3.31E-02	5.76E-02	115.29	not significant
1823	SUCLG2	-1.19	1.27E-06	4.76E-06	1475.29	not significant
1824	MRPL21	-1.19	1.71E-05	5.49E-05	946.30	not significant
1825	TCEB1	-1.19	1.72E-10	9.91E-10	3078.51	not significant
1826	TDP2	-1.19	1.19E-07	5.05E-07	1971.24	not significant
1827	ZNF468	-1.19	4.50E-06	1.57E-05	971.69	not significant
1828	KIAA0754	-1.19	4.40E-09	2.18E-08	1832.17	not significant
1829	AGK	-1.19	3.17E-06	1.13E-05	944.76	not significant
1830	LTB4R	-1.19	4.82E-03	1.01E-02	423.89	not significant
1831	DHCR7	-1.19	3.31E-09	1.66E-08	2101.55	not significant
1832	CUL2	-1.19	5.88E-11	3.53E-10	2450.31	not significant
1833	INCENP	-1.19	7.32E-17	7.37E-16	6251.19	not significant
1834	SLAIN2	-1.19	2.68E-10	1.51E-09	2452.36	not significant
1835	PHLDA3	-1.19	5.35E-03	1.11E-02	277.36	not significant
1836	GPR65	-1.19	3.20E-03	6.97E-03	326.76	not significant

1837	PRAME	-1.19	6.96E-02	1.11E-01	27.21	not significant
1838	MTM1	-1.19	8.54E-03	1.70E-02	239.10	not significant
1839	FOS	-1.19	6.16E-02	9.98E-02	59.59	not significant
1840	EIF4E2	-1.19	2.18E-08	1.01E-07	2328.20	not significant
1841	UBE2E1	-1.19	1.34E-12	9.37E-12	3886.01	not significant
1842	DPH3	-1.19	1.04E-07	4.43E-07	1482.49	not significant
1843	S100A4	-1.19	6.67E-02	1.07E-01	23.54	not significant
1844	PBK	-1.19	1.76E-11	1.11E-10	2799.76	not significant
1845	SAP130	-1.19	4.37E-08	1.95E-07	1940.25	not significant
1846	UNC119	-1.19	1.26E-04	3.55E-04	670.94	not significant
1847	MRPS7	-1.19	5.70E-10	3.11E-09	2886.14	not significant
1848	RAB3D	-1.19	2.96E-02	5.22E-02	128.41	not significant
1849	GAA	-1.19	1.41E-05	4.60E-05	1396.78	not significant
1850	PCYT1A	-1.19	2.88E-04	7.62E-04	553.94	not significant
1851	SMIM3	-1.19	5.49E-04	1.38E-03	473.71	not significant
1852	SEC23A	-1.19	9.14E-09	4.42E-08	1802.50	not significant
1853	SDCBP2-AS1	-1.19	4.58E-02	7.68E-02	92.94	not significant
1854	BAG2	-1.19	2.79E-04	7.39E-04	569.78	not significant
1855	ABCF1	-1.19	2.20E-11	1.37E-10	2553.10	not significant
1856	TNPO1	-1.19	3.83E-15	3.36E-14	10306.31	not significant
1857	MRPL14	-1.19	1.36E-06	5.08E-06	1210.73	not significant
1858	TREML1	-1.19	6.05E-02	9.82E-02	18.69	not significant
1859	COPS4	-1.19	4.11E-08	1.84E-07	1899.42	not significant
1860	PPP1R35	-1.19	1.95E-07	8.05E-07	1528.54	not significant
1861	CCDC84	-1.19	8.55E-03	1.70E-02	242.58	not significant
1862	PXN-AS1	-1.19	1.22E-02	2.36E-02	224.79	not significant
1863	AAAS	-1.19	2.13E-12	1.46E-11	3179.18	not significant
1864	MBTPS2	-1.19	3.11E-04	8.19E-04	591.13	not significant
1865	DPY30	-1.19	3.58E-06	1.26E-05	1159.71	not significant
1866	UTP6	-1.19	2.21E-06	8.00E-06	1566.11	not significant
1867	CEBPZ	-1.19	2.33E-10	1.33E-09	2902.58	not significant
1868	ZNF778	-1.19	1.54E-02	2.90E-02	198.11	not significant
1869	PSMB9	-1.19	7.93E-05	2.31E-04	996.97	not significant
1870	JTB	-1.19	3.48E-12	2.34E-11	4045.75	not significant
1871	NAP1L5	-1.19	1.98E-03	4.47E-03	382.63	not significant
1872	GET4	-1.19	7.19E-10	3.86E-09	2288.94	not significant
1873	PPIE	-1.19	7.06E-08	3.07E-07	1499.32	not significant
1874	EXOSC3	-1.19	9.55E-08	4.09E-07	1567.11	not significant
1875	WWOX	-1.19	2.09E-04	5.68E-04	577.84	not significant
1876	COX11	-1.19	1.75E-09	9.06E-09	2136.77	not significant
1877	FAM129B	-1.19	1.38E-04	3.87E-04	711.83	not significant
1878	MED6	-1.19	1.69E-06	6.23E-06	1291.68	not significant
1879	THAP1	-1.19	2.55E-05	8.00E-05	803.20	not significant
1880	C12orf43	-1.19	1.08E-06	4.06E-06	1186.19	not significant
1881	PTBP1	-1.19	6.71E-19	7.91E-18	24443.61	not significant
1882	AAGAB	-1.19	2.72E-09	1.38E-08	2415.73	not significant
1883	HIST1H4L	-1.19	4.69E-02	7.85E-02	13.36	not significant
1884	PWP2	-1.19	4.69E-07	1.85E-06	1222.95	not significant
1885	PPIA	-1.19	8.61E-12	5.60E-11	33642.47	not significant
1886	YKT6	-1.19	4.58E-12	3.05E-11	4969.46	not significant
1887	B2M	-1.19	1.89E-12	1.30E-11	37012.77	not significant
1888	ECHS1	-1.19	2.96E-08	1.35E-07	1954.63	not significant
1889	SRFBP1	-1.19	1.26E-04	3.55E-04	675.58	not significant
1890	ITGB1BP2	-1.19	6.58E-02	1.06E-01	66.37	not significant
1891	TDRD7	-1.19	4.61E-03	9.74E-03	295.99	not significant
1892	COX8A	-1.19	2.14E-10	1.22E-09	5498.16	not significant
1893	ZCCHC5	-1.19	5.88E-02	9.57E-02	16.88	not significant
1894	RAD23B	-1.19	2.17E-15	1.93E-14	5857.88	not significant
1895	LIMD1-AS1	-1.19	7.53E-02	1.19E-01	39.45	not significant
1896	MROH8	-1.19	5.14E-02	8.52E-02	89.96	not significant
1897	HCAR1	-1.19	2.31E-02	4.17E-02	156.70	not significant
1898	DHX9	-1.19	3.93E-15	3.44E-14	17809.03	not significant
1899	C15orf39	-1.19	5.50E-08	2.43E-07	1694.33	not significant
1900	CLINT1	-1.19	1.57E-16	1.54E-15	8470.61	not significant
1901	DIABLO	-1.19	3.45E-08	1.56E-07	2514.76	not significant
1902	TYW3	-1.19	1.44E-07	6.05E-07	1959.98	not significant
1903	CAAP1	-1.19	2.85E-07	1.15E-06	1530.63	not significant
1904	ARPC5	-1.19	7.09E-13	5.07E-12	7855.06	not significant
1905	MIR210HG	-1.19	3.24E-02	5.66E-02	125.69	not significant
1906	AIDA	-1.19	1.75E-04	4.82E-04	673.60	not significant
1907	PRR22	-1.19	5.77E-02	9.42E-02	81.38	not significant
1908	GLIPR1	-1.19	2.76E-04	7.31E-04	568.19	not significant
1909	TP53I11	-1.19	1.52E-08	7.09E-08	1818.58	not significant
1910	MCM6	-1.19	4.41E-13	3.21E-12	16431.03	not significant
1911	COPS7A	-1.19	5.21E-06	1.79E-05	1164.15	not significant
1912	CFDP1	-1.19	5.14E-09	2.54E-08	3405.46	not significant
1913	RAC2	-1.19	2.72E-14	2.21E-13	13375.59	not significant
1914	SBDSP1	-1.19	6.56E-03	1.34E-02	289.85	not significant
1915	FAM149B1	-1.19	2.07E-04	5.62E-04	603.54	not significant
1916	EOMES	-1.19	6.84E-03	1.39E-02	280.54	not significant
1917	ASCC2	-1.19	5.57E-11	3.35E-10	3144.62	not significant
1918	FAM104B	-1.19	1.79E-03	4.07E-03	409.71	not significant
1919	ADPRHL2	-1.19	1.70E-05	5.47E-05	1032.76	not significant
1920	POLR1A	-1.19	1.11E-08	5.30E-08	3138.89	not significant
1921	VTI1B	-1.19	3.76E-09	1.88E-08	2027.70	not significant
1922	EBP	-1.19	5.91E-04	1.47E-03	532.98	not significant
1923	LACE1	-1.19	5.62E-02	9.21E-02	88.40	not significant
1924	TMEM63A	-1.19	1.95E-04	5.33E-04	715.06	not significant

1925	STXBP5	-1.19	1.57E-03	3.62E-03	475.54	not significant
1926	DNAJC8	-1.19	4.03E-14	3.21E-13	5936.17	not significant
1927	OAZ2	-1.19	7.62E-07	2.92E-06	1404.86	not significant
1928	SLC38A5	-1.19	1.76E-04	4.86E-04	683.00	not significant
1929	TMEM11	-1.18	4.42E-04	1.13E-03	586.81	not significant
1930	ARL4D	-1.18	4.85E-02	8.09E-02	99.43	not significant
1931	KCTD9	-1.18	4.97E-11	3.01E-10	2884.93	not significant
1932	FRMD6	-1.18	7.80E-02	1.23E-01	42.61	not significant
1933	BCAS2	-1.18	5.39E-07	2.10E-06	1499.71	not significant
1934	SMYD5	-1.18	5.50E-07	2.15E-06	1480.30	not significant
1935	DERA	-1.18	1.02E-05	3.39E-05	985.98	not significant
1936	C6orf223	-1.18	2.07E-06	7.52E-06	1219.47	not significant
1937	NDUFS1	-1.18	4.69E-11	2.85E-10	3123.30	not significant
1938	RNPEP	-1.18	7.25E-04	1.78E-03	499.98	not significant
1939	ZNF23	-1.18	7.77E-03	1.56E-02	280.14	not significant
1940	EIF2B2	-1.18	2.69E-07	1.09E-06	1618.77	not significant
1941	INTS2	-1.18	7.80E-10	4.17E-09	3785.65	not significant
1942	ASIC1	-1.18	4.69E-06	1.63E-05	1405.69	not significant
1943	TTC27	-1.18	1.53E-06	5.69E-06	1258.15	not significant
1944	PSMA5	-1.18	6.22E-13	4.47E-12	5570.93	not significant
1945	TOMM34	-1.18	1.56E-07	6.51E-07	1683.40	not significant
1946	BRMS1L	-1.18	4.48E-03	9.50E-03	325.17	not significant
1947	AP2M1	-1.18	6.54E-13	4.70E-12	8008.82	not significant
1948	DOCK2	-1.18	1.52E-13	1.16E-12	13040.05	not significant
1949	RBM42	-1.18	6.29E-08	2.75E-07	2415.92	not significant
1950	SLCO4A1	-1.18	1.54E-07	6.44E-07	1587.72	not significant
1951	UPRT	-1.18	1.48E-05	4.80E-05	984.78	not significant
1952	LIMK1	-1.18	4.94E-03	1.04E-02	324.09	not significant
1953	GTF2H3	-1.18	1.27E-07	5.35E-07	2569.23	not significant
1954	SIDT1	-1.18	5.45E-05	1.63E-04	823.58	not significant
1955	E2F4	-1.18	2.88E-13	2.13E-12	5243.22	not significant
1956	ACADVL	-1.18	1.25E-11	7.97E-11	4276.62	not significant
1957	HAUS7	-1.18	8.03E-03	1.61E-02	278.39	not significant
1958	HDAC9	-1.18	1.25E-03	2.93E-03	445.08	not significant
1959	EEFSEC	-1.18	4.22E-06	1.47E-05	1108.50	not significant
1960	CPSF6	-1.18	4.67E-09	2.31E-08	8115.09	not significant
1961	SEC24A	-1.18	3.05E-08	1.39E-07	1891.32	not significant
1962	DDX39A	-1.18	7.22E-16	6.70E-15	8555.52	not significant
1963	CCDC167	-1.18	1.46E-07	6.11E-07	1900.90	not significant
1964	CKAP5	-1.18	7.42E-10	3.98E-09	12985.50	not significant
1965	AP1G1	-1.18	6.37E-11	3.81E-10	3723.74	not significant
1966	SPRED2	-1.18	6.77E-07	2.61E-06	1329.30	not significant
1967	PIK3R6	-1.18	6.17E-04	1.53E-03	560.39	not significant
1968	ARF4	-1.18	5.59E-10	3.05E-09	2577.30	not significant
1969	TRA2A	-1.18	3.48E-10	1.94E-09	3475.78	not significant
1970	STRA13	-1.18	2.85E-10	1.61E-09	2974.90	not significant
1971	IPO13	-1.18	1.88E-06	6.87E-06	1377.64	not significant
1972	UBE2K	-1.18	1.63E-12	1.13E-11	4965.10	not significant
1973	NRN1	-1.18	1.06E-13	8.17E-13	4711.62	not significant
1974	PDIA6	-1.18	9.85E-11	5.79E-10	10884.88	not significant
1975	MRPL55	-1.18	3.08E-04	8.10E-04	684.23	not significant
1976	POLR3H	-1.18	2.03E-07	8.33E-07	2229.38	not significant
1977	ARHGAP30	-1.18	1.42E-12	9.89E-12	9061.96	not significant
1978	VRK2	-1.18	6.43E-04	1.59E-03	520.84	not significant
1979	PLEKHH2	-1.18	8.29E-02	1.30E-01	44.18	not significant
1980	UQCC1	-1.18	1.29E-08	6.10E-08	2140.76	not significant
1981	KIAA1524	-1.18	5.77E-10	3.14E-09	2964.15	not significant
1982	SOD2	-1.18	9.24E-08	3.96E-07	1843.62	not significant
1983	ICE2	-1.18	1.05E-11	6.81E-11	3502.51	not significant
1984	GORASP2	-1.18	5.58E-13	4.02E-12	4380.83	not significant
1985	CLCN2	-1.18	2.88E-02	5.09E-02	172.61	not significant
1986	THOC7	-1.18	6.51E-10	3.52E-09	2884.81	not significant
1987	RNASEH1	-1.18	5.54E-07	2.16E-06	1541.81	not significant
1988	KTN1	-1.18	7.53E-11	4.47E-10	9378.49	not significant
1989	LINC01481	-1.18	3.77E-02	6.46E-02	128.12	not significant
1990	METTL2A	-1.18	2.53E-05	7.95E-05	919.94	not significant
1991	LRP6	-1.18	1.01E-06	3.81E-06	1473.61	not significant
1992	CLP1	-1.18	1.48E-03	3.43E-03	475.78	not significant
1993	PRPF31	-1.18	2.46E-05	7.72E-05	1224.50	not significant
1994	ATXN1	-1.18	1.26E-02	2.43E-02	287.12	not significant
1995	CAPN1	-1.18	9.42E-12	6.11E-11	4229.35	not significant
1996	XPO1	-1.18	5.97E-17	6.09E-16	19566.39	not significant
1997	C5	-1.18	3.56E-02	6.13E-02	142.02	not significant
1998	LINC00892	-1.18	8.24E-02	1.29E-01	28.07	not significant
1999	RAC1	-1.18	1.09E-13	8.36E-13	5582.69	not significant
2000	POLK	-1.18	1.66E-06	6.13E-06	1393.85	not significant
2001	IMP3	-1.18	5.96E-08	2.62E-07	1881.82	not significant
2002	CCDC47	-1.18	3.24E-11	1.99E-10	5180.73	not significant
2003	NRBP1	-1.18	2.76E-09	1.40E-08	2270.21	not significant
2004	NFKBIB	-1.18	7.89E-06	2.66E-05	1048.63	not significant
2005	PARN	-1.18	2.98E-10	1.68E-09	2597.21	not significant
2006	AHCTF1P1	-1.18	8.52E-02	1.33E-01	39.47	not significant
2007	ISCA2	-1.18	1.04E-04	2.98E-04	814.56	not significant
2008	INTS5	-1.18	2.67E-05	8.36E-05	920.64	not significant
2009	DESI1	-1.18	3.71E-09	1.86E-08	2196.64	not significant
2010	TXN	-1.18	1.18E-08	5.60E-08	3945.33	not significant
2011	LOC100130744	-1.18	3.32E-02	5.78E-02	165.88	not significant
2012	U2AF2	-1.18	1.45E-13	1.10E-12	17756.15	not significant

2013	NUFIP1	-1.18	1.63E-04	4.52E-04	704.71	not significant
2014	FKBP8	-1.18	4.42E-13	3.22E-12	7066.16	not significant
2015	KDELR2	-1.18	1.07E-10	6.28E-10	2881.80	not significant
2016	OCIAD2	-1.18	1.08E-06	4.08E-06	1961.67	not significant
2017	NECAP2	-1.18	6.06E-08	2.66E-07	2346.73	not significant
2018	ERP27	-1.18	4.70E-02	7.86E-02	111.03	not significant
2019	SUB1	-1.18	2.69E-13	2.00E-12	9191.28	not significant
2020	ACO2	-1.18	8.16E-14	6.33E-13	5503.97	not significant
2021	WFIKKN1	-1.18	8.81E-02	1.37E-01	31.27	not significant
2022	GLI1	-1.18	7.93E-02	1.25E-01	56.63	not significant
2023	METTL15	-1.18	4.67E-03	9.86E-03	382.78	not significant
2024	LOC100379224	-1.18	8.31E-02	1.30E-01	50.17	not significant
2025	NARS	-1.18	5.00E-14	3.96E-13	6865.52	not significant
2026	NDUFA9	-1.18	4.91E-09	2.43E-08	2869.97	not significant
2027	DSE	-1.18	4.04E-02	6.86E-02	130.14	not significant
2028	CD79A	-1.18	9.95E-03	1.95E-02	278.27	not significant
2029	AMPD2	-1.18	2.01E-08	9.31E-08	2293.11	not significant
2030	SETBP1	-1.18	5.97E-02	9.70E-02	92.98	not significant
2031	MPZL3	-1.18	4.06E-02	6.89E-02	133.87	not significant
2032	ADIPOR2	-1.18	1.22E-14	1.02E-13	6602.83	not significant
2033	INTS10	-1.18	2.64E-10	1.49E-09	2712.67	not significant
2034	LONP1	-1.18	1.32E-11	8.43E-11	4189.58	not significant
2035	TRMT6	-1.18	1.14E-07	4.82E-07	1775.33	not significant
2036	RABL3	-1.18	2.11E-07	8.66E-07	1640.44	not significant
2037	RAB38	-1.18	8.86E-02	1.37E-01	38.92	not significant
2038	NPIPB3	-1.18	2.69E-02	4.78E-02	213.76	not significant
2039	TRIM16	-1.18	7.90E-03	1.59E-02	294.21	not significant
2040	KIF11	-1.18	4.78E-15	4.15E-14	11577.53	not significant
2041	XPO6	-1.18	9.04E-13	6.40E-12	6154.75	not significant
2042	IRF2BPL	-1.18	5.12E-07	2.00E-06	1711.77	not significant
2043	PPIF	-1.18	7.84E-13	5.58E-12	5335.17	not significant
2044	BRCA2	-1.18	2.66E-07	1.08E-06	2808.68	not significant
2045	SEC11C	-1.18	1.29E-05	4.23E-05	1144.78	not significant
2046	IMMP1L	-1.18	1.17E-03	2.76E-03	559.81	not significant
2047	BZW1	-1.18	8.46E-14	6.56E-13	8557.18	not significant
2048	CCDC7	-1.18	4.27E-02	7.22E-02	124.26	not significant
2049	AKT1S1	-1.18	1.86E-03	4.22E-03	475.88	not significant
2050	NOTCH3	-1.18	2.02E-05	6.43E-05	1266.30	not significant
2051	TMEM63B	-1.18	5.28E-03	1.10E-02	338.89	not significant
2052	RPA3	-1.18	1.55E-06	5.73E-06	1722.27	not significant
2053	IDI1	-1.18	7.56E-10	4.05E-09	4373.83	not significant
2054	UBE2T	-1.18	1.88E-09	9.69E-09	2530.35	not significant
2055	NDRG3	-1.18	5.04E-09	2.49E-08	2975.40	not significant
2056	LAS1L	-1.18	1.51E-08	7.07E-08	2287.19	not significant
2057	CEP83	-1.18	1.02E-05	3.37E-05	1065.72	not significant
2058	PHF23	-1.18	7.56E-06	2.55E-05	1099.14	not significant
2059	FAM98B	-1.18	1.83E-07	7.57E-07	2232.48	not significant
2060	CSNK2A1	-1.18	8.97E-14	6.92E-13	5525.37	not significant
2061	NPRL3	-1.18	4.66E-09	2.31E-08	2223.09	not significant
2062	RAB31	-1.18	8.76E-02	1.36E-01	43.49	not significant
2063	DNAJB11	-1.18	9.86E-07	3.74E-06	2420.14	not significant
2064	GRK5	-1.17	6.54E-08	2.85E-07	2329.67	not significant
2065	MYL6	-1.17	5.70E-14	4.49E-13	8760.68	not significant
2066	CHCHD4	-1.17	5.65E-05	1.69E-04	847.33	not significant
2067	STK3	-1.17	8.04E-06	2.71E-05	1210.26	not significant
2068	SUPV3L1	-1.17	9.53E-07	3.62E-06	1358.90	not significant
2069	NELFCD	-1.17	9.74E-10	5.15E-09	2964.66	not significant
2070	SAFB	-1.17	3.57E-13	2.61E-12	5887.16	not significant
2071	STOML2	-1.17	1.33E-08	6.28E-08	3662.66	not significant
2072	PARVG	-1.17	2.65E-10	1.50E-09	3183.62	not significant
2073	HAX1	-1.17	1.13E-09	5.92E-09	2769.55	not significant
2074	KHSRP	-1.17	1.00E-15	9.20E-15	16631.96	not significant
2075	DDX49	-1.17	3.11E-07	1.25E-06	1768.55	not significant
2076	TXNDC17	-1.17	1.88E-05	6.03E-05	1103.17	not significant
2077	C19orf24	-1.17	4.22E-04	1.08E-03	942.64	not significant
2078	LINC01431	-1.17	6.83E-02	1.09E-01	16.75	not significant
2079	SLC39A10	-1.17	6.35E-08	2.77E-07	2195.85	not significant
2080	SDAD1	-1.17	6.30E-10	3.41E-09	2907.28	not significant
2081	NHP2	-1.17	1.19E-09	6.25E-09	4017.97	not significant
2082	MRPS33	-1.17	1.36E-05	4.44E-05	1305.81	not significant
2083	BUD31	-1.17	9.47E-08	4.06E-07	2819.43	not significant
2084	ATXN7L1	-1.17	9.55E-04	2.29E-03	569.13	not significant
2085	TAF3	-1.17	1.99E-06	7.27E-06	1506.52	not significant
2086	MNAT1	-1.17	2.11E-04	5.72E-04	917.24	not significant
2087	SYNCRIP	-1.17	6.89E-15	5.92E-14	21807.82	not significant
2088	HDDC2	-1.17	6.23E-08	2.73E-07	1901.14	not significant
2089	ZNF831	-1.17	2.10E-02	3.83E-02	200.55	not significant
2090	FASN	-1.17	2.14E-02	3.89E-02	23856.48	not significant
2091	MTX1	-1.17	3.82E-03	8.21E-03	380.51	not significant
2092	DHCR24	-1.17	6.78E-11	4.05E-10	5448.94	not significant
2093	CCDC18	-1.17	4.40E-05	1.34E-04	982.83	not significant
2094	NSDHL	-1.17	1.41E-02	2.69E-02	252.80	not significant
2095	MIEF1	-1.17	4.25E-09	2.11E-08	3466.03	not significant
2096	PITPNA	-1.17	9.49E-11	5.59E-10	3539.40	not significant
2097	PSMD13	-1.17	2.85E-09	1.45E-08	4190.30	not significant
2098	IL17RA	-1.17	5.31E-09	2.62E-08	2286.75	not significant
2099	GPS1	-1.17	2.93E-12	1.98E-11	5078.46	not significant
2100	TMA7	-1.17	8.66E-03	1.72E-02	2557.33	not significant

2101	NKIRAS1	-1.17	6.55E-02	1.05E-01	94.05	not significant
2102	LOC100506603	-1.17	4.76E-02	7.96E-02	128.31	not significant
2103	DPH2	-1.17	4.99E-07	1.96E-06	1592.67	not significant
2104	IFIH1	-1.17	1.47E-03	3.42E-03	507.73	not significant
2105	CHST1	-1.17	8.51E-02	1.33E-01	63.04	not significant
2106	TIPRL	-1.17	2.62E-12	1.78E-11	4180.24	not significant
2107	MTRR	-1.17	8.58E-07	3.27E-06	1650.76	not significant
2108	MBOAT7	-1.17	3.66E-04	9.51E-04	673.73	not significant
2109	NAGA	-1.17	2.23E-04	6.04E-04	747.52	not significant
2110	ALYREF	-1.17	4.72E-11	2.87E-10	9653.73	not significant
2111	BNIP2	-1.17	1.54E-07	6.43E-07	2485.88	not significant
2112	ITSN1	-1.17	2.59E-04	6.93E-04	761.87	not significant
2113	TRNAU1AP	-1.17	1.07E-04	3.04E-04	834.09	not significant
2114	MTAP	-1.17	6.34E-10	3.43E-09	2897.94	not significant
2115	ATAD3A	-1.17	3.56E-06	1.26E-05	1980.86	not significant
2116	DYRK3	-1.17	9.41E-02	1.45E-01	37.95	not significant
2117	PICALM	-1.17	2.01E-11	1.26E-10	4211.15	not significant
2118	DEF8	-1.17	6.38E-02	1.03E-01	95.21	not significant
2119	BTBD10	-1.17	5.15E-05	1.54E-04	967.64	not significant
2120	CABIN1	-1.17	3.26E-08	1.48E-07	4169.55	not significant
2121	FGF11	-1.17	6.24E-02	1.01E-01	106.31	not significant
2122	CORO6	-1.17	6.74E-02	1.08E-01	100.40	not significant
2123	SNX11	-1.17	4.87E-04	1.24E-03	682.63	not significant
2124	RHOF	-1.17	2.58E-08	1.18E-07	2635.22	not significant
2125	CECR5	-1.17	2.82E-07	1.14E-06	2537.40	not significant
2126	POLA1	-1.17	4.90E-11	2.97E-10	4980.07	not significant
2127	GTF2E1	-1.17	6.27E-05	1.86E-04	897.26	not significant
2128	ALKBH3	-1.17	3.11E-05	9.64E-05	1084.14	not significant
2129	RNASEL	-1.17	4.74E-03	9.99E-03	371.51	not significant
2130	ZNHIT6	-1.17	1.16E-07	4.93E-07	2032.13	not significant
2131	SBF2	-1.17	1.74E-04	4.81E-04	798.93	not significant
2132	TMEM70	-1.17	5.20E-07	2.04E-06	1974.60	not significant
2133	VPS25	-1.17	1.55E-07	6.48E-07	1760.97	not significant
2134	TMEM104	-1.17	3.44E-06	1.22E-05	1312.93	not significant
2135	NRXN2	-1.17	1.31E-02	2.50E-02	260.33	not significant
2136	EFNA3	-1.17	7.54E-02	1.19E-01	77.31	not significant
2137	ELAVL1	-1.17	1.41E-12	9.87E-12	7496.43	not significant
2138	ATPAF2	-1.17	2.06E-03	4.64E-03	478.38	not significant
2139	TBXAS1	-1.17	8.82E-02	1.37E-01	62.46	not significant
2140	COX10	-1.17	2.10E-04	5.70E-04	759.90	not significant
2141	MRPS18B	-1.17	2.91E-04	7.69E-04	718.14	not significant
2142	SAE1	-1.17	1.79E-10	1.03E-09	10017.00	not significant
2143	UBE2D3	-1.17	2.70E-16	2.59E-15	13923.47	not significant
2144	TMED2	-1.17	3.74E-13	2.73E-12	10909.28	not significant
2145	ENOX1	-1.17	7.74E-02	1.22E-01	74.70	not significant
2146	ERCC6L	-1.17	5.03E-08	2.23E-07	2084.42	not significant
2147	IRF5	-1.17	9.17E-02	1.41E-01	26.72	not significant
2148	CHCHD1	-1.17	1.84E-04	5.04E-04	930.44	not significant
2149	ACOX3	-1.17	3.99E-03	8.54E-03	401.33	not significant
2150	IER2	-1.17	3.58E-08	1.62E-07	2601.97	not significant
2151	AP3B1	-1.17	2.25E-10	1.28E-09	3657.64	not significant
2152	CKAP2	-1.17	1.78E-11	1.12E-10	5533.06	not significant
2153	CD300A	-1.17	1.54E-06	5.69E-06	1558.53	not significant
2154	RND3	-1.17	1.44E-02	2.74E-02	267.49	not significant
2155	TACC1	-1.17	1.27E-11	8.13E-11	7980.43	not significant
2156	MRPS5	-1.17	5.40E-09	2.66E-08	2741.72	not significant
2157	LOC100506325	-1.17	9.15E-02	1.41E-01	27.86	not significant
2158	POFUT1	-1.17	7.04E-10	3.79E-09	3461.72	not significant
2159	JHDM1D-AS1	-1.17	5.09E-02	8.44E-02	136.21	not significant
2160	TBCB	-1.17	3.95E-07	1.57E-06	2488.33	not significant
2161	MARS2	-1.17	2.25E-05	7.10E-05	1163.02	not significant
2162	PIGP	-1.17	1.62E-03	3.72E-03	555.22	not significant
2163	SACM1L	-1.17	1.41E-11	9.00E-11	4408.27	not significant
2164	C1orf109	-1.17	1.65E-05	5.32E-05	1184.43	not significant
2165	ARHGAP11A	-1.17	5.34E-09	2.63E-08	4329.72	not significant
2166	ZNF185	-1.17	5.84E-02	9.52E-02	13.64	not significant
2167	RPAP2	-1.17	2.57E-04	6.88E-04	829.86	not significant
2168	ARHGAP10	-1.17	8.61E-03	1.71E-02	313.30	not significant
2169	TCP1	-1.17	1.10E-11	7.08E-11	16454.37	not significant
2170	ALKBH1	-1.17	1.25E-03	2.94E-03	550.10	not significant
2171	FAM103A1	-1.17	3.04E-03	6.64E-03	469.66	not significant
2172	SLC25A44	-1.17	4.22E-06	1.47E-05	1404.07	not significant
2173	TFEC	-1.17	1.43E-08	6.69E-08	6851.84	not significant
2174	CACNA1D	-1.17	9.86E-02	1.51E-01	34.39	not significant
2175	TMEM183A	-1.17	3.77E-02	6.45E-02	181.59	not significant
2176	SRRD	-1.17	1.08E-03	2.56E-03	681.50	not significant
2177	DDX55	-1.17	4.53E-07	1.79E-06	2605.81	not significant
2178	MRPL11	-1.17	1.84E-08	8.55E-08	3015.05	not significant
2179	PNPO	-1.17	1.02E-06	3.86E-06	1723.44	not significant
2180	ZNF664	-1.17	4.54E-14	3.60E-13	11148.71	not significant
2181	PARP11	-1.17	4.83E-05	1.45E-04	1115.80	not significant
2182	LRRC20	-1.17	4.04E-06	1.41E-05	1508.26	not significant
2183	RAB1A	-1.17	1.26E-06	4.73E-06	2592.69	not significant
2184	NFKBIE	-1.17	1.41E-02	2.68E-02	267.91	not significant
2185	TRIP12	-1.17	3.75E-14	3.01E-13	8895.20	not significant
2186	ATP6AP1L	-1.17	1.67E-02	3.13E-02	253.33	not significant
2187	CERS4	-1.17	5.20E-02	8.60E-02	132.06	not significant
2188	FAR1	-1.17	8.09E-10	4.31E-09	4666.61	not significant

2189	DCPS	-1.17	7.70E-05	2.25E-04	994.53	not significant
2190	NT5DC3	-1.17	1.25E-02	2.40E-02	291.18	not significant
2191	BBS9	-1.17	4.69E-02	7.86E-02	148.53	not significant
2192	CCDC74A	-1.17	5.51E-02	9.05E-02	123.39	not significant
2193	RPL17	-1.17	2.89E-02	5.11E-02	216.34	not significant
2194	GUSBP1	-1.17	1.96E-02	3.59E-02	241.64	not significant
2195	MRPL18	-1.17	7.09E-07	2.73E-06	1802.06	not significant
2196	BEND6	-1.17	5.82E-02	9.49E-02	12.53	not significant
2197	SVIL-AS1	-1.17	1.21E-04	3.41E-04	922.54	not significant
2198	HLA-H	-1.17	3.80E-02	6.50E-02	181.31	not significant
2199	LSM6	-1.17	1.22E-05	4.01E-05	1631.24	not significant
2200	ISG15	-1.17	4.59E-05	1.39E-04	1251.19	not significant
2201	PIGX	-1.16	4.03E-08	1.81E-07	2753.31	not significant
2202	GGT1	-1.16	5.11E-03	1.07E-02	496.66	not significant
2203	LONRF1	-1.16	4.25E-04	1.09E-03	721.84	not significant
2204	PSMB1	-1.16	9.94E-07	3.77E-06	4123.46	not significant
2205	SLC25A30	-1.16	4.56E-05	1.38E-04	1029.22	not significant
2206	MRPS9	-1.16	1.63E-05	5.27E-05	1237.99	not significant
2207	ACSL4	-1.16	1.20E-07	5.09E-07	2743.11	not significant
2208	HECTD3	-1.16	6.64E-05	1.96E-04	1041.16	not significant
2209	POLR2I	-1.16	2.05E-04	5.58E-04	945.77	not significant
2210	BCLAF1	-1.16	7.05E-11	4.20E-10	10849.40	not significant
2211	ATRIP	-1.16	4.89E-04	1.24E-03	691.28	not significant
2212	RCAN1	-1.16	8.94E-06	2.99E-05	1577.49	not significant
2213	TBK1	-1.16	1.73E-05	5.57E-05	1235.87	not significant
2214	KIF23	-1.16	1.57E-07	6.54E-07	2634.54	not significant
2215	FERMT2	-1.16	9.92E-02	1.51E-01	51.83	not significant
2216	SNRPD3	-1.16	2.47E-09	1.26E-08	7228.12	not significant
2217	NDUFB1	-1.16	6.24E-05	1.85E-04	1127.95	not significant
2218	PARS2	-1.16	2.89E-02	5.11E-02	198.41	not significant
2219	ERI3	-1.16	1.70E-06	6.27E-06	1571.62	not significant
2220	PFAS	-1.16	3.03E-10	1.70E-09	4545.06	not significant
2221	PRPF4	-1.16	1.18E-08	5.61E-08	2430.85	not significant
2222	RAB33A	-1.16	8.81E-03	1.75E-02	327.78	not significant
2223	GEMIN5	-1.16	2.14E-06	7.78E-06	1985.93	not significant
2224	KPTN	-1.16	5.33E-03	1.11E-02	397.59	not significant
2225	LRP1	-1.16	1.02E-01	1.55E-01	30.60	not significant
2226	FAM115C	-1.16	5.44E-02	8.96E-02	142.97	not significant
2227	DPP8	-1.16	7.76E-06	2.62E-05	1423.25	not significant
2228	TRAF4	-1.16	7.68E-05	2.24E-04	960.42	not significant
2229	CLDN12	-1.16	4.43E-03	9.39E-03	431.48	not significant
2230	TRMT13	-1.16	2.60E-04	6.96E-04	1137.68	not significant
2231	KIAA1161	-1.16	1.75E-02	3.25E-02	261.33	not significant
2232	LZTS1	-1.16	8.58E-10	4.55E-09	4216.48	not significant
2233	CCER2	-1.16	8.03E-02	1.26E-01	17.08	not significant
2234	ARHGAP15	-1.16	3.34E-08	1.51E-07	4125.75	not significant
2235	SNAPIN	-1.16	1.05E-04	3.00E-04	964.34	not significant
2236	CNDP2	-1.16	7.44E-12	4.87E-11	5894.96	not significant
2237	NAA25	-1.16	1.05E-07	4.46E-07	2307.48	not significant
2238	PTER	-1.16	2.67E-06	9.57E-06	1492.63	not significant
2239	GALM	-1.16	2.94E-05	9.15E-05	1142.19	not significant
2240	STK10	-1.16	1.46E-08	6.84E-08	2922.67	not significant
2241	SLC29A2	-1.16	9.85E-02	1.51E-01	63.05	not significant
2242	IFT74	-1.16	6.44E-03	1.32E-02	378.09	not significant
2243	NAE1	-1.16	9.48E-10	5.01E-09	3945.48	not significant
2244	TSPYL2	-1.16	8.05E-02	1.26E-01	82.68	not significant
2245	TTK	-1.16	9.40E-09	4.53E-08	3488.92	not significant
2246	TOMM40L	-1.16	3.38E-04	8.83E-04	745.13	not significant
2247	TBL3	-1.16	3.16E-06	1.12E-05	1550.49	not significant
2248	MTMR10	-1.16	1.51E-06	5.60E-06	1622.49	not significant
2249	TARS2	-1.16	6.98E-05	2.05E-04	980.42	not significant
2250	POP7	-1.16	1.86E-05	5.96E-05	1457.31	not significant
2251	VEGFC	-1.16	3.79E-02	6.49E-02	189.69	not significant
2252	CSK	-1.16	3.48E-12	2.34E-11	5392.91	not significant
2253	WDR17	-1.16	5.11E-02	8.47E-02	159.02	not significant
2254	ALG14	-1.16	1.08E-02	2.11E-02	320.45	not significant
2255	MKKS	-1.16	9.55E-06	3.18E-05	1880.31	not significant
2256	CUL1	-1.16	6.26E-09	3.06E-08	3857.99	not significant
2257	UQCRC1	-1.16	3.99E-10	2.21E-09	4535.60	not significant
2258	CEACAM21	-1.16	6.54E-02	1.05E-01	14.91	not significant
2259	MTF1	-1.16	2.44E-04	6.54E-04	835.91	not significant
2260	CWC22	-1.16	8.34E-06	2.80E-05	1389.58	not significant
2261	CTNNA1	-1.16	2.49E-08	1.14E-07	3238.26	not significant
2262	BCHE	-1.16	1.03E-04	2.94E-04	968.05	not significant
2263	MRPS11	-1.16	1.19E-04	3.37E-04	1018.98	not significant
2264	RAB3A	-1.16	1.02E-01	1.56E-01	53.35	not significant
2265	IWS1	-1.16	2.05E-07	8.43E-07	3466.09	not significant
2266	DDB1	-1.16	8.48E-16	7.82E-15	14074.11	not significant
2267	EFTUD2	-1.16	8.86E-14	6.85E-13	7273.55	not significant
2268	PEA15	-1.16	1.45E-05	4.69E-05	1342.81	not significant
2269	CCAR1	-1.16	1.01E-08	4.86E-08	6629.95	not significant
2270	MAPKBP1	-1.16	1.77E-04	4.87E-04	1051.00	not significant
2271	DDX41	-1.16	8.88E-09	4.30E-08	3499.11	not significant
2272	NDUFA5	-1.16	1.77E-06	6.51E-06	2452.32	not significant
2273	NTAN1	-1.16	5.95E-05	1.77E-04	1188.75	not significant
2274	GATAD2A	-1.16	6.82E-14	5.33E-13	8418.48	not significant
2275	ZNF563	-1.16	9.78E-02	1.50E-01	62.72	not significant
2276	ARMCX6	-1.16	4.59E-02	7.70E-02	164.02	not significant

2277	SMIM4	-1.16	5.59E-02	9.17E-02	135.77	not significant
2278	CORO2A	-1.16	4.93E-06	1.70E-05	1555.03	not significant
2279	TMEM169	-1.16	8.44E-02	1.32E-01	20.09	not significant
2280	COX6A1	-1.16	2.63E-06	9.43E-06	3262.70	not significant
2281	PAICS	-1.16	8.82E-12	5.73E-11	24734.62	not significant
2282	SH3PXD2A-AS1	-1.16	4.26E-02	7.21E-02	9.69	not significant
2283	NOSIP	-1.16	3.37E-05	1.04E-04	1324.90	not significant
2284	GADD45B	-1.16	2.39E-03	5.32E-03	538.15	not significant
2285	NDUFS7	-1.16	2.06E-05	6.56E-05	1551.16	not significant
2286	TNFRSF10B	-1.16	1.04E-01	1.58E-01	27.69	not significant
2287	CSNK1G3	-1.16	6.24E-03	1.28E-02	436.30	not significant
2288	SLC39A7	-1.16	5.16E-04	1.30E-03	729.42	not significant
2289	THOC6	-1.16	6.55E-06	2.23E-05	1447.18	not significant
2290	ASTN2	-1.16	7.02E-02	1.12E-01	105.95	not significant
2291	YWHAB	-1.16	7.44E-14	5.80E-13	21892.66	not significant
2292	RAD50	-1.16	4.79E-08	2.13E-07	3499.71	not significant
2293	GNB4	-1.16	1.40E-09	7.31E-09	5344.23	not significant
2294	FAM50A	-1.16	8.87E-04	2.14E-03	703.32	not significant
2295	DBF4B	-1.16	3.18E-06	1.13E-05	1661.12	not significant
2296	FTSJ2	-1.16	5.92E-05	1.77E-04	1708.07	not significant
2297	HERC6	-1.16	4.17E-02	7.06E-02	172.78	not significant
2298	VTA1	-1.16	9.98E-09	4.79E-08	3249.23	not significant
2299	MAD2L1BP	-1.16	8.78E-04	2.12E-03	646.46	not significant
2300	ANKRD13C	-1.16	6.10E-05	1.81E-04	1074.68	not significant
2301	TTI1	-1.16	9.21E-10	4.88E-09	3414.01	not significant
2302	USP39	-1.16	3.93E-10	2.18E-09	4974.18	not significant
2303	CA11	-1.16	2.17E-02	3.95E-02	246.05	not significant
2304	GAN	-1.16	3.34E-02	5.82E-02	212.70	not significant
2305	ESPL1	-1.16	4.52E-07	1.79E-06	6634.47	not significant
2306	C14orf169	-1.16	2.19E-05	6.93E-05	1213.56	not significant
2307	RNF181	-1.16	2.70E-04	7.19E-04	866.70	not significant
2308	PRPF38B	-1.16	5.87E-07	2.28E-06	4074.82	not significant
2309	MFAP1	-1.16	2.02E-06	7.35E-06	2015.96	not significant
2310	HPS3	-1.16	1.91E-05	6.10E-05	1342.20	not significant
2311	MTG2	-1.16	5.38E-04	1.36E-03	781.46	not significant
2312	SPCS1	-1.16	8.10E-08	3.49E-07	3346.26	not significant
2313	TRAPPC9	-1.16	1.04E-07	4.44E-07	2250.43	not significant
2314	NDUFA2	-1.16	1.49E-05	4.84E-05	1783.02	not significant
2315	VPRBP	-1.16	1.59E-04	4.41E-04	916.77	not significant
2316	LINC00426	-1.16	7.12E-03	1.44E-02	382.73	not significant
2317	RCL1	-1.16	1.32E-04	3.70E-04	977.04	not significant
2318	SPRYD3	-1.16	6.67E-04	1.65E-03	707.66	not significant
2319	LLPH	-1.16	9.42E-06	3.14E-05	1432.87	not significant
2320	SLC9A3R1	-1.16	7.19E-13	5.13E-12	15188.04	not significant
2321	LOC100996286	-1.16	2.19E-03	4.91E-03	791.91	not significant
2322	POU2F2	-1.16	8.30E-02	1.30E-01	94.77	not significant
2323	YOD1	-1.16	2.88E-05	8.98E-05	1578.06	not significant
2324	SETMAR	-1.16	3.48E-04	9.07E-04	781.54	not significant
2325	CYTH4	-1.16	1.08E-01	1.63E-01	33.18	not significant
2326	VRK3	-1.16	2.44E-05	7.67E-05	1280.14	not significant
2327	POLDIP2	-1.16	2.79E-05	8.72E-05	1379.44	not significant
2328	IK	-1.16	2.49E-09	1.27E-08	4176.06	not significant
2329	MGST2	-1.16	4.01E-02	6.82E-02	216.43	not significant
2330	PRPF8	-1.16	1.10E-02	2.15E-02	22179.95	not significant
2331	LINC01184	-1.16	1.87E-02	3.45E-02	305.42	not significant
2332	STRADB	-1.16	1.09E-03	2.59E-03	642.06	not significant
2333	TRIM21	-1.16	7.49E-04	1.83E-03	796.64	not significant
2334	AP3S1	-1.16	1.99E-07	8.19E-07	2396.55	not significant
2335	MVK	-1.16	1.56E-03	3.60E-03	719.16	not significant
2336	ZNF511	-1.16	8.14E-04	1.98E-03	702.52	not significant
2337	ALG5	-1.16	2.36E-04	6.34E-04	1220.52	not significant
2338	TFPT	-1.16	2.23E-02	4.05E-02	268.32	not significant
2339	HSF4	-1.16	3.11E-02	5.46E-02	276.59	not significant
2340	NPR2	-1.16	9.58E-02	1.47E-01	98.17	not significant
2341	MRPL19	-1.16	4.62E-07	1.82E-06	2502.10	not significant
2342	PSMA8	-1.16	4.80E-03	1.01E-02	452.67	not significant
2343	ZC3HC1	-1.16	5.37E-04	1.35E-03	809.39	not significant
2344	ZNF101	-1.16	1.93E-05	6.18E-05	1388.18	not significant
2345	TRIM65	-1.16	1.74E-06	6.40E-06	2291.99	not significant
2346	ADCY10P1	-1.16	1.03E-01	1.56E-01	64.11	not significant
2347	NR2C2AP	-1.16	4.98E-04	1.26E-03	808.91	not significant
2348	PISD	-1.16	9.27E-06	3.09E-05	1537.85	not significant
2349	RPL7L1	-1.16	3.49E-05	1.07E-04	1519.66	not significant
2350	CTNNBL1	-1.16	4.48E-08	2.00E-07	3108.11	not significant
2351	CCDC109B	-1.16	2.75E-07	1.12E-06	3125.80	not significant
2352	FADS1	-1.16	9.18E-12	5.95E-11	7950.05	not significant
2353	RNPS1	-1.16	6.18E-10	3.35E-09	7478.26	not significant
2354	RBM12	-1.16	1.43E-10	8.28E-10	7467.85	not significant
2355	AKR1B1	-1.16	1.75E-09	9.04E-09	4317.50	not significant
2356	LRRC47	-1.16	8.19E-08	3.53E-07	2429.13	not significant
2357	CIAPIN1	-1.16	1.03E-05	3.41E-05	1768.29	not significant
2358	CCDC117	-1.16	7.94E-10	4.24E-09	3957.11	not significant
2359	UBE2M	-1.16	5.05E-08	2.24E-07	3821.88	not significant
2360	WDR92	-1.16	2.73E-03	6.01E-03	591.44	not significant
2361	SUOX	-1.16	1.13E-01	1.69E-01	33.85	not significant
2362	EED	-1.16	1.01E-04	2.90E-04	1181.89	not significant
2363	NFKB1	-1.15	4.06E-08	1.82E-07	2542.43	not significant
2364	PRPF38A	-1.15	1.02E-10	5.96E-10	4718.12	not significant

2365	MTOR	-1.15	2.61E-06	9.37E-06	4210.90	not significant
2366	IKBIP	-1.15	2.74E-04	7.27E-04	1091.35	not significant
2367	UROD	-1.15	1.37E-04	3.83E-04	1075.93	not significant
2368	MYO1A	-1.15	1.13E-01	1.69E-01	29.55	not significant
2369	EML5	-1.15	2.50E-02	4.49E-02	280.38	not significant
2370	C9orf41	-1.15	1.06E-03	2.53E-03	766.83	not significant
2371	MAPK1IP1L	-1.15	1.52E-09	7.86E-09	5805.09	not significant
2372	CAPZA2	-1.15	7.61E-09	3.70E-08	3394.19	not significant
2373	RAB11FIP4	-1.15	1.11E-01	1.67E-01	31.83	not significant
2374	RCOR2	-1.15	6.88E-02	1.10E-01	125.18	not significant
2375	IQCE	-1.15	3.36E-04	8.79E-04	935.87	not significant
2376	ISG20L2	-1.15	1.57E-06	5.79E-06	1930.12	not significant
2377	TBC1D4	-1.15	4.11E-06	1.44E-05	1713.93	not significant
2378	MDFI	-1.15	5.05E-06	1.74E-05	1711.58	not significant
2379	UQCC3	-1.15	1.03E-02	2.02E-02	469.89	not significant
2380	AFAP1L2	-1.15	1.10E-01	1.66E-01	26.22	not significant
2381	ATP6V1B2	-1.15	1.31E-08	6.21E-08	2934.81	not significant
2382	43710_4150	-1.15	2.31E-11	1.44E-10	12137.52	not significant
2383	RAET1K	-1.15	9.20E-02	1.42E-01	92.01	not significant
2384	ADD3	-1.15	1.65E-13	1.25E-12	9120.82	not significant
2385	GORASP1	-1.15	1.35E-02	2.57E-02	382.65	not significant
2386	STK4	-1.15	2.92E-13	2.16E-12	7773.96	not significant
2387	SSU72	-1.15	2.78E-09	1.41E-08	3783.94	not significant
2388	FAM86C1	-1.15	6.63E-02	1.06E-01	129.63	not significant
2389	RPS6KA4	-1.15	5.23E-06	1.80E-05	1696.95	not significant
2390	PARP1	-1.15	1.25E-13	9.52E-13	11465.33	not significant
2391	TRIP6	-1.15	1.14E-01	1.71E-01	29.58	not significant
2392	ARHGEF25	-1.15	1.08E-01	1.63E-01	67.37	not significant
2393	DESI2	-1.15	2.09E-08	9.67E-08	3904.32	not significant
2394	NUP188	-1.15	2.28E-10	1.30E-09	5305.61	not significant
2395	SLA2	-1.15	2.58E-08	1.18E-07	4005.42	not significant
2396	SCRN1	-1.15	7.53E-02	1.19E-01	114.11	not significant
2397	ST6GALNAC6	-1.15	3.49E-03	7.55E-03	518.04	not significant
2398	NSFL1C	-1.15	8.77E-07	3.34E-06	2063.58	not significant
2399	MDC1	-1.15	6.92E-03	1.41E-02	440.49	not significant
2400	TMED10	-1.15	1.67E-14	1.38E-13	14724.44	not significant
2401	CYB5R3	-1.15	5.71E-09	2.80E-08	4982.33	not significant
2402	NOTCH2NL	-1.15	8.03E-02	1.26E-01	120.75	not significant
2403	ISCU	-1.15	5.94E-08	2.61E-07	2697.75	not significant
2404	GABPB2	-1.15	1.31E-02	2.51E-02	338.37	not significant
2405	NOL8	-1.15	3.54E-06	1.25E-05	1912.57	not significant
2406	VPS8	-1.15	5.13E-04	1.30E-03	832.41	not significant
2407	CCDC6	-1.15	1.94E-05	6.18E-05	1412.21	not significant
2408	GBAS	-1.15	1.55E-07	6.49E-07	2854.41	not significant
2409	ENTPD5	-1.15	2.64E-02	4.71E-02	253.94	not significant
2410	RBBP7	-1.15	1.09E-09	5.75E-09	10249.38	not significant
2411	INPP5A	-1.15	3.41E-03	7.39E-03	541.66	not significant
2412	SF1	-1.15	3.27E-13	2.40E-12	16293.28	not significant
2413	TDRKH	-1.15	9.46E-04	2.27E-03	724.67	not significant
2414	ATF7IP2	-1.15	2.29E-03	5.11E-03	629.47	not significant
2415	CCDC125	-1.15	7.50E-02	1.19E-01	124.26	not significant
2416	TRAPPC4	-1.15	4.46E-02	7.51E-02	198.46	not significant
2417	PMS2CL	-1.15	1.44E-02	2.74E-02	403.73	not significant
2418	RGS19	-1.15	5.94E-04	1.48E-03	1334.80	not significant
2419	ABCB8	-1.15	1.26E-04	3.55E-04	1388.53	not significant
2420	NRBF2	-1.15	4.03E-03	8.62E-03	545.72	not significant
2421	RABEP1	-1.15	9.78E-09	4.70E-08	5172.07	not significant
2422	R3HCC1L	-1.15	1.12E-04	3.17E-04	1070.62	not significant
2423	TBC1D7	-1.15	2.76E-03	6.09E-03	571.57	not significant
2424	ESF1	-1.15	1.33E-05	4.36E-05	1816.93	not significant
2425	WDR44	-1.15	2.75E-04	7.30E-04	924.17	not significant
2426	CCNK	-1.15	2.44E-10	1.38E-09	4666.02	not significant
2427	NUDT9	-1.15	1.54E-03	3.55E-03	821.91	not significant
2428	MTMR1	-1.15	3.10E-03	6.78E-03	563.56	not significant
2429	NDUFA13	-1.15	7.88E-03	1.58E-02	3595.16	not significant
2430	BCAP31	-1.15	9.54E-06	3.17E-05	2402.07	not significant
2431	ANKRD27	-1.15	1.14E-05	3.75E-05	1662.47	not significant
2432	CBWD5	-1.15	1.14E-01	1.71E-01	28.46	not significant
2433	STYXL1	-1.15	1.25E-02	2.40E-02	348.10	not significant
2434	SART3	-1.15	3.25E-10	1.82E-09	5670.07	not significant
2435	PPP1CC	-1.15	3.17E-11	1.95E-10	12064.25	not significant
2436	GDF11	-1.15	1.47E-04	4.11E-04	1413.85	not significant
2437	BNIP3	-1.15	1.65E-04	4.57E-04	992.08	not significant
2438	ABHD14B	-1.15	7.79E-05	2.27E-04	1211.58	not significant
2439	AKIRIN2	-1.15	1.36E-04	3.82E-04	1053.54	not significant
2440	AEBP2	-1.15	1.98E-06	7.22E-06	2925.74	not significant
2441	SPTLC1	-1.15	1.07E-04	3.06E-04	1254.64	not significant
2442	CYSTM1	-1.15	5.66E-02	9.26E-02	159.41	not significant
2443	NUP107	-1.15	2.93E-08	1.34E-07	5469.12	not significant
2444	UNC13D	-1.15	4.38E-13	3.19E-12	9384.49	not significant
2445	CHMP4B	-1.15	2.04E-08	9.44E-08	5667.06	not significant
2446	ZCCHC9	-1.15	1.04E-05	3.43E-05	1541.82	not significant
2447	MBNL1-AS1	-1.15	1.13E-01	1.70E-01	25.19	not significant
2448	OGFOD2	-1.15	7.88E-04	1.92E-03	865.55	not significant
2449	C16orf72	-1.15	1.17E-04	3.31E-04	1452.60	not significant
2450	HPDL	-1.15	5.71E-02	9.33E-02	182.65	not significant
2451	CDK7	-1.15	1.03E-02	2.01E-02	492.79	not significant
2452	YWHAQ	-1.15	1.73E-11	1.09E-10	17560.08	not significant

2453	SLC4A1AP	-1.15	1.01E-04	2.91E-04	1098.42	not significant
2454	FOSL2	-1.15	1.07E-01	1.62E-01	74.01	not significant
2455	RELL2	-1.15	7.55E-02	1.19E-01	143.41	not significant
2456	IGSF9B	-1.15	2.47E-02	4.44E-02	294.11	not significant
2457	MGAT2	-1.15	2.85E-06	1.02E-05	1982.35	not significant
2458	SLC25A12	-1.15	1.99E-05	6.34E-05	1605.18	not significant
2459	GYS1	-1.15	4.24E-06	1.48E-05	1933.43	not significant
2460	SNW1	-1.15	7.05E-07	2.72E-06	2791.94	not significant
2461	FBLN7	-1.15	1.22E-01	1.81E-01	50.74	not significant
2462	LAP3	-1.15	1.67E-05	5.38E-05	1574.20	not significant
2463	MICU2	-1.15	5.70E-05	1.70E-04	1372.66	not significant
2464	SPRYD7	-1.15	1.05E-01	1.60E-01	87.61	not significant
2465	NF1	-1.15	5.05E-09	2.50E-08	4382.48	not significant
2466	RHNO1	-1.15	1.31E-08	6.18E-08	3177.59	not significant
2467	SLIRP	-1.15	1.86E-03	4.23E-03	776.37	not significant
2468	PPIL2	-1.15	5.33E-07	2.08E-06	2774.10	not significant
2469	MINPP1	-1.15	1.86E-04	5.09E-04	1098.55	not significant
2470	TRAF1	-1.15	1.11E-01	1.66E-01	75.75	not significant
2471	SMIM11	-1.15	1.92E-03	4.35E-03	764.83	not significant
2472	RPAP1	-1.15	2.11E-05	6.70E-05	1607.91	not significant
2473	AGA	-1.15	2.50E-03	5.55E-03	597.76	not significant
2474	PTPLAD2	-1.15	8.53E-05	2.48E-04	1428.87	not significant
2475	RGS18	-1.15	1.23E-01	1.83E-01	51.37	not significant
2476	NBPF3	-1.15	7.83E-03	1.57E-02	447.53	not significant
2477	ZNF106	-1.15	2.67E-07	1.09E-06	2798.79	not significant
2478	PGM2	-1.15	3.82E-07	1.52E-06	2623.07	not significant
2479	SLFN5	-1.15	1.21E-06	4.56E-06	2456.90	not significant
2480	ACTR3B	-1.15	3.15E-02	5.51E-02	253.00	not significant
2481	TGFB1	-1.15	6.04E-07	2.34E-06	3494.31	not significant
2482	YIF1A	-1.15	1.41E-04	3.95E-04	1150.68	not significant
2483	HIST1H2BL	-1.15	1.14E-01	1.70E-01	24.04	not significant
2484	NGLY1	-1.15	2.38E-07	9.72E-07	2629.66	not significant
2485	SUCLA2	-1.15	8.07E-06	2.71E-05	1945.10	not significant
2486	LOC100131691	-1.15	1.03E-01	1.57E-01	88.78	not significant
2487	FAM212A	-1.15	1.20E-01	1.78E-01	59.95	not significant
2488	PRKAG1	-1.15	1.84E-06	6.75E-06	2067.82	not significant
2489	ADCK5	-1.15	7.34E-02	1.16E-01	148.88	not significant
2490	C19orf70	-1.15	1.53E-03	3.53E-03	755.35	not significant
2491	ATP7B	-1.15	8.45E-02	1.32E-01	14.63	not significant
2492	ZNF37A	-1.15	2.56E-06	9.22E-06	2061.38	not significant
2493	CEBPZOS	-1.15	7.74E-06	2.61E-05	1688.49	not significant
2494	FAM86EP	-1.15	1.18E-01	1.76E-01	67.93	not significant
2495	DHX37	-1.15	1.51E-09	7.85E-09	3934.90	not significant
2496	DECR1	-1.15	3.35E-05	1.03E-04	1809.39	not significant
2497	FUT8-AS1	-1.15	1.28E-01	1.89E-01	45.40	not significant
2498	FAM175B	-1.15	6.93E-05	2.04E-04	1218.14	not significant
2499	DOCK10	-1.15	5.03E-09	2.49E-08	3939.23	not significant
2500	CD55	-1.15	2.36E-02	4.25E-02	311.29	not significant
2501	CCSER2	-1.15	2.52E-06	9.06E-06	2033.15	not significant
2502	CHD5	-1.15	1.28E-01	1.89E-01	51.85	not significant
2503	TMC6	-1.15	1.90E-05	6.09E-05	2096.95	not significant
2504	ALDH9A1	-1.15	6.32E-07	2.45E-06	2362.25	not significant
2505	LOC100507316	-1.15	7.79E-02	1.23E-01	126.59	not significant
2506	RFX2	-1.15	9.72E-02	1.49E-01	97.85	not significant
2507	AURKAIP1	-1.15	7.21E-05	2.12E-04	2574.04	not significant
2508	PPP1R12A	-1.15	1.13E-09	5.95E-09	5532.18	not significant
2509	PSMD10	-1.15	3.49E-05	1.07E-04	1448.90	not significant
2510	EPHX1	-1.15	9.36E-02	1.44E-01	108.15	not significant
2511	OPN3	-1.15	9.13E-04	2.20E-03	855.87	not significant
2512	SPOCD1	-1.15	5.46E-02	8.99E-02	190.88	not significant
2513	APEH	-1.15	2.78E-08	1.27E-07	4046.44	not significant
2514	GNB2	-1.15	5.47E-08	2.42E-07	5408.44	not significant
2515	DHDDS	-1.15	2.72E-04	7.24E-04	1041.64	not significant
2516	NUF2	-1.15	3.58E-06	1.26E-05	2814.41	not significant
2517	FAM58A	-1.15	3.94E-02	6.72E-02	226.48	not significant
2518	PLEKHA5	-1.14	3.28E-03	7.12E-03	599.05	not significant
2519	UBP1	-1.14	9.34E-09	4.50E-08	4189.27	not significant
2520	ACLY	-1.14	2.78E-10	1.57E-09	6086.78	not significant
2521	DGKH	-1.14	5.86E-02	9.55E-02	1157.60	not significant
2522	PIGN	-1.14	4.49E-05	1.36E-04	1667.34	not significant
2523	CCDC181	-1.14	1.31E-01	1.92E-01	36.00	not significant
2524	AMER1	-1.14	2.31E-03	5.15E-03	653.49	not significant
2525	NAA38	-1.14	1.65E-03	3.78E-03	863.25	not significant
2526	ANP32C	-1.14	1.24E-01	1.84E-01	30.05	not significant
2527	LMNB1	-1.14	2.14E-12	1.47E-11	18847.54	not significant
2528	AMOTL2	-1.14	1.07E-01	1.62E-01	20.45	not significant
2529	UBE3A	-1.14	6.50E-09	3.17E-08	4375.69	not significant
2530	ST3GAL6	-1.14	6.37E-02	1.03E-01	11.09	not significant
2531	VAV3	-1.14	4.12E-05	1.26E-04	1545.88	not significant
2532	UBE2C	-1.14	2.04E-08	9.43E-08	6911.69	not significant
2533	RPS6KA3	-1.14	7.08E-10	3.81E-09	7277.67	not significant
2534	GMFB	-1.14	7.78E-06	2.62E-05	2119.18	not significant
2535	TFAM	-1.14	5.83E-08	2.57E-07	3948.21	not significant
2536	KCNN3	-1.14	3.69E-02	6.34E-02	7.66	not significant
2537	UBA5	-1.14	3.94E-06	1.38E-05	1889.98	not significant
2538	MTERF2	-1.14	6.25E-02	1.01E-01	175.88	not significant
2539	HSPA9	-1.14	1.78E-09	9.16E-09	15873.51	not significant
2540	USP45	-1.14	4.84E-03	1.02E-02	665.52	not significant

2541	FUNDC2	-1.14	6.50E-03	1.33E-02	656.62	not significant
2542	NSUN6	-1.14	7.86E-03	1.58E-02	503.76	not significant
2543	CCDC66	-1.14	2.73E-03	6.03E-03	814.71	not significant
2544	TSEN54	-1.14	5.17E-06	1.78E-05	2056.02	not significant
2545	PDHX	-1.14	5.55E-04	1.39E-03	944.08	not significant
2546	SERPINB8	-1.14	1.31E-01	1.92E-01	57.20	not significant
2547	EIF4A3	-1.14	1.63E-07	6.79E-07	6211.27	not significant
2548	MFN2	-1.14	1.18E-08	5.59E-08	4303.51	not significant
2549	SIGLEC8	-1.14	6.24E-02	1.01E-01	10.00	not significant
2550	FDXR	-1.14	9.97E-04	2.38E-03	786.89	not significant
2551	SNUPN	-1.14	3.82E-04	9.88E-04	1289.01	not significant
2552	RRP1B	-1.14	4.02E-09	2.00E-08	4883.58	not significant
2553	CD70	-1.14	6.43E-02	1.04E-01	164.93	not significant
2554	PRPSAP2	-1.14	9.04E-05	2.61E-04	1668.46	not significant
2555	FKBP14	-1.14	3.01E-02	5.29E-02	301.16	not significant
2556	TMEM41A	-1.14	3.01E-03	6.59E-03	671.36	not significant
2557	PLRG1	-1.14	1.35E-05	4.41E-05	2190.80	not significant
2558	PIGT	-1.14	6.72E-07	2.60E-06	2663.45	not significant
2559	GGPS1	-1.14	2.07E-04	5.62E-04	1132.58	not significant
2560	PIGO	-1.14	1.03E-03	2.45E-03	956.25	not significant
2561	PLAG1	-1.14	1.31E-01	1.92E-01	60.87	not significant
2562	SLC27A5	-1.14	3.21E-02	5.61E-02	267.18	not significant
2563	GCFC2	-1.14	3.94E-04	1.02E-03	1008.67	not significant
2564	MAGED1	-1.14	3.78E-04	9.78E-04	1088.28	not significant
2565	CCDC138	-1.14	4.23E-04	1.09E-03	1084.95	not significant
2566	SLMAP	-1.14	6.35E-06	2.17E-05	2238.59	not significant
2567	MPI	-1.14	2.22E-03	4.96E-03	757.13	not significant
2568	GLMN	-1.14	6.72E-03	1.37E-02	602.40	not significant
2569	AP2S1	-1.14	2.10E-05	6.68E-05	2915.43	not significant
2570	SETD3	-1.14	5.87E-07	2.28E-06	2731.96	not significant
2571	SLC10A7	-1.14	1.85E-03	4.21E-03	743.54	not significant
2572	GABPB1	-1.14	3.06E-05	9.50E-05	1760.93	not significant
2573	ZCCHC2	-1.14	1.56E-03	3.61E-03	731.23	not significant
2574	YWHAH	-1.14	3.32E-08	1.50E-07	4756.34	not significant
2575	SFXN4	-1.14	3.50E-05	1.08E-04	1485.02	not significant
2576	MRPL50	-1.14	6.21E-03	1.28E-02	511.12	not significant
2577	CHMP4A	-1.14	8.82E-05	2.55E-04	1453.76	not significant
2578	BAG4	-1.14	3.47E-04	9.06E-04	1128.69	not significant
2579	RGS5	-1.14	1.05E-01	1.60E-01	96.58	not significant
2580	OAZ1	-1.14	2.13E-06	7.75E-06	22045.06	not significant
2581	GPD2	-1.14	2.85E-02	5.05E-02	305.34	not significant
2582	MYL12A	-1.14	9.60E-10	5.08E-09	5376.47	not significant
2583	HSPB1	-1.14	5.03E-06	1.74E-05	2749.49	not significant
2584	APTX	-1.14	1.78E-04	4.90E-04	1216.15	not significant
2585	SYNE4	-1.14	1.23E-01	1.82E-01	24.67	not significant
2586	LIPA	-1.14	6.18E-06	2.11E-05	2870.49	not significant
2587	ALDH18A1	-1.14	4.91E-10	2.70E-09	5966.83	not significant
2588	PRPF40A	-1.14	4.72E-10	2.60E-09	6611.12	not significant
2589	HMGN2	-1.14	3.73E-08	1.68E-07	14047.09	not significant
2590	EZR	-1.14	1.89E-12	1.30E-11	15338.22	not significant
2591	ARMC9	-1.14	1.13E-01	1.70E-01	89.46	not significant
2592	SALL2	-1.14	3.90E-03	8.36E-03	631.56	not significant
2593	PSME1	-1.14	4.28E-09	2.13E-08	10319.71	not significant
2594	GTF3C4	-1.14	1.57E-04	4.38E-04	1206.71	not significant
2595	LOC100507600	-1.14	9.10E-08	3.91E-07	3841.87	not significant
2596	SNX8	-1.14	4.15E-04	1.07E-03	1146.97	not significant
2597	TCEA2	-1.14	1.44E-02	2.73E-02	460.00	not significant
2598	EFCAB13	-1.14	7.34E-02	1.16E-01	157.13	not significant
2599	KDM1A	-1.14	1.03E-10	6.05E-10	7350.19	not significant
2600	WDR7	-1.14	1.70E-05	5.47E-05	1902.20	not significant
2601	MICU1	-1.14	5.08E-06	1.75E-05	2480.08	not significant
2602	SDHC	-1.14	1.95E-04	5.33E-04	1338.10	not significant
2603	ITM2C	-1.14	3.01E-07	1.21E-06	4937.44	not significant
2604	TCERG1	-1.14	6.14E-07	2.38E-06	5815.41	not significant
2605	OCRL	-1.14	7.76E-02	1.22E-01	151.34	not significant
2606	SPTY2D1	-1.14	3.28E-05	1.01E-04	1716.87	not significant
2607	NELFE	-1.14	1.01E-04	2.90E-04	1575.48	not significant
2608	BRMS1	-1.14	6.82E-06	2.32E-05	2597.01	not significant
2609	NRD1	-1.14	2.90E-10	1.63E-09	6697.83	not significant
2610	NKRF	-1.14	1.90E-04	5.20E-04	1150.26	not significant
2611	STAMBP	-1.14	4.83E-06	1.67E-05	2187.47	not significant
2612	KNSTRN	-1.14	9.68E-05	2.79E-04	1506.71	not significant
2613	APH1B	-1.14	1.48E-02	2.80E-02	405.87	not significant
2614	KIAA0930	-1.14	3.18E-06	1.13E-05	3241.44	not significant
2615	PDE6B	-1.14	1.78E-02	3.30E-02	366.50	not significant
2616	SRSF2	-1.14	6.82E-08	2.97E-07	20511.44	not significant
2617	DDA1	-1.14	9.64E-06	3.21E-05	1961.67	not significant
2618	OSBPL11	-1.14	7.17E-06	2.43E-05	1917.55	not significant
2619	MTHFD2L	-1.14	4.46E-02	7.51E-02	234.50	not significant
2620	LOC100507424	-1.14	1.34E-01	1.96E-01	63.08	not significant
2621	LHFPL2	-1.14	5.52E-02	9.06E-02	9.41	not significant
2622	UTP23	-1.14	7.14E-06	2.42E-05	2050.49	not significant
2623	ARL5A	-1.14	2.15E-06	7.80E-06	2998.30	not significant
2624	PPHLN1	-1.14	3.27E-08	1.48E-07	4110.03	not significant
2625	TAF1A	-1.14	8.81E-03	1.75E-02	536.67	not significant
2626	COX6C	-1.14	2.34E-02	4.22E-02	4181.52	not significant
2627	RAB10	-1.14	3.72E-10	2.07E-09	6596.77	not significant
2628	WFS1	-1.14	1.42E-01	2.07E-01	46.39	not significant

2629	C4orf29	-1.14	6.34E-03	1.30E-02	659.66	not significant
2630	LCP2	-1.14	3.21E-08	1.46E-07	4299.35	not significant
2631	SIPA1L2	-1.14	1.38E-01	2.02E-01	32.64	not significant
2632	PLIN3	-1.14	2.55E-06	9.16E-06	2801.95	not significant
2633	DNM3	-1.14	1.42E-01	2.07E-01	42.71	not significant
2634	ERMP1	-1.14	2.09E-02	3.82E-02	380.28	not significant
2635	QRSL1	-1.14	1.03E-04	2.94E-04	1367.78	not significant
2636	ABCD2	-1.14	1.42E-01	2.07E-01	45.96	not significant
2637	WWP2	-1.14	1.42E-05	4.61E-05	1949.44	not significant
2638	MTMR6	-1.14	4.59E-07	1.81E-06	2863.66	not significant
2639	DHRS7B	-1.14	5.93E-02	9.66E-02	208.39	not significant
2640	NDUFA1	-1.14	2.87E-02	5.08E-02	2033.27	not significant
2641	XRCC5	-1.14	1.45E-10	8.39E-10	24516.97	not significant
2642	LY96	-1.14	9.25E-02	1.43E-01	152.14	not significant
2643	ARPC3	-1.14	3.99E-08	1.79E-07	10515.63	not significant
2644	CNTROB	-1.14	7.29E-07	2.80E-06	2807.18	not significant
2645	NUPL2	-1.14	3.95E-04	1.02E-03	1103.94	not significant
2646	AFTPH	-1.14	4.95E-04	1.26E-03	1416.28	not significant
2647	GEMIN4	-1.14	1.51E-06	5.61E-06	2488.96	not significant
2648	TADA2A	-1.14	5.47E-04	1.38E-03	1001.09	not significant
2649	QTRTD1	-1.14	8.47E-05	2.46E-04	1480.19	not significant
2650	TESC	-1.14	9.08E-07	3.45E-06	4199.51	not significant
2651	DCTN1	-1.14	5.99E-10	3.26E-09	7200.21	not significant
2652	HAR1A	-1.14	9.70E-02	1.49E-01	123.46	not significant
2653	F2RL1	-1.14	1.46E-01	2.11E-01	50.58	not significant
2654	HDAC2	-1.14	3.05E-09	1.54E-08	8386.83	not significant
2655	TIMP1	-1.14	8.06E-02	1.26E-01	155.40	not significant
2656	ARL6IP1	-1.14	2.11E-09	1.08E-08	11580.28	not significant
2657	PDRG1	-1.14	5.03E-03	1.05E-02	950.13	not significant
2658	TOMM22	-1.14	1.25E-07	5.28E-07	4576.38	not significant
2659	DDX56	-1.14	7.88E-06	2.65E-05	2820.41	not significant
2660	SH3KBP1	-1.14	5.58E-10	3.05E-09	7732.32	not significant
2661	ZNF197-AS1	-1.14	6.04E-02	9.81E-02	9.30	not significant
2662	MED19	-1.14	1.06E-02	2.07E-02	541.91	not significant
2663	G3BP1	-1.14	4.09E-09	2.04E-08	9003.74	not significant
2664	RDH13	-1.14	1.12E-01	1.68E-01	102.92	not significant
2665	UROS	-1.14	3.83E-05	1.17E-04	1644.82	not significant
2666	CSNK2A3	-1.14	1.31E-01	1.92E-01	80.81	not significant
2667	PNPLA7	-1.14	1.44E-01	2.09E-01	32.95	not significant
2668	CANT1	-1.14	2.77E-07	1.12E-06	4535.62	not significant
2669	SGPP1	-1.14	4.92E-04	1.25E-03	1360.01	not significant
2670	RGS14	-1.14	1.67E-04	4.63E-04	1392.63	not significant
2671	ATP8B3	-1.14	2.41E-03	5.37E-03	882.62	not significant
2672	MRPL40	-1.14	1.05E-02	2.06E-02	527.66	not significant
2673	SMEK2	-1.14	1.42E-08	6.64E-08	5578.50	not significant
2674	CUTC	-1.14	5.86E-03	1.21E-02	813.95	not significant
2675	TRNT1	-1.14	3.14E-04	8.25E-04	1195.47	not significant
2676	ZNF542P	-1.14	1.01E-03	2.41E-03	1038.31	not significant
2677	KMT2C	-1.14	1.05E-02	2.05E-02	3960.38	not significant
2678	PPAT	-1.14	1.54E-05	5.00E-05	2981.05	not significant
2679	NDUFA11	-1.14	1.82E-06	6.66E-06	2542.21	not significant
2680	GPR124	-1.14	5.09E-06	1.76E-05	2670.98	not significant
2681	COMMD8	-1.14	7.91E-04	1.93E-03	1063.46	not significant
2682	TMEM14B	-1.14	9.25E-05	2.67E-04	2072.95	not significant
2683	ABHD15	-1.13	1.42E-02	2.69E-02	475.33	not significant
2684	PMFBP1	-1.13	1.09E-01	1.64E-01	110.32	not significant
2685	PDCD11	-1.13	6.23E-08	2.73E-07	5398.80	not significant
2686	FYN	-1.13	1.52E-08	7.11E-08	4283.33	not significant
2687	SRSF9	-1.13	1.05E-02	2.05E-02	6517.29	not significant
2688	U2AF1	-1.13	2.41E-05	7.57E-05	3557.48	not significant
2689	RAPGEF5	-1.13	9.89E-06	3.28E-05	2133.68	not significant
2690	FLAD1	-1.13	2.12E-03	4.77E-03	758.04	not significant
2691	MLF2	-1.13	2.14E-07	8.77E-07	5452.36	not significant
2692	CAND1	-1.13	4.66E-11	2.83E-10	9805.58	not significant
2693	SDCCAG8	-1.13	1.15E-02	2.23E-02	478.21	not significant
2694	PPP2R5E	-1.13	2.96E-07	1.19E-06	3465.42	not significant
2695	ERF	-1.13	8.26E-05	2.40E-04	1774.37	not significant
2696	PSMD5	-1.13	4.86E-04	1.24E-03	1089.25	not significant
2697	VASP	-1.13	2.58E-04	6.91E-04	2071.54	not significant
2698	SLC37A2	-1.13	1.51E-01	2.18E-01	51.04	not significant
2699	ARTN	-1.13	1.33E-01	1.95E-01	23.31	not significant
2700	ATF1	-1.13	7.27E-05	2.13E-04	1625.58	not significant
2701	SRPK1	-1.13	2.17E-09	1.11E-08	6854.42	not significant
2702	WDR33	-1.13	6.77E-08	2.95E-07	4043.79	not significant
2703	STK17A	-1.13	1.74E-07	7.23E-07	3313.62	not significant
2704	RBM26	-1.13	4.42E-05	1.34E-04	3842.93	not significant
2705	TERF1	-1.13	9.12E-06	3.05E-05	2464.31	not significant
2706	CTR9	-1.13	2.57E-06	9.22E-06	4710.60	not significant
2707	AGL	-1.13	4.43E-04	1.13E-03	1788.35	not significant
2708	SENP3	-1.13	4.75E-03	1.00E-02	703.54	not significant
2709	NAPSA	-1.13	1.02E-01	1.56E-01	15.40	not significant
2710	TSEN2	-1.13	2.00E-02	3.67E-02	406.49	not significant
2711	SLC9A1	-1.13	1.51E-03	3.50E-03	946.07	not significant
2712	ZNF18	-1.13	2.60E-02	4.64E-02	339.02	not significant
2713	ENOPH1	-1.13	7.27E-07	2.80E-06	3750.80	not significant
2714	PFKFB3	-1.13	3.77E-04	9.78E-04	1145.08	not significant
2715	SCG5	-1.13	8.02E-02	1.26E-01	11.26	not significant
2716	GINS1	-1.13	2.43E-07	9.95E-07	4088.04	not significant

2717	IQGAP1	-1.13	2.19E-09	1.12E-08	14182.22	not significant
2718	HBS1L	-1.13	1.45E-05	4.71E-05	3796.22	not significant
2719	G3BP2	-1.13	2.00E-10	1.14E-09	8209.68	not significant
2720	RBM43	-1.13	2.27E-02	4.11E-02	419.30	not significant
2721	HSPE1	-1.13	4.69E-02	7.85E-02	1465.01	not significant
2722	SYMPK	-1.13	2.32E-08	1.07E-07	4384.50	not significant
2723	DAXX	-1.13	5.99E-03	1.23E-02	617.31	not significant
2724	TAF6L	-1.13	2.55E-03	5.65E-03	833.12	not significant
2725	EPN2	-1.13	9.46E-03	1.87E-02	551.94	not significant
2726	FDXACB1	-1.13	1.50E-01	2.17E-01	32.27	not significant
2727	LGMN	-1.13	1.17E-01	1.74E-01	17.64	not significant
2728	ZW10	-1.13	2.56E-04	6.85E-04	1470.92	not significant
2729	THUMPD2	-1.13	3.76E-03	8.10E-03	712.23	not significant
2730	RBM27	-1.13	2.57E-07	1.05E-06	3387.22	not significant
2731	PFKP	-1.13	1.73E-08	8.04E-08	5681.30	not significant
2732	TARDBP	-1.13	9.46E-09	4.55E-08	8733.74	not significant
2733	NDUFAF5	-1.13	1.20E-02	2.31E-02	540.19	not significant
2734	ZFR	-1.13	2.86E-08	1.31E-07	5323.00	not significant
2735	CAT	-1.13	3.31E-07	1.33E-06	3469.33	not significant
2736	KDM4A-AS1	-1.13	1.57E-01	2.25E-01	51.27	not significant
2737	RAD51B	-1.13	3.52E-02	6.07E-02	342.08	not significant
2738	TRAPPC2L	-1.13	1.80E-03	4.10E-03	934.05	not significant
2739	LATS2	-1.13	1.55E-01	2.22E-01	40.98	not significant
2740	RRN3	-1.13	1.72E-05	5.54E-05	2184.14	not significant
2741	CARD11	-1.13	1.26E-05	4.12E-05	2877.13	not significant
2742	DDX19A	-1.13	1.20E-05	3.96E-05	2703.51	not significant
2743	HARBI1	-1.13	1.33E-01	1.95E-01	92.55	not significant
2744	INIP	-1.13	2.57E-03	5.70E-03	933.74	not significant
2745	ABCC4	-1.13	2.52E-04	6.74E-04	1303.27	not significant
2746	DOK3	-1.13	1.52E-01	2.19E-01	67.68	not significant
2747	EMC3	-1.13	1.90E-04	5.20E-04	1449.95	not significant
2748	ORAOV1	-1.13	7.60E-03	1.53E-02	599.78	not significant
2749	TBC1D10C	-1.13	2.54E-06	9.14E-06	3413.98	not significant
2750	MRPS30	-1.13	7.43E-04	1.82E-03	1053.93	not significant
2751	GDPD1	-1.13	1.08E-01	1.64E-01	125.38	not significant
2752	MRS2	-1.13	4.70E-04	1.20E-03	1673.02	not significant
2753	ZDHHC14	-1.13	1.39E-01	2.04E-01	82.46	not significant
2754	SRSF4	-1.13	6.04E-08	2.65E-07	6352.04	not significant
2755	PPIG	-1.13	2.04E-06	7.42E-06	3517.22	not significant
2756	TSC22D3	-1.13	1.45E-01	2.11E-01	26.89	not significant
2757	TULP4	-1.13	3.87E-03	8.32E-03	840.50	not significant
2758	MAD1L1	-1.13	2.77E-04	7.35E-04	1690.02	not significant
2759	ATP6V1C1	-1.13	2.90E-06	1.04E-05	3477.75	not significant
2760	NOC3L	-1.13	5.76E-04	1.44E-03	1600.81	not significant
2761	SDHA	-1.13	1.13E-06	4.25E-06	4164.47	not significant
2762	APOBEC3F	-1.13	1.55E-02	2.91E-02	552.38	not significant
2763	PUS7L	-1.13	5.98E-04	1.49E-03	1104.45	not significant
2764	MCOLN2	-1.13	1.57E-01	2.25E-01	31.37	not significant
2765	LDLRAP1	-1.13	1.26E-01	1.86E-01	20.17	not significant
2766	UBQLN1	-1.13	1.43E-08	6.71E-08	6029.65	not significant
2767	TBC1D22B	-1.13	1.24E-05	4.08E-05	2179.74	not significant
2768	REEP3	-1.13	6.30E-04	1.56E-03	1206.83	not significant
2769	MDH1	-1.13	1.40E-06	5.23E-06	6493.69	not significant
2770	UPF2	-1.13	5.88E-05	1.76E-04	1943.87	not significant
2771	M6PR	-1.13	1.04E-06	3.94E-06	4261.94	not significant
2772	TFB2M	-1.13	3.96E-03	8.49E-03	771.38	not significant
2773	43715_9262	-1.13	1.18E-08	5.62E-08	11256.85	not significant
2774	SEC24D	-1.13	4.92E-05	1.48E-04	1828.93	not significant
2775	SYDE2	-1.13	9.14E-02	1.41E-01	182.40	not significant
2776	GPN3	-1.13	2.32E-04	6.26E-04	1687.63	not significant
2777	KCTD5	-1.13	5.04E-04	1.28E-03	1585.65	not significant
2778	C6orf1	-1.13	2.78E-02	4.93E-02	387.18	not significant
2779	FAM32A	-1.13	3.33E-06	1.18E-05	3375.12	not significant
2780	C1orf61	-1.13	1.27E-01	1.88E-01	17.95	not significant
2781	TCF25	-1.13	1.24E-05	4.07E-05	2756.27	not significant
2782	SPATA2	-1.13	3.45E-03	7.47E-03	792.24	not significant
2783	RPS6KB2	-1.13	6.77E-06	2.30E-05	2466.93	not significant
2784	SZRD1	-1.13	1.33E-07	5.58E-07	7143.89	not significant
2785	TSR2	-1.13	9.40E-04	2.26E-03	1590.95	not significant
2786	PAAF1	-1.13	8.84E-03	1.75E-02	636.45	not significant
2787	GUCY1A3	-1.13	4.53E-03	9.59E-03	756.80	not significant
2788	ATG7	-1.13	1.38E-02	2.62E-02	498.59	not significant
2789	NUDT4	-1.13	1.62E-01	2.32E-01	63.46	not significant
2790	HIST1H2BF	-1.13	1.54E-01	2.21E-01	28.30	not significant
2791	ARMCX5	-1.13	6.02E-03	1.24E-02	652.74	not significant
2792	STMN3	-1.13	1.44E-06	5.36E-06	3516.78	not significant
2793	CCRL2	-1.13	7.60E-02	1.20E-01	192.49	not significant
2794	TRIB3	-1.13	5.94E-04	1.48E-03	1244.69	not significant
2795	MIS12	-1.13	4.22E-05	1.29E-04	1978.06	not significant
2796	RRP1	-1.13	2.10E-03	4.73E-03	915.26	not significant
2797	APOM	-1.13	1.64E-01	2.34E-01	38.70	not significant
2798	RIOK2	-1.13	3.56E-04	9.27E-04	1519.63	not significant
2799	HNRNPR	-1.13	2.86E-08	1.30E-07	19171.17	not significant
2800	DUSP19	-1.13	1.11E-01	1.67E-01	140.35	not significant
2801	STAG3	-1.13	2.39E-02	4.30E-02	426.26	not significant
2802	RAB7A	-1.13	3.52E-07	1.41E-06	8786.30	not significant
2803	DHFR	-1.13	8.50E-07	3.24E-06	4693.91	not significant
2804	FGGY	-1.13	6.72E-02	1.08E-01	229.14	not significant

2805	HCFC1R1	-1.13	2.60E-02	4.64E-02	432.40	not significant
2806	RAD51C	-1.13	2.22E-05	7.04E-05	2418.34	not significant
2807	LINC00659	-1.13	1.43E-01	2.09E-01	86.32	not significant
2808	NACC1	-1.13	4.97E-05	1.50E-04	5163.87	not significant
2809	TNRC6C-AS1	-1.13	9.30E-02	1.43E-01	171.19	not significant
2810	TOP2B	-1.13	2.06E-08	9.54E-08	15168.70	not significant
2811	RLIM	-1.13	7.58E-05	2.22E-04	2558.68	not significant
2812	SNTB1	-1.13	1.28E-01	1.90E-01	121.18	not significant
2813	NOL7	-1.13	1.66E-04	4.59E-04	1872.23	not significant
2814	UBE2J2	-1.13	4.10E-05	1.25E-04	2616.91	not significant
2815	TGM1	-1.13	1.67E-01	2.38E-01	38.15	not significant
2816	PEAK1	-1.13	2.12E-03	4.78E-03	1153.98	not significant
2817	PTGES3	-1.13	4.68E-06	1.63E-05	22235.66	not significant
2818	RIC8A	-1.13	1.15E-06	4.31E-06	3446.37	not significant
2819	THYN1	-1.13	5.21E-04	1.32E-03	1747.14	not significant
2820	RPL23	-1.13	1.49E-05	4.83E-05	20513.13	not significant
2821	MTFR1L	-1.13	9.90E-04	2.37E-03	1077.47	not significant
2822	ZC3H11A	-1.13	5.00E-08	2.22E-07	5526.11	not significant
2823	LOC101927021	-1.13	1.13E-01	1.69E-01	147.20	not significant
2824	PIM3	-1.13	8.34E-05	2.43E-04	2230.15	not significant
2825	SHOC2	-1.13	8.93E-05	2.58E-04	1967.40	not significant
2826	TMEM126B	-1.13	1.47E-03	3.41E-03	1061.33	not significant
2827	ERV3-1	-1.13	4.53E-02	7.62E-02	428.17	not significant
2828	NPIPB5	-1.13	1.25E-01	1.85E-01	144.10	not significant
2829	YIPF1	-1.13	4.06E-03	8.67E-03	825.35	not significant
2830	RHOG	-1.13	5.68E-05	1.70E-04	3886.21	not significant
2831	KIRREL	-1.13	1.03E-04	2.96E-04	1694.46	not significant
2832	CDC23	-1.13	1.94E-06	7.08E-06	3150.21	not significant
2833	TRIAP1	-1.13	5.50E-04	1.38E-03	1675.77	not significant
2834	ATP5F1	-1.13	7.72E-07	2.95E-06	6424.09	not significant
2835	FAM78A	-1.13	6.67E-04	1.65E-03	1365.87	not significant
2836	TAF9B	-1.13	3.48E-02	6.02E-02	346.42	not significant
2837	EIF1AX	-1.13	8.76E-06	2.93E-05	2625.95	not significant
2838	TMX2	-1.13	1.40E-05	4.56E-05	2465.07	not significant
2839	SPNS2	-1.13	1.61E-01	2.30E-01	89.96	not significant
2840	FNDC3B	-1.13	7.64E-02	1.21E-01	236.06	not significant
2841	APOL6	-1.13	3.93E-07	1.56E-06	5484.23	not significant
2842	GNPDA1	-1.13	3.85E-06	1.35E-05	3121.38	not significant
2843	C2orf44	-1.13	3.88E-04	1.00E-03	1495.75	not significant
2844	DENND1A	-1.13	1.50E-03	3.47E-03	983.33	not significant
2845	TMEM33	-1.13	9.11E-07	3.46E-06	3871.92	not significant
2846	MELK	-1.13	1.54E-06	5.71E-06	3999.38	not significant
2847	ALG6	-1.13	3.01E-04	7.93E-04	1426.10	not significant
2848	FRMPD2	-1.13	1.09E-01	1.64E-01	14.62	not significant
2849	GTF2A1	-1.13	1.50E-07	6.29E-07	4776.88	not significant
2850	CLTB	-1.12	7.53E-04	1.84E-03	1431.70	not significant
2851	SLAIN1	-1.12	4.65E-05	1.40E-04	2230.76	not significant
2852	RGCC	-1.12	5.20E-03	1.09E-02	771.71	not significant
2853	MRPL42	-1.12	2.40E-06	8.65E-06	3312.39	not significant
2854	STRBP	-1.12	2.36E-05	7.42E-05	3203.77	not significant
2855	ANAPC5	-1.12	1.64E-07	6.81E-07	5834.96	not significant
2856	PRPS1	-1.12	1.80E-05	5.77E-05	2913.84	not significant
2857	PIAS3	-1.12	1.02E-01	1.55E-01	166.91	not significant
2858	ARRDC4	-1.12	1.74E-01	2.46E-01	38.96	not significant
2859	EFR3A	-1.12	7.28E-08	3.15E-07	5541.93	not significant
2860	SSSCA1	-1.12	1.39E-02	2.64E-02	622.49	not significant
2861	CYTIP	-1.12	7.22E-02	1.15E-01	8.78	not significant
2862	CHST15	-1.12	5.71E-02	9.32E-02	8.08	not significant
2863	TBPL1	-1.12	4.73E-03	9.98E-03	834.87	not significant
2864	DPM2	-1.12	1.05E-03	2.50E-03	1114.95	not significant
2865	PREP	-1.12	3.83E-06	1.35E-05	2957.50	not significant
2866	C11orf96	-1.12	1.30E-01	1.91E-01	126.48	not significant
2867	C1orf174	-1.12	2.43E-04	6.51E-04	1481.22	not significant
2868	SERPINI1	-1.12	1.67E-01	2.38E-01	32.30	not significant
2869	BYSL	-1.12	6.40E-05	1.90E-04	2038.94	not significant
2870	APOL3	-1.12	4.51E-04	1.15E-03	1432.98	not significant
2871	TSPAN2	-1.12	5.54E-02	9.10E-02	267.18	not significant
2872	MIF4GD	-1.12	5.91E-04	1.47E-03	1390.03	not significant
2873	MREG	-1.12	8.82E-03	1.75E-02	650.50	not significant
2874	ARHGAP12	-1.12	1.23E-02	2.36E-02	591.90	not significant
2875	LINC01128	-1.12	2.09E-02	3.81E-02	482.16	not significant
2876	TMEM198B	-1.12	3.21E-02	5.61E-02	615.58	not significant
2877	GPS2	-1.12	5.51E-05	1.65E-04	2001.85	not significant
2878	RNF4	-1.12	1.59E-05	5.13E-05	3888.57	not significant
2879	TBL1X	-1.12	6.38E-05	1.89E-04	2273.88	not significant
2880	ATP13A1	-1.12	2.08E-05	6.60E-05	2861.01	not significant
2881	C6orf57	-1.12	7.22E-02	1.15E-01	236.40	not significant
2882	FDFT1	-1.12	9.37E-09	4.51E-08	15250.71	not significant
2883	COMMD7	-1.12	1.04E-04	2.96E-04	2083.04	not significant
2884	JMJD8	-1.12	1.01E-03	2.40E-03	1295.75	not significant
2885	HSD17B8	-1.12	5.34E-02	8.80E-02	296.15	not significant
2886	TMEM55A	-1.12	2.44E-02	4.39E-02	447.36	not significant
2887	WBSCR22	-1.12	7.61E-04	1.85E-03	1528.46	not significant
2888	RAP2C	-1.12	3.78E-04	9.81E-04	1652.27	not significant
2889	VARS2	-1.12	7.40E-04	1.81E-03	1224.64	not significant
2890	APOPT1	-1.12	3.88E-03	8.33E-03	986.54	not significant
2891	SH2D3A	-1.12	1.54E-01	2.22E-01	88.38	not significant
2892	MRPL38	-1.12	1.03E-04	2.95E-04	3078.11	not significant

2893	DNAAF2	-1.12	2.78E-02	4.94E-02	410.38	not significant
2894	CAPN15	-1.12	5.80E-06	1.99E-05	3133.14	not significant
2895	STAG3L5P	-1.12	1.51E-01	2.17E-01	20.48	not significant
2896	PLOD1	-1.12	2.97E-03	6.50E-03	891.83	not significant
2897	SLC44A1	-1.12	1.19E-02	2.29E-02	640.26	not significant
2898	IMPA1	-1.12	1.27E-04	3.57E-04	1816.99	not significant
2899	ATL2	-1.12	2.61E-06	9.36E-06	3391.85	not significant
2900	EXTL2	-1.12	3.86E-03	8.28E-03	891.66	not significant
2901	C6orf120	-1.12	1.77E-03	4.04E-03	1294.15	not significant
2902	TRAF3IP3	-1.12	4.94E-06	1.71E-05	3459.54	not significant
2903	OTOF	-1.12	8.30E-02	1.30E-01	9.57	not significant
2904	MAPK6	-1.12	1.38E-06	5.14E-06	3818.74	not significant
2905	DNAJA2	-1.12	3.58E-05	1.10E-04	3118.77	not significant
2906	ACBD6	-1.12	1.53E-04	4.26E-04	1774.14	not significant
2907	TGS1	-1.12	1.04E-05	3.44E-05	2970.07	not significant
2908	PURA	-1.12	9.67E-04	2.32E-03	1285.46	not significant
2909	ACTR3C	-1.12	1.25E-01	1.85E-01	17.04	not significant
2910	PYCRL	-1.12	6.77E-02	1.08E-01	354.04	not significant
2911	DEXI	-1.12	8.99E-03	1.78E-02	715.35	not significant
2912	DYNC1LI1	-1.12	1.20E-04	3.39E-04	2119.36	not significant
2913	PYROXD1	-1.12	4.23E-02	7.16E-02	364.72	not significant
2914	DHX16	-1.12	6.36E-03	1.30E-02	715.05	not significant
2915	EYA3	-1.12	4.44E-04	1.14E-03	1739.82	not significant
2916	PITRM1	-1.12	8.29E-06	2.78E-05	2900.93	not significant
2917	DHX33	-1.12	3.91E-05	1.20E-04	2743.75	not significant
2918	ERAL1	-1.12	1.87E-04	5.12E-04	1827.31	not significant
2919	TMEM44-AS1	-1.12	1.74E-01	2.46E-01	29.08	not significant
2920	SUV39H2	-1.12	8.58E-05	2.49E-04	1866.33	not significant
2921	RRP7A	-1.12	3.85E-06	1.35E-05	5927.62	not significant
2922	RIN1	-1.12	1.48E-01	2.15E-01	20.23	not significant
2923	CCNH	-1.12	5.02E-03	1.05E-02	843.38	not significant
2924	PIGF	-1.12	2.92E-02	5.16E-02	491.50	not significant
2925	ZMAT3	-1.12	2.30E-04	6.21E-04	3018.13	not significant
2926	URI1	-1.12	2.67E-06	9.56E-06	3487.94	not significant
2927	FAM83D	-1.12	3.12E-03	6.81E-03	1024.52	not significant
2928	SERAC1	-1.12	4.28E-02	7.22E-02	349.86	not significant
2929	IKBKAP	-1.12	4.87E-05	1.47E-04	2283.74	not significant
2930	EPRS	-1.12	2.54E-06	9.14E-06	6491.57	not significant
2931	BUB1B	-1.12	2.50E-06	9.00E-06	3992.37	not significant
2932	CENPI	-1.12	8.44E-03	1.68E-02	732.44	not significant
2933	PRPF3	-1.12	8.97E-02	1.39E-01	928.95	not significant
2934	NTHL1	-1.12	9.80E-03	1.93E-02	723.16	not significant
2935	ACTL6A	-1.12	1.34E-06	5.00E-06	3476.00	not significant
2936	FAM120B	-1.12	2.70E-04	7.19E-04	1757.52	not significant
2937	CMTM4	-1.12	1.70E-01	2.41E-01	78.16	not significant
2938	TMOD3	-1.12	6.16E-06	2.11E-05	3264.88	not significant
2939	PIK3R1	-1.12	3.34E-07	1.34E-06	5509.55	not significant
2940	CENPP	-1.12	8.83E-03	1.75E-02	702.46	not significant
2941	TLN1	-1.12	2.59E-02	4.63E-02	14904.83	not significant
2942	MCM7	-1.12	3.75E-10	2.08E-09	24102.62	not significant
2943	RNF166	-1.12	8.47E-04	2.05E-03	1337.82	not significant
2944	RPL36AL	-1.12	3.22E-04	8.44E-04	4202.49	not significant
2945	PRRC2C	-1.12	6.72E-02	1.08E-01	15743.40	not significant
2946	PLEC	-1.12	9.96E-02	1.52E-01	205.83	not significant
2947	PYCR2	-1.12	4.15E-06	1.45E-05	4524.35	not significant
2948	CASC14	-1.12	1.86E-01	2.60E-01	55.19	not significant
2949	MED26	-1.12	1.76E-02	3.27E-02	572.07	not significant
2950	PDHB	-1.12	1.15E-04	3.25E-04	2510.28	not significant
2951	STARD4	-1.12	2.32E-04	6.25E-04	1737.95	not significant
2952	MOB3C	-1.12	1.26E-01	1.87E-01	138.79	not significant
2953	PDCD6	-1.12	1.58E-04	4.39E-04	2590.76	not significant
2954	DEK	-1.12	2.05E-06	7.48E-06	18322.30	not significant
2955	GAPVD1	-1.12	3.89E-04	1.01E-03	2123.43	not significant
2956	EAF2	-1.12	1.68E-01	2.39E-01	82.17	not significant
2957	NOP14	-1.12	2.73E-07	1.11E-06	4713.03	not significant
2958	CEP70	-1.12	2.32E-05	7.32E-05	2513.23	not significant
2959	GPR160	-1.12	5.98E-02	9.72E-02	285.34	not significant
2960	SRSF10	-1.12	7.09E-04	1.74E-03	1406.08	not significant
2961	SCAMP3	-1.12	2.15E-03	4.84E-03	1356.46	not significant
2962	LOC653712	-1.12	1.56E-01	2.24E-01	20.13	not significant
2963	ASIC3	-1.12	1.88E-01	2.62E-01	49.01	not significant
2964	ZNF544	-1.12	1.13E-03	2.68E-03	1613.80	not significant
2965	EHD1	-1.12	1.29E-05	4.22E-05	3604.40	not significant
2966	CHEK2	-1.12	1.81E-03	4.12E-03	1096.32	not significant
2967	TMA16	-1.12	8.44E-04	2.05E-03	1440.07	not significant
2968	RAB14	-1.12	3.96E-05	1.21E-04	2429.99	not significant
2969	PIK3R4	-1.12	1.50E-04	4.19E-04	1870.47	not significant
2970	NME7	-1.12	3.53E-02	6.09E-02	432.02	not significant
2971	EDEM3	-1.12	1.71E-06	6.28E-06	4324.93	not significant
2972	TMCO1	-1.12	2.83E-06	1.01E-05	6439.54	not significant
2973	NSF	-1.12	3.42E-04	8.92E-04	1524.91	not significant
2974	PROSER1	-1.12	7.31E-07	2.81E-06	4875.72	not significant
2975	SMARCA2	-1.12	1.05E-01	1.59E-01	181.98	not significant
2976	LOH12CR1	-1.12	8.35E-02	1.30E-01	233.37	not significant
2977	ELOF1	-1.12	1.07E-03	2.54E-03	1373.38	not significant
2978	UTP18	-1.12	8.19E-05	2.38E-04	2513.16	not significant
2979	EMC6	-1.12	4.91E-03	1.03E-02	1195.45	not significant
2980	CDC26	-1.12	1.15E-01	1.72E-01	169.52	not significant

2981	XRRA1	-1.12	5.33E-03	1.11E-02	996.48	not significant
2982	CITED2	-1.12	1.46E-02	2.77E-02	581.05	not significant
2983	NBPF15	-1.12	1.81E-01	2.54E-01	27.67	not significant
2984	PPFIA3	-1.12	8.66E-02	1.35E-01	232.53	not significant
2985	INPP4A	-1.12	3.45E-05	1.06E-04	2936.99	not significant
2986	43709_19983	-1.12	5.20E-07	2.04E-06	6758.31	not significant
2987	NT5C3B	-1.12	1.45E-02	2.75E-02	741.77	not significant
2988	PRMT6	-1.12	1.97E-03	4.46E-03	1218.92	not significant
2989	C17orf75	-1.12	2.30E-03	5.14E-03	1248.91	not significant
2990	C21orf67	-1.12	1.22E-01	1.82E-01	157.02	not significant
2991	NABP2	-1.12	1.29E-04	3.62E-04	2591.30	not significant
2992	DPAGT1	-1.12	4.77E-04	1.21E-03	1573.92	not significant
2993	TNFAIP1	-1.12	1.66E-01	2.37E-01	95.44	not significant
2994	RAD23A	-1.12	1.06E-06	4.00E-06	5086.37	not significant
2995	SOD1	-1.12	3.31E-05	1.02E-04	7795.55	not significant
2996	RBM3	-1.12	1.58E-04	4.38E-04	2006.55	not significant
2997	DNTTIP1	-1.12	1.13E-03	2.68E-03	1355.24	not significant
2998	FAM35A	-1.12	1.85E-03	4.20E-03	1297.76	not significant
2999	CDCA4	-1.12	1.15E-04	3.27E-04	2277.50	not significant
3000	F3	-1.12	1.19E-01	1.77E-01	12.78	not significant
3001	IDH3B	-1.12	3.07E-05	9.52E-05	3280.39	not significant
3002	TFDP1	-1.12	4.95E-07	1.94E-06	11113.99	not significant
3003	GUCA1B	-1.12	1.80E-01	2.54E-01	83.51	not significant
3004	ANGEL1	-1.12	7.22E-03	1.46E-02	805.14	not significant
3005	ANP32A	-1.12	3.11E-06	1.11E-05	7469.17	not significant
3006	TMEM128	-1.12	2.02E-02	3.71E-02	548.68	not significant
3007	JUNB	-1.12	1.79E-04	4.93E-04	2545.84	not significant
3008	TOM1	-1.12	5.16E-03	1.08E-02	866.01	not significant
3009	FBXO41	-1.12	4.78E-04	1.22E-03	2536.12	not significant
3010	TEX261	-1.12	5.09E-02	8.44E-02	384.26	not significant
3011	SLC20A2	-1.12	3.85E-04	9.96E-04	1798.50	not significant
3012	PSMD6-AS2	-1.12	1.98E-01	2.74E-01	47.22	not significant
3013	RNF157	-1.12	9.74E-06	3.24E-05	3501.66	not significant
3014	P4HA1	-1.12	4.73E-04	1.21E-03	1727.56	not significant
3015	USP25	-1.12	2.82E-05	8.79E-05	2772.73	not significant
3016	PARG	-1.12	8.98E-03	1.78E-02	784.13	not significant
3017	MYADM	-1.12	1.40E-03	3.27E-03	1394.17	not significant
3018	CCZ1	-1.12	1.60E-01	2.29E-01	112.32	not significant
3019	ALDH3A2	-1.12	1.31E-01	1.93E-01	14.77	not significant
3020	FAM200A	-1.12	4.07E-02	6.90E-02	389.41	not significant
3021	SF3A3	-1.12	1.03E-06	3.90E-06	6968.80	not significant
3022	TOLLIP-AS1	-1.12	1.71E-01	2.42E-01	23.54	not significant
3023	ANKRD40	-1.12	6.63E-05	1.96E-04	3057.80	not significant
3024	SPTA1	-1.12	5.72E-02	9.34E-02	350.74	not significant
3025	COX19	-1.12	2.14E-03	4.80E-03	1451.90	not significant
3026	PPP4C	-1.12	8.28E-06	2.78E-05	4622.62	not significant
3027	LOC100419583	-1.12	1.32E-02	2.53E-02	672.38	not significant
3028	INAFM2	-1.12	5.86E-02	9.55E-02	315.54	not significant
3029	SLC25A25-AS1	-1.12	1.21E-01	1.80E-01	248.45	not significant
3030	TUBGCP2	-1.12	6.79E-05	2.00E-04	2361.72	not significant
3031	BRWD3	-1.12	1.18E-02	2.28E-02	761.53	not significant
3032	TTC21A	-1.12	1.07E-01	1.61E-01	10.80	not significant
3033	CAMTA1	-1.12	9.35E-03	1.85E-02	769.65	not significant
3034	ARV1	-1.12	1.07E-02	2.08E-02	754.54	not significant
3035	YIF1B	-1.12	1.80E-03	4.09E-03	1645.80	not significant
3036	EML4	-1.12	2.35E-04	6.33E-04	2500.23	not significant
3037	RBM33	-1.12	1.68E-04	4.65E-04	4504.27	not significant
3038	STXBP2	-1.11	5.62E-04	1.41E-03	1486.51	not significant
3039	PDE12	-1.11	2.15E-04	5.82E-04	1981.25	not significant
3040	NUP155	-1.11	3.92E-05	1.20E-04	2701.64	not significant
3041	DBT	-1.11	3.43E-03	7.43E-03	1186.83	not significant
3042	SORBS2	-1.11	1.08E-01	1.63E-01	191.72	not significant
3043	CSGALNACT1	-1.11	1.11E-01	1.67E-01	11.28	not significant
3044	SNRPB2	-1.11	2.86E-05	8.91E-05	4070.62	not significant
3045	PIK3R2	-1.11	2.23E-04	6.03E-04	1959.21	not significant
3046	UBE4A	-1.11	1.39E-03	3.25E-03	1385.65	not significant
3047	PFKFB1	-1.11	1.71E-01	2.42E-01	21.52	not significant
3048	IL20RB	-1.11	1.99E-01	2.75E-01	39.91	not significant
3049	FH	-1.11	6.98E-05	2.05E-04	2700.13	not significant
3050	ADA	-1.11	8.26E-08	3.56E-07	23796.17	not significant
3051	CHCHD7	-1.11	6.49E-04	1.60E-03	1708.62	not significant
3052	HTT	-1.11	3.06E-04	8.06E-04	3924.41	not significant
3053	ADAM19	-1.11	3.04E-06	1.08E-05	4519.17	not significant
3054	UBXN2B	-1.11	1.89E-04	5.16E-04	2141.74	not significant
3055	PRR14	-1.11	7.15E-04	1.75E-03	1763.26	not significant
3056	PTPN12	-1.11	2.02E-01	2.79E-01	59.53	not significant
3057	SNHG17	-1.11	2.13E-02	3.89E-02	551.65	not significant
3058	LRP8	-1.11	1.07E-03	2.54E-03	2618.19	not significant
3059	NNT	-1.11	8.83E-07	3.36E-06	6470.76	not significant
3060	PCID2	-1.11	4.84E-05	1.46E-04	2480.63	not significant
3061	MAP6D1	-1.11	2.03E-01	2.81E-01	53.25	not significant
3062	CRIPAK	-1.11	1.40E-01	2.04E-01	165.95	not significant
3063	RRBP1	-1.11	7.21E-03	1.46E-02	884.88	not significant
3064	WDR53	-1.11	3.16E-02	5.52E-02	455.57	not significant
3065	SNRNP25	-1.11	6.38E-04	1.58E-03	1659.87	not significant
3066	CSRP2BP	-1.11	2.91E-03	6.39E-03	1086.26	not significant
3067	COMTD1	-1.11	1.05E-01	1.60E-01	245.55	not significant
3068	TMEM109	-1.11	9.43E-06	3.14E-05	5032.36	not significant

3069	FLOT1	-1.11	1.13E-03	2.69E-03	1457.40	not significant
3070	SSRP1	-1.11	3.92E-07	1.56E-06	14450.57	not significant
3071	PDCD2L	-1.11	5.94E-02	9.66E-02	353.41	not significant
3072	METTL13	-1.11	8.23E-04	2.00E-03	2305.26	not significant
3073	NBEAL1	-1.11	1.06E-01	1.61E-01	264.01	not significant
3074	TRIM62	-1.11	2.50E-02	4.48E-02	528.32	not significant
3075	ZNF281	-1.11	1.33E-03	3.12E-03	1351.85	not significant
3076	MON1B	-1.11	5.53E-04	1.39E-03	1641.69	not significant
3077	CD82	-1.11	5.32E-05	1.59E-04	5335.33	not significant
3078	CDKL1	-1.11	1.36E-01	1.99E-01	157.61	not significant
3079	HRAS	-1.11	1.42E-02	2.70E-02	748.19	not significant
3080	GIN1	-1.11	2.02E-01	2.79E-01	34.37	not significant
3081	LOC643387	-1.11	9.71E-02	1.49E-01	10.80	not significant
3082	LRWD1	-1.11	8.01E-04	1.95E-03	1486.40	not significant
3083	GSTCD	-1.11	4.10E-03	8.74E-03	1038.51	not significant
3084	OAS2	-1.11	5.46E-06	1.87E-05	3700.43	not significant
3085	POU3F2	-1.11	3.49E-02	6.03E-02	458.54	not significant
3086	TBCK	-1.11	8.14E-03	1.63E-02	895.93	not significant
3087	TXNDC12	-1.11	1.07E-05	3.54E-05	3578.03	not significant
3088	LSG1	-1.11	2.67E-04	7.11E-04	2504.98	not significant
3089	MAP2K1	-1.11	5.38E-04	1.35E-03	2110.87	not significant
3090	WDR83	-1.11	3.20E-02	5.59E-02	486.44	not significant
3091	C14orf119	-1.11	1.31E-03	3.06E-03	1347.10	not significant
3092	ESYT1	-1.11	1.47E-07	6.16E-07	10218.63	not significant
3093	ESD	-1.11	8.59E-05	2.49E-04	5782.03	not significant
3094	SLC25A22	-1.11	1.22E-03	2.88E-03	1461.04	not significant
3095	KLC1	-1.11	3.14E-05	9.72E-05	3141.08	not significant
3096	IFT20	-1.11	1.44E-01	2.10E-01	147.45	not significant
3097	GLRX	-1.11	1.11E-03	2.64E-03	1483.97	not significant
3098	TSKU	-1.11	1.05E-01	1.60E-01	209.83	not significant
3099	MAP2K6	-1.11	2.66E-02	4.74E-02	539.72	not significant
3100	AGFG1	-1.11	4.50E-05	1.36E-04	3320.69	not significant
3101	NCLN	-1.11	6.26E-05	1.86E-04	3911.90	not significant
3102	EDRF1	-1.11	5.45E-03	1.13E-02	1442.94	not significant
3103	APOBEC3C	-1.11	2.46E-04	6.59E-04	2026.60	not significant
3104	MMP14	-1.11	2.05E-01	2.83E-01	35.73	not significant
3105	MSL3P1	-1.11	2.60E-02	4.65E-02	579.04	not significant
3106	TSEN15	-1.11	5.78E-05	1.72E-04	2541.18	not significant
3107	TMEM200A	-1.11	1.46E-01	2.11E-01	146.29	not significant
3108	CHCHD3	-1.11	1.03E-05	3.41E-05	4965.91	not significant
3109	RARRES3	-1.11	4.17E-03	8.89E-03	1045.77	not significant
3110	AOC2	-1.11	2.06E-01	2.83E-01	33.27	not significant
3111	PCF11	-1.11	1.04E-04	2.96E-04	3366.20	not significant
3112	NOC4L	-1.11	2.20E-03	4.94E-03	1288.69	not significant
3113	SLBP	-1.11	1.46E-05	4.74E-05	7488.27	not significant
3114	PIN1	-1.11	2.56E-04	6.85E-04	2713.49	not significant
3115	HCFC1	-1.11	1.19E-03	2.81E-03	2568.33	not significant
3116	DAAM1	-1.11	3.27E-02	5.70E-02	503.59	not significant
3117	COPS7B	-1.11	9.76E-05	2.81E-04	2844.60	not significant
3118	GPR180	-1.11	6.27E-04	1.56E-03	1724.13	not significant
3119	DNM2	-1.11	1.66E-07	6.92E-07	8172.96	not significant
3120	OTUD5	-1.11	2.07E-02	3.78E-02	611.77	not significant
3121	GFM1	-1.11	1.73E-04	4.79E-04	2354.62	not significant
3122	MSH6	-1.11	2.15E-06	7.79E-06	4618.70	not significant
3123	GTF2B	-1.11	1.58E-03	3.64E-03	1576.10	not significant
3124	C16orf91	-1.11	3.86E-02	6.60E-02	453.93	not significant
3125	ANKRD44	-1.11	6.77E-03	1.38E-02	922.99	not significant
3126	PPM1F	-1.11	7.68E-04	1.87E-03	1869.93	not significant
3127	SENCR	-1.11	1.38E-01	2.02E-01	13.32	not significant
3128	NOM1	-1.11	4.93E-04	1.25E-03	2016.76	not significant
3129	ARRB1	-1.11	2.63E-04	7.02E-04	2474.75	not significant
3130	NDUFS8	-1.11	2.40E-04	6.46E-04	2070.61	not significant
3131	FUNDC1	-1.11	2.83E-02	5.01E-02	586.34	not significant
3132	ZMYM1	-1.11	1.14E-02	2.22E-02	876.01	not significant
3133	BTN1A1	-1.11	9.38E-02	1.44E-01	9.69	not significant
3134	PNLDC1	-1.11	1.30E-01	1.92E-01	12.57	not significant
3135	SRP19	-1.11	9.11E-04	2.19E-03	1622.63	not significant
3136	NAPA	-1.11	3.33E-04	8.72E-04	2618.49	not significant
3137	AGAP5	-1.11	2.14E-01	2.93E-01	49.22	not significant
3138	LARP4B	-1.11	1.66E-06	6.13E-06	5147.05	not significant
3139	TTLL4	-1.11	5.69E-04	1.42E-03	1870.91	not significant
3140	SNX18	-1.11	6.46E-02	1.04E-01	384.33	not significant
3141	IPPK	-1.11	5.62E-02	9.20E-02	374.15	not significant
3142	FAM53C	-1.11	7.24E-04	1.77E-03	1700.88	not significant
3143	ATP2A2	-1.11	4.06E-07	1.61E-06	11072.17	not significant
3144	BCORL1	-1.11	5.53E-03	1.15E-02	1245.80	not significant
3145	UBC	-1.11	6.97E-05	2.05E-04	13186.41	not significant
3146	LOC339803	-1.11	1.02E-01	1.55E-01	237.74	not significant
3147	WDR36	-1.11	2.97E-05	9.22E-05	3144.64	not significant
3148	DEDD	-1.11	7.26E-04	1.78E-03	1838.06	not significant
3149	GRAP	-1.11	2.08E-03	4.69E-03	1328.64	not significant
3150	EIF4G2	-1.11	1.99E-07	8.19E-07	51470.27	not significant
3151	SMC5	-1.11	3.57E-05	1.10E-04	4099.00	not significant
3152	RPS6KC1	-1.11	2.02E-02	3.70E-02	618.91	not significant
3153	TNIP2	-1.11	1.15E-02	2.24E-02	1118.84	not significant
3154	DPM3	-1.11	7.39E-02	1.17E-01	330.12	not significant
3155	MRRF	-1.11	2.82E-02	5.00E-02	615.84	not significant
3156	FAM210A	-1.11	2.38E-03	5.29E-03	1265.89	not significant

3157	PIGW	-1.11	1.72E-01	2.44E-01	18.74	not significant
3158	PTCD3	-1.11	2.48E-04	6.65E-04	5088.48	not significant
3159	LOC285484	-1.11	1.49E-01	2.15E-01	14.98	not significant
3160	WRNIP1	-1.11	2.03E-04	5.54E-04	3472.39	not significant
3161	UBA3	-1.11	1.60E-03	3.68E-03	1548.14	not significant
3162	IPO4	-1.11	4.38E-04	1.12E-03	2168.27	not significant
3163	ILKAP	-1.11	2.21E-03	4.95E-03	1361.58	not significant
3164	C2orf76	-1.11	1.09E-01	1.64E-01	243.87	not significant
3165	ACAA2	-1.11	4.51E-05	1.37E-04	3355.57	not significant
3166	USO1	-1.11	1.75E-04	4.82E-04	3180.78	not significant
3167	ATRAID	-1.11	7.24E-04	1.77E-03	1945.33	not significant
3168	CSTB	-1.11	2.00E-03	4.51E-03	2070.11	not significant
3169	C17orf51	-1.11	1.94E-01	2.69E-01	22.43	not significant
3170	MTX2	-1.11	7.90E-03	1.59E-02	1066.26	not significant
3171	CROCC	-1.11	1.18E-02	2.27E-02	868.95	not significant
3172	ZGLP1	-1.11	2.21E-01	3.01E-01	43.03	not significant
3173	MCPH1	-1.11	1.72E-03	3.93E-03	1528.41	not significant
3174	EXOSC10	-1.11	4.69E-04	1.20E-03	3461.81	not significant
3175	RDH11	-1.11	1.68E-05	5.41E-05	3983.56	not significant
3176	CWC15	-1.11	1.63E-02	3.05E-02	701.31	not significant
3177	COPRS	-1.11	1.22E-02	2.34E-02	835.73	not significant
3178	FAM91A1	-1.11	5.35E-04	1.35E-03	3104.68	not significant
3179	C11orf24	-1.11	1.03E-01	1.57E-01	241.74	not significant
3180	C2orf42	-1.11	7.04E-02	1.12E-01	362.07	not significant
3181	CHPT1	-1.11	9.92E-03	1.95E-02	881.53	not significant
3182	TRMT61B	-1.11	5.14E-02	8.51E-02	402.40	not significant
3183	XPO7	-1.11	4.19E-06	1.47E-05	4731.19	not significant
3184	MCCC2	-1.11	2.63E-03	5.82E-03	1271.57	not significant
3185	PLAGL2	-1.11	7.43E-05	2.18E-04	4783.89	not significant
3186	SRSF7	-1.11	7.56E-08	3.27E-07	9895.57	not significant
3187	SMIM8	-1.11	5.45E-02	8.97E-02	387.92	not significant
3188	BAZ1A	-1.11	1.70E-05	5.47E-05	5738.36	not significant
3189	RRP15	-1.11	4.05E-03	8.65E-03	1317.89	not significant
3190	UBAP1	-1.11	7.96E-04	1.93E-03	1705.58	not significant
3191	UFSP2	-1.11	1.49E-02	2.81E-02	755.09	not significant
3192	URB1	-1.11	4.81E-03	1.01E-02	2237.52	not significant
3193	LOC100506990	-1.11	1.18E-01	1.76E-01	220.67	not significant
3194	NPPA-AS1	-1.11	1.73E-01	2.45E-01	17.77	not significant
3195	TMEM223	-1.11	5.27E-02	8.70E-02	480.52	not significant
3196	TUFM	-1.11	4.60E-05	1.39E-04	7973.73	not significant
3197	ANKRD26	-1.11	4.22E-03	8.97E-03	1126.08	not significant
3198	YWHAZ	-1.11	1.07E-07	4.56E-07	36086.92	not significant
3199	ACAD9	-1.11	7.05E-04	1.73E-03	1817.25	not significant
3200	LOC101927919	-1.11	1.76E-01	2.49E-01	21.21	not significant
3201	LINC00116	-1.11	1.75E-01	2.47E-01	138.03	not significant
3202	SURF1	-1.11	5.32E-02	8.78E-02	429.27	not significant
3203	ST6GALNAC4	-1.11	2.05E-01	2.83E-01	89.62	not significant
3204	PRKAR1B	-1.11	4.12E-04	1.06E-03	3162.25	not significant
3205	BLVRB	-1.11	2.02E-01	2.79E-01	97.57	not significant
3206	C1QL1	-1.11	2.25E-01	3.06E-01	45.49	not significant
3207	ARHGEF7	-1.11	2.12E-04	5.75E-04	3063.38	not significant
3208	ADPRHL1	-1.11	2.22E-01	3.02E-01	34.09	not significant
3209	DRG1	-1.11	1.48E-03	3.43E-03	2474.62	not significant
3210	SAMD4A	-1.11	1.48E-01	2.14E-01	13.02	not significant
3211	C12orf29	-1.11	1.62E-03	3.72E-03	1444.65	not significant
3212	SOCS2-AS1	-1.11	2.17E-01	2.96E-01	75.86	not significant
3213	RPS6KB1	-1.11	1.01E-04	2.90E-04	4047.48	not significant
3214	ECD	-1.11	3.92E-03	8.40E-03	1255.13	not significant
3215	PARK7	-1.11	4.86E-04	1.23E-03	4482.60	not significant
3216	KLHL3	-1.11	2.89E-02	5.10E-02	628.30	not significant
3217	43723_1041	-1.11	2.03E-05	6.45E-05	6768.24	not significant
3218	GNAS	-1.11	4.20E-07	1.67E-06	25838.85	not significant
3219	NLGN4X	-1.11	1.02E-01	1.55E-01	272.47	not significant
3220	SNX19	-1.11	4.56E-05	1.38E-04	3256.49	not significant
3221	MRGBP	-1.11	3.42E-03	7.41E-03	1297.94	not significant
3222	PFDN1	-1.11	5.68E-04	1.42E-03	2305.11	not significant
3223	NDC80	-1.11	2.39E-04	6.42E-04	2954.07	not significant
3224	NADK	-1.11	1.47E-04	4.11E-04	2802.01	not significant
3225	THAP5	-1.11	1.93E-03	4.36E-03	1558.05	not significant
3226	BCDIN3D	-1.11	1.03E-01	1.56E-01	270.56	not significant
3227	ZDHHC16	-1.11	1.74E-03	3.97E-03	1670.04	not significant
3228	MYL12B	-1.11	2.45E-05	7.70E-05	8213.46	not significant
3229	IRAK3	-1.10	9.79E-02	1.50E-01	8.46	not significant
3230	NET1	-1.10	6.10E-04	1.52E-03	3180.28	not significant
3231	HIST1H2BG	-1.10	1.75E-01	2.47E-01	16.15	not significant
3232	FEZ2	-1.10	2.29E-02	4.15E-02	663.81	not significant
3233	LINC00341	-1.10	1.90E-01	2.65E-01	116.82	not significant
3234	AP5M1	-1.10	2.34E-04	6.31E-04	2537.02	not significant
3235	ARPC4	-1.10	4.06E-04	1.05E-03	3121.31	not significant
3236	NBPF10	-1.10	2.30E-01	3.11E-01	61.65	not significant
3237	ATP2A3	-1.10	6.55E-06	2.23E-05	17755.17	not significant
3238	ZNRD1-AS1	-1.10	1.90E-01	2.65E-01	20.52	not significant
3239	MLLT1	-1.10	9.68E-06	3.22E-05	5148.26	not significant
3240	NCK1-AS1	-1.10	2.10E-01	2.88E-01	93.13	not significant
3241	YIPF5	-1.10	2.79E-03	6.14E-03	1304.87	not significant
3242	PRUNE2	-1.10	2.65E-02	4.72E-02	866.07	not significant
3243	SAMM50	-1.10	1.18E-03	2.78E-03	1974.39	not significant
3244	RAPGEF6	-1.10	1.46E-03	3.39E-03	1788.17	not significant

3245	FLJ38122	-1.10	1.86E-01	2.60E-01	130.40	not significant
3246	GNAI3	-1.10	1.31E-04	3.68E-04	5259.71	not significant
3247	U2SURP	-1.10	4.48E-05	1.36E-04	8670.72	not significant
3248	RBM25	-1.10	1.48E-04	4.14E-04	6486.03	not significant
3249	GMEB2	-1.10	4.66E-03	9.84E-03	1253.55	not significant
3250	TTC26	-1.10	2.54E-02	4.54E-02	627.48	not significant
3251	C9orf172	-1.10	1.88E-01	2.63E-01	18.33	not significant
3252	ALS2CR12	-1.10	1.13E-01	1.69E-01	9.97	not significant
3253	DGKE	-1.10	1.43E-01	2.08E-01	1933.47	not significant
3254	CHMP1A	-1.10	3.47E-04	9.04E-04	3124.40	not significant
3255	BAIAP2-AS1	-1.10	7.30E-02	1.16E-01	352.27	not significant
3256	TPM3P9	-1.10	1.33E-02	2.54E-02	852.30	not significant
3257	PIK3CB	-1.10	1.71E-03	3.92E-03	1534.36	not significant
3258	MIR17HG	-1.10	2.36E-01	3.18E-01	288.54	not significant
3259	TMSB4X	-1.10	2.24E-04	6.04E-04	40361.32	not significant
3260	DTWD2	-1.10	4.39E-02	7.40E-02	530.31	not significant
3261	DNMT1	-1.10	2.76E-04	7.32E-04	16503.48	not significant
3262	TRIM52-AS1	-1.10	5.77E-02	9.43E-02	461.79	not significant
3263	TXN2	-1.10	2.23E-04	6.03E-04	2695.22	not significant
3264	SCYL3	-1.10	5.17E-02	8.55E-02	475.96	not significant
3265	LOC100505549	-1.10	9.65E-02	1.48E-01	324.76	not significant
3266	CPEB4	-1.10	7.66E-02	1.21E-01	345.53	not significant
3267	SLC7A5P1	-1.10	2.40E-01	3.22E-01	48.14	not significant
3268	RAB5A	-1.10	1.58E-03	3.65E-03	1875.68	not significant
3269	NCKIPSD	-1.10	1.08E-02	2.10E-02	958.69	not significant
3270	PCBP1	-1.10	4.85E-06	1.68E-05	13158.05	not significant
3271	ZNF232	-1.10	4.42E-02	7.44E-02	586.86	not significant
3272	ADSL	-1.10	2.65E-04	7.06E-04	4470.45	not significant
3273	PTP4A1	-1.10	1.15E-05	3.78E-05	7067.64	not significant
3274	ELMOD3	-1.10	3.46E-02	5.99E-02	560.44	not significant
3275	MAP3K4	-1.10	2.17E-03	4.88E-03	1536.22	not significant
3276	PEF1	-1.10	9.72E-04	2.33E-03	2144.64	not significant
3277	HLA-G	-1.10	1.08E-01	1.63E-01	8.85	not significant
3278	AAR2	-1.10	5.02E-04	1.27E-03	2637.61	not significant
3279	C10orf91	-1.10	2.04E-01	2.81E-01	20.62	not significant
3280	POC5	-1.10	1.89E-02	3.48E-02	846.38	not significant
3281	C9orf64	-1.10	1.64E-02	3.07E-02	848.51	not significant
3282	LAPTM5	-1.10	4.70E-06	1.63E-05	13234.32	not significant
3283	MAGT1	-1.10	3.49E-02	6.03E-02	562.27	not significant
3284	EPDR1	-1.10	9.62E-03	1.89E-02	1143.71	not significant
3285	CPOX	-1.10	8.42E-03	1.68E-02	1223.97	not significant
3286	NUFIP2	-1.10	3.42E-02	5.93E-02	7152.85	not significant
3287	RPTOR	-1.10	1.08E-05	3.56E-05	7475.39	not significant
3288	SOCS7	-1.10	1.61E-01	2.31E-01	175.60	not significant
3289	KCNQ1OT1	-1.10	2.40E-01	3.23E-01	36.62	not significant
3290	TRPM7	-1.10	1.49E-05	4.85E-05	5058.59	not significant
3291	ANGEL2	-1.10	8.60E-03	1.71E-02	1201.97	not significant
3292	HERPUD1	-1.10	1.25E-03	2.93E-03	1831.44	not significant
3293	URB2	-1.10	7.27E-04	1.78E-03	2159.05	not significant
3294	RP9	-1.10	6.40E-02	1.03E-01	461.77	not significant
3295	PRRT2	-1.10	1.10E-01	1.65E-01	8.99	not significant
3296	VMP1	-1.10	6.41E-04	1.59E-03	3091.06	not significant
3297	ALMS1	-1.10	1.72E-03	3.92E-03	2522.71	not significant
3298	PDXK	-1.10	8.26E-03	1.65E-02	1068.87	not significant
3299	IFIT3	-1.10	3.72E-02	6.39E-02	597.05	not significant
3300	CBX4	-1.10	1.43E-03	3.33E-03	2476.95	not significant
3301	MMADHC	-1.10	6.26E-04	1.55E-03	2258.09	not significant
3302	ACTA2	-1.10	2.42E-01	3.25E-01	37.59	not significant
3303	KXD1	-1.10	2.92E-04	7.71E-04	2890.74	not significant
3304	WIPI1	-1.10	1.51E-01	2.18E-01	202.38	not significant
3305	CUL4A	-1.10	3.99E-05	1.22E-04	4037.75	not significant
3306	DIS3	-1.10	1.06E-04	3.01E-04	3255.20	not significant
3307	CRLF3	-1.10	3.18E-04	8.35E-04	2520.56	not significant
3308	GPBP1	-1.10	1.77E-04	4.88E-04	4828.22	not significant
3309	B3GNT9	-1.10	2.33E-01	3.15E-01	90.15	not significant
3310	KLHL12	-1.10	2.52E-03	5.59E-03	1680.82	not significant
3311	SNHG16	-1.10	2.18E-03	4.89E-03	1695.62	not significant
3312	ACY1	-1.10	1.77E-01	2.49E-01	16.22	not significant
3313	COPE	-1.10	7.54E-05	2.21E-04	4986.75	not significant
3314	MYH9	-1.10	1.47E-01	2.13E-01	20782.64	not significant
3315	ZNF438	-1.10	6.43E-02	1.04E-01	476.54	not significant
3316	ANXA5	-1.10	7.23E-05	2.12E-04	4209.07	not significant
3317	TFAP4	-1.10	1.11E-02	2.16E-02	943.19	not significant
3318	MAPK8IP2	-1.10	2.03E-01	2.81E-01	18.85	not significant
3319	DGCR6	-1.10	1.97E-01	2.73E-01	20.02	not significant
3320	NEXN	-1.10	1.17E-03	2.77E-03	2008.31	not significant
3321	GMEB1	-1.10	3.08E-02	5.40E-02	620.72	not significant
3322	KIDINS220	-1.10	1.29E-05	4.23E-05	4650.31	not significant
3323	LINC01260	-1.10	1.45E-02	2.74E-02	857.33	not significant
3324	AQR	-1.10	1.79E-03	4.08E-03	2355.96	not significant
3325	CEP63	-1.10	2.63E-03	5.82E-03	1712.66	not significant
3326	TRMT44	-1.10	8.11E-02	1.27E-01	382.01	not significant
3327	TDP1	-1.10	6.26E-04	1.55E-03	2848.78	not significant
3328	ABR	-1.10	7.36E-04	1.80E-03	2209.19	not significant
3329	ELOVL1	-1.10	1.45E-03	3.37E-03	1852.68	not significant
3330	CYB561A3	-1.10	4.58E-03	9.69E-03	2448.33	not significant
3331	GLO1	-1.10	5.15E-05	1.55E-04	8536.10	not significant
3332	COPB1	-1.10	2.48E-06	8.93E-06	7150.05	not significant

3333	POLR2K	-1.10	4.20E-04	1.08E-03	2687.23	not significant
3334	LRRCC1	-1.10	8.70E-04	2.10E-03	2202.56	not significant
3335	C6orf136	-1.10	1.86E-01	2.60E-01	164.35	not significant
3336	DST	-1.10	1.69E-01	2.40E-01	13.54	not significant
3337	UQCRC2	-1.10	9.48E-05	2.73E-04	8986.81	not significant
3338	UGGT1	-1.10	3.40E-05	1.05E-04	6129.78	not significant
3339	ARL1	-1.10	5.94E-04	1.48E-03	2197.33	not significant
3340	MORF4L1	-1.10	2.74E-05	8.55E-05	5193.56	not significant
3341	COG7	-1.10	4.29E-02	7.24E-02	666.01	not significant
3342	UFSP1	-1.10	1.81E-01	2.54E-01	14.52	not significant
3343	ELP5	-1.10	3.05E-03	6.66E-03	2637.83	not significant
3344	FAM213B	-1.10	1.32E-02	2.53E-02	1194.85	not significant
3345	SMU1	-1.10	2.18E-04	5.91E-04	3568.74	not significant
3346	SLC35B1	-1.10	9.47E-03	1.87E-02	1074.35	not significant
3347	PSMF1	-1.10	3.14E-05	9.74E-05	6977.45	not significant
3348	CDYL	-1.10	1.40E-02	2.67E-02	909.62	not significant
3349	GNG2	-1.10	2.49E-06	8.96E-06	12329.85	not significant
3350	C3orf58	-1.10	5.33E-02	8.80E-02	504.16	not significant
3351	DIP2B	-1.10	6.14E-04	1.53E-03	3737.15	not significant
3352	BTBD3	-1.10	1.91E-02	3.52E-02	892.31	not significant
3353	MRPL54	-1.10	3.07E-02	5.39E-02	851.02	not significant
3354	SHFM1	-1.10	9.40E-03	1.86E-02	2145.98	not significant
3355	SRI	-1.10	7.50E-04	1.83E-03	2747.48	not significant
3356	PPP1R15B	-1.10	8.33E-05	2.42E-04	4438.34	not significant
3357	GUF1	-1.10	8.57E-04	2.07E-03	2378.64	not significant
3358	CUEDC1	-1.10	2.56E-01	3.41E-01	39.15	not significant
3359	CD80	-1.10	2.24E-01	3.05E-01	22.74	not significant
3360	VIMP	-1.10	1.91E-02	3.52E-02	849.45	not significant
3361	43717_21856	-1.10	2.07E-05	6.59E-05	55293.88	not significant
3362	KIN	-1.10	2.73E-02	4.86E-02	742.23	not significant
3363	CHMP7	-1.10	9.64E-04	2.31E-03	2928.10	not significant
3364	ZKSCAN5	-1.10	8.41E-03	1.68E-02	1318.20	not significant
3365	SLC25A17	-1.10	3.10E-03	6.78E-03	1539.40	not significant
3366	PPP4R1L	-1.10	2.36E-01	3.18E-01	28.27	not significant
3367	RNF126	-1.10	7.92E-04	1.93E-03	2455.15	not significant
3368	ATP5O	-1.10	6.32E-05	1.88E-04	5019.20	not significant
3369	RSG1	-1.10	2.49E-01	3.32E-01	80.54	not significant
3370	DIEXF	-1.10	9.43E-03	1.86E-02	1158.97	not significant
3371	CASP6	-1.10	2.13E-02	3.88E-02	1158.27	not significant
3372	NSL1	-1.10	3.46E-04	9.03E-04	2848.39	not significant
3373	IQCG	-1.10	2.32E-01	3.13E-01	97.82	not significant
3374	LOC100506136	-1.10	1.64E-01	2.34E-01	11.95	not significant
3375	MDM2	-1.10	2.30E-04	6.19E-04	5360.10	not significant
3376	TM9SF2	-1.10	4.44E-05	1.35E-04	6451.39	not significant
3377	METTL6	-1.10	2.79E-02	4.95E-02	816.18	not significant
3378	PEBP1	-1.10	2.30E-04	6.20E-04	9512.14	not significant
3379	YME1L1	-1.10	1.39E-05	4.53E-05	9789.72	not significant
3380	SLC35A2	-1.10	2.61E-01	3.47E-01	53.94	not significant
3381	TTLL5	-1.10	7.17E-03	1.45E-02	1397.09	not significant
3382	SYNGAP1	-1.10	1.37E-01	2.01E-01	311.68	not significant
3383	TSC22D4	-1.10	6.04E-04	1.50E-03	3216.67	not significant
3384	TUSC2	-1.10	1.88E-01	2.63E-01	162.01	not significant
3385	CDK1	-1.10	1.33E-05	4.37E-05	7183.78	not significant
3386	RAPGEFL1	-1.10	2.33E-01	3.15E-01	103.06	not significant
3387	ASTE1	-1.10	6.58E-02	1.06E-01	464.00	not significant
3388	SNF8	-1.10	7.54E-03	1.52E-02	2136.50	not significant
3389	RAP1GDS1	-1.10	2.97E-05	9.22E-05	4499.59	not significant
3390	ICOS	-1.10	1.74E-04	4.81E-04	5060.01	not significant
3391	SLK	-1.10	4.55E-04	1.16E-03	3821.84	not significant
3392	ATOX1	-1.10	6.62E-02	1.06E-01	537.86	not significant
3393	STT3A	-1.10	1.75E-05	5.63E-05	5598.00	not significant
3394	PIK3R3	-1.10	6.44E-03	1.32E-02	1646.98	not significant
3395	FBXO38	-1.10	1.23E-02	2.37E-02	1339.50	not significant
3396	SAPCD2	-1.10	7.40E-03	1.49E-02	1353.18	not significant
3397	PNKD	-1.10	3.25E-02	5.67E-02	788.69	not significant
3398	SNX4	-1.10	2.70E-03	5.96E-03	1742.30	not significant
3399	HEMK1	-1.10	2.27E-02	4.11E-02	1323.18	not significant
3400	MARK3	-1.10	9.39E-04	2.26E-03	2396.29	not significant
3401	SRF	-1.10	1.23E-03	2.89E-03	3500.29	not significant
3402	ZNF330	-1.10	6.14E-03	1.26E-02	1753.82	not significant
3403	SGK1	-1.10	2.64E-01	3.49E-01	56.44	not significant
3404	PDSS2	-1.10	1.56E-01	2.24E-01	234.57	not significant
3405	PAGR1	-1.10	4.88E-03	1.03E-02	2301.07	not significant
3406	TOR1A	-1.10	1.27E-03	2.99E-03	2489.87	not significant
3407	SKA1	-1.10	9.87E-02	1.51E-01	351.96	not significant
3408	DCTN6	-1.10	2.24E-02	4.06E-02	813.51	not significant
3409	ARL11	-1.10	9.25E-02	1.43E-01	379.55	not significant
3410	TIPARP	-1.10	8.37E-02	1.31E-01	411.88	not significant
3411	KRIT1	-1.10	1.46E-03	3.39E-03	2266.50	not significant
3412	LMTK2	-1.10	3.75E-03	8.08E-03	2005.93	not significant
3413	RNF8	-1.10	6.78E-03	1.38E-02	1421.85	not significant
3414	CLTCL1	-1.10	2.59E-01	3.44E-01	70.16	not significant
3415	FLYWCH2	-1.10	3.30E-02	5.75E-02	815.53	not significant
3416	MAD2L1	-1.10	3.06E-04	8.05E-04	4624.93	not significant
3417	RAB35	-1.10	3.57E-04	9.29E-04	3680.50	not significant
3418	ZNF470	-1.10	1.75E-01	2.47E-01	199.72	not significant
3419	EXOSC9	-1.10	4.76E-04	1.21E-03	2840.53	not significant
3420	ARL4A	-1.10	1.50E-01	2.17E-01	254.27	not significant

3421	BCL2L13	-1.10	3.20E-03	6.98E-03	1798.15	not significant
3422	EXOC2	-1.10	5.95E-04	1.48E-03	2399.15	not significant
3423	SLC7A1	-1.10	6.84E-06	2.33E-05	9320.82	not significant
3424	RHOV	-1.10	2.29E-01	3.10E-01	21.02	not significant
3425	LGALSL	-1.10	2.28E-01	3.09E-01	20.02	not significant
3426	ANAPC11	-1.10	1.15E-01	1.72E-01	1856.09	not significant
3427	SHKBP1	-1.09	7.33E-04	1.79E-03	3087.71	not significant
3428	TCEANC	-1.09	2.27E-01	3.09E-01	119.10	not significant
3429	LYRM7	-1.09	2.76E-04	7.31E-04	3041.06	not significant
3430	EME1	-1.09	2.58E-02	4.61E-02	858.17	not significant
3431	ORMDL2	-1.09	3.69E-02	6.34E-02	678.73	not significant
3432	TMEM161B-AS1	-1.09	2.56E-01	3.41E-01	88.15	not significant
3433	HAUS6	-1.09	8.27E-05	2.40E-04	3873.03	not significant
3434	POLR3A	-1.09	1.68E-03	3.85E-03	2380.40	not significant
3435	AATF	-1.09	1.26E-04	3.54E-04	5121.15	not significant
3436	ZNF155	-1.09	1.27E-01	1.87E-01	288.44	not significant
3437	TMEM135	-1.09	9.74E-04	2.33E-03	2241.76	not significant
3438	DGKZ	-1.09	7.72E-05	2.25E-04	6191.93	not significant
3439	C19orf40	-1.09	1.40E-01	2.04E-01	270.68	not significant
3440	CNOT2	-1.09	1.91E-04	5.22E-04	4549.50	not significant
3441	DR1	-1.09	9.31E-06	3.10E-05	7062.41	not significant
3442	DRG2	-1.09	3.11E-03	6.78E-03	1858.29	not significant
3443	ZNF275	-1.09	2.60E-01	3.45E-01	30.03	not significant
3444	DCAKD	-1.09	2.12E-02	3.86E-02	1136.81	not significant
3445	FAM104A	-1.09	1.88E-03	4.26E-03	3027.37	not significant
3446	UBE2I	-1.09	2.31E-05	7.30E-05	7460.00	not significant
3447	C3orf38	-1.09	1.13E-02	2.20E-02	1176.44	not significant
3448	CD200R1	-1.09	1.30E-01	1.91E-01	341.49	not significant
3449	ETAA1	-1.09	1.57E-02	2.94E-02	1112.80	not significant
3450	ACADM	-1.09	1.05E-04	3.00E-04	4086.32	not significant
3451	SNX1	-1.09	1.11E-04	3.15E-04	4029.45	not significant
3452	MED25	-1.09	9.14E-03	1.81E-02	1367.49	not significant
3453	TBRG1	-1.09	5.32E-03	1.11E-02	1813.19	not significant
3454	FUBP1	-1.09	2.31E-04	6.23E-04	7371.39	not significant
3455	KARS	-1.09	2.19E-04	5.94E-04	9575.60	not significant
3456	LOC100506746	-1.09	2.36E-01	3.18E-01	21.05	not significant
3457	MTMR2	-1.09	6.45E-04	1.60E-03	2693.15	not significant
3458	ORC4	-1.09	1.10E-02	2.15E-02	1217.96	not significant
3459	ADAT2	-1.09	4.23E-02	7.16E-02	785.68	not significant
3460	RAB3GAP1	-1.09	4.07E-03	8.69E-03	1677.18	not significant
3461	EDEM2	-1.09	6.39E-03	1.31E-02	1382.68	not significant
3462	SIT1	-1.09	4.82E-02	8.05E-02	602.99	not significant
3463	RETSAT	-1.09	3.83E-02	6.56E-02	679.26	not significant
3464	TALDO1	-1.09	5.12E-04	1.30E-03	4655.74	not significant
3465	ID1	-1.09	1.94E-01	2.70E-01	13.99	not significant
3466	MIER1	-1.09	1.60E-03	3.68E-03	2466.55	not significant
3467	OMA1	-1.09	2.10E-02	3.83E-02	904.20	not significant
3468	TMEM209	-1.09	8.37E-05	2.43E-04	4611.80	not significant
3469	APC	-1.09	1.00E-02	1.97E-02	1435.07	not significant
3470	UBE2D1	-1.09	2.70E-02	4.81E-02	836.62	not significant
3471	POLR2A	-1.09	1.82E-01	2.55E-01	11304.51	not significant
3472	SLC35B4	-1.09	5.30E-04	1.34E-03	2903.07	not significant
3473	TMEM261	-1.09	6.84E-03	1.39E-02	1764.17	not significant
3474	IRAK4	-1.09	7.39E-04	1.81E-03	2958.85	not significant
3475	ZDHHC5	-1.09	7.82E-05	2.28E-04	5352.40	not significant
3476	DNAJC19	-1.09	2.89E-02	5.11E-02	865.38	not significant
3477	HJURP	-1.09	1.52E-04	4.23E-04	3843.25	not significant
3478	KCTD10	-1.09	3.48E-04	9.08E-04	3227.34	not significant
3479	MED18	-1.09	4.69E-02	7.86E-02	644.67	not significant
3480	MOCS3	-1.09	1.10E-01	1.66E-01	352.15	not significant
3481	FOXN3-AS1	-1.09	2.50E-01	3.34E-01	24.10	not significant
3482	PMS1	-1.09	7.86E-03	1.58E-02	1590.00	not significant
3483	NPFF	-1.09	2.51E-01	3.35E-01	22.64	not significant
3484	MSTO1	-1.09	2.72E-01	3.58E-01	77.08	not significant
3485	FGFR3	-1.09	1.92E-01	2.67E-01	216.98	not significant
3486	ATP6V0A1	-1.09	2.82E-01	3.70E-01	57.67	not significant
3487	TBCE	-1.09	2.81E-02	4.97E-02	910.92	not significant
3488	ILF2	-1.09	1.00E-05	3.33E-05	17892.16	not significant
3489	GPR35	-1.09	2.80E-01	3.68E-01	38.39	not significant
3490	TGFBRAP1	-1.09	2.28E-03	5.10E-03	2428.23	not significant
3491	CDON	-1.09	8.19E-02	1.28E-01	462.75	not significant
3492	BPHL	-1.09	1.44E-01	2.10E-01	274.01	not significant
3493	BBS7	-1.09	3.24E-02	5.66E-02	849.43	not significant
3494	CHCHD2	-1.09	2.02E-04	5.50E-04	11009.96	not significant
3495	RAB23	-1.09	1.11E-01	1.67E-01	377.37	not significant
3496	WDR41	-1.09	3.95E-03	8.46E-03	1777.42	not significant
3497	CCT4	-1.09	1.28E-04	3.60E-04	11287.49	not significant
3498	STK16	-1.09	4.55E-02	7.64E-02	681.47	not significant
3499	XPNPEP1	-1.09	3.39E-04	8.87E-04	3550.95	not significant
3500	TIMM13	-1.09	4.93E-03	1.03E-02	2492.08	not significant
3501	ZNF385C	-1.09	1.57E-01	2.25E-01	10.68	not significant
3502	TGDS	-1.09	2.99E-02	5.27E-02	997.93	not significant
3503	RBX1	-1.09	7.95E-03	1.60E-02	1929.43	not significant
3504	GLCE	-1.09	2.84E-01	3.72E-01	59.12	not significant
3505	TTI2	-1.09	1.83E-02	3.38E-02	1138.05	not significant
3506	BCL10	-1.09	4.75E-02	7.94E-02	670.59	not significant
3507	CRYGS	-1.09	2.82E-01	3.70E-01	38.75	not significant
3508	LRRC42	-1.09	1.29E-02	2.47E-02	1252.42	not significant

3509	HDAC4	-1.09	8.76E-05	2.54E-04	6556.50	not significant
3510	CNIH4	-1.09	4.61E-02	7.73E-02	715.72	not significant
3511	RPA2	-1.09	1.12E-03	2.66E-03	4990.90	not significant
3512	SSBP3	-1.09	2.86E-05	8.92E-05	7384.43	not significant
3513	COPG1	-1.09	3.79E-04	9.82E-04	4112.12	not significant
3514	EIF1AD	-1.09	6.07E-03	1.25E-02	1901.47	not significant
3515	VAC14	-1.09	6.26E-03	1.28E-02	1523.67	not significant
3516	CA5BP1	-1.09	2.44E-01	3.27E-01	131.41	not significant
3517	TRAF2	-1.09	1.39E-02	2.65E-02	1142.30	not significant
3518	DDX59	-1.09	2.56E-02	4.59E-02	954.14	not significant
3519	HDLBP	-1.09	6.77E-05	2.00E-04	6521.30	not significant
3520	FAM120AOS	-1.09	1.06E-02	2.07E-02	1265.04	not significant
3521	VPS53	-1.09	6.68E-03	1.36E-02	1564.11	not significant
3522	HEBP1	-1.09	1.62E-01	2.32E-01	10.83	not significant
3523	ARFRP1	-1.09	2.39E-02	4.31E-02	1097.04	not significant
3524	SNHG11	-1.09	1.07E-01	1.61E-01	429.92	not significant
3525	NCKAP5L	-1.09	1.15E-02	2.23E-02	1522.15	not significant
3526	PUS10	-1.09	1.09E-01	1.64E-01	387.05	not significant
3527	PIM2	-1.09	2.88E-01	3.76E-01	43.66	not significant
3528	HNRNPUL1	-1.09	4.22E-06	1.47E-05	23949.85	not significant
3529	OXSR1	-1.09	1.07E-04	3.04E-04	6513.68	not significant
3530	NDNL2	-1.09	3.95E-02	6.73E-02	833.00	not significant
3531	EXOC5	-1.09	9.64E-05	2.78E-04	5875.19	not significant
3532	SYNJ2	-1.09	8.25E-04	2.00E-03	3111.33	not significant
3533	CD164	-1.09	4.04E-05	1.23E-04	11983.81	not significant
3534	ESRRA	-1.09	3.14E-02	5.50E-02	900.30	not significant
3535	TCEA3	-1.09	2.93E-01	3.82E-01	52.72	not significant
3536	SRSF11	-1.09	2.04E-03	4.60E-03	7076.67	not significant
3537	GLRX3	-1.09	1.40E-03	3.26E-03	2556.47	not significant
3538	ATP2A1	-1.09	1.48E-01	2.15E-01	297.92	not significant
3539	CCDC163P	-1.09	1.70E-01	2.42E-01	260.97	not significant
3540	ARF5	-1.09	9.13E-04	2.20E-03	3831.67	not significant
3541	RMI1	-1.09	3.82E-03	8.22E-03	1987.37	not significant
3542	RBBP6	-1.09	9.23E-04	2.22E-03	4875.31	not significant
3543	TFG	-1.09	1.90E-03	4.30E-03	2356.57	not significant
3544	VPS36	-1.09	7.96E-04	1.93E-03	3106.56	not significant
3545	HIST1H2BO	-1.09	2.71E-01	3.57E-01	24.26	not significant
3546	PRCC	-1.09	7.94E-04	1.93E-03	3151.18	not significant
3547	CYB5B	-1.09	2.26E-04	6.09E-04	6826.78	not significant
3548	DUSP18	-1.09	2.12E-01	2.90E-01	179.15	not significant
3549	CEP76	-1.09	5.23E-02	8.64E-02	682.37	not significant
3550	GATB	-1.09	3.19E-02	5.58E-02	817.92	not significant
3551	TMEM167A	-1.09	6.46E-05	1.91E-04	4930.38	not significant
3552	ATG4C	-1.09	3.34E-02	5.81E-02	918.27	not significant
3553	WDR60	-1.09	5.26E-02	8.69E-02	666.25	not significant
3554	PITX1	-1.09	2.24E-01	3.05E-01	163.41	not significant
3555	POC1B	-1.09	6.95E-03	1.41E-02	1525.03	not significant
3556	GGNBP2	-1.09	4.52E-02	7.59E-02	799.24	not significant
3557	ABI3	-1.09	3.62E-02	6.22E-02	945.23	not significant
3558	FES	-1.09	2.98E-01	3.87E-01	43.85	not significant
3559	WWC3	-1.09	1.37E-02	2.61E-02	1380.44	not significant
3560	STAMBPL1	-1.09	9.81E-03	1.93E-02	1449.27	not significant
3561	MTFR1	-1.09	5.42E-02	8.93E-02	672.09	not significant
3562	INO80	-1.09	4.66E-03	9.84E-03	1938.95	not significant
3563	DHODH	-1.09	8.49E-02	1.32E-01	473.15	not significant
3564	SMAP2	-1.09	7.48E-04	1.83E-03	3074.72	not significant
3565	EMR1	-1.09	2.84E-01	3.72E-01	28.75	not significant
3566	LEO1	-1.09	1.13E-02	2.19E-02	1526.86	not significant
3567	LOC102724297	-1.09	2.16E-01	2.96E-01	13.84	not significant
3568	SLC30A6	-1.09	6.24E-03	1.28E-02	1828.48	not significant
3569	DENND1C	-1.09	7.52E-04	1.83E-03	3301.76	not significant
3570	HSD17B12	-1.09	5.00E-04	1.27E-03	3212.73	not significant
3571	VPS29	-1.09	2.99E-03	6.55E-03	2190.97	not significant
3572	DTNBP1	-1.09	4.53E-02	7.61E-02	744.92	not significant
3573	KMT2D	-1.09	1.39E-01	2.03E-01	8438.98	not significant
3574	PHTF2	-1.09	3.76E-03	8.10E-03	2135.95	not significant
3575	WDR20	-1.09	8.29E-02	1.30E-01	548.79	not significant
3576	HELB	-1.09	1.57E-01	2.25E-01	290.71	not significant
3577	KIAA0586	-1.09	1.43E-02	2.71E-02	1373.19	not significant
3578	KIAA1033	-1.09	1.03E-03	2.46E-03	2863.05	not significant
3579	PSMG3-AS1	-1.09	1.11E-01	1.67E-01	479.93	not significant
3580	MAP3K2	-1.09	1.04E-02	2.04E-02	2281.83	not significant
3581	AGPAT3	-1.09	1.25E-03	2.94E-03	2753.49	not significant
3582	FAN1	-1.09	1.47E-02	2.78E-02	1313.63	not significant
3583	RHBDD1	-1.09	1.16E-02	2.25E-02	1468.47	not significant
3584	MPP7	-1.09	3.02E-01	3.92E-01	45.44	not significant
3585	TOPORS	-1.09	1.21E-02	2.33E-02	1477.00	not significant
3586	NDUFB10	-1.09	4.21E-03	8.95E-03	2439.46	not significant
3587	METTL16	-1.09	5.12E-03	1.07E-02	2298.85	not significant
3588	MIR503HG	-1.09	2.45E-01	3.28E-01	17.33	not significant
3589	LYPLA1	-1.09	1.10E-03	2.61E-03	3908.08	not significant
3590	BLOC1S2	-1.09	2.31E-02	4.17E-02	1332.69	not significant
3591	FKBP7	-1.09	1.97E-01	2.74E-01	237.73	not significant
3592	RPL35	-1.09	7.05E-04	1.73E-03	13393.70	not significant
3593	ZNF146	-1.09	1.58E-03	3.63E-03	7077.17	not significant
3594	WSB2	-1.09	4.18E-03	8.90E-03	2503.69	not significant
3595	SMEK1	-1.09	1.44E-04	4.03E-04	5726.35	not significant
3596	GPR19	-1.09	1.98E-01	2.74E-01	217.77	not significant

3597	UQCRHL	-1.09	1.14E-01	1.70E-01	417.69	not significant
3598	LINS	-1.09	1.45E-01	2.11E-01	409.25	not significant
3599	PPP3R1	-1.09	1.28E-04	3.61E-04	5584.20	not significant
3600	MVD	-1.09	1.14E-02	2.20E-02	1377.89	not significant
3601	CALU	-1.09	3.63E-04	9.45E-04	5203.13	not significant
3602	ZBTB24	-1.09	1.54E-02	2.90E-02	1369.28	not significant
3603	TRAPPC3	-1.09	4.11E-03	8.77E-03	2031.82	not significant
3604	PPP5C	-1.09	3.96E-03	8.48E-03	2866.33	not significant
3605	USP32	-1.09	5.64E-04	1.41E-03	3703.11	not significant
3606	GFPT1	-1.09	2.60E-03	5.76E-03	2919.67	not significant
3607	ABHD13	-1.09	6.80E-03	1.39E-02	1636.60	not significant
3608	STX17	-1.09	7.30E-03	1.48E-02	1693.48	not significant
3609	RNF26	-1.09	6.85E-03	1.39E-02	2360.77	not significant
3610	SETSIP	-1.09	3.05E-01	3.94E-01	35.99	not significant
3611	TAF6	-1.09	5.81E-04	1.45E-03	4043.48	not significant
3612	TMEM65	-1.09	1.80E-02	3.34E-02	1493.34	not significant
3613	CASP3	-1.09	8.74E-04	2.11E-03	5084.20	not significant
3614	BMPR2	-1.09	5.35E-02	8.83E-02	719.96	not significant
3615	SUMO1P3	-1.09	2.84E-01	3.72E-01	26.65	not significant
3616	ZNF485	-1.09	2.12E-01	2.91E-01	206.65	not significant
3617	GALNT2	-1.09	6.33E-05	1.88E-04	10985.18	not significant
3618	KLHL8	-1.09	1.13E-02	2.19E-02	1501.02	not significant
3619	LOC728485	-1.09	2.14E-01	2.93E-01	214.84	not significant
3620	NID2	-1.09	2.00E-01	2.77E-01	224.57	not significant
3621	PTPN22	-1.09	1.49E-02	2.82E-02	1366.94	not significant
3622	UBE2G1	-1.09	6.46E-04	1.60E-03	4033.28	not significant
3623	KDM4C	-1.09	1.90E-02	3.50E-02	1321.67	not significant
3624	LOC100507002	-1.09	2.72E-01	3.58E-01	21.49	not significant
3625	OSGEPL1	-1.08	1.08E-01	1.64E-01	498.56	not significant
3626	ACADSB	-1.08	3.53E-02	6.10E-02	1085.47	not significant
3627	FBXO24	-1.08	2.07E-01	2.85E-01	12.78	not significant
3628	EFCAB11	-1.08	2.09E-01	2.87E-01	226.01	not significant
3629	RAPGEF4	-1.08	2.99E-01	3.88E-01	32.78	not significant
3630	ANKEF1	-1.08	2.28E-01	3.09E-01	181.03	not significant
3631	ARHGAP25	-1.08	2.49E-02	4.46E-02	1052.04	not significant
3632	PTAFR	-1.08	2.02E-01	2.79E-01	11.24	not significant
3633	HUS1	-1.08	3.96E-02	6.74E-02	913.47	not significant
3634	IRF3	-1.08	8.36E-03	1.67E-02	1712.46	not significant
3635	MYCBP2	-1.08	7.31E-02	1.16E-01	6824.78	not significant
3636	PPP1R21	-1.08	4.91E-02	8.17E-02	773.76	not significant
3637	PRMT7	-1.08	9.11E-03	1.80E-02	1608.65	not significant
3638	MPDU1	-1.08	1.19E-02	2.29E-02	1416.40	not significant
3639	NRADDP	-1.08	1.79E-01	2.52E-01	9.97	not significant
3640	TUBGCP4	-1.08	7.48E-03	1.51E-02	1830.51	not significant
3641	SNAI3-AS1	-1.08	3.08E-01	3.97E-01	35.04	not significant
3642	SS18L2	-1.08	5.68E-02	9.28E-02	853.36	not significant
3643	SLC6A19	-1.08	2.79E-01	3.67E-01	22.63	not significant
3644	MSRB2	-1.08	1.53E-01	2.20E-01	400.80	not significant
3645	SIRT4	-1.08	2.42E-01	3.25E-01	16.20	not significant
3646	CSNK1A1	-1.08	2.16E-04	5.85E-04	7298.74	not significant
3647	NGDN	-1.08	1.86E-02	3.43E-02	1582.67	not significant
3648	CRK	-1.08	5.23E-02	8.64E-02	755.08	not significant
3649	NRAS	-1.08	3.20E-05	9.90E-05	9421.41	not significant
3650	DDX5	-1.08	4.41E-04	1.13E-03	16407.42	not significant
3651	TMEM138	-1.08	5.79E-02	9.44E-02	726.69	not significant
3652	ABL2	-1.08	3.46E-02	6.00E-02	1042.87	not significant
3653	PPP2R5B	-1.08	1.72E-01	2.44E-01	290.29	not significant
3654	RPP40	-1.08	1.84E-01	2.58E-01	258.94	not significant
3655	PCDHGA10	-1.08	1.77E-01	2.49E-01	9.20	not significant
3656	FOXP4	-1.08	2.84E-03	6.24E-03	3121.10	not significant
3657	ZNF148	-1.08	5.78E-03	1.19E-02	2674.34	not significant
3658	NEDD1	-1.08	2.78E-04	7.37E-04	4537.51	not significant
3659	NDEL1	-1.08	2.21E-02	4.02E-02	1265.01	not significant
3660	MAP2K4	-1.08	1.54E-02	2.89E-02	1696.45	not significant
3661	VANGL1	-1.08	3.50E-05	1.08E-04	10893.26	not significant
3662	XRCC3	-1.08	3.02E-03	6.61E-03	2379.27	not significant
3663	AARD	-1.08	1.80E-01	2.54E-01	278.91	not significant
3664	HIST1H4C	-1.08	2.85E-01	3.73E-01	23.08	not significant
3665	TXNDC9	-1.08	4.33E-02	7.30E-02	957.28	not significant
3666	LOC100506083	-1.08	3.22E-01	4.13E-01	48.26	not significant
3667	ZDHHC6	-1.08	7.02E-03	1.43E-02	2615.44	not significant
3668	MMS22L	-1.08	1.69E-03	3.88E-03	3319.81	not significant
3669	S100A6	-1.08	2.53E-01	3.37E-01	16.66	not significant
3670	GPR176	-1.08	2.05E-01	2.82E-01	232.20	not significant
3671	DYNLT1	-1.08	1.87E-01	2.61E-01	309.42	not significant
3672	ZNF658	-1.08	3.22E-01	4.13E-01	48.35	not significant
3673	PXK	-1.08	1.30E-03	3.05E-03	3554.57	not significant
3674	B3GNT1	-1.08	1.91E-01	2.65E-01	270.28	not significant
3675	RPL8	-1.08	7.16E-04	1.76E-03	39864.77	not significant
3676	DUS3L	-1.08	6.47E-03	1.32E-02	1823.18	not significant
3677	SNX2	-1.08	3.63E-02	6.24E-02	1328.02	not significant
3678	GSR	-1.08	4.44E-04	1.14E-03	4669.91	not significant
3679	ZNF207	-1.08	2.34E-04	6.29E-04	9082.52	not significant
3680	METTL18	-1.08	9.52E-02	1.46E-01	521.41	not significant
3681	BAZ1B	-1.08	1.51E-03	3.49E-03	3270.03	not significant
3682	SAP18	-1.08	8.40E-04	2.04E-03	4791.29	not significant
3683	SMC2	-1.08	2.72E-04	7.24E-04	6514.77	not significant
3684	MAFF	-1.08	3.13E-01	4.03E-01	31.34	not significant

3685	GHITM	-1.08	9.32E-04	2.24E-03	6140.25	not significant
3686	PTGER2	-1.08	1.82E-01	2.56E-01	293.48	not significant
3687	C12orf65	-1.08	3.76E-02	6.45E-02	1142.76	not significant
3688	CILP2	-1.08	1.81E-01	2.55E-01	10.05	not significant
3689	SRGAP2D	-1.08	3.19E-01	4.10E-01	37.04	not significant
3690	CDC40	-1.08	1.31E-02	2.52E-02	1943.26	not significant
3691	P2RX7	-1.08	1.66E-01	2.36E-01	315.32	not significant
3692	UBE2G2	-1.08	1.42E-01	2.07E-01	396.15	not significant
3693	KIAA1522	-1.08	2.69E-01	3.55E-01	18.02	not significant
3694	USP47	-1.08	9.77E-04	2.34E-03	3870.21	not significant
3695	TAF5L	-1.08	5.13E-03	1.07E-02	2233.67	not significant
3696	PAFAH2	-1.08	5.98E-03	1.23E-02	1951.88	not significant
3697	SAMD10	-1.08	1.90E-01	2.65E-01	301.81	not significant
3698	MOB3A	-1.08	1.05E-02	2.06E-02	2158.89	not significant
3699	HMGN1	-1.08	1.13E-03	2.69E-03	11972.23	not significant
3700	C10orf76	-1.08	1.52E-02	2.87E-02	1453.51	not significant
3701	GPALPP1	-1.08	3.49E-02	6.03E-02	1094.57	not significant
3702	DCAF7	-1.08	1.39E-04	3.89E-04	15099.51	not significant
3703	IER5	-1.08	1.20E-02	2.32E-02	1793.16	not significant
3704	OTUB1	-1.08	3.26E-03	7.10E-03	2910.92	not significant
3705	ZCCHC4	-1.08	1.15E-01	1.72E-01	488.01	not significant
3706	KCNK12	-1.08	2.71E-01	3.58E-01	19.00	not significant
3707	FBXL18	-1.08	2.94E-02	5.18E-02	1071.07	not significant
3708	CYFIP2	-1.08	1.37E-04	3.84E-04	20178.67	not significant
3709	ANAPC4	-1.08	2.43E-02	4.38E-02	1295.12	not significant
3710	LIG3	-1.08	4.90E-03	1.03E-02	2130.03	not significant
3711	HDAC1	-1.08	3.82E-05	1.17E-04	10287.16	not significant
3712	DERL2	-1.08	6.27E-02	1.01E-01	883.24	not significant
3713	NR2F6	-1.08	1.51E-01	2.18E-01	419.87	not significant
3714	YRDC	-1.08	3.46E-02	5.99E-02	1149.86	not significant
3715	PRPF40B	-1.08	2.70E-01	3.56E-01	141.70	not significant
3716	CCND2	-1.08	2.33E-01	3.15E-01	13.19	not significant
3717	LOC727896	-1.08	2.69E-01	3.55E-01	17.76	not significant
3718	POU2F1	-1.08	2.57E-02	4.60E-02	1719.01	not significant
3719	LOC100506674	-1.08	1.80E-01	2.53E-01	9.34	not significant
3720	DPYD	-1.08	2.71E-03	5.98E-03	2621.71	not significant
3721	GNPDA2	-1.08	1.48E-01	2.14E-01	359.60	not significant
3722	CDV3	-1.08	6.84E-04	1.68E-03	10455.38	not significant
3723	TXNDC11	-1.08	2.15E-02	3.91E-02	1390.56	not significant
3724	MOB1A	-1.08	1.86E-03	4.23E-03	4207.91	not significant
3725	DNAJC10	-1.08	1.52E-03	3.53E-03	3133.06	not significant
3726	RPN2	-1.08	2.60E-04	6.94E-04	15841.84	not significant
3727	CRKL	-1.08	1.80E-04	4.94E-04	6461.90	not significant
3728	LOC100288842	-1.08	2.75E-01	3.61E-01	19.75	not significant
3729	HEYL	-1.08	3.29E-01	4.20E-01	42.87	not significant
3730	ASB6	-1.08	5.29E-02	8.73E-02	857.13	not significant
3731	TXLNG	-1.08	5.44E-03	1.13E-02	2141.42	not significant
3732	NUDT22	-1.08	6.88E-02	1.10E-01	712.26	not significant
3733	THRAP3	-1.08	2.01E-04	5.47E-04	11704.11	not significant
3734	DLD	-1.08	3.93E-03	8.42E-03	4476.12	not significant
3735	MFSD5	-1.08	5.13E-02	8.50E-02	819.06	not significant
3736	PELP1	-1.08	1.36E-03	3.17E-03	4150.86	not significant
3737	RPL23AP82	-1.08	3.12E-01	4.03E-01	28.12	not significant
3738	GLIPR1L2	-1.08	3.00E-01	3.89E-01	23.75	not significant
3739	HDAC11	-1.08	2.86E-01	3.74E-01	135.06	not significant
3740	VAPA	-1.08	7.12E-04	1.75E-03	7578.20	not significant
3741	RAB2A	-1.08	8.52E-03	1.70E-02	2520.18	not significant
3742	HEATR6	-1.08	7.97E-02	1.25E-01	679.82	not significant
3743	MRPL43	-1.08	1.55E-02	2.91E-02	1511.04	not significant
3744	MDN1	-1.08	2.87E-01	3.75E-01	4015.03	not significant
3745	RNGTT	-1.08	3.09E-03	6.75E-03	3085.77	not significant
3746	PMS2	-1.08	5.19E-02	8.58E-02	797.17	not significant
3747	CHRNA6	-1.08	3.07E-01	3.97E-01	109.35	not significant
3748	CBX6	-1.08	1.77E-02	3.28E-02	1867.42	not significant
3749	TIGD4	-1.08	3.29E-01	4.20E-01	68.54	not significant
3750	FANCM	-1.08	7.36E-02	1.17E-01	831.57	not significant
3751	TFIP11	-1.08	9.43E-03	1.86E-02	1819.92	not significant
3752	H2AFY	-1.08	1.68E-04	4.64E-04	16510.92	not significant
3753	WDR55	-1.08	6.55E-02	1.05E-01	927.99	not significant
3754	PPP1R13B	-1.08	3.29E-01	4.20E-01	72.61	not significant
3755	SSC4D	-1.08	2.89E-01	3.77E-01	20.55	not significant
3756	ZNF774	-1.08	3.35E-01	4.27E-01	40.30	not significant
3757	KIAA2018	-1.08	1.11E-02	2.16E-02	1976.21	not significant
3758	AKAP11	-1.08	2.76E-02	4.91E-02	1674.38	not significant
3759	TSNAXIP1	-1.08	2.86E-01	3.74E-01	21.30	not significant
3760	CDC37	-1.08	1.99E-04	5.42E-04	6722.07	not significant
3761	PPP4R1	-1.08	8.72E-04	2.11E-03	4169.71	not significant
3762	EIF4G3	-1.08	4.35E-03	9.23E-03	2748.36	not significant
3763	CHEK1	-1.08	9.30E-04	2.24E-03	6445.55	not significant
3764	MBP	-1.08	3.20E-01	4.11E-01	96.21	not significant
3765	PPWD1	-1.08	2.04E-02	3.73E-02	1437.74	not significant
3766	TXLNA	-1.08	5.12E-04	1.30E-03	4889.11	not significant
3767	C11orf73	-1.08	3.85E-02	6.59E-02	1068.25	not significant
3768	SV2B	-1.08	2.71E-01	3.57E-01	18.62	not significant
3769	CDC73	-1.08	1.24E-02	2.38E-02	1801.62	not significant
3770	TXNL4B	-1.08	1.68E-02	3.13E-02	1539.33	not significant
3771	NELFB	-1.08	9.93E-03	1.95E-02	1990.12	not significant
3772	MTF2	-1.08	4.20E-04	1.08E-03	5522.06	not significant

3773	MFSD2A	-1.08	2.60E-01	3.45E-01	168.40	not significant
3774	BRD4	-1.08	1.49E-03	3.45E-03	4795.98	not significant
3775	ASPM	-1.08	5.70E-03	1.18E-02	10466.62	not significant
3776	KIFC3	-1.08	2.68E-01	3.54E-01	18.69	not significant
3777	RIOK3	-1.08	8.11E-03	1.62E-02	1967.36	not significant
3778	GABPA	-1.08	1.05E-02	2.06E-02	2325.95	not significant
3779	BABAM1	-1.08	1.69E-02	3.15E-02	2246.15	not significant
3780	CNP	-1.08	1.31E-01	1.93E-01	453.55	not significant
3781	ZSWIM8-AS1	-1.08	3.42E-01	4.33E-01	56.88	not significant
3782	GNPTAB	-1.08	2.45E-04	6.56E-04	7674.20	not significant
3783	LRRC16B	-1.08	2.78E-01	3.65E-01	194.79	not significant
3784	DROSHA	-1.08	8.96E-04	2.16E-03	3940.99	not significant
3785	HIST1H2BI	-1.08	2.74E-01	3.61E-01	16.03	not significant
3786	KTN1-AS1	-1.08	3.43E-01	4.34E-01	50.49	not significant
3787	GPR157	-1.08	3.40E-01	4.31E-01	71.84	not significant
3788	ATP6V1D	-1.08	2.04E-02	3.74E-02	1787.34	not significant
3789	PAXIP1	-1.08	1.59E-03	3.67E-03	3379.64	not significant
3790	CDR2	-1.08	1.04E-02	2.04E-02	2141.35	not significant
3791	PARP4	-1.08	3.65E-03	7.88E-03	4630.82	not significant
3792	LOC100506804	-1.08	2.86E-01	3.74E-01	18.67	not significant
3793	RALGAPA1	-1.08	3.42E-01	4.33E-01	68.56	not significant
3794	CLPTM1	-1.08	3.78E-03	8.14E-03	3126.85	not significant
3795	LRRC58	-1.08	5.77E-04	1.44E-03	7903.73	not significant
3796	XPO4	-1.08	1.58E-02	2.97E-02	2765.40	not significant
3797	VPS72	-1.08	3.97E-02	6.76E-02	1395.32	not significant
3798	DDX46	-1.08	1.14E-03	2.71E-03	6570.79	not significant
3799	MB21D2	-1.08	3.45E-01	4.36E-01	54.02	not significant
3800	SFXN2	-1.08	5.00E-02	8.32E-02	896.91	not significant
3801	PEX26	-1.08	6.03E-03	1.24E-02	2368.00	not significant
3802	LARP1	-1.08	5.51E-04	1.38E-03	16264.99	not significant
3803	TCFL5	-1.08	2.78E-02	4.94E-02	1180.87	not significant
3804	CNOT7	-1.08	5.53E-04	1.39E-03	8195.28	not significant
3805	CD27-AS1	-1.08	1.68E-01	2.39E-01	361.18	not significant
3806	OPA3	-1.08	3.77E-02	6.46E-02	1075.02	not significant
3807	DNAH1	-1.08	1.07E-01	1.62E-01	788.08	not significant
3808	NXT2	-1.08	4.59E-02	7.70E-02	992.07	not significant
3809	SATB2	-1.08	3.46E-01	4.38E-01	65.77	not significant
3810	DNAJB4	-1.08	2.28E-01	3.10E-01	232.37	not significant
3811	PCYOX1	-1.08	1.89E-02	3.49E-02	1644.55	not significant
3812	FAM132A	-1.08	1.74E-01	2.46E-01	7.82	not significant
3813	LAT	-1.08	6.66E-04	1.64E-03	8885.16	not significant
3814	EIF3J-AS1	-1.08	3.28E-01	4.19E-01	92.59	not significant
3815	RALY	-1.08	3.56E-04	9.28E-04	18913.74	not significant
3816	MTHFR	-1.08	4.23E-02	7.16E-02	1030.71	not significant
3817	FAHD2CP	-1.08	3.50E-01	4.41E-01	61.12	not significant
3818	ACP6	-1.08	3.04E-01	3.94E-01	130.71	not significant
3819	PARD3	-1.08	4.69E-03	9.90E-03	3027.02	not significant
3820	NXT1	-1.08	3.50E-02	6.04E-02	1176.08	not significant
3821	L3MBTL2	-1.08	1.46E-02	2.76E-02	1708.07	not significant
3822	BSG	-1.08	3.36E-03	7.31E-03	8642.71	not significant
3823	C14orf80	-1.08	2.53E-01	3.37E-01	199.12	not significant
3824	NR1D1	-1.08	1.87E-01	2.61E-01	349.20	not significant
3825	SMG1	-1.08	6.89E-03	1.40E-02	7497.76	not significant
3826	GTF2H1	-1.08	7.91E-03	1.59E-02	2116.36	not significant
3827	PHB2	-1.08	2.64E-03	5.85E-03	4883.16	not significant
3828	SMG1P3	-1.08	3.42E-01	4.34E-01	106.64	not significant
3829	HSDL2	-1.08	3.06E-02	5.38E-02	1243.07	not significant
3830	PLXNB2	-1.08	2.81E-01	3.68E-01	17.58	not significant
3831	HCG18	-1.08	3.51E-01	4.43E-01	52.28	not significant
3832	SKA3	-1.08	2.29E-03	5.11E-03	3609.95	not significant
3833	YDJC	-1.08	3.25E-02	5.67E-02	1192.64	not significant
3834	SIKE1	-1.08	2.70E-03	5.96E-03	3511.55	not significant
3835	DNAJC15	-1.08	1.49E-01	2.16E-01	443.61	not significant
3836	ZNF613	-1.08	2.13E-01	2.92E-01	270.05	not significant
3837	TANC2	-1.08	1.92E-01	2.67E-01	310.87	not significant
3838	ESCO1	-1.08	1.59E-02	2.98E-02	1817.80	not significant
3839	CDK5RAP1	-1.08	2.62E-02	4.68E-02	1264.45	not significant
3840	BTN2A1	-1.08	2.92E-02	5.15E-02	1303.68	not significant
3841	GEN1	-1.08	2.68E-01	3.54E-01	2308.57	not significant
3842	SF3B3	-1.08	4.41E-03	9.36E-03	13853.76	not significant
3843	OGFOD1	-1.08	7.28E-03	1.47E-02	2309.08	not significant
3844	NCDN	-1.08	3.03E-02	5.32E-02	1610.95	not significant
3845	ROCK1	-1.08	6.55E-04	1.62E-03	6806.36	not significant
3846	SEL1L	-1.08	7.43E-04	1.82E-03	5007.11	not significant
3847	TRIM27	-1.08	9.89E-02	1.51E-01	643.93	not significant
3848	UFM1	-1.08	3.59E-03	7.75E-03	2886.05	not significant
3849	KPNA6	-1.08	7.18E-03	1.46E-02	2733.86	not significant
3850	FIBP	-1.08	8.85E-03	1.76E-02	3210.16	not significant
3851	FKTN	-1.08	9.64E-02	1.48E-01	648.75	not significant
3852	ARMC7	-1.08	6.32E-02	1.02E-01	912.65	not significant
3853	SOAT1	-1.08	3.55E-03	7.67E-03	3200.48	not significant
3854	LITAF	-1.08	6.95E-02	1.11E-01	803.94	not significant
3855	CCT8	-1.08	1.35E-04	3.78E-04	13125.41	not significant
3856	CEP41	-1.08	1.48E-01	2.14E-01	455.95	not significant
3857	SLX4	-1.08	1.27E-01	1.87E-01	822.32	not significant
3858	MAN1A2	-1.08	2.04E-02	3.74E-02	1488.69	not significant
3859	TEX30	-1.08	5.14E-02	8.52E-02	1022.35	not significant
3860	DCTPP1	-1.08	8.52E-03	1.70E-02	3312.36	not significant

3861	MPC2	-1.08	6.15E-03	1.26E-02	3157.15	not significant
3862	COG3	-1.08	2.09E-02	3.81E-02	1453.51	not significant
3863	NUP62	-1.08	3.66E-04	9.51E-04	7691.40	not significant
3864	MGA	-1.08	1.67E-02	3.13E-02	3191.49	not significant
3865	INTS6	-1.08	1.91E-02	3.52E-02	1798.36	not significant
3866	FBXL19	-1.08	1.45E-02	2.75E-02	3403.92	not significant
3867	GNB1L	-1.08	7.12E-02	1.13E-01	793.86	not significant
3868	VPS35	-1.08	7.73E-04	1.88E-03	5313.69	not significant
3869	CCR4	-1.08	3.13E-01	4.03E-01	132.03	not significant
3870	LSM5	-1.08	5.70E-03	1.18E-02	3151.44	not significant
3871	STIM2	-1.08	5.24E-02	8.65E-02	1047.59	not significant
3872	MCUR1	-1.08	5.82E-03	1.20E-02	3122.65	not significant
3873	ATXN10	-1.08	8.14E-03	1.63E-02	6042.27	not significant
3874	PEX6	-1.08	9.72E-02	1.49E-01	699.83	not significant
3875	ELK4	-1.08	4.30E-03	9.14E-03	3374.04	not significant
3876	ICA1	-1.08	2.04E-01	2.81E-01	9.46	not significant
3877	DDIAS	-1.08	2.34E-02	4.23E-02	1588.03	not significant
3878	BAZ2A	-1.08	9.79E-04	2.34E-03	5927.16	not significant
3879	LIN7C	-1.08	8.76E-02	1.36E-01	869.69	not significant
3880	MOCS1	-1.08	4.10E-02	6.96E-02	1161.79	not significant
3881	MAN1B1-AS1	-1.08	3.17E-01	4.08E-01	22.84	not significant
3882	STX1A	-1.08	2.38E-01	3.20E-01	10.63	not significant
3883	HNRNPH1	-1.08	1.43E-04	3.99E-04	29210.87	not significant
3884	AP3D1	-1.07	1.47E-03	3.41E-03	6758.85	not significant
3885	CCDC91	-1.07	5.22E-02	8.63E-02	1228.11	not significant
3886	SMC1A	-1.07	2.35E-03	5.24E-03	4340.59	not significant
3887	BAG6	-1.07	2.71E-03	5.98E-03	4409.94	not significant
3888	PFDN2	-1.07	6.38E-02	1.03E-01	1336.73	not significant
3889	SNPH	-1.07	3.13E-01	4.04E-01	136.42	not significant
3890	CHERP	-1.07	1.59E-03	3.66E-03	5277.26	not significant
3891	HIST1H2AG	-1.07	3.65E-01	4.57E-01	44.90	not significant
3892	HIP1	-1.07	2.91E-01	3.80E-01	16.51	not significant
3893	PDLIM5	-1.07	5.24E-02	8.66E-02	987.82	not significant
3894	SCAMP2	-1.07	3.61E-02	6.21E-02	1409.45	not significant
3895	CLASP2	-1.07	7.20E-03	1.46E-02	2879.85	not significant
3896	RSBN1L	-1.07	4.43E-02	7.47E-02	1305.99	not significant
3897	GAS5-AS1	-1.07	3.64E-01	4.56E-01	37.82	not significant
3898	CDK5	-1.07	8.10E-02	1.27E-01	801.23	not significant
3899	TIGD6	-1.07	3.09E-01	3.99E-01	146.16	not significant
3900	ATP1B3	-1.07	2.68E-03	5.92E-03	4874.94	not significant
3901	NOS3	-1.07	3.16E-01	4.07E-01	146.06	not significant
3902	SDCCAG3	-1.07	4.79E-02	8.01E-02	1213.74	not significant
3903	DYRK4	-1.07	1.37E-01	2.01E-01	529.55	not significant
3904	ECH1	-1.07	2.39E-02	4.31E-02	2837.48	not significant
3905	C6orf211	-1.07	3.48E-02	6.02E-02	1599.87	not significant
3906	NHP2L1	-1.07	2.44E-03	5.42E-03	5201.90	not significant
3907	SLC6A8	-1.07	2.38E-01	3.20E-01	11.05	not significant
3908	KIAA0895	-1.07	2.67E-01	3.53E-01	220.68	not significant
3909	NSD1	-1.07	4.09E-03	8.73E-03	5163.02	not significant
3910	GTF3C3	-1.07	5.78E-03	1.19E-02	2782.48	not significant
3911	GOLGA7	-1.07	2.76E-03	6.08E-03	3527.05	not significant
3912	SLC25A42	-1.07	9.21E-02	1.42E-01	718.78	not significant
3913	FUBP3	-1.07	1.67E-02	3.12E-02	2152.05	not significant
3914	PHAX	-1.07	5.58E-02	9.16E-02	1297.31	not significant
3915	MTA2	-1.07	3.61E-04	9.37E-04	9748.08	not significant
3916	CD151	-1.07	2.52E-01	3.36E-01	247.75	not significant
3917	TMEM186	-1.07	1.71E-01	2.42E-01	417.10	not significant
3918	TMED9	-1.07	2.27E-01	3.08E-01	2589.50	not significant
3919	CTSV	-1.07	2.80E-01	3.68E-01	14.04	not significant
3920	EZH2	-1.07	4.42E-04	1.13E-03	7493.93	not significant
3921	LMBRD2	-1.07	7.65E-02	1.21E-01	805.83	not significant
3922	CPS1	-1.07	2.95E-01	3.84E-01	172.77	not significant
3923	NUP98	-1.07	4.96E-04	1.26E-03	7458.68	not significant
3924	TRAT1	-1.07	1.19E-02	2.29E-02	2435.51	not significant
3925	TAOK3	-1.07	8.54E-04	2.07E-03	5052.41	not significant
3926	CAMSAP2	-1.07	3.37E-01	4.28E-01	23.77	not significant
3927	SLC23A1	-1.07	3.50E-01	4.41E-01	139.43	not significant
3928	RANBP2	-1.07	1.79E-03	4.07E-03	6563.08	not significant
3929	NUTM2D	-1.07	3.20E-01	4.11E-01	19.55	not significant
3930	ACOT2	-1.07	2.78E-01	3.65E-01	214.24	not significant
3931	STK39	-1.07	2.07E-03	4.67E-03	3730.90	not significant
3932	TNPO3	-1.07	1.29E-03	3.02E-03	6752.36	not significant
3933	PINK1-AS	-1.07	1.99E-01	2.75E-01	347.30	not significant
3934	IKZF5	-1.07	1.01E-01	1.54E-01	913.57	not significant
3935	IGF1R	-1.07	3.25E-02	5.68E-02	1520.47	not significant
3936	PANO	-1.07	3.69E-01	4.61E-01	70.62	not significant
3937	KCNAB2	-1.07	9.86E-04	2.36E-03	9973.16	not significant
3938	ATRN	-1.07	3.43E-01	4.34E-01	115.47	not significant
3939	SLC33A1	-1.07	6.01E-02	9.76E-02	999.59	not significant
3940	WDR5	-1.07	7.42E-03	1.50E-02	3132.78	not significant
3941	MCM10	-1.07	3.47E-03	7.50E-03	4417.09	not significant
3942	TMCO6	-1.07	1.04E-01	1.58E-01	697.63	not significant
3943	TTC7B	-1.07	3.74E-01	4.66E-01	64.43	not significant
3944	LIF	-1.07	9.51E-02	1.46E-01	863.58	not significant
3945	UBE2O	-1.07	7.05E-03	1.43E-02	3362.81	not significant
3946	RAP1B	-1.07	3.81E-03	8.19E-03	3765.58	not significant
3947	CRYGN	-1.07	3.14E-01	4.05E-01	17.86	not significant
3948	UBIAD1	-1.07	5.45E-02	8.97E-02	1291.34	not significant

3949	AKR7L	-1.07	3.52E-01	4.44E-01	26.83	not significant
3950	PRAM1	-1.07	3.52E-01	4.44E-01	25.84	not significant
3951	HMG20A	-1.07	1.75E-02	3.25E-02	2012.03	not significant
3952	FER	-1.07	2.28E-01	3.09E-01	290.02	not significant
3953	ZBTB7A	-1.07	4.92E-02	8.18E-02	1554.13	not significant
3954	SLTM	-1.07	3.02E-03	6.61E-03	5059.46	not significant
3955	EMC1	-1.07	3.49E-02	6.04E-02	1914.76	not significant
3956	DARS	-1.07	2.72E-03	6.00E-03	4725.34	not significant
3957	LOC101927151	-1.07	1.83E-01	2.57E-01	465.28	not significant
3958	LRRC8C	-1.07	4.15E-02	7.03E-02	1345.33	not significant
3959	HSP90B2P	-1.07	3.74E-01	4.66E-01	80.78	not significant
3960	COPZ1	-1.07	8.62E-03	1.71E-02	4741.47	not significant
3961	STRN3	-1.07	6.66E-02	1.07E-01	983.62	not significant
3962	DCTN5	-1.07	1.91E-03	4.34E-03	4525.67	not significant
3963	NUP153	-1.07	1.59E-03	3.67E-03	6965.64	not significant
3964	TOR1AIP2	-1.07	2.06E-02	3.77E-02	1841.84	not significant
3965	AVPI1	-1.07	3.05E-01	3.95E-01	15.85	not significant
3966	ZNF467	-1.07	3.38E-01	4.29E-01	20.39	not significant
3967	MTRF1	-1.07	1.66E-01	2.36E-01	484.41	not significant
3968	CYP2R1	-1.07	3.77E-01	4.68E-01	75.72	not significant
3969	LAMTOR5	-1.07	2.54E-02	4.54E-02	2141.43	not significant
3970	RBCK1	-1.07	2.81E-03	6.18E-03	4978.53	not significant
3971	KLHL7-AS1	-1.07	3.83E-01	4.75E-01	45.01	not significant
3972	AP2B1	-1.07	4.90E-03	1.03E-02	4568.26	not significant
3973	ZWILCH	-1.07	1.91E-02	3.52E-02	2294.25	not significant
3974	SKAP1	-1.07	2.99E-02	5.26E-02	1588.85	not significant
3975	FBXO4	-1.07	2.21E-01	3.01E-01	314.56	not significant
3976	GABRR2	-1.07	3.26E-01	4.17E-01	18.91	not significant
3977	PDS5A	-1.07	1.51E-03	3.50E-03	12862.70	not significant
3978	LOC102723703	-1.07	1.71E-01	2.43E-01	8.52	not significant
3979	CYB5R4	-1.07	6.34E-02	1.02E-01	998.72	not significant
3980	SNRPD1	-1.07	2.53E-02	4.53E-02	4777.06	not significant
3981	GANC	-1.07	1.98E-01	2.74E-01	368.35	not significant
3982	LARP1B	-1.07	6.15E-02	9.96E-02	1067.21	not significant
3983	PTGR2	-1.07	2.09E-01	2.87E-01	347.86	not significant
3984	IKZF3	-1.07	1.10E-01	1.66E-01	710.13	not significant
3985	UBL4A	-1.07	1.85E-01	2.58E-01	480.87	not significant
3986	LOC113230	-1.07	2.22E-01	3.02E-01	9.21	not significant
3987	C1orf122	-1.07	1.06E-01	1.61E-01	806.43	not significant
3988	NAMPT	-1.07	4.65E-02	7.79E-02	1739.48	not significant
3989	SEC14L1	-1.07	4.05E-03	8.65E-03	3926.94	not significant
3990	CDC25A	-1.07	2.48E-03	5.52E-03	4343.46	not significant
3991	OXLD1	-1.07	2.22E-01	3.03E-01	345.98	not significant
3992	RASSF5	-1.07	1.13E-01	1.69E-01	691.52	not significant
3993	LYRM1	-1.07	7.78E-02	1.22E-01	1012.37	not significant
3994	PMVK	-1.07	6.13E-02	9.93E-02	1424.19	not significant
3995	KIF2A	-1.07	1.28E-03	3.00E-03	6924.06	not significant
3996	TMEM161A	-1.07	6.05E-02	9.82E-02	1052.75	not significant
3997	BCL11A	-1.07	1.13E-01	1.70E-01	759.54	not significant
3998	SF3B4	-1.07	1.15E-01	1.71E-01	757.97	not significant
3999	PGAM1P5	-1.07	2.63E-01	3.49E-01	11.74	not significant
4000	NEK9	-1.07	2.86E-03	6.28E-03	4443.70	not significant
4001	TK1	-1.07	3.52E-02	6.09E-02	1394.55	not significant
4002	CEP350	-1.07	4.68E-03	9.88E-03	4586.61	not significant
4003	GCLM	-1.07	6.05E-02	9.82E-02	1255.93	not significant
4004	ACER3	-1.07	3.31E-01	4.23E-01	150.31	not significant
4005	FBXL17	-1.07	5.45E-02	8.97E-02	1158.14	not significant
4006	SEC22B	-1.07	1.80E-01	2.53E-01	452.30	not significant
4007	HNRNPUL2	-1.07	3.83E-03	8.23E-03	4917.81	not significant
4008	OTUD6B-AS1	-1.07	3.33E-02	5.80E-02	1708.24	not significant
4009	SIPA1L1	-1.07	3.24E-02	5.66E-02	1640.75	not significant
4010	HIST1H2BE	-1.07	3.81E-01	4.73E-01	32.28	not significant
4011	MTPAP	-1.07	4.73E-02	7.92E-02	1299.41	not significant
4012	AP1M1	-1.07	8.73E-03	1.74E-02	4022.19	not significant
4013	EID2	-1.07	1.21E-01	1.80E-01	770.82	not significant
4014	AMN1	-1.07	2.06E-01	2.83E-01	423.99	not significant
4015	MAP4K5	-1.07	2.02E-02	3.70E-02	1879.00	not significant
4016	GLYR1	-1.07	5.52E-03	1.15E-02	3713.51	not significant
4017	EIF2AK2	-1.07	8.15E-03	1.63E-02	2911.74	not significant
4018	DBR1	-1.07	6.32E-02	1.02E-01	1246.30	not significant
4019	SEMA4G	-1.07	2.69E-01	3.55E-01	11.77	not significant
4020	NADSYN1	-1.07	3.63E-02	6.25E-02	1477.98	not significant
4021	KCNRG	-1.07	3.83E-01	4.75E-01	34.16	not significant
4022	LOC100128239	-1.07	3.23E-01	4.14E-01	16.49	not significant
4023	IFNGR1	-1.07	1.06E-01	1.61E-01	750.88	not significant
4024	MRPS31	-1.07	5.65E-02	9.24E-02	1131.02	not significant
4025	ADARB2	-1.07	3.72E-01	4.64E-01	27.90	not significant
4026	SF3B5	-1.07	2.27E-02	4.11E-02	3164.20	not significant
4027	CMTM3	-1.07	4.09E-03	8.72E-03	5300.69	not significant
4028	CAD	-1.07	2.87E-01	3.75E-01	7148.43	not significant
4029	ARMC2	-1.07	3.63E-01	4.55E-01	117.44	not significant
4030	NEMF	-1.07	3.42E-02	5.94E-02	2019.79	not significant
4031	SUPT20H	-1.07	9.17E-03	1.81E-02	2973.81	not significant
4032	NAA20	-1.07	2.39E-02	4.30E-02	2271.12	not significant
4033	GCN1L1	-1.07	1.99E-01	2.75E-01	9018.64	not significant
4034	STXBP3	-1.07	3.10E-02	5.43E-02	1812.74	not significant
4035	UBR3	-1.07	3.65E-02	6.27E-02	1477.16	not significant
4036	B3GNT2	-1.07	9.89E-03	1.94E-02	2899.07	not significant

4037	TRRAP	-1.07	2.76E-01	3.63E-01	7939.17	not significant
4038	CFAP44	-1.07	3.00E-01	3.89E-01	307.38	not significant
4039	LCLAT1	-1.07	7.67E-02	1.21E-01	974.30	not significant
4040	AOC3	-1.07	3.79E-01	4.71E-01	27.43	not significant
4041	NUTM2B-AS1	-1.07	2.34E-01	3.15E-01	378.99	not significant
4042	WDR37	-1.07	7.22E-02	1.15E-01	1071.26	not significant
4043	ANKRD11	-1.07	4.04E-03	8.64E-03	5683.16	not significant
4044	SF3B2	-1.07	7.50E-04	1.83E-03	12060.38	not significant
4045	LOC100507634	-1.07	3.62E-01	4.54E-01	21.62	not significant
4046	BANF1	-1.07	2.74E-02	4.86E-02	3253.07	not significant
4047	TMCO3	-1.07	5.21E-02	8.62E-02	1364.14	not significant
4048	MCM4	-1.07	4.03E-04	1.04E-03	29324.93	not significant
4049	RPN1	-1.07	1.76E-03	4.03E-03	9352.43	not significant
4050	GNL3L	-1.07	2.43E-02	4.37E-02	1809.26	not significant
4051	PROZ	-1.07	3.87E-01	4.80E-01	31.89	not significant
4052	SH2B3	-1.07	2.24E-02	4.07E-02	2481.01	not significant
4053	SELP	-1.07	3.74E-01	4.66E-01	26.98	not significant
4054	PCGF5	-1.07	4.51E-03	9.56E-03	7283.20	not significant
4055	CEP164	-1.07	9.28E-02	1.43E-01	887.45	not significant
4056	CYB5R1	-1.07	2.24E-01	3.05E-01	368.42	not significant
4057	PLXND1	-1.07	7.80E-02	1.23E-01	960.34	not significant
4058	MED16	-1.07	2.35E-02	4.23E-02	2491.42	not significant
4059	PLEKHH1	-1.07	2.79E-01	3.67E-01	11.34	not significant
4060	CACNB3	-1.07	7.13E-02	1.13E-01	988.87	not significant
4061	CEP89	-1.07	2.44E-01	3.28E-01	345.33	not significant
4062	FKBP11	-1.07	1.25E-01	1.85E-01	661.93	not significant
4063	NPAS1	-1.07	3.66E-01	4.58E-01	22.71	not significant
4064	FRA10AC1	-1.07	1.34E-01	1.97E-01	701.22	not significant
4065	ANXA7	-1.07	1.41E-02	2.68E-02	2660.47	not significant
4066	TNK2	-1.07	4.01E-02	6.82E-02	1545.96	not significant
4067	ABAT	-1.07	1.19E-01	1.77E-01	704.59	not significant
4068	CACNB4	-1.07	3.66E-01	4.57E-01	21.70	not significant
4069	AFMID	-1.07	2.32E-01	3.13E-01	346.12	not significant
4070	CEP85L	-1.07	3.66E-02	6.29E-02	2285.03	not significant
4071	ARIH2	-1.07	4.59E-03	9.72E-03	3844.97	not significant
4072	ISCA1	-1.07	9.25E-02	1.43E-01	842.50	not significant
4073	LOC101926928	-1.07	2.80E-01	3.68E-01	12.98	not significant
4074	ITSN2	-1.07	1.90E-02	3.51E-02	2159.84	not significant
4075	CBX3	-1.07	7.63E-03	1.54E-02	16674.87	not significant
4076	PLK3	-1.07	2.58E-01	3.43E-01	310.00	not significant
4077	MLH3	-1.07	4.67E-02	7.84E-02	1497.61	not significant
4078	PALB2	-1.07	6.70E-02	1.07E-01	1182.62	not significant
4079	SRD5A1	-1.07	1.72E-01	2.44E-01	535.73	not significant
4080	CENPK	-1.07	5.45E-02	8.97E-02	1961.91	not significant
4081	ARMC8	-1.07	2.45E-02	4.41E-02	1939.57	not significant
4082	COMMD9	-1.07	5.98E-02	9.72E-02	1312.93	not significant
4083	PPARD	-1.07	1.63E-01	2.32E-01	577.59	not significant
4084	NHLRC2	-1.07	3.55E-01	4.47E-01	712.23	not significant
4085	IRAK1BP1	-1.07	2.36E-01	3.18E-01	363.62	not significant
4086	SLC19A1	-1.07	4.88E-02	8.13E-02	1519.44	not significant
4087	SLC27A3	-1.07	3.10E-01	4.01E-01	13.15	not significant
4088	ARHGEF17	-1.07	4.10E-01	5.02E-01	45.13	not significant
4089	GDPGP1	-1.07	3.93E-01	4.85E-01	28.98	not significant
4090	ILF3-AS1	-1.07	2.35E-01	3.17E-01	393.68	not significant
4091	ANAPC10	-1.07	1.32E-01	1.94E-01	658.32	not significant
4092	LOC401134	-1.07	2.60E-01	3.45E-01	9.20	not significant
4093	SPEG	-1.07	2.61E-01	3.46E-01	9.81	not significant
4094	PHF21A	-1.07	9.01E-02	1.39E-01	1035.49	not significant
4095	HTATSF1P2	-1.07	4.00E-01	4.92E-01	87.33	not significant
4096	FBXO28	-1.07	6.91E-02	1.10E-01	1226.83	not significant
4097	SEC24C	-1.07	3.17E-03	6.92E-03	5504.23	not significant
4098	LINC-PINT	-1.07	3.19E-01	4.10E-01	14.13	not significant
4099	USP34	-1.07	1.00E-02	1.96E-02	6864.03	not significant
4100	LOC102724467	-1.07	2.53E-01	3.37E-01	9.11	not significant
4101	LOC101060498	-1.07	3.80E-01	4.72E-01	23.69	not significant
4102	GRB10	-1.07	4.09E-01	5.01E-01	71.70	not significant
4103	SERTAD3	-1.07	4.09E-01	5.01E-01	71.78	not significant
4104	COPS8	-1.07	2.21E-02	4.01E-02	2826.53	not significant
4105	WAS	-1.07	5.20E-02	8.61E-02	1298.90	not significant
4106	IFNAR2	-1.07	2.09E-02	3.82E-02	2415.00	not significant
4107	HMGB3	-1.07	8.71E-02	1.35E-01	1023.62	not significant
4108	RTN4R	-1.07	2.99E-01	3.88E-01	258.04	not significant
4109	MYT1L	-1.07	2.64E-01	3.50E-01	356.85	not significant
4110	HAVCR2	-1.07	3.96E-01	4.88E-01	28.94	not significant
4111	ATP8B2	-1.07	5.81E-03	1.20E-02	3889.97	not significant
4112	MED31	-1.07	2.86E-01	3.74E-01	257.87	not significant
4113	SOX7	-1.07	3.15E-01	4.05E-01	12.91	not significant
4114	SNAP23	-1.07	3.18E-02	5.56E-02	1758.54	not significant
4115	CSPP1	-1.07	7.02E-02	1.12E-01	1592.49	not significant
4116	TPD52L2	-1.07	1.97E-02	3.62E-02	2931.02	not significant
4117	DCAF4L1	-1.07	3.88E-01	4.81E-01	24.39	not significant
4118	LOC100289092	-1.07	3.91E-01	4.83E-01	116.84	not significant
4119	TRIM25	-1.07	4.08E-03	8.72E-03	5891.88	not significant
4120	LPCAT1	-1.07	1.21E-02	2.32E-02	7074.85	not significant
4121	LINC00977	-1.07	8.01E-02	1.26E-01	1044.30	not significant
4122	ZC3H12A	-1.07	3.16E-01	4.07E-01	221.27	not significant
4123	FUT10	-1.07	2.01E-01	2.78E-01	476.04	not significant
4124	MBNL2	-1.07	1.09E-01	1.64E-01	1079.11	not significant

4125	DRP2	-1.07	3.86E-01	4.78E-01	127.83	not significant
4126	DCAF10	-1.07	3.74E-02	6.41E-02	1626.60	not significant
4127	HIST1H1B	-1.07	4.21E-01	5.13E-01	54.41	not significant
4128	SMIM12	-1.07	7.90E-02	1.24E-01	1182.89	not significant
4129	UFL1	-1.07	2.19E-02	3.98E-02	2382.62	not significant
4130	NSUN5	-1.07	1.57E-01	2.25E-01	618.21	not significant
4131	OGFR	-1.07	2.44E-02	4.39E-02	2721.81	not significant
4132	MFSD12	-1.07	1.22E-01	1.82E-01	903.67	not significant
4133	EPB41	-1.07	4.10E-03	8.74E-03	8146.08	not significant
4134	ZNF117	-1.07	1.51E-01	2.17E-01	1163.98	not significant
4135	PHF20L1	-1.07	4.56E-03	9.66E-03	5600.12	not significant
4136	DDX47	-1.07	1.92E-02	3.53E-02	2292.23	not significant
4137	RPIA	-1.07	3.86E-02	6.59E-02	3166.38	not significant
4138	TYW5	-1.07	2.08E-01	2.86E-01	466.70	not significant
4139	NDUFS4	-1.07	1.37E-01	2.01E-01	948.44	not significant
4140	BCL2L12	-1.07	7.21E-02	1.15E-01	1277.47	not significant
4141	GPR97	-1.07	3.34E-01	4.25E-01	14.69	not significant
4142	XPA	-1.07	1.73E-01	2.45E-01	663.23	not significant
4143	RSRC1	-1.06	7.06E-02	1.12E-01	1270.52	not significant
4144	SNRPF	-1.06	2.38E-01	3.20E-01	4676.54	not significant
4145	MAML3	-1.06	2.39E-01	3.22E-01	391.92	not significant
4146	SUMF1	-1.06	3.52E-01	4.44E-01	189.45	not significant
4147	NIP7	-1.06	2.40E-02	4.32E-02	2413.33	not significant
4148	ELP3	-1.06	3.07E-02	5.38E-02	2094.39	not significant
4149	GCSHP3	-1.06	3.66E-01	4.58E-01	157.52	not significant
4150	ZNF705E	-1.06	2.66E-01	3.52E-01	9.17	not significant
4151	WDR62	-1.06	2.22E-01	3.02E-01	3420.57	not significant
4152	JAKMIP1	-1.06	3.23E-02	5.65E-02	2875.09	not significant
4153	COMT	-1.06	4.32E-02	7.30E-02	2315.75	not significant
4154	GTF2H2	-1.06	4.29E-01	5.21E-01	56.65	not significant
4155	MYO19	-1.06	1.31E-01	1.93E-01	756.59	not significant
4156	SCAF11	-1.06	1.72E-03	3.93E-03	9804.02	not significant
4157	LMAN2	-1.06	1.66E-02	3.09E-02	5693.04	not significant
4158	LRRC37A2	-1.06	4.28E-01	5.20E-01	49.31	not significant
4159	ARHGAP21	-1.06	3.98E-02	6.78E-02	2521.53	not significant
4160	TXNRD1	-1.06	2.64E-03	5.83E-03	12001.75	not significant
4161	MGME1	-1.06	7.50E-02	1.19E-01	1760.70	not significant
4162	LINC01516	-1.06	3.13E-01	4.04E-01	11.94	not significant
4163	SDHAF2	-1.06	6.19E-02	1.00E-01	1433.00	not significant
4164	COTL1	-1.06	1.97E-03	4.45E-03	8962.67	not significant
4165	HRH2	-1.06	2.28E-01	3.09E-01	8.37	not significant
4166	KLRAP1	-1.06	4.11E-01	5.03E-01	144.42	not significant
4167	DIAPH1	-1.06	5.90E-04	1.47E-03	17699.60	not significant
4168	UBXN2A	-1.06	8.61E-02	1.34E-01	1151.10	not significant
4169	COMMD2	-1.06	4.56E-02	7.66E-02	1615.58	not significant
4170	RGS12	-1.06	4.24E-01	5.16E-01	35.83	not significant
4171	CTDSPL2	-1.06	6.76E-03	1.38E-02	4246.51	not significant
4172	RNF144A-AS1	-1.06	2.22E-01	3.02E-01	450.85	not significant
4173	NDC1	-1.06	5.20E-03	1.09E-02	4818.35	not significant
4174	SENP2	-1.06	4.81E-02	8.03E-02	2081.50	not significant
4175	CCDC127	-1.06	2.05E-01	2.83E-01	474.90	not significant
4176	SHCBP1	-1.06	2.60E-02	4.64E-02	2944.84	not significant
4177	FSTL3	-1.06	3.96E-01	4.87E-01	127.18	not significant
4178	ATIC	-1.06	3.23E-03	7.04E-03	6463.05	not significant
4179	TBC1D5	-1.06	7.48E-03	1.51E-02	5424.34	not significant
4180	CNST	-1.06	3.70E-02	6.35E-02	1828.35	not significant
4181	RBMS2	-1.06	1.98E-01	2.75E-01	581.78	not significant
4182	ABCF3	-1.06	8.49E-02	1.32E-01	1090.24	not significant
4183	SET	-1.06	1.96E-03	4.44E-03	25694.29	not significant
4184	TRMT2A	-1.06	3.34E-02	5.81E-02	2052.99	not significant
4185	SOX12	-1.06	7.65E-02	1.21E-01	1200.41	not significant
4186	MORC2	-1.06	5.59E-02	9.16E-02	1846.12	not significant
4187	LRR1	-1.06	4.58E-02	7.68E-02	1741.46	not significant
4188	HCFC2	-1.06	1.70E-01	2.42E-01	610.82	not significant
4189	HIST1H3I	-1.06	4.11E-01	5.03E-01	27.70	not significant
4190	MAP7D3	-1.06	4.32E-02	7.30E-02	1840.82	not significant
4191	WEE1	-1.06	1.37E-02	2.62E-02	4139.36	not significant
4192	ZZZ3	-1.06	3.84E-02	6.57E-02	2130.44	not significant
4193	AMD1	-1.06	2.05E-03	4.63E-03	8397.72	not significant
4194	ITPRIP	-1.06	1.55E-01	2.22E-01	695.28	not significant
4195	FAM122B	-1.06	1.02E-02	2.00E-02	5461.97	not significant
4196	C3orf62	-1.06	2.65E-01	3.50E-01	387.68	not significant
4197	AGGF1	-1.06	9.82E-03	1.93E-02	3627.53	not significant
4198	BRD2	-1.06	2.14E-02	3.89E-02	2711.00	not significant
4199	LOC654342	-1.06	4.33E-01	5.25E-01	79.85	not significant
4200	FEM1B	-1.06	3.59E-02	6.18E-02	1878.75	not significant
4201	SLC35G1	-1.06	3.81E-01	4.73E-01	176.05	not significant
4202	MRPL27	-1.06	1.43E-01	2.08E-01	941.09	not significant
4203	TMBIM6	-1.06	6.91E-03	1.41E-02	31265.69	not significant
4204	ZSWIM7	-1.06	1.99E-01	2.75E-01	537.72	not significant
4205	QRICH1	-1.06	1.09E-02	2.11E-02	4210.10	not significant
4206	RAD21-AS1	-1.06	3.77E-01	4.69E-01	19.25	not significant
4207	TAB2	-1.06	2.11E-02	3.86E-02	2785.35	not significant
4208	C16orf95	-1.06	4.13E-01	5.04E-01	112.52	not significant
4209	XYLT1	-1.06	3.38E-01	4.30E-01	13.94	not significant
4210	HIST1H2BN	-1.06	4.11E-01	5.03E-01	25.66	not significant
4211	PTGES3L	-1.06	3.17E-01	4.08E-01	11.26	not significant
4212	FUT8	-1.06	2.52E-02	4.52E-02	2875.89	not significant

4213	UBE2Q1	-1.06	2.12E-02	3.87E-02	2922.48	not significant
4214	ALG11	-1.06	3.69E-01	4.61E-01	173.70	not significant
4215	LINC00936	-1.06	3.83E-01	4.75E-01	19.96	not significant
4216	TMEM62	-1.06	4.32E-01	5.24E-01	82.08	not significant
4217	PRR14L	-1.06	4.77E-02	7.98E-02	2378.72	not significant
4218	KLF16	-1.06	8.50E-02	1.32E-01	1432.77	not significant
4219	CANX	-1.06	6.95E-04	1.71E-03	28315.48	not significant
4220	HIST1H2AI	-1.06	3.89E-01	4.81E-01	19.51	not significant
4221	TRADD	-1.06	3.26E-01	4.17E-01	314.96	not significant
4222	DEGS1	-1.06	6.26E-02	1.01E-01	2183.29	not significant
4223	BRAP	-1.06	5.97E-02	9.71E-02	1818.08	not significant
4224	PCCB	-1.06	2.76E-02	4.90E-02	2524.45	not significant
4225	PTMA	-1.06	2.60E-03	5.77E-03	83042.12	not significant
4226	LOC100288637	-1.06	1.41E-01	2.06E-01	801.26	not significant
4227	SMAD6	-1.06	1.47E-01	2.13E-01	917.35	not significant
4228	LAMA2	-1.06	3.35E-01	4.27E-01	13.85	not significant
4229	ILF3	-1.06	1.82E-02	3.36E-02	26000.53	not significant
4230	C9orf69	-1.06	6.40E-02	1.03E-01	1488.95	not significant
4231	CDK6	-1.06	1.33E-02	2.55E-02	59852.66	not significant
4232	PIGG	-1.06	8.06E-02	1.26E-01	1197.85	not significant
4233	AMMECR1L	-1.06	5.53E-02	9.08E-02	1629.76	not significant
4234	NCAPH	-1.06	5.09E-03	1.07E-02	5465.02	not significant
4235	WBSCR16	-1.06	2.77E-01	3.64E-01	389.28	not significant
4236	UBAP2	-1.06	1.33E-02	2.55E-02	3663.80	not significant
4237	POM121	-1.06	1.03E-01	1.57E-01	1071.35	not significant
4238	BRD9	-1.06	3.51E-02	6.06E-02	2079.53	not significant
4239	LBR	-1.06	1.42E-03	3.30E-03	17991.69	not significant
4240	ULBP2	-1.06	4.44E-01	5.36E-01	86.65	not significant
4241	ATP6V1A	-1.06	4.05E-02	6.88E-02	2075.90	not significant
4242	HDHD3	-1.06	3.22E-01	4.13E-01	267.97	not significant
4243	HIST1H4E	-1.06	4.49E-01	5.41E-01	43.60	not significant
4244	SIGMAR1	-1.06	2.56E-02	4.59E-02	3339.84	not significant
4245	HNRNPH3	-1.06	9.50E-03	1.87E-02	9785.76	not significant
4246	INO80D	-1.06	1.90E-01	2.65E-01	1003.08	not significant
4247	CDC6	-1.06	1.51E-02	2.84E-02	3636.58	not significant
4248	AHCYL1	-1.06	2.21E-02	4.03E-02	4160.85	not significant
4249	FAM168B	-1.06	2.37E-02	4.27E-02	7735.52	not significant
4250	LOC341056	-1.06	4.09E-01	5.01E-01	21.14	not significant
4251	AKT2	-1.06	6.63E-03	1.35E-02	6192.58	not significant
4252	STS	-1.06	2.24E-01	3.05E-01	492.25	not significant
4253	FASTKD2	-1.06	1.10E-01	1.66E-01	1211.72	not significant
4254	PSMD9	-1.06	6.08E-02	9.86E-02	2150.52	not significant
4255	REXO1	-1.06	2.58E-02	4.61E-02	2795.37	not significant
4256	LINC01024	-1.06	3.24E-01	4.15E-01	10.93	not significant
4257	NACAP1	-1.06	4.52E-01	5.44E-01	67.37	not significant
4258	DENND3	-1.06	2.15E-01	2.95E-01	585.09	not significant
4259	RNF125	-1.06	3.10E-01	4.00E-01	313.85	not significant
4260	TYW1	-1.06	1.63E-01	2.33E-01	849.89	not significant
4261	RNU6-2	-1.06	3.47E-01	4.39E-01	14.23	not significant
4262	C17orf58	-1.06	4.00E-01	4.92E-01	21.41	not significant
4263	CPB2-AS1	-1.06	4.51E-01	5.43E-01	40.44	not significant
4264	RAB3GAP2	-1.06	2.22E-02	4.03E-02	2738.62	not significant
4265	PPP1R3D	-1.06	4.52E-01	5.44E-01	68.68	not significant
4266	NCAPG2	-1.06	7.38E-03	1.49E-02	8259.13	not significant
4267	PRRC2A	-1.06	1.85E-02	3.42E-02	7309.14	not significant
4268	ARHGAP26	-1.06	7.02E-02	1.12E-01	1433.76	not significant
4269	TMEM251	-1.06	2.25E-01	3.06E-01	489.56	not significant
4270	CREB3	-1.06	1.69E-01	2.40E-01	893.15	not significant
4271	CXorf40B	-1.06	4.28E-01	5.20E-01	110.92	not significant
4272	RALGAPB	-1.06	2.71E-02	4.83E-02	4811.17	not significant
4273	ATMIN	-1.06	3.18E-02	5.57E-02	2246.51	not significant
4274	SEC61G	-1.06	3.41E-01	4.32E-01	1531.62	not significant
4275	PDE6D	-1.06	5.57E-02	9.15E-02	1743.69	not significant
4276	MED7	-1.06	2.76E-01	3.63E-01	363.15	not significant
4277	RAB5C	-1.06	7.50E-02	1.19E-01	1847.58	not significant
4278	PIP4K2C	-1.06	1.19E-01	1.77E-01	968.90	not significant
4279	NEK7	-1.06	1.65E-02	3.08E-02	4617.04	not significant
4280	ZNF584	-1.06	2.92E-01	3.80E-01	343.66	not significant
4281	ZNF839	-1.06	2.65E-01	3.51E-01	401.86	not significant
4282	ADAM8	-1.06	4.57E-01	5.49E-01	47.03	not significant
4283	LOC101928063	-1.06	4.37E-01	5.29E-01	26.96	not significant
4284	NKAP	-1.06	1.63E-01	2.33E-01	759.71	not significant
4285	NAPA-AS1	-1.06	4.55E-01	5.46E-01	79.79	not significant
4286	GNG7	-1.06	2.93E-01	3.81E-01	9.47	not significant
4287	RPP30	-1.06	8.30E-02	1.30E-01	1629.54	not significant
4288	WDR63	-1.06	2.90E-01	3.78E-01	8.84	not significant
4289	PPP1R8	-1.06	2.27E-02	4.12E-02	3304.64	not significant
4290	SRPR	-1.06	7.04E-03	1.43E-02	6233.02	not significant
4291	ZNF267	-1.06	1.42E-01	2.07E-01	917.16	not significant
4292	PIGS	-1.06	7.76E-02	1.22E-01	1569.22	not significant
4293	ZNF79	-1.06	3.43E-01	4.34E-01	271.68	not significant
4294	FBL	-1.06	1.94E-01	2.69E-01	8352.38	not significant
4295	FAM192A	-1.06	1.21E-02	2.33E-02	4256.30	not significant
4296	PCNA	-1.06	1.82E-02	3.36E-02	27680.27	not significant
4297	NAPG	-1.06	6.67E-02	1.07E-01	1627.36	not significant
4298	AFG3L2	-1.06	4.84E-02	8.07E-02	2760.88	not significant
4299	MC1R	-1.06	4.30E-01	5.22E-01	25.51	not significant
4300	TMEM50A	-1.06	1.11E-02	2.16E-02	4188.46	not significant

4301	SLC52A2	-1.06	4.05E-01	4.97E-01	162.25	not significant
4302	PI4KB	-1.06	3.96E-02	6.75E-02	2648.58	not significant
4303	ANGPT1	-1.06	2.51E-01	3.35E-01	474.06	not significant
4304	PLCG2	-1.06	4.59E-01	5.50E-01	77.25	not significant
4305	MAP1LC3B2	-1.06	4.08E-01	5.00E-01	19.83	not significant
4306	CCDC168	-1.06	4.67E-01	5.58E-01	55.78	not significant
4307	TRIM71	-1.06	4.05E-01	4.97E-01	159.82	not significant
4308	RBM45	-1.06	2.66E-01	3.52E-01	427.62	not significant
4309	ATG10	-1.06	2.28E-01	3.09E-01	519.34	not significant
4310	DTD2	-1.06	1.71E-01	2.43E-01	789.66	not significant
4311	CREG1	-1.06	1.23E-01	1.82E-01	1200.83	not significant
4312	FAM220A	-1.06	1.94E-01	2.69E-01	692.94	not significant
4313	EEF2K	-1.06	8.59E-02	1.34E-01	1671.15	not significant
4314	B3GALT6	-1.06	1.53E-01	2.20E-01	1318.40	not significant
4315	MBD1	-1.06	3.02E-02	5.31E-02	3243.98	not significant
4316	SASH3	-1.06	4.60E-03	9.73E-03	20809.34	not significant
4317	SLC16A7	-1.06	7.42E-02	1.18E-01	1821.31	not significant
4318	TLR3	-1.06	3.36E-01	4.27E-01	305.51	not significant
4319	EIF3I	-1.06	2.12E-02	3.86E-02	8468.54	not significant
4320	PCTP	-1.06	2.39E-01	3.21E-01	497.86	not significant
4321	CCDC12	-1.06	1.27E-01	1.88E-01	1217.19	not significant
4322	LMAN2L	-1.06	2.11E-01	2.89E-01	679.79	not significant
4323	NSMCE1	-1.06	8.75E-02	1.36E-01	1496.95	not significant
4324	CCAR2	-1.06	4.06E-03	8.67E-03	9246.64	not significant
4325	AKTIP	-1.06	3.36E-01	4.27E-01	294.10	not significant
4326	RPGR	-1.06	2.65E-01	3.51E-01	450.99	not significant
4327	ANKDD1A	-1.06	4.73E-01	5.65E-01	55.37	not significant
4328	ASRGL1	-1.06	7.82E-02	1.23E-01	2074.26	not significant
4329	HLA-DMA	-1.06	4.67E-01	5.58E-01	37.69	not significant
4330	YTHDF2	-1.06	1.54E-02	2.90E-02	4100.29	not significant
4331	ERMARD	-1.06	3.23E-01	4.14E-01	388.14	not significant
4332	CEBPB	-1.06	3.20E-01	4.11E-01	450.67	not significant
4333	NFATC3	-1.06	1.37E-02	2.61E-02	7063.21	not significant
4334	DNAJC24	-1.06	1.49E-01	2.15E-01	860.76	not significant
4335	C16orf13	-1.06	6.78E-02	1.08E-01	1673.21	not significant
4336	KDM1B	-1.06	1.62E-01	2.32E-01	878.91	not significant
4337	AMH	-1.06	4.43E-01	5.35E-01	697.62	not significant
4338	WAC-AS1	-1.06	2.71E-01	3.57E-01	420.80	not significant
4339	FZR1	-1.06	3.92E-02	6.69E-02	2639.07	not significant
4340	TRIM35	-1.06	7.38E-02	1.17E-01	2157.41	not significant
4341	HAUS2	-1.06	6.15E-02	9.96E-02	1923.37	not significant
4342	DDX52	-1.06	6.61E-02	1.06E-01	1894.71	not significant
4343	MRPL44	-1.06	1.45E-01	2.11E-01	1055.82	not significant
4344	SUPT6H	-1.06	2.37E-02	4.28E-02	5275.06	not significant
4345	UQCRH	-1.06	3.94E-02	6.72E-02	4317.84	not significant
4346	NFYA	-1.06	1.69E-02	3.16E-02	4801.82	not significant
4347	CDK13	-1.06	3.90E-02	6.66E-02	2972.27	not significant
4348	KIF5A	-1.06	4.60E-01	5.52E-01	31.17	not significant
4349	LOC143666	-1.06	4.00E-01	4.92E-01	17.03	not significant
4350	C3AR1	-1.06	3.96E-01	4.88E-01	16.04	not significant
4351	MTMR4	-1.06	1.79E-02	3.31E-02	4281.61	not significant
4352	CCDC25	-1.06	3.98E-02	6.77E-02	2666.06	not significant
4353	ATAD1	-1.06	1.91E-02	3.51E-02	4041.77	not significant
4354	AASDHPPT	-1.06	4.69E-02	7.86E-02	3078.59	not significant
4355	RNMTL1	-1.06	1.87E-01	2.61E-01	740.85	not significant
4356	MACF1	-1.06	5.27E-02	8.71E-02	10176.53	not significant
4357	AGPAT1	-1.06	3.30E-01	4.21E-01	315.00	not significant
4358	CIDECP	-1.06	4.12E-01	5.03E-01	182.48	not significant
4359	NUP205	-1.06	1.69E-02	3.14E-02	8522.53	not significant
4360	FAM45B	-1.06	4.05E-01	4.97E-01	246.00	not significant
4361	RBM17	-1.06	1.28E-02	2.46E-02	5476.91	not significant
4362	DENND6B	-1.06	4.48E-01	5.40E-01	26.34	not significant
4363	CCRN4L	-1.06	3.92E-01	4.84E-01	212.11	not significant
4364	TRMT112	-1.06	5.77E-02	9.42E-02	2965.23	not significant
4365	PIP4K2B	-1.06	1.11E-02	2.15E-02	5694.07	not significant
4366	ATP2B4	-1.06	1.58E-02	2.96E-02	7449.72	not significant
4367	GSTA4	-1.06	4.21E-01	5.13E-01	161.61	not significant
4368	ZNF415	-1.06	2.74E-01	3.61E-01	450.19	not significant
4369	CNOT3	-1.06	1.07E-01	1.62E-01	1282.20	not significant
4370	C2orf69	-1.06	2.12E-01	2.91E-01	701.37	not significant
4371	NUPL1	-1.06	6.97E-03	1.42E-02	6525.17	not significant
4372	AK8	-1.06	3.71E-01	4.62E-01	12.34	not significant
4373	SEC31A	-1.06	7.43E-03	1.50E-02	6059.44	not significant
4374	ZP3	-1.06	4.53E-01	5.45E-01	27.62	not significant
4375	PAF1	-1.06	5.06E-02	8.40E-02	2192.00	not significant
4376	TSSC4	-1.06	1.84E-01	2.58E-01	860.39	not significant
4377	SEC63	-1.06	1.61E-02	3.01E-02	4819.86	not significant
4378	UNG	-1.06	1.27E-02	2.43E-02	6998.98	not significant
4379	TBP	-1.06	1.65E-01	2.36E-01	875.33	not significant
4380	TANGO2	-1.06	1.85E-01	2.59E-01	806.67	not significant
4381	PRDX2	-1.06	1.89E-02	3.48E-02	4530.96	not significant
4382	RNF25	-1.06	2.99E-01	3.88E-01	441.50	not significant
4383	SRP68	-1.06	1.23E-02	2.38E-02	6052.18	not significant
4384	FRYL	-1.06	2.96E-01	3.84E-01	4702.14	not significant
4385	CKS1B	-1.06	1.42E-01	2.07E-01	1598.58	not significant
4386	RPRD1A	-1.06	5.79E-02	9.46E-02	2353.14	not significant
4387	MAP4	-1.06	2.35E-02	4.25E-02	8272.14	not significant
4388	PIGA	-1.06	2.78E-01	3.65E-01	485.24	not significant

4389	MDK	-1.06	4.47E-01	5.39E-01	145.53	not significant
4390	NPTN	-1.06	1.27E-01	1.87E-01	1273.32	not significant
4391	TPGS2	-1.06	1.56E-02	2.92E-02	5768.18	not significant
4392	PVRL3	-1.06	1.19E-01	1.78E-01	1189.97	not significant
4393	LOC643770	-1.06	3.41E-01	4.32E-01	9.55	not significant
4394	MYH7B	-1.06	3.47E-01	4.38E-01	9.94	not significant
4395	TMEM50B	-1.06	3.43E-01	4.34E-01	299.07	not significant
4396	L2HGDH	-1.06	1.35E-01	1.98E-01	1134.37	not significant
4397	RABGAP1	-1.06	7.33E-02	1.16E-01	1728.29	not significant
4398	ADAP1	-1.06	4.77E-01	5.68E-01	33.73	not significant
4399	NECAB3	-1.06	2.70E-01	3.56E-01	745.97	not significant
4400	METTL17	-1.06	7.05E-02	1.12E-01	2255.21	not significant
4401	ADD1	-1.06	4.63E-03	9.78E-03	9403.91	not significant
4402	IFT122	-1.06	1.27E-01	1.88E-01	1122.31	not significant
4403	SRCAP	-1.06	1.70E-02	3.16E-02	7727.86	not significant
4404	SLC39A11	-1.06	1.91E-01	2.66E-01	866.78	not significant
4405	LIAS	-1.06	2.48E-01	3.32E-01	676.03	not significant
4406	DPH1	-1.05	2.82E-01	3.70E-01	456.47	not significant
4407	DUS4L	-1.05	2.19E-01	2.99E-01	656.15	not significant
4408	FAM207A	-1.05	2.18E-01	2.98E-01	710.42	not significant
4409	LINC00152	-1.05	4.32E-01	5.24E-01	171.50	not significant
4410	DUSP7	-1.05	1.64E-01	2.34E-01	1325.50	not significant
4411	SRSF3	-1.05	8.63E-03	1.72E-02	21848.67	not significant
4412	CFAP20	-1.05	6.47E-02	1.04E-01	3294.12	not significant
4413	SRPRB	-1.05	8.71E-02	1.35E-01	2175.60	not significant
4414	TCTEX1D2	-1.05	4.01E-01	4.93E-01	220.65	not significant
4415	ATXN3	-1.05	9.24E-02	1.42E-01	1483.97	not significant
4416	ZNF28	-1.05	1.64E-01	2.34E-01	1035.10	not significant
4417	LAMTOR1	-1.05	7.08E-02	1.13E-01	2239.18	not significant
4418	SP100	-1.05	5.54E-02	9.10E-02	2217.06	not significant
4419	UBR5	-1.05	2.40E-01	3.22E-01	7820.83	not significant
4420	TMED8	-1.05	3.22E-01	4.13E-01	380.32	not significant
4421	RIC1	-1.05	8.35E-02	1.30E-01	1596.99	not significant
4422	ACER2	-1.05	4.34E-01	5.26E-01	162.14	not significant
4423	LRP5L	-1.05	4.02E-01	4.93E-01	222.65	not significant
4424	DRAP1	-1.05	5.95E-02	9.69E-02	3564.54	not significant
4425	SLC26A11	-1.05	3.27E-01	4.18E-01	8.71	not significant
4426	CCDC116	-1.05	4.73E-01	5.64E-01	27.96	not significant
4427	STARD7	-1.05	2.01E-02	3.68E-02	11509.45	not significant
4428	FOXP1	-1.05	1.35E-01	1.98E-01	1112.84	not significant
4429	BTRC	-1.05	1.57E-01	2.25E-01	988.52	not significant
4430	PGGT1B	-1.05	2.31E-01	3.13E-01	756.29	not significant
4431	KLHDC10	-1.05	1.46E-01	2.11E-01	1077.42	not significant
4432	KCTD3	-1.05	1.77E-01	2.49E-01	866.95	not significant
4433	LOC115110	-1.05	4.83E-01	5.74E-01	33.50	not significant
4434	DMC1	-1.05	2.30E-01	3.11E-01	614.00	not significant
4435	SGOL1	-1.05	7.08E-02	1.13E-01	1902.96	not significant
4436	SEPHS1	-1.05	1.70E-02	3.17E-02	5457.39	not significant
4437	TICAM1	-1.05	3.29E-01	4.20E-01	357.84	not significant
4438	MID1IP1	-1.05	4.81E-02	8.03E-02	3231.59	not significant
4439	UFD1L	-1.05	5.60E-02	9.18E-02	2483.44	not significant
4440	CIPC	-1.05	1.43E-01	2.08E-01	1158.29	not significant
4441	COL4A3BP	-1.05	6.67E-02	1.07E-01	2553.16	not significant
4442	RAB6A	-1.05	3.44E-02	5.96E-02	4051.09	not significant
4443	RRP8	-1.05	2.09E-01	2.87E-01	727.93	not significant
4444	ASB8	-1.05	1.22E-01	1.81E-01	1477.40	not significant
4445	SUPT16H	-1.05	1.13E-02	2.19E-02	14794.36	not significant
4446	SWSAP1	-1.05	4.73E-01	5.64E-01	119.00	not significant
4447	ICE1	-1.05	4.06E-02	6.89E-02	3893.71	not significant
4448	OVCA2	-1.05	5.02E-01	5.92E-01	52.87	not significant
4449	GTF2H5	-1.05	2.83E-01	3.71E-01	572.70	not significant
4450	TIAF1	-1.05	3.39E-01	4.30E-01	8.46	not significant
4451	CD6	-1.05	3.95E-02	6.72E-02	3591.40	not significant
4452	SPAG5	-1.05	9.51E-03	1.87E-02	6750.55	not significant
4453	TMEM72	-1.05	5.03E-01	5.93E-01	51.58	not significant
4454	KCTD6	-1.05	4.58E-01	5.49E-01	168.61	not significant
4455	SHMT2	-1.05	1.66E-02	3.09E-02	9569.94	not significant
4456	C2CD2L	-1.05	2.02E-01	2.79E-01	851.92	not significant
4457	HNRNPA3	-1.05	2.46E-02	4.42E-02	23023.18	not significant
4458	BNIP1	-1.05	3.03E-01	3.92E-01	446.52	not significant
4459	DDTL	-1.05	3.30E-01	4.21E-01	9.82	not significant
4460	OTULIN	-1.05	7.00E-02	1.12E-01	2375.14	not significant
4461	PC	-1.05	2.01E-01	2.78E-01	846.17	not significant
4462	FAM189B	-1.05	3.60E-01	4.52E-01	458.91	not significant
4463	NUBP1	-1.05	3.07E-01	3.97E-01	448.16	not significant
4464	FHL1	-1.05	8.55E-02	1.33E-01	2112.75	not significant
4465	LHPP	-1.05	3.49E-01	4.41E-01	356.32	not significant
4466	ARFGEF1	-1.05	1.64E-02	3.07E-02	5440.10	not significant
4467	USP8	-1.05	9.98E-02	1.52E-01	1850.24	not significant
4468	KIAA2013	-1.05	1.10E-01	1.66E-01	1801.77	not significant
4469	ATP8A2	-1.05	2.47E-01	3.31E-01	632.85	not significant
4470	TRAFD1	-1.05	5.70E-02	9.31E-02	2483.94	not significant
4471	GLDN	-1.05	4.86E-01	5.76E-01	117.87	not significant
4472	UGDH	-1.05	2.42E-01	3.25E-01	661.67	not significant
4473	LRSAM1	-1.05	2.66E-01	3.52E-01	549.10	not significant
4474	MRPL37	-1.05	2.20E-02	4.01E-02	5265.75	not significant
4475	CCDC82	-1.05	1.05E-01	1.59E-01	1516.29	not significant
4476	DNPH1	-1.05	2.40E-01	3.22E-01	636.89	not significant

4477	GNPAT	-1.05	5.56E-02	9.13E-02	2716.87	not significant
4478	FBXO31	-1.05	1.36E-01	1.99E-01	1223.65	not significant
4479	BIRC2	-1.05	1.09E-01	1.64E-01	1571.19	not significant
4480	RSRC2	-1.05	7.47E-02	1.18E-01	3854.08	not significant
4481	SON	-1.05	4.99E-02	8.30E-02	18909.50	not significant
4482	MAPRE2	-1.05	2.28E-02	4.12E-02	5723.75	not significant
4483	GPR155	-1.05	2.23E-01	3.03E-01	758.51	not significant
4484	TRAM2-AS1	-1.05	5.08E-01	5.97E-01	96.00	not significant
4485	C15orf37	-1.05	5.03E-01	5.93E-01	91.41	not significant
4486	RHBDD3	-1.05	2.00E-01	2.77E-01	847.12	not significant
4487	ACSL5	-1.05	3.88E-02	6.62E-02	3239.14	not significant
4488	FEN1	-1.05	2.62E-01	3.47E-01	7743.56	not significant
4489	UBQLN4	-1.05	5.83E-02	9.51E-02	2450.72	not significant
4490	RAN	-1.05	2.45E-02	4.41E-02	29007.40	not significant
4491	HHIP	-1.05	1.04E-01	1.59E-01	1583.47	not significant
4492	XAF1	-1.05	1.42E-01	2.07E-01	1463.70	not significant
4493	MFSD3	-1.05	3.52E-01	4.44E-01	357.93	not significant
4494	PTTG1IP	-1.05	5.16E-02	8.55E-02	2798.66	not significant
4495	DICER1	-1.05	5.51E-02	9.06E-02	5947.68	not significant
4496	ATP6V0B	-1.05	8.06E-02	1.26E-01	2982.98	not significant
4497	C9orf78	-1.05	4.78E-02	8.00E-02	5351.93	not significant
4498	FCHO1	-1.05	1.33E-01	1.95E-01	1645.63	not significant
4499	RTN4RL1	-1.05	4.99E-01	5.88E-01	29.65	not significant
4500	DUSP11	-1.05	2.19E-01	2.98E-01	814.37	not significant
4501	RHOA	-1.05	5.10E-03	1.07E-02	21260.64	not significant
4502	TLL1	-1.05	4.78E-01	5.69E-01	21.14	not significant
4503	TMEM184B	-1.05	1.69E-01	2.39E-01	1285.14	not significant
4504	TM2D2	-1.05	2.20E-01	3.00E-01	804.45	not significant
4505	VAMP5	-1.05	1.62E-01	2.31E-01	1085.21	not significant
4506	DTWD1	-1.05	3.65E-01	4.57E-01	365.18	not significant
4507	THOC1	-1.05	1.10E-01	1.65E-01	1815.93	not significant
4508	PRPF18	-1.05	2.01E-01	2.78E-01	925.91	not significant
4509	ZNF202	-1.05	2.37E-01	3.19E-01	808.87	not significant
4510	LRBA	-1.05	9.08E-02	1.40E-01	3484.92	not significant
4511	BBS12	-1.05	5.19E-01	6.08E-01	45.42	not significant
4512	GCHFR	-1.05	3.66E-01	4.58E-01	355.35	not significant
4513	SYAP1	-1.05	2.04E-01	2.81E-01	1003.37	not significant
4514	JAM3	-1.05	3.91E-02	6.68E-02	3805.23	not significant
4515	TPRKB	-1.05	2.18E-01	2.98E-01	1347.43	not significant
4516	CSRP1	-1.05	9.30E-02	1.43E-01	2154.94	not significant
4517	MUL1	-1.05	2.89E-01	3.77E-01	638.94	not significant
4518	PCMT1	-1.05	6.67E-02	1.07E-01	3693.31	not significant
4519	STK38	-1.05	5.47E-02	9.00E-02	2926.30	not significant
4520	TP53RK	-1.05	1.27E-01	1.88E-01	1615.09	not significant
4521	SEC16A	-1.05	9.26E-02	1.43E-01	4655.37	not significant
4522	BAX	-1.05	8.50E-02	1.32E-01	2370.17	not significant
4523	CCDC71	-1.05	2.75E-01	3.62E-01	601.87	not significant
4524	PHF5A	-1.05	1.45E-01	2.11E-01	2810.51	not significant
4525	TET1	-1.05	2.17E-01	2.96E-01	816.54	not significant
4526	OSTM1	-1.05	1.41E-01	2.06E-01	1442.59	not significant
4527	GRB2	-1.05	3.54E-02	6.11E-02	15653.09	not significant
4528	UBE2D2	-1.05	3.62E-02	6.23E-02	6412.68	not significant
4529	THEMIS	-1.05	5.74E-02	9.38E-02	2869.07	not significant
4530	SNRPD2	-1.05	7.51E-02	1.19E-01	6293.38	not significant
4531	MYOM1	-1.05	4.66E-01	5.58E-01	17.99	not significant
4532	C11orf49	-1.05	2.06E-01	2.84E-01	906.25	not significant
4533	FLNA	-1.05	6.51E-02	1.05E-01	7750.21	not significant
4534	AKAP8	-1.05	1.12E-01	1.68E-01	1627.46	not significant
4535	TMSB10	-1.05	3.50E-02	6.06E-02	18766.11	not significant
4536	THAP2	-1.05	4.55E-01	5.47E-01	208.21	not significant
4537	TADA3	-1.05	9.04E-02	1.40E-01	2467.21	not significant
4538	CCDC85C	-1.05	1.18E-01	1.76E-01	2633.61	not significant
4539	OSTF1	-1.05	1.24E-01	1.83E-01	2013.00	not significant
4540	GDE1	-1.05	8.77E-02	1.36E-01	2333.24	not significant
4541	SRSF6	-1.05	2.41E-02	4.34E-02	14598.16	not significant
4542	C19orf71	-1.05	5.14E-01	6.03E-01	31.86	not significant
4543	CDC16	-1.05	1.27E-01	1.87E-01	2263.09	not significant
4544	TRIM38	-1.05	1.73E-01	2.45E-01	1248.06	not significant
4545	GNB1	-1.05	1.94E-02	3.56E-02	22227.28	not significant
4546	ZNF121	-1.05	5.22E-01	6.10E-01	426.14	not significant
4547	THOC2	-1.05	3.19E-02	5.58E-02	5940.91	not significant
4548	LPXN	-1.05	3.83E-02	6.56E-02	3818.89	not significant
4549	CUL5	-1.05	1.29E-01	1.91E-01	1661.90	not significant
4550	ATG4A	-1.05	3.24E-01	4.15E-01	477.31	not significant
4551	ARL3	-1.05	3.27E-01	4.18E-01	463.79	not significant
4552	DIS3L2	-1.05	1.73E-01	2.45E-01	1179.63	not significant
4553	ATP11B	-1.05	2.43E-02	4.38E-02	7735.33	not significant
4554	TCF7	-1.05	8.59E-03	1.71E-02	43046.99	not significant
4555	PPP1R18	-1.05	3.98E-01	4.90E-01	328.63	not significant
4556	ADAMTS7	-1.05	4.33E-01	5.25E-01	14.01	not significant
4557	CDK8	-1.05	2.06E-01	2.84E-01	1039.31	not significant
4558	RHOBTB1	-1.05	3.75E-01	4.67E-01	348.68	not significant
4559	MTO1	-1.05	1.29E-01	1.91E-01	1630.96	not significant
4560	AKIRIN1	-1.05	9.71E-02	1.49E-01	2641.46	not significant
4561	TWF2	-1.05	1.43E-01	2.09E-01	3088.17	not significant
4562	SRRM1	-1.05	4.89E-02	8.15E-02	5571.64	not significant
4563	KIF2C	-1.05	2.07E-02	3.79E-02	5601.76	not significant
4564	YY1	-1.05	2.64E-02	4.71E-02	6657.25	not significant

4565	PDK3	-1.05	1.51E-01	2.18E-01	1584.89	not significant
4566	JAKMIP3	-1.05	5.36E-01	6.23E-01	47.83	not significant
4567	NAAA	-1.05	4.12E-01	5.03E-01	287.46	not significant
4568	MED30	-1.05	1.91E-01	2.66E-01	1316.81	not significant
4569	MANEA	-1.05	1.24E-01	1.84E-01	1894.17	not significant
4570	HOMER2	-1.05	3.57E-01	4.48E-01	429.42	not significant
4571	TRIM3	-1.05	5.36E-01	6.23E-01	76.55	not significant
4572	BRAT1	-1.05	9.98E-02	1.52E-01	2454.53	not significant
4573	SELT	-1.05	6.60E-02	1.06E-01	3070.89	not significant
4574	ITGAE	-1.05	6.89E-02	1.10E-01	3299.92	not significant
4575	SMG1P1	-1.05	5.34E-01	6.22E-01	72.45	not significant
4576	ATR	-1.05	1.19E-01	1.78E-01	2055.94	not significant
4577	PPP1R3B	-1.05	2.88E-01	3.76E-01	615.50	not significant
4578	TCEA1	-1.05	8.33E-02	1.30E-01	3238.86	not significant
4579	LPIN1	-1.05	3.74E-02	6.42E-02	4819.19	not significant
4580	CCDC136	-1.05	2.82E-01	3.70E-01	844.41	not significant
4581	FOPNL	-1.05	5.05E-02	8.39E-02	3781.33	not significant
4582	CLDND2	-1.05	4.00E-01	4.92E-01	9.65	not significant
4583	CSNK1G2	-1.05	5.58E-02	9.15E-02	6106.18	not significant
4584	TBC1D31	-1.05	1.76E-01	2.48E-01	1265.91	not significant
4585	USP6NL	-1.05	1.66E-01	2.36E-01	1607.37	not significant
4586	NOVA1	-1.05	5.04E-01	5.94E-01	143.66	not significant
4587	NAF1	-1.05	2.11E-01	2.89E-01	960.57	not significant
4588	APBA2	-1.05	1.56E-01	2.24E-01	1323.38	not significant
4589	WDR74	-1.05	1.57E-01	2.25E-01	1384.53	not significant
4590	TBC1D25	-1.05	5.43E-01	6.29E-01	50.59	not significant
4591	TRPV2	-1.05	1.63E-01	2.33E-01	1286.29	not significant
4592	POLR2H	-1.05	1.51E-01	2.17E-01	1834.51	not significant
4593	MRPL53	-1.05	2.93E-01	3.81E-01	667.70	not significant
4594	RFC4	-1.05	8.72E-02	1.35E-01	3442.09	not significant
4595	CDH26	-1.05	4.34E-01	5.26E-01	12.60	not significant
4596	YBX2	-1.05	5.27E-01	6.15E-01	100.11	not significant
4597	TMEM81	-1.05	5.36E-01	6.24E-01	93.27	not significant
4598	LRRC63	-1.05	5.46E-01	6.32E-01	43.82	not significant
4599	EIF3D	-1.05	2.59E-02	4.63E-02	10425.93	not significant
4600	MUM1	-1.05	1.58E-01	2.26E-01	1328.70	not significant
4601	RNF141	-1.05	2.22E-01	3.03E-01	940.46	not significant
4602	APP	-1.05	5.24E-01	6.12E-01	26.53	not significant
4603	NKIRAS2	-1.05	4.71E-01	5.63E-01	258.43	not significant
4604	ZNF263	-1.05	1.59E-01	2.28E-01	1510.37	not significant
4605	PGBD1	-1.05	3.62E-01	4.54E-01	426.93	not significant
4606	HAS3	-1.05	5.50E-01	6.36E-01	49.71	not significant
4607	DBNL	-1.05	5.39E-02	8.89E-02	6315.73	not significant
4608	MCTS1	-1.05	1.45E-01	2.11E-01	1818.38	not significant
4609	REV3L	-1.05	1.06E-01	1.61E-01	2351.21	not significant
4610	ANKRD32	-1.05	1.57E-01	2.26E-01	1441.68	not significant
4611	TMEM127	-1.05	1.59E-01	2.28E-01	1625.54	not significant
4612	LMAN1	-1.05	2.67E-02	4.76E-02	8213.33	not significant
4613	DOCK9	-1.05	2.07E-01	2.84E-01	1174.09	not significant
4614	ABHD17A	-1.05	2.06E-01	2.84E-01	1028.78	not significant
4615	LRRC38	-1.05	5.38E-01	6.25E-01	32.87	not significant
4616	MAF1	-1.05	7.10E-02	1.13E-01	5007.22	not significant
4617	AIFM2	-1.05	5.41E-01	6.28E-01	87.59	not significant
4618	STAU2	-1.05	2.70E-02	4.81E-02	5803.02	not significant
4619	MAGED2	-1.05	1.10E-01	1.65E-01	2134.62	not significant
4620	SLC35E3	-1.05	3.90E-01	4.83E-01	411.70	not significant
4621	ERGIC2	-1.05	1.93E-01	2.68E-01	1162.49	not significant
4622	WBP4	-1.05	1.95E-01	2.70E-01	1291.02	not significant
4623	OST4	-1.05	6.94E-02	1.11E-01	3006.82	not significant
4624	ELMO3	-1.05	5.40E-01	6.27E-01	122.42	not significant
4625	PTPN11	-1.05	8.98E-02	1.39E-01	14315.15	not significant
4626	DHX36	-1.05	9.37E-02	1.44E-01	2475.36	not significant
4627	CMTM6	-1.05	3.33E-02	5.80E-02	7932.02	not significant
4628	C19orf10	-1.05	1.58E-01	2.26E-01	1692.46	not significant
4629	LPCAT3	-1.05	3.17E-01	4.07E-01	580.47	not significant
4630	GLA	-1.05	4.84E-01	5.75E-01	201.41	not significant
4631	SH3D21	-1.05	5.56E-01	6.41E-01	59.77	not significant
4632	TNFAIP8L2	-1.05	5.23E-01	6.11E-01	23.15	not significant
4633	UAP1	-1.05	1.96E-01	2.71E-01	1330.51	not significant
4634	ZPR1	-1.05	1.48E-01	2.14E-01	1550.77	not significant
4635	USP31	-1.05	3.02E-01	3.92E-01	610.35	not significant
4636	IPO9	-1.05	4.21E-02	7.12E-02	4978.07	not significant
4637	ERICH1	-1.05	1.88E-01	2.62E-01	1372.17	not significant
4638	TAF10	-1.05	1.59E-01	2.28E-01	2296.36	not significant
4639	SV2A	-1.05	3.65E-01	4.57E-01	446.51	not significant
4640	ZCCHC10	-1.05	1.97E-01	2.73E-01	1126.44	not significant
4641	KIAA1024	-1.05	5.49E-01	6.35E-01	87.98	not significant
4642	INO80E	-1.05	9.29E-02	1.43E-01	2486.12	not significant
4643	PORCN	-1.05	5.57E-01	6.42E-01	43.99	not significant
4644	LAMTOR4	-1.05	1.73E-01	2.45E-01	1498.81	not significant
4645	SLC22A5	-1.05	4.22E-01	5.14E-01	313.73	not significant
4646	CCDC88A	-1.05	4.02E-01	4.93E-01	4522.94	not significant
4647	LRRC37A3	-1.05	5.61E-01	6.46E-01	59.13	not significant
4648	RAD18	-1.05	7.80E-02	1.23E-01	2698.46	not significant
4649	NCOA6	-1.05	9.17E-02	1.42E-01	5158.08	not significant
4650	HORMAD2	-1.05	4.62E-01	5.54E-01	13.16	not significant
4651	UBE2A	-1.05	4.94E-02	8.22E-02	4370.68	not significant
4652	SMAD5	-1.05	3.79E-01	4.70E-01	445.64	not significant

4653	FNTB	-1.05	5.62E-01	6.46E-01	44.21	not significant
4654	FIP1L1	-1.05	7.01E-02	1.12E-01	3216.92	not significant
4655	GTF2F2	-1.05	2.19E-01	2.99E-01	1459.01	not significant
4656	GALNT10	-1.05	1.97E-01	2.73E-01	1312.20	not significant
4657	TTC30B	-1.05	5.54E-01	6.39E-01	94.40	not significant
4658	PSMG4	-1.05	2.88E-01	3.76E-01	736.24	not significant
4659	ARF6	-1.05	3.47E-02	6.01E-02	6736.43	not significant
4660	GBP4	-1.05	1.28E-01	1.89E-01	1901.30	not significant
4661	ACOT8	-1.05	2.71E-01	3.57E-01	825.87	not significant
4662	HIF1A	-1.05	5.48E-02	9.02E-02	4136.60	not significant
4663	PRR34-AS1	-1.05	5.48E-01	6.34E-01	110.06	not significant
4664	ERCC3	-1.05	1.06E-01	1.61E-01	2662.59	not significant
4665	ZNF689	-1.05	1.73E-01	2.45E-01	1425.96	not significant
4666	RASSF1	-1.05	4.12E-01	5.03E-01	365.26	not significant
4667	SLC25A51	-1.05	3.57E-01	4.49E-01	504.11	not significant
4668	UBA2	-1.04	5.22E-02	8.63E-02	8613.27	not significant
4669	UBA6	-1.04	1.08E-01	1.63E-01	3422.29	not significant
4670	USP1	-1.04	4.10E-02	6.95E-02	9140.61	not significant
4671	GJA3	-1.04	5.44E-01	6.30E-01	26.49	not significant
4672	TMEM131	-1.04	7.68E-02	1.21E-01	3233.46	not significant
4673	VPS37A	-1.04	2.05E-01	2.83E-01	1516.87	not significant
4674	OSM	-1.04	2.55E-01	3.40E-01	860.13	not significant
4675	TMEM184C	-1.04	1.63E-01	2.33E-01	1695.75	not significant
4676	VSIG10L	-1.04	5.65E-01	6.49E-01	41.96	not significant
4677	AKNA	-1.04	5.41E-02	8.92E-02	8684.11	not significant
4678	REXO2	-1.04	2.96E-01	3.84E-01	820.38	not significant
4679	NMNAT1	-1.04	4.03E-01	4.95E-01	391.65	not significant
4680	PPP1CB	-1.04	3.87E-02	6.61E-02	7328.08	not significant
4681	SLC39A3	-1.04	1.99E-01	2.75E-01	1396.22	not significant
4682	GMPS	-1.04	6.45E-02	1.04E-01	4198.08	not significant
4683	IL21R	-1.04	5.67E-01	6.51E-01	37.80	not significant
4684	SKA2	-1.04	4.50E-02	7.58E-02	5850.49	not significant
4685	UGP2	-1.04	5.32E-02	8.78E-02	12797.60	not significant
4686	SIRT5	-1.04	3.61E-01	4.53E-01	545.86	not significant
4687	COA1	-1.04	1.20E-01	1.79E-01	3458.66	not significant
4688	POLR2C	-1.04	8.65E-02	1.34E-01	4047.28	not significant
4689	GINS2	-1.04	1.23E-01	1.83E-01	3108.57	not significant
4690	RNF14	-1.04	1.38E-01	2.02E-01	1932.68	not significant
4691	RNF144B	-1.04	5.05E-01	5.95E-01	16.24	not significant
4692	TTPAL	-1.04	2.30E-01	3.11E-01	1123.78	not significant
4693	SCNM1	-1.04	4.72E-01	5.64E-01	12.27	not significant
4694	RASSF3	-1.04	1.64E-01	2.34E-01	1896.42	not significant
4695	DSTYK	-1.04	4.83E-01	5.73E-01	243.61	not significant
4696	KRCC1	-1.04	3.17E-01	4.08E-01	650.19	not significant
4697	GNAZ	-1.04	4.65E-01	5.57E-01	11.97	not significant
4698	RPA1	-1.04	5.37E-02	8.86E-02	11675.76	not significant
4699	SORBS3	-1.04	1.18E-01	1.76E-01	2130.05	not significant
4700	KIF9-AS1	-1.04	5.51E-01	6.36E-01	26.20	not significant
4701	GNL1	-1.04	2.61E-01	3.46E-01	1040.64	not significant
4702	ANKFN1	-1.04	3.10E-01	4.00E-01	689.79	not significant
4703	MED11	-1.04	4.38E-01	5.30E-01	340.70	not significant
4704	FAM83G	-1.04	5.08E-01	5.97E-01	197.22	not significant
4705	NFE2L3	-1.04	4.88E-01	5.78E-01	244.48	not significant
4706	TMEM2	-1.04	3.36E-01	4.27E-01	660.09	not significant
4707	TIMM10B	-1.04	1.37E-01	2.00E-01	1913.86	not significant
4708	ZNF396	-1.04	4.19E-01	5.11E-01	8.21	not significant
4709	MFAP3	-1.04	1.47E-01	2.13E-01	1894.75	not significant
4710	USP16	-1.04	1.06E-01	1.61E-01	2462.87	not significant
4711	SLC35F6	-1.04	2.35E-01	3.17E-01	1063.05	not significant
4712	SLC35G2	-1.04	5.25E-01	6.13E-01	172.08	not significant
4713	TTC8	-1.04	5.65E-01	6.49E-01	105.91	not significant
4714	NF2	-1.04	1.65E-01	2.35E-01	2275.08	not significant
4715	GGA1	-1.04	2.11E-01	2.89E-01	1565.47	not significant
4716	RNASEH2B	-1.04	4.88E-02	8.14E-02	6627.55	not significant
4717	TRAF3IP1	-1.04	3.75E-01	4.67E-01	515.81	not significant
4718	B4GALT7	-1.04	4.61E-01	5.53E-01	295.65	not significant
4719	LOC728730	-1.04	5.83E-01	6.65E-01	54.41	not significant
4720	EIF2B4	-1.04	2.99E-01	3.88E-01	796.91	not significant
4721	USP43	-1.04	5.68E-01	6.51E-01	32.66	not significant
4722	ISPD	-1.04	5.57E-01	6.42E-01	132.61	not significant
4723	ANTXR2	-1.04	5.72E-01	6.56E-01	36.59	not significant
4724	MESDC2	-1.04	1.92E-01	2.67E-01	2274.49	not significant
4725	EP300-AS1	-1.04	5.62E-01	6.46E-01	31.24	not significant
4726	MIF-AS1	-1.04	5.12E-01	6.01E-01	375.27	not significant
4727	C1orf123	-1.04	2.97E-01	3.86E-01	865.22	not significant
4728	USP15	-1.04	1.37E-01	2.00E-01	3185.37	not significant
4729	MBD3	-1.04	7.25E-02	1.15E-01	5272.49	not significant
4730	CCDC186	-1.04	3.74E-01	4.66E-01	564.62	not significant
4731	SMDT1	-1.04	5.05E-01	5.94E-01	240.78	not significant
4732	RBMXL1	-1.04	2.27E-01	3.08E-01	1448.02	not significant
4733	HELLS	-1.04	1.30E-01	1.91E-01	2393.67	not significant
4734	MBIP	-1.04	3.21E-01	4.12E-01	769.71	not significant
4735	AES	-1.04	8.96E-02	1.39E-01	15217.33	not significant
4736	CHKB-AS1	-1.04	5.83E-01	6.65E-01	34.33	not significant
4737	STRN	-1.04	1.15E-01	1.72E-01	3984.48	not significant
4738	CEP83-AS1	-1.04	5.54E-01	6.39E-01	22.69	not significant
4739	TP53INP2	-1.04	5.03E-01	5.93E-01	238.11	not significant
4740	DET1	-1.04	5.49E-01	6.35E-01	164.96	not significant

4741	STYX	-1.04	1.78E-01	2.50E-01	1849.34	not significant
4742	TPI1P2	-1.04	5.90E-01	6.72E-01	43.44	not significant
4743	RER1	-1.04	1.22E-01	1.81E-01	3832.18	not significant
4744	LPAR4	-1.04	5.40E-01	6.27E-01	19.38	not significant
4745	HMGB1	-1.04	7.83E-02	1.23E-01	19601.01	not significant
4746	TRIM2	-1.04	5.81E-01	6.64E-01	30.98	not significant
4747	CTTNBP2NL	-1.04	5.32E-01	6.20E-01	186.82	not significant
4748	KATNB1	-1.04	2.53E-01	3.37E-01	1069.42	not significant
4749	MTHFD1	-1.04	3.86E-02	6.59E-02	9808.54	not significant
4750	SLC9A6	-1.04	5.59E-01	6.44E-01	142.38	not significant
4751	MANSC1	-1.04	4.51E-01	5.43E-01	9.08	not significant
4752	SNX29	-1.04	2.61E-01	3.46E-01	1096.16	not significant
4753	GTDC1	-1.04	4.97E-01	5.87E-01	277.84	not significant
4754	LINC01144	-1.04	5.65E-01	6.49E-01	22.98	not significant
4755	PBRM1	-1.04	8.05E-02	1.26E-01	8729.17	not significant
4756	TPM1	-1.04	5.95E-01	6.76E-01	47.31	not significant
4757	TMEM102	-1.04	4.98E-01	5.88E-01	339.48	not significant
4758	ZNF639	-1.04	1.62E-01	2.32E-01	2131.56	not significant
4759	STON2	-1.04	5.96E-01	6.77E-01	57.26	not significant
4760	C9orf156	-1.04	4.93E-01	5.84E-01	278.41	not significant
4761	SBNO1	-1.04	1.04E-01	1.58E-01	4651.41	not significant
4762	SCARNA9	-1.04	5.40E-01	6.27E-01	18.05	not significant
4763	COX5A	-1.04	1.16E-01	1.73E-01	3372.58	not significant
4764	POLG2	-1.04	5.42E-01	6.29E-01	179.43	not significant
4765	TTC30A	-1.04	5.98E-01	6.78E-01	60.58	not significant
4766	RILPL2	-1.04	2.86E-01	3.74E-01	1056.07	not significant
4767	HSBP1	-1.04	1.64E-01	2.34E-01	1864.21	not significant
4768	ATP5C1	-1.04	5.47E-02	9.00E-02	7884.49	not significant
4769	RNF13	-1.04	2.86E-01	3.75E-01	1004.05	not significant
4770	PLEKHA4	-1.04	6.01E-01	6.80E-01	58.34	not significant
4771	TRMT10B	-1.04	4.64E-01	5.56E-01	401.92	not significant
4772	ERCC8	-1.04	3.40E-01	4.32E-01	701.38	not significant
4773	RFC2	-1.04	2.16E-01	2.95E-01	1891.10	not significant
4774	LRRC16A	-1.04	5.51E-01	6.37E-01	18.45	not significant
4775	ZSCAN30	-1.04	3.84E-01	4.76E-01	680.49	not significant
4776	ZSWIM1	-1.04	4.12E-01	5.04E-01	463.35	not significant
4777	APOOL	-1.04	2.93E-01	3.81E-01	899.86	not significant
4778	PDS5B	-1.04	1.65E-01	2.35E-01	4175.88	not significant
4779	ZSCAN5A	-1.04	5.65E-01	6.49E-01	144.51	not significant
4780	LSM7	-1.04	5.30E-01	6.18E-01	1912.11	not significant
4781	NLRP14	-1.04	6.01E-01	6.81E-01	72.78	not significant
4782	GIMAP7	-1.04	1.18E-01	1.75E-01	7868.25	not significant
4783	TBC1D23	-1.04	2.70E-01	3.56E-01	1196.09	not significant
4784	ERCC2	-1.04	2.90E-01	3.78E-01	1003.32	not significant
4785	TRAPPC12	-1.04	2.61E-01	3.46E-01	1329.97	not significant
4786	SCMH1	-1.04	1.34E-01	1.96E-01	2749.46	not significant
4787	ZRANB2	-1.04	1.07E-01	1.62E-01	5937.93	not significant
4788	EHBP1L1	-1.04	1.17E-01	1.75E-01	2756.24	not significant
4789	FAF1	-1.04	9.52E-02	1.46E-01	3554.47	not significant
4790	LMNB2	-1.04	9.20E-02	1.42E-01	11841.44	not significant
4791	RNMT	-1.04	1.46E-01	2.12E-01	3538.37	not significant
4792	SLC16A13	-1.04	5.23E-01	6.12E-01	231.04	not significant
4793	YAE1D1	-1.04	5.20E-01	6.08E-01	237.05	not significant
4794	PSMC6	-1.04	1.50E-01	2.17E-01	2495.64	not significant
4795	SIRT3	-1.04	4.48E-01	5.40E-01	397.39	not significant
4796	C9orf89	-1.04	4.56E-01	5.48E-01	392.92	not significant
4797	RNF157-AS1	-1.04	4.84E-01	5.74E-01	11.12	not significant
4798	ATRX	-1.04	3.35E-01	4.27E-01	812.86	not significant
4799	MCF2	-1.04	5.91E-01	6.72E-01	28.61	not significant
4800	RPP14	-1.04	2.48E-01	3.32E-01	1259.15	not significant
4801	MANBAL	-1.04	4.17E-01	5.08E-01	525.18	not significant
4802	AVEN	-1.04	4.32E-01	5.24E-01	466.91	not significant
4803	SH3BP5L	-1.04	1.76E-01	2.49E-01	1823.07	not significant
4804	BBS4	-1.04	4.42E-01	5.35E-01	417.75	not significant
4805	PTPRVP	-1.04	5.87E-01	6.69E-01	30.95	not significant
4806	AMZ2P1	-1.04	3.96E-01	4.88E-01	591.83	not significant
4807	ITGA9-AS1	-1.04	5.88E-01	6.69E-01	27.04	not significant
4808	DECR2	-1.04	4.50E-01	5.43E-01	398.14	not significant
4809	MED4	-1.04	1.26E-01	1.87E-01	3357.48	not significant
4810	LINC00662	-1.04	5.78E-01	6.61E-01	147.39	not significant
4811	SMIM19	-1.04	4.00E-01	4.91E-01	594.75	not significant
4812	TRIP11	-1.04	2.76E-01	3.63E-01	1293.95	not significant
4813	TOMM70A	-1.04	6.07E-02	9.85E-02	6432.55	not significant
4814	AUNIP	-1.04	4.43E-01	5.36E-01	413.13	not significant
4815	AMDHD1	-1.04	5.15E-01	6.03E-01	11.74	not significant
4816	PIEZO1	-1.04	3.95E-01	4.87E-01	9867.00	not significant
4817	NAA16	-1.04	3.39E-01	4.30E-01	1462.54	not significant
4818	CDKN2AIP	-1.04	2.04E-01	2.82E-01	1655.57	not significant
4819	RFX7	-1.04	1.60E-01	2.29E-01	3413.65	not significant
4820	APAF1	-1.04	1.83E-01	2.56E-01	2047.78	not significant
4821	GLB1	-1.04	2.57E-01	3.42E-01	1440.10	not significant
4822	NLRP1	-1.04	4.95E-01	5.85E-01	346.08	not significant
4823	ZMYND19	-1.04	3.37E-01	4.29E-01	850.62	not significant
4824	ZSCAN22	-1.04	5.90E-01	6.72E-01	126.96	not significant
4825	BRI3BP	-1.04	2.26E-01	3.07E-01	1506.77	not significant
4826	EMC4	-1.04	1.98E-01	2.75E-01	1737.36	not significant
4827	SP110	-1.04	2.37E-01	3.19E-01	1551.67	not significant
4828	ELOVL4	-1.04	2.66E-01	3.52E-01	1271.02	not significant

4829	RNF34	-1.04	5.50E-01	6.35E-01	231.35	not significant
4830	ITCH	-1.04	8.04E-02	1.26E-01	5535.78	not significant
4831	GLE1	-1.04	1.73E-01	2.45E-01	2541.48	not significant
4832	SLC43A2	-1.04	5.47E-01	6.33E-01	213.82	not significant
4833	TMED5	-1.04	6.75E-02	1.08E-01	5802.32	not significant
4834	NDUFA10	-1.04	1.33E-01	1.95E-01	2728.46	not significant
4835	LRRC8B	-1.04	4.30E-01	5.22E-01	469.45	not significant
4836	MCM2	-1.04	5.89E-02	9.59E-02	16370.09	not significant
4837	ZC3H4	-1.04	1.52E-01	2.19E-01	3103.90	not significant
4838	COA5	-1.04	3.24E-01	4.15E-01	978.97	not significant
4839	BIN3	-1.04	3.38E-01	4.30E-01	1058.59	not significant
4840	CAST	-1.04	3.27E-01	4.18E-01	970.37	not significant
4841	FAM126B	-1.04	2.56E-01	3.40E-01	1690.44	not significant
4842	ZNF654	-1.04	3.19E-01	4.10E-01	964.99	not significant
4843	RAG2	-1.04	6.16E-01	6.94E-01	39.29	not significant
4844	BROX	-1.04	3.61E-01	4.53E-01	911.76	not significant
4845	SLC7A6OS	-1.04	4.29E-01	5.21E-01	504.20	not significant
4846	PLOD3	-1.04	5.61E-01	6.45E-01	184.77	not significant
4847	C6orf106	-1.04	1.99E-01	2.75E-01	4172.64	not significant
4848	LRRIQ3	-1.04	5.91E-01	6.72E-01	25.30	not significant
4849	LOC100506730	-1.04	5.66E-01	6.50E-01	185.62	not significant
4850	SNRPA	-1.04	6.80E-02	1.09E-01	5586.90	not significant
4851	AK9	-1.04	6.05E-01	6.85E-01	108.95	not significant
4852	GBF1	-1.04	5.06E-01	5.96E-01	3431.89	not significant
4853	RPRD2	-1.04	2.30E-01	3.11E-01	2409.98	not significant
4854	LYRM4	-1.04	3.20E-01	4.11E-01	927.16	not significant
4855	CHRNA10	-1.04	5.79E-01	6.62E-01	20.39	not significant
4856	KATNA1	-1.04	2.97E-01	3.86E-01	1020.20	not significant
4857	PHKA1	-1.04	6.17E-01	6.95E-01	39.18	not significant
4858	DHX30	-1.04	9.49E-02	1.46E-01	4924.22	not significant
4859	NEK6	-1.04	5.40E-01	6.27E-01	234.07	not significant
4860	BAIAP2	-1.04	5.26E-01	6.14E-01	287.76	not significant
4861	TMEM150A	-1.04	5.27E-01	6.15E-01	12.01	not significant
4862	RARS2	-1.04	3.05E-01	3.95E-01	1006.27	not significant
4863	MCMBP	-1.04	1.10E-01	1.65E-01	7084.73	not significant
4864	TMEM154	-1.04	3.54E-01	4.46E-01	810.96	not significant
4865	ECT2	-1.04	9.72E-02	1.49E-01	4599.69	not significant
4866	UBN1	-1.04	9.20E-02	1.42E-01	5065.70	not significant
4867	MSS51	-1.04	6.27E-01	7.03E-01	51.66	not significant
4868	GCSH	-1.04	6.12E-01	6.90E-01	97.86	not significant
4869	CCDC152	-1.04	2.32E-01	3.14E-01	2102.60	not significant
4870	DCAF5	-1.04	2.09E-01	2.87E-01	2920.64	not significant
4871	KCTD20	-1.04	8.88E-02	1.38E-01	6363.06	not significant
4872	ARFGEF2	-1.04	1.26E-01	1.87E-01	4183.95	not significant
4873	PLP2	-1.04	3.97E-01	4.88E-01	714.09	not significant
4874	RNF187	-1.04	1.22E-01	1.82E-01	5207.16	not significant
4875	R3HDM4	-1.04	2.68E-01	3.54E-01	1287.83	not significant
4876	MLX	-1.04	1.86E-01	2.61E-01	2666.43	not significant
4877	FUT11	-1.04	6.27E-01	7.03E-01	46.53	not significant
4878	MBLAC2	-1.04	4.13E-01	5.04E-01	574.46	not significant
4879	RAVER1	-1.04	1.07E-01	1.62E-01	9233.09	not significant
4880	FAM208A	-1.04	9.38E-02	1.44E-01	6650.07	not significant
4881	RBM23	-1.04	1.66E-01	2.36E-01	2881.31	not significant
4882	C8orf58	-1.04	6.18E-01	6.95E-01	97.78	not significant
4883	FRG1	-1.04	3.56E-01	4.48E-01	1181.48	not significant
4884	FAM212B	-1.04	5.84E-01	6.66E-01	167.62	not significant
4885	INPP5K	-1.04	2.78E-01	3.66E-01	1560.64	not significant
4886	SHB	-1.04	5.49E-01	6.35E-01	13.49	not significant
4887	BTBD7	-1.04	3.51E-01	4.43E-01	861.52	not significant
4888	SLC38A6	-1.04	5.33E-01	6.20E-01	276.84	not significant
4889	FBXO18	-1.04	2.04E-01	2.81E-01	2249.69	not significant
4890	FBXO9	-1.04	1.78E-01	2.51E-01	2387.26	not significant
4891	FAM96A	-1.04	2.27E-01	3.09E-01	1646.47	not significant
4892	NOMO2	-1.04	5.36E-01	6.23E-01	288.95	not significant
4893	GOLGA5	-1.04	3.34E-01	4.26E-01	892.68	not significant
4894	WIPF2	-1.04	2.20E-01	3.00E-01	1716.60	not significant
4895	BST2	-1.04	5.07E-01	5.97E-01	1809.66	not significant
4896	MED1	-1.04	1.18E-01	1.76E-01	7840.03	not significant
4897	HIST1H4A	-1.04	6.31E-01	7.08E-01	42.51	not significant
4898	BCL2L15	-1.04	5.87E-01	6.69E-01	19.48	not significant
4899	ST3GAL2	-1.04	2.32E-01	3.14E-01	1718.08	not significant
4900	PSD4	-1.04	8.74E-02	1.36E-01	6839.22	not significant
4901	NDUFV1	-1.04	8.61E-02	1.34E-01	5078.89	not significant
4902	FAM199X	-1.04	6.13E-01	6.91E-01	125.95	not significant
4903	LYRM5	-1.04	5.05E-01	5.94E-01	339.27	not significant
4904	GSS	-1.04	1.71E-01	2.43E-01	2781.16	not significant
4905	LOC730202	-1.04	5.72E-01	6.56E-01	17.99	not significant
4906	GS1-259H13.2	-1.04	6.30E-01	7.06E-01	87.01	not significant
4907	UCK2	-1.04	1.35E-01	1.97E-01	5530.63	not significant
4908	UTP14A	-1.04	1.99E-01	2.75E-01	2131.81	not significant
4909	GTPBP3	-1.04	3.65E-01	4.57E-01	1167.70	not significant
4910	GZMA	-1.04	5.80E-01	6.63E-01	188.72	not significant
4911	LINC00665	-1.04	5.08E-01	5.97E-01	342.19	not significant
4912	RNF113A	-1.04	3.81E-01	4.73E-01	824.85	not significant
4913	ZNF800	-1.04	2.66E-01	3.52E-01	1457.02	not significant
4914	GTF2I	-1.04	1.64E-01	2.34E-01	3693.32	not significant
4915	SNX3	-1.04	1.29E-01	1.91E-01	4100.96	not significant
4916	AP4E1	-1.04	3.41E-01	4.32E-01	977.91	not significant

4917	SLC25A39	-1.04	1.51E-01	2.18E-01	3251.46	not significant
4918	ARMC4	-1.04	6.34E-01	7.10E-01	81.30	not significant
4919	FAF2	-1.04	1.51E-01	2.18E-01	2954.32	not significant
4920	MPHOSPH8	-1.04	2.35E-01	3.17E-01	1919.15	not significant
4921	LIME1	-1.04	3.31E-01	4.22E-01	1321.53	not significant
4922	ZNF75A	-1.04	4.99E-01	5.88E-01	400.02	not significant
4923	LOC646214	-1.04	6.29E-01	7.06E-01	31.16	not significant
4924	TFCP2	-1.04	1.36E-01	1.99E-01	4658.99	not significant
4925	RPUSD1	-1.04	3.20E-01	4.11E-01	1372.39	not significant
4926	KLHDC3	-1.04	1.28E-01	1.88E-01	5177.18	not significant
4927	FAM208B	-1.04	2.05E-01	2.82E-01	3776.61	not significant
4928	GTPBP10	-1.04	3.13E-01	4.04E-01	1111.74	not significant
4929	MECP2	-1.04	6.29E-01	7.06E-01	106.33	not significant
4930	CD320	-1.04	2.55E-01	3.40E-01	1944.71	not significant
4931	ROCK2	-1.04	2.53E-01	3.37E-01	1981.05	not significant
4932	ZNF22	-1.04	1.08E-01	1.63E-01	5292.24	not significant
4933	CLEC16A	-1.04	1.96E-01	2.72E-01	2284.69	not significant
4934	LOC284009	-1.04	4.73E-01	5.64E-01	7.33	not significant
4935	ATP11A	-1.04	2.62E-01	3.47E-01	2346.48	not significant
4936	GPR3	-1.04	6.45E-01	7.19E-01	63.19	not significant
4937	GABBR1	-1.04	6.46E-01	7.20E-01	71.32	not significant
4938	ZNF720	-1.04	5.10E-01	5.99E-01	381.89	not significant
4939	SLC39A1	-1.04	1.91E-01	2.66E-01	2932.64	not significant
4940	DDX51	-1.04	2.30E-01	3.12E-01	2267.91	not significant
4941	ERCC6L2	-1.04	3.28E-01	4.19E-01	1157.46	not significant
4942	RAB8B	-1.04	1.33E-01	1.96E-01	4388.82	not significant
4943	OXTR	-1.04	6.36E-01	7.11E-01	116.78	not significant
4944	NAA35	-1.04	3.34E-01	4.25E-01	1037.40	not significant
4945	FGL2	-1.04	5.16E-01	6.04E-01	365.69	not significant
4946	EIF3M	-1.04	1.36E-01	1.99E-01	11526.42	not significant
4947	TRIP4	-1.04	5.01E-01	5.91E-01	508.93	not significant
4948	HSPB11	-1.04	2.59E-01	3.45E-01	1601.60	not significant
4949	SPEN	-1.04	2.39E-01	3.22E-01	7991.68	not significant
4950	KIF5B	-1.04	9.28E-02	1.43E-01	8810.90	not significant
4951	PAK2	-1.04	1.09E-01	1.64E-01	11852.42	not significant
4952	LIMS1	-1.04	2.16E-01	2.95E-01	2654.88	not significant
4953	CHAF1A	-1.04	1.18E-01	1.75E-01	5804.43	not significant
4954	GBP1P1	-1.04	6.42E-01	7.17E-01	34.75	not significant
4955	PIBF1	-1.04	4.30E-01	5.22E-01	730.65	not significant
4956	ZNF507	-1.04	2.58E-01	3.43E-01	1917.01	not significant
4957	GRAMD3	-1.04	6.46E-01	7.20E-01	95.83	not significant
4958	KIAA1467	-1.03	5.99E-01	6.79E-01	180.99	not significant
4959	FAM86DP	-1.03	6.03E-01	6.83E-01	213.20	not significant
4960	RING1	-1.03	4.88E-01	5.78E-01	483.28	not significant
4961	TAGLN	-1.03	6.37E-01	7.12E-01	30.05	not significant
4962	FAM86HP	-1.03	6.43E-01	7.18E-01	33.41	not significant
4963	EP300	-1.03	4.77E-01	5.68E-01	3628.54	not significant
4964	COQ7	-1.03	4.55E-01	5.47E-01	556.93	not significant
4965	ZNF546	-1.03	5.99E-01	6.79E-01	191.57	not significant
4966	LOC100506321	-1.03	5.99E-01	6.79E-01	17.96	not significant
4967	PMEL	-1.03	5.28E-01	6.16E-01	8.93	not significant
4968	RPSAP9	-1.03	5.77E-01	6.61E-01	12.88	not significant
4969	COX7C	-1.03	2.11E-01	2.90E-01	5638.67	not significant
4970	RRAGA	-1.03	3.26E-01	4.18E-01	1262.38	not significant
4971	HSPD1	-1.03	1.56E-01	2.24E-01	27736.70	not significant
4972	CRTC2	-1.03	3.35E-01	4.26E-01	1342.45	not significant
4973	RACGAP1P	-1.03	5.69E-01	6.53E-01	12.35	not significant
4974	SMG1P2	-1.03	6.60E-01	7.33E-01	58.01	not significant
4975	ATAD2	-1.03	9.63E-02	1.48E-01	12999.15	not significant
4976	UNC45A	-1.03	2.46E-01	3.29E-01	2258.45	not significant
4977	ATXN7L3	-1.03	1.88E-01	2.62E-01	3658.28	not significant
4978	G6PC3	-1.03	5.81E-01	6.63E-01	245.86	not significant
4979	NPEPPS	-1.03	1.58E-01	2.26E-01	3711.30	not significant
4980	NDUFB5	-1.03	2.50E-01	3.34E-01	2438.74	not significant
4981	MAP10	-1.03	4.67E-01	5.58E-01	587.18	not significant
4982	CDIPT-AS1	-1.03	5.80E-01	6.63E-01	13.41	not significant
4983	IFT81	-1.03	4.93E-01	5.83E-01	491.05	not significant
4984	TAF5	-1.03	4.12E-01	5.04E-01	958.40	not significant
4985	UHRF1	-1.03	1.47E-01	2.13E-01	9063.93	not significant
4986	SMIM7	-1.03	3.71E-01	4.63E-01	1315.12	not significant
4987	HIST1H2AE	-1.03	6.56E-01	7.28E-01	34.83	not significant
4988	LRPAP1	-1.03	2.26E-01	3.06E-01	2217.06	not significant
4989	DNM1L	-1.03	1.86E-01	2.60E-01	2949.95	not significant
4990	HIST1H1E	-1.03	6.64E-01	7.36E-01	74.79	not significant
4991	HVCN1	-1.03	4.56E-01	5.47E-01	646.89	not significant
4992	ZNF665	-1.03	5.81E-01	6.64E-01	267.11	not significant
4993	A1BG-AS1	-1.03	5.92E-01	6.73E-01	256.82	not significant
4994	CCDC102A	-1.03	4.71E-01	5.63E-01	559.24	not significant
4995	ETS2	-1.03	9.87E-02	1.51E-01	10072.70	not significant
4996	NOL3	-1.03	6.67E-01	7.38E-01	83.64	not significant
4997	C16orf70	-1.03	3.74E-01	4.66E-01	993.00	not significant
4998	MMP15	-1.03	6.53E-01	7.27E-01	31.51	not significant
4999	ITLN1	-1.03	5.62E-01	6.46E-01	11.27	not significant
5000	NUDT19	-1.03	5.04E-01	5.93E-01	501.00	not significant
5001	INTS3	-1.03	3.79E-01	4.70E-01	1076.91	not significant
5002	IPP	-1.03	4.47E-01	5.39E-01	649.49	not significant
5003	GLUD1	-1.03	1.22E-01	1.82E-01	6158.48	not significant
5004	TSPAN5	-1.03	2.55E-01	3.39E-01	2133.78	not significant

5005	IL2RG	-1.03	7.84E-02	1.23E-01	14586.50	not significant
5006	PMS2P1	-1.03	3.28E-01	4.19E-01	1418.37	not significant
5007	TMEM126A	-1.03	5.17E-01	6.05E-01	695.96	not significant
5008	SPTSSA	-1.03	3.53E-01	4.45E-01	1212.21	not significant
5009	ICMT	-1.03	1.76E-01	2.48E-01	7232.44	not significant
5010	ANKRD17	-1.03	2.44E-01	3.28E-01	5845.04	not significant
5011	C18orf25	-1.03	3.66E-01	4.58E-01	1671.93	not significant
5012	LOC100133315	-1.03	6.61E-01	7.33E-01	96.08	not significant
5013	NOL12	-1.03	3.93E-01	4.85E-01	1178.84	not significant
5014	DNAH10	-1.03	6.62E-01	7.34E-01	38.72	not significant
5015	OTX1	-1.03	6.34E-01	7.10E-01	153.42	not significant
5016	PECR	-1.03	6.53E-01	7.27E-01	113.96	not significant
5017	N4BP2L2-IT2	-1.03	6.69E-01	7.39E-01	89.92	not significant
5018	VPS41	-1.03	2.52E-01	3.37E-01	2224.52	not significant
5019	GSTM2	-1.03	6.66E-01	7.37E-01	83.00	not significant
5020	NPEPL1	-1.03	5.56E-01	6.41E-01	9.95	not significant
5021	METTL23	-1.03	3.57E-01	4.49E-01	1189.90	not significant
5022	EGR2	-1.03	5.53E-01	6.39E-01	10.10	not significant
5023	CYP4F11	-1.03	5.53E-01	6.38E-01	9.32	not significant
5024	LZIC	-1.03	3.96E-01	4.88E-01	1056.40	not significant
5025	KMT2A	-1.03	4.79E-01	5.70E-01	774.05	not significant
5026	TMEM8A	-1.03	3.28E-01	4.19E-01	1833.67	not significant
5027	CCT3	-1.03	1.75E-01	2.48E-01	18388.93	not significant
5028	NAGLU	-1.03	5.94E-01	6.74E-01	249.63	not significant
5029	MATR3	-1.03	1.06E-01	1.60E-01	27414.02	not significant
5030	CXorf38	-1.03	3.06E-01	3.95E-01	1545.73	not significant
5031	MCAM	-1.03	6.68E-01	7.39E-01	38.33	not significant
5032	LINC00944	-1.03	6.32E-01	7.08E-01	164.78	not significant
5033	PHKB	-1.03	2.22E-01	3.02E-01	3069.87	not significant
5034	GFM2	-1.03	3.33E-01	4.24E-01	1741.72	not significant
5035	FOXJ3	-1.03	1.79E-01	2.52E-01	3690.82	not significant
5036	BCL7B	-1.03	4.39E-01	5.31E-01	741.62	not significant
5037	WDFY1	-1.03	2.92E-01	3.81E-01	1631.19	not significant
5038	GOLGA4	-1.03	2.40E-01	3.23E-01	3355.69	not significant
5039	DDX20	-1.03	3.23E-01	4.14E-01	1484.43	not significant
5040	MCFD2	-1.03	1.95E-01	2.71E-01	4261.52	not significant
5041	ENPP3	-1.03	6.54E-01	7.27E-01	26.36	not significant
5042	KIFC1	-1.03	2.68E-01	3.54E-01	2013.26	not significant
5043	NDUFAF6	-1.03	4.81E-01	5.72E-01	607.35	not significant
5044	FAM13A	-1.03	6.69E-01	7.39E-01	40.22	not significant
5045	DUSP12	-1.03	4.54E-01	5.46E-01	708.25	not significant
5046	RHBDL1	-1.03	6.48E-01	7.22E-01	182.44	not significant
5047	KIF13B	-1.03	2.72E-01	3.59E-01	1962.25	not significant
5048	C5orf51	-1.03	2.95E-01	3.84E-01	1985.76	not significant
5049	TMEM68	-1.03	3.67E-01	4.58E-01	1141.49	not significant
5050	CDKAL1	-1.03	4.10E-01	5.02E-01	1051.67	not significant
5051	LINC01366	-1.03	5.82E-01	6.65E-01	282.74	not significant
5052	ZNF200	-1.03	4.03E-01	4.95E-01	973.79	not significant
5053	CIRBP-AS1	-1.03	5.43E-01	6.29E-01	8.27	not significant
5054	MID1IP1-AS1	-1.03	5.79E-01	6.62E-01	11.82	not significant
5055	KDM5C	-1.03	3.23E-01	4.15E-01	1588.78	not significant
5056	CTDSPL	-1.03	3.97E-01	4.89E-01	963.42	not significant
5057	TEFM	-1.03	6.16E-01	6.94E-01	231.25	not significant
5058	NUP50	-1.03	1.23E-01	1.83E-01	8900.09	not significant
5059	SEC23B	-1.03	2.18E-01	2.98E-01	3047.22	not significant
5060	SMIM20	-1.03	5.03E-01	5.93E-01	617.02	not significant
5061	FHOD1	-1.03	3.14E-01	4.04E-01	1572.02	not significant
5062	PCDH9	-1.03	6.81E-01	7.50E-01	54.13	not significant
5063	DNAJC3	-1.03	2.64E-01	3.49E-01	2217.37	not significant
5064	ABLIM2	-1.03	5.88E-01	6.69E-01	11.44	not significant
5065	DMTN	-1.03	6.63E-01	7.35E-01	31.38	not significant
5066	HIST1H2BM	-1.03	6.36E-01	7.11E-01	19.48	not significant
5067	COA3	-1.03	5.04E-01	5.94E-01	525.03	not significant
5068	KCNAB3	-1.03	6.09E-01	6.88E-01	263.98	not significant
5069	UQCC2	-1.03	4.18E-01	5.10E-01	976.97	not significant
5070	ZSCAN20	-1.03	6.60E-01	7.33E-01	135.52	not significant
5071	DIAPH2	-1.03	4.66E-01	5.58E-01	803.32	not significant
5072	DPP4	-1.03	1.26E-01	1.86E-01	6513.08	not significant
5073	43531_3536	-1.03	1.38E-01	2.02E-01	5424.44	not significant
5074	ORC2	-1.03	2.95E-01	3.84E-01	2098.29	not significant
5075	GLTP	-1.03	3.68E-01	4.60E-01	1613.14	not significant
5076	SKI	-1.03	5.40E-01	6.27E-01	423.51	not significant
5077	PTGES2	-1.03	4.56E-01	5.48E-01	887.49	not significant
5078	ANKRD36BP2	-1.03	6.65E-01	7.37E-01	25.66	not significant
5079	LURAP1	-1.03	6.26E-01	7.03E-01	15.32	not significant
5080	ZDHHC7	-1.03	3.05E-01	3.95E-01	1945.43	not significant
5081	DDX3X	-1.03	1.67E-01	2.38E-01	14882.91	not significant
5082	TUBGCP5	-1.03	5.03E-01	5.93E-01	708.70	not significant
5083	RFWD2	-1.03	3.36E-01	4.27E-01	1791.20	not significant
5084	SLC35F2	-1.03	4.05E-01	4.97E-01	1029.19	not significant
5085	TAF1A-AS1	-1.03	6.30E-01	7.06E-01	16.20	not significant
5086	SNX20	-1.03	6.41E-01	7.16E-01	205.28	not significant
5087	ZSCAN21	-1.03	6.21E-01	6.98E-01	255.76	not significant
5088	DNAJC13	-1.03	2.48E-01	3.32E-01	3242.60	not significant
5089	PTPN1	-1.03	1.97E-01	2.73E-01	4385.87	not significant
5090	GK5	-1.03	3.53E-01	4.45E-01	1432.49	not significant
5091	MTA1	-1.03	2.55E-01	3.40E-01	2568.32	not significant
5092	NADK2	-1.03	3.85E-01	4.77E-01	1604.83	not significant

5093	KIF22	-1.03	1.54E-01	2.21E-01	7320.75	not significant
5094	IQCD	-1.03	6.58E-01	7.31E-01	20.51	not significant
5095	MRPS16	-1.03	1.99E-01	2.75E-01	4264.14	not significant
5096	EZR-AS1	-1.03	5.52E-01	6.38E-01	8.46	not significant
5097	TMEM63C	-1.03	5.44E-01	6.30E-01	8.66	not significant
5098	NEIL3	-1.03	2.55E-01	3.39E-01	2959.77	not significant
5099	ZNF808	-1.03	5.94E-01	6.75E-01	462.30	not significant
5100	TNPO2	-1.03	2.49E-01	3.33E-01	6824.89	not significant
5101	VKORC1	-1.03	3.72E-01	4.64E-01	1531.81	not significant
5102	EBPL	-1.03	4.83E-01	5.73E-01	1175.67	not significant
5103	YTHDC1	-1.03	3.93E-01	4.85E-01	1161.16	not significant
5104	SQLE	-1.03	2.39E-01	3.22E-01	5111.99	not significant
5105	C2orf81	-1.03	6.93E-01	7.60E-01	53.60	not significant
5106	RACGAP1	-1.03	1.84E-01	2.58E-01	7750.52	not significant
5107	ENTPD6	-1.03	3.08E-01	3.97E-01	1986.23	not significant
5108	BSN	-1.03	6.89E-01	7.57E-01	38.39	not significant
5109	TBC1D20	-1.03	2.68E-01	3.54E-01	2364.28	not significant
5110	PANK3	-1.03	3.30E-01	4.21E-01	2374.61	not significant
5111	LIPC	-1.03	6.97E-01	7.62E-01	65.72	not significant
5112	DNAJC7	-1.03	3.56E-01	4.47E-01	1941.17	not significant
5113	PFKFB2	-1.03	6.31E-01	7.08E-01	242.53	not significant
5114	CALHM2	-1.03	5.16E-01	6.05E-01	579.00	not significant
5115	HSPA2	-1.03	6.98E-01	7.63E-01	49.59	not significant
5116	SREBF2	-1.03	1.54E-01	2.21E-01	12272.23	not significant
5117	TBC1D9	-1.03	5.80E-01	6.63E-01	374.44	not significant
5118	MKLN1	-1.03	3.09E-01	3.99E-01	2766.54	not significant
5119	DOT1L	-1.03	2.44E-01	3.27E-01	5001.39	not significant
5120	GMPPB	-1.03	4.86E-01	5.77E-01	696.31	not significant
5121	SAV1	-1.03	5.08E-01	5.97E-01	609.61	not significant
5122	C5orf28	-1.03	5.66E-01	6.50E-01	425.81	not significant
5123	FHIT	-1.03	5.09E-01	5.98E-01	655.44	not significant
5124	CYP4F35P	-1.03	6.32E-01	7.08E-01	13.71	not significant
5125	UBR7	-1.03	1.78E-01	2.51E-01	7039.96	not significant
5126	BPNT1	-1.03	4.04E-01	4.95E-01	1128.88	not significant
5127	CSNK1D	-1.03	1.81E-01	2.54E-01	6582.27	not significant
5128	MKS1	-1.03	4.76E-01	5.67E-01	834.91	not significant
5129	ORC6	-1.03	3.16E-01	4.07E-01	1894.79	not significant
5130	CACTIN	-1.03	3.46E-01	4.38E-01	1659.83	not significant
5131	FAM188A	-1.03	5.34E-01	6.21E-01	547.84	not significant
5132	LOC100507462	-1.03	7.01E-01	7.66E-01	45.31	not significant
5133	NUP160	-1.03	2.08E-01	2.86E-01	6245.15	not significant
5134	TNFRSF21	-1.03	4.29E-01	5.21E-01	1142.36	not significant
5135	SCAF4	-1.03	2.85E-01	3.73E-01	4511.88	not significant
5136	HIST1H4F	-1.03	4.01E-01	4.93E-01	11.66	not significant
5137	OTUB2	-1.03	6.95E-01	7.61E-01	97.02	not significant
5138	ADO	-1.03	3.75E-01	4.67E-01	1380.12	not significant
5139	DCLRE1C	-1.03	3.82E-01	4.74E-01	1365.78	not significant
5140	ZBTB2	-1.03	3.42E-01	4.34E-01	1688.55	not significant
5141	PRNP	-1.03	6.06E-01	6.85E-01	334.73	not significant
5142	OCEL1	-1.03	6.98E-01	7.63E-01	106.92	not significant
5143	MSMO1	-1.03	3.56E-01	4.48E-01	1881.03	not significant
5144	C11orf65	-1.03	6.47E-01	7.21E-01	15.09	not significant
5145	ZNF252P	-1.03	4.40E-01	5.32E-01	1056.25	not significant
5146	CALM2	-1.03	2.38E-01	3.20E-01	19656.37	not significant
5147	SIRT7	-1.03	5.12E-01	6.01E-01	824.31	not significant
5148	THAP11	-1.03	3.92E-01	4.84E-01	1996.74	not significant
5149	KIF4B	-1.03	6.56E-01	7.29E-01	16.81	not significant
5150	TARBP1	-1.03	3.24E-01	4.15E-01	2492.65	not significant
5151	NCOR1	-1.03	1.86E-01	2.60E-01	9300.03	not significant
5152	ZNF761	-1.03	3.95E-01	4.87E-01	1389.24	not significant
5153	TERF2	-1.03	3.03E-01	3.92E-01	2144.83	not significant
5154	ORAI1	-1.03	7.04E-01	7.69E-01	80.13	not significant
5155	LOC100507195	-1.03	6.01E-01	6.81E-01	9.43	not significant
5156	DYNC1I2	-1.03	3.24E-01	4.15E-01	2039.47	not significant
5157	MCM3AP	-1.03	2.62E-01	3.48E-01	3042.98	not significant
5158	HIP1R	-1.03	2.97E-01	3.86E-01	3819.73	not significant
5159	C11orf71	-1.03	6.80E-01	7.49E-01	146.07	not significant
5160	GIGYF2	-1.03	2.66E-01	3.52E-01	3380.95	not significant
5161	BTN2A2	-1.03	5.66E-01	6.50E-01	460.07	not significant
5162	SLC39A9	-1.03	2.03E-01	2.81E-01	4110.73	not significant
5163	PRPF6	-1.03	2.64E-01	3.50E-01	3526.16	not significant
5164	PAIP2B	-1.03	7.09E-01	7.72E-01	51.54	not significant
5165	PA2G4P4	-1.03	6.94E-01	7.61E-01	118.28	not significant
5166	OMG	-1.03	6.35E-01	7.11E-01	12.69	not significant
5167	DCLRE1B	-1.03	4.26E-01	5.18E-01	1422.54	not significant
5168	ALG13	-1.03	4.69E-01	5.61E-01	1126.15	not significant
5169	RCOR1	-1.03	3.15E-01	4.06E-01	2863.87	not significant
5170	SLC5A6	-1.03	3.15E-01	4.06E-01	2497.48	not significant
5171	KIAA1211L	-1.03	6.93E-01	7.60E-01	26.53	not significant
5172	SAMD9L	-1.03	4.96E-01	5.86E-01	923.22	not significant
5173	CEP78	-1.03	3.43E-01	4.34E-01	1850.41	not significant
5174	NCAPG	-1.03	2.44E-01	3.28E-01	4829.22	not significant
5175	GSN	-1.03	6.15E-01	6.93E-01	10.97	not significant
5176	ZNF815P	-1.03	7.04E-01	7.69E-01	33.37	not significant
5177	FBXO45	-1.03	3.25E-01	4.16E-01	2415.67	not significant
5178	TSR3	-1.03	4.32E-01	5.24E-01	1306.71	not significant
5179	GCC1	-1.03	4.55E-01	5.47E-01	1005.18	not significant
5180	LCOR	-1.03	4.78E-01	5.69E-01	918.47	not significant

5181	SOBP	-1.03	4.88E-01	5.78E-01	895.40	not significant
5182	SLC35A4	-1.03	2.94E-01	3.83E-01	3999.26	not significant
5183	VPS26A	-1.03	3.70E-01	4.62E-01	2139.38	not significant
5184	GRPEL2	-1.03	5.72E-01	6.56E-01	476.19	not significant
5185	EXOC6B	-1.03	6.22E-01	6.99E-01	324.09	not significant
5186	ANLN	-1.03	2.55E-01	3.40E-01	3938.73	not significant
5187	WDHD1	-1.03	2.34E-01	3.16E-01	4426.85	not significant
5188	EMC2	-1.03	5.58E-01	6.43E-01	551.43	not significant
5189	CLCN5	-1.03	7.05E-01	7.69E-01	33.51	not significant
5190	KANSL3	-1.03	1.98E-01	2.75E-01	5967.23	not significant
5191	ARFIP2	-1.03	3.66E-01	4.58E-01	1646.24	not significant
5192	SNX25	-1.03	4.97E-01	5.87E-01	806.66	not significant
5193	RCC1	-1.03	2.46E-01	3.29E-01	5972.50	not significant
5194	LINC01337	-1.03	6.40E-01	7.16E-01	11.94	not significant
5195	RBM4B	-1.03	6.33E-01	7.09E-01	355.62	not significant
5196	TMEM182	-1.03	6.93E-01	7.60E-01	151.48	not significant
5197	OGG1	-1.03	6.20E-01	6.97E-01	346.97	not significant
5198	STXBP1	-1.03	5.75E-01	6.58E-01	483.87	not significant
5199	SCML1	-1.03	6.13E-01	6.91E-01	358.70	not significant
5200	UBTF	-1.03	1.82E-01	2.56E-01	10117.56	not significant
5201	CLPX	-1.03	4.41E-01	5.34E-01	1386.58	not significant
5202	P2RX1	-1.03	6.97E-01	7.63E-01	139.81	not significant
5203	ARAF	-1.03	3.46E-01	4.37E-01	1917.76	not significant
5204	NUCB2	-1.03	3.12E-01	4.02E-01	22033.90	not significant
5205	KCTD18	-1.03	4.97E-01	5.87E-01	835.15	not significant
5206	SUPT5H	-1.03	2.14E-01	2.93E-01	4681.57	not significant
5207	PUS3	-1.03	5.70E-01	6.54E-01	519.03	not significant
5208	FUK	-1.03	6.13E-01	6.91E-01	399.63	not significant
5209	UBE2F	-1.03	4.85E-01	5.75E-01	869.69	not significant
5210	SPOCK2	-1.03	7.15E-01	7.78E-01	102.55	not significant
5211	SLC9B1	-1.03	7.16E-01	7.79E-01	42.19	not significant
5212	DAZAP2	-1.03	2.39E-01	3.21E-01	12382.68	not significant
5213	KCNQ4	-1.03	6.72E-01	7.42E-01	17.36	not significant
5214	MAPK1	-1.03	1.98E-01	2.74E-01	10348.67	not significant
5215	COQ4	-1.03	5.69E-01	6.53E-01	584.28	not significant
5216	PRR3	-1.03	6.55E-01	7.28E-01	246.27	not significant
5217	ACIN1	-1.03	1.91E-01	2.66E-01	10696.57	not significant
5218	CORO7	-1.03	5.79E-01	6.62E-01	486.09	not significant
5219	YTHDF1	-1.03	3.07E-01	3.96E-01	2545.86	not significant
5220	NBPF8	-1.03	7.00E-01	7.65E-01	22.10	not significant
5221	MLST8	-1.03	3.69E-01	4.61E-01	1943.34	not significant
5222	ERICH5	-1.03	6.93E-01	7.60E-01	22.84	not significant
5223	TYW1B	-1.03	7.29E-01	7.89E-01	60.32	not significant
5224	CHTOP	-1.03	2.78E-01	3.65E-01	3493.80	not significant
5225	LINC00471	-1.03	6.76E-01	7.45E-01	16.16	not significant
5226	HIST1H2AL	-1.03	6.79E-01	7.48E-01	17.26	not significant
5227	ABCA2	-1.03	7.27E-01	7.88E-01	42.17	not significant
5228	EIF2AK1	-1.03	1.46E-01	2.11E-01	11362.80	not significant
5229	ZNF69	-1.03	7.09E-01	7.73E-01	137.56	not significant
5230	LRRC40	-1.03	4.06E-01	4.98E-01	1834.11	not significant
5231	ZC3HAV1L	-1.03	5.64E-01	6.49E-01	831.34	not significant
5232	SOS1	-1.03	3.73E-01	4.65E-01	2381.61	not significant
5233	DNAJC5	-1.03	3.44E-01	4.35E-01	3512.31	not significant
5234	PSAP	-1.03	2.61E-01	3.46E-01	30553.03	not significant
5235	CCDC90B	-1.03	4.63E-01	5.55E-01	1295.63	not significant
5236	GPX7	-1.03	4.34E-01	5.26E-01	1266.52	not significant
5237	URGCP	-1.03	4.69E-01	5.60E-01	1259.00	not significant
5238	FGFRL1	-1.03	5.74E-01	6.57E-01	549.15	not significant
5239	WDR82	-1.03	2.16E-01	2.95E-01	11309.60	not significant
5240	SYNGR1	-1.03	6.28E-01	7.04E-01	10.47	not significant
5241	POF1B	-1.03	5.45E-01	6.31E-01	769.10	not significant
5242	MGAT1	-1.03	3.37E-01	4.28E-01	3904.46	not significant
5243	CREB3L2	-1.03	3.37E-01	4.29E-01	2627.75	not significant
5244	CELF1	-1.03	2.56E-01	3.41E-01	6059.15	not significant
5245	FAM222B	-1.03	5.44E-01	6.31E-01	743.37	not significant
5246	COA6	-1.03	5.60E-01	6.44E-01	859.00	not significant
5247	GMFG	-1.03	3.33E-01	4.24E-01	3862.83	not significant
5248	CCND3	-1.03	2.15E-01	2.95E-01	31289.14	not significant
5249	GTF3C1	-1.03	3.91E-01	4.83E-01	4497.07	not significant
5250	CCNY	-1.03	2.58E-01	3.43E-01	5017.47	not significant
5251	ZMYND10	-1.03	6.98E-01	7.63E-01	17.83	not significant
5252	SEC61A1	-1.03	2.19E-01	2.99E-01	10176.45	not significant
5253	NEO1	-1.03	6.50E-01	7.24E-01	11.18	not significant
5254	RASGRF1	-1.03	6.36E-01	7.11E-01	10.07	not significant
5255	RAB11FIP1	-1.03	2.38E-01	3.21E-01	10761.97	not significant
5256	UBR1	-1.03	4.66E-01	5.58E-01	1559.06	not significant
5257	SMURF2	-1.03	5.45E-01	6.31E-01	765.42	not significant
5258	STOX1	-1.03	6.84E-01	7.52E-01	233.35	not significant
5259	NIPBL	-1.03	3.24E-01	4.16E-01	6402.85	not significant
5260	RDH5	-1.03	7.33E-01	7.93E-01	32.19	not significant
5261	LSM12	-1.03	6.83E-01	7.51E-01	229.99	not significant
5262	ZNF526	-1.03	6.17E-01	6.94E-01	463.37	not significant
5263	SNIP1	-1.03	5.18E-01	6.06E-01	875.46	not significant
5264	DDR1	-1.03	7.41E-01	7.99E-01	71.11	not significant
5265	RTFDC1	-1.03	3.69E-01	4.61E-01	3174.67	not significant
5266	C4orf48	-1.03	6.25E-01	7.02E-01	415.39	not significant
5267	RNF40	-1.03	2.73E-01	3.60E-01	5435.58	not significant
5268	ATP13A3	-1.03	2.48E-01	3.32E-01	9555.85	not significant

5269	NDUFAF3	-1.03	4.87E-01	5.77E-01	1311.54	not significant
5270	HERC1	-1.03	4.28E-01	5.20E-01	2458.19	not significant
5271	BDNF-AS	-1.03	7.22E-01	7.84E-01	23.67	not significant
5272	DUSP10	-1.03	7.44E-01	8.01E-01	52.74	not significant
5273	SC5D	-1.02	4.12E-01	5.03E-01	1693.44	not significant
5274	TRAPPC13	-1.02	4.87E-01	5.77E-01	1168.06	not significant
5275	ARRB2	-1.02	2.80E-01	3.68E-01	4286.95	not significant
5276	DLGAP1-AS2	-1.02	6.63E-01	7.35E-01	10.55	not significant
5277	UBE2H	-1.02	4.26E-01	5.18E-01	2154.63	not significant
5278	UBE3B	-1.02	4.24E-01	5.16E-01	1735.31	not significant
5279	HIST1H4H	-1.02	7.40E-01	7.98E-01	47.54	not significant
5280	TBL1XR1	-1.02	2.91E-01	3.80E-01	6910.08	not significant
5281	CNR2	-1.02	7.40E-01	7.98E-01	87.85	not significant
5282	CPNE5	-1.02	7.40E-01	7.98E-01	100.08	not significant
5283	ZMYM4	-1.02	3.16E-01	4.06E-01	4305.34	not significant
5284	ECE2	-1.02	6.84E-01	7.52E-01	312.69	not significant
5285	RBM39	-1.02	1.96E-01	2.72E-01	14130.63	not significant
5286	MAP2K7	-1.02	3.69E-01	4.61E-01	2245.35	not significant
5287	LOC100506469	-1.02	7.17E-01	7.80E-01	183.46	not significant
5288	TSPAN10	-1.02	6.40E-01	7.16E-01	9.76	not significant
5289	BIRC6	-1.02	3.81E-01	4.73E-01	5017.87	not significant
5290	ADNP2	-1.02	3.36E-01	4.27E-01	2811.84	not significant
5291	HIST1H2BJ	-1.02	7.27E-01	7.88E-01	26.34	not significant
5292	VWA8	-1.02	5.16E-01	6.05E-01	1173.81	not significant
5293	RPS14P3	-1.02	7.39E-01	7.98E-01	127.14	not significant
5294	BBIP1	-1.02	6.47E-01	7.22E-01	409.04	not significant
5295	SENP8	-1.02	7.52E-01	8.08E-01	62.86	not significant
5296	ALKBH5	-1.02	3.90E-01	4.83E-01	4521.86	not significant
5297	ASNA1	-1.02	4.27E-01	5.20E-01	2149.94	not significant
5298	ZBTB39	-1.02	4.60E-01	5.51E-01	1397.55	not significant
5299	ZNF391	-1.02	7.23E-01	7.85E-01	158.39	not significant
5300	SUSD4	-1.02	6.69E-01	7.39E-01	313.44	not significant
5301	AKAP10	-1.02	5.10E-01	5.99E-01	990.88	not significant
5302	INTS7	-1.02	3.52E-01	4.44E-01	2704.63	not significant
5303	GNN	-1.02	7.06E-01	7.71E-01	15.67	not significant
5304	ZBED8	-1.02	7.50E-01	8.06E-01	100.04	not significant
5305	AKR7A2	-1.02	4.31E-01	5.23E-01	2061.96	not significant
5306	MAEA	-1.02	3.72E-01	4.64E-01	2629.50	not significant
5307	VAV1	-1.02	2.74E-01	3.61E-01	5259.72	not significant
5308	CCDC132	-1.02	5.32E-01	6.20E-01	912.83	not significant
5309	RNF138	-1.02	3.40E-01	4.31E-01	4336.05	not significant
5310	KLHL36	-1.02	7.04E-01	7.69E-01	241.54	not significant
5311	DEF6	-1.02	3.29E-01	4.20E-01	4005.23	not significant
5312	SMARCE1	-1.02	2.37E-01	3.19E-01	10458.52	not significant
5313	PTS	-1.02	6.06E-01	6.85E-01	549.43	not significant
5314	VTI1A	-1.02	5.01E-01	5.91E-01	1125.63	not significant
5315	TEX14	-1.02	7.08E-01	7.72E-01	17.74	not significant
5316	CFP	-1.02	6.92E-01	7.59E-01	12.64	not significant
5317	LOC101930452	-1.02	7.30E-01	7.90E-01	21.38	not significant
5318	UCP3	-1.02	7.56E-01	8.11E-01	94.42	not significant
5319	UXS1	-1.02	4.53E-01	5.45E-01	1643.21	not significant
5320	SETD2	-1.02	4.03E-01	4.95E-01	5768.42	not significant
5321	RALA	-1.02	3.87E-01	4.80E-01	3867.27	not significant
5322	CLASRP	-1.02	5.22E-01	6.11E-01	1959.21	not significant
5323	MIA3	-1.02	3.76E-01	4.68E-01	2799.89	not significant
5324	LINC00996	-1.02	7.10E-01	7.74E-01	16.57	not significant
5325	WAPAL	-1.02	2.82E-01	3.70E-01	5213.15	not significant
5326	STARD10	-1.02	7.29E-01	7.89E-01	165.91	not significant
5327	MR1	-1.02	5.41E-01	6.28E-01	945.91	not significant
5328	RANBP3	-1.02	3.60E-01	4.52E-01	2828.48	not significant
5329	UHRF1BP1	-1.02	4.15E-01	5.06E-01	2315.63	not significant
5330	ACAP2	-1.02	3.36E-01	4.27E-01	5360.20	not significant
5331	GNA15	-1.02	3.19E-01	4.10E-01	12445.30	not significant
5332	ECI1	-1.02	7.28E-01	7.89E-01	18.99	not significant
5333	USP9X	-1.02	4.21E-01	5.13E-01	5133.14	not significant
5334	CRCP	-1.02	3.99E-01	4.91E-01	2266.90	not significant
5335	PPCS	-1.02	5.90E-01	6.72E-01	675.22	not significant
5336	DMPK	-1.02	6.35E-01	7.10E-01	486.95	not significant
5337	AREL1	-1.02	3.71E-01	4.62E-01	2914.52	not significant
5338	GAK	-1.02	3.68E-01	4.60E-01	3751.05	not significant
5339	NFKBIA	-1.02	4.93E-01	5.83E-01	1254.48	not significant
5340	PEX7	-1.02	7.29E-01	7.90E-01	205.47	not significant
5341	RAPGEF1	-1.02	3.96E-01	4.88E-01	3095.12	not significant
5342	ALAS1	-1.02	4.75E-01	5.66E-01	1476.01	not significant
5343	ZC3H18	-1.02	3.40E-01	4.32E-01	4570.45	not significant
5344	EVI5	-1.02	7.63E-01	8.17E-01	110.14	not significant
5345	TECR	-1.02	4.09E-01	5.01E-01	3203.37	not significant
5346	PIP5K1A	-1.02	2.98E-01	3.87E-01	4453.81	not significant
5347	GLB1L	-1.02	7.67E-01	8.21E-01	69.95	not significant
5348	ALDH4A1	-1.02	6.77E-01	7.47E-01	369.84	not significant
5349	ZNF597	-1.02	7.59E-01	8.14E-01	117.18	not significant
5350	ATP1A1-AS1	-1.02	7.57E-01	8.12E-01	117.30	not significant
5351	VPS16	-1.02	5.13E-01	6.02E-01	1446.64	not significant
5352	FNBP4	-1.02	4.77E-01	5.68E-01	4100.89	not significant
5353	TMEM120B	-1.02	4.86E-01	5.76E-01	1524.83	not significant
5354	PCYT2	-1.02	4.14E-01	5.06E-01	2486.22	not significant
5355	CCDC11	-1.02	6.91E-01	7.58E-01	10.68	not significant
5356	TRAPPC5	-1.02	5.97E-01	6.77E-01	754.68	not significant

5357	ESCO2	-1.02	4.12E-01	5.03E-01	2863.31	not significant
5358	MCM3	-1.02	2.17E-01	2.96E-01	24256.23	not significant
5359	RFC5	-1.02	3.13E-01	4.04E-01	5007.91	not significant
5360	MTIF2	-1.02	5.84E-01	6.66E-01	792.61	not significant
5361	RIPK1	-1.02	4.84E-01	5.75E-01	1480.00	not significant
5362	TRIM46	-1.02	7.31E-01	7.91E-01	216.19	not significant
5363	LYSMD3	-1.02	5.47E-01	6.33E-01	1083.20	not significant
5364	HID1	-1.02	6.72E-01	7.41E-01	9.15	not significant
5365	HSP90AB1	-1.02	2.90E-01	3.78E-01	55189.07	not significant
5366	CLSTN3	-1.02	5.39E-01	6.26E-01	1200.06	not significant
5367	RAB3B	-1.02	7.45E-01	8.02E-01	21.32	not significant
5368	SOGA3	-1.02	5.96E-01	6.76E-01	761.27	not significant
5369	PPP1R2P3	-1.02	7.47E-01	8.03E-01	20.62	not significant
5370	MAPRE1	-1.02	2.89E-01	3.77E-01	14017.64	not significant
5371	LOC101929512	-1.02	7.25E-01	7.86E-01	15.43	not significant
5372	PGS1	-1.02	5.14E-01	6.02E-01	1347.75	not significant
5373	H2AFY2	-1.02	7.11E-01	7.75E-01	13.29	not significant
5374	CNPY2	-1.02	4.55E-01	5.47E-01	1998.08	not significant
5375	SLC4A4	-1.02	5.10E-01	5.99E-01	1348.02	not significant
5376	SLC16A4	-1.02	6.77E-01	7.46E-01	10.06	not significant
5377	C12orf73	-1.02	6.15E-01	6.93E-01	626.57	not significant
5378	RPL23AP7	-1.02	7.73E-01	8.25E-01	72.32	not significant
5379	ZSWIM3	-1.02	7.30E-01	7.90E-01	241.19	not significant
5380	UBR4	-1.02	7.59E-01	8.14E-01	6852.04	not significant
5381	EXOSC2	-1.02	5.08E-01	5.97E-01	1447.24	not significant
5382	GTSE1	-1.02	3.65E-01	4.57E-01	3711.89	not significant
5383	NPLOC4	-1.02	3.48E-01	4.40E-01	8366.27	not significant
5384	PIGV	-1.02	6.96E-01	7.62E-01	340.84	not significant
5385	OSBPL5	-1.02	4.33E-01	5.25E-01	2742.81	not significant
5386	TEF	-1.02	7.02E-01	7.67E-01	312.27	not significant
5387	PTPRG	-1.02	7.78E-01	8.30E-01	56.45	not significant
5388	MGMT	-1.02	5.84E-01	6.66E-01	1001.95	not significant
5389	KCNIP2-AS1	-1.02	6.80E-01	7.49E-01	8.29	not significant
5390	RHPN1	-1.02	6.96E-01	7.62E-01	2902.23	not significant
5391	MRPL33	-1.02	5.42E-01	6.28E-01	1322.19	not significant
5392	ADAMTSL5	-1.02	7.67E-01	8.20E-01	28.61	not significant
5393	HTATSF1	-1.02	6.67E-01	7.38E-01	5769.02	not significant
5394	RNF10	-1.02	3.29E-01	4.20E-01	6826.29	not significant
5395	FAM214B	-1.02	7.72E-01	8.25E-01	107.55	not significant
5396	ZNF790	-1.02	7.40E-01	7.98E-01	248.31	not significant
5397	HSF1	-1.02	4.87E-01	5.77E-01	2524.41	not significant
5398	C1QTNF6	-1.02	7.27E-01	7.88E-01	14.03	not significant
5399	SLC25A43	-1.02	7.65E-01	8.19E-01	142.22	not significant
5400	SART1	-1.02	4.75E-01	5.66E-01	3873.86	not significant
5401	CASC5	-1.02	4.81E-01	5.72E-01	3380.23	not significant
5402	KANK1	-1.02	7.79E-01	8.30E-01	92.92	not significant
5403	PMP22	-1.02	7.77E-01	8.29E-01	36.57	not significant
5404	TMTC2	-1.02	7.52E-01	8.09E-01	19.13	not significant
5405	FAM86JP	-1.02	7.80E-01	8.31E-01	38.85	not significant
5406	PKNOX1	-1.02	6.07E-01	6.86E-01	828.70	not significant
5407	IFITM1	-1.02	4.13E-01	5.04E-01	7375.91	not significant
5408	RPA3OS	-1.02	5.82E-01	6.64E-01	976.52	not significant
5409	RBM44	-1.02	7.76E-01	8.28E-01	33.29	not significant
5410	RABGGTB	-1.02	5.11E-01	6.00E-01	1950.56	not significant
5411	ZNF286A	-1.02	6.06E-01	6.85E-01	845.94	not significant
5412	LOC100507501	-1.02	7.86E-01	8.36E-01	53.20	not significant
5413	C11orf94	-1.02	7.00E-01	7.65E-01	9.86	not significant
5414	NUSAP1	-1.02	3.59E-01	4.51E-01	10059.51	not significant
5415	HMGA1	-1.02	2.65E-01	3.50E-01	15573.88	not significant
5416	CCDC13	-1.02	7.41E-01	7.99E-01	14.39	not significant
5417	CNBP	-1.02	4.07E-01	4.99E-01	14589.55	not significant
5418	EIF4H	-1.02	5.95E-01	6.76E-01	1046.33	not significant
5419	C19orf83	-1.02	7.56E-01	8.12E-01	18.72	not significant
5420	CHRAC1	-1.02	4.25E-01	5.17E-01	3859.54	not significant
5421	PIGU	-1.02	5.16E-01	6.04E-01	1700.49	not significant
5422	WHSC1	-1.02	3.63E-01	4.55E-01	17056.60	not significant
5423	ZFYVE21	-1.02	6.65E-01	7.37E-01	572.47	not significant
5424	SRP9	-1.02	3.73E-01	4.65E-01	7726.82	not significant
5425	ECE1	-1.02	4.62E-01	5.54E-01	2579.38	not significant
5426	VAPB	-1.02	4.68E-01	5.59E-01	2185.48	not significant
5427	ARFIP1	-1.02	5.81E-01	6.64E-01	1065.89	not significant
5428	DCUN1D3	-1.02	7.72E-01	8.25E-01	145.52	not significant
5429	MIS18BP1	-1.02	4.65E-01	5.57E-01	2901.32	not significant
5430	LOC100507547	-1.02	6.81E-01	7.49E-01	7.33	not significant
5431	PRKAA1	-1.02	5.39E-01	6.26E-01	3106.35	not significant
5432	OSBPL9	-1.02	4.68E-01	5.59E-01	2163.99	not significant
5433	SETX	-1.02	4.55E-01	5.47E-01	4618.42	not significant
5434	ENPP4	-1.02	6.32E-01	7.08E-01	784.02	not significant
5435	COQ10B	-1.02	6.58E-01	7.31E-01	623.49	not significant
5436	OR2AG2	-1.02	7.10E-01	7.73E-01	9.26	not significant
5437	NSUN3	-1.02	7.45E-01	8.02E-01	249.88	not significant
5438	RB1	-1.02	3.13E-01	4.03E-01	17336.15	not significant
5439	MAPK9	-1.02	4.45E-01	5.38E-01	2719.81	not significant
5440	CHST10	-1.02	5.78E-01	6.61E-01	1207.94	not significant
5441	SCRN3	-1.02	6.89E-01	7.56E-01	533.59	not significant
5442	SLC31A1	-1.02	5.58E-01	6.43E-01	1343.08	not significant
5443	CCM2	-1.02	4.70E-01	5.61E-01	3237.75	not significant
5444	C19orf47	-1.02	5.95E-01	6.76E-01	1053.91	not significant

5445	MALAT1	-1.02	7.75E-01	8.27E-01	8853.88	not significant
5446	JKAMP	-1.02	5.83E-01	6.65E-01	1065.83	not significant
5447	TANC1	-1.02	7.40E-01	7.98E-01	12.33	not significant
5448	THAP7-AS1	-1.02	7.75E-01	8.27E-01	21.74	not significant
5449	CEBPG	-1.02	5.35E-01	6.22E-01	1970.11	not significant
5450	SMG8	-1.02	5.67E-01	6.51E-01	1289.40	not significant
5451	LINC00173	-1.02	7.97E-01	8.46E-01	42.48	not significant
5452	C14orf1	-1.02	5.72E-01	6.56E-01	1428.87	not significant
5453	SPCS2	-1.02	5.90E-01	6.72E-01	1509.47	not significant
5454	PANK4	-1.02	5.99E-01	6.79E-01	1064.77	not significant
5455	ZC3H13	-1.02	4.18E-01	5.10E-01	4511.37	not significant
5456	MIR181A2HG	-1.02	7.44E-01	8.01E-01	11.98	not significant
5457	ITGB3BP	-1.02	6.23E-01	7.00E-01	991.47	not significant
5458	ARL6IP4	-1.02	4.38E-01	5.30E-01	5787.76	not significant
5459	ARHGAP17	-1.02	4.63E-01	5.55E-01	2734.27	not significant
5460	LRRC61	-1.02	5.43E-01	6.29E-01	2083.72	not significant
5461	INTS4	-1.02	6.00E-01	6.80E-01	1156.21	not significant
5462	AIG1	-1.02	7.12E-01	7.76E-01	433.62	not significant
5463	TMEM39B	-1.02	5.74E-01	6.57E-01	1537.80	not significant
5464	CMAS	-1.02	5.79E-01	6.62E-01	1724.85	not significant
5465	DARS-AS1	-1.02	7.95E-01	8.44E-01	38.18	not significant
5466	AP3M1	-1.02	3.62E-01	4.55E-01	5691.32	not significant
5467	ABHD14A	-1.02	7.53E-01	8.09E-01	256.73	not significant
5468	CMTR2	-1.02	5.62E-01	6.46E-01	1419.60	not significant
5469	IFIT5	-1.02	6.77E-01	7.46E-01	578.32	not significant
5470	LMBR1	-1.02	4.96E-01	5.86E-01	2332.27	not significant
5471	GPR125	-1.02	5.38E-01	6.25E-01	1641.54	not significant
5472	MPZ	-1.02	8.00E-01	8.48E-01	39.54	not significant
5473	ZBTB34	-1.02	6.71E-01	7.41E-01	784.13	not significant
5474	KCTD21-AS1	-1.02	7.80E-01	8.31E-01	20.34	not significant
5475	ERP44	-1.02	5.31E-01	6.19E-01	1956.65	not significant
5476	ALG1	-1.02	5.95E-01	6.75E-01	1152.84	not significant
5477	KIAA1614	-1.02	7.41E-01	7.99E-01	11.77	not significant
5478	PPTC7	-1.02	4.95E-01	5.85E-01	3395.25	not significant
5479	LOC101928370	-1.02	7.50E-01	8.07E-01	11.58	not significant
5480	C7orf73	-1.02	4.70E-01	5.62E-01	2913.31	not significant
5481	TP53BP1	-1.02	5.45E-01	6.31E-01	2197.67	not significant
5482	NUDT15	-1.02	6.05E-01	6.85E-01	1662.70	not significant
5483	SLC25A16	-1.02	7.15E-01	7.78E-01	447.39	not significant
5484	RBM15	-1.02	5.87E-01	6.69E-01	1517.49	not significant
5485	TXNRD2	-1.02	7.31E-01	7.91E-01	379.32	not significant
5486	JAKMIP2	-1.02	7.03E-01	7.68E-01	535.49	not significant
5487	PDXDC1	-1.02	5.06E-01	5.96E-01	2582.41	not significant
5488	FKBP1AP1	-1.02	8.02E-01	8.49E-01	35.25	not significant
5489	TMEM38A	-1.02	7.30E-01	7.90E-01	9.87	not significant
5490	ARL6	-1.02	8.08E-01	8.54E-01	77.34	not significant
5491	ADH5	-1.02	4.56E-01	5.47E-01	4271.00	not significant
5492	MYOM2	-1.02	7.89E-01	8.39E-01	170.10	not significant
5493	SLC9B2	-1.02	5.67E-01	6.51E-01	1756.32	not significant
5494	LRCH3	-1.02	6.65E-01	7.37E-01	735.99	not significant
5495	ITGAL	-1.02	5.56E-01	6.42E-01	3674.05	not significant
5496	ROM1	-1.02	7.83E-01	8.33E-01	17.29	not significant
5497	HMGB2	-1.02	4.75E-01	5.67E-01	33418.73	not significant
5498	HIVEP3	-1.02	4.74E-01	5.66E-01	3930.29	not significant
5499	TOPBP1	-1.02	3.91E-01	4.84E-01	10195.12	not significant
5500	RSPH3	-1.02	8.10E-01	8.55E-01	92.55	not significant
5501	TMEM230	-1.02	4.22E-01	5.13E-01	5019.43	not significant
5502	GMDS	-1.02	5.92E-01	6.73E-01	1553.97	not significant
5503	ABT1	-1.02	7.65E-01	8.19E-01	279.98	not significant
5504	HIC2	-1.02	6.85E-01	7.53E-01	624.37	not significant
5505	SNHG15	-1.02	5.96E-01	6.76E-01	1269.43	not significant
5506	TMEM161B	-1.02	6.58E-01	7.31E-01	843.94	not significant
5507	ILDR2	-1.02	6.98E-01	7.64E-01	644.06	not significant
5508	ZDHHC20	-1.02	4.26E-01	5.18E-01	7009.38	not significant
5509	PRPF39	-1.02	6.14E-01	6.92E-01	2088.24	not significant
5510	MRPL57	-1.02	5.85E-01	6.67E-01	2317.24	not significant
5511	SCAF1	-1.02	5.28E-01	6.16E-01	3438.96	not significant
5512	CCBL1	-1.02	7.32E-01	7.92E-01	398.11	not significant
5513	PRG2	-1.02	8.10E-01	8.55E-01	34.62	not significant
5514	TMEM147	-1.02	5.91E-01	6.72E-01	1711.10	not significant
5515	ELAC1	-1.02	7.95E-01	8.43E-01	183.86	not significant
5516	PWP1	-1.02	5.09E-01	5.98E-01	2936.29	not significant
5517	TRIM28	-1.02	3.76E-01	4.68E-01	26508.90	not significant
5518	ZWINT	-1.02	4.34E-01	5.26E-01	7429.64	not significant
5519	WAC	-1.02	3.68E-01	4.60E-01	9101.39	not significant
5520	ANKRD46	-1.02	5.81E-01	6.64E-01	1587.69	not significant
5521	LRRC69	-1.02	8.07E-01	8.52E-01	26.18	not significant
5522	MYO1F	-1.02	8.20E-01	8.64E-01	67.29	not significant
5523	PARD6A	-1.02	7.77E-01	8.28E-01	261.77	not significant
5524	TNRC6B	-1.02	5.91E-01	6.72E-01	1807.56	not significant
5525	UBE4B	-1.02	5.25E-01	6.13E-01	2595.83	not significant
5526	RNF168	-1.02	5.13E-01	6.02E-01	2667.54	not significant
5527	PCNXL3	-1.02	5.59E-01	6.44E-01	3453.28	not significant
5528	CTD-2201I18.1	-1.02	8.06E-01	8.52E-01	24.92	not significant
5529	SMOX	-1.02	8.04E-01	8.50E-01	151.62	not significant
5530	SUMO3	-1.02	5.07E-01	5.97E-01	4656.04	not significant
5531	FGFR1OP2	-1.02	5.30E-01	6.18E-01	3049.36	not significant
5532	ACTA2-AS1	-1.02	7.75E-01	8.27E-01	13.43	not significant

5533	ZBTB43	-1.02	7.02E-01	7.67E-01	621.15	not significant
5534	CASP8AP2	-1.02	4.75E-01	5.66E-01	4104.40	not significant
5535	ARHGAP39	-1.02	7.98E-01	8.46E-01	19.16	not significant
5536	ZNF609	-1.02	5.33E-01	6.21E-01	2941.82	not significant
5537	MAX	-1.02	4.42E-01	5.34E-01	5249.55	not significant
5538	CBX8	-1.02	7.42E-01	8.00E-01	433.89	not significant
5539	CDKN2B-AS1	-1.02	8.01E-01	8.48E-01	20.52	not significant
5540	TMEM232	-1.02	7.98E-01	8.46E-01	18.82	not significant
5541	RAD21	-1.02	4.00E-01	4.92E-01	38629.44	not significant
5542	FXYD5	-1.02	5.23E-01	6.11E-01	2883.37	not significant
5543	MAP3K7	-1.02	4.92E-01	5.82E-01	3291.78	not significant
5544	LSM14A	-1.02	5.96E-01	6.76E-01	1938.65	not significant
5545	TOR2A	-1.02	6.97E-01	7.63E-01	710.40	not significant
5546	NAP1L4	-1.02	4.84E-01	5.74E-01	8993.02	not significant
5547	PRKRIR	-1.02	5.31E-01	6.19E-01	3102.11	not significant
5548	SLC25A33	-1.02	7.62E-01	8.17E-01	373.84	not significant
5549	C17orf67	-1.02	8.07E-01	8.52E-01	178.30	not significant
5550	SENP6	-1.02	4.65E-01	5.56E-01	5116.39	not significant
5551	FCER1G	-1.02	7.25E-01	7.87E-01	6.79	not significant
5552	RNF11	-1.02	5.57E-01	6.42E-01	2150.46	not significant
5553	CREBBP	-1.02	5.78E-01	6.62E-01	3347.23	not significant
5554	CLN5	-1.02	7.37E-01	7.96E-01	535.16	not significant
5555	TIMM17B	-1.02	7.47E-01	8.04E-01	450.71	not significant
5556	KIAA1191	-1.02	5.81E-01	6.64E-01	1843.92	not significant
5557	RNF165	-1.02	8.09E-01	8.54E-01	20.42	not significant
5558	GNMT	-1.02	8.19E-01	8.62E-01	26.57	not significant
5559	LAGE3	-1.02	7.80E-01	8.31E-01	328.85	not significant
5560	CASC4	-1.02	5.63E-01	6.48E-01	2223.75	not significant
5561	GPATCH11	-1.02	6.21E-01	6.98E-01	1749.64	not significant
5562	RASA2	-1.02	6.37E-01	7.12E-01	1555.05	not significant
5563	SENP5	-1.02	5.74E-01	6.57E-01	2191.57	not significant
5564	OSBPL8	-1.02	4.86E-01	5.76E-01	8290.13	not significant
5565	EFTUD1	-1.02	6.53E-01	7.27E-01	1273.15	not significant
5566	DIS3L	-1.02	6.08E-01	6.87E-01	1903.57	not significant
5567	HERC2P3	-1.02	8.01E-01	8.48E-01	15.15	not significant
5568	PIAS1	-1.02	6.62E-01	7.34E-01	1035.26	not significant
5569	TIGD2	-1.02	8.23E-01	8.66E-01	127.34	not significant
5570	COX4I1	-1.02	5.58E-01	6.43E-01	8313.38	not significant
5571	METTL22	-1.02	7.59E-01	8.14E-01	465.00	not significant
5572	SRP72	-1.02	4.24E-01	5.16E-01	7921.06	not significant
5573	GSKIP	-1.02	6.82E-01	7.51E-01	1109.52	not significant
5574	IL1RAP	-1.02	8.36E-01	8.76E-01	55.90	not significant
5575	VPS37B	-1.02	5.11E-01	6.00E-01	3562.34	not significant
5576	TAF1	-1.02	6.12E-01	6.90E-01	2493.99	not significant
5577	NPIPA5	-1.02	8.20E-01	8.64E-01	156.46	not significant
5578	UPP1	-1.02	8.31E-01	8.72E-01	29.93	not significant
5579	MAP3K14-AS1	-1.02	8.04E-01	8.51E-01	222.27	not significant
5580	ASGR1	-1.02	7.56E-01	8.11E-01	7.72	not significant
5581	SENP1	-1.02	5.39E-01	6.26E-01	3702.32	not significant
5582	ARL16	-1.02	6.70E-01	7.40E-01	1233.60	not significant
5583	RAB18	-1.02	6.00E-01	6.79E-01	1967.75	not significant
5584	USP46-AS1	-1.02	7.81E-01	8.32E-01	11.23	not significant
5585	BANP	-1.02	7.43E-01	8.01E-01	573.20	not significant
5586	RNF139	-1.02	6.11E-01	6.90E-01	1834.56	not significant
5587	LRCH1	-1.02	6.35E-01	7.10E-01	1462.38	not significant
5588	MCAT	-1.02	7.34E-01	7.93E-01	601.99	not significant
5589	CCDC65	-1.02	7.71E-01	8.24E-01	8.91	not significant
5590	LY6G5B	-1.02	8.01E-01	8.48E-01	14.11	not significant
5591	TMBIM1	-1.02	7.40E-01	7.98E-01	589.22	not significant
5592	TUSC5	-1.02	7.79E-01	8.30E-01	366.55	not significant
5593	CEP57L1	-1.02	6.89E-01	7.57E-01	1044.46	not significant
5594	TMEM242	-1.02	8.35E-01	8.75E-01	121.98	not significant
5595	INF2	-1.02	5.99E-01	6.79E-01	2593.22	not significant
5596	UBAC1	-1.02	6.89E-01	7.57E-01	1124.33	not significant
5597	C8orf76	-1.02	8.32E-01	8.73E-01	97.36	not significant
5598	ZNF660	-1.02	7.90E-01	8.40E-01	10.61	not significant
5599	DDX50	-1.02	5.85E-01	6.67E-01	3471.26	not significant
5600	ARMCX5-GPRASF	-1.01	8.37E-01	8.77E-01	32.53	not significant
5601	SMNDC1	-1.01	6.00E-01	6.80E-01	2370.06	not significant
5602	VPS4A	-1.01	5.81E-01	6.63E-01	3462.67	not significant
5603	ANAPC16	-1.01	5.71E-01	6.55E-01	3674.46	not significant
5604	FAIM	-1.01	8.22E-01	8.65E-01	195.40	not significant
5605	CUEDC2	-1.01	5.75E-01	6.59E-01	2473.83	not significant
5606	PET100	-1.01	7.31E-01	7.91E-01	663.32	not significant
5607	SLAMF1	-1.01	7.84E-01	8.34E-01	343.03	not significant
5608	TMLHE	-1.01	8.43E-01	8.82E-01	74.59	not significant
5609	GDAP2	-1.01	7.26E-01	7.87E-01	716.23	not significant
5610	RECQL	-1.01	5.45E-01	6.31E-01	3492.83	not significant
5611	CD274	-1.01	8.45E-01	8.83E-01	43.87	not significant
5612	ACOT9	-1.01	8.07E-01	8.53E-01	250.50	not significant
5613	CHID1	-1.01	6.44E-01	7.19E-01	1479.16	not significant
5614	FAM149A	-1.01	8.35E-01	8.75E-01	131.57	not significant
5615	VKORC1L1	-1.01	5.42E-01	6.29E-01	3623.81	not significant
5616	FAM3C	-1.01	7.97E-01	8.46E-01	313.27	not significant
5617	MRPS26	-1.01	6.65E-01	7.37E-01	1976.21	not significant
5618	VPS37C	-1.01	8.32E-01	8.73E-01	163.03	not significant
5619	STAM2	-1.01	7.22E-01	7.84E-01	831.61	not significant
5620	CSNK1G1	-1.01	6.52E-01	7.25E-01	1932.13	not significant

5621	MED8	-1.01	7.03E-01	7.68E-01	942.87	not significant
5622	MTMR9	-1.01	7.34E-01	7.94E-01	946.88	not significant
5623	PTEN	-1.01	5.04E-01	5.94E-01	12482.63	not significant
5624	ZNF598	-1.01	6.04E-01	6.84E-01	2602.64	not significant
5625	SMYD2	-1.01	6.10E-01	6.88E-01	2031.22	not significant
5626	KHK	-1.01	8.29E-01	8.70E-01	176.47	not significant
5627	TADA1	-1.01	7.08E-01	7.72E-01	1067.30	not significant
5628	NCOA7	-1.01	6.76E-01	7.45E-01	1256.99	not significant
5629	MIIP	-1.01	7.16E-01	7.79E-01	880.91	not significant
5630	QSER1	-1.01	6.61E-01	7.33E-01	1913.41	not significant
5631	COLGALT1	-1.01	5.58E-01	6.42E-01	3576.45	not significant
5632	ZNF576	-1.01	8.04E-01	8.51E-01	365.79	not significant
5633	GPRIN1	-1.01	7.97E-01	8.45E-01	10.44	not significant
5634	GOLPH3	-1.01	5.72E-01	6.56E-01	3504.10	not significant
5635	KIF18B	-1.01	7.69E-01	8.23E-01	4498.27	not significant
5636	RRM2B	-1.01	7.40E-01	7.98E-01	717.16	not significant
5637	TAPT1-AS1	-1.01	8.54E-01	8.90E-01	77.54	not significant
5638	PITPNA-AS1	-1.01	8.18E-01	8.62E-01	267.80	not significant
5639	RFXANK	-1.01	7.05E-01	7.69E-01	1047.77	not significant
5640	NUP85	-1.01	5.74E-01	6.57E-01	4107.89	not significant
5641	RABL6	-1.01	5.84E-01	6.66E-01	3440.07	not significant
5642	GRIK5	-1.01	8.21E-01	8.64E-01	12.96	not significant
5643	SMG6	-1.01	5.93E-01	6.74E-01	2978.91	not significant
5644	TMED10P1	-1.01	8.31E-01	8.72E-01	16.35	not significant
5645	PPA1	-1.01	5.75E-01	6.59E-01	8138.38	not significant
5646	MSL1	-1.01	5.56E-01	6.41E-01	3997.25	not significant
5647	LINC00909	-1.01	7.71E-01	8.24E-01	596.01	not significant
5648	TMEM177	-1.01	8.31E-01	8.72E-01	256.02	not significant
5649	DLX4	-1.01	8.22E-01	8.65E-01	12.86	not significant
5650	EPS8L1	-1.01	8.55E-01	8.91E-01	106.38	not significant
5651	SNX17	-1.01	6.18E-01	6.95E-01	4378.37	not significant
5652	OCLM	-1.01	8.41E-01	8.80E-01	21.32	not significant
5653	SCEL	-1.01	6.57E-01	7.30E-01	1927.06	not significant
5654	DCUN1D1	-1.01	6.78E-01	7.47E-01	1536.07	not significant
5655	GANAB	-1.01	5.07E-01	5.96E-01	14261.71	not significant
5656	CNIH3	-1.01	8.47E-01	8.85E-01	23.96	not significant
5657	MSRB1	-1.01	8.05E-01	8.51E-01	375.90	not significant
5658	TPTEP1	-1.01	7.63E-01	8.17E-01	647.91	not significant
5659	SLC25A1	-1.01	7.59E-01	8.14E-01	801.77	not significant
5660	MAPKAPK5	-1.01	6.41E-01	7.16E-01	2435.93	not significant
5661	SLC43A1	-1.01	8.43E-01	8.82E-01	199.27	not significant
5662	ENTPD1-AS1	-1.01	8.62E-01	8.97E-01	68.90	not significant
5663	HOOK3	-1.01	6.35E-01	7.11E-01	2871.59	not significant
5664	TNFSF8	-1.01	8.52E-01	8.89E-01	132.44	not significant
5665	EMC9	-1.01	7.87E-01	8.37E-01	482.26	not significant
5666	PDK1	-1.01	6.70E-01	7.40E-01	1657.46	not significant
5667	TECPR2	-1.01	7.63E-01	8.17E-01	711.43	not significant
5668	TRIM47	-1.01	8.63E-01	8.97E-01	75.18	not significant
5669	SEC22C	-1.01	6.69E-01	7.39E-01	2252.94	not significant
5670	MRPL32	-1.01	7.30E-01	7.90E-01	1304.30	not significant
5671	BMP1	-1.01	8.15E-01	8.59E-01	334.79	not significant
5672	VWA9	-1.01	6.78E-01	7.47E-01	1747.28	not significant
5673	LLGL2	-1.01	8.63E-01	8.97E-01	82.36	not significant
5674	ALDH16A1	-1.01	7.10E-01	7.73E-01	1530.36	not significant
5675	NDUFB2	-1.01	8.36E-01	8.76E-01	1268.77	not significant
5676	MFHAS1	-1.01	6.17E-01	6.95E-01	5551.03	not significant
5677	RAB9A	-1.01	8.14E-01	8.59E-01	361.12	not significant
5678	UBB	-1.01	4.75E-01	5.66E-01	21311.40	not significant
5679	CDC45	-1.01	6.16E-01	6.94E-01	4135.75	not significant
5680	SMUG1	-1.01	7.93E-01	8.42E-01	480.60	not significant
5681	HIST1H4B	-1.01	8.05E-01	8.51E-01	8.56	not significant
5682	SCLT1	-1.01	7.39E-01	7.98E-01	924.11	not significant
5683	PCDH18	-1.01	8.65E-01	8.99E-01	39.49	not significant
5684	NPM1	-1.01	6.05E-01	6.85E-01	31786.21	not significant
5685	CS	-1.01	4.90E-01	5.80E-01	10607.57	not significant
5686	PRDM8	-1.01	8.66E-01	9.00E-01	75.91	not significant
5687	MRFAP1L1	-1.01	6.83E-01	7.52E-01	2276.02	not significant
5688	VPS54	-1.01	7.31E-01	7.91E-01	1189.13	not significant
5689	RPGRIP1L	-1.01	8.05E-01	8.51E-01	418.81	not significant
5690	GPANK1	-1.01	8.62E-01	8.97E-01	115.06	not significant
5691	C9orf40	-1.01	7.29E-01	7.90E-01	1154.97	not significant
5692	CD7	-1.01	5.93E-01	6.74E-01	7428.31	not significant
5693	VWA5A	-1.01	8.67E-01	9.00E-01	36.14	not significant
5694	DHX38	-1.01	6.26E-01	7.03E-01	3033.94	not significant
5695	PFKL	-1.01	6.63E-01	7.35E-01	2442.59	not significant
5696	ULK4	-1.01	8.50E-01	8.88E-01	207.76	not significant
5697	CALML4	-1.01	8.27E-01	8.69E-01	340.47	not significant
5698	ZFP91	-1.01	6.19E-01	6.97E-01	3455.08	not significant
5699	ERI2	-1.01	7.21E-01	7.83E-01	1210.48	not significant
5700	TLE3	-1.01	5.92E-01	6.73E-01	8571.96	not significant
5701	DTX2	-1.01	8.01E-01	8.48E-01	646.58	not significant
5702	PARP9	-1.01	6.47E-01	7.22E-01	2751.94	not significant
5703	NAPRT	-1.01	8.27E-01	8.69E-01	403.66	not significant
5704	FGFR4	-1.01	8.62E-01	8.96E-01	25.41	not significant
5705	ZNF256	-1.01	8.36E-01	8.76E-01	321.82	not significant
5706	FBXO48	-1.01	8.60E-01	8.95E-01	158.73	not significant
5707	PELI1	-1.01	8.05E-01	8.51E-01	493.97	not significant
5708	SECISBP2	-1.01	7.03E-01	7.67E-01	1880.74	not significant

5709	C6orf163	-1.01	8.36E-01	8.76E-01	11.47	not significant
5710	TEX2	-1.01	7.08E-01	7.72E-01	1505.58	not significant
5711	RALBP1	-1.01	6.31E-01	7.08E-01	4925.88	not significant
5712	VPS9D1	-1.01	8.76E-01	9.07E-01	75.81	not significant
5713	LTBP1	-1.01	8.81E-01	9.10E-01	109.11	not significant
5714	RC3H1	-1.01	7.40E-01	7.98E-01	1646.09	not significant
5715	SIRT6	-1.01	7.73E-01	8.25E-01	920.69	not significant
5716	LINC00467	-1.01	8.77E-01	9.08E-01	58.83	not significant
5717	C14orf2	-1.01	6.89E-01	7.57E-01	3408.04	not significant
5718	CMTM2	-1.01	8.39E-01	8.78E-01	12.00	not significant
5719	PUM2	-1.01	5.63E-01	6.48E-01	9936.58	not significant
5720	GAS8	-1.01	8.74E-01	9.05E-01	33.15	not significant
5721	CHD1	-1.01	6.51E-01	7.25E-01	4487.67	not significant
5722	POLB	-1.01	7.33E-01	7.92E-01	1351.22	not significant
5723	FMO4	-1.01	8.78E-01	9.08E-01	39.11	not significant
5724	HELZ	-1.01	6.48E-01	7.23E-01	9015.86	not significant
5725	FBXO25	-1.01	7.02E-01	7.67E-01	2656.62	not significant
5726	LOC344967	-1.01	8.51E-01	8.88E-01	14.26	not significant
5727	ATAD2B	-1.01	7.27E-01	7.88E-01	1729.04	not significant
5728	NRSN2-AS1	-1.01	8.74E-01	9.06E-01	29.42	not significant
5729	PXDN	-1.01	6.51E-01	7.25E-01	3588.06	not significant
5730	EPN1	-1.01	6.79E-01	7.48E-01	2728.31	not significant
5731	C19orf18	-1.01	8.37E-01	8.77E-01	10.25	not significant
5732	CTPS1	-1.01	6.22E-01	6.99E-01	6683.76	not significant
5733	NDN	-1.01	8.43E-01	8.81E-01	362.40	not significant
5734	CBY1	-1.01	8.76E-01	9.07E-01	130.47	not significant
5735	ITGB3	-1.01	8.82E-01	9.11E-01	42.87	not significant
5736	UTP14C	-1.01	7.70E-01	8.24E-01	1107.36	not significant
5737	SCLY	-1.01	8.39E-01	8.78E-01	9.80	not significant
5738	ZFAND6	-1.01	7.38E-01	7.97E-01	1355.10	not significant
5739	DUSP5P1	-1.01	8.74E-01	9.05E-01	23.55	not significant
5740	SLC39A8	-1.01	6.65E-01	7.37E-01	3544.75	not significant
5741	OSBP	-1.01	6.69E-01	7.39E-01	3182.68	not significant
5742	TRAPPC8	-1.01	6.82E-01	7.50E-01	2583.75	not significant
5743	GLT8D1	-1.01	7.66E-01	8.20E-01	1224.45	not significant
5744	ALPK3	-1.01	8.49E-01	8.86E-01	13.18	not significant
5745	LETM1	-1.01	6.20E-01	6.97E-01	4986.97	not significant
5746	PREX1	-1.01	6.88E-01	7.56E-01	3163.21	not significant
5747	DDX6	-1.01	7.40E-01	7.98E-01	1952.67	not significant
5748	FXN	-1.01	8.76E-01	9.07E-01	219.04	not significant
5749	FAM134B	-1.01	7.26E-01	7.87E-01	1803.65	not significant
5750	ZNF287	-1.01	8.58E-01	8.94E-01	299.77	not significant
5751	ZNF343	-1.01	8.16E-01	8.60E-01	595.69	not significant
5752	NEDD4	-1.01	7.43E-01	8.01E-01	1553.37	not significant
5753	RAB19	-1.01	8.86E-01	9.14E-01	37.53	not significant
5754	KIAA1586	-1.01	8.23E-01	8.66E-01	535.12	not significant
5755	NBEAL2	-1.01	8.62E-01	8.97E-01	7269.94	not significant
5756	REV1	-1.01	7.57E-01	8.12E-01	1390.13	not significant
5757	FIS1	-1.01	7.67E-01	8.21E-01	1670.05	not significant
5758	ACBD7	-1.01	7.55E-01	8.11E-01	1444.77	not significant
5759	VPS9D1-AS1	-1.01	8.63E-01	8.97E-01	394.72	not significant
5760	UNC93B1	-1.01	8.86E-01	9.14E-01	23.39	not significant
5761	SERGEF	-1.01	8.32E-01	8.73E-01	525.44	not significant
5762	GFRA3	-1.01	8.63E-01	8.97E-01	12.31	not significant
5763	ATP5A1	-1.01	6.98E-01	7.63E-01	20511.17	not significant
5764	GMPR2	-1.01	7.69E-01	8.22E-01	1757.56	not significant
5765	LASP1	-1.01	6.67E-01	7.38E-01	10470.30	not significant
5766	PPP3CA	-1.01	7.63E-01	8.17E-01	1544.60	not significant
5767	HIST1H4D	-1.01	8.58E-01	8.94E-01	9.96	not significant
5768	ZNF134	-1.01	7.99E-01	8.47E-01	1039.71	not significant
5769	SLC37A4	-1.01	8.91E-01	9.18E-01	144.45	not significant
5770	TCF7L2	-1.01	8.47E-01	8.85E-01	435.45	not significant
5771	HEATR5A	-1.01	8.71E-01	9.03E-01	276.35	not significant
5772	RBMXL2	-1.01	8.54E-01	8.91E-01	8.59	not significant
5773	HIST1H3D	-1.01	8.92E-01	9.19E-01	26.44	not significant
5774	BBS5	-1.01	8.86E-01	9.14E-01	210.29	not significant
5775	PPP6C	-1.01	7.09E-01	7.72E-01	3513.85	not significant
5776	AZIN1	-1.01	5.83E-01	6.65E-01	15959.22	not significant
5777	ZNF137P	-1.01	8.68E-01	9.01E-01	323.37	not significant
5778	EXOC6	-1.01	7.94E-01	8.43E-01	1113.59	not significant
5779	ITPK1	-1.01	7.45E-01	8.02E-01	2482.54	not significant
5780	IGF2BP3	-1.01	8.96E-01	9.21E-01	28.46	not significant
5781	PPP1R11	-1.01	8.95E-01	9.21E-01	165.10	not significant
5782	CENPBD1	-1.01	8.77E-01	9.07E-01	284.59	not significant
5783	MGAT3	-1.01	8.96E-01	9.21E-01	27.22	not significant
5784	SATB1	-1.01	7.42E-01	8.00E-01	2314.30	not significant
5785	PITRM1-AS1	-1.01	9.01E-01	9.25E-01	36.61	not significant
5786	TLN2	-1.01	9.02E-01	9.25E-01	94.65	not significant
5787	ATXN1L	-1.01	7.32E-01	7.92E-01	2867.69	not significant
5788	MAFK	-1.01	7.24E-01	7.86E-01	2904.44	not significant
5789	XRCC6BP1	-1.01	8.68E-01	9.01E-01	353.76	not significant
5790	SMARCAD1	-1.01	7.12E-01	7.75E-01	4162.67	not significant
5791	ZNF257	-1.01	8.90E-01	9.17E-01	180.83	not significant
5792	NUP214	-1.01	8.68E-01	9.01E-01	3065.32	not significant
5793	GOLGA2	-1.01	7.71E-01	8.24E-01	1740.11	not significant
5794	YY2	-1.01	9.02E-01	9.26E-01	118.22	not significant
5795	DEPDC4	-1.01	9.07E-01	9.30E-01	48.97	not significant
5796	POU4F1	-1.01	9.00E-01	9.24E-01	27.80	not significant

5797	ARID2	-1.01	7.39E-01	7.98E-01	4507.41	not significant
5798	GPN1	-1.01	7.75E-01	8.27E-01	1667.38	not significant
5799	MUSTN1	-1.01	8.92E-01	9.19E-01	18.84	not significant
5800	SMARCA4	-1.01	7.38E-01	7.97E-01	14073.12	not significant
5801	ARL6IP6	-1.01	7.73E-01	8.25E-01	2541.65	not significant
5802	PTPN14	-1.01	8.95E-01	9.21E-01	200.46	not significant
5803	MDM1	-1.01	7.82E-01	8.32E-01	1538.52	not significant
5804	MRPS35	-1.01	7.60E-01	8.14E-01	2793.17	not significant
5805	HMCES	-1.01	7.76E-01	8.28E-01	2901.29	not significant
5806	KRTCAP3	-1.01	8.95E-01	9.21E-01	18.04	not significant
5807	C11orf58	-1.01	7.09E-01	7.72E-01	5846.44	not significant
5808	SELPLG	-1.01	7.25E-01	7.86E-01	5772.73	not significant
5809	ZNF84	-1.01	9.06E-01	9.29E-01	110.75	not significant
5810	CYB561D1	-1.01	8.55E-01	8.91E-01	595.36	not significant
5811	EXOSC4	-1.01	9.11E-01	9.33E-01	67.38	not significant
5812	TP53TG1	-1.01	8.93E-01	9.19E-01	253.48	not significant
5813	FBXO42	-1.01	8.20E-01	8.64E-01	1040.94	not significant
5814	PXYLP1	-1.01	7.54E-01	8.10E-01	3088.28	not significant
5815	FUS	-1.01	7.22E-01	7.84E-01	20406.32	not significant
5816	NLGN2	-1.01	8.58E-01	8.94E-01	595.91	not significant
5817	RAC3	-1.01	8.85E-01	9.14E-01	365.67	not significant
5818	WASF2	-1.01	7.12E-01	7.75E-01	8569.48	not significant
5819	DBP	-1.01	8.52E-01	8.89E-01	696.34	not significant
5820	HNRNPF	-1.01	7.08E-01	7.72E-01	22331.94	not significant
5821	PWWP2B	-1.01	8.80E-01	9.10E-01	452.33	not significant
5822	PRDX6	-1.01	7.30E-01	7.90E-01	5586.24	not significant
5823	NMRK1	-1.01	9.01E-01	9.25E-01	248.90	not significant
5824	EMC7	-1.01	8.44E-01	8.82E-01	952.29	not significant
5825	SP4	-1.01	7.98E-01	8.46E-01	2102.56	not significant
5826	PM20D2	-1.01	7.25E-01	7.87E-01	4766.94	not significant
5827	HSF2BP	-1.01	9.07E-01	9.30E-01	18.56	not significant
5828	ITPKA	-1.01	9.08E-01	9.30E-01	21.70	not significant
5829	CD97	-1.01	8.29E-01	8.71E-01	1887.42	not significant
5830	KIAA0100	-1.01	7.14E-01	7.77E-01	9395.56	not significant
5831	IFT43	-1.01	9.15E-01	9.35E-01	131.01	not significant
5832	CUTA	-1.01	8.09E-01	8.55E-01	1569.92	not significant
5833	HAUS1	-1.01	7.94E-01	8.43E-01	2115.45	not significant
5834	DKFZP434I0714	-1.01	9.10E-01	9.32E-01	227.61	not significant
5835	MBOAT2	-1.01	8.32E-01	8.73E-01	1368.41	not significant
5836	KIF9	-1.01	9.12E-01	9.33E-01	176.83	not significant
5837	IST1	-1.01	7.48E-01	8.05E-01	4218.78	not significant
5838	ACAT2	-1.01	7.85E-01	8.35E-01	3513.17	not significant
5839	RUNX1	-1.01	7.42E-01	8.00E-01	8879.31	not significant
5840	HARS	-1.01	7.96E-01	8.45E-01	2348.58	not significant
5841	HOXB-AS1	-1.01	9.23E-01	9.42E-01	40.60	not significant
5842	FBXO5	-1.01	7.91E-01	8.41E-01	2922.45	not significant
5843	PAX8-AS1	-1.01	8.44E-01	8.82E-01	1371.25	not significant
5844	SAYSD1	-1.01	8.71E-01	9.04E-01	636.03	not significant
5845	LRRC17	-1.01	9.05E-01	9.28E-01	12.92	not significant
5846	WDR24	-1.01	8.64E-01	8.98E-01	943.19	not significant
5847	TEX10	-1.01	8.54E-01	8.91E-01	1085.23	not significant
5848	CCDC64	-1.01	8.43E-01	8.81E-01	995.97	not significant
5849	KLHDC1	-1.01	9.24E-01	9.43E-01	45.82	not significant
5850	MAN2B2	-1.01	8.26E-01	8.68E-01	1639.67	not significant
5851	TEX9	-1.01	9.26E-01	9.44E-01	65.86	not significant
5852	CD2AP	-1.01	7.91E-01	8.40E-01	4227.68	not significant
5853	LPAR2	-1.01	9.14E-01	9.35E-01	277.57	not significant
5854	ARHGAP23	-1.01	9.05E-01	9.28E-01	266.99	not significant
5855	ARL14EP	-1.01	8.54E-01	8.91E-01	1026.14	not significant
5856	TMEM134	-1.01	8.71E-01	9.04E-01	735.29	not significant
5857	ZNF616	-1.01	8.78E-01	9.08E-01	641.13	not significant
5858	SCARNA10	-1.01	9.04E-01	9.27E-01	11.81	not significant
5859	ACTR10	-1.01	8.53E-01	8.90E-01	1114.45	not significant
5860	PYROXD2	-1.01	9.21E-01	9.41E-01	163.38	not significant
5861	POU2AF1	-1.01	8.74E-01	9.05E-01	746.60	not significant
5862	SACS	-1.01	8.87E-01	9.15E-01	5801.67	not significant
5863	MYNN	-1.01	8.67E-01	9.00E-01	852.38	not significant
5864	NMRAL1	-1.01	8.02E-01	8.49E-01	3140.83	not significant
5865	C16orf87	-1.01	8.93E-01	9.19E-01	550.05	not significant
5866	N4BP1	-1.01	8.25E-01	8.67E-01	1914.74	not significant
5867	USP38	-1.01	8.25E-01	8.67E-01	2087.86	not significant
5868	ARNTL	-1.01	9.01E-01	9.25E-01	479.35	not significant
5869	ZNF182	-1.01	9.29E-01	9.47E-01	31.13	not significant
5870	ZNF596	-1.01	9.24E-01	9.43E-01	170.19	not significant
5871	CMPK1	-1.01	8.00E-01	8.48E-01	5141.03	not significant
5872	BTD	-1.01	9.25E-01	9.44E-01	165.61	not significant
5873	SNX22	-1.01	9.19E-01	9.39E-01	84.86	not significant
5874	CASZ1	-1.01	9.00E-01	9.24E-01	423.37	not significant
5875	NECAP1	-1.01	8.95E-01	9.21E-01	737.16	not significant
5876	WRAP73	-1.01	8.75E-01	9.06E-01	1140.44	not significant
5877	ALOX15P1	-1.01	9.32E-01	9.49E-01	23.63	not significant
5878	HMGCR	-1.01	7.84E-01	8.35E-01	7015.20	not significant
5879	IQCH	-1.01	9.38E-01	9.52E-01	42.91	not significant
5880	ZNF416	-1.01	9.20E-01	9.39E-01	290.96	not significant
5881	WDR83OS	-1.01	8.69E-01	9.01E-01	1493.87	not significant
5882	ADAM9	-1.01	8.89E-01	9.16E-01	829.17	not significant
5883	DGCR6L	-1.01	8.95E-01	9.21E-01	652.62	not significant
5884	AP2A2	-1.01	8.55E-01	8.91E-01	1678.65	not significant

5885	MIPEPP3	-1.01	9.40E-01	9.54E-01	62.59	not significant
5886	ABI1	-1.01	8.31E-01	8.72E-01	2678.40	not significant
5887	VWCE	-1.01	9.28E-01	9.46E-01	226.45	not significant
5888	LOC100652758	-1.01	9.37E-01	9.52E-01	28.95	not significant
5889	THAP8	-1.01	9.29E-01	9.47E-01	248.12	not significant
5890	NCOR2	-1.01	8.06E-01	8.52E-01	7874.50	not significant
5891	ANKRD42	-1.01	9.41E-01	9.55E-01	71.39	not significant
5892	USP28	-1.01	8.75E-01	9.06E-01	1303.20	not significant
5893	CENPBD1P1	-1.01	8.81E-01	9.10E-01	1101.55	not significant
5894	COQ6	-1.01	9.13E-01	9.34E-01	404.54	not significant
5895	EXOSC5	-1.01	9.02E-01	9.26E-01	675.11	not significant
5896	ZNF638	-1.01	8.16E-01	8.60E-01	3957.45	not significant
5897	TCEAL8	-1.01	8.58E-01	8.94E-01	1837.16	not significant
5898	SLMO2	-1.01	8.55E-01	8.91E-01	2510.79	not significant
5899	MED24	-1.01	8.30E-01	8.71E-01	4230.58	not significant
5900	FAM172A	-1.01	8.69E-01	9.01E-01	1538.96	not significant
5901	CHRNA3	-1.01	9.40E-01	9.54E-01	27.34	not significant
5902	ATP6V0E1	-1.01	8.64E-01	8.98E-01	2211.68	not significant
5903	TOR1B	-1.01	8.83E-01	9.12E-01	1053.33	not significant
5904	TBCD	-1.01	7.79E-01	8.30E-01	9692.97	not significant
5905	ENSA	-1.01	8.35E-01	8.75E-01	6465.51	not significant
5906	KREMEN2	-1.01	9.38E-01	9.53E-01	19.53	not significant
5907	FARS2	-1.01	9.17E-01	9.37E-01	481.83	not significant
5908	LARP7	-1.01	8.55E-01	8.91E-01	2244.04	not significant
5909	TATDN3	-1.01	8.95E-01	9.21E-01	956.36	not significant
5910	UPF3B	-1.00	8.85E-01	9.13E-01	1415.44	not significant
5911	RSL1D1	-1.00	8.42E-01	8.80E-01	7849.12	not significant
5912	MAPK13	-1.00	9.47E-01	9.60E-01	75.14	not significant
5913	LTN1	-1.00	8.98E-01	9.22E-01	1937.95	not significant
5914	RAB28	-1.00	8.98E-01	9.22E-01	1117.00	not significant
5915	CHD4	-1.00	8.43E-01	8.81E-01	18782.07	not significant
5916	NSUN4	-1.00	8.88E-01	9.15E-01	1558.96	not significant
5917	DCAF11	-1.00	8.59E-01	8.95E-01	4242.17	not significant
5918	MAST4	-1.00	9.14E-01	9.35E-01	1024.29	not significant
5919	CHCHD5	-1.00	9.51E-01	9.63E-01	115.88	not significant
5920	STARD3NL	-1.00	8.85E-01	9.13E-01	2490.45	not significant
5921	PLD3	-1.00	9.02E-01	9.25E-01	1207.15	not significant
5922	CBWD6	-1.00	9.50E-01	9.63E-01	27.93	not significant
5923	SRRM5	-1.00	9.45E-01	9.58E-01	18.60	not significant
5924	KIAA0922	-1.00	8.54E-01	8.91E-01	4826.56	not significant
5925	UBFD1	-1.00	8.62E-01	8.97E-01	3921.50	not significant
5926	MRPS22	-1.00	9.15E-01	9.36E-01	947.48	not significant
5927	RNF2	-1.00	9.02E-01	9.25E-01	1398.43	not significant
5928	VPS13A	-1.00	8.90E-01	9.17E-01	3210.00	not significant
5929	43711_25571	-1.00	9.56E-01	9.67E-01	49.84	not significant
5930	SLC12A7	-1.00	8.97E-01	9.22E-01	1819.33	not significant
5931	ZNF567	-1.00	9.26E-01	9.45E-01	619.21	not significant
5932	SCAF8	-1.00	8.61E-01	8.96E-01	3478.45	not significant
5933	SMC3	-1.00	8.62E-01	8.97E-01	7571.08	not significant
5934	LIMK2	-1.00	8.96E-01	9.21E-01	1700.80	not significant
5935	LTB4R2	-1.00	9.57E-01	9.68E-01	87.02	not significant
5936	TERC	-1.00	9.34E-01	9.50E-01	7.60	not significant
5937	HERC4	-1.00	9.02E-01	9.26E-01	1573.55	not significant
5938	GTF2H4	-1.00	9.28E-01	9.46E-01	620.09	not significant
5939	SARS2	-1.00	9.23E-01	9.43E-01	768.51	not significant
5940	AMN	-1.00	9.49E-01	9.62E-01	227.03	not significant
5941	ZNF329	-1.00	9.33E-01	9.50E-01	674.69	not significant
5942	C18orf8	-1.00	9.13E-01	9.34E-01	1165.63	not significant
5943	NDUFS2	-1.00	8.95E-01	9.21E-01	2180.41	not significant
5944	PNRC2	-1.00	9.31E-01	9.48E-01	632.38	not significant
5945	LTA	-1.00	9.59E-01	9.69E-01	81.26	not significant
5946	RAB44	-1.00	9.57E-01	9.68E-01	162.48	not significant
5947	MKL1	-1.00	8.95E-01	9.21E-01	2231.62	not significant
5948	NUCB1	-1.00	8.73E-01	9.05E-01	5102.45	not significant
5949	RGL4	-1.00	9.22E-01	9.41E-01	1071.40	not significant
5950	RBAK	-1.00	9.26E-01	9.44E-01	1232.93	not significant
5951	FASTK	-1.00	9.17E-01	9.38E-01	1692.87	not significant
5952	FBXO34	-1.00	9.15E-01	9.36E-01	1477.39	not significant
5953	LEPREL4	-1.00	9.48E-01	9.61E-01	10.58	not significant
5954	RSAD1	-1.00	9.08E-01	9.30E-01	1720.24	not significant
5955	TXNDC5	-1.00	9.61E-01	9.71E-01	45.99	not significant
5956	ERO1L	-1.00	8.95E-01	9.21E-01	4389.05	not significant
5957	TNRC6A	-1.00	8.96E-01	9.21E-01	2624.15	not significant
5958	CYP4V2	-1.00	9.24E-01	9.44E-01	1056.87	not significant
5959	TMEM179B	-1.00	9.38E-01	9.52E-01	694.04	not significant
5960	SKIV2L	-1.00	9.40E-01	9.54E-01	687.32	not significant
5961	PRDM2	-1.00	9.32E-01	9.49E-01	1184.34	not significant
5962	NFIX	-1.00	9.26E-01	9.44E-01	1277.92	not significant
5963	SLC25A13	-1.00	9.47E-01	9.60E-01	545.05	not significant
5964	DNAJB14	-1.00	9.15E-01	9.35E-01	2498.71	not significant
5965	RASA1	-1.00	9.39E-01	9.53E-01	919.03	not significant
5966	PBDC1	-1.00	9.66E-01	9.74E-01	148.62	not significant
5967	YTHDF3	-1.00	9.19E-01	9.39E-01	2412.65	not significant
5968	IFRD1	-1.00	9.34E-01	9.50E-01	1082.17	not significant
5969	EIF1	-1.00	9.09E-01	9.31E-01	21677.99	not significant
5970	CDK12	-1.00	9.18E-01	9.38E-01	4393.32	not significant
5971	RPL13P5	-1.00	9.58E-01	9.68E-01	8.78	not significant
5972	C7orf25	-1.00	9.61E-01	9.70E-01	330.16	not significant

5973	WDR11	-1.00	9.35E-01	9.51E-01	1435.85	not significant
5974	PIKFYVE	-1.00	9.08E-01	9.30E-01	5786.59	not significant
5975	LINC00565	-1.00	9.64E-01	9.73E-01	13.36	not significant
5976	ZNF668	-1.00	9.55E-01	9.66E-01	805.58	not significant
5977	PPIP5K2	-1.00	9.36E-01	9.52E-01	1518.15	not significant
5978	LOC399715	-1.00	9.68E-01	9.76E-01	19.44	not significant
5979	SLC39A4	-1.00	9.72E-01	9.79E-01	105.85	not significant
5980	SLC30A9	-1.00	9.33E-01	9.50E-01	2335.94	not significant
5981	SGK2	-1.00	9.65E-01	9.73E-01	12.53	not significant
5982	DCP1B	-1.00	9.60E-01	9.70E-01	492.59	not significant
5983	REEP6	-1.00	9.73E-01	9.80E-01	41.58	not significant
5984	KANSL2	-1.00	9.32E-01	9.49E-01	2225.66	not significant
5985	NMT1	-1.00	9.14E-01	9.35E-01	5897.74	not significant
5986	SPATA13	-1.00	9.33E-01	9.50E-01	3585.80	not significant
5987	LINC00539	-1.00	9.73E-01	9.80E-01	28.55	not significant
5988	MYH3	-1.00	9.75E-01	9.81E-01	121.02	not significant
5989	IER3IP1	-1.00	9.36E-01	9.52E-01	1877.90	not significant
5990	TTC39C	-1.00	9.58E-01	9.69E-01	741.19	not significant
5991	TRANK1	-1.00	9.43E-01	9.57E-01	2148.17	not significant
5992	MOK	-1.00	9.68E-01	9.76E-01	10.56	not significant
5993	HM13	-1.00	9.32E-01	9.49E-01	4813.98	not significant
5994	C19orf25	-1.00	9.58E-01	9.69E-01	818.63	not significant
5995	JOSD2	-1.00	9.71E-01	9.78E-01	291.92	not significant
5996	WBP11P1	-1.00	9.70E-01	9.77E-01	10.89	not significant
5997	SDHD	-1.00	9.44E-01	9.57E-01	3315.50	not significant
5998	POLG	-1.00	9.33E-01	9.50E-01	4889.94	not significant
5999	EP400NL	-1.00	9.72E-01	9.79E-01	327.19	not significant
6000	PSMD4	-1.00	9.45E-01	9.58E-01	3685.58	not significant
6001	FGFBP3	-1.00	9.79E-01	9.84E-01	74.65	not significant
6002	MED14OS	-1.00	9.69E-01	9.76E-01	8.80	not significant
6003	TSG101	-1.00	9.53E-01	9.65E-01	1603.23	not significant
6004	TATDN1	-1.00	9.68E-01	9.76E-01	630.80	not significant
6005	ATP2B1	-1.00	9.54E-01	9.66E-01	2332.55	not significant
6006	LCK	-1.00	9.40E-01	9.54E-01	22340.72	not significant
6007	ZNF142	-1.00	9.60E-01	9.70E-01	1953.35	not significant
6008	UBL3	-1.00	9.63E-01	9.72E-01	1057.83	not significant
6009	PTPDC1	-1.00	9.73E-01	9.79E-01	422.74	not significant
6010	LOC101929715	-1.00	9.73E-01	9.79E-01	8.49	not significant
6011	CTSA	-1.00	9.56E-01	9.67E-01	2249.96	not significant
6012	TNFSF12	-1.00	9.76E-01	9.82E-01	12.32	not significant
6013	CSRP2	-1.00	9.77E-01	9.83E-01	14.21	not significant
6014	CCT6B	-1.00	9.71E-01	9.78E-01	9.75	not significant
6015	CBFB	-1.00	9.45E-01	9.58E-01	10115.85	not significant
6016	POLR2M	-1.00	9.82E-01	9.87E-01	95.79	not significant
6017	ARSK	-1.00	9.76E-01	9.82E-01	502.19	not significant
6018	HIATL1	-1.00	9.61E-01	9.71E-01	3494.43	not significant
6019	CEACAM1	-1.00	9.80E-01	9.85E-01	48.03	not significant
6020	ATF6	-1.00	9.53E-01	9.65E-01	3424.55	not significant
6021	FBF1	-1.00	9.70E-01	9.78E-01	1113.01	not significant
6022	GAPDH	-1.00	9.86E-01	9.90E-01	189970.30	not significant
6023	RAD17	-1.00	9.64E-01	9.73E-01	1111.55	not significant
6024	CACTIN-AS1	-1.00	9.83E-01	9.87E-01	15.19	not significant
6025	AARS2	-1.00	9.72E-01	9.79E-01	1741.64	not significant
6026	RINT1	-1.00	9.79E-01	9.84E-01	1160.12	not significant
6027	ASCC1	-1.00	9.76E-01	9.82E-01	1063.50	not significant
6028	LOC100506023	-1.00	9.87E-01	9.91E-01	33.67	not significant
6029	TOX4	-1.00	9.69E-01	9.76E-01	2917.47	not significant
6030	CYB561D2	-1.00	9.85E-01	9.89E-01	552.04	not significant
6031	EEA1	-1.00	9.75E-01	9.81E-01	1690.10	not significant
6032	KSR1	-1.00	9.90E-01	9.92E-01	153.42	not significant
6033	SLC25A34	-1.00	9.90E-01	9.92E-01	32.28	not significant
6034	BLOC1S4	-1.00	9.88E-01	9.91E-01	522.58	not significant
6035	SCP2	-1.00	9.81E-01	9.86E-01	3483.17	not significant
6036	WDR78	-1.00	9.90E-01	9.92E-01	12.62	not significant
6037	NT5C2	-1.00	9.80E-01	9.85E-01	3623.23	not significant
6038	GRSF1	-1.00	9.75E-01	9.81E-01	9593.21	not significant
6039	MPHOSPH9	-1.00	9.75E-01	9.81E-01	3892.11	not significant
6040	SIX3-AS1	-1.00	9.92E-01	9.94E-01	45.48	not significant
6041	PER3	-1.00	9.93E-01	9.95E-01	20.91	not significant
6042	ZNF561-AS1	-1.00	9.94E-01	9.96E-01	98.91	not significant
6043	SLC16A3	-1.00	9.93E-01	9.95E-01	503.26	not significant
6044	TGIF2	-1.00	9.90E-01	9.92E-01	1957.32	not significant
6045	NXPE3	-1.00	9.92E-01	9.95E-01	2703.71	not significant
6046	BLVRA	-1.00	9.94E-01	9.96E-01	1037.60	not significant
6047	ZBTB38	-1.00	9.96E-01	9.97E-01	27.31	not significant
6048	PTPMT1	-1.00	9.89E-01	9.92E-01	1526.67	not significant
6049	SQRDL	-1.00	1.00E+00	1.00E+00	822.44	not significant
6050	PAFAH1B1	-1.00	9.94E-01	9.95E-01	7874.65	not significant
6051	THUMPD1	-1.00	9.95E-01	9.96E-01	3289.34	not significant
6052	CIT	-1.00	9.97E-01	9.98E-01	6202.43	not significant
6053	CMTR1	-1.00	9.97E-01	9.98E-01	4343.41	not significant
6054	KLF6	1.00	9.94E-01	9.96E-01	3690.75	not significant
6055	C19orf12	1.00	9.93E-01	9.95E-01	772.45	not significant
6056	MYO5C	1.00	9.99E-01	9.99E-01	184.75	not significant
6057	GHDC	1.00	9.99E-01	9.99E-01	654.60	not significant
6058	SMIM13	1.00	9.98E-01	9.99E-01	1021.96	not significant
6059	SETD1A	1.00	9.95E-01	9.96E-01	3773.08	not significant
6060	LYG1	1.00	9.99E-01	9.99E-01	54.65	not significant

6061	FBXL3	1.00	9.95E-01	9.96E-01	2546.28	not significant
6062	ATP6AP2	1.00	9.94E-01	9.95E-01	2553.52	not significant
6063	UGCG	1.00	9.95E-01	9.96E-01	514.98	not significant
6064	CSDE1	1.00	9.96E-01	9.97E-01	23782.02	not significant
6065	INSL3	1.00	9.97E-01	9.97E-01	11.03	not significant
6066	RALGDS	1.00	9.90E-01	9.93E-01	2044.25	not significant
6067	FGFR1OP	1.00	9.92E-01	9.94E-01	1267.20	not significant
6068	PDCD2	1.00	9.89E-01	9.92E-01	3182.38	not significant
6069	ERI1	1.00	9.90E-01	9.93E-01	2411.05	not significant
6070	TCP11L2	1.00	9.97E-01	9.97E-01	30.91	not significant
6071	PTPRA	1.00	9.84E-01	9.88E-01	5534.23	not significant
6072	PRPS2	1.00	9.83E-01	9.87E-01	4205.29	not significant
6073	SLC35B3	1.00	9.93E-01	9.95E-01	347.69	not significant
6074	CCDC97	1.00	9.85E-01	9.89E-01	2326.74	not significant
6075	BDP1	1.00	9.88E-01	9.91E-01	1078.57	not significant
6076	SPSB2	1.00	9.94E-01	9.95E-01	16.91	not significant
6077	ING2	1.00	9.89E-01	9.92E-01	590.62	not significant
6078	SPTAN1	1.00	9.95E-01	9.96E-01	12316.86	not significant
6079	TAF4B	1.00	9.69E-01	9.76E-01	1678.74	not significant
6080	PRKAR2A	1.00	9.78E-01	9.84E-01	818.35	not significant
6081	PRR34	1.00	9.90E-01	9.93E-01	15.17	not significant
6082	NIM1K	1.00	9.88E-01	9.91E-01	8.65	not significant
6083	PDLIM2	1.00	9.82E-01	9.86E-01	1040.31	not significant
6084	SIVA1	1.00	9.72E-01	9.79E-01	3692.96	not significant
6085	ARMC10	1.00	9.78E-01	9.84E-01	1584.88	not significant
6086	ARSB	1.00	9.77E-01	9.83E-01	1435.06	not significant
6087	RBMS1	1.00	9.70E-01	9.77E-01	2959.75	not significant
6088	AGBL3	1.00	9.93E-01	9.95E-01	33.00	not significant
6089	TMPO	1.00	9.59E-01	9.69E-01	38427.56	not significant
6090	FAM185A	1.00	9.87E-01	9.91E-01	203.10	not significant
6091	NDUFB2-AS1	1.00	9.89E-01	9.92E-01	32.86	not significant
6092	OCIAD1	1.00	9.62E-01	9.71E-01	5381.41	not significant
6093	ZNF276	1.00	9.86E-01	9.90E-01	2023.73	not significant
6094	YY1AP1	1.00	9.63E-01	9.72E-01	2520.83	not significant
6095	CAPG	1.00	9.60E-01	9.70E-01	3651.48	not significant
6096	IMPA2	1.00	9.86E-01	9.90E-01	24.91	not significant
6097	LOC100294362	1.00	9.83E-01	9.87E-01	14.20	not significant
6098	PAN2	1.00	9.81E-01	9.85E-01	2932.42	not significant
6099	NAGK	1.00	9.74E-01	9.80E-01	634.88	not significant
6100	SUFU	1.00	9.65E-01	9.73E-01	1257.47	not significant
6101	TERT	1.00	9.82E-01	9.87E-01	198.97	not significant
6102	TMX1	1.00	9.49E-01	9.62E-01	4666.93	not significant
6103	SGSM3	1.00	9.62E-01	9.71E-01	2258.20	not significant
6104	UVRAG	1.00	9.61E-01	9.71E-01	1250.99	not significant
6105	NCBP2-AS2	1.00	9.59E-01	9.69E-01	802.72	not significant
6106	HOMEZ	1.00	9.77E-01	9.83E-01	398.56	not significant
6107	CEBPB-AS1	1.00	9.79E-01	9.84E-01	25.55	not significant
6108	TMEM258	1.00	9.57E-01	9.68E-01	1481.36	not significant
6109	KCNIP2	1.00	9.79E-01	9.84E-01	31.83	not significant
6110	SAMD8	1.00	9.55E-01	9.66E-01	819.56	not significant
6111	ORMDL3	1.00	9.34E-01	9.50E-01	6900.61	not significant
6112	TYRO3	1.00	9.63E-01	9.72E-01	634.51	not significant
6113	SLC25A10	1.00	9.52E-01	9.64E-01	1542.21	not significant
6114	SLX4IP	1.00	9.70E-01	9.77E-01	193.94	not significant
6115	CBX1	1.00	9.37E-01	9.52E-01	10184.21	not significant
6116	PHF14	1.00	9.22E-01	9.41E-01	3606.20	not significant
6117	SVIL	1.00	9.49E-01	9.62E-01	826.79	not significant
6118	KCMF1	1.00	9.27E-01	9.45E-01	1985.69	not significant
6119	KIF1C	1.00	9.38E-01	9.52E-01	1767.00	not significant
6120	STX18-AS1	1.00	9.74E-01	9.80E-01	96.19	not significant
6121	GUSBP4	1.00	9.70E-01	9.77E-01	220.17	not significant
6122	DNAJB12	1.00	9.38E-01	9.53E-01	1504.63	not significant
6123	PJA1	1.00	9.67E-01	9.75E-01	271.68	not significant
6124	NUDCD3	1.00	9.21E-01	9.41E-01	2677.46	not significant
6125	LOC100129083	1.00	9.63E-01	9.72E-01	11.15	not significant
6126	CTNNB1	1.00	9.10E-01	9.32E-01	4058.18	not significant
6127	KCNMB3	1.00	9.66E-01	9.75E-01	17.22	not significant
6128	PRUNE	1.00	9.34E-01	9.50E-01	1323.19	not significant
6129	KIAA1279	1.00	9.46E-01	9.59E-01	741.36	not significant
6130	BECN1	1.00	9.15E-01	9.36E-01	2303.47	not significant
6131	SURF2	1.00	9.64E-01	9.73E-01	179.58	not significant
6132	ZNF35	1.00	9.60E-01	9.70E-01	13.43	not significant
6133	AVL9	1.00	9.49E-01	9.62E-01	814.29	not significant
6134	CTBP1-AS2	1.00	9.36E-01	9.52E-01	883.51	not significant
6135	LRP5	1.00	9.41E-01	9.55E-01	730.22	not significant
6136	DUSP22	1.00	9.34E-01	9.50E-01	1029.24	not significant
6137	PAX6	1.00	9.54E-01	9.65E-01	9.62	not significant
6138	LOC100996351	1.00	9.60E-01	9.70E-01	17.45	not significant
6139	CKAP2L	1.00	8.95E-01	9.21E-01	3104.15	not significant
6140	FBXW7	1.00	9.26E-01	9.44E-01	1311.12	not significant
6141	TAF4	1.00	9.09E-01	9.31E-01	2274.19	not significant
6142	AGO3	1.00	9.37E-01	9.52E-01	661.34	not significant
6143	CLSPN	1.00	8.78E-01	9.08E-01	4744.17	not significant
6144	CHN1	1.00	9.66E-01	9.74E-01	36.57	not significant
6145	CCDC114	1.00	9.62E-01	9.71E-01	25.57	not significant
6146	MIAT	1.00	9.62E-01	9.71E-01	144.35	not significant
6147	FTO	1.00	9.04E-01	9.28E-01	2260.30	not significant
6148	RNF24	1.00	9.09E-01	9.31E-01	1500.96	not significant

6149	LOC101060091	1.00	9.58E-01	9.69E-01	18.14	not significant
6150	RDX	1.00	9.64E-01	9.73E-01	64.65	not significant
6151	VPS13D	1.00	9.06E-01	9.29E-01	2416.34	not significant
6152	ITFG3	1.00	9.22E-01	9.41E-01	954.56	not significant
6153	CHAF1B	1.00	8.91E-01	9.18E-01	2555.19	not significant
6154	LOC102606465	1.00	9.45E-01	9.59E-01	339.07	not significant
6155	UPF1	1.00	8.65E-01	8.99E-01	10270.27	not significant
6156	TCF20	1.00	9.58E-01	9.69E-01	121.05	not significant
6157	BAG5	1.00	8.80E-01	9.10E-01	2886.73	not significant
6158	LRTOMT	1.00	9.49E-01	9.62E-01	278.09	not significant
6159	GGA3	1.00	8.80E-01	9.10E-01	4081.91	not significant
6160	PDE1B	1.00	9.59E-01	9.69E-01	676.19	not significant
6161	MAP7D1	1.00	8.51E-01	8.88E-01	6512.24	not significant
6162	EAPP	1.00	9.09E-01	9.31E-01	1318.16	not significant
6163	RFC3	1.00	8.64E-01	8.98E-01	3827.65	not significant
6164	SPAG6	1.00	9.40E-01	9.54E-01	8.91	not significant
6165	C9orf114	1.00	8.97E-01	9.22E-01	1594.29	not significant
6166	ZC3H7B	1.00	8.48E-01	8.86E-01	6671.67	not significant
6167	DCTN2	1.00	8.58E-01	8.94E-01	5000.09	not significant
6168	APEX2	1.00	9.06E-01	9.29E-01	1473.68	not significant
6169	PITPNM3	1.00	9.58E-01	9.68E-01	35.07	not significant
6170	HIST1H3H	1.00	9.51E-01	9.63E-01	18.92	not significant
6171	CDC34	1.00	9.14E-01	9.35E-01	1004.27	not significant
6172	RBM10	1.00	8.92E-01	9.19E-01	1870.10	not significant
6173	CAPN2	1.00	9.37E-01	9.52E-01	8.33	not significant
6174	POLH	1.00	8.76E-01	9.07E-01	2538.20	not significant
6175	YLPM1	1.00	9.34E-01	9.50E-01	5615.35	not significant
6176	PRKRA	1.00	9.14E-01	9.35E-01	1017.48	not significant
6177	ZNF433	1.00	9.47E-01	9.60E-01	14.59	not significant
6178	LOC100132352	1.00	9.57E-01	9.68E-01	34.19	not significant
6179	RPL23AP53	1.00	9.11E-01	9.32E-01	1019.59	not significant
6180	C1orf162	1.00	9.51E-01	9.63E-01	22.80	not significant
6181	OAT	1.00	8.89E-01	9.16E-01	1676.52	not significant
6182	JPH1	1.00	8.95E-01	9.21E-01	1657.25	not significant
6183	MPZL1	1.00	8.50E-01	8.88E-01	4029.81	not significant
6184	THAP7	1.00	9.10E-01	9.32E-01	887.09	not significant
6185	AIMP1	1.00	8.77E-01	9.07E-01	2633.09	not significant
6186	LOC101929125	1.00	9.44E-01	9.58E-01	15.13	not significant
6187	ARMC12	1.00	9.51E-01	9.63E-01	31.15	not significant
6188	TMEM214	1.00	8.93E-01	9.19E-01	1545.91	not significant
6189	FBXO32	1.00	9.49E-01	9.62E-01	133.62	not significant
6190	QRICH2	1.00	9.36E-01	9.52E-01	328.71	not significant
6191	SKP1P2	1.00	9.36E-01	9.52E-01	10.83	not significant
6192	MPLKIP	1.00	8.99E-01	9.23E-01	1328.68	not significant
6193	TMIGD2	1.00	9.34E-01	9.50E-01	206.46	not significant
6194	HYAL2	1.00	9.52E-01	9.64E-01	50.28	not significant
6195	GORAB	1.00	9.26E-01	9.45E-01	473.77	not significant
6196	APBB1	1.00	9.48E-01	9.61E-01	119.20	not significant
6197	RPL18A	1.00	8.31E-01	8.72E-01	15401.24	not significant
6198	SREK1	1.00	8.73E-01	9.05E-01	4207.98	not significant
6199	RFTN2	1.00	9.29E-01	9.47E-01	11.25	not significant
6200	PCM1	1.00	8.05E-01	8.51E-01	10530.37	not significant
6201	WDR31	1.00	9.42E-01	9.56E-01	21.79	not significant
6202	TECTA	1.01	9.39E-01	9.54E-01	16.60	not significant
6203	CAPRIN1	1.01	7.90E-01	8.40E-01	19864.39	not significant
6204	CCDC142	1.01	9.33E-01	9.50E-01	278.08	not significant
6205	ATP6V0D1	1.01	8.65E-01	8.99E-01	1627.73	not significant
6206	NDUFA6-AS1	1.01	9.31E-01	9.48E-01	11.79	not significant
6207	CPPED1	1.01	8.91E-01	9.17E-01	978.49	not significant
6208	PGAP2	1.01	8.88E-01	9.15E-01	1092.06	not significant
6209	NCAPD3	1.01	8.11E-01	8.55E-01	9625.52	not significant
6210	VEGFB	1.01	8.68E-01	9.01E-01	1607.41	not significant
6211	EDC3	1.01	8.66E-01	8.99E-01	1671.55	not significant
6212	LIPE	1.01	9.25E-01	9.44E-01	417.81	not significant
6213	BCL2L1	1.01	8.23E-01	8.65E-01	7177.95	not significant
6214	ST20	1.01	9.30E-01	9.47E-01	190.63	not significant
6215	GLUD2	1.01	9.38E-01	9.53E-01	145.06	not significant
6216	ETV4	1.01	9.25E-01	9.44E-01	12.21	not significant
6217	C1orf35	1.01	8.83E-01	9.12E-01	989.14	not significant
6218	TTC23	1.01	9.39E-01	9.53E-01	41.51	not significant
6219	TMEM17	1.01	9.16E-01	9.36E-01	9.86	not significant
6220	RALY-AS1	1.01	9.37E-01	9.52E-01	26.31	not significant
6221	PAFAH1B2	1.01	8.27E-01	8.69E-01	2555.68	not significant
6222	SNX27	1.01	8.75E-01	9.06E-01	1134.06	not significant
6223	LUC7L2	1.01	9.34E-01	9.50E-01	747.47	not significant
6224	STK17B	1.01	7.78E-01	8.30E-01	8187.80	not significant
6225	LOC100288798	1.01	9.37E-01	9.52E-01	145.31	not significant
6226	GGH	1.01	8.61E-01	8.96E-01	1602.81	not significant
6227	PAK4	1.01	8.76E-01	9.07E-01	936.14	not significant
6228	RALGAPA2	1.01	8.66E-01	8.99E-01	1260.40	not significant
6229	MLH1	1.01	8.16E-01	8.60E-01	3330.61	not significant
6230	CCDC9	1.01	8.95E-01	9.21E-01	651.56	not significant
6231	STXBP4	1.01	9.27E-01	9.46E-01	208.96	not significant
6232	LINC00667	1.01	8.86E-01	9.14E-01	740.34	not significant
6233	TRAM1	1.01	7.50E-01	8.06E-01	17498.67	not significant
6234	KLHL32	1.01	9.33E-01	9.50E-01	32.45	not significant
6235	SEC62	1.01	8.17E-01	8.61E-01	3560.61	not significant
6236	DNPEP	1.01	8.38E-01	8.78E-01	1908.54	not significant

6237	PPP1R12C	1.01	8.37E-01	8.77E-01	2634.35	not significant
6238	HIRIP3	1.01	8.23E-01	8.66E-01	2336.54	not significant
6239	ERLIN1	1.01	8.36E-01	8.76E-01	1718.21	not significant
6240	BSPRY	1.01	9.34E-01	9.50E-01	78.26	not significant
6241	CWF19L1	1.01	8.29E-01	8.71E-01	1819.15	not significant
6242	CRAT	1.01	9.14E-01	9.35E-01	294.20	not significant
6243	DSCR9	1.01	9.25E-01	9.44E-01	19.07	not significant
6244	ZBTB48	1.01	8.84E-01	9.13E-01	634.37	not significant
6245	ASB12	1.01	9.26E-01	9.44E-01	21.89	not significant
6246	SLC2A6	1.01	9.09E-01	9.31E-01	10.19	not significant
6247	GPATCH8	1.01	7.88E-01	8.38E-01	3950.97	not significant
6248	ZC3H7A	1.01	7.94E-01	8.43E-01	3613.03	not significant
6249	TINCR	1.01	9.30E-01	9.48E-01	31.66	not significant
6250	CFD	1.01	8.98E-01	9.22E-01	8.60	not significant
6251	LOC100288069	1.01	9.09E-01	9.31E-01	11.73	not significant
6252	MAP2K2	1.01	7.79E-01	8.30E-01	4824.07	not significant
6253	POT1	1.01	8.14E-01	8.58E-01	2496.14	not significant
6254	ZNF326	1.01	8.10E-01	8.55E-01	2188.24	not significant
6255	PAQR6	1.01	9.29E-01	9.47E-01	287.71	not significant
6256	ASNS	1.01	8.82E-01	9.11E-01	691.32	not significant
6257	C6orf226	1.01	9.24E-01	9.44E-01	131.95	not significant
6258	SF3B1	1.01	7.43E-01	8.00E-01	19105.44	not significant
6259	GNA12	1.01	8.08E-01	8.54E-01	2721.71	not significant
6260	PRKACB	1.01	7.63E-01	8.17E-01	5341.25	not significant
6261	OIP5	1.01	8.87E-01	9.15E-01	507.89	not significant
6262	LRMP	1.01	8.14E-01	8.59E-01	1758.13	not significant
6263	TAX1BP1	1.01	7.97E-01	8.45E-01	3925.41	not significant
6264	KLHL21	1.01	8.66E-01	9.00E-01	832.14	not significant
6265	EPS15L1	1.01	8.24E-01	8.66E-01	1598.17	not significant
6266	ACSM3	1.01	8.98E-01	9.22E-01	10.24	not significant
6267	PAPD7	1.01	8.39E-01	8.78E-01	1656.07	not significant
6268	CD109	1.01	9.11E-01	9.33E-01	226.99	not significant
6269	NUCB1-AS1	1.01	8.87E-01	9.15E-01	9.75	not significant
6270	PDZD8	1.01	8.36E-01	8.76E-01	1416.63	not significant
6271	DZIP1	1.01	8.81E-01	9.10E-01	475.60	not significant
6272	CXCR5	1.01	9.14E-01	9.35E-01	21.46	not significant
6273	ARSG	1.01	8.76E-01	9.07E-01	507.44	not significant
6274	PRMT9	1.01	8.82E-01	9.11E-01	487.13	not significant
6275	MASTL	1.01	8.03E-01	8.50E-01	2142.40	not significant
6276	FAM71E1	1.01	9.04E-01	9.27E-01	15.92	not significant
6277	MYLIP	1.01	8.86E-01	9.14E-01	8.79	not significant
6278	VBP1	1.01	8.59E-01	8.94E-01	881.86	not significant
6279	IPMK	1.01	8.73E-01	9.05E-01	550.02	not significant
6280	ENTPD3-AS1	1.01	8.79E-01	9.09E-01	8.60	not significant
6281	DAP	1.01	7.72E-01	8.25E-01	3252.64	not significant
6282	PSMB4	1.01	7.47E-01	8.04E-01	5556.02	not significant
6283	C11orf31	1.01	7.98E-01	8.46E-01	3509.58	not significant
6284	DLG4	1.01	8.59E-01	8.94E-01	682.36	not significant
6285	BMS1P4	1.01	9.11E-01	9.33E-01	138.48	not significant
6286	CENPH	1.01	7.79E-01	8.30E-01	2672.43	not significant
6287	MLYCD	1.01	8.90E-01	9.17E-01	308.57	not significant
6288	FIG4	1.01	8.39E-01	8.78E-01	843.93	not significant
6289	MAP3K9	1.01	8.44E-01	8.82E-01	878.80	not significant
6290	GPN2	1.01	8.51E-01	8.88E-01	707.19	not significant
6291	PLCG1-AS1	1.01	9.18E-01	9.38E-01	31.77	not significant
6292	MMD	1.01	7.86E-01	8.36E-01	2245.97	not significant
6293	SASS6	1.01	8.12E-01	8.57E-01	1732.64	not significant
6294	DMXL2	1.01	8.17E-01	8.61E-01	1680.81	not significant
6295	SNRNP35	1.01	8.65E-01	8.99E-01	525.30	not significant
6296	CASKIN2	1.01	8.14E-01	8.58E-01	1283.44	not significant
6297	TTC5	1.01	8.49E-01	8.87E-01	679.86	not significant
6298	BTBD2	1.01	7.18E-01	7.81E-01	5283.04	not significant
6299	TMEM87B	1.01	8.01E-01	8.48E-01	1391.65	not significant
6300	GAL3ST4	1.01	8.85E-01	9.13E-01	392.04	not significant
6301	CYB5RL	1.01	8.71E-01	9.03E-01	488.45	not significant
6302	UBE2D4	1.01	8.75E-01	9.06E-01	361.32	not significant
6303	C9orf85	1.01	8.77E-01	9.07E-01	414.89	not significant
6304	BLOC1S3	1.01	8.88E-01	9.15E-01	278.40	not significant
6305	ING1	1.01	8.19E-01	8.62E-01	1099.42	not significant
6306	TMEM143	1.01	8.80E-01	9.10E-01	397.89	not significant
6307	SCARF1	1.01	8.81E-01	9.10E-01	10.86	not significant
6308	ZNF587B	1.01	8.90E-01	9.17E-01	318.52	not significant
6309	CLEC11A	1.01	9.08E-01	9.30E-01	40.61	not significant
6310	CDK11A	1.01	8.83E-01	9.12E-01	320.30	not significant
6311	PQLC1	1.01	8.06E-01	8.52E-01	1398.84	not significant
6312	ADAMTS13	1.01	8.60E-01	8.95E-01	8.05	not significant
6313	TNRC18	1.01	7.04E-01	7.69E-01	5391.77	not significant
6314	BRF2	1.01	8.30E-01	8.71E-01	749.32	not significant
6315	NAA30	1.01	8.06E-01	8.52E-01	1441.51	not significant
6316	CHD8	1.01	7.41E-01	7.99E-01	5730.63	not significant
6317	TMOD1	1.01	8.86E-01	9.14E-01	15.04	not significant
6318	CLEC4A	1.01	8.66E-01	8.99E-01	9.46	not significant
6319	WDR13	1.01	8.88E-01	9.15E-01	222.62	not significant
6320	TRPM2	1.01	8.00E-01	8.48E-01	1279.65	not significant
6321	NUP54	1.01	7.35E-01	7.94E-01	2616.56	not significant
6322	ADCY3	1.01	7.49E-01	8.06E-01	1941.22	not significant
6323	MGC57346	1.01	8.79E-01	9.09E-01	247.56	not significant
6324	SLC27A1	1.01	9.01E-01	9.25E-01	107.51	not significant

6325	HYKK	1.01	8.96E-01	9.21E-01	25.58	not significant
6326	PAPD4	1.01	7.26E-01	7.87E-01	2730.55	not significant
6327	ZNF780A	1.01	8.65E-01	8.99E-01	391.97	not significant
6328	PIGH	1.01	8.19E-01	8.63E-01	921.56	not significant
6329	ZNF280B	1.01	8.92E-01	9.18E-01	176.49	not significant
6330	FAM129A	1.01	8.28E-01	8.70E-01	717.28	not significant
6331	EDA2R	1.01	8.84E-01	9.13E-01	16.33	not significant
6332	CD38	1.01	7.45E-01	8.02E-01	1911.39	not significant
6333	FAM118A	1.01	7.92E-01	8.41E-01	1118.09	not significant
6334	AACS	1.01	7.72E-01	8.25E-01	1438.58	not significant
6335	GCAT	1.01	8.72E-01	9.04E-01	252.48	not significant
6336	MTERF1	1.01	8.58E-01	8.94E-01	401.63	not significant
6337	MLEC	1.01	6.73E-01	7.42E-01	16734.99	not significant
6338	FCHO2	1.01	8.58E-01	8.94E-01	9.62	not significant
6339	RBKS	1.01	8.98E-01	9.22E-01	78.48	not significant
6340	SMAP1	1.01	7.43E-01	8.00E-01	1980.59	not significant
6341	GOLPH3L	1.01	7.77E-01	8.29E-01	1354.28	not significant
6342	ERCC1	1.01	7.48E-01	8.04E-01	1694.33	not significant
6343	FANCD2	1.01	7.03E-01	7.68E-01	4831.63	not significant
6344	CYSLTR2	1.01	8.61E-01	8.96E-01	307.71	not significant
6345	ZNF775	1.01	8.31E-01	8.72E-01	660.22	not significant
6346	ZNF611	1.01	8.05E-01	8.51E-01	737.48	not significant
6347	MORF4L2-AS1	1.01	8.97E-01	9.22E-01	50.20	not significant
6348	HDGF	1.01	6.67E-01	7.38E-01	13729.62	not significant
6349	STRADA	1.01	7.27E-01	7.88E-01	2085.44	not significant
6350	B4GALT5	1.01	7.94E-01	8.43E-01	849.08	not significant
6351	ADAM17	1.01	7.55E-01	8.11E-01	1573.71	not significant
6352	KCTD11	1.01	8.72E-01	9.04E-01	226.25	not significant
6353	LOC642236	1.01	8.91E-01	9.18E-01	33.56	not significant
6354	GRK6	1.01	6.91E-01	7.58E-01	4042.15	not significant
6355	ST7L	1.01	8.41E-01	8.80E-01	432.42	not significant
6356	PEX12	1.01	8.63E-01	8.97E-01	269.62	not significant
6357	FBXW11	1.01	7.54E-01	8.10E-01	1646.76	not significant
6358	MED17	1.01	7.78E-01	8.29E-01	1111.16	not significant
6359	SLC25A37	1.01	8.48E-01	8.86E-01	358.84	not significant
6360	LINC00888	1.01	8.78E-01	9.08E-01	165.77	not significant
6361	AAMP	1.01	7.26E-01	7.88E-01	3092.55	not significant
6362	URM1	1.01	7.10E-01	7.73E-01	2581.91	not significant
6363	ASXL2	1.01	7.52E-01	8.09E-01	2286.39	not significant
6364	C5orf22	1.01	7.60E-01	8.15E-01	1510.18	not significant
6365	PSMG3	1.01	7.46E-01	8.02E-01	1714.23	not significant
6366	MYD88	1.01	6.67E-01	7.38E-01	3589.16	not significant
6367	NUDT17	1.01	8.71E-01	9.03E-01	17.19	not significant
6368	RAF1	1.01	6.07E-01	6.86E-01	5955.80	not significant
6369	NCK1	1.01	7.37E-01	7.96E-01	1761.91	not significant
6370	AHCY	1.01	6.68E-01	7.39E-01	12847.98	not significant
6371	KRR1	1.01	7.02E-01	7.67E-01	3844.77	not significant
6372	ANKS1A	1.01	7.83E-01	8.33E-01	858.88	not significant
6373	LTBP4	1.01	8.46E-01	8.84E-01	335.40	not significant
6374	CDK9	1.01	7.26E-01	7.88E-01	1903.08	not significant
6375	ISYNA1	1.01	8.90E-01	9.17E-01	52.48	not significant
6376	PCOLCE	1.01	8.88E-01	9.16E-01	45.37	not significant
6377	POLR3F	1.01	8.21E-01	8.64E-01	544.53	not significant
6378	AGBL2	1.01	8.85E-01	9.14E-01	94.37	not significant
6379	CTRL	1.01	8.88E-01	9.15E-01	66.31	not significant
6380	CCDC159	1.01	8.88E-01	9.15E-01	61.80	not significant
6381	LOC100129534	1.01	7.35E-01	7.94E-01	11.87	not significant
6382	SPHK2	1.01	7.63E-01	8.17E-01	1150.60	not significant
6383	DEDD2	1.01	7.93E-01	8.42E-01	821.26	not significant
6384	IDH1-AS1	1.01	8.65E-01	8.99E-01	15.97	not significant
6385	TSPAN33	1.01	7.92E-01	8.42E-01	917.25	not significant
6386	ZNF585A	1.01	8.15E-01	8.59E-01	543.20	not significant
6387	TAF11	1.01	7.34E-01	7.93E-01	1366.05	not significant
6388	BZW2	1.01	5.97E-01	6.77E-01	6901.59	not significant
6389	C14orf142	1.01	7.74E-01	8.27E-01	1099.71	not significant
6390	NFYB	1.01	6.53E-01	7.27E-01	2863.10	not significant
6391	DBIL5P	1.01	8.80E-01	9.10E-01	35.18	not significant
6392	TMEM106C	1.01	5.79E-01	6.62E-01	7793.38	not significant
6393	SLC10A3	1.01	8.62E-01	8.97E-01	17.69	not significant
6394	ZCCHC6	1.01	7.53E-01	8.10E-01	1259.42	not significant
6395	GFOD1	1.01	8.70E-01	9.03E-01	138.68	not significant
6396	RBFADN	1.01	8.26E-01	8.68E-01	8.93	not significant
6397	BCKDK	1.01	7.60E-01	8.15E-01	910.04	not significant
6398	MAP3K11	1.01	6.94E-01	7.60E-01	2726.91	not significant
6399	LINC01011	1.01	8.70E-01	9.02E-01	24.41	not significant
6400	SLC16A5	1.01	8.72E-01	9.04E-01	113.35	not significant
6401	BRICD5	1.01	8.87E-01	9.15E-01	108.56	not significant
6402	CFL2	1.01	8.42E-01	8.81E-01	292.15	not significant
6403	TICRR	1.01	7.22E-01	7.84E-01	2390.32	not significant
6404	ACD	1.01	7.41E-01	7.99E-01	1166.38	not significant
6405	METTL10	1.01	7.66E-01	8.20E-01	1027.16	not significant
6406	SNRNP27	1.01	6.72E-01	7.42E-01	1984.60	not significant
6407	ATP1B1	1.01	8.74E-01	9.05E-01	94.53	not significant
6408	C9orf9	1.01	8.41E-01	8.80E-01	292.65	not significant
6409	RHOC	1.01	7.19E-01	7.82E-01	1659.29	not significant
6410	PHYH	1.01	8.43E-01	8.82E-01	287.02	not significant
6411	RBBP8	1.01	5.91E-01	6.72E-01	4306.58	not significant
6412	PHLDB2	1.01	8.01E-01	8.48E-01	544.53	not significant

6413	TMEM203	1.01	7.36E-01	7.95E-01	1228.26	not significant
6414	PML	1.01	6.62E-01	7.34E-01	2431.46	not significant
6415	C3orf35	1.01	8.33E-01	8.74E-01	11.18	not significant
6416	SLU7	1.01	6.61E-01	7.33E-01	2364.20	not significant
6417	RBL1	1.01	6.06E-01	6.85E-01	4586.19	not significant
6418	AZI2	1.01	6.63E-01	7.35E-01	2576.88	not significant
6419	NUP210	1.01	6.06E-01	6.85E-01	22826.07	not significant
6420	LOC100128568	1.01	8.53E-01	8.90E-01	21.25	not significant
6421	TVP23B	1.01	8.53E-01	8.90E-01	230.80	not significant
6422	MCMDC2	1.01	8.28E-01	8.70E-01	12.34	not significant
6423	LINC00926	1.01	8.73E-01	9.04E-01	54.06	not significant
6424	PRKD2	1.01	6.10E-01	6.88E-01	3602.23	not significant
6425	VPS13B	1.01	8.13E-01	8.58E-01	2861.25	not significant
6426	LOC100129917	1.01	8.63E-01	8.97E-01	135.77	not significant
6427	HPS1	1.01	6.91E-01	7.58E-01	1600.99	not significant
6428	PSIP1	1.01	5.83E-01	6.65E-01	11214.75	not significant
6429	ATG12	1.01	6.84E-01	7.52E-01	1788.87	not significant
6430	LOC101928068	1.01	8.59E-01	8.94E-01	24.78	not significant
6431	CNKSR1	1.01	8.26E-01	8.68E-01	11.11	not significant
6432	HCLS1	1.01	6.49E-01	7.23E-01	6016.36	not significant
6433	ATF3	1.01	7.79E-01	8.30E-01	582.12	not significant
6434	ASB13	1.01	7.98E-01	8.46E-01	605.72	not significant
6435	MCL1	1.01	5.46E-01	6.32E-01	5581.82	not significant
6436	SREK1IP1	1.01	5.95E-01	6.76E-01	3635.07	not significant
6437	RBBP5	1.01	6.54E-01	7.27E-01	2115.91	not significant
6438	LRFN1	1.01	8.16E-01	8.60E-01	334.10	not significant
6439	TSC2	1.01	8.06E-01	8.52E-01	2510.84	not significant
6440	XYLT2	1.01	7.39E-01	7.97E-01	968.52	not significant
6441	TTF1	1.01	6.52E-01	7.25E-01	2215.73	not significant
6442	RBM6	1.01	5.58E-01	6.43E-01	4890.31	not significant
6443	ARHGEF1	1.01	5.95E-01	6.76E-01	3720.09	not significant
6444	SIAH2	1.01	6.75E-01	7.45E-01	2483.40	not significant
6445	LOC100129697	1.01	8.39E-01	8.78E-01	17.11	not significant
6446	EXO5	1.01	7.60E-01	8.15E-01	697.47	not significant
6447	CALR	1.01	5.79E-01	6.62E-01	41076.61	not significant
6448	ORMDL1	1.01	6.05E-01	6.85E-01	2928.81	not significant
6449	CCDC157	1.01	8.55E-01	8.91E-01	127.33	not significant
6450	CLPTM1L	1.01	6.08E-01	6.86E-01	8017.20	not significant
6451	MICALL1	1.01	7.65E-01	8.19E-01	677.06	not significant
6452	KCNK5	1.01	6.92E-01	7.59E-01	1314.28	not significant
6453	SLC41A1	1.01	6.71E-01	7.41E-01	1830.54	not significant
6454	MRPS21	1.01	8.17E-01	8.61E-01	290.95	not significant
6455	RPL6	1.01	6.08E-01	6.87E-01	19195.34	not significant
6456	DCUN1D2	1.01	7.32E-01	7.92E-01	808.01	not significant
6457	GOSR1	1.01	6.45E-01	7.19E-01	1823.95	not significant
6458	ELMOD2	1.01	6.56E-01	7.29E-01	1891.44	not significant
6459	CDC5L	1.01	5.66E-01	6.50E-01	4625.46	not significant
6460	FNIP2	1.01	6.75E-01	7.45E-01	1453.83	not significant
6461	C19orf43	1.01	6.32E-01	7.08E-01	6497.37	not significant
6462	EVL	1.01	4.81E-01	5.72E-01	20512.90	not significant
6463	OTUD7B	1.01	8.59E-01	8.94E-01	53.35	not significant
6464	GNA11	1.01	8.39E-01	8.78E-01	41.04	not significant
6465	ATAD3B	1.01	7.56E-01	8.12E-01	834.79	not significant
6466	LOC654841	1.01	8.34E-01	8.75E-01	17.71	not significant
6467	TMEM9B	1.01	7.53E-01	8.09E-01	752.79	not significant
6468	MAPK7	1.01	7.17E-01	7.80E-01	959.21	not significant
6469	DLG1	1.01	5.78E-01	6.61E-01	3352.16	not significant
6470	PCNP	1.01	5.59E-01	6.44E-01	6476.86	not significant
6471	PPP1R16A	1.01	7.62E-01	8.17E-01	598.60	not significant
6472	MSH2	1.01	5.51E-01	6.37E-01	7272.98	not significant
6473	LINC00094	1.01	7.65E-01	8.19E-01	543.11	not significant
6474	TLX2	1.01	8.20E-01	8.63E-01	13.72	not significant
6475	EXD2	1.01	7.73E-01	8.26E-01	534.47	not significant
6476	TMEM168	1.01	7.15E-01	7.78E-01	890.81	not significant
6477	SNHG10	1.01	8.25E-01	8.67E-01	228.13	not significant
6478	CYP4F29P	1.01	8.36E-01	8.76E-01	20.90	not significant
6479	HCN2	1.01	8.50E-01	8.88E-01	28.85	not significant
6480	CRYBG3	1.01	7.85E-01	8.35E-01	8.25	not significant
6481	PKIA	1.01	6.20E-01	6.97E-01	2180.36	not significant
6482	TYSND1	1.01	6.95E-01	7.61E-01	1132.23	not significant
6483	CENPL	1.01	7.03E-01	7.68E-01	1064.33	not significant
6484	NCOA1	1.01	5.78E-01	6.61E-01	3100.48	not significant
6485	RGMA	1.01	8.33E-01	8.74E-01	166.63	not significant
6486	YJEFN3	1.01	8.49E-01	8.86E-01	111.93	not significant
6487	TMEM206	1.01	6.82E-01	7.50E-01	1390.47	not significant
6488	SHISA5	1.01	5.82E-01	6.64E-01	4664.48	not significant
6489	LEPROTL1	1.01	5.33E-01	6.20E-01	3826.04	not significant
6490	VPS33B	1.01	7.82E-01	8.32E-01	472.68	not significant
6491	F12	1.01	7.99E-01	8.47E-01	10.89	not significant
6492	ZNF846	1.01	8.45E-01	8.83E-01	103.04	not significant
6493	ATP1A3	1.01	7.86E-01	8.36E-01	359.82	not significant
6494	ZFAND4	1.01	7.24E-01	7.86E-01	898.87	not significant
6495	FGF14-AS2	1.01	8.50E-01	8.87E-01	59.70	not significant
6496	SPCS3	1.01	4.43E-01	5.36E-01	9456.79	not significant
6497	BICD2	1.01	6.07E-01	6.86E-01	2384.05	not significant
6498	BUB3	1.01	4.59E-01	5.50E-01	9778.76	not significant
6499	LOC100240735	1.01	8.49E-01	8.86E-01	66.09	not significant
6500	RASGEF1A	1.01	7.81E-01	8.32E-01	8.63	not significant

6501	AGO2	1.01	6.64E-01	7.35E-01	1366.42	not significant
6502	MAT2A	1.01	7.71E-01	8.24E-01	14187.57	not significant
6503	ETV3	1.01	8.04E-01	8.51E-01	326.55	not significant
6504	DDB2	1.01	6.06E-01	6.85E-01	2090.47	not significant
6505	DGCR11	1.01	8.37E-01	8.77E-01	26.97	not significant
6506	CCNYL1	1.01	7.42E-01	8.00E-01	606.91	not significant
6507	GAB3	1.01	8.43E-01	8.81E-01	92.84	not significant
6508	EFCAB12	1.01	8.25E-01	8.67E-01	19.08	not significant
6509	DFFA	1.01	6.13E-01	6.91E-01	2140.64	not significant
6510	HSD17B1	1.01	8.23E-01	8.66E-01	18.48	not significant
6511	CFAP97	1.01	5.35E-01	6.22E-01	3626.09	not significant
6512	TNFRSF25	1.02	7.71E-01	8.24E-01	409.54	not significant
6513	DDX26B	1.02	8.13E-01	8.58E-01	221.46	not significant
6514	MITD1	1.02	6.93E-01	7.60E-01	895.31	not significant
6515	TOP3B	1.02	6.83E-01	7.52E-01	1064.48	not significant
6516	CASS4	1.02	8.29E-01	8.70E-01	23.56	not significant
6517	AHRR	1.02	8.03E-01	8.50E-01	244.46	not significant
6518	CECR6	1.02	8.40E-01	8.79E-01	41.10	not significant
6519	LRRFIP2	1.02	6.52E-01	7.25E-01	1459.46	not significant
6520	USP48	1.02	5.23E-01	6.11E-01	3494.39	not significant
6521	CNPPD1	1.02	6.01E-01	6.80E-01	2107.68	not significant
6522	JUN	1.02	8.35E-01	8.75E-01	37.97	not significant
6523	AURKC	1.02	8.08E-01	8.53E-01	16.13	not significant
6524	C17orf80	1.02	6.14E-01	6.92E-01	2206.42	not significant
6525	OSGEP	1.02	6.19E-01	6.97E-01	1815.65	not significant
6526	CAHM	1.02	7.61E-01	8.15E-01	8.63	not significant
6527	SLC35A3	1.02	6.68E-01	7.39E-01	1462.35	not significant
6528	FSCN1	1.02	7.86E-01	8.36E-01	11.96	not significant
6529	PTENP1	1.02	8.35E-01	8.75E-01	84.98	not significant
6530	ATF5	1.02	7.58E-01	8.13E-01	425.01	not significant
6531	SYCP2L	1.02	7.83E-01	8.33E-01	11.22	not significant
6532	SFT2D1	1.02	6.23E-01	7.00E-01	1596.26	not significant
6533	MAPK3	1.02	5.42E-01	6.28E-01	3091.37	not significant
6534	SEL1L3	1.02	7.93E-01	8.42E-01	13.28	not significant
6535	SLC8B1	1.02	6.09E-01	6.87E-01	1635.73	not significant
6536	GSTK1	1.02	5.85E-01	6.67E-01	2143.32	not significant
6537	GNA13	1.02	4.62E-01	5.54E-01	11511.07	not significant
6538	FAM3A	1.02	7.97E-01	8.45E-01	239.32	not significant
6539	TUT1	1.02	7.07E-01	7.71E-01	763.78	not significant
6540	BBS2	1.02	6.95E-01	7.61E-01	849.39	not significant
6541	EP400	1.02	7.76E-01	8.28E-01	6451.43	not significant
6542	NBEA	1.02	7.93E-01	8.42E-01	264.60	not significant
6543	ZNF562	1.02	7.07E-01	7.71E-01	713.00	not significant
6544	TM9SF4	1.02	5.19E-01	6.07E-01	3503.39	not significant
6545	ORC3	1.02	6.25E-01	7.02E-01	1462.60	not significant
6546	ZCWPW2	1.02	7.95E-01	8.43E-01	14.71	not significant
6547	NUDT13	1.02	8.02E-01	8.49E-01	18.30	not significant
6548	MFSD10	1.02	6.89E-01	7.56E-01	966.03	not significant
6549	ANKFY1	1.02	6.13E-01	6.91E-01	3188.28	not significant
6550	FEM1A	1.02	5.89E-01	6.71E-01	1923.32	not significant
6551	XXYLT1	1.02	6.76E-01	7.45E-01	884.46	not significant
6552	MERTK	1.02	8.30E-01	8.72E-01	71.08	not significant
6553	HKR1	1.02	6.76E-01	7.45E-01	992.69	not significant
6554	TBL2	1.02	8.01E-01	8.48E-01	199.47	not significant
6555	GLOD4	1.02	5.47E-01	6.33E-01	2802.19	not significant
6556	SMARCD2	1.02	4.76E-01	5.67E-01	6757.16	not significant
6557	SUGP1	1.02	6.68E-01	7.39E-01	1116.89	not significant
6558	NUP133	1.02	4.92E-01	5.82E-01	3620.15	not significant
6559	COL15A1	1.02	7.63E-01	8.17E-01	10.05	not significant
6560	WDR59	1.02	5.46E-01	6.32E-01	2430.05	not significant
6561	HIST1H3B	1.02	8.21E-01	8.64E-01	36.51	not significant
6562	DFNB59	1.02	8.22E-01	8.65E-01	33.88	not significant
6563	KAT2B	1.02	7.68E-01	8.21E-01	395.03	not significant
6564	SETD9	1.02	8.23E-01	8.66E-01	107.12	not significant
6565	PRKCQ	1.02	5.53E-01	6.39E-01	2261.11	not significant
6566	MBTPS1	1.02	4.52E-01	5.44E-01	5458.62	not significant
6567	ECM1	1.02	7.90E-01	8.40E-01	18.62	not significant
6568	FAM21A	1.02	8.17E-01	8.61E-01	110.70	not significant
6569	ZFP41	1.02	7.35E-01	7.94E-01	481.47	not significant
6570	PI4KA	1.02	4.86E-01	5.77E-01	5736.76	not significant
6571	IMPAD1	1.02	4.40E-01	5.33E-01	4865.81	not significant
6572	TMEM216	1.02	8.08E-01	8.54E-01	23.46	not significant
6573	PGP	1.02	6.05E-01	6.85E-01	1521.31	not significant
6574	SLC25A24	1.02	5.59E-01	6.44E-01	1911.54	not significant
6575	SGMS1	1.02	7.90E-01	8.40E-01	227.60	not significant
6576	CARKD	1.02	6.21E-01	6.98E-01	1271.57	not significant
6577	SBF1	1.02	4.98E-01	5.88E-01	8181.91	not significant
6578	ENAH	1.02	7.16E-01	7.78E-01	546.40	not significant
6579	TROAP	1.02	7.37E-01	7.96E-01	3851.19	not significant
6580	CA5B	1.02	8.11E-01	8.56E-01	133.21	not significant
6581	PROB1	1.02	8.21E-01	8.64E-01	50.16	not significant
6582	TPST2	1.02	5.85E-01	6.67E-01	1527.97	not significant
6583	CHST7	1.02	7.96E-01	8.44E-01	174.99	not significant
6584	UNC119B	1.02	5.02E-01	5.92E-01	5377.29	not significant
6585	PSMB8-AS1	1.02	8.15E-01	8.60E-01	38.58	not significant
6586	ZNF398	1.02	6.50E-01	7.24E-01	922.41	not significant
6587	RNF185	1.02	5.98E-01	6.77E-01	1474.94	not significant
6588	SPOPL	1.02	6.95E-01	7.61E-01	667.59	not significant

6589	ARL8B	1.02	4.47E-01	5.39E-01	3777.85	not significant
6590	ARL2	1.02	7.33E-01	7.93E-01	443.13	not significant
6591	ZNF124	1.02	7.14E-01	7.77E-01	552.68	not significant
6592	FAM63A	1.02	7.89E-01	8.39E-01	19.38	not significant
6593	SDF4	1.02	4.98E-01	5.88E-01	2915.73	not significant
6594	LOC339862	1.02	6.18E-01	6.95E-01	1204.98	not significant
6595	ST7	1.02	7.68E-01	8.21E-01	15.15	not significant
6596	C11orf48	1.02	8.16E-01	8.60E-01	73.48	not significant
6597	TMEM39A	1.02	6.12E-01	6.91E-01	1229.21	not significant
6598	MGC27345	1.02	7.34E-01	7.93E-01	530.21	not significant
6599	TMEM53	1.02	8.14E-01	8.59E-01	40.32	not significant
6600	QKI	1.02	4.70E-01	5.62E-01	4755.60	not significant
6601	PRSS36	1.02	7.56E-01	8.12E-01	11.31	not significant
6602	FREM1	1.02	7.68E-01	8.21E-01	13.54	not significant
6603	PARP12	1.02	5.09E-01	5.98E-01	2415.24	not significant
6604	FBXW9	1.02	7.74E-01	8.26E-01	217.17	not significant
6605	POLQ	1.02	5.53E-01	6.38E-01	2566.25	not significant
6606	USE1	1.02	7.41E-01	7.99E-01	361.83	not significant
6607	DNAJC18	1.02	6.95E-01	7.61E-01	564.50	not significant
6608	ME2	1.02	3.73E-01	4.65E-01	6147.74	not significant
6609	SMA4	1.02	7.55E-01	8.11E-01	12.09	not significant
6610	CHKB	1.02	7.29E-01	7.90E-01	9.32	not significant
6611	ZBTB14	1.02	6.11E-01	6.90E-01	1092.43	not significant
6612	HDHD2	1.02	5.22E-01	6.10E-01	2528.88	not significant
6613	RAB22A	1.02	5.61E-01	6.46E-01	1763.38	not significant
6614	C15orf40	1.02	7.42E-01	8.00E-01	365.90	not significant
6615	EPHB4	1.02	7.94E-01	8.43E-01	158.90	not significant
6616	IGFBP6	1.02	7.73E-01	8.25E-01	211.11	not significant
6617	CCDC94	1.02	6.35E-01	7.11E-01	932.53	not significant
6618	SAMSN1	1.02	5.70E-01	6.54E-01	1443.93	not significant
6619	GNB5	1.02	6.44E-01	7.18E-01	864.82	not significant
6620	SMARCD3	1.02	8.08E-01	8.54E-01	52.23	not significant
6621	MIOX	1.02	7.21E-01	7.84E-01	8.53	not significant
6622	PRKAR2B	1.02	5.60E-01	6.45E-01	1639.52	not significant
6623	MXI1	1.02	7.50E-01	8.06E-01	265.57	not significant
6624	HIPK3	1.02	4.90E-01	5.80E-01	3140.64	not significant
6625	BVES	1.02	8.07E-01	8.53E-01	45.84	not significant
6626	LHFPL1	1.02	8.00E-01	8.48E-01	38.22	not significant
6627	EIF6	1.02	4.81E-01	5.72E-01	3333.56	not significant
6628	POM121C	1.02	6.14E-01	6.92E-01	973.12	not significant
6629	RILP	1.02	7.88E-01	8.38E-01	23.13	not significant
6630	MAP3K15	1.02	7.99E-01	8.47E-01	31.46	not significant
6631	GYPC	1.02	5.35E-01	6.22E-01	1719.86	not significant
6632	NUTM2A-AS1	1.02	6.65E-01	7.37E-01	712.38	not significant
6633	DNAL1	1.02	6.95E-01	7.61E-01	527.72	not significant
6634	ERCC5	1.02	8.00E-01	8.48E-01	95.46	not significant
6635	IFT88	1.02	7.29E-01	7.90E-01	385.14	not significant
6636	FOXK2	1.02	3.69E-01	4.61E-01	7395.53	not significant
6637	HELQ	1.02	6.85E-01	7.53E-01	535.97	not significant
6638	LINC01176	1.02	7.66E-01	8.19E-01	16.15	not significant
6639	LPP	1.02	7.55E-01	8.11E-01	1675.99	not significant
6640	TTC18	1.02	7.53E-01	8.09E-01	13.67	not significant
6641	TARBP2	1.02	5.57E-01	6.42E-01	1657.64	not significant
6642	TIMM9	1.02	6.22E-01	7.00E-01	1189.31	not significant
6643	AASDH	1.02	6.60E-01	7.32E-01	649.37	not significant
6644	ZNF57	1.02	7.56E-01	8.11E-01	240.82	not significant
6645	LOC100506472	1.02	8.00E-01	8.47E-01	69.75	not significant
6646	BEX4	1.02	5.51E-01	6.37E-01	1830.94	not significant
6647	POMGNT2	1.02	6.79E-01	7.48E-01	790.37	not significant
6648	DGCR8	1.02	4.97E-01	5.87E-01	2366.34	not significant
6649	MIOS	1.02	5.96E-01	6.76E-01	1004.53	not significant
6650	POU6F1	1.02	7.97E-01	8.46E-01	60.50	not significant
6651	VPS18	1.02	6.35E-01	7.10E-01	808.96	not significant
6652	ACBD3	1.02	5.35E-01	6.22E-01	1527.92	not significant
6653	CNNM4	1.02	6.00E-01	6.79E-01	944.61	not significant
6654	H2AFV	1.02	3.68E-01	4.60E-01	11600.83	not significant
6655	LRP4	1.02	7.08E-01	7.72E-01	8.92	not significant
6656	MPRIP	1.02	3.96E-01	4.88E-01	7270.52	not significant
6657	LOC101927166	1.02	7.49E-01	8.05E-01	14.10	not significant
6658	RASAL1	1.02	5.36E-01	6.23E-01	2113.44	not significant
6659	FBXO22	1.02	7.03E-01	7.68E-01	400.58	not significant
6660	SETD8	1.02	4.69E-01	5.60E-01	2461.01	not significant
6661	POMT1	1.02	6.25E-01	7.02E-01	813.40	not significant
6662	C5orf66	1.02	7.55E-01	8.11E-01	16.03	not significant
6663	ZBTB49	1.02	7.40E-01	7.98E-01	253.77	not significant
6664	ZNF607	1.02	6.69E-01	7.39E-01	540.57	not significant
6665	VMA21	1.02	4.06E-01	4.98E-01	3577.12	not significant
6666	ZNF174	1.02	6.67E-01	7.38E-01	547.00	not significant
6667	SELK	1.02	6.11E-01	6.90E-01	910.46	not significant
6668	SNAPC1	1.02	6.54E-01	7.27E-01	651.61	not significant
6669	BAIAP2L2	1.02	7.86E-01	8.36E-01	36.88	not significant
6670	SH3BGRL	1.02	4.37E-01	5.29E-01	4217.71	not significant
6671	MED23	1.02	5.42E-01	6.28E-01	1994.02	not significant
6672	TOMM20	1.02	3.56E-01	4.48E-01	7447.04	not significant
6673	PBX2	1.02	6.17E-01	6.95E-01	963.40	not significant
6674	SP140L	1.02	5.91E-01	6.72E-01	1249.19	not significant
6675	PHLPP2	1.02	6.70E-01	7.40E-01	753.55	not significant
6676	LOC100499484	1.02	7.19E-01	7.82E-01	11.28	not significant

6677	PIPSL	1.02	7.87E-01	8.37E-01	44.33	not significant
6678	DNAJC21	1.02	4.69E-01	5.60E-01	2103.92	not significant
6679	NEK11	1.02	7.26E-01	7.87E-01	12.42	not significant
6680	RAD1	1.02	4.44E-01	5.36E-01	2406.93	not significant
6681	IFNGR2	1.02	7.13E-01	7.76E-01	339.61	not significant
6682	FOXRED2	1.02	4.01E-01	4.93E-01	3752.61	not significant
6683	GATC	1.02	4.94E-01	5.84E-01	2310.00	not significant
6684	TBCC	1.02	6.71E-01	7.41E-01	459.26	not significant
6685	MFSD9	1.02	6.70E-01	7.40E-01	511.96	not significant
6686	PSMA1	1.02	3.57E-01	4.49E-01	6719.52	not significant
6687	MKRN2	1.02	4.45E-01	5.37E-01	2433.28	not significant
6688	RAB11FIP2	1.02	5.70E-01	6.53E-01	1052.01	not significant
6689	ADD3-AS1	1.02	7.27E-01	7.88E-01	12.78	not significant
6690	NTN5	1.02	7.78E-01	8.29E-01	32.50	not significant
6691	LINC01521	1.02	6.66E-01	7.37E-01	481.09	not significant
6692	ZFAT	1.02	6.60E-01	7.33E-01	516.48	not significant
6693	MED13	1.02	3.70E-01	4.62E-01	6505.08	not significant
6694	CLSTN1	1.02	2.81E-01	3.68E-01	11547.96	not significant
6695	SLFNL1-AS1	1.02	7.81E-01	8.32E-01	59.37	not significant
6696	LCMT2	1.02	6.40E-01	7.15E-01	617.08	not significant
6697	CPSF3	1.02	4.29E-01	5.21E-01	3068.43	not significant
6698	NOP9	1.02	4.24E-01	5.16E-01	2877.13	not significant
6699	SLC6A6	1.02	4.18E-01	5.10E-01	2913.40	not significant
6700	ZNF525	1.02	6.08E-01	6.86E-01	788.27	not significant
6701	ZNF317	1.02	4.37E-01	5.29E-01	2195.13	not significant
6702	BCO2	1.02	7.64E-01	8.18E-01	24.52	not significant
6703	EIF3A	1.02	2.52E-01	3.36E-01	23007.64	not significant
6704	HCK	1.02	6.87E-01	7.54E-01	9.85	not significant
6705	ATP6V1C2	1.02	7.15E-01	7.78E-01	13.33	not significant
6706	SNAP29	1.02	4.90E-01	5.80E-01	2024.87	not significant
6707	PARP14	1.02	3.85E-01	4.77E-01	5593.28	not significant
6708	RTN4	1.02	2.99E-01	3.88E-01	9364.78	not significant
6709	APPL1	1.02	3.28E-01	4.20E-01	4651.33	not significant
6710	PET117	1.02	7.63E-01	8.17E-01	125.20	not significant
6711	IFNAR1	1.02	3.63E-01	4.55E-01	3857.66	not significant
6712	KLHL23	1.02	7.74E-01	8.27E-01	43.96	not significant
6713	LOC101928784	1.02	7.60E-01	8.15E-01	26.02	not significant
6714	ITK	1.02	2.89E-01	3.78E-01	6715.86	not significant
6715	GPR89A	1.02	7.55E-01	8.11E-01	27.97	not significant
6716	SLC26A4	1.02	7.36E-01	7.95E-01	17.10	not significant
6717	VLDLR-AS1	1.02	7.17E-01	7.80E-01	13.69	not significant
6718	BAP1	1.02	3.34E-01	4.25E-01	5490.59	not significant
6719	PLXDC1	1.02	7.75E-01	8.27E-01	78.48	not significant
6720	SUV39H1	1.02	7.21E-01	7.83E-01	258.36	not significant
6721	TLL2	1.02	7.00E-01	7.65E-01	10.73	not significant
6722	C1QTNF4	1.02	7.14E-01	7.77E-01	12.79	not significant
6723	PDE7A	1.02	2.82E-01	3.70E-01	7320.15	not significant
6724	DENND1B	1.02	3.78E-01	4.70E-01	3738.61	not significant
6725	PIN4P1	1.02	6.97E-01	7.63E-01	10.34	not significant
6726	ANKIB1	1.02	3.79E-01	4.70E-01	3147.37	not significant
6727	C16orf62	1.02	4.48E-01	5.40E-01	2160.63	not significant
6728	RGS3	1.02	6.81E-01	7.50E-01	396.74	not significant
6729	ANKRD33B	1.02	5.44E-01	6.31E-01	1114.92	not significant
6730	PIK3CA	1.02	5.12E-01	6.00E-01	1454.08	not significant
6731	NCOA2	1.02	4.78E-01	5.69E-01	1908.30	not significant
6732	SAMD3	1.02	6.95E-01	7.61E-01	10.42	not significant
6733	PDCD6IP	1.02	4.01E-01	4.92E-01	4269.53	not significant
6734	SPN	1.02	2.64E-01	3.50E-01	20333.10	not significant
6735	PTRH1	1.02	7.24E-01	7.86E-01	222.47	not significant
6736	CLIC5	1.02	7.62E-01	8.17E-01	99.74	not significant
6737	MAGI2	1.02	6.61E-01	7.33E-01	8.07	not significant
6738	MTMR14	1.02	4.97E-01	5.87E-01	1455.41	not significant
6739	TARSL2	1.02	6.89E-01	7.56E-01	360.08	not significant
6740	PIK3R5	1.02	4.64E-01	5.55E-01	1796.13	not significant
6741	POLRMT	1.02	4.30E-01	5.22E-01	2411.14	not significant
6742	RAP2B	1.02	5.50E-01	6.36E-01	1224.90	not significant
6743	FAM20B	1.02	4.48E-01	5.40E-01	2628.89	not significant
6744	PELO	1.02	4.52E-01	5.44E-01	1852.30	not significant
6745	EDC4	1.02	4.00E-01	4.92E-01	5359.20	not significant
6746	C9orf142	1.02	5.52E-01	6.38E-01	948.47	not significant
6747	ZNF585B	1.02	6.05E-01	6.85E-01	709.53	not significant
6748	VDAC3	1.02	3.16E-01	4.07E-01	7231.48	not significant
6749	TRIM5	1.02	4.64E-01	5.56E-01	1843.65	not significant
6750	CCDC183	1.02	6.77E-01	7.46E-01	9.75	not significant
6751	LDHB	1.02	4.51E-01	5.43E-01	32914.87	not significant
6752	SRC	1.02	6.72E-01	7.42E-01	365.39	not significant
6753	FAM71F2	1.02	6.49E-01	7.23E-01	8.00	not significant
6754	APMAP	1.02	3.97E-01	4.89E-01	3400.45	not significant
6755	UBA6-AS1	1.02	6.40E-01	7.15E-01	465.82	not significant
6756	CHRNB1	1.02	6.54E-01	7.27E-01	447.35	not significant
6757	SLC9A8	1.02	5.45E-01	6.31E-01	1055.06	not significant
6758	AGAP2	1.02	3.65E-01	4.57E-01	3411.47	not significant
6759	LOH12CR2	1.02	7.16E-01	7.79E-01	14.80	not significant
6760	RWDD3	1.02	6.99E-01	7.64E-01	278.84	not significant
6761	CTCF	1.02	2.95E-01	3.84E-01	5511.67	not significant
6762	DCAF13P3	1.02	7.06E-01	7.70E-01	13.20	not significant
6763	CEP250	1.02	3.28E-01	4.19E-01	4423.70	not significant
6764	FAM179B	1.02	7.38E-01	7.97E-01	143.56	not significant

6765	ZNF786	1.02	6.90E-01	7.57E-01	307.40	not significant
6766	KBTBD7	1.02	6.34E-01	7.10E-01	477.60	not significant
6767	PNN	1.02	3.69E-01	4.61E-01	8550.54	not significant
6768	LINC00641	1.02	6.55E-01	7.28E-01	613.30	not significant
6769	HEATR5B	1.02	5.07E-01	5.97E-01	1292.21	not significant
6770	ZNF583	1.02	7.21E-01	7.83E-01	197.02	not significant
6771	DSTN	1.02	4.02E-01	4.94E-01	3092.50	not significant
6772	TMEM141	1.02	6.78E-01	7.47E-01	316.60	not significant
6773	DDIT3	1.02	6.76E-01	7.45E-01	316.99	not significant
6774	ATG2B	1.02	5.05E-01	5.95E-01	1851.61	not significant
6775	ERLIN2	1.02	4.47E-01	5.39E-01	1656.98	not significant
6776	BLM	1.02	4.03E-01	4.94E-01	2971.45	not significant
6777	SOCS4	1.02	6.44E-01	7.19E-01	2598.55	not significant
6778	MCCC1	1.02	5.20E-01	6.08E-01	1049.93	not significant
6779	LINC01120	1.02	7.21E-01	7.83E-01	201.26	not significant
6780	TMED3	1.02	4.67E-01	5.59E-01	1525.48	not significant
6781	OSBPL3	1.02	5.07E-01	5.97E-01	1963.22	not significant
6782	SNHG21	1.02	7.32E-01	7.92E-01	148.13	not significant
6783	RTEL1	1.02	7.54E-01	8.10E-01	57.97	not significant
6784	QDPR	1.02	5.43E-01	6.29E-01	842.23	not significant
6785	ABHD8	1.02	6.54E-01	7.27E-01	388.49	not significant
6786	FAM107B	1.02	4.42E-01	5.35E-01	1750.80	not significant
6787	DDHD2	1.02	3.61E-01	4.53E-01	2867.01	not significant
6788	RAB21	1.02	3.93E-01	4.85E-01	2682.05	not significant
6789	SCN8A	1.02	6.06E-01	6.85E-01	654.24	not significant
6790	NLRC3	1.02	3.92E-01	4.84E-01	2437.00	not significant
6791	MYH10	1.02	4.11E-01	5.03E-01	3299.27	not significant
6792	MAP1LC3B	1.02	3.89E-01	4.82E-01	2286.80	not significant
6793	PHF10	1.02	3.78E-01	4.70E-01	2415.49	not significant
6794	USP42	1.02	4.27E-01	5.19E-01	2074.43	not significant
6795	RNFT2	1.02	6.86E-01	7.54E-01	247.36	not significant
6796	STIM1	1.02	3.06E-01	3.96E-01	5815.31	not significant
6797	PACSIN2	1.02	3.58E-01	4.50E-01	2974.35	not significant
6798	GCA	1.02	6.68E-01	7.39E-01	310.99	not significant
6799	CCDC126	1.02	6.96E-01	7.62E-01	224.63	not significant
6800	CXCR4	1.02	2.69E-01	3.55E-01	8177.39	not significant
6801	SPG21	1.02	3.82E-01	4.74E-01	2319.84	not significant
6802	ITPA	1.02	4.48E-01	5.40E-01	1576.20	not significant
6803	TRIP10	1.02	6.81E-01	7.50E-01	276.11	not significant
6804	PCDHGA6	1.02	6.64E-01	7.35E-01	10.53	not significant
6805	ADIPOR1	1.02	2.89E-01	3.77E-01	3967.78	not significant
6806	SH3GL1	1.02	4.52E-01	5.44E-01	1382.96	not significant
6807	SKP2	1.02	3.04E-01	3.93E-01	3442.08	not significant
6808	PATL1	1.02	2.90E-01	3.78E-01	4127.80	not significant
6809	ELMO2	1.03	4.04E-01	4.96E-01	1930.23	not significant
6810	CLCN6	1.03	5.83E-01	6.65E-01	714.48	not significant
6811	NME2	1.03	7.45E-01	8.02E-01	72.94	not significant
6812	EPS8L2	1.03	6.98E-01	7.63E-01	15.39	not significant
6813	MSL3	1.03	4.74E-01	5.65E-01	1201.04	not significant
6814	ACTR6	1.03	4.98E-01	5.88E-01	1362.49	not significant
6815	HIRA	1.03	2.67E-01	3.53E-01	5357.61	not significant
6816	BLMH	1.03	2.96E-01	3.85E-01	4234.30	not significant
6817	SOCS3	1.03	7.26E-01	7.87E-01	26.39	not significant
6818	SCAND1	1.03	4.98E-01	5.88E-01	1287.12	not significant
6819	DYNC2LI1	1.03	7.35E-01	7.94E-01	105.85	not significant
6820	HMGXB4	1.03	3.49E-01	4.41E-01	2863.05	not significant
6821	RNF20	1.03	4.14E-01	5.06E-01	1751.65	not significant
6822	NFXL1	1.03	5.64E-01	6.49E-01	674.50	not significant
6823	LPCAT4	1.03	5.40E-01	6.26E-01	1054.08	not significant
6824	UBE2E3	1.03	6.25E-01	7.02E-01	440.46	not significant
6825	ZUFSP	1.03	5.51E-01	6.36E-01	743.63	not significant
6826	RNF152	1.03	6.66E-01	7.38E-01	12.81	not significant
6827	NOXO1	1.03	6.75E-01	7.45E-01	13.18	not significant
6828	CWC25	1.03	4.73E-01	5.64E-01	1268.19	not significant
6829	ZDHHC2	1.03	3.43E-01	4.34E-01	2608.74	not significant
6830	CCHCR1	1.03	5.40E-01	6.26E-01	805.17	not significant
6831	GPA33	1.03	6.74E-01	7.43E-01	256.59	not significant
6832	USP9Y	1.03	4.77E-01	5.68E-01	2500.32	not significant
6833	TNNT3	1.03	7.13E-01	7.77E-01	26.51	not significant
6834	ZNF407	1.03	5.20E-01	6.08E-01	851.99	not significant
6835	KLKB1	1.03	7.01E-01	7.66E-01	19.26	not significant
6836	IDH3G	1.03	4.86E-01	5.76E-01	1189.37	not significant
6837	IFI35	1.03	6.54E-01	7.27E-01	324.52	not significant
6838	COG5	1.03	3.93E-01	4.85E-01	1854.98	not significant
6839	AQP4-AS1	1.03	7.08E-01	7.72E-01	23.04	not significant
6840	SAMD1	1.03	3.97E-01	4.89E-01	1691.31	not significant
6841	PAQR3	1.03	3.35E-01	4.26E-01	2497.02	not significant
6842	FLJ44635	1.03	7.34E-01	7.93E-01	85.67	not significant
6843	ENY2	1.03	3.30E-01	4.21E-01	3712.99	not significant
6844	EDF1	1.03	3.68E-01	4.60E-01	3134.48	not significant
6845	NTNG2	1.03	7.28E-01	7.89E-01	34.68	not significant
6846	MCRS1	1.03	3.32E-01	4.24E-01	3601.24	not significant
6847	ELMSAN1	1.03	4.15E-01	5.06E-01	1938.97	not significant
6848	C19orf73	1.03	6.50E-01	7.24E-01	11.25	not significant
6849	PATL2	1.03	7.23E-01	7.85E-01	29.19	not significant
6850	PIGC	1.03	4.64E-01	5.55E-01	1284.58	not significant
6851	PPM1G	1.03	2.08E-01	2.86E-01	9455.71	not significant
6852	APBA3	1.03	5.41E-01	6.28E-01	696.27	not significant

6853	SLC35D2	1.03	6.49E-01	7.23E-01	11.76	not significant
6854	PIK3CD	1.03	2.20E-01	3.01E-01	4953.53	not significant
6855	TKT	1.03	2.39E-01	3.21E-01	7991.13	not significant
6856	CES2	1.03	4.46E-01	5.38E-01	1396.11	not significant
6857	LOC101927391	1.03	6.61E-01	7.33E-01	14.07	not significant
6858	ENPP1	1.03	7.27E-01	7.88E-01	40.02	not significant
6859	CLASP1	1.03	3.45E-01	4.36E-01	3409.67	not significant
6860	PTCH2	1.03	6.73E-01	7.43E-01	15.42	not significant
6861	GPR108	1.03	4.08E-01	5.00E-01	1660.90	not significant
6862	SLC26A2	1.03	4.67E-01	5.58E-01	1155.47	not significant
6863	KAT8	1.03	4.39E-01	5.31E-01	1443.85	not significant
6864	ZFC3H1	1.03	6.71E-01	7.41E-01	3825.78	not significant
6865	CAMTA2	1.03	4.56E-01	5.48E-01	1269.19	not significant
6866	NFE2L1	1.03	2.28E-01	3.09E-01	4536.86	not significant
6867	SMARCB1	1.03	3.31E-01	4.22E-01	3816.14	not significant
6868	NUDT3	1.03	6.79E-01	7.48E-01	214.67	not significant
6869	SPRED3	1.03	6.56E-01	7.28E-01	12.89	not significant
6870	LIN37	1.03	6.94E-01	7.61E-01	189.88	not significant
6871	N6AMT1	1.03	6.74E-01	7.43E-01	224.90	not significant
6872	UBLCP1	1.03	4.33E-01	5.25E-01	1911.17	not significant
6873	NPM3	1.03	4.32E-01	5.24E-01	1760.91	not significant
6874	GAMT	1.03	3.76E-01	4.68E-01	2100.86	not significant
6875	ATP6V0C	1.03	3.96E-01	4.87E-01	3963.51	not significant
6876	C15orf62	1.03	7.21E-01	7.84E-01	37.21	not significant
6877	GPATCH1	1.03	5.14E-01	6.03E-01	738.90	not significant
6878	PIAS2	1.03	4.26E-01	5.18E-01	1228.44	not significant
6879	GJC2	1.03	7.16E-01	7.79E-01	40.53	not significant
6880	MEPCE	1.03	2.59E-01	3.45E-01	3474.59	not significant
6881	PAK1	1.03	3.35E-01	4.26E-01	2827.48	not significant
6882	LATS1	1.03	4.01E-01	4.93E-01	1568.74	not significant
6883	EMILIN2	1.03	5.32E-01	6.20E-01	704.89	not significant
6884	ATF2	1.03	2.20E-01	3.00E-01	5327.26	not significant
6885	SLC16A1-AS1	1.03	6.93E-01	7.60E-01	150.29	not significant
6886	TRIM41	1.03	3.06E-01	3.95E-01	2553.14	not significant
6887	C7orf31	1.03	5.42E-01	6.28E-01	581.51	not significant
6888	TATDN2	1.03	3.23E-01	4.14E-01	4820.32	not significant
6889	ADRBK2	1.03	2.12E-01	2.91E-01	16406.70	not significant
6890	MSANTD4	1.03	5.08E-01	5.97E-01	778.71	not significant
6891	GINS3	1.03	3.76E-01	4.68E-01	1605.83	not significant
6892	SMARCD1	1.03	1.88E-01	2.63E-01	10275.09	not significant
6893	PTPN6	1.03	4.02E-01	4.93E-01	1484.61	not significant
6894	LOC100506474	1.03	7.18E-01	7.81E-01	71.50	not significant
6895	KATNAL1	1.03	4.81E-01	5.72E-01	1021.07	not significant
6896	IMMP2L	1.03	6.48E-01	7.23E-01	249.29	not significant
6897	EPM2A	1.03	4.85E-01	5.75E-01	987.48	not significant
6898	HIST1H3G	1.03	6.89E-01	7.56E-01	21.99	not significant
6899	ARMC6	1.03	2.91E-01	3.79E-01	2881.98	not significant
6900	ZNF140	1.03	5.40E-01	6.26E-01	639.16	not significant
6901	ZNHIT2	1.03	6.82E-01	7.51E-01	194.17	not significant
6902	ASB7	1.03	5.16E-01	6.04E-01	735.90	not significant
6903	CDK17	1.03	3.38E-01	4.29E-01	2398.07	not significant
6904	MAN2C1	1.03	6.81E-01	7.50E-01	814.37	not significant
6905	PRDM4	1.03	3.60E-01	4.52E-01	1740.72	not significant
6906	BTBD1	1.03	2.94E-01	3.83E-01	3199.89	not significant
6907	PGAP1	1.03	5.37E-01	6.24E-01	893.56	not significant
6908	PRPF4B	1.03	2.85E-01	3.73E-01	6199.32	not significant
6909	SOAT2	1.03	6.27E-01	7.04E-01	289.65	not significant
6910	SEC24B	1.03	3.37E-01	4.28E-01	2064.30	not significant
6911	SEMA4D	1.03	1.89E-01	2.63E-01	7952.50	not significant
6912	CERS6-AS1	1.03	6.44E-01	7.19E-01	13.76	not significant
6913	PRDM10	1.03	5.21E-01	6.10E-01	712.14	not significant
6914	KLC2	1.03	3.53E-01	4.45E-01	2309.15	not significant
6915	ZNF771	1.03	6.98E-01	7.63E-01	142.48	not significant
6916	NCF2	1.03	6.42E-01	7.17E-01	13.65	not significant
6917	ZXDC	1.03	4.63E-01	5.55E-01	1208.29	not significant
6918	PPP1R10	1.03	4.77E-01	5.68E-01	870.21	not significant
6919	KIAA0391	1.03	3.48E-01	4.40E-01	1967.53	not significant
6920	KLHDC7B	1.03	6.26E-01	7.02E-01	12.97	not significant
6921	IL10RB	1.03	3.32E-01	4.24E-01	2204.01	not significant
6922	PPM1B	1.03	3.40E-01	4.32E-01	2344.14	not significant
6923	CMYA5	1.03	6.95E-01	7.61E-01	31.14	not significant
6924	LETM2	1.03	6.40E-01	7.16E-01	240.69	not significant
6925	HAUS8	1.03	5.34E-01	6.22E-01	910.11	not significant
6926	GDAP1	1.03	4.49E-01	5.41E-01	1019.90	not significant
6927	ZNF432	1.03	6.41E-01	7.16E-01	272.15	not significant
6928	SUZ12	1.03	2.18E-01	2.97E-01	6699.89	not significant
6929	NRIP3	1.03	5.90E-01	6.72E-01	9.82	not significant
6930	CRIP1	1.03	5.05E-01	5.95E-01	705.81	not significant
6931	KCTD13	1.03	5.29E-01	6.17E-01	618.86	not significant
6932	CRYBB2P1	1.03	4.94E-01	5.84E-01	879.39	not significant
6933	CASC10	1.03	6.69E-01	7.39E-01	18.80	not significant
6934	THAP9	1.03	5.96E-01	6.76E-01	379.47	not significant
6935	POMZP3	1.03	6.92E-01	7.59E-01	115.88	not significant
6936	LNX2	1.03	4.55E-01	5.47E-01	940.13	not significant
6937	ATP5E	1.03	6.90E-01	7.58E-01	108.13	not significant
6938	FBXO33	1.03	3.54E-01	4.46E-01	1593.88	not significant
6939	CATSPER2P1	1.03	6.52E-01	7.25E-01	16.17	not significant
6940	CHCHD6	1.03	5.84E-01	6.66E-01	401.64	not significant

6941	KIAA0232	1.03	2.73E-01	3.60E-01	2669.74	not significant
6942	RBM18	1.03	4.06E-01	4.97E-01	1135.54	not significant
6943	IREB2	1.03	2.18E-01	2.97E-01	4221.73	not significant
6944	ZNF749	1.03	5.96E-01	6.77E-01	431.83	not significant
6945	UBE3D	1.03	6.51E-01	7.25E-01	209.10	not significant
6946	ZGPAT	1.03	4.30E-01	5.22E-01	1214.64	not significant
6947	ALDH3B2	1.03	7.06E-01	7.70E-01	59.31	not significant
6948	PANK1	1.03	4.59E-01	5.51E-01	1002.70	not significant
6949	COL9A3	1.03	7.06E-01	7.70E-01	62.62	not significant
6950	STIL	1.03	2.34E-01	3.15E-01	3286.06	not significant
6951	RBPJ	1.03	2.89E-01	3.78E-01	3295.21	not significant
6952	TRIM11	1.03	3.93E-01	4.85E-01	1278.15	not significant
6953	ZIC2	1.03	7.03E-01	7.68E-01	65.83	not significant
6954	APOE	1.03	6.55E-01	7.28E-01	16.89	not significant
6955	CCDC17	1.03	6.98E-01	7.64E-01	37.62	not significant
6956	FAM206A	1.03	5.69E-01	6.53E-01	525.57	not significant
6957	LINC01278	1.03	6.55E-01	7.28E-01	17.15	not significant
6958	PQLC3	1.03	4.46E-01	5.39E-01	907.46	not significant
6959	RRAGC	1.03	4.20E-01	5.12E-01	1309.27	not significant
6960	MIR497HG	1.03	5.88E-01	6.69E-01	10.58	not significant
6961	ZNF192P1	1.03	6.54E-01	7.27E-01	16.80	not significant
6962	APTR	1.03	6.36E-01	7.11E-01	206.40	not significant
6963	FBXO11	1.03	3.34E-01	4.26E-01	2201.96	not significant
6964	TTC13	1.03	5.33E-01	6.21E-01	612.14	not significant
6965	TTLL13	1.03	5.71E-01	6.54E-01	8.18	not significant
6966	RNF138P1	1.03	6.56E-01	7.28E-01	17.49	not significant
6967	RPE	1.03	3.50E-01	4.42E-01	1584.92	not significant
6968	MAST2	1.03	2.82E-01	3.70E-01	2331.46	not significant
6969	ZBTB25	1.03	6.07E-01	6.86E-01	318.43	not significant
6970	HILPDA	1.03	4.48E-01	5.40E-01	926.58	not significant
6971	OPA1	1.03	1.79E-01	2.51E-01	4974.26	not significant
6972	FKBP15	1.03	4.31E-01	5.23E-01	1039.20	not significant
6973	TRIM32	1.03	5.53E-01	6.39E-01	504.37	not significant
6974	KLHL31	1.03	6.35E-01	7.11E-01	14.37	not significant
6975	ANKRD22	1.03	6.94E-01	7.60E-01	85.95	not significant
6976	RNF216P1	1.03	4.42E-01	5.34E-01	991.18	not significant
6977	LAMC3	1.03	6.32E-01	7.08E-01	14.66	not significant
6978	CAPN5	1.03	6.96E-01	7.62E-01	51.19	not significant
6979	RNASE4	1.03	5.97E-01	6.77E-01	11.24	not significant
6980	CCDC74B	1.03	6.86E-01	7.54E-01	31.26	not significant
6981	PRKCI	1.03	2.73E-01	3.60E-01	2298.56	not significant
6982	GSTZ1	1.03	5.68E-01	6.52E-01	426.43	not significant
6983	KIAA1328	1.03	6.22E-01	6.99E-01	275.79	not significant
6984	DUSP4	1.03	6.93E-01	7.60E-01	46.39	not significant
6985	LINC01420	1.03	3.92E-01	4.84E-01	1166.48	not significant
6986	ZNF444	1.03	3.78E-01	4.69E-01	1472.09	not significant
6987	TTTY14	1.03	6.55E-01	7.28E-01	19.67	not significant
6988	C16orf58	1.03	3.41E-01	4.32E-01	1722.32	not significant
6989	SCRIB	1.03	2.86E-01	3.74E-01	2130.50	not significant
6990	RNF111	1.03	4.05E-01	4.97E-01	1047.08	not significant
6991	CTH	1.03	6.21E-01	6.98E-01	15.00	not significant
6992	DNAH17	1.03	6.87E-01	7.54E-01	86.90	not significant
6993	CPSF4	1.03	2.92E-01	3.80E-01	2416.40	not significant
6994	C1orf53	1.03	6.90E-01	7.58E-01	45.87	not significant
6995	KIF3C	1.03	4.20E-01	5.12E-01	974.21	not significant
6996	ZNF565	1.03	6.91E-01	7.58E-01	59.95	not significant
6997	TAF1B	1.03	4.18E-01	5.10E-01	940.44	not significant
6998	TFAP2E	1.03	6.84E-01	7.52E-01	84.57	not significant
6999	CLK3	1.03	3.40E-01	4.31E-01	1648.59	not significant
7000	ARPP19	1.03	1.38E-01	2.02E-01	9619.77	not significant
7001	CD3D	1.03	1.74E-01	2.46E-01	14907.74	not significant
7002	PLEKHF2	1.03	3.64E-01	4.56E-01	1299.62	not significant
7003	STUB1	1.03	2.84E-01	3.72E-01	1983.51	not significant
7004	PHF11	1.03	4.09E-01	5.01E-01	1321.44	not significant
7005	USP36	1.03	2.34E-01	3.16E-01	4435.32	not significant
7006	MAPK14	1.03	1.79E-01	2.51E-01	4452.18	not significant
7007	PI4K2A	1.03	4.10E-01	5.02E-01	1108.79	not significant
7008	FRG1B	1.03	4.13E-01	5.04E-01	1025.71	not significant
7009	ABHD10	1.03	2.65E-01	3.51E-01	2273.50	not significant
7010	PALM	1.03	6.82E-01	7.50E-01	90.55	not significant
7011	NIT2	1.03	3.99E-01	4.91E-01	1024.10	not significant
7012	SGK494	1.03	6.73E-01	7.43E-01	212.44	not significant
7013	TMX3	1.03	2.09E-01	2.87E-01	3287.66	not significant
7014	RHEB	1.03	3.15E-01	4.06E-01	1989.84	not significant
7015	C14orf166	1.03	2.30E-01	3.12E-01	6433.42	not significant
7016	KCNA6	1.03	6.68E-01	7.39E-01	29.13	not significant
7017	FOXM1	1.03	1.20E-01	1.78E-01	7195.26	not significant
7018	DMBT1	1.03	5.94E-01	6.74E-01	12.30	not significant
7019	LINC01372	1.03	5.90E-01	6.72E-01	11.40	not significant
7020	GSK3B	1.03	1.42E-01	2.07E-01	6820.80	not significant
7021	ZNF286B	1.03	6.70E-01	7.41E-01	100.21	not significant
7022	GIMAP1	1.03	2.43E-01	3.27E-01	5213.42	not significant
7023	PIN4	1.03	4.91E-01	5.82E-01	581.06	not significant
7024	PRG4	1.03	6.15E-01	6.93E-01	237.81	not significant
7025	FLVCR2	1.03	6.46E-01	7.21E-01	23.43	not significant
7026	ZNF540	1.03	6.80E-01	7.49E-01	63.55	not significant
7027	THOC3	1.03	5.53E-01	6.39E-01	490.44	not significant
7028	ITGB5	1.03	6.15E-01	6.93E-01	15.97	not significant

7029	OGFRP1	1.03	6.36E-01	7.11E-01	20.10	not significant
7030	LOC100335030	1.03	6.42E-01	7.17E-01	21.34	not significant
7031	YEATS4	1.03	2.32E-01	3.14E-01	2730.93	not significant
7032	XKR9	1.03	5.58E-01	6.43E-01	9.49	not significant
7033	MARK2	1.03	2.04E-01	2.81E-01	3168.81	not significant
7034	ETV5	1.03	6.73E-01	7.43E-01	69.65	not significant
7035	POLR2G	1.03	2.70E-01	3.56E-01	3186.02	not significant
7036	SLC1A4	1.03	1.06E-01	1.61E-01	7760.13	not significant
7037	SETD5	1.03	2.48E-01	3.32E-01	5097.22	not significant
7038	GSTO1	1.03	2.65E-01	3.51E-01	2476.87	not significant
7039	RNASEH2B-AS1	1.03	6.26E-01	7.03E-01	17.54	not significant
7040	PLA2G15	1.03	5.72E-01	6.56E-01	337.21	not significant
7041	SURF4	1.03	4.16E-01	5.07E-01	831.08	not significant
7042	ANO10	1.03	5.78E-01	6.61E-01	11.18	not significant
7043	NDUFAF7	1.03	4.62E-01	5.54E-01	647.47	not significant
7044	GPSM3	1.03	5.80E-01	6.63E-01	276.64	not significant
7045	SOWAHA	1.03	6.51E-01	7.25E-01	127.97	not significant
7046	PWWP2A	1.03	3.71E-01	4.63E-01	1064.11	not significant
7047	MORC4	1.03	4.80E-01	5.71E-01	607.37	not significant
7048	PPIL3	1.03	3.29E-01	4.20E-01	1380.46	not significant
7049	ZNF621	1.03	5.35E-01	6.22E-01	402.56	not significant
7050	PPT1	1.03	1.54E-01	2.22E-01	7173.95	not significant
7051	ADAR	1.03	1.46E-01	2.11E-01	17662.44	not significant
7052	ARIH1	1.03	1.96E-01	2.72E-01	2902.57	not significant
7053	ASAP1	1.03	2.54E-01	3.39E-01	2154.58	not significant
7054	ZC3H14	1.03	2.28E-01	3.09E-01	2414.18	not significant
7055	RPRD1B	1.03	1.89E-01	2.64E-01	3049.42	not significant
7056	ZMYM6	1.03	4.46E-01	5.38E-01	873.53	not significant
7057	SYNPO2	1.03	6.69E-01	7.39E-01	57.06	not significant
7058	ABRACL	1.03	1.51E-01	2.17E-01	5248.30	not significant
7059	CRHR1-IT1	1.03	6.57E-01	7.29E-01	31.26	not significant
7060	RLF	1.03	3.41E-01	4.32E-01	1155.23	not significant
7061	LRP10	1.03	3.43E-01	4.34E-01	1429.83	not significant
7062	HADHA	1.03	1.20E-01	1.78E-01	7970.44	not significant
7063	GAL3ST3	1.03	5.42E-01	6.28E-01	9.20	not significant
7064	CPT1B	1.03	6.67E-01	7.38E-01	56.84	not significant
7065	SLC35C2	1.03	2.87E-01	3.76E-01	1902.26	not significant
7066	C11orf54	1.03	3.74E-01	4.66E-01	1043.00	not significant
7067	TOLLIP	1.03	2.83E-01	3.70E-01	1623.10	not significant
7068	ZNF233	1.03	6.63E-01	7.35E-01	37.73	not significant
7069	SNHG20	1.03	5.96E-01	6.76E-01	336.31	not significant
7070	ANKRD31	1.03	6.26E-01	7.03E-01	20.71	not significant
7071	LINC00880	1.03	5.27E-01	6.16E-01	8.93	not significant
7072	TRIM14	1.03	1.20E-01	1.79E-01	5707.60	not significant
7073	PPAN	1.03	5.96E-01	6.76E-01	206.78	not significant
7074	TMEM191A	1.03	5.35E-01	6.23E-01	8.74	not significant
7075	CCDC112	1.03	4.59E-01	5.50E-01	592.41	not significant
7076	ZNF582-AS1	1.03	6.62E-01	7.34E-01	76.64	not significant
7077	ZFYVE19	1.03	4.21E-01	5.12E-01	769.49	not significant
7078	DNLZ	1.03	4.71E-01	5.62E-01	562.90	not significant
7079	CATSPERB	1.03	5.68E-01	6.52E-01	12.38	not significant
7080	NOMO3	1.03	6.44E-01	7.19E-01	112.79	not significant
7081	CHD2	1.03	2.72E-01	3.58E-01	2699.33	not significant
7082	SLC12A5	1.03	6.43E-01	7.18E-01	33.56	not significant
7083	IFI16	1.03	1.28E-01	1.89E-01	13561.91	not significant
7084	WDR47	1.03	4.72E-01	5.63E-01	544.36	not significant
7085	LOC101927365	1.03	6.42E-01	7.17E-01	117.77	not significant
7086	HIVEP1	1.03	5.74E-01	6.57E-01	275.65	not significant
7087	PSTPIP1	1.03	5.24E-01	6.12E-01	479.60	not significant
7088	SMURF1	1.03	4.47E-01	5.40E-01	691.06	not significant
7089	CD247	1.03	1.85E-01	2.59E-01	8442.75	not significant
7090	GPR135	1.03	5.93E-01	6.74E-01	14.86	not significant
7091	ELL	1.03	3.60E-01	4.52E-01	987.02	not significant
7092	KMT2B	1.03	5.18E-01	6.07E-01	3250.69	not significant
7093	KNTC1	1.03	5.55E-01	6.40E-01	8029.90	not significant
7094	ZDHHC9	1.03	4.37E-01	5.29E-01	703.91	not significant
7095	SP2	1.03	2.74E-01	3.60E-01	1601.81	not significant
7096	TMEM185B	1.03	2.06E-01	2.83E-01	2516.35	not significant
7097	DOCK9-AS2	1.03	6.21E-01	6.98E-01	21.88	not significant
7098	PPP2CB	1.03	2.69E-01	3.55E-01	2465.40	not significant
7099	CCDC102B	1.03	6.59E-01	7.32E-01	56.94	not significant
7100	FAM178A	1.03	2.46E-01	3.29E-01	3704.63	not significant
7101	FBXO21	1.03	2.21E-01	3.01E-01	2211.37	not significant
7102	PRMT2	1.03	2.58E-01	3.42E-01	1731.38	not significant
7103	PIP4K2A	1.03	1.15E-01	1.72E-01	5840.27	not significant
7104	TEX21P	1.03	4.85E-01	5.76E-01	8.41	not significant
7105	ZNF687	1.03	3.14E-01	4.04E-01	1337.08	not significant
7106	ARNT	1.03	2.58E-01	3.43E-01	1751.98	not significant
7107	KIAA0556	1.03	4.80E-01	5.71E-01	490.10	not significant
7108	CRNKL1	1.03	2.49E-01	3.32E-01	1751.50	not significant
7109	PHEX	1.03	6.41E-01	7.16E-01	29.49	not significant
7110	HDGFRP2	1.03	2.14E-01	2.93E-01	3250.32	not significant
7111	SMCO4	1.03	6.53E-01	7.27E-01	40.31	not significant
7112	SLC30A5	1.03	1.56E-01	2.24E-01	3325.54	not significant
7113	FAHD1	1.03	4.85E-01	5.75E-01	487.37	not significant
7114	DSN1	1.03	1.75E-01	2.47E-01	2819.14	not significant
7115	FAT1	1.03	1.80E-01	2.54E-01	8289.19	not significant
7116	PSENEN	1.03	4.61E-01	5.53E-01	728.97	not significant

7117	RCN1	1.03	3.12E-01	4.03E-01	1391.35	not significant
7118	GMCL1	1.04	2.16E-01	2.96E-01	2168.76	not significant
7119	ALMS1-IT1	1.04	6.38E-01	7.14E-01	29.36	not significant
7120	CD53	1.04	1.79E-01	2.52E-01	4515.46	not significant
7121	PHF8	1.04	4.37E-01	5.29E-01	596.15	not significant
7122	PCNT	1.04	2.62E-01	3.47E-01	3145.70	not significant
7123	IRF2BP1	1.04	2.55E-01	3.40E-01	1974.50	not significant
7124	EIF4EBP2	1.04	8.86E-02	1.37E-01	13206.21	not significant
7125	SNX12	1.04	3.92E-01	4.84E-01	964.74	not significant
7126	PRICKLE3	1.04	6.47E-01	7.21E-01	45.01	not significant
7127	LCMT1-AS1	1.04	6.33E-01	7.09E-01	29.15	not significant
7128	ZNFX1	1.04	3.39E-01	4.30E-01	1980.44	not significant
7129	SAMD9	1.04	1.47E-01	2.13E-01	3349.63	not significant
7130	RMND5A	1.04	1.31E-01	1.93E-01	5471.28	not significant
7131	NRN1L	1.04	5.00E-01	5.90E-01	8.68	not significant
7132	PROSER3	1.04	4.80E-01	5.71E-01	534.15	not significant
7133	C2orf49	1.04	2.63E-01	3.49E-01	1606.87	not significant
7134	ELP6	1.04	2.72E-01	3.58E-01	1679.87	not significant
7135	COLQ	1.04	6.51E-01	7.25E-01	51.49	not significant
7136	APITD1	1.04	6.17E-01	6.95E-01	143.91	not significant
7137	SETDB2	1.04	3.70E-01	4.62E-01	866.85	not significant
7138	EIF4EBP3	1.04	5.63E-01	6.47E-01	13.41	not significant
7139	ZNF138	1.04	3.37E-01	4.28E-01	1195.56	not significant
7140	ALKBH4	1.04	4.49E-01	5.41E-01	560.73	not significant
7141	HNRNPDL	1.04	8.99E-02	1.39E-01	16162.28	not significant
7142	PPP2R5C	1.04	1.16E-01	1.74E-01	6205.94	not significant
7143	SLC16A6	1.04	5.66E-01	6.50E-01	13.70	not significant
7144	FOXO3B	1.04	4.83E-01	5.73E-01	510.09	not significant
7145	TSTD3	1.04	6.32E-01	7.08E-01	29.95	not significant
7146	LINC01001	1.04	5.52E-01	6.38E-01	11.94	not significant
7147	LOC101928103	1.04	6.34E-01	7.10E-01	102.07	not significant
7148	APPBP2	1.04	1.78E-01	2.51E-01	2805.07	not significant
7149	RTCB	1.04	1.92E-01	2.67E-01	3414.97	not significant
7150	PHRF1	1.04	1.66E-01	2.37E-01	3858.70	not significant
7151	FAHD2A	1.04	3.88E-01	4.81E-01	744.92	not significant
7152	PLCB3	1.04	4.47E-01	5.39E-01	582.30	not significant
7153	AOAH	1.04	6.45E-01	7.20E-01	54.59	not significant
7154	UBN2	1.04	3.39E-01	4.30E-01	1201.33	not significant
7155	POLR2J4	1.04	5.49E-01	6.35E-01	337.43	not significant
7156	BOD1L1	1.04	2.62E-01	3.48E-01	3128.59	not significant
7157	PRX	1.04	6.30E-01	7.06E-01	109.47	not significant
7158	SRRM2	1.04	5.54E-01	6.39E-01	29892.15	not significant
7159	KIAA0247	1.04	2.54E-01	3.38E-01	1697.87	not significant
7160	ZNF410	1.04	2.41E-01	3.24E-01	1856.95	not significant
7161	MAP1S	1.04	2.43E-01	3.27E-01	1713.44	not significant
7162	KBTBD2	1.04	2.15E-01	2.94E-01	2282.61	not significant
7163	AMACR	1.04	6.23E-01	7.00E-01	29.91	not significant
7164	ANKRD54	1.04	3.93E-01	4.85E-01	720.49	not significant
7165	NRSN2	1.04	6.41E-01	7.16E-01	54.57	not significant
7166	DYNC1H1	1.04	6.32E-01	7.08E-01	9939.20	not significant
7167	LOC652276	1.04	6.33E-01	7.09E-01	90.39	not significant
7168	CCDC153	1.04	5.11E-01	6.00E-01	10.12	not significant
7169	KIAA0825	1.04	6.25E-01	7.02E-01	32.32	not significant
7170	DND1	1.04	6.27E-01	7.03E-01	34.19	not significant
7171	POPDC2	1.04	6.05E-01	6.85E-01	24.26	not significant
7172	AKIP1	1.04	4.52E-01	5.44E-01	574.80	not significant
7173	C1orf56	1.04	6.26E-01	7.03E-01	34.21	not significant
7174	ADNP	1.04	8.13E-02	1.27E-01	6170.53	not significant
7175	ATP13A2	1.04	2.57E-01	3.42E-01	1839.72	not significant
7176	SQSTM1	1.04	2.37E-01	3.20E-01	1894.12	not significant
7177	ADAP2	1.04	4.75E-01	5.66E-01	8.54	not significant
7178	RPEL1	1.04	5.00E-01	5.90E-01	9.77	not significant
7179	MFAP4	1.04	2.16E-01	2.95E-01	1939.51	not significant
7180	IBTK	1.04	1.61E-01	2.30E-01	3146.40	not significant
7181	LEF1	1.04	5.22E-02	8.63E-02	26364.27	not significant
7182	SIDT2	1.04	4.83E-01	5.73E-01	401.69	not significant
7183	PLCL2	1.04	2.27E-01	3.09E-01	1852.63	not significant
7184	COX16	1.04	6.28E-01	7.04E-01	148.28	not significant
7185	LEMD2	1.04	1.88E-01	2.62E-01	2617.40	not significant
7186	LGALS3BP	1.04	7.75E-02	1.22E-01	9551.72	not significant
7187	SMARCA5-AS1	1.04	5.78E-01	6.62E-01	20.85	not significant
7188	SF3A1	1.04	7.86E-02	1.24E-01	8161.02	not significant
7189	CLOCK	1.04	4.45E-01	5.37E-01	549.80	not significant
7190	RNF5P1	1.04	5.78E-01	6.62E-01	18.43	not significant
7191	ZNF318	1.04	2.35E-01	3.17E-01	2211.32	not significant
7192	CCDC174	1.04	3.47E-01	4.39E-01	916.27	not significant
7193	SPIRE1	1.04	4.79E-01	5.70E-01	8.92	not significant
7194	FOXK1	1.04	2.06E-01	2.84E-01	2338.39	not significant
7195	RWDD2A	1.04	6.15E-01	6.93E-01	110.40	not significant
7196	SMS	1.04	1.54E-01	2.21E-01	3847.40	not significant
7197	SNRNP48	1.04	1.14E-01	1.70E-01	4327.54	not significant
7198	TLK1	1.04	1.30E-01	1.91E-01	4511.24	not significant
7199	HPGD	1.04	5.92E-01	6.73E-01	145.66	not significant
7200	TTC16	1.04	5.34E-01	6.22E-01	400.80	not significant
7201	MYC	1.04	5.59E-02	9.16E-02	11612.71	not significant
7202	HAR1B	1.04	6.05E-01	6.84E-01	26.79	not significant
7203	FLVCR1-AS1	1.04	6.23E-01	7.00E-01	42.09	not significant
7204	LIG4	1.04	1.23E-01	1.83E-01	3635.40	not significant

7205	UBE2J1	1.04	1.54E-01	2.21E-01	2783.34	not significant
7206	C1QTNF3-AMACR	1.04	4.93E-01	5.83E-01	10.13	not significant
7207	RBM19	1.04	1.81E-01	2.54E-01	2337.91	not significant
7208	SRRM2-AS1	1.04	5.33E-01	6.21E-01	13.30	not significant
7209	ANKRD24	1.04	4.79E-01	5.70E-01	9.77	not significant
7210	DDX23	1.04	7.63E-02	1.21E-01	11966.15	not significant
7211	ZNF394	1.04	4.07E-01	4.99E-01	599.08	not significant
7212	TTC7A	1.04	1.14E-01	1.71E-01	7947.72	not significant
7213	NFRKB	1.04	1.78E-01	2.51E-01	2108.29	not significant
7214	MBLAC1	1.04	6.20E-01	6.97E-01	76.23	not significant
7215	HYLS1	1.04	5.26E-01	6.15E-01	254.88	not significant
7216	ARPC1A	1.04	1.81E-01	2.55E-01	2558.72	not significant
7217	SNX6	1.04	1.68E-01	2.39E-01	2443.86	not significant
7218	ARMC1	1.04	8.50E-02	1.32E-01	4320.99	not significant
7219	MPP1	1.04	2.44E-01	3.27E-01	1377.02	not significant
7220	PAGE5	1.04	6.17E-01	6.94E-01	44.16	not significant
7221	CETN2	1.04	5.96E-01	6.76E-01	114.83	not significant
7222	MYOZ3	1.04	6.07E-01	6.86E-01	32.59	not significant
7223	MTCL1	1.04	6.07E-01	6.86E-01	93.52	not significant
7224	NAA60	1.04	1.65E-01	2.35E-01	2824.88	not significant
7225	FBXO10	1.04	4.86E-01	5.76E-01	343.34	not significant
7226	AKAP7	1.04	4.71E-01	5.62E-01	411.11	not significant
7227	C7orf49	1.04	2.66E-01	3.52E-01	1855.27	not significant
7228	UGT3A2	1.04	5.92E-01	6.73E-01	117.79	not significant
7229	TMEM60	1.04	3.87E-01	4.80E-01	620.55	not significant
7230	NPAT	1.04	2.16E-01	2.96E-01	2142.01	not significant
7231	WDR66	1.04	5.42E-01	6.28E-01	15.18	not significant
7232	AGPAT2	1.04	4.82E-01	5.73E-01	374.39	not significant
7233	RPS6KA1	1.04	1.23E-01	1.82E-01	3939.78	not significant
7234	LY86	1.04	4.64E-01	5.56E-01	8.61	not significant
7235	ZNF580	1.04	3.95E-01	4.87E-01	714.93	not significant
7236	IPO9-AS1	1.04	5.75E-01	6.59E-01	23.84	not significant
7237	EML6	1.04	4.90E-01	5.81E-01	317.61	not significant
7238	IKBKG	1.04	5.92E-01	6.73E-01	112.93	not significant
7239	DYNLT3	1.04	5.98E-01	6.78E-01	30.84	not significant
7240	MX1	1.04	5.50E-01	6.36E-01	216.47	not significant
7241	PSMB5	1.04	2.66E-01	3.52E-01	1337.58	not significant
7242	TUSC3	1.04	2.23E-01	3.03E-01	1836.57	not significant
7243	ZSWIM5	1.04	5.79E-01	6.62E-01	145.55	not significant
7244	ALKBH6	1.04	4.65E-01	5.56E-01	381.69	not significant
7245	FBXL5	1.04	1.91E-01	2.66E-01	1747.94	not significant
7246	GALNT7	1.04	1.53E-01	2.21E-01	2561.91	not significant
7247	PSPN	1.04	5.07E-01	5.97E-01	11.73	not significant
7248	LOC101929057	1.04	6.09E-01	6.88E-01	49.23	not significant
7249	PTBP3	1.04	7.98E-02	1.25E-01	9532.88	not significant
7250	MKL2	1.04	2.19E-01	2.99E-01	1859.49	not significant
7251	YEATS2	1.04	8.86E-02	1.37E-01	5348.95	not significant
7252	MYO18A	1.04	1.31E-01	1.92E-01	4539.46	not significant
7253	SUV420H1	1.04	2.17E-01	2.96E-01	1656.91	not significant
7254	JAK1	1.04	8.41E-02	1.31E-01	5335.73	not significant
7255	CAMKK2	1.04	7.76E-02	1.22E-01	5014.04	not significant
7256	TMF1	1.04	2.29E-01	3.10E-01	1728.86	not significant
7257	ZBTB44	1.04	1.11E-01	1.66E-01	6134.00	not significant
7258	PANK2	1.04	2.23E-01	3.04E-01	1500.90	not significant
7259	MYLK-AS1	1.04	6.07E-01	6.86E-01	64.37	not significant
7260	SLC38A1	1.04	3.48E-02	6.02E-02	20729.32	not significant
7261	ANP32A-IT1	1.04	5.27E-01	6.15E-01	16.21	not significant
7262	PPM1L	1.04	5.82E-01	6.64E-01	153.46	not significant
7263	SNAP47	1.04	3.18E-01	4.09E-01	846.03	not significant
7264	ATG16L1	1.04	3.19E-01	4.10E-01	840.88	not significant
7265	ABCB10	1.04	1.87E-01	2.61E-01	2277.57	not significant
7266	LXN	1.04	5.78E-01	6.62E-01	118.65	not significant
7267	SP1	1.04	1.02E-01	1.56E-01	6950.73	not significant
7268	NUB1	1.04	6.87E-02	1.10E-01	5063.06	not significant
7269	TOR1AIP1	1.04	1.03E-01	1.57E-01	3803.74	not significant
7270	DFFB	1.04	4.83E-01	5.73E-01	328.43	not significant
7271	SULT1A2	1.04	5.57E-01	6.42E-01	19.10	not significant
7272	C12orf49	1.04	1.67E-01	2.37E-01	2126.55	not significant
7273	HOXB4	1.04	3.74E-01	4.66E-01	806.95	not significant
7274	SCOC	1.04	1.57E-01	2.26E-01	2500.53	not significant
7275	MCM3AP-AS1	1.04	5.62E-01	6.46E-01	147.29	not significant
7276	CWF19L2	1.04	3.55E-01	4.46E-01	647.97	not significant
7277	WDYHV1	1.04	3.06E-01	3.95E-01	984.31	not significant
7278	MALT1	1.04	2.29E-01	3.10E-01	1303.36	not significant
7279	MGC12916	1.04	5.29E-01	6.17E-01	17.61	not significant
7280	PPM1A	1.04	8.77E-02	1.36E-01	5036.37	not significant
7281	PCDHGA11	1.04	5.95E-01	6.76E-01	45.69	not significant
7282	ZNF2	1.04	5.03E-01	5.93E-01	246.42	not significant
7283	HSD17B6	1.04	5.14E-01	6.03E-01	255.03	not significant
7284	NUMB	1.04	7.72E-02	1.22E-01	3775.64	not significant
7285	PINK1	1.04	4.64E-01	5.55E-01	387.72	not significant
7286	AP4S1	1.04	3.78E-01	4.70E-01	573.09	not significant
7287	RBM41	1.04	3.53E-01	4.45E-01	745.98	not significant
7288	POLD1	1.04	8.26E-02	1.29E-01	5721.18	not significant
7289	KAT5	1.04	1.92E-01	2.68E-01	1753.17	not significant
7290	LOC100289511	1.04	5.38E-01	6.25E-01	22.74	not significant
7291	ZNF572	1.04	5.83E-01	6.65E-01	31.75	not significant
7292	CIAO1	1.04	9.39E-02	1.44E-01	3978.35	not significant

7293	PRKXP1	1.04	5.16E-01	6.04E-01	284.45	not significant
7294	KIAA1429	1.04	9.62E-02	1.47E-01	3452.62	not significant
7295	GDPD5	1.04	2.56E-01	3.40E-01	1094.34	not significant
7296	PTPLB	1.04	3.16E-01	4.06E-01	736.74	not significant
7297	BLOC1S1	1.04	3.69E-01	4.60E-01	596.64	not significant
7298	PPCDC	1.04	4.31E-01	5.23E-01	383.52	not significant
7299	SERPINH1	1.04	5.84E-01	6.66E-01	87.99	not significant
7300	DSCC1	1.04	1.40E-01	2.04E-01	2174.20	not significant
7301	STK11	1.04	1.35E-01	1.98E-01	2803.52	not significant
7302	FAM98C	1.04	5.24E-01	6.12E-01	187.66	not significant
7303	PPP1R32	1.04	5.91E-01	6.72E-01	56.86	not significant
7304	FIZ1	1.04	3.62E-01	4.54E-01	609.42	not significant
7305	ABCB6	1.04	4.83E-01	5.74E-01	260.70	not significant
7306	MAP4K4	1.04	3.27E-02	5.69E-02	9075.42	not significant
7307	USP33	1.04	1.51E-01	2.18E-01	2594.61	not significant
7308	LOC389247	1.04	5.10E-01	5.99E-01	14.50	not significant
7309	ARFGAP2	1.04	1.06E-01	1.60E-01	3106.01	not significant
7310	AK1	1.04	5.86E-01	6.67E-01	78.91	not significant
7311	THADA	1.04	1.50E-01	2.16E-01	2162.14	not significant
7312	LSMEM1	1.04	5.62E-01	6.47E-01	26.55	not significant
7313	LOC148413	1.04	3.01E-01	3.90E-01	846.64	not significant
7314	LINC00174	1.04	5.39E-01	6.26E-01	180.21	not significant
7315	PTOV1	1.04	1.07E-01	1.61E-01	4188.74	not significant
7316	AKAP9	1.04	1.54E-01	2.21E-01	3231.79	not significant
7317	CACNB2	1.04	5.41E-01	6.27E-01	162.74	not significant
7318	NSMAF	1.04	6.07E-02	9.84E-02	4079.26	not significant
7319	CASKIN1	1.04	5.70E-01	6.54E-01	31.69	not significant
7320	AGAP2-AS1	1.04	5.13E-01	6.01E-01	14.94	not significant
7321	RNF169	1.04	1.41E-01	2.05E-01	1963.01	not significant
7322	TUBA8	1.04	5.85E-01	6.67E-01	51.04	not significant
7323	PRSS53	1.04	5.57E-01	6.42E-01	176.47	not significant
7324	EMD	1.04	3.34E-01	4.25E-01	746.80	not significant
7325	CCDC23	1.04	3.88E-01	4.81E-01	489.32	not significant
7326	TMCC1	1.04	3.62E-01	4.54E-01	587.38	not significant
7327	RNF103-CHMP3	1.04	4.22E-01	5.13E-01	8.85	not significant
7328	FAM115A	1.04	2.79E-01	3.66E-01	919.56	not significant
7329	SNRPE	1.04	2.44E-01	3.28E-01	1700.56	not significant
7330	FAM151B	1.04	5.55E-01	6.40E-01	25.51	not significant
7331	BCDIN3D-AS1	1.04	5.24E-01	6.12E-01	17.65	not significant
7332	CD81	1.04	1.30E-01	1.91E-01	4961.03	not significant
7333	RELA	1.04	9.37E-02	1.44E-01	2966.03	not significant
7334	MED9	1.04	2.37E-01	3.19E-01	1147.41	not significant
7335	SLC7A5P2	1.04	5.76E-01	6.59E-01	77.49	not significant
7336	CNN3	1.04	1.38E-01	2.01E-01	2389.41	not significant
7337	SCAP	1.04	1.20E-01	1.78E-01	4217.59	not significant
7338	IGIP	1.04	5.91E-01	6.72E-01	80.11	not significant
7339	NME4	1.04	2.19E-01	2.99E-01	1480.54	not significant
7340	PDPK1	1.04	1.77E-01	2.49E-01	2110.94	not significant
7341	MVP	1.04	4.71E-01	5.63E-01	285.00	not significant
7342	CREB1	1.04	9.79E-02	1.50E-01	3286.18	not significant
7343	PCNX	1.04	1.13E-01	1.69E-01	2486.87	not significant
7344	MED22	1.04	5.59E-01	6.44E-01	109.61	not significant
7345	TMTC4	1.04	2.68E-01	3.54E-01	1012.53	not significant
7346	NT5C3A	1.04	2.44E-01	3.28E-01	1061.05	not significant
7347	AKAP13	1.04	1.32E-01	1.95E-01	3169.81	not significant
7348	ZNF793	1.04	5.00E-01	5.90E-01	14.71	not significant
7349	ZKSCAN3	1.04	4.67E-01	5.58E-01	284.16	not significant
7350	RPL27	1.04	3.49E-02	6.03E-02	15068.79	not significant
7351	VGF	1.04	4.72E-01	5.63E-01	12.46	not significant
7352	ZFP37	1.04	5.49E-01	6.35E-01	123.46	not significant
7353	ALAD	1.04	2.10E-01	2.88E-01	1322.02	not significant
7354	LANCL1	1.04	4.48E-02	7.54E-02	5127.72	not significant
7355	WRB	1.04	2.49E-01	3.33E-01	1070.66	not significant
7356	CASP7	1.04	1.60E-01	2.29E-01	1746.80	not significant
7357	STMN1	1.04	5.94E-02	9.66E-02	62874.60	not significant
7358	TMEM199	1.04	5.07E-01	5.97E-01	189.86	not significant
7359	BICD1	1.04	3.33E-01	4.25E-01	618.60	not significant
7360	HIVEP2	1.04	1.02E-01	1.55E-01	2693.91	not significant
7361	GM2A	1.04	1.47E-01	2.12E-01	2184.07	not significant
7362	OPRL1	1.04	5.18E-01	6.06E-01	21.91	not significant
7363	CCDC134	1.04	4.51E-01	5.43E-01	311.88	not significant
7364	NFIL3	1.04	5.72E-01	6.55E-01	45.82	not significant
7365	RABGGTA	1.04	3.06E-01	3.95E-01	666.41	not significant
7366	RAD54L2	1.04	2.64E-01	3.50E-01	1021.25	not significant
7367	FBXW5	1.04	1.88E-01	2.62E-01	1604.77	not significant
7368	LOC101928020	1.04	4.99E-01	5.89E-01	17.77	not significant
7369	SIK2	1.04	1.93E-01	2.68E-01	1317.40	not significant
7370	GDPD3	1.04	5.62E-01	6.46E-01	110.60	not significant
7371	ARID3A	1.04	2.47E-01	3.31E-01	1009.68	not significant
7372	WDR73	1.04	3.69E-01	4.60E-01	469.69	not significant
7373	ZNF271	1.04	1.53E-01	2.20E-01	1631.79	not significant
7374	YIPF2	1.04	3.15E-01	4.05E-01	662.93	not significant
7375	BZRAP1	1.04	4.96E-01	5.86E-01	2140.00	not significant
7376	NFAT5	1.04	4.84E-01	5.74E-01	1741.40	not significant
7377	MYRF	1.04	5.65E-01	6.49E-01	40.31	not significant
7378	GUCY2D	1.04	4.89E-01	5.79E-01	14.20	not significant
7379	SHARPIN	1.04	2.49E-01	3.33E-01	1104.05	not significant
7380	LOC729732	1.04	4.83E-01	5.74E-01	13.60	not significant

7381	ZNF550	1.05	2.48E-01	3.32E-01	916.86	not significant
7382	FZD6	1.05	8.71E-02	1.35E-01	3041.96	not significant
7383	NUDT21	1.05	3.55E-02	6.12E-02	13505.93	not significant
7384	FAM127B	1.05	4.42E-01	5.34E-01	295.61	not significant
7385	MTHFSD	1.05	3.34E-01	4.26E-01	567.94	not significant
7386	ARMCX3	1.05	5.39E-01	6.26E-01	117.37	not significant
7387	MLLT10	1.05	8.70E-02	1.35E-01	2734.13	not significant
7388	TUBGCP3	1.05	1.02E-01	1.55E-01	2342.10	not significant
7389	TENC1	1.05	5.08E-01	5.97E-01	17.94	not significant
7390	XPNPEP2	1.05	1.56E-01	2.25E-01	1734.19	not significant
7391	DYNLL2	1.05	1.29E-01	1.91E-01	6030.34	not significant
7392	GALNT8	1.05	5.27E-01	6.15E-01	21.35	not significant
7393	VPS26B	1.05	6.24E-02	1.01E-01	5362.11	not significant
7394	GPKOW	1.05	4.30E-01	5.22E-01	318.22	not significant
7395	RWDD1	1.05	1.41E-01	2.05E-01	2645.86	not significant
7396	LOC646762	1.05	4.22E-01	5.13E-01	9.81	not significant
7397	LOC728392	1.05	5.61E-01	6.46E-01	52.35	not significant
7398	RABGAP1L	1.05	2.28E-01	3.09E-01	1033.62	not significant
7399	TUBA1A	1.05	6.41E-02	1.03E-01	6443.99	not significant
7400	STK31	1.05	4.32E-01	5.24E-01	10.17	not significant
7401	PEMT	1.05	2.79E-01	3.67E-01	728.03	not significant
7402	RIT1	1.05	2.25E-01	3.06E-01	957.66	not significant
7403	SPG20	1.05	5.19E-01	6.07E-01	21.22	not significant
7404	TPTE2P5	1.05	5.17E-01	6.06E-01	21.18	not significant
7405	TMOD4	1.05	5.30E-01	6.18E-01	24.29	not significant
7406	EGLN1	1.05	1.90E-01	2.65E-01	1334.85	not significant
7407	FTO-IT1	1.05	4.39E-01	5.31E-01	11.52	not significant
7408	FAM76B	1.05	1.84E-01	2.58E-01	1265.17	not significant
7409	PDXP	1.05	1.58E-01	2.27E-01	2783.29	not significant
7410	SCARNA17	1.05	5.17E-01	6.05E-01	22.22	not significant
7411	HMGXB3	1.05	1.72E-01	2.43E-01	2157.98	not significant
7412	SFSWAP	1.05	8.86E-02	1.37E-01	3040.56	not significant
7413	CDKL5	1.05	4.89E-01	5.79E-01	17.52	not significant
7414	PDE8A	1.05	3.69E-01	4.61E-01	464.30	not significant
7415	TPP2	1.05	1.06E-01	1.61E-01	3893.25	not significant
7416	ANKMY2	1.05	1.33E-01	1.95E-01	1737.79	not significant
7417	STX10	1.05	1.11E-01	1.67E-01	2658.69	not significant
7418	FLJ37035	1.05	5.06E-01	5.95E-01	21.72	not significant
7419	PRR19	1.05	5.54E-01	6.39E-01	65.78	not significant
7420	TNFRSF1A	1.05	1.25E-01	1.86E-01	1917.22	not significant
7421	PHF6	1.05	6.01E-02	9.76E-02	4460.45	not significant
7422	LOC100130357	1.05	5.21E-01	6.09E-01	24.02	not significant
7423	SLC4A2	1.05	6.14E-02	9.94E-02	4095.82	not significant
7424	SEC11A	1.05	1.18E-01	1.75E-01	2283.56	not significant
7425	CDC7	1.05	7.83E-02	1.23E-01	3318.85	not significant
7426	EDEM1	1.05	5.47E-02	9.01E-02	9765.60	not significant
7427	GINS4	1.05	1.04E-01	1.58E-01	2541.89	not significant
7428	ASB1	1.05	1.57E-01	2.25E-01	1461.71	not significant
7429	PXMP2	1.05	1.44E-01	2.09E-01	1848.62	not significant
7430	LINC01252	1.05	4.79E-01	5.70E-01	15.82	not significant
7431	ZMIZ2	1.05	3.62E-01	4.54E-01	3044.91	not significant
7432	LMNTD2	1.05	4.86E-01	5.76E-01	16.57	not significant
7433	HEIH	1.05	2.46E-01	3.29E-01	850.78	not significant
7434	ZNF141	1.05	4.71E-01	5.63E-01	14.62	not significant
7435	UBE2L6	1.05	3.37E-02	5.85E-02	6153.91	not significant
7436	NAV1	1.05	4.83E-01	5.73E-01	16.20	not significant
7437	LOC146880	1.05	5.35E-01	6.22E-01	1053.49	not significant
7438	DPEP2	1.05	5.43E-01	6.29E-01	36.38	not significant
7439	PPP1R2	1.05	1.75E-01	2.47E-01	1381.33	not significant
7440	LOC101927221	1.05	3.59E-01	4.51E-01	7.96	not significant
7441	PKN3	1.05	3.74E-01	4.66E-01	446.08	not significant
7442	ACO1	1.05	1.44E-01	2.09E-01	1459.03	not significant
7443	MRPL30	1.05	1.32E-01	1.94E-01	2291.00	not significant
7444	PDCL	1.05	2.18E-01	2.98E-01	1021.08	not significant
7445	TIAM2	1.05	4.46E-01	5.38E-01	243.07	not significant
7446	LYSMD2	1.05	3.03E-01	3.92E-01	676.49	not significant
7447	GZF1	1.05	2.63E-01	3.49E-01	761.53	not significant
7448	LRCH4	1.05	8.19E-02	1.28E-01	3641.80	not significant
7449	DTD1	1.05	4.14E-01	5.05E-01	10.32	not significant
7450	SUCO	1.05	1.01E-01	1.54E-01	1979.53	not significant
7451	ZNF19	1.05	5.29E-01	6.17E-01	29.91	not significant
7452	SRD5A3	1.05	3.63E-01	4.55E-01	413.56	not significant
7453	LRIT3	1.05	4.46E-01	5.38E-01	13.14	not significant
7454	KMT2E	1.05	3.01E-02	5.30E-02	5719.20	not significant
7455	HIF1AN	1.05	2.99E-02	5.26E-02	4784.57	not significant
7456	ETV2	1.05	4.82E-01	5.73E-01	17.76	not significant
7457	SHPRH	1.05	1.18E-01	1.76E-01	2646.28	not significant
7458	EXOC8	1.05	2.24E-01	3.05E-01	966.56	not significant
7459	GRIPAP1	1.05	1.85E-01	2.60E-01	1118.01	not significant
7460	TMEM9	1.05	2.29E-01	3.10E-01	835.05	not significant
7461	CDK11B	1.05	2.56E-01	3.40E-01	815.78	not significant
7462	PPP3CC	1.05	2.48E-01	3.32E-01	833.34	not significant
7463	OBSCN	1.05	1.67E-01	2.37E-01	2035.60	not significant
7464	NDFIP2	1.05	5.82E-02	9.49E-02	3326.77	not significant
7465	UNC5CL	1.05	5.35E-01	6.22E-01	107.83	not significant
7466	MYCBPAP	1.05	5.32E-01	6.20E-01	87.40	not significant
7467	IP6K1	1.05	1.09E-01	1.64E-01	1782.43	not significant
7468	ZNF45	1.05	2.05E-01	2.82E-01	1084.84	not significant

7469	SNRK	1.05	1.35E-01	1.97E-01	1458.67	not significant
7470	DAPK3	1.05	2.27E-01	3.08E-01	997.87	not significant
7471	AKR1A1	1.05	6.63E-02	1.06E-01	2744.41	not significant
7472	VCPIP1	1.05	1.41E-01	2.06E-01	1817.32	not significant
7473	SLC48A1	1.05	5.15E-01	6.04E-01	114.19	not significant
7474	GUSBP3	1.05	5.37E-01	6.25E-01	68.53	not significant
7475	C16orf46	1.05	5.35E-01	6.22E-01	73.42	not significant
7476	CREBL2	1.05	2.41E-01	3.24E-01	838.96	not significant
7477	TMEM218	1.05	2.74E-01	3.60E-01	629.52	not significant
7478	LPPR2	1.05	4.38E-01	5.30E-01	12.64	not significant
7479	ZNF845	1.05	3.12E-01	4.03E-01	527.07	not significant
7480	SCN9A	1.05	5.21E-02	8.62E-02	3551.86	not significant
7481	CA13	1.05	5.33E-01	6.21E-01	37.78	not significant
7482	REPS1	1.05	7.09E-02	1.13E-01	2789.67	not significant
7483	ZNF335	1.05	1.07E-01	1.61E-01	2295.52	not significant
7484	SEPSECS	1.05	2.15E-01	2.95E-01	868.13	not significant
7485	CLIP1	1.05	9.01E-02	1.39E-01	2438.17	not significant
7486	LOC101928767	1.05	5.37E-01	6.24E-01	62.90	not significant
7487	TSKS	1.05	4.51E-01	5.43E-01	224.67	not significant
7488	FAM168A	1.05	4.43E-02	7.46E-02	4001.16	not significant
7489	METAP1	1.05	4.40E-02	7.42E-02	4025.13	not significant
7490	TRAM2	1.05	9.70E-02	1.49E-01	1984.53	not significant
7491	PPFIA1	1.05	1.44E-01	2.09E-01	1517.24	not significant
7492	SCYL1	1.05	8.47E-02	1.32E-01	2287.20	not significant
7493	LOC101929767	1.05	5.28E-01	6.16E-01	83.71	not significant
7494	KIAA1731	1.05	1.29E-01	1.91E-01	1846.72	not significant
7495	FAM46C	1.05	4.36E-01	5.28E-01	14.15	not significant
7496	ZNF449	1.05	4.52E-01	5.44E-01	14.63	not significant
7497	NDUFS3	1.05	1.02E-01	1.56E-01	2555.10	not significant
7498	HMGN4	1.05	4.21E-02	7.13E-02	4748.51	not significant
7499	CMIP	1.05	3.17E-02	5.55E-02	4223.03	not significant
7500	ATP6V1F	1.05	8.56E-02	1.33E-01	2841.82	not significant
7501	LIX1L	1.05	3.91E-01	4.83E-01	354.35	not significant
7502	PEX3	1.05	2.97E-01	3.86E-01	560.08	not significant
7503	RIMKLA	1.05	5.00E-01	5.90E-01	26.51	not significant
7504	LINC00969	1.05	5.28E-01	6.16E-01	41.31	not significant
7505	BBC3	1.05	5.28E-01	6.16E-01	77.13	not significant
7506	PGRMC2	1.05	7.70E-02	1.21E-01	2713.61	not significant
7507	BCAP29	1.05	8.85E-02	1.37E-01	2184.10	not significant
7508	SLC2A4RG	1.05	2.52E-01	3.37E-01	741.62	not significant
7509	MAZ	1.05	4.03E-02	6.85E-02	21468.32	not significant
7510	TBC1D3P1-DHX4	1.05	5.20E-01	6.08E-01	35.11	not significant
7511	LOC389705	1.05	4.87E-01	5.77E-01	21.39	not significant
7512	TAF7	1.05	5.02E-02	8.34E-02	7259.17	not significant
7513	TOB2	1.05	1.78E-01	2.51E-01	1153.07	not significant
7514	FLT1	1.05	1.62E-01	2.31E-01	1174.21	not significant
7515	METTL21B	1.05	3.25E-01	4.16E-01	515.29	not significant
7516	BAHD1	1.05	1.73E-01	2.45E-01	1554.86	not significant
7517	TBC1D14	1.05	3.85E-02	6.59E-02	4204.55	not significant
7518	TMEM167B	1.05	9.38E-02	1.44E-01	1966.20	not significant
7519	SEMA3G	1.05	4.59E-01	5.50E-01	16.92	not significant
7520	NOXRED1	1.05	3.91E-01	4.83E-01	10.37	not significant
7521	PLXNB3	1.05	4.59E-01	5.50E-01	15.93	not significant
7522	LIMD1	1.05	3.37E-02	5.85E-02	3844.81	not significant
7523	LOC101928069	1.05	5.13E-01	6.01E-01	32.48	not significant
7524	CXorf56	1.05	2.21E-01	3.01E-01	904.69	not significant
7525	METTL21A	1.05	2.24E-01	3.05E-01	895.44	not significant
7526	SS18	1.05	8.46E-02	1.32E-01	3176.11	not significant
7527	CA8	1.05	4.53E-01	5.45E-01	182.52	not significant
7528	YTHDF3-AS1	1.05	4.90E-01	5.80E-01	22.67	not significant
7529	MX2	1.05	5.10E-01	5.98E-01	91.04	not significant
7530	TIAL1	1.05	2.87E-02	5.08E-02	5748.73	not significant
7531	FAM66D	1.05	4.50E-01	5.42E-01	15.98	not significant
7532	TPR	1.05	8.18E-02	1.28E-01	12375.73	not significant
7533	ZSCAN32	1.05	1.88E-01	2.62E-01	997.90	not significant
7534	GEMIN8	1.05	2.97E-01	3.86E-01	520.91	not significant
7535	PVT1	1.05	4.22E-01	5.14E-01	235.91	not significant
7536	ANKAR	1.05	5.23E-01	6.11E-01	50.61	not significant
7537	WDR45B	1.05	6.57E-02	1.06E-01	2284.17	not significant
7538	NCAPD2	1.05	1.17E-02	2.26E-02	19264.77	not significant
7539	MIR181A1HG	1.05	4.95E-01	5.85E-01	26.41	not significant
7540	RNASEH2A	1.05	1.23E-01	1.83E-01	2491.22	not significant
7541	C10orf88	1.05	3.14E-01	4.04E-01	527.99	not significant
7542	PGBD4	1.05	4.74E-01	5.65E-01	152.46	not significant
7543	NDE1	1.05	9.60E-02	1.47E-01	1968.49	not significant
7544	CLDN15	1.05	2.28E-01	3.09E-01	775.05	not significant
7545	MAML1	1.05	4.59E-02	7.71E-02	3688.12	not significant
7546	STON1	1.05	5.17E-01	6.05E-01	53.85	not significant
7547	LINC01436	1.05	4.97E-01	5.87E-01	109.82	not significant
7548	IVD	1.05	1.10E-01	1.66E-01	2102.89	not significant
7549	IRF9	1.05	3.90E-01	4.83E-01	284.58	not significant
7550	CDK4	1.05	2.58E-02	4.61E-02	7509.78	not significant
7551	BCRP3	1.05	3.55E-01	4.46E-01	8.51	not significant
7552	C19orf68	1.05	3.36E-01	4.27E-01	504.78	not significant
7553	PCSK7	1.05	9.39E-02	1.44E-01	1683.56	not significant
7554	NUBP2	1.05	7.21E-02	1.14E-01	2434.77	not significant
7555	ZNF292	1.05	9.34E-02	1.44E-01	3085.36	not significant
7556	LINC01125	1.05	4.14E-01	5.06E-01	12.49	not significant

7557	NANOS3	1.05	4.30E-01	5.22E-01	14.12	not significant
7558	TRPC3	1.05	5.10E-01	5.99E-01	38.02	not significant
7559	LINC00910	1.05	5.07E-01	5.97E-01	38.68	not significant
7560	FAM219A	1.05	2.58E-01	3.43E-01	648.73	not significant
7561	LOC100133331	1.05	5.16E-01	6.04E-01	50.17	not significant
7562	ARL8A	1.05	1.53E-01	2.21E-01	1152.77	not significant
7563	MAVS	1.05	3.44E-02	5.97E-02	6349.67	not significant
7564	S100A13	1.05	5.13E-01	6.02E-01	64.32	not significant
7565	LOC101927550	1.05	5.09E-01	5.98E-01	71.61	not significant
7566	PTPN2	1.05	4.55E-02	7.65E-02	2910.68	not significant
7567	STX6	1.05	8.51E-02	1.33E-01	2763.90	not significant
7568	TM9SF1	1.05	1.45E-01	2.10E-01	1253.15	not significant
7569	CEP104	1.05	6.78E-02	1.08E-01	2203.87	not significant
7570	ZNF337	1.05	1.94E-01	2.70E-01	975.54	not significant
7571	AQPEP	1.05	4.24E-01	5.16E-01	13.74	not significant
7572	TTF2	1.05	4.31E-02	7.28E-02	4698.53	not significant
7573	TGFB3	1.05	5.08E-01	5.97E-01	41.74	not significant
7574	PLEKHO1	1.05	1.88E-01	2.63E-01	960.54	not significant
7575	SNRNP200	1.05	7.74E-02	1.22E-01	20620.46	not significant
7576	MEX3C	1.05	6.63E-02	1.06E-01	3134.30	not significant
7577	ZNF573	1.05	4.95E-01	5.85E-01	91.57	not significant
7578	GUCY1B3	1.05	1.13E-01	1.69E-01	1438.79	not significant
7579	RPL36	1.05	2.84E-01	3.72E-01	15672.15	not significant
7580	TMEM243	1.05	1.76E-01	2.48E-01	929.33	not significant
7581	RFX8	1.05	4.92E-01	5.82E-01	148.00	not significant
7582	PEX19	1.05	7.45E-02	1.18E-01	2050.78	not significant
7583	S1PR2	1.05	5.08E-01	5.97E-01	64.18	not significant
7584	C3orf33	1.05	4.75E-01	5.66E-01	122.63	not significant
7585	HEXB	1.05	9.14E-02	1.41E-01	2005.03	not significant
7586	NABP1	1.05	3.00E-01	3.89E-01	472.08	not significant
7587	PHC3	1.05	3.86E-01	4.78E-01	2293.02	not significant
7588	DNM1P46	1.05	4.87E-01	5.77E-01	26.94	not significant
7589	COG1	1.05	1.48E-01	2.14E-01	1326.50	not significant
7590	RFC1	1.05	1.53E-02	2.88E-02	8068.57	not significant
7591	MOB1B	1.05	2.70E-02	4.80E-02	5432.66	not significant
7592	COPS3	1.05	2.52E-02	4.52E-02	5589.45	not significant
7593	TRIM26	1.05	3.28E-01	4.19E-01	417.51	not significant
7594	BTN3A3	1.05	1.60E-01	2.29E-01	1015.88	not significant
7595	E2F6	1.05	1.46E-01	2.11E-01	1058.12	not significant
7596	ASF1B	1.05	3.05E-02	5.36E-02	6159.90	not significant
7597	PRKCA	1.05	1.73E-02	3.22E-02	7984.71	not significant
7598	PARP15	1.05	4.59E-01	5.51E-01	149.61	not significant
7599	ZYG11B	1.05	2.44E-01	3.27E-01	747.13	not significant
7600	PLCD1	1.05	5.04E-01	5.94E-01	59.92	not significant
7601	R3HCC1	1.05	9.13E-02	1.41E-01	1704.56	not significant
7602	LEAP2	1.05	4.76E-01	5.67E-01	25.93	not significant
7603	STX12	1.05	2.29E-01	3.10E-01	661.86	not significant
7604	LTBP3	1.05	4.95E-01	5.85E-01	93.15	not significant
7605	PANX1	1.05	1.00E-01	1.53E-01	1442.17	not significant
7606	EXO1	1.05	3.96E-02	6.75E-02	3841.93	not significant
7607	FAM204A	1.05	1.17E-01	1.74E-01	1283.35	not significant
7608	DTX4	1.05	3.64E-01	4.56E-01	10.44	not significant
7609	ZNF513	1.05	3.85E-01	4.77E-01	254.12	not significant
7610	RSBN1	1.05	8.56E-02	1.33E-01	1854.09	not significant
7611	WDR26	1.05	3.25E-02	5.67E-02	5498.72	not significant
7612	HS3ST3B1	1.05	3.62E-01	4.55E-01	10.53	not significant
7613	RCAN3	1.05	1.69E-01	2.41E-01	1075.23	not significant
7614	E2F3	1.05	2.85E-02	5.04E-02	3598.67	not significant
7615	SPECC1L	1.05	1.27E-01	1.88E-01	1261.24	not significant
7616	NPB	1.05	3.91E-01	4.84E-01	14.25	not significant
7617	TCAIM	1.05	1.24E-01	1.84E-01	1264.40	not significant
7618	CLK2P	1.05	4.11E-01	5.03E-01	14.27	not significant
7619	LOC103344931	1.05	3.34E-01	4.26E-01	343.43	not significant
7620	SAMD15	1.05	3.35E-01	4.26E-01	9.85	not significant
7621	ALG9	1.05	2.52E-01	3.36E-01	555.88	not significant
7622	CCDC30	1.05	3.88E-01	4.80E-01	12.22	not significant
7623	ZC3H6	1.05	2.69E-01	3.55E-01	569.30	not significant
7624	PBX3	1.05	1.75E-01	2.47E-01	845.69	not significant
7625	UPF3A	1.05	1.75E-01	2.48E-01	886.87	not significant
7626	INVS	1.05	2.57E-01	3.42E-01	546.68	not significant
7627	EHMT1	1.05	4.82E-02	8.04E-02	2648.43	not significant
7628	DLEU7-AS1	1.05	3.22E-01	4.13E-01	9.26	not significant
7629	ZNF25	1.05	3.83E-01	4.75E-01	245.65	not significant
7630	CRELD1	1.05	3.95E-01	4.87E-01	236.32	not significant
7631	F8	1.05	4.79E-01	5.70E-01	33.86	not significant
7632	CCDC106	1.05	3.43E-01	4.34E-01	344.53	not significant
7633	FTX	1.05	4.57E-01	5.49E-01	24.88	not significant
7634	MAPK8	1.05	1.99E-02	3.64E-02	4224.63	not significant
7635	TBCA	1.06	4.48E-02	7.54E-02	4131.44	not significant
7636	INTS6-AS1	1.06	4.78E-01	5.69E-01	31.25	not significant
7637	TMPRSS5	1.06	3.65E-01	4.57E-01	11.13	not significant
7638	DGCR2	1.06	6.43E-02	1.04E-01	2508.76	not significant
7639	ZNF429	1.06	3.23E-01	4.14E-01	383.56	not significant
7640	EPS15	1.06	3.10E-02	5.43E-02	3275.87	not significant
7641	DPF1	1.06	4.60E-01	5.51E-01	129.33	not significant
7642	BRCA1	1.06	1.47E-02	2.78E-02	5261.44	not significant
7643	PNPLA6	1.06	7.59E-02	1.20E-01	2307.18	not significant
7644	LRRC37A	1.06	4.06E-01	4.97E-01	15.98	not significant

7645	NOL9	1.06	1.73E-01	2.45E-01	1037.18	not significant
7646	SPAG1	1.06	2.50E-01	3.34E-01	531.72	not significant
7647	COX15	1.06	5.84E-02	9.52E-02	2028.77	not significant
7648	BZRAP1-AS1	1.06	1.88E-01	2.63E-01	805.16	not significant
7649	SIK3	1.06	1.78E-01	2.50E-01	1128.12	not significant
7650	RASA3	1.06	4.22E-02	7.14E-02	3599.63	not significant
7651	KLHL5	1.06	1.33E-01	1.95E-01	1104.49	not significant
7652	LOC100130691	1.06	4.83E-01	5.73E-01	37.85	not significant
7653	SAP30	1.06	2.05E-01	2.83E-01	850.94	not significant
7654	DSCR3	1.06	3.08E-02	5.40E-02	3437.50	not significant
7655	NMI	1.06	4.01E-02	6.82E-02	2800.27	not significant
7656	SAP30L-AS1	1.06	3.29E-01	4.20E-01	9.08	not significant
7657	GLG1	1.06	3.85E-02	6.59E-02	3107.03	not significant
7658	ZNF347	1.06	1.28E-01	1.89E-01	1138.33	not significant
7659	SSR1	1.06	8.51E-03	1.69E-02	8941.48	not significant
7660	POLA2	1.06	2.60E-02	4.64E-02	3214.82	not significant
7661	TCTE3	1.06	3.32E-01	4.24E-01	9.63	not significant
7662	SMAD2	1.06	1.95E-02	3.59E-02	4336.76	not significant
7663	CFAP36	1.06	2.29E-01	3.11E-01	607.41	not significant
7664	GOPC	1.06	3.06E-02	5.38E-02	2842.18	not significant
7665	SLC43A3	1.06	8.94E-03	1.77E-02	7944.62	not significant
7666	ESYT2	1.06	4.80E-03	1.01E-02	13049.21	not significant
7667	TTC3	1.06	7.22E-03	1.46E-02	8160.05	not significant
7668	DUS1L	1.06	1.37E-02	2.61E-02	5021.77	not significant
7669	SRBD1	1.06	6.84E-02	1.09E-01	1987.86	not significant
7670	TM2D1	1.06	2.34E-01	3.15E-01	592.90	not significant
7671	KIF26B	1.06	3.43E-01	4.34E-01	10.27	not significant
7672	AGPAT6	1.06	3.16E-02	5.53E-02	3331.79	not significant
7673	PJA2	1.06	1.37E-02	2.62E-02	5134.40	not significant
7674	RAB11A	1.06	5.94E-02	9.67E-02	3824.38	not significant
7675	SKIDA1	1.06	4.45E-01	5.37E-01	24.07	not significant
7676	CISD2	1.06	1.35E-01	1.98E-01	980.39	not significant
7677	CACNA2D4	1.06	4.77E-01	5.68E-01	42.90	not significant
7678	ZNF225	1.06	3.74E-01	4.66E-01	256.11	not significant
7679	CNOT4	1.06	1.44E-01	2.10E-01	944.08	not significant
7680	YTHDC2	1.06	8.73E-02	1.36E-01	2552.50	not significant
7681	STOML1	1.06	3.61E-01	4.53E-01	273.74	not significant
7682	PRRC1	1.06	3.00E-02	5.28E-02	3273.03	not significant
7683	CTU1	1.06	3.20E-01	4.11E-01	346.22	not significant
7684	TRIM36	1.06	3.82E-01	4.74E-01	235.96	not significant
7685	FBXO44	1.06	1.02E-01	1.55E-01	1420.83	not significant
7686	BLZF1	1.06	2.45E-01	3.29E-01	581.38	not significant
7687	NUP62CL	1.06	4.60E-01	5.52E-01	30.91	not significant
7688	THOP1	1.06	3.89E-02	6.65E-02	3065.14	not significant
7689	CDC25C	1.06	2.78E-01	3.65E-01	526.12	not significant
7690	LOC728554	1.06	3.43E-01	4.34E-01	296.19	not significant
7691	ZC3H8	1.06	1.02E-01	1.56E-01	1505.40	not significant
7692	LOC100133985	1.06	3.56E-01	4.48E-01	14.72	not significant
7693	CD3G	1.06	1.34E-02	2.57E-02	6196.01	not significant
7694	SLC31A2	1.06	4.15E-01	5.06E-01	183.77	not significant
7695	RHOT2	1.06	7.91E-02	1.24E-01	2635.71	not significant
7696	CPTP	1.06	3.09E-01	4.00E-01	389.39	not significant
7697	SCML2	1.06	4.86E-02	8.10E-02	2102.08	not significant
7698	MFF	1.06	3.47E-02	6.00E-02	2567.64	not significant
7699	CYP4F22	1.06	3.32E-01	4.23E-01	10.61	not significant
7700	HHLA3	1.06	4.07E-01	4.99E-01	172.92	not significant
7701	ANKRD13B	1.06	2.14E-01	2.93E-01	725.47	not significant
7702	HECTD2	1.06	4.74E-01	5.65E-01	68.44	not significant
7703	FLJ37201	1.06	3.79E-01	4.70E-01	13.57	not significant
7704	JADE3	1.06	4.20E-01	5.12E-01	158.75	not significant
7705	C11orf80	1.06	2.14E-01	2.93E-01	602.76	not significant
7706	MRPS25	1.06	3.90E-02	6.66E-02	2539.94	not significant
7707	BET1	1.06	1.69E-01	2.40E-01	849.70	not significant
7708	CBLL1	1.06	2.87E-02	5.07E-02	2758.66	not significant
7709	ZNF165	1.06	3.62E-01	4.54E-01	12.20	not significant
7710	BTF3	1.06	4.05E-02	6.88E-02	20247.97	not significant
7711	MAP3K10	1.06	2.50E-01	3.34E-01	606.01	not significant
7712	EXOC3	1.06	7.03E-02	1.12E-01	1822.06	not significant
7713	ICAM1	1.06	3.99E-01	4.91E-01	192.76	not significant
7714	PHF20	1.06	1.50E-02	2.82E-02	3800.09	not significant
7715	TIGD3	1.06	4.74E-01	5.65E-01	50.22	not significant
7716	ZNF383	1.06	3.69E-01	4.61E-01	238.58	not significant
7717	HMHA1	1.06	7.09E-03	1.44E-02	9281.35	not significant
7718	FAM122A	1.06	2.11E-01	2.90E-01	598.12	not significant
7719	EIF3K	1.06	2.89E-02	5.11E-02	5084.35	not significant
7720	TRPC1	1.06	4.13E-01	5.05E-01	18.81	not significant
7721	PTPLAD1	1.06	8.22E-03	1.64E-02	6899.84	not significant
7722	SLC25A15	1.06	6.19E-02	1.00E-01	2128.65	not significant
7723	ZMAT2	1.06	4.45E-02	7.49E-02	3483.55	not significant
7724	HPRT1	1.06	2.04E-02	3.73E-02	3878.73	not significant
7725	CHSY1	1.06	3.50E-02	6.04E-02	2992.58	not significant
7726	MAP3K6	1.06	3.63E-01	4.55E-01	12.84	not significant
7727	MCF2L	1.06	3.97E-01	4.89E-01	16.89	not significant
7728	CCDC62	1.06	4.64E-01	5.56E-01	37.30	not significant
7729	CDK5RAP2	1.06	4.28E-02	7.23E-02	3189.57	not significant
7730	ZFYVE20	1.06	1.93E-01	2.69E-01	659.07	not significant
7731	C22orf46	1.06	1.33E-01	1.95E-01	1055.77	not significant
7732	OTUD3	1.06	1.53E-01	2.20E-01	1045.86	not significant

7733	RNF208	1.06	3.78E-01	4.70E-01	14.31	not significant
7734	LKAAEAR1	1.06	3.17E-01	4.07E-01	10.83	not significant
7735	FNBP1	1.06	5.07E-03	1.06E-02	9086.53	not significant
7736	TBC1D10B	1.06	3.76E-02	6.45E-02	3357.83	not significant
7737	SPATA5	1.06	1.18E-01	1.76E-01	1055.60	not significant
7738	DTL	1.06	3.53E-03	7.63E-03	7204.49	not significant
7739	WDR35	1.06	4.01E-01	4.93E-01	173.95	not significant
7740	PIP5KL1	1.06	3.64E-01	4.56E-01	13.49	not significant
7741	ASPHD2	1.06	3.74E-01	4.66E-01	204.52	not significant
7742	PTHLH	1.06	3.53E-01	4.45E-01	12.38	not significant
7743	C15orf61	1.06	3.45E-01	4.36E-01	290.17	not significant
7744	RHBDD2	1.06	3.22E-01	4.13E-01	331.94	not significant
7745	ZNF440	1.06	3.29E-01	4.20E-01	280.83	not significant
7746	ARID4A	1.06	7.15E-02	1.14E-01	1623.28	not significant
7747	C17orf96	1.06	3.07E-01	3.97E-01	341.74	not significant
7748	PPME1	1.06	6.68E-02	1.07E-01	1678.78	not significant
7749	MCC	1.06	3.28E-01	4.19E-01	285.57	not significant
7750	NEK4	1.06	9.62E-02	1.47E-01	1310.17	not significant
7751	LRP2BP	1.06	4.48E-01	5.40E-01	31.63	not significant
7752	ZNF702P	1.06	3.53E-01	4.45E-01	259.08	not significant
7753	MTL5	1.06	4.55E-01	5.46E-01	82.36	not significant
7754	FAM179A	1.06	3.65E-01	4.57E-01	205.03	not significant
7755	CCNDBP1	1.06	1.12E-01	1.68E-01	1080.70	not significant
7756	ABI2	1.06	5.46E-03	1.13E-02	7745.84	not significant
7757	COPA	1.06	4.42E-03	9.38E-03	7489.00	not significant
7758	LOC407835	1.06	4.53E-01	5.45E-01	36.05	not significant
7759	TBC1D2	1.06	4.36E-01	5.29E-01	27.25	not significant
7760	SYVN1	1.06	6.64E-02	1.07E-01	1726.92	not significant
7761	RIF1	1.06	3.42E-02	5.94E-02	6405.99	not significant
7762	TRMT11	1.06	1.85E-01	2.59E-01	760.73	not significant
7763	TRAPPC10	1.06	5.41E-02	8.92E-02	2255.29	not significant
7764	ZNF692	1.06	2.34E-01	3.15E-01	754.23	not significant
7765	REPIN1	1.06	1.76E-02	3.27E-02	4970.27	not significant
7766	ATP7A	1.06	4.11E-01	5.03E-01	138.15	not significant
7767	TMEM30A	1.06	9.35E-03	1.85E-02	5020.66	not significant
7768	INPP5F	1.06	1.70E-01	2.41E-01	694.94	not significant
7769	MED20	1.06	6.35E-02	1.02E-01	1662.13	not significant
7770	KIAA1715	1.06	4.74E-02	7.92E-02	2176.42	not significant
7771	RASGRP1	1.06	1.42E-02	2.69E-02	4145.81	not significant
7772	MTMR12	1.06	4.92E-02	8.19E-02	1932.32	not significant
7773	FXR2	1.06	4.10E-02	6.95E-02	1971.44	not significant
7774	LINC00884	1.06	4.32E-01	5.24E-01	26.40	not significant
7775	CCDC43	1.06	8.48E-02	1.32E-01	1363.78	not significant
7776	PLEKHA2	1.06	1.28E-02	2.45E-02	7585.50	not significant
7777	MID1	1.06	4.20E-01	5.12E-01	22.70	not significant
7778	SEMA6A-AS1	1.06	3.89E-01	4.81E-01	17.04	not significant
7779	SLC25A4	1.06	3.94E-01	4.86E-01	162.42	not significant
7780	FBXL8	1.06	4.52E-01	5.44E-01	93.97	not significant
7781	ALS2	1.06	1.06E-01	1.61E-01	1081.72	not significant
7782	KDM2A	1.06	1.68E-02	3.14E-02	4845.68	not significant
7783	ZCCHC8	1.06	5.61E-02	9.19E-02	1926.32	not significant
7784	CLCN3	1.06	9.50E-03	1.87E-02	4924.47	not significant
7785	KLHDC8B	1.06	3.28E-01	4.19E-01	11.98	not significant
7786	D2HGDH	1.06	2.06E-01	2.83E-01	691.47	not significant
7787	LZTFL1	1.06	2.45E-01	3.28E-01	3341.09	not significant
7788	ARFGAP1	1.06	2.87E-02	5.08E-02	3533.41	not significant
7789	STK25	1.06	1.79E-02	3.32E-02	3144.73	not significant
7790	KIFAP3	1.06	9.40E-02	1.45E-01	1142.47	not significant
7791	ZFPL1	1.06	1.95E-01	2.71E-01	608.17	not significant
7792	PAXIP1-AS1	1.06	4.36E-01	5.28E-01	396.60	not significant
7793	FOXO1	1.06	3.03E-01	3.92E-01	10.41	not significant
7794	CHIC1	1.06	2.88E-01	3.76E-01	365.58	not significant
7795	FNTA	1.06	2.30E-02	4.16E-02	2573.98	not significant
7796	RHOT1	1.06	2.67E-02	4.75E-02	2419.85	not significant
7797	GTPBP8	1.06	1.65E-01	2.36E-01	809.19	not significant
7798	HIST1H2BD	1.06	4.39E-01	5.31E-01	89.21	not significant
7799	MTCH1	1.06	4.92E-03	1.03E-02	7386.64	not significant
7800	SEPT7-AS1	1.06	3.83E-01	4.75E-01	16.93	not significant
7801	PSKH1	1.06	7.38E-02	1.17E-01	1368.77	not significant
7802	MUT	1.06	1.05E-01	1.60E-01	1128.66	not significant
7803	SAMD13	1.06	3.94E-01	4.86E-01	164.05	not significant
7804	KLHL15	1.06	9.16E-02	1.41E-01	1178.48	not significant
7805	TOR3A	1.06	5.96E-02	9.70E-02	2708.46	not significant
7806	PAQR7	1.06	4.47E-01	5.39E-01	47.44	not significant
7807	CDC42SE2	1.06	4.50E-03	9.54E-03	10555.89	not significant
7808	PPP2R3C	1.06	6.19E-02	1.00E-01	1585.90	not significant
7809	PDZD4	1.06	4.14E-01	5.05E-01	23.05	not significant
7810	GPT2	1.06	1.62E-01	2.32E-01	733.50	not significant
7811	HERC2	1.06	9.25E-02	1.43E-01	2020.15	not significant
7812	RABL2B	1.06	4.46E-01	5.38E-01	41.77	not significant
7813	POGLUT1	1.06	1.05E-01	1.60E-01	1107.46	not significant
7814	AKAP8L	1.06	3.55E-02	6.12E-02	2423.27	not significant
7815	ANTXR1	1.06	4.13E-02	7.00E-02	1914.99	not significant
7816	HEG1	1.06	6.24E-02	1.01E-01	1478.57	not significant
7817	TMEM217	1.06	2.33E-01	3.14E-01	452.73	not significant
7818	PIM1	1.06	3.61E-03	7.79E-03	6376.33	not significant
7819	TPCN2	1.06	2.27E-01	3.08E-01	469.95	not significant
7820	FAM177A1	1.06	2.23E-01	3.03E-01	473.60	not significant

7821	MAT2B	1.06	1.54E-02	2.90E-02	3795.61	not significant
7822	CDKL3	1.06	4.35E-01	5.27E-01	87.03	not significant
7823	WDPCP	1.06	3.39E-01	4.30E-01	233.03	not significant
7824	ARNTL2	1.06	5.74E-02	9.38E-02	1776.31	not significant
7825	PEX14	1.06	1.10E-01	1.66E-01	996.69	not significant
7826	UBXN7	1.06	9.57E-02	1.47E-01	1525.24	not significant
7827	TMEM208	1.06	1.83E-01	2.57E-01	962.78	not significant
7828	CSTF2T	1.06	1.91E-02	3.51E-02	3024.70	not significant
7829	MIER3	1.06	9.19E-02	1.42E-01	1198.84	not significant
7830	ZNF568	1.06	3.26E-01	4.17E-01	239.39	not significant
7831	SSX2IP	1.06	6.87E-02	1.10E-01	1285.89	not significant
7832	ACY3	1.06	4.27E-01	5.19E-01	88.76	not significant
7833	ZNF324	1.06	2.57E-01	3.42E-01	421.82	not significant
7834	ASF1A	1.06	2.30E-02	4.16E-02	2949.32	not significant
7835	ZNF382	1.06	2.60E-01	3.45E-01	444.97	not significant
7836	GLTSCR1	1.06	1.52E-01	2.19E-01	714.44	not significant
7837	EMC10	1.06	5.70E-02	9.32E-02	2935.92	not significant
7838	ZNF622	1.06	1.16E-01	1.74E-01	964.41	not significant
7839	SUV420H2	1.06	1.29E-01	1.91E-01	813.19	not significant
7840	TAF1L	1.06	2.92E-01	3.80E-01	10.88	not significant
7841	PCDHGB3	1.06	3.00E-01	3.89E-01	9.98	not significant
7842	DLGAP4	1.06	7.20E-02	1.14E-01	1315.41	not significant
7843	PRKAR2A-AS1	1.06	3.52E-01	4.44E-01	15.53	not significant
7844	MGC16142	1.06	4.06E-01	4.98E-01	24.46	not significant
7845	MTMR8	1.06	3.93E-01	4.85E-01	130.20	not significant
7846	PWAR5	1.06	3.92E-01	4.84E-01	146.01	not significant
7847	UBAP1L	1.06	3.92E-01	4.84E-01	23.27	not significant
7848	ATAD5	1.06	4.37E-02	7.37E-02	3418.97	not significant
7849	LOXL2	1.06	4.39E-01	5.31E-01	54.06	not significant
7850	LOC93622	1.06	8.44E-02	1.32E-01	1193.23	not significant
7851	CASK	1.06	1.28E-01	1.90E-01	805.55	not significant
7852	TAOK1	1.06	3.56E-02	6.14E-02	4051.23	not significant
7853	CDKN2A	1.06	1.50E-01	2.17E-01	789.87	not significant
7854	ZNF829	1.06	2.81E-01	3.69E-01	308.15	not significant
7855	C1orf27	1.06	9.43E-02	1.45E-01	1027.86	not significant
7856	SIPA1	1.06	1.54E-01	2.21E-01	668.12	not significant
7857	BMP2K	1.06	6.31E-02	1.02E-01	1457.84	not significant
7858	SARDH	1.06	4.20E-01	5.12E-01	93.19	not significant
7859	FPGS	1.06	5.06E-02	8.40E-02	1660.72	not significant
7860	TXNDC16	1.06	1.14E-01	1.71E-01	882.05	not significant
7861	BIN2	1.06	4.33E-02	7.32E-02	1815.18	not significant
7862	TTC9	1.06	1.66E-01	2.36E-01	621.01	not significant
7863	NARFL	1.06	1.26E-01	1.86E-01	800.86	not significant
7864	ITM2A	1.06	3.39E-03	7.35E-03	9448.64	not significant
7865	DAK	1.06	1.28E-01	1.89E-01	769.96	not significant
7866	ACBD5	1.06	7.92E-02	1.24E-01	1244.23	not significant
7867	TMED7	1.06	4.93E-02	8.20E-02	1534.29	not significant
7868	PRKAB2	1.06	4.24E-01	5.16E-01	41.42	not significant
7869	C6orf147	1.06	3.69E-01	4.61E-01	161.97	not significant
7870	LPIN2	1.06	1.44E-02	2.73E-02	3124.28	not significant
7871	FBXW2	1.06	2.57E-02	4.59E-02	2981.06	not significant
7872	KATNBL1	1.06	1.13E-01	1.69E-01	866.56	not significant
7873	GFPT2	1.06	4.25E-01	5.17E-01	35.32	not significant
7874	CD226	1.06	3.33E-01	4.24E-01	218.57	not significant
7875	DNAH6	1.06	3.84E-01	4.76E-01	19.60	not significant
7876	TASP1	1.06	1.46E-01	2.11E-01	772.71	not significant
7877	DLG2	1.06	2.70E-01	3.56E-01	8.92	not significant
7878	RFWD3	1.06	2.83E-03	6.23E-03	7631.42	not significant
7879	OBFC1	1.06	4.01E-02	6.83E-02	1650.35	not significant
7880	NPR3	1.06	2.84E-01	3.72E-01	10.45	not significant
7881	NEU3	1.06	7.47E-02	1.18E-01	1576.71	not significant
7882	CXXC1	1.06	3.02E-02	5.31E-02	2686.94	not significant
7883	COL7A1	1.06	4.28E-01	5.20E-01	403.70	not significant
7884	EIF3G	1.06	5.81E-03	1.20E-02	5860.68	not significant
7885	IFT172	1.06	2.93E-01	3.82E-01	316.10	not significant
7886	FAM53A	1.06	4.28E-01	5.21E-01	47.28	not significant
7887	PLXNA1	1.06	3.59E-02	6.18E-02	2495.51	not significant
7888	CNEP1R1	1.06	1.44E-01	2.10E-01	738.58	not significant
7889	KCTD19	1.06	2.87E-01	3.75E-01	280.42	not significant
7890	KDM7A	1.06	1.10E-01	1.65E-01	860.48	not significant
7891	FAM169A	1.06	4.41E-02	7.44E-02	2105.76	not significant
7892	FAM109A	1.06	3.88E-01	4.80E-01	131.82	not significant
7893	ZNF599	1.06	3.54E-01	4.46E-01	168.56	not significant
7894	KIAA1257	1.06	3.48E-01	4.39E-01	15.44	not significant
7895	TINAGL1	1.06	4.20E-01	5.12E-01	41.44	not significant
7896	LOC554206	1.06	3.80E-01	4.72E-01	22.56	not significant
7897	MRPL34	1.06	6.70E-02	1.07E-01	1770.62	not significant
7898	AKT3	1.07	6.03E-02	9.79E-02	1529.28	not significant
7899	ESYT3	1.07	4.18E-01	5.10E-01	41.65	not significant
7900	CMC4	1.07	4.12E-01	5.04E-01	34.70	not significant
7901	KCTD2	1.07	4.51E-02	7.58E-02	2394.48	not significant
7902	SND1	1.07	1.68E-03	3.84E-03	11219.45	not significant
7903	TMEM115	1.07	1.16E-01	1.73E-01	940.26	not significant
7904	GSE1	1.07	1.97E-02	3.62E-02	5889.18	not significant
7905	PGAM2	1.07	2.38E-01	3.21E-01	8.77	not significant
7906	CELF2	1.07	1.08E-02	2.11E-02	9803.83	not significant
7907	NDUFV2-AS1	1.07	3.11E-01	4.01E-01	13.16	not significant
7908	BCL11B	1.07	3.18E-03	6.93E-03	9597.09	not significant

7909	ZMYND8	1.07	8.80E-02	1.37E-01	1041.36	not significant
7910	FANCB	1.07	2.06E-01	2.84E-01	481.51	not significant
7911	AAMDC	1.07	3.81E-01	4.73E-01	125.99	not significant
7912	CD99L2	1.07	2.87E-01	3.75E-01	293.23	not significant
7913	RGS2	1.07	3.93E-01	4.85E-01	111.55	not significant
7914	KCTD17	1.07	2.11E-01	2.89E-01	431.25	not significant
7915	DLL3	1.07	4.19E-01	5.10E-01	45.90	not significant
7916	SLC11A2	1.07	3.70E-02	6.35E-02	2424.19	not significant
7917	FLT3	1.07	3.93E-01	4.85E-01	27.02	not significant
7918	DCAF17	1.07	2.99E-02	5.26E-02	1828.25	not significant
7919	ACVR1B	1.07	3.02E-02	5.31E-02	1893.72	not significant
7920	L3HYPDH	1.07	3.83E-01	4.75E-01	116.07	not significant
7921	ZFPM2	1.07	3.92E-01	4.84E-01	105.87	not significant
7922	CAPN7	1.07	4.28E-02	7.22E-02	1648.35	not significant
7923	ATP5D	1.07	2.46E-01	3.30E-01	2358.30	not significant
7924	NFIA	1.07	2.90E-01	3.78E-01	11.04	not significant
7925	ZKSCAN7	1.07	3.58E-01	4.50E-01	147.72	not significant
7926	NAIF1	1.07	1.74E-01	2.46E-01	552.81	not significant
7927	WDR76	1.07	1.36E-02	2.60E-02	2663.31	not significant
7928	POLD3	1.07	1.31E-02	2.50E-02	2760.33	not significant
7929	OTUD4	1.07	3.26E-02	5.69E-02	2669.98	not significant
7930	JMJD7	1.07	4.08E-01	4.99E-01	84.31	not significant
7931	MST1L	1.07	3.34E-01	4.25E-01	15.18	not significant
7932	BDH1	1.07	5.84E-02	9.52E-02	1279.41	not significant
7933	B3GALNT2	1.07	2.66E-02	4.74E-02	2101.98	not significant
7934	MDGA1	1.07	3.98E-01	4.90E-01	92.80	not significant
7935	MGST3	1.07	1.87E-01	2.62E-01	465.27	not significant
7936	TSN	1.07	6.11E-03	1.26E-02	4543.40	not significant
7937	TMEM67	1.07	2.28E-01	3.10E-01	374.07	not significant
7938	ZNF559	1.07	1.53E-01	2.20E-01	611.26	not significant
7939	AUP1	1.07	1.60E-02	3.00E-02	4017.07	not significant
7940	FBXO30	1.07	1.30E-01	1.91E-01	758.24	not significant
7941	TM7SF3	1.07	1.43E-03	3.33E-03	11494.29	not significant
7942	LINC00476	1.07	3.21E-01	4.12E-01	204.07	not significant
7943	SLC46A3	1.07	1.09E-01	1.64E-01	836.16	not significant
7944	CBX3P2	1.07	4.07E-01	4.99E-01	37.09	not significant
7945	CENPM	1.07	2.26E-02	4.09E-02	2626.10	not significant
7946	ANKRD49	1.07	1.57E-01	2.26E-01	774.10	not significant
7947	TRMT2B	1.07	3.82E-02	6.54E-02	1644.00	not significant
7948	ACTR5	1.07	1.31E-01	1.92E-01	673.72	not significant
7949	ZNF423	1.07	4.19E-02	7.09E-02	1762.33	not significant
7950	H3F3C	1.07	4.10E-01	5.02E-01	50.15	not significant
7951	PRC1	1.07	7.32E-03	1.48E-02	3275.77	not significant
7952	SMCR8	1.07	1.63E-02	3.05E-02	2568.12	not significant
7953	DHX8	1.07	1.48E-02	2.80E-02	2647.95	not significant
7954	SLC16A10	1.07	2.40E-01	3.22E-01	407.32	not significant
7955	SLC8A1	1.07	3.53E-01	4.45E-01	157.81	not significant
7956	PI4K2B	1.07	1.70E-02	3.17E-02	2657.47	not significant
7957	IL11RA	1.07	3.43E-01	4.34E-01	173.37	not significant
7958	WASH2P	1.07	3.94E-01	4.86E-01	96.68	not significant
7959	TMEM120A	1.07	2.94E-01	3.83E-01	227.80	not significant
7960	PLEKHA3	1.07	1.48E-01	2.15E-01	615.76	not significant
7961	RANBP10	1.07	2.11E-02	3.86E-02	1987.92	not significant
7962	FBXO7	1.07	1.84E-02	3.40E-02	3918.14	not significant
7963	C8orf59	1.07	4.01E-02	6.82E-02	1719.07	not significant
7964	C18orf54	1.07	1.67E-01	2.38E-01	574.32	not significant
7965	ARHGEF9	1.07	3.33E-01	4.24E-01	170.39	not significant
7966	OXCT1	1.07	1.49E-02	2.81E-02	4788.92	not significant
7967	CDC42SE1	1.07	5.07E-03	1.06E-02	3673.60	not significant
7968	IL6ST	1.07	1.54E-01	2.21E-01	714.28	not significant
7969	TM9SF3	1.07	1.98E-03	4.47E-03	7809.68	not significant
7970	STARD4-AS1	1.07	4.08E-01	4.99E-01	54.25	not significant
7971	LOC100129148	1.07	3.98E-01	4.90E-01	53.72	not significant
7972	SMG5	1.07	3.21E-03	7.00E-03	5867.61	not significant
7973	LSM2	1.07	7.01E-02	1.12E-01	1020.72	not significant
7974	LOC729970	1.07	3.26E-01	4.17E-01	18.57	not significant
7975	CTBP1-AS	1.07	3.74E-01	4.66E-01	34.16	not significant
7976	PCDHGB1	1.07	3.07E-01	3.97E-01	13.49	not significant
7977	ZNF557	1.07	1.82E-01	2.55E-01	452.92	not significant
7978	PLEKHF1	1.07	1.43E-01	2.08E-01	586.79	not significant
7979	FBXW4P1	1.07	3.84E-01	4.76E-01	29.38	not significant
7980	SLC7A3	1.07	4.03E-01	4.95E-01	46.92	not significant
7981	XIAP	1.07	3.80E-02	6.51E-02	2442.64	not significant
7982	KDM6B	1.07	7.40E-02	1.17E-01	1173.80	not significant
7983	SHPK	1.07	1.06E-01	1.61E-01	784.22	not significant
7984	RNASET2	1.07	9.89E-02	1.51E-01	816.08	not significant
7985	ENTPD1	1.07	2.96E-01	3.85E-01	12.89	not significant
7986	AFF4	1.07	2.52E-02	4.52E-02	3875.06	not significant
7987	LINC00337	1.07	3.11E-01	4.01E-01	13.87	not significant
7988	PTPRF	1.07	3.95E-01	4.87E-01	74.40	not significant
7989	CTNNAL1	1.07	5.50E-02	9.05E-02	1381.25	not significant
7990	LOC101927572	1.07	4.00E-01	4.92E-01	50.89	not significant
7991	SYNE2	1.07	2.39E-01	3.22E-01	6887.37	not significant
7992	EMILIN1	1.07	3.69E-01	4.61E-01	27.21	not significant
7993	ZNF7	1.07	1.30E-01	1.92E-01	785.43	not significant
7994	TUBD1	1.07	1.80E-01	2.54E-01	460.46	not significant
7995	ARHGAP31	1.07	3.96E-01	4.88E-01	41.04	not significant
7996	CDCA7	1.07	1.17E-03	2.76E-03	11288.48	not significant

7997	ALCAM	1.07	1.11E-01	1.67E-01	737.68	not significant
7998	HECTD4	1.07	2.86E-01	3.74E-01	3694.85	not significant
7999	ZFAND3	1.07	1.06E-02	2.06E-02	2951.51	not significant
8000	MGAT5	1.07	1.19E-02	2.29E-02	3076.00	not significant
8001	PAPOLG	1.07	4.35E-02	7.34E-02	1445.43	not significant
8002	PSTK	1.07	3.25E-01	4.16E-01	189.26	not significant
8003	TBC1D22A	1.07	6.24E-02	1.01E-01	1144.03	not significant
8004	LOC100129518	1.07	3.95E-01	4.87E-01	42.36	not significant
8005	DBH-AS1	1.07	3.97E-01	4.89E-01	57.34	not significant
8006	USP30	1.07	9.82E-02	1.50E-01	879.62	not significant
8007	MED29	1.07	3.60E-02	6.20E-02	1577.00	not significant
8008	GPR158	1.07	3.58E-01	4.50E-01	23.42	not significant
8009	HMBOX1	1.07	1.23E-01	1.83E-01	749.51	not significant
8010	STARD7-AS1	1.07	3.36E-01	4.27E-01	149.44	not significant
8011	APLP2	1.07	2.76E-03	6.07E-03	6323.22	not significant
8012	SEC22A	1.07	1.57E-01	2.25E-01	497.57	not significant
8013	TRAF3	1.07	6.40E-03	1.31E-02	4499.70	not significant
8014	ZNF197	1.07	5.05E-02	8.39E-02	1339.55	not significant
8015	TSHR	1.07	2.23E-02	4.04E-02	1711.94	not significant
8016	CSNK2B	1.07	7.33E-03	1.48E-02	2885.78	not significant
8017	NUTM2A	1.07	3.10E-01	4.00E-01	16.28	not significant
8018	ETS1	1.07	6.14E-04	1.53E-03	20603.79	not significant
8019	FAM217B	1.07	8.19E-03	1.64E-02	4023.73	not significant
8020	EXTL3	1.07	1.25E-02	2.40E-02	2799.48	not significant
8021	SELO	1.07	1.62E-01	2.32E-01	770.56	not significant
8022	CPEB3	1.07	3.27E-01	4.18E-01	153.36	not significant
8023	TMEM245	1.07	5.39E-03	1.12E-02	3531.32	not significant
8024	ACADS	1.07	8.54E-02	1.33E-01	800.22	not significant
8025	RNF121	1.07	1.28E-01	1.89E-01	633.21	not significant
8026	LYRM2	1.07	2.74E-02	4.88E-02	1696.58	not significant
8027	PNISR	1.07	1.54E-01	2.22E-01	6134.41	not significant
8028	TMEM19	1.07	1.35E-02	2.58E-02	2090.08	not significant
8029	MED28	1.07	9.95E-03	1.95E-02	2692.62	not significant
8030	PDCL3P4	1.07	3.79E-01	4.70E-01	37.61	not significant
8031	BEND4	1.07	2.87E-02	5.08E-02	1816.68	not significant
8032	PLK4	1.07	2.07E-03	4.67E-03	4563.66	not significant
8033	FAM120C	1.07	3.85E-01	4.77E-01	51.51	not significant
8034	ARID1A	1.07	1.60E-01	2.29E-01	11272.22	not significant
8035	UVSSA	1.07	1.76E-01	2.49E-01	465.45	not significant
8036	EXOC1	1.07	8.05E-02	1.26E-01	924.46	not significant
8037	VPS28	1.07	6.70E-02	1.07E-01	1133.85	not significant
8038	DIP2C	1.07	3.86E-01	4.78E-01	55.44	not significant
8039	TBC1D30	1.07	2.33E-01	3.15E-01	9.66	not significant
8040	B9D1	1.07	3.86E-01	4.78E-01	59.11	not significant
8041	PRKAR1A	1.07	1.77E-03	4.03E-03	9152.18	not significant
8042	PDP1	1.07	1.79E-02	3.33E-02	1975.45	not significant
8043	PPP6R2	1.07	1.62E-02	3.04E-02	2826.45	not significant
8044	PHIP	1.07	2.49E-01	3.33E-01	4631.39	not significant
8045	ARHGAP1	1.07	1.87E-02	3.46E-02	2048.28	not significant
8046	ATP6V1H	1.07	3.34E-02	5.81E-02	1982.37	not significant
8047	BBS10	1.07	1.34E-01	1.96E-01	656.48	not significant
8048	MEN1	1.07	1.35E-02	2.58E-02	3551.27	not significant
8049	ARHGAP44	1.07	3.57E-01	4.49E-01	27.63	not significant
8050	ADAMTS17	1.07	2.85E-01	3.73E-01	13.48	not significant
8051	TNFSF14	1.07	3.42E-01	4.33E-01	26.87	not significant
8052	GIT1	1.07	2.85E-03	6.25E-03	4708.66	not significant
8053	SP3	1.07	8.50E-04	2.06E-03	5300.26	not significant
8054	LOC729218	1.07	1.12E-01	1.68E-01	765.19	not significant
8055	GPR68	1.07	1.26E-01	1.87E-01	622.60	not significant
8056	SPINT1	1.07	3.82E-01	4.74E-01	49.22	not significant
8057	MBD4	1.07	1.38E-02	2.63E-02	2261.00	not significant
8058	BTAF1	1.07	2.02E-01	2.79E-01	4329.03	not significant
8059	PAXBP1	1.07	2.00E-01	2.77E-01	2700.35	not significant
8060	CHN2	1.07	8.02E-03	1.61E-02	2520.74	not significant
8061	CASP1	1.07	1.36E-01	1.99E-01	565.89	not significant
8062	ZNF724P	1.07	3.66E-01	4.58E-01	74.19	not significant
8063	LOC653653	1.07	2.98E-01	3.86E-01	15.07	not significant
8064	LAMP3	1.07	1.84E-01	2.58E-01	406.21	not significant
8065	TRMT1	1.07	4.04E-02	6.87E-02	1681.82	not significant
8066	PTPN4	1.07	3.47E-02	6.01E-02	1436.59	not significant
8067	TSPAN14	1.07	1.47E-02	2.78E-02	2040.94	not significant
8068	NFIB	1.07	2.68E-01	3.54E-01	11.91	not significant
8069	SCUBE1	1.07	3.05E-01	3.95E-01	15.98	not significant
8070	KLHL7	1.07	3.45E-02	5.98E-02	1660.21	not significant
8071	UTRN	1.07	1.52E-01	2.19E-01	4155.30	not significant
8072	ACOT1	1.07	3.50E-01	4.42E-01	28.98	not significant
8073	DHRS3	1.07	2.52E-01	3.37E-01	257.12	not significant
8074	ILVBL	1.07	7.25E-02	1.15E-01	1214.40	not significant
8075	DDX3Y	1.07	3.21E-03	6.99E-03	6839.68	not significant
8076	SLC23A3	1.07	3.47E-01	4.38E-01	24.58	not significant
8077	WDR70	1.07	8.59E-02	1.34E-01	898.60	not significant
8078	TMEM42	1.07	2.65E-01	3.51E-01	224.67	not significant
8079	CXorf65	1.07	3.77E-01	4.69E-01	64.56	not significant
8080	HMGCS1	1.07	3.55E-03	7.66E-03	7957.72	not significant
8081	ZC3HAV1	1.07	1.29E-01	1.90E-01	7850.20	not significant
8082	SPATA33	1.07	2.08E-01	2.86E-01	355.29	not significant
8083	OS9	1.07	1.56E-03	3.61E-03	4372.60	not significant
8084	KLF13	1.07	5.67E-03	1.17E-02	6263.65	not significant

8085	SLC6A16	1.07	3.74E-01	4.66E-01	43.71	not significant
8086	CENPN	1.07	6.51E-03	1.33E-02	3631.27	not significant
8087	BBX	1.07	7.99E-03	1.60E-02	2692.31	not significant
8088	MBNL3	1.07	1.20E-02	2.32E-02	5657.74	not significant
8089	LOC100129034	1.07	1.79E-01	2.52E-01	383.59	not significant
8090	SPG7	1.07	1.78E-02	3.29E-02	1927.74	not significant
8091	TNK1	1.07	3.63E-01	4.55E-01	82.97	not significant
8092	IAH1	1.07	6.36E-02	1.03E-01	1154.97	not significant
8093	POMGNT1	1.07	8.00E-03	1.60E-02	2569.17	not significant
8094	EEPD1	1.07	2.66E-02	4.73E-02	1584.58	not significant
8095	FMNL3	1.07	4.60E-03	9.73E-03	3522.32	not significant
8096	GCLC	1.07	1.52E-02	2.86E-02	2147.85	not significant
8097	MSANTD2	1.07	2.81E-01	3.69E-01	241.61	not significant
8098	LEMD3	1.07	8.48E-03	1.69E-02	2414.32	not significant
8099	TGFBR2	1.07	7.41E-02	1.17E-01	798.49	not significant
8100	ZNF737	1.07	3.71E-01	4.63E-01	54.20	not significant
8101	ZBTB21	1.07	3.40E-02	5.90E-02	1412.59	not significant
8102	MADD	1.07	5.33E-03	1.11E-02	2980.97	not significant
8103	BARD1	1.07	1.88E-02	3.47E-02	1717.54	not significant
8104	LAMTOR3	1.07	3.14E-02	5.50E-02	1461.68	not significant
8105	RIMKLB	1.07	9.40E-02	1.45E-01	1002.72	not significant
8106	TBC1D2B	1.07	1.85E-02	3.42E-02	1705.33	not significant
8107	SSBP2	1.07	1.56E-02	2.94E-02	2104.88	not significant
8108	SIRT2	1.07	1.93E-02	3.55E-02	1658.19	not significant
8109	DQX1	1.07	2.22E-01	3.02E-01	9.63	not significant
8110	DNAJC12	1.07	3.67E-01	4.59E-01	37.34	not significant
8111	AFG3L1P	1.07	7.19E-02	1.14E-01	974.89	not significant
8112	TMBIM4	1.07	2.31E-02	4.17E-02	1578.17	not significant
8113	CPSF3L	1.07	1.29E-02	2.47E-02	2454.84	not significant
8114	AGFG2	1.07	8.76E-02	1.36E-01	708.42	not significant
8115	NUP50-AS1	1.07	1.93E-01	2.69E-01	381.04	not significant
8116	NANOS1	1.07	2.50E-01	3.34E-01	242.35	not significant
8117	DDX11	1.07	3.56E-02	6.14E-02	2876.18	not significant
8118	LOC100507437	1.07	2.34E-01	3.16E-01	10.62	not significant
8119	SMG9	1.07	7.24E-03	1.46E-02	2417.96	not significant
8120	GRK4	1.07	3.52E-01	4.44E-01	99.95	not significant
8121	GSK3A	1.07	3.44E-03	7.45E-03	3565.45	not significant
8122	ZNF592	1.07	1.60E-02	2.99E-02	1886.82	not significant
8123	PAX9	1.07	1.43E-01	2.09E-01	483.81	not significant
8124	MED21	1.07	2.17E-02	3.94E-02	1677.81	not significant
8125	NPIPA1	1.07	3.56E-01	4.47E-01	82.97	not significant
8126	CPT1A	1.07	7.09E-03	1.44E-02	3614.66	not significant
8127	ZNF620	1.07	2.73E-01	3.59E-01	17.43	not significant
8128	MIR4435-1HG	1.07	3.31E-01	4.22E-01	127.40	not significant
8129	LINC01237	1.08	3.64E-01	4.56E-01	61.88	not significant
8130	PLCH2	1.08	2.60E-01	3.45E-01	12.53	not significant
8131	LIN9	1.08	4.78E-02	8.00E-02	1088.83	not significant
8132	ARGLU1	1.08	1.83E-01	2.56E-01	5796.48	not significant
8133	ANKS3	1.08	2.17E-01	2.96E-01	283.10	not significant
8134	LOXL1-AS1	1.08	3.40E-01	4.31E-01	100.54	not significant
8135	CACFD1	1.08	2.81E-01	3.68E-01	16.08	not significant
8136	SPTLC2	1.08	3.54E-03	7.66E-03	4289.49	not significant
8137	LOC100130705	1.08	3.56E-01	4.48E-01	34.11	not significant
8138	C6orf62	1.08	1.01E-03	2.41E-03	6205.13	not significant
8139	ERLEC1	1.08	1.30E-02	2.49E-02	2227.35	not significant
8140	RAB3IP	1.08	1.70E-02	3.17E-02	1673.63	not significant
8141	MSH3	1.08	2.26E-02	4.09E-02	1441.12	not significant
8142	PCDH10	1.08	3.57E-01	4.49E-01	72.91	not significant
8143	CAMK2G	1.08	1.51E-02	2.85E-02	2272.28	not significant
8144	RNLS	1.08	2.22E-03	4.96E-03	4760.15	not significant
8145	BHLHB9	1.08	2.14E-01	2.93E-01	302.48	not significant
8146	NRROS	1.08	6.10E-04	1.52E-03	5601.43	not significant
8147	ADAL	1.08	1.22E-01	1.81E-01	531.73	not significant
8148	NEGR1	1.08	2.03E-01	2.81E-01	8.90	not significant
8149	WTIP	1.08	3.64E-01	4.56E-01	56.20	not significant
8150	PABPN1	1.08	1.31E-01	1.92E-01	654.25	not significant
8151	CATSPER2	1.08	1.69E-01	2.40E-01	7.30	not significant
8152	LOC401127	1.08	3.06E-01	3.96E-01	18.55	not significant
8153	AFF3	1.08	3.23E-02	5.65E-02	1462.19	not significant
8154	ELK1	1.08	9.88E-03	1.94E-02	2233.91	not significant
8155	AP2A1	1.08	5.71E-03	1.18E-02	3161.69	not significant
8156	CNTLN	1.08	4.79E-02	8.01E-02	996.44	not significant
8157	NVL	1.08	2.04E-02	3.73E-02	1571.78	not significant
8158	CCDC154	1.08	2.87E-01	3.75E-01	16.83	not significant
8159	MFSD6	1.08	5.34E-03	1.11E-02	3558.36	not significant
8160	HLA-J	1.08	2.31E-01	3.13E-01	10.43	not significant
8161	SNAPC3	1.08	2.62E-02	4.68E-02	1382.59	not significant
8162	PRRT4	1.08	3.48E-01	4.40E-01	32.90	not significant
8163	ZDHHC18	1.08	1.74E-02	3.23E-02	2031.82	not significant
8164	TMEM116	1.08	1.94E-01	2.69E-01	331.77	not significant
8165	RUSC1	1.08	4.35E-02	7.34E-02	1122.18	not significant
8166	GOLGA3	1.08	3.14E-04	8.25E-04	7469.24	not significant
8167	STK24	1.08	7.57E-04	1.85E-03	7181.70	not significant
8168	FAM127A	1.08	2.80E-01	3.67E-01	170.95	not significant
8169	ATP11C	1.08	1.67E-02	3.12E-02	2053.11	not significant
8170	AGAP6	1.08	3.46E-01	4.38E-01	81.14	not significant
8171	RAB40B	1.08	3.59E-01	4.51E-01	46.65	not significant
8172	LINC00672	1.08	3.57E-01	4.49E-01	50.37	not significant

8173	SYPL1	1.08	9.79E-04	2.34E-03	8101.11	not significant
8174	LRRC46	1.08	3.54E-01	4.46E-01	43.56	not significant
8175	SLC25A11	1.08	1.20E-02	2.32E-02	2075.22	not significant
8176	MED14	1.08	6.26E-03	1.28E-02	3194.10	not significant
8177	DLGAP1-AS1	1.08	3.49E-01	4.40E-01	83.99	not significant
8178	MAP3K5	1.08	3.57E-01	4.48E-01	52.43	not significant
8179	LYST	1.08	1.47E-01	2.13E-01	460.41	not significant
8180	TTBK2	1.08	1.25E-01	1.85E-01	505.48	not significant
8181	MFN1	1.08	5.17E-02	8.56E-02	939.34	not significant
8182	CARD8	1.08	1.47E-02	2.78E-02	2004.87	not significant
8183	DOC2GP	1.08	2.24E-01	3.04E-01	10.91	not significant
8184	NLGN4Y	1.08	2.00E-01	2.77E-01	330.03	not significant
8185	ZNF215	1.08	1.20E-01	1.79E-01	519.63	not significant
8186	FAM161A	1.08	1.21E-01	1.80E-01	531.78	not significant
8187	CD72	1.08	2.91E-01	3.79E-01	18.31	not significant
8188	WASH3P	1.08	2.62E-01	3.47E-01	187.48	not significant
8189	COPS5	1.08	9.05E-03	1.79E-02	3312.23	not significant
8190	ZNF813	1.08	1.02E-01	1.55E-01	619.50	not significant
8191	SDF2	1.08	4.94E-02	8.22E-02	1017.83	not significant
8192	NENF	1.08	5.96E-02	9.70E-02	1148.58	not significant
8193	IFT80	1.08	3.57E-02	6.15E-02	1192.11	not significant
8194	RB1CC1	1.08	2.62E-03	5.81E-03	3023.75	not significant
8195	ERI3-IT1	1.08	2.75E-01	3.61E-01	16.55	not significant
8196	RMDN1	1.08	1.11E-02	2.15E-02	1894.80	not significant
8197	MSTO2P	1.08	2.87E-01	3.76E-01	160.32	not significant
8198	ZCCHC11	1.08	1.31E-03	3.06E-03	4501.12	not significant
8199	RAD51	1.08	1.19E-02	2.29E-02	1929.48	not significant
8200	CTBP1	1.08	3.85E-03	8.28E-03	8980.72	not significant
8201	STRN4	1.08	3.62E-03	7.80E-03	3545.92	not significant
8202	UBE2Z	1.08	5.30E-03	1.11E-02	2856.96	not significant
8203	CCDC15	1.08	1.25E-01	1.85E-01	540.78	not significant
8204	FAM171B	1.08	3.50E-01	4.41E-01	49.52	not significant
8205	SMCO2	1.08	2.45E-01	3.28E-01	13.54	not significant
8206	UCKL1	1.08	3.47E-02	6.00E-02	1130.34	not significant
8207	LOC145783	1.08	2.33E-01	3.15E-01	283.51	not significant
8208	HPS6	1.08	9.11E-02	1.41E-01	612.52	not significant
8209	FRMD8	1.08	1.63E-02	3.04E-02	1754.97	not significant
8210	RABGEF1	1.08	8.12E-03	1.62E-02	2026.82	not significant
8211	C1orf43	1.08	2.97E-03	6.50E-03	7677.25	not significant
8212	THAP3	1.08	1.09E-01	1.64E-01	529.19	not significant
8213	SDR39U1	1.08	2.74E-02	4.87E-02	1269.93	not significant
8214	RNF41	1.08	1.45E-02	2.75E-02	1822.70	not significant
8215	TCF3	1.08	2.69E-04	7.16E-04	12446.61	not significant
8216	ZNF669	1.08	9.23E-02	1.42E-01	613.77	not significant
8217	LUC7L	1.08	2.87E-02	5.07E-02	1801.06	not significant
8218	TPO	1.08	1.81E-01	2.54E-01	320.16	not significant
8219	CYP2U1	1.08	8.99E-02	1.39E-01	626.73	not significant
8220	DIXDC1	1.08	3.26E-01	4.18E-01	30.23	not significant
8221	FAXDC2	1.08	1.89E-01	2.63E-01	9.11	not significant
8222	PEX10	1.08	1.03E-01	1.57E-01	585.45	not significant
8223	EVI5L	1.08	6.10E-02	9.89E-02	840.94	not significant
8224	TMEM164	1.08	7.66E-04	1.86E-03	5723.11	not significant
8225	DHX35	1.08	2.74E-02	4.87E-02	1492.72	not significant
8226	SMARCC1	1.08	3.49E-04	9.09E-04	15005.31	not significant
8227	MYO9A	1.08	3.34E-02	5.81E-02	1193.83	not significant
8228	TTC3P1	1.08	3.15E-01	4.06E-01	24.11	not significant
8229	RPL22L1	1.08	3.94E-03	8.44E-03	3980.73	not significant
8230	QSOX1	1.08	7.09E-02	1.13E-01	815.83	not significant
8231	PTPN23	1.08	2.62E-02	4.67E-02	2312.37	not significant
8232	ZNF766	1.08	3.02E-02	5.30E-02	1210.77	not significant
8233	CGGBP1	1.08	9.63E-05	2.77E-04	10207.64	not significant
8234	SLC25A38	1.08	2.06E-03	4.64E-03	3646.66	not significant
8235	CTC-338M12.4	1.08	3.20E-01	4.11E-01	93.93	not significant
8236	FLJ22184	1.08	2.26E-01	3.07E-01	11.31	not significant
8237	DOCK4	1.08	3.30E-01	4.21E-01	30.68	not significant
8238	ANKRD20A5P	1.08	3.15E-01	4.05E-01	108.72	not significant
8239	DTX2P1-UPK3BP	1.08	3.20E-01	4.11E-01	85.15	not significant
8240	ZNF24	1.08	6.35E-04	1.57E-03	4761.20	not significant
8241	ZNF510	1.08	6.78E-02	1.08E-01	729.94	not significant
8242	SLC12A2	1.08	2.80E-02	4.96E-02	1264.92	not significant
8243	RND1	1.08	3.39E-01	4.30E-01	44.59	not significant
8244	MRPS2	1.08	1.80E-02	3.35E-02	1553.17	not significant
8245	PHF13	1.08	2.10E-02	3.83E-02	1447.69	not significant
8246	LOC101926996	1.08	1.92E-01	2.67E-01	9.78	not significant
8247	RHOBTB2	1.08	2.68E-01	3.54E-01	160.01	not significant
8248	TRAIP	1.08	4.51E-02	7.58E-02	1045.30	not significant
8249	TMEM27	1.08	1.95E-01	2.71E-01	10.48	not significant
8250	GABARAPL2	1.08	9.53E-03	1.88E-02	1867.65	not significant
8251	B4GALT4	1.08	1.37E-01	2.00E-01	450.80	not significant
8252	LIPT1	1.08	2.07E-01	2.85E-01	251.32	not significant
8253	ANP32AP1	1.08	2.88E-01	3.76E-01	19.84	not significant
8254	ZNF76	1.08	8.07E-03	1.62E-02	2116.48	not significant
8255	GALNT3	1.08	2.47E-01	3.30E-01	14.25	not significant
8256	PSEN1	1.08	6.23E-03	1.28E-02	2147.61	not significant
8257	SAT1	1.08	2.30E-02	4.17E-02	1283.94	not significant
8258	ATE1	1.08	1.88E-02	3.48E-02	1487.98	not significant
8259	USP18	1.08	1.05E-01	1.59E-01	548.25	not significant
8260	SCN3A	1.08	3.29E-01	4.20E-01	76.84	not significant

8261	TRIM37	1.08	2.36E-03	5.26E-03	2948.05	not significant
8262	ITGB7	1.08	2.46E-01	3.29E-01	193.87	not significant
8263	IL27RA	1.08	2.82E-02	4.99E-02	1670.41	not significant
8264	TCHP	1.08	1.71E-02	3.18E-02	1814.62	not significant
8265	MLLT6	1.08	5.19E-04	1.31E-03	7756.84	not significant
8266	EIF1B-AS1	1.08	1.70E-01	2.41E-01	8.45	not significant
8267	PPARA	1.08	2.51E-01	3.35E-01	187.95	not significant
8268	ZNF81	1.08	2.27E-01	3.09E-01	13.68	not significant
8269	BCKDHA	1.08	5.19E-02	8.59E-02	801.79	not significant
8270	FAM171A2	1.08	2.56E-01	3.41E-01	204.75	not significant
8271	CIB2	1.08	2.12E-01	2.91E-01	11.06	not significant
8272	ZNF235	1.08	2.63E-01	3.48E-01	164.57	not significant
8273	GPR83	1.08	2.56E-01	3.41E-01	16.22	not significant
8274	TSC1	1.08	5.93E-02	9.66E-02	928.05	not significant
8275	ZBED4	1.08	1.69E-04	4.66E-04	7242.79	not significant
8276	NCKAP1L	1.08	1.20E-04	3.39E-04	7421.64	not significant
8277	IQCC	1.08	1.32E-01	1.95E-01	423.61	not significant
8278	MYO5A	1.08	1.87E-02	3.45E-02	1687.85	not significant
8279	ZNF569	1.08	6.40E-02	1.03E-01	868.49	not significant
8280	CCT6P3	1.08	3.03E-01	3.92E-01	130.98	not significant
8281	AFF1	1.08	2.26E-03	5.05E-03	5043.23	not significant
8282	CAMK1D	1.08	8.04E-02	1.26E-01	679.01	not significant
8283	COMMD4	1.08	3.70E-02	6.35E-02	949.22	not significant
8284	HMG20B	1.08	1.17E-02	2.26E-02	2049.91	not significant
8285	COPS2	1.08	5.44E-03	1.13E-02	2143.72	not significant
8286	RNF170	1.08	6.78E-02	1.08E-01	773.46	not significant
8287	FICD	1.08	3.24E-01	4.15E-01	74.71	not significant
8288	SLC22A23	1.08	1.58E-01	2.27E-01	350.18	not significant
8289	ECSIT	1.08	4.59E-02	7.70E-02	963.14	not significant
8290	RTCA-AS1	1.08	2.77E-01	3.64E-01	20.00	not significant
8291	USP19	1.08	1.66E-03	3.82E-03	2986.09	not significant
8292	UHMK1	1.08	2.14E-03	4.81E-03	7940.95	not significant
8293	ACOX1	1.08	1.87E-03	4.24E-03	3201.65	not significant
8294	MYPOP	1.08	9.73E-02	1.49E-01	529.96	not significant
8295	TMC8	1.08	4.32E-03	9.17E-03	5717.42	not significant
8296	ANAPC2	1.08	8.21E-02	1.28E-01	980.26	not significant
8297	KAT2A	1.08	1.36E-02	2.59E-02	1563.87	not significant
8298	CLTA	1.08	1.17E-03	2.77E-03	4539.54	not significant
8299	ACTA1	1.08	1.94E-01	2.70E-01	9.83	not significant
8300	DCP1A	1.08	1.53E-01	2.21E-01	340.49	not significant
8301	FOXD2	1.08	2.92E-01	3.81E-01	29.07	not significant
8302	ATP10A	1.08	5.58E-02	9.15E-02	765.61	not significant
8303	MCM8	1.08	1.36E-03	3.18E-03	4713.08	not significant
8304	ZNF460	1.08	2.85E-01	3.73E-01	119.28	not significant
8305	PEX5	1.08	8.17E-03	1.63E-02	2295.25	not significant
8306	DOCK7	1.08	4.07E-02	6.91E-02	1214.72	not significant
8307	ZMYND11	1.08	1.87E-03	4.24E-03	2850.53	not significant
8308	ADAM10	1.08	1.17E-03	2.76E-03	5107.70	not significant
8309	STX18	1.08	3.59E-02	6.18E-02	986.40	not significant
8310	LRRC23	1.08	3.21E-01	4.12E-01	39.09	not significant
8311	PIK3C3	1.08	2.83E-02	5.02E-02	1055.88	not significant
8312	ZBTB37	1.08	2.91E-01	3.80E-01	122.66	not significant
8313	CPNE3	1.08	2.24E-04	6.06E-04	5460.28	not significant
8314	LOC644656	1.08	3.24E-01	4.15E-01	44.62	not significant
8315	CPD	1.08	1.40E-03	3.26E-03	3178.45	not significant
8316	MFSD1	1.08	3.63E-02	6.24E-02	1003.66	not significant
8317	ANKRD13D	1.08	1.41E-02	2.68E-02	1842.96	not significant
8318	FBXO3	1.08	1.34E-01	1.97E-01	398.51	not significant
8319	MAFB	1.08	3.00E-01	3.89E-01	26.13	not significant
8320	FZD2	1.08	1.75E-01	2.47E-01	295.58	not significant
8321	ITM2B	1.08	8.11E-05	2.36E-04	16675.85	not significant
8322	PLEKHA7	1.08	3.08E-01	3.98E-01	108.69	not significant
8323	SLA	1.08	5.97E-03	1.23E-02	1976.87	not significant
8324	CEP95	1.08	3.93E-02	6.71E-02	1162.70	not significant
8325	LRPPRC	1.08	1.25E-05	4.10E-05	13138.94	not significant
8326	TRAPPC2P1	1.08	2.80E-01	3.68E-01	156.29	not significant
8327	TSC22D2	1.08	7.46E-02	1.18E-01	621.96	not significant
8328	ZFAND5	1.08	3.04E-03	6.64E-03	2697.59	not significant
8329	PAXBP1-AS1	1.08	3.10E-01	4.00E-01	30.97	not significant
8330	REEP5	1.08	1.15E-02	2.23E-02	1547.70	not significant
8331	VPS4B	1.08	1.54E-03	3.57E-03	4303.45	not significant
8332	LENG1	1.08	2.90E-01	3.78E-01	104.35	not significant
8333	SNAPC4	1.08	8.17E-02	1.28E-01	633.56	not significant
8334	NCOA3	1.08	4.66E-03	9.85E-03	2051.76	not significant
8335	PGD	1.08	7.64E-05	2.23E-04	10859.00	not significant
8336	TEX12	1.08	1.74E-01	2.47E-01	9.87	not significant
8337	TARP	1.08	7.86E-02	1.24E-01	707.28	not significant
8338	PHLDA1	1.08	3.01E-01	3.90E-01	29.54	not significant
8339	AUTS2	1.08	3.14E-01	4.05E-01	71.73	not significant
8340	TINF2	1.08	1.98E-03	4.48E-03	2776.82	not significant
8341	EIF2AK3	1.08	2.06E-02	3.77E-02	1556.70	not significant
8342	HIPK2	1.08	3.96E-03	8.48E-03	3947.91	not significant
8343	APOL2	1.08	7.84E-03	1.58E-02	1872.76	not significant
8344	ZBTB18	1.08	1.44E-02	2.73E-02	1410.53	not significant
8345	TPM4	1.08	6.41E-05	1.90E-04	10244.62	not significant
8346	C21orf2	1.08	1.23E-01	1.82E-01	410.24	not significant
8347	DMWD	1.08	3.53E-02	6.09E-02	889.55	not significant
8348	GIMAP5	1.08	2.94E-01	3.82E-01	26.94	not significant

8349	ADAM22	1.08	6.38E-03	1.31E-02	2106.75	not significant
8350	PRKX	1.08	3.48E-03	7.53E-03	2567.18	not significant
8351	NMNAT3	1.08	2.93E-01	3.82E-01	25.34	not significant
8352	PITPNM1	1.08	1.29E-03	3.03E-03	3412.51	not significant
8353	CLHC1	1.08	1.95E-01	2.71E-01	246.41	not significant
8354	TUBG2	1.08	1.77E-01	2.50E-01	291.45	not significant
8355	SLC9C1	1.08	2.10E-01	2.89E-01	12.21	not significant
8356	MBD5	1.08	1.42E-01	2.07E-01	342.01	not significant
8357	RCE1	1.08	5.59E-02	9.17E-02	742.98	not significant
8358	MEF2D	1.08	7.03E-03	1.43E-02	1809.00	not significant
8359	NR4A1	1.08	1.48E-01	2.15E-01	7.70	not significant
8360	PIAS4	1.08	3.37E-02	5.85E-02	929.80	not significant
8361	UBL7	1.08	1.58E-02	2.96E-02	1601.33	not significant
8362	HARS2	1.08	2.90E-02	5.13E-02	1010.55	not significant
8363	LINC00563	1.08	2.98E-01	3.87E-01	89.67	not significant
8364	ASH1L-AS1	1.08	3.15E-01	4.05E-01	51.63	not significant
8365	DDOST	1.08	5.07E-04	1.28E-03	6758.98	not significant
8366	ADNP-AS1	1.08	2.84E-01	3.72E-01	23.75	not significant
8367	ZNF236	1.08	2.35E-02	4.24E-02	1339.62	not significant
8368	RRM1	1.08	1.53E-05	4.96E-05	15343.56	not significant
8369	ZDHHC23	1.08	1.28E-01	1.89E-01	409.64	not significant
8370	YIPF6	1.08	6.20E-02	1.00E-01	685.15	not significant
8371	TRIM8	1.09	3.43E-02	5.95E-02	973.72	not significant
8372	ENOX2	1.09	8.53E-02	1.33E-01	776.07	not significant
8373	PLSCR1	1.09	1.87E-02	3.46E-02	1308.80	not significant
8374	EFCAB14	1.09	4.85E-04	1.23E-03	5403.33	not significant
8375	IFITM10	1.09	3.08E-01	3.98E-01	37.17	not significant
8376	TULP3	1.09	5.68E-02	9.29E-02	673.75	not significant
8377	DUSP28	1.09	2.41E-01	3.23E-01	156.06	not significant
8378	SERTAD2	1.09	1.14E-02	2.22E-02	1553.87	not significant
8379	TMEM110	1.09	1.55E-02	2.90E-02	1265.09	not significant
8380	COL11A2	1.09	2.81E-01	3.68E-01	24.12	not significant
8381	PDF	1.09	2.35E-01	3.17E-01	188.65	not significant
8382	C1RL-AS1	1.09	1.87E-01	2.61E-01	306.83	not significant
8383	TOP3A	1.09	9.44E-04	2.27E-03	3381.95	not significant
8384	DYNLL1-AS1	1.09	2.84E-01	3.72E-01	104.59	not significant
8385	E2F2	1.09	1.39E-04	3.88E-04	5436.28	not significant
8386	HERPUD2	1.09	1.16E-02	2.25E-02	1432.94	not significant
8387	MRPS31P5	1.09	9.38E-02	1.44E-01	474.64	not significant
8388	SERP1	1.09	3.17E-05	9.83E-05	10138.33	not significant
8389	TMEM222	1.09	1.61E-02	3.02E-02	1218.24	not significant
8390	BOLA1	1.09	2.87E-01	3.75E-01	27.93	not significant
8391	TJP2	1.09	5.62E-02	9.20E-02	671.40	not significant
8392	DUSP16	1.09	2.03E-01	2.80E-01	208.24	not significant
8393	ZNF791	1.09	1.42E-01	2.07E-01	355.97	not significant
8394	RNF114	1.09	2.77E-04	7.34E-04	4584.91	not significant
8395	LOC439994	1.09	3.05E-01	3.94E-01	63.71	not significant
8396	NOD1	1.09	1.86E-02	3.44E-02	1141.45	not significant
8397	TMEM248	1.09	1.02E-04	2.92E-04	6327.49	not significant
8398	RSF1	1.09	2.04E-02	3.73E-02	1502.74	not significant
8399	NME6	1.09	7.16E-02	1.14E-01	610.43	not significant
8400	RUNX2	1.09	7.96E-03	1.60E-02	2583.26	not significant
8401	ZNF14	1.09	1.44E-01	2.09E-01	333.59	not significant
8402	CDC25B	1.09	6.58E-05	1.95E-04	13657.80	not significant
8403	OLA1	1.09	1.37E-03	3.21E-03	5201.93	not significant
8404	ANXA11	1.09	6.65E-04	1.64E-03	3812.35	not significant
8405	SMPD3	1.09	3.07E-01	3.97E-01	50.95	not significant
8406	PPM1N	1.09	1.82E-01	2.55E-01	11.22	not significant
8407	WDR27	1.09	1.33E-01	1.95E-01	457.04	not significant
8408	HSPA13	1.09	7.56E-04	1.84E-03	3246.30	not significant
8409	TMEM38B	1.09	5.17E-02	8.55E-02	888.69	not significant
8410	C7orf26	1.09	4.32E-03	9.17E-03	1849.17	not significant
8411	SMYD3	1.09	4.46E-02	7.50E-02	1035.18	not significant
8412	ATG4B	1.09	1.51E-03	3.49E-03	2691.57	not significant
8413	BEND3	1.09	2.02E-01	2.79E-01	12.31	not significant
8414	SRSF5	1.09	2.90E-05	9.03E-05	11915.69	not significant
8415	LPP-AS2	1.09	3.00E-01	3.89E-01	75.68	not significant
8416	CHM	1.09	2.97E-02	5.24E-02	878.80	not significant
8417	ZNF77	1.09	1.82E-01	2.55E-01	234.41	not significant
8418	SEMA4F	1.09	1.87E-01	2.62E-01	255.67	not significant
8419	TCN2	1.09	2.26E-01	3.07E-01	16.36	not significant
8420	ATN1	1.09	8.21E-02	1.28E-01	522.48	not significant
8421	COG4	1.09	1.79E-02	3.32E-02	1301.59	not significant
8422	TMOD2	1.09	4.34E-02	7.33E-02	944.15	not significant
8423	NR3C1	1.09	2.37E-03	5.28E-03	2291.90	not significant
8424	RBM28	1.09	8.86E-03	1.76E-02	1551.05	not significant
8425	ATP2C1	1.09	6.04E-04	1.50E-03	3754.09	not significant
8426	RPL12	1.09	3.35E-04	8.78E-04	16360.10	not significant
8427	SAMHD1	1.09	2.98E-01	3.87E-01	37.34	not significant
8428	SLC35E1	1.09	1.16E-03	2.75E-03	2712.91	not significant
8429	GAS6-AS1	1.09	3.02E-01	3.91E-01	50.43	not significant
8430	CAPS2	1.09	2.39E-01	3.21E-01	149.25	not significant
8431	NELFA	1.09	1.44E-02	2.73E-02	1659.97	not significant
8432	POLD4	1.09	4.87E-02	8.13E-02	679.38	not significant
8433	PIK3C2A	1.09	4.50E-02	7.57E-02	1012.72	not significant
8434	KRI1	1.09	1.48E-03	3.44E-03	2788.67	not significant
8435	TRIM16L	1.09	2.99E-01	3.88E-01	51.74	not significant
8436	TPRN	1.09	6.05E-02	9.82E-02	603.94	not significant

8437	SLC35A5	1.09	8.00E-03	1.60E-02	1627.05	not significant
8438	LINC00920	1.09	2.55E-01	3.40E-01	119.72	not significant
8439	NSMCE2	1.09	3.37E-02	5.85E-02	984.70	not significant
8440	AOX2P	1.09	1.81E-01	2.54E-01	11.74	not significant
8441	ZNF614	1.09	1.51E-02	2.84E-02	1229.45	not significant
8442	MCM5	1.09	9.08E-06	3.03E-05	12071.86	not significant
8443	NSA2	1.09	8.85E-04	2.14E-03	3806.84	not significant
8444	GUSBP9	1.09	2.96E-01	3.85E-01	48.76	not significant
8445	MYL6B	1.09	3.47E-03	7.50E-03	3601.59	not significant
8446	LLGL1	1.09	5.14E-03	1.08E-02	2220.92	not significant
8447	FAM134C	1.09	8.58E-03	1.71E-02	1666.72	not significant
8448	PLCXD2	1.09	2.97E-01	3.86E-01	59.27	not significant
8449	ZNF408	1.09	1.08E-01	1.63E-01	392.26	not significant
8450	SUDS3	1.09	4.87E-04	1.24E-03	3451.43	not significant
8451	DIRC2	1.09	2.24E-01	3.05E-01	156.21	not significant
8452	CLCC1	1.09	1.17E-01	1.74E-01	367.58	not significant
8453	MRPS36	1.09	1.17E-01	1.75E-01	378.73	not significant
8454	LOC100287944	1.09	1.65E-01	2.36E-01	10.77	not significant
8455	PTPRD	1.09	2.87E-01	3.75E-01	34.20	not significant
8456	AKAP5	1.09	1.05E-01	1.60E-01	417.30	not significant
8457	SEMA7A	1.09	2.89E-03	6.34E-03	2034.03	not significant
8458	DRICH1	1.09	2.53E-01	3.38E-01	21.68	not significant
8459	NEDD9	1.09	2.38E-02	4.30E-02	937.67	not significant
8460	VAV2	1.09	1.83E-01	2.56E-01	11.23	not significant
8461	CTAGE5	1.09	2.26E-02	4.09E-02	1099.59	not significant
8462	ZNF26	1.09	2.90E-01	3.78E-01	61.76	not significant
8463	LRFN4	1.09	9.34E-03	1.85E-02	1618.71	not significant
8464	CDK20	1.09	2.94E-01	3.83E-01	48.12	not significant
8465	AP1AR	1.09	8.32E-03	1.66E-02	1413.73	not significant
8466	WHAMMP1	1.09	2.85E-01	3.74E-01	90.98	not significant
8467	TSPAN31	1.09	1.16E-01	1.73E-01	423.72	not significant
8468	MRPL15	1.09	1.24E-02	2.39E-02	2365.08	not significant
8469	RXRB	1.09	1.10E-01	1.65E-01	381.65	not significant
8470	BTBD6	1.09	1.34E-02	2.56E-02	1156.39	not significant
8471	GRAMD4	1.09	1.73E-04	4.78E-04	5952.61	not significant
8472	SHMT1	1.09	3.85E-03	8.27E-03	1845.99	not significant
8473	HOXC4	1.09	1.53E-01	2.20E-01	282.31	not significant
8474	MTBP	1.09	1.19E-02	2.30E-02	1281.10	not significant
8475	TOE1	1.09	6.16E-03	1.27E-02	1554.43	not significant
8476	MIS18A	1.09	4.90E-03	1.03E-02	1774.00	not significant
8477	GCC2	1.09	5.99E-03	1.23E-02	1580.40	not significant
8478	GATA3-AS1	1.09	2.18E-01	2.97E-01	16.43	not significant
8479	LOC256880	1.09	2.73E-01	3.59E-01	27.69	not significant
8480	SSH2	1.09	5.74E-04	1.44E-03	3330.90	not significant
8481	LOC102723701	1.09	2.62E-01	3.48E-01	27.71	not significant
8482	TMEM184A	1.09	1.82E-01	2.55E-01	12.72	not significant
8483	RNF149	1.09	5.01E-03	1.05E-02	1700.61	not significant
8484	RAD9A	1.09	7.38E-03	1.49E-02	1715.52	not significant
8485	LOC100129931	1.09	1.76E-01	2.49E-01	12.03	not significant
8486	ZMYM3	1.09	2.33E-03	5.19E-03	3478.53	not significant
8487	ZNF44	1.09	1.07E-01	1.62E-01	387.08	not significant
8488	ZNF674-AS1	1.09	2.19E-01	2.99E-01	161.40	not significant
8489	LCAT	1.09	2.69E-01	3.55E-01	104.60	not significant
8490	H1F0	1.09	2.39E-01	3.22E-01	130.33	not significant
8491	CELSR3	1.09	6.25E-03	1.28E-02	2229.50	not significant
8492	METTL14	1.09	1.40E-02	2.66E-02	1116.01	not significant
8493	CC2D1B	1.09	9.84E-03	1.93E-02	1324.83	not significant
8494	SLC9A7	1.09	9.67E-02	1.48E-01	396.74	not significant
8495	C1orf86	1.09	1.43E-02	2.71E-02	1514.10	not significant
8496	SBNO2	1.09	1.44E-02	2.73E-02	1733.19	not significant
8497	CDK10	1.09	8.59E-03	1.71E-02	1466.09	not significant
8498	TMX4	1.09	1.85E-01	2.59E-01	205.27	not significant
8499	SSR4	1.09	1.41E-03	3.29E-03	2462.60	not significant
8500	IGHMBP2	1.09	2.82E-02	5.00E-02	873.01	not significant
8501	NR2C2	1.09	4.06E-04	1.05E-03	4002.40	not significant
8502	PYGB	1.09	3.13E-03	6.84E-03	1882.03	not significant
8503	CAMSAP1	1.09	1.58E-03	3.64E-03	2335.67	not significant
8504	ORAI2	1.09	1.24E-03	2.92E-03	3749.77	not significant
8505	PPM1D	1.09	5.04E-03	1.06E-02	1645.43	not significant
8506	NNT-AS1	1.09	3.94E-02	6.72E-02	698.50	not significant
8507	RNF216	1.09	7.93E-04	1.93E-03	3353.97	not significant
8508	RASA4	1.09	2.47E-01	3.30E-01	21.40	not significant
8509	KDM3B	1.09	5.32E-04	1.34E-03	5021.84	not significant
8510	SPATA7	1.09	2.00E-01	2.77E-01	187.45	not significant
8511	DOCK11	1.09	8.53E-04	2.06E-03	2543.74	not significant
8512	RAPH1	1.09	1.14E-01	1.71E-01	413.48	not significant
8513	SIN3A	1.09	2.54E-05	7.97E-05	5236.73	not significant
8514	GMIP	1.09	3.14E-02	5.50E-02	896.42	not significant
8515	TBC1D24	1.09	4.39E-02	7.41E-02	753.25	not significant
8516	NFX1	1.09	1.42E-03	3.30E-03	2438.66	not significant
8517	RNF220	1.09	1.72E-03	3.93E-03	2996.36	not significant
8518	CYBRD1	1.09	7.95E-02	1.25E-01	444.09	not significant
8519	TBC1D10A	1.09	5.92E-03	1.22E-02	1559.80	not significant
8520	ING5	1.09	1.72E-03	3.92E-03	2099.81	not significant
8521	SYTL1	1.09	5.45E-02	8.98E-02	757.29	not significant
8522	TMEM181	1.09	6.33E-03	1.30E-02	1734.08	not significant
8523	ZNF160	1.09	1.51E-02	2.84E-02	1242.82	not significant
8524	MYSM1	1.09	1.29E-01	1.90E-01	1960.62	not significant

8525	DTNB	1.09	6.64E-02	1.07E-01	517.55	not significant
8526	LINC01341	1.09	1.52E-01	2.20E-01	9.79	not significant
8527	CERS6	1.09	4.23E-05	1.29E-04	6759.74	not significant
8528	SCYL2	1.09	4.50E-04	1.15E-03	3213.89	not significant
8529	ZNF551	1.09	1.27E-02	2.43E-02	1132.03	not significant
8530	ZNF570	1.09	1.97E-01	2.74E-01	185.05	not significant
8531	UXT-AS1	1.09	1.95E-01	2.71E-01	13.86	not significant
8532	TTTY10	1.09	1.50E-01	2.17E-01	9.61	not significant
8533	SLC45A4	1.09	1.73E-03	3.96E-03	2072.07	not significant
8534	UNK	1.09	3.50E-04	9.11E-04	3772.72	not significant
8535	VEZT	1.09	2.84E-04	7.52E-04	4303.39	not significant
8536	IGF2R	1.09	7.62E-02	1.20E-01	8735.32	not significant
8537	RARA-AS1	1.09	1.70E-01	2.41E-01	13.27	not significant
8538	B4GALT1	1.09	4.77E-03	1.01E-02	1489.54	not significant
8539	THAP6	1.09	9.95E-02	1.52E-01	379.20	not significant
8540	BRPF1	1.09	1.31E-03	3.06E-03	2364.76	not significant
8541	ZC3H3	1.09	1.22E-02	2.35E-02	1436.57	not significant
8542	LOC100130872	1.09	2.77E-02	4.92E-02	955.24	not significant
8543	LRFN3	1.09	5.42E-02	8.93E-02	566.67	not significant
8544	ZAP70	1.09	2.73E-04	7.25E-04	9588.48	not significant
8545	MINK1	1.09	1.30E-02	2.49E-02	1642.82	not significant
8546	DMTF1	1.09	1.45E-01	2.10E-01	3049.60	not significant
8547	KIF15	1.09	2.09E-05	6.63E-05	7090.76	not significant
8548	MON2	1.09	1.16E-01	1.74E-01	2556.07	not significant
8549	LRP12	1.09	1.86E-02	3.44E-02	1051.06	not significant
8550	FMR1	1.09	6.54E-02	1.05E-01	513.04	not significant
8551	RIC8B	1.09	1.41E-02	2.69E-02	1194.47	not significant
8552	LCORL	1.09	3.47E-02	6.01E-02	686.64	not significant
8553	UBXN4	1.09	1.52E-05	4.93E-05	8094.53	not significant
8554	TSEN34	1.09	2.05E-01	2.82E-01	156.65	not significant
8555	CASP2	1.09	4.26E-05	1.30E-04	7687.91	not significant
8556	WDR64	1.09	2.56E-01	3.40E-01	28.05	not significant
8557	FAM60A	1.09	1.21E-04	3.42E-04	4748.09	not significant
8558	IPCEF1	1.09	3.43E-02	5.95E-02	806.11	not significant
8559	NSMCE4A	1.09	3.98E-03	8.53E-03	1733.18	not significant
8560	ZNF674	1.09	2.41E-01	3.23E-01	120.27	not significant
8561	RERE	1.09	2.14E-02	3.90E-02	1463.32	not significant
8562	TTC37	1.09	1.23E-04	3.47E-04	4112.14	not significant
8563	ABHD4	1.09	2.28E-01	3.10E-01	135.38	not significant
8564	PHTF1	1.09	2.53E-01	3.37E-01	92.45	not significant
8565	LOC100996579	1.09	4.07E-02	6.90E-02	636.17	not significant
8566	CARHSP1	1.09	1.58E-04	4.40E-04	7439.12	not significant
8567	C14orf79	1.09	2.00E-01	2.77E-01	16.48	not significant
8568	PAXIP1OS	1.09	1.04E-01	1.58E-01	404.43	not significant
8569	ZNF589	1.09	3.55E-02	6.12E-02	791.99	not significant
8570	PDIK1L	1.10	6.97E-03	1.42E-02	1567.44	not significant
8571	RCHY1	1.10	8.46E-03	1.69E-02	1391.61	not significant
8572	PITHD1	1.10	2.21E-03	4.95E-03	2158.38	not significant
8573	DPH7	1.10	2.54E-02	4.54E-02	814.70	not significant
8574	JAK2	1.10	2.49E-02	4.46E-02	854.09	not significant
8575	CFLAR	1.10	1.40E-02	2.67E-02	1158.14	not significant
8576	ATXN2	1.10	9.49E-03	1.87E-02	1745.69	not significant
8577	BRD7	1.10	6.06E-04	1.51E-03	3757.96	not significant
8578	ARAP2	1.10	7.32E-03	1.48E-02	1323.07	not significant
8579	STX7	1.10	3.66E-02	6.29E-02	671.21	not significant
8580	ZNF530	1.10	7.70E-02	1.21E-01	435.09	not significant
8581	C1GALT1	1.10	4.23E-04	1.09E-03	2766.83	not significant
8582	PLAA	1.10	3.45E-03	7.48E-03	1834.78	not significant
8583	MEF2A	1.10	4.10E-04	1.06E-03	3368.09	not significant
8584	MBD6	1.10	9.10E-03	1.80E-02	2403.69	not significant
8585	CD2BP2	1.10	6.73E-04	1.66E-03	3153.38	not significant
8586	TRAM1L1	1.10	2.66E-01	3.52E-01	43.62	not significant
8587	JPX	1.10	2.13E-01	2.92E-01	142.31	not significant
8588	RAB11B-AS1	1.10	2.15E-01	2.94E-01	133.70	not significant
8589	ACTR8	1.10	1.21E-02	2.34E-02	1114.28	not significant
8590	STK38L	1.10	6.77E-04	1.67E-03	2266.32	not significant
8591	COMMD6	1.10	5.03E-03	1.05E-02	1581.59	not significant
8592	LRRC29	1.10	2.35E-01	3.17E-01	24.04	not significant
8593	ZNF746	1.10	1.39E-02	2.65E-02	1044.96	not significant
8594	C21orf128	1.10	2.24E-01	3.04E-01	20.84	not significant
8595	ZNF571	1.10	2.24E-01	3.05E-01	110.49	not significant
8596	ARL10	1.10	1.90E-01	2.64E-01	164.35	not significant
8597	NIPSNAP1	1.10	6.29E-05	1.87E-04	4458.39	not significant
8598	LOC100506606	1.10	2.45E-01	3.29E-01	26.41	not significant
8599	TET3	1.10	1.69E-04	4.67E-04	3920.19	not significant
8600	LINC01003	1.10	1.22E-01	1.82E-01	275.69	not significant
8601	TMEM123	1.10	7.39E-06	2.50E-05	24346.00	not significant
8602	XRCC2	1.10	8.33E-03	1.66E-02	1990.17	not significant
8603	ELF4	1.10	1.14E-03	2.70E-03	2017.21	not significant
8604	FAM227B	1.10	2.62E-01	3.48E-01	44.09	not significant
8605	LOC100287098	1.10	1.72E-01	2.44E-01	13.46	not significant
8606	ZKSCAN4	1.10	1.34E-01	1.97E-01	254.41	not significant
8607	CLNS1A	1.10	8.89E-04	2.15E-03	4625.40	not significant
8608	PILRB	1.10	2.35E-01	3.17E-01	24.77	not significant
8609	LOC101927027	1.10	6.28E-02	1.02E-01	643.14	not significant
8610	CNTRL	1.10	3.30E-04	8.65E-04	3420.66	not significant
8611	CMTM8	1.10	7.97E-02	1.25E-01	452.90	not significant
8612	ZNF830	1.10	3.65E-02	6.27E-02	683.16	not significant

8613	APLF	1.10	1.50E-01	2.16E-01	232.26	not significant
8614	PIK3CG	1.10	6.78E-04	1.67E-03	2962.70	not significant
8615	ZNF706	1.10	8.54E-04	2.07E-03	2258.49	not significant
8616	MRI1	1.10	7.92E-03	1.59E-02	1467.83	not significant
8617	ANKRD16	1.10	9.15E-02	1.41E-01	375.22	not significant
8618	LOC728613	1.10	2.09E-01	2.87E-01	134.40	not significant
8619	ZSCAN29	1.10	7.30E-03	1.48E-02	1374.36	not significant
8620	F11R	1.10	2.13E-02	3.88E-02	798.87	not significant
8621	VANGL2	1.10	1.46E-01	2.12E-01	227.29	not significant
8622	WASL	1.10	5.07E-02	8.41E-02	510.09	not significant
8623	SLC25A35	1.10	2.07E-01	2.84E-01	153.31	not significant
8624	FLYWCH1	1.10	7.88E-03	1.58E-02	1166.52	not significant
8625	PPP1R9B	1.10	1.35E-03	3.15E-03	2325.52	not significant
8626	CCDC115	1.10	1.58E-02	2.97E-02	981.91	not significant
8627	FYTTD1	1.10	2.50E-03	5.55E-03	1975.16	not significant
8628	DENND4C	1.10	3.80E-04	9.85E-04	2716.45	not significant
8629	LINC00265	1.10	5.14E-02	8.52E-02	584.46	not significant
8630	ZNF17	1.10	9.71E-02	1.49E-01	376.01	not significant
8631	TMEM189	1.10	9.96E-03	1.96E-02	1379.99	not significant
8632	RNASEK	1.10	2.35E-01	3.17E-01	25.45	not significant
8633	BCAS3	1.10	4.84E-02	8.07E-02	521.10	not significant
8634	CRBN	1.10	6.17E-03	1.27E-02	1301.10	not significant
8635	TYMP	1.10	1.55E-01	2.23E-01	13.29	not significant
8636	TNFSF10	1.10	5.58E-05	1.67E-04	7190.09	not significant
8637	RBM34	1.10	6.20E-03	1.27E-02	1376.58	not significant
8638	PRKY	1.10	1.47E-02	2.78E-02	1023.67	not significant
8639	VAT1	1.10	2.15E-05	6.82E-05	4617.94	not significant
8640	ITGB1	1.10	6.35E-05	1.88E-04	6179.05	not significant
8641	SPAST	1.10	9.89E-04	2.37E-03	2402.83	not significant
8642	C11orf57	1.10	6.10E-04	1.52E-03	2252.91	not significant
8643	JMJD4	1.10	5.08E-02	8.42E-02	571.93	not significant
8644	TMEM185A	1.10	2.48E-01	3.31E-01	68.59	not significant
8645	SERHL2	1.10	2.47E-02	4.44E-02	752.57	not significant
8646	TYK2	1.10	2.71E-04	7.20E-04	3915.09	not significant
8647	H2AFX	1.10	3.82E-04	9.89E-04	10303.89	not significant
8648	PLIN2	1.10	1.87E-03	4.24E-03	2483.64	not significant
8649	FAAH2	1.10	1.81E-01	2.54E-01	156.55	not significant
8650	NAPEPLD	1.10	6.51E-02	1.05E-01	685.13	not significant
8651	DNAJC14	1.10	2.82E-04	7.45E-04	3229.12	not significant
8652	FEM1C	1.10	1.55E-02	2.92E-02	910.39	not significant
8653	NASP	1.10	9.82E-04	2.35E-03	15349.12	not significant
8654	TGFBR1	1.10	5.79E-03	1.20E-02	1484.44	not significant
8655	FOXO3	1.10	2.10E-02	3.83E-02	802.26	not significant
8656	ITPR3	1.10	8.54E-02	1.33E-01	5295.20	not significant
8657	CDK16	1.10	1.03E-03	2.45E-03	2081.11	not significant
8658	PHOSPHO2	1.10	2.36E-01	3.18E-01	81.62	not significant
8659	BAZ2B	1.10	1.72E-02	3.21E-02	863.17	not significant
8660	DAGLB	1.10	2.95E-02	5.20E-02	679.50	not significant
8661	FZD1	1.10	1.34E-01	1.96E-01	230.09	not significant
8662	IPW	1.10	8.92E-02	1.38E-01	358.16	not significant
8663	PAX8	1.10	1.06E-01	1.61E-01	281.36	not significant
8664	ADRBK1	1.10	7.14E-06	2.42E-05	15959.91	not significant
8665	ZSCAN25	1.10	2.25E-03	5.03E-03	1626.43	not significant
8666	BTG2	1.10	1.83E-01	2.57E-01	158.94	not significant
8667	KIAA1551	1.10	2.33E-05	7.36E-05	4938.83	not significant
8668	ZNF781	1.10	2.44E-01	3.27E-01	64.74	not significant
8669	ZNF181	1.10	8.04E-02	1.26E-01	359.79	not significant
8670	GUSBP2	1.10	2.44E-01	3.28E-01	36.15	not significant
8671	PHF3	1.10	3.48E-05	1.07E-04	4600.58	not significant
8672	AIM1	1.10	4.81E-05	1.45E-04	3658.53	not significant
8673	RPL41	1.10	2.13E-01	2.92E-01	4142.52	not significant
8674	USP21	1.10	3.43E-03	7.43E-03	1470.01	not significant
8675	EIF4B	1.10	3.69E-06	1.30E-05	18833.96	not significant
8676	SPIN2B	1.10	2.23E-01	3.04E-01	100.22	not significant
8677	ROBO3	1.10	3.54E-02	6.11E-02	650.47	not significant
8678	MRPS18A	1.10	5.13E-03	1.07E-02	1277.36	not significant
8679	YARS2	1.10	1.90E-02	3.50E-02	763.30	not significant
8680	HIAT1	1.10	6.86E-05	2.02E-04	3580.19	not significant
8681	ZNF628	1.10	9.16E-02	1.41E-01	330.64	not significant
8682	TLK2	1.10	1.76E-03	4.02E-03	1705.13	not significant
8683	SPRY1	1.10	7.59E-02	1.20E-01	361.60	not significant
8684	CTSC	1.10	6.49E-05	1.92E-04	4411.03	not significant
8685	MKRN1	1.10	2.61E-04	6.96E-04	2809.76	not significant
8686	CDIP1	1.10	7.83E-02	1.23E-01	362.26	not significant
8687	PLCG1	1.10	1.16E-05	3.81E-05	12336.53	not significant
8688	VSIG10	1.10	2.13E-01	2.92E-01	99.01	not significant
8689	HNRNPA1L2	1.10	4.09E-02	6.94E-02	551.17	not significant
8690	SLC39A13	1.10	1.82E-02	3.36E-02	782.38	not significant
8691	ZNF543	1.10	1.24E-01	1.84E-01	243.70	not significant
8692	ARRDC2	1.10	2.67E-02	4.75E-02	680.89	not significant
8693	FANCF	1.10	9.61E-03	1.89E-02	1063.85	not significant
8694	PSMB7	1.10	1.20E-03	2.83E-03	2866.97	not significant
8695	MAP4K2	1.10	4.70E-03	9.93E-03	1281.64	not significant
8696	LY75	1.10	4.83E-02	8.05E-02	476.75	not significant
8697	NXF1	1.10	5.98E-04	1.49E-03	3744.03	not significant
8698	NAGPA	1.10	4.48E-02	7.54E-02	492.10	not significant
8699	KLF12	1.10	3.17E-04	8.32E-04	4038.94	not significant
8700	SDHAF1	1.10	4.90E-02	8.17E-02	532.27	not significant

8701	TP53BP2	1.10	1.13E-04	3.21E-04	2764.39	not significant
8702	VAMP4	1.10	1.07E-02	2.10E-02	912.73	not significant
8703	TRAPPC11	1.10	6.47E-04	1.60E-03	1999.23	not significant
8704	NMD3	1.10	3.67E-04	9.53E-04	2531.00	not significant
8705	TMEM237	1.10	2.42E-04	6.48E-04	2492.61	not significant
8706	SLC26A6	1.10	3.20E-02	5.60E-02	842.68	not significant
8707	ZNF274	1.10	5.02E-02	8.34E-02	460.49	not significant
8708	SH3BP2	1.10	3.60E-03	7.77E-03	2056.09	not significant
8709	GLCCI1	1.10	2.95E-03	6.47E-03	1364.46	not significant
8710	INTS1	1.10	6.25E-04	1.55E-03	6973.81	not significant
8711	FAM21C	1.10	1.12E-01	1.69E-01	282.51	not significant
8712	RSPRY1	1.10	2.98E-03	6.51E-03	1408.86	not significant
8713	AP4B1	1.10	2.05E-02	3.76E-02	955.17	not significant
8714	NEK1	1.10	6.48E-03	1.33E-02	1283.94	not significant
8715	GON4L	1.10	5.96E-04	1.48E-03	2041.61	not significant
8716	TMEM55B	1.10	9.76E-03	1.92E-02	954.74	not significant
8717	CD8A	1.10	1.94E-05	6.19E-05	4625.00	not significant
8718	FAM195B	1.10	3.21E-04	8.43E-04	2272.24	not significant
8719	GOLGA2P7	1.10	1.85E-01	2.58E-01	17.86	not significant
8720	ZNF3	1.10	4.67E-04	1.19E-03	2177.48	not significant
8721	CDADC1	1.10	2.94E-02	5.19E-02	623.15	not significant
8722	ALKBH2	1.10	2.01E-02	3.68E-02	804.60	not significant
8723	TCEAL3	1.10	2.36E-01	3.18E-01	63.60	not significant
8724	DOLPP1	1.10	1.35E-02	2.58E-02	918.95	not significant
8725	PLTP	1.10	2.35E-01	3.17E-01	70.99	not significant
8726	EPHA5	1.10	1.69E-01	2.41E-01	14.50	not significant
8727	PLCB2	1.10	7.23E-03	1.46E-02	1479.43	not significant
8728	RPL23P8	1.10	2.32E-01	3.13E-01	66.39	not significant
8729	FBXL4	1.10	2.22E-02	4.03E-02	691.14	not significant
8730	SEMA4B	1.10	6.68E-02	1.07E-01	413.31	not significant
8731	AP3M2	1.10	3.56E-03	7.69E-03	1337.83	not significant
8732	ZNF264	1.10	8.82E-03	1.75E-02	1006.04	not significant
8733	APOL1	1.10	8.02E-03	1.61E-02	1003.18	not significant
8734	CLIC4	1.10	2.62E-04	6.99E-04	2245.50	not significant
8735	MYEOV2	1.10	3.46E-03	7.48E-03	1392.59	not significant
8736	LOC101926935	1.10	9.82E-02	1.50E-01	8.50	not significant
8737	TCEANC2	1.10	8.94E-03	1.77E-02	940.72	not significant
8738	ANAPC13	1.10	2.55E-03	5.64E-03	1610.27	not significant
8739	ASB9	1.10	3.27E-02	5.70E-02	541.68	not significant
8740	CHAMP1	1.10	2.16E-01	2.95E-01	80.20	not significant
8741	B3GALTL	1.10	8.03E-03	1.61E-02	1111.27	not significant
8742	TMEM69	1.10	7.51E-03	1.51E-02	1092.12	not significant
8743	OGDHL	1.10	5.69E-02	9.30E-02	441.74	not significant
8744	DCTN4	1.10	1.49E-03	3.45E-03	1846.44	not significant
8745	ANKH	1.10	1.31E-04	3.68E-04	2636.76	not significant
8746	CCDC96	1.10	2.29E-01	3.10E-01	63.78	not significant
8747	NFATC2	1.10	3.82E-04	9.89E-04	2682.54	not significant
8748	LOC100131655	1.10	2.30E-01	3.11E-01	39.92	not significant
8749	IFIT2	1.10	6.58E-02	1.06E-01	405.00	not significant
8750	C21orf33	1.10	3.75E-03	8.08E-03	1322.38	not significant
8751	ZNF484	1.10	1.93E-01	2.69E-01	115.86	not significant
8752	SCAMP5	1.10	5.97E-02	9.71E-02	416.93	not significant
8753	OPTN	1.10	2.72E-04	7.23E-04	2358.10	not significant
8754	TADA2B	1.11	6.63E-03	1.35E-02	1039.79	not significant
8755	NICN1	1.11	2.31E-02	4.17E-02	739.03	not significant
8756	OSCP1	1.11	2.33E-01	3.15E-01	44.85	not significant
8757	NDOR1	1.11	4.72E-03	9.96E-03	2536.41	not significant
8758	CES3	1.11	3.35E-02	5.83E-02	595.04	not significant
8759	SAP30BP	1.11	2.85E-04	7.53E-04	2481.76	not significant
8760	MTR	1.11	4.96E-03	1.04E-02	2086.09	not significant
8761	FANCC	1.11	5.30E-03	1.11E-02	1073.62	not significant
8762	CEP85	1.11	1.76E-04	4.85E-04	2891.94	not significant
8763	ZNF770	1.11	5.35E-04	1.35E-03	2019.95	not significant
8764	SSH1	1.11	4.95E-04	1.26E-03	2229.13	not significant
8765	C20orf196	1.11	8.59E-02	1.34E-01	314.62	not significant
8766	REXO4	1.11	6.17E-02	1.00E-01	402.86	not significant
8767	C19orf52	1.11	2.26E-02	4.09E-02	673.99	not significant
8768	UBTD2	1.11	5.42E-03	1.13E-02	1255.39	not significant
8769	CCNL1	1.11	1.26E-01	1.86E-01	3974.59	not significant
8770	AP5S1	1.11	1.30E-02	2.49E-02	864.67	not significant
8771	CNNM2	1.11	1.50E-01	2.16E-01	167.88	not significant
8772	QTRT1	1.11	1.22E-02	2.35E-02	857.89	not significant
8773	DRAM1	1.11	2.28E-01	3.10E-01	42.22	not significant
8774	HPS5	1.11	5.11E-03	1.07E-02	1063.77	not significant
8775	C10orf25	1.11	7.16E-02	1.14E-01	363.45	not significant
8776	APIP	1.11	2.07E-03	4.67E-03	1531.19	not significant
8777	RAPGEF2	1.11	3.92E-03	8.40E-03	1206.73	not significant
8778	ADSS	1.11	6.73E-05	1.99E-04	3603.88	not significant
8779	ARL2BP	1.11	3.26E-04	8.54E-04	2206.37	not significant
8780	LOC284454	1.11	1.58E-01	2.26E-01	14.18	not significant
8781	GK	1.11	8.67E-02	1.35E-01	339.44	not significant
8782	CSTF3-AS1	1.11	2.10E-01	2.88E-01	83.42	not significant
8783	ITPKC	1.11	9.09E-02	1.40E-01	361.48	not significant
8784	ANKRD28	1.11	2.23E-05	7.05E-05	6071.00	not significant
8785	CTC1	1.11	6.65E-02	1.07E-01	1980.51	not significant
8786	SOCS1	1.11	7.00E-02	1.12E-01	2949.90	not significant
8787	UNC50	1.11	6.56E-03	1.34E-02	1150.03	not significant
8788	ZRSR2	1.11	8.64E-02	1.34E-01	287.48	not significant

8789	ZNF841	1.11	1.94E-01	2.70E-01	470.83	not significant
8790	TJAP1	1.11	2.85E-03	6.26E-03	1377.22	not significant
8791	RPL19P12	1.11	1.98E-01	2.74E-01	112.83	not significant
8792	CEP135	1.11	6.32E-04	1.57E-03	2127.86	not significant
8793	HECTD1	1.11	9.31E-04	2.24E-03	2938.16	not significant
8794	PYHIN1	1.11	1.56E-03	3.60E-03	1484.08	not significant
8795	NUMBL	1.11	8.48E-02	1.32E-01	287.47	not significant
8796	LINC00051	1.11	2.24E-01	3.04E-01	38.98	not significant
8797	HPCAL1	1.11	3.53E-03	7.62E-03	1302.74	not significant
8798	CD84	1.11	2.13E-05	6.76E-05	3571.28	not significant
8799	STAG2	1.11	2.93E-06	1.05E-05	15205.88	not significant
8800	BRPF3	1.11	8.82E-04	2.13E-03	1743.87	not significant
8801	HS6ST1	1.11	1.03E-04	2.95E-04	4996.40	not significant
8802	LOC100128494	1.11	2.07E-01	2.85E-01	116.61	not significant
8803	WDR19	1.11	4.18E-02	7.08E-02	496.60	not significant
8804	UBR2	1.11	1.02E-03	2.43E-03	2557.74	not significant
8805	PDDC1	1.11	5.72E-04	1.43E-03	2242.44	not significant
8806	ZBTB3	1.11	1.68E-01	2.39E-01	135.37	not significant
8807	PRKCH	1.11	4.03E-06	1.41E-05	11623.83	not significant
8808	ZNF805	1.11	9.43E-02	1.45E-01	297.22	not significant
8809	ZNF213-AS1	1.11	2.08E-01	2.86E-01	78.04	not significant
8810	NDRG4	1.11	2.15E-01	2.94E-01	68.28	not significant
8811	MORC3	1.11	2.28E-04	6.16E-04	2468.09	not significant
8812	HGH1	1.11	2.19E-01	2.99E-01	35.91	not significant
8813	DDHD1	1.11	1.39E-03	3.24E-03	3069.20	not significant
8814	MARVELD1	1.11	1.62E-01	2.31E-01	164.75	not significant
8815	NBAS	1.11	1.56E-03	3.59E-03	1748.94	not significant
8816	CPSF7	1.11	1.52E-06	5.65E-06	7684.65	not significant
8817	PIFO	1.11	1.86E-01	2.60E-01	19.87	not significant
8818	GCDH	1.11	3.66E-03	7.90E-03	1206.82	not significant
8819	SLC7A7	1.11	1.06E-01	1.60E-01	9.62	not significant
8820	CATSPER3	1.11	2.08E-01	2.86E-01	28.69	not significant
8821	SUGT1	1.11	1.81E-03	4.12E-03	1763.90	not significant
8822	RRAGD	1.11	1.51E-03	3.50E-03	1374.76	not significant
8823	DCAF8	1.11	6.38E-04	1.58E-03	3384.15	not significant
8824	CYB5D1	1.11	9.31E-03	1.84E-02	914.26	not significant
8825	RPL37A	1.11	9.47E-05	2.73E-04	23817.45	not significant
8826	ARHGAP32	1.11	3.31E-04	8.66E-04	2239.41	not significant
8827	TPP1	1.11	1.04E-05	3.43E-05	3958.53	not significant
8828	ZNF707	1.11	2.19E-01	2.99E-01	46.10	not significant
8829	SEMA6C	1.11	1.94E-01	2.70E-01	91.76	not significant
8830	PAQR4	1.11	2.78E-04	7.37E-04	2102.30	not significant
8831	RTKN	1.11	1.78E-01	2.50E-01	20.61	not significant
8832	FLII	1.11	9.08E-07	3.45E-06	6359.29	not significant
8833	RFX1	1.11	2.44E-02	4.39E-02	655.87	not significant
8834	PRIM2	1.11	1.78E-03	4.07E-03	1516.52	not significant
8835	RPL38	1.11	8.90E-06	2.98E-05	15663.81	not significant
8836	LINC00963	1.11	9.48E-02	1.46E-01	9.29	not significant
8837	TRIM56	1.11	5.85E-04	1.46E-03	1780.33	not significant
8838	ZYX	1.11	7.29E-02	1.16E-01	318.60	not significant
8839	FAM195A	1.11	1.72E-01	2.44E-01	20.47	not significant
8840	MAP2K5	1.11	2.21E-03	4.95E-03	1240.41	not significant
8841	NUCKS1	1.11	7.12E-06	2.42E-05	23057.94	not significant
8842	CUL4B	1.11	1.38E-04	3.86E-04	3154.18	not significant
8843	C4orf46	1.11	9.78E-05	2.81E-04	2988.66	not significant
8844	MRPL9	1.11	9.00E-05	2.60E-04	2743.91	not significant
8845	CERKL	1.11	1.76E-01	2.48E-01	25.33	not significant
8846	WRN	1.11	7.14E-04	1.75E-03	2319.64	not significant
8847	CDIPT	1.11	6.10E-04	1.52E-03	2634.90	not significant
8848	LINC00630	1.11	1.76E-01	2.49E-01	105.84	not significant
8849	SOCS5	1.11	1.62E-02	3.03E-02	712.75	not significant
8850	ENC1	1.11	1.75E-02	3.26E-02	649.94	not significant
8851	LINC00950	1.11	1.10E-01	1.66E-01	10.64	not significant
8852	MSL2	1.11	5.88E-08	2.59E-07	7868.34	not significant
8853	ADAT1	1.11	4.02E-03	8.61E-03	1016.65	not significant
8854	LOC100507557	1.11	1.92E-01	2.67E-01	25.34	not significant
8855	FAM53B	1.11	6.81E-04	1.68E-03	2505.30	not significant
8856	RYBP	1.11	1.44E-03	3.34E-03	1509.41	not significant
8857	TYMS	1.11	7.47E-06	2.52E-05	27827.08	not significant
8858	ATP9B	1.11	9.58E-03	1.89E-02	814.69	not significant
8859	SZT2	1.11	1.24E-01	1.84E-01	1715.06	not significant
8860	UAP1L1	1.11	1.98E-01	2.74E-01	27.27	not significant
8861	ST5	1.11	1.44E-01	2.10E-01	14.17	not significant
8862	COG6	1.11	8.17E-03	1.63E-02	903.22	not significant
8863	NFYC-AS1	1.11	1.89E-01	2.64E-01	121.16	not significant
8864	SGPL1	1.11	7.56E-04	1.84E-03	1543.43	not significant
8865	UBA52	1.11	1.39E-04	3.89E-04	16496.43	not significant
8866	LOC101928812	1.11	1.58E-01	2.27E-01	16.25	not significant
8867	NKD2	1.11	7.22E-03	1.46E-02	943.59	not significant
8868	ZNF772	1.11	1.64E-02	3.07E-02	655.42	not significant
8869	KDM4A	1.11	6.14E-04	1.53E-03	1977.28	not significant
8870	DCAF15	1.11	2.35E-04	6.32E-04	3155.77	not significant
8871	ZNF217	1.11	6.69E-05	1.98E-04	3094.79	not significant
8872	MICA	1.11	2.12E-01	2.91E-01	51.06	not significant
8873	BUD13	1.11	7.04E-04	1.73E-03	1718.07	not significant
8874	RELL1	1.11	8.54E-02	1.33E-01	275.44	not significant
8875	KLHL26	1.11	6.11E-02	9.90E-02	382.55	not significant
8876	LAMP1	1.11	8.03E-06	2.70E-05	5364.32	not significant

8877	LOC100506124	1.11	2.09E-01	2.87E-01	40.32	not significant
8878	SLC38A9	1.11	3.24E-03	7.05E-03	1092.34	not significant
8879	WASH1	1.11	1.76E-01	2.48E-01	111.39	not significant
8880	MUC1	1.11	1.36E-01	1.99E-01	12.86	not significant
8881	NLGN3	1.11	1.56E-01	2.24E-01	143.15	not significant
8882	ARL5B	1.11	4.09E-03	8.73E-03	1266.13	not significant
8883	LOC100506476	1.11	1.24E-01	1.84E-01	12.00	not significant
8884	STK36	1.11	1.17E-01	1.75E-01	231.50	not significant
8885	PLAUR	1.11	7.15E-02	1.14E-01	318.44	not significant
8886	IRF2	1.11	7.01E-04	1.72E-03	1751.87	not significant
8887	PDE4DIP	1.11	5.50E-02	9.05E-02	404.55	not significant
8888	ZNF195	1.11	2.02E-03	4.56E-03	1389.38	not significant
8889	FUOM	1.11	1.57E-01	2.25E-01	137.38	not significant
8890	GPC1	1.11	1.82E-01	2.55E-01	94.42	not significant
8891	FLJ37453	1.11	1.40E-01	2.05E-01	156.89	not significant
8892	GPR17	1.11	2.07E-01	2.84E-01	45.93	not significant
8893	GLB1L2	1.11	1.08E-01	1.63E-01	213.57	not significant
8894	DXO	1.11	1.74E-01	2.46E-01	105.14	not significant
8895	PGM1	1.11	6.33E-05	1.88E-04	2479.27	not significant
8896	43714_12910	1.11	4.54E-09	2.25E-08	22381.28	not significant
8897	ZNF180	1.11	4.16E-02	7.06E-02	486.43	not significant
8898	ZNF765	1.11	1.73E-02	3.22E-02	606.91	not significant
8899	CCDC146	1.11	2.49E-02	4.47E-02	562.60	not significant
8900	KLHDC4	1.11	5.51E-04	1.39E-03	1627.64	not significant
8901	VLDLR	1.11	5.86E-02	9.54E-02	342.18	not significant
8902	TMEM263	1.11	1.77E-05	5.68E-05	3479.61	not significant
8903	KBTBD6	1.11	3.40E-02	5.91E-02	555.28	not significant
8904	SLC39A6	1.11	1.59E-05	5.13E-05	4704.14	not significant
8905	TERF2IP	1.11	1.26E-04	3.56E-04	4920.64	not significant
8906	DTX3L	1.11	5.72E-06	1.96E-05	4233.82	not significant
8907	HAUS5	1.11	1.27E-04	3.59E-04	2383.97	not significant
8908	NIPSNAP3A	1.11	4.63E-03	9.79E-03	941.31	not significant
8909	TRIM33	1.11	3.97E-04	1.02E-03	4033.87	not significant
8910	CMAHP	1.11	1.60E-03	3.68E-03	2855.42	not significant
8911	TMEM43	1.11	1.95E-04	5.31E-04	2103.20	not significant
8912	TMEM106B	1.11	1.08E-04	3.06E-04	2405.73	not significant
8913	DCAF12	1.11	1.43E-05	4.66E-05	4365.59	not significant
8914	PARP3	1.11	1.57E-02	2.95E-02	657.43	not significant
8915	ZBTB40	1.11	1.80E-03	4.11E-03	2378.05	not significant
8916	LINC00526	1.11	1.94E-01	2.70E-01	77.58	not significant
8917	LINC01137	1.11	1.97E-01	2.73E-01	31.44	not significant
8918	ENKD1	1.11	6.80E-02	1.09E-01	316.91	not significant
8919	ADAM11	1.11	1.41E-01	2.05E-01	14.20	not significant
8920	ARRDC1-AS1	1.11	4.10E-02	6.96E-02	399.73	not significant
8921	BMPR1A	1.11	3.69E-02	6.34E-02	449.67	not significant
8922	CCDC22	1.11	5.44E-02	8.97E-02	362.98	not significant
8923	KIF3A	1.11	1.00E-04	2.88E-04	2322.74	not significant
8924	TYMSOS	1.11	1.57E-01	2.25E-01	125.90	not significant
8925	GATSL3	1.11	5.72E-03	1.18E-02	878.50	not significant
8926	CERK	1.11	4.75E-06	1.65E-05	4223.41	not significant
8927	STK32C	1.11	1.17E-01	1.75E-01	12.89	not significant
8928	CEP162	1.11	1.54E-02	2.90E-02	623.64	not significant
8929	FADS3	1.11	2.04E-01	2.81E-01	57.65	not significant
8930	PGRMC1	1.11	8.66E-05	2.51E-04	2548.06	not significant
8931	PEX2	1.11	3.33E-04	8.71E-04	2476.91	not significant
8932	LAMP2	1.11	9.16E-06	3.06E-05	4291.42	not significant
8933	WHAMM	1.11	4.80E-02	8.02E-02	394.64	not significant
8934	ZSCAN18	1.11	1.65E-03	3.78E-03	1225.38	not significant
8935	MAP3K1	1.11	6.07E-02	9.85E-02	340.67	not significant
8936	SMCHD1	1.11	6.06E-06	2.07E-05	8969.68	not significant
8937	BET1L	1.11	9.94E-04	2.38E-03	1677.21	not significant
8938	ZHX2	1.11	8.17E-02	1.28E-01	258.07	not significant
8939	ZNF615	1.11	2.06E-02	3.76E-02	539.46	not significant
8940	KIAA0226	1.11	2.54E-03	5.63E-03	1402.37	not significant
8941	LIN52	1.11	1.19E-02	2.29E-02	726.45	not significant
8942	TMUB1	1.11	3.89E-04	1.01E-03	2087.74	not significant
8943	PLEKHA8	1.11	5.63E-04	1.41E-03	1773.38	not significant
8944	CLN3	1.11	1.64E-03	3.76E-03	1262.01	not significant
8945	RAD52	1.11	1.68E-02	3.13E-02	727.01	not significant
8946	TSTD2	1.11	5.40E-03	1.12E-02	1007.50	not significant
8947	RAB27A	1.11	3.21E-04	8.43E-04	1815.77	not significant
8948	ARID3B	1.11	1.28E-04	3.61E-04	2056.00	not significant
8949	RUSC1-AS1	1.11	1.50E-01	2.17E-01	16.10	not significant
8950	ZMIZ1	1.11	2.92E-06	1.04E-05	7231.40	not significant
8951	ZBTB45	1.11	4.91E-02	8.17E-02	427.62	not significant
8952	PCYOX1L	1.11	4.07E-02	6.90E-02	463.91	not significant
8953	CD59	1.11	6.77E-04	1.67E-03	1938.06	not significant
8954	AGTPBP1	1.11	1.55E-03	3.58E-03	1309.40	not significant
8955	RNF7	1.11	9.90E-04	2.37E-03	1507.50	not significant
8956	DHRS11	1.12	1.91E-01	2.65E-01	67.34	not significant
8957	NKTR	1.12	1.61E-01	2.30E-01	5182.03	not significant
8958	MGC72080	1.12	5.98E-02	9.72E-02	307.18	not significant
8959	ZNF865	1.12	9.99E-03	1.96E-02	742.47	not significant
8960	ZDHHC17	1.12	2.03E-04	5.54E-04	1862.35	not significant
8961	C17orf85	1.12	3.57E-06	1.26E-05	4429.85	not significant
8962	VHL	1.12	2.04E-06	7.43E-06	5516.95	not significant
8963	DENND4B	1.12	2.38E-04	6.40E-04	4119.87	not significant
8964	SYNJ1	1.12	5.66E-03	1.17E-02	1010.67	not significant

8965	PTCH1	1.12	1.54E-01	2.22E-01	117.45	not significant
8966	XPC	1.12	1.21E-03	2.86E-03	1258.05	not significant
8967	PRTFDC1	1.12	4.77E-03	1.01E-02	1059.10	not significant
8968	PGM3	1.12	2.65E-02	4.73E-02	531.08	not significant
8969	PINLYP	1.12	4.30E-02	7.27E-02	412.82	not significant
8970	ZNF213	1.12	3.08E-02	5.41E-02	503.16	not significant
8971	SUGP2	1.12	1.10E-01	1.65E-01	5792.06	not significant
8972	NLRX1	1.12	5.88E-03	1.21E-02	924.79	not significant
8973	DEAF1	1.12	2.28E-03	5.10E-03	1257.32	not significant
8974	OSGIN2	1.12	1.51E-03	3.49E-03	1468.39	not significant
8975	RSL24D1	1.12	2.08E-05	6.60E-05	4084.36	not significant
8976	IQCH-AS1	1.12	1.10E-01	1.65E-01	197.63	not significant
8977	DNAJB2	1.12	9.32E-03	1.84E-02	865.79	not significant
8978	SIPA1L3	1.12	1.43E-03	3.33E-03	1458.89	not significant
8979	EPC1	1.12	8.43E-04	2.04E-03	1775.04	not significant
8980	JADE2	1.12	1.73E-06	6.37E-06	4832.03	not significant
8981	ATP8A1	1.12	3.95E-03	8.46E-03	1069.33	not significant
8982	PRRG4	1.12	4.72E-02	7.90E-02	346.32	not significant
8983	HDAC10	1.12	7.35E-03	1.48E-02	1206.68	not significant
8984	SMG1P5	1.12	1.41E-01	2.05E-01	17.43	not significant
8985	ZNF552	1.12	9.50E-02	1.46E-01	222.03	not significant
8986	FBXO36	1.12	1.70E-01	2.42E-01	92.27	not significant
8987	TBC1D15	1.12	1.25E-04	3.54E-04	2010.81	not significant
8988	CD1A	1.12	5.66E-04	1.42E-03	1828.60	not significant
8989	ZNF710	1.12	6.63E-03	1.35E-02	859.44	not significant
8990	SSR3	1.12	5.06E-07	1.99E-06	6569.21	not significant
8991	GCSAM	1.12	8.59E-04	2.08E-03	1572.35	not significant
8992	LOC101927621	1.12	1.79E-01	2.52E-01	83.19	not significant
8993	FAM24B	1.12	9.33E-02	1.44E-01	229.32	not significant
8994	EFNB1	1.12	7.14E-02	1.14E-01	258.89	not significant
8995	SLC3A2	1.12	1.41E-06	5.26E-06	5047.78	not significant
8996	OARD1	1.12	2.79E-03	6.15E-03	1338.25	not significant
8997	SLC2A11	1.12	1.11E-01	1.66E-01	221.73	not significant
8998	REEP2	1.12	3.90E-02	6.66E-02	438.57	not significant
8999	WIZ	1.12	9.23E-05	2.67E-04	2110.32	not significant
9000	LEPRE1	1.12	1.45E-03	3.37E-03	1301.20	not significant
9001	C2orf15	1.12	1.72E-01	2.44E-01	24.19	not significant
9002	BSCL2	1.12	1.46E-01	2.12E-01	121.12	not significant
9003	LMF1	1.12	6.06E-02	9.83E-02	309.68	not significant
9004	SLC25A25	1.12	3.53E-03	7.63E-03	976.25	not significant
9005	H3F3B	1.12	1.83E-07	7.58E-07	38721.49	not significant
9006	GLI4	1.12	1.95E-02	3.59E-02	645.30	not significant
9007	TRIM44	1.12	1.91E-01	2.66E-01	56.88	not significant
9008	PAIP1	1.12	2.88E-03	6.32E-03	1206.00	not significant
9009	C9orf91	1.12	1.71E-03	3.91E-03	1170.55	not significant
9010	REC8	1.12	1.82E-02	3.36E-02	649.70	not significant
9011	P2RY11	1.12	1.77E-01	2.50E-01	87.16	not significant
9012	TROVE2	1.12	2.95E-03	6.47E-03	1147.88	not significant
9013	GUCD1	1.12	3.00E-05	9.33E-05	3661.91	not significant
9014	CRY1	1.12	1.29E-04	3.64E-04	1970.17	not significant
9015	TTC21B	1.12	2.11E-03	4.74E-03	1245.25	not significant
9016	SLC30A4	1.12	9.85E-02	1.51E-01	191.58	not significant
9017	CHD9	1.12	3.30E-05	1.02E-04	3095.56	not significant
9018	AURKAPS1	1.12	1.89E-01	2.64E-01	37.55	not significant
9019	BRF1	1.12	6.34E-04	1.57E-03	1576.29	not significant
9020	MYL5	1.12	1.90E-01	2.65E-01	44.67	not significant
9021	USP37	1.12	9.74E-05	2.80E-04	2235.31	not significant
9022	KCNK6	1.12	1.60E-01	2.28E-01	98.05	not significant
9023	GTF2F1	1.12	1.85E-06	6.77E-06	4487.26	not significant
9024	SAMD4B	1.12	1.12E-04	3.17E-04	2136.81	not significant
9025	OSTC	1.12	3.33E-05	1.03E-04	3997.66	not significant
9026	TSSC1	1.12	2.89E-04	7.63E-04	2269.16	not significant
9027	RYK	1.12	4.77E-04	1.21E-03	1446.62	not significant
9028	TTC33	1.12	1.78E-03	4.05E-03	1229.39	not significant
9029	RAB39B	1.12	1.82E-01	2.55E-01	32.99	not significant
9030	IRAK1	1.12	4.18E-04	1.08E-03	1769.12	not significant
9031	PBX4	1.12	1.19E-01	1.77E-01	157.44	not significant
9032	ZNRF2	1.12	1.31E-03	3.07E-03	1502.28	not significant
9033	MTMR3	1.12	4.54E-04	1.16E-03	1808.59	not significant
9034	PPP2R1A	1.12	1.93E-06	7.06E-06	7516.73	not significant
9035	ITFG1	1.12	1.87E-03	4.24E-03	1529.94	not significant
9036	ICK	1.12	1.48E-02	2.80E-02	610.95	not significant
9037	P4HB	1.12	7.00E-08	3.04E-07	27890.83	not significant
9038	POLE4	1.12	5.32E-03	1.11E-02	809.59	not significant
9039	DEPDC5	1.12	4.09E-03	8.73E-03	937.50	not significant
9040	C15orf57	1.12	5.63E-02	9.22E-02	320.40	not significant
9041	KIAA1462	1.12	4.48E-02	7.53E-02	352.60	not significant
9042	PTGER4	1.12	4.05E-06	1.42E-05	5443.60	not significant
9043	CDPF1	1.12	6.83E-02	1.09E-01	267.87	not significant
9044	SDHAP2	1.12	1.70E-01	2.41E-01	82.15	not significant
9045	BCL2A1	1.12	1.85E-01	2.59E-01	52.38	not significant
9046	POLN	1.12	1.79E-01	2.52E-01	42.17	not significant
9047	EIF4ENIF1	1.12	4.59E-04	1.17E-03	1534.95	not significant
9048	TMEM160	1.12	8.42E-03	1.68E-02	919.37	not significant
9049	WIPF1	1.12	1.15E-07	4.86E-07	11707.83	not significant
9050	C5orf15	1.12	1.51E-04	4.21E-04	1736.32	not significant
9051	PLEKHA1	1.12	1.83E-01	2.57E-01	44.46	not significant
9052	ANKRD12	1.12	3.78E-05	1.16E-04	2483.00	not significant

9053	LOC100507564	1.12	1.17E-01	1.75E-01	14.21	not significant
9054	ZNF853	1.12	1.76E-01	2.48E-01	32.56	not significant
9055	AHCYL2	1.12	1.07E-03	2.54E-03	1341.39	not significant
9056	ZNF574	1.12	1.24E-02	2.39E-02	670.41	not significant
9057	COMMD5	1.12	4.73E-02	7.91E-02	357.42	not significant
9058	THRIL	1.12	1.43E-01	2.09E-01	23.89	not significant
9059	SPATS2	1.12	4.34E-04	1.11E-03	1458.15	not significant
9060	DGKA	1.12	3.94E-02	6.72E-02	5898.20	not significant
9061	RRM2	1.12	7.10E-08	3.08E-07	20641.00	not significant
9062	PTBP2	1.12	4.49E-03	9.52E-03	893.68	not significant
9063	SLC5A3	1.12	2.58E-02	4.62E-02	5188.97	not significant
9064	LRRC1	1.12	3.44E-02	5.97E-02	382.36	not significant
9065	NFATC1	1.12	1.32E-03	3.09E-03	1388.12	not significant
9066	PLEK	1.12	1.26E-01	1.87E-01	15.16	not significant
9067	IFT22	1.12	1.96E-02	3.60E-02	514.53	not significant
9068	TDRD3	1.12	1.07E-02	2.08E-02	628.66	not significant
9069	CEP152	1.12	1.50E-05	4.85E-05	2612.25	not significant
9070	PAIP2	1.12	4.60E-07	1.82E-06	8559.06	not significant
9071	TRABD	1.12	7.65E-07	2.93E-06	4065.63	not significant
9072	PTPN9	1.12	4.13E-04	1.06E-03	1937.99	not significant
9073	WDTC1	1.12	4.40E-05	1.34E-04	3222.50	not significant
9074	PI4KAP2	1.12	9.69E-02	1.49E-01	196.42	not significant
9075	SPPL3	1.12	7.51E-06	2.54E-05	3749.49	not significant
9076	ZNF512	1.12	2.74E-06	9.83E-06	3346.96	not significant
9077	VAMP3	1.12	2.92E-03	6.40E-03	978.10	not significant
9078	XRN2	1.12	2.33E-09	1.19E-08	9215.83	not significant
9079	RDH14	1.12	1.78E-01	2.51E-01	61.73	not significant
9080	THOC5	1.12	9.04E-05	2.61E-04	1912.76	not significant
9081	NUDT2	1.12	7.83E-03	1.57E-02	860.95	not significant
9082	CACNB1	1.12	2.36E-02	4.25E-02	541.49	not significant
9083	TPT1-AS1	1.12	7.01E-02	1.12E-01	235.52	not significant
9084	UBAC2	1.12	4.59E-06	1.59E-05	3098.44	not significant
9085	SIMC1	1.12	2.30E-02	4.16E-02	474.15	not significant
9086	SLC22A18	1.12	1.55E-01	2.22E-01	99.06	not significant
9087	KAT6A	1.12	7.43E-08	3.22E-07	8826.85	not significant
9088	MTHFS	1.12	1.67E-01	2.37E-01	27.10	not significant
9089	AQP11	1.12	1.43E-01	2.08E-01	20.70	not significant
9090	BCOR	1.12	3.00E-05	9.33E-05	4740.27	not significant
9091	SFT2D2	1.12	3.86E-02	6.59E-02	353.76	not significant
9092	IL16	1.12	2.35E-05	7.41E-05	2325.52	not significant
9093	BRD8	1.12	3.96E-05	1.21E-04	2797.73	not significant
9094	CEP290	1.12	3.18E-03	6.92E-03	1246.46	not significant
9095	IDS	1.12	2.76E-02	4.90E-02	413.87	not significant
9096	CC2D1A	1.12	9.90E-04	2.37E-03	1457.21	not significant
9097	RUFY1	1.12	9.57E-05	2.76E-04	1991.81	not significant
9098	USP46	1.12	3.97E-02	6.77E-02	332.49	not significant
9099	RANBP9	1.12	7.19E-07	2.77E-06	3708.63	not significant
9100	DUSP14	1.12	6.71E-03	1.37E-02	813.02	not significant
9101	GPR107	1.12	6.88E-03	1.40E-02	691.30	not significant
9102	CENPB	1.12	1.39E-04	3.88E-04	5156.58	not significant
9103	COX14	1.12	8.05E-03	1.61E-02	690.28	not significant
9104	CTDSP2	1.12	1.14E-06	4.28E-06	14808.67	not significant
9105	TRMT12	1.12	1.34E-02	2.57E-02	550.11	not significant
9106	SLC18B1	1.12	9.77E-03	1.92E-02	624.87	not significant
9107	TMEM25	1.12	1.59E-01	2.27E-01	27.08	not significant
9108	CLGN	1.12	1.50E-03	3.47E-03	1364.19	not significant
9109	TCP11L1	1.12	1.06E-02	2.06E-02	670.51	not significant
9110	TBC1D13	1.12	5.69E-03	1.18E-02	877.32	not significant
9111	ERG	1.12	1.06E-03	2.53E-03	1673.71	not significant
9112	LINC01215	1.12	2.70E-04	7.19E-04	1566.91	not significant
9113	DAG1	1.12	3.76E-03	8.09E-03	889.90	not significant
9114	UBALD2	1.12	3.75E-07	1.50E-06	5050.64	not significant
9115	AEBP1	1.12	2.61E-02	4.66E-02	27805.30	not significant
9116	USF1	1.12	3.99E-05	1.22E-04	2581.06	not significant
9117	FAM213A	1.12	2.44E-04	6.54E-04	1486.62	not significant
9118	PPP1R12B	1.12	4.07E-03	8.69E-03	785.57	not significant
9119	DAPP1	1.12	1.02E-01	1.56E-01	158.34	not significant
9120	RASSF2	1.12	6.56E-06	2.23E-05	2969.58	not significant
9121	RAI1	1.12	3.18E-05	9.85E-05	2706.49	not significant
9122	SNTB2	1.12	1.83E-03	4.16E-03	1303.80	not significant
9123	TCEAL1	1.12	1.26E-01	1.86E-01	128.43	not significant
9124	VIM-AS1	1.12	1.53E-01	2.20E-01	416.35	not significant
9125	SLC25A28	1.12	1.24E-02	2.39E-02	652.39	not significant
9126	DUT	1.12	1.17E-06	4.39E-06	7000.27	not significant
9127	RNF38	1.12	7.08E-05	2.08E-04	1949.13	not significant
9128	C19orf60	1.12	7.86E-03	1.58E-02	668.11	not significant
9129	PRR11	1.12	1.97E-07	8.15E-07	10500.40	not significant
9130	TFE3	1.12	6.91E-02	1.10E-01	230.13	not significant
9131	BRAF	1.12	1.77E-02	3.28E-02	482.74	not significant
9132	HLCS	1.12	1.64E-03	3.76E-03	1018.73	not significant
9133	STX16	1.12	5.18E-05	1.55E-04	2989.90	not significant
9134	CENPO	1.12	5.52E-07	2.15E-06	3806.69	not significant
9135	KIAA1919	1.12	3.55E-02	6.13E-02	422.03	not significant
9136	WDR81	1.12	1.30E-03	3.05E-03	1102.11	not significant
9137	UBE2V1	1.12	1.62E-01	2.32E-01	77.78	not significant
9138	TSPAN4	1.12	1.81E-02	3.36E-02	528.14	not significant
9139	LRRC37BP1	1.12	5.47E-03	1.14E-02	767.27	not significant
9140	RP2	1.13	1.45E-01	2.11E-01	107.18	not significant

9141	CCL28	1.13	1.66E-01	2.36E-01	30.58	not significant
9142	EPB41L5	1.13	4.19E-03	8.91E-03	868.96	not significant
9143	KLHL28	1.13	7.54E-03	1.52E-02	675.90	not significant
9144	SMKR1	1.13	1.50E-01	2.16E-01	22.77	not significant
9145	NISCH	1.13	9.60E-05	2.77E-04	4822.15	not significant
9146	ZCCHC3	1.13	1.36E-05	4.45E-05	3057.31	not significant
9147	ARHGAP35	1.13	4.46E-06	1.55E-05	3839.80	not significant
9148	C11orf30	1.13	3.63E-04	9.43E-04	2021.04	not significant
9149	VPS52	1.13	8.63E-03	1.72E-02	635.02	not significant
9150	GRAP2	1.13	1.09E-07	4.65E-07	7496.57	not significant
9151	SH2B1	1.13	5.86E-02	9.55E-02	2177.55	not significant
9152	B4GALT3	1.13	1.31E-03	3.08E-03	1102.75	not significant
9153	ACAA1	1.13	3.43E-05	1.06E-04	2210.40	not significant
9154	RUNX3	1.13	7.74E-05	2.26E-04	1929.38	not significant
9155	SLC17A5	1.13	4.98E-02	8.29E-02	305.76	not significant
9156	VAMP1	1.13	1.46E-01	2.12E-01	1291.37	not significant
9157	ALDH8A1	1.13	1.68E-01	2.39E-01	35.87	not significant
9158	ARHGEF19	1.13	8.04E-02	1.26E-01	192.41	not significant
9159	NDUFB11	1.13	3.55E-03	7.67E-03	829.44	not significant
9160	MZT2A	1.13	2.90E-04	7.67E-04	2390.51	not significant
9161	CLMN	1.13	1.69E-01	2.40E-01	37.86	not significant
9162	EPHB6	1.13	1.37E-05	4.45E-05	3362.19	not significant
9163	ARMC5	1.13	1.03E-02	2.02E-02	615.38	not significant
9164	ATF7IP	1.13	9.37E-05	2.70E-04	3033.05	not significant
9165	AGO1	1.13	1.35E-05	4.41E-05	3088.01	not significant
9166	ZBTB5	1.13	2.18E-04	5.91E-04	1542.19	not significant
9167	ZNF780B	1.13	1.45E-01	2.10E-01	677.71	not significant
9168	NR1H2	1.13	1.85E-04	5.09E-04	1778.26	not significant
9169	UQCRB	1.13	2.32E-02	4.18E-02	5322.44	not significant
9170	FAM92A1	1.13	1.62E-02	3.03E-02	478.54	not significant
9171	UBXN8	1.13	1.55E-02	2.91E-02	497.74	not significant
9172	LOC100507577	1.13	1.60E-01	2.29E-01	73.10	not significant
9173	INO80B	1.13	1.17E-01	1.75E-01	14.85	not significant
9174	SLC15A4	1.13	2.20E-03	4.94E-03	963.21	not significant
9175	MCM9	1.13	8.69E-04	2.10E-03	1089.66	not significant
9176	JMJD1C-AS1	1.13	6.94E-02	1.11E-01	8.84	not significant
9177	AGPAT4	1.13	1.40E-01	2.04E-01	97.57	not significant
9178	PHF12	1.13	1.37E-05	4.48E-05	2521.25	not significant
9179	MAPKAPK2	1.13	3.53E-03	7.63E-03	777.55	not significant
9180	POLE	1.13	4.98E-02	8.28E-02	12005.19	not significant
9181	KDM5A	1.13	9.29E-08	3.99E-07	5090.96	not significant
9182	QSOX2	1.13	2.35E-03	5.24E-03	1048.34	not significant
9183	C1orf198	1.13	3.36E-03	7.31E-03	1038.14	not significant
9184	SLC35A1	1.13	8.80E-03	1.75E-02	584.08	not significant
9185	GIT2	1.13	5.39E-07	2.10E-06	3774.75	not significant
9186	ETHE1	1.13	2.25E-02	4.09E-02	426.70	not significant
9187	GPBP1L1	1.13	3.18E-09	1.60E-08	6268.24	not significant
9188	NBN	1.13	9.90E-06	3.29E-05	3531.68	not significant
9189	TSNARE1	1.13	3.22E-02	5.63E-02	360.19	not significant
9190	TRIM59	1.13	4.34E-03	9.21E-03	807.80	not significant
9191	FLJ27354	1.13	1.32E-01	1.93E-01	18.11	not significant
9192	LINC00618	1.13	1.23E-01	1.82E-01	16.24	not significant
9193	TTC19	1.13	1.34E-05	4.39E-05	2295.72	not significant
9194	C1QTNF3	1.13	7.13E-02	1.13E-01	217.18	not significant
9195	ZZEF1	1.13	2.58E-05	8.10E-05	3773.40	not significant
9196	PTCD1	1.13	7.06E-02	1.12E-01	9.38	not significant
9197	LAG3	1.13	1.03E-01	1.57E-01	13.05	not significant
9198	ABHD11	1.13	1.59E-01	2.27E-01	63.52	not significant
9199	RBM48	1.13	8.94E-03	1.77E-02	573.69	not significant
9200	RCOR3	1.13	4.75E-04	1.21E-03	1251.86	not significant
9201	FRAT2	1.13	3.63E-02	6.25E-02	370.02	not significant
9202	FURIN	1.13	2.51E-03	5.56E-03	1056.88	not significant
9203	ZRANB1	1.13	8.82E-05	2.55E-04	1731.73	not significant
9204	CTBS	1.13	4.94E-03	1.04E-02	755.99	not significant
9205	BTBD9	1.13	2.54E-02	4.56E-02	403.61	not significant
9206	EFNA4	1.13	1.39E-01	2.04E-01	92.20	not significant
9207	RUNDC1	1.13	2.09E-03	4.71E-03	863.40	not significant
9208	SCARF2	1.13	1.60E-01	2.29E-01	31.83	not significant
9209	LOC100506159	1.13	1.53E-01	2.20E-01	80.94	not significant
9210	RNF146	1.13	1.48E-02	2.79E-02	512.16	not significant
9211	MTG1	1.13	5.35E-04	1.35E-03	1277.02	not significant
9212	OSBPL2	1.13	1.71E-03	3.92E-03	1034.17	not significant
9213	KDM8	1.13	6.41E-02	1.03E-01	225.37	not significant
9214	TCF12	1.13	9.45E-09	4.55E-08	7035.75	not significant
9215	RPARP-AS1	1.13	1.59E-02	2.97E-02	484.12	not significant
9216	PUSL1	1.13	5.17E-03	1.08E-02	741.05	not significant
9217	MEF2BNB	1.13	9.23E-02	1.42E-01	154.21	not significant
9218	HLTF	1.13	3.02E-08	1.37E-07	5064.07	not significant
9219	FBXW8	1.13	3.00E-04	7.92E-04	1278.91	not significant
9220	TRIM24	1.13	6.43E-08	2.81E-07	4597.83	not significant
9221	PABPC4	1.13	3.01E-09	1.52E-08	7261.74	not significant
9222	LINC01012	1.13	1.42E-01	2.07E-01	21.73	not significant
9223	TBC1D8	1.13	1.05E-02	2.06E-02	556.28	not significant
9224	AKR7A3	1.13	1.10E-01	1.65E-01	15.05	not significant
9225	LSM14B	1.13	1.98E-05	6.30E-05	2080.43	not significant
9226	FAM89A	1.13	7.38E-02	1.17E-01	198.45	not significant
9227	CYP20A1	1.13	6.50E-04	1.61E-03	1159.02	not significant
9228	SNX16	1.13	4.27E-02	7.22E-02	336.63	not significant

9229	RGP1	1.13	2.43E-02	4.38E-02	391.10	not significant
9230	SPAG16	1.13	2.06E-02	3.76E-02	473.22	not significant
9231	EHD2	1.13	1.12E-03	2.66E-03	980.00	not significant
9232	EMBP1	1.13	9.26E-02	1.43E-01	12.03	not significant
9233	WTAP	1.13	6.14E-07	2.38E-06	4375.42	not significant
9234	ZFY	1.13	1.93E-03	4.37E-03	993.73	not significant
9235	PKMYT1	1.13	1.35E-05	4.41E-05	4624.67	not significant
9236	SPPL2A	1.13	9.61E-04	2.30E-03	998.09	not significant
9237	FANCL	1.13	7.69E-04	1.87E-03	1083.29	not significant
9238	FAM102A	1.13	4.07E-04	1.05E-03	1472.99	not significant
9239	USP11	1.13	5.58E-08	2.47E-07	5010.13	not significant
9240	SPAG4	1.13	1.51E-01	2.17E-01	27.92	not significant
9241	DENND6A	1.13	2.19E-05	6.92E-05	1885.36	not significant
9242	TSTD1	1.13	1.04E-02	2.04E-02	584.89	not significant
9243	MGRN1	1.13	1.60E-05	5.18E-05	2224.44	not significant
9244	ANKRD39	1.13	2.37E-02	4.28E-02	407.38	not significant
9245	CNOT10	1.13	5.76E-06	1.97E-05	2385.98	not significant
9246	C14orf93	1.13	1.14E-01	1.71E-01	137.51	not significant
9247	MLXIP	1.13	3.73E-06	1.31E-05	4679.25	not significant
9248	HNRNPLL	1.13	6.68E-05	1.97E-04	3895.29	not significant
9249	GBA	1.13	4.68E-02	7.84E-02	292.66	not significant
9250	ZNF91	1.13	2.80E-04	7.42E-04	1413.62	not significant
9251	SAAL1	1.13	6.29E-05	1.87E-04	1930.11	not significant
9252	ANKRD50	1.13	3.46E-04	9.03E-04	1267.01	not significant
9253	ZNF655	1.13	2.23E-05	7.06E-05	4003.78	not significant
9254	FANCG	1.13	3.52E-06	1.24E-05	3041.57	not significant
9255	LOC283070	1.13	4.79E-03	1.01E-02	657.47	not significant
9256	FNBP1L	1.13	2.06E-04	5.61E-04	1440.01	not significant
9257	KLHL20	1.13	1.20E-02	2.32E-02	497.65	not significant
9258	CSRNP2	1.13	9.99E-05	2.87E-04	1774.44	not significant
9259	LOC101926963	1.13	8.28E-02	1.29E-01	189.88	not significant
9260	CNPY4	1.13	1.43E-02	2.71E-02	535.94	not significant
9261	MIRLET7BHG	1.13	1.40E-01	2.04E-01	25.09	not significant
9262	ERBB2IP	1.13	8.04E-08	3.47E-07	6401.29	not significant
9263	DVL1	1.13	2.34E-04	6.30E-04	1505.67	not significant
9264	RASSF7	1.13	2.62E-02	4.68E-02	380.31	not significant
9265	ZNF773	1.13	5.16E-02	8.55E-02	248.57	not significant
9266	PAFAH1B3	1.13	1.88E-05	6.02E-05	2094.33	not significant
9267	SORT1	1.13	1.02E-07	4.36E-07	4120.00	not significant
9268	ITGB2-AS1	1.13	9.78E-02	1.50E-01	187.18	not significant
9269	TNKS	1.13	2.38E-04	6.39E-04	2322.27	not significant
9270	ERGIC1	1.13	9.47E-10	5.01E-09	16063.80	not significant
9271	LOC648987	1.13	4.71E-03	9.94E-03	654.50	not significant
9272	SPAG9	1.13	1.14E-05	3.75E-05	2172.09	not significant
9273	PXMP4	1.13	2.37E-03	5.29E-03	892.43	not significant
9274	ARID1B	1.13	4.40E-07	1.74E-06	4716.25	not significant
9275	WBP2	1.13	2.26E-07	9.28E-07	4762.46	not significant
9276	C9orf163	1.13	5.28E-02	8.72E-02	8.77	not significant
9277	PRSS57	1.13	1.52E-01	2.19E-01	57.64	not significant
9278	CHRNE	1.13	5.07E-02	8.41E-02	7.70	not significant
9279	STARD5	1.13	1.44E-01	2.09E-01	80.57	not significant
9280	SPNS1	1.13	3.55E-04	9.24E-04	1415.84	not significant
9281	EXOC4	1.13	4.45E-07	1.76E-06	3696.64	not significant
9282	THTPA	1.13	3.86E-02	6.59E-02	283.99	not significant
9283	SLFN12	1.13	1.04E-02	2.03E-02	540.18	not significant
9284	NCOA4	1.13	1.44E-04	4.04E-04	1535.00	not significant
9285	ZNF501	1.13	9.80E-02	1.50E-01	147.85	not significant
9286	C1orf145	1.13	9.98E-02	1.52E-01	14.84	not significant
9287	ERO1LB	1.13	1.08E-01	1.63E-01	137.78	not significant
9288	WBP1L	1.13	3.80E-05	1.16E-04	2042.46	not significant
9289	AZIN2	1.13	5.88E-02	9.58E-02	214.85	not significant
9290	PPP2R2D	1.13	2.23E-02	4.05E-02	371.48	not significant
9291	PLEKHJ1	1.13	7.00E-05	2.06E-04	2909.41	not significant
9292	GAS7	1.13	4.05E-07	1.61E-06	5219.52	not significant
9293	LOC101929698	1.13	1.31E-01	1.92E-01	20.13	not significant
9294	PMS2P3	1.13	9.57E-02	1.47E-01	138.86	not significant
9295	NIT1	1.13	1.32E-03	3.08E-03	926.75	not significant
9296	GRHPR	1.13	7.05E-04	1.73E-03	1427.86	not significant
9297	BAD	1.13	9.09E-04	2.19E-03	1214.28	not significant
9298	PPIL4	1.13	3.97E-03	8.50E-03	784.89	not significant
9299	DHRS12	1.13	1.40E-01	2.05E-01	75.23	not significant
9300	DMXL1	1.13	3.31E-05	1.02E-04	2796.52	not significant
9301	C4orf3	1.13	4.71E-04	1.20E-03	2205.72	not significant
9302	AXIN1	1.13	7.46E-05	2.18E-04	1531.63	not significant
9303	SPICE1	1.13	5.23E-03	1.09E-02	804.63	not significant
9304	FAM57B	1.13	1.23E-01	1.83E-01	94.54	not significant
9305	GID8	1.13	8.67E-07	3.31E-06	3857.99	not significant
9306	HSF2	1.13	2.14E-04	5.82E-04	1744.41	not significant
9307	EIF5A2	1.13	1.85E-03	4.20E-03	812.58	not significant
9308	FAM65B	1.13	4.50E-07	1.78E-06	3075.14	not significant
9309	BLOC1S6	1.13	5.95E-06	2.04E-05	3376.57	not significant
9310	MED15	1.13	7.92E-06	2.67E-05	2154.58	not significant
9311	IL18BP	1.13	2.34E-02	4.22E-02	441.08	not significant
9312	CHFR	1.13	1.47E-07	6.18E-07	6160.33	not significant
9313	MMGT1	1.13	1.44E-01	2.09E-01	63.18	not significant
9314	HOXB3	1.13	3.53E-02	6.10E-02	359.22	not significant
9315	ITGA6	1.13	1.62E-03	3.72E-03	890.49	not significant
9316	ATP6V1G1	1.13	7.19E-06	2.44E-05	2530.76	not significant

9317	CDKN2C	1.13	1.92E-06	7.04E-06	3257.35	not significant
9318	SLC2A1	1.13	2.73E-04	7.26E-04	1239.85	not significant
9319	ATF7	1.13	6.68E-05	1.97E-04	1747.49	not significant
9320	ACYP2	1.13	1.01E-01	1.55E-01	122.85	not significant
9321	ISL2	1.13	8.26E-02	1.29E-01	161.44	not significant
9322	WHSC1L1	1.13	7.49E-10	4.01E-09	5795.87	not significant
9323	CLK2	1.13	2.97E-03	6.51E-03	894.11	not significant
9324	HERC2P9	1.13	8.70E-02	1.35E-01	161.97	not significant
9325	UBASH3A	1.14	7.10E-04	1.74E-03	1128.06	not significant
9326	SLC15A2	1.14	1.51E-01	2.18E-01	47.29	not significant
9327	SKOR1	1.14	1.25E-01	1.86E-01	22.85	not significant
9328	ATF4	1.14	1.67E-08	7.78E-08	16503.44	not significant
9329	MOGS	1.14	2.66E-04	7.08E-04	1839.52	not significant
9330	RWDD4	1.14	4.66E-03	9.84E-03	627.28	not significant
9331	ANKRD37	1.14	1.37E-01	2.01E-01	70.08	not significant
9332	PIGB	1.14	2.92E-02	5.15E-02	311.92	not significant
9333	NPAS2	1.14	7.45E-04	1.82E-03	1074.23	not significant
9334	CENPC	1.14	7.72E-05	2.25E-04	1590.68	not significant
9335	HGS	1.14	4.84E-06	1.68E-05	3585.75	not significant
9336	RPS10	1.14	6.96E-02	1.11E-01	195.12	not significant
9337	ZNF610	1.14	2.46E-02	4.43E-02	341.60	not significant
9338	SARNP	1.14	2.01E-06	7.35E-06	2851.81	not significant
9339	DPH5	1.14	1.21E-04	3.41E-04	1579.81	not significant
9340	ADCK4	1.14	5.29E-03	1.10E-02	585.35	not significant
9341	UFC1	1.14	2.62E-05	8.20E-05	2098.88	not significant
9342	LOC101926943	1.14	8.77E-02	1.36E-01	13.27	not significant
9343	ARMCX2	1.14	1.00E-01	1.53E-01	15.21	not significant
9344	ATG9A	1.14	2.26E-04	6.11E-04	1236.76	not significant
9345	BOD1	1.14	1.39E-03	3.24E-03	829.05	not significant
9346	CDC14A	1.14	1.72E-02	3.21E-02	462.53	not significant
9347	TRPC4AP	1.14	1.68E-08	7.85E-08	5303.91	not significant
9348	GCH1	1.14	1.48E-06	5.50E-06	2761.08	not significant
9349	LZTS3	1.14	1.01E-01	1.54E-01	16.02	not significant
9350	MIR600HG	1.14	2.81E-02	4.97E-02	304.49	not significant
9351	DDX60	1.14	1.21E-04	3.42E-04	1438.06	not significant
9352	RNF167	1.14	1.02E-06	3.86E-06	3973.98	not significant
9353	LOC101928378	1.14	8.88E-02	1.38E-01	178.99	not significant
9354	SPTBN1	1.14	2.95E-06	1.05E-05	19501.93	not significant
9355	CCDC73	1.14	1.11E-01	1.67E-01	23.13	not significant
9356	C5orf30	1.14	1.45E-01	2.10E-01	41.86	not significant
9357	MCOLN1	1.14	7.28E-03	1.47E-02	558.08	not significant
9358	GOLT1B	1.14	2.33E-04	6.29E-04	1325.12	not significant
9359	RILPL1	1.14	8.29E-02	1.30E-01	150.62	not significant
9360	PRKD3	1.14	1.40E-07	5.89E-07	3206.55	not significant
9361	ZDHHC21	1.14	3.05E-02	5.35E-02	313.90	not significant
9362	KIAA0907	1.14	3.02E-02	5.31E-02	2601.22	not significant
9363	BTF3L4	1.14	3.52E-06	1.24E-05	2691.86	not significant
9364	MORN1	1.14	1.39E-01	2.04E-01	57.26	not significant
9365	SUMF2	1.14	7.21E-09	3.51E-08	5415.43	not significant
9366	NRDE2	1.14	3.37E-03	7.31E-03	674.66	not significant
9367	KCNC4	1.14	1.37E-02	2.62E-02	417.33	not significant
9368	ZNF227	1.14	1.05E-03	2.50E-03	1094.67	not significant
9369	ULK1	1.14	3.67E-06	1.29E-05	3824.26	not significant
9370	PRR12	1.14	8.45E-06	2.83E-05	3143.85	not significant
9371	SPATA25	1.14	1.09E-01	1.65E-01	17.10	not significant
9372	WDR34	1.14	8.34E-07	3.18E-06	3076.73	not significant
9373	DOCK8	1.14	7.25E-10	3.89E-09	14249.09	not significant
9374	NFKBID	1.14	5.66E-02	9.26E-02	207.17	not significant
9375	DYRK1A	1.14	5.64E-08	2.49E-07	3686.52	not significant
9376	RECK	1.14	8.34E-04	2.02E-03	968.85	not significant
9377	MGAT4B	1.14	1.96E-04	5.34E-04	1317.59	not significant
9378	CCDC88C	1.14	2.48E-08	1.14E-07	5165.99	not significant
9379	HADHB	1.14	2.33E-06	8.42E-06	2712.46	not significant
9380	SPG11	1.14	8.90E-06	2.98E-05	1850.07	not significant
9381	C15orf41	1.14	1.09E-02	2.12E-02	454.07	not significant
9382	CHPF2	1.14	2.55E-04	6.83E-04	1404.21	not significant
9383	BLCAP	1.14	1.32E-04	3.72E-04	1650.42	not significant
9384	ZNF862	1.14	4.99E-03	1.05E-02	597.01	not significant
9385	CEP120	1.14	5.13E-05	1.54E-04	1461.12	not significant
9386	TTN-AS1	1.14	3.06E-02	5.38E-02	294.42	not significant
9387	GXYLT2	1.14	1.02E-04	2.92E-04	1382.95	not significant
9388	SNAPC2	1.14	4.06E-03	8.68E-03	640.45	not significant
9389	COMMD3	1.14	1.24E-03	2.92E-03	864.74	not significant
9390	SMYD4	1.14	4.27E-05	1.30E-04	1493.87	not significant
9391	ZNF606	1.14	1.15E-02	2.23E-02	456.48	not significant
9392	ZNF273	1.14	3.94E-05	1.20E-04	1614.76	not significant
9393	PABPC4L	1.14	2.84E-03	6.25E-03	726.14	not significant
9394	DNAJC9	1.14	3.45E-07	1.39E-06	5557.11	not significant
9395	ASH1L	1.14	2.12E-02	3.87E-02	1917.18	not significant
9396	ZNF527	1.14	1.22E-02	2.34E-02	453.18	not significant
9397	ADAMTS10	1.14	1.21E-02	2.32E-02	438.17	not significant
9398	C20orf197	1.14	1.92E-02	3.54E-02	380.93	not significant
9399	PGPEP1L	1.14	1.40E-01	2.04E-01	36.15	not significant
9400	SYNRG	1.14	1.76E-07	7.30E-07	3811.33	not significant
9401	WASH7P	1.14	1.35E-01	1.98E-01	29.79	not significant
9402	FAM160B2	1.14	3.73E-04	9.67E-04	1560.89	not significant
9403	NDFIP1	1.14	1.41E-09	7.34E-09	6156.46	not significant
9404	PRDM15	1.14	7.10E-03	1.44E-02	547.62	not significant

9405	TRAPPC6A	1.14	2.92E-02	5.16E-02	447.21	not significant
9406	ZFP36L2	1.14	6.42E-08	2.80E-07	3609.26	not significant
9407	RAD51D	1.14	2.04E-03	4.59E-03	811.12	not significant
9408	HS2ST1	1.14	3.44E-08	1.56E-07	3909.35	not significant
9409	RPL13A	1.14	3.19E-09	1.61E-08	7062.22	not significant
9410	POLR3C	1.14	6.63E-03	1.35E-02	556.61	not significant
9411	CCDC120	1.14	9.89E-02	1.51E-01	110.73	not significant
9412	FAM8A1	1.14	2.13E-03	4.79E-03	724.15	not significant
9413	FUZ	1.14	6.25E-04	1.55E-03	998.63	not significant
9414	TMEM170B	1.14	5.69E-04	1.43E-03	1279.73	not significant
9415	TAB3	1.14	1.34E-05	4.39E-05	1985.65	not significant
9416	ZNF331	1.14	3.39E-03	7.35E-03	1022.29	not significant
9417	RELT	1.14	1.11E-03	2.63E-03	888.94	not significant
9418	CGRRF1	1.14	3.94E-02	6.71E-02	250.97	not significant
9419	ACAP3	1.14	3.92E-04	1.01E-03	1702.96	not significant
9420	TAF1C	1.14	4.59E-02	7.71E-02	2391.65	not significant
9421	NCK2	1.14	2.01E-04	5.49E-04	1169.33	not significant
9422	VPS39	1.14	4.46E-06	1.55E-05	2259.17	not significant
9423	C14orf159	1.14	9.78E-06	3.25E-05	2017.13	not significant
9424	ANKLE2	1.14	2.98E-10	1.67E-09	6043.62	not significant
9425	MIDN	1.14	4.20E-06	1.47E-05	2667.32	not significant
9426	DNASE2	1.14	9.23E-04	2.22E-03	1251.96	not significant
9427	POLI	1.14	1.76E-02	3.26E-02	406.85	not significant
9428	ZFP1	1.14	1.95E-05	6.21E-05	1754.92	not significant
9429	IRS1	1.14	1.05E-02	2.05E-02	453.93	not significant
9430	KAT6B	1.14	3.02E-06	1.07E-05	2985.84	not significant
9431	L3MBTL3	1.14	8.96E-04	2.16E-03	877.29	not significant
9432	SLC38A7	1.14	1.03E-02	2.03E-02	449.23	not significant
9433	YES1	1.14	2.63E-03	5.82E-03	707.56	not significant
9434	CBR3	1.14	1.19E-01	1.77E-01	77.27	not significant
9435	PTPRE	1.14	7.08E-03	1.44E-02	543.56	not significant
9436	GGCX	1.14	4.16E-03	8.85E-03	623.65	not significant
9437	LRP11	1.14	9.64E-07	3.66E-06	2975.21	not significant
9438	DCTD	1.14	3.24E-07	1.30E-06	2958.51	not significant
9439	SSFA2	1.14	2.79E-03	6.15E-03	693.97	not significant
9440	RPSA	1.14	2.20E-06	7.98E-06	24020.26	not significant
9441	ZNF624	1.14	3.37E-02	5.85E-02	288.07	not significant
9442	ZNF558	1.14	8.18E-02	1.28E-01	135.98	not significant
9443	RNF19B	1.14	1.41E-03	3.28E-03	801.11	not significant
9444	CSNK1E	1.14	1.11E-06	4.19E-06	2489.77	not significant
9445	EOGT	1.14	9.92E-02	1.51E-01	104.51	not significant
9446	FAM111B	1.14	1.97E-04	5.36E-04	1132.00	not significant
9447	C21orf91	1.14	5.47E-06	1.88E-05	2066.06	not significant
9448	MVB12A	1.14	9.54E-03	1.88E-02	432.12	not significant
9449	FAM76A	1.14	3.90E-03	8.36E-03	651.66	not significant
9450	KHDRBS1	1.14	5.20E-10	2.85E-09	19878.15	not significant
9451	ZNF818P	1.14	2.09E-02	3.81E-02	331.47	not significant
9452	BCL2	1.14	3.11E-08	1.41E-07	4217.45	not significant
9453	IFI27L2	1.14	3.49E-02	6.03E-02	255.34	not significant
9454	AGPAT5	1.14	7.04E-10	3.79E-09	5796.48	not significant
9455	C17orf62	1.14	4.49E-09	2.23E-08	5889.22	not significant
9456	TAB1	1.14	9.18E-05	2.65E-04	1309.42	not significant
9457	PFDN5	1.14	2.95E-06	1.05E-05	4864.67	not significant
9458	TCTN3	1.14	1.72E-04	4.75E-04	1116.15	not significant
9459	LRRC34	1.14	3.54E-02	6.11E-02	254.27	not significant
9460	PHACTR4	1.14	5.74E-07	2.23E-06	2381.17	not significant
9461	RBFA	1.14	5.30E-04	1.34E-03	1001.81	not significant
9462	RICTOR	1.14	3.25E-02	5.67E-02	1872.21	not significant
9463	CRY2	1.14	9.73E-04	2.33E-03	849.29	not significant
9464	PMEPA1	1.14	2.61E-05	8.18E-05	2138.05	not significant
9465	PHF7	1.14	1.68E-03	3.84E-03	785.87	not significant
9466	ZNF675	1.14	8.89E-04	2.15E-03	900.49	not significant
9467	CCDC85B	1.14	9.36E-04	2.25E-03	1073.33	not significant
9468	LZTR1	1.14	6.30E-05	1.87E-04	1634.43	not significant
9469	RTN3	1.14	2.38E-08	1.10E-07	8112.62	not significant
9470	DIP2A	1.14	3.41E-04	8.91E-04	1356.40	not significant
9471	GALC	1.14	1.39E-02	2.65E-02	367.16	not significant
9472	ZNF768	1.14	6.00E-03	1.24E-02	487.19	not significant
9473	ZNF419	1.14	2.16E-02	3.92E-02	310.85	not significant
9474	DOCK5	1.14	8.98E-03	1.78E-02	506.06	not significant
9475	ACACB	1.14	4.51E-03	9.55E-03	533.30	not significant
9476	LOC100506844	1.14	1.79E-05	5.73E-05	1931.48	not significant
9477	ZNF691	1.14	2.83E-02	5.01E-02	293.58	not significant
9478	BCKDHB	1.14	2.73E-04	7.26E-04	1168.21	not significant
9479	DNAJC16	1.14	1.74E-03	3.97E-03	701.97	not significant
9480	LOC100270804	1.15	1.31E-01	1.92E-01	38.54	not significant
9481	VPS13C	1.15	2.60E-06	9.33E-06	5024.52	not significant
9482	MTHFD2	1.15	1.12E-09	5.87E-09	7822.39	not significant
9483	HIGD2A	1.15	2.31E-05	7.30E-05	2405.25	not significant
9484	RPS7	1.15	7.76E-03	1.56E-02	18892.07	not significant
9485	ZNF461	1.15	6.07E-02	9.84E-02	224.93	not significant
9486	TRIM9	1.15	1.30E-01	1.91E-01	38.17	not significant
9487	CD46	1.15	5.11E-08	2.26E-07	4779.34	not significant
9488	SCGB3A1	1.15	1.04E-02	2.04E-02	417.11	not significant
9489	FBXL12	1.15	2.09E-03	4.71E-03	675.34	not significant
9490	GOLGA1	1.15	7.63E-03	1.54E-02	519.66	not significant
9491	CDK2	1.15	1.53E-11	9.69E-11	7329.18	not significant
9492	C9orf43	1.15	6.24E-02	1.01E-01	10.61	not significant

9493	ZNF680	1.15	1.77E-04	4.87E-04	1067.73	not significant
9494	RTF1	1.15	2.51E-08	1.15E-07	4531.07	not significant
9495	RABL2A	1.15	1.15E-01	1.72E-01	73.96	not significant
9496	FLOT2	1.15	1.76E-04	4.86E-04	1172.49	not significant
9497	ISY1	1.15	6.07E-04	1.51E-03	989.15	not significant
9498	SUPT7L	1.15	3.99E-05	1.22E-04	1739.68	not significant
9499	DMAP1	1.15	1.71E-03	3.92E-03	866.20	not significant
9500	RBBP4	1.15	4.96E-13	3.59E-12	18248.56	not significant
9501	KLHL25	1.15	1.43E-02	2.72E-02	353.40	not significant
9502	TEP1	1.15	9.12E-04	2.20E-03	1330.48	not significant
9503	ARL17A	1.15	5.75E-02	9.40E-02	182.28	not significant
9504	ADPGK	1.15	3.78E-05	1.16E-04	1570.98	not significant
9505	RBM12B	1.15	3.03E-06	1.08E-05	2212.99	not significant
9506	DYNC1LI2	1.15	1.79E-04	4.93E-04	2026.08	not significant
9507	POMT2	1.15	3.95E-03	8.46E-03	568.79	not significant
9508	ZSCAN31	1.15	1.24E-01	1.83E-01	54.22	not significant
9509	CENPT	1.15	4.84E-02	8.07E-02	1601.50	not significant
9510	RUFY2	1.15	2.47E-02	4.44E-02	387.85	not significant
9511	SECISBP2L	1.15	3.35E-05	1.03E-04	2064.89	not significant
9512	KIAA0430	1.15	3.22E-06	1.14E-05	3101.93	not significant
9513	MAN2A1	1.15	2.85E-07	1.15E-06	2497.75	not significant
9514	DRAM2	1.15	4.77E-05	1.44E-04	1348.02	not significant
9515	ABHD2	1.15	4.54E-08	2.03E-07	3120.16	not significant
9516	GNAQ	1.15	2.17E-10	1.24E-09	6579.03	not significant
9517	DCUN1D4	1.15	3.59E-03	7.75E-03	698.27	not significant
9518	C7orf60	1.15	5.81E-04	1.45E-03	921.77	not significant
9519	CD58	1.15	2.02E-02	3.70E-02	1693.16	not significant
9520	ZNF436	1.15	1.75E-02	3.25E-02	332.81	not significant
9521	TRAF7	1.15	3.68E-09	1.84E-08	5017.89	not significant
9522	LDB1	1.15	7.52E-06	2.54E-05	3686.81	not significant
9523	LOC102724814	1.15	9.55E-02	1.47E-01	107.29	not significant
9524	CTDNEP1	1.15	2.55E-09	1.30E-08	6277.49	not significant
9525	43719_6028	1.15	4.00E-03	8.55E-03	592.65	not significant
9526	RASAL3	1.15	8.53E-06	2.86E-05	1761.85	not significant
9527	POFUT2	1.15	1.45E-02	2.75E-02	408.72	not significant
9528	ZNF764	1.15	5.12E-03	1.07E-02	557.55	not significant
9529	UBE2Q2	1.15	2.92E-06	1.05E-05	1832.46	not significant
9530	AMBRA1	1.15	2.00E-06	7.30E-06	2079.57	not significant
9531	ATG2A	1.15	2.44E-04	6.54E-04	1077.05	not significant
9532	PEX1	1.15	1.76E-05	5.65E-05	1814.48	not significant
9533	CD1E	1.15	2.98E-11	1.84E-10	24595.60	not significant
9534	PSPC1	1.15	3.42E-07	1.37E-06	2379.98	not significant
9535	CEPT1	1.15	5.38E-07	2.10E-06	2495.44	not significant
9536	PTK7	1.15	3.82E-06	1.34E-05	2386.52	not significant
9537	BNIP3L	1.15	4.64E-08	2.07E-07	3388.75	not significant
9538	RPL4	1.15	5.80E-09	2.84E-08	39626.73	not significant
9539	FTL	1.15	2.87E-08	1.31E-07	11968.79	not significant
9540	SUGT1P3	1.15	8.53E-02	1.33E-01	14.83	not significant
9541	FUT4	1.15	4.45E-05	1.35E-04	1569.19	not significant
9542	IRF2BP2	1.15	8.77E-07	3.34E-06	3201.43	not significant
9543	MIB1	1.15	5.02E-08	2.23E-07	3480.77	not significant
9544	USP22	1.15	5.79E-11	3.47E-10	11972.69	not significant
9545	CCNJ	1.15	1.24E-03	2.91E-03	724.86	not significant
9546	HENMT1	1.15	1.03E-05	3.41E-05	1741.37	not significant
9547	DOPEY2	1.15	5.44E-05	1.63E-04	1554.86	not significant
9548	APPL2	1.15	2.40E-04	6.44E-04	1169.88	not significant
9549	ZNF879	1.15	1.08E-01	1.64E-01	26.09	not significant
9550	RPS19	1.15	1.41E-06	5.24E-06	15833.81	not significant
9551	SMARCC2	1.15	1.12E-06	4.23E-06	10055.72	not significant
9552	ZBTB7C	1.15	1.16E-01	1.73E-01	61.56	not significant
9553	RCC2	1.15	4.30E-10	2.37E-09	16031.86	not significant
9554	HIPK1	1.15	2.58E-07	1.05E-06	4715.00	not significant
9555	CLIC1	1.15	1.16E-06	4.37E-06	2305.50	not significant
9556	IFITM3	1.15	1.20E-01	1.79E-01	37.67	not significant
9557	CRNDE	1.15	2.70E-05	8.45E-05	1663.36	not significant
9558	LOC728024	1.15	1.21E-01	1.81E-01	46.71	not significant
9559	CDAN1	1.15	2.58E-05	8.07E-05	1425.12	not significant
9560	WDR48	1.15	1.54E-06	5.69E-06	1989.07	not significant
9561	C9orf72	1.15	1.05E-01	1.59E-01	303.61	not significant
9562	TAZ	1.15	1.53E-02	2.88E-02	348.86	not significant
9563	STRIP1	1.15	4.52E-06	1.57E-05	1755.03	not significant
9564	PLXNA3	1.15	2.49E-02	4.46E-02	327.71	not significant
9565	CIC	1.15	4.62E-07	1.82E-06	2968.63	not significant
9566	EID1	1.15	7.83E-10	4.19E-09	4454.98	not significant
9567	PTPRCAP	1.15	2.78E-07	1.13E-06	6404.34	not significant
9568	ZNF320	1.15	1.06E-05	3.51E-05	1687.28	not significant
9569	MDP1	1.15	1.17E-01	1.74E-01	29.63	not significant
9570	MAP3K14	1.15	2.28E-03	5.09E-03	595.72	not significant
9571	PI4KAP1	1.15	8.99E-02	1.39E-01	101.15	not significant
9572	MIER2	1.15	4.24E-04	1.09E-03	832.03	not significant
9573	IGFLR1	1.15	6.17E-02	9.99E-02	142.55	not significant
9574	GRAMD1C	1.15	6.18E-02	1.00E-01	139.21	not significant
9575	ZBTB11	1.15	7.41E-06	2.51E-05	1978.96	not significant
9576	CHURC1	1.15	3.41E-06	1.21E-05	1775.35	not significant
9577	ZNF700	1.15	2.93E-03	6.41E-03	630.24	not significant
9578	LOC150776	1.15	8.86E-03	1.76E-02	479.20	not significant
9579	MSI2	1.15	1.25E-09	6.55E-09	6311.61	not significant
9580	TEX264	1.15	2.47E-05	7.76E-05	1369.86	not significant

9581	ZNF641	1.15	7.13E-03	1.45E-02	434.64	not significant
9582	RNF123	1.15	4.31E-06	1.50E-05	1602.48	not significant
9583	EVPL	1.15	1.40E-03	3.26E-03	800.99	not significant
9584	ACP2	1.15	2.72E-03	6.00E-03	594.99	not significant
9585	MESDC1	1.15	9.43E-06	3.14E-05	2656.11	not significant
9586	RABAC1	1.15	1.48E-02	2.80E-02	340.86	not significant
9587	PRSS21	1.15	4.77E-04	1.21E-03	863.18	not significant
9588	ZNF487	1.15	1.17E-01	1.74E-01	45.18	not significant
9589	FBXL14	1.15	6.08E-04	1.51E-03	1077.74	not significant
9590	RIN3	1.15	4.72E-08	2.10E-07	3022.36	not significant
9591	TTLL1	1.15	1.03E-02	2.03E-02	370.29	not significant
9592	MOAP1	1.15	6.19E-05	1.84E-04	1360.00	not significant
9593	CUX1	1.15	2.07E-06	7.52E-06	1753.86	not significant
9594	POLR2J3	1.15	1.74E-02	3.24E-02	328.10	not significant
9595	ZNF709	1.15	4.42E-02	7.45E-02	187.91	not significant
9596	DDX42	1.15	3.02E-13	2.22E-12	7547.59	not significant
9597	MRE11A	1.15	1.47E-06	5.47E-06	3004.52	not significant
9598	TESK1	1.15	1.80E-04	4.94E-04	931.36	not significant
9599	PUM1	1.15	1.43E-08	6.70E-08	3923.31	not significant
9600	HINT3	1.15	6.28E-04	1.56E-03	853.42	not significant
9601	RCN2	1.15	1.28E-08	6.04E-08	3250.34	not significant
9602	SLC44A2	1.15	4.40E-10	2.43E-09	3789.87	not significant
9603	STX2	1.15	3.13E-05	9.70E-05	1579.80	not significant
9604	BPTF	1.15	5.58E-08	2.46E-07	8782.53	not significant
9605	SIN3B	1.15	5.98E-06	2.05E-05	1656.77	not significant
9606	SMIM17	1.15	1.14E-01	1.71E-01	38.77	not significant
9607	POGK	1.15	3.71E-09	1.86E-08	3501.73	not significant
9608	RFFL	1.15	1.10E-01	1.66E-01	59.51	not significant
9609	GATAD2B	1.15	6.92E-03	1.41E-02	487.35	not significant
9610	NIPAL3	1.15	5.36E-05	1.61E-04	1090.30	not significant
9611	ZNF528	1.15	4.68E-02	7.84E-02	172.60	not significant
9612	CYP51A1	1.15	3.05E-04	8.05E-04	1070.83	not significant
9613	JMJD1C	1.15	7.03E-06	2.39E-05	2932.04	not significant
9614	ZNF341	1.16	3.49E-02	6.03E-02	198.33	not significant
9615	ITPKB	1.16	1.13E-04	3.21E-04	972.41	not significant
9616	RCBTB2	1.16	1.19E-11	7.65E-11	23312.92	not significant
9617	C2orf68	1.16	1.79E-07	7.43E-07	2236.63	not significant
9618	KDM4B	1.16	4.78E-06	1.65E-05	1827.68	not significant
9619	NKX3-2	1.16	6.47E-02	1.04E-01	12.16	not significant
9620	ZNF880	1.16	1.08E-02	2.11E-02	344.87	not significant
9621	RTTN	1.16	6.65E-06	2.27E-05	1526.21	not significant
9622	POC1A	1.16	1.16E-06	4.37E-06	1978.54	not significant
9623	CYHR1	1.16	3.49E-04	9.09E-04	818.05	not significant
9624	ARHGEF2	1.16	4.57E-10	2.52E-09	4265.60	not significant
9625	SYNJ2BP	1.16	8.20E-06	2.75E-05	1769.30	not significant
9626	AKT1	1.16	4.82E-12	3.21E-11	9490.46	not significant
9627	C19orf54	1.16	1.84E-04	5.04E-04	999.28	not significant
9628	CELSR2	1.16	1.67E-04	4.63E-04	989.21	not significant
9629	KAT7	1.16	2.48E-07	1.01E-06	2527.88	not significant
9630	ZNF730	1.16	1.22E-02	2.35E-02	328.38	not significant
9631	PHKG2	1.16	8.08E-05	2.35E-04	1051.97	not significant
9632	CHIC2	1.16	1.27E-02	2.43E-02	328.14	not significant
9633	ZNF350	1.16	2.31E-02	4.17E-02	273.22	not significant
9634	INO80C	1.16	4.94E-03	1.04E-02	456.09	not significant
9635	SMG1P7	1.16	7.98E-02	1.25E-01	103.65	not significant
9636	PLAGL1	1.16	3.68E-04	9.55E-04	871.06	not significant
9637	ZNF670	1.16	1.77E-02	3.28E-02	342.38	not significant
9638	EIF2D	1.16	5.38E-06	1.85E-05	1509.95	not significant
9639	ZNF644	1.16	9.17E-08	3.94E-07	2441.81	not significant
9640	TMEM192	1.16	1.21E-02	2.34E-02	395.61	not significant
9641	MOSPD2	1.16	5.67E-03	1.17E-02	434.18	not significant
9642	PARP8	1.16	5.04E-07	1.98E-06	2095.92	not significant
9643	FLVCR1	1.16	4.43E-04	1.13E-03	1003.24	not significant
9644	PCMTD2	1.16	1.33E-06	4.96E-06	1837.48	not significant
9645	NOTCH1	1.16	5.94E-03	1.22E-02	13481.21	not significant
9646	C1orf159	1.16	3.37E-03	7.31E-03	526.15	not significant
9647	CKMT2-AS1	1.16	3.79E-02	6.49E-02	190.29	not significant
9648	ABHD3	1.16	9.44E-07	3.59E-06	2103.19	not significant
9649	C12orf45	1.16	1.05E-02	2.05E-02	408.77	not significant
9650	ANKRD9	1.16	1.12E-01	1.68E-01	33.84	not significant
9651	ACSS1	1.16	1.31E-08	6.19E-08	6574.07	not significant
9652	MYBL1	1.16	5.47E-04	1.38E-03	1066.27	not significant
9653	ACP1	1.16	4.27E-10	2.36E-09	6798.43	not significant
9654	PARP16	1.16	6.76E-05	2.00E-04	1067.61	not significant
9655	PNPLA8	1.16	3.33E-05	1.03E-04	1238.85	not significant
9656	CEP128	1.16	3.28E-06	1.16E-05	1791.41	not significant
9657	ATP6AP1	1.16	1.02E-03	2.43E-03	651.87	not significant
9658	ESR2	1.16	8.36E-02	1.31E-01	18.83	not significant
9659	TIA1	1.16	7.30E-07	2.81E-06	6214.63	not significant
9660	PRRG2	1.16	4.27E-02	7.22E-02	9.14	not significant
9661	ZMYM6NB	1.16	1.97E-03	4.45E-03	605.55	not significant
9662	SLC2A13	1.16	3.53E-03	7.63E-03	483.57	not significant
9663	MEX3D	1.16	3.34E-05	1.03E-04	1587.41	not significant
9664	SEC24B-AS1	1.16	1.09E-01	1.64E-01	31.65	not significant
9665	BDH2	1.16	1.91E-04	5.23E-04	945.71	not significant
9666	CCDC176	1.16	3.34E-02	5.82E-02	207.47	not significant
9667	PPM1E	1.16	7.72E-02	1.22E-01	107.18	not significant
9668	WDFY2	1.16	1.07E-03	2.54E-03	617.63	not significant

9669	BTN3A2	1.16	7.85E-08	3.39E-07	2290.02	not significant
9670	NPC1	1.16	6.97E-05	2.05E-04	1079.55	not significant
9671	GLIS2	1.16	1.04E-01	1.58E-01	53.79	not significant
9672	GPC6	1.16	9.66E-02	1.48E-01	67.44	not significant
9673	LOC389765	1.16	8.86E-02	1.37E-01	85.78	not significant
9674	OIP5-AS1	1.16	1.26E-07	5.31E-07	2393.83	not significant
9675	SEMA4A	1.16	1.11E-02	2.15E-02	335.09	not significant
9676	ZNF714	1.16	1.30E-07	5.47E-07	2371.49	not significant
9677	GPATCH2	1.16	2.31E-03	5.16E-03	609.40	not significant
9678	LINC01222	1.16	1.10E-01	1.66E-01	36.24	not significant
9679	RCBTB1	1.16	3.49E-07	1.40E-06	2182.44	not significant
9680	ITGA7	1.16	1.07E-01	1.62E-01	47.05	not significant
9681	ZNF837	1.16	3.26E-02	5.68E-02	215.97	not significant
9682	FUCA1	1.16	1.42E-02	2.70E-02	317.50	not significant
9683	RAD54L	1.16	2.59E-10	1.47E-09	4853.45	not significant
9684	CASP10	1.16	1.63E-07	6.80E-07	2352.37	not significant
9685	SYNE3	1.16	3.02E-02	5.31E-02	215.60	not significant
9686	IPO5	1.16	6.10E-16	5.70E-15	15418.85	not significant
9687	LINC00669	1.16	6.66E-02	1.07E-01	111.12	not significant
9688	RPS4Y1	1.16	4.95E-11	3.00E-10	13560.06	not significant
9689	LOC642361	1.16	1.04E-01	1.58E-01	57.85	not significant
9690	RABIF	1.16	2.92E-04	7.72E-04	821.48	not significant
9691	ZNF814	1.16	2.96E-03	6.48E-03	550.68	not significant
9692	ZNF417	1.16	1.64E-03	3.76E-03	640.50	not significant
9693	ZNF71	1.16	2.81E-04	7.43E-04	853.41	not significant
9694	ZFP64	1.16	6.21E-04	1.54E-03	744.72	not significant
9695	TRIM13	1.16	4.99E-05	1.50E-04	1141.76	not significant
9696	SNX30	1.16	6.47E-03	1.32E-02	411.78	not significant
9697	METAP2	1.16	4.55E-12	3.03E-11	7614.11	not significant
9698	WNK1	1.16	9.79E-11	5.76E-10	18698.29	not significant
9699	FBRS	1.16	8.68E-09	4.20E-08	3461.81	not significant
9700	CCS	1.16	1.09E-02	2.12E-02	376.09	not significant
9701	FLJ42351	1.16	5.80E-02	9.46E-02	11.40	not significant
9702	LINC00294	1.16	2.37E-03	5.29E-03	556.72	not significant
9703	PIGL	1.16	2.65E-02	4.72E-02	235.75	not significant
9704	FAM95C	1.16	4.80E-02	8.02E-02	10.28	not significant
9705	TTLL3	1.16	5.45E-02	8.97E-02	163.60	not significant
9706	ANO5	1.16	8.28E-03	1.65E-02	355.94	not significant
9707	VDAC2	1.16	3.05E-06	1.09E-05	1738.89	not significant
9708	NONO	1.16	2.31E-16	2.23E-15	31227.44	not significant
9709	FBXO46	1.16	1.09E-04	3.09E-04	935.45	not significant
9710	SCAPER	1.16	6.02E-05	1.79E-04	1002.38	not significant
9711	RBM4	1.16	1.02E-04	2.92E-04	931.68	not significant
9712	SCAI	1.16	2.93E-02	5.17E-02	1624.05	not significant
9713	CXorf57	1.16	5.39E-03	1.12E-02	508.40	not significant
9714	CD5	1.16	1.17E-11	7.51E-11	6930.11	not significant
9715	TIGD5	1.16	1.57E-02	2.94E-02	345.27	not significant
9716	MYO9B	1.16	3.82E-08	1.72E-07	7319.47	not significant
9717	LOC728743	1.16	6.94E-06	2.36E-05	1828.19	not significant
9718	USP4	1.16	9.95E-09	4.78E-08	2812.67	not significant
9719	METTL25	1.16	1.02E-02	2.00E-02	348.27	not significant
9720	SMAD4	1.16	3.22E-08	1.46E-07	3044.18	not significant
9721	CD1C	1.16	1.19E-06	4.48E-06	1935.53	not significant
9722	CCNT1	1.16	6.89E-10	3.71E-09	4292.95	not significant
9723	ZNF787	1.16	6.53E-05	1.93E-04	1126.78	not significant
9724	ZNF254	1.16	2.11E-05	6.70E-05	1276.32	not significant
9725	EID2B	1.16	7.14E-02	1.13E-01	105.29	not significant
9726	EPHX2	1.16	6.25E-04	1.55E-03	655.94	not significant
9727	DAP3	1.16	2.31E-11	1.43E-10	4293.51	not significant
9728	SIGIRR	1.16	1.86E-06	6.82E-06	1621.36	not significant
9729	CD83	1.16	4.47E-05	1.36E-04	1609.45	not significant
9730	ZNF816	1.16	5.85E-03	1.21E-02	391.89	not significant
9731	CRTC1	1.16	2.35E-03	5.25E-03	525.77	not significant
9732	PWARSN	1.16	1.02E-01	1.55E-01	49.61	not significant
9733	KRBOX4	1.16	1.49E-03	3.44E-03	598.49	not significant
9734	LYPD5	1.16	8.42E-02	1.31E-01	20.41	not significant
9735	ZNF696	1.16	1.61E-03	3.69E-03	592.07	not significant
9736	ZNF304	1.16	1.01E-03	2.42E-03	622.35	not significant
9737	ADCK2	1.16	1.12E-05	3.69E-05	1750.12	not significant
9738	CDH4	1.16	9.96E-06	3.30E-05	1493.44	not significant
9739	MMP24-AS1	1.16	3.25E-04	8.51E-04	728.94	not significant
9740	HSH2D	1.16	4.66E-02	7.81E-02	149.35	not significant
9741	JOSD1	1.16	4.54E-08	2.03E-07	2814.17	not significant
9742	ARL13B	1.16	1.99E-03	4.49E-03	544.85	not significant
9743	ZNRD1	1.16	9.05E-03	1.79E-02	331.08	not significant
9744	IQGAP2	1.16	1.72E-11	1.08E-10	5575.77	not significant
9745	PRKCQ-AS1	1.16	6.70E-05	1.98E-04	1145.36	not significant
9746	PPP1R13L	1.16	1.30E-02	2.49E-02	328.35	not significant
9747	DNASE1L2	1.16	9.56E-02	1.47E-01	60.74	not significant
9748	TPRA1	1.16	1.90E-04	5.21E-04	944.57	not significant
9749	ARHGAP27	1.16	9.61E-05	2.77E-04	909.47	not significant
9750	UBXN6	1.16	5.05E-07	1.98E-06	2466.65	not significant
9751	AHNAK	1.16	1.12E-02	2.18E-02	330.31	not significant
9752	DNAJC27	1.16	1.88E-02	3.48E-02	259.67	not significant
9753	RPL15	1.16	7.60E-14	5.91E-13	18745.31	not significant
9754	ZNF212	1.16	4.09E-04	1.05E-03	784.96	not significant
9755	ODF2L	1.16	2.13E-04	5.77E-04	823.92	not significant
9756	TM2D3	1.16	8.80E-05	2.55E-04	1005.89	not significant

9757	IPO8	1.16	1.41E-08	6.63E-08	2815.53	not significant
9758	ZDHHC12	1.16	1.13E-04	3.20E-04	1170.18	not significant
9759	NLK	1.16	1.81E-06	6.65E-06	1791.34	not significant
9760	GNRH1	1.16	7.08E-02	1.13E-01	106.51	not significant
9761	TTTY15	1.16	1.32E-06	4.94E-06	1602.32	not significant
9762	ZNF234	1.16	9.01E-04	2.17E-03	693.60	not significant
9763	TMEM140	1.16	6.81E-02	1.09E-01	105.47	not significant
9764	CKLF	1.16	1.78E-04	4.90E-04	1007.53	not significant
9765	SNX5	1.16	9.29E-11	5.48E-10	5386.27	not significant
9766	PHKA2	1.16	7.40E-07	2.84E-06	1666.24	not significant
9767	SLC25A45	1.16	4.18E-03	8.90E-03	496.64	not significant
9768	C11orf84	1.16	1.36E-09	7.09E-09	3251.35	not significant
9769	GABRA5	1.16	7.14E-03	1.45E-02	349.29	not significant
9770	TMEM259	1.16	9.40E-04	2.26E-03	6425.30	not significant
9771	ELF1	1.16	2.92E-11	1.80E-10	5378.00	not significant
9772	CCDC42	1.16	4.34E-02	7.33E-02	11.18	not significant
9773	SFMBT2	1.16	3.15E-07	1.27E-06	2277.61	not significant
9774	TWSG1	1.16	1.33E-05	4.37E-05	1306.84	not significant
9775	ZFYVE26	1.16	1.83E-04	5.03E-04	1239.57	not significant
9776	FAM222A	1.16	3.08E-02	5.41E-02	197.33	not significant
9777	C8orf88	1.16	3.01E-05	9.35E-05	1166.57	not significant
9778	ZBED6	1.16	2.55E-04	6.84E-04	810.78	not significant
9779	LYSMD4	1.16	8.04E-03	1.61E-02	370.23	not significant
9780	ZNF131	1.17	3.88E-07	1.55E-06	2280.79	not significant
9781	RC3H2	1.17	1.84E-06	6.74E-06	1461.88	not significant
9782	LAX1	1.17	1.06E-05	3.50E-05	1233.45	not significant
9783	THAP4	1.17	7.64E-07	2.93E-06	1794.39	not significant
9784	KIF7	1.17	6.12E-04	1.52E-03	658.90	not significant
9785	RPS26	1.17	4.47E-12	2.98E-11	5778.43	not significant
9786	STAU1	1.17	3.83E-11	2.34E-10	4572.86	not significant
9787	CCP110	1.17	3.81E-11	2.33E-10	4708.89	not significant
9788	PCBP4	1.17	3.86E-03	8.29E-03	468.73	not significant
9789	CTNS	1.17	4.72E-04	1.20E-03	723.70	not significant
9790	RPS2	1.17	8.72E-10	4.63E-09	44348.97	not significant
9791	ZNF34	1.17	6.73E-02	1.08E-01	102.27	not significant
9792	RPS16	1.17	2.29E-13	1.71E-12	20239.25	not significant
9793	RPSAP58	1.17	5.54E-03	1.15E-02	428.91	not significant
9794	TMEM219	1.17	1.36E-05	4.45E-05	1224.01	not significant
9795	DNAJC27-AS1	1.17	4.06E-02	6.89E-02	9.66	not significant
9796	MAL	1.17	8.04E-14	6.25E-13	13709.48	not significant
9797	PAPSS1	1.17	1.35E-08	6.37E-08	2524.47	not significant
9798	STAT1	1.17	1.87E-12	1.29E-11	6614.59	not significant
9799	KIAA0753	1.17	2.21E-04	5.99E-04	846.89	not significant
9800	N4BP2L2	1.17	2.33E-08	1.08E-07	2694.20	not significant
9801	SLC35B2	1.17	5.79E-06	1.98E-05	1570.79	not significant
9802	ABCC2	1.17	6.71E-02	1.08E-01	118.18	not significant
9803	SLC36A4	1.17	1.36E-04	3.82E-04	839.98	not significant
9804	CLDND1	1.17	8.69E-07	3.31E-06	1684.81	not significant
9805	RBMX	1.17	9.50E-14	7.33E-13	23084.34	not significant
9806	HP1BP3	1.17	3.25E-16	3.09E-15	16514.72	not significant
9807	HADH	1.17	2.01E-12	1.38E-11	5145.13	not significant
9808	MAPT	1.17	8.31E-02	1.30E-01	21.73	not significant
9809	PPM1M	1.17	8.71E-05	2.53E-04	1026.56	not significant
9810	NIPA1	1.17	9.54E-07	3.62E-06	1559.68	not significant
9811	LCMT1	1.17	5.35E-05	1.60E-04	1098.17	not significant
9812	CCDC81	1.17	9.45E-02	1.45E-01	27.05	not significant
9813	CSAD	1.17	5.04E-02	8.37E-02	182.17	not significant
9814	ZNF678	1.17	1.03E-04	2.95E-04	956.23	not significant
9815	ARHGAP4	1.17	3.59E-08	1.62E-07	2648.80	not significant
9816	LOC399491	1.17	8.82E-03	1.75E-02	369.53	not significant
9817	ZNF107	1.17	2.56E-08	1.18E-07	5323.24	not significant
9818	RPS18	1.17	7.35E-04	1.80E-03	24946.48	not significant
9819	STK11IP	1.17	1.44E-03	3.34E-03	750.57	not significant
9820	ZNF74	1.17	8.82E-05	2.55E-04	1041.82	not significant
9821	METRN	1.17	4.69E-02	7.86E-02	160.68	not significant
9822	CNOT8	1.17	7.34E-11	4.37E-10	4602.13	not significant
9823	GSDMB	1.17	4.20E-02	7.11E-02	674.96	not significant
9824	KIAA1841	1.17	7.14E-03	1.45E-02	327.76	not significant
9825	SCART1	1.17	2.50E-02	4.48E-02	1149.82	not significant
9826	RPS27A	1.17	7.77E-09	3.77E-08	14377.30	not significant
9827	RPPH1	1.17	9.70E-02	1.49E-01	35.32	not significant
9828	SLC12A9	1.17	8.36E-04	2.03E-03	639.16	not significant
9829	DHX58	1.17	3.72E-02	6.38E-02	154.26	not significant
9830	C22orf24	1.17	9.43E-02	1.45E-01	48.24	not significant
9831	HPS4	1.17	2.12E-09	1.09E-08	3461.07	not significant
9832	EFCAB7	1.17	5.15E-03	1.08E-02	377.03	not significant
9833	RGPD3	1.17	6.99E-05	2.06E-04	1154.08	not significant
9834	IL4R	1.17	1.98E-06	7.23E-06	1552.65	not significant
9835	CCDC14	1.17	1.35E-02	2.59E-02	3156.48	not significant
9836	RPS27	1.17	1.76E-14	1.45E-13	16718.35	not significant
9837	SLC4A8	1.17	2.84E-02	5.03E-02	192.51	not significant
9838	ZEB1	1.17	3.46E-10	1.93E-09	3957.51	not significant
9839	EPC2	1.17	9.39E-06	3.13E-05	1151.44	not significant
9840	TBC1D9B	1.17	1.23E-10	7.19E-10	3845.41	not significant
9841	FN3KRP	1.17	1.37E-07	5.78E-07	2826.82	not significant
9842	PTPN18	1.17	2.00E-07	8.24E-07	1799.48	not significant
9843	LINC01126	1.17	5.92E-02	9.64E-02	15.17	not significant
9844	KDM3A	1.17	1.31E-08	6.18E-08	4215.15	not significant

9845	ARHGAP9	1.17	1.21E-07	5.13E-07	2201.53	not significant
9846	ENGASE	1.17	7.80E-02	1.23E-01	18.41	not significant
9847	MED12L	1.17	1.92E-04	5.25E-04	894.42	not significant
9848	HAUS3	1.17	3.19E-06	1.13E-05	1426.94	not significant
9849	RAB15	1.17	4.01E-08	1.80E-07	2273.65	not significant
9850	CCDC101	1.17	2.78E-04	7.36E-04	734.65	not significant
9851	SCGB1B2P	1.17	5.61E-02	9.20E-02	13.08	not significant
9852	E4F1	1.17	1.56E-05	5.05E-05	1099.65	not significant
9853	TRAPPC6B	1.17	1.10E-06	4.13E-06	1480.20	not significant
9854	PRCP	1.17	5.63E-05	1.68E-04	920.67	not significant
9855	ZDHHC8	1.17	1.35E-05	4.41E-05	1910.10	not significant
9856	FDX1	1.17	3.85E-04	9.96E-04	712.18	not significant
9857	FGF17	1.17	6.41E-02	1.03E-01	15.03	not significant
9858	C1orf101	1.17	9.44E-02	1.45E-01	32.86	not significant
9859	SERINC3	1.17	1.12E-12	7.93E-12	4644.49	not significant
9860	ZNF354A	1.17	4.41E-03	9.37E-03	410.98	not significant
9861	PCBD1	1.17	6.94E-03	1.41E-02	332.90	not significant
9862	OSR2	1.17	5.82E-02	9.49E-02	103.52	not significant
9863	PARP10	1.17	1.08E-03	2.56E-03	555.34	not significant
9864	UCN	1.17	9.02E-02	1.39E-01	50.51	not significant
9865	NFYC	1.17	1.88E-08	8.75E-08	2065.25	not significant
9866	MAP3K3	1.17	5.17E-09	2.55E-08	2519.83	not significant
9867	SNX13	1.17	1.75E-06	6.42E-06	1443.65	not significant
9868	CLIP2	1.17	8.04E-02	1.26E-01	67.57	not significant
9869	SMARCAL1	1.17	1.34E-05	4.39E-05	1245.66	not significant
9870	SETD4	1.17	2.13E-03	4.79E-03	475.61	not significant
9871	CABLES2	1.17	5.39E-06	1.85E-05	1296.21	not significant
9872	NPM2	1.17	8.15E-02	1.28E-01	20.79	not significant
9873	RAB11B	1.17	4.86E-09	2.41E-08	3670.01	not significant
9874	EXOC7	1.17	2.50E-13	1.86E-12	9079.80	not significant
9875	ANTXRLP1	1.17	7.88E-02	1.24E-01	21.60	not significant
9876	ZNF189	1.17	1.35E-03	3.17E-03	492.17	not significant
9877	CCDC71L	1.17	8.09E-05	2.36E-04	857.59	not significant
9878	KDM6A	1.17	1.61E-06	5.95E-06	1374.53	not significant
9879	STX5	1.17	2.44E-05	7.68E-05	1129.52	not significant
9880	MOV10	1.17	8.60E-08	3.70E-07	4266.23	not significant
9881	FCHSD2	1.17	7.52E-11	4.47E-10	3321.46	not significant
9882	PCNA-AS1	1.17	8.62E-02	1.34E-01	38.66	not significant
9883	RPL24	1.17	3.10E-09	1.57E-08	13194.01	not significant
9884	LRRC45	1.17	2.82E-07	1.14E-06	1919.05	not significant
9885	CXorf21	1.17	8.97E-02	1.39E-01	45.35	not significant
9886	KLHL42	1.17	2.75E-07	1.12E-06	1885.88	not significant
9887	EML2	1.17	4.20E-04	1.08E-03	665.74	not significant
9888	RRN3P1	1.17	6.19E-03	1.27E-02	422.18	not significant
9889	TMEM201	1.17	1.58E-07	6.57E-07	1929.13	not significant
9890	POLDIP3	1.17	3.55E-11	2.18E-10	5830.89	not significant
9891	C15orf52	1.17	7.74E-02	1.22E-01	18.88	not significant
9892	ZC4H2	1.17	7.90E-06	2.66E-05	1233.83	not significant
9893	SEC61A2	1.17	8.56E-03	1.70E-02	295.17	not significant
9894	USP12	1.17	6.09E-09	2.98E-08	2664.77	not significant
9895	EEF1D	1.17	1.37E-11	8.72E-11	14261.67	not significant
9896	STARD3	1.17	1.16E-09	6.07E-09	2862.21	not significant
9897	ZNF75D	1.17	8.83E-02	1.37E-01	48.34	not significant
9898	HCN3	1.17	7.96E-02	1.25E-01	21.70	not significant
9899	ANKHD1	1.17	2.22E-02	4.03E-02	228.02	not significant
9900	ABHD17B	1.17	1.68E-08	7.83E-08	2093.25	not significant
9901	PHLPP1	1.17	2.79E-02	4.96E-02	180.83	not significant
9902	ZNF226	1.17	6.50E-04	1.60E-03	575.13	not significant
9903	PHKG1	1.17	8.86E-02	1.37E-01	47.77	not significant
9904	JADE1	1.17	4.48E-08	2.00E-07	2516.12	not significant
9905	SENP7	1.17	1.02E-06	3.85E-06	1484.77	not significant
9906	PEX13	1.17	9.54E-04	2.29E-03	558.82	not significant
9907	ASXL1	1.17	5.13E-10	2.81E-09	6856.16	not significant
9908	ZNF836	1.17	1.45E-02	2.75E-02	290.91	not significant
9909	SEPW1	1.17	1.24E-07	5.23E-07	2805.90	not significant
9910	EBLN3	1.17	7.60E-11	4.51E-10	3672.37	not significant
9911	TIPARP-AS1	1.17	5.67E-02	9.27E-02	14.08	not significant
9912	ZDHHC13	1.17	3.45E-06	1.22E-05	1210.70	not significant
9913	MAP4K3	1.17	1.57E-04	4.37E-04	772.00	not significant
9914	ZNF518A	1.17	6.41E-02	1.03E-01	85.56	not significant
9915	ARRDC3-AS1	1.17	8.65E-02	1.35E-01	28.66	not significant
9916	ZNF395	1.18	3.26E-11	2.00E-10	3501.72	not significant
9917	LDLRAD4	1.18	4.40E-15	3.84E-14	7896.51	not significant
9918	TMEFF1	1.18	8.52E-02	1.33E-01	30.21	not significant
9919	CBX5	1.18	1.46E-11	9.28E-11	24273.90	not significant
9920	COIL	1.18	7.46E-06	2.52E-05	1350.56	not significant
9921	UBE2R2	1.18	1.10E-14	9.22E-14	5807.35	not significant
9922	RPL19	1.18	1.43E-10	8.26E-10	52827.59	not significant
9923	SPRYD4	1.18	1.13E-02	2.19E-02	267.96	not significant
9924	RAB40C	1.18	3.68E-04	9.56E-04	600.98	not significant
9925	GOLGA6L5P	1.18	4.90E-02	8.16E-02	12.55	not significant
9926	ZNF420	1.18	4.14E-03	8.83E-03	367.95	not significant
9927	RLTPR	1.18	8.08E-10	4.30E-09	9290.34	not significant
9928	NFATC2IP	1.18	1.76E-02	3.27E-02	3449.70	not significant
9929	RPS6	1.18	3.51E-09	1.76E-08	68179.33	not significant
9930	CARNS1	1.18	7.12E-02	1.13E-01	71.32	not significant
9931	ZDHHC4	1.18	2.98E-06	1.06E-05	1603.72	not significant
9932	VEZF1	1.18	1.46E-12	1.02E-11	4260.28	not significant

9933	MRPS27	1.18	8.28E-12	5.39E-11	3943.96	not significant
9934	ABHD16A	1.18	5.40E-05	1.62E-04	980.88	not significant
9935	RPS3A	1.18	2.40E-03	5.33E-03	18091.03	not significant
9936	EAF1	1.18	1.17E-08	5.55E-08	2259.67	not significant
9937	TSPYL1	1.18	3.24E-08	1.47E-07	2107.17	not significant
9938	WDR54	1.18	8.08E-05	2.35E-04	775.60	not significant
9939	ZNF283	1.18	4.07E-02	6.91E-02	134.00	not significant
9940	H1FX	1.18	4.03E-04	1.04E-03	12443.20	not significant
9941	ADI1	1.18	9.32E-08	4.00E-07	2541.48	not significant
9942	CRACR2A	1.18	1.01E-04	2.90E-04	743.14	not significant
9943	ZSCAN4	1.18	5.99E-02	9.73E-02	19.20	not significant
9944	GUSB	1.18	3.04E-09	1.54E-08	2604.42	not significant
9945	VGLL4	1.18	8.32E-09	4.03E-08	2107.18	not significant
9946	FBXL15	1.18	1.33E-02	2.54E-02	246.51	not significant
9947	ENTPD4	1.18	4.61E-07	1.82E-06	2719.20	not significant
9948	TMEM260	1.18	3.70E-04	9.60E-04	595.22	not significant
9949	MACROD1	1.18	4.60E-03	9.73E-03	376.49	not significant
9950	ZNF564	1.18	5.73E-03	1.19E-02	313.91	not significant
9951	CDS2	1.18	7.29E-13	5.20E-12	4409.59	not significant
9952	TPRG1L	1.18	1.11E-04	3.15E-04	766.75	not significant
9953	C1orf112	1.18	7.56E-08	3.27E-07	1870.55	not significant
9954	XRN1	1.18	4.98E-08	2.21E-07	2855.80	not significant
9955	POT1-AS1	1.18	7.82E-02	1.23E-01	22.39	not significant
9956	PGLS	1.18	1.15E-08	5.49E-08	2645.74	not significant
9957	PRRT3	1.18	7.53E-02	1.19E-01	66.64	not significant
9958	TAOK2	1.18	2.22E-09	1.14E-08	3293.21	not significant
9959	SCAMP4	1.18	1.30E-06	4.87E-06	1874.79	not significant
9960	ZNF492	1.18	2.52E-02	4.51E-02	166.08	not significant
9961	ELF2	1.18	7.55E-07	2.89E-06	1454.78	not significant
9962	ZNF688	1.18	1.84E-02	3.41E-02	199.07	not significant
9963	CUL9	1.18	1.45E-02	2.74E-02	1649.63	not significant
9964	SDCBP	1.18	4.70E-10	2.59E-09	3583.92	not significant
9965	ASH2L	1.18	1.05E-10	6.17E-10	3626.26	not significant
9966	ZACN	1.18	7.72E-02	1.22E-01	25.88	not significant
9967	PEX11B	1.18	6.57E-02	1.06E-01	84.02	not significant
9968	ALG10	1.18	1.31E-03	3.07E-03	458.61	not significant
9969	LEPROT	1.18	3.34E-04	8.73E-04	612.30	not significant
9970	KIFC2	1.18	1.49E-02	2.82E-02	1128.36	not significant
9971	DLST	1.18	1.95E-13	1.46E-12	4451.09	not significant
9972	PNMA2	1.18	3.79E-10	2.10E-09	2955.31	not significant
9973	NDST2	1.18	2.48E-06	8.94E-06	1382.31	not significant
9974	PER2	1.18	8.47E-06	2.84E-05	1074.22	not significant
9975	AP1G2	1.18	4.12E-06	1.44E-05	2415.49	not significant
9976	EME2	1.18	4.15E-02	7.04E-02	120.83	not significant
9977	RPLP0	1.18	3.03E-12	2.05E-11	53871.84	not significant
9978	CERS5	1.18	4.65E-07	1.83E-06	1988.57	not significant
9979	ZMYM2	1.18	3.23E-11	1.99E-10	5090.00	not significant
9980	FBXL13	1.18	7.95E-02	1.25E-01	51.74	not significant
9981	CCNT2-AS1	1.18	3.30E-02	5.76E-02	142.45	not significant
9982	GFI1	1.18	2.08E-07	8.53E-07	1596.17	not significant
9983	PGM2L1	1.18	1.90E-06	6.95E-06	1519.26	not significant
9984	43716_7153	1.18	3.95E-15	3.45E-14	6195.91	not significant
9985	RBM38	1.18	2.89E-04	7.62E-04	652.90	not significant
9986	PLEKHM2	1.18	6.45E-10	3.49E-09	2646.54	not significant
9987	XAB2	1.18	4.33E-09	2.15E-08	2614.55	not significant
9988	ZNF33A	1.18	2.95E-07	1.19E-06	2234.74	not significant
9989	SERPINB1	1.18	6.20E-11	3.71E-10	3629.64	not significant
9990	WIBG	1.18	3.55E-05	1.09E-04	833.92	not significant
9991	GLTSCR1L	1.18	3.50E-06	1.24E-05	1174.97	not significant
9992	DHRS7	1.18	1.23E-05	4.04E-05	1249.68	not significant
9993	CTSF	1.18	6.99E-02	1.11E-01	19.75	not significant
9994	MTERF4	1.18	4.37E-06	1.52E-05	1144.76	not significant
9995	EBLN2	1.18	5.98E-02	9.72E-02	91.99	not significant
9996	CHMP6	1.18	5.25E-05	1.57E-04	819.30	not significant
9997	FAM73B	1.18	7.81E-06	2.63E-05	1101.66	not significant
9998	SUMO2	1.18	1.59E-12	1.10E-11	8577.46	not significant
9999	LYRM9	1.18	7.64E-02	1.21E-01	50.66	not significant
10000	VCPKMT	1.18	1.17E-03	2.76E-03	493.41	not significant
10001	LINC00959	1.18	5.79E-02	9.44E-02	86.07	not significant
10002	ARHGEF18	1.18	1.46E-10	8.41E-10	3749.02	not significant
10003	LOC100996437	1.18	4.87E-02	8.13E-02	13.46	not significant
10004	FAM117B	1.18	4.98E-06	1.72E-05	1381.65	not significant
10005	PIP5K1C	1.18	3.02E-06	1.07E-05	1197.99	not significant
10006	ARID4B	1.18	3.17E-09	1.60E-08	2688.50	not significant
10007	FIGNL1	1.18	1.01E-08	4.84E-08	2861.85	not significant
10008	FLJ42627	1.18	3.71E-02	6.36E-02	122.63	not significant
10009	ANKRD13A	1.18	3.73E-14	2.99E-13	5575.82	not significant
10010	FAM66B	1.18	7.68E-02	1.21E-01	53.16	not significant
10011	PROX1	1.18	6.56E-02	1.06E-01	72.36	not significant
10012	FAM110C	1.18	7.69E-03	1.55E-02	263.42	not significant
10013	PCYT1B	1.18	2.26E-02	4.10E-02	166.17	not significant
10014	DCK	1.18	2.31E-17	2.42E-16	8943.01	not significant
10015	YAF2	1.18	6.80E-06	2.31E-05	1198.75	not significant
10016	ENDOV	1.18	1.50E-02	2.84E-02	208.16	not significant
10017	TRAF6	1.18	1.15E-05	3.80E-05	970.66	not significant
10018	MFSD8	1.18	4.35E-04	1.12E-03	600.67	not significant
10019	FAM133B	1.18	7.66E-02	1.21E-01	48.41	not significant
10020	PKN2	1.18	1.95E-05	6.22E-05	1714.32	not significant

10021	HAGH	1.18	5.38E-05	1.61E-04	949.50	not significant
10022	TNRC6C	1.18	4.98E-11	3.01E-10	3469.98	not significant
10023	LRRC14	1.18	1.95E-07	8.05E-07	1910.51	not significant
10024	LIG1	1.18	1.73E-13	1.31E-12	6690.66	not significant
10025	LRIG2	1.18	2.75E-04	7.30E-04	690.93	not significant
10026	PYGO2	1.18	3.21E-09	1.61E-08	2292.19	not significant
10027	ZBTB10	1.18	6.70E-07	2.59E-06	1286.51	not significant
10028	SYCP2	1.18	1.75E-02	3.24E-02	3760.24	not significant
10029	KBTBD4	1.18	7.30E-06	2.47E-05	981.78	not significant
10030	CCDC57	1.18	2.07E-05	6.59E-05	944.72	not significant
10031	SCNN1D	1.18	5.68E-02	9.29E-02	107.40	not significant
10032	KDM2B	1.18	6.21E-07	2.41E-06	1246.83	not significant
10033	MEGF9	1.18	1.05E-08	5.01E-08	2350.20	not significant
10034	MAN2B1	1.18	5.26E-07	2.06E-06	1488.73	not significant
10035	ANKLE1	1.18	6.28E-08	2.75E-07	1603.98	not significant
10036	LAMB2P1	1.18	7.26E-02	1.15E-01	21.85	not significant
10037	GABARAP	1.18	1.53E-09	7.94E-09	3439.67	not significant
10038	GPR63	1.18	7.85E-05	2.29E-04	887.69	not significant
10039	TMCC1-AS1	1.18	3.07E-02	5.39E-02	138.51	not significant
10040	TNKS2	1.18	7.26E-12	4.75E-11	4469.88	not significant
10041	IRX3	1.18	1.36E-05	4.44E-05	888.13	not significant
10042	SNX10	1.18	2.58E-06	9.27E-06	1332.01	not significant
10043	ZNF587	1.18	3.66E-05	1.12E-04	1060.81	not significant
10044	CCSAP	1.18	6.19E-12	4.08E-11	3818.36	not significant
10045	CCDC69	1.18	3.43E-09	1.72E-08	3248.66	not significant
10046	SUPT3H	1.19	9.10E-06	3.04E-05	1053.57	not significant
10047	SIAH1	1.19	1.95E-04	5.31E-04	640.06	not significant
10048	NRL	1.19	5.01E-02	8.33E-02	92.63	not significant
10049	TAPBP	1.19	1.23E-05	4.03E-05	978.78	not significant
10050	KLC4	1.19	5.58E-04	1.40E-03	557.87	not significant
10051	UBQLN2	1.19	8.23E-07	3.14E-06	2079.03	not significant
10052	TELO2	1.19	7.20E-08	3.12E-07	1914.22	not significant
10053	RRP7B	1.19	9.30E-04	2.24E-03	583.32	not significant
10054	ACAD8	1.19	1.10E-05	3.63E-05	946.03	not significant
10055	ZFP82	1.19	3.81E-04	9.88E-04	563.65	not significant
10056	ZNF776	1.19	2.66E-07	1.08E-06	1365.02	not significant
10057	PTAR1	1.19	1.02E-07	4.37E-07	2477.95	not significant
10058	IFI27L1	1.19	2.25E-03	5.03E-03	392.10	not significant
10059	SFMBT1	1.19	3.88E-08	1.74E-07	1777.88	not significant
10060	PTPRJ	1.19	3.32E-02	5.77E-02	9.52	not significant
10061	P2RX5-TAX1BP3	1.19	1.34E-02	2.56E-02	209.04	not significant
10062	CTSD	1.19	1.14E-11	7.33E-11	4975.74	not significant
10063	YIPF3	1.19	5.00E-10	2.74E-09	2253.23	not significant
10064	ZBTB4	1.19	3.79E-06	1.33E-05	1216.46	not significant
10065	PODXL	1.19	7.35E-03	1.48E-02	274.88	not significant
10066	HOOK2	1.19	4.07E-02	6.90E-02	114.33	not significant
10067	SLC23A2	1.19	3.47E-10	1.94E-09	3233.42	not significant
10068	THAP9-AS1	1.19	4.96E-05	1.49E-04	1157.63	not significant
10069	RFX5	1.19	4.58E-13	3.32E-12	3821.96	not significant
10070	PIWIL4	1.19	5.06E-02	8.40E-02	88.74	not significant
10071	FAM200B	1.19	3.19E-04	8.38E-04	570.11	not significant
10072	ZNF284	1.19	2.29E-02	4.14E-02	167.35	not significant
10073	FBN1	1.19	1.21E-03	2.85E-03	439.35	not significant
10074	PLEKHM1	1.19	3.52E-07	1.41E-06	1304.83	not significant
10075	SIRT1	1.19	5.74E-07	2.23E-06	1358.52	not significant
10076	MAD2L2	1.19	4.82E-11	2.93E-10	6551.58	not significant
10077	KPNA5	1.19	1.31E-03	3.07E-03	463.49	not significant
10078	LDOC1L	1.19	7.15E-15	6.13E-14	7116.54	not significant
10079	RCCD1	1.19	1.89E-06	6.92E-06	1102.08	not significant
10080	HKDC1	1.19	5.14E-02	8.52E-02	83.63	not significant
10081	ZBTB6	1.19	2.45E-04	6.56E-04	608.51	not significant
10082	TMEM87A	1.19	1.20E-08	5.68E-08	1900.91	not significant
10083	GDF9	1.19	7.69E-02	1.21E-01	38.98	not significant
10084	IKZF1	1.19	4.97E-18	5.53E-17	16264.70	not significant
10085	SLC25A14	1.19	3.42E-04	8.94E-04	534.87	not significant
10086	PPP1R37	1.19	1.92E-05	6.14E-05	837.11	not significant
10087	ZIK1	1.19	5.14E-06	1.77E-05	1099.75	not significant
10088	NAA40	1.19	9.50E-09	4.57E-08	2018.99	not significant
10089	TTC28-AS1	1.19	9.69E-05	2.79E-04	803.65	not significant
10090	FBRSL1	1.19	7.24E-11	4.31E-10	3155.83	not significant
10091	STRIP2	1.19	5.07E-03	1.06E-02	428.16	not significant
10092	TMEM79	1.19	9.38E-03	1.85E-02	233.20	not significant
10093	HINT1	1.19	7.90E-12	5.16E-11	11734.29	not significant
10094	LPGAT1	1.19	2.23E-09	1.14E-08	2155.16	not significant
10095	RPL32	1.19	1.88E-13	1.41E-12	22244.01	not significant
10096	ZNF384	1.19	8.04E-12	5.25E-11	3002.63	not significant
10097	KHNYN	1.19	1.47E-09	7.62E-09	3234.19	not significant
10098	FXR1	1.19	2.18E-12	1.50E-11	6033.27	not significant
10099	GVINP1	1.19	6.06E-05	1.80E-04	1044.96	not significant
10100	HNRNPA0	1.19	6.76E-10	3.65E-09	18338.51	not significant
10101	FANCA	1.19	2.51E-03	5.58E-03	2330.80	not significant
10102	SULT1A1	1.19	8.21E-03	1.64E-02	254.67	not significant
10103	SPIN1	1.19	1.26E-14	1.05E-13	4999.70	not significant
10104	PSMD5-AS1	1.19	3.63E-08	1.64E-07	1562.37	not significant
10105	SLC25A26	1.19	1.06E-03	2.51E-03	456.89	not significant
10106	GNE	1.19	5.48E-09	2.69E-08	1889.71	not significant
10107	CENPU	1.19	1.26E-12	8.84E-12	4957.85	not significant
10108	INSIG2	1.19	1.05E-04	3.00E-04	684.80	not significant

10109	RGPD4	1.19	7.44E-02	1.18E-01	38.71	not significant
10110	FRS2	1.19	5.69E-07	2.21E-06	1226.64	not significant
10111	VIPAS39	1.19	2.98E-06	1.06E-05	1083.46	not significant
10112	ZNF671	1.19	1.94E-04	5.29E-04	590.90	not significant
10113	HTRA2	1.19	1.18E-06	4.42E-06	1509.98	not significant
10114	CHD1L	1.19	7.30E-07	2.80E-06	1323.04	not significant
10115	ACAP1	1.19	3.17E-16	3.01E-15	6512.33	not significant
10116	ACTR1B	1.19	3.39E-09	1.70E-08	2384.73	not significant
10117	ERN1	1.19	9.09E-07	3.45E-06	1236.09	not significant
10118	PTRHD1	1.19	2.78E-04	7.36E-04	584.41	not significant
10119	RAB2B	1.19	1.93E-05	6.18E-05	879.70	not significant
10120	NUDT9P1	1.19	7.49E-02	1.19E-01	33.18	not significant
10121	HDGFRP3	1.19	2.30E-09	1.17E-08	2490.12	not significant
10122	TXNDC15	1.19	2.52E-07	1.03E-06	1334.34	not significant
10123	CECR1	1.19	6.74E-12	4.42E-11	3187.55	not significant
10124	BCL7A	1.19	1.07E-13	8.20E-13	4293.27	not significant
10125	C3orf17	1.19	1.34E-09	7.00E-09	1964.24	not significant
10126	VNN2	1.19	5.53E-03	1.15E-02	273.87	not significant
10127	WDR6	1.19	1.20E-14	1.00E-13	8775.74	not significant
10128	MAN1A1	1.19	6.71E-14	5.25E-13	4851.99	not significant
10129	TBCEL	1.19	1.43E-03	3.33E-03	406.92	not significant
10130	ALG12	1.19	1.30E-05	4.27E-05	946.61	not significant
10131	CCNT2	1.19	1.67E-08	7.79E-08	2590.61	not significant
10132	SVIP	1.19	6.99E-06	2.37E-05	885.18	not significant
10133	SLAMF6	1.19	1.87E-07	7.75E-07	1737.67	not significant
10134	FAM73A	1.19	1.26E-04	3.55E-04	648.34	not significant
10135	ATXN2L	1.19	7.97E-11	4.73E-10	16013.74	not significant
10136	NTSR1	1.19	6.74E-03	1.37E-02	245.02	not significant
10137	ZNF169	1.19	5.50E-02	9.04E-02	77.18	not significant
10138	TMEM59	1.19	6.90E-09	3.36E-08	2797.86	not significant
10139	KIAA2026	1.19	6.43E-06	2.19E-05	1107.79	not significant
10140	ZFX	1.19	9.93E-08	4.25E-07	1575.46	not significant
10141	PHF1	1.19	2.83E-03	6.23E-03	333.01	not significant
10142	USP3	1.19	4.77E-07	1.88E-06	1265.10	not significant
10143	TMEM234	1.19	4.90E-02	8.16E-02	88.99	not significant
10144	EIF3H	1.19	2.55E-12	1.74E-11	12763.97	not significant
10145	ZNF451	1.19	1.41E-08	6.61E-08	2145.38	not significant
10146	FBXO8	1.19	1.41E-03	3.29E-03	400.32	not significant
10147	SNHG8	1.19	4.07E-10	2.25E-09	2305.45	not significant
10148	IQGAP3	1.19	3.55E-02	6.12E-02	1075.12	not significant
10149	TMEM41B	1.19	9.96E-08	4.26E-07	1700.55	not significant
10150	RMDN3	1.19	4.69E-08	2.09E-07	1526.15	not significant
10151	BTG3	1.19	1.27E-06	4.77E-06	1117.51	not significant
10152	C2CD3	1.19	2.09E-09	1.07E-08	2236.21	not significant
10153	GXYLT1	1.19	9.52E-11	5.60E-10	2565.56	not significant
10154	KIAA1468	1.19	1.09E-02	2.12E-02	1033.11	not significant
10155	ASB3	1.19	5.19E-02	8.59E-02	74.29	not significant
10156	EXT2	1.19	3.95E-07	1.57E-06	1463.96	not significant
10157	RPS15	1.19	3.48E-11	2.13E-10	11754.56	not significant
10158	SCAMP1	1.19	4.05E-09	2.02E-08	1811.58	not significant
10159	LOC645513	1.19	4.86E-03	1.02E-02	281.22	not significant
10160	IGSF8	1.19	3.45E-07	1.38E-06	1261.69	not significant
10161	NCSTN	1.19	1.91E-08	8.86E-08	2147.17	not significant
10162	ZNF367	1.19	1.45E-09	7.52E-09	1891.86	not significant
10163	ANO9	1.19	4.80E-02	8.02E-02	97.53	not significant
10164	FYB	1.19	1.65E-14	1.36E-13	5537.57	not significant
10165	ST13	1.19	6.49E-18	7.13E-17	9787.14	not significant
10166	USF2	1.19	8.03E-12	5.24E-11	4100.71	not significant
10167	GBP3	1.19	1.21E-04	3.42E-04	590.48	not significant
10168	LOC100128288	1.19	6.73E-02	1.08E-01	55.95	not significant
10169	CBL	1.19	7.92E-10	4.23E-09	6082.81	not significant
10170	NPHP4	1.19	2.36E-06	8.51E-06	1200.67	not significant
10171	GOLGA2P5	1.19	1.91E-02	3.51E-02	1125.73	not significant
10172	OXA1L	1.19	5.57E-14	4.39E-13	3459.05	not significant
10173	HIATL2	1.19	3.71E-02	6.37E-02	106.82	not significant
10174	PEX16	1.19	8.13E-05	2.37E-04	673.23	not significant
10175	ZNF260	1.19	9.19E-09	4.44E-08	1743.78	not significant
10176	PRRC2B	1.19	9.27E-18	1.01E-16	7856.89	not significant
10177	ZNF354B	1.20	1.36E-03	3.17E-03	459.60	not significant
10178	MEAF6	1.20	2.60E-12	1.77E-11	3391.88	not significant
10179	NUDT16L1	1.20	1.66E-05	5.36E-05	920.74	not significant
10180	GPR137	1.20	2.23E-05	7.06E-05	818.25	not significant
10181	MZT2B	1.20	5.56E-04	1.40E-03	3765.61	not significant
10182	LOC653160	1.20	6.54E-02	1.05E-01	65.82	not significant
10183	SETD1B	1.20	1.48E-11	9.39E-11	3861.62	not significant
10184	UCK1	1.20	4.52E-07	1.79E-06	1333.87	not significant
10185	FANCI	1.20	3.89E-18	4.37E-17	6647.88	not significant
10186	BRIP1	1.20	1.36E-15	1.24E-14	4635.83	not significant
10187	ZNF490	1.20	5.37E-03	1.12E-02	264.11	not significant
10188	ZNF184	1.20	3.52E-07	1.41E-06	1182.11	not significant
10189	ZXDA	1.20	1.52E-02	2.86E-02	173.34	not significant
10190	GPHN	1.20	5.53E-02	9.08E-02	17.05	not significant
10191	ATXN7L2	1.20	1.11E-03	2.64E-03	402.01	not significant
10192	TP53	1.20	1.57E-15	1.41E-14	6058.10	not significant
10193	TONSL	1.20	1.94E-08	9.02E-08	3151.39	not significant
10194	TRIM45	1.20	6.44E-02	1.04E-01	50.40	not significant
10195	EFCAB5	1.20	2.46E-02	4.41E-02	143.08	not significant
10196	SPSB1	1.20	3.70E-05	1.14E-04	704.26	not significant

10197	PNPLA2	1.20	1.92E-07	7.96E-07	1557.82	not significant
10198	ENOSF1	1.20	8.47E-06	2.84E-05	1366.82	not significant
10199	PP7080	1.20	1.76E-05	5.65E-05	783.99	not significant
10200	EHMT2	1.20	5.41E-11	3.26E-10	2527.24	not significant
10201	RPL27A	1.20	1.32E-12	9.24E-12	19669.54	not significant
10202	KLHL9	1.20	8.66E-11	5.11E-10	2426.16	not significant
10203	PHACTR3	1.20	3.19E-10	1.78E-09	3026.46	not significant
10204	ZNF136	1.20	2.14E-05	6.77E-05	988.00	not significant
10205	LOC100507053	1.20	6.36E-02	1.03E-01	20.92	not significant
10206	MZT1	1.20	6.58E-12	4.33E-11	3707.20	not significant
10207	AP5Z1	1.20	1.31E-07	5.49E-07	1601.39	not significant
10208	ORAI3	1.20	5.97E-03	1.23E-02	280.52	not significant
10209	ZNF268	1.20	1.48E-06	5.51E-06	1477.64	not significant
10210	HDAC6	1.20	9.31E-05	2.69E-04	662.29	not significant
10211	LOC100289230	1.20	6.96E-02	1.11E-01	35.04	not significant
10212	ANKZF1	1.20	2.36E-06	8.52E-06	1164.35	not significant
10213	NIN	1.20	5.53E-14	4.36E-13	4200.38	not significant
10214	RNF144A	1.20	1.84E-15	1.64E-14	4256.21	not significant
10215	NFKBIZ	1.20	6.65E-02	1.07E-01	45.98	not significant
10216	KLF5	1.20	1.48E-02	2.80E-02	172.16	not significant
10217	SH3YL1	1.20	1.69E-04	4.67E-04	604.50	not significant
10218	AP5B1	1.20	2.74E-07	1.11E-06	1536.78	not significant
10219	C10orf35	1.20	1.05E-02	2.06E-02	208.30	not significant
10220	TMEM194B	1.20	1.53E-07	6.40E-07	1384.62	not significant
10221	RPL5	1.20	3.57E-15	3.14E-14	35246.85	not significant
10222	TRIM23	1.20	3.94E-04	1.02E-03	483.71	not significant
10223	KIAA1109	1.20	3.15E-09	1.59E-08	2893.14	not significant
10224	VAMP2	1.20	3.41E-08	1.54E-07	1512.63	not significant
10225	FKRP	1.20	1.15E-05	3.80E-05	843.20	not significant
10226	ZNF133	1.20	3.40E-03	7.37E-03	305.48	not significant
10227	SLC30A7	1.20	2.41E-06	8.69E-06	1731.55	not significant
10228	ZC3H12B	1.20	1.10E-02	2.15E-02	193.48	not significant
10229	GPATCH2L	1.20	4.94E-09	2.45E-08	2208.82	not significant
10230	EML3	1.20	1.25E-08	5.91E-08	2145.45	not significant
10231	UBXN11	1.20	1.42E-03	3.30E-03	411.62	not significant
10232	ZKSCAN2	1.20	1.06E-05	3.51E-05	845.20	not significant
10233	PHACTR2	1.20	4.26E-02	7.21E-02	89.66	not significant
10234	POGZ	1.20	2.86E-04	7.56E-04	4188.93	not significant
10235	RAB4A	1.20	6.59E-07	2.55E-06	1270.64	not significant
10236	GRINA	1.20	3.18E-03	6.94E-03	309.18	not significant
10237	CEP72	1.20	2.62E-05	8.21E-05	708.99	not significant
10238	DHX40	1.20	8.76E-13	6.22E-12	2784.16	not significant
10239	ZHX1-C8orf76	1.20	6.66E-02	1.07E-01	31.78	not significant
10240	LOC101927497	1.20	5.89E-08	2.59E-07	1407.31	not significant
10241	BTBD8	1.20	6.25E-02	1.01E-01	23.30	not significant
10242	MST1R	1.20	4.60E-02	7.72E-02	80.03	not significant
10243	LEF1-AS1	1.20	9.58E-03	1.89E-02	291.14	not significant
10244	CIRBP	1.20	2.24E-18	2.56E-17	6201.20	not significant
10245	TESPA1	1.20	3.70E-18	4.17E-17	11307.99	not significant
10246	SFR1	1.20	2.17E-03	4.86E-03	364.01	not significant
10247	C1orf50	1.20	1.24E-03	2.93E-03	371.60	not significant
10248	ATP5G2	1.20	1.04E-15	9.51E-15	10844.20	not significant
10249	LUC7L3	1.20	5.08E-04	1.28E-03	6343.67	not significant
10250	TAS2R5	1.20	4.65E-02	7.81E-02	14.27	not significant
10251	ZNF747	1.20	2.64E-05	8.25E-05	704.53	not significant
10252	CENPJ	1.20	1.84E-07	7.60E-07	1641.70	not significant
10253	ST3GAL4	1.20	5.93E-07	2.30E-06	1050.30	not significant
10254	PLEKHM3	1.20	4.93E-05	1.48E-04	677.29	not significant
10255	STAG3L2	1.20	1.15E-02	2.23E-02	260.66	not significant
10256	LOC285074	1.20	4.17E-04	1.07E-03	517.70	not significant
10257	ZGRF1	1.20	1.27E-07	5.36E-07	2219.00	not significant
10258	FAM13B	1.20	2.27E-12	1.56E-11	3279.37	not significant
10259	CLEC2B	1.20	2.65E-04	7.06E-04	561.47	not significant
10260	NEDD4L	1.20	1.68E-02	3.14E-02	169.36	not significant
10261	ZNF677	1.20	3.64E-02	6.27E-02	92.85	not significant
10262	BIK	1.20	1.10E-04	3.13E-04	610.44	not significant
10263	LINC01108	1.20	5.59E-02	9.16E-02	18.42	not significant
10264	DNASE1L1	1.20	6.53E-02	1.05E-01	37.86	not significant
10265	NUMA1	1.20	2.51E-10	1.42E-09	11931.65	not significant
10266	ZNF891	1.20	4.51E-03	9.55E-03	258.63	not significant
10267	RPL29	1.20	3.01E-14	2.43E-13	15682.11	not significant
10268	LOC642852	1.20	5.70E-04	1.43E-03	468.73	not significant
10269	CD47	1.20	4.88E-23	7.58E-22	10970.87	not significant
10270	ARHGAP11B	1.20	1.13E-02	2.19E-02	186.25	not significant
10271	TTC24	1.20	2.50E-03	5.54E-03	322.60	not significant
10272	CDC42EP2	1.20	4.64E-02	7.78E-02	71.32	not significant
10273	TGOLN2	1.20	2.85E-21	3.93E-20	9057.99	not significant
10274	FCHSD1	1.20	1.19E-02	2.29E-02	191.24	not significant
10275	SYS1	1.20	2.76E-07	1.12E-06	1302.46	not significant
10276	PON2	1.20	9.63E-03	1.89E-02	218.50	not significant
10277	ZNF428	1.20	1.27E-07	5.36E-07	1996.66	not significant
10278	SLFN11	1.20	1.78E-16	1.74E-15	7040.64	not significant
10279	SDHAP3	1.20	2.22E-02	4.04E-02	143.74	not significant
10280	NFKB2	1.20	9.83E-05	2.83E-04	655.16	not significant
10281	YBEY	1.20	5.69E-03	1.18E-02	241.20	not significant
10282	PTGER3	1.20	6.41E-02	1.03E-01	32.88	not significant
10283	MAGEH1	1.20	2.29E-05	7.23E-05	727.25	not significant
10284	IKBKB	1.20	1.10E-13	8.43E-13	3156.00	not significant

10285	WRAP53	1.20	3.82E-07	1.52E-06	1202.80	not significant
10286	FAM102B	1.20	4.91E-13	3.55E-12	3152.16	not significant
10287	PSMB10	1.21	2.10E-08	9.71E-08	2600.59	not significant
10288	ST8SIA4	1.21	1.04E-11	6.72E-11	2288.91	not significant
10289	TBC1D1	1.21	5.23E-16	4.90E-15	5126.39	not significant
10290	SAP25	1.21	4.35E-02	7.34E-02	380.89	not significant
10291	GIMAP8	1.21	9.01E-11	5.31E-10	2751.36	not significant
10292	UBOX5	1.21	4.55E-05	1.38E-04	628.85	not significant
10293	SGSM2	1.21	3.71E-08	1.67E-07	2736.62	not significant
10294	TTC39B	1.21	1.28E-03	3.02E-03	394.99	not significant
10295	EXOSC6	1.21	3.75E-07	1.50E-06	1110.68	not significant
10296	HACL1	1.21	1.63E-04	4.51E-04	517.23	not significant
10297	GGCT	1.21	2.15E-08	9.95E-08	2717.79	not significant
10298	ZNF512B	1.21	5.32E-09	2.62E-08	3394.26	not significant
10299	FSD1L	1.21	5.99E-03	1.23E-02	232.51	not significant
10300	RPL28	1.21	3.95E-13	2.89E-12	18043.88	not significant
10301	PPOX	1.21	3.26E-04	8.55E-04	559.63	not significant
10302	WSB1	1.21	2.12E-04	5.75E-04	4137.91	not significant
10303	PROCA1	1.21	2.93E-02	5.16E-02	122.01	not significant
10304	TRAF3IP2-AS1	1.21	1.05E-04	3.00E-04	559.20	not significant
10305	SSSCA1-AS1	1.21	5.67E-02	9.28E-02	21.39	not significant
10306	TRAK1	1.21	2.63E-03	5.82E-03	285.08	not significant
10307	NUP43	1.21	6.15E-13	4.42E-12	3192.96	not significant
10308	TMEM97	1.21	9.94E-03	1.95E-02	181.34	not significant
10309	SLC25A3	1.21	6.07E-17	6.18E-16	19192.97	not significant
10310	TTC17	1.21	1.18E-12	8.32E-12	3014.59	not significant
10311	SMAD3	1.21	2.83E-05	8.82E-05	700.20	not significant
10312	ZNF211	1.21	1.35E-05	4.41E-05	682.42	not significant
10313	C7orf43	1.21	3.63E-05	1.11E-04	972.10	not significant
10314	CROCCP2	1.21	1.49E-04	4.15E-04	554.32	not significant
10315	CCDC130	1.21	1.38E-05	4.49E-05	847.97	not significant
10316	AHI1	1.21	1.66E-03	3.82E-03	320.57	not significant
10317	TSSK6	1.21	5.13E-03	1.07E-02	236.65	not significant
10318	ANP32B	1.21	3.86E-15	3.38E-14	18250.66	not significant
10319	MUTYH	1.21	8.83E-07	3.36E-06	1149.96	not significant
10320	CD1D	1.21	4.35E-04	1.11E-03	474.20	not significant
10321	TRIM68	1.21	3.60E-05	1.11E-04	674.89	not significant
10322	TMEM194A	1.21	7.15E-21	9.66E-20	9831.44	not significant
10323	RAD9B	1.21	6.12E-02	9.92E-02	29.21	not significant
10324	PRAF2	1.21	1.02E-03	2.44E-03	354.87	not significant
10325	NACA	1.21	9.37E-05	2.70E-04	27906.47	not significant
10326	TET2	1.21	1.13E-06	4.25E-06	1198.94	not significant
10327	DHRS4L1	1.21	5.07E-02	8.41E-02	59.26	not significant
10328	ZNF219	1.21	9.46E-06	3.15E-05	834.88	not significant
10329	ZFP69B	1.21	3.50E-03	7.57E-03	249.36	not significant
10330	IFT52	1.21	6.43E-08	2.81E-07	1395.48	not significant
10331	OXR1	1.21	2.63E-10	1.49E-09	1929.68	not significant
10332	GTPBP2	1.21	1.46E-08	6.85E-08	2041.72	not significant
10333	CYP4F2	1.21	2.50E-02	4.48E-02	125.15	not significant
10334	MRFAP1	1.21	2.35E-11	1.46E-10	4329.37	not significant
10335	ZNF48	1.21	8.38E-07	3.20E-06	947.77	not significant
10336	LNPEP	1.21	1.06E-10	6.20E-10	2228.63	not significant
10337	ATF6B	1.21	2.70E-08	1.23E-07	1603.40	not significant
10338	ACBD4	1.21	2.36E-03	5.26E-03	316.54	not significant
10339	PLEKHG5	1.21	5.09E-02	8.44E-02	54.66	not significant
10340	DNMBP	1.21	4.48E-05	1.36E-04	597.42	not significant
10341	MED13L	1.21	1.93E-18	2.21E-17	8217.88	not significant
10342	TSPYL5	1.21	1.91E-13	1.44E-12	2564.64	not significant
10343	AKAP2	1.21	5.10E-02	8.45E-02	19.85	not significant
10344	LYPD3	1.21	5.92E-02	9.63E-02	34.18	not significant
10345	TAPBPL	1.21	2.14E-06	7.76E-06	894.36	not significant
10346	ST3GAL5	1.21	8.31E-06	2.79E-05	760.15	not significant
10347	SH3GLB2	1.21	7.94E-10	4.24E-09	2097.30	not significant
10348	EXOG	1.21	1.52E-04	4.22E-04	640.14	not significant
10349	B3GAT3	1.21	4.15E-08	1.86E-07	1334.11	not significant
10350	FAM111A	1.21	1.37E-15	1.24E-14	5571.52	not significant
10351	C8orf44	1.21	4.41E-02	7.43E-02	84.07	not significant
10352	REL	1.21	1.52E-08	7.09E-08	1620.37	not significant
10353	LOC100132356	1.21	5.57E-02	9.14E-02	46.11	not significant
10354	SPON2	1.21	3.35E-02	5.82E-02	93.63	not significant
10355	C17orf59	1.21	3.40E-04	8.89E-04	431.28	not significant
10356	DIDO1	1.21	8.28E-12	5.39E-11	4992.30	not significant
10357	C16orf59	1.21	1.85E-06	6.79E-06	970.16	not significant
10358	PITPNC1	1.21	1.48E-13	1.13E-12	3148.72	not significant
10359	PPP1R15A	1.21	1.43E-05	4.64E-05	690.25	not significant
10360	GFOD2	1.21	1.11E-07	4.70E-07	1113.80	not significant
10361	RAB5B	1.21	1.72E-19	2.12E-18	5266.23	not significant
10362	DLG5	1.21	3.04E-08	1.39E-07	1403.01	not significant
10363	RAB9B	1.21	3.90E-04	1.01E-03	416.54	not significant
10364	PVRIG	1.21	2.31E-11	1.43E-10	2462.44	not significant
10365	GNS	1.21	3.88E-16	3.66E-15	3800.94	not significant
10366	ZER1	1.21	1.99E-07	8.19E-07	1067.43	not significant
10367	NCAPH2	1.21	8.88E-18	9.64E-17	5125.11	not significant
10368	KCNN4	1.21	1.75E-04	4.83E-04	480.44	not significant
10369	GPX4	1.21	2.05E-14	1.67E-13	5366.47	not significant
10370	CCNI	1.21	1.20E-20	1.59E-19	12122.13	not significant
10371	MROH1	1.21	5.57E-03	1.15E-02	235.95	not significant
10372	CHMP3	1.22	5.61E-02	9.19E-02	36.34	not significant

10373	RPL10A	1.22	2.68E-20	3.49E-19	16758.75	not significant
10374	ZNF740	1.22	4.95E-12	3.29E-11	2836.49	not significant
10375	ZNF157	1.22	5.67E-02	9.28E-02	31.10	not significant
10376	GTSE1-AS1	1.22	4.65E-02	7.81E-02	18.08	not significant
10377	STX3	1.22	5.48E-02	9.02E-02	39.01	not significant
10378	TSHZ1	1.22	7.33E-09	3.56E-08	1747.90	not significant
10379	SMPD1	1.22	3.61E-02	6.22E-02	75.65	not significant
10380	LOC100507217	1.22	3.44E-06	1.22E-05	901.10	not significant
10381	FBXL20	1.22	2.45E-05	7.69E-05	632.81	not significant
10382	LOC100287042	1.22	1.64E-02	3.07E-02	145.16	not significant
10383	GDI2	1.22	3.81E-22	5.57E-21	14683.77	not significant
10384	PCMTD1	1.22	1.25E-08	5.91E-08	1563.82	not significant
10385	FGR	1.22	3.11E-04	8.17E-04	425.75	not significant
10386	SF3A2	1.22	2.65E-16	2.54E-15	7540.78	not significant
10387	OVGP1	1.22	4.73E-02	7.92E-02	59.62	not significant
10388	RPS13	1.22	1.27E-16	1.26E-15	14601.28	not significant
10389	ZFAND2B	1.22	1.78E-06	6.55E-06	896.52	not significant
10390	CLUAP1	1.22	6.98E-06	2.37E-05	732.46	not significant
10391	LTA4H	1.22	4.58E-14	3.64E-13	4070.53	not significant
10392	LRRC41	1.22	5.30E-12	3.51E-11	2571.65	not significant
10393	HR	1.22	5.55E-02	9.10E-02	32.98	not significant
10394	MNT	1.22	5.85E-06	2.00E-05	825.48	not significant
10395	CCDC77	1.22	2.67E-06	9.57E-06	863.65	not significant
10396	PLD6	1.22	4.81E-02	8.03E-02	53.27	not significant
10397	LOC101928710	1.22	5.63E-03	1.17E-02	261.59	not significant
10398	LANCL2	1.22	2.95E-05	9.19E-05	693.63	not significant
10399	ZNF547	1.22	3.46E-02	6.00E-02	77.27	not significant
10400	KHDC1	1.22	1.54E-02	2.90E-02	136.11	not significant
10401	STXBP5L	1.22	5.51E-02	9.05E-02	39.48	not significant
10402	LOC100507530	1.22	3.99E-02	6.79E-02	66.63	not significant
10403	NAPB	1.22	2.18E-05	6.91E-05	642.97	not significant
10404	F2R	1.22	6.06E-10	3.29E-09	1581.92	not significant
10405	RINL	1.22	4.85E-05	1.46E-04	580.40	not significant
10406	IL7R	1.22	8.16E-04	1.98E-03	364.32	not significant
10407	UXT	1.22	4.84E-11	2.93E-10	1811.92	not significant
10408	DNA2	1.22	1.29E-11	8.27E-11	3215.21	not significant
10409	LINC00339	1.22	2.02E-03	4.55E-03	273.08	not significant
10410	PLEKHM1P	1.22	1.01E-03	2.40E-03	497.59	not significant
10411	DCAF16	1.22	3.82E-12	2.56E-11	2999.76	not significant
10412	ANKRD18DP	1.22	4.05E-02	6.88E-02	71.71	not significant
10413	P2RX4	1.22	5.65E-07	2.20E-06	860.65	not significant
10414	KEAP1	1.22	1.19E-10	6.93E-10	2728.26	not significant
10415	CYP2D7P	1.22	5.47E-02	9.01E-02	26.39	not significant
10416	FAM135A	1.22	2.15E-04	5.83E-04	435.92	not significant
10417	BTN3A1	1.22	1.73E-09	8.94E-09	1617.32	not significant
10418	RAET1E-AS1	1.22	5.23E-02	8.64E-02	22.95	not significant
10419	RECQL5	1.22	1.57E-07	6.54E-07	1328.71	not significant
10420	FGD5-AS1	1.22	7.38E-23	1.13E-21	6366.93	not significant
10421	CDK5R1	1.22	1.99E-03	4.50E-03	274.91	not significant
10422	RPS11	1.22	2.77E-21	3.82E-20	30771.93	not significant
10423	ABCA4	1.22	5.15E-02	8.53E-02	41.05	not significant
10424	TSC22D1-AS1	1.22	3.19E-02	5.58E-02	11.98	not significant
10425	GCNT4	1.22	3.24E-02	5.65E-02	80.42	not significant
10426	PTDSS2	1.22	9.06E-09	4.38E-08	1251.62	not significant
10427	AFF2	1.22	1.81E-04	4.97E-04	454.86	not significant
10428	NPTN-IT1	1.22	5.00E-02	8.32E-02	52.81	not significant
10429	ALG10B	1.22	8.89E-08	3.82E-07	1406.50	not significant
10430	JRKL	1.22	3.75E-07	1.50E-06	885.43	not significant
10431	UBE2W	1.22	9.63E-08	4.12E-07	1136.97	not significant
10432	USP20	1.22	4.56E-21	6.24E-20	6048.61	not significant
10433	RPS24	1.22	2.59E-12	1.76E-11	18378.46	not significant
10434	LOC100130950	1.22	5.35E-02	8.83E-02	25.54	not significant
10435	RAP2A	1.22	1.57E-11	9.94E-11	2056.55	not significant
10436	NFIC	1.22	2.18E-09	1.12E-08	1450.24	not significant
10437	SH3GLB1	1.22	2.03E-16	1.97E-15	3681.89	not significant
10438	PSMA2	1.22	1.91E-11	1.20E-10	6713.77	not significant
10439	MGEA5	1.22	1.13E-15	1.03E-14	5071.34	not significant
10440	ZNF222	1.22	1.17E-02	2.26E-02	141.16	not significant
10441	MRC2	1.22	9.33E-09	4.50E-08	2033.27	not significant
10442	RALGPS2	1.22	1.70E-10	9.79E-10	1682.43	not significant
10443	CASD1	1.22	8.14E-14	6.32E-13	2500.55	not significant
10444	MT2A	1.22	1.92E-04	5.25E-04	12755.09	not significant
10445	EEF1G	1.22	1.45E-18	1.68E-17	18356.50	not significant
10446	SCAMP1-AS1	1.22	7.35E-04	1.80E-03	368.21	not significant
10447	CBX2	1.22	2.17E-03	4.87E-03	288.07	not significant
10448	ZNF316	1.22	2.28E-13	1.70E-12	2366.75	not significant
10449	ZNF582	1.22	6.43E-03	1.32E-02	178.98	not significant
10450	SMIM14	1.22	8.36E-03	1.67E-02	177.79	not significant
10451	PLA2G12A	1.22	5.79E-05	1.73E-04	505.46	not significant
10452	ZFYVE16	1.22	5.59E-06	1.92E-05	772.71	not significant
10453	NR5A1	1.22	2.23E-02	4.06E-02	101.31	not significant
10454	ATP6V0A2	1.22	3.26E-14	2.63E-13	3040.85	not significant
10455	ZNF823	1.22	2.46E-03	5.48E-03	242.41	not significant
10456	CROT	1.22	4.79E-05	1.44E-04	543.99	not significant
10457	RPLP2	1.22	5.11E-05	1.54E-04	21664.39	not significant
10458	RAB30-AS1	1.22	1.58E-02	2.96E-02	123.83	not significant
10459	KCNA3	1.22	1.56E-16	1.53E-15	4573.46	not significant
10460	CAPN10	1.22	1.74E-07	7.21E-07	955.50	not significant

10461	ARHGEF39	1.22	4.30E-04	1.10E-03	375.95	not significant
10462	OSBP2	1.22	1.60E-02	2.99E-02	129.97	not significant
10463	PTPRC	1.22	3.13E-26	5.98E-25	12514.57	not significant
10464	PRR29	1.22	4.83E-02	8.06E-02	46.88	not significant
10465	ADPRM	1.23	6.08E-03	1.25E-02	184.97	not significant
10466	EFCAB2	1.23	7.26E-05	2.13E-04	469.38	not significant
10467	CCDC34	1.23	5.26E-09	2.59E-08	1525.13	not significant
10468	CDC37L1	1.23	4.81E-03	1.01E-02	198.34	not significant
10469	HMGN3-AS1	1.23	5.04E-02	8.37E-02	36.63	not significant
10470	ANKMY1	1.23	3.94E-05	1.20E-04	512.21	not significant
10471	KANSL1	1.23	1.48E-07	6.19E-07	1039.26	not significant
10472	RECQL4	1.23	2.04E-10	1.17E-09	3501.87	not significant
10473	MYEF2	1.23	1.13E-07	4.81E-07	1896.46	not significant
10474	GUSBP11	1.23	1.53E-02	2.88E-02	1019.06	not significant
10475	ZRANB3	1.23	1.35E-04	3.80E-04	472.60	not significant
10476	FLCN	1.23	9.23E-09	4.46E-08	1225.34	not significant
10477	STK35	1.23	4.85E-12	3.23E-11	2061.56	not significant
10478	RRNAD1	1.23	7.45E-06	2.52E-05	621.76	not significant
10479	RPL7A	1.23	1.35E-19	1.68E-18	19205.94	not significant
10480	BAG1	1.23	7.42E-10	3.98E-09	1612.50	not significant
10481	S100PBP	1.23	1.08E-12	7.61E-12	2616.66	not significant
10482	FAM13A-AS1	1.23	5.05E-02	8.38E-02	29.56	not significant
10483	ZNF493	1.23	1.32E-09	6.87E-09	1377.73	not significant
10484	FLI1	1.23	4.15E-17	4.27E-16	3748.31	not significant
10485	TIMELESS	1.23	1.85E-28	4.06E-27	11718.68	not significant
10486	FAM110A	1.23	6.83E-08	2.97E-07	978.94	not significant
10487	UHRF1BP1L	1.23	1.16E-09	6.09E-09	1334.41	not significant
10488	ERAP2	1.23	6.10E-29	1.38E-27	13969.10	not significant
10489	DCP2	1.23	1.41E-14	1.17E-13	7532.74	not significant
10490	DDX17	1.23	4.54E-13	3.29E-12	21461.59	not significant
10491	NETO2	1.23	1.37E-09	7.13E-09	1571.84	not significant
10492	RAB33B	1.23	6.82E-05	2.01E-04	504.37	not significant
10493	ABCC10	1.23	5.65E-06	1.94E-05	813.67	not significant
10494	ZFP62	1.23	7.93E-07	3.03E-06	1268.15	not significant
10495	TRIM22	1.23	2.53E-11	1.57E-10	2479.77	not significant
10496	RNF150	1.23	4.07E-04	1.05E-03	345.35	not significant
10497	POLR1D	1.23	9.53E-20	1.20E-18	5402.70	not significant
10498	ACVR2B-AS1	1.23	4.81E-02	8.03E-02	29.64	not significant
10499	ZNF549	1.23	1.22E-05	4.02E-05	603.82	not significant
10500	IQCB1	1.23	2.73E-10	1.54E-09	1476.02	not significant
10501	TMPPE	1.23	1.32E-02	2.53E-02	137.67	not significant
10502	CHMP5	1.23	5.77E-10	3.14E-09	1358.81	not significant
10503	NGRN	1.23	1.05E-12	7.43E-12	2494.34	not significant
10504	TIRAP	1.23	4.50E-02	7.56E-02	19.05	not significant
10505	ZNF575	1.23	6.33E-03	1.30E-02	168.42	not significant
10506	ZNF782	1.23	5.41E-03	1.13E-02	192.79	not significant
10507	COX10-AS1	1.23	4.88E-04	1.24E-03	379.63	not significant
10508	LRRC57	1.23	1.96E-05	6.24E-05	542.50	not significant
10509	JAGN1	1.23	2.42E-08	1.11E-07	1375.52	not significant
10510	KIF24	1.23	3.33E-08	1.51E-07	1105.75	not significant
10511	SLC12A4	1.23	2.00E-07	8.24E-07	1018.98	not significant
10512	FAM184A	1.23	1.07E-04	3.06E-04	441.93	not significant
10513	FMNL1	1.23	1.65E-22	2.47E-21	10285.75	not significant
10514	SFI1	1.23	4.23E-03	8.99E-03	2337.73	not significant
10515	CALCOCO2	1.23	1.50E-20	1.98E-19	4477.46	not significant
10516	DPP7	1.23	9.46E-12	6.13E-11	2527.24	not significant
10517	GPR56	1.23	8.42E-16	7.78E-15	3214.05	not significant
10518	TMEM14C	1.23	3.34E-12	2.24E-11	2096.15	not significant
10519	RPS18P9	1.23	3.99E-02	6.79E-02	53.60	not significant
10520	INPP5B	1.23	2.90E-10	1.64E-09	1388.76	not significant
10521	CCT6P1	1.23	1.95E-02	3.58E-02	105.71	not significant
10522	NARF	1.23	3.94E-17	4.07E-16	3970.37	not significant
10523	CTNNBIP1	1.23	1.88E-07	7.79E-07	1145.18	not significant
10524	PACS2	1.23	1.24E-05	4.08E-05	587.62	not significant
10525	ZFHX3	1.23	4.01E-03	8.59E-03	230.19	not significant
10526	HERC3	1.23	9.72E-08	4.16E-07	1049.91	not significant
10527	WDR91	1.23	3.24E-05	1.00E-04	562.72	not significant
10528	DDX54	1.23	1.33E-19	1.65E-18	6858.60	not significant
10529	DNMT3A	1.23	4.93E-18	5.49E-17	3881.93	not significant
10530	CEP192	1.23	5.17E-13	3.73E-12	4136.89	not significant
10531	AGBL5	1.23	1.13E-13	8.67E-13	2241.78	not significant
10532	PARD6B	1.23	2.10E-02	3.83E-02	90.18	not significant
10533	LRRC39	1.23	4.75E-02	7.95E-02	30.41	not significant
10534	NBR1	1.23	1.05E-14	8.83E-14	3277.97	not significant
10535	GABPB1-AS1	1.23	1.20E-03	2.82E-03	270.14	not significant
10536	RASGRP2	1.23	1.20E-10	6.99E-10	1666.37	not significant
10537	YIPF4	1.23	7.89E-08	3.41E-07	1119.12	not significant
10538	DBH	1.23	2.44E-02	4.38E-02	10.54	not significant
10539	SEC14L1P1	1.23	4.17E-02	7.06E-02	47.13	not significant
10540	SYNE1	1.24	3.50E-09	1.76E-08	1687.69	not significant
10541	PARP2	1.24	1.21E-11	7.78E-11	1723.08	not significant
10542	ITFG2	1.24	2.29E-07	9.38E-07	902.83	not significant
10543	TBC1D32	1.24	1.75E-03	4.00E-03	262.05	not significant
10544	C11orf95	1.24	2.68E-11	1.66E-10	1607.64	not significant
10545	GABRB3	1.24	3.94E-09	1.97E-08	1207.67	not significant
10546	ZKSCAN8	1.24	1.48E-12	1.03E-11	2530.35	not significant
10547	MIB2	1.24	3.07E-08	1.40E-07	1252.98	not significant
10548	ADAMTS1	1.24	1.18E-17	1.27E-16	3836.14	not significant

10549	THUMPD3-AS1	1.24	5.18E-04	1.31E-03	399.80	not significant
10550	RPL9	1.24	6.83E-15	5.87E-14	19651.94	not significant
10551	KIAA0319L	1.24	4.23E-10	2.34E-09	1418.35	not significant
10552	PURB	1.24	1.13E-05	3.74E-05	4929.76	not significant
10553	ACVR1	1.24	1.62E-03	3.73E-03	239.03	not significant
10554	SLC24A1	1.24	5.29E-04	1.34E-03	307.83	not significant
10555	TTL	1.24	6.58E-14	5.16E-13	2031.49	not significant
10556	RAVER2	1.24	2.47E-02	4.43E-02	10.00	not significant
10557	EPAS1	1.24	1.42E-15	1.29E-14	3305.53	not significant
10558	SLC4A7	1.24	5.36E-13	3.86E-12	4990.44	not significant
10559	SNX21	1.24	2.69E-02	4.78E-02	11.05	not significant
10560	MAP3K12	1.24	4.62E-06	1.60E-05	650.12	not significant
10561	SRPK2	1.24	3.61E-25	6.53E-24	9036.62	not significant
10562	CEP44	1.24	1.98E-08	9.19E-08	1126.94	not significant
10563	MAPK8IP3	1.24	4.57E-03	9.67E-03	2266.40	not significant
10564	DHPS	1.24	1.70E-16	1.66E-15	2889.29	not significant
10565	TRG-AS1	1.24	3.62E-18	4.08E-17	4382.57	not significant
10566	HACE1	1.24	3.57E-16	3.38E-15	2694.11	not significant
10567	C22orf29	1.24	6.41E-14	5.03E-13	2783.80	not significant
10568	GJC1	1.24	5.02E-16	4.71E-15	2642.03	not significant
10569	EXOSC1	1.24	2.62E-07	1.07E-06	873.87	not significant
10570	DVL2	1.24	1.17E-16	1.16E-15	3708.45	not significant
10571	SAMD12	1.24	3.18E-02	5.56E-02	63.61	not significant
10572	ZFP30	1.24	5.80E-07	2.25E-06	730.28	not significant
10573	SPIDR	1.24	4.95E-13	3.58E-12	1981.32	not significant
10574	EPOR	1.24	3.68E-03	7.93E-03	181.07	not significant
10575	ZNF397	1.24	1.52E-06	5.63E-06	790.17	not significant
10576	TRPV1	1.24	1.04E-03	2.48E-03	280.38	not significant
10577	ZNF517	1.24	1.81E-02	3.36E-02	96.89	not significant
10578	KIF21A	1.24	5.18E-04	1.31E-03	336.85	not significant
10579	ASPSCR1	1.24	2.88E-07	1.17E-06	942.59	not significant
10580	CERS2	1.24	6.31E-23	9.72E-22	7979.04	not significant
10581	ARFGAP3	1.24	9.94E-16	9.12E-15	4700.86	not significant
10582	KLHL2	1.24	4.42E-04	1.13E-03	316.75	not significant
10583	C1RL	1.24	1.69E-03	3.88E-03	231.83	not significant
10584	FAU	1.24	9.69E-17	9.67E-16	8552.32	not significant
10585	CNNM3	1.24	1.26E-12	8.88E-12	2364.57	not significant
10586	MFSD11	1.24	4.57E-10	2.52E-09	1329.73	not significant
10587	FECH	1.24	6.30E-10	3.41E-09	1357.10	not significant
10588	CD3E	1.24	6.82E-19	8.04E-18	26655.52	not significant
10589	DICER1-AS1	1.24	2.98E-02	5.25E-02	63.17	not significant
10590	C19orf44	1.24	1.66E-03	3.81E-03	238.31	not significant
10591	SUN1	1.24	1.92E-16	1.87E-15	3057.51	not significant
10592	GYG1	1.24	7.13E-04	1.75E-03	274.30	not significant
10593	GTPBP1	1.24	6.66E-15	5.73E-14	2508.22	not significant
10594	MURC	1.24	3.19E-02	5.58E-02	58.62	not significant
10595	ZBED5	1.24	5.49E-04	1.38E-03	1713.59	not significant
10596	ZNF623	1.24	1.78E-08	8.29E-08	1011.83	not significant
10597	P4HTM	1.24	2.30E-02	4.16E-02	83.22	not significant
10598	JUND	1.24	2.20E-14	1.80E-13	6304.98	not significant
10599	TAF1D	1.24	1.37E-12	9.58E-12	1741.65	not significant
10600	CRYZL1	1.24	1.05E-07	4.46E-07	861.52	not significant
10601	ZNF594	1.24	4.15E-03	8.84E-03	186.72	not significant
10602	SRY	1.24	2.87E-02	5.08E-02	67.53	not significant
10603	RNF44	1.24	1.69E-17	1.80E-16	5425.18	not significant
10604	TRIOBP	1.24	1.24E-12	8.73E-12	1953.64	not significant
10605	ZNF37BP	1.24	1.25E-02	2.41E-02	1977.95	not significant
10606	RANBP6	1.24	3.05E-12	2.06E-11	2341.79	not significant
10607	OGN	1.24	6.67E-06	2.27E-05	535.09	not significant
10608	ADAM21	1.24	4.04E-02	6.87E-02	19.30	not significant
10609	CAPRIN2	1.24	1.04E-03	2.49E-03	378.39	not significant
10610	SLC38A2	1.24	2.42E-25	4.40E-24	20634.42	not significant
10611	PPM1K	1.24	1.66E-12	1.15E-11	1938.51	not significant
10612	ZFP90	1.24	6.83E-10	3.69E-09	1390.32	not significant
10613	HHIP-AS1	1.24	1.06E-13	8.17E-13	2188.38	not significant
10614	RALGPS1	1.24	1.07E-07	4.57E-07	1218.07	not significant
10615	ELOVL5	1.24	3.32E-32	9.16E-31	22531.06	not significant
10616	SGCB	1.24	5.58E-11	3.35E-10	1367.27	not significant
10617	DLGAP4-AS1	1.24	4.28E-02	7.24E-02	24.67	not significant
10618	IDH2	1.24	7.30E-21	9.86E-20	15307.12	not significant
10619	RNF115	1.24	6.11E-05	1.82E-04	416.40	not significant
10620	CNOT6	1.24	1.80E-26	3.49E-25	10992.22	not significant
10621	ZNF586	1.24	5.74E-07	2.23E-06	687.08	not significant
10622	RPLP1	1.24	3.99E-14	3.19E-13	26590.05	not significant
10623	CDK18	1.25	1.38E-06	5.15E-06	651.95	not significant
10624	QPCTL	1.25	5.45E-04	1.37E-03	296.77	not significant
10625	RFXAP	1.25	1.50E-07	6.26E-07	851.72	not significant
10626	CDCA7L	1.25	5.65E-27	1.14E-25	9354.78	not significant
10627	TCF19	1.25	1.31E-08	6.19E-08	1006.65	not significant
10628	KIAA0195	1.25	9.53E-22	1.36E-20	5242.61	not significant
10629	PDE4D	1.25	3.61E-07	1.44E-06	781.11	not significant
10630	TIAM1	1.25	6.41E-07	2.48E-06	725.55	not significant
10631	SLFN13	1.25	4.29E-09	2.13E-08	1290.99	not significant
10632	UIMC1	1.25	1.47E-10	8.47E-10	1531.17	not significant
10633	SERINC1	1.25	6.21E-16	5.79E-15	3191.72	not significant
10634	PCGF6	1.25	7.58E-06	2.56E-05	547.59	not significant
10635	RBL2	1.25	2.18E-27	4.50E-26	8091.08	not significant
10636	TMTC3	1.25	2.39E-05	7.52E-05	495.17	not significant

10637	ATAT1	1.25	2.56E-04	6.86E-04	322.28	not significant
10638	SH3GL1P1	1.25	3.88E-02	6.62E-02	20.54	not significant
10639	METTL3	1.25	7.53E-08	3.26E-07	1579.28	not significant
10640	ERCC6	1.25	1.03E-04	2.95E-04	413.58	not significant
10641	VOPP1	1.25	1.26E-05	4.14E-05	712.68	not significant
10642	HSDL1	1.25	2.05E-19	2.52E-18	3181.05	not significant
10643	TMEM170A	1.25	5.19E-05	1.56E-04	453.09	not significant
10644	ZFYVE27	1.25	5.74E-11	3.45E-10	1359.62	not significant
10645	SLC37A3	1.25	2.33E-12	1.59E-11	1595.28	not significant
10646	FOXJ2	1.25	9.92E-12	6.42E-11	1514.17	not significant
10647	MARCKSL1	1.25	5.16E-18	5.71E-17	13861.13	not significant
10648	SFT2D3	1.25	2.40E-05	7.55E-05	577.05	not significant
10649	WIPI2	1.25	6.59E-19	7.79E-18	3564.15	not significant
10650	RNASEH2C	1.25	1.03E-09	5.43E-09	1526.26	not significant
10651	TPT1	1.25	1.37E-15	1.24E-14	96852.18	not significant
10652	EMB	1.25	5.53E-25	9.89E-24	5101.57	not significant
10653	ZMYM5	1.25	7.13E-08	3.09E-07	869.51	not significant
10654	MMS19	1.25	1.11E-17	1.21E-16	2883.22	not significant
10655	DSCAML1	1.25	1.62E-02	3.03E-02	97.72	not significant
10656	PSMC3IP	1.25	1.93E-09	9.90E-09	1061.42	not significant
10657	DPF2	1.25	7.04E-18	7.72E-17	3156.16	not significant
10658	WDSUB1	1.25	1.77E-04	4.88E-04	346.15	not significant
10659	DERL1	1.25	4.79E-19	5.72E-18	4111.45	not significant
10660	RPS8	1.25	3.16E-15	2.78E-14	40609.17	not significant
10661	ITGAV	1.25	5.44E-03	1.13E-02	154.20	not significant
10662	OSER1	1.25	1.62E-08	7.56E-08	961.28	not significant
10663	ZNF414	1.25	1.24E-06	4.66E-06	619.70	not significant
10664	ARL4C	1.25	4.62E-29	1.06E-27	12844.01	not significant
10665	ZAK	1.25	6.83E-17	6.91E-16	3319.93	not significant
10666	CRYL1	1.25	3.14E-03	6.84E-03	182.17	not significant
10667	RPL30	1.25	4.92E-19	5.86E-18	25746.55	not significant
10668	SUZ12P1	1.25	6.63E-05	1.96E-04	495.54	not significant
10669	COX7A2L	1.25	6.95E-20	8.82E-19	5222.14	not significant
10670	STAG3L1	1.25	2.91E-02	5.14E-02	61.97	not significant
10671	SLC35F5	1.25	3.07E-06	1.09E-05	664.97	not significant
10672	GOLGB1	1.25	2.71E-12	1.84E-11	2377.24	not significant
10673	COPG2	1.25	1.46E-06	5.42E-06	588.09	not significant
10674	LRRC37A4P	1.25	4.64E-11	2.82E-10	2787.88	not significant
10675	PMS2P5	1.25	3.43E-03	7.43E-03	167.07	not significant
10676	ENO3	1.25	3.67E-04	9.54E-04	336.33	not significant
10677	GATAD1	1.25	2.46E-08	1.13E-07	837.04	not significant
10678	ENO2	1.25	3.80E-08	1.71E-07	840.16	not significant
10679	NEURL4	1.25	1.08E-09	5.68E-09	1714.55	not significant
10680	CDCA5	1.25	1.39E-26	2.73E-25	9418.29	not significant
10681	RGPD1	1.25	4.85E-03	1.02E-02	189.12	not significant
10682	CCDC93	1.25	2.94E-16	2.80E-15	2341.07	not significant
10683	PCGF3	1.25	1.18E-14	9.90E-14	2169.32	not significant
10684	APH1A	1.25	4.53E-07	1.79E-06	777.73	not significant
10685	FAM129C	1.25	1.73E-02	3.23E-02	93.77	not significant
10686	SYCE1L	1.25	3.12E-02	5.46E-02	49.57	not significant
10687	DAND5	1.25	3.39E-02	5.89E-02	16.61	not significant
10688	SNN	1.25	5.28E-11	3.18E-10	2233.45	not significant
10689	LOC440434	1.25	2.94E-02	5.19E-02	58.56	not significant
10690	LOC729603	1.25	1.49E-02	2.81E-02	116.34	not significant
10691	TMEM26-AS1	1.25	2.79E-02	4.94E-02	13.15	not significant
10692	RAB12	1.25	2.19E-04	5.94E-04	382.91	not significant
10693	POLR3D	1.25	6.85E-12	4.49E-11	1604.37	not significant
10694	RPL7	1.25	3.53E-15	3.11E-14	24172.25	not significant
10695	LRRC8A	1.25	6.20E-10	3.36E-09	1121.17	not significant
10696	TCTA	1.26	5.45E-07	2.13E-06	724.99	not significant
10697	USP13	1.26	1.18E-13	9.04E-13	1806.52	not significant
10698	MAN1B1	1.26	2.96E-08	1.35E-07	909.08	not significant
10699	CDKN2D	1.26	5.83E-12	3.86E-11	1735.34	not significant
10700	TXLNGY	1.26	1.88E-03	4.26E-03	6623.38	not significant
10701	ACTG1P4	1.26	2.97E-02	5.24E-02	13.15	not significant
10702	PYCARD	1.26	1.87E-03	4.25E-03	193.42	not significant
10703	RMND5B	1.26	1.48E-06	5.49E-06	617.43	not significant
10704	STAC3	1.26	2.64E-03	5.83E-03	217.40	not significant
10705	DHTKD1	1.26	1.67E-14	1.38E-13	2086.06	not significant
10706	ZNF100	1.26	1.68E-02	3.14E-02	81.60	not significant
10707	SLC9A5	1.26	4.00E-02	6.80E-02	28.67	not significant
10708	ZNF708	1.26	1.67E-06	6.14E-06	758.09	not significant
10709	SCCPDH	1.26	4.02E-14	3.20E-13	3892.78	not significant
10710	GIMAP4	1.26	1.83E-30	4.53E-29	11973.22	not significant
10711	ZNF833P	1.26	2.42E-02	4.36E-02	62.71	not significant
10712	CEP170	1.26	1.45E-06	5.39E-06	623.59	not significant
10713	CLK1	1.26	1.11E-08	5.31E-08	1682.48	not significant
10714	KLF2	1.26	1.58E-04	4.40E-04	349.61	not significant
10715	WNT3	1.26	8.24E-05	2.40E-04	355.72	not significant
10716	BRK1	1.26	5.28E-19	6.28E-18	4284.60	not significant
10717	DTX1	1.26	7.62E-34	2.40E-32	12290.68	not significant
10718	DPY19L4	1.26	4.97E-10	2.73E-09	1428.82	not significant
10719	PTDSS1	1.26	9.01E-26	1.68E-24	5938.06	not significant
10720	KIZ	1.26	2.09E-08	9.67E-08	822.64	not significant
10721	ABHD5	1.26	1.06E-06	4.00E-06	609.04	not significant
10722	CAMK2D	1.26	4.99E-11	3.01E-10	1286.17	not significant
10723	ZNF282	1.26	1.70E-14	1.40E-13	2262.57	not significant
10724	KIAA1143	1.26	8.85E-16	8.15E-15	2202.92	not significant

10725	RNPEPL1	1.26	5.73E-13	4.13E-12	2393.81	not significant
10726	RAB43	1.26	1.76E-02	3.28E-02	77.54	not significant
10727	ALG1L	1.26	3.82E-02	6.53E-02	23.09	not significant
10728	RPS3	1.26	2.61E-18	2.96E-17	43805.94	not significant
10729	CASC3	1.26	1.05E-23	1.72E-22	5256.56	not significant
10730	EEF1A1	1.26	1.88E-24	3.22E-23	147547.41	not significant
10731	EZH1	1.26	7.33E-04	1.79E-03	1261.94	not significant
10732	ZBTB41	1.26	1.50E-08	7.01E-08	923.71	not significant
10733	SOS2	1.26	2.52E-15	2.23E-14	2154.77	not significant
10734	APEX1	1.26	1.21E-24	2.09E-23	8663.43	not significant
10735	N4BP2	1.26	1.01E-26	2.01E-25	5754.07	not significant
10736	DGKD	1.26	5.21E-17	5.33E-16	2871.66	not significant
10737	STT3B	1.26	3.02E-33	8.96E-32	20485.16	not significant
10738	HSPBAP1	1.26	6.31E-04	1.56E-03	257.21	not significant
10739	GGT7	1.26	2.42E-09	1.23E-08	1188.81	not significant
10740	BCR	1.26	1.22E-19	1.52E-18	3696.63	not significant
10741	ALKBH7	1.26	1.55E-07	6.47E-07	1096.88	not significant
10742	AP1S2	1.26	7.26E-12	4.75E-11	1344.55	not significant
10743	FAM89B	1.26	1.73E-09	8.93E-09	1279.86	not significant
10744	ADAMTS6	1.26	1.20E-02	2.32E-02	103.54	not significant
10745	DHRS13	1.26	3.98E-07	1.58E-06	662.78	not significant
10746	FGD1	1.26	2.59E-02	4.62E-02	59.02	not significant
10747	ZNF701	1.26	2.41E-08	1.11E-07	866.21	not significant
10748	UHRF2	1.26	1.43E-05	4.65E-05	2857.32	not significant
10749	MAPKAPK5-AS1	1.26	4.65E-10	2.56E-09	1131.03	not significant
10750	C11orf68	1.26	7.69E-07	2.94E-06	760.68	not significant
10751	CLN6	1.26	1.33E-15	1.21E-14	2279.66	not significant
10752	TFDP2	1.26	8.06E-30	1.93E-28	14256.57	not significant
10753	NT5C	1.26	3.52E-10	1.96E-09	1054.42	not significant
10754	TTLL7	1.26	9.02E-03	1.79E-02	113.97	not significant
10755	ANKRA2	1.26	1.14E-05	3.77E-05	498.76	not significant
10756	C14orf28	1.26	4.60E-03	9.73E-03	136.71	not significant
10757	DYM	1.26	1.15E-17	1.24E-16	2670.39	not significant
10758	RNF19A	1.26	7.52E-14	5.85E-13	1718.49	not significant
10759	FAM160B1	1.26	4.22E-11	2.57E-10	2236.55	not significant
10760	MFI2	1.26	7.16E-06	2.43E-05	470.30	not significant
10761	FOXN3	1.26	4.90E-23	7.61E-22	4604.13	not significant
10762	ZNF605	1.27	3.72E-07	1.49E-06	742.59	not significant
10763	PSD	1.27	3.67E-02	6.31E-02	26.14	not significant
10764	TMEM129	1.27	2.70E-08	1.24E-07	921.73	not significant
10765	PKD1P1	1.27	5.99E-04	1.49E-03	288.31	not significant
10766	ZNF699	1.27	7.98E-03	1.60E-02	111.97	not significant
10767	C9orf16	1.27	1.39E-12	9.71E-12	1538.22	not significant
10768	TBC1D17	1.27	1.64E-06	6.04E-06	557.86	not significant
10769	ZNF777	1.27	7.18E-07	2.76E-06	762.22	not significant
10770	CASP4	1.27	4.10E-11	2.50E-10	1268.24	not significant
10771	TSPAN7	1.27	6.37E-19	7.52E-18	5932.29	not significant
10772	ZNF555	1.27	5.51E-03	1.14E-02	129.51	not significant
10773	TAPT1	1.27	2.58E-15	2.29E-14	1916.99	not significant
10774	PDXDC2P	1.27	1.91E-02	3.51E-02	318.50	not significant
10775	EPG5	1.27	1.39E-10	8.09E-10	1595.31	not significant
10776	IRF1	1.27	3.29E-27	6.70E-26	8330.52	not significant
10777	GLT1D1	1.27	1.68E-05	5.41E-05	453.79	not significant
10778	TTC9C	1.27	2.02E-10	1.16E-09	1061.30	not significant
10779	HIST1H1C	1.27	2.61E-03	5.78E-03	167.43	not significant
10780	APLN	1.27	2.85E-12	1.93E-11	1707.08	not significant
10781	RPS28	1.27	1.59E-15	1.43E-14	10825.41	not significant
10782	E2F7	1.27	4.04E-05	1.23E-04	2197.78	not significant
10783	TMEM57	1.27	5.29E-16	4.96E-15	2094.98	not significant
10784	RPP25L	1.27	9.80E-06	3.26E-05	525.72	not significant
10785	GLUL	1.27	9.73E-36	3.43E-34	31386.94	not significant
10786	ZC3H10	1.27	4.72E-05	1.43E-04	354.44	not significant
10787	SWT1	1.27	1.18E-03	2.78E-03	196.36	not significant
10788	TECPR1	1.27	1.36E-10	7.90E-10	1545.98	not significant
10789	SUN2	1.27	3.75E-24	6.33E-23	5221.53	not significant
10790	RGS10	1.27	3.07E-18	3.48E-17	3359.51	not significant
10791	MEGF8	1.27	2.45E-08	1.13E-07	928.08	not significant
10792	TBX19	1.27	1.06E-02	2.08E-02	91.83	not significant
10793	SLC25A40	1.27	8.98E-23	1.37E-21	3486.87	not significant
10794	VIM	1.27	3.56E-36	1.29E-34	38939.62	not significant
10795	C20orf96	1.27	2.29E-06	8.29E-06	670.24	not significant
10796	BIN1	1.27	4.89E-08	2.18E-07	788.67	not significant
10797	LOC100506639	1.27	1.80E-03	4.09E-03	183.51	not significant
10798	ZNF736	1.27	1.51E-11	9.59E-11	1436.19	not significant
10799	ZFP36L1	1.27	1.24E-09	6.50E-09	955.36	not significant
10800	NSUN5P2	1.27	6.43E-03	1.32E-02	128.74	not significant
10801	SPSB4	1.27	9.75E-03	1.92E-02	94.84	not significant
10802	RBM22	1.27	5.71E-21	7.78E-20	3240.94	not significant
10803	CUBN	1.27	1.08E-02	2.10E-02	92.44	not significant
10804	LAIR1	1.27	1.05E-10	6.13E-10	1225.00	not significant
10805	LINC00528	1.27	2.78E-04	7.37E-04	292.30	not significant
10806	ZNF346	1.27	1.27E-11	8.09E-11	1248.56	not significant
10807	GMDS-AS1	1.27	1.87E-02	3.45E-02	74.98	not significant
10808	ERAP1	1.27	1.28E-25	2.37E-24	5056.21	not significant
10809	FGD3	1.27	9.35E-10	4.95E-09	1046.15	not significant
10810	CTHRC1	1.27	7.22E-10	3.88E-09	1055.69	not significant
10811	LOC389906	1.27	4.15E-04	1.07E-03	243.97	not significant
10812	RBM5	1.27	4.05E-16	3.82E-15	3305.38	not significant

10813	MED12	1.27	4.33E-04	1.11E-03	3289.10	not significant
10814	ATXN7L3B	1.27	5.41E-35	1.81E-33	9258.77	not significant
10815	ANKRD10	1.27	1.96E-16	1.90E-15	2840.00	not significant
10816	UNKL	1.27	9.16E-06	3.06E-05	586.01	not significant
10817	PACRGL	1.27	4.44E-05	1.35E-04	357.00	not significant
10818	XYLB	1.27	3.41E-08	1.54E-07	731.46	not significant
10819	LOC81691	1.27	8.89E-09	4.30E-08	850.17	not significant
10820	ZBED3	1.27	1.01E-04	2.90E-04	318.67	not significant
10821	JRK	1.27	2.16E-04	5.85E-04	393.80	not significant
10822	PCBD2	1.27	7.22E-07	2.78E-06	579.37	not significant
10823	YPEL4	1.27	3.35E-02	5.83E-02	21.12	not significant
10824	TNFAIP8	1.27	4.52E-26	8.53E-25	4202.60	not significant
10825	A1BG	1.27	3.89E-05	1.19E-04	397.95	not significant
10826	CMPK2	1.27	6.40E-22	9.24E-21	2985.60	not significant
10827	REST	1.27	8.81E-21	1.18E-19	3514.75	not significant
10828	FANCE	1.27	1.70E-07	7.08E-07	627.70	not significant
10829	CPSF1	1.27	7.32E-17	7.37E-16	4450.64	not significant
10830	PKN1	1.27	1.73E-23	2.78E-22	8104.66	not significant
10831	HMX3	1.27	2.47E-02	4.44E-02	62.15	not significant
10832	JARID2	1.27	1.60E-29	3.78E-28	5568.27	not significant
10833	THBS3	1.28	4.19E-03	8.91E-03	130.03	not significant
10834	SARM1	1.28	1.51E-02	2.85E-02	79.37	not significant
10835	TSC22D1	1.28	1.49E-16	1.47E-15	2264.88	not significant
10836	ARAP1	1.28	7.79E-07	2.98E-06	4874.12	not significant
10837	FAM193A	1.28	7.07E-12	4.63E-11	2047.29	not significant
10838	ZNF431	1.28	2.92E-09	1.48E-08	1126.24	not significant
10839	ELMO1	1.28	1.99E-35	6.88E-34	9019.65	not significant
10840	SAP30L	1.28	1.83E-14	1.51E-13	2263.40	not significant
10841	KIAA1407	1.28	1.29E-02	2.48E-02	83.17	not significant
10842	H6PD	1.28	5.81E-19	6.89E-18	2575.14	not significant
10843	PCDHGB2	1.28	3.17E-02	5.55E-02	32.58	not significant
10844	BAHCC1	1.28	5.27E-21	7.20E-20	3209.33	not significant
10845	ATG13	1.28	2.62E-20	3.42E-19	2743.88	not significant
10846	ALDH5A1	1.28	1.45E-22	2.18E-21	3313.23	not significant
10847	CBFA2T2	1.28	1.66E-15	1.49E-14	2121.99	not significant
10848	ZNF280D	1.28	8.70E-14	6.73E-13	1505.00	not significant
10849	BIVM	1.28	2.98E-04	7.85E-04	253.67	not significant
10850	ZNF92	1.28	1.12E-15	1.02E-14	2040.37	not significant
10851	THEM6	1.28	9.86E-10	5.21E-09	968.08	not significant
10852	FAM131A	1.28	5.11E-04	1.29E-03	253.03	not significant
10853	PABPC1	1.28	1.15E-39	4.95E-38	72273.04	not significant
10854	KHDRBS3	1.28	2.41E-02	4.35E-02	48.32	not significant
10855	ATL3	1.28	3.33E-28	7.23E-27	5777.15	not significant
10856	DENND5A	1.28	5.02E-28	1.08E-26	4847.05	not significant
10857	LOC100652768	1.28	3.31E-02	5.76E-02	20.19	not significant
10858	ZNHIT3	1.28	1.77E-05	5.68E-05	367.06	not significant
10859	ZNF280C	1.28	4.53E-06	1.58E-05	492.03	not significant
10860	TXNL1	1.28	6.96E-21	9.41E-20	3244.12	not significant
10861	FAM189A1	1.28	2.85E-02	5.04E-02	38.14	not significant
10862	HERC5	1.28	8.87E-16	8.15E-15	2465.00	not significant
10863	RHOH	1.28	3.94E-25	7.08E-24	4153.74	not significant
10864	LMF2	1.28	3.25E-12	2.19E-11	2244.46	not significant
10865	KLHL17	1.28	2.33E-06	8.42E-06	672.95	not significant
10866	LOC100505812	1.28	1.03E-04	2.95E-04	287.87	not significant
10867	RPL37	1.28	1.86E-18	2.14E-17	20118.11	not significant
10868	C12orf10	1.28	1.80E-12	1.24E-11	1419.92	not significant
10869	BBS1	1.28	7.32E-05	2.15E-04	375.35	not significant
10870	ZBTB1	1.28	4.36E-21	5.99E-20	3282.09	not significant
10871	PACS1	1.28	1.34E-15	1.22E-14	1874.04	not significant
10872	MESP1	1.28	2.65E-02	4.72E-02	43.48	not significant
10873	TOM1L2	1.28	1.25E-06	4.69E-06	507.39	not significant
10874	RAP1GAP	1.28	3.05E-29	7.03E-28	5263.24	not significant
10875	CECR7	1.28	1.53E-02	2.89E-02	70.17	not significant
10876	TMED4	1.28	4.36E-18	4.87E-17	2012.67	not significant
10877	RPL18	1.28	2.72E-27	5.56E-26	21264.69	not significant
10878	MBOAT1	1.28	7.28E-08	3.15E-07	716.31	not significant
10879	RPS5	1.28	2.27E-21	3.17E-20	25147.37	not significant
10880	PATZ1	1.28	1.59E-17	1.69E-16	3133.76	not significant
10881	UBE2Q2P1	1.28	2.24E-02	4.07E-02	53.90	not significant
10882	MAP9	1.28	4.51E-06	1.57E-05	435.24	not significant
10883	ARHGAP29	1.28	3.05E-02	5.35E-02	18.35	not significant
10884	DGAT2	1.28	3.47E-04	9.06E-04	245.68	not significant
10885	GSDMD	1.28	4.95E-18	5.50E-17	2782.41	not significant
10886	LRRC28	1.28	3.00E-13	2.21E-12	1804.50	not significant
10887	ANO6	1.28	6.35E-32	1.72E-30	5562.22	not significant
10888	DNAH11	1.28	2.77E-02	4.92E-02	14.14	not significant
10889	ZNF561	1.28	9.31E-09	4.49E-08	712.64	not significant
10890	NR2C1	1.28	2.54E-03	5.63E-03	1623.05	not significant
10891	RPL23A	1.28	8.62E-20	1.09E-18	9697.55	not significant
10892	MPND	1.28	5.35E-08	2.37E-07	734.16	not significant
10893	P2RY10	1.28	1.73E-07	7.20E-07	574.19	not significant
10894	CEP131	1.28	1.39E-10	8.07E-10	1647.78	not significant
10895	CCDC121	1.29	3.25E-02	5.67E-02	24.58	not significant
10896	UBL7-AS1	1.29	9.25E-05	2.67E-04	283.93	not significant
10897	QARS	1.29	1.12E-33	3.49E-32	6444.89	not significant
10898	LHX4-AS1	1.29	1.50E-03	3.48E-03	203.88	not significant
10899	ZNF430	1.29	5.11E-12	3.39E-11	1267.55	not significant
10900	NMT2	1.29	1.89E-11	1.18E-10	1035.84	not significant

10901	TRAPPC2	1.29	1.11E-08	5.31E-08	756.36	not significant
10902	DPYSL2	1.29	2.29E-25	4.18E-24	3741.11	not significant
10903	TOMM7	1.29	2.52E-12	1.72E-11	2381.16	not significant
10904	BMF	1.29	1.97E-02	3.61E-02	54.16	not significant
10905	TMEM8B	1.29	2.01E-05	6.39E-05	348.75	not significant
10906	SLC35D1	1.29	4.85E-19	5.80E-18	2332.79	not significant
10907	LOC100506127	1.29	5.75E-03	1.19E-02	111.51	not significant
10908	KLHL6	1.29	1.43E-17	1.53E-16	2625.97	not significant
10909	MTA3	1.29	7.60E-25	1.33E-23	3526.39	not significant
10910	ZNF579	1.29	1.58E-05	5.11E-05	383.47	not significant
10911	ZNF253	1.29	1.03E-08	4.93E-08	784.00	not significant
10912	PNMA1	1.29	2.43E-14	1.97E-13	1598.26	not significant
10913	TEN1-CDK3	1.29	2.81E-02	4.97E-02	37.99	not significant
10914	NUDT18	1.29	6.87E-05	2.02E-04	330.37	not significant
10915	DVL3	1.29	4.58E-21	6.26E-20	4835.26	not significant
10916	PKD2	1.29	1.39E-08	6.52E-08	774.29	not significant
10917	ZNF672	1.29	9.96E-19	1.17E-17	2393.49	not significant
10918	PAN3	1.29	1.20E-21	1.70E-20	2928.70	not significant
10919	LMO2	1.29	2.15E-24	3.68E-23	7455.23	not significant
10920	SEPT7P2	1.29	3.15E-06	1.12E-05	445.67	not significant
10921	APBB3	1.29	8.28E-05	2.41E-04	373.50	not significant
10922	GALT	1.29	6.63E-07	2.56E-06	617.85	not significant
10923	ACSF2	1.29	2.43E-08	1.12E-07	737.27	not significant
10924	NHEJ1	1.29	6.35E-09	3.10E-08	709.47	not significant
10925	NEK8	1.29	6.48E-03	1.33E-02	97.53	not significant
10926	C2CD2	1.29	6.46E-04	1.60E-03	210.61	not significant
10927	FAM134A	1.29	2.72E-21	3.77E-20	3447.25	not significant
10928	LINC00638	1.29	1.84E-02	3.40E-02	56.19	not significant
10929	DCBLD2	1.29	6.85E-07	2.64E-06	568.04	not significant
10930	ICA1L	1.29	7.54E-07	2.89E-06	485.29	not significant
10931	LPAR5	1.29	8.94E-11	5.28E-10	944.42	not significant
10932	NUDT8	1.29	1.01E-04	2.90E-04	344.46	not significant
10933	LINC00657	1.29	3.66E-36	1.32E-34	11863.01	not significant
10934	SORL1	1.29	4.57E-19	5.48E-18	3767.73	not significant
10935	ACRC	1.29	1.96E-02	3.59E-02	54.55	not significant
10936	ZNF439	1.29	7.39E-05	2.16E-04	398.69	not significant
10937	EIF1B	1.29	9.27E-11	5.47E-10	1518.04	not significant
10938	GIMAP6	1.29	2.31E-29	5.37E-28	4955.06	not significant
10939	PCSK5	1.29	4.30E-04	1.10E-03	217.03	not significant
10940	AJUBA	1.29	2.35E-05	7.40E-05	380.82	not significant
10941	ZNF8	1.29	4.63E-05	1.40E-04	324.71	not significant
10942	MAU2	1.29	3.38E-22	4.96E-21	3141.55	not significant
10943	LOC642846	1.29	2.88E-03	6.32E-03	834.49	not significant
10944	TUBB	1.29	7.73E-18	8.44E-17	12417.24	not significant
10945	MBTD1	1.29	5.14E-18	5.69E-17	2391.74	not significant
10946	ZNF653	1.29	1.31E-04	3.68E-04	258.42	not significant
10947	ZNF442	1.29	1.42E-02	2.70E-02	65.54	not significant
10948	PASK	1.29	2.21E-14	1.80E-13	1534.20	not significant
10949	ZNF726	1.29	1.15E-04	3.25E-04	266.08	not significant
10950	SEC1P	1.29	2.23E-02	4.04E-02	11.38	not significant
10951	LSM8	1.29	2.53E-24	4.31E-23	3381.57	not significant
10952	ARRDC1	1.29	1.20E-07	5.06E-07	634.51	not significant
10953	TCTN2	1.29	1.55E-03	3.58E-03	151.74	not significant
10954	HSCB	1.29	2.40E-05	7.55E-05	355.03	not significant
10955	SSR2	1.29	2.28E-29	5.31E-28	6706.83	not significant
10956	U2AF1L4	1.29	1.41E-04	3.95E-04	280.21	not significant
10957	ZNF426	1.29	6.72E-08	2.93E-07	588.81	not significant
10958	ZNF12	1.29	1.37E-15	1.24E-14	1780.47	not significant
10959	CHML	1.29	3.90E-25	7.04E-24	3981.45	not significant
10960	PGPEP1	1.29	1.33E-13	1.01E-12	1353.19	not significant
10961	RSAD2	1.29	6.42E-16	5.99E-15	1621.24	not significant
10962	UTY	1.29	3.09E-09	1.56E-08	1220.39	not significant
10963	LINC00861	1.29	2.56E-03	5.68E-03	163.23	not significant
10964	ELP2	1.29	2.33E-17	2.45E-16	1892.63	not significant
10965	GPAA1	1.29	1.04E-09	5.47E-09	808.23	not significant
10966	LOC101928865	1.29	1.57E-02	2.95E-02	66.37	not significant
10967	RORA	1.29	3.82E-11	2.34E-10	1283.80	not significant
10968	EEF2	1.29	7.61E-33	2.21E-31	110535.15	not significant
10969	UBE2B	1.29	8.78E-16	8.09E-15	2159.72	not significant
10970	LOC374443	1.29	1.83E-03	4.15E-03	170.15	not significant
10971	FAM174A	1.30	2.90E-03	6.35E-03	132.83	not significant
10972	CRTC3	1.30	2.32E-18	2.64E-17	2070.42	not significant
10973	NAB1	1.30	3.08E-15	2.72E-14	1800.53	not significant
10974	DONSON	1.30	3.79E-16	3.58E-15	1681.75	not significant
10975	NAT9	1.30	1.03E-10	6.07E-10	937.75	not significant
10976	MDM4	1.30	2.18E-05	6.91E-05	2196.70	not significant
10977	SNX24	1.30	3.51E-03	7.58E-03	117.48	not significant
10978	ZNF566	1.30	1.46E-06	5.43E-06	458.34	not significant
10979	ZNF441	1.30	6.85E-04	1.68E-03	202.39	not significant
10980	NLE1	1.30	1.32E-13	1.01E-12	1280.18	not significant
10981	SYT1	1.30	6.61E-12	4.35E-11	995.79	not significant
10982	LOC493754	1.30	5.06E-08	2.24E-07	578.05	not significant
10983	ZADH2	1.30	2.65E-13	1.97E-12	1247.85	not significant
10984	PIDD1	1.30	1.63E-14	1.35E-13	2143.68	not significant
10985	BCL2L11	1.30	2.20E-12	1.50E-11	1222.53	not significant
10986	BMI1	1.30	1.38E-04	3.86E-04	276.54	not significant
10987	FLJ31306	1.30	7.02E-13	5.02E-12	1602.93	not significant
10988	TMEM107	1.30	6.60E-05	1.95E-04	305.49	not significant

10989	RMND1	1.30	5.31E-07	2.08E-06	529.50	not significant
10990	IRGQ	1.30	1.77E-08	8.25E-08	656.33	not significant
10991	AGAP3	1.30	3.58E-06	1.26E-05	398.42	not significant
10992	NBPF12	1.30	2.36E-02	4.25E-02	39.28	not significant
10993	ITGB4	1.30	1.62E-02	3.03E-02	58.65	not significant
10994	GDI1	1.30	1.97E-10	1.13E-09	864.35	not significant
10995	HNRNPA1	1.30	2.89E-19	3.53E-18	2534.62	not significant
10996	ISG20	1.30	1.21E-03	2.85E-03	159.46	not significant
10997	PAWR	1.30	6.44E-11	3.85E-10	901.10	not significant
10998	CPNE1	1.30	2.89E-34	9.36E-33	5844.79	not significant
10999	ASPDH	1.30	5.57E-03	1.16E-02	96.35	not significant
11000	CIR1	1.30	6.60E-12	4.34E-11	1183.59	not significant
11001	DGCR14	1.30	8.25E-11	4.88E-10	1030.95	not significant
11002	DDT	1.30	1.35E-08	6.38E-08	743.01	not significant
11003	GID4	1.30	3.53E-13	2.58E-12	1228.89	not significant
11004	ERP29	1.30	2.45E-22	3.63E-21	7753.78	not significant
11005	SIX3	1.30	1.37E-06	5.13E-06	436.85	not significant
11006	NPC2	1.30	4.03E-11	2.46E-10	1152.88	not significant
11007	CENPQ	1.30	2.63E-11	1.63E-10	967.56	not significant
11008	KDELR1	1.30	7.30E-23	1.12E-21	3465.45	not significant
11009	TOX	1.30	2.98E-33	8.88E-32	7548.49	not significant
11010	C5orf34	1.30	1.62E-06	5.98E-06	444.25	not significant
11011	RPL13	1.30	2.53E-18	2.88E-17	40439.67	not significant
11012	PNKP	1.30	1.93E-09	9.90E-09	754.75	not significant
11013	AMOT	1.30	2.44E-14	1.99E-13	1270.68	not significant
11014	RPL14	1.30	2.68E-27	5.50E-26	16347.32	not significant
11015	TMEM175	1.30	6.01E-08	2.64E-07	636.55	not significant
11016	ING3	1.30	2.60E-12	1.77E-11	1022.09	not significant
11017	LMBRD1	1.30	7.17E-13	5.12E-12	1145.89	not significant
11018	MEI1	1.30	1.56E-02	2.94E-02	58.39	not significant
11019	KIAA1958	1.30	5.49E-10	3.00E-09	861.33	not significant
11020	SH2D1A	1.30	4.58E-37	1.75E-35	14779.95	not significant
11021	ZCCHC7	1.30	5.21E-12	3.45E-11	1094.50	not significant
11022	FRS3	1.30	1.04E-03	2.48E-03	156.86	not significant
11023	CDC42BPG	1.31	7.38E-05	2.16E-04	254.04	not significant
11024	GADD45A	1.31	1.71E-03	3.90E-03	137.75	not significant
11025	RPS4X	1.31	2.93E-31	7.60E-30	33106.11	not significant
11026	PEX5L	1.31	3.76E-23	5.90E-22	3330.58	not significant
11027	VPS51	1.31	3.17E-17	3.28E-16	3813.03	not significant
11028	LRRC27	1.31	1.60E-03	3.69E-03	142.72	not significant
11029	RPS6KA5	1.31	2.51E-06	9.04E-06	442.01	not significant
11030	INPP5E	1.31	1.20E-08	5.70E-08	807.51	not significant
11031	GNPTG	1.31	8.41E-10	4.47E-09	736.17	not significant
11032	ZNF266	1.31	4.27E-20	5.47E-19	2608.24	not significant
11033	GBAP1	1.31	1.16E-03	2.74E-03	153.21	not significant
11034	SETDB1	1.31	6.35E-19	7.51E-18	2138.35	not significant
11035	ZNF767P	1.31	1.88E-03	4.26E-03	750.09	not significant
11036	MTURN	1.31	1.16E-04	3.29E-04	254.30	not significant
11037	TMED1	1.31	2.97E-06	1.06E-05	389.76	not significant
11038	ULK3	1.31	1.54E-13	1.17E-12	1488.77	not significant
11039	IRX5	1.31	4.56E-07	1.80E-06	538.02	not significant
11040	EMC3-AS1	1.31	1.95E-11	1.22E-10	998.05	not significant
11041	TVP23C	1.31	2.15E-03	4.82E-03	130.55	not significant
11042	TRIM69	1.31	1.74E-02	3.24E-02	46.97	not significant
11043	FZD5	1.31	1.37E-03	3.21E-03	152.06	not significant
11044	LIN54	1.31	8.85E-21	1.19E-19	2709.83	not significant
11045	LMBR1L	1.31	7.20E-14	5.61E-13	1159.55	not significant
11046	LY9	1.31	2.22E-06	8.03E-06	416.44	not significant
11047	LOC100130987	1.31	2.50E-02	4.48E-02	31.18	not significant
11048	FAM117A	1.31	1.23E-18	1.43E-17	1723.97	not significant
11049	GPLD1	1.31	5.47E-03	1.14E-02	104.90	not significant
11050	ENTHD2	1.31	5.11E-10	2.80E-09	1015.35	not significant
11051	MPPE1	1.31	2.59E-08	1.19E-07	572.83	not significant
11052	ZNF852	1.31	2.02E-04	5.50E-04	225.17	not significant
11053	STAG3L5P-PVRIG	1.31	1.50E-04	4.18E-04	1180.25	not significant
11054	RAB11FIP3	1.31	7.63E-22	1.10E-20	2347.67	not significant
11055	KDELC2	1.31	4.03E-23	6.29E-22	3651.99	not significant
11056	CHD6	1.31	1.66E-33	5.05E-32	4797.46	not significant
11057	ZSWIM4	1.31	2.82E-07	1.14E-06	496.88	not significant
11058	ZNF646	1.31	1.46E-17	1.56E-16	1621.04	not significant
11059	ZMAT1	1.31	1.29E-03	3.04E-03	156.65	not significant
11060	PCIF1	1.31	1.86E-22	2.78E-21	2908.63	not significant
11061	RABEP2	1.31	1.56E-09	8.10E-09	654.52	not significant
11062	ABL1	1.31	1.97E-24	3.38E-23	3813.51	not significant
11063	SLC41A3	1.31	1.71E-14	1.41E-13	1271.09	not significant
11064	DDX12P	1.31	1.79E-03	4.08E-03	1141.08	not significant
11065	SH3PXD2A	1.31	7.49E-25	1.31E-23	3069.12	not significant
11066	TSPAN3	1.31	1.90E-22	2.84E-21	4104.21	not significant
11067	SARAF	1.31	5.95E-31	1.52E-29	8143.49	not significant
11068	SHROOM1	1.31	2.28E-02	4.13E-02	34.90	not significant
11069	ACYP1	1.31	6.64E-11	3.97E-10	822.65	not significant
11070	43529_13977	1.31	1.51E-20	1.99E-19	2024.36	not significant
11071	AMOTL1	1.31	7.65E-05	2.24E-04	245.49	not significant
11072	LOC283922	1.31	1.56E-03	3.60E-03	140.53	not significant
11073	PDPR	1.31	2.62E-28	5.73E-27	4258.76	not significant
11074	DISP1	1.31	6.49E-04	1.60E-03	162.95	not significant
11075	CNOT6L	1.32	1.85E-22	2.76E-21	2569.12	not significant
11076	DGAT1	1.32	1.43E-12	1.00E-11	1012.74	not significant

11077	RNF31	1.32	6.32E-20	8.03E-19	2670.80	not significant
11078	IFI44	1.32	4.00E-10	2.21E-09	729.33	not significant
11079	GPATCH3	1.32	8.54E-08	3.68E-07	598.98	not significant
11080	FAM57A	1.32	1.67E-05	5.39E-05	307.49	not significant
11081	DTX3	1.32	1.43E-17	1.53E-16	2067.13	not significant
11082	LOC100133091	1.32	2.52E-03	5.58E-03	112.83	not significant
11083	TMEM254	1.32	1.86E-10	1.06E-09	731.82	not significant
11084	LINC01232	1.32	5.69E-03	1.18E-02	87.62	not significant
11085	ABCA7	1.32	1.42E-12	9.89E-12	1545.29	not significant
11086	POLM	1.32	6.28E-25	1.12E-23	4107.60	not significant
11087	HEXDC	1.32	4.04E-14	3.22E-13	1234.06	not significant
11088	NOB1	1.32	8.26E-28	1.76E-26	3369.06	not significant
11089	C2CD5	1.32	2.97E-19	3.62E-18	2968.81	not significant
11090	ZFAND2A	1.32	4.88E-05	1.47E-04	256.65	not significant
11091	CNIH1	1.32	2.58E-27	5.32E-26	3754.36	not significant
11092	C11orf1	1.32	6.18E-04	1.54E-03	159.93	not significant
11093	AK3	1.32	4.18E-21	5.76E-20	1942.13	not significant
11094	ZNF224	1.32	2.83E-03	6.23E-03	554.95	not significant
11095	STAT2	1.32	4.52E-16	4.25E-15	2468.68	not significant
11096	KIAA0368	1.32	6.51E-27	1.30E-25	3158.30	not significant
11097	SAC3D1	1.32	1.75E-12	1.20E-11	1441.53	not significant
11098	DDX11L2	1.32	2.57E-02	4.59E-02	25.93	not significant
11099	TTC32	1.32	2.86E-05	8.92E-05	270.73	not significant
11100	RBBP9	1.32	2.60E-14	2.11E-13	1198.90	not significant
11101	NLRC5	1.32	7.84E-24	1.29E-22	2834.76	not significant
11102	ZXDB	1.32	1.29E-06	4.84E-06	399.56	not significant
11103	POLR1E	1.32	7.08E-16	6.58E-15	1764.00	not significant
11104	C18orf21	1.32	3.06E-10	1.71E-09	718.27	not significant
11105	GINM1	1.32	1.83E-10	1.05E-09	721.06	not significant
11106	RMI2	1.32	2.37E-15	2.11E-14	1526.86	not significant
11107	RPS15A	1.32	5.02E-31	1.29E-29	16247.95	not significant
11108	ST3GAL3	1.32	1.03E-07	4.41E-07	498.87	not significant
11109	ZNF302	1.32	7.75E-16	7.18E-15	1272.43	not significant
11110	RPS14	1.32	1.27E-30	3.16E-29	18277.19	not significant
11111	RCSD1	1.32	1.56E-31	4.13E-30	7383.69	not significant
11112	PRKCSH	1.32	2.20E-37	8.58E-36	9453.11	not significant
11113	RENBP	1.32	2.18E-03	4.90E-03	130.51	not significant
11114	ZNF506	1.32	6.66E-12	4.38E-11	1071.83	not significant
11115	CHST11	1.32	1.75E-37	6.89E-36	18500.97	not significant
11116	C22orf34	1.32	1.08E-04	3.08E-04	228.85	not significant
11117	CDKN1C	1.32	1.90E-02	3.50E-02	12.34	not significant
11118	GTF3C5	1.32	6.49E-39	2.71E-37	7231.80	not significant
11119	SLC14A1	1.32	1.07E-03	2.55E-03	142.94	not significant
11120	TAL1	1.32	3.13E-07	1.26E-06	463.44	not significant
11121	ZFYVE1	1.32	4.58E-13	3.32E-12	1001.44	not significant
11122	MEX3A	1.32	2.57E-16	2.46E-15	1329.63	not significant
11123	CLK4	1.32	7.79E-08	3.37E-07	531.12	not significant
11124	C7orf55	1.32	2.84E-03	6.23E-03	106.71	not significant
11125	LOC100287015	1.32	9.05E-04	2.18E-03	150.01	not significant
11126	ATG4D	1.32	2.71E-16	2.59E-15	1420.43	not significant
11127	LIMS2	1.32	1.59E-10	9.16E-10	791.50	not significant
11128	LOC644961	1.33	5.23E-03	1.09E-02	85.17	not significant
11129	JAK3	1.33	1.37E-11	8.74E-11	1160.42	not significant
11130	SMAGP	1.33	1.93E-06	7.06E-06	366.92	not significant
11131	C19orf66	1.33	4.24E-18	4.75E-17	1578.33	not significant
11132	PCBP2	1.33	8.29E-54	5.96E-52	26809.86	not significant
11133	ZNF362	1.33	1.71E-18	1.98E-17	1820.99	not significant
11134	CTDSP1	1.33	2.97E-24	5.03E-23	2743.56	not significant
11135	GUCY1B2	1.33	9.75E-03	1.92E-02	63.69	not significant
11136	ZDHHC15	1.33	1.64E-04	4.55E-04	209.38	not significant
11137	RRN3P3	1.33	6.96E-05	2.05E-04	252.54	not significant
11138	PHC2	1.33	4.59E-28	9.90E-27	3933.89	not significant
11139	PIGM	1.33	2.07E-10	1.18E-09	855.04	not significant
11140	TNIP1	1.33	1.43E-33	4.40E-32	4011.42	not significant
11141	GNB2L1	1.33	1.13E-31	3.02E-30	36811.33	not significant
11142	EVA1B	1.33	2.34E-02	4.23E-02	16.24	not significant
11143	PTCHD2	1.33	8.38E-12	5.45E-11	974.48	not significant
11144	POMK	1.33	2.41E-04	6.46E-04	185.99	not significant
11145	PELI2	1.33	1.78E-26	3.46E-25	2464.12	not significant
11146	PHYKPL	1.33	1.45E-14	1.21E-13	1261.67	not significant
11147	RPAIN	1.33	3.11E-20	4.00E-19	1833.50	not significant
11148	MAGEF1	1.33	2.55E-09	1.30E-08	622.19	not significant
11149	FBXL6	1.33	2.96E-04	7.80E-04	178.75	not significant
11150	TMEM101	1.33	7.57E-08	3.27E-07	462.38	not significant
11151	ABCC1	1.33	7.05E-27	1.41E-25	7122.25	not significant
11152	LYSMD1	1.33	1.95E-08	9.05E-08	546.14	not significant
11153	RPL3	1.33	7.30E-34	2.31E-32	56790.01	not significant
11154	TMSB15B	1.33	3.94E-03	8.44E-03	90.80	not significant
11155	NBR2	1.33	7.32E-03	1.48E-02	76.20	not significant
11156	ABHD12	1.33	2.09E-20	2.73E-19	2293.90	not significant
11157	LINC00938	1.33	4.37E-14	3.47E-13	1173.89	not significant
11158	PIK3IP1	1.33	5.76E-03	1.19E-02	79.78	not significant
11159	DDX58	1.33	1.15E-19	1.44E-18	1759.54	not significant
11160	C5orf45	1.33	1.84E-04	5.06E-04	215.10	not significant
11161	RPS25	1.33	4.13E-06	1.44E-05	7551.94	not significant
11162	SCD5	1.33	4.76E-19	5.70E-18	2102.06	not significant
11163	SLIT1	1.33	2.82E-33	8.45E-32	11926.06	not significant
11164	DNAJB9	1.33	3.49E-06	1.23E-05	358.36	not significant

11165	CBLB	1.33	2.80E-05	8.75E-05	256.86	not significant
11166	ZDBF2	1.33	2.06E-02	3.77E-02	30.52	not significant
11167	XKR8	1.33	4.84E-07	1.90E-06	420.55	not significant
11168	HECA	1.33	1.21E-24	2.09E-23	2704.37	not significant
11169	CXorf23	1.34	2.74E-05	8.55E-05	266.40	not significant
11170	43532_13639	1.34	1.53E-04	4.26E-04	217.63	not significant
11171	CCBL2	1.34	1.26E-13	9.60E-13	1023.18	not significant
11172	GPR137B	1.34	2.60E-05	8.13E-05	270.38	not significant
11173	VPS11	1.34	2.72E-07	1.11E-06	401.66	not significant
11174	AMT	1.34	1.80E-03	4.11E-03	116.64	not significant
11175	LINC01000	1.34	6.55E-04	1.62E-03	1923.86	not significant
11176	SEC31B	1.34	2.16E-03	4.86E-03	15660.34	not significant
11177	ZFAND1	1.34	8.20E-15	6.98E-14	1099.38	not significant
11178	ZNF175	1.34	5.06E-11	3.06E-10	768.76	not significant
11179	VIPR2	1.34	8.57E-32	2.31E-30	3606.81	not significant
11180	MGAT4A	1.34	2.61E-40	1.17E-38	6887.74	not significant
11181	RPL22	1.34	8.05E-28	1.72E-26	6627.68	not significant
11182	CTXN1	1.34	4.74E-04	1.21E-03	230.58	not significant
11183	ASAP2	1.34	3.17E-05	9.83E-05	237.13	not significant
11184	AIP	1.34	7.39E-28	1.58E-26	4184.09	not significant
11185	ABLIM1	1.34	3.11E-35	1.05E-33	6007.26	not significant
11186	FLJ22447	1.34	2.32E-02	4.18E-02	21.10	not significant
11187	CHST12	1.34	3.20E-18	3.62E-17	3173.43	not significant
11188	PTPRK	1.34	8.61E-25	1.50E-23	2198.47	not significant
11189	TMEM180	1.34	1.38E-09	7.16E-09	586.32	not significant
11190	INPPL1	1.34	2.07E-33	6.27E-32	4351.55	not significant
11191	PDCD7	1.34	3.21E-26	6.12E-25	2867.51	not significant
11192	FAM69B	1.34	4.83E-06	1.67E-05	296.90	not significant
11193	PCSK4	1.34	2.26E-04	6.11E-04	255.51	not significant
11194	LOC101929099	1.34	2.05E-02	3.75E-02	28.61	not significant
11195	C5orf24	1.34	1.22E-14	1.02E-13	1637.50	not significant
11196	ZCWPW1	1.34	4.42E-03	9.38E-03	82.18	not significant
11197	LOC284023	1.34	2.89E-06	1.03E-05	322.04	not significant
11198	ICAM3	1.34	4.08E-27	8.24E-26	3685.52	not significant
11199	MARK4	1.34	5.15E-18	5.71E-17	1623.07	not significant
11200	ALG1L2	1.34	2.04E-02	3.74E-02	12.86	not significant
11201	MUS81	1.34	3.23E-17	3.35E-16	1473.29	not significant
11202	IPO7	1.34	4.21E-54	3.08E-52	17570.66	not significant
11203	ASL	1.34	1.37E-03	3.19E-03	116.11	not significant
11204	RPS10P7	1.34	5.42E-03	1.13E-02	72.68	not significant
11205	ATM	1.34	5.53E-07	2.16E-06	4581.05	not significant
11206	ALDH6A1	1.34	1.02E-12	7.25E-12	835.53	not significant
11207	ZNF524	1.34	5.03E-04	1.27E-03	152.43	not significant
11208	ZNF319	1.34	6.04E-10	3.28E-09	598.16	not significant
11209	ST8SIA1	1.34	2.62E-03	5.80E-03	95.94	not significant
11210	SLC8A1-AS1	1.34	3.06E-05	9.50E-05	229.80	not significant
11211	CDKL2	1.34	2.18E-02	3.97E-02	22.35	not significant
11212	PSMG2	1.34	1.64E-26	3.19E-25	2555.54	not significant
11213	ZNF32	1.34	2.55E-14	2.07E-13	983.93	not significant
11214	CD69	1.34	1.26E-15	1.14E-14	1418.60	not significant
11215	TTYH3	1.34	4.08E-27	8.24E-26	3782.10	not significant
11216	FAM167A	1.34	2.07E-02	3.78E-02	26.31	not significant
11217	ZBTB20	1.34	1.85E-03	4.21E-03	105.31	not significant
11218	CCDC183-AS1	1.34	1.98E-02	3.64E-02	31.74	not significant
11219	RNF214	1.34	2.84E-11	1.76E-10	830.00	not significant
11220	ZNF627	1.35	5.17E-09	2.55E-08	512.02	not significant
11221	CCR8	1.35	1.69E-15	1.52E-14	1213.10	not significant
11222	WBP1	1.35	8.06E-03	1.61E-02	64.49	not significant
11223	KIAA1875	1.35	1.36E-02	2.60E-02	49.36	not significant
11224	FGD5	1.35	3.99E-09	1.99E-08	517.94	not significant
11225	HES6	1.35	8.23E-06	2.77E-05	308.50	not significant
11226	ZNF43	1.35	1.19E-11	7.66E-11	758.90	not significant
11227	WDR90	1.35	2.48E-03	5.52E-03	1707.79	not significant
11228	TP53I3	1.35	2.80E-03	6.16E-03	91.27	not significant
11229	RPL11	1.35	1.77E-10	1.02E-09	26346.99	not significant
11230	C5orf56	1.35	3.18E-19	3.86E-18	1458.22	not significant
11231	LMO7	1.35	2.70E-09	1.37E-08	658.83	not significant
11232	LOC401320	1.35	1.57E-04	4.37E-04	205.28	not significant
11233	MIR155HG	1.35	2.21E-04	5.98E-04	174.97	not significant
11234	SMAD1	1.35	2.97E-10	1.67E-09	640.44	not significant
11235	LOC155060	1.35	6.53E-03	1.34E-02	335.31	not significant
11236	RPS9	1.35	5.72E-25	1.02E-23	7952.03	not significant
11237	MANEAL	1.35	1.51E-11	9.59E-11	795.08	not significant
11238	LINC00324	1.35	1.05E-02	2.06E-02	50.46	not significant
11239	ZNF682	1.35	4.07E-06	1.42E-05	308.07	not significant
11240	SDHAP1	1.35	1.69E-04	4.66E-04	184.46	not significant
11241	CCDC171	1.35	1.63E-05	5.27E-05	249.66	not significant
11242	SPAG7	1.35	1.03E-14	8.66E-14	1448.01	not significant
11243	LOC220729	1.35	6.56E-07	2.54E-06	539.17	not significant
11244	LINC00649	1.35	5.82E-12	3.85E-11	805.81	not significant
11245	CD96	1.35	1.00E-46	5.49E-45	8212.99	not significant
11246	PRPSAP1	1.35	5.50E-25	9.86E-24	2816.40	not significant
11247	CEL	1.35	3.13E-03	6.82E-03	87.72	not significant
11248	FLT4	1.35	5.00E-18	5.56E-17	1378.77	not significant
11249	N4BP3	1.35	4.48E-03	9.50E-03	80.43	not significant
11250	MAFG	1.35	2.80E-24	4.75E-23	1946.95	not significant
11251	GKAP1	1.35	7.63E-05	2.23E-04	187.95	not significant
11252	XKR5	1.35	4.19E-04	1.08E-03	145.83	not significant

11253	PKD1	1.35	5.89E-22	8.51E-21	2981.64	not significant
11254	LAPTM4A	1.36	4.66E-18	5.19E-17	1299.49	not significant
11255	RPS21	1.36	2.16E-33	6.51E-32	10375.52	not significant
11256	ZNF799	1.36	4.42E-05	1.34E-04	249.64	not significant
11257	MNS1	1.36	4.79E-03	1.01E-02	81.21	not significant
11258	TRIM4	1.36	1.31E-17	1.41E-16	1456.51	not significant
11259	RNF130	1.36	2.67E-22	3.92E-21	2679.42	not significant
11260	CCNE2	1.36	2.72E-31	7.08E-30	2879.27	not significant
11261	RPUSD4	1.36	1.38E-19	1.71E-18	1502.75	not significant
11262	C10orf32	1.36	7.75E-13	5.52E-12	936.40	not significant
11263	ZNF445	1.36	1.87E-23	2.99E-22	2734.99	not significant
11264	PRORSD1P	1.36	1.89E-02	3.49E-02	29.44	not significant
11265	ZNF618	1.36	6.60E-03	1.35E-02	60.28	not significant
11266	NAT14	1.36	2.00E-08	9.28E-08	701.56	not significant
11267	ACTG1	1.36	1.05E-34	3.48E-33	26487.33	not significant
11268	ARID5A	1.36	3.29E-13	2.41E-12	876.17	not significant
11269	BSDC1	1.36	1.10E-23	1.79E-22	1953.76	not significant
11270	LENG8	1.36	7.98E-04	1.94E-03	1369.29	not significant
11271	RAB24	1.36	1.21E-14	1.01E-13	989.59	not significant
11272	CCNL2	1.36	5.29E-07	2.07E-06	2901.89	not significant
11273	PLEKHG4	1.36	4.63E-30	1.13E-28	3460.82	not significant
11274	LOC100506713	1.36	8.39E-03	1.67E-02	52.66	not significant
11275	ZNF850	1.36	7.17E-07	2.76E-06	419.75	not significant
11276	SOCS6	1.36	9.89E-06	3.28E-05	288.25	not significant
11277	HNRNPU-AS1	1.36	9.68E-03	1.91E-02	1391.16	not significant
11278	NOL4L	1.36	9.40E-06	3.13E-05	2352.61	not significant
11279	KMT2E-AS1	1.36	4.39E-04	1.12E-03	140.72	not significant
11280	RGL2	1.36	3.47E-06	1.23E-05	283.52	not significant
11281	ASAH1	1.36	4.04E-16	3.81E-15	1121.85	not significant
11282	MCF2L2	1.36	3.15E-03	6.88E-03	81.00	not significant
11283	ARHGAP33	1.36	2.62E-03	5.80E-03	2231.21	not significant
11284	ZNF514	1.36	1.11E-04	3.15E-04	216.79	not significant
11285	PDCD4-AS1	1.36	2.62E-04	7.00E-04	164.28	not significant
11286	RNF103	1.36	5.93E-08	2.61E-07	442.97	not significant
11287	C16orf52	1.36	2.25E-07	9.23E-07	368.41	not significant
11288	WDR5B	1.36	8.16E-06	2.74E-05	333.96	not significant
11289	EIF3E	1.36	1.88E-36	6.95E-35	14676.53	not significant
11290	FAM84B	1.36	5.37E-04	1.35E-03	131.59	not significant
11291	ICAM2	1.36	6.30E-30	1.52E-28	6135.47	not significant
11292	BRD3	1.36	5.17E-29	1.18E-27	2658.50	not significant
11293	SLC30A1	1.36	4.19E-11	2.56E-10	691.24	not significant
11294	DNAL4	1.36	5.00E-08	2.22E-07	410.16	not significant
11295	LBH	1.36	9.23E-22	1.32E-20	2350.32	not significant
11296	ZNF230	1.36	1.32E-06	4.94E-06	321.68	not significant
11297	NS3BP	1.36	7.30E-03	1.48E-02	65.42	not significant
11298	SMO	1.36	6.77E-22	9.75E-21	1752.63	not significant
11299	CNPY3	1.36	1.75E-37	6.89E-36	4213.68	not significant
11300	RORB	1.36	1.47E-03	3.41E-03	98.65	not significant
11301	USP49	1.36	1.11E-30	2.78E-29	4275.13	not significant
11302	ZNF681	1.36	7.64E-14	5.94E-13	909.98	not significant
11303	HINFP	1.36	2.04E-11	1.28E-10	653.00	not significant
11304	TP53I13	1.37	3.55E-17	3.67E-16	1427.20	not significant
11305	COQ10A	1.37	1.28E-08	6.05E-08	478.06	not significant
11306	GIGYF1	1.37	1.41E-04	3.95E-04	4706.17	not significant
11307	MRPL45	1.37	3.33E-08	1.51E-07	429.27	not significant
11308	TM7SF2	1.37	3.69E-07	1.48E-06	330.95	not significant
11309	TMEM106A	1.37	3.64E-08	1.64E-07	404.07	not significant
11310	CD1B	1.37	1.99E-55	1.54E-53	7564.17	not significant
11311	SH3BP5-AS1	1.37	7.13E-03	1.45E-02	218.93	not significant
11312	MND1	1.37	3.15E-19	3.82E-18	1710.15	not significant
11313	MLLT11	1.37	8.96E-22	1.28E-20	2265.54	not significant
11314	LINC00342	1.37	1.63E-03	3.75E-03	469.16	not significant
11315	CD2	1.37	8.60E-36	3.05E-34	5869.21	not significant
11316	RSRP1	1.37	1.85E-14	1.52E-13	1229.82	not significant
11317	SLC25A5	1.37	1.63E-50	1.04E-48	19411.31	not significant
11318	MT1X	1.37	6.51E-21	8.82E-20	3124.56	not significant
11319	NDST3	1.37	1.99E-22	2.97E-21	1684.35	not significant
11320	ST6GAL1	1.37	1.78E-38	7.34E-37	4325.47	not significant
11321	C14orf39	1.37	1.31E-03	3.07E-03	111.17	not significant
11322	ZNF738	1.37	1.99E-19	2.45E-18	1782.62	not significant
11323	C5orf42	1.37	8.10E-18	8.83E-17	1693.70	not significant
11324	PCNXL2	1.37	2.42E-16	2.33E-15	1004.97	not significant
11325	PMS2P4	1.37	4.16E-03	8.85E-03	71.37	not significant
11326	NSUN5P1	1.37	1.22E-04	3.43E-04	179.83	not significant
11327	CYLD	1.37	1.40E-16	1.38E-15	1281.40	not significant
11328	ZNF473	1.37	2.69E-20	3.50E-19	1328.80	not significant
11329	TAF8	1.37	1.60E-22	2.40E-21	1721.95	not significant
11330	ZNF324B	1.37	3.68E-05	1.13E-04	225.60	not significant
11331	RFX3	1.37	1.47E-09	7.64E-09	660.42	not significant
11332	HSD17B7P2	1.37	2.59E-04	6.93E-04	143.25	not significant
11333	ZNF500	1.37	2.64E-06	9.45E-06	325.74	not significant
11334	STAG3L4	1.37	5.49E-07	2.14E-06	338.50	not significant
11335	METTL9	1.37	2.01E-36	7.41E-35	6570.79	not significant
11336	ANO8	1.37	3.71E-06	1.30E-05	329.52	not significant
11337	LOC90834	1.37	3.27E-03	7.11E-03	96.00	not significant
11338	AMFR	1.37	3.00E-33	8.93E-32	3850.01	not significant
11339	SNTG2	1.37	2.46E-06	8.89E-06	276.09	not significant
11340	ITGA4	1.37	2.76E-67	2.93E-65	38395.06	not significant

11341	C21orf58	1.38	2.87E-16	2.74E-15	1252.53	not significant
11342	VN1R1	1.38	1.95E-02	3.58E-02	17.64	not significant
11343	PTK2B	1.38	3.79E-52	2.57E-50	5766.04	not significant
11344	ZNF83	1.38	1.60E-15	1.44E-14	1538.67	not significant
11345	BACH1	1.38	6.04E-24	1.00E-22	1764.57	not significant
11346	E2F1	1.38	1.92E-44	9.97E-43	4578.58	not significant
11347	ZFP3	1.38	5.47E-03	1.14E-02	61.86	not significant
11348	NT5DC1	1.38	1.41E-11	8.95E-11	651.10	not significant
11349	ZNF789	1.38	5.58E-06	1.92E-05	324.85	not significant
11350	RPL35A	1.38	2.07E-31	5.45E-30	13287.96	not significant
11351	CHTF18	1.38	9.32E-09	4.49E-08	2584.61	not significant
11352	CENPV	1.38	3.77E-28	8.18E-27	2863.37	not significant
11353	SUGT1P1	1.38	6.67E-03	1.36E-02	58.28	not significant
11354	CHST14	1.38	8.10E-16	7.49E-15	923.32	not significant
11355	ATXN7	1.38	3.10E-16	2.95E-15	1678.85	not significant
11356	PMF1	1.38	1.16E-10	6.75E-10	549.46	not significant
11357	SS18L1	1.38	1.70E-15	1.53E-14	1076.85	not significant
11358	ZNF784	1.38	7.60E-04	1.85E-03	111.10	not significant
11359	NRM	1.38	6.92E-05	2.04E-04	175.17	not significant
11360	PABPC3	1.38	7.34E-07	2.82E-06	291.65	not significant
11361	CSGALNACT2	1.38	8.82E-30	2.10E-28	2534.92	not significant
11362	GCNT1	1.38	7.43E-10	3.98E-09	496.39	not significant
11363	TTC14	1.38	3.19E-05	9.88E-05	3200.15	not significant
11364	DPY19L3	1.38	1.69E-18	1.95E-17	1239.60	not significant
11365	CYTH1	1.38	4.37E-61	3.87E-59	8880.71	not significant
11366	SP140	1.38	2.11E-13	1.58E-12	711.53	not significant
11367	SNHG12	1.38	2.45E-06	8.85E-06	340.55	not significant
11368	TMUB2	1.38	2.30E-14	1.88E-13	895.97	not significant
11369	EPSTI1	1.38	5.69E-41	2.59E-39	3501.32	not significant
11370	PCNXL4	1.38	1.27E-43	6.24E-42	4141.73	not significant
11371	RPS20	1.38	1.67E-11	1.05E-10	20483.35	not significant
11372	CD48	1.38	4.38E-31	1.13E-29	2810.66	not significant
11373	UBASH3B	1.38	1.54E-59	1.31E-57	10803.15	not significant
11374	NHLRC3	1.38	2.35E-13	1.75E-12	969.65	not significant
11375	BACE1-AS	1.38	1.09E-02	2.12E-02	40.48	not significant
11376	COL18A1	1.38	6.77E-04	1.67E-03	119.97	not significant
11377	ANKRD23	1.38	9.07E-04	2.19E-03	121.98	not significant
11378	MKRN3	1.38	2.93E-09	1.48E-08	457.59	not significant
11379	RNPC3	1.38	2.41E-08	1.11E-07	521.66	not significant
11380	METTL12	1.38	2.81E-03	6.18E-03	76.16	not significant
11381	LOC100128361	1.38	2.41E-05	7.58E-05	211.35	not significant
11382	KIAA1107	1.38	6.07E-04	1.51E-03	124.02	not significant
11383	ZNF783	1.38	6.58E-07	2.54E-06	384.32	not significant
11384	SLC37A1	1.38	2.54E-11	1.58E-10	583.97	not significant
11385	ZNF718	1.38	2.67E-03	5.90E-03	76.42	not significant
11386	CHMP1B	1.38	1.49E-26	2.91E-25	1920.80	not significant
11387	UBALD1	1.38	2.34E-07	9.56E-07	327.51	not significant
11388	DHRS1	1.38	3.65E-06	1.28E-05	258.40	not significant
11389	TMSB15A	1.39	2.47E-05	7.76E-05	195.15	not significant
11390	MPG	1.39	1.42E-17	1.52E-16	1206.51	not significant
11391	LRRC75A	1.39	4.12E-03	8.78E-03	65.46	not significant
11392	NBPF1	1.39	7.53E-18	8.23E-17	1024.29	not significant
11393	P2RX5	1.39	3.78E-37	1.46E-35	3250.92	not significant
11394	TMEM64	1.39	5.55E-08	2.45E-07	358.25	not significant
11395	LMO4	1.39	4.23E-05	1.29E-04	176.00	not significant
11396	AP4M1	1.39	2.97E-10	1.67E-09	581.81	not significant
11397	CRIPT	1.39	5.82E-10	3.17E-09	471.21	not significant
11398	CCDC61	1.39	4.52E-08	2.02E-07	348.35	not significant
11399	GPR161	1.39	1.05E-06	3.97E-06	293.52	not significant
11400	FNIP1	1.39	4.14E-18	4.64E-17	1154.40	not significant
11401	PPDPF	1.39	3.18E-19	3.86E-18	1405.14	not significant
11402	MVB12B	1.39	2.05E-17	2.16E-16	1556.19	not significant
11403	PTCRA	1.39	5.37E-03	1.12E-02	56.12	not significant
11404	DOPEY1	1.39	2.05E-15	1.83E-14	893.77	not significant
11405	CDKN1B	1.39	6.09E-25	1.09E-23	1704.01	not significant
11406	CAPS	1.39	3.09E-03	6.75E-03	74.90	not significant
11407	TSLP	1.39	9.51E-04	2.28E-03	95.67	not significant
11408	NR1D2	1.39	2.08E-10	1.19E-09	620.61	not significant
11409	LOC100129550	1.39	6.91E-04	1.70E-03	107.54	not significant
11410	PQBP1	1.39	7.58E-11	4.50E-10	520.68	not significant
11411	FBXW4	1.39	1.43E-16	1.41E-15	1440.22	not significant
11412	CCDC150	1.39	1.13E-07	4.81E-07	407.32	not significant
11413	ATHL1	1.39	3.14E-05	9.72E-05	6475.29	not significant
11414	GFER	1.39	8.22E-15	6.99E-14	920.97	not significant
11415	CASC15	1.39	2.94E-19	3.58E-18	1223.67	not significant
11416	SLC25A36	1.39	2.46E-35	8.38E-34	4354.87	not significant
11417	MAST3	1.39	1.15E-12	8.11E-12	745.14	not significant
11418	CSNK2A2	1.39	2.74E-23	4.34E-22	1789.22	not significant
11419	ZNF497	1.39	1.19E-04	3.36E-04	153.76	not significant
11420	RPS23	1.39	1.02E-09	5.39E-09	15741.85	not significant
11421	SPPL2B	1.39	4.56E-18	5.09E-17	1840.64	not significant
11422	C8orf82	1.39	7.97E-17	8.00E-16	906.83	not significant
11423	CEP97	1.39	7.47E-20	9.47E-19	1292.48	not significant
11424	RPS12	1.39	2.66E-40	1.19E-38	25781.43	not significant
11425	EVI2B	1.39	7.85E-28	1.68E-26	1764.60	not significant
11426	KIAA1656	1.39	9.42E-03	1.86E-02	44.54	not significant
11427	TBC1D19	1.40	5.17E-09	2.55E-08	392.93	not significant
11428	ZBTB8A	1.40	7.62E-15	6.51E-14	808.92	not significant

11429	GAB1	1.40	4.05E-03	8.65E-03	63.80	not significant
11430	TMEM9B-AS1	1.40	2.71E-03	5.98E-03	72.86	not significant
11431	EEF1B2	1.40	3.02E-34	9.75E-33	14246.99	not significant
11432	ZKSCAN1	1.40	6.83E-53	4.77E-51	5912.46	not significant
11433	PHLDB3	1.40	6.33E-06	2.16E-05	241.09	not significant
11434	CDK19	1.40	2.56E-29	5.94E-28	2185.56	not significant
11435	PDK2	1.40	1.93E-07	7.96E-07	323.94	not significant
11436	RAD51AP1	1.40	1.99E-36	7.36E-35	2676.86	not significant
11437	LOC729296	1.40	1.88E-03	4.26E-03	77.79	not significant
11438	PBLD	1.40	1.15E-03	2.73E-03	97.54	not significant
11439	FAM221A	1.40	1.33E-08	6.26E-08	377.56	not significant
11440	PTPLA	1.40	9.06E-06	3.03E-05	223.23	not significant
11441	KLF7	1.40	1.27E-02	2.44E-02	32.23	not significant
11442	LINC01004	1.40	1.08E-04	3.06E-04	208.01	not significant
11443	DLEU2L	1.40	1.56E-02	2.93E-02	24.06	not significant
11444	DGKQ	1.40	1.18E-20	1.57E-19	1363.97	not significant
11445	IBA57	1.40	7.73E-11	4.59E-10	531.75	not significant
11446	RCN3	1.40	3.34E-03	7.25E-03	68.74	not significant
11447	TRAF5	1.40	4.25E-21	5.84E-20	1996.83	not significant
11448	HIST1H2BK	1.40	4.92E-08	2.19E-07	342.99	not significant
11449	KLHDC2	1.40	9.02E-21	1.21E-19	1193.63	not significant
11450	KRBA2	1.40	1.17E-03	2.76E-03	88.26	not significant
11451	TTC31	1.40	8.12E-20	1.03E-18	1339.10	not significant
11452	CAPN10-AS1	1.40	1.75E-03	3.99E-03	80.51	not significant
11453	RPS29	1.40	4.77E-06	1.65E-05	8052.98	not significant
11454	KRBA1	1.40	4.34E-13	3.17E-12	634.53	not significant
11455	PLA2G6	1.40	3.84E-15	3.37E-14	1182.96	not significant
11456	RPL26	1.40	6.96E-35	2.32E-33	13903.33	not significant
11457	ZBTB42	1.40	2.03E-06	7.39E-06	295.36	not significant
11458	VASH2	1.40	4.10E-24	6.88E-23	1423.75	not significant
11459	OGT	1.40	1.89E-04	5.19E-04	11004.96	not significant
11460	TUBGCP6	1.40	3.35E-06	1.19E-05	2952.35	not significant
11461	SBK1	1.40	1.28E-27	2.68E-26	2068.17	not significant
11462	KIAA0895L	1.40	2.01E-14	1.65E-13	1299.26	not significant
11463	KDM5D	1.41	1.13E-36	4.24E-35	3522.51	not significant
11464	NOP14-AS1	1.41	7.98E-06	2.69E-05	201.79	not significant
11465	CAMK4	1.41	1.17E-25	2.17E-24	1531.08	not significant
11466	PPAPDC2	1.41	5.28E-10	2.89E-09	456.89	not significant
11467	TOPORS-AS1	1.41	4.35E-05	1.32E-04	176.33	not significant
11468	FAM193B	1.41	1.39E-04	3.89E-04	2766.38	not significant
11469	MTSS1L	1.41	2.10E-15	1.87E-14	815.74	not significant
11470	SLC29A3	1.41	3.39E-07	1.36E-06	287.55	not significant
11471	GSG2	1.41	1.27E-27	2.68E-26	1859.50	not significant
11472	TRPT1	1.41	5.88E-12	3.88E-11	548.28	not significant
11473	AGO4	1.41	5.35E-26	1.00E-24	2037.27	not significant
11474	CNTD1	1.41	1.58E-02	2.96E-02	11.35	not significant
11475	ZNF529	1.41	1.55E-17	1.65E-16	1149.19	not significant
11476	TMEM80	1.41	6.89E-07	2.66E-06	299.07	not significant
11477	LINC00883	1.41	9.57E-05	2.76E-04	151.43	not significant
11478	SRGAP3	1.41	2.62E-04	6.99E-04	120.38	not significant
11479	FNDC3A	1.41	1.51E-35	5.25E-34	3175.22	not significant
11480	ZNF519	1.41	3.18E-12	2.15E-11	678.68	not significant
11481	MDFIC	1.41	1.77E-43	8.69E-42	7070.31	not significant
11482	LOC100132077	1.41	4.94E-03	1.04E-02	56.69	not significant
11483	PQLC2	1.41	6.58E-05	1.95E-04	154.43	not significant
11484	TUFT1	1.41	1.41E-02	2.69E-02	26.33	not significant
11485	LINC01115	1.41	8.95E-04	2.16E-03	91.12	not significant
11486	S1PR3	1.41	5.95E-15	5.13E-14	736.23	not significant
11487	MOB2	1.41	5.40E-12	3.58E-11	541.21	not significant
11488	LGALS9	1.41	2.72E-32	7.62E-31	2027.95	not significant
11489	HES4	1.41	7.15E-19	8.41E-18	1062.82	not significant
11490	HEXA	1.41	7.73E-27	1.54E-25	1804.48	not significant
11491	NEAT1	1.41	2.40E-04	6.44E-04	4055.14	not significant
11492	NPHP3	1.41	1.26E-03	2.96E-03	99.56	not significant
11493	C16orf93	1.41	9.34E-04	2.25E-03	88.20	not significant
11494	SNX14	1.41	3.84E-19	4.63E-18	1119.73	not significant
11495	CADM4	1.41	1.83E-03	4.16E-03	77.17	not significant
11496	SVOPL	1.41	1.38E-08	6.51E-08	448.00	not significant
11497	ABCD4	1.41	2.61E-23	4.14E-22	1320.42	not significant
11498	PRKAB1	1.41	4.25E-42	2.00E-40	3601.84	not significant
11499	RPL32P3	1.41	4.47E-06	1.56E-05	247.91	not significant
11500	GSC	1.41	9.08E-06	3.03E-05	203.97	not significant
11501	DBN1	1.41	2.30E-38	9.39E-37	4217.25	not significant
11502	ZSCAN26	1.41	1.98E-07	8.15E-07	301.94	not significant
11503	FHL3	1.41	1.09E-06	4.12E-06	241.06	not significant
11504	N4BP2L1	1.41	4.00E-14	3.20E-13	800.85	not significant
11505	KCTD7	1.41	3.04E-20	3.93E-19	1129.39	not significant
11506	PLEKHA8P1	1.41	1.34E-07	5.65E-07	298.02	not significant
11507	KDSR	1.41	2.51E-24	4.28E-23	1810.16	not significant
11508	MYB	1.42	1.10E-70	1.31E-68	18020.66	not significant
11509	RRAGB	1.42	6.79E-06	2.31E-05	210.62	not significant
11510	NT5M	1.42	5.24E-11	3.16E-10	565.92	not significant
11511	STK19	1.42	2.30E-03	5.13E-03	72.81	not significant
11512	VCAN	1.42	1.50E-04	4.17E-04	127.85	not significant
11513	DNAJC4	1.42	8.53E-07	3.25E-06	267.40	not significant
11514	PHF19	1.42	6.43E-40	2.82E-38	4239.88	not significant
11515	BOLA3-AS1	1.42	1.19E-02	2.31E-02	30.33	not significant
11516	SELL	1.42	1.16E-47	6.57E-46	14689.26	not significant

11517	ERGIC3	1.42	7.35E-50	4.58E-48	4834.53	not significant
11518	MSANTD3	1.42	2.73E-07	1.11E-06	270.61	not significant
11519	ZNF443	1.42	1.89E-09	9.71E-09	388.94	not significant
11520	PRIM1	1.42	6.01E-34	1.91E-32	2317.29	not significant
11521	PHF2	1.42	7.56E-44	3.80E-42	3710.90	not significant
11522	VILL	1.42	9.80E-12	6.34E-11	719.64	not significant
11523	SYNC	1.42	1.46E-02	2.76E-02	22.78	not significant
11524	RAB32	1.42	2.73E-14	2.21E-13	903.71	not significant
11525	NREP	1.42	1.39E-55	1.08E-53	5176.15	not significant
11526	HS1BP3	1.42	6.53E-09	3.19E-08	366.73	not significant
11527	ATG14	1.42	7.64E-10	4.09E-09	504.11	not significant
11528	PIGQ	1.42	9.45E-17	9.46E-16	935.12	not significant
11529	TIFA	1.42	1.50E-21	2.12E-20	1187.94	not significant
11530	FBXO43	1.42	3.71E-10	2.06E-09	488.94	not significant
11531	ZNF248	1.42	2.10E-16	2.04E-15	812.97	not significant
11532	PFDN4	1.42	8.92E-15	7.57E-14	789.58	not significant
11533	NAP1L1	1.42	1.37E-53	9.75E-52	49414.15	not significant
11534	KCNMB4	1.42	2.59E-08	1.19E-07	326.97	not significant
11535	CEP57	1.43	1.20E-59	1.04E-57	4890.96	not significant
11536	MXD3	1.43	9.25E-29	2.07E-27	1744.61	not significant
11537	LOC100630918	1.43	1.66E-03	3.82E-03	72.41	not significant
11538	DKFZP586I1420	1.43	5.05E-14	4.00E-13	621.39	not significant
11539	WDR45	1.43	3.00E-07	1.21E-06	257.20	not significant
11540	IKZF2	1.43	3.79E-53	2.68E-51	13602.88	not significant
11541	C22orf15	1.43	7.69E-03	1.55E-02	37.38	not significant
11542	IL12RB1	1.43	3.09E-20	3.99E-19	1067.61	not significant
11543	PHC1	1.43	1.14E-11	7.36E-11	510.71	not significant
11544	APCDD1	1.43	3.53E-05	1.09E-04	153.25	not significant
11545	TUG1	1.43	8.69E-47	4.78E-45	13570.48	not significant
11546	PRSS27	1.43	1.42E-02	2.69E-02	21.83	not significant
11547	C1orf21	1.43	9.40E-05	2.71E-04	125.37	not significant
11548	LINC01096	1.43	3.48E-03	7.54E-03	53.16	not significant
11549	EIF2S3	1.43	2.07E-73	2.60E-71	8745.13	not significant
11550	CLUHP3	1.43	2.56E-09	1.30E-08	383.60	not significant
11551	TRIM52	1.43	2.95E-09	1.50E-08	490.87	not significant
11552	R3HDM2	1.43	3.51E-31	9.06E-30	2716.09	not significant
11553	EFEMP2	1.43	5.14E-03	1.08E-02	44.79	not significant
11554	FAM228B	1.43	3.78E-03	8.14E-03	50.44	not significant
11555	LRRC75A-AS1	1.43	1.24E-59	1.06E-57	24033.19	not significant
11556	TIGD1	1.43	8.28E-09	4.02E-08	390.77	not significant
11557	BFAR	1.43	3.15E-39	1.34E-37	2648.57	not significant
11558	EIF2A	1.43	6.49E-54	4.72E-52	4508.91	not significant
11559	ACAD11	1.44	3.89E-03	8.36E-03	56.11	not significant
11560	ZFPM1	1.44	1.83E-05	5.85E-05	180.28	not significant
11561	PITPNM2	1.44	2.26E-46	1.23E-44	5223.70	not significant
11562	ZNF251	1.44	5.67E-13	4.08E-12	658.16	not significant
11563	ANKRD36B	1.44	5.59E-08	2.47E-07	325.40	not significant
11564	HGSNAT	1.44	2.56E-31	6.69E-30	1716.75	not significant
11565	ABCC5	1.44	6.85E-16	6.37E-15	869.25	not significant
11566	BHLHE23	1.44	1.14E-02	2.22E-02	26.01	not significant
11567	CARF	1.44	7.93E-12	5.18E-11	572.94	not significant
11568	TFAP2C	1.44	3.42E-17	3.54E-16	820.04	not significant
11569	RAB37	1.44	2.71E-54	2.00E-52	5539.55	not significant
11570	KCNH2	1.44	6.04E-15	5.21E-14	733.90	not significant
11571	CTSW	1.44	1.06E-02	2.08E-02	28.29	not significant
11572	FAM122C	1.44	2.83E-07	1.14E-06	252.12	not significant
11573	INSR	1.44	7.29E-17	7.35E-16	791.13	not significant
11574	VSX1	1.44	1.24E-02	2.38E-02	24.60	not significant
11575	ZNRF1	1.44	7.12E-54	5.14E-52	5777.71	not significant
11576	CHPF	1.44	2.22E-03	4.98E-03	61.52	not significant
11577	TRIQK	1.44	1.13E-11	7.29E-11	464.40	not significant
11578	MIR4674HG	1.44	2.39E-03	5.33E-03	57.60	not significant
11579	CCDC28A	1.44	2.24E-16	2.16E-15	798.02	not significant
11580	EIF3L	1.44	2.55E-55	1.96E-53	16953.17	not significant
11581	KIAA1683	1.44	1.49E-02	2.82E-02	12.47	not significant
11582	CLIP3	1.44	5.72E-08	2.52E-07	299.13	not significant
11583	CIZ1	1.44	1.55E-48	9.01E-47	3230.50	not significant
11584	HESX1	1.44	8.82E-03	1.75E-02	32.43	not significant
11585	NEU1	1.44	9.69E-07	3.68E-06	223.51	not significant
11586	TRPV3	1.44	1.38E-02	2.63E-02	20.22	not significant
11587	EIF4E3	1.44	1.68E-12	1.16E-11	556.14	not significant
11588	NCKAP1	1.44	1.50E-12	1.04E-11	525.62	not significant
11589	ZBTB17	1.45	2.48E-26	4.77E-25	1419.12	not significant
11590	CTSO	1.45	1.38E-02	2.63E-02	19.30	not significant
11591	C6orf132	1.45	2.72E-03	6.01E-03	61.14	not significant
11592	E2F8	1.45	2.76E-32	7.69E-31	2025.04	not significant
11593	GLB1L3	1.45	4.04E-03	8.64E-03	49.49	not significant
11594	SMPD2	1.45	1.76E-09	9.06E-09	345.04	not significant
11595	SPC24	1.45	2.92E-18	3.31E-17	815.43	not significant
11596	SLC40A1	1.45	8.63E-35	2.86E-33	1827.45	not significant
11597	DPY19L1	1.45	1.42E-03	3.31E-03	66.58	not significant
11598	ZSCAN16-AS1	1.45	7.08E-09	3.45E-08	306.91	not significant
11599	EFNB2	1.45	1.20E-07	5.09E-07	252.74	not significant
11600	TCIRG1	1.45	5.40E-12	3.57E-11	3526.75	not significant
11601	FAM160A2	1.45	4.49E-11	2.73E-10	565.75	not significant
11602	STAT3	1.45	5.60E-82	9.25E-80	11282.36	not significant
11603	SFXN5	1.45	9.83E-09	4.72E-08	322.58	not significant
11604	FAM219B	1.45	1.46E-18	1.69E-17	1120.92	not significant

11605	SYF2	1.45	4.00E-30	9.75E-29	2222.55	not significant
11606	HIST1H2AC	1.45	9.12E-03	1.80E-02	30.22	not significant
11607	CASP8	1.45	2.79E-32	7.76E-31	2320.81	not significant
11608	SKIL	1.45	6.33E-10	3.43E-09	361.79	not significant
11609	LOC728323	1.45	4.82E-03	1.02E-02	49.00	not significant
11610	SIX5	1.45	1.96E-06	7.17E-06	199.87	not significant
11611	TRO	1.46	1.03E-12	7.29E-12	489.46	not significant
11612	CYFIP1	1.46	6.13E-06	2.10E-05	186.80	not significant
11613	ZNF695	1.46	8.29E-07	3.17E-06	221.93	not significant
11614	ZNF713	1.46	1.40E-05	4.56E-05	166.34	not significant
11615	ZNF354C	1.46	5.88E-12	3.88E-11	438.33	not significant
11616	TSPYL4	1.46	3.78E-44	1.94E-42	2487.31	not significant
11617	RPL31	1.46	1.70E-15	1.53E-14	18102.94	not significant
11618	INAFM1	1.46	2.56E-09	1.30E-08	360.86	not significant
11619	CASP9	1.46	3.21E-06	1.14E-05	183.77	not significant
11620	IDNK	1.46	7.49E-04	1.83E-03	77.64	not significant
11621	PDGFA	1.46	7.38E-03	1.49E-02	33.25	not significant
11622	GATA3	1.46	1.91E-68	2.08E-66	7440.24	not significant
11623	EIF3F	1.46	7.24E-60	6.28E-58	5717.42	not significant
11624	ATP5SL	1.46	9.77E-07	3.70E-06	219.18	not significant
11625	LSM11	1.46	8.27E-15	7.03E-14	578.15	not significant
11626	DENND2D	1.46	4.83E-75	6.48E-73	8279.84	not significant
11627	FSTL1	1.46	6.96E-16	6.47E-15	682.22	not significant
11628	EMID1	1.46	2.12E-23	3.38E-22	1224.88	not significant
11629	IRS2	1.46	4.68E-19	5.61E-18	876.95	not significant
11630	TLR5	1.46	1.59E-03	3.66E-03	65.66	not significant
11631	LOC101929140	1.46	2.81E-03	6.19E-03	51.03	not significant
11632	PPAPDC1B	1.47	2.35E-22	3.48E-21	1117.42	not significant
11633	KLHL22	1.47	4.44E-15	3.87E-14	690.55	not significant
11634	CD44	1.47	3.71E-19	4.48E-18	837.42	not significant
11635	SLC35E2B	1.47	2.55E-47	1.43E-45	3425.34	not significant
11636	RASSF8	1.47	8.39E-13	5.96E-12	493.34	not significant
11637	HMX2	1.47	1.74E-03	3.96E-03	58.44	not significant
11638	PCBP3	1.47	1.74E-18	2.01E-17	721.37	not significant
11639	CDK5RAP3	1.47	2.01E-07	8.25E-07	6581.97	not significant
11640	HSD11B1L	1.47	1.92E-03	4.36E-03	54.36	not significant
11641	FRMD4A	1.47	1.27E-23	2.05E-22	1019.82	not significant
11642	ATP5S	1.47	2.42E-10	1.38E-09	381.51	not significant
11643	RAD51-AS1	1.47	5.45E-03	1.13E-02	41.06	not significant
11644	LOC100128398	1.47	2.05E-05	6.53E-05	210.55	not significant
11645	EPCAM	1.47	2.21E-03	4.94E-03	52.76	not significant
11646	ZNF785	1.47	1.07E-09	5.63E-09	378.38	not significant
11647	GRASP	1.47	1.97E-04	5.38E-04	95.19	not significant
11648	C22orf39	1.47	1.21E-37	4.81E-36	2093.48	not significant
11649	CRTAP	1.47	1.08E-51	7.15E-50	4240.37	not significant
11650	GLUD1P3	1.47	6.31E-03	1.29E-02	133.19	not significant
11651	PFN2	1.47	9.36E-08	4.01E-07	228.10	not significant
11652	ZNF554	1.47	1.94E-04	5.30E-04	99.86	not significant
11653	KIAA0141	1.48	2.54E-36	9.30E-35	1999.67	not significant
11654	MRPL10	1.48	4.61E-32	1.26E-30	1652.62	not significant
11655	GATS	1.48	1.88E-29	4.41E-28	1511.11	not significant
11656	ASPRV1	1.48	1.77E-04	4.86E-04	105.09	not significant
11657	MYO1G	1.48	1.26E-61	1.14E-59	9281.91	not significant
11658	CCDC88B	1.48	1.16E-25	2.16E-24	1292.70	not significant
11659	RTKN2	1.48	8.43E-29	1.89E-27	1783.82	not significant
11660	IPO5P1	1.48	4.14E-23	6.46E-22	1152.76	not significant
11661	MFAP2	1.48	1.35E-02	2.58E-02	13.16	not significant
11662	43530_6595	1.48	4.22E-16	3.98E-15	6503.23	not significant
11663	AMDHD2	1.48	2.78E-17	2.90E-16	757.50	not significant
11664	BRD1	1.48	5.59E-49	3.31E-47	3298.33	not significant
11665	LOC101928736	1.48	1.60E-05	5.17E-05	138.25	not significant
11666	RELB	1.48	4.80E-10	2.63E-09	321.32	not significant
11667	DZANK1	1.48	1.17E-04	3.32E-04	102.52	not significant
11668	IFT140	1.48	1.57E-12	1.09E-11	615.92	not significant
11669	SNHG1	1.48	2.43E-13	1.81E-12	7170.17	not significant
11670	NIFK-AS1	1.48	4.06E-12	2.72E-11	421.07	not significant
11671	SPAG8	1.48	1.16E-02	2.24E-02	20.38	not significant
11672	RUFY3	1.48	1.69E-49	1.03E-47	3686.72	not significant
11673	KCNG3	1.48	8.96E-05	2.59E-04	111.35	not significant
11674	CBX7	1.49	6.40E-08	2.80E-07	227.63	not significant
11675	SOGA1	1.49	2.21E-26	4.26E-25	1327.77	not significant
11676	SLC18A2	1.49	5.56E-39	2.34E-37	2186.97	not significant
11677	CREBZF	1.49	1.85E-11	1.16E-10	3726.89	not significant
11678	NACA2	1.49	3.68E-03	7.94E-03	40.39	not significant
11679	MAST1	1.49	5.54E-04	1.39E-03	71.20	not significant
11680	RASA4CP	1.49	1.26E-07	5.31E-07	241.12	not significant
11681	TP53INP1	1.49	4.40E-30	1.07E-28	1324.40	not significant
11682	MIEF2	1.49	1.05E-10	6.16E-10	362.18	not significant
11683	RTCA	1.49	1.68E-36	6.24E-35	1665.12	not significant
11684	DDX11-AS1	1.49	6.58E-03	1.34E-02	31.95	not significant
11685	PPIEL	1.49	1.09E-03	2.58E-03	257.18	not significant
11686	IL15	1.49	1.41E-08	6.61E-08	255.18	not significant
11687	GPRASP1	1.49	3.46E-18	3.91E-17	806.12	not significant
11688	PMPCB	1.49	5.13E-56	4.09E-54	4053.04	not significant
11689	VMAC	1.49	1.88E-05	6.02E-05	134.81	not significant
11690	ETV6	1.49	3.66E-41	1.69E-39	2303.01	not significant
11691	IFFO1	1.49	4.48E-13	3.26E-12	648.80	not significant
11692	LIN7B	1.49	5.62E-04	1.41E-03	80.03	not significant

11693	GS1-24F4.2	1.49	4.29E-05	1.30E-04	117.14	not significant
11694	CUL7	1.49	7.10E-25	1.25E-23	1187.10	not significant
11695	MIR646HG	1.49	8.07E-21	1.09E-19	803.16	not significant
11696	C20orf203	1.49	2.18E-03	4.89E-03	49.24	not significant
11697	RNF122	1.49	1.57E-11	9.91E-11	371.00	not significant
11698	ZFHX2	1.49	4.48E-05	1.36E-04	116.37	not significant
11699	SCRN2	1.49	2.13E-16	2.07E-15	626.74	not significant
11700	C17orf70	1.49	2.80E-44	1.44E-42	2203.70	not significant
11701	CCNB1IP1	1.49	9.21E-44	4.61E-42	2515.09	not significant
11702	SEPSECS-AS1	1.50	1.56E-03	3.61E-03	53.48	not significant
11703	ERICH6-AS1	1.50	2.63E-03	5.82E-03	45.28	not significant
11704	OSBPL7	1.50	5.18E-14	4.09E-13	677.19	not significant
11705	ZSWIM8	1.50	4.03E-11	2.46E-10	2576.56	not significant
11706	SDK2	1.50	8.70E-05	2.52E-04	99.99	not significant
11707	HAGHL	1.50	6.50E-03	1.33E-02	30.51	not significant
11708	WARS2	1.50	3.81E-19	4.59E-18	744.33	not significant
11709	HSPA8	1.50	3.35E-68	3.59E-66	135890.00	not significant
11710	OFD1	1.50	3.59E-20	4.62E-19	1111.49	not significant
11711	MRPL45P2	1.50	2.26E-03	5.06E-03	49.21	not significant
11712	EIF4A2	1.50	2.17E-64	2.18E-62	11824.36	not significant
11713	DDRGK1	1.50	7.73E-30	1.85E-28	1772.50	not significant
11714	NFKBIL1	1.50	2.09E-04	5.68E-04	88.44	not significant
11715	PLEKHG2	1.50	3.74E-12	2.51E-11	3187.50	not significant
11716	PDCD4	1.50	6.08E-43	2.93E-41	2254.61	not significant
11717	ZSCAN2	1.50	2.95E-17	3.06E-16	607.54	Increased
11718	LOC100507419	1.50	5.06E-09	2.50E-08	258.42	Increased
11719	LOC101927599	1.50	3.09E-05	9.58E-05	120.92	Increased
11720	SDE2	1.50	2.89E-39	1.23E-37	2022.62	Increased
11721	RBM7	1.50	9.52E-28	2.02E-26	1132.54	Increased
11722	ZNF85	1.50	1.53E-03	3.54E-03	52.47	Increased
11723	IP6K2	1.50	3.10E-40	1.37E-38	3133.16	Increased
11724	FLJ32255	1.50	9.99E-21	1.33E-19	974.25	Increased
11725	DUSP1	1.50	4.04E-17	4.16E-16	592.57	Increased
11726	LRRN1	1.50	2.29E-03	5.11E-03	46.55	Increased
11727	C16orf54	1.51	1.01E-31	2.71E-30	1596.40	Increased
11728	THG1L	1.51	2.76E-12	1.88E-11	400.96	Increased
11729	RTP4	1.51	7.86E-11	4.66E-10	325.15	Increased
11730	NINL	1.51	3.31E-48	1.91E-46	2949.17	Increased
11731	ZFP2	1.51	2.93E-03	6.42E-03	46.88	Increased
11732	BRWD1	1.51	2.12E-45	1.13E-43	2687.00	Increased
11733	PMM1	1.51	1.81E-20	2.38E-19	818.62	Increased
11734	ARSA	1.51	1.03E-11	6.64E-11	483.38	Increased
11735	CLCN7	1.51	1.07E-45	5.70E-44	2252.40	Increased
11736	FAM214A	1.51	6.87E-17	6.94E-16	556.13	Increased
11737	ZNF250	1.51	4.07E-11	2.48E-10	328.17	Increased
11738	ARIH2OS	1.51	5.62E-04	1.41E-03	64.83	Increased
11739	LOC101927815	1.52	1.76E-05	5.65E-05	127.29	Increased
11740	NME3	1.52	6.28E-07	2.43E-06	188.09	Increased
11741	SHANK3	1.52	2.89E-11	1.78E-10	354.23	Increased
11742	RFNG	1.52	4.52E-24	7.56E-23	1208.55	Increased
11743	C17orf53	1.52	2.10E-18	2.40E-17	625.90	Increased
11744	TMEM159	1.52	3.79E-14	3.03E-13	462.30	Increased
11745	LOC101927204	1.52	4.70E-14	3.73E-13	450.81	Increased
11746	HERC2P2	1.52	1.57E-14	1.30E-13	532.03	Increased
11747	PTPRN2	1.52	1.64E-28	3.62E-27	1060.86	Increased
11748	CEP68	1.52	7.35E-25	1.29E-23	911.39	Increased
11749	RPL39	1.52	1.66E-14	1.37E-13	616.98	Increased
11750	LINC00493	1.52	9.14E-30	2.18E-28	1293.02	Increased
11751	OGFOD3	1.52	3.93E-33	1.16E-31	1336.69	Increased
11752	KIAA1549	1.52	1.13E-09	5.95E-09	314.33	Increased
11753	CD244	1.52	1.60E-47	9.02E-46	2306.47	Increased
11754	STAT5B	1.52	4.32E-98	1.06E-95	10904.51	Increased
11755	CROCCP3	1.52	5.12E-05	1.54E-04	134.50	Increased
11756	DPY19L2P2	1.52	2.34E-24	3.99E-23	968.29	Increased
11757	BRI3	1.52	2.75E-23	4.35E-22	984.12	Increased
11758	TIMP2	1.52	1.94E-11	1.22E-10	347.44	Increased
11759	CLIP4	1.52	9.97E-25	1.74E-23	1059.40	Increased
11760	DLG3	1.52	5.29E-31	1.35E-29	1395.32	Increased
11761	PDE3B	1.52	1.56E-04	4.34E-04	85.53	Increased
11762	LOC100506123	1.53	1.17E-02	2.27E-02	43.87	Increased
11763	COL6A3	1.53	3.21E-03	6.98E-03	37.93	Increased
11764	ST3GAL1	1.53	7.13E-56	5.62E-54	2482.14	Increased
11765	ZNF418	1.53	6.15E-12	4.05E-11	347.87	Increased
11766	C1orf228	1.53	8.36E-56	6.55E-54	4101.44	Increased
11767	C1orf213	1.53	2.25E-04	6.08E-04	74.39	Increased
11768	STARD9	1.53	1.04E-14	8.74E-14	568.52	Increased
11769	CAMK2N2	1.53	5.66E-04	1.42E-03	66.12	Increased
11770	SLC25A5-AS1	1.53	4.59E-04	1.17E-03	77.74	Increased
11771	PARP6	1.53	1.36E-08	6.39E-08	1161.54	Increased
11772	LINC00663	1.53	1.42E-03	3.30E-03	49.77	Increased
11773	GRAMD1A	1.53	3.68E-48	2.11E-46	3047.21	Increased
11774	C19orf48	1.54	7.93E-73	9.79E-71	4831.93	Increased
11775	FAM66C	1.54	5.97E-03	1.23E-02	26.32	Increased
11776	ZNF711	1.54	6.89E-47	3.83E-45	2876.85	Increased
11777	S1PR4	1.54	3.08E-10	1.73E-09	1702.22	Increased
11778	TSGA10	1.54	1.14E-04	3.22E-04	82.58	Increased
11779	LOC400863	1.54	5.68E-04	1.42E-03	63.81	Increased
11780	RPL34	1.54	8.06E-55	6.04E-53	10550.40	Increased

11781	ACVR2B	1.54	6.70E-37	2.54E-35	1772.22	Increased
11782	CAPN3	1.54	9.45E-04	2.27E-03	54.60	Increased
11783	ZNF10	1.54	1.93E-23	3.08E-22	754.11	Increased
11784	KIAA0355	1.54	5.28E-16	4.94E-15	469.69	Increased
11785	ADCK3	1.54	1.25E-25	2.32E-24	863.05	Increased
11786	EGFL7	1.54	1.14E-02	2.22E-02	13.16	Increased
11787	IMPDH2	1.54	2.87E-87	5.49E-85	12127.26	Increased
11788	MICB	1.54	2.70E-09	1.37E-08	253.03	Increased
11789	RASGEF1B	1.55	3.03E-10	1.70E-09	274.28	Increased
11790	ORC1	1.55	1.46E-61	1.31E-59	4116.17	Increased
11791	CFTR	1.55	2.36E-79	3.66E-77	12338.94	Increased
11792	LOC101927181	1.55	7.50E-13	5.35E-12	389.85	Increased
11793	LINC01089	1.55	2.99E-05	9.29E-05	729.59	Increased
11794	ACSF3	1.55	6.44E-64	6.40E-62	3298.89	Increased
11795	LINC00921	1.55	2.38E-03	5.31E-03	38.87	Increased
11796	GPR113	1.55	4.90E-10	2.69E-09	271.24	Increased
11797	APOBR	1.55	4.51E-21	6.19E-20	728.14	Increased
11798	ZNF33B	1.55	1.39E-26	2.73E-25	1090.67	Increased
11799	GPC2	1.55	5.50E-18	6.07E-17	580.08	Increased
11800	PPP1R3E	1.55	8.35E-16	7.72E-15	546.15	Increased
11801	LOC730183	1.55	8.04E-03	1.61E-02	21.58	Increased
11802	ZNF135	1.55	4.79E-04	1.22E-03	59.08	Increased
11803	CPNE7	1.55	1.73E-23	2.78E-22	736.04	Increased
11804	MYO15B	1.56	3.24E-03	7.05E-03	34.17	Increased
11805	FAM210B	1.56	9.93E-09	4.77E-08	232.41	Increased
11806	SESTD1	1.56	9.13E-24	1.50E-22	847.41	Increased
11807	FAM227A	1.56	9.58E-04	2.30E-03	59.54	Increased
11808	PAQR8	1.56	2.42E-30	5.95E-29	1233.74	Increased
11809	DCHS1	1.56	8.27E-42	3.87E-40	2345.41	Increased
11810	COL6A4P1	1.56	1.28E-03	3.00E-03	46.03	Increased
11811	ZNF93	1.56	1.76E-28	3.87E-27	1041.78	Increased
11812	TLE4	1.56	9.54E-12	6.17E-11	315.88	Increased
11813	GOLGA8A	1.56	1.01E-04	2.91E-04	857.96	Increased
11814	BRSK1	1.56	9.56E-08	4.09E-07	182.23	Increased
11815	PCBP1-AS1	1.56	2.64E-13	1.96E-12	359.24	Increased
11816	SH2D3C	1.56	5.75E-41	2.61E-39	1471.47	Increased
11817	KIAA0101	1.56	6.07E-53	4.26E-51	5181.29	Increased
11818	TK2	1.57	8.05E-11	4.76E-10	369.07	Increased
11819	BACH2	1.57	1.25E-17	1.35E-16	533.51	Increased
11820	ZNF345	1.57	5.44E-10	2.97E-09	243.05	Increased
11821	ATG9B	1.57	2.09E-04	5.67E-04	76.15	Increased
11822	CTSS	1.57	5.36E-27	1.08E-25	1033.83	Increased
11823	CCNE1	1.57	1.32E-18	1.54E-17	527.35	Increased
11824	TENM1	1.57	8.90E-31	2.25E-29	1008.24	Increased
11825	ZNF154	1.57	1.31E-25	2.41E-24	1165.37	Increased
11826	BEND5	1.57	6.73E-13	4.82E-12	365.68	Increased
11827	HEPACAM	1.57	1.15E-03	2.72E-03	44.57	Increased
11828	FAM19A2	1.57	1.06E-11	6.87E-11	293.18	Increased
11829	GBA2	1.57	5.17E-26	9.70E-25	819.23	Increased
11830	RASSF8-AS1	1.57	5.05E-03	1.06E-02	28.14	Increased
11831	KIAA1147	1.57	2.09E-04	5.67E-04	67.68	Increased
11832	LOC646719	1.58	4.78E-07	1.88E-06	884.76	Increased
11833	USP51	1.58	3.51E-10	1.95E-09	265.38	Increased
11834	TMSB4Y	1.58	8.36E-07	3.19E-06	135.83	Increased
11835	CRAMP1L	1.58	3.10E-42	1.47E-40	1865.72	Increased
11836	GAB2	1.58	3.96E-145	3.02E-142	41937.35	Increased
11837	RBMX2	1.58	8.61E-42	4.01E-40	1551.45	Increased
11838	QPRT	1.58	9.32E-44	4.65E-42	1899.61	Increased
11839	TMEM18	1.58	9.60E-50	5.89E-48	2189.00	Increased
11840	CNIH2	1.58	8.19E-06	2.75E-05	107.93	Increased
11841	LOC100506688	1.58	1.23E-36	4.60E-35	1219.30	Increased
11842	LOC728752	1.58	3.15E-06	1.12E-05	119.28	Increased
11843	SHISA2	1.58	3.06E-119	1.39E-116	10032.83	Increased
11844	ZDHHC24	1.58	6.68E-17	6.77E-16	617.57	Increased
11845	TGIF1	1.58	6.04E-11	3.62E-10	272.38	Increased
11846	TMEM256	1.58	9.58E-17	9.58E-16	472.39	Increased
11847	PAN3-AS1	1.59	7.35E-05	2.15E-04	89.58	Increased
11848	SCAND2P	1.59	3.45E-07	1.38E-06	152.86	Increased
11849	BCORP1	1.59	1.40E-13	1.06E-12	451.16	Increased
11850	FAM229A	1.59	2.27E-04	6.14E-04	63.59	Increased
11851	LOC102723927	1.59	3.58E-06	1.26E-05	163.19	Increased
11852	SATB1-AS1	1.59	2.95E-04	7.78E-04	61.64	Increased
11853	CBFA2T3	1.59	3.92E-109	1.37E-106	9553.71	Increased
11854	KANSL1L	1.59	2.70E-10	1.53E-09	249.78	Increased
11855	CD28	1.59	2.53E-98	6.31E-96	9745.66	Increased
11856	NSG1	1.60	5.51E-03	1.14E-02	22.70	Increased
11857	HDAC7	1.60	3.80E-103	1.03E-100	7577.58	Increased
11858	C12orf57	1.60	5.18E-14	4.10E-13	378.63	Increased
11859	ZFP14	1.60	9.17E-20	1.16E-18	571.43	Increased
11860	UBA7	1.60	1.28E-41	5.94E-40	2538.46	Increased
11861	DNAJC1	1.60	2.07E-26	3.99E-25	1058.22	Increased
11862	LOC101929374	1.60	1.21E-04	3.42E-04	72.82	Increased
11863	LOC100132078	1.60	6.82E-03	1.39E-02	19.15	Increased
11864	AHSA2	1.60	7.02E-05	2.06E-04	2486.52	Increased
11865	HDAC5	1.60	4.65E-24	7.76E-23	690.90	Increased
11866	PGBD2	1.60	1.95E-07	8.04E-07	168.48	Increased
11867	NEK10	1.60	1.02E-03	2.43E-03	43.97	Increased
11868	KCNK1	1.61	9.78E-64	9.63E-62	2363.73	Increased

11869	FAM175A	1.61	3.45E-23	5.43E-22	651.12	Increased
11870	KIF27	1.61	3.86E-08	1.73E-07	170.17	Increased
11871	GAREML	1.61	4.63E-13	3.36E-12	311.55	Increased
11872	LRRC24	1.61	1.13E-04	3.22E-04	73.80	Increased
11873	PRR5	1.61	2.89E-16	2.75E-15	429.22	Increased
11874	LOC100131564	1.61	1.10E-05	3.64E-05	486.68	Increased
11875	ATP13A4	1.61	1.27E-03	2.99E-03	38.76	Increased
11876	COL9A2	1.61	6.07E-05	1.81E-04	77.04	Increased
11877	C1orf85	1.61	3.29E-23	5.19E-22	733.43	Increased
11878	PIGZ	1.61	6.25E-06	2.13E-05	100.10	Increased
11879	SLC12A6	1.62	1.89E-84	3.35E-82	4310.46	Increased
11880	ZNF827	1.62	1.05E-07	4.46E-07	158.32	Increased
11881	PABPC1L	1.62	6.30E-05	1.87E-04	1227.71	Increased
11882	ZFAS1	1.62	5.81E-91	1.22E-88	4490.09	Increased
11883	CMTM1	1.62	2.26E-11	1.41E-10	269.26	Increased
11884	BAI2	1.62	4.80E-40	2.12E-38	1367.34	Increased
11885	LOC153684	1.63	1.42E-06	5.28E-06	127.82	Increased
11886	FOXD2-AS1	1.63	2.48E-20	3.24E-19	527.27	Increased
11887	LRRC56	1.63	1.76E-04	4.85E-04	61.08	Increased
11888	UBXN1	1.63	2.85E-58	2.35E-56	2949.02	Increased
11889	LIMD2	1.63	3.52E-103	9.76E-101	4533.04	Increased
11890	LINC00664	1.63	1.49E-11	9.45E-11	241.52	Increased
11891	PDE10A	1.64	1.84E-04	5.05E-04	58.55	Increased
11892	TNFAIP3	1.64	8.11E-66	8.25E-64	2686.36	Increased
11893	IRF7	1.64	1.41E-10	8.15E-10	232.85	Increased
11894	ZNF792	1.64	1.86E-16	1.81E-15	397.13	Increased
11895	FAM173A	1.64	3.88E-07	1.55E-06	127.09	Increased
11896	IVNS1ABP	1.64	8.14E-106	2.49E-103	5869.32	Increased
11897	HAUS4	1.64	1.80E-42	8.59E-41	1650.13	Increased
11898	PTGIS	1.64	1.37E-26	2.70E-25	710.11	Increased
11899	ZNF322	1.64	3.77E-04	9.77E-04	50.34	Increased
11900	L3MBTL1	1.65	6.39E-09	3.12E-08	192.01	Increased
11901	GPCPD1	1.65	2.81E-37	1.09E-35	1189.46	Increased
11902	SOX4	1.65	9.88E-113	4.16E-110	21521.62	Increased
11903	TXK	1.65	2.14E-05	6.80E-05	92.31	Increased
11904	BTG1	1.65	1.16E-77	1.69E-75	6024.85	Increased
11905	ZNF446	1.65	8.61E-14	6.66E-13	351.99	Increased
11906	RNF139-AS1	1.65	4.86E-04	1.24E-03	53.90	Increased
11907	LINC01355	1.65	6.83E-07	2.64E-06	148.43	Increased
11908	LOC100288152	1.65	2.15E-05	6.81E-05	80.83	Increased
11909	MICAL1	1.66	9.91E-14	7.64E-13	2058.93	Increased
11910	CYP2E1	1.66	1.06E-04	3.01E-04	67.89	Increased
11911	LRRC37B	1.66	1.31E-32	3.75E-31	880.33	Increased
11912	PCED1A	1.66	3.42E-35	1.15E-33	1298.44	Increased
11913	FCGRT	1.66	4.10E-32	1.13E-30	1048.66	Increased
11914	EPM2AIP1	1.66	2.64E-11	1.63E-10	2537.14	Increased
11915	CKB	1.67	7.02E-10	3.78E-09	208.28	Increased
11916	CALCOCO1	1.67	4.20E-29	9.64E-28	708.26	Increased
11917	GAS5	1.67	1.74E-80	2.83E-78	3766.08	Increased
11918	DRAXIN	1.67	1.23E-17	1.33E-16	400.32	Increased
11919	CDKN2B	1.67	7.37E-04	1.80E-03	38.62	Increased
11920	GLTSCR2	1.67	1.72E-77	2.45E-75	15723.05	Increased
11921	HLA-E	1.67	1.30E-56	1.04E-54	2059.48	Increased
11922	YPEL5	1.67	3.41E-36	1.24E-34	903.15	Increased
11923	MAPK11	1.67	1.46E-12	1.02E-11	258.37	Increased
11924	FAM161B	1.67	5.26E-11	3.17E-10	212.40	Increased
11925	SPSB3	1.67	5.47E-32	1.49E-30	1006.97	Increased
11926	FBXL19-AS1	1.67	5.45E-08	2.41E-07	160.31	Increased
11927	RASIP1	1.67	7.96E-04	1.93E-03	41.23	Increased
11928	MANEA-AS1	1.68	6.55E-04	1.62E-03	48.68	Increased
11929	RFX3-AS1	1.68	3.50E-10	1.95E-09	189.73	Increased
11930	MYO18B	1.68	1.49E-72	1.82E-70	18879.47	Increased
11931	C18orf32	1.68	2.75E-03	6.07E-03	27.18	Increased
11932	NOG	1.68	6.83E-03	1.39E-02	14.92	Increased
11933	LPAR1	1.68	1.30E-03	3.05E-03	33.60	Increased
11934	CREB3L3	1.68	2.92E-14	2.36E-13	328.58	Increased
11935	FLJ10038	1.68	1.93E-17	2.04E-16	384.05	Increased
11936	PDCD1	1.68	2.89E-05	9.00E-05	71.42	Increased
11937	ZNF491	1.68	3.50E-06	1.24E-05	124.31	Increased
11938	PICK1	1.68	3.22E-14	2.60E-13	291.26	Increased
11939	ANKRD36	1.69	4.30E-05	1.31E-04	425.02	Increased
11940	MANBA	1.69	7.03E-35	2.34E-33	872.86	Increased
11941	ADAMTS7P1	1.69	7.42E-03	1.50E-02	13.66	Increased
11942	MT1G	1.69	8.53E-23	1.30E-21	4019.65	Increased
11943	LOC100499489	1.69	2.10E-06	7.62E-06	94.78	Increased
11944	TXLNB	1.69	2.20E-08	1.02E-07	141.93	Increased
11945	ZBTB26	1.69	2.51E-18	2.85E-17	412.72	Increased
11946	USP30-AS1	1.70	1.52E-07	6.36E-07	125.50	Increased
11947	C2orf48	1.70	8.99E-13	6.38E-12	257.40	Increased
11948	LINC00634	1.70	1.80E-04	4.94E-04	54.86	Increased
11949	SLC25A29	1.70	4.48E-83	7.82E-81	2815.96	Increased
11950	STAM	1.70	1.06E-35	3.71E-34	829.90	Increased
11951	IZUMO1	1.70	5.63E-03	1.17E-02	16.17	Increased
11952	ZNF821	1.70	3.16E-06	1.12E-05	94.22	Increased
11953	TSPY26P	1.70	6.26E-08	2.74E-07	123.83	Increased
11954	PNRC1	1.70	3.89E-20	5.00E-19	412.91	Increased
11955	MAMSTR	1.70	2.91E-03	6.39E-03	24.58	Increased
11956	SLC4A5	1.70	2.13E-03	4.78E-03	27.08	Increased

11957	ARID5B	1.71	5.75E-62	5.24E-60	1817.37	Increased
11958	ZNF548	1.71	1.85E-37	7.24E-36	1025.94	Increased
11959	YPEL2	1.71	3.29E-03	7.14E-03	22.28	Increased
11960	TEX19	1.71	2.60E-32	7.29E-31	759.79	Increased
11961	FAAH	1.71	3.94E-23	6.17E-22	526.87	Increased
11962	JMY	1.71	9.32E-38	3.76E-36	978.82	Increased
11963	PLCL1	1.71	2.44E-10	1.38E-09	174.21	Increased
11964	RGS1	1.71	4.41E-05	1.34E-04	64.66	Increased
11965	SHC4	1.71	4.24E-04	1.09E-03	50.93	Increased
11966	LINC00847	1.71	8.76E-36	3.10E-34	888.80	Increased
11967	CCR9	1.71	1.33E-99	3.38E-97	4877.95	Increased
11968	PRKCE	1.72	4.14E-85	7.43E-83	2778.24	Increased
11969	GPR153	1.72	1.81E-29	4.25E-28	639.79	Increased
11970	SPATA20	1.72	4.90E-05	1.48E-04	61.65	Increased
11971	ZNF763	1.72	6.49E-06	2.21E-05	77.41	Increased
11972	KIAA1211	1.72	5.20E-12	3.45E-11	212.78	Increased
11973	FMNL2	1.73	3.08E-12	2.08E-11	212.82	Increased
11974	CYTH2	1.73	8.57E-69	9.69E-67	2837.31	Increased
11975	SLC29A4	1.73	1.74E-15	1.56E-14	284.64	Increased
11976	CELF6	1.73	6.19E-09	3.03E-08	184.06	Increased
11977	ING4	1.73	1.46E-32	4.17E-31	1011.64	Increased
11978	BCL2L2	1.73	1.03E-03	2.46E-03	30.44	Increased
11979	LOC730101	1.74	1.45E-51	9.50E-50	1270.65	Increased
11980	GIMAP2	1.74	7.41E-92	1.59E-89	4517.29	Increased
11981	CLEC2D	1.74	1.74E-30	4.32E-29	829.96	Increased
11982	XRCC1	1.74	3.64E-59	3.07E-57	1933.18	Increased
11983	CCNG1	1.74	1.74E-117	7.58E-115	5139.86	Increased
11984	ZNF70	1.74	1.68E-11	1.06E-10	227.03	Increased
11985	YPEL3	1.74	3.16E-14	2.55E-13	266.85	Increased
11986	RPL10	1.75	7.29E-18	7.98E-17	11902.47	Increased
11987	CR2	1.75	3.21E-82	5.44E-80	2076.64	Increased
11988	GLYCTK	1.75	1.60E-16	1.57E-15	297.39	Increased
11989	CD37	1.75	1.02E-71	1.24E-69	1820.86	Increased
11990	ABCB7	1.75	3.67E-52	2.51E-50	1195.90	Increased
11991	ERVK13-1	1.75	1.61E-14	1.33E-13	271.88	Increased
11992	RNF215	1.76	3.95E-09	1.98E-08	137.15	Increased
11993	FAM132B	1.76	7.78E-06	2.62E-05	70.24	Increased
11994	GOLGA8B	1.76	4.13E-07	1.64E-06	885.00	Increased
11995	NPHP3-ACAD11	1.76	6.44E-04	1.59E-03	39.21	Increased
11996	ITGA1	1.76	4.74E-125	2.52E-122	6413.07	Increased
11997	ADAM1A	1.76	1.16E-14	9.72E-14	271.41	Increased
11998	HBP1	1.77	2.25E-35	7.75E-34	756.27	Increased
11999	SYCE2	1.77	8.88E-10	4.71E-09	151.60	Increased
12000	MIATNB	1.77	2.45E-10	1.39E-09	154.58	Increased
12001	SHF	1.77	2.96E-07	1.19E-06	97.08	Increased
12002	HEMGN	1.77	3.21E-15	2.83E-14	264.84	Increased
12003	ZNF333	1.77	9.50E-15	8.05E-14	272.68	Increased
12004	MST1	1.77	1.96E-07	8.10E-07	102.78	Increased
12005	DNASE1	1.77	1.04E-31	2.79E-30	690.02	Increased
12006	LOC100506548	1.77	2.63E-70	3.12E-68	2038.66	Increased
12007	MAN2A2	1.78	1.17E-20	1.55E-19	2086.08	Increased
12008	TRIB2	1.78	7.41E-159	6.97E-156	8802.57	Increased
12009	EPB41L4A	1.78	3.58E-14	2.88E-13	269.54	Increased
12010	DDAH2	1.78	7.44E-33	2.17E-31	834.25	Increased
12011	PILRA	1.78	1.44E-08	6.74E-08	121.47	Increased
12012	UCP2	1.78	2.51E-86	4.65E-84	2989.78	Increased
12013	PBXIP1	1.78	1.79E-97	4.29E-95	2414.93	Increased
12014	HYMAI	1.78	5.04E-03	1.06E-02	14.49	Increased
12015	TMEM44	1.79	3.05E-32	8.44E-31	676.73	Increased
12016	MEX3B	1.79	2.76E-10	1.56E-09	181.18	Increased
12017	LOC202181	1.79	4.01E-07	1.59E-06	387.48	Increased
12018	GPR174	1.79	2.35E-52	1.62E-50	1106.09	Increased
12019	ATG16L2	1.79	2.39E-13	1.78E-12	1399.61	Increased
12020	CXXC5	1.79	2.88E-42	1.37E-40	920.07	Increased
12021	ACRBP	1.80	7.35E-04	1.80E-03	35.87	Increased
12022	ELL3	1.80	4.66E-06	1.62E-05	70.04	Increased
12023	MFSD4	1.80	9.04E-04	2.18E-03	27.38	Increased
12024	PON1	1.80	1.95E-06	7.12E-06	78.01	Increased
12025	GPR137C	1.80	3.91E-06	1.37E-05	68.17	Increased
12026	DYRK1B	1.80	2.33E-12	1.59E-11	227.59	Increased
12027	DALRD3	1.80	3.81E-24	6.41E-23	453.70	Increased
12028	ASB16-AS1	1.81	1.26E-23	2.05E-22	508.77	Increased
12029	LOC100507373	1.81	3.84E-14	3.07E-13	213.19	Increased
12030	HIC1	1.81	3.84E-04	9.93E-04	34.14	Increased
12031	ARRDC3	1.81	1.23E-51	8.11E-50	1409.73	Increased
12032	ABCA13	1.81	7.50E-03	1.51E-02	11.39	Increased
12033	IGBP1	1.81	6.56E-80	1.04E-77	2102.87	Increased
12034	SPHK1	1.81	8.42E-10	4.48E-09	134.45	Increased
12035	GPR18	1.82	4.64E-07	1.83E-06	84.36	Increased
12036	ERBB2	1.82	5.19E-18	5.74E-17	288.73	Increased
12037	NOA1	1.82	6.34E-95	1.41E-92	2474.10	Increased
12038	LINC00954	1.82	3.11E-04	8.19E-04	37.03	Increased
12039	SPTBN2	1.82	1.82E-95	4.12E-93	2347.32	Increased
12040	OTUD1	1.82	1.69E-05	5.45E-05	56.65	Increased
12041	EVI2A	1.82	1.94E-43	9.43E-42	846.12	Increased
12042	PGAP3	1.83	5.20E-29	1.18E-27	512.73	Increased
12043	MXD1	1.83	2.21E-18	2.53E-17	308.67	Increased
12044	CELF5	1.83	2.94E-06	1.05E-05	71.96	Increased

12045	S1PR1	1.83	1.06E-103	3.02E-101	2392.25	Increased
12046	TMEM238	1.83	4.89E-05	1.47E-04	51.28	Increased
12047	TMEM132D	1.83	5.87E-23	9.07E-22	472.79	Increased
12048	CAMLG	1.83	1.59E-65	1.61E-63	2087.65	Increased
12049	EPB41L4A-AS1	1.84	5.10E-37	1.95E-35	725.03	Increased
12050	TTYH2	1.84	1.30E-22	1.97E-21	407.01	Increased
12051	ERMAP	1.84	1.15E-17	1.25E-16	275.43	Increased
12052	ABTB2	1.84	8.25E-12	5.38E-11	171.66	Increased
12053	MORN3	1.84	1.53E-03	3.53E-03	22.10	Increased
12054	MZF1	1.85	8.75E-24	1.44E-22	488.90	Increased
12055	PTP4A3	1.85	1.31E-42	6.29E-41	829.89	Increased
12056	NXN	1.85	4.37E-07	1.73E-06	84.73	Increased
12057	ALDH1A2	1.85	5.65E-32	1.54E-30	665.79	Increased
12058	IL4	1.85	1.18E-07	5.02E-07	95.51	Increased
12059	MXD4	1.85	7.87E-37	2.98E-35	650.17	Increased
12060	FAIM3	1.86	4.11E-34	1.32E-32	581.06	Increased
12061	DPEP1	1.86	7.45E-06	2.52E-05	57.93	Increased
12062	C9orf47	1.86	2.71E-03	5.99E-03	19.01	Increased
12063	CCDC42B	1.86	1.80E-12	1.24E-11	171.91	Increased
12064	RDM1	1.87	5.66E-07	2.20E-06	80.20	Increased
12065	TMEM91	1.87	1.59E-06	5.86E-06	69.01	Increased
12066	MYLK4	1.87	1.81E-04	4.97E-04	34.77	Increased
12067	CHI3L2	1.87	3.19E-163	3.54E-160	38177.48	Increased
12068	FIGNL2	1.87	5.08E-08	2.25E-07	96.85	Increased
12069	SERINC5	1.87	1.80E-205	3.15E-202	9645.68	Increased
12070	FLJ20021	1.88	4.55E-06	1.58E-05	63.36	Increased
12071	LOC101928150	1.88	8.82E-03	1.75E-02	7.93	Increased
12072	AMY2B	1.88	3.39E-06	1.20E-05	75.04	Increased
12073	HHAT	1.89	3.71E-12	2.49E-11	160.43	Increased
12074	HDC	1.89	9.45E-04	2.27E-03	25.02	Increased
12075	ZBED6CL	1.89	1.48E-66	1.53E-64	1270.66	Increased
12076	LOC100130992	1.89	4.59E-04	1.17E-03	29.28	Increased
12077	UMODL1	1.89	9.99E-19	1.17E-17	259.57	Increased
12078	LOC100049716	1.90	9.23E-05	2.67E-04	37.66	Increased
12079	BCL6	1.90	8.30E-11	4.91E-10	133.71	Increased
12080	ZNF16	1.90	6.46E-21	8.77E-20	327.34	Increased
12081	EXPH5	1.90	1.21E-07	5.14E-07	80.98	Increased
12082	APOLD1	1.91	1.20E-11	7.72E-11	166.64	Increased
12083	CEBPE	1.91	8.85E-06	2.96E-05	53.51	Increased
12084	TMEM254-AS1	1.91	5.55E-04	1.39E-03	27.33	Increased
12085	HSD17B11	1.91	1.93E-82	3.33E-80	1449.81	Increased
12086	KLF8	1.91	1.62E-03	3.73E-03	18.69	Increased
12087	ZNF704	1.91	1.15E-20	1.53E-19	296.13	Increased
12088	TNFRSF13C	1.92	1.39E-05	4.53E-05	63.86	Increased
12089	OLFM2	1.92	1.88E-05	6.01E-05	46.47	Increased
12090	TNFRSF14	1.93	2.34E-87	4.53E-85	1699.28	Increased
12091	LOC100131289	1.93	4.41E-10	2.43E-09	113.36	Increased
12092	TESK2	1.93	5.70E-24	9.48E-23	345.10	Increased
12093	SLC35E2	1.93	4.83E-44	2.47E-42	735.74	Increased
12094	FGFR1	1.93	1.12E-06	4.23E-06	63.62	Increased
12095	ZEB1-AS1	1.94	9.46E-44	4.70E-42	653.68	Increased
12096	GUCY1A2	1.94	3.67E-08	1.65E-07	86.88	Increased
12097	CACNA1I	1.94	2.02E-05	6.44E-05	47.38	Increased
12098	CCNG2	1.94	3.86E-90	7.86E-88	1563.19	Increased
12099	DFNA5	1.94	1.94E-05	6.20E-05	47.89	Increased
12100	RIPK4	1.95	5.25E-10	2.87E-09	117.05	Increased
12101	TPM2	1.95	1.72E-15	1.54E-14	265.47	Increased
12102	HYI	1.95	7.41E-33	2.16E-31	452.87	Increased
12103	C1R	1.95	4.43E-24	7.42E-23	319.74	Increased
12104	CACNA1A	1.96	3.73E-04	9.66E-04	25.83	Increased
12105	SNHG5	1.97	2.82E-74	3.70E-72	1179.63	Increased
12106	C19orf57	1.97	1.18E-23	1.92E-22	330.91	Increased
12107	FRAT1	1.98	1.25E-15	1.14E-14	202.14	Increased
12108	MICALL2	1.98	2.52E-13	1.87E-12	159.82	Increased
12109	ZNF496	1.99	2.32E-78	3.45E-76	1665.14	Increased
12110	RTP5	1.99	1.08E-09	5.69E-09	101.41	Increased
12111	ZNF581	1.99	1.35E-52	9.37E-51	843.58	Increased
12112	FOXD4	2.00	3.38E-03	7.34E-03	12.49	Increased
12113	TOB1-AS1	2.00	1.44E-05	4.68E-05	42.51	Increased
12114	IL23A	2.00	5.33E-11	3.21E-10	122.94	Increased
12115	LINC00473	2.00	5.02E-04	1.27E-03	23.36	Increased
12116	EFHC1	2.01	7.82E-24	1.29E-22	351.72	Increased
12117	RHEBL1	2.02	4.35E-13	3.17E-12	139.54	Increased
12118	PDE4A	2.02	1.56E-14	1.29E-13	159.07	Increased
12119	LINC00462	2.02	8.42E-04	2.04E-03	23.55	Increased
12120	NHLRC4	2.02	7.25E-06	2.46E-05	51.00	Increased
12121	ZNF425	2.02	1.94E-08	9.02E-08	87.33	Increased
12122	CTTN	2.03	2.43E-10	1.38E-09	111.27	Increased
12123	IDUA	2.03	1.03E-25	1.91E-24	399.58	Increased
12124	ZNF844	2.03	1.15E-03	2.73E-03	17.86	Increased
12125	MFGE8	2.03	4.18E-110	1.60E-107	1975.54	Increased
12126	LOC440311	2.03	8.70E-09	4.21E-08	80.81	Increased
12127	CD68	2.04	1.16E-09	6.09E-09	100.05	Increased
12128	LOC101927768	2.05	1.16E-03	2.74E-03	19.03	Increased
12129	HAPLN3	2.05	5.44E-06	1.87E-05	46.51	Increased
12130	SNHG6	2.05	3.82E-97	8.98E-95	3651.89	Increased
12131	LOC100130476	2.05	7.78E-17	7.82E-16	198.85	Increased
12132	LETMD1	2.06	2.32E-164	2.84E-161	3210.33	Increased

12133	WNT8B	2.08	2.66E-06	9.52E-06	47.92	Increased
12134	ARHGAP19-SLIT1	2.09	4.71E-05	1.42E-04	36.03	Increased
12135	SCN7A	2.10	2.61E-152	2.13E-149	3673.98	Increased
12136	CREBRF	2.10	3.37E-25	6.11E-24	307.66	Increased
12137	LOC101927415	2.10	9.40E-05	2.71E-04	28.32	Increased
12138	LPAR6	2.11	5.83E-107	1.83E-104	2727.76	Increased
12139	SIGLEC6	2.11	1.32E-110	5.19E-108	2022.91	Increased
12140	MST1P2	2.12	2.25E-05	7.11E-05	35.22	Increased
12141	FAM20C	2.13	5.30E-05	1.59E-04	31.24	Increased
12142	PRDM11	2.13	3.88E-08	1.74E-07	65.57	Increased
12143	C12orf76	2.13	7.35E-36	2.63E-34	388.47	Increased
12144	LRRC36	2.13	6.65E-04	1.64E-03	18.40	Increased
12145	CDT1	2.14	5.45E-214	1.11E-210	11729.87	Increased
12146	TIGD7	2.15	2.00E-13	1.50E-12	123.53	Increased
12147	MAP3K8	2.15	1.46E-06	5.42E-06	47.69	Increased
12148	CD40LG	2.17	3.24E-127	1.80E-124	2963.17	Increased
12149	CREB3L4	2.17	4.51E-31	1.16E-29	344.52	Increased
12150	ABTB1	2.18	5.11E-38	2.08E-36	423.66	Increased
12151	KCTD1	2.19	1.40E-100	3.63E-98	1582.37	Increased
12152	IGLL1	2.19	2.07E-111	8.44E-109	1976.37	Increased
12153	ZNF277	2.19	1.20E-94	2.62E-92	1281.97	Increased
12154	PCGF1	2.19	1.49E-44	7.80E-43	495.44	Increased
12155	DERL3	2.20	6.44E-13	4.63E-12	108.29	Increased
12156	YPEL1	2.20	1.95E-104	5.81E-102	1320.86	Increased
12157	TMEM26	2.20	6.53E-91	1.35E-88	1040.88	Increased
12158	LOC100131347	2.20	1.09E-04	3.10E-04	26.60	Increased
12159	C17orf100	2.21	2.11E-07	8.66E-07	51.53	Increased
12160	LRRC70	2.22	1.08E-07	4.62E-07	57.15	Increased
12161	MT1E	2.23	4.21E-86	7.67E-84	1598.96	Increased
12162	TEC	2.23	2.17E-12	1.49E-11	101.32	Increased
12163	PCAT18	2.24	2.03E-79	3.17E-77	961.76	Increased
12164	MT1H	2.24	3.28E-22	4.81E-21	2304.39	Increased
12165	ZNF521	2.25	4.73E-09	2.34E-08	67.09	Increased
12166	LOC400685	2.25	5.80E-07	2.25E-06	44.69	Increased
12167	SCARB2	2.26	4.24E-63	4.08E-61	649.14	Increased
12168	LOC729683	2.26	1.21E-12	8.50E-12	111.05	Increased
12169	CACNA1C-AS2	2.27	2.04E-04	5.55E-04	20.46	Increased
12170	C16orf86	2.28	1.38E-04	3.85E-04	22.15	Increased
12171	SLC20A1	2.29	0.00E+00	0.00E+00	5506.61	Increased
12172	PPP1R16B	2.30	6.23E-101	1.65E-98	1494.69	Increased
12173	HEXIM2	2.30	2.06E-19	2.53E-18	184.24	Increased
12174	H1FX-AS1	2.36	7.06E-14	5.51E-13	108.53	Increased
12175	LOC100130093	2.38	2.03E-04	5.52E-04	18.55	Increased
12176	NEURL1B	2.39	1.19E-24	2.06E-23	204.88	Increased
12177	ANGPTL6	2.44	3.22E-23	5.08E-22	181.99	Increased
12178	PLXNB1	2.45	5.43E-20	6.93E-19	171.56	Increased
12179	FCGBP	2.46	9.15E-49	5.35E-47	453.98	Increased
12180	NEURL2	2.49	1.93E-09	9.94E-09	58.48	Increased
12181	ADSSL1	2.49	8.57E-10	4.55E-09	59.62	Increased
12182	KLHL24	2.52	1.27E-77	1.82E-75	783.04	Increased
12183	TCAM1P	2.55	1.39E-17	1.50E-16	116.91	Increased
12184	SNHG7	2.55	2.39E-224	5.84E-221	2373.42	Increased
12185	STAT5A	2.56	0.00E+00	0.00E+00	19149.66	Increased
12186	JUP	2.56	1.51E-04	4.21E-04	18.43	Increased
12187	CDH24	2.57	5.41E-41	2.48E-39	305.04	Increased
12188	FOXB1	2.58	5.82E-08	2.56E-07	43.69	Increased
12189	C6orf48	2.59	6.06E-125	2.96E-122	1349.35	Increased
12190	TPGS1	2.59	3.22E-13	2.37E-12	303.50	Increased
12191	ANXA2R	2.61	9.44E-124	4.44E-121	1033.61	Increased
12192	CKAP4	2.62	2.94E-05	9.15E-05	21.69	Increased
12193	NATD1	2.65	1.35E-62	1.28E-60	451.55	Increased
12194	LINC01226	2.69	3.64E-07	1.46E-06	35.36	Increased
12195	ATP6V0A4	2.74	3.22E-159	3.28E-156	1230.51	Increased
12196	PI16	2.75	3.60E-08	1.62E-07	39.23	Increased
12197	DNTT	2.76	0.00E+00	0.00E+00	8501.85	Increased
12198	OSER1-AS1	2.78	1.33E-11	8.50E-11	59.13	Increased
12199	SERINC2	2.81	7.28E-05	2.14E-04	17.42	Increased
12200	HSD17B14	2.88	3.82E-14	3.06E-13	73.04	Increased
12201	PGLYRP4	2.98	3.47E-04	9.06E-04	11.50	Increased
12202	HOMER3	2.99	2.64E-08	1.21E-07	33.99	Increased
12203	CACNA1C-AS1	3.00	1.59E-11	1.00E-10	54.65	Increased
12204	MT1F	3.01	1.30E-10	7.56E-10	50.13	Increased
12205	MFI2-AS1	3.03	2.56E-16	2.46E-15	94.97	Increased
12206	RAB26	3.04	4.82E-05	1.45E-04	15.90	Increased
12207	PPIL6	3.04	3.29E-04	8.61E-04	12.49	Increased
12208	FMN1	3.20	1.40E-06	5.21E-06	21.84	Increased
12209	TDRD9	3.34	2.68E-17	2.80E-16	74.80	Increased
12210	KIAA1644	3.54	1.32E-08	6.23E-08	29.89	Increased
12211	LOC63930	3.85	7.06E-11	4.21E-10	34.97	Increased
12212	SYT11	4.11	6.18E-52	4.13E-50	203.79	Increased
12213	CR1	4.18	2.97E-13	2.19E-12	40.41	Increased
12214	IL17D	4.31	1.31E-09	6.85E-09	26.63	Increased
12215	LINC00304	4.45	9.17E-05	2.65E-04	9.23	Increased
12216	BCL3	4.70	4.99E-07	1.96E-06	17.77	Increased
12217	GRIN2D	5.44	2.81E-05	8.76E-05	9.28	Increased
12218	DAAM2	7.70	3.81E-07	1.52E-06	12.16	Increased
12219	RSPH4A	8.35	5.05E-05	1.52E-04	7.37	Increased

Supplementary Table 7D: Gene expression changes induced by RZ-2994 vs. DMSO at Day 1 on KOPTK1 cells.
Significance estimated based on DESeq2 (apeglm shrunken fold change) padj < 0.10. Effect of RZ-2994 on gene expression: decreased if log2FoldChange < -1.2, Increased if log2FoldChange > 1.2. Base mean is the average DESeq2 normalized reads in DMSO replicates. Expressed genes have at least 10 reads in at least three replicate samples. Shown are the expressed genes at Day 1 ranked by RZ-2994 vs. DMSO log2FoldChange

#	Gene symbol (hg19)	log2FoldChange RZ-2994 vs. DMSO Day1 DESeq2 apeglm	pvalue RZ-2994 vs. DMSO Day1 DESeq2	padj RZ-2994 vs. DMSO Day1 DESeq2	baseMean RZ-2994 vs. DMSO Day1 DESeq2	RZ-2994 effect on gene expression at Day 1
1	H19	-1.49	6.11E-26	8.73E-23	1097.71	Decreased
2	PLK1	-1.40	1.02E-41	5.12E-38	3361.99	Decreased
3	CDC20	-1.38	8.36E-42	5.12E-38	4745.60	Decreased
4	RPS14P3	-1.36	7.28E-04	1.01E-02	109.59	Decreased
5	NOTCH3	-1.35	1.87E-08	1.77E-06	410.66	Decreased
6	LOC100129148	-1.35	3.12E-03	NA	66.35	Decreased
7	EIF5AL1	-1.34	3.40E-04	5.68E-03	131.17	Decreased
8	SLC35F3	-1.30	5.94E-08	4.57E-06	538.34	Decreased
9	SMTN	-1.28	5.86E-07	3.13E-05	522.29	Decreased
10	AK4	-1.28	1.45E-03	1.67E-02	132.14	Decreased
11	CCNB1	-1.28	5.12E-21	4.65E-18	4162.64	Decreased
12	AURKA	-1.26	6.31E-14	1.97E-11	1696.83	Decreased
13	PIF1	-1.25	2.08E-04	3.90E-03	255.81	Decreased
14	FAM64A	-1.25	1.32E-06	6.25E-05	584.83	Decreased
15	IKZF4	-1.24	1.47E-09	1.77E-07	1338.90	Decreased
16	RSC1A1	-1.24	3.48E-04	5.77E-03	333.76	Decreased
17	CENPE	-1.23	4.55E-05	1.15E-03	3056.20	Decreased
18	ZNF286B	-1.23	3.28E-03	3.00E-02	128.23	Decreased
19	KPNA2	-1.22	6.06E-17	3.03E-14	4822.25	Decreased
20	RARA	-1.22	2.90E-08	2.50E-06	1099.92	Decreased
21	MKNK2	-1.21	2.01E-18	1.26E-15	5086.75	Decreased
22	GPATCH4	-1.21	1.74E-11	3.34E-09	3038.84	Decreased
23	PTPN3	-1.21	2.57E-05	7.31E-04	532.71	Decreased
24	HMMR	-1.21	2.78E-10	3.86E-08	1773.31	Decreased
25	CDCA2	-1.20	1.14E-11	2.38E-09	2459.98	Decreased
26	PTTG1	-1.20	6.24E-08	4.69E-06	1712.72	Decreased
27	MICAL2	-1.19	7.70E-07	3.87E-05	1213.92	not significant
28	BHLHE40	-1.19	8.16E-07	4.04E-05	1058.66	not significant
29	RRP9	-1.19	6.55E-08	4.85E-06	2419.53	not significant
30	LONRF2	-1.18	8.48E-06	2.91E-04	1372.42	not significant
31	KIF4A	-1.18	5.15E-10	6.96E-08	2403.26	not significant
32	TPMT	-1.18	1.98E-04	3.73E-03	531.65	not significant
33	NOL10	-1.18	1.95E-09	2.30E-07	2197.56	not significant
34	SFPQ	-1.18	1.31E-19	1.09E-16	19192.10	not significant
35	WT1	-1.18	3.26E-05	8.68E-04	789.26	not significant
36	CCNB2	-1.18	4.08E-08	3.32E-06	2063.68	not significant
37	SPDL1	-1.18	4.54E-08	3.61E-06	2166.22	not significant
38	AMER1	-1.18	2.66E-05	7.46E-04	784.26	not significant
39	CCDC86	-1.18	6.87E-12	1.46E-09	3681.49	not significant
40	ZNF256	-1.17	1.59E-03	1.79E-02	305.72	not significant
41	UBE2C	-1.17	3.94E-09	4.33E-07	4418.09	not significant
42	SENP3	-1.17	2.81E-05	7.72E-04	884.32	not significant
43	LDHA	-1.17	4.58E-17	2.41E-14	40022.09	not significant
44	PNO1	-1.17	5.65E-08	4.38E-06	1988.73	not significant
45	RPF2	-1.17	5.30E-07	2.85E-05	2277.09	not significant
46	PRR11	-1.17	4.43E-12	1.03E-09	5110.96	not significant
47	CDKN3	-1.17	1.58E-05	5.04E-04	1094.98	not significant
48	ZHX1	-1.17	1.57E-10	2.32E-08	4640.36	not significant
49	C12orf5	-1.17	3.40E-04	5.68E-03	542.46	not significant
50	PCF11	-1.17	1.32E-07	8.82E-06	3141.38	not significant
51	CKS2	-1.17	1.56E-07	1.00E-05	2988.92	not significant
52	TFAP2E	-1.17	7.90E-03	5.67E-02	105.56	not significant
53	PKI55	-1.16	1.98E-03	2.09E-02	390.62	not significant
54	KIF20A	-1.16	9.09E-07	4.46E-05	1483.98	not significant
55	TUBA1C	-1.16	5.10E-10	6.96E-08	6588.75	not significant
56	ZNF587B	-1.16	1.66E-03	1.85E-02	362.10	not significant
57	MAK16	-1.16	1.54E-10	2.30E-08	3598.19	not significant
58	NCR3LG1	-1.16	6.30E-04	9.01E-03	842.72	not significant
59	TAMM41	-1.16	3.28E-03	3.00E-02	260.68	not significant
60	TOP2A	-1.16	3.48E-11	5.80E-09	28280.91	not significant
61	ENPEP	-1.16	9.74E-08	6.87E-06	2233.16	not significant
62	DMPK	-1.16	1.47E-03	1.69E-02	407.80	not significant
63	LOC90784	-1.15	1.33E-03	1.57E-02	423.60	not significant
64	LIF	-1.15	3.61E-07	2.08E-05	3672.10	not significant
65	CDR2	-1.15	2.33E-06	9.88E-05	1809.15	not significant
66	PRKCD	-1.15	5.03E-03	4.08E-02	236.02	not significant
67	SUSD4	-1.15	3.22E-03	2.96E-02	327.16	not significant
68	TXNIP	-1.15	6.43E-04	9.14E-03	605.14	not significant
69	PAK1IP1	-1.15	5.56E-06	2.10E-04	1835.04	not significant
70	ODC1	-1.15	6.83E-10	8.76E-08	16060.26	not significant
71	AHDC1	-1.15	4.53E-06	1.80E-04	1751.89	not significant
72	SAPCD2	-1.15	2.98E-05	8.09E-04	1150.72	not significant
73	NOP16	-1.15	7.75E-07	3.88E-05	2271.19	not significant
74	LYAR	-1.15	1.84E-06	8.21E-05	3138.34	not significant
75	SGOL2	-1.15	5.12E-07	2.78E-05	3657.96	not significant

76	KCNJ11	-1.15	5.69E-09	6.06E-07	4238.70	not significant
77	OGG1	-1.15	5.78E-03	4.52E-02	264.21	not significant
78	POLR3G	-1.14	2.77E-05	7.65E-04	1277.85	not significant
79	PLAGL2	-1.14	1.47E-07	9.53E-06	4944.25	not significant
80	EBNA1BP2	-1.14	1.01E-07	7.04E-06	4412.88	not significant
81	LOC100128361	-1.14	8.72E-03	6.04E-02	152.80	not significant
82	AMIGO3	-1.14	9.24E-04	1.20E-02	632.72	not significant
83	TUBB4B	-1.14	3.12E-09	3.64E-07	5686.77	not significant
84	TPX2	-1.14	2.82E-12	7.23E-10	11367.67	not significant
85	MGC27345	-1.14	1.26E-03	1.50E-02	558.14	not significant
86	PSRC1	-1.14	5.40E-04	8.10E-03	752.21	not significant
87	ZFR	-1.14	7.84E-10	9.93E-08	5458.79	not significant
88	TAF12	-1.14	1.05E-04	2.26E-03	1141.95	not significant
89	MTF1	-1.14	1.78E-04	3.41E-03	1101.86	not significant
90	PPARGC1B	-1.14	1.72E-03	1.89E-02	833.43	not significant
91	CSNK1G1	-1.14	5.58E-05	1.35E-03	1894.29	not significant
92	HN1	-1.14	4.59E-07	2.52E-05	7896.67	not significant
93	DNTTIP2	-1.14	1.33E-07	8.84E-06	3112.82	not significant
94	C12orf4	-1.14	3.01E-04	5.25E-03	924.76	not significant
95	PTPN7	-1.14	5.77E-12	1.25E-09	12551.84	not significant
96	TUBA4A	-1.14	9.21E-04	1.20E-02	666.32	not significant
97	NFS1	-1.14	2.10E-04	3.92E-03	997.56	not significant
98	ARHGAP11A	-1.14	1.35E-06	6.31E-05	3465.38	not significant
99	CDCA8	-1.14	1.06E-07	7.34E-06	3486.74	not significant
100	C10orf2	-1.13	2.13E-06	9.25E-05	2192.94	not significant
101	KBTBD8	-1.13	7.94E-04	1.08E-02	717.62	not significant
102	HSPA5	-1.13	2.51E-11	4.56E-09	13779.34	not significant
103	NEU3	-1.13	5.44E-04	8.11E-03	1453.69	not significant
104	TAF9B	-1.13	6.40E-03	4.85E-02	274.04	not significant
105	CCNF	-1.13	9.92E-07	4.82E-05	2888.92	not significant
106	DLGAP5	-1.13	7.01E-07	3.56E-05	2673.02	not significant
107	MIEF1	-1.13	9.32E-08	6.67E-06	4144.14	not significant
108	DCAF13	-1.13	6.26E-06	2.29E-04	3198.67	not significant
109	UTP14A	-1.13	2.22E-06	9.55E-05	2392.85	not significant
110	GEMIN5	-1.13	6.21E-06	2.28E-04	2371.43	not significant
111	KIF23	-1.13	3.10E-05	8.31E-04	1891.05	not significant
112	BMS1	-1.13	4.51E-07	2.52E-05	4427.51	not significant
113	NOLC1	-1.13	3.32E-12	8.10E-10	15983.21	not significant
114	GLS	-1.13	3.71E-09	4.13E-07	8254.68	not significant
115	POLR1B	-1.13	6.03E-06	2.23E-04	2614.15	not significant
116	EIF5	-1.13	3.21E-11	5.54E-09	16188.24	not significant
117	AEN	-1.13	2.47E-05	7.15E-04	2154.62	not significant
118	ZNF37A	-1.13	3.17E-04	5.40E-03	2138.48	not significant
119	KIF20B	-1.13	3.52E-06	1.43E-04	3047.85	not significant
120	UBE2S	-1.13	3.67E-05	9.54E-04	4572.40	not significant
121	ANKRD52	-1.13	6.21E-06	2.28E-04	6809.97	not significant
122	PITPNA	-1.13	6.75E-07	3.44E-05	3444.82	not significant
123	POLR3H	-1.13	5.73E-06	2.15E-04	2817.85	not significant
124	PDSS1	-1.13	5.43E-04	8.11E-03	915.17	not significant
125	DDX21	-1.13	8.52E-10	1.07E-07	17492.87	not significant
126	GTPBP4	-1.13	2.78E-08	2.42E-06	5456.89	not significant
127	MRPL35	-1.13	1.36E-05	4.46E-04	2116.58	not significant
128	TRMT44	-1.12	4.86E-03	3.97E-02	401.88	not significant
129	BAIAP2-AS1	-1.12	7.16E-03	5.29E-02	312.40	not significant
130	PHLDA3	-1.12	3.37E-03	3.05E-02	502.02	not significant
131	TWISTNB	-1.12	7.39E-06	2.64E-04	2402.19	not significant
132	NOL6	-1.12	4.43E-08	3.57E-06	4826.43	not significant
133	SLC22A5	-1.12	6.74E-03	5.05E-02	353.90	not significant
134	ARCN1	-1.12	2.81E-04	4.96E-03	1433.76	not significant
135	RNF145	-1.12	1.35E-07	8.86E-06	4934.73	not significant
136	GRPEL1	-1.12	1.09E-04	2.33E-03	1841.19	not significant
137	HSPE1	-1.12	7.85E-05	1.78E-03	2333.95	not significant
138	PKM	-1.12	2.17E-08	2.03E-06	20249.05	not significant
139	LGALS1	-1.12	1.87E-03	2.01E-02	799.35	not significant
140	FARSB	-1.12	1.88E-06	8.34E-05	3669.07	not significant
141	KIF14	-1.12	5.13E-05	1.26E-03	2928.86	not significant
142	IL2RB	-1.12	2.54E-05	7.27E-04	2011.68	not significant
143	RXRA	-1.12	3.42E-03	3.07E-02	584.93	not significant
144	MDC1	-1.12	5.56E-03	4.38E-02	407.02	not significant
145	RITA1	-1.12	1.19E-04	2.47E-03	1846.22	not significant
146	WDR75	-1.12	1.09E-05	3.59E-04	2492.19	not significant
147	DKC1	-1.12	1.35E-06	6.31E-05	3753.12	not significant
148	CCDC6	-1.12	1.53E-04	3.04E-03	1524.74	not significant
149	TOMM34	-1.12	1.86E-04	3.55E-03	1917.25	not significant
150	TMEM229B	-1.12	8.09E-04	1.10E-02	989.16	not significant
151	HSPA4	-1.12	4.01E-08	3.31E-06	8152.47	not significant
152	TCEB3	-1.12	2.84E-05	7.76E-04	2832.33	not significant
153	TACC3	-1.12	2.56E-08	2.26E-06	6524.32	not significant
154	CENPA	-1.12	4.86E-04	7.48E-03	1132.61	not significant
155	NAA50	-1.12	6.41E-10	8.34E-08	12424.31	not significant
156	ZC3HAV1L	-1.12	1.85E-03	2.00E-02	898.87	not significant
157	IGF1R	-1.12	5.55E-05	1.35E-03	2003.03	not significant
158	ESF1	-1.12	9.45E-05	2.07E-03	2169.01	not significant
159	HNRNPM	-1.12	2.26E-08	2.09E-06	16146.55	not significant
160	GDF11	-1.12	2.68E-04	4.77E-03	1559.83	not significant
161	DDX18	-1.12	5.50E-08	4.30E-06	6540.87	not significant
162	SMEK2	-1.12	5.99E-08	4.57E-06	5939.95	not significant
163	R3HDM1	-1.12	7.88E-06	2.75E-04	4491.34	not significant

164	BIRC5	-1.12	4.77E-06	1.86E-04	7416.09	not significant
165	BUB1	-1.12	1.49E-07	9.63E-06	5342.91	not significant
166	SNRNP40	-1.12	2.08E-05	6.27E-04	3225.66	not significant
167	PAPOLA	-1.11	8.86E-09	8.87E-07	10734.10	not significant
168	GTF2H1	-1.11	4.00E-05	1.03E-03	2258.14	not significant
169	DHX34	-1.11	1.93E-04	3.67E-03	1545.83	not significant
170	TRMT61A	-1.11	3.58E-04	5.90E-03	1458.54	not significant
171	SIK1	-1.11	8.72E-03	6.04E-02	325.57	not significant
172	TFRC	-1.11	1.77E-07	1.10E-05	35439.15	not significant
173	LLPH	-1.11	3.99E-04	6.40E-03	1525.99	not significant
174	GALNS	-1.11	9.84E-03	6.57E-02	294.82	not significant
175	C3orf18	-1.11	1.95E-03	2.07E-02	893.53	not significant
176	SIKE1	-1.11	2.78E-06	1.17E-04	3926.27	not significant
177	KIAA2018	-1.11	1.19E-03	1.44E-02	1782.23	not significant
178	LCLAT1	-1.11	2.08E-03	2.17E-02	1131.11	not significant
179	ATP6V1B2	-1.11	2.24E-05	6.67E-04	3344.22	not significant
180	PSME3	-1.11	3.44E-09	3.87E-07	9502.01	not significant
181	GTF3C4	-1.11	5.86E-04	8.57E-03	1332.71	not significant
182	PPAN	-1.11	9.03E-03	6.19E-02	356.39	not significant
183	TOMM40	-1.11	6.79E-06	2.45E-04	6491.95	not significant
184	TBRG4	-1.11	3.67E-06	1.48E-04	5032.23	not significant
185	SSBP1	-1.11	2.15E-04	4.01E-03	2945.43	not significant
186	RRP12	-1.11	5.73E-06	2.15E-04	3595.24	not significant
187	ZMAT3	-1.11	6.39E-05	1.51E-03	3022.12	not significant
188	WDR43	-1.11	1.51E-06	6.90E-05	4857.82	not significant
189	FNDC3B	-1.11	1.09E-02	7.06E-02	277.60	not significant
190	OSM	-1.11	2.42E-06	1.02E-04	6108.18	not significant
191	ARHGAP19	-1.11	1.88E-04	3.58E-03	1933.54	not significant
192	DEPDC1	-1.11	4.75E-04	7.37E-03	1318.84	not significant
193	PSMC1	-1.11	1.68E-03	1.87E-02	1002.08	not significant
194	PRMT5	-1.11	3.32E-06	1.36E-04	4413.20	not significant
195	CHKA	-1.11	2.39E-03	2.43E-02	895.77	not significant
196	NEIL2	-1.11	3.62E-03	3.21E-02	736.27	not significant
197	NUFIP1	-1.11	2.66E-03	2.60E-02	790.63	not significant
198	SAR1A	-1.11	2.94E-06	1.22E-04	4195.36	not significant
199	GPI	-1.11	5.88E-09	6.10E-07	17056.77	not significant
200	DYNLL1	-1.11	6.68E-05	1.57E-03	4863.47	not significant
201	CNOT1	-1.11	1.08E-05	3.57E-04	15709.31	not significant
202	LPHN1	-1.11	7.93E-03	5.67E-02	428.64	not significant
203	WDR74	-1.11	5.59E-04	8.31E-03	1744.18	not significant
204	CNTROB	-1.11	6.45E-05	1.52E-03	2360.62	not significant
205	MAPKAPK3	-1.11	8.03E-07	4.00E-05	9397.35	not significant
206	FAM126B	-1.11	2.25E-04	4.15E-03	2196.46	not significant
207	PMM2	-1.11	1.03E-05	3.47E-04	3874.90	not significant
208	C9orf41	-1.11	3.31E-03	3.01E-02	751.92	not significant
209	ETF1	-1.11	1.77E-07	1.10E-05	7060.87	not significant
210	UCHL5	-1.11	8.55E-06	2.93E-04	4083.80	not significant
211	RHOU	-1.11	3.95E-03	3.41E-02	694.82	not significant
212	TAF4B	-1.10	8.68E-04	1.15E-02	1455.13	not significant
213	GOSR2	-1.10	1.65E-04	3.22E-03	2060.71	not significant
214	H1F0	-1.10	1.26E-02	7.80E-02	140.21	not significant
215	EIF5A	-1.10	4.79E-06	1.86E-04	16446.39	not significant
216	ARRB1	-1.10	2.82E-05	7.72E-04	3282.20	not significant
217	HEATR1	-1.10	1.06E-04	2.28E-03	5541.29	not significant
218	GRWD1	-1.10	7.37E-05	1.70E-03	3567.34	not significant
219	PSMD2	-1.10	1.31E-07	8.79E-06	9949.55	not significant
220	RASGRP3	-1.10	1.39E-02	8.40E-02	204.49	not significant
221	FAM83D	-1.10	4.31E-03	3.65E-02	802.95	not significant
222	IKZF3	-1.10	3.89E-03	3.37E-02	920.68	not significant
223	ATXN1L	-1.10	1.13E-03	1.39E-02	2305.68	not significant
224	ZNHIT6	-1.10	2.91E-04	5.12E-03	2448.18	not significant
225	TRIM25	-1.10	7.04E-06	2.53E-04	5233.59	not significant
226	DPH2	-1.10	1.66E-04	3.24E-03	2562.35	not significant
227	DGCR8	-1.10	1.38E-04	2.80E-03	2948.32	not significant
228	CACUL1	-1.10	7.51E-04	1.03E-02	1698.05	not significant
229	GPAM	-1.10	1.03E-03	1.30E-02	1568.16	not significant
230	RRP36	-1.10	4.15E-04	6.58E-03	2428.36	not significant
231	XPO6	-1.10	5.51E-06	2.09E-04	6215.68	not significant
232	MSL1	-1.10	2.73E-05	7.60E-04	3665.76	not significant
233	RPL23	-1.10	1.10E-04	2.33E-03	16952.17	not significant
234	RBMXL1	-1.10	1.66E-03	1.85E-02	1171.46	not significant
235	SYNCRIP	-1.10	1.12E-07	7.70E-06	22048.64	not significant
236	SERBP1	-1.10	3.72E-08	3.12E-06	18393.64	not significant
237	WDR77	-1.10	4.79E-06	1.86E-04	4852.68	not significant
238	POLR1A	-1.10	1.73E-04	3.35E-03	4283.02	not significant
239	POLR3B	-1.10	1.43E-03	1.65E-02	1229.37	not significant
240	ALMS1	-1.10	2.32E-03	2.38E-02	2507.73	not significant
241	ERCC8	-1.10	5.62E-03	4.42E-02	708.50	not significant
242	CKAP5	-1.10	3.84E-05	9.91E-04	10159.78	not significant
243	RANGAP1	-1.10	1.66E-05	5.24E-04	7870.82	not significant
244	QSER1	-1.10	1.08E-03	1.34E-02	1835.78	not significant
245	SPRTN	-1.10	5.37E-03	4.27E-02	734.13	not significant
246	INTS8	-1.10	4.96E-04	7.60E-03	1787.69	not significant
247	DDIT4	-1.10	3.33E-03	3.02E-02	1014.84	not significant
248	HSP90AA1	-1.10	1.30E-07	8.79E-06	132378.11	not significant
249	KPNA4	-1.10	2.28E-06	9.74E-05	6625.58	not significant
250	ARL6IP1	-1.10	5.34E-06	2.05E-04	8553.49	not significant
251	SEC31A	-1.10	1.98E-05	6.05E-04	6045.71	not significant

252	BTRC	-1.10	3.19E-03	2.94E-02	965.26	not significant
253	PPP2R5A	-1.10	1.11E-04	2.35E-03	2657.01	not significant
254	PARPBP	-1.10	4.43E-04	6.94E-03	1817.85	not significant
255	TDP2	-1.10	3.49E-04	5.79E-03	2049.10	not significant
256	ZNF542P	-1.10	1.11E-03	1.37E-02	1452.32	not significant
257	HSPH1	-1.10	7.05E-08	5.15E-06	23980.71	not significant
258	SVIL-AS1	-1.10	2.52E-03	2.51E-02	1142.03	not significant
259	ZNF28	-1.10	3.86E-03	3.36E-02	984.12	not significant
260	NME1	-1.10	1.54E-03	1.76E-02	2211.46	not significant
261	NRBF2	-1.10	8.03E-03	5.72E-02	605.20	not significant
262	KPNA3	-1.10	9.38E-06	3.19E-04	4748.53	not significant
263	NAA15	-1.10	7.36E-06	2.64E-04	7627.99	not significant
264	MBNL1	-1.10	3.22E-07	1.88E-05	29697.62	not significant
265	PMEPA1	-1.10	3.29E-03	3.00E-02	1625.48	not significant
266	ZNF480	-1.10	1.20E-03	1.45E-02	1750.27	not significant
267	DNAJB1	-1.10	1.04E-05	3.48E-04	5325.11	not significant
268	NSRP1	-1.10	3.61E-03	3.21E-02	964.88	not significant
269	EIF2S1	-1.10	4.73E-06	1.86E-04	6380.67	not significant
270	KLHL18	-1.10	2.28E-03	2.35E-02	1183.15	not significant
271	AGK	-1.10	4.35E-03	3.67E-02	946.03	not significant
272	MYBBP1A	-1.10	7.41E-06	2.64E-04	7030.80	not significant
273	PIK3R3	-1.10	8.02E-04	1.09E-02	1836.96	not significant
274	FAM98A	-1.10	5.65E-04	8.36E-03	2007.92	not significant
275	RGS6	-1.10	1.58E-02	9.20E-02	239.94	not significant
276	ZNF671	-1.10	9.28E-03	6.30E-02	584.21	not significant
277	IPMK	-1.10	8.43E-03	5.93E-02	611.32	not significant
278	TTC1	-1.09	6.14E-04	8.82E-03	2373.62	not significant
279	CDK6	-1.09	1.59E-04	3.14E-03	57773.41	not significant
280	LOC100507600	-1.09	1.15E-04	2.41E-03	3675.91	not significant
281	TRIM35	-1.09	3.46E-04	5.75E-03	2405.50	not significant
282	CHORDC1	-1.09	7.93E-05	1.78E-03	3590.90	not significant
283	KIF3B	-1.09	2.69E-03	2.62E-02	1302.86	not significant
284	C18orf25	-1.09	1.19E-03	1.44E-02	2059.79	not significant
285	STAG1	-1.09	3.96E-04	6.38E-03	3458.22	not significant
286	DHX33	-1.09	2.20E-04	4.08E-03	3880.25	not significant
287	PTP4A1	-1.09	5.37E-06	2.05E-04	7970.87	not significant
288	FAM53C	-1.09	1.62E-03	1.82E-02	1562.81	not significant
289	DYRK2	-1.09	1.13E-03	1.39E-02	1722.76	not significant
290	UBE2K	-1.09	1.88E-05	5.80E-04	5119.42	not significant
291	TRUB1	-1.09	2.45E-03	2.47E-02	1432.02	not significant
292	MAPKAP1	-1.09	4.39E-04	6.90E-03	2919.22	not significant
293	PKP4	-1.09	2.46E-03	2.47E-02	1567.14	not significant
294	ZMAT5	-1.09	8.73E-03	6.04E-02	725.82	not significant
295	SSB	-1.09	2.81E-05	7.72E-04	5659.96	not significant
296	EIF4G2	-1.09	9.31E-08	6.67E-06	57858.65	not significant
297	ABCE1	-1.09	1.30E-06	6.18E-05	7776.38	not significant
298	RSL1D1	-1.09	7.70E-06	2.71E-04	7847.72	not significant
299	NAT10	-1.09	2.75E-06	1.16E-04	7637.12	not significant
300	DDIAS	-1.09	1.51E-03	1.72E-02	1638.82	not significant
301	MBD2	-1.09	1.63E-04	3.19E-03	3356.80	not significant
302	ARMC7	-1.09	4.02E-03	3.45E-02	1005.99	not significant
303	PPP4R2	-1.09	5.76E-04	8.46E-03	2048.47	not significant
304	PTP4A2	-1.09	3.12E-07	1.84E-05	37127.22	not significant
305	OIP5	-1.09	1.35E-02	8.19E-02	435.20	not significant
306	IPO4	-1.09	7.86E-05	1.78E-03	3741.45	not significant
307	CIRH1A	-1.09	3.75E-04	6.17E-03	2543.93	not significant
308	MPHOSPH10	-1.09	8.45E-04	1.13E-02	2252.42	not significant
309	SCEL	-1.09	3.91E-03	3.38E-02	1117.11	not significant
310	CIAPIN1	-1.09	2.10E-03	2.18E-02	2110.11	not significant
311	EIF3B	-1.09	7.77E-06	2.73E-04	13688.80	not significant
312	CCDC85C	-1.09	9.66E-04	1.25E-02	1858.46	not significant
313	ZFP82	-1.09	1.10E-02	7.11E-02	568.06	not significant
314	DEPDC1B	-1.09	1.48E-03	1.70E-02	1636.97	not significant
315	STYX	-1.09	1.08E-03	1.34E-02	1769.13	not significant
316	EIF3J	-1.09	1.60E-04	3.14E-03	3591.50	not significant
317	ABCF2	-1.09	3.87E-05	9.95E-04	6029.11	not significant
318	ARHGEF3	-1.09	7.40E-04	1.02E-02	2113.12	not significant
319	ETS2	-1.09	1.64E-06	7.38E-05	9275.81	not significant
320	ARSB	-1.09	1.64E-03	1.83E-02	1856.78	not significant
321	LRRC59	-1.09	2.01E-06	8.79E-05	11170.57	not significant
322	CCNA2	-1.09	2.64E-05	7.46E-04	6149.69	not significant
323	SLC25A19	-1.09	1.47E-03	1.69E-02	1892.88	not significant
324	DCAF4	-1.09	5.60E-03	4.41E-02	916.40	not significant
325	EIF2B4	-1.09	4.23E-03	3.60E-02	1023.38	not significant
326	ASUN	-1.09	3.94E-04	6.38E-03	2550.34	not significant
327	METTL16	-1.09	2.80E-04	4.95E-03	2742.19	not significant
328	TRAK2	-1.09	2.59E-03	2.56E-02	1322.89	not significant
329	NOC3L	-1.09	8.83E-04	1.16E-02	2022.84	not significant
330	PNPT1	-1.09	4.91E-04	7.55E-03	2537.67	not significant
331	CCT5	-1.09	1.77E-05	5.52E-04	19602.47	not significant
332	KCTD21	-1.09	1.71E-02	9.63E-02	332.17	not significant
333	IARS	-1.09	4.78E-06	1.86E-04	9483.73	not significant
334	DDX49	-1.09	1.71E-03	1.88E-02	2466.53	not significant
335	DPP8	-1.09	3.34E-03	3.02E-02	1467.89	not significant
336	KCTD9	-1.09	9.99E-04	1.28E-02	2770.60	not significant
337	DIEXF	-1.09	2.52E-03	2.51E-02	1434.68	not significant
338	LARP4	-1.09	3.33E-05	8.83E-04	7384.73	not significant
339	ETNK1	-1.09	3.28E-04	5.54E-03	4567.62	not significant

340	MRPL3	-1.09	4.25E-05	1.09E-03	5518.30	not significant
341	DDX56	-1.09	2.38E-04	4.36E-03	3772.73	not significant
342	MBP	-1.09	1.76E-02	9.86E-02	303.98	not significant
343	ATRIP	-1.09	1.21E-02	7.58E-02	586.53	not significant
344	CEP85L	-1.09	1.98E-03	2.09E-02	2543.72	not significant
345	SLC25A44	-1.09	1.59E-03	1.79E-02	1743.21	not significant
346	CCT6A	-1.09	1.06E-06	5.14E-05	19488.56	not significant
347	RSU1	-1.09	4.18E-04	6.62E-03	2533.14	not significant
348	EFTUD2	-1.09	4.12E-06	1.65E-04	8940.44	not significant
349	PLEKHB2	-1.09	5.59E-05	1.35E-03	5902.07	not significant
350	HK2	-1.09	1.49E-03	1.70E-02	2006.06	not significant
351	DNAJC11	-1.09	6.45E-04	9.14E-03	2631.72	not significant
352	ZNF23	-1.09	1.79E-02	9.94E-02	316.54	not significant
353	EIF5A2	-1.09	7.77E-03	5.62E-02	936.31	not significant
354	UTP23	-1.09	6.86E-04	9.61E-03	2278.62	not significant
355	NRF1	-1.09	3.38E-03	3.05E-02	1264.57	not significant
356	MCCC2	-1.09	3.97E-03	3.42E-02	1397.21	not significant
357	FKBP4	-1.09	6.17E-05	1.46E-03	11331.60	not significant
358	CD3EAP	-1.09	4.30E-03	3.64E-02	1152.41	not significant
359	HEXIM1	-1.09	8.83E-04	1.16E-02	2500.86	not significant
360	SRRT	-1.09	4.36E-06	1.74E-04	9690.36	not significant
361	SBDS	-1.09	5.04E-03	4.08E-02	1122.76	not significant
362	RBM27	-1.09	9.16E-04	1.20E-02	3735.36	not significant
363	NFATC3	-1.09	9.96E-05	2.16E-03	6906.46	not significant
364	TOP1	-1.09	8.37E-06	2.90E-04	10377.10	not significant
365	ZNF569	-1.09	7.32E-03	5.37E-02	856.01	not significant
366	HSP90B1	-1.09	4.05E-06	1.63E-04	26220.11	not significant
367	DDX10	-1.09	2.46E-03	2.47E-02	1784.23	not significant
368	NOP14	-1.09	9.03E-05	2.00E-03	5599.57	not significant
369	LIN28B	-1.09	3.29E-04	5.54E-03	2948.97	not significant
370	DUSP3	-1.09	1.49E-02	8.82E-02	550.35	not significant
371	KLHL8	-1.09	2.78E-03	2.67E-02	1621.42	not significant
372	ZCCHC2	-1.09	9.45E-03	6.39E-02	838.25	not significant
373	ZNF207	-1.09	9.46E-06	3.20E-04	8486.59	not significant
374	TNPO1	-1.09	4.43E-05	1.12E-03	11597.32	not significant
375	SKIV2L2	-1.09	3.98E-04	6.40E-03	3562.11	not significant
376	LARP1B	-1.09	8.14E-03	5.78E-02	867.61	not significant
377	PPIF	-1.09	1.18E-04	2.46E-03	5598.09	not significant
378	ACACA	-1.09	7.86E-04	1.07E-02	4978.44	not significant
379	SHOC2	-1.09	1.60E-03	1.80E-02	1947.10	not significant
380	AMPD2	-1.08	6.83E-04	9.59E-03	2871.74	not significant
381	XPO5	-1.08	1.47E-04	2.95E-03	5864.40	not significant
382	COX11	-1.08	3.01E-03	2.83E-02	2066.09	not significant
383	MED13	-1.08	1.71E-03	1.88E-02	6726.67	not significant
384	COX10	-1.08	1.03E-02	6.79E-02	783.30	not significant
385	GPSM2	-1.08	7.73E-03	5.60E-02	951.29	not significant
386	LTV1	-1.08	1.26E-03	1.50E-02	2468.34	not significant
387	ARF3	-1.08	8.42E-06	2.90E-04	9288.04	not significant
388	LRRC58	-1.08	4.36E-04	6.87E-03	8250.86	not significant
389	TTK	-1.08	1.40E-03	1.63E-02	2362.97	not significant
390	ZNFX1	-1.08	1.18E-03	1.43E-02	2496.36	not significant
391	EGLN3	-1.08	1.65E-02	9.43E-02	470.34	not significant
392	NEK2	-1.08	3.22E-03	2.96E-02	1509.25	not significant
393	USP14	-1.08	3.34E-05	8.83E-04	6388.42	not significant
394	PSMD11	-1.08	4.98E-05	1.24E-03	5581.01	not significant
395	COX20	-1.08	4.94E-03	4.02E-02	1223.68	not significant
396	SNX29	-1.08	8.73E-03	6.04E-02	934.77	not significant
397	SOD2	-1.08	2.34E-03	2.40E-02	1819.44	not significant
398	BAG4	-1.08	2.99E-03	2.81E-02	1512.99	not significant
399	YBX1	-1.08	5.71E-04	8.40E-03	47683.48	not significant
400	ZBTB34	-1.08	1.06E-02	6.92E-02	875.54	not significant
401	RRP7A	-1.08	1.41E-04	2.84E-03	6952.31	not significant
402	HIVEP3	-1.08	8.53E-04	1.14E-02	3649.00	not significant
403	SNX2	-1.08	7.02E-03	5.22E-02	1131.01	not significant
404	AAK1	-1.08	6.91E-03	5.15E-02	2189.27	not significant
405	VAPB	-1.08	1.81E-03	1.96E-02	1949.26	not significant
406	ANAPC1	-1.08	1.25E-03	1.50E-02	2825.02	not significant
407	MTMR9	-1.08	7.51E-03	5.49E-02	1080.55	not significant
408	PAICS	-1.08	1.96E-06	8.59E-05	25461.14	not significant
409	KIN	-1.08	1.19E-02	7.53E-02	747.38	not significant
410	ZNF286A	-1.08	8.49E-03	5.94E-02	921.99	not significant
411	ZSCAN5A	-1.08	1.63E-02	9.37E-02	165.67	not significant
412	IMPDH1	-1.08	7.91E-03	5.67E-02	1048.30	not significant
413	GZF1	-1.08	9.76E-03	6.54E-02	872.15	not significant
414	IQSEC1	-1.08	5.30E-03	4.23E-02	2035.82	not significant
415	RASAL1	-1.08	2.47E-03	2.48E-02	2176.68	not significant
416	GABPB1	-1.08	3.31E-03	3.01E-02	1754.98	not significant
417	UBAP2L	-1.08	1.92E-04	3.65E-03	9216.32	not significant
418	CLUH	-1.08	5.90E-05	1.41E-03	6705.73	not significant
419	ATP5J2	-1.08	4.73E-03	3.89E-02	2260.88	not significant
420	EWSR1	-1.08	4.36E-05	1.11E-03	11230.16	not significant
421	CYCS	-1.08	9.87E-05	2.15E-03	10374.45	not significant
422	TRMT10C	-1.08	3.08E-03	2.87E-02	1943.99	not significant
423	SAP130	-1.08	3.21E-03	2.96E-02	1853.29	not significant
424	UBE2L3	-1.08	2.31E-04	4.26E-03	5264.62	not significant
425	PHB	-1.08	1.71E-03	1.88E-02	8714.40	not significant
426	PPP1R8	-1.08	5.87E-04	8.57E-03	3482.15	not significant
427	NOL8	-1.08	2.17E-03	2.25E-02	1963.46	not significant

428	TCOF1	-1.08	5.83E-05	1.40E-03	7850.31	not significant
429	PSMD12	-1.08	5.70E-04	8.40E-03	3585.66	not significant
430	WDR46	-1.08	6.68E-03	5.03E-02	1303.71	not significant
431	TAF15	-1.08	3.52E-04	5.81E-03	4361.89	not significant
432	CALM1	-1.08	2.65E-05	7.46E-04	7843.77	not significant
433	POP1	-1.08	4.22E-03	3.60E-02	1678.82	not significant
434	SEC24A	-1.08	2.76E-03	2.66E-02	2234.42	not significant
435	FAM136A	-1.08	8.89E-04	1.17E-02	4292.39	not significant
436	PPAT	-1.08	6.02E-04	8.71E-03	3672.49	not significant
437	PEA15	-1.08	7.45E-03	5.45E-02	1557.40	not significant
438	ARPC5L	-1.08	4.13E-03	3.54E-02	2025.35	not significant
439	OTUD6B	-1.08	1.90E-03	2.04E-02	2076.64	not significant
440	PPRC1	-1.08	1.56E-03	1.78E-02	3753.14	not significant
441	ARIH1	-1.08	1.08E-03	1.34E-02	2946.27	not significant
442	WDR3	-1.08	2.59E-04	4.65E-03	4028.09	not significant
443	HDLBP	-1.08	3.07E-04	5.30E-03	6532.70	not significant
444	E2F5	-1.08	1.98E-02	1.06E-01	667.85	not significant
445	RC3H1	-1.08	3.41E-03	3.07E-02	1769.29	not significant
446	GSPT1	-1.08	2.11E-05	6.31E-04	9760.60	not significant
447	SLC7A6	-1.08	4.45E-03	3.73E-02	2795.92	not significant
448	STRAP	-1.08	2.46E-04	4.48E-03	6537.00	not significant
449	GIPC1	-1.08	6.43E-03	4.87E-02	1383.37	not significant
450	EDC3	-1.08	3.62E-03	3.21E-02	1598.21	not significant
451	ZMYM4	-1.08	1.23E-03	1.48E-02	3793.29	not significant
452	INO80	-1.08	1.93E-03	2.07E-02	2221.49	not significant
453	UBE3C	-1.08	5.83E-04	8.55E-03	4284.51	not significant
454	DBF4	-1.08	7.28E-04	1.01E-02	3102.93	not significant
455	ZNF117	-1.08	1.55E-02	9.09E-02	1030.19	not significant
456	PROSER1	-1.08	1.08E-03	1.34E-02	4979.43	not significant
457	NCOA1	-1.08	2.88E-03	2.74E-02	2944.90	not significant
458	FARSA	-1.08	1.46E-04	2.94E-03	5985.54	not significant
459	NOP58	-1.08	1.73E-04	3.35E-03	6497.12	not significant
460	TARDBP	-1.08	3.09E-05	8.30E-04	9865.67	not significant
461	KARS	-1.08	9.99E-05	2.16E-03	10790.66	not significant
462	CCDC59	-1.08	2.63E-03	2.58E-02	2051.56	not significant
463	NOP2	-1.08	3.96E-04	6.38E-03	4232.45	not significant
464	UBFD1	-1.08	3.38E-04	5.66E-03	4095.06	not significant
465	SLC27A4	-1.08	7.17E-03	5.29E-02	1282.63	not significant
466	ATF4	-1.08	3.90E-04	6.34E-03	19035.48	not significant
467	SLC25A12	-1.08	5.36E-03	4.26E-02	1602.14	not significant
468	GLRX3	-1.08	3.85E-03	3.35E-02	3233.39	not significant
469	KPNB1	-1.08	9.87E-06	3.32E-04	26241.38	not significant
470	GOT2	-1.08	1.95E-05	6.01E-04	9049.79	not significant
471	PES1	-1.08	8.67E-04	1.15E-02	4487.75	not significant
472	CBWD1	-1.08	2.26E-02	1.17E-01	373.39	not significant
473	SRFBP1	-1.08	1.20E-02	7.55E-02	871.85	not significant
474	CCDC157	-1.08	1.97E-02	1.05E-01	197.63	not significant
475	TGFBR1	-1.08	3.27E-03	2.99E-02	1895.48	not significant
476	FAM208B	-1.08	4.07E-03	3.49E-02	4522.28	not significant
477	CHUK	-1.08	2.42E-03	2.46E-02	2793.10	not significant
478	DPP9	-1.08	4.15E-04	6.58E-03	4043.84	not significant
479	CRLS1	-1.08	4.24E-03	3.60E-02	2239.09	not significant
480	API5	-1.08	7.60E-05	1.73E-03	7561.31	not significant
481	XPOT	-1.08	1.65E-05	5.24E-04	11123.04	not significant
482	CDC123	-1.08	5.94E-04	8.65E-03	4940.40	not significant
483	DHX37	-1.08	2.09E-04	3.92E-03	5219.77	not significant
484	APOOL	-1.08	1.20E-02	7.57E-02	872.24	not significant
485	TRIAP1	-1.08	7.71E-03	5.59E-02	1899.63	not significant
486	E2F4	-1.08	2.08E-04	3.90E-03	6401.29	not significant
487	PGAM1	-1.08	1.65E-03	1.85E-02	2947.76	not significant
488	CCT2	-1.08	9.02E-05	2.00E-03	17477.63	not significant
489	SORD	-1.08	9.30E-03	6.31E-02	1112.70	not significant
490	FAM175B	-1.08	7.61E-03	5.54E-02	1335.68	not significant
491	DHX9	-1.08	7.45E-06	2.65E-04	20862.63	not significant
492	GAR1	-1.08	9.37E-03	6.35E-02	2394.70	not significant
493	TSR1	-1.08	2.72E-04	4.84E-03	4701.91	not significant
494	PFKFB3	-1.08	8.50E-03	5.94E-02	1238.39	not significant
495	PA2G4	-1.08	2.25E-05	6.67E-04	23801.58	not significant
496	DTWD2	-1.08	2.04E-02	1.08E-01	576.77	not significant
497	C15orf39	-1.08	2.82E-03	2.70E-02	1977.41	not significant
498	POFUT1	-1.08	1.03E-03	1.30E-02	3867.87	not significant
499	PITPNB	-1.08	6.33E-03	4.82E-02	1528.81	not significant
500	DNAJC2	-1.08	4.41E-03	3.71E-02	2303.46	not significant
501	ANKRD13C	-1.08	8.48E-03	5.94E-02	1216.02	not significant
502	NDUFA12	-1.08	3.11E-03	2.89E-02	3005.03	not significant
503	LARP4B	-1.08	3.76E-04	6.18E-03	5457.97	not significant
504	TNFAIP8L1	-1.08	2.40E-02	1.21E-01	371.62	not significant
505	LYRM7	-1.08	1.62E-03	1.82E-02	2778.00	not significant
506	SNX11	-1.08	1.98E-02	1.06E-01	725.86	not significant
507	C1orf131	-1.08	1.33E-02	8.14E-02	1052.12	not significant
508	TGS1	-1.08	9.77E-04	1.26E-02	3104.82	not significant
509	NUP93	-1.08	1.07E-03	1.34E-02	4099.77	not significant
510	NCOA5	-1.08	1.05E-03	1.31E-02	4321.65	not significant
511	SNRNP48	-1.08	8.16E-04	1.10E-02	3933.93	not significant
512	MRTO4	-1.08	1.57E-03	1.78E-02	5262.39	not significant
513	SHQ1	-1.08	7.36E-04	1.02E-02	4270.72	not significant
514	IPP	-1.08	2.30E-02	1.18E-01	470.00	not significant
515	MRPL17	-1.08	5.73E-03	4.49E-02	2178.73	not significant

516	ZNF267	-1.08	1.68E-02	9.56E-02	846.51	not significant
517	TRIP13	-1.08	1.88E-03	2.02E-02	2625.91	not significant
518	RACGAP1	-1.08	3.18E-04	5.41E-03	5440.05	not significant
519	GNL3L	-1.07	2.89E-03	2.74E-02	2489.82	not significant
520	ASPM	-1.07	2.64E-02	1.29E-01	5947.86	not significant
521	EAF1	-1.07	2.51E-03	2.51E-02	2355.97	not significant
522	ZNF343	-1.07	1.91E-02	1.04E-01	700.40	not significant
523	SRF	-1.07	1.87E-03	2.02E-02	3297.27	not significant
524	RAB10	-1.07	1.19E-04	2.47E-03	7294.15	not significant
525	TIMM21	-1.07	8.50E-03	5.94E-02	1286.89	not significant
526	TACC1	-1.07	2.05E-03	2.15E-02	8973.71	not significant
527	CRK	-1.07	1.37E-02	8.30E-02	947.85	not significant
528	IPO11	-1.07	1.45E-02	8.63E-02	983.05	not significant
529	FADD	-1.07	9.66E-03	6.51E-02	1331.21	not significant
530	NSUN2	-1.07	2.56E-04	4.62E-03	6271.67	not significant
531	PPP6R3	-1.07	5.97E-04	8.68E-03	5527.02	not significant
532	AK2	-1.07	9.32E-05	2.05E-03	10493.04	not significant
533	METTL13	-1.07	2.81E-03	2.69E-02	2738.50	not significant
534	PUS1	-1.07	3.76E-03	3.28E-02	2624.97	not significant
535	ZNF148	-1.07	2.45E-03	2.47E-02	2634.77	not significant
536	EIF5B	-1.07	4.19E-04	6.62E-03	7503.90	not significant
537	DDI2	-1.07	2.46E-02	1.24E-01	569.02	not significant
538	WDR12	-1.07	5.29E-03	4.22E-02	2316.13	not significant
539	TRUB2	-1.07	1.33E-02	8.12E-02	1240.72	not significant
540	PLEKHF1	-1.07	1.06E-02	6.92E-02	1233.43	not significant
541	RRS1	-1.07	3.73E-03	3.27E-02	3016.62	not significant
542	RRN3	-1.07	2.54E-03	2.52E-02	2517.65	not significant
543	EIF4A3	-1.07	7.07E-04	9.87E-03	6864.09	not significant
544	TNPO3	-1.07	4.68E-04	7.29E-03	6271.54	not significant
545	WASF1	-1.07	5.11E-03	4.11E-02	1754.44	not significant
546	MAP3K2	-1.07	4.77E-03	3.91E-02	2536.83	not significant
547	ELMOD2	-1.07	5.66E-03	4.45E-02	1656.98	not significant
548	SNRPD3	-1.07	3.10E-04	5.33E-03	7403.28	not significant
549	SLC19A2	-1.07	2.22E-02	1.15E-01	633.21	not significant
550	AFF3	-1.07	1.24E-02	7.73E-02	1317.49	not significant
551	EIF4G1	-1.07	5.01E-05	1.24E-03	25806.46	not significant
552	PPP2CA	-1.07	4.58E-04	7.16E-03	11719.25	not significant
553	ARHGDIA	-1.07	4.11E-04	6.55E-03	27613.93	not significant
554	TOB2	-1.07	7.91E-03	5.67E-02	1482.36	not significant
555	KIF2C	-1.07	1.17E-03	1.42E-02	3758.95	not significant
556	EIF4ENIF1	-1.07	8.79E-03	6.07E-02	1394.00	not significant
557	PPP1CC	-1.07	1.28E-04	2.62E-03	9564.27	not significant
558	PRR14L	-1.07	1.12E-02	7.21E-02	2478.14	not significant
559	ZNF271	-1.07	7.11E-03	5.26E-02	1589.79	not significant
560	CCRN4L	-1.07	2.57E-02	1.27E-01	324.28	not significant
561	DNAJA1	-1.07	2.07E-04	3.89E-03	14616.57	not significant
562	ZC3H8	-1.07	7.53E-03	5.50E-02	1571.57	not significant
563	NPTN	-1.07	9.85E-03	6.57E-02	1353.86	not significant
564	PSMF1	-1.07	2.50E-04	4.54E-03	7427.04	not significant
565	PPP2R5E	-1.07	2.70E-03	2.62E-02	3256.40	not significant
566	TARS	-1.07	1.92E-04	3.65E-03	8518.12	not significant
567	WDR89	-1.07	1.13E-02	7.22E-02	1297.29	not significant
568	MAP2K4	-1.07	5.87E-03	4.57E-02	1775.12	not significant
569	ATP5B	-1.07	3.17E-04	5.40E-03	39110.47	not significant
570	CEP70	-1.07	1.09E-02	7.08E-02	1462.61	not significant
571	EIF2AK2	-1.07	6.33E-03	4.82E-02	3366.36	not significant
572	SMC4	-1.07	4.78E-04	7.40E-03	12717.90	not significant
573	GNL3	-1.07	2.88E-04	5.07E-03	6061.99	not significant
574	MTHFD1L	-1.07	2.05E-03	2.15E-02	3098.19	not significant
575	ILF2	-1.07	8.75E-04	1.15E-02	17947.22	not significant
576	ANKRD40	-1.07	1.60E-03	1.80E-02	3248.43	not significant
577	SLA2	-1.07	1.81E-03	1.96E-02	4951.17	not significant
578	TAF3	-1.07	8.50E-03	5.94E-02	1665.55	not significant
579	TFAM	-1.07	1.29E-03	1.53E-02	4222.00	not significant
580	YKT6	-1.07	5.94E-04	8.65E-03	5260.58	not significant
581	PPP1R10	-1.07	1.63E-02	9.37E-02	901.94	not significant
582	CALM2	-1.07	7.36E-04	1.02E-02	18340.79	not significant
583	TPM3	-1.07	7.19E-05	1.66E-03	32376.64	not significant
584	MAD2L1BP	-1.07	2.35E-02	1.20E-01	727.81	not significant
585	PUS7	-1.07	4.22E-03	3.60E-02	2220.75	not significant
586	PGAM5	-1.07	3.05E-04	5.28E-03	5812.84	not significant
587	LAS1L	-1.07	3.04E-03	2.85E-02	2659.98	not significant
588	PPP2R5D	-1.07	2.36E-03	2.41E-02	3560.77	not significant
589	COG8	-1.07	2.50E-02	1.25E-01	567.12	not significant
590	PDLIM5	-1.07	1.54E-02	9.05E-02	1053.11	not significant
591	EIF2S2	-1.07	9.38E-04	1.22E-02	7242.18	not significant
592	RCC1	-1.07	9.33E-04	1.21E-02	5751.59	not significant
593	KCTD5	-1.07	7.18E-03	5.29E-02	1856.02	not significant
594	ZNF398	-1.07	1.69E-02	9.57E-02	965.47	not significant
595	DDX52	-1.07	4.83E-03	3.95E-02	2189.21	not significant
596	STIP1	-1.07	4.43E-05	1.12E-03	15838.33	not significant
597	UTP15	-1.07	1.07E-02	6.98E-02	1404.30	not significant
598	DDX1	-1.07	1.31E-03	1.56E-02	4534.42	not significant
599	RPRD1B	-1.07	1.96E-03	2.08E-02	3382.67	not significant
600	DHX15	-1.07	7.18E-05	1.66E-03	13020.48	not significant
601	NIFK	-1.07	3.61E-03	3.21E-02	2869.51	not significant
602	POLDIP2	-1.07	1.05E-02	6.88E-02	1535.10	not significant
603	SLK	-1.07	3.62E-03	3.21E-02	3357.07	not significant

604	CUL3	-1.07	1.07E-03	1.34E-02	3952.25	not significant
605	LSP1	-1.07	1.78E-03	1.94E-02	3818.91	not significant
606	PAFAH1B1	-1.07	2.63E-04	4.70E-03	7358.81	not significant
607	FBXL18	-1.07	1.27E-02	7.85E-02	1246.51	not significant
608	MDM2	-1.07	6.40E-04	9.11E-03	6259.07	not significant
609	RRAS2	-1.07	2.31E-02	1.19E-01	669.38	not significant
610	TAF5L	-1.07	4.32E-03	3.65E-02	2252.65	not significant
611	UBA1	-1.07	3.17E-04	5.40E-03	6792.60	not significant
612	KPNA6	-1.07	2.01E-03	2.12E-02	3362.04	not significant
613	MTIF2	-1.07	2.03E-02	1.08E-01	830.25	not significant
614	RBM14	-1.07	1.13E-03	1.39E-02	5160.87	not significant
615	BCLAF1	-1.07	6.94E-04	9.70E-03	12305.84	not significant
616	DCTN5	-1.07	1.10E-03	1.36E-02	4805.02	not significant
617	G2E3	-1.07	1.43E-02	8.54E-02	1271.55	not significant
618	CSE1L	-1.07	2.58E-04	4.63E-03	9562.44	not significant
619	ZHX3	-1.07	1.90E-02	1.03E-01	1116.10	not significant
620	AHSA1	-1.07	1.34E-03	1.58E-02	8871.65	not significant
621	FLT3LG	-1.07	2.45E-02	1.23E-01	646.57	not significant
622	CDC27	-1.07	1.08E-03	1.34E-02	4231.70	not significant
623	ZNF468	-1.07	1.63E-02	9.37E-02	1018.24	not significant
624	JMJD6	-1.07	1.09E-02	7.06E-02	1412.58	not significant
625	AURKB	-1.07	5.91E-03	4.59E-02	3108.90	not significant
626	MED1	-1.07	5.06E-03	4.09E-02	7599.71	not significant
627	WDR7	-1.07	8.95E-03	6.16E-02	1991.47	not significant
628	FAM35A	-1.07	1.13E-02	7.22E-02	1484.26	not significant
629	DBF4B	-1.07	1.29E-02	7.97E-02	1348.39	not significant
630	NUDC	-1.07	2.63E-03	2.58E-02	8556.83	not significant
631	ZNF350	-1.07	2.65E-02	1.29E-01	231.31	not significant
632	SPRYD3	-1.07	2.09E-02	1.10E-01	861.47	not significant
633	POLR2C	-1.07	3.57E-03	3.18E-02	4251.45	not significant
634	TOR1AIP2	-1.07	7.06E-03	5.24E-02	2035.30	not significant
635	FBXW2	-1.07	4.61E-03	3.83E-02	2846.34	not significant
636	MRPL19	-1.07	3.54E-03	3.17E-02	2686.36	not significant
637	ENO1	-1.07	1.27E-03	1.51E-02	107675.50	not significant
638	USP10	-1.07	1.05E-03	1.32E-02	4303.36	not significant
639	SBDSP1	-1.07	2.96E-02	1.39E-01	327.28	not significant
640	FAM172A	-1.07	1.55E-02	9.07E-02	1218.41	not significant
641	MARS	-1.07	1.25E-04	2.58E-03	12505.90	not significant
642	BORA	-1.07	1.52E-02	8.96E-02	1142.73	not significant
643	UBP1	-1.07	1.24E-03	1.49E-02	4172.95	not significant
644	GTF2A1	-1.07	9.60E-04	1.24E-02	4705.09	not significant
645	RPAP3	-1.07	2.84E-03	2.71E-02	3098.08	not significant
646	SEPHS2	-1.07	3.71E-03	3.26E-02	3078.10	not significant
647	TRIT1	-1.07	1.80E-02	9.99E-02	1117.18	not significant
648	SUV39H2	-1.07	1.26E-02	7.81E-02	1706.47	not significant
649	WWP1	-1.07	9.09E-03	6.21E-02	1735.23	not significant
650	VPS53	-1.07	7.20E-03	5.30E-02	1818.87	not significant
651	SMG7	-1.07	1.74E-03	1.91E-02	6425.68	not significant
652	TEX2	-1.07	1.10E-02	7.10E-02	1662.79	not significant
653	RAB11FIP2	-1.07	1.48E-02	8.77E-02	1218.56	not significant
654	MARK3	-1.07	6.24E-03	4.78E-02	2499.87	not significant
655	KNSTRN	-1.07	1.66E-02	9.50E-02	1113.53	not significant
656	EYA3	-1.07	1.13E-02	7.22E-02	1752.92	not significant
657	ZNF551	-1.07	1.83E-02	1.01E-01	1280.64	not significant
658	PSMC2	-1.07	1.37E-03	1.60E-02	5096.78	not significant
659	CHD1	-1.07	3.59E-03	3.20E-02	4456.25	not significant
660	NOP56	-1.07	4.81E-05	1.20E-03	15971.29	not significant
661	ASB6	-1.07	1.82E-02	1.00E-01	1071.01	not significant
662	AMMECR1L	-1.07	8.26E-03	5.84E-02	1860.69	not significant
663	BYSL	-1.07	4.66E-03	3.85E-02	2771.78	not significant
664	NCBP2	-1.07	9.98E-04	1.28E-02	6095.32	not significant
665	C12orf66	-1.07	3.10E-02	1.43E-01	445.94	not significant
666	CBX6	-1.07	7.52E-03	5.49E-02	2287.05	not significant
667	PTPN11	-1.07	1.04E-03	1.31E-02	12519.58	not significant
668	MRPL51	-1.07	1.23E-02	7.67E-02	3352.05	not significant
669	RSBN1L	-1.07	1.27E-02	7.86E-02	1428.53	not significant
670	SENP5	-1.07	7.08E-03	5.24E-02	2492.35	not significant
671	ALKBH8	-1.07	2.28E-02	1.18E-01	866.34	not significant
672	ARHGEF6	-1.07	1.08E-03	1.34E-02	8877.78	not significant
673	RRP15	-1.07	8.45E-03	5.94E-02	1792.64	not significant
674	PPP2R4	-1.07	4.52E-03	3.77E-02	3919.31	not significant
675	KIF5B	-1.07	1.03E-03	1.30E-02	8318.38	not significant
676	ANAPC10	-1.07	2.94E-02	1.38E-01	637.00	not significant
677	LETM1	-1.07	1.08E-03	1.34E-02	4914.76	not significant
678	POLR3A	-1.07	6.72E-03	5.04E-02	2735.11	not significant
679	URB2	-1.07	3.64E-03	3.22E-02	3217.77	not significant
680	RLF	-1.07	1.71E-02	9.63E-02	1200.92	not significant
681	PRPF4	-1.07	3.91E-03	3.38E-02	2948.17	not significant
682	TRIP12	-1.07	4.64E-03	3.84E-02	8775.33	not significant
683	PDHA1	-1.07	4.92E-03	4.00E-02	3739.89	not significant
684	RQCD1	-1.07	1.57E-03	1.78E-02	5722.18	not significant
685	CABIN1	-1.07	2.45E-03	2.47E-02	4117.98	not significant
686	UBC	-1.07	5.63E-04	8.34E-03	11633.27	not significant
687	RNF11	-1.07	1.00E-02	6.64E-02	2102.65	not significant
688	DYNC1LI1	-1.07	8.25E-03	5.83E-02	2139.90	not significant
689	TBL1XR1	-1.07	5.06E-04	7.73E-03	7267.29	not significant
690	C7orf31	-1.07	3.29E-02	1.48E-01	453.46	not significant
691	BAIAP2	-1.07	3.13E-02	1.44E-01	504.62	not significant

692	CENPL	-1.07	1.88E-02	1.03E-01	1040.75	not significant
693	POLR2B	-1.07	6.58E-04	9.32E-03	7700.52	not significant
694	SMAD5	-1.07	3.20E-02	1.46E-01	494.42	not significant
695	GOSR1	-1.07	8.62E-03	6.01E-02	1963.20	not significant
696	PRKACA	-1.07	8.01E-03	5.71E-02	3509.63	not significant
697	GNL2	-1.07	6.81E-03	5.09E-02	2580.62	not significant
698	NRBP1	-1.07	5.15E-03	4.13E-02	2463.57	not significant
699	DDX46	-1.07	2.91E-03	2.76E-02	5982.80	not significant
700	SSH3	-1.07	1.64E-02	9.39E-02	131.64	not significant
701	TIMM23	-1.07	2.20E-02	1.15E-01	182.83	not significant
702	RHOBTB2	-1.07	2.61E-02	1.28E-01	210.63	not significant
703	RNASEH1	-1.07	1.12E-02	7.21E-02	1681.92	not significant
704	PAPD5	-1.07	1.81E-02	1.00E-01	1175.96	not significant
705	SPTY2D1	-1.07	7.80E-03	5.63E-02	2051.92	not significant
706	POLR2D	-1.07	2.58E-03	2.55E-02	4010.82	not significant
707	PRPF8	-1.07	4.46E-03	3.73E-02	24672.30	not significant
708	SMU1	-1.07	2.38E-03	2.43E-02	3794.09	not significant
709	ID2	-1.07	2.48E-02	1.24E-01	189.39	not significant
710	ZDHHC3	-1.07	8.48E-03	5.94E-02	2589.89	not significant
711	NUS1	-1.07	5.70E-03	4.48E-02	2450.45	not significant
712	UTP20	-1.07	5.57E-03	4.39E-02	5303.57	not significant
713	PSMC5	-1.07	1.36E-03	1.59E-02	8608.39	not significant
714	YARS	-1.07	7.13E-04	9.93E-03	11744.72	not significant
715	ANKS1A	-1.06	2.83E-02	1.35E-01	844.74	not significant
716	ALDH1B1	-1.06	2.74E-02	1.32E-01	204.39	not significant
717	SUPT5H	-1.06	1.33E-03	1.57E-02	4823.77	not significant
718	LSM1	-1.06	1.24E-02	7.74E-02	2237.45	not significant
719	RARS	-1.06	7.15E-03	5.28E-02	2698.85	not significant
720	UCHL3	-1.06	2.38E-02	1.21E-01	1209.97	not significant
721	HMOX2	-1.06	1.79E-02	9.94E-02	1698.09	not significant
722	PSMC3	-1.06	3.54E-03	3.17E-02	8049.65	not significant
723	DENR	-1.06	1.81E-03	1.96E-02	9641.37	not significant
724	KIF11	-1.06	6.75E-04	9.49E-03	7726.31	not significant
725	UBE2G1	-1.06	2.83E-03	2.71E-02	3789.35	not significant
726	LOC100506844	-1.06	2.64E-02	1.29E-01	1191.86	not significant
727	TCP1	-1.06	5.04E-04	7.72E-03	18865.75	not significant
728	NSA2	-1.06	4.63E-03	3.84E-02	3488.07	not significant
729	LRRC61	-1.06	7.98E-03	5.70E-02	2601.56	not significant
730	TAF2	-1.06	6.12E-03	4.71E-02	3169.45	not significant
731	DDX27	-1.06	2.84E-03	2.71E-02	3699.83	not significant
732	INCENP	-1.06	2.45E-03	2.47E-02	4570.05	not significant
733	GAPVD1	-1.06	1.05E-02	6.88E-02	2215.15	not significant
734	PREPL	-1.06	6.33E-03	4.82E-02	2636.84	not significant
735	LARP1	-1.06	5.09E-03	4.10E-02	19703.55	not significant
736	MRPS35	-1.06	5.98E-03	4.63E-02	2805.18	not significant
737	43710_4150	-1.06	3.02E-04	5.25E-03	11369.11	not significant
738	DTX1	-1.06	1.74E-04	3.35E-03	15248.83	not significant
739	DESI2	-1.06	2.70E-03	2.62E-02	3748.02	not significant
740	KTN1	-1.06	4.46E-03	3.74E-02	7784.29	not significant
741	C3orf62	-1.06	3.58E-02	1.58E-01	388.88	not significant
742	BCCIP	-1.06	5.03E-03	4.08E-02	4533.37	not significant
743	CSTF2	-1.06	1.83E-02	1.01E-01	1263.46	not significant
744	PRR13	-1.06	8.77E-03	6.06E-02	3163.13	not significant
745	FBXO28	-1.06	1.55E-02	9.09E-02	1504.33	not significant
746	MRPS23	-1.06	1.07E-02	6.96E-02	2890.95	not significant
747	ASCC3	-1.06	5.31E-03	4.23E-02	6141.31	not significant
748	FLNB	-1.06	1.67E-02	9.52E-02	3873.98	not significant
749	ZNF138	-1.06	2.50E-02	1.25E-01	1154.47	not significant
750	RAPGEF5	-1.06	1.81E-02	1.00E-01	1855.77	not significant
751	PSMD6	-1.06	7.12E-03	5.26E-02	3135.33	not significant
752	ZNF614	-1.06	2.41E-02	1.22E-01	1341.28	not significant
753	TLR9	-1.06	3.29E-02	1.48E-01	278.35	not significant
754	UMPS	-1.06	1.21E-02	7.58E-02	1989.17	not significant
755	LTB	-1.06	3.09E-02	1.43E-01	850.96	not significant
756	RCL1	-1.06	2.28E-02	1.18E-01	1180.88	not significant
757	SRSF10	-1.06	1.91E-02	1.04E-01	1452.25	not significant
758	RUVBL1	-1.06	5.74E-03	4.50E-02	4239.58	not significant
759	FAM91A1	-1.06	5.52E-03	4.36E-02	3785.11	not significant
760	SERHL2	-1.06	3.66E-02	1.59E-01	429.33	not significant
761	MICAL3	-1.06	3.40E-02	1.52E-01	634.37	not significant
762	KLHDC10	-1.06	2.54E-02	1.26E-01	1212.89	not significant
763	DDB1	-1.06	3.52E-04	5.81E-03	15457.96	not significant
764	LMAN2L	-1.06	2.71E-02	1.31E-01	879.58	not significant
765	RLIM	-1.06	1.34E-02	8.19E-02	2812.48	not significant
766	ZNF800	-1.06	2.08E-02	1.10E-01	1605.56	not significant
767	CRKL	-1.06	1.37E-03	1.60E-02	6754.79	not significant
768	FAR1	-1.06	2.30E-03	2.37E-02	4885.23	not significant
769	CLTC	-1.06	2.04E-03	2.14E-02	18043.46	not significant
770	NOMO1	-1.06	2.75E-02	1.32E-01	956.79	not significant
771	CCDC88A	-1.06	1.05E-02	6.91E-02	3415.24	not significant
772	DUSP7	-1.06	1.59E-02	9.23E-02	1672.10	not significant
773	CAPZA1	-1.06	8.74E-04	1.15E-02	11948.28	not significant
774	MEMO1	-1.06	3.52E-02	1.56E-01	655.32	not significant
775	MRPL47	-1.06	1.99E-02	1.06E-01	1606.01	not significant
776	TYW1	-1.06	2.84E-02	1.35E-01	924.49	not significant
777	DDX28	-1.06	2.96E-02	1.39E-01	927.68	not significant
778	HMG20A	-1.06	1.23E-02	7.66E-02	1866.64	not significant
779	C8orf33	-1.06	3.75E-03	3.28E-02	7769.99	not significant

780	FCF1	-1.06	9.76E-03	6.54E-02	2524.80	not significant
781	DCXR	-1.06	2.96E-02	1.39E-01	1433.28	not significant
782	TSSC4	-1.06	2.78E-02	1.33E-01	1101.47	not significant
783	INTS12	-1.06	3.15E-02	1.44E-01	787.26	not significant
784	PIK3C2A	-1.06	2.92E-02	1.38E-01	1005.51	not significant
785	PRELID1	-1.06	1.21E-02	7.58E-02	4759.57	not significant
786	CLASP2	-1.06	1.03E-02	6.83E-02	2372.50	not significant
787	FKBP1A	-1.06	1.35E-03	1.59E-02	13550.41	not significant
788	EIF2AK4	-1.06	1.00E-02	6.64E-02	2443.60	not significant
789	SLC39A14	-1.06	4.19E-03	3.57E-02	4778.72	not significant
790	HNRNPC	-1.06	1.43E-03	1.65E-02	21780.92	not significant
791	PPP1R12A	-1.06	3.25E-03	2.98E-02	5350.36	not significant
792	FTSJ3	-1.06	1.70E-03	1.88E-02	6090.38	not significant
793	PTGES3	-1.06	6.63E-04	9.35E-03	25522.88	not significant
794	FOXN2	-1.06	1.02E-02	6.76E-02	2821.65	not significant
795	AEBP2	-1.06	6.45E-03	4.88E-02	2898.89	not significant
796	PPP4R1	-1.06	3.91E-03	3.38E-02	3957.84	not significant
797	CDV3	-1.06	1.04E-03	1.31E-02	10740.39	not significant
798	ARHGAP5	-1.06	1.63E-02	9.37E-02	3010.26	not significant
799	SPAG5	-1.06	2.78E-03	2.67E-02	5111.75	not significant
800	HSF1	-1.06	1.25E-02	7.78E-02	2315.15	not significant
801	BRMS1	-1.06	1.34E-02	8.17E-02	3190.44	not significant
802	RNF219	-1.06	1.37E-02	8.28E-02	2016.75	not significant
803	LRRFIP2	-1.06	2.37E-02	1.20E-01	1233.84	not significant
804	RABL3	-1.06	2.21E-02	1.15E-01	1397.96	not significant
805	NAE1	-1.06	6.78E-03	5.08E-02	3543.02	not significant
806	HSPA9	-1.06	4.11E-04	6.55E-03	20295.31	not significant
807	NUDT5	-1.06	1.13E-02	7.23E-02	2823.73	not significant
808	NUP35	-1.06	3.08E-02	1.43E-01	917.14	not significant
809	SUPT6H	-1.06	2.66E-03	2.60E-02	6023.57	not significant
810	EIF2B3	-1.06	2.14E-02	1.13E-01	1423.48	not significant
811	DEDD	-1.06	1.70E-02	9.61E-02	1845.19	not significant
812	RDH10	-1.06	1.71E-02	9.66E-02	2106.35	not significant
813	SRPK1	-1.06	2.73E-03	2.63E-02	6763.37	not significant
814	FAM168B	-1.06	1.78E-03	1.94E-02	7240.70	not significant
815	NCOR1	-1.06	9.95E-03	6.62E-02	8123.91	not significant
816	PIK3R1	-1.06	3.99E-03	3.44E-02	5669.66	not significant
817	CHTF8	-1.06	1.94E-03	2.07E-02	5279.41	not significant
818	SPATA2	-1.06	2.76E-02	1.33E-01	1101.81	not significant
819	CDK12	-1.06	1.14E-02	7.25E-02	4976.34	not significant
820	CREBBP	-1.06	1.79E-02	9.94E-02	3559.70	not significant
821	XPO4	-1.06	1.63E-02	9.37E-02	3045.29	not significant
822	C9orf78	-1.06	5.39E-03	4.27E-02	6594.11	not significant
823	GART	-1.06	2.59E-03	2.56E-02	6196.78	not significant
824	ZNF525	-1.06	3.53E-02	1.56E-01	844.78	not significant
825	NCL	-1.06	2.54E-03	2.53E-02	60155.46	not significant
826	MGA	-1.06	1.97E-02	1.06E-01	3183.09	not significant
827	DLAT	-1.06	2.79E-02	1.34E-01	1201.40	not significant
828	CMC2	-1.06	2.50E-02	1.25E-01	1604.22	not significant
829	HN1L	-1.06	4.66E-03	3.85E-02	5108.57	not significant
830	CORO1C	-1.06	1.81E-03	1.96E-02	6017.51	not significant
831	CCNJ	-1.06	3.02E-02	1.41E-01	1031.05	not significant
832	OGFOD1	-1.06	8.67E-03	6.02E-02	2652.71	not significant
833	RABEP1	-1.06	6.16E-03	4.73E-02	4341.97	not significant
834	DCAF7	-1.06	1.99E-03	2.10E-02	12153.44	not significant
835	NANP	-1.06	2.61E-02	1.28E-01	1270.70	not significant
836	MTCH2	-1.06	6.23E-03	4.78E-02	3890.73	not significant
837	LNX2	-1.06	3.28E-02	1.48E-01	875.57	not significant
838	NSD1	-1.06	1.63E-02	9.37E-02	4469.27	not significant
839	ZNF74	-1.06	2.49E-02	1.24E-01	1233.92	not significant
840	POMP	-1.06	5.19E-03	4.16E-02	5218.66	not significant
841	GNPNAT1	-1.06	7.69E-03	5.58E-02	3233.58	not significant
842	ESRRA	-1.06	2.84E-02	1.35E-01	1261.09	not significant
843	SAMD8	-1.06	3.54E-02	1.57E-01	811.28	not significant
844	ENC1	-1.06	3.74E-02	1.62E-01	752.18	not significant
845	CNN2	-1.06	6.29E-03	4.81E-02	3639.82	not significant
846	ESPL1	-1.06	7.11E-03	5.26E-02	4665.46	not significant
847	TTLL12	-1.06	2.56E-03	2.53E-02	7439.27	not significant
848	PCGF5	-1.06	3.81E-03	3.32E-02	5728.93	not significant
849	CWF19L1	-1.06	2.35E-02	1.20E-01	1789.92	not significant
850	DNAJB6	-1.06	1.71E-03	1.88E-02	8289.09	not significant
851	IDH3A	-1.06	8.23E-03	5.83E-02	3231.39	not significant
852	AATF	-1.06	6.13E-03	4.72E-02	4863.01	not significant
853	PRPF19	-1.06	2.96E-03	2.79E-02	11249.78	not significant
854	DNMT3B	-1.06	1.67E-02	9.52E-02	2475.14	not significant
855	AAMP	-1.06	8.70E-03	6.04E-02	3699.19	not significant
856	MRPL4	-1.06	1.36E-02	8.25E-02	4430.39	not significant
857	PDCD2	-1.06	1.82E-02	1.01E-01	3053.54	not significant
858	CD300A	-1.06	9.52E-03	6.43E-02	3935.80	not significant
859	USPL1	-1.06	1.43E-02	8.54E-02	2039.87	not significant
860	LMNB2	-1.06	2.21E-03	2.29E-02	11026.18	not significant
861	ZNF202	-1.06	3.05E-02	1.42E-01	1126.60	not significant
862	ZNF146	-1.06	6.41E-03	4.86E-02	7223.50	not significant
863	PGM2	-1.06	1.06E-02	6.92E-02	2733.92	not significant
864	BAZ1A	-1.06	8.10E-03	5.76E-02	5515.87	not significant
865	FH	-1.06	1.29E-02	7.93E-02	3096.96	not significant
866	SF3A3	-1.06	2.10E-03	2.18E-02	7575.87	not significant
867	HDAC8	-1.06	3.08E-02	1.42E-01	191.78	not significant

868	UBXN7	-1.06	3.37E-02	1.51E-01	1211.92	not significant
869	MAP3K4	-1.06	1.99E-02	1.06E-01	1712.69	not significant
870	DENND4A	-1.06	4.47E-02	1.83E-01	563.08	not significant
871	SF3B4	-1.06	3.60E-02	1.58E-01	885.07	not significant
872	ZFP91	-1.06	8.95E-03	6.16E-02	3687.57	not significant
873	CSNK2A1	-1.06	3.75E-03	3.28E-02	5527.40	not significant
874	PLAC8	-1.06	3.29E-02	1.48E-01	214.60	not significant
875	PRR5	-1.06	4.48E-02	1.83E-01	449.63	not significant
876	NOL7	-1.06	1.53E-02	9.02E-02	2217.40	not significant
877	RUVBL2	-1.06	1.45E-02	8.62E-02	5926.71	not significant
878	RRP1B	-1.06	4.72E-03	3.89E-02	5245.76	not significant
879	RPGRIP1L	-1.06	4.54E-02	1.85E-01	426.70	not significant
880	RNF4	-1.06	8.29E-03	5.85E-02	4216.61	not significant
881	SMARCA5	-1.06	2.08E-03	2.17E-02	11077.32	not significant
882	RIOK2	-1.06	2.16E-02	1.13E-01	1583.77	not significant
883	NKRF	-1.06	2.84E-02	1.35E-01	1290.55	not significant
884	UBAP1	-1.06	2.67E-02	1.30E-01	1568.62	not significant
885	UQCC1	-1.06	1.33E-02	8.12E-02	2365.96	not significant
886	ELP4	-1.06	3.82E-02	1.65E-01	881.67	not significant
887	JUN	-1.06	3.28E-02	1.48E-01	196.50	not significant
888	NARS2	-1.06	2.27E-02	1.17E-01	1584.39	not significant
889	CINP	-1.06	4.25E-02	1.77E-01	958.33	not significant
890	PROSC	-1.06	8.09E-03	5.75E-02	5715.10	not significant
891	VAPA	-1.06	4.00E-03	3.44E-02	6724.65	not significant
892	ECHDC1	-1.06	7.19E-03	5.29E-02	3599.45	not significant
893	PSMD9	-1.06	2.25E-02	1.17E-01	2275.33	not significant
894	UQCRFS1	-1.06	1.77E-02	9.89E-02	2810.06	not significant
895	C16orf72	-1.06	2.09E-02	1.10E-01	1904.31	not significant
896	AGPS	-1.06	1.34E-02	8.17E-02	3718.93	not significant
897	MFAP1	-1.06	1.90E-02	1.03E-01	1838.79	not significant
898	ZC3H7B	-1.06	3.28E-03	3.00E-02	6441.45	not significant
899	RABEPK	-1.06	3.70E-02	1.61E-01	1105.54	not significant
900	BAZ1B	-1.06	1.49E-02	8.82E-02	3079.32	not significant
901	LPP	-1.06	3.92E-02	1.67E-01	1526.28	not significant
902	MTOR	-1.06	2.19E-02	1.14E-01	4675.82	not significant
903	ALDOA	-1.06	7.66E-03	5.57E-02	32627.54	not significant
904	DCAF6	-1.06	3.37E-02	1.51E-01	1160.43	not significant
905	TARBP1	-1.06	1.44E-02	8.62E-02	2564.03	not significant
906	SOCS4	-1.06	1.86E-02	1.02E-01	3437.32	not significant
907	SLC25A32	-1.06	1.04E-02	6.87E-02	3400.77	not significant
908	PLK3	-1.06	4.65E-02	1.87E-01	595.17	not significant
909	PURA	-1.06	2.79E-02	1.34E-01	1447.79	not significant
910	SPATA13	-1.06	1.48E-02	8.77E-02	3452.96	not significant
911	NSF	-1.06	2.83E-02	1.35E-01	1358.47	not significant
912	STK4	-1.06	8.21E-03	5.82E-02	7964.21	not significant
913	C10orf54	-1.06	2.00E-02	1.07E-01	1914.85	not significant
914	L3MBTL2	-1.06	1.96E-02	1.05E-01	2090.29	not significant
915	EI24	-1.06	1.42E-02	8.50E-02	2435.49	not significant
916	SAP18	-1.06	1.72E-02	9.68E-02	4655.76	not significant
917	ZNF91	-1.06	3.60E-02	1.58E-01	1311.97	not significant
918	PUS7L	-1.06	4.26E-02	1.77E-01	1332.25	not significant
919	ZNF252P	-1.06	3.71E-02	1.61E-01	1159.29	not significant
920	UBE2V2	-1.06	9.04E-03	6.20E-02	4940.10	not significant
921	SF1	-1.06	8.27E-04	1.11E-02	15636.84	not significant
922	ZDHHC9	-1.06	4.64E-02	1.87E-01	700.71	not significant
923	POU2F1	-1.06	3.83E-02	1.65E-01	1504.74	not significant
924	MKLN1	-1.06	1.99E-02	1.06E-01	2710.46	not significant
925	TATDN2	-1.06	8.37E-03	5.90E-02	4429.21	not significant
926	ACADSB	-1.06	4.14E-02	1.74E-01	909.56	not significant
927	QRSL1	-1.06	3.24E-02	1.47E-01	1528.33	not significant
928	MARS2	-1.06	2.81E-02	1.35E-01	1452.70	not significant
929	MEX3C	-1.06	1.64E-02	9.39E-02	2923.03	not significant
930	WDR82	-1.06	1.32E-03	1.56E-02	11300.62	not significant
931	USP16	-1.06	2.15E-02	1.13E-01	2008.98	not significant
932	GOLGA4	-1.06	2.57E-02	1.27E-01	3140.56	not significant
933	CELF1	-1.06	9.76E-03	6.54E-02	6417.24	not significant
934	GFPT1	-1.06	1.70E-02	9.60E-02	3449.28	not significant
935	UBAP2	-1.06	1.72E-02	9.68E-02	3500.20	not significant
936	ZNF641	-1.06	5.17E-02	2.01E-01	441.56	not significant
937	MRPS30	-1.06	3.51E-02	1.56E-01	1226.21	not significant
938	TPI1	-1.06	1.11E-02	7.14E-02	6903.61	not significant
939	WDR33	-1.06	9.21E-03	6.27E-02	4005.42	not significant
940	RPS27L	-1.05	4.16E-02	1.74E-01	1044.88	not significant
941	VCP	-1.05	2.49E-03	2.49E-02	18519.62	not significant
942	FASTKD3	-1.05	4.17E-02	1.75E-01	906.15	not significant
943	KIAA1524	-1.05	1.91E-02	1.04E-01	2598.38	not significant
944	POLR2A	-1.05	4.86E-02	1.93E-01	11921.21	not significant
945	ZIK1	-1.05	3.82E-02	1.65E-01	1071.15	not significant
946	YLPM1	-1.05	2.76E-02	1.33E-01	4938.67	not significant
947	SH3BGRL3	-1.05	1.35E-02	8.19E-02	8224.37	not significant
948	TAF13	-1.05	4.76E-02	1.90E-01	350.26	not significant
949	MTMR2	-1.05	1.35E-02	8.19E-02	2911.38	not significant
950	CORO1A	-1.05	4.96E-03	4.02E-02	18520.35	not significant
951	SRSF1	-1.05	2.05E-03	2.15E-02	26977.68	not significant
952	GLTP	-1.05	3.21E-02	1.46E-01	1530.72	not significant
953	PDCD11	-1.05	9.09E-03	6.21E-02	6993.65	not significant
954	ERI2	-1.05	4.20E-02	1.75E-01	977.84	not significant
955	DHX57	-1.05	3.95E-02	1.68E-01	1163.05	not significant

956	YOD1	-1.05	3.22E-02	1.46E-01	1673.69	not significant
957	FKTN	-1.05	5.12E-02	2.00E-01	659.28	not significant
958	ZNF134	-1.05	4.32E-02	1.79E-01	1133.67	not significant
959	KRAS	-1.05	1.41E-02	8.45E-02	3434.76	not significant
960	PIGA	-1.05	5.23E-02	2.03E-01	512.02	not significant
961	VRK3	-1.05	4.09E-02	1.72E-01	1103.12	not significant
962	SNX12	-1.05	4.15E-02	1.74E-01	1032.23	not significant
963	ANKRD33B	-1.05	3.81E-02	1.64E-01	1573.57	not significant
964	ESD	-1.05	9.53E-03	6.44E-02	4990.84	not significant
965	SLC35A4	-1.05	6.71E-03	5.04E-02	4515.08	not significant
966	MFN2	-1.05	9.93E-03	6.61E-02	4860.39	not significant
967	DLEU1	-1.05	4.89E-02	1.94E-01	858.42	not significant
968	ZNF544	-1.05	3.09E-02	1.43E-01	1831.48	not significant
969	ISOC1	-1.05	2.96E-02	1.39E-01	1658.94	not significant
970	ZNF429	-1.05	3.99E-02	1.69E-01	256.30	not significant
971	LCP2	-1.05	7.84E-03	5.65E-02	5427.00	not significant
972	ICE1	-1.05	2.58E-02	1.27E-01	4244.00	not significant
973	AP5M1	-1.05	1.82E-02	1.00E-01	2532.78	not significant
974	DDX24	-1.05	5.14E-03	4.13E-02	6092.19	not significant
975	MRPL12	-1.05	2.52E-02	1.25E-01	5350.83	not significant
976	HIGD1A	-1.05	1.92E-02	1.04E-01	3989.03	not significant
977	STOML2	-1.05	1.87E-02	1.03E-01	4585.49	not significant
978	CARS2	-1.05	2.64E-02	1.29E-01	1735.96	not significant
979	SLC41A1	-1.05	3.18E-02	1.45E-01	2248.93	not significant
980	SLC35C1	-1.05	3.26E-02	1.48E-01	1494.62	not significant
981	SART3	-1.05	6.10E-03	4.70E-02	6198.69	not significant
982	LARS	-1.05	3.09E-03	2.87E-02	8103.11	not significant
983	COA7	-1.05	4.72E-02	1.89E-01	857.71	not significant
984	NCBP1	-1.05	1.05E-02	6.88E-02	3820.41	not significant
985	PPARD	-1.05	5.11E-02	2.00E-01	709.31	not significant
986	C12orf43	-1.05	3.13E-02	1.44E-01	1593.99	not significant
987	TMEM167B	-1.05	2.36E-02	1.20E-01	2051.89	not significant
988	POLH	-1.05	2.33E-02	1.19E-01	2134.26	not significant
989	LOC100288637	-1.05	5.43E-02	2.08E-01	558.34	not significant
990	SLC25A15	-1.05	2.66E-02	1.29E-01	1939.41	not significant
991	INO80D	-1.05	4.07E-02	1.71E-01	1092.40	not significant
992	TNPO2	-1.05	1.10E-02	7.11E-02	7920.43	not significant
993	TWF1	-1.05	4.91E-02	1.94E-01	822.22	not significant
994	MAPK1	-1.05	2.76E-03	2.66E-02	9329.63	not significant
995	SREK1IP1	-1.05	1.41E-02	8.45E-02	3164.39	not significant
996	PRKACB	-1.05	1.37E-02	8.30E-02	3875.82	not significant
997	ZHX2	-1.05	5.13E-02	2.00E-01	329.30	not significant
998	AKAP1	-1.05	2.28E-02	1.18E-01	4340.95	not significant
999	SNHG16	-1.05	3.13E-02	1.44E-01	2250.76	not significant
1000	NT5DC2	-1.05	3.18E-02	1.45E-01	1586.44	not significant
1001	UBE2Q1	-1.05	1.45E-02	8.65E-02	3091.36	not significant
1002	FOXM1	-1.05	9.72E-03	6.52E-02	5396.49	not significant
1003	CAB39	-1.05	3.82E-03	3.32E-02	7278.95	not significant
1004	DMWD	-1.05	5.41E-02	2.08E-01	731.31	not significant
1005	ZNF281	-1.05	3.30E-02	1.49E-01	1551.37	not significant
1006	URB1	-1.05	2.69E-02	1.30E-01	2903.81	not significant
1007	CCNK	-1.05	1.26E-02	7.83E-02	4447.49	not significant
1008	ZC3H15	-1.05	1.37E-02	8.30E-02	3875.88	not significant
1009	STARD7	-1.05	2.93E-03	2.77E-02	12325.16	not significant
1010	ATP13A3	-1.05	1.84E-02	1.01E-01	9047.73	not significant
1011	ATP2A2	-1.05	1.38E-02	8.35E-02	14094.89	not significant
1012	FTSJ2	-1.05	3.38E-02	1.51E-01	1860.88	not significant
1013	NCOA7	-1.05	4.07E-02	1.71E-01	1438.73	not significant
1014	ZNF714	-1.05	3.37E-02	1.51E-01	2087.50	not significant
1015	SEC14L1	-1.05	1.12E-02	7.19E-02	4830.33	not significant
1016	LCT	-1.05	5.55E-02	2.11E-01	438.86	not significant
1017	WDR4	-1.05	4.78E-02	1.91E-01	951.94	not significant
1018	C1orf109	-1.05	3.52E-02	1.56E-01	1503.13	not significant
1019	ATPAF1	-1.05	2.83E-02	1.35E-01	2068.96	not significant
1020	PBX3	-1.05	5.65E-02	2.13E-01	593.79	not significant
1021	SAR1B	-1.05	3.93E-02	1.67E-01	1622.34	not significant
1022	SEH1L	-1.05	8.71E-03	6.04E-02	4893.67	not significant
1023	PAFAH2	-1.05	2.85E-02	1.36E-01	1826.09	not significant
1024	LONP2	-1.05	2.19E-02	1.14E-01	3260.50	not significant
1025	RNF216P1	-1.05	4.65E-02	1.87E-01	1182.93	not significant
1026	MPV17	-1.05	4.77E-02	1.90E-01	1047.96	not significant
1027	OAT	-1.05	3.68E-02	1.60E-01	1670.27	not significant
1028	ANP32A	-1.05	1.32E-02	8.09E-02	6609.00	not significant
1029	C7orf50	-1.05	5.17E-02	2.01E-01	1237.80	not significant
1030	ZNF562	-1.05	5.62E-02	2.13E-01	836.29	not significant
1031	RCOR1	-1.05	1.97E-02	1.06E-01	3144.77	not significant
1032	PPTC7	-1.05	2.35E-02	1.20E-01	3499.15	not significant
1033	YWHAB	-1.05	3.05E-03	2.86E-02	21853.62	not significant
1034	RAB23	-1.05	5.86E-02	2.18E-01	462.08	not significant
1035	OTUD3	-1.05	5.54E-02	2.11E-01	902.69	not significant
1036	YBX3	-1.05	2.86E-02	1.36E-01	2653.96	not significant
1037	DDX55	-1.05	1.89E-02	1.03E-01	2976.64	not significant
1038	AXIN2	-1.05	1.84E-02	1.01E-01	116.71	not significant
1039	ZNF143	-1.05	5.30E-02	2.04E-01	836.41	not significant
1040	LSG1	-1.05	1.60E-02	9.26E-02	3196.31	not significant
1041	USP36	-1.05	1.12E-02	7.21E-02	5452.97	not significant
1042	NUP98	-1.05	1.01E-02	6.68E-02	7116.87	not significant
1043	TAB2	-1.05	2.61E-02	1.28E-01	2381.35	not significant

1044	CBX4	-1.05	2.31E-02	1.19E-01	2805.97	not significant
1045	KPNA1	-1.05	1.23E-02	7.66E-02	4092.17	not significant
1046	ATG3	-1.05	2.16E-02	1.13E-01	3787.29	not significant
1047	LRRC47	-1.05	2.41E-02	1.22E-01	2776.96	not significant
1048	MED27	-1.05	6.14E-02	2.25E-01	700.58	not significant
1049	CDK2AP1	-1.05	2.69E-02	1.30E-01	3707.10	not significant
1050	HSPA14	-1.05	1.80E-02	9.99E-02	3392.01	not significant
1051	OXSR1	-1.05	1.18E-02	7.47E-02	5540.47	not significant
1052	PTEN	-1.05	4.15E-03	3.55E-02	9196.21	not significant
1053	LRCH3	-1.05	5.97E-02	2.21E-01	626.97	not significant
1054	NAMPT	-1.05	3.33E-02	1.50E-01	1757.16	not significant
1055	CCR7	-1.05	5.99E-02	2.21E-01	608.17	not significant
1056	TNFRSF8	-1.05	4.30E-02	1.79E-01	1288.28	not significant
1057	GTF3C6	-1.05	2.87E-02	1.36E-01	2774.39	not significant
1058	PSMD14	-1.05	1.90E-02	1.03E-01	4483.16	not significant
1059	RBBP6	-1.05	2.70E-02	1.31E-01	4952.25	not significant
1060	CCDC47	-1.05	9.12E-03	6.22E-02	6085.83	not significant
1061	IQCE	-1.05	5.13E-02	2.00E-01	998.95	not significant
1062	CTU2	-1.05	5.46E-02	2.09E-01	1227.25	not significant
1063	SMC5	-1.05	2.16E-02	1.13E-01	3739.65	not significant
1064	DCUN1D3	-1.05	4.01E-02	1.70E-01	201.25	not significant
1065	EML5	-1.05	4.82E-02	1.92E-01	246.24	not significant
1066	LOC101927482	-1.05	7.43E-02	2.54E-01	312.75	not significant
1067	MRPS12	-1.05	5.23E-02	2.03E-01	1665.12	not significant
1068	NUDCD1	-1.05	2.02E-02	1.07E-01	3185.98	not significant
1069	CENPF	-1.05	6.41E-02	2.31E-01	10726.35	not significant
1070	SCO1	-1.05	4.70E-02	1.89E-01	1416.04	not significant
1071	PPIL1	-1.05	3.02E-02	1.41E-01	2133.91	not significant
1072	NOC2L	-1.05	9.90E-03	6.60E-02	4984.18	not significant
1073	ZNF22	-1.05	8.96E-03	6.16E-02	5008.53	not significant
1074	TOMM22	-1.05	3.09E-02	1.43E-01	6110.72	not significant
1075	PSMD4	-1.05	2.19E-02	1.14E-01	4132.78	not significant
1076	POLR2E	-1.05	1.13E-02	7.22E-02	7354.70	not significant
1077	ISG20L2	-1.05	2.67E-02	1.30E-01	2360.82	not significant
1078	RNF169	-1.05	4.55E-02	1.85E-01	1872.60	not significant
1079	RNF6	-1.05	2.70E-02	1.31E-01	2984.92	not significant
1080	ATG101	-1.05	5.69E-02	2.15E-01	1128.05	not significant
1081	FAM222B	-1.05	5.81E-02	2.17E-01	819.11	not significant
1082	LDLRAD4	-1.05	1.03E-02	6.82E-02	6713.91	not significant
1083	AKAP8	-1.05	4.19E-02	1.75E-01	1774.33	not significant
1084	TIMM44	-1.05	3.55E-02	1.57E-01	2235.29	not significant
1085	CDK8	-1.05	5.63E-02	2.13E-01	1069.05	not significant
1086	PSME2	-1.05	2.16E-02	1.13E-01	8817.80	not significant
1087	LRP6	-1.05	5.50E-02	2.10E-01	1485.96	not significant
1088	TTLL5	-1.05	4.90E-02	1.94E-01	1316.87	not significant
1089	RREB1	-1.05	4.72E-02	1.89E-01	1442.76	not significant
1090	FYTTD1	-1.05	3.14E-02	1.44E-01	2106.64	not significant
1091	CTR9	-1.05	2.20E-02	1.15E-01	4518.06	not significant
1092	ZKSCAN5	-1.05	5.24E-02	2.03E-01	1197.91	not significant
1093	BZW1	-1.05	1.04E-02	6.83E-02	9224.85	not significant
1094	BAK1	-1.05	4.88E-02	1.94E-01	1534.56	not significant
1095	SLC39A10	-1.05	4.64E-02	1.87E-01	1668.40	not significant
1096	C17orf80	-1.05	2.61E-02	1.28E-01	2534.98	not significant
1097	FAM104A	-1.05	2.25E-02	1.17E-01	2868.06	not significant
1098	MLH3	-1.05	4.39E-02	1.81E-01	1411.09	not significant
1099	YWHAE	-1.05	1.13E-02	7.22E-02	18029.36	not significant
1100	PRKRIR	-1.05	3.17E-02	1.45E-01	2972.76	not significant
1101	RAB21	-1.05	2.48E-02	1.24E-01	2772.53	not significant
1102	SH3KBP1	-1.05	1.17E-02	7.42E-02	5876.70	not significant
1103	AP2B1	-1.05	3.43E-02	1.53E-01	4082.64	not significant
1104	DCAF10	-1.05	5.31E-02	2.05E-01	1383.36	not significant
1105	SLC9B2	-1.05	3.92E-02	1.67E-01	1693.92	not significant
1106	RAB8A	-1.05	1.88E-02	1.03E-01	5132.35	not significant
1107	UHMK1	-1.05	1.65E-02	9.43E-02	7989.75	not significant
1108	UBQLN4	-1.05	2.56E-02	1.27E-01	2620.38	not significant
1109	XRCC5	-1.05	2.28E-03	2.35E-02	24812.24	not significant
1110	RPP14	-1.05	4.57E-02	1.86E-01	1559.69	not significant
1111	PRKDC	-1.05	3.14E-02	1.44E-01	33430.80	not significant
1112	PRPF3	-1.05	6.29E-02	2.28E-01	919.83	not significant
1113	MFNG	-1.05	4.02E-02	1.70E-01	2271.37	not significant
1114	ELK4	-1.05	3.10E-02	1.43E-01	3611.87	not significant
1115	ZMPSTE24	-1.05	3.03E-02	1.41E-01	3227.53	not significant
1116	ZNF518B	-1.05	5.44E-02	2.08E-01	1520.15	not significant
1117	GTSE1	-1.05	3.05E-02	1.42E-01	2596.57	not significant
1118	HDAC2	-1.05	7.70E-03	5.58E-02	8086.20	not significant
1119	YWHAG	-1.05	3.96E-03	3.42E-02	21241.11	not significant
1120	RPS4Y1	-1.05	1.79E-02	9.94E-02	11507.90	not significant
1121	TOMM70A	-1.05	8.90E-03	6.14E-02	6580.67	not significant
1122	ABHD5	-1.05	6.87E-02	2.42E-01	669.78	not significant
1123	RNPS1	-1.05	1.74E-02	9.74E-02	7531.25	not significant
1124	AMD1	-1.05	9.08E-03	6.21E-02	8880.85	not significant
1125	ABCF1	-1.05	3.14E-02	1.44E-01	3037.03	not significant
1126	STX18	-1.05	6.29E-02	2.28E-01	956.48	not significant
1127	HDHD1	-1.05	4.49E-02	1.84E-01	1585.79	not significant
1128	SKA3	-1.05	4.09E-02	1.72E-01	2501.23	not significant
1129	LRRFIP1	-1.05	1.99E-02	1.06E-01	5916.49	not significant
1130	WAPAL	-1.05	1.80E-02	9.98E-02	5063.94	not significant
1131	GNG2	-1.05	4.83E-03	3.95E-02	11270.86	not significant

1132	BID	-1.05	2.91E-02	1.38E-01	3952.81	not significant
1133	ZC3H11A	-1.05	1.59E-02	9.25E-02	5256.31	not significant
1134	HNRNPAB	-1.05	1.01E-02	6.71E-02	17676.90	not significant
1135	LINC00665	-1.05	6.73E-02	2.39E-01	415.33	not significant
1136	KLF10	-1.05	4.60E-02	1.86E-01	1514.97	not significant
1137	PRPF38A	-1.05	1.79E-02	9.94E-02	4477.62	not significant
1138	PDP2	-1.05	5.14E-02	2.00E-01	1672.81	not significant
1139	IMP4	-1.05	3.39E-02	1.51E-01	2293.45	not significant
1140	MRPL49	-1.05	3.12E-02	1.44E-01	3477.99	not significant
1141	ERAL1	-1.05	3.58E-02	1.58E-01	2040.01	not significant
1142	TFEC	-1.05	1.72E-02	9.67E-02	7266.20	not significant
1143	ITCH	-1.05	1.59E-02	9.23E-02	5352.22	not significant
1144	MPV17L2	-1.05	5.76E-02	2.16E-01	1170.99	not significant
1145	SENP2	-1.05	3.96E-02	1.68E-01	1949.91	not significant
1146	MYD88	-1.05	1.81E-02	1.00E-01	3781.50	not significant
1147	CEP350	-1.05	4.18E-02	1.75E-01	4252.07	not significant
1148	NUPL1	-1.05	1.69E-02	9.60E-02	6792.34	not significant
1149	ZNF664	-1.05	1.32E-02	8.08E-02	10467.93	not significant
1150	PTGIS	-1.05	8.75E-03	6.05E-02	8244.57	not significant
1151	BTBD3	-1.05	6.31E-02	2.28E-01	962.82	not significant
1152	PLS1	-1.05	5.46E-02	2.09E-01	1556.44	not significant
1153	APTX	-1.05	5.04E-02	1.98E-01	1415.04	not significant
1154	FBXL3	-1.05	3.77E-02	1.63E-01	2423.17	not significant
1155	HCFC1	-1.05	4.63E-02	1.87E-01	2761.99	not significant
1156	NUFIP2	-1.05	7.06E-02	2.46E-01	7933.93	not significant
1157	RAB14	-1.05	3.24E-02	1.47E-01	2736.50	not significant
1158	PSMD1	-1.05	1.92E-02	1.04E-01	6319.36	not significant
1159	DCTN1	-1.05	9.32E-03	6.32E-02	7196.55	not significant
1160	EMC8	-1.05	4.57E-02	1.86E-01	1983.80	not significant
1161	PPFIA1	-1.05	4.82E-02	1.92E-01	1657.33	not significant
1162	GTF3C2	-1.05	2.53E-02	1.26E-01	3566.38	not significant
1163	ARHGAP30	-1.05	9.11E-03	6.21E-02	9391.58	not significant
1164	TTPAL	-1.05	5.36E-02	2.06E-01	1459.52	not significant
1165	HDAC4	-1.05	2.44E-02	1.23E-01	6222.03	not significant
1166	EMC9	-1.05	6.88E-02	2.42E-01	401.43	not significant
1167	BCS1L	-1.05	6.98E-02	2.45E-01	846.34	not significant
1168	ATP5C1	-1.05	1.79E-02	9.94E-02	7645.87	not significant
1169	PICALM	-1.05	2.50E-02	1.25E-01	3937.26	not significant
1170	TERF2	-1.05	4.01E-02	1.70E-01	2101.07	not significant
1171	KIF1B	-1.05	7.35E-02	2.53E-01	1037.30	not significant
1172	PTER	-1.05	6.01E-02	2.21E-01	1355.07	not significant
1173	ALG8	-1.05	4.66E-02	1.87E-01	1704.50	not significant
1174	PINK1-AS	-1.05	6.94E-02	2.44E-01	419.19	not significant
1175	ZNF761	-1.05	6.85E-02	2.41E-01	1256.79	not significant
1176	SETMAR	-1.05	7.08E-02	2.47E-01	774.22	not significant
1177	ATP5F1	-1.05	2.99E-02	1.40E-01	6445.63	not significant
1178	ZNF585A	-1.05	7.25E-02	2.51E-01	598.92	not significant
1179	NDE1	-1.05	5.57E-02	2.11E-01	1497.45	not significant
1180	ZNF347	-1.05	6.24E-02	2.27E-01	1082.26	not significant
1181	MCFD2	-1.05	2.29E-02	1.18E-01	3975.68	not significant
1182	ALKBH1	-1.05	7.38E-02	2.53E-01	569.21	not significant
1183	TRA2B	-1.05	1.20E-02	7.54E-02	13614.30	not significant
1184	INPP5A	-1.05	7.43E-02	2.54E-01	581.62	not significant
1185	DPH3	-1.05	5.10E-02	2.00E-01	1860.36	not significant
1186	ARL5A	-1.05	2.65E-02	1.29E-01	3153.27	not significant
1187	SGTA	-1.05	3.73E-02	1.62E-01	4615.56	not significant
1188	NUSAP1	-1.05	1.72E-02	9.68E-02	5423.03	not significant
1189	RBM25	-1.05	1.89E-02	1.03E-01	7354.08	not significant
1190	TIMM50	-1.05	5.33E-02	2.06E-01	2745.12	not significant
1191	IDE	-1.05	5.20E-02	2.02E-01	2095.56	not significant
1192	WBP11	-1.05	1.40E-02	8.42E-02	6691.50	not significant
1193	HMGXB3	-1.05	4.02E-02	1.70E-01	2460.31	not significant
1194	RUNX3	-1.05	3.67E-02	1.60E-01	2736.08	not significant
1195	PSMD5	-1.05	5.98E-02	2.21E-01	1416.93	not significant
1196	UBIAD1	-1.05	5.86E-02	2.18E-01	1459.02	not significant
1197	MCM3AP	-1.05	3.84E-02	1.65E-01	3152.32	not significant
1198	FAM120A	-1.05	1.43E-02	8.54E-02	7957.84	not significant
1199	BRWD3	-1.05	7.50E-02	2.55E-01	786.51	not significant
1200	CUX1	-1.05	5.98E-02	2.21E-01	1253.22	not significant
1201	KIAA0020	-1.05	2.75E-02	1.32E-01	3406.66	not significant
1202	KRR1	-1.05	2.66E-02	1.29E-01	3654.03	not significant
1203	NOVA1	-1.05	3.13E-02	1.44E-01	137.57	not significant
1204	NBEAL1	-1.05	6.73E-02	2.39E-01	270.64	not significant
1205	NFKBIB	-1.05	6.22E-02	2.27E-01	1393.58	not significant
1206	C20orf27	-1.05	5.41E-02	2.08E-01	3292.49	not significant
1207	MLLT10	-1.05	3.99E-02	1.69E-01	2316.94	not significant
1208	ZNF616	-1.05	7.69E-02	2.60E-01	631.25	not significant
1209	MAPKAPK5	-1.05	4.04E-02	1.70E-01	2486.06	not significant
1210	GRPEL2	-1.05	7.64E-02	2.59E-01	665.13	not significant
1211	IP6K1	-1.05	4.96E-02	1.96E-01	1985.52	not significant
1212	TYW3	-1.05	4.10E-02	1.72E-01	2410.06	not significant
1213	RPS6KA3	-1.05	3.60E-02	1.58E-01	6539.89	not significant
1214	RFX7	-1.05	5.63E-02	2.13E-01	2895.88	not significant
1215	CBLL1	-1.05	4.71E-02	1.89E-01	2633.11	not significant
1216	PSMC6	-1.05	3.50E-02	1.56E-01	3055.29	not significant
1217	PFAS	-1.05	2.08E-02	1.10E-01	6219.36	not significant
1218	WARS	-1.05	2.79E-02	1.34E-01	3830.50	not significant
1219	AP2M1	-1.05	1.83E-02	1.01E-01	8939.03	not significant

1220	CYFIP2	-1.05	1.52E-02	8.95E-02	16276.38	not significant
1221	MAGOH	-1.05	4.42E-02	1.82E-01	2642.15	not significant
1222	CNOT11	-1.05	3.97E-02	1.69E-01	3841.25	not significant
1223	PTMA	-1.05	2.54E-02	1.26E-01	72149.33	not significant
1224	LCOR	-1.05	7.86E-02	2.63E-01	816.56	not significant
1225	NDUFAB1	-1.05	5.55E-02	2.11E-01	3202.92	not significant
1226	SDHAF2	-1.05	6.61E-02	2.36E-01	1481.19	not significant
1227	PHC3	-1.05	6.26E-02	2.28E-01	2468.65	not significant
1228	EIF1AD	-1.05	4.23E-02	1.76E-01	2361.25	not significant
1229	PPP2R2A	-1.05	3.54E-02	1.56E-01	3034.48	not significant
1230	RBM26-AS1	-1.04	2.37E-02	1.20E-01	114.59	not significant
1231	RPL7L1	-1.04	5.60E-02	2.12E-01	1682.19	not significant
1232	FEM1A	-1.04	4.35E-02	1.80E-01	2322.57	not significant
1233	POU3F2	-1.04	7.15E-02	2.49E-01	339.87	not significant
1234	EHD4	-1.04	7.51E-02	2.55E-01	402.12	not significant
1235	TRIM14	-1.04	2.52E-02	1.26E-01	4560.87	not significant
1236	TBC1D13	-1.04	7.37E-02	2.53E-01	919.56	not significant
1237	TIMM17A	-1.04	5.74E-02	2.16E-01	2564.28	not significant
1238	SH3TC1	-1.04	7.73E-02	2.61E-01	414.35	not significant
1239	GTF2I	-1.04	3.84E-02	1.65E-01	3480.66	not significant
1240	NEK9	-1.04	3.05E-02	1.42E-01	3901.60	not significant
1241	CHD4	-1.04	1.70E-02	9.61E-02	17981.41	not significant
1242	PDS5A	-1.04	1.22E-02	7.62E-02	11264.81	not significant
1243	B4GALT5	-1.04	7.39E-02	2.53E-01	960.91	not significant
1244	IPW	-1.04	6.74E-02	2.39E-01	293.96	not significant
1245	MSANTD4	-1.04	7.83E-02	2.63E-01	894.28	not significant
1246	TGIF2	-1.04	4.66E-02	1.87E-01	2165.33	not significant
1247	CLIP1	-1.04	4.58E-02	1.86E-01	2465.44	not significant
1248	CDC25B	-1.04	1.20E-02	7.54E-02	8282.27	not significant
1249	CRADD	-1.04	6.06E-02	2.23E-01	270.75	not significant
1250	CHCHD10	-1.04	8.20E-02	2.71E-01	735.28	not significant
1251	TSC22D2	-1.04	8.10E-02	2.69E-01	593.03	not significant
1252	FANCM	-1.04	7.85E-02	2.63E-01	874.57	not significant
1253	UROS	-1.04	6.14E-02	2.25E-01	1587.03	not significant
1254	AP1G1	-1.04	4.71E-02	1.89E-01	4219.16	not significant
1255	DESI1	-1.04	4.55E-02	1.85E-01	2566.13	not significant
1256	AHCTF1	-1.04	4.03E-02	1.70E-01	3229.29	not significant
1257	FAM72B	-1.04	2.96E-02	1.39E-01	135.88	not significant
1258	EEF1E1	-1.04	8.12E-02	2.69E-01	512.91	not significant
1259	NFE2L2	-1.04	4.69E-02	1.89E-01	2192.35	not significant
1260	TRAF3IP1	-1.04	8.42E-02	2.76E-01	582.33	not significant
1261	OXNAD1	-1.04	8.09E-02	2.69E-01	760.95	not significant
1262	RPP30	-1.04	6.30E-02	2.28E-01	1725.74	not significant
1263	FZR1	-1.04	4.71E-02	1.89E-01	2101.97	not significant
1264	PRMT1	-1.04	3.52E-02	1.56E-01	10678.83	not significant
1265	CCDC137	-1.04	4.72E-02	1.89E-01	2545.49	not significant
1266	CDK13	-1.04	4.94E-02	1.95E-01	2947.80	not significant
1267	MON1A	-1.04	8.30E-02	2.73E-01	723.37	not significant
1268	SET	-1.04	1.51E-02	8.94E-02	24551.75	not significant
1269	PFDN2	-1.04	8.00E-02	2.67E-01	1482.20	not significant
1270	ANKRD12	-1.04	7.45E-02	2.54E-01	2209.88	not significant
1271	CCT4	-1.04	2.67E-02	1.30E-01	12195.72	not significant
1272	PPWD1	-1.04	6.59E-02	2.35E-01	1567.67	not significant
1273	MCUR1	-1.04	3.84E-02	1.65E-01	3250.26	not significant
1274	CEP170	-1.04	8.30E-02	2.73E-01	515.29	not significant
1275	ERCC4	-1.04	8.42E-02	2.76E-01	821.24	not significant
1276	ZNF611	-1.04	8.28E-02	2.73E-01	692.14	not significant
1277	PPP1R7	-1.04	5.06E-02	1.99E-01	2292.34	not significant
1278	TGFBRAP1	-1.04	5.22E-02	2.03E-01	2187.29	not significant
1279	EIF6	-1.04	4.17E-02	1.74E-01	4350.01	not significant
1280	CDC42	-1.04	2.31E-02	1.19E-01	6532.33	not significant
1281	MRPL36	-1.04	9.56E-02	2.99E-01	592.45	not significant
1282	COPS8	-1.04	5.43E-02	2.08E-01	2746.32	not significant
1283	C2orf44	-1.04	5.96E-02	2.21E-01	1595.31	not significant
1284	RPF1	-1.04	6.67E-02	2.37E-01	2410.25	not significant
1285	PPFIBP1	-1.04	6.83E-02	2.41E-01	1479.72	not significant
1286	CD3G	-1.04	2.80E-02	1.34E-01	6364.92	not significant
1287	LRRCC1	-1.04	7.31E-02	2.52E-01	1496.30	not significant
1288	SLC25A17	-1.04	6.48E-02	2.33E-01	1539.03	not significant
1289	UBN1	-1.04	3.62E-02	1.59E-01	4860.75	not significant
1290	KLF16	-1.04	7.00E-02	2.45E-01	1552.14	not significant
1291	PRPF40A	-1.04	1.69E-02	9.60E-02	6809.72	not significant
1292	PNPO	-1.04	5.57E-02	2.11E-01	2244.18	not significant
1293	AKR1B1	-1.04	3.39E-02	1.51E-01	4455.30	not significant
1294	CASP3	-1.04	2.42E-02	1.22E-01	5869.30	not significant
1295	MMACHC	-1.04	8.49E-02	2.77E-01	535.92	not significant
1296	PNP	-1.04	3.52E-02	1.56E-01	4567.97	not significant
1297	TRMT12	-1.04	8.66E-02	2.81E-01	554.11	not significant
1298	ACTN1	-1.04	8.54E-02	2.78E-01	845.96	not significant
1299	AKIRIN1	-1.04	4.86E-02	1.93E-01	2536.01	not significant
1300	ZC3H4	-1.04	4.99E-02	1.97E-01	3587.64	not significant
1301	EPT1	-1.04	4.24E-02	1.76E-01	4898.73	not significant
1302	CNP	-1.04	8.31E-02	2.73E-01	419.43	not significant
1303	MRPS18C	-1.04	8.54E-02	2.78E-01	886.79	not significant
1304	TBC1D20	-1.04	5.01E-02	1.97E-01	2364.53	not significant
1305	DYNLL2	-1.04	3.00E-02	1.40E-01	5672.89	not significant
1306	G3BP2	-1.04	1.61E-02	9.29E-02	8605.18	not significant
1307	STS	-1.04	8.71E-02	2.82E-01	825.67	not significant

1308	SORBS2	-1.04	4.03E-02	1.70E-01	151.93	not significant
1309	DCLRE1C	-1.04	8.44E-02	2.76E-01	1262.00	not significant
1310	TSTA3	-1.04	6.81E-02	2.41E-01	1859.11	not significant
1311	TERF1	-1.04	5.55E-02	2.11E-01	2097.05	not significant
1312	MTMR4	-1.04	3.14E-02	1.44E-01	4552.08	not significant
1313	QTRTD1	-1.04	6.77E-02	2.40E-01	1851.08	not significant
1314	MALT1	-1.04	7.98E-02	2.67E-01	1238.24	not significant
1315	FBL	-1.04	5.13E-02	2.00E-01	8771.04	not significant
1316	KATNA1	-1.04	8.86E-02	2.85E-01	866.87	not significant
1317	NFYC	-1.04	6.69E-02	2.38E-01	1905.81	not significant
1318	ZNF592	-1.04	6.89E-02	2.42E-01	1818.64	not significant
1319	NET1	-1.04	4.78E-02	1.91E-01	2557.82	not significant
1320	MFAP3	-1.04	5.24E-02	2.03E-01	2279.18	not significant
1321	TUBA1B	-1.04	3.00E-02	1.40E-01	57429.41	not significant
1322	UBE3A	-1.04	3.15E-02	1.44E-01	4772.75	not significant
1323	UBE2F	-1.04	9.04E-02	2.88E-01	733.61	not significant
1324	KIAA0040	-1.04	8.27E-02	2.73E-01	1000.22	not significant
1325	STXBP3	-1.04	6.61E-02	2.36E-01	1592.91	not significant
1326	DDHD1	-1.04	7.70E-02	2.60E-01	2381.95	not significant
1327	ERI3	-1.04	7.76E-02	2.61E-01	1753.07	not significant
1328	MAP7D3	-1.04	7.17E-02	2.49E-01	1732.50	not significant
1329	TBC1D5	-1.04	5.46E-02	2.09E-01	4400.04	not significant
1330	MYC	-1.04	1.87E-02	1.02E-01	9908.72	not significant
1331	CXorf38	-1.04	7.18E-02	2.49E-01	1438.17	not significant
1332	HTT	-1.04	5.73E-02	2.16E-01	4133.39	not significant
1333	NRAS	-1.04	1.48E-02	8.80E-02	9119.57	not significant
1334	RBM12	-1.04	2.16E-02	1.13E-01	6724.22	not significant
1335	ZSCAN25	-1.04	6.67E-02	2.37E-01	1734.88	not significant
1336	KIF18B	-1.04	4.96E-02	1.96E-01	3595.45	not significant
1337	CCT7	-1.04	1.62E-02	9.33E-02	18068.38	not significant
1338	NUP188	-1.04	4.49E-02	1.84E-01	5813.25	not significant
1339	NLN	-1.04	7.36E-02	2.53E-01	1693.30	not significant
1340	ZRANB1	-1.04	6.56E-02	2.35E-01	1672.56	not significant
1341	TFDP1	-1.04	1.81E-02	1.00E-01	11639.42	not significant
1342	WDFY1	-1.04	8.65E-02	2.81E-01	1242.50	not significant
1343	RANGRF	-1.04	7.55E-02	2.57E-01	1965.44	not significant
1344	EHD1	-1.04	5.25E-02	2.03E-01	3359.20	not significant
1345	SS18L2	-1.04	9.00E-02	2.87E-01	916.37	not significant
1346	CEBPZOS	-1.04	7.50E-02	2.55E-01	1354.29	not significant
1347	ACBD3	-1.04	6.86E-02	2.42E-01	1551.61	not significant
1348	MBD1	-1.04	3.96E-02	1.69E-01	3499.81	not significant
1349	GABPB2	-1.04	7.19E-02	2.49E-01	283.92	not significant
1350	CYC1	-1.04	5.49E-02	2.09E-01	5676.26	not significant
1351	HNRNPH3	-1.04	2.89E-02	1.37E-01	8217.58	not significant
1352	PHF20L1	-1.04	2.97E-02	1.39E-01	5289.90	not significant
1353	BCL9L	-1.04	9.41E-02	2.96E-01	883.63	not significant
1354	PLIN2	-1.04	5.97E-02	2.21E-01	2166.81	not significant
1355	PDCD6IP	-1.04	4.85E-02	1.93E-01	4086.43	not significant
1356	CCAR1	-1.04	3.20E-02	1.46E-01	6379.28	not significant
1357	HNRNPU	-1.04	1.50E-02	8.89E-02	42179.04	not significant
1358	FGD6	-1.04	8.45E-02	2.76E-01	412.46	not significant
1359	MAZ	-1.04	2.91E-02	1.37E-01	17478.88	not significant
1360	FXN	-1.04	6.83E-02	2.41E-01	234.39	not significant
1361	PARL	-1.04	6.74E-02	2.39E-01	1667.17	not significant
1362	KDM2A	-1.04	3.82E-02	1.64E-01	5222.46	not significant
1363	PQBP1	-1.04	9.36E-02	2.95E-01	556.88	not significant
1364	ITPKC	-1.04	8.60E-02	2.80E-01	347.55	not significant
1365	COG7	-1.04	9.58E-02	2.99E-01	645.16	not significant
1366	AKIRIN2	-1.04	8.44E-02	2.76E-01	1123.00	not significant
1367	CISH	-1.04	1.22E-02	7.62E-02	14908.98	not significant
1368	RRP1	-1.04	9.21E-02	2.92E-01	1137.11	not significant
1369	ABAT	-1.04	9.55E-02	2.99E-01	624.96	not significant
1370	SENP1	-1.04	5.51E-02	2.10E-01	3819.26	not significant
1371	KCNAB2	-1.04	1.51E-02	8.90E-02	9256.56	not significant
1372	SLC2A3	-1.04	9.55E-02	2.99E-01	959.09	not significant
1373	SMYD3	-1.04	8.94E-02	2.86E-01	1085.78	not significant
1374	VPS35	-1.04	3.40E-02	1.52E-01	5224.11	not significant
1375	MRPS9	-1.04	8.14E-02	2.70E-01	1276.20	not significant
1376	SLC35B4	-1.04	6.18E-02	2.26E-01	3193.92	not significant
1377	PHF14	-1.04	4.30E-02	1.79E-01	3367.03	not significant
1378	FGD5	-1.04	9.82E-02	3.05E-01	644.99	not significant
1379	HDAC3	-1.04	5.19E-02	2.02E-01	2695.08	not significant
1380	DR1	-1.04	2.50E-02	1.25E-01	7015.03	not significant
1381	ALKBH3	-1.04	8.75E-02	2.83E-01	1104.40	not significant
1382	LIMD1	-1.04	4.01E-02	1.70E-01	3684.42	not significant
1383	TBCD	-1.04	1.99E-02	1.06E-01	8062.11	not significant
1384	CPS1	-1.04	4.73E-02	1.89E-01	165.02	not significant
1385	ZNF814	-1.04	9.41E-02	2.96E-01	626.00	not significant
1386	CISD1	-1.04	8.93E-02	2.86E-01	1103.34	not significant
1387	ZNF587	-1.04	9.59E-02	2.99E-01	1000.67	not significant
1388	ARID2	-1.04	7.14E-02	2.48E-01	4546.19	not significant
1389	RNF166	-1.04	7.84E-02	2.63E-01	1440.42	not significant
1390	GATAD2A	-1.04	1.68E-02	9.54E-02	9644.98	not significant
1391	DYRK4	-1.04	9.84E-02	3.05E-01	613.73	not significant
1392	GPN1	-1.04	7.15E-02	2.49E-01	1856.85	not significant
1393	STK17A	-1.04	5.38E-02	2.07E-01	3416.90	not significant
1394	HNRNPD	-1.04	2.33E-02	1.19E-01	21309.32	not significant
1395	RIC8A	-1.04	4.23E-02	1.76E-01	3884.83	not significant

1396	POLG	-1.04	3.67E-02	1.60E-01	4769.87	not significant
1397	UMODL1	-1.04	1.13E-02	NA	74.18	not significant
1398	PSMA6	-1.04	3.17E-02	1.45E-01	8289.73	not significant
1399	MAT2A	-1.04	2.56E-02	1.27E-01	15053.92	not significant
1400	SLC6A20	-1.04	6.37E-02	2.30E-01	206.45	not significant
1401	ZNF174	-1.04	9.58E-02	2.99E-01	542.19	not significant
1402	TUBB4A	-1.04	5.62E-02	2.13E-01	172.60	not significant
1403	AMMECR1	-1.04	9.22E-02	2.92E-01	491.55	not significant
1404	SRSF3	-1.04	2.63E-02	1.29E-01	19819.45	not significant
1405	RNF8	-1.04	9.02E-02	2.87E-01	1320.70	not significant
1406	ASB8	-1.04	8.29E-02	2.73E-01	1431.74	not significant
1407	PPID	-1.04	7.39E-02	2.53E-01	2552.92	not significant
1408	MEPCE	-1.04	4.32E-02	1.79E-01	3789.54	not significant
1409	MPHOSPH8	-1.04	7.44E-02	2.54E-01	1768.51	not significant
1410	KIFC1	-1.04	8.20E-02	2.71E-01	1463.90	not significant
1411	CRCP	-1.04	6.21E-02	2.26E-01	2254.42	not significant
1412	UBTF	-1.04	2.22E-02	1.15E-01	9719.60	not significant
1413	RBM41	-1.04	1.00E-01	3.09E-01	765.86	not significant
1414	LRRC8D	-1.04	8.11E-02	2.69E-01	1663.26	not significant
1415	ATXN7L3	-1.04	4.40E-02	1.81E-01	3545.17	not significant
1416	MORC2	-1.04	6.96E-02	2.44E-01	1919.93	not significant
1417	CARM1	-1.04	5.11E-02	2.00E-01	3726.86	not significant
1418	POGLUT1	-1.04	9.41E-02	2.96E-01	1366.27	not significant
1419	ACTR3	-1.04	2.12E-02	1.12E-01	10483.27	not significant
1420	IDH3B	-1.04	6.74E-02	2.39E-01	3519.26	not significant
1421	PRMT3	-1.04	8.81E-02	2.84E-01	1483.06	not significant
1422	DYRK1A	-1.04	4.58E-02	1.86E-01	3785.40	not significant
1423	NOL11	-1.04	3.04E-02	1.41E-01	6832.02	not significant
1424	SPNS2	-1.04	2.75E-02	1.32E-01	143.17	not significant
1425	UTP18	-1.04	6.27E-02	2.28E-01	2759.82	not significant
1426	ODF2	-1.04	4.71E-02	1.89E-01	3425.81	not significant
1427	PSMD3	-1.04	2.37E-02	1.21E-01	8798.58	not significant
1428	XPNPEP3	-1.04	9.86E-02	3.06E-01	492.87	not significant
1429	AIMP2	-1.04	7.89E-02	2.64E-01	1815.38	not significant
1430	DDX3X	-1.04	2.82E-02	1.35E-01	14427.53	not significant
1431	MPZL3	-1.04	5.79E-02	2.17E-01	189.99	not significant
1432	FOCAD	-1.04	8.82E-02	2.84E-01	1328.80	not significant
1433	SETD8	-1.04	7.94E-02	2.66E-01	2028.89	not significant
1434	RNF26	-1.04	7.27E-02	2.51E-01	1888.47	not significant
1435	DCP1A	-1.04	8.19E-02	2.71E-01	324.15	not significant
1436	SNHG3	-1.04	8.39E-02	2.75E-01	2639.43	not significant
1437	C21orf59	-1.04	7.58E-02	2.57E-01	2272.21	not significant
1438	RGS14	-1.04	8.49E-02	2.77E-01	1541.28	not significant
1439	MAP4K1	-1.04	7.15E-02	2.49E-01	2601.57	not significant
1440	RPS6KB1	-1.04	5.11E-02	2.00E-01	3674.60	not significant
1441	COG3	-1.04	9.11E-02	2.89E-01	1373.34	not significant
1442	USP47	-1.04	7.20E-02	2.49E-01	3880.54	not significant
1443	ATMIN	-1.04	7.06E-02	2.46E-01	2143.76	not significant
1444	TTC26	-1.04	1.06E-01	3.20E-01	673.97	not significant
1445	AGO2	-1.04	1.06E-01	3.20E-01	1246.33	not significant
1446	KCTD2	-1.04	7.23E-02	2.50E-01	2202.48	not significant
1447	EFHD2	-1.04	7.23E-02	2.50E-01	2912.95	not significant
1448	SLMAP	-1.04	7.14E-02	2.48E-01	2081.07	not significant
1449	BAP1	-1.04	3.80E-02	1.64E-01	5311.38	not significant
1450	PPP6R1	-1.04	1.60E-02	9.29E-02	18886.25	not significant
1451	MTX1	-1.04	1.02E-01	3.11E-01	474.24	not significant
1452	PPIP5K2	-1.04	8.87E-02	2.85E-01	1472.06	not significant
1453	PRPF6	-1.04	5.66E-02	2.13E-01	3696.80	not significant
1454	PPIG	-1.04	6.54E-02	2.34E-01	3068.92	not significant
1455	NUP214	-1.04	9.12E-02	2.89E-01	3117.44	not significant
1456	PSMC4	-1.04	4.87E-02	1.94E-01	5013.29	not significant
1457	XRCC6	-1.04	3.26E-02	1.47E-01	22199.72	not significant
1458	PUM2	-1.04	2.84E-02	1.35E-01	9412.40	not significant
1459	POC5	-1.04	1.09E-01	3.25E-01	850.79	not significant
1460	EPHB1	-1.04	7.44E-02	2.54E-01	233.73	not significant
1461	CYHR1	-1.04	1.09E-01	3.25E-01	724.95	not significant
1462	PPP1R3B	-1.04	1.06E-01	3.19E-01	516.71	not significant
1463	TRDMT1	-1.04	1.09E-01	3.26E-01	776.31	not significant
1464	EIF4E	-1.04	1.00E-01	3.09E-01	1515.52	not significant
1465	CMSS1	-1.04	8.83E-02	2.84E-01	2097.84	not significant
1466	TAF6	-1.04	4.34E-02	1.80E-01	4238.05	not significant
1467	NANS	-1.04	1.11E-01	3.29E-01	664.13	not significant
1468	PSMD10	-1.04	1.02E-01	3.11E-01	1358.26	not significant
1469	ZNF609	-1.04	8.38E-02	2.75E-01	2867.03	not significant
1470	IPO13	-1.04	8.06E-02	2.68E-01	1861.08	not significant
1471	CAP1	-1.04	2.13E-02	1.12E-01	10656.08	not significant
1472	ARMC1	-1.04	5.70E-02	2.15E-01	4140.90	not significant
1473	PGK1	-1.04	3.63E-02	1.59E-01	14050.24	not significant
1474	SF3B3	-1.04	1.55E-02	9.09E-02	14685.47	not significant
1475	NHEJ1	-1.04	1.11E-01	3.29E-01	712.77	not significant
1476	ACOT7	-1.04	5.34E-02	2.06E-01	6932.40	not significant
1477	BATF	-1.04	1.12E-01	3.31E-01	879.93	not significant
1478	MOSPD1	-1.04	1.28E-01	3.59E-01	587.24	not significant
1479	FGFR1OP	-1.04	9.86E-02	3.05E-01	1268.17	not significant
1480	ICMT	-1.04	3.64E-02	1.59E-01	7489.01	not significant
1481	CBFB	-1.04	2.47E-02	1.24E-01	10797.61	not significant
1482	ACTR2	-1.04	1.29E-02	7.93E-02	18394.38	not significant
1483	NOSIP	-1.04	1.08E-01	3.23E-01	1581.76	not significant

1484	GEN1	-1.04	1.06E-01	3.19E-01	2024.50	not significant
1485	CALM3	-1.04	3.73E-02	1.62E-01	17252.11	not significant
1486	RAF1	-1.04	3.20E-02	1.46E-01	5833.42	not significant
1487	GTF2F2	-1.04	9.73E-02	3.03E-01	1551.57	not significant
1488	SUV420H1	-1.04	1.00E-01	3.09E-01	1271.38	not significant
1489	MOB1B	-1.04	6.31E-02	2.29E-01	4253.73	not significant
1490	HSP90AB1	-1.04	1.12E-02	7.21E-02	78889.81	not significant
1491	FHL2	-1.04	8.36E-02	2.75E-01	257.80	not significant
1492	KCTD10	-1.04	6.35E-02	2.29E-01	3107.47	not significant
1493	PTPN1	-1.04	4.38E-02	1.81E-01	4307.91	not significant
1494	GNAQ	-1.04	5.02E-02	1.98E-01	5281.43	not significant
1495	CCDC112	-1.04	1.01E-01	3.09E-01	390.95	not significant
1496	UTP14C	-1.04	1.05E-01	3.17E-01	1276.29	not significant
1497	PPIL2	-1.04	6.50E-02	2.33E-01	2849.22	not significant
1498	GNB4	-1.04	4.07E-02	1.71E-01	5418.66	not significant
1499	FLAD1	-1.04	1.06E-01	3.20E-01	1037.66	not significant
1500	TSR2	-1.04	9.25E-02	2.92E-01	1616.58	not significant
1501	STRBP	-1.04	7.00E-02	2.45E-01	2717.54	not significant
1502	NUP43	-1.04	6.37E-02	2.30E-01	3123.89	not significant
1503	ASRGL1	-1.04	8.88E-02	2.85E-01	1736.22	not significant
1504	CDC23	-1.04	6.14E-02	2.25E-01	3024.58	not significant
1505	HNRNPR	-1.04	2.48E-02	1.24E-01	17702.80	not significant
1506	AP3D1	-1.04	3.23E-02	1.47E-01	6470.37	not significant
1507	TMEM126A	-1.04	1.14E-01	3.35E-01	799.26	not significant
1508	BOLA3	-1.04	1.11E-01	3.28E-01	1103.54	not significant
1509	VDAC2	-1.04	1.01E-01	3.09E-01	1793.13	not significant
1510	LRRC28	-1.04	1.15E-01	3.35E-01	916.77	not significant
1511	HOMER1	-1.04	1.02E-01	3.11E-01	1240.16	not significant
1512	TUBGCP2	-1.04	7.08E-02	2.47E-01	2440.29	not significant
1513	RCHY1	-1.04	1.03E-01	3.14E-01	1338.68	not significant
1514	CASP7	-1.04	8.86E-02	2.85E-01	1692.28	not significant
1515	NDUFA5	-1.04	8.80E-02	2.84E-01	2548.40	not significant
1516	RPAP1	-1.04	8.74E-02	2.83E-01	1839.69	not significant
1517	MANF	-1.04	1.09E-01	3.25E-01	1330.20	not significant
1518	FDXR	-1.04	1.15E-01	3.35E-01	831.73	not significant
1519	ETFA	-1.04	8.68E-02	2.82E-01	3148.90	not significant
1520	PIGT	-1.04	7.05E-02	2.46E-01	3271.78	not significant
1521	AGFG1	-1.04	5.94E-02	2.20E-01	3747.12	not significant
1522	KANSL3	-1.04	4.06E-02	1.71E-01	5686.59	not significant
1523	HS6ST1	-1.04	3.74E-02	1.62E-01	6115.11	not significant
1524	AP3S1	-1.04	9.70E-02	3.02E-01	2205.39	not significant
1525	LINC01420	-1.04	1.14E-01	3.35E-01	1077.43	not significant
1526	C1orf198	-1.04	1.15E-01	3.36E-01	854.68	not significant
1527	NIPA2	-1.04	5.88E-02	2.19E-01	3650.87	not significant
1528	HNRNPK	-1.04	2.15E-02	1.13E-01	34184.53	not significant
1529	ZNF829	-1.04	8.56E-02	2.79E-01	280.67	not significant
1530	INTS6	-1.04	1.03E-01	3.13E-01	1624.84	not significant
1531	VDAC1	-1.04	3.39E-02	1.51E-01	8795.20	not significant
1532	LINC01132	-1.04	9.72E-02	3.02E-01	417.08	not significant
1533	FBXO41	-1.04	8.45E-02	2.76E-01	2650.60	not significant
1534	CAPRIN1	-1.04	2.92E-02	1.38E-01	19819.25	not significant
1535	SBNO1	-1.04	6.51E-02	2.33E-01	4982.14	not significant
1536	PARS2	-1.04	9.09E-02	2.89E-01	274.08	not significant
1537	ZMYM6	-1.04	1.19E-01	3.43E-01	932.26	not significant
1538	PCYT1A	-1.04	1.20E-01	3.45E-01	668.57	not significant
1539	GTF2A2	-1.04	1.10E-01	3.27E-01	1426.64	not significant
1540	PSPC1	-1.04	9.88E-02	3.06E-01	1598.69	not significant
1541	NCDN	-1.04	9.36E-02	2.95E-01	1700.92	not significant
1542	NPEPPS	-1.04	6.09E-02	2.23E-01	3388.11	not significant
1543	POLA1	-1.04	6.61E-02	2.36E-01	4809.71	not significant
1544	PPME1	-1.04	9.97E-02	3.08E-01	1563.89	not significant
1545	PYCR1	-1.04	8.66E-02	2.81E-01	2253.11	not significant
1546	FBXO45	-1.04	7.65E-02	2.59E-01	2749.77	not significant
1547	TMOD3	-1.04	8.73E-02	2.83E-01	3121.20	not significant
1548	MTA2	-1.04	2.53E-02	1.26E-01	9492.48	not significant
1549	NARS	-1.04	2.83E-02	1.35E-01	9668.44	not significant
1550	PTBP1	-1.04	2.05E-02	1.09E-01	27546.09	not significant
1551	SLC25A46	-1.04	7.31E-02	2.52E-01	2945.62	not significant
1552	PDLIM2	-1.04	1.09E-01	3.26E-01	1505.75	not significant
1553	UBA5	-1.04	9.44E-02	2.96E-01	1959.98	not significant
1554	AREL1	-1.04	7.58E-02	2.57E-01	2973.55	not significant
1555	ADAM19	-1.04	5.50E-02	2.10E-01	12167.70	not significant
1556	CPSF2	-1.04	4.48E-02	1.84E-01	5681.76	not significant
1557	DICER1	-1.04	8.97E-02	2.87E-01	6383.48	not significant
1558	FIP1L1	-1.04	8.21E-02	2.71E-01	3032.30	not significant
1559	RAD23B	-1.04	6.15E-02	2.25E-01	5640.16	not significant
1560	TMEM167A	-1.04	4.63E-02	1.87E-01	4861.10	not significant
1561	ZFYVE21	-1.04	1.17E-01	3.40E-01	493.48	not significant
1562	IQCB1	-1.04	1.08E-01	3.24E-01	1378.18	not significant
1563	ADH5	-1.04	7.73E-02	2.61E-01	3975.31	not significant
1564	UBE2D3	-1.04	4.73E-02	1.89E-01	14661.71	not significant
1565	RAB30	-1.04	6.40E-02	2.30E-01	184.22	not significant
1566	CENPP	-1.04	1.18E-01	3.40E-01	561.46	not significant
1567	TRMT13	-1.04	1.16E-01	3.37E-01	1259.71	not significant
1568	THAP11	-1.04	1.03E-01	3.13E-01	2221.63	not significant
1569	MLEC	-1.04	4.95E-02	1.96E-01	16772.72	not significant
1570	DYNLRB1	-1.04	8.46E-02	2.76E-01	2887.18	not significant
1571	LATS1	-1.04	1.03E-01	3.13E-01	1801.98	not significant

1572	NUP88	-1.04	8.52E-02	2.78E-01	2214.76	not significant
1573	AP1B1	-1.04	4.42E-02	1.82E-01	6279.98	not significant
1574	KDM1A	-1.04	3.52E-02	1.56E-01	6724.29	not significant
1575	BRIX1	-1.04	8.41E-02	2.76E-01	2688.23	not significant
1576	MKRN2	-1.04	8.78E-02	2.83E-01	2488.16	not significant
1577	PRKCH	-1.04	2.44E-02	1.23E-01	13590.72	not significant
1578	CD63	-1.04	1.01E-01	3.09E-01	2510.22	not significant
1579	SDHB	-1.04	1.06E-01	3.20E-01	3175.65	not significant
1580	DIMT1	-1.04	1.11E-01	3.29E-01	1306.32	not significant
1581	PRMT7	-1.04	1.02E-01	3.11E-01	1609.73	not significant
1582	FASTKD1	-1.04	1.02E-01	3.12E-01	1592.63	not significant
1583	EPB41L2	-1.04	8.45E-02	2.76E-01	4015.57	not significant
1584	NDUFC2	-1.04	1.23E-01	3.52E-01	1024.94	not significant
1585	SRP14	-1.04	8.98E-02	2.87E-01	5366.01	not significant
1586	RPRD1A	-1.04	8.95E-02	2.86E-01	2286.54	not significant
1587	YY1AP1	-1.04	8.95E-02	2.86E-01	2137.93	not significant
1588	LGALS8	-1.04	1.03E-01	3.13E-01	1994.38	not significant
1589	XPO1	-1.04	3.78E-02	1.63E-01	20347.66	not significant
1590	RTN4IP1	-1.04	7.82E-02	2.63E-01	210.58	not significant
1591	ARHGEF7	-1.04	7.02E-02	2.46E-01	3272.78	not significant
1592	TMED5	-1.04	4.28E-02	1.78E-01	6462.77	not significant
1593	ATP5I	-1.04	1.17E-01	3.39E-01	2119.69	not significant
1594	HSPA4L	-1.04	1.13E-01	3.33E-01	1382.72	not significant
1595	RAB5C	-1.04	9.67E-02	3.02E-01	2024.12	not significant
1596	PRDX1	-1.04	5.70E-02	2.15E-01	15509.13	not significant
1597	RBMX	-1.04	2.38E-02	1.21E-01	17136.97	not significant
1598	RYK	-1.04	1.15E-01	3.36E-01	1232.05	not significant
1599	NSFL1C	-1.04	7.57E-02	2.57E-01	2768.01	not significant
1600	NOMO3	-1.04	5.09E-02	1.99E-01	137.56	not significant
1601	CCDC58	-1.04	1.29E-01	3.61E-01	863.74	not significant
1602	CLPX	-1.04	1.16E-01	3.37E-01	1291.03	not significant
1603	DRG1	-1.04	8.14E-02	2.70E-01	2725.96	not significant
1604	IKBKAP	-1.04	8.56E-02	2.79E-01	2373.96	not significant
1605	GLYR1	-1.04	5.96E-02	2.21E-01	3911.05	not significant
1606	NUPL2	-1.04	1.14E-01	3.35E-01	1071.69	not significant
1607	RHBDD3	-1.04	1.21E-01	3.47E-01	1197.94	not significant
1608	PIP4K2B	-1.04	5.74E-02	2.16E-01	6043.69	not significant
1609	ARPP19	-1.04	3.20E-02	1.46E-01	9458.38	not significant
1610	GARS	-1.04	2.89E-02	1.37E-01	11879.20	not significant
1611	HSD17B10	-1.04	1.30E-01	3.62E-01	1008.32	not significant
1612	RCAN1	-1.04	1.17E-01	3.39E-01	1318.23	not significant
1613	SRP54	-1.04	8.24E-02	2.72E-01	2950.75	not significant
1614	INTS10	-1.04	8.85E-02	2.85E-01	2764.65	not significant
1615	GSK3B	-1.04	5.48E-02	2.09E-01	6522.40	not significant
1616	MRPL1	-1.04	1.24E-01	3.52E-01	1092.34	not significant
1617	VWA8	-1.04	1.22E-01	3.49E-01	1136.49	not significant
1618	UBE2E1	-1.04	9.92E-02	3.07E-01	3149.92	not significant
1619	BUB3	-1.04	5.72E-02	2.15E-01	7771.71	not significant
1620	CWC22	-1.04	1.07E-01	3.22E-01	1546.41	not significant
1621	CLEC16A	-1.04	9.58E-02	2.99E-01	2412.73	not significant
1622	ATG5	-1.04	1.04E-01	3.16E-01	1685.86	not significant
1623	NIP7	-1.04	9.12E-02	2.89E-01	2983.68	not significant
1624	MCU	-1.04	1.32E-01	3.65E-01	847.98	not significant
1625	RNF111	-1.04	1.29E-01	3.61E-01	1219.43	not significant
1626	CHMP7	-1.04	7.61E-02	2.58E-01	3349.29	not significant
1627	BCAT1	-1.04	6.94E-02	2.44E-01	4498.62	not significant
1628	EXOSC5	-1.04	1.32E-01	3.67E-01	889.92	not significant
1629	MED29	-1.04	1.13E-01	3.32E-01	1507.03	not significant
1630	EIF3I	-1.04	7.57E-02	2.57E-01	10081.24	not significant
1631	RAB6A	-1.04	6.97E-02	2.44E-01	3812.34	not significant
1632	POLE3	-1.04	5.86E-02	2.18E-01	7430.03	not significant
1633	WDR1	-1.04	3.07E-02	1.42E-01	13990.57	not significant
1634	YRDC	-1.04	1.15E-01	3.36E-01	1779.29	not significant
1635	ZNF142	-1.04	1.16E-01	3.38E-01	1991.45	not significant
1636	C1orf52	-1.04	1.33E-01	3.67E-01	1057.03	not significant
1637	ABL2	-1.04	1.34E-01	3.70E-01	1114.68	not significant
1638	TNRC6A	-1.04	1.23E-01	3.50E-01	2616.05	not significant
1639	PIGG	-1.04	1.26E-01	3.56E-01	1332.19	not significant
1640	EPHX4	-1.04	7.25E-02	2.51E-01	178.37	not significant
1641	TBC1D4	-1.04	1.23E-01	3.51E-01	1289.01	not significant
1642	GDAP2	-1.04	1.36E-01	3.73E-01	770.39	not significant
1643	ARFGEF1	-1.04	7.22E-02	2.50E-01	4902.18	not significant
1644	PRDM2	-1.04	1.33E-01	3.67E-01	1260.54	not significant
1645	GOT1	-1.04	1.16E-01	3.38E-01	1889.79	not significant
1646	GATB	-1.04	1.29E-01	3.61E-01	796.06	not significant
1647	UTP11L	-1.04	1.09E-01	3.25E-01	2288.76	not significant
1648	NAB2	-1.04	1.22E-01	3.49E-01	1644.90	not significant
1649	VAT1	-1.04	1.01E-01	3.10E-01	2273.64	not significant
1650	NF2	-1.04	9.41E-02	2.96E-01	2530.47	not significant
1651	EFCAB14	-1.04	7.29E-02	2.51E-01	4891.63	not significant
1652	ZNF546	-1.04	1.46E-01	3.90E-01	197.08	not significant
1653	SPOPL	-1.04	1.37E-01	3.75E-01	628.85	not significant
1654	KIF2A	-1.04	6.13E-02	2.25E-01	5266.73	not significant
1655	HIC2	-1.04	1.36E-01	3.73E-01	652.29	not significant
1656	RIOK1	-1.04	9.43E-02	2.96E-01	2840.55	not significant
1657	PEX5	-1.04	1.07E-01	3.21E-01	1911.74	not significant
1658	EXOC5	-1.04	7.64E-02	2.59E-01	5156.44	not significant
1659	PAQR3	-1.03	1.13E-01	3.32E-01	2294.58	not significant

1660	POP4	-1.03	1.12E-01	3.31E-01	2035.76	not significant
1661	SUPT4H1	-1.03	7.76E-02	2.61E-01	6377.82	not significant
1662	AGPAT3	-1.03	9.41E-02	2.96E-01	2745.85	not significant
1663	DSE	-1.03	3.64E-02	1.59E-01	113.95	not significant
1664	GPR155	-1.03	1.31E-01	3.65E-01	482.66	not significant
1665	MRPL39	-1.03	1.30E-01	3.63E-01	1245.13	not significant
1666	NLE1	-1.03	1.27E-01	3.58E-01	1390.14	not significant
1667	DHX29	-1.03	1.26E-01	3.56E-01	1485.22	not significant
1668	FAM126A	-1.03	1.17E-01	3.39E-01	1748.71	not significant
1669	MYO1B	-1.03	1.02E-01	3.11E-01	2264.71	not significant
1670	ASCC2	-1.03	7.55E-02	2.57E-01	3505.29	not significant
1671	ZNF493	-1.03	1.38E-01	3.77E-01	1071.82	not significant
1672	RPS2	-1.03	7.06E-02	2.46E-01	41376.24	not significant
1673	REV3L	-1.03	1.23E-01	3.51E-01	2364.28	not significant
1674	ALG3	-1.03	1.17E-01	3.39E-01	1840.10	not significant
1675	ZCCHC3	-1.03	9.65E-02	3.01E-01	2857.93	not significant
1676	USP24	-1.03	8.92E-02	2.86E-01	5694.20	not significant
1677	FNBP1	-1.03	4.51E-02	1.84E-01	8044.04	not significant
1678	CTSH	-1.03	1.25E-01	3.54E-01	1436.22	not significant
1679	RNF41	-1.03	1.17E-01	3.40E-01	1851.85	not significant
1680	KNOP1	-1.03	1.28E-01	3.60E-01	1210.75	not significant
1681	CEP55	-1.03	8.84E-02	2.85E-01	3806.45	not significant
1682	POLR3F	-1.03	1.40E-01	3.81E-01	759.17	not significant
1683	DNM2	-1.03	5.15E-02	2.01E-01	8053.26	not significant
1684	CLSTN3	-1.03	1.31E-01	3.64E-01	1430.71	not significant
1685	ZWILCH	-1.03	1.19E-01	3.44E-01	2039.16	not significant
1686	CDCA3	-1.03	1.10E-01	3.26E-01	302.46	not significant
1687	CDC40	-1.03	1.14E-01	3.35E-01	1688.18	not significant
1688	SLAIN2	-1.03	1.06E-01	3.19E-01	2436.32	not significant
1689	KCTD11	-1.03	8.26E-02	2.73E-01	186.62	not significant
1690	RFK	-1.03	1.19E-01	3.44E-01	1767.24	not significant
1691	C17orf75	-1.03	1.33E-01	3.68E-01	1189.85	not significant
1692	INTS3	-1.03	1.31E-01	3.65E-01	1279.55	not significant
1693	POLR1C	-1.03	1.43E-01	3.86E-01	1067.14	not significant
1694	SUGP1	-1.03	1.24E-01	3.52E-01	1073.38	not significant
1695	HOOK3	-1.03	1.30E-01	3.62E-01	2912.25	not significant
1696	ADIPOR2	-1.03	5.77E-02	2.16E-01	6439.38	not significant
1697	ERGIC2	-1.03	1.30E-01	3.62E-01	1499.73	not significant
1698	ARIH2	-1.03	8.86E-02	2.85E-01	3536.89	not significant
1699	HEATR2	-1.03	9.86E-02	3.05E-01	2637.22	not significant
1700	CAMKK2	-1.03	8.96E-02	2.87E-01	4608.51	not significant
1701	ZNF383	-1.03	9.84E-02	3.05E-01	240.96	not significant
1702	CCSER2	-1.03	1.33E-01	3.68E-01	2191.92	not significant
1703	SENP6	-1.03	8.88E-02	2.85E-01	4409.32	not significant
1704	NUP50	-1.03	6.01E-02	2.21E-01	7950.82	not significant
1705	TBRG1	-1.03	1.21E-01	3.48E-01	2002.72	not significant
1706	TMEM186	-1.03	1.42E-01	3.84E-01	488.37	not significant
1707	CFLAR	-1.03	1.21E-01	3.48E-01	1133.32	not significant
1708	STAMBP	-1.03	1.13E-01	3.32E-01	2145.76	not significant
1709	SASH3	-1.03	4.14E-02	1.74E-01	24247.58	not significant
1710	ZNF808	-1.03	1.23E-01	3.52E-01	390.37	not significant
1711	DLEU2	-1.03	1.37E-01	3.75E-01	650.87	not significant
1712	EIF4H	-1.03	1.44E-01	3.88E-01	982.74	not significant
1713	DARS2	-1.03	5.81E-01	NA	24.54	not significant
1714	TET1	-1.03	1.46E-01	3.91E-01	720.04	not significant
1715	ATIC	-1.03	5.93E-02	2.20E-01	6986.59	not significant
1716	LOC100130744	-1.03	7.39E-02	2.53E-01	166.48	not significant
1717	UGDH	-1.03	1.51E-01	3.98E-01	845.67	not significant
1718	ACBD7	-1.03	1.49E-01	3.96E-01	954.52	not significant
1719	TBPL1	-1.03	1.45E-01	3.90E-01	942.34	not significant
1720	ARHGDIB	-1.03	4.96E-02	1.96E-01	35642.96	not significant
1721	RNF138	-1.03	7.82E-02	2.63E-01	3986.57	not significant
1722	RAB11FIP1	-1.03	6.78E-02	2.40E-01	13626.32	not significant
1723	PINX1	-1.03	1.46E-01	3.90E-01	1148.97	not significant
1724	TRMT6	-1.03	1.26E-01	3.56E-01	2043.16	not significant
1725	HIF1AN	-1.03	9.35E-02	2.95E-01	3997.96	not significant
1726	ZPR1	-1.03	1.24E-01	3.52E-01	1722.00	not significant
1727	EEA1	-1.03	1.39E-01	3.80E-01	1782.55	not significant
1728	ROCK2	-1.03	1.37E-01	3.75E-01	1847.65	not significant
1729	C1QBP	-1.03	9.49E-02	2.97E-01	15640.66	not significant
1730	CACTIN	-1.03	1.26E-01	3.55E-01	1831.51	not significant
1731	CKAP2L	-1.03	1.30E-01	3.63E-01	1916.74	not significant
1732	EIF2B1	-1.03	8.32E-02	2.73E-01	4694.24	not significant
1733	SREBF1	-1.03	9.34E-02	2.95E-01	4284.17	not significant
1734	CISD3	-1.03	1.50E-01	3.97E-01	1858.94	not significant
1735	DNAJC8	-1.03	1.21E-01	3.47E-01	5382.96	not significant
1736	ANXA2	-1.03	1.26E-01	3.56E-01	314.30	not significant
1737	MTO1	-1.03	1.30E-01	3.63E-01	1836.59	not significant
1738	DNAJA2	-1.03	1.09E-01	3.25E-01	3553.76	not significant
1739	RAPGEF1	-1.03	1.24E-01	3.53E-01	2571.85	not significant
1740	GRK5	-1.03	1.15E-01	3.36E-01	2278.08	not significant
1741	FAM199X	-1.03	5.78E-02	2.16E-01	136.77	not significant
1742	ARID3B	-1.03	1.24E-01	3.52E-01	2325.09	not significant
1743	NUTF2	-1.03	1.10E-01	3.28E-01	5349.82	not significant
1744	CCT8	-1.03	5.76E-02	2.16E-01	13860.19	not significant
1745	TMEM203	-1.03	1.49E-01	3.96E-01	1343.10	not significant
1746	PREB	-1.03	1.24E-01	3.52E-01	2709.38	not significant
1747	FUBP3	-1.03	1.30E-01	3.63E-01	2027.51	not significant

1748	OSBPL8	-1.03	8.80E-02	2.84E-01	7715.22	not significant
1749	TMEM164	-1.03	9.10E-02	2.89E-01	4757.78	not significant
1750	USP7	-1.03	4.63E-02	1.87E-01	10468.00	not significant
1751	PTMS	-1.03	1.07E-01	3.21E-01	233.17	not significant
1752	KCNAB3	-1.03	9.96E-02	3.08E-01	199.78	not significant
1753	RPP38	-1.03	1.43E-01	3.86E-01	464.42	not significant
1754	ZFP64	-1.03	1.56E-01	4.04E-01	740.85	not significant
1755	FRS2	-1.03	1.51E-01	3.99E-01	1115.70	not significant
1756	YME1L1	-1.03	5.51E-02	2.10E-01	9059.60	not significant
1757	VTI1A	-1.03	1.46E-01	3.90E-01	1234.74	not significant
1758	RNMT	-1.03	1.13E-01	3.33E-01	3169.16	not significant
1759	CENPI	-1.03	1.38E-01	3.78E-01	604.79	not significant
1760	CCZ1B	-1.03	1.56E-01	4.04E-01	718.33	not significant
1761	ARV1	-1.03	1.51E-01	3.99E-01	651.63	not significant
1762	HARS	-1.03	1.26E-01	3.56E-01	2401.24	not significant
1763	TIPRL	-1.03	9.42E-02	2.96E-01	4054.66	not significant
1764	CCNYL1	-1.03	1.55E-01	4.04E-01	646.84	not significant
1765	HCCS	-1.03	1.57E-01	4.05E-01	672.89	not significant
1766	MRPL20	-1.03	1.38E-01	3.77E-01	2854.86	not significant
1767	SMG6	-1.03	1.11E-01	3.29E-01	2835.00	not significant
1768	BDP1	-1.03	1.56E-01	4.04E-01	935.81	not significant
1769	MRPL22	-1.03	1.55E-01	4.03E-01	1237.38	not significant
1770	SNRNP25	-1.03	1.51E-01	3.98E-01	2041.10	not significant
1771	TMEM71	-1.03	9.70E-02	3.02E-01	183.92	not significant
1772	MPC1	-1.03	1.56E-01	4.04E-01	1565.83	not significant
1773	AGO3	-1.03	1.54E-01	4.03E-01	647.67	not significant
1774	SUPT20H	-1.03	1.26E-01	3.56E-01	2575.35	not significant
1775	SMPD4	-1.03	1.01E-01	3.09E-01	3920.54	not significant
1776	KHSRP	-1.03	5.73E-02	2.16E-01	15769.34	not significant
1777	RPAP2	-1.03	1.62E-01	4.12E-01	814.08	not significant
1778	ZDHHC18	-1.03	1.35E-01	3.71E-01	2001.76	not significant
1779	RAC1	-1.03	1.13E-01	3.33E-01	5270.03	not significant
1780	CLN8	-1.03	1.40E-01	3.81E-01	465.80	not significant
1781	PLEKHO2	-1.03	1.60E-01	4.10E-01	779.89	not significant
1782	SEC16A	-1.03	1.10E-01	3.27E-01	5592.82	not significant
1783	CGN	-1.03	1.41E-01	3.82E-01	374.47	not significant
1784	EPB41	-1.03	1.02E-01	3.12E-01	7411.08	not significant
1785	MAPRE1	-1.03	5.93E-02	2.20E-01	12724.09	not significant
1786	GMEB1	-1.03	1.47E-01	3.93E-01	522.48	not significant
1787	PHF23	-1.03	1.72E-01	4.26E-01	1237.41	not significant
1788	CDK2AP2	-1.03	1.33E-01	3.67E-01	4671.08	not significant
1789	SMYD5	-1.03	1.42E-01	3.84E-01	1802.64	not significant
1790	SLA	-1.03	1.04E-01	3.16E-01	3312.97	not significant
1791	SLTM	-1.03	1.07E-01	3.21E-01	4354.53	not significant
1792	PRKCB	-1.03	9.15E-02	2.90E-01	7671.96	not significant
1793	SUPT16H	-1.03	5.85E-02	2.18E-01	13624.90	not significant
1794	SCLT1	-1.03	1.63E-01	4.13E-01	812.49	not significant
1795	RFWD2	-1.03	1.41E-01	3.83E-01	1567.37	not significant
1796	TAOK1	-1.03	1.40E-01	3.81E-01	3667.74	not significant
1797	NME6	-1.03	1.64E-01	4.16E-01	702.58	not significant
1798	ARPC4	-1.03	1.42E-01	3.84E-01	3742.24	not significant
1799	LCK	-1.03	5.43E-02	2.08E-01	21650.40	not significant
1800	PSMD7	-1.03	1.04E-01	3.15E-01	5099.83	not significant
1801	ACER2	-1.03	1.04E-01	3.16E-01	163.36	not significant
1802	MT2A	-1.03	2.02E-01	4.67E-01	34834.43	not significant
1803	BZRAP1-AS1	-1.03	1.63E-01	4.14E-01	625.49	not significant
1804	PWP2	-1.03	1.61E-01	4.11E-01	1602.38	not significant
1805	CEP164	-1.03	1.65E-01	4.17E-01	905.73	not significant
1806	EGLN1	-1.03	1.59E-01	4.08E-01	1072.99	not significant
1807	MTMR1	-1.03	1.61E-01	4.11E-01	561.29	not significant
1808	MRPS2	-1.03	1.55E-01	4.04E-01	1439.65	not significant
1809	METTL2B	-1.03	1.64E-01	4.14E-01	1006.59	not significant
1810	KLHL21	-1.03	1.55E-01	4.03E-01	965.50	not significant
1811	THAP4	-1.03	1.47E-01	3.91E-01	1662.86	not significant
1812	ZNF197	-1.03	1.53E-01	4.01E-01	1308.02	not significant
1813	AKNA	-1.03	7.34E-02	2.52E-01	8882.48	not significant
1814	ZNF416	-1.03	1.41E-01	3.83E-01	358.65	not significant
1815	TARBP2	-1.03	1.62E-01	4.13E-01	1766.55	not significant
1816	SUFU	-1.03	1.57E-01	4.05E-01	1018.32	not significant
1817	GGA2	-1.03	1.67E-01	4.20E-01	692.49	not significant
1818	HSPBP1	-1.03	1.50E-01	3.97E-01	2101.06	not significant
1819	FAM98B	-1.03	1.38E-01	3.76E-01	2102.86	not significant
1820	BICD1	-1.03	2.08E-01	4.73E-01	565.93	not significant
1821	CAMKK1	-1.03	7.24E-02	2.51E-01	138.43	not significant
1822	RAB29	-1.03	1.73E-01	4.28E-01	960.38	not significant
1823	MATR3	-1.03	5.95E-02	2.21E-01	24871.43	not significant
1824	CCT3	-1.03	6.57E-02	2.35E-01	21332.67	not significant
1825	EXOC8	-1.03	1.68E-01	4.22E-01	1167.47	not significant
1826	ADK	-1.03	1.49E-01	3.95E-01	1650.52	not significant
1827	SLAIN1	-1.03	1.46E-01	3.90E-01	1947.45	not significant
1828	RPL7	-1.03	1.23E-01	3.52E-01	16638.34	not significant
1829	WDR20	-1.03	1.72E-01	4.26E-01	657.08	not significant
1830	KIF1C	-1.03	1.52E-01	3.99E-01	1814.05	not significant
1831	ANKRD46	-1.03	1.59E-01	4.07E-01	1457.80	not significant
1832	MED4	-1.03	1.25E-01	3.53E-01	3254.05	not significant
1833	MOB3A	-1.03	1.30E-01	3.63E-01	2758.35	not significant
1834	AZIN1	-1.03	4.56E-02	1.85E-01	18035.01	not significant
1835	SBF2	-1.03	1.68E-01	4.21E-01	631.47	not significant

1836	SLC25A51	-1.03	4.72E-01	NA	71.42	not significant
1837	RBBP5	-1.03	1.42E-01	3.84E-01	2101.99	not significant
1838	ATP8A2	-1.03	1.51E-01	3.98E-01	437.08	not significant
1839	DHDDS	-1.03	1.61E-01	4.11E-01	1342.47	not significant
1840	TOX4	-1.03	1.23E-01	3.51E-01	2750.19	not significant
1841	PITRM1	-1.03	1.26E-01	3.55E-01	2761.36	not significant
1842	BTBD1	-1.03	1.18E-01	3.41E-01	2826.02	not significant
1843	EIF3A	-1.03	6.79E-02	2.40E-01	21163.01	not significant
1844	CS	-1.03	5.99E-02	2.21E-01	10431.78	not significant
1845	LRTOMT	-1.03	1.12E-01	3.31E-01	225.93	not significant
1846	TYW5	-1.03	1.60E-01	4.10E-01	457.39	not significant
1847	ANKMY2	-1.03	1.65E-01	4.16E-01	1457.26	not significant
1848	RYBP	-1.03	1.63E-01	4.13E-01	1365.45	not significant
1849	ZNF106	-1.03	1.63E-01	4.14E-01	2535.82	not significant
1850	SMG8	-1.03	1.50E-01	3.97E-01	1680.30	not significant
1851	SEL1L	-1.03	1.24E-01	3.53E-01	5506.16	not significant
1852	SZRD1	-1.03	9.07E-02	2.88E-01	6966.21	not significant
1853	ZNF324	-1.03	1.70E-01	4.24E-01	530.63	not significant
1854	BCAT2	-1.03	1.75E-01	4.30E-01	1009.58	not significant
1855	SPAST	-1.03	1.61E-01	4.12E-01	2036.89	not significant
1856	FAM13B	-1.03	1.25E-01	3.55E-01	3163.53	not significant
1857	TET3	-1.03	1.63E-01	4.14E-01	3341.87	not significant
1858	UBR3	-1.03	1.66E-01	4.19E-01	1731.03	not significant
1859	NETO2	-1.03	1.61E-01	4.11E-01	1654.82	not significant
1860	COPS2	-1.03	1.55E-01	4.03E-01	1977.02	not significant
1861	EIF3D	-1.03	1.04E-01	3.16E-01	9928.68	not significant
1862	MCC	-1.03	1.43E-01	3.86E-01	317.45	not significant
1863	TSEN2	-1.03	1.67E-01	4.20E-01	466.69	not significant
1864	GPR17	-1.03	1.01E-02	NA	53.12	not significant
1865	AQR	-1.03	1.55E-01	4.04E-01	2338.92	not significant
1866	SEC24C	-1.03	1.21E-01	3.47E-01	6271.10	not significant
1867	CCSAP	-1.03	1.34E-01	3.69E-01	2865.27	not significant
1868	NACAP1	-1.03	1.70E-02	NA	62.41	not significant
1869	GYG2	-1.03	1.52E-01	3.99E-01	369.61	not significant
1870	ITPR2	-1.03	1.66E-01	4.18E-01	2601.38	not significant
1871	VPS25	-1.03	1.56E-01	4.04E-01	1884.22	not significant
1872	SOS1	-1.03	1.72E-01	4.26E-01	2124.50	not significant
1873	RSBN1	-1.03	1.58E-01	4.06E-01	1547.29	not significant
1874	SON	-1.03	1.05E-01	3.18E-01	19350.90	not significant
1875	HSPD1	-1.03	7.29E-02	2.51E-01	32105.34	not significant
1876	CCDC18	-1.03	2.00E-01	4.64E-01	583.63	not significant
1877	ZNF436	-1.03	1.64E-01	4.15E-01	403.91	not significant
1878	ITPR1	-1.03	1.81E-01	4.38E-01	936.00	not significant
1879	FAM76B	-1.03	1.72E-01	4.26E-01	1192.85	not significant
1880	PISD	-1.03	1.48E-01	3.93E-01	2329.10	not significant
1881	TBC1D14	-1.03	1.15E-01	3.36E-01	3559.83	not significant
1882	ARPC2	-1.03	7.40E-02	2.53E-01	12756.44	not significant
1883	ATP5EP2	-1.03	5.72E-02	NA	87.50	not significant
1884	CFDP1	-1.03	1.52E-01	4.00E-01	3026.79	not significant
1885	WIPF2	-1.03	1.75E-01	4.30E-01	1538.76	not significant
1886	RBM10	-1.03	1.55E-01	4.03E-01	1777.69	not significant
1887	SMCR8	-1.03	1.55E-01	4.04E-01	2714.99	not significant
1888	TTLL4	-1.03	1.73E-01	4.27E-01	2139.93	not significant
1889	TCERG1	-1.03	1.14E-01	3.35E-01	5832.84	not significant
1890	RASSF4	-1.03	1.14E-01	3.34E-01	214.50	not significant
1891	KANSL2	-1.03	1.42E-01	3.84E-01	2378.57	not significant
1892	RNF20	-1.03	1.58E-01	4.06E-01	1723.12	not significant
1893	ARF1	-1.03	1.08E-01	3.24E-01	13515.96	not significant
1894	HCFC2	-1.03	1.82E-01	4.40E-01	744.84	not significant
1895	ANKEF1	-1.03	1.49E-01	3.95E-01	250.73	not significant
1896	CLIP3	-1.03	1.34E-01	3.70E-01	253.01	not significant
1897	ZNF304	-1.03	1.83E-01	4.41E-01	736.80	not significant
1898	RC3H2	-1.03	1.79E-01	4.36E-01	1548.81	not significant
1899	43533_16638	-1.03	1.63E-01	4.13E-01	1783.04	not significant
1900	MTMR10	-1.03	1.69E-01	4.23E-01	1526.79	not significant
1901	KLC2	-1.03	1.44E-01	3.86E-01	2641.87	not significant
1902	CBX1	-1.03	8.44E-02	2.76E-01	8205.95	not significant
1903	SNTB2	-1.03	1.80E-01	4.37E-01	1063.20	not significant
1904	MLKL	-1.03	1.79E-01	4.36E-01	986.95	not significant
1905	GTPBP10	-1.03	1.60E-01	4.09E-01	1209.99	not significant
1906	PPP2CB	-1.03	1.38E-01	3.76E-01	2890.61	not significant
1907	ZCCHC17	-1.03	1.76E-01	4.31E-01	1318.61	not significant
1908	AAR2	-1.03	1.33E-01	3.67E-01	2859.78	not significant
1909	CACYBP	-1.03	1.21E-01	3.48E-01	5671.28	not significant
1910	ZNF644	-1.03	1.49E-01	3.96E-01	2647.68	not significant
1911	TLN1	-1.03	1.14E-01	3.35E-01	16525.05	not significant
1912	HMGA1	-1.03	8.31E-02	2.73E-01	10156.56	not significant
1913	HIST1H2BH	-1.03	6.88E-02	2.42E-01	128.85	not significant
1914	DDIT3	-1.03	1.61E-01	4.11E-01	428.89	not significant
1915	CUL5	-1.03	1.64E-01	4.16E-01	1713.46	not significant
1916	MPP6	-1.03	1.68E-01	4.21E-01	463.97	not significant
1917	ALYREF	-1.03	1.41E-01	3.83E-01	10475.63	not significant
1918	SLC5A6	-1.03	1.35E-01	3.72E-01	3841.61	not significant
1919	ZNF137P	-1.03	1.42E-01	3.84E-01	279.92	not significant
1920	ZNF189	-1.03	1.71E-01	4.25E-01	520.87	not significant
1921	GAS7	-1.03	1.39E-01	3.79E-01	3347.43	not significant
1922	S100A11	-1.03	1.93E-01	4.55E-01	898.97	not significant
1923	LOC339862	-1.03	1.91E-01	4.51E-01	886.79	not significant

1924	SRM	-1.03	1.57E-01	4.05E-01	7122.26	not significant
1925	WDR5	-1.03	1.34E-01	3.70E-01	3196.65	not significant
1926	TFCP2	-1.03	1.16E-01	3.38E-01	4363.29	not significant
1927	MKI67	-1.03	1.09E-01	3.25E-01	21745.85	not significant
1928	ZNF778	-1.03	1.19E-01	3.45E-01	210.37	not significant
1929	GEMIN4	-1.03	1.49E-01	3.95E-01	2675.97	not significant
1930	NDUFS1	-1.03	1.16E-01	3.37E-01	3562.49	not significant
1931	ELAC2	-1.03	1.10E-01	3.28E-01	4642.00	not significant
1932	UTP6	-1.03	1.72E-01	4.26E-01	1967.47	not significant
1933	PYGB	-1.03	1.61E-01	4.11E-01	2026.37	not significant
1934	MYO7B	-1.03	6.43E-02	2.31E-01	35337.26	not significant
1935	TTC27	-1.03	1.82E-01	4.39E-01	1443.80	not significant
1936	HMCES	-1.03	1.58E-01	4.07E-01	2772.98	not significant
1937	KXD1	-1.03	1.52E-01	3.99E-01	2756.02	not significant
1938	FUBP1	-1.03	1.05E-01	3.18E-01	7566.61	not significant
1939	TULP4	-1.03	1.91E-01	4.51E-01	913.48	not significant
1940	C16orf70	-1.03	1.94E-01	4.56E-01	1107.21	not significant
1941	MCPH1	-1.03	1.76E-01	4.32E-01	1603.49	not significant
1942	MRPL13	-1.03	1.67E-01	4.20E-01	2474.62	not significant
1943	YTHDF3	-1.03	1.51E-01	3.98E-01	2635.93	not significant
1944	RGS3	-1.03	1.88E-01	4.47E-01	660.05	not significant
1945	TRMT5	-1.03	1.95E-01	4.57E-01	763.93	not significant
1946	ZNF254	-1.03	1.80E-01	4.37E-01	1243.25	not significant
1947	KIDINS220	-1.03	1.45E-01	3.88E-01	4160.66	not significant
1948	RNF40	-1.03	1.05E-01	3.18E-01	5755.58	not significant
1949	DHX30	-1.03	1.15E-01	3.36E-01	5616.94	not significant
1950	SOX12	-1.03	1.88E-01	4.48E-01	1029.74	not significant
1951	RINT1	-1.03	1.83E-01	4.40E-01	1381.67	not significant
1952	CIPC	-1.03	1.84E-01	4.42E-01	1175.74	not significant
1953	EIF1AX	-1.03	1.48E-01	3.94E-01	2916.44	not significant
1954	ZDHHC5	-1.03	1.38E-01	3.76E-01	6142.55	not significant
1955	MTRF1L	-1.03	1.53E-01	4.01E-01	292.11	not significant
1956	NAF1	-1.03	1.88E-01	4.47E-01	1117.97	not significant
1957	RNH1	-1.03	1.45E-01	3.88E-01	3037.59	not significant
1958	FBXO18	-1.03	1.79E-01	4.36E-01	2001.25	not significant
1959	ST6GALNAC6	-1.03	1.81E-01	4.38E-01	529.48	not significant
1960	C5orf22	-1.03	1.80E-01	4.37E-01	1466.28	not significant
1961	ATP6V1D	-1.03	1.68E-01	4.21E-01	1691.02	not significant
1962	SH3PXD2A	-1.03	1.71E-01	4.25E-01	2150.12	not significant
1963	CFAP97	-1.03	1.39E-01	3.79E-01	3048.03	not significant
1964	NT5DC3	-1.03	1.74E-01	4.30E-01	390.98	not significant
1965	TFB2M	-1.03	2.04E-01	4.70E-01	974.15	not significant
1966	MSN	-1.03	9.18E-02	2.91E-01	41851.88	not significant
1967	INPP1	-1.03	7.19E-02	2.49E-01	117.29	not significant
1968	MAP1A	-1.03	1.84E-01	4.42E-01	6156.22	not significant
1969	EMC3-AS1	-1.03	2.00E-01	4.64E-01	683.18	not significant
1970	SLC35D1	-1.03	1.76E-01	4.32E-01	2075.91	not significant
1971	USP38	-1.03	1.75E-01	4.31E-01	2403.09	not significant
1972	APPL1	-1.03	1.35E-01	3.72E-01	4179.68	not significant
1973	BPGM	-1.03	1.94E-01	4.56E-01	721.21	not significant
1974	CDK5RAP1	-1.03	1.84E-01	4.41E-01	1310.59	not significant
1975	WEE1	-1.03	1.21E-01	3.48E-01	4067.80	not significant
1976	TRAPPC8	-1.03	1.63E-01	4.14E-01	2363.17	not significant
1977	BUB1B	-1.03	1.56E-01	4.04E-01	2798.01	not significant
1978	TMTC3	-1.03	1.94E-01	4.55E-01	582.03	not significant
1979	NTMT1	-1.03	1.98E-01	4.62E-01	783.47	not significant
1980	NKD2	-1.03	1.89E-01	4.48E-01	615.30	not significant
1981	TAP1	-1.03	2.20E-01	4.86E-01	940.22	not significant
1982	MYO5A	-1.03	1.87E-01	4.46E-01	1423.88	not significant
1983	PIM3	-1.03	1.62E-01	4.13E-01	2710.58	not significant
1984	NACC1	-1.03	1.22E-01	3.50E-01	5243.57	not significant
1985	RANBP2	-1.03	1.52E-01	4.00E-01	7315.18	not significant
1986	RPTOR	-1.03	1.21E-01	3.48E-01	8082.23	not significant
1987	INPP5D	-1.03	1.00E-01	3.09E-01	8178.66	not significant
1988	PBDC1	-1.03	1.07E-01	3.21E-01	172.77	not significant
1989	USP18	-1.03	2.09E-01	4.74E-01	579.91	not significant
1990	IKZF5	-1.03	1.94E-01	4.56E-01	975.17	not significant
1991	EBAG9	-1.03	1.70E-01	4.24E-01	1531.15	not significant
1992	PIK3R4	-1.03	1.91E-01	4.51E-01	2032.53	not significant
1993	NPRL3	-1.03	1.58E-01	4.07E-01	2495.31	not significant
1994	BRPF3	-1.03	1.82E-01	4.40E-01	1741.84	not significant
1995	PRCC	-1.03	1.47E-01	3.92E-01	3218.00	not significant
1996	TRIM37	-1.03	1.58E-01	4.06E-01	3028.81	not significant
1997	BZW2	-1.03	1.29E-01	3.62E-01	6842.67	not significant
1998	OTUB2	-1.03	5.44E-02	NA	100.29	not significant
1999	ZNF440	-1.03	1.53E-01	4.01E-01	289.22	not significant
2000	ZNF839	-1.03	1.85E-01	4.43E-01	397.86	not significant
2001	SLC35F2	-1.03	1.92E-01	4.53E-01	1151.30	not significant
2002	CDKAL1	-1.03	1.89E-01	4.48E-01	1249.01	not significant
2003	ZCRB1	-1.03	1.69E-01	4.23E-01	2305.71	not significant
2004	FAF1	-1.03	1.56E-01	4.04E-01	3664.62	not significant
2005	GTF3A	-1.03	1.24E-01	3.52E-01	12101.80	not significant
2006	RAD50	-1.03	1.69E-01	4.23E-01	2752.55	not significant
2007	ALDH18A1	-1.03	1.14E-01	3.34E-01	6247.77	not significant
2008	FAM168A	-1.03	1.56E-01	4.04E-01	3109.32	not significant
2009	USP54	-1.03	1.85E-01	4.44E-01	495.68	not significant
2010	ZNHIT1	-1.03	1.99E-01	4.63E-01	1628.29	not significant
2011	NGDN	-1.03	1.83E-01	4.40E-01	1749.82	not significant

2012	DNAJC7	-1.03	1.85E-01	4.44E-01	1817.24	not significant
2013	MAP3K11	-1.03	1.44E-01	3.88E-01	2836.01	not significant
2014	PSMG3-AS1	-1.03	1.71E-01	4.25E-01	304.99	not significant
2015	ZFAND4	-1.03	2.10E-01	4.74E-01	852.97	not significant
2016	C1orf174	-1.03	1.91E-01	4.51E-01	1516.82	not significant
2017	USMG5	-1.03	1.77E-01	4.32E-01	3414.90	not significant
2018	MAF	-1.03	2.90E-02	NA	71.56	not significant
2019	DRG2	-1.03	1.71E-01	4.25E-01	2033.60	not significant
2020	FTO	-1.03	1.59E-01	4.08E-01	2379.53	not significant
2021	PDCD2L	-1.03	1.81E-01	4.38E-01	416.68	not significant
2022	VPS54	-1.03	2.00E-01	4.64E-01	995.28	not significant
2023	TSFM	-1.03	2.01E-01	4.65E-01	1569.58	not significant
2024	TUBG1	-1.03	1.72E-01	4.26E-01	2020.55	not significant
2025	GLRX2	-1.03	1.76E-01	4.31E-01	368.39	not significant
2026	TUBGCP4	-1.03	2.00E-01	4.64E-01	1621.78	not significant
2027	CHP1	-1.03	1.72E-01	4.26E-01	2035.99	not significant
2028	PEBP1	-1.03	1.25E-01	3.55E-01	10288.82	not significant
2029	USP39	-1.03	1.23E-01	3.52E-01	5036.06	not significant
2030	LOC100128494	-1.03	4.07E-02	NA	88.13	not significant
2031	MROH6	-1.03	1.94E-01	4.56E-01	504.53	not significant
2032	ZNF845	-1.03	2.03E-01	4.68E-01	583.16	not significant
2033	GNL1	-1.03	2.08E-01	4.73E-01	1015.18	not significant
2034	ERC1	-1.03	2.09E-01	4.73E-01	820.73	not significant
2035	EIF4E2	-1.03	1.89E-01	4.49E-01	2394.41	not significant
2036	COX6B1	-1.03	1.67E-01	4.20E-01	4238.67	not significant
2037	CCDC97	-1.03	1.71E-01	4.25E-01	2290.99	not significant
2038	GLUD1	-1.03	1.16E-01	3.38E-01	5326.57	not significant
2039	CSNK1A1	-1.03	9.37E-02	2.95E-01	7480.30	not significant
2040	SLC29A1	-1.03	1.16E-01	3.37E-01	7391.95	not significant
2041	ZNF263	-1.03	1.86E-01	4.44E-01	1695.30	not significant
2042	FAM149B1	-1.03	1.87E-01	4.46E-01	418.67	not significant
2043	ZNF423	-1.03	2.10E-01	4.74E-01	1148.12	not significant
2044	SHCBP1	-1.03	1.67E-01	4.19E-01	2433.73	not significant
2045	PSME4	-1.03	1.78E-01	4.34E-01	3899.12	not significant
2046	FOXJ3	-1.03	1.73E-01	4.27E-01	3595.67	not significant
2047	SH2B3	-1.03	1.63E-01	4.13E-01	3119.26	not significant
2048	PAPSS2	-1.03	5.94E-02	NA	97.97	not significant
2049	ZSCAN21	-1.03	1.28E-01	3.60E-01	228.74	not significant
2050	RWDD2B	-1.03	1.98E-01	4.62E-01	478.87	not significant
2051	RPL8	-1.03	1.75E-01	4.31E-01	40748.78	not significant
2052	TMEM165	-1.03	1.79E-01	4.36E-01	2610.43	not significant
2053	ZSWIM1	-1.03	1.97E-01	4.60E-01	485.22	not significant
2054	ZNF136	-1.03	2.08E-01	4.73E-01	793.10	not significant
2055	COQ9	-1.03	2.09E-01	4.73E-01	788.42	not significant
2056	GNG5	-1.03	1.68E-01	4.21E-01	4530.93	not significant
2057	GDE1	-1.03	1.69E-01	4.23E-01	2318.70	not significant
2058	FOXRED2	-1.03	1.59E-01	4.07E-01	3810.61	not significant
2059	DEF8	-1.03	7.37E-02	2.53E-01	105.48	not significant
2060	HEATR6	-1.03	2.15E-01	4.81E-01	770.61	not significant
2061	APOBEC3G	-1.03	1.99E-01	4.63E-01	1363.82	not significant
2062	MRPS11	-1.03	2.36E-01	5.03E-01	1053.99	not significant
2063	SDAD1	-1.03	1.52E-01	4.00E-01	3125.30	not significant
2064	SERAC1	-1.03	1.91E-01	4.52E-01	457.71	not significant
2065	NDUFAF4	-1.03	2.02E-01	4.67E-01	1358.04	not significant
2066	ING1	-1.03	2.07E-01	4.72E-01	1044.54	not significant
2067	UCK2	-1.03	1.24E-01	3.52E-01	5819.48	not significant
2068	OGDH	-1.03	1.33E-01	3.68E-01	5485.81	not significant
2069	SRXN1	-1.03	1.54E-01	4.02E-01	266.19	not significant
2070	TRMT61B	-1.03	1.80E-01	4.37E-01	309.57	not significant
2071	PWWP2A	-1.03	2.10E-01	4.74E-01	963.27	not significant
2072	MED14	-1.03	1.63E-01	4.14E-01	2784.06	not significant
2073	MAVS	-1.03	1.72E-01	4.26E-01	6174.37	not significant
2074	VDAC3	-1.03	1.42E-01	3.84E-01	6581.58	not significant
2075	GIT1	-1.03	1.33E-01	3.68E-01	4388.49	not significant
2076	GLRX5	-1.03	1.94E-01	4.56E-01	2505.25	not significant
2077	ANKRD27	-1.03	2.02E-01	4.66E-01	1509.27	not significant
2078	UNC13D	-1.03	9.24E-02	2.92E-01	10984.05	not significant
2079	ADARB1	-1.03	2.13E-01	4.78E-01	1287.96	not significant
2080	GCC1	-1.03	1.89E-01	4.49E-01	1176.78	not significant
2081	SKP1	-1.03	1.40E-01	3.81E-01	8735.83	not significant
2082	NUP153	-1.03	1.63E-01	4.14E-01	8500.82	not significant
2083	LTA	-1.03	1.02E-01	3.12E-01	147.30	not significant
2084	PPAP2B	-1.03	7.71E-02	2.60E-01	119.61	not significant
2085	EMG1	-1.03	2.20E-01	4.87E-01	704.85	not significant
2086	DNAL1	-1.03	2.08E-01	4.73E-01	560.40	not significant
2087	TIPIN	-1.03	2.11E-01	4.75E-01	873.87	not significant
2088	SNHG17	-1.03	2.16E-01	4.82E-01	941.56	not significant
2089	PTPLB	-1.03	2.19E-01	4.86E-01	768.38	not significant
2090	UBR1	-1.03	2.07E-01	4.72E-01	1685.17	not significant
2091	LDOC1L	-1.03	1.23E-01	3.51E-01	5627.26	not significant
2092	SPATA33	-1.03	1.86E-01	4.45E-01	365.00	not significant
2093	KCTD3	-1.03	2.40E-01	5.08E-01	875.28	not significant
2094	EIF2B2	-1.03	2.02E-01	4.67E-01	1885.87	not significant
2095	UBB	-1.03	2.36E-01	5.03E-01	20909.88	not significant
2096	SNX8	-1.03	2.30E-01	4.97E-01	1063.54	not significant
2097	RIC1	-1.03	2.05E-01	4.70E-01	1502.12	not significant
2098	WSB2	-1.03	1.96E-01	4.59E-01	2057.80	not significant
2099	RPUSD1	-1.03	2.06E-01	4.71E-01	1876.59	not significant

2100	CNTRL	-1.03	1.98E-01	4.62E-01	2390.89	not significant
2101	C12orf45	-1.03	1.96E-01	4.58E-01	396.28	not significant
2102	EXTL2	-1.03	2.20E-01	4.86E-01	910.72	not significant
2103	MRPL28	-1.03	1.89E-01	4.48E-01	2810.77	not significant
2104	ZBTB39	-1.03	2.07E-01	4.72E-01	1448.06	not significant
2105	ZNF260	-1.03	1.98E-01	4.62E-01	2045.54	not significant
2106	NRD1	-1.03	1.36E-01	3.73E-01	6062.25	not significant
2107	ZNF547	-1.03	9.31E-02	2.94E-01	136.98	not significant
2108	CRACR2A	-1.03	2.10E-01	4.74E-01	762.62	not significant
2109	PARN	-1.03	2.00E-01	4.64E-01	2045.19	not significant
2110	ZZZ3	-1.03	1.96E-01	4.59E-01	2324.55	not significant
2111	USP34	-1.03	1.75E-01	4.30E-01	5939.30	not significant
2112	LINC00909	-1.03	2.20E-01	4.87E-01	675.13	not significant
2113	SIDT1	-1.03	2.17E-01	4.84E-01	806.99	not significant
2114	FASTKD5	-1.03	2.42E-01	5.10E-01	1100.48	not significant
2115	MYBL2	-1.03	1.11E-01	3.29E-01	11818.89	not significant
2116	CSNK1D	-1.03	1.15E-01	3.36E-01	6898.22	not significant
2117	DDX47	-1.03	1.86E-01	4.45E-01	2724.90	not significant
2118	ZNF776	-1.03	2.28E-01	4.95E-01	1241.08	not significant
2119	EEFSEC	-1.03	2.34E-01	5.01E-01	1114.13	not significant
2120	ZNF41	-1.03	2.16E-01	4.82E-01	590.70	not significant
2121	TXLNG	-1.03	2.04E-01	4.69E-01	2120.67	not significant
2122	STK39	-1.03	1.70E-01	4.24E-01	3134.70	not significant
2123	TDG	-1.03	1.45E-01	3.89E-01	4064.03	not significant
2124	TFDP2	-1.03	1.40E-01	3.81E-01	5714.32	not significant
2125	ANGPT1	-1.03	2.11E-01	4.75E-01	522.52	not significant
2126	INPP5F	-1.03	2.22E-01	4.89E-01	661.70	not significant
2127	PITHD1	-1.03	2.07E-01	4.72E-01	2249.99	not significant
2128	LARS2	-1.03	1.73E-01	4.27E-01	2893.12	not significant
2129	BTF3	-1.03	1.54E-01	4.02E-01	16681.97	not significant
2130	FDX1L	-1.03	2.11E-01	4.75E-01	634.03	not significant
2131	SRA1	-1.03	2.19E-01	4.86E-01	1012.99	not significant
2132	PFDN1	-1.03	2.01E-01	4.65E-01	2059.01	not significant
2133	B3GALNT2	-1.03	2.08E-01	4.73E-01	1887.01	not significant
2134	SCAF11	-1.03	1.39E-01	3.79E-01	8802.38	not significant
2135	MIPEP	-1.03	2.14E-01	4.80E-01	544.71	not significant
2136	PRKAR2A	-1.03	2.25E-01	4.92E-01	771.34	not significant
2137	TARS2	-1.03	2.44E-01	5.12E-01	990.12	not significant
2138	MRPL42	-1.03	2.01E-01	4.66E-01	2777.77	not significant
2139	ATXN3	-1.03	2.14E-01	4.79E-01	1236.67	not significant
2140	SPAG9	-1.03	2.15E-01	4.81E-01	1957.47	not significant
2141	DBP	-1.03	2.80E-01	5.51E-01	547.03	not significant
2142	ERICH1	-1.03	2.26E-01	4.94E-01	1238.68	not significant
2143	VKORC1L1	-1.03	1.78E-01	4.35E-01	3529.57	not significant
2144	PLEKHA8	-1.03	2.11E-01	4.75E-01	1654.20	not significant
2145	COPS4	-1.03	2.12E-01	4.77E-01	1822.53	not significant
2146	STRN3	-1.03	2.60E-01	5.30E-01	1049.14	not significant
2147	DDX19A	-1.03	1.66E-01	4.18E-01	3187.68	not significant
2148	HMGN5	-1.03	2.13E-01	4.79E-01	792.56	not significant
2149	IFT57	-1.03	2.44E-01	5.12E-01	572.24	not significant
2150	THOC6	-1.03	2.16E-01	4.82E-01	1728.16	not significant
2151	TBL3	-1.03	2.01E-01	4.65E-01	2175.55	not significant
2152	SAFB	-1.03	1.34E-01	3.70E-01	6288.44	not significant
2153	FTH1	-1.03	2.91E-01	5.62E-01	28286.13	not significant
2154	TMEM5	-1.03	2.31E-01	4.99E-01	811.94	not significant
2155	AP3M1	-1.03	1.46E-01	3.90E-01	5123.12	not significant
2156	SCPEP1	-1.03	2.19E-01	4.86E-01	517.07	not significant
2157	NPRL2	-1.03	2.27E-01	4.95E-01	866.17	not significant
2158	MED9	-1.03	2.31E-01	4.99E-01	1041.89	not significant
2159	PRKCA	-1.03	1.90E-01	4.50E-01	6621.00	not significant
2160	PAPD4	-1.03	1.92E-01	4.52E-01	2473.14	not significant
2161	DDX41	-1.03	1.57E-01	4.05E-01	4281.29	not significant
2162	SLC7A6OS	-1.03	2.20E-01	4.87E-01	535.05	not significant
2163	ZNF124	-1.03	2.32E-01	4.99E-01	660.28	not significant
2164	MAGOHB	-1.03	2.30E-01	4.98E-01	1792.34	not significant
2165	AKAP10	-1.03	2.29E-01	4.96E-01	1068.38	not significant
2166	AFF4	-1.03	2.13E-01	4.78E-01	3650.26	not significant
2167	GCLM	-1.03	2.02E-01	4.67E-01	1660.01	not significant
2168	TMEM41A	-1.03	2.29E-01	4.97E-01	829.74	not significant
2169	MPP5	-1.03	2.31E-01	4.99E-01	789.46	not significant
2170	ANKRD44	-1.03	2.66E-01	5.37E-01	912.87	not significant
2171	SH3BP5L	-1.03	2.21E-01	4.87E-01	1826.34	not significant
2172	ELMO2	-1.03	2.07E-01	4.71E-01	2066.66	not significant
2173	RAB1A	-1.03	1.99E-01	4.63E-01	2622.05	not significant
2174	AASDHPPT	-1.03	1.81E-01	4.39E-01	3172.52	not significant
2175	43715_9262	-1.03	1.10E-01	3.27E-01	10214.93	not significant
2176	LINC00426	-1.03	1.42E-01	3.84E-01	183.43	not significant
2177	TRIM16	-1.03	1.76E-01	4.31E-01	264.45	not significant
2178	TMEM241	-1.03	2.06E-01	4.71E-01	396.84	not significant
2179	GCFC2	-1.03	2.18E-01	4.84E-01	882.90	not significant
2180	POLR3D	-1.03	2.15E-01	4.81E-01	1796.41	not significant
2181	OLA1	-1.03	1.66E-01	4.18E-01	4986.32	not significant
2182	C12orf49	-1.03	2.00E-01	4.64E-01	2166.52	not significant
2183	CFL1	-1.03	1.57E-01	4.05E-01	34631.71	not significant
2184	RALGAPB	-1.03	1.73E-01	4.27E-01	4895.54	not significant
2185	DNAJA3	-1.03	1.55E-01	4.03E-01	4922.46	not significant
2186	PIM1	-1.03	1.12E-01	3.32E-01	8825.56	not significant
2187	VPS13B	-1.03	2.27E-01	4.95E-01	2535.76	not significant

2188	ACTR1A	-1.03	1.75E-01	4.31E-01	5326.25	not significant
2189	ACSL4	-1.03	1.76E-01	4.31E-01	2682.74	not significant
2190	TSKU	-1.03	1.80E-01	4.37E-01	255.73	not significant
2191	MIIP	-1.03	2.31E-01	4.99E-01	1067.79	not significant
2192	MRPS7	-1.03	2.17E-01	4.83E-01	3965.55	not significant
2193	MYEF2	-1.03	2.24E-01	4.92E-01	1258.65	not significant
2194	NCOA6	-1.03	2.17E-01	4.83E-01	4275.25	not significant
2195	SFXN1	-1.03	1.55E-01	4.04E-01	4760.05	not significant
2196	MPRIP	-1.03	2.20E-01	4.87E-01	6601.44	not significant
2197	LACTB	-1.03	1.33E-01	3.67E-01	164.47	not significant
2198	AK6	-1.03	2.00E-01	4.64E-01	335.58	not significant
2199	ATG7	-1.03	2.23E-01	4.89E-01	509.65	not significant
2200	UTP3	-1.03	2.06E-01	4.71E-01	2067.93	not significant
2201	NCAPG	-1.03	1.62E-01	4.13E-01	3704.62	not significant
2202	ZNF460	-1.03	5.88E-02	2.19E-01	136.68	not significant
2203	AP5B1	-1.03	2.27E-01	4.95E-01	1186.01	not significant
2204	ELOF1	-1.03	2.28E-01	4.95E-01	1467.36	not significant
2205	RNGTT	-1.03	2.00E-01	4.64E-01	2876.84	not significant
2206	FKBP3	-1.03	1.98E-01	4.62E-01	2474.61	not significant
2207	VTA1	-1.03	1.83E-01	4.40E-01	3326.01	not significant
2208	CTRL	-1.03	4.80E-02	NA	74.39	not significant
2209	LOC100506603	-1.03	8.07E-02	2.68E-01	106.40	not significant
2210	ZNF765	-1.03	2.40E-01	5.08E-01	709.75	not significant
2211	SUGT1	-1.03	2.26E-01	4.94E-01	1909.02	not significant
2212	REXO1	-1.03	1.77E-01	4.33E-01	3324.94	not significant
2213	SRSF11	-1.03	1.29E-01	3.60E-01	6702.77	not significant
2214	RGMA	-1.03	9.07E-02	2.88E-01	114.75	not significant
2215	TLDC1	-1.03	1.26E-01	3.56E-01	162.80	not significant
2216	ITGB1BP1	-1.03	2.37E-01	5.04E-01	3083.40	not significant
2217	TNRC6C	-1.03	2.26E-01	4.94E-01	3334.21	not significant
2218	NEK1	-1.03	2.29E-01	4.97E-01	1114.02	not significant
2219	CECR5	-1.03	2.12E-01	4.76E-01	2925.42	not significant
2220	DDX51	-1.03	2.00E-01	4.64E-01	2704.64	not significant
2221	USB1	-1.03	1.75E-01	4.30E-01	3636.13	not significant
2222	IFT27	-1.03	1.96E-01	4.59E-01	320.80	not significant
2223	TMEM237	-1.03	2.30E-01	4.97E-01	1817.99	not significant
2224	ARF4	-1.03	1.88E-01	4.48E-01	3340.10	not significant
2225	CLPP	-1.03	2.05E-01	4.70E-01	3112.07	not significant
2226	VPS26A	-1.03	2.13E-01	4.79E-01	2241.69	not significant
2227	TMEM184C	-1.03	2.36E-01	5.03E-01	1852.94	not significant
2228	SERP1	-1.03	1.34E-01	3.69E-01	10080.63	not significant
2229	EIF1	-1.03	1.63E-01	4.14E-01	24295.09	not significant
2230	PHLPP2	-1.03	2.44E-01	5.11E-01	808.24	not significant
2231	RIPK1	-1.03	2.31E-01	4.99E-01	1405.04	not significant
2232	SNAP29	-1.03	2.30E-01	4.98E-01	1675.62	not significant
2233	HNRNPUL2	-1.03	2.04E-01	4.70E-01	4292.57	not significant
2234	ADAR	-1.03	1.71E-01	4.25E-01	16261.84	not significant
2235	HYOU1	-1.03	1.78E-01	4.35E-01	4913.48	not significant
2236	SOBP	-1.03	2.43E-01	5.11E-01	771.19	not significant
2237	LRWD1	-1.03	2.33E-01	5.00E-01	1840.98	not significant
2238	IVD	-1.03	2.14E-01	4.79E-01	2186.61	not significant
2239	DPP3	-1.03	1.92E-01	4.53E-01	4228.62	not significant
2240	KIF3A	-1.03	2.20E-01	4.86E-01	2155.02	not significant
2241	ALKBH5	-1.03	1.65E-01	4.17E-01	4751.54	not significant
2242	AP1S1	-1.03	2.43E-01	5.11E-01	1462.83	not significant
2243	ATP5G1	-1.03	2.33E-01	5.01E-01	2735.16	not significant
2244	ZNF101	-1.03	2.69E-01	5.39E-01	1079.71	not significant
2245	SLC30A6	-1.03	2.28E-01	4.95E-01	2095.22	not significant
2246	RNF10	-1.03	1.49E-01	3.96E-01	5839.68	not significant
2247	NCAPD2	-1.03	1.58E-01	4.06E-01	12848.82	not significant
2248	ZNF420	-1.03	2.20E-01	4.87E-01	423.29	not significant
2249	FAM162A	-1.03	2.46E-01	5.14E-01	1191.91	not significant
2250	RFXANK	-1.03	2.39E-01	5.07E-01	1207.01	not significant
2251	TMPO-AS1	-1.03	2.40E-01	5.08E-01	829.32	not significant
2252	GGPS1	-1.03	2.65E-01	5.36E-01	1015.50	not significant
2253	GATC	-1.03	2.11E-01	4.75E-01	2115.86	not significant
2254	SF3B6	-1.03	2.00E-01	4.64E-01	2827.25	not significant
2255	CNST	-1.03	2.28E-01	4.95E-01	1768.81	not significant
2256	COPZ1	-1.03	1.88E-01	4.47E-01	4429.71	not significant
2257	CCDC25	-1.03	2.06E-01	4.71E-01	2316.50	not significant
2258	BICD2	-1.03	2.10E-01	4.74E-01	2322.06	not significant
2259	SEC14L2	-1.03	2.32E-01	4.99E-01	465.05	not significant
2260	NDUFAF6	-1.03	2.47E-01	5.15E-01	731.11	not significant
2261	DOLPP1	-1.03	2.70E-01	5.40E-01	1018.14	not significant
2262	CUL2	-1.03	2.06E-01	4.71E-01	2567.39	not significant
2263	UBQLN1	-1.03	1.54E-01	4.02E-01	5486.74	not significant
2264	ANKRD16	-1.03	2.04E-01	4.69E-01	337.30	not significant
2265	POLR2J	-1.03	2.39E-01	5.07E-01	1233.98	not significant
2266	RAB11FIP3	-1.03	2.29E-01	4.96E-01	1809.50	not significant
2267	LUZP1	-1.03	1.98E-01	4.62E-01	2859.89	not significant
2268	ZBTB44	-1.03	1.82E-01	4.40E-01	4972.18	not significant
2269	YWHAZ	-1.03	1.05E-01	3.17E-01	32033.04	not significant
2270	ZNF45	-1.03	2.46E-01	5.14E-01	1204.97	not significant
2271	TLK2	-1.03	2.34E-01	5.01E-01	1645.28	not significant
2272	APRT	-1.03	2.23E-01	4.91E-01	4187.75	not significant
2273	RAE1	-1.03	2.09E-01	4.74E-01	2942.57	not significant
2274	NFYB	-1.03	2.22E-01	4.89E-01	1934.45	not significant
2275	RGL1	-1.03	9.14E-02	2.90E-01	110.83	not significant

2276	FAM65A	-1.03	2.59E-01	5.28E-01	821.85	not significant
2277	POM121C	-1.03	2.58E-01	5.28E-01	872.97	not significant
2278	TPD52	-1.03	1.98E-01	4.62E-01	3151.88	not significant
2279	HDAC1	-1.03	1.51E-01	3.98E-01	8791.73	not significant
2280	TRIM62	-1.03	2.40E-01	5.08E-01	546.40	not significant
2281	PMS2	-1.03	2.53E-01	5.22E-01	697.71	not significant
2282	DARS	-1.03	1.79E-01	4.36E-01	4675.54	not significant
2283	NUDT21	-1.03	1.36E-01	3.74E-01	11319.25	not significant
2284	NOMO2	-1.03	2.08E-01	4.72E-01	337.22	not significant
2285	RANBP1	-1.03	1.87E-01	4.46E-01	9573.86	not significant
2286	PPIA	-1.03	1.68E-01	4.21E-01	27779.23	not significant
2287	PFKFB4	-1.02	5.58E-02	NA	78.69	not significant
2288	ZNF257	-1.02	1.52E-01	3.99E-01	172.17	not significant
2289	LOC728485	-1.02	1.64E-01	4.15E-01	205.39	not significant
2290	DZIP3	-1.02	2.28E-01	4.95E-01	523.36	not significant
2291	MYBL1	-1.02	2.55E-01	5.23E-01	1142.29	not significant
2292	SQSTM1	-1.02	2.33E-01	5.00E-01	1956.88	not significant
2293	NAPG	-1.02	2.35E-01	5.02E-01	1753.33	not significant
2294	PRKX	-1.02	2.18E-01	4.84E-01	2337.80	not significant
2295	PAFAH1B2	-1.02	2.06E-01	4.71E-01	2638.96	not significant
2296	C6orf106	-1.02	1.90E-01	4.50E-01	3980.80	not significant
2297	RBM26	-1.02	1.90E-01	4.50E-01	4276.68	not significant
2298	ZNF385A	-1.02	8.12E-02	2.69E-01	107.50	not significant
2299	TBL2	-1.02	1.68E-01	4.21E-01	224.97	not significant
2300	C2orf47	-1.02	2.53E-01	5.21E-01	637.59	not significant
2301	ENAH	-1.02	3.00E-01	5.70E-01	524.32	not significant
2302	MRPL46	-1.02	2.48E-01	5.16E-01	637.99	not significant
2303	EMC4	-1.02	2.33E-01	5.00E-01	1970.97	not significant
2304	PSMA5	-1.02	1.81E-01	4.38E-01	6466.45	not significant
2305	ZNF317	-1.02	2.15E-01	4.81E-01	2401.36	not significant
2306	GRB2	-1.02	1.28E-01	3.59E-01	15646.58	not significant
2307	MT1G	-1.02	2.60E-01	5.29E-01	15256.97	not significant
2308	MLF2	-1.02	2.00E-01	4.64E-01	5137.17	not significant
2309	AIMP1	-1.02	1.95E-01	4.57E-01	2757.20	not significant
2310	PSMB2	-1.02	1.61E-01	4.11E-01	10731.97	not significant
2311	IRF1	-1.02	1.51E-01	3.98E-01	8419.49	not significant
2312	ZNF552	-1.02	1.55E-01	4.04E-01	186.65	not significant
2313	BBS9	-1.02	1.34E-01	3.70E-01	154.16	not significant
2314	LINC00977	-1.02	2.52E-01	5.21E-01	629.42	not significant
2315	PLIN3	-1.02	2.37E-01	5.05E-01	1965.35	not significant
2316	AFTPH	-1.02	2.42E-01	5.10E-01	1324.45	not significant
2317	JMJD8	-1.02	2.44E-01	5.11E-01	1489.43	not significant
2318	SNW1	-1.02	2.18E-01	4.85E-01	2661.38	not significant
2319	SLC16A1	-1.02	1.76E-01	4.31E-01	8578.47	not significant
2320	CAD	-1.02	1.67E-01	4.20E-01	9339.62	not significant
2321	COQ3	-1.02	2.45E-01	5.13E-01	490.04	not significant
2322	TMEM138	-1.02	2.53E-01	5.21E-01	858.81	not significant
2323	ERCC3	-1.02	2.02E-01	4.67E-01	2742.01	not significant
2324	MAP4	-1.02	1.57E-01	4.05E-01	8133.37	not significant
2325	PKNOX1	-1.02	2.53E-01	5.22E-01	663.26	not significant
2326	PLAGL1	-1.02	2.54E-01	5.22E-01	651.26	not significant
2327	MED21	-1.02	2.44E-01	5.12E-01	1296.08	not significant
2328	LIN7C	-1.02	2.53E-01	5.22E-01	1168.97	not significant
2329	PRDX6	-1.02	2.12E-01	4.77E-01	5672.66	not significant
2330	CENPO	-1.02	2.00E-01	4.64E-01	3196.75	not significant
2331	CCDC117	-1.02	1.76E-01	4.31E-01	3970.13	not significant
2332	DDX3Y	-1.02	1.96E-01	4.58E-01	5905.94	not significant
2333	SCMH1	-1.02	2.39E-01	5.07E-01	2133.10	not significant
2334	PPP5C	-1.02	2.05E-01	4.70E-01	3399.77	not significant
2335	JTB	-1.02	2.03E-01	4.69E-01	4822.38	not significant
2336	VANGL1	-1.02	1.71E-01	4.25E-01	10734.50	not significant
2337	STX8	-1.02	2.50E-01	5.18E-01	611.30	not significant
2338	GPD1L	-1.02	2.57E-01	5.25E-01	637.26	not significant
2339	ZNF330	-1.02	2.43E-01	5.11E-01	1690.82	not significant
2340	ARL5B	-1.02	2.71E-01	5.42E-01	1580.78	not significant
2341	SNRPC	-1.02	2.14E-01	4.79E-01	4192.04	not significant
2342	BCORL1	-1.02	2.47E-01	5.15E-01	1400.00	not significant
2343	UBA2	-1.02	1.78E-01	4.34E-01	7276.14	not significant
2344	PFKFB2	-1.02	1.58E-01	4.06E-01	185.64	not significant
2345	MED26	-1.02	2.57E-01	5.25E-01	653.66	not significant
2346	RAP1A	-1.02	2.47E-01	5.15E-01	2132.92	not significant
2347	RAD51C	-1.02	2.31E-01	4.99E-01	2100.86	not significant
2348	PSMA4	-1.02	1.89E-01	4.49E-01	5103.07	not significant
2349	HK1	-1.02	1.98E-01	4.62E-01	3518.27	not significant
2350	CCDC163P	-1.02	1.74E-01	4.30E-01	200.20	not significant
2351	ZNF593	-1.02	2.38E-01	5.06E-01	437.20	not significant
2352	BAG3	-1.02	2.59E-01	5.28E-01	893.54	not significant
2353	MTAP	-1.02	2.10E-01	4.74E-01	3316.33	not significant
2354	CYP27B1	-1.02	1.44E-01	3.87E-01	159.06	not significant
2355	FGR	-1.02	1.70E-01	4.24E-01	190.56	not significant
2356	USP46	-1.02	2.22E-01	4.89E-01	347.75	not significant
2357	DHRS4-AS1	-1.02	2.71E-01	5.42E-01	745.85	not significant
2358	SPATA5	-1.02	2.51E-01	5.20E-01	1283.03	not significant
2359	EIF1AY	-1.02	2.40E-01	5.08E-01	3511.12	not significant
2360	COPS5	-1.02	2.19E-01	4.86E-01	3412.81	not significant
2361	OTUD4	-1.02	2.42E-01	5.10E-01	2702.74	not significant
2362	PRPF38B	-1.02	1.90E-01	4.49E-01	4078.69	not significant
2363	ARMC8	-1.02	2.45E-01	5.13E-01	2054.05	not significant

2364	IL17RA	-1.02	2.42E-01	5.11E-01	2618.11	not significant
2365	SDHD	-1.02	2.11E-01	4.75E-01	3292.27	not significant
2366	ANAPC5	-1.02	1.87E-01	4.45E-01	5853.82	not significant
2367	RIMBP2	-1.02	6.91E-02	NA	84.66	not significant
2368	CDKL1	-1.02	1.42E-01	3.84E-01	172.92	not significant
2369	TMED8	-1.02	2.14E-01	4.79E-01	350.62	not significant
2370	LOC103344931	-1.02	2.24E-01	4.91E-01	314.89	not significant
2371	DHX16	-1.02	2.67E-01	5.38E-01	832.66	not significant
2372	PIK3CB	-1.02	2.52E-01	5.21E-01	1376.19	not significant
2373	H3F3B	-1.02	1.85E-01	4.44E-01	29262.64	not significant
2374	COX16	-1.02	1.16E-01	3.38E-01	160.28	not significant
2375	XXYLT1	-1.02	2.70E-01	5.40E-01	935.76	not significant
2376	ANP32E	-1.02	2.66E-01	5.37E-01	1583.57	not significant
2377	MRPS17	-1.02	2.69E-01	5.39E-01	862.87	not significant
2378	FNBP1L	-1.02	2.66E-01	5.37E-01	1167.34	not significant
2379	URI1	-1.02	2.34E-01	5.01E-01	3255.96	not significant
2380	ATAD3A	-1.02	2.32E-01	4.99E-01	3008.34	not significant
2381	FUS	-1.02	1.58E-01	4.06E-01	17571.80	not significant
2382	GNB1	-1.02	1.64E-01	4.14E-01	20046.78	not significant
2383	ZNF567	-1.02	2.64E-01	5.35E-01	606.70	not significant
2384	EMC3	-1.02	2.80E-01	5.51E-01	1569.06	not significant
2385	NOM1	-1.02	2.37E-01	5.05E-01	2487.49	not significant
2386	CHERP	-1.02	1.86E-01	4.44E-01	5918.28	not significant
2387	ZNF736	-1.02	2.58E-01	5.27E-01	1433.91	not significant
2388	SLC9A3R1	-1.02	1.37E-01	3.75E-01	14308.29	not significant
2389	ATP6AP1L	-1.02	1.50E-01	3.97E-01	160.36	not significant
2390	COMMD1	-1.02	2.56E-01	5.24E-01	485.92	not significant
2391	NR2F6	-1.02	2.52E-01	5.21E-01	434.30	not significant
2392	ZNF526	-1.02	2.68E-01	5.39E-01	621.58	not significant
2393	TROAP	-1.02	2.54E-01	5.23E-01	2647.87	not significant
2394	RELA	-1.02	2.31E-01	4.99E-01	2826.67	not significant
2395	CERK	-1.02	2.13E-01	4.78E-01	3820.45	not significant
2396	GAPDH	-1.02	2.06E-01	4.71E-01	183429.09	not significant
2397	SNX20	-1.02	1.68E-01	4.21E-01	170.72	not significant
2398	CEP19	-1.02	2.34E-01	5.01E-01	340.83	not significant
2399	IFRD2	-1.02	2.62E-01	5.32E-01	1225.49	not significant
2400	TPD52L2	-1.02	2.46E-01	5.13E-01	3006.15	not significant
2401	MPHOSPH9	-1.02	2.28E-01	4.95E-01	3183.13	not significant
2402	ARHGAP11B	-1.02	1.24E-01	3.52E-01	124.55	not significant
2403	ANKRD42	-1.02	1.28E-01	3.60E-01	138.17	not significant
2404	ZNF530	-1.02	2.61E-01	5.31E-01	470.81	not significant
2405	ALDOC	-1.02	2.40E-01	5.08E-01	373.04	not significant
2406	TCEB2	-1.02	2.66E-01	5.37E-01	2690.02	not significant
2407	LYPLA2	-1.02	2.54E-01	5.23E-01	2167.25	not significant
2408	ZNF605	-1.02	2.61E-01	5.30E-01	491.91	not significant
2409	SLC25A20	-1.02	2.69E-01	5.40E-01	1080.65	not significant
2410	LOC100996286	-1.02	2.74E-01	5.44E-01	815.79	not significant
2411	ZNF788	-1.02	2.73E-01	5.43E-01	648.70	not significant
2412	CREM	-1.02	2.78E-01	5.48E-01	955.44	not significant
2413	SERF2	-1.02	2.67E-01	5.38E-01	3946.58	not significant
2414	ZDHHC6	-1.02	2.32E-01	5.00E-01	2689.45	not significant
2415	B3GNT2	-1.02	2.40E-01	5.08E-01	2569.41	not significant
2416	ZC3H14	-1.02	2.49E-01	5.17E-01	2196.28	not significant
2417	CSK	-1.02	2.08E-01	4.73E-01	5983.98	not significant
2418	SEMA7A	-1.02	2.43E-01	5.11E-01	2758.99	not significant
2419	EXD2	-1.02	2.71E-01	5.42E-01	548.53	not significant
2420	HMBS	-1.02	2.78E-01	5.48E-01	1283.38	not significant
2421	VBP1	-1.02	2.92E-01	5.64E-01	864.26	not significant
2422	COA4	-1.02	2.74E-01	5.45E-01	1435.86	not significant
2423	ZNF501	-1.02	1.91E-01	4.51E-01	201.81	not significant
2424	PPP1R13L	-1.02	2.05E-01	4.70E-01	240.24	not significant
2425	CCDC92	-1.02	2.68E-01	5.39E-01	1181.40	not significant
2426	COPS6	-1.02	2.50E-01	5.18E-01	3750.87	not significant
2427	AIFM1	-1.02	2.51E-01	5.20E-01	2039.04	not significant
2428	RABGEF1	-1.02	2.53E-01	5.21E-01	1959.65	not significant
2429	BRAP	-1.02	2.66E-01	5.37E-01	1812.84	not significant
2430	VPS26B	-1.02	2.13E-01	4.78E-01	3955.32	not significant
2431	KCTD20	-1.02	1.91E-01	4.51E-01	5713.31	not significant
2432	LPCAT3	-1.02	2.66E-01	5.37E-01	527.76	not significant
2433	BPNT1	-1.02	2.68E-01	5.39E-01	1230.47	not significant
2434	AKT3	-1.02	2.75E-01	5.45E-01	1138.24	not significant
2435	C12orf29	-1.02	2.71E-01	5.42E-01	1562.56	not significant
2436	ZNF674	-1.02	1.30E-01	3.62E-01	121.54	not significant
2437	TRIM32	-1.02	2.68E-01	5.39E-01	527.19	not significant
2438	ZCCHC4	-1.02	2.74E-01	5.45E-01	549.41	not significant
2439	TBC1D22A	-1.02	2.82E-01	5.53E-01	1083.47	not significant
2440	ANKRD54	-1.02	2.78E-01	5.48E-01	769.41	not significant
2441	PDRG1	-1.02	2.78E-01	5.48E-01	1146.75	not significant
2442	EIF3G	-1.02	2.23E-01	4.90E-01	6195.72	not significant
2443	YWHAH	-1.02	2.17E-01	4.83E-01	5282.22	not significant
2444	N4BP1	-1.02	2.68E-01	5.39E-01	1762.18	not significant
2445	CPSF6	-1.02	1.86E-01	4.44E-01	7368.13	not significant
2446	AHRR	-1.02	2.24E-01	4.92E-01	266.32	not significant
2447	KCNMB4	-1.02	1.79E-01	4.36E-01	181.29	not significant
2448	COQ6	-1.02	2.71E-01	5.42E-01	510.27	not significant
2449	C10orf88	-1.02	2.93E-01	5.64E-01	568.58	not significant
2450	RNF185	-1.02	2.68E-01	5.38E-01	1357.04	not significant
2451	ATL2	-1.02	2.38E-01	5.06E-01	2963.48	not significant

2452	SFSWAP	-1.02	2.35E-01	5.02E-01	3019.97	not significant
2453	ZSWIM3	-1.02	2.45E-01	5.13E-01	347.24	not significant
2454	CASC5	-1.02	2.82E-01	5.53E-01	2302.79	not significant
2455	SETD2	-1.02	2.65E-01	5.36E-01	5197.70	not significant
2456	PRRC2A	-1.02	2.19E-01	4.86E-01	6318.55	not significant
2457	HNRNPA3	-1.02	1.89E-01	4.48E-01	20697.53	not significant
2458	ACSL3	-1.02	2.43E-01	5.11E-01	3130.64	not significant
2459	STXBP4	-1.02	2.04E-01	4.69E-01	213.42	not significant
2460	ITGB3BP	-1.02	2.63E-01	5.33E-01	821.14	not significant
2461	OPA3	-1.02	2.83E-01	5.53E-01	1229.31	not significant
2462	C2orf43	-1.02	2.69E-01	5.40E-01	1934.06	not significant
2463	SH3PXD2B	-1.02	6.73E-02	NA	70.87	not significant
2464	RAB4A	-1.02	2.82E-01	5.53E-01	849.00	not significant
2465	APOBEC3D	-1.02	2.84E-01	5.54E-01	617.46	not significant
2466	UBN2	-1.02	2.90E-01	5.61E-01	1068.20	not significant
2467	NFXL1	-1.02	2.85E-01	5.55E-01	778.48	not significant
2468	MCMBP	-1.02	1.80E-01	4.37E-01	6836.25	not significant
2469	DGKZ	-1.02	1.86E-01	4.44E-01	5602.33	not significant
2470	CALU	-1.02	1.94E-01	4.55E-01	5908.63	not significant
2471	CCDC181	-1.02	5.73E-02	NA	65.63	not significant
2472	SESN1	-1.02	2.82E-01	5.53E-01	577.66	not significant
2473	NLGN4X	-1.02	2.72E-01	5.43E-01	517.93	not significant
2474	ATRX	-1.02	2.71E-01	5.42E-01	711.41	not significant
2475	EPC2	-1.02	2.82E-01	5.53E-01	1066.46	not significant
2476	PCYOX1	-1.02	2.71E-01	5.42E-01	1392.54	not significant
2477	QKI	-1.02	2.13E-01	4.78E-01	4207.64	not significant
2478	GTSF1	-1.02	2.19E-01	4.86E-01	247.27	not significant
2479	G6PD	-1.02	2.85E-01	5.55E-01	1567.35	not significant
2480	UPF2	-1.02	2.84E-01	5.54E-01	1748.46	not significant
2481	DNAJB11	-1.02	2.34E-01	5.01E-01	3464.21	not significant
2482	RHOQ	-1.02	2.49E-01	5.16E-01	298.79	not significant
2483	LINC00641	-1.02	2.55E-01	5.24E-01	359.19	not significant
2484	RILPL2	-1.02	2.85E-01	5.55E-01	1596.87	not significant
2485	FAM120AOS	-1.02	2.77E-01	5.47E-01	1263.89	not significant
2486	DCLRE1A	-1.02	2.73E-01	5.43E-01	1345.84	not significant
2487	LZTFL1	-1.02	2.49E-01	5.16E-01	2945.19	not significant
2488	CCDC152	-1.02	2.66E-01	5.37E-01	2034.42	not significant
2489	CTSB	-1.02	1.98E-01	4.62E-01	4982.16	not significant
2490	HIATL2	-1.02	1.61E-01	NA	94.60	not significant
2491	CREB3L3	-1.02	1.47E-01	3.92E-01	131.49	not significant
2492	ZNF17	-1.02	2.59E-01	5.28E-01	367.63	not significant
2493	SH3BP1	-1.02	2.82E-01	5.52E-01	1284.58	not significant
2494	HPS3	-1.02	2.92E-01	5.64E-01	1142.13	not significant
2495	IRAK1	-1.02	2.81E-01	5.52E-01	1654.81	not significant
2496	EARS2	-1.02	2.72E-01	5.42E-01	1642.06	not significant
2497	OAS2	-1.02	2.61E-01	5.30E-01	2965.82	not significant
2498	NAA60	-1.02	2.45E-01	5.13E-01	2723.11	not significant
2499	MORF4L2	-1.02	2.19E-01	4.86E-01	5461.11	not significant
2500	U2SURP	-1.02	1.89E-01	4.48E-01	7740.67	not significant
2501	ATG4A	-1.02	2.73E-01	5.43E-01	493.37	not significant
2502	PMS2CL	-1.02	2.57E-01	5.26E-01	374.63	not significant
2503	EXOSC3	-1.02	2.77E-01	5.47E-01	2056.36	not significant
2504	CHMP2A	-1.02	2.84E-01	5.54E-01	1222.34	not significant
2505	VPRBP	-1.02	2.99E-01	5.70E-01	951.74	not significant
2506	KIRREL	-1.02	3.17E-01	5.87E-01	1259.08	not significant
2507	CASC4	-1.02	2.81E-01	5.51E-01	1805.26	not significant
2508	HBS1L	-1.02	2.34E-01	5.01E-01	3573.31	not significant
2509	UBASH3B	-1.02	1.70E-01	4.24E-01	11822.81	not significant
2510	CHCHD6	-1.02	2.64E-01	5.35E-01	425.33	not significant
2511	METTL21B	-1.02	2.76E-01	5.46E-01	491.53	not significant
2512	TMOD2	-1.02	2.88E-01	5.59E-01	859.95	not significant
2513	PIGN	-1.02	3.06E-01	5.78E-01	1584.67	not significant
2514	TSPYL5	-1.02	2.54E-01	5.22E-01	2495.91	not significant
2515	MIER1	-1.02	2.61E-01	5.31E-01	2308.91	not significant
2516	CD2AP	-1.02	2.42E-01	5.10E-01	3901.23	not significant
2517	CNOT2	-1.02	2.28E-01	4.95E-01	4350.12	not significant
2518	EP300	-1.02	2.76E-01	5.47E-01	3658.60	not significant
2519	TAGAP	-1.02	2.93E-01	5.64E-01	580.09	not significant
2520	HIBCH	-1.02	3.00E-01	5.70E-01	1008.34	not significant
2521	BBX	-1.02	2.92E-01	5.63E-01	2814.57	not significant
2522	TBC1D22B	-1.02	2.73E-01	5.43E-01	1920.68	not significant
2523	BAG5	-1.02	2.48E-01	5.16E-01	3021.43	not significant
2524	ZSCAN22	-1.02	1.77E-01	4.34E-01	178.21	not significant
2525	BECN1	-1.02	2.85E-01	5.56E-01	2061.03	not significant
2526	GNAI3	-1.02	2.32E-01	4.99E-01	4873.04	not significant
2527	SLC39A9	-1.02	2.47E-01	5.15E-01	4218.56	not significant
2528	DOK4	-1.02	2.44E-01	5.12E-01	270.48	not significant
2529	FAM3C	-1.02	2.56E-01	5.25E-01	328.96	not significant
2530	HIPK2	-1.02	2.81E-01	5.52E-01	3387.16	not significant
2531	ZNF770	-1.02	2.70E-01	5.41E-01	2322.44	not significant
2532	CCNY	-1.02	2.28E-01	4.95E-01	4177.29	not significant
2533	PSD4	-1.02	2.33E-01	5.01E-01	6976.43	not significant
2534	SIPA1L2	-1.02	2.76E-02	NA	44.07	not significant
2535	RARG	-1.02	1.57E-01	4.05E-01	138.32	not significant
2536	FRRS1	-1.02	2.08E-01	4.73E-01	208.16	not significant
2537	ZMYM1	-1.02	3.00E-01	5.70E-01	664.61	not significant
2538	PAF1	-1.02	2.88E-01	5.59E-01	2352.56	not significant
2539	ACTR8	-1.02	2.93E-01	5.65E-01	1261.00	not significant

2540	USP42	-1.02	2.77E-01	5.47E-01	2152.75	not significant
2541	LSM11	-1.02	2.60E-01	5.30E-01	491.30	not significant
2542	ZNF584	-1.02	2.92E-01	5.64E-01	523.57	not significant
2543	MKNK1	-1.02	2.89E-01	5.60E-01	520.39	not significant
2544	COMMD9	-1.02	2.86E-01	5.57E-01	1351.53	not significant
2545	CCDC66	-1.02	2.87E-01	5.58E-01	805.27	not significant
2546	THOC5	-1.02	3.03E-01	5.74E-01	1830.15	not significant
2547	EIF4G3	-1.02	2.82E-01	5.53E-01	2994.05	not significant
2548	ANKIB1	-1.02	2.72E-01	5.42E-01	2823.43	not significant
2549	GORASP2	-1.02	2.24E-01	4.91E-01	4465.93	not significant
2550	GPBP1	-1.02	2.24E-01	4.91E-01	4285.74	not significant
2551	SMARCE1	-1.02	1.83E-01	4.41E-01	8472.30	not significant
2552	ATRN	-1.02	1.26E-01	3.55E-01	115.44	not significant
2553	SPSB1	-1.02	2.99E-01	5.70E-01	566.30	not significant
2554	SOGA1	-1.02	2.92E-01	5.63E-01	1044.73	not significant
2555	ZNF675	-1.02	3.06E-01	5.78E-01	941.29	not significant
2556	ATP6V0E2	-1.02	2.95E-01	5.66E-01	1163.91	not significant
2557	FNIP2	-1.02	2.90E-01	5.62E-01	1283.20	not significant
2558	ZBTB48	-1.02	2.71E-01	5.42E-01	644.88	not significant
2559	TBC1D23	-1.02	3.06E-01	5.78E-01	1084.49	not significant
2560	LRR1	-1.02	2.92E-01	5.63E-01	1692.32	not significant
2561	SNRPA1	-1.02	2.86E-01	5.57E-01	2455.64	not significant
2562	NCOA2	-1.02	2.92E-01	5.64E-01	1850.88	not significant
2563	CFAP36	-1.02	2.84E-01	5.55E-01	529.78	not significant
2564	PHF5A	-1.02	2.80E-01	5.51E-01	2970.77	not significant
2565	CAPZA2	-1.02	2.75E-01	5.46E-01	3532.57	not significant
2566	FBXO5	-1.02	2.76E-01	5.47E-01	2525.92	not significant
2567	GLE1	-1.02	2.88E-01	5.59E-01	2171.24	not significant
2568	PSMD13	-1.02	2.43E-01	5.11E-01	5520.33	not significant
2569	PC	-1.02	3.11E-01	5.83E-01	941.36	not significant
2570	PDCL3	-1.02	2.97E-01	5.68E-01	1297.12	not significant
2571	SLC4A1AP	-1.02	3.07E-01	5.78E-01	1170.73	not significant
2572	FBXO42	-1.02	3.09E-01	5.80E-01	984.98	not significant
2573	C9orf114	-1.02	2.87E-01	5.58E-01	2011.03	not significant
2574	MRPL38	-1.02	2.92E-01	5.63E-01	3450.23	not significant
2575	SNRPB2	-1.02	2.51E-01	5.19E-01	4501.79	not significant
2576	LOC728084	-1.02	2.75E-01	5.46E-01	2865.05	not significant
2577	VPS36	-1.02	2.57E-01	5.26E-01	3033.88	not significant
2578	OXSM	-1.02	2.48E-01	5.16E-01	311.42	not significant
2579	NKG7	-1.02	2.93E-01	5.64E-01	1348.84	not significant
2580	CSDE1	-1.02	1.74E-01	4.30E-01	21064.67	not significant
2581	COMMD10	-1.02	3.12E-01	5.84E-01	850.40	not significant
2582	GEMIN6	-1.02	3.13E-01	5.84E-01	791.03	not significant
2583	CTDP1	-1.02	2.96E-01	5.66E-01	1881.64	not significant
2584	ZNF689	-1.02	2.96E-01	5.67E-01	1481.83	not significant
2585	APOL6	-1.02	2.79E-01	5.50E-01	7191.87	not significant
2586	DLD	-1.02	2.45E-01	5.12E-01	4525.51	not significant
2587	GHITM	-1.02	2.65E-01	5.35E-01	6778.69	not significant
2588	TESPA1	-1.02	2.23E-01	4.89E-01	8072.08	not significant
2589	GREB1	-1.02	2.21E-01	4.88E-01	229.39	not significant
2590	COA6	-1.02	3.11E-01	5.83E-01	895.54	not significant
2591	CDYL	-1.02	3.13E-01	5.84E-01	909.55	not significant
2592	XRRA1	-1.02	3.14E-01	5.85E-01	913.60	not significant
2593	CAAP1	-1.02	2.85E-01	5.55E-01	1604.82	not significant
2594	C11orf58	-1.02	2.64E-01	5.35E-01	5897.52	not significant
2595	43717_21856	-1.02	2.05E-01	4.70E-01	41632.66	not significant
2596	UBE2E2	-1.02	3.07E-01	5.78E-01	650.81	not significant
2597	NEXN	-1.02	3.10E-01	5.81E-01	1794.56	not significant
2598	ZRANB2	-1.02	2.23E-01	4.90E-01	6086.96	not significant
2599	ADM5	-1.02	2.51E-01	5.19E-01	257.99	not significant
2600	POR	-1.02	3.07E-01	5.78E-01	561.44	not significant
2601	CSNK1G3	-1.02	2.87E-01	5.58E-01	419.25	not significant
2602	SNUPN	-1.02	3.13E-01	5.85E-01	1213.63	not significant
2603	CNNM4	-1.02	3.16E-01	5.86E-01	925.69	not significant
2604	AAGAB	-1.02	2.81E-01	5.51E-01	2731.73	not significant
2605	KIF22	-1.02	2.40E-01	5.08E-01	5594.20	not significant
2606	CCDC176	-1.02	1.48E-01	3.94E-01	115.99	not significant
2607	RPP40	-1.02	2.73E-01	5.43E-01	336.80	not significant
2608	CBWD2	-1.02	3.10E-01	5.81E-01	578.06	not significant
2609	FAM118B	-1.02	3.15E-01	5.86E-01	810.36	not significant
2610	RNF121	-1.02	3.24E-01	5.93E-01	661.30	not significant
2611	NFIX	-1.02	3.16E-01	5.86E-01	843.99	not significant
2612	INIP	-1.02	3.16E-01	5.86E-01	984.89	not significant
2613	SMURF2	-1.02	3.16E-01	5.86E-01	1023.82	not significant
2614	GTF2E2	-1.02	2.90E-01	5.62E-01	2306.59	not significant
2615	CSRNP2	-1.02	2.92E-01	5.64E-01	2132.83	not significant
2616	ATP6V1C1	-1.02	2.60E-01	5.30E-01	3436.91	not significant
2617	IRF8	-1.02	1.20E-01	NA	94.49	not significant
2618	LYPLAL1	-1.02	2.22E-01	4.89E-01	212.20	not significant
2619	COPRS	-1.02	3.09E-01	5.80E-01	882.98	not significant
2620	RNF25	-1.02	3.14E-01	5.85E-01	609.32	not significant
2621	LINC01128	-1.02	3.03E-01	5.75E-01	494.84	not significant
2622	MIR646HG	-1.02	3.23E-01	5.93E-01	792.49	not significant
2623	MGME1	-1.02	3.06E-01	5.78E-01	1234.77	not significant
2624	ING5	-1.02	2.92E-01	5.64E-01	2255.54	not significant
2625	NIPBL	-1.02	2.97E-01	5.67E-01	5602.02	not significant
2626	MAP4K4	-1.02	2.54E-01	5.22E-01	8789.87	not significant
2627	NPLOC4	-1.02	2.08E-01	4.73E-01	9318.42	not significant

2628	C19orf40	-1.02	3.00E-01	5.70E-01	290.91	not significant
2629	SDF2L1	-1.02	3.25E-01	5.94E-01	1143.04	not significant
2630	PGS1	-1.02	3.02E-01	5.73E-01	1341.33	not significant
2631	ZNF710	-1.02	3.22E-01	5.91E-01	913.60	not significant
2632	CHCHD4	-1.02	3.20E-01	5.89E-01	956.08	not significant
2633	UBE2D1	-1.02	3.20E-01	5.89E-01	870.94	not significant
2634	RALGAPA2	-1.02	3.18E-01	5.88E-01	1125.64	not significant
2635	PFKM	-1.02	2.93E-01	5.64E-01	2215.30	not significant
2636	AGO1	-1.02	3.00E-01	5.71E-01	2677.93	not significant
2637	PPHLN1	-1.02	2.46E-01	5.14E-01	3948.58	not significant
2638	SNRNP200	-1.02	2.39E-01	5.07E-01	19884.71	not significant
2639	COPA	-1.02	2.40E-01	5.08E-01	7590.02	not significant
2640	DYNLL1-AS1	-1.02	1.28E-01	3.59E-01	111.20	not significant
2641	LRSAM1	-1.02	2.50E-01	5.19E-01	587.80	not significant
2642	DCPS	-1.02	3.24E-01	5.93E-01	847.92	not significant
2643	DUSP6	-1.02	1.72E-01	4.26E-01	13961.74	not significant
2644	SNHG4	-1.02	2.42E-01	5.10E-01	250.24	not significant
2645	SLC25A33	-1.02	2.69E-01	5.40E-01	370.59	not significant
2646	VPS37A	-1.02	3.18E-01	5.87E-01	1729.30	not significant
2647	MCM10	-1.02	2.34E-01	5.01E-01	4682.78	not significant
2648	BRCC3	-1.02	2.39E-01	5.08E-01	237.36	not significant
2649	SRP19	-1.02	3.10E-01	5.81E-01	1838.24	not significant
2650	SART1	-1.02	2.76E-01	5.47E-01	3953.60	not significant
2651	RAPGEF6	-1.02	3.12E-01	5.84E-01	2197.21	not significant
2652	BCL7C	-1.02	3.19E-01	5.88E-01	837.77	not significant
2653	NDUFS4	-1.02	3.25E-01	5.93E-01	884.29	not significant
2654	NTSR1	-1.02	3.31E-01	5.99E-01	551.67	not significant
2655	CWC27	-1.02	3.15E-01	5.86E-01	1961.98	not significant
2656	KLHL15	-1.02	3.23E-01	5.93E-01	1097.06	not significant
2657	C2CD3	-1.02	3.17E-01	5.87E-01	2111.79	not significant
2658	CHCHD3	-1.02	2.74E-01	5.44E-01	5500.24	not significant
2659	P2RY11	-1.02	1.43E-01	3.86E-01	105.96	not significant
2660	TRAF1	-1.02	2.31E-01	4.99E-01	206.09	not significant
2661	ANKRD17	-1.02	3.05E-01	5.77E-01	6026.37	not significant
2662	FOXP1	-1.02	3.27E-01	5.95E-01	1019.78	not significant
2663	TXNDC11	-1.02	3.10E-01	5.81E-01	1344.07	not significant
2664	SEC22C	-1.02	3.10E-01	5.81E-01	1914.97	not significant
2665	LOC100507424	-1.02	4.84E-02	NA	54.68	not significant
2666	ZNF490	-1.02	2.69E-01	5.39E-01	289.85	not significant
2667	ASB7	-1.02	3.28E-01	5.96E-01	732.13	not significant
2668	TXNL4B	-1.02	3.17E-01	5.86E-01	1480.41	not significant
2669	WRNIP1	-1.02	2.98E-01	5.68E-01	3042.25	not significant
2670	PLRG1	-1.02	2.88E-01	5.59E-01	2501.28	not significant
2671	QRICH1	-1.02	2.58E-01	5.26E-01	4224.37	not significant
2672	ITGB2	-1.02	2.69E-01	5.40E-01	4033.60	not significant
2673	FAM86C2P	-1.02	1.44E-01	3.87E-01	110.28	not significant
2674	CLPB	-1.02	3.29E-01	5.97E-01	1177.07	not significant
2675	ACAA2	-1.02	3.23E-01	5.93E-01	2985.96	not significant
2676	GCN1L1	-1.02	2.74E-01	5.44E-01	10887.76	not significant
2677	NR6A1	-1.02	1.15E-01	NA	87.32	not significant
2678	ARL4A	-1.02	2.48E-01	5.16E-01	238.91	not significant
2679	PTPRU	-1.02	3.07E-01	5.78E-01	400.15	not significant
2680	NAA10	-1.02	3.26E-01	5.95E-01	1668.05	not significant
2681	ABCC4	-1.02	3.31E-01	5.99E-01	1489.93	not significant
2682	HEBP2	-1.02	2.34E-01	5.01E-01	218.07	not significant
2683	SH2D2A	-1.02	2.96E-01	5.67E-01	354.99	not significant
2684	MRPL21	-1.02	3.16E-01	5.86E-01	1163.15	not significant
2685	TOMM5	-1.02	3.11E-01	5.82E-01	4750.79	not significant
2686	NCK1	-1.02	3.38E-01	6.06E-01	1509.02	not significant
2687	TPP2	-1.02	2.94E-01	5.65E-01	4029.42	not significant
2688	CCDC124	-1.02	3.18E-01	5.88E-01	3476.88	not significant
2689	STRA13	-1.02	3.17E-01	5.86E-01	3845.57	not significant
2690	RALGDS	-1.02	3.16E-01	5.86E-01	2024.96	not significant
2691	FKBP5	-1.02	2.69E-01	5.40E-01	5206.64	not significant
2692	CIDECP	-1.02	2.09E-01	4.73E-01	200.64	not significant
2693	LZTS2	-1.02	3.15E-01	5.86E-01	421.65	not significant
2694	THAP7	-1.02	3.36E-01	6.04E-01	1099.81	not significant
2695	MREG	-1.02	3.36E-01	6.04E-01	719.80	not significant
2696	DCTN6	-1.02	3.35E-01	6.04E-01	717.88	not significant
2697	PDXK	-1.02	3.37E-01	6.05E-01	1072.24	not significant
2698	KRIT1	-1.02	3.21E-01	5.91E-01	2002.47	not significant
2699	ERH	-1.02	2.76E-01	5.47E-01	8599.18	not significant
2700	TXLNA	-1.02	2.54E-01	5.23E-01	5899.28	not significant
2701	LIMK1	-1.02	2.96E-01	5.67E-01	358.25	not significant
2702	SRR	-1.02	3.06E-01	5.78E-01	399.13	not significant
2703	PDZD11	-1.02	3.38E-01	6.06E-01	1025.40	not significant
2704	ASTE1	-1.02	3.28E-01	5.96E-01	568.98	not significant
2705	HAT1	-1.02	2.69E-01	5.39E-01	3685.94	not significant
2706	SRSF4	-1.02	2.34E-01	5.01E-01	7095.32	not significant
2707	POM121	-1.02	2.44E-01	5.12E-01	1079.49	not significant
2708	SMIM24	-1.02	3.35E-01	6.04E-01	1081.79	not significant
2709	PARG	-1.02	3.39E-01	6.06E-01	817.26	not significant
2710	PARD3	-1.02	3.18E-01	5.87E-01	2195.21	not significant
2711	ZNF12	-1.02	3.30E-01	5.98E-01	1639.76	not significant
2712	OAS3	-1.02	2.62E-01	5.32E-01	7344.92	not significant
2713	ROCK1	-1.02	3.70E-01	6.35E-01	5897.16	not significant
2714	CDK11A	-1.02	3.05E-01	5.77E-01	363.30	not significant
2715	SPATA5L1	-1.02	3.10E-01	5.81E-01	385.73	not significant

2716	KIF18A	-1.02	3.39E-01	6.07E-01	1020.09	not significant
2717	TMEM39B	-1.02	3.36E-01	6.04E-01	1279.44	not significant
2718	PSMB7	-1.02	3.01E-01	5.71E-01	3049.07	not significant
2719	DHX8	-1.02	3.27E-01	5.95E-01	2194.07	not significant
2720	ARHGAP15	-1.02	3.08E-01	5.80E-01	3081.32	not significant
2721	SETD3	-1.02	3.21E-01	5.90E-01	2812.83	not significant
2722	YTHDF2	-1.02	2.70E-01	5.41E-01	4023.46	not significant
2723	RDH13	-1.02	1.40E-01	3.81E-01	111.71	not significant
2724	MORN2	-1.02	1.09E-01	NA	86.27	not significant
2725	ZNF417	-1.02	3.32E-01	5.99E-01	580.59	not significant
2726	SNAP23	-1.02	3.27E-01	5.95E-01	1572.14	not significant
2727	UVRAG	-1.02	3.37E-01	6.05E-01	1252.48	not significant
2728	RNF14	-1.02	3.47E-01	6.13E-01	1812.44	not significant
2729	ZNF107	-1.02	3.16E-01	5.86E-01	4464.86	not significant
2730	SSH2	-1.02	3.21E-01	5.91E-01	3001.93	not significant
2731	SSR4P1	-1.02	6.43E-02	NA	59.49	not significant
2732	PIWIL3	-1.02	1.46E-01	3.90E-01	115.42	not significant
2733	ATG4B	-1.02	3.17E-01	5.87E-01	2562.27	not significant
2734	DMXL1	-1.02	3.29E-01	5.97E-01	2085.51	not significant
2735	NAA30	-1.02	3.70E-01	6.34E-01	1532.72	not significant
2736	ANXA6	-1.02	2.17E-01	4.83E-01	9922.13	not significant
2737	WAC	-1.02	2.59E-01	5.28E-01	7858.09	not significant
2738	TEX9	-1.02	9.90E-02	NA	73.66	not significant
2739	ATP5G3	-1.02	3.35E-01	6.04E-01	8566.20	not significant
2740	U2AF1	-1.02	3.08E-01	5.79E-01	3516.02	not significant
2741	PREP	-1.02	3.14E-01	5.85E-01	2759.63	not significant
2742	FPGT	-1.02	2.95E-01	5.66E-01	307.46	not significant
2743	SKIL	-1.02	3.35E-01	6.04E-01	547.05	not significant
2744	KDM1B	-1.02	3.39E-01	6.07E-01	593.19	not significant
2745	MAN1A2	-1.02	3.38E-01	6.06E-01	1569.90	not significant
2746	FAM20B	-1.02	2.98E-01	5.69E-01	2571.30	not significant
2747	LIMS1	-1.02	3.30E-01	5.97E-01	2121.81	not significant
2748	TMEM104	-1.02	3.39E-01	6.07E-01	1663.83	not significant
2749	NDUFAF2	-1.02	3.30E-01	5.97E-01	470.81	not significant
2750	ECHS1	-1.02	3.42E-01	6.09E-01	2083.57	not significant
2751	ADAT2	-1.02	3.48E-01	6.15E-01	871.45	not significant
2752	PAPD7	-1.02	3.45E-01	6.11E-01	1509.47	not significant
2753	STK35	-1.02	3.39E-01	6.07E-01	2336.47	not significant
2754	HJURP	-1.02	3.27E-01	5.96E-01	3015.23	not significant
2755	TMX2	-1.02	2.97E-01	5.68E-01	2924.03	not significant
2756	NBN	-1.02	2.71E-01	5.41E-01	4137.06	not significant
2757	WASF2	-1.02	2.73E-01	5.43E-01	6997.16	not significant
2758	FAM216A	-1.02	3.51E-01	6.18E-01	949.67	not significant
2759	UBE2J2	-1.02	3.24E-01	5.93E-01	2828.59	not significant
2760	CEP78	-1.02	3.34E-01	6.03E-01	1588.27	not significant
2761	DIP2B	-1.02	3.25E-01	5.94E-01	3777.03	not significant
2762	CDK5RAP2	-1.02	3.37E-01	6.05E-01	2078.62	not significant
2763	DFFA	-1.02	3.22E-01	5.92E-01	2416.82	not significant
2764	FAM178A	-1.02	3.05E-01	5.77E-01	3852.03	not significant
2765	CDK1	-1.02	2.54E-01	5.23E-01	5460.39	not significant
2766	ZNF235	-1.02	2.07E-01	4.71E-01	212.42	not significant
2767	IRAK1BP1	-1.02	3.16E-01	5.86E-01	358.63	not significant
2768	ZNF670	-1.02	3.01E-01	5.71E-01	331.83	not significant
2769	NTHL1	-1.02	3.53E-01	6.19E-01	913.74	not significant
2770	SPOP	-1.02	3.32E-01	6.00E-01	2081.47	not significant
2771	GMPS	-1.02	2.92E-01	5.63E-01	3691.22	not significant
2772	TMEM33	-1.02	2.88E-01	5.59E-01	4813.60	not significant
2773	BRMS1L	-1.02	3.21E-01	5.91E-01	389.87	not significant
2774	CCDC51	-1.02	3.29E-01	5.97E-01	528.09	not significant
2775	UBE2G2	-1.02	3.26E-01	5.94E-01	440.30	not significant
2776	METTL4	-1.02	3.53E-01	6.19E-01	880.24	not significant
2777	MRPL18	-1.02	3.52E-01	6.19E-01	2030.24	not significant
2778	OAZ2	-1.02	3.50E-01	6.17E-01	1270.98	not significant
2779	PRKAR2B	-1.02	3.54E-01	6.19E-01	1061.70	not significant
2780	FLVCR1	-1.02	3.52E-01	6.19E-01	985.26	not significant
2781	RHOG	-1.02	3.14E-01	5.85E-01	3672.38	not significant
2782	SEC13	-1.02	3.04E-01	5.76E-01	4147.94	not significant
2783	PLEKHA2	-1.02	2.42E-01	5.10E-01	7000.38	not significant
2784	LRPPRC	-1.02	2.10E-01	4.74E-01	12913.07	not significant
2785	LOC100131691	-1.02	1.27E-01	NA	88.55	not significant
2786	FBXO30	-1.02	3.55E-01	6.21E-01	920.35	not significant
2787	UQCRH	-1.02	3.28E-01	5.96E-01	4935.57	not significant
2788	PARVG	-1.02	3.26E-01	5.94E-01	3022.33	not significant
2789	TMEM68	-1.02	3.53E-01	6.19E-01	1261.27	not significant
2790	SS18	-1.02	3.17E-01	5.87E-01	2803.86	not significant
2791	RAB7A	-1.02	2.72E-01	5.43E-01	7630.71	not significant
2792	PCM1	-1.02	2.71E-01	5.42E-01	8271.20	not significant
2793	MTSS1	-1.02	1.50E-01	NA	94.57	not significant
2794	GAN	-1.02	2.37E-01	5.04E-01	221.62	not significant
2795	NKIRAS1	-1.02	2.09E-01	4.74E-01	150.35	not significant
2796	NAT1	-1.02	3.32E-01	6.00E-01	416.01	not significant
2797	GALNT6	-1.02	3.42E-01	6.09E-01	2097.55	not significant
2798	GPS1	-1.02	2.88E-01	5.59E-01	6693.01	not significant
2799	GLMN	-1.02	3.50E-01	6.17E-01	582.98	not significant
2800	TTC5	-1.02	3.68E-01	6.33E-01	743.79	not significant
2801	MRPL23	-1.02	3.53E-01	6.19E-01	2442.49	not significant
2802	TXNL4A	-1.02	3.39E-01	6.06E-01	3794.42	not significant
2803	SNF8	-1.02	3.48E-01	6.15E-01	2377.53	not significant

2804	MCM4	-1.02	2.00E-01	4.64E-01	28517.12	not significant
2805	CD80	-1.02	9.74E-02	NA	67.48	not significant
2806	APOO	-1.02	3.57E-01	6.22E-01	665.22	not significant
2807	DCTN4	-1.02	3.42E-01	6.09E-01	1808.08	not significant
2808	RTCB	-1.02	3.16E-01	5.86E-01	3359.44	not significant
2809	PDPK1	-1.02	3.51E-01	6.18E-01	1991.80	not significant
2810	GOLGA3	-1.02	2.50E-01	5.18E-01	8362.35	not significant
2811	ARL10	-1.02	1.84E-01	4.42E-01	137.97	not significant
2812	LINC00944	-1.02	2.09E-01	4.74E-01	149.79	not significant
2813	NF1	-1.02	3.47E-01	6.14E-01	4429.42	not significant
2814	CEP89	-1.02	3.20E-01	5.89E-01	349.96	not significant
2815	ARMC5	-1.02	3.59E-01	6.25E-01	793.83	not significant
2816	TAF1	-1.02	3.50E-01	6.17E-01	2132.71	not significant
2817	GSR	-1.02	2.76E-01	5.47E-01	5531.64	not significant
2818	ATP6V1E2	-1.02	2.16E-01	4.82E-01	143.46	not significant
2819	FAM63B	-1.02	2.84E-01	5.55E-01	272.33	not significant
2820	AUNIP	-1.02	3.36E-01	6.04E-01	412.24	not significant
2821	RBM42	-1.02	3.51E-01	6.18E-01	2836.89	not significant
2822	CD320	-1.02	3.40E-01	6.08E-01	2609.39	not significant
2823	SNRPD1	-1.02	3.27E-01	5.95E-01	4319.04	not significant
2824	SIAH2	-1.02	3.44E-01	6.10E-01	2342.93	not significant
2825	AAMDC	-1.02	1.87E-01	4.45E-01	120.70	not significant
2826	OTUD5	-1.02	3.53E-01	6.19E-01	556.22	not significant
2827	KLHL12	-1.02	3.49E-01	6.15E-01	1426.48	not significant
2828	FOPNL	-1.02	3.08E-01	5.80E-01	3307.16	not significant
2829	ERBB2IP	-1.02	3.32E-01	6.00E-01	5293.50	not significant
2830	HNRNPL	-1.02	2.55E-01	5.24E-01	16718.41	not significant
2831	PLCG1-AS1	-1.02	4.20E-02	NA	49.64	not significant
2832	RAB12	-1.02	3.57E-01	6.23E-01	537.67	not significant
2833	ATF1	-1.02	3.67E-01	6.32E-01	1737.57	not significant
2834	CUL1	-1.02	3.13E-01	5.84E-01	3722.15	not significant
2835	C17orf96	-1.02	3.07E-01	5.79E-01	447.99	not significant
2836	C12orf65	-1.02	3.68E-01	6.32E-01	1032.83	not significant
2837	CCDC138	-1.02	3.69E-01	6.33E-01	934.67	not significant
2838	SLC25A22	-1.02	3.55E-01	6.21E-01	1861.49	not significant
2839	ASAP1	-1.02	3.65E-01	6.30E-01	1860.17	not significant
2840	MDH2	-1.02	3.25E-01	5.94E-01	4853.39	not significant
2841	XIAP	-1.02	3.49E-01	6.16E-01	2503.76	not significant
2842	HMGB1	-1.02	2.51E-01	5.19E-01	13669.09	not significant
2843	KIAA1024	-1.02	1.44E-01	NA	92.53	not significant
2844	CLP1	-1.02	3.57E-01	6.22E-01	544.70	not significant
2845	HINT3	-1.02	3.70E-01	6.35E-01	681.03	not significant
2846	MRPL48	-1.02	3.67E-01	6.31E-01	1766.01	not significant
2847	NDUFA9	-1.02	3.30E-01	5.98E-01	3625.30	not significant
2848	PEF1	-1.02	3.42E-01	6.09E-01	2487.93	not significant
2849	SETX	-1.02	3.40E-01	6.07E-01	4355.00	not significant
2850	ADRBK2	-1.02	2.95E-01	5.66E-01	15292.86	not significant
2851	CCDC84	-1.02	2.96E-01	5.67E-01	258.82	not significant
2852	ZNF586	-1.02	3.58E-01	6.23E-01	527.71	not significant
2853	POLR3K	-1.02	3.66E-01	6.30E-01	1443.77	not significant
2854	DCUN1D5	-1.02	3.72E-01	6.37E-01	1838.00	not significant
2855	ARHGAP26	-1.02	3.54E-01	6.19E-01	1420.77	not significant
2856	CCNC	-1.02	3.24E-01	5.93E-01	3889.94	not significant
2857	UBE2O	-1.02	3.35E-01	6.04E-01	3544.49	not significant
2858	FGF11	-1.02	9.63E-02	NA	63.26	not significant
2859	ACTR3B	-1.02	2.84E-01	5.54E-01	244.40	not significant
2860	SLC25A37	-1.02	3.41E-01	6.08E-01	377.51	not significant
2861	DGUOK	-1.02	3.64E-01	6.28E-01	1982.71	not significant
2862	CUTC	-1.02	3.73E-01	6.38E-01	863.04	not significant
2863	ZBTB40	-1.02	3.72E-01	6.37E-01	2648.13	not significant
2864	SCFD1	-1.02	4.03E-01	6.62E-01	1519.27	not significant
2865	ADSL	-1.02	3.15E-01	5.86E-01	4983.28	not significant
2866	ZAK	-1.02	3.51E-01	6.18E-01	2287.97	not significant
2867	SSBP3	-1.02	3.37E-01	6.05E-01	5908.72	not significant
2868	CDC25A	-1.02	2.86E-01	5.57E-01	4927.86	not significant
2869	MLLT1	-1.02	2.98E-01	5.68E-01	4894.57	not significant
2870	E2F3	-1.02	3.06E-01	5.78E-01	3855.36	not significant
2871	TMEM99	-1.02	2.85E-01	5.55E-01	234.13	not significant
2872	THAP3	-1.02	3.21E-01	5.91E-01	530.70	not significant
2873	SLC36A1	-1.02	3.53E-01	6.19E-01	479.27	not significant
2874	SAMM50	-1.02	3.65E-01	6.29E-01	2225.45	not significant
2875	RAD18	-1.02	3.60E-01	6.25E-01	2232.88	not significant
2876	ANTXR1	-1.02	3.75E-01	6.39E-01	2521.52	not significant
2877	GSK3A	-1.02	3.42E-01	6.08E-01	3318.76	not significant
2878	SUCLG1	-1.02	3.41E-01	6.08E-01	3266.87	not significant
2879	CEBPZ	-1.02	3.41E-01	6.08E-01	3006.15	not significant
2880	SCYL2	-1.02	3.41E-01	6.08E-01	3256.10	not significant
2881	ATP1A1-AS1	-1.02	1.56E-01	4.04E-01	115.40	not significant
2882	STARD7-AS1	-1.02	2.24E-01	4.91E-01	145.99	not significant
2883	CETN3	-1.02	3.78E-01	6.43E-01	857.04	not significant
2884	UBL3	-1.02	3.78E-01	6.43E-01	886.70	not significant
2885	NACA	-1.02	3.26E-01	5.94E-01	21863.78	not significant
2886	BAZ2A	-1.02	3.58E-01	6.23E-01	4719.11	not significant
2887	NAA25	-1.02	3.46E-01	6.12E-01	2891.25	not significant
2888	VPS9D1	-1.02	1.42E-01	NA	86.01	not significant
2889	CD27	-1.02	2.04E-01	4.69E-01	113.13	not significant
2890	JADE3	-1.02	2.48E-01	5.15E-01	173.47	not significant
2891	CEP112	-1.02	3.07E-01	5.79E-01	262.39	not significant

2892	SLC25A13	-1.02	3.70E-01	6.35E-01	574.84	not significant
2893	RNF19B	-1.02	3.92E-01	6.53E-01	736.51	not significant
2894	DDX20	-1.02	3.63E-01	6.27E-01	1785.54	not significant
2895	ERI1	-1.02	3.50E-01	6.17E-01	2524.42	not significant
2896	MSH2	-1.02	2.82E-01	5.52E-01	6867.11	not significant
2897	SF3A1	-1.02	2.59E-01	5.28E-01	8770.02	not significant
2898	EXOSC8	-1.02	3.66E-01	6.30E-01	2050.57	not significant
2899	ATF7	-1.02	3.80E-01	6.44E-01	1595.80	not significant
2900	NDC1	-1.02	3.40E-01	6.08E-01	4307.44	not significant
2901	NAP1L4	-1.02	2.98E-01	5.68E-01	8676.93	not significant
2902	TAOK3	-1.02	3.07E-01	5.78E-01	4550.78	not significant
2903	MTERF1	-1.02	3.54E-01	6.20E-01	423.91	not significant
2904	CHCHD7	-1.02	3.80E-01	6.44E-01	1261.68	not significant
2905	ZNF407	-1.02	3.81E-01	6.45E-01	880.40	not significant
2906	UBE2Z	-1.02	3.42E-01	6.09E-01	2591.82	not significant
2907	SMAP2	-1.02	3.37E-01	6.05E-01	2728.57	not significant
2908	CAND1	-1.02	3.00E-01	5.70E-01	11095.53	not significant
2909	MAPK8	-1.02	3.48E-01	6.15E-01	4930.08	not significant
2910	CCDC102A	-1.02	3.77E-01	6.42E-01	400.80	not significant
2911	BTBD7	-1.02	3.83E-01	6.46E-01	905.86	not significant
2912	SUCLA2	-1.02	3.62E-01	6.27E-01	2120.38	not significant
2913	SLC9A1	-1.02	3.84E-01	6.46E-01	1215.53	not significant
2914	STX6	-1.02	3.56E-01	6.21E-01	2905.42	not significant
2915	BCL2L1	-1.02	2.68E-01	5.38E-01	8707.58	not significant
2916	NUP62	-1.02	2.64E-01	5.35E-01	7557.36	not significant
2917	CSTF2T	-1.02	3.30E-01	5.97E-01	2870.20	not significant
2918	COL4A3BP	-1.02	3.55E-01	6.21E-01	2368.81	not significant
2919	CHST2	-1.02	3.49E-01	6.16E-01	4550.88	not significant
2920	PM20D2	-1.02	3.31E-01	5.99E-01	3746.91	not significant
2921	PSMA2	-1.02	3.36E-01	6.04E-01	6641.18	not significant
2922	SDHA	-1.02	3.41E-01	6.08E-01	3728.30	not significant
2923	FLNA	-1.02	3.21E-01	5.91E-01	13415.94	not significant
2924	THUMPD3	-1.02	3.60E-01	6.25E-01	2753.66	not significant
2925	EDC4	-1.02	2.95E-01	5.66E-01	5479.89	not significant
2926	TMPRSS3	-1.02	1.48E-01	NA	83.70	not significant
2927	ZNF140	-1.02	3.83E-01	6.46E-01	653.47	not significant
2928	GPX1	-1.02	3.83E-01	6.46E-01	2979.62	not significant
2929	TRERF1	-1.02	3.85E-01	6.47E-01	800.96	not significant
2930	SHISA5	-1.02	3.34E-01	6.03E-01	4240.95	not significant
2931	CSPP1	-1.02	3.81E-01	6.45E-01	1532.45	not significant
2932	PGRMC2	-1.02	3.51E-01	6.18E-01	2513.02	not significant
2933	ZBTB24	-1.02	4.19E-01	6.75E-01	1490.68	not significant
2934	NCAPH	-1.02	3.27E-01	5.95E-01	3929.37	not significant
2935	DIS3	-1.02	3.52E-01	6.19E-01	3307.83	not significant
2936	PAK2	-1.02	2.92E-01	5.64E-01	11435.67	not significant
2937	ING2	-1.02	3.32E-01	5.99E-01	532.57	not significant
2938	VRK2	-1.02	3.33E-01	6.00E-01	562.12	not significant
2939	BAHD1	-1.02	3.80E-01	6.44E-01	1502.03	not significant
2940	NDUFA10	-1.02	3.57E-01	6.23E-01	2528.51	not significant
2941	LSM5	-1.02	3.61E-01	6.26E-01	2883.25	not significant
2942	CERS6	-1.02	3.60E-01	6.25E-01	6092.90	not significant
2943	ENOPH1	-1.02	3.20E-01	5.89E-01	4156.12	not significant
2944	CHCHD2	-1.02	3.81E-01	6.45E-01	13171.30	not significant
2945	BCAS2	-1.02	3.82E-01	6.45E-01	1796.00	not significant
2946	NIPA1	-1.02	3.74E-01	6.39E-01	1421.58	not significant
2947	ZNF507	-1.02	3.85E-01	6.47E-01	2164.68	not significant
2948	SETD7	-1.02	3.86E-01	6.48E-01	1797.39	not significant
2949	KIAA0196	-1.02	3.64E-01	6.28E-01	2972.83	not significant
2950	AP3B1	-1.02	3.49E-01	6.16E-01	3585.93	not significant
2951	LINC00341	-1.02	2.01E-01	4.65E-01	117.50	not significant
2952	OAS1	-1.02	2.62E-01	5.32E-01	166.13	not significant
2953	C10orf12	-1.02	3.62E-01	6.26E-01	601.35	not significant
2954	PRADC1	-1.02	3.94E-01	6.54E-01	826.65	not significant
2955	RNF141	-1.02	3.91E-01	6.52E-01	716.02	not significant
2956	PRPSAP2	-1.02	3.74E-01	6.39E-01	1421.89	not significant
2957	MRPS15	-1.02	3.87E-01	6.48E-01	3487.22	not significant
2958	TMEM70	-1.02	3.84E-01	6.46E-01	2319.65	not significant
2959	TSN	-1.02	3.24E-01	5.93E-01	4641.28	not significant
2960	PPP2R1B	-1.02	3.56E-01	6.22E-01	2661.68	not significant
2961	HNRNPUL1	-1.02	2.78E-01	5.48E-01	18953.80	not significant
2962	DENND6B	-1.02	7.04E-02	NA	45.81	not significant
2963	MIPEPP3	-1.02	1.54E-01	NA	81.18	not significant
2964	TEF	-1.02	3.25E-01	5.93E-01	293.56	not significant
2965	AHNAK	-1.02	3.64E-01	6.28E-01	397.70	not significant
2966	UBAC1	-1.02	3.96E-01	6.55E-01	932.46	not significant
2967	TULP3	-1.02	3.94E-01	6.54E-01	696.84	not significant
2968	SIRT2	-1.02	3.92E-01	6.53E-01	1518.89	not significant
2969	PLGRKT	-1.02	2.94E-01	5.65E-01	438.39	not significant
2970	TIGD5	-1.02	3.44E-01	6.11E-01	367.71	not significant
2971	PSMG1	-1.02	3.87E-01	6.48E-01	1906.36	not significant
2972	CHMP4B	-1.02	3.56E-01	6.21E-01	5078.83	not significant
2973	PRDM4	-1.02	3.91E-01	6.52E-01	1746.39	not significant
2974	M6PR	-1.02	3.38E-01	6.06E-01	4915.05	not significant
2975	CYB5R3	-1.02	3.36E-01	6.04E-01	4284.60	not significant
2976	SLC9A6	-1.02	2.31E-01	4.99E-01	123.97	not significant
2977	KLHL29	-1.02	1.96E-01	4.59E-01	110.82	not significant
2978	HELZ2	-1.02	2.92E-01	5.64E-01	222.29	not significant
2979	ELK1	-1.02	3.86E-01	6.48E-01	2066.98	not significant

2980	UPRT	-1.02	3.98E-01	6.58E-01	1013.48	not significant
2981	SIRT1	-1.02	3.94E-01	6.54E-01	1315.91	not significant
2982	SMEK1	-1.02	3.31E-01	5.99E-01	6304.87	not significant
2983	LRRC69	-1.02	2.13E-02	NA	27.38	not significant
2984	IQCH	-1.02	3.21E-02	NA	34.70	not significant
2985	WDR61	-1.02	4.02E-01	6.61E-01	1454.72	not significant
2986	ILK	-1.02	3.94E-01	6.54E-01	1671.04	not significant
2987	TPCN1	-1.02	4.00E-01	6.59E-01	922.56	not significant
2988	NEMF	-1.02	3.99E-01	6.59E-01	1857.18	not significant
2989	MRS2	-1.02	3.80E-01	6.44E-01	1888.75	not significant
2990	SSBP4	-1.02	3.63E-01	6.28E-01	4543.98	not significant
2991	TTF2	-1.02	3.68E-01	6.33E-01	3773.60	not significant
2992	TTI1	-1.02	3.68E-01	6.33E-01	3578.58	not significant
2993	MTF2	-1.02	3.01E-01	5.72E-01	5762.81	not significant
2994	SACM1L	-1.02	3.31E-01	5.99E-01	4859.57	not significant
2995	LOC100379224	-1.02	1.13E-01	NA	73.05	not significant
2996	IFIH1	-1.02	3.92E-01	6.53E-01	548.84	not significant
2997	ZNF426	-1.02	3.91E-01	6.52E-01	559.76	not significant
2998	SGPL1	-1.02	3.85E-01	6.47E-01	1611.76	not significant
2999	TMEM39A	-1.02	3.93E-01	6.54E-01	1516.58	not significant
3000	WDR41	-1.02	3.87E-01	6.48E-01	1860.42	not significant
3001	CDK4	-1.02	3.57E-01	6.23E-01	9009.99	not significant
3002	TMEM65	-1.02	3.91E-01	6.52E-01	1734.72	not significant
3003	ALDH5A1	-1.02	3.75E-01	6.40E-01	2354.92	not significant
3004	FEM1B	-1.02	3.84E-01	6.46E-01	2285.15	not significant
3005	PDE12	-1.02	3.98E-01	6.58E-01	2517.65	not significant
3006	ZFP69	-1.02	2.63E-01	5.34E-01	173.49	not significant
3007	TMEM199	-1.02	4.05E-01	6.63E-01	227.33	not significant
3008	C2orf76	-1.02	3.12E-01	5.84E-01	224.80	not significant
3009	SRRD	-1.02	3.97E-01	6.56E-01	609.02	not significant
3010	RASSF5	-1.02	3.94E-01	6.54E-01	737.50	not significant
3011	BTBD10	-1.02	4.02E-01	6.61E-01	1082.70	not significant
3012	NGLY1	-1.02	3.83E-01	6.46E-01	2075.55	not significant
3013	TRAF3	-1.02	3.41E-01	6.08E-01	3914.75	not significant
3014	43714_12910	-1.02	3.03E-01	5.75E-01	15264.44	not significant
3015	C5orf66	-1.02	1.44E-02	NA	35.23	not significant
3016	FUCA1	-1.02	3.45E-01	6.11E-01	279.27	not significant
3017	TRIM27	-1.02	3.97E-01	6.56E-01	587.04	not significant
3018	SSU72	-1.02	3.74E-01	6.39E-01	3678.97	not significant
3019	PCMT1	-1.02	3.65E-01	6.29E-01	3427.26	not significant
3020	NUP155	-1.02	3.90E-01	6.52E-01	3099.33	not significant
3021	TMEM141	-1.02	3.56E-01	6.21E-01	348.05	not significant
3022	RNF34	-1.02	3.40E-01	6.07E-01	266.38	not significant
3023	TRIM26	-1.02	3.86E-01	6.48E-01	462.33	not significant
3024	CRYZ	-1.02	4.08E-01	6.66E-01	1147.82	not significant
3025	PTRH2	-1.02	4.08E-01	6.66E-01	1093.83	not significant
3026	INTS9	-1.02	3.95E-01	6.55E-01	1489.68	not significant
3027	SMIM12	-1.02	4.05E-01	6.63E-01	1325.98	not significant
3028	EPDR1	-1.02	3.89E-01	6.50E-01	1432.03	not significant
3029	SAE1	-1.02	3.26E-01	5.95E-01	9427.22	not significant
3030	GPATCH8	-1.02	3.91E-01	6.52E-01	3285.53	not significant
3031	NUDT4	-1.02	1.22E-01	NA	61.41	not significant
3032	FAM177A1	-1.02	3.87E-01	6.48E-01	460.06	not significant
3033	OTUD6B-AS1	-1.02	4.12E-01	6.70E-01	1564.29	not significant
3034	VARS	-1.02	3.63E-01	6.27E-01	3398.70	not significant
3035	ZBTB11	-1.02	3.79E-01	6.44E-01	2320.30	not significant
3036	SCAF1	-1.02	3.63E-01	6.28E-01	3709.92	not significant
3037	TBC1D2B	-1.02	3.95E-01	6.54E-01	2109.62	not significant
3038	PTPN14	-1.02	2.99E-01	5.70E-01	187.51	not significant
3039	ZNF155	-1.02	3.52E-01	6.19E-01	334.80	not significant
3040	MT1X	-1.02	4.18E-01	6.73E-01	9540.35	not significant
3041	TRAP1	-1.02	3.74E-01	6.38E-01	2921.66	not significant
3042	ESCO1	-1.02	4.05E-01	6.63E-01	1628.44	not significant
3043	FAM60A	-1.02	3.58E-01	6.23E-01	4195.84	not significant
3044	MAP6D1	-1.02	1.31E-01	NA	67.13	not significant
3045	ARHGAP31	-1.02	1.73E-01	NA	82.07	not significant
3046	IFT46	-1.02	3.56E-01	6.22E-01	287.67	not significant
3047	ZNF8	-1.02	3.48E-01	6.15E-01	313.45	not significant
3048	BBS4	-1.02	3.71E-01	6.36E-01	346.39	not significant
3049	TRIP4	-1.02	3.97E-01	6.56E-01	499.64	not significant
3050	ZNF566	-1.02	3.94E-01	6.54E-01	481.53	not significant
3051	ACOT13	-1.02	4.11E-01	6.69E-01	696.14	not significant
3052	TBP	-1.02	4.14E-01	6.72E-01	1054.11	not significant
3053	LSM10	-1.02	4.20E-01	6.75E-01	1133.16	not significant
3054	IGLL1	-1.02	4.16E-01	6.72E-01	1426.91	not significant
3055	CENPN	-1.02	3.80E-01	6.44E-01	3141.54	not significant
3056	VPS33A	-1.02	3.97E-01	6.57E-01	1911.08	not significant
3057	HERPUD1	-1.02	3.81E-01	6.45E-01	2658.42	not significant
3058	CTCF	-1.02	3.37E-01	6.05E-01	4915.28	not significant
3059	FSD1L	-1.02	4.45E-01	6.96E-01	195.66	not significant
3060	ENPP1	-1.02	3.70E-01	6.35E-01	368.70	not significant
3061	RTKN2	-1.02	4.16E-01	6.72E-01	1039.06	not significant
3062	MLLT3	-1.02	4.01E-01	6.60E-01	1856.22	not significant
3063	PRDX3	-1.02	3.51E-01	6.18E-01	9035.68	not significant
3064	CA6	-1.02	9.90E-02	NA	51.00	not significant
3065	IFFO2	-1.02	2.77E-01	5.47E-01	166.00	not significant
3066	METTL22	-1.02	4.00E-01	6.59E-01	474.57	not significant
3067	WDR47	-1.02	4.16E-01	6.73E-01	682.71	not significant

3068	MBIP	-1.02	4.17E-01	6.73E-01	778.08	not significant
3069	COPS7A	-1.02	4.16E-01	6.73E-01	1260.87	not significant
3070	PSMB4	-1.02	3.90E-01	6.51E-01	6709.83	not significant
3071	FYN	-1.02	3.77E-01	6.42E-01	4039.56	not significant
3072	PPP1CA	-1.02	4.31E-01	6.85E-01	10945.92	not significant
3073	PIP5K1A	-1.02	3.60E-01	6.25E-01	4686.72	not significant
3074	ADNP	-1.02	3.53E-01	6.19E-01	6215.03	not significant
3075	ANGPTL2	-1.02	2.11E-01	4.75E-01	103.23	not significant
3076	DNAH17	-1.02	1.98E-01	NA	95.33	not significant
3077	HELZ	-1.02	4.19E-01	6.74E-01	7032.69	not significant
3078	NDUFA8	-1.02	4.23E-01	6.78E-01	1048.03	not significant
3079	NXT2	-1.02	4.20E-01	6.75E-01	955.38	not significant
3080	ERCC2	-1.02	4.20E-01	6.75E-01	944.55	not significant
3081	MRPS5	-1.02	3.93E-01	6.54E-01	2556.57	not significant
3082	WWP2	-1.02	4.04E-01	6.63E-01	1808.26	not significant
3083	SLU7	-1.02	4.01E-01	6.60E-01	2005.84	not significant
3084	ZWINT	-1.02	3.45E-01	6.12E-01	7229.12	not significant
3085	CPNE3	-1.02	3.60E-01	6.25E-01	4621.65	not significant
3086	PPIP5K1	-1.02	2.95E-01	5.66E-01	173.99	not significant
3087	MRPS22	-1.02	4.21E-01	6.76E-01	1020.14	not significant
3088	TCEB1	-1.02	4.04E-01	6.62E-01	3101.49	not significant
3089	STAT6	-1.02	3.48E-01	6.15E-01	5018.73	not significant
3090	PRG4	-1.02	7.14E-02	NA	43.47	not significant
3091	DMD	-1.02	2.95E-01	5.66E-01	168.76	not significant
3092	CYB5RL	-1.02	4.03E-01	6.62E-01	499.85	not significant
3093	PDCD5	-1.02	4.23E-01	6.78E-01	1540.05	not significant
3094	ZUFSP	-1.02	4.13E-01	6.71E-01	740.01	not significant
3095	METTL5	-1.02	4.23E-01	6.78E-01	923.34	not significant
3096	RWDD1	-1.02	3.95E-01	6.55E-01	2455.87	not significant
3097	PRC1	-1.02	4.02E-01	6.61E-01	2305.31	not significant
3098	PPM1F	-1.02	4.11E-01	6.69E-01	1744.29	not significant
3099	VMA21	-1.02	3.61E-01	6.25E-01	4183.85	not significant
3100	USP1	-1.02	3.29E-01	5.97E-01	9047.32	not significant
3101	KPNA5	-1.02	3.59E-01	6.24E-01	429.73	not significant
3102	RPGR	-1.02	4.59E-01	7.06E-01	473.65	not significant
3103	MALSU1	-1.02	4.26E-01	6.79E-01	974.64	not significant
3104	PPIH	-1.02	4.06E-01	6.64E-01	2242.31	not significant
3105	DCLRE1B	-1.02	4.12E-01	6.69E-01	1609.82	not significant
3106	IFT122	-1.02	4.24E-01	6.79E-01	977.93	not significant
3107	NADK	-1.02	3.84E-01	6.46E-01	3049.89	not significant
3108	NLRC3	-1.02	3.99E-01	6.59E-01	2491.66	not significant
3109	CAPN3	-1.02	8.81E-02	NA	47.81	not significant
3110	C2orf74	-1.02	2.56E-01	5.25E-01	130.72	not significant
3111	GABARAPL1	-1.02	3.04E-01	5.76E-01	205.29	not significant
3112	CBX2	-1.02	3.61E-01	6.26E-01	269.28	not significant
3113	RBAK	-1.02	4.30E-01	6.84E-01	1222.10	not significant
3114	COX19	-1.02	4.09E-01	6.67E-01	1414.61	not significant
3115	HADHB	-1.02	4.05E-01	6.64E-01	2310.99	not significant
3116	USP37	-1.02	4.09E-01	6.67E-01	2482.49	not significant
3117	MMGT1	-1.02	1.38E-01	NA	62.50	not significant
3118	ZNF805	-1.02	3.93E-01	6.54E-01	401.06	not significant
3119	USP8	-1.02	4.15E-01	6.72E-01	1734.43	not significant
3120	TAGLN2	-1.02	3.66E-01	6.30E-01	10610.48	not significant
3121	YWHAQ	-1.02	3.57E-01	6.22E-01	16589.25	not significant
3122	SH3BP5-AS1	-1.02	3.02E-01	5.73E-01	195.17	not significant
3123	C19orf44	-1.02	3.48E-01	6.15E-01	246.22	not significant
3124	FRG1B	-1.02	4.59E-01	7.06E-01	764.59	not significant
3125	POLR2F	-1.02	4.34E-01	6.88E-01	2266.70	not significant
3126	DECR1	-1.02	4.12E-01	6.70E-01	1419.50	not significant
3127	RALBP1	-1.02	3.88E-01	6.49E-01	3503.36	not significant
3128	MST4	-1.02	3.36E-01	6.04E-01	5992.94	not significant
3129	RBPJ	-1.02	4.10E-01	6.68E-01	3300.31	not significant
3130	TYW1B	-1.02	1.11E-01	NA	52.80	not significant
3131	DDA1	-1.02	4.25E-01	6.79E-01	1944.69	not significant
3132	HPS4	-1.02	4.11E-01	6.69E-01	2602.73	not significant
3133	TRAFD1	-1.02	4.04E-01	6.63E-01	2386.16	not significant
3134	PARP9	-1.02	4.07E-01	6.65E-01	2438.67	not significant
3135	CTPS1	-1.02	3.27E-01	5.95E-01	7378.99	not significant
3136	GCSH	-1.02	2.19E-01	4.86E-01	103.28	not significant
3137	CA5BP1	-1.02	2.76E-01	5.46E-01	137.85	not significant
3138	ZNF880	-1.02	3.52E-01	6.19E-01	248.26	not significant
3139	IQCC	-1.02	3.99E-01	6.59E-01	411.80	not significant
3140	ZNF786	-1.02	3.79E-01	6.44E-01	365.04	not significant
3141	TCP11L1	-1.02	4.04E-01	6.63E-01	630.76	not significant
3142	NDUFS5	-1.02	4.29E-01	6.82E-01	2622.40	not significant
3143	GSTCD	-1.02	4.34E-01	6.88E-01	1061.54	not significant
3144	SMC2	-1.02	3.59E-01	6.24E-01	5486.09	not significant
3145	LOC100996351	-1.02	4.08E-02	NA	32.55	not significant
3146	ZSCAN20	-1.02	2.82E-01	5.53E-01	147.79	not significant
3147	NKAP	-1.02	4.01E-01	6.60E-01	758.46	not significant
3148	ILKAP	-1.02	4.34E-01	6.88E-01	1549.98	not significant
3149	SLC38A5	-1.02	4.36E-01	6.88E-01	1050.24	not significant
3150	LMBR1	-1.02	4.17E-01	6.73E-01	2009.23	not significant
3151	ATXN10	-1.02	3.79E-01	6.44E-01	5586.84	not significant
3152	DCAF12	-1.02	3.81E-01	6.45E-01	3841.04	not significant
3153	HIRA	-1.02	3.62E-01	6.26E-01	4863.77	not significant
3154	TBKBP1	-1.02	1.12E-01	NA	53.41	not significant
3155	ZNF799	-1.02	3.71E-01	6.36E-01	270.09	not significant

3156	RWDD4	-1.02	4.31E-01	6.85E-01	638.99	not significant
3157	ZNF227	-1.02	4.42E-01	6.93E-01	935.24	not significant
3158	EXOSC7	-1.02	4.36E-01	6.89E-01	1158.57	not significant
3159	MED10	-1.02	4.37E-01	6.89E-01	2008.75	not significant
3160	ZNF7	-1.02	4.36E-01	6.89E-01	945.28	not significant
3161	HEATR3	-1.02	4.36E-01	6.89E-01	1181.33	not significant
3162	OSBPL11	-1.02	4.25E-01	6.79E-01	2115.70	not significant
3163	SPATS2	-1.02	4.38E-01	6.90E-01	1105.07	not significant
3164	MIOS	-1.02	4.40E-01	6.92E-01	928.88	not significant
3165	CSTF1	-1.02	4.22E-01	6.77E-01	1408.10	not significant
3166	RFWD3	-1.02	3.55E-01	6.21E-01	6648.81	not significant
3167	TMED2	-1.02	3.16E-01	5.86E-01	12232.91	not significant
3168	MECR	-1.02	4.40E-01	6.92E-01	663.44	not significant
3169	TGDS	-1.02	4.40E-01	6.92E-01	1046.85	not significant
3170	DIABLO	-1.02	4.21E-01	6.76E-01	2576.81	not significant
3171	BTAF1	-1.02	4.07E-01	6.66E-01	4451.23	not significant
3172	PIK3R2	-1.02	4.29E-01	6.83E-01	1486.34	not significant
3173	SOCS7	-1.02	3.15E-01	5.86E-01	168.31	not significant
3174	LIMS2	-1.02	4.42E-01	6.93E-01	828.09	not significant
3175	GFOD2	-1.02	4.45E-01	6.96E-01	1067.83	not significant
3176	DNPEP	-1.02	4.14E-01	6.72E-01	2639.17	not significant
3177	KIAA1191	-1.02	4.29E-01	6.82E-01	1732.55	not significant
3178	TTTY15	-1.02	4.42E-01	6.93E-01	1519.92	not significant
3179	GTF2F1	-1.02	3.81E-01	6.45E-01	4408.73	not significant
3180	MOB1A	-1.02	4.00E-01	6.60E-01	4274.32	not significant
3181	HKDC1	-1.02	2.56E-01	5.25E-01	117.87	not significant
3182	ZNF596	-1.02	3.16E-01	5.86E-01	166.99	not significant
3183	STEAP1B	-1.02	2.12E-01	NA	90.32	not significant
3184	SCFD2	-1.02	4.43E-01	6.94E-01	1028.76	not significant
3185	RRAGC	-1.02	4.42E-01	6.93E-01	1266.85	not significant
3186	SP4	-1.02	4.32E-01	6.85E-01	1937.56	not significant
3187	GRSF1	-1.02	3.47E-01	6.14E-01	7254.47	not significant
3188	CDC73	-1.02	4.27E-01	6.81E-01	2075.33	not significant
3189	APPBP2	-1.02	4.10E-01	6.68E-01	2628.00	not significant
3190	TPM1	-1.02	1.17E-01	NA	50.57	not significant
3191	WBP5	-1.02	3.56E-01	6.22E-01	219.88	not significant
3192	TUBD1	-1.02	4.16E-01	6.72E-01	396.47	not significant
3193	TRIM59	-1.02	4.46E-01	6.96E-01	689.69	not significant
3194	SIK3	-1.02	4.47E-01	6.97E-01	995.72	not significant
3195	ARHGAP17	-1.02	4.08E-01	6.66E-01	2470.33	not significant
3196	IMPAD1	-1.02	4.10E-01	6.68E-01	5354.68	not significant
3197	PUM1	-1.02	3.87E-01	6.48E-01	3804.62	not significant
3198	G3BP1	-1.02	3.35E-01	6.04E-01	11515.61	not significant
3199	MROH8	-1.02	2.06E-01	NA	84.99	not significant
3200	ACP6	-1.02	2.52E-01	5.21E-01	140.57	not significant
3201	TMEM189	-1.02	4.49E-01	6.99E-01	1308.82	not significant
3202	DNAJC24	-1.02	4.48E-01	6.98E-01	861.48	not significant
3203	SMAP1	-1.02	4.37E-01	6.90E-01	1707.70	not significant
3204	PIGK	-1.02	4.29E-01	6.83E-01	1396.38	not significant
3205	PPA1	-1.02	3.94E-01	6.54E-01	8495.69	not significant
3206	ARMC4	-1.02	1.64E-01	NA	65.08	not significant
3207	CLEC12A	-1.02	2.42E-01	NA	99.28	not significant
3208	ZNF121	-1.02	2.71E-01	5.41E-01	556.42	not significant
3209	C19orf24	-1.02	4.47E-01	6.97E-01	1268.05	not significant
3210	SKI	-1.02	4.21E-01	6.76E-01	398.82	not significant
3211	ATP6V1E1	-1.02	4.28E-01	6.82E-01	3324.20	not significant
3212	MKRN1	-1.02	4.26E-01	6.79E-01	2690.01	not significant
3213	RBM22	-1.02	4.10E-01	6.68E-01	3032.28	not significant
3214	HNRNPA2B1	-1.02	4.12E-01	6.69E-01	66003.26	not significant
3215	MIR22HG	-1.02	1.38E-01	NA	60.66	not significant
3216	CCDC62	-1.02	1.23E-01	NA	58.16	not significant
3217	RABIF	-1.02	4.53E-01	7.02E-01	853.71	not significant
3218	ANAPC15	-1.02	4.50E-01	6.99E-01	1540.19	not significant
3219	STX10	-1.02	4.44E-01	6.95E-01	1959.20	not significant
3220	CAPN7	-1.02	4.51E-01	7.00E-01	1640.62	not significant
3221	SP1	-1.02	4.07E-01	6.66E-01	5867.65	not significant
3222	MAST2	-1.02	4.50E-01	6.99E-01	2178.64	not significant
3223	ZC3H18	-1.02	3.74E-01	6.38E-01	4764.85	not significant
3224	PELP1	-1.02	3.91E-01	6.52E-01	4768.78	not significant
3225	SF3B2	-1.02	3.46E-01	6.13E-01	12596.77	not significant
3226	BPTF	-1.02	4.60E-01	7.07E-01	6693.61	not significant
3227	GPRIN3	-1.02	3.86E-01	6.48E-01	300.54	not significant
3228	CYB561D1	-1.02	4.45E-01	6.96E-01	582.02	not significant
3229	COMMD2	-1.02	4.61E-01	7.07E-01	1724.17	not significant
3230	PSMD8	-1.02	4.11E-01	6.69E-01	6023.00	not significant
3231	SYMPK	-1.02	3.91E-01	6.52E-01	4127.31	not significant
3232	NUP133	-1.02	4.11E-01	6.69E-01	3299.07	not significant
3233	BRD2	-1.02	4.48E-01	6.98E-01	2772.11	not significant
3234	RFX3-AS1	-1.02	1.74E-01	NA	66.52	not significant
3235	DNTTIP1	-1.02	4.85E-01	7.26E-01	1331.27	not significant
3236	SERTAD2	-1.02	4.56E-01	7.04E-01	1424.14	not significant
3237	ZNF264	-1.02	4.54E-01	7.03E-01	1249.20	not significant
3238	PAG1	-1.02	4.09E-01	6.67E-01	5894.33	not significant
3239	TEX14	-1.02	2.37E-02	NA	23.34	not significant
3240	TNFSF14	-1.02	1.47E-01	NA	60.03	not significant
3241	ADAM1A	-1.02	3.95E-01	6.55E-01	233.16	not significant
3242	HOMER2	-1.02	4.04E-01	6.63E-01	395.64	not significant
3243	ZNF585B	-1.02	4.53E-01	7.02E-01	649.44	not significant

3244	MYO1C	-1.02	4.58E-01	7.05E-01	778.08	not significant
3245	CRY2	-1.02	4.57E-01	7.05E-01	999.65	not significant
3246	TIMMDC1	-1.02	4.67E-01	7.12E-01	1699.46	not significant
3247	ITGAE	-1.02	4.33E-01	6.87E-01	3277.78	not significant
3248	ATG12	-1.02	4.48E-01	6.98E-01	1701.92	not significant
3249	BEND4	-1.02	4.57E-01	7.05E-01	1546.02	not significant
3250	EHD3	-1.02	2.43E-01	5.11E-01	104.59	not significant
3251	METTL7A	-1.02	2.23E-01	NA	91.18	not significant
3252	CWC15	-1.02	4.38E-01	6.90E-01	701.78	not significant
3253	SIRT5	-1.02	4.47E-01	6.97E-01	462.85	not significant
3254	UFSP2	-1.02	4.61E-01	7.07E-01	779.76	not significant
3255	SOCS2	-1.02	4.43E-01	6.93E-01	2443.57	not significant
3256	MAPKBP1	-1.02	4.57E-01	7.05E-01	1211.29	not significant
3257	GPR68	-1.02	4.49E-01	6.99E-01	1480.70	not significant
3258	TANK	-1.02	4.45E-01	6.96E-01	1821.04	not significant
3259	SRSF6	-1.02	3.27E-01	5.95E-01	13397.24	not significant
3260	AOC3	-1.02	7.69E-02	NA	36.63	not significant
3261	FBLN5	-1.02	2.56E-01	5.24E-01	122.15	not significant
3262	MXI1	-1.02	3.67E-01	6.31E-01	208.22	not significant
3263	ZNF79	-1.02	4.01E-01	6.60E-01	323.87	not significant
3264	NDUFA7	-1.02	4.66E-01	7.11E-01	1205.20	not significant
3265	PUS3	-1.02	4.54E-01	7.03E-01	583.35	not significant
3266	TMEM110	-1.02	4.61E-01	7.07E-01	1187.75	not significant
3267	EXOSC10	-1.02	4.15E-01	6.72E-01	3639.10	not significant
3268	AIFM2	-1.02	1.61E-01	NA	60.56	not significant
3269	FAM206A	-1.02	4.55E-01	7.04E-01	582.20	not significant
3270	EMC2	-1.02	4.59E-01	7.06E-01	522.36	not significant
3271	GZMA	-1.02	4.64E-01	7.10E-01	1025.70	not significant
3272	SLC25A30	-1.02	4.63E-01	7.09E-01	1176.95	not significant
3273	LAP3	-1.02	4.52E-01	7.01E-01	1939.81	not significant
3274	PHF20	-1.02	4.35E-01	6.88E-01	3095.68	not significant
3275	SSRP1	-1.02	3.73E-01	6.38E-01	14645.18	not significant
3276	ZNF564	-1.01	3.97E-01	6.56E-01	292.87	not significant
3277	CHRNA9	-1.01	4.06E-01	6.64E-01	278.47	not significant
3278	ZNF543	-1.01	4.12E-01	6.69E-01	350.63	not significant
3279	COQ5	-1.01	4.57E-01	7.05E-01	756.09	not significant
3280	TPM3P9	-1.01	4.64E-01	7.10E-01	767.65	not significant
3281	RBM15	-1.01	4.75E-01	7.17E-01	1319.39	not significant
3282	DGKE	-1.01	4.65E-01	7.11E-01	1970.33	not significant
3283	MRPS25	-1.01	4.32E-01	6.85E-01	2556.84	not significant
3284	TAX1BP1	-1.01	4.24E-01	6.78E-01	3237.91	not significant
3285	EMC1	-1.01	4.48E-01	6.98E-01	2620.52	not significant
3286	CHD8	-1.01	4.25E-01	6.79E-01	5730.94	not significant
3287	NFKBIE	-1.01	4.27E-01	6.81E-01	340.90	not significant
3288	APOPT1	-1.01	4.69E-01	7.13E-01	1022.86	not significant
3289	C2orf49	-1.01	4.58E-01	7.05E-01	1717.68	not significant
3290	PI4KB	-1.01	4.35E-01	6.88E-01	2536.47	not significant
3291	LAT	-1.01	3.69E-01	6.33E-01	10834.66	not significant
3292	ZNF638	-1.01	4.34E-01	6.88E-01	3254.33	not significant
3293	TPI1P2	-1.01	9.23E-02	NA	44.70	not significant
3294	GBP5	-1.01	4.58E-01	7.05E-01	547.20	not significant
3295	NDUFAF1	-1.01	4.38E-01	6.90E-01	390.03	not significant
3296	TCFL5	-1.01	4.70E-01	7.14E-01	899.07	not significant
3297	L2HGDH	-1.01	4.67E-01	7.12E-01	1206.34	not significant
3298	HAUS2	-1.01	4.52E-01	7.01E-01	1950.40	not significant
3299	RHOT1	-1.01	4.58E-01	7.05E-01	1980.45	not significant
3300	MCAM	-1.01	9.10E-02	NA	40.23	not significant
3301	WNK1	-1.01	3.91E-01	6.52E-01	18000.57	not significant
3302	FBXO31	-1.01	4.69E-01	7.14E-01	1249.97	not significant
3303	COASY	-1.01	4.35E-01	6.88E-01	2969.65	not significant
3304	GOLGA7	-1.01	4.28E-01	6.82E-01	3299.00	not significant
3305	NPM1	-1.01	4.26E-01	6.80E-01	34066.24	not significant
3306	DTX3L	-1.01	4.39E-01	6.92E-01	3864.44	not significant
3307	SPRY4	-1.01	1.36E-01	NA	49.67	not significant
3308	SERTAD1	-1.01	2.95E-01	5.66E-01	140.82	not significant
3309	SACS	-1.01	4.63E-01	7.09E-01	5736.67	not significant
3310	CAMTA1	-1.01	4.68E-01	7.13E-01	688.51	not significant
3311	RCOR3	-1.01	4.73E-01	7.16E-01	1188.09	not significant
3312	TCEAL4	-1.01	2.72E-01	5.43E-01	109.21	not significant
3313	APTR	-1.01	3.45E-01	6.12E-01	184.59	not significant
3314	PRRC2C	-1.01	2.97E-01	5.68E-01	17871.84	not significant
3315	WASH3P	-1.01	4.10E-01	6.68E-01	181.37	not significant
3316	METTL15	-1.01	4.44E-01	6.95E-01	387.59	not significant
3317	NSUN5	-1.01	4.65E-01	7.11E-01	699.15	not significant
3318	ZNF415	-1.01	4.53E-01	7.02E-01	427.71	not significant
3319	MRRF	-1.01	4.76E-01	7.18E-01	658.51	not significant
3320	INTS5	-1.01	4.74E-01	7.17E-01	1091.44	not significant
3321	LEO1	-1.01	4.71E-01	7.15E-01	1540.48	not significant
3322	RSF1	-1.01	4.74E-01	7.17E-01	1328.01	not significant
3323	PTPN4	-1.01	4.42E-01	6.93E-01	1653.83	not significant
3324	PARP14	-1.01	4.21E-01	6.76E-01	6448.19	not significant
3325	MTDH	-1.01	3.86E-01	6.48E-01	16497.93	not significant
3326	GNA13	-1.01	3.83E-01	6.46E-01	8861.11	not significant
3327	TTLL11	-1.01	3.17E-01	5.86E-01	135.50	not significant
3328	ZBTB25	-1.01	4.14E-01	6.72E-01	279.66	not significant
3329	FEZ2	-1.01	4.44E-01	6.95E-01	527.09	not significant
3330	SIDT2	-1.01	4.29E-01	6.82E-01	306.23	not significant
3331	DAAM1	-1.01	4.64E-01	7.10E-01	535.06	not significant

3332	ZNF268	-1.01	4.77E-01	7.19E-01	1466.93	not significant
3333	ARRB2	-1.01	4.34E-01	6.88E-01	3852.59	not significant
3334	RAP1GDS1	-1.01	4.02E-01	6.61E-01	3844.48	not significant
3335	HNRNPH1	-1.01	3.62E-01	6.26E-01	26115.00	not significant
3336	BLOC1S2	-1.01	4.79E-01	7.21E-01	1412.95	not significant
3337	APC	-1.01	4.80E-01	7.22E-01	1693.84	not significant
3338	SCAMP3	-1.01	4.76E-01	7.18E-01	1596.55	not significant
3339	CMTM3	-1.01	4.21E-01	6.76E-01	5558.58	not significant
3340	SFMBT2	-1.01	4.67E-01	7.12E-01	3143.05	not significant
3341	TLK1	-1.01	4.35E-01	6.88E-01	3693.86	not significant
3342	ELAVL1	-1.01	3.87E-01	6.48E-01	8441.45	not significant
3343	WT1-AS	-1.01	5.26E-02	NA	29.91	not significant
3344	FAHD2B	-1.01	3.35E-01	6.04E-01	149.33	not significant
3345	CORO7	-1.01	4.67E-01	7.12E-01	506.16	not significant
3346	ZFYVE19	-1.01	4.81E-01	7.22E-01	790.45	not significant
3347	TCF7L2	-1.01	4.48E-01	6.98E-01	389.81	not significant
3348	EDARADD	-1.01	4.35E-01	6.88E-01	404.04	not significant
3349	MRPL2	-1.01	4.82E-01	7.22E-01	910.28	not significant
3350	HKR1	-1.01	4.81E-01	7.22E-01	835.52	not significant
3351	SP110	-1.01	4.68E-01	7.13E-01	1457.34	not significant
3352	CREB1	-1.01	4.59E-01	7.06E-01	2839.53	not significant
3353	TLE3	-1.01	4.16E-01	6.73E-01	8201.91	not significant
3354	GPATCH1	-1.01	4.87E-01	7.26E-01	731.94	not significant
3355	IMP3	-1.01	4.81E-01	7.22E-01	2242.07	not significant
3356	MTERF3	-1.01	4.68E-01	7.13E-01	1430.54	not significant
3357	CHSY1	-1.01	4.70E-01	7.14E-01	3462.27	not significant
3358	PLCXD2	-1.01	1.73E-01	NA	62.43	not significant
3359	LINC01184	-1.01	3.90E-01	6.52E-01	203.86	not significant
3360	LOC283070	-1.01	4.27E-01	6.81E-01	276.08	not significant
3361	TBCCD1	-1.01	4.83E-01	7.24E-01	644.06	not significant
3362	C11orf54	-1.01	4.84E-01	7.24E-01	856.86	not significant
3363	SH3BGRL	-1.01	4.55E-01	7.04E-01	2677.74	not significant
3364	RAB11A	-1.01	4.45E-01	6.96E-01	3168.22	not significant
3365	NUCKS1	-1.01	3.67E-01	6.31E-01	16400.69	not significant
3366	ZNF850	-1.01	4.30E-01	6.83E-01	306.49	not significant
3367	REXO2	-1.01	5.37E-01	7.61E-01	792.59	not significant
3368	SNRPE	-1.01	4.80E-01	7.22E-01	1688.68	not significant
3369	CCDC69	-1.01	4.77E-01	7.19E-01	1904.48	not significant
3370	PRKCI	-1.01	4.74E-01	7.16E-01	2027.83	not significant
3371	TP53BP1	-1.01	4.77E-01	7.19E-01	2260.70	not significant
3372	TMEM185B	-1.01	4.65E-01	7.11E-01	2887.68	not significant
3373	TRIM28	-1.01	4.29E-01	6.83E-01	29239.64	not significant
3374	N6AMT2	-1.01	4.34E-01	6.88E-01	456.66	not significant
3375	NAP1L5	-1.01	4.39E-01	6.92E-01	349.04	not significant
3376	ADPRHL2	-1.01	4.89E-01	7.29E-01	1228.06	not significant
3377	CLOCK	-1.01	4.81E-01	7.22E-01	556.13	not significant
3378	SDHC	-1.01	4.89E-01	7.28E-01	1307.90	not significant
3379	MICU1	-1.01	4.66E-01	7.12E-01	2230.72	not significant
3380	SMG9	-1.01	4.65E-01	7.11E-01	2589.23	not significant
3381	CELF2	-1.01	4.68E-01	7.12E-01	11845.07	not significant
3382	GNAI2	-1.01	4.47E-01	6.97E-01	4044.75	not significant
3383	GCLC	-1.01	4.65E-01	7.11E-01	2381.93	not significant
3384	RUNX1	-1.01	4.32E-01	6.86E-01	8938.11	not significant
3385	KLF9	-1.01	1.12E-01	NA	39.97	not significant
3386	ZNF713	-1.01	3.26E-01	5.94E-01	132.27	not significant
3387	TCP10L	-1.01	2.06E-01	NA	72.90	not significant
3388	ZNF253	-1.01	4.89E-01	7.29E-01	640.17	not significant
3389	LOC100419583	-1.01	4.74E-01	7.17E-01	488.48	not significant
3390	CXorf56	-1.01	4.92E-01	7.31E-01	933.83	not significant
3391	PPA2	-1.01	5.21E-01	7.51E-01	1117.56	not significant
3392	MRPS31	-1.01	4.93E-01	7.31E-01	1012.78	not significant
3393	AP4S1	-1.01	4.83E-01	7.24E-01	561.19	not significant
3394	SGOL1	-1.01	4.90E-01	7.29E-01	1394.15	not significant
3395	INO80E	-1.01	4.91E-01	7.30E-01	2456.72	not significant
3396	USP5	-1.01	4.66E-01	7.11E-01	2570.33	not significant
3397	KLHL42	-1.01	4.86E-01	7.26E-01	1806.26	not significant
3398	TRAM2	-1.01	4.88E-01	7.28E-01	1929.88	not significant
3399	SIT1	-1.01	4.86E-01	7.26E-01	591.81	not significant
3400	LIX1L	-1.01	4.50E-01	6.99E-01	350.90	not significant
3401	FOXO3B	-1.01	4.83E-01	7.24E-01	598.47	not significant
3402	KIAA1429	-1.01	4.57E-01	7.05E-01	3461.58	not significant
3403	PPP1R15B	-1.01	4.60E-01	7.07E-01	5490.27	not significant
3404	CELSR3	-1.01	4.78E-01	7.20E-01	2926.62	not significant
3405	LANCL1	-1.01	4.43E-01	6.94E-01	3708.49	not significant
3406	SUZ12	-1.01	4.15E-01	6.72E-01	5971.65	not significant
3407	CBY1	-1.01	3.18E-01	5.87E-01	123.20	not significant
3408	ZFP69B	-1.01	3.86E-01	6.48E-01	183.99	not significant
3409	CMTM8	-1.01	4.58E-01	7.05E-01	357.77	not significant
3410	RASSF1	-1.01	4.71E-01	7.14E-01	441.35	not significant
3411	RPS26	-1.01	4.76E-01	7.18E-01	4935.40	not significant
3412	RNF139	-1.01	4.89E-01	7.29E-01	1513.37	not significant
3413	GIMAP7	-1.01	4.30E-01	6.84E-01	6518.05	not significant
3414	ZNF438	-1.01	4.42E-01	6.93E-01	329.51	not significant
3415	MRPL50	-1.01	4.62E-01	7.08E-01	526.39	not significant
3416	ZNF431	-1.01	4.70E-01	7.14E-01	984.53	not significant
3417	R3HCC1L	-1.01	4.97E-01	7.35E-01	1113.73	not significant
3418	EMD	-1.01	4.95E-01	7.33E-01	698.71	not significant
3419	SAFB2	-1.01	4.52E-01	7.01E-01	3208.85	not significant

3420	PTPRA	-1.01	4.33E-01	6.87E-01	4487.60	not significant
3421	MED22	-1.01	3.28E-01	5.96E-01	125.42	not significant
3422	FAM8A1	-1.01	4.72E-01	7.15E-01	419.91	not significant
3423	KIAA0556	-1.01	4.65E-01	7.11E-01	508.73	not significant
3424	SRD5A1	-1.01	4.91E-01	7.30E-01	566.13	not significant
3425	UBE4A	-1.01	4.87E-01	7.27E-01	1377.42	not significant
3426	MTG2	-1.01	5.00E-01	7.36E-01	836.72	not significant
3427	TMEM184B	-1.01	4.97E-01	7.35E-01	1360.86	not significant
3428	UQCRC2	-1.01	4.41E-01	6.92E-01	7581.88	not significant
3429	YY1	-1.01	4.26E-01	6.80E-01	5910.19	not significant
3430	FHL3	-1.01	4.01E-01	6.60E-01	203.18	not significant
3431	COL6A3	-1.01	3.59E-01	6.24E-01	152.37	not significant
3432	HELB	-1.01	4.15E-01	6.72E-01	236.44	not significant
3433	CDC14A	-1.01	4.74E-01	7.16E-01	418.32	not significant
3434	FBXO38	-1.01	4.99E-01	7.36E-01	1414.86	not significant
3435	ZNF654	-1.01	4.99E-01	7.36E-01	890.55	not significant
3436	SLC30A1	-1.01	4.89E-01	7.28E-01	1382.96	not significant
3437	FAR2	-1.01	4.89E-01	7.28E-01	1822.33	not significant
3438	CLINT1	-1.01	4.03E-01	6.62E-01	8484.47	not significant
3439	CASKIN1	-1.01	4.76E-02	NA	31.22	not significant
3440	SRGAP2D	-1.01	1.07E-01	NA	36.85	not significant
3441	NETO1	-1.01	2.56E-01	NA	90.11	not significant
3442	DOK3	-1.01	3.21E-01	5.91E-01	120.35	not significant
3443	PCNA-AS1	-1.01	1.91E-01	NA	66.56	not significant
3444	KLF12	-1.01	4.95E-01	7.33E-01	3298.83	not significant
3445	ADSS	-1.01	4.64E-01	7.10E-01	3439.15	not significant
3446	SMARCD2	-1.01	4.34E-01	6.88E-01	6617.76	not significant
3447	SLFN12L	-1.01	1.75E-01	4.31E-01	233.68	not significant
3448	FOSL2	-1.01	3.10E-01	5.81E-01	113.35	not significant
3449	HERC6	-1.01	3.71E-01	6.36E-01	175.89	not significant
3450	FAM200A	-1.01	5.16E-01	7.47E-01	447.90	not significant
3451	CSRNP1	-1.01	4.71E-01	7.15E-01	385.44	not significant
3452	CYP2U1	-1.01	4.64E-01	7.10E-01	487.09	not significant
3453	ZDHHC20	-1.01	4.64E-01	7.10E-01	5456.14	not significant
3454	PTBP3	-1.01	4.29E-01	6.82E-01	8119.69	not significant
3455	SENP8	-1.01	1.75E-01	NA	53.76	not significant
3456	BMP10	-1.01	1.38E-01	NA	52.74	not significant
3457	PIK3AP1	-1.01	3.69E-01	6.33E-01	162.82	not significant
3458	TADA2A	-1.01	5.06E-01	7.40E-01	784.69	not significant
3459	KBTBD6	-1.01	5.06E-01	7.40E-01	763.15	not significant
3460	EML4	-1.01	4.83E-01	7.24E-01	2684.70	not significant
3461	DSCR9	-1.01	6.19E-02	NA	27.58	not significant
3462	DCAF4L1	-1.01	1.03E-01	NA	34.38	not significant
3463	DUSP4	-1.01	2.91E-01	NA	91.09	not significant
3464	PIAS3	-1.01	3.51E-01	6.18E-01	133.20	not significant
3465	RBMS2	-1.01	4.89E-01	7.28E-01	423.61	not significant
3466	ALAD	-1.01	5.11E-01	7.44E-01	897.81	not significant
3467	THAP6	-1.01	5.05E-01	7.39E-01	500.86	not significant
3468	SLMO2	-1.01	5.01E-01	7.37E-01	2668.81	not significant
3469	NDC80	-1.01	4.98E-01	7.35E-01	2043.94	not significant
3470	CDCA4	-1.01	4.99E-01	7.36E-01	2310.31	not significant
3471	SMC1A	-1.01	4.75E-01	7.17E-01	3711.34	not significant
3472	TAF4	-1.01	4.99E-01	7.36E-01	2091.33	not significant
3473	ATP7A	-1.01	3.13E-01	5.84E-01	105.08	not significant
3474	AOC2	-1.01	1.41E-01	NA	46.81	not significant
3475	DHRS4L2	-1.01	4.80E-01	7.21E-01	525.28	not significant
3476	FKBP15	-1.01	5.13E-01	7.45E-01	996.44	not significant
3477	CAPG	-1.01	4.87E-01	7.26E-01	4670.81	not significant
3478	HDGF	-1.01	4.40E-01	6.92E-01	9708.82	not significant
3479	UBE2N	-1.01	4.32E-01	6.86E-01	8378.31	not significant
3480	GNA12	-1.01	5.50E-01	7.70E-01	2664.23	not significant
3481	NUBPL	-1.01	4.42E-01	6.93E-01	294.17	not significant
3482	PSMB3	-1.01	4.78E-01	7.20E-01	4594.94	not significant
3483	C8orf59	-1.01	5.15E-01	7.46E-01	1602.88	not significant
3484	ZNF561	-1.01	5.11E-01	7.44E-01	744.41	not significant
3485	CYB5D1	-1.01	5.14E-01	7.46E-01	793.03	not significant
3486	ZNF329	-1.01	5.12E-01	7.45E-01	705.79	not significant
3487	ATP5O	-1.01	5.38E-01	7.61E-01	4437.36	not significant
3488	ZNF92	-1.01	5.09E-01	7.43E-01	2052.59	not significant
3489	PDP1	-1.01	5.04E-01	7.39E-01	1735.95	not significant
3490	AP1M1	-1.01	4.73E-01	7.16E-01	3877.70	not significant
3491	UPF1	-1.01	4.17E-01	6.73E-01	11801.79	not significant
3492	HIST1H2BC	-1.01	1.08E-01	NA	35.26	not significant
3493	ZFYVE9	-1.01	3.82E-01	6.45E-01	150.88	not significant
3494	UNC45A	-1.01	5.00E-01	7.36E-01	2380.35	not significant
3495	NRP1	-1.01	9.00E-02	NA	30.63	not significant
3496	TUBB2A	-1.01	2.27E-01	NA	66.34	not significant
3497	BBS5	-1.01	4.38E-01	6.90E-01	278.64	not significant
3498	GRAP	-1.01	5.00E-01	7.36E-01	1171.16	not significant
3499	NDUFAF7	-1.01	5.14E-01	7.46E-01	599.49	not significant
3500	EXOG	-1.01	5.10E-01	7.44E-01	609.79	not significant
3501	CDKN2AIPNL	-1.01	5.21E-01	7.51E-01	1099.38	not significant
3502	NSMCE2	-1.01	5.32E-01	7.58E-01	745.18	not significant
3503	PDHX	-1.01	5.21E-01	7.51E-01	998.53	not significant
3504	RPS6KC1	-1.01	5.10E-01	7.44E-01	588.39	not significant
3505	NABP2	-1.01	5.02E-01	7.38E-01	2972.04	not significant
3506	SPTLC1	-1.01	5.16E-01	7.47E-01	1457.73	not significant
3507	TRA2A	-1.01	4.72E-01	7.15E-01	3339.73	not significant

3508	INTS7	-1.01	4.85E-01	7.26E-01	3016.25	not significant
3509	OTULIN	-1.01	5.03E-01	7.39E-01	2603.51	not significant
3510	ZBTB7A	-1.01	5.41E-01	7.63E-01	1722.37	not significant
3511	ILF3	-1.01	3.91E-01	6.52E-01	28041.52	not significant
3512	PRKCE	-1.01	4.53E-01	7.02E-01	6095.30	not significant
3513	GRASP	-1.01	1.50E-01	NA	45.34	not significant
3514	DDX6	-1.01	4.61E-01	7.07E-01	1765.36	not significant
3515	RPL26L1	-1.01	5.10E-01	7.44E-01	629.94	not significant
3516	STRADB	-1.01	5.13E-01	7.45E-01	507.62	not significant
3517	ARL8A	-1.01	5.20E-01	7.50E-01	1043.42	not significant
3518	AP1AR	-1.01	5.19E-01	7.49E-01	1316.53	not significant
3519	CEP85	-1.01	5.07E-01	7.41E-01	2690.18	not significant
3520	MSI2	-1.01	4.94E-01	7.32E-01	5374.13	not significant
3521	ANLN	-1.01	4.82E-01	7.23E-01	3313.85	not significant
3522	CSF2	-1.01	1.62E-02	NA	15.49	not significant
3523	LOC103611081	-1.01	4.46E-01	6.96E-01	240.52	not significant
3524	PARD6A	-1.01	4.15E-01	6.72E-01	282.58	not significant
3525	RGP1	-1.01	4.73E-01	7.16E-01	322.26	not significant
3526	PRMT9	-1.01	5.06E-01	7.40E-01	450.23	not significant
3527	TMEM11	-1.01	5.17E-01	7.47E-01	653.31	not significant
3528	UBXN2A	-1.01	5.18E-01	7.48E-01	1036.27	not significant
3529	NCKIPSD	-1.01	5.21E-01	7.51E-01	1025.97	not significant
3530	RABGGTB	-1.01	5.02E-01	7.38E-01	2549.99	not significant
3531	EPSTI1	-1.01	4.94E-01	7.32E-01	3459.85	not significant
3532	EHBP1	-1.01	5.23E-01	7.52E-01	1032.89	not significant
3533	HHIP	-1.01	5.07E-01	7.42E-01	1976.47	not significant
3534	HECTD3	-1.01	5.22E-01	7.51E-01	1181.31	not significant
3535	LONP1	-1.01	4.70E-01	7.14E-01	5203.53	not significant
3536	CNBP	-1.01	4.52E-01	7.01E-01	15065.37	not significant
3537	FERMT3	-1.01	4.31E-01	6.85E-01	7231.17	not significant
3538	C9orf172	-1.01	4.33E-02	NA	20.72	not significant
3539	FSD1	-1.01	4.81E-01	7.22E-01	313.47	not significant
3540	C11orf24	-1.01	4.94E-01	7.32E-01	379.93	not significant
3541	CHD9	-1.01	5.28E-01	7.56E-01	3222.55	not significant
3542	C4orf33	-1.01	5.04E-01	7.39E-01	447.81	not significant
3543	BCL2L12	-1.01	5.28E-01	7.55E-01	1186.32	not significant
3544	EPB41L5	-1.01	5.21E-01	7.51E-01	764.02	not significant
3545	THOC1	-1.01	5.16E-01	7.47E-01	1912.03	not significant
3546	GNB2	-1.01	4.77E-01	7.19E-01	6090.01	not significant
3547	RASGRP2	-1.01	5.22E-01	7.51E-01	1294.77	not significant
3548	PEX7	-1.01	4.01E-01	6.60E-01	179.76	not significant
3549	ACY3	-1.01	3.78E-01	6.43E-01	138.05	not significant
3550	PVT1	-1.01	4.42E-01	6.93E-01	226.52	not significant
3551	ARHGAP10	-1.01	4.72E-01	7.15E-01	289.34	not significant
3552	ADAL	-1.01	4.99E-01	7.36E-01	483.25	not significant
3553	SNX30	-1.01	4.55E-01	7.04E-01	273.25	not significant
3554	ZNF621	-1.01	4.99E-01	7.36E-01	417.85	not significant
3555	CCDC91	-1.01	5.25E-01	7.53E-01	1245.71	not significant
3556	YTHDF1	-1.01	4.94E-01	7.33E-01	3045.26	not significant
3557	MYH10	-1.01	5.09E-01	7.43E-01	2597.12	not significant
3558	LINC00116	-1.01	4.18E-01	6.73E-01	191.72	not significant
3559	C19orf12	-1.01	5.26E-01	7.54E-01	772.32	not significant
3560	CIB1	-1.01	5.14E-01	7.46E-01	2932.02	not significant
3561	SCP2	-1.01	4.88E-01	7.28E-01	3251.34	not significant
3562	FNBP4	-1.01	5.13E-01	7.45E-01	3541.43	not significant
3563	SETD1A	-1.01	5.00E-01	7.36E-01	3858.24	not significant
3564	ZMYND10	-1.01	5.28E-02	NA	22.89	not significant
3565	C17orf51	-1.01	8.53E-02	NA	30.16	not significant
3566	EXOSC4	-1.01	2.82E-01	NA	90.72	not significant
3567	CBWD6	-1.01	1.04E-01	NA	34.40	not significant
3568	GCSHP3	-1.01	3.84E-01	6.47E-01	160.21	not significant
3569	SWI5	-1.01	4.60E-01	7.07E-01	278.96	not significant
3570	RPUSD2	-1.01	5.15E-01	7.46E-01	498.54	not significant
3571	URGCP	-1.01	5.31E-01	7.57E-01	1211.11	not significant
3572	UBE2W	-1.01	5.30E-01	7.57E-01	1184.88	not significant
3573	NEK4	-1.01	5.29E-01	7.56E-01	1238.54	not significant
3574	PPP3CB	-1.01	5.21E-01	7.51E-01	1638.71	not significant
3575	ZNF236	-1.01	5.22E-01	7.51E-01	1246.62	not significant
3576	BNIP2	-1.01	5.10E-01	7.44E-01	2572.39	not significant
3577	REPS1	-1.01	5.06E-01	7.40E-01	2429.19	not significant
3578	ARFGAP1	-1.01	4.82E-01	7.22E-01	3851.99	not significant
3579	TTC30A	-1.01	2.30E-01	NA	66.66	not significant
3580	ZNF408	-1.01	4.96E-01	7.33E-01	507.55	not significant
3581	HELQ	-1.01	5.28E-01	7.55E-01	532.94	not significant
3582	RGPD3	-1.01	5.26E-01	7.54E-01	548.71	not significant
3583	MFSD9	-1.01	5.25E-01	7.54E-01	550.48	not significant
3584	POP5	-1.01	5.34E-01	7.59E-01	968.97	not significant
3585	PRPF18	-1.01	5.32E-01	7.58E-01	882.26	not significant
3586	POP7	-1.01	5.34E-01	7.59E-01	1668.76	not significant
3587	BMS1P20	-1.01	5.32E-01	7.58E-01	920.91	not significant
3588	RPL12	-1.01	5.09E-01	7.43E-01	13159.91	not significant
3589	FAM102B	-1.01	5.08E-01	7.43E-01	2469.49	not significant
3590	CCP110	-1.01	5.06E-01	7.40E-01	4402.94	not significant
3591	WDR92	-1.01	5.20E-01	7.50E-01	559.33	not significant
3592	PIGH	-1.01	5.34E-01	7.59E-01	957.22	not significant
3593	CNIH4	-1.01	5.34E-01	7.59E-01	780.46	not significant
3594	MAPK9	-1.01	5.14E-01	7.46E-01	2531.63	not significant
3595	TRPM7	-1.01	5.12E-01	7.44E-01	4930.46	not significant

3596	PIM2	-1.01	1.65E-01	NA	43.35	not significant
3597	ABCD1	-1.01	3.19E-01	NA	97.45	not significant
3598	PEX3	-1.01	3.12E-01	5.84E-01	464.05	not significant
3599	RND3	-1.01	4.87E-01	7.26E-01	308.02	not significant
3600	MMAA	-1.01	4.98E-01	7.35E-01	409.02	not significant
3601	NME7	-1.01	5.26E-01	7.54E-01	492.67	not significant
3602	COG2	-1.01	5.37E-01	7.61E-01	1377.50	not significant
3603	KIAA0907	-1.01	5.23E-01	7.52E-01	2312.85	not significant
3604	SMNDC1	-1.01	5.17E-01	7.47E-01	2462.89	not significant
3605	SIPA1L1	-1.01	5.65E-01	7.80E-01	1534.73	not significant
3606	FAM49B	-1.01	4.38E-01	6.90E-01	10348.96	not significant
3607	KLHL13	-1.01	3.38E-01	6.06E-01	114.57	not significant
3608	KLLN	-1.01	4.62E-01	7.09E-01	246.94	not significant
3609	PLBD2	-1.01	5.70E-01	7.83E-01	234.80	not significant
3610	MPP1	-1.01	5.37E-01	7.61E-01	779.21	not significant
3611	LZIC	-1.01	5.40E-01	7.63E-01	1078.95	not significant
3612	TRAPPC13	-1.01	5.40E-01	7.63E-01	1206.94	not significant
3613	APOL3	-1.01	5.39E-01	7.62E-01	1230.09	not significant
3614	ANAPC7	-1.01	5.04E-01	7.39E-01	4350.68	not significant
3615	SNX3	-1.01	5.03E-01	7.38E-01	4078.17	not significant
3616	BRD4	-1.01	5.12E-01	7.44E-01	4626.02	not significant
3617	DOCK2	-1.01	4.74E-01	7.17E-01	12026.06	not significant
3618	STAU1	-1.01	4.86E-01	7.26E-01	4518.12	not significant
3619	LOC101927550	-1.01	2.27E-01	NA	61.54	not significant
3620	ANKRD49	-1.01	5.40E-01	7.63E-01	782.51	not significant
3621	VPS9D1-AS1	-1.01	5.15E-01	7.46E-01	556.16	not significant
3622	CEP162	-1.01	5.35E-01	7.60E-01	508.38	not significant
3623	C4orf27	-1.01	5.39E-01	7.62E-01	1336.34	not significant
3624	TMEM126B	-1.01	5.43E-01	7.64E-01	1197.93	not significant
3625	ACAD9	-1.01	5.36E-01	7.61E-01	1911.32	not significant
3626	CIAO1	-1.01	5.03E-01	7.38E-01	4267.83	not significant
3627	ZNF658	-1.01	2.24E-01	NA	63.88	not significant
3628	TPK1	-1.01	3.20E-01	NA	87.93	not significant
3629	PAXIP1OS	-1.01	4.91E-01	7.30E-01	322.85	not significant
3630	NDUFV2	-1.01	5.38E-01	7.62E-01	2668.96	not significant
3631	ACAT1	-1.01	5.40E-01	7.63E-01	1432.68	not significant
3632	LYPLA1	-1.01	5.30E-01	7.56E-01	4006.35	not significant
3633	CASP8AP2	-1.01	5.17E-01	7.47E-01	3840.35	not significant
3634	COPB2	-1.01	5.01E-01	7.37E-01	4892.58	not significant
3635	MRM1	-1.01	2.95E-01	NA	95.68	not significant
3636	PIGF	-1.01	4.91E-01	7.30E-01	443.79	not significant
3637	BTBD9	-1.01	5.24E-01	7.52E-01	442.19	not significant
3638	FAM69A	-1.01	5.62E-01	7.78E-01	679.33	not significant
3639	MAEA	-1.01	5.27E-01	7.54E-01	2444.93	not significant
3640	STK3	-1.01	5.45E-01	7.66E-01	1079.20	not significant
3641	NDEL1	-1.01	5.45E-01	7.65E-01	1279.45	not significant
3642	NMT1	-1.01	4.74E-01	7.17E-01	6378.01	not significant
3643	LYPD3	-1.01	7.44E-02	NA	25.01	not significant
3644	LOC100294362	-1.01	5.58E-02	NA	22.61	not significant
3645	PCSK5	-1.01	3.48E-01	6.15E-01	106.88	not significant
3646	DPH5	-1.01	5.48E-01	7.68E-01	1174.58	not significant
3647	C19orf53	-1.01	5.36E-01	7.61E-01	2979.04	not significant
3648	ZNF195	-1.01	5.46E-01	7.67E-01	1491.68	not significant
3649	SLC39A1	-1.01	5.08E-01	7.43E-01	3138.30	not significant
3650	NELFCD	-1.01	5.26E-01	7.54E-01	2860.79	not significant
3651	ADNP2	-1.01	2.12E-01	NA	23.52	not significant
3652	IKBKG	-1.01	3.62E-01	6.26E-01	114.83	not significant
3653	NLGN3	-1.01	3.14E-01	NA	92.24	not significant
3654	LOC100506730	-1.01	4.04E-01	6.63E-01	128.15	not significant
3655	FAM57A	-1.01	4.89E-01	7.28E-01	304.91	not significant
3656	NOL12	-1.01	5.47E-01	7.67E-01	1228.97	not significant
3657	OGFR	-1.01	5.40E-01	7.63E-01	2764.04	not significant
3658	ANGEL2	-1.01	5.49E-01	7.69E-01	1383.13	not significant
3659	DNAJC3	-1.01	5.41E-01	7.63E-01	2904.25	not significant
3660	GYS1	-1.01	5.48E-01	7.68E-01	1909.66	not significant
3661	ZC3HC1	-1.01	5.44E-01	7.65E-01	907.67	not significant
3662	GNPDA2	-1.01	5.27E-01	7.55E-01	421.05	not significant
3663	DIAPH2	-1.01	5.43E-01	7.64E-01	838.62	not significant
3664	TIMM22	-1.01	5.54E-01	7.72E-01	949.06	not significant
3665	RIC8B	-1.01	5.52E-01	7.71E-01	1249.42	not significant
3666	APIP	-1.01	5.51E-01	7.71E-01	1292.47	not significant
3667	UFC1	-1.01	5.47E-01	7.67E-01	2043.03	not significant
3668	ERCC6L2	-1.01	5.52E-01	7.71E-01	1113.43	not significant
3669	VARS2	-1.01	5.51E-01	7.70E-01	1398.77	not significant
3670	GON4L	-1.01	5.56E-01	7.74E-01	1843.22	not significant
3671	PXYLP1	-1.01	5.33E-01	7.59E-01	2479.70	not significant
3672	SP2	-1.01	5.51E-01	7.71E-01	1306.07	not significant
3673	SOD1	-1.01	5.21E-01	7.51E-01	7857.79	not significant
3674	PITRM1-AS1	-1.01	1.72E-01	NA	42.65	not significant
3675	ZNF583	-1.01	3.78E-01	6.43E-01	265.35	not significant
3676	PINK1	-1.01	4.93E-01	7.32E-01	296.43	not significant
3677	LINC01260	-1.01	5.79E-01	7.88E-01	733.55	not significant
3678	SLIRP	-1.01	5.44E-01	7.65E-01	980.19	not significant
3679	ELP5	-1.01	5.44E-01	7.65E-01	2757.73	not significant
3680	AP2A2	-1.01	5.54E-01	7.72E-01	1347.94	not significant
3681	MTPAP	-1.01	5.54E-01	7.72E-01	1555.96	not significant
3682	CALR	-1.01	4.44E-01	6.95E-01	51588.53	not significant
3683	TFEB	-1.01	5.09E-01	7.43E-01	295.38	not significant

3684	DECR2	-1.01	5.29E-01	7.56E-01	390.20	not significant
3685	MRPL41	-1.01	5.35E-01	7.61E-01	629.56	not significant
3686	TIMM9	-1.01	5.60E-01	7.77E-01	1158.64	not significant
3687	PBK	-1.01	5.39E-01	7.62E-01	2326.53	not significant
3688	NOTCH2	-1.01	5.59E-01	7.77E-01	2841.75	not significant
3689	TOPBP1	-1.01	4.91E-01	7.30E-01	8819.68	not significant
3690	FAM189B	-1.01	5.37E-01	7.61E-01	441.46	not significant
3691	FARP2	-1.01	5.03E-01	7.38E-01	292.76	not significant
3692	PDIA5	-1.01	5.59E-01	7.76E-01	986.11	not significant
3693	UGGT1	-1.01	5.32E-01	7.58E-01	6590.18	not significant
3694	RBM23	-1.01	5.24E-01	7.52E-01	2909.89	not significant
3695	UBXN2B	-1.01	5.58E-01	7.76E-01	2003.67	not significant
3696	SPRYD7	-1.01	3.58E-01	6.23E-01	107.46	not significant
3697	ACER3	-1.01	4.14E-01	6.72E-01	153.66	not significant
3698	DUSP18	-1.01	4.56E-01	7.04E-01	185.94	not significant
3699	EXOC6B	-1.01	4.84E-01	7.24E-01	305.12	not significant
3700	CPEB4	-1.01	5.34E-01	7.59E-01	466.32	not significant
3701	RPL38	-1.01	6.18E-01	8.14E-01	13679.04	not significant
3702	NEDD8	-1.01	5.59E-01	7.77E-01	1869.75	not significant
3703	CCDC186	-1.01	5.32E-01	7.58E-01	555.50	not significant
3704	FBXL14	-1.01	5.59E-01	7.77E-01	1083.38	not significant
3705	GPATCH2L	-1.01	5.60E-01	7.77E-01	1874.89	not significant
3706	ASNSD1	-1.01	5.43E-01	7.64E-01	2572.51	not significant
3707	NCOA4	-1.01	5.59E-01	7.77E-01	1357.82	not significant
3708	POLD2	-1.01	5.26E-01	7.54E-01	6608.95	not significant
3709	ACTB	-1.01	4.64E-01	7.11E-01	184351.29	not significant
3710	POLDIP3	-1.01	5.07E-01	7.41E-01	4882.02	not significant
3711	PEX19	-1.01	5.50E-01	7.70E-01	2099.04	not significant
3712	PBRM1	-1.01	5.25E-01	7.54E-01	8124.53	not significant
3713	ADAMTS1	-1.01	5.27E-01	7.55E-01	4159.94	not significant
3714	ANKRD28	-1.01	5.05E-01	7.39E-01	6331.62	not significant
3715	MYH9	-1.01	5.28E-01	7.56E-01	23816.23	not significant
3716	IL10RA	-1.01	1.33E-01	NA	31.54	not significant
3717	PRR29	-1.01	2.21E-01	NA	62.47	not significant
3718	IL18R1	-1.01	3.12E-01	NA	81.46	not significant
3719	NMB	-1.01	3.18E-01	NA	90.22	not significant
3720	TRIM71	-1.01	4.17E-01	6.73E-01	152.77	not significant
3721	FKBP7	-1.01	4.99E-01	7.36E-01	257.95	not significant
3722	PMVK	-1.01	5.66E-01	7.81E-01	1278.37	not significant
3723	RPE	-1.01	5.43E-01	7.64E-01	1652.64	not significant
3724	RAB3GAP2	-1.01	5.52E-01	7.71E-01	2604.19	not significant
3725	ZSCAN30	-1.01	5.41E-01	7.63E-01	423.60	not significant
3726	SUPV3L1	-1.01	5.63E-01	7.79E-01	1595.65	not significant
3727	PIAS2	-1.01	5.65E-01	7.80E-01	1143.26	not significant
3728	INPP4A	-1.01	5.66E-01	7.81E-01	2329.13	not significant
3729	NEDD1	-1.01	5.03E-01	7.38E-01	3843.91	not significant
3730	LOC643387	-1.01	1.43E-02	NA	12.60	not significant
3731	ZNF699	-1.01	3.42E-01	NA	97.11	not significant
3732	NHP2L1	-1.01	3.31E-01	5.98E-01	5443.66	not significant
3733	SIGLEC12	-1.01	5.41E-01	7.63E-01	388.04	not significant
3734	ACBD6	-1.01	5.68E-01	7.82E-01	1697.75	not significant
3735	APOL2	-1.01	5.61E-01	7.78E-01	1815.87	not significant
3736	FRYL	-1.01	5.57E-01	7.75E-01	4758.46	not significant
3737	ZFAND3	-1.01	5.44E-01	7.65E-01	2568.31	not significant
3738	GNB1L	-1.01	5.67E-01	7.81E-01	698.64	not significant
3739	ZNF529	-1.01	5.68E-01	7.82E-01	952.11	not significant
3740	BLOC1S3	-1.01	6.80E-01	8.50E-01	364.87	not significant
3741	MANEA	-1.01	5.71E-01	7.83E-01	2045.64	not significant
3742	LDHB	-1.01	5.21E-01	7.51E-01	29528.64	not significant
3743	GUCA1B	-1.01	2.96E-01	NA	68.80	not significant
3744	ZNF575	-1.01	3.82E-01	6.45E-01	119.68	not significant
3745	SSSCA1	-1.01	5.70E-01	7.83E-01	872.69	not significant
3746	DCTN3	-1.01	5.67E-01	7.81E-01	1477.24	not significant
3747	RGL4	-1.01	5.73E-01	7.84E-01	1124.99	not significant
3748	TIAM1	-1.01	5.71E-01	7.83E-01	758.93	not significant
3749	ZNF746	-1.01	5.73E-01	7.84E-01	1179.54	not significant
3750	CENPBD1P1	-1.01	5.72E-01	7.83E-01	1196.76	not significant
3751	DDHD2	-1.01	5.67E-01	7.81E-01	2097.11	not significant
3752	LMTK2	-1.01	5.71E-01	7.83E-01	2108.80	not significant
3753	ABR	-1.01	5.65E-01	7.80E-01	1794.10	not significant
3754	NPPA-AS1	-1.01	1.50E-01	NA	32.69	not significant
3755	LMLN	-1.01	4.43E-01	6.94E-01	144.09	not significant
3756	PGBD1	-1.01	5.23E-01	7.52E-01	405.88	not significant
3757	FAH	-1.01	5.71E-01	7.83E-01	1056.84	not significant
3758	TMEM217	-1.01	5.67E-01	7.81E-01	468.86	not significant
3759	SNX17	-1.01	4.95E-01	7.33E-01	4648.80	not significant
3760	STOM	-1.01	5.75E-01	7.86E-01	836.28	not significant
3761	HDDC2	-1.01	5.69E-01	7.83E-01	2185.02	not significant
3762	RAP1B	-1.01	5.60E-01	7.77E-01	3307.36	not significant
3763	DNAJC5	-1.01	5.50E-01	7.70E-01	3635.58	not significant
3764	XPR1	-1.01	5.61E-01	7.78E-01	2179.49	not significant
3765	ZYG11B	-1.01	4.41E-01	6.92E-01	432.28	not significant
3766	TBCE	-1.01	5.75E-01	7.86E-01	820.08	not significant
3767	CNOT7	-1.01	4.85E-01	7.26E-01	7786.70	not significant
3768	GFM1	-1.01	5.54E-01	7.72E-01	2674.59	not significant
3769	ATF6	-1.01	5.52E-01	7.71E-01	3222.91	not significant
3770	TTLL13	-1.01	6.80E-03	NA	9.82	not significant
3771	MYOM2	-1.01	3.93E-01	6.54E-01	114.87	not significant

3772	PA2G4P4	-1.01	4.50E-01	6.99E-01	150.45	not significant
3773	ST3GAL4-AS1	-1.01	4.07E-01	6.65E-01	115.92	not significant
3774	BCL9	-1.01	4.36E-01	6.89E-01	144.23	not significant
3775	FKBP14	-1.01	5.42E-01	7.64E-01	372.32	not significant
3776	ZDHHC16	-1.01	5.76E-01	7.86E-01	1971.32	not significant
3777	EED	-1.01	5.82E-01	7.90E-01	1476.97	not significant
3778	DBT	-1.01	5.80E-01	7.89E-01	1103.92	not significant
3779	TCF12	-1.01	5.43E-01	7.64E-01	5013.06	not significant
3780	EZR	-1.01	4.76E-01	7.18E-01	15263.54	not significant
3781	PIPSL	-1.01	2.26E-01	NA	48.92	not significant
3782	ARMC2	-1.01	3.72E-01	NA	93.62	not significant
3783	TMEM183A	-1.01	4.44E-01	6.95E-01	152.58	not significant
3784	MTERF2	-1.01	4.25E-01	6.79E-01	124.34	not significant
3785	LOC100996324	-1.01	4.55E-01	7.04E-01	170.89	not significant
3786	ZNF665	-1.01	4.84E-01	7.24E-01	227.30	not significant
3787	TOMM6	-1.01	5.66E-01	7.81E-01	4777.18	not significant
3788	EIF2B5	-1.01	5.59E-01	7.77E-01	2441.09	not significant
3789	VPS41	-1.01	5.73E-01	7.84E-01	2033.38	not significant
3790	ME2	-1.01	5.28E-01	7.55E-01	5467.25	not significant
3791	EFR3A	-1.01	5.48E-01	7.68E-01	5021.43	not significant
3792	TRAPPC4	-1.01	5.10E-01	7.44E-01	248.29	not significant
3793	MYO5C	-1.01	4.79E-01	7.21E-01	190.60	not significant
3794	C9orf156	-1.01	5.44E-01	7.65E-01	349.86	not significant
3795	ACOX3	-1.01	5.64E-01	7.80E-01	431.54	not significant
3796	RAPH1	-1.01	5.39E-01	7.62E-01	345.62	not significant
3797	DTYMK	-1.01	5.71E-01	7.83E-01	2738.41	not significant
3798	PKIA	-1.01	5.76E-01	7.87E-01	1716.49	not significant
3799	MTRR	-1.01	5.75E-01	7.86E-01	1933.37	not significant
3800	FBXW7	-1.01	5.82E-01	7.90E-01	1474.13	not significant
3801	RNF43	-1.01	1.35E-01	NA	29.53	not significant
3802	ZNF75A	-1.01	5.51E-01	7.71E-01	396.15	not significant
3803	SHFM1	-1.01	5.91E-01	7.97E-01	2163.49	not significant
3804	FAM129B	-1.01	5.85E-01	7.93E-01	1397.24	not significant
3805	TRAF4	-1.01	5.87E-01	7.94E-01	1330.23	not significant
3806	BROX	-1.01	5.86E-01	7.93E-01	990.01	not significant
3807	XAF1	-1.01	5.91E-01	7.97E-01	1582.35	not significant
3808	PYCR2	-1.01	5.59E-01	7.77E-01	4595.50	not significant
3809	TCEA1	-1.01	5.66E-01	7.81E-01	2970.00	not significant
3810	SNRK-AS1	-1.01	3.62E-02	NA	14.75	not significant
3811	RGS2	-1.01	2.81E-01	NA	78.66	not significant
3812	ZNF485	-1.01	5.31E-01	7.57E-01	282.71	not significant
3813	PARP12	-1.01	5.77E-01	7.87E-01	1984.64	not significant
3814	FMNL3	-1.01	5.71E-01	7.83E-01	3149.04	not significant
3815	ADD1	-1.01	5.05E-01	7.40E-01	7467.42	not significant
3816	TRAF7	-1.01	5.43E-01	7.64E-01	4589.21	not significant
3817	GPR114	-1.01	1.38E-01	NA	34.40	not significant
3818	CORO6	-1.01	2.03E-01	NA	38.07	not significant
3819	KMT2D	-1.01	5.17E-01	7.47E-01	9824.45	not significant
3820	RHOBTB3	-1.01	4.64E-01	7.11E-01	151.15	not significant
3821	FAM127B	-1.01	5.46E-01	7.67E-01	337.46	not significant
3822	SPEN	-1.01	5.04E-01	7.39E-01	8146.57	not significant
3823	REEP2	-1.01	5.30E-01	7.56E-01	271.88	not significant
3824	C1GALT1C1	-1.01	5.64E-01	7.80E-01	411.48	not significant
3825	DPY30	-1.01	5.89E-01	7.96E-01	1094.01	not significant
3826	TAP2	-1.01	5.92E-01	7.98E-01	885.24	not significant
3827	NREP	-1.01	5.53E-01	7.72E-01	3590.15	not significant
3828	PTTG1IP	-1.01	5.69E-01	7.83E-01	2648.32	not significant
3829	SPINT1	-1.01	1.53E-01	NA	34.54	not significant
3830	DNAJC4	-1.01	5.16E-01	7.47E-01	219.84	not significant
3831	DMTN	-1.01	1.20E-01	NA	25.12	not significant
3832	PLCD3	-1.01	4.85E-01	7.26E-01	176.93	not significant
3833	CTTNBP2NL	-1.01	5.17E-01	7.47E-01	269.88	not significant
3834	MED16	-1.01	5.92E-01	7.98E-01	2460.00	not significant
3835	CEBPG	-1.01	5.82E-01	7.90E-01	2321.00	not significant
3836	CTNNBL1	-1.01	5.75E-01	7.86E-01	3244.11	not significant
3837	TMEM216	-1.01	4.21E-02	NA	15.55	not significant
3838	ZNF618	-1.01	2.18E-01	NA	45.95	not significant
3839	ZBTB37	-1.01	4.11E-01	6.69E-01	107.73	not significant
3840	GRAMD3	-1.01	4.00E-01	NA	100.47	not significant
3841	ATP5L	-1.01	5.20E-01	7.51E-01	1866.18	not significant
3842	ZNF791	-1.01	4.80E-01	7.22E-01	399.75	not significant
3843	SGMS1	-1.01	5.22E-01	7.51E-01	261.36	not significant
3844	CYSLTR2	-1.01	5.29E-01	7.56E-01	266.99	not significant
3845	NDUFB3	-1.01	5.96E-01	8.01E-01	1699.02	not significant
3846	FAM32A	-1.01	5.85E-01	7.93E-01	3298.98	not significant
3847	ZXDC	-1.01	5.46E-01	7.67E-01	1137.10	not significant
3848	MRPS10	-1.01	5.87E-01	7.94E-01	2025.20	not significant
3849	MFSD5	-1.01	5.97E-01	8.02E-01	1076.95	not significant
3850	LRRC41	-1.01	5.83E-01	7.91E-01	2648.03	not significant
3851	SRCAP	-1.01	5.89E-01	7.96E-01	7971.51	not significant
3852	GPR75	-1.01	3.33E-01	NA	77.59	not significant
3853	TRIM36	-1.01	5.22E-01	7.51E-01	247.28	not significant
3854	DENND1A	-1.01	5.97E-01	8.02E-01	909.04	not significant
3855	DNAH1	-1.01	5.73E-01	7.84E-01	528.86	not significant
3856	RSRC1	-1.01	5.97E-01	8.02E-01	1139.38	not significant
3857	ARPC1B	-1.01	5.48E-01	7.68E-01	7499.34	not significant
3858	IRAK4	-1.01	5.77E-01	7.87E-01	2503.62	not significant
3859	PRR7	-1.01	4.34E-01	6.88E-01	126.69	not significant

3860	UBE3D	-1.01	5.00E-01	7.36E-01	204.45	not significant
3861	ABHD14A	-1.01	5.52E-01	7.71E-01	297.90	not significant
3862	HRSP12	-1.01	5.75E-01	7.86E-01	551.80	not significant
3863	TOB1	-1.01	5.73E-01	7.84E-01	425.22	not significant
3864	KAT6A	-1.01	6.47E-01	8.32E-01	7438.13	not significant
3865	YDJC	-1.01	6.01E-01	8.02E-01	1278.67	not significant
3866	ORC4	-1.01	5.99E-01	8.02E-01	1265.81	not significant
3867	CHAC2	-1.01	6.00E-01	8.02E-01	845.17	not significant
3868	MFF	-1.01	5.88E-01	7.95E-01	2194.86	not significant
3869	ALS2	-1.01	6.01E-01	8.02E-01	1038.44	not significant
3870	SUDS3	-1.01	5.64E-01	7.80E-01	3417.12	not significant
3871	SKP2	-1.01	5.72E-01	7.83E-01	3605.27	not significant
3872	RAC2	-1.01	5.49E-01	7.69E-01	11999.50	not significant
3873	IREB2	-1.01	5.63E-01	7.79E-01	4432.83	not significant
3874	NECAB1	-1.01	7.98E-03	NA	9.13	not significant
3875	SERPINB8	-1.01	3.17E-01	NA	65.68	not significant
3876	IFT22	-1.01	5.89E-01	7.96E-01	567.94	not significant
3877	BATF3	-1.01	6.07E-01	8.06E-01	960.79	not significant
3878	GNGT2	-1.01	5.89E-01	7.96E-01	526.97	not significant
3879	RAB2B	-1.01	6.00E-01	8.02E-01	972.65	not significant
3880	AQP3	-1.01	5.85E-01	7.93E-01	2930.90	not significant
3881	SCAF8	-1.01	5.86E-01	7.94E-01	3089.33	not significant
3882	CSNK2A3	-1.01	3.31E-01	NA	77.04	not significant
3883	ACOT9	-1.01	5.28E-01	7.55E-01	259.97	not significant
3884	MYH3	-1.01	4.80E-01	7.22E-01	168.11	not significant
3885	PABPC3	-1.01	4.90E-01	7.29E-01	190.53	not significant
3886	TMEM192	-1.01	5.84E-01	7.92E-01	444.52	not significant
3887	OCIAD2	-1.01	6.04E-01	8.04E-01	2031.62	not significant
3888	CSRP1	-1.01	6.03E-01	8.03E-01	2489.36	not significant
3889	RAD1	-1.01	5.88E-01	7.95E-01	2433.10	not significant
3890	KDM6B	-1.01	6.05E-01	8.05E-01	1243.78	not significant
3891	DNAJC14	-1.01	5.79E-01	7.88E-01	3308.79	not significant
3892	SCARB1	-1.01	6.02E-01	8.03E-01	1414.82	not significant
3893	ACLY	-1.01	5.47E-01	7.67E-01	6272.13	not significant
3894	FITM2	-1.01	1.76E-01	NA	32.54	not significant
3895	ATF5	-1.01	5.97E-01	8.02E-01	596.03	not significant
3896	PHF21A	-1.01	6.08E-01	8.07E-01	879.73	not significant
3897	SEPHS1	-1.01	5.68E-01	7.82E-01	4752.67	not significant
3898	FGD1	-1.01	2.40E-01	NA	46.97	not significant
3899	TUBA8	-1.01	2.52E-01	NA	43.51	not significant
3900	ARMCX5-GPRASP2	-1.01	1.85E-01	NA	33.08	not significant
3901	RPL23P8	-1.01	3.08E-01	NA	58.98	not significant
3902	PRDM1	-1.01	5.19E-01	7.49E-01	215.04	not significant
3903	ALG11	-1.01	5.02E-01	7.38E-01	192.57	not significant
3904	EXO5	-1.01	6.08E-01	8.07E-01	754.97	not significant
3905	NUDT1	-1.01	6.07E-01	8.07E-01	2190.20	not significant
3906	TRIM38	-1.01	6.07E-01	8.07E-01	1161.91	not significant
3907	CHMP1A	-1.01	5.93E-01	7.98E-01	3417.99	not significant
3908	CDC42SE1	-1.01	5.56E-01	7.74E-01	3565.08	not significant
3909	PALB2	-1.01	6.09E-01	8.08E-01	1281.24	not significant
3910	DNM1L	-1.01	5.91E-01	7.97E-01	2876.93	not significant
3911	ZNF165	-1.01	6.27E-02	NA	16.65	not significant
3912	CXCR3	-1.01	9.65E-02	NA	20.83	not significant
3913	LINC01465	-1.01	2.32E-02	NA	11.62	not significant
3914	NDUFB2-AS1	-1.01	2.48E-01	NA	41.91	not significant
3915	GDPD1	-1.01	4.74E-01	7.16E-01	136.80	not significant
3916	NGFRAP1	-1.01	5.83E-01	7.91E-01	446.23	not significant
3917	ZNF470	-1.01	5.72E-01	7.83E-01	234.66	not significant
3918	HEATR5A	-1.01	5.62E-01	7.78E-01	311.40	not significant
3919	CHM	-1.01	6.13E-01	8.10E-01	869.93	not significant
3920	HMGN3	-1.01	6.02E-01	8.03E-01	3358.54	not significant
3921	IKBIP	-1.01	6.11E-01	8.09E-01	1167.62	not significant
3922	ZSCAN32	-1.01	6.12E-01	8.09E-01	892.98	not significant
3923	HEG1	-1.01	6.15E-01	8.12E-01	1215.28	not significant
3924	ARMC6	-1.01	5.96E-01	8.01E-01	3217.10	not significant
3925	KIF15	-1.01	5.79E-01	7.88E-01	3992.83	not significant
3926	ARHGAP35	-1.01	6.03E-01	8.03E-01	3195.50	not significant
3927	SP3	-1.01	6.09E-01	8.08E-01	4930.37	not significant
3928	SATB2	-1.01	3.98E-01	6.58E-01	108.54	not significant
3929	DZANK1	-1.01	4.51E-01	7.01E-01	119.18	not significant
3930	PRDM10	-1.01	6.02E-01	8.03E-01	721.70	not significant
3931	VPS37B	-1.01	5.65E-01	7.80E-01	3778.35	not significant
3932	TMEM131	-1.01	6.16E-01	8.13E-01	2844.78	not significant
3933	BLMH	-1.01	5.98E-01	8.02E-01	4291.29	not significant
3934	RABGAP1	-1.01	6.21E-01	8.15E-01	1675.88	not significant
3935	ARL8B	-1.01	5.79E-01	7.88E-01	3539.24	not significant
3936	DCAF5	-1.01	6.01E-01	8.02E-01	2285.23	not significant
3937	COPS7B	-1.01	5.81E-01	7.90E-01	3082.03	not significant
3938	ZSWIM8-AS1	-1.01	2.03E-01	NA	38.61	not significant
3939	ZBTB38	-1.01	1.74E-01	NA	29.34	not significant
3940	FAM227A	-1.01	3.14E-01	NA	58.83	not significant
3941	PET117	-1.01	4.38E-01	6.90E-01	109.24	not significant
3942	KCNC4	-1.01	5.94E-01	7.99E-01	428.72	not significant
3943	DOHH	-1.01	6.17E-01	8.13E-01	1345.22	not significant
3944	TIGD4	-1.01	3.29E-01	NA	61.10	not significant
3945	JOSD2	-1.01	5.72E-01	7.83E-01	303.43	not significant
3946	PCDH18	-1.01	3.24E-01	NA	60.93	not significant
3947	TMEM251	-1.01	5.92E-01	7.98E-01	473.75	not significant

3948	NSL1	-1.01	6.12E-01	8.10E-01	2493.16	not significant
3949	NVL	-1.01	6.20E-01	8.15E-01	1620.12	not significant
3950	ECD	-1.01	6.17E-01	8.13E-01	1248.07	not significant
3951	CD6	-1.01	5.69E-01	7.83E-01	3669.84	not significant
3952	KHDRBS1	-1.01	5.28E-01	7.55E-01	16435.98	not significant
3953	SCUBE1	-1.01	5.72E-02	NA	14.59	not significant
3954	AHCTF1P1	-1.01	2.52E-01	NA	43.21	not significant
3955	ZNF484	-1.01	4.60E-01	7.07E-01	139.25	not significant
3956	FAM212B	-1.01	5.23E-01	7.52E-01	177.68	not significant
3957	USP45	-1.01	6.19E-01	8.14E-01	709.52	not significant
3958	ZCCHC9	-1.01	6.18E-01	8.14E-01	1425.59	not significant
3959	SNX27	-1.01	6.02E-01	8.03E-01	1396.52	not significant
3960	TXNL1	-1.01	6.28E-01	8.19E-01	3126.17	not significant
3961	MKLN1-AS	-1.01	2.35E-01	NA	37.64	not significant
3962	NUDT6	-1.01	5.57E-01	7.75E-01	240.10	not significant
3963	ZNF280B	-1.01	5.43E-01	7.64E-01	244.26	not significant
3964	DTWD1	-1.01	5.91E-01	7.98E-01	352.27	not significant
3965	BIRC6	-1.01	5.98E-01	8.02E-01	5242.66	not significant
3966	FAM222A	-1.01	5.79E-01	7.88E-01	349.73	not significant
3967	TTN-AS1	-1.01	5.58E-01	7.76E-01	261.59	not significant
3968	C14orf64	-1.01	5.74E-01	7.85E-01	318.54	not significant
3969	ATXN7L1	-1.01	5.94E-01	7.99E-01	410.03	not significant
3970	ZNF783	-1.01	5.98E-01	8.02E-01	375.90	not significant
3971	METTL2A	-1.01	6.27E-01	8.18E-01	1020.27	not significant
3972	C19orf47	-1.01	6.24E-01	8.16E-01	1148.52	not significant
3973	OSGEP	-1.01	6.12E-01	8.09E-01	2105.49	not significant
3974	43716_7153	-1.01	5.81E-01	7.90E-01	4398.52	not significant
3975	METAP2	-1.01	5.43E-01	7.64E-01	7043.82	not significant
3976	TMOD4	-1.01	1.12E-01	NA	20.53	not significant
3977	MED4-AS1	-1.01	8.28E-02	NA	22.11	not significant
3978	NINJ1	-1.01	5.70E-01	7.83E-01	263.19	not significant
3979	MCTS2P	-1.01	5.53E-01	7.72E-01	263.30	not significant
3980	MRPL11	-1.01	5.87E-01	7.94E-01	3638.52	not significant
3981	GLDN	-1.01	4.96E-01	7.34E-01	154.43	not significant
3982	MTFR1L	-1.01	6.24E-01	8.16E-01	1034.80	not significant
3983	TTC19	-1.01	6.19E-01	8.14E-01	2037.69	not significant
3984	ZFAND5	-1.01	6.00E-01	8.02E-01	3014.64	not significant
3985	SYNJ2BP	-1.01	6.20E-01	8.14E-01	1843.69	not significant
3986	C6orf62	-1.01	5.62E-01	7.78E-01	5858.21	not significant
3987	CCDC168	-1.01	3.83E-01	NA	73.91	not significant
3988	NTRK1	-1.01	4.70E-01	7.14E-01	118.82	not significant
3989	CD226	-1.01	5.14E-01	7.46E-01	184.38	not significant
3990	SLC8A1-AS1	-1.01	5.13E-01	7.45E-01	155.70	not significant
3991	STRA6	-1.01	5.16E-01	7.47E-01	178.96	not significant
3992	ZNF852	-1.01	5.08E-01	7.42E-01	206.51	not significant
3993	TFB1M	-1.01	5.93E-01	7.99E-01	354.17	not significant
3994	GNG4	-1.01	6.25E-01	8.17E-01	865.90	not significant
3995	ZNF701	-1.01	5.99E-01	8.02E-01	651.02	not significant
3996	R3HDM4	-1.01	6.28E-01	8.19E-01	1288.14	not significant
3997	GNA15	-1.01	6.24E-01	8.16E-01	15298.92	not significant
3998	SENP3-EIF4A1	-1.01	4.22E-02	NA	12.05	not significant
3999	USH1C	-1.01	2.41E-01	NA	36.99	not significant
4000	SFXN3	-1.01	2.92E-01	NA	52.06	not significant
4001	STON2	-1.01	3.68E-01	NA	63.51	not significant
4002	FAM171B	-1.01	2.05E-01	NA	33.45	not significant
4003	DOCK4	-1.01	3.43E-01	NA	59.96	not significant
4004	RGS12	-1.01	2.07E-01	NA	35.18	not significant
4005	GXYLT2	-1.01	5.68E-01	7.82E-01	731.08	not significant
4006	ZDHHC21	-1.01	6.05E-01	8.05E-01	396.26	not significant
4007	TSTD2	-1.01	6.31E-01	8.21E-01	961.43	not significant
4008	PANK3	-1.01	6.32E-01	8.22E-01	2441.55	not significant
4009	PER2	-1.01	6.32E-01	8.22E-01	1336.06	not significant
4010	THOP1	-1.01	5.99E-01	8.02E-01	3176.64	not significant
4011	GLO1	-1.01	5.79E-01	7.88E-01	7491.46	not significant
4012	NT5C2	-1.01	6.13E-01	8.10E-01	2902.41	not significant
4013	NUCB1-AS1	-1.01	7.04E-02	NA	15.43	not significant
4014	ZNF563	-1.01	2.50E-01	NA	39.34	not significant
4015	FUT10	-1.01	4.19E-01	6.75E-01	488.64	not significant
4016	SGK494	-1.01	5.36E-01	7.61E-01	208.21	not significant
4017	ECI2	-1.01	6.36E-01	8.23E-01	1567.55	not significant
4018	STX17	-1.01	6.38E-01	8.25E-01	1464.23	not significant
4019	AAAS	-1.01	6.07E-01	8.07E-01	3049.55	not significant
4020	CANX	-1.01	5.91E-01	7.97E-01	34219.67	not significant
4021	MT1E	-1.01	5.82E-01	7.90E-01	3038.93	not significant
4022	TPRN	-1.01	6.19E-01	8.14E-01	559.68	not significant
4023	BRCA2	-1.01	5.98E-01	8.02E-01	2387.74	not significant
4024	KIAA1919	-1.01	5.99E-01	8.02E-01	427.35	not significant
4025	CHIC1	-1.01	6.17E-01	8.13E-01	451.11	not significant
4026	IFRD1	-1.01	6.34E-01	8.23E-01	1357.32	not significant
4027	SP100	-1.01	6.27E-01	8.19E-01	1859.11	not significant
4028	ZNF318	-1.01	6.36E-01	8.24E-01	1650.38	not significant
4029	STRN	-1.01	6.32E-01	8.22E-01	3272.69	not significant
4030	AGL	-1.01	6.34E-01	8.23E-01	1700.20	not significant
4031	HIPK3	-1.01	6.19E-01	8.14E-01	3073.34	not significant
4032	RPL37A	-1.01	8.32E-01	9.29E-01	20283.87	not significant
4033	ZNF283	-1.01	5.02E-01	7.38E-01	134.72	not significant
4034	UBA6-AS1	-1.01	6.14E-01	8.10E-01	417.59	not significant
4035	NDRG3	-1.01	6.26E-01	8.18E-01	2349.73	not significant

4036	MRPL30	-1.01	6.25E-01	8.17E-01	2219.12	not significant
4037	FAM120C	-1.01	3.38E-01	NA	53.64	not significant
4038	TIMM8B	-1.01	5.61E-01	7.78E-01	1260.31	not significant
4039	PRR22	-1.01	4.92E-01	7.31E-01	135.34	not significant
4040	PDSS2	-1.01	5.82E-01	7.90E-01	266.24	not significant
4041	MRPL14	-1.01	6.39E-01	8.27E-01	1321.67	not significant
4042	KIAA1462	-1.01	6.14E-01	8.11E-01	390.96	not significant
4043	AP1S2	-1.01	6.40E-01	8.27E-01	983.41	not significant
4044	ERCC1	-1.01	6.52E-01	8.35E-01	1681.84	not significant
4045	TIPARP	-1.01	6.19E-01	8.14E-01	438.75	not significant
4046	IWS1	-1.01	6.15E-01	8.12E-01	3427.88	not significant
4047	UFM1	-1.01	6.10E-01	8.09E-01	3213.87	not significant
4048	MECP2	-1.01	4.84E-01	7.25E-01	116.99	not significant
4049	SURF6	-1.01	5.62E-01	7.78E-01	207.90	not significant
4050	ZNF397	-1.01	6.37E-01	8.24E-01	737.63	not significant
4051	GADD45B	-1.01	6.39E-01	8.26E-01	546.20	not significant
4052	SRSF9	-1.01	6.25E-01	8.17E-01	6918.28	not significant
4053	GUCD1	-1.01	6.22E-01	8.15E-01	3504.44	not significant
4054	EIF3H	-1.01	5.77E-01	7.87E-01	8817.83	not significant
4055	HIST1H2BM	-1.01	1.22E-01	NA	20.81	not significant
4056	HMGN3-AS1	-1.01	2.57E-01	NA	37.76	not significant
4057	THSD1	-1.01	2.43E-01	NA	33.86	not significant
4058	GTDC1	-1.01	6.62E-01	8.41E-01	254.38	not significant
4059	DCUN1D2	-1.01	6.42E-01	8.28E-01	652.06	not significant
4060	COX10-AS1	-1.01	5.91E-01	7.98E-01	293.11	not significant
4061	VPS45	-1.01	6.42E-01	8.28E-01	657.31	not significant
4062	EPS15L1	-1.01	6.43E-01	8.30E-01	1448.58	not significant
4063	ANGEL1	-1.01	6.22E-01	8.15E-01	680.98	not significant
4064	CAPNS1	-1.01	6.22E-01	8.15E-01	7086.80	not significant
4065	TNFRSF21	-1.01	6.46E-01	8.32E-01	939.99	not significant
4066	CD7	-1.01	6.20E-01	8.15E-01	6140.00	not significant
4067	SAP30L	-1.01	6.43E-01	8.29E-01	1486.05	not significant
4068	ZNF335	-1.01	6.37E-01	8.24E-01	2702.92	not significant
4069	PPP2R5C	-1.01	6.22E-01	8.15E-01	4157.47	not significant
4070	TXNRD1	-1.01	5.53E-01	7.71E-01	12654.54	not significant
4071	HARBI1	-1.01	4.74E-01	7.17E-01	111.48	not significant
4072	FAM58A	-1.01	5.85E-01	7.93E-01	255.58	not significant
4073	LSM12	-1.01	5.85E-01	7.93E-01	241.03	not significant
4074	MRPL24	-1.01	6.48E-01	8.32E-01	1143.94	not significant
4075	ZW10	-1.01	6.45E-01	8.31E-01	1593.28	not significant
4076	MAP7D1	-1.01	5.99E-01	8.02E-01	6031.19	not significant
4077	RFC3	-1.01	6.17E-01	8.13E-01	3514.32	not significant
4078	TOP2B	-1.01	6.18E-01	8.14E-01	11709.26	not significant
4079	SEPP1	-1.01	2.48E-02	NA	11.16	not significant
4080	LOC440600	-1.01	1.30E-01	NA	21.07	not significant
4081	KBTBD3	-1.01	3.45E-01	NA	53.83	not significant
4082	PEPD	-1.01	6.50E-01	8.33E-01	1372.27	not significant
4083	ALG2	-1.01	6.48E-01	8.32E-01	741.25	not significant
4084	NGRN	-1.01	6.37E-01	8.24E-01	2424.93	not significant
4085	ATF7IP	-1.01	6.48E-01	8.32E-01	2580.05	not significant
4086	RALA	-1.01	6.23E-01	8.15E-01	3369.88	not significant
4087	SCAP	-1.01	6.46E-01	8.31E-01	4596.31	not significant
4088	ZFP36L2	-1.01	6.15E-01	8.12E-01	3736.08	not significant
4089	CCR5	-1.01	1.18E-01	NA	18.87	not significant
4090	MIF-AS1	-1.01	9.27E-01	9.73E-01	1053.24	not significant
4091	SOWAHA	-1.01	3.68E-01	NA	64.96	not significant
4092	LOC407835	-1.01	1.73E-01	NA	28.51	not significant
4093	SH3BP5	-1.01	4.15E-01	NA	91.69	not significant
4094	ONECUT2	-1.01	5.16E-01	7.47E-01	132.62	not significant
4095	NQO1	-1.01	5.53E-01	7.72E-01	259.36	not significant
4096	FAM200B	-1.01	6.03E-01	8.03E-01	295.79	not significant
4097	UHRF1BP1	-1.01	6.53E-01	8.36E-01	2362.50	not significant
4098	MB21D2	-1.01	3.91E-01	NA	62.72	not significant
4099	KIAA1614	-1.01	1.74E-01	NA	23.74	not significant
4100	IQCG	-1.01	4.38E-01	NA	80.95	not significant
4101	SEMA4F	-1.01	5.63E-01	7.79E-01	177.74	not significant
4102	FYCO1	-1.01	6.01E-01	8.02E-01	1638.86	not significant
4103	MLYCD	-1.01	6.14E-01	8.11E-01	325.25	not significant
4104	MAST4	-1.01	6.53E-01	8.36E-01	1259.62	not significant
4105	GBE1	-1.01	6.65E-01	8.42E-01	1620.51	not significant
4106	ZKSCAN8	-1.01	6.59E-01	8.39E-01	2136.71	not significant
4107	KIF13B	-1.01	6.50E-01	8.33E-01	1761.13	not significant
4108	CLSPN	-1.01	6.44E-01	8.30E-01	5106.09	not significant
4109	SRPRB	-1.01	6.32E-01	8.22E-01	3129.01	not significant
4110	COL15A1	-1.01	1.32E-01	NA	19.09	not significant
4111	ARL4D	-1.01	4.44E-01	NA	84.16	not significant
4112	RAPGEFL1	-1.01	4.42E-01	6.93E-01	141.84	not significant
4113	COL5A2	-1.01	4.96E-01	7.33E-01	113.89	not significant
4114	UBE2E3	-1.01	6.26E-01	8.18E-01	363.17	not significant
4115	BRE	-1.01	6.54E-01	8.36E-01	794.24	not significant
4116	TADA2B	-1.01	6.58E-01	8.39E-01	912.64	not significant
4117	SNRPF	-1.01	6.48E-01	8.32E-01	4941.39	not significant
4118	APBB1IP	-1.01	6.59E-01	8.39E-01	1609.83	not significant
4119	USP31	-1.01	6.74E-01	8.47E-01	688.75	not significant
4120	LYSMD3	-1.01	6.59E-01	8.39E-01	1214.02	not significant
4121	GTF2H3	-1.01	6.35E-01	8.23E-01	2532.33	not significant
4122	LGALSL	-1.01	1.39E-01	NA	19.64	not significant
4123	MAFB	-1.01	1.78E-01	NA	23.09	not significant

4124	43711_25571	-1.01	1.97E-01	NA	25.70	not significant
4125	SNX33	-1.01	4.00E-01	NA	62.99	not significant
4126	KCNJ14	-1.01	4.82E-01	NA	96.22	not significant
4127	ZNF391	-1.01	5.41E-01	7.63E-01	147.48	not significant
4128	MSL3P1	-1.01	6.44E-01	8.30E-01	502.87	not significant
4129	HMGB3	-1.01	6.58E-01	8.39E-01	713.46	not significant
4130	SNX1	-1.01	6.21E-01	8.15E-01	3456.99	not significant
4131	SRSF7	-1.01	6.12E-01	8.10E-01	9606.18	not significant
4132	KIF5A	-1.01	1.45E-01	NA	19.35	not significant
4133	SMARCA5-AS1	-1.01	1.36E-01	NA	26.43	not significant
4134	LOXL2	-1.01	4.58E-01	NA	85.97	not significant
4135	PHACTR2	-1.01	4.64E-01	NA	90.71	not significant
4136	TPT1-AS1	-1.01	5.51E-01	7.71E-01	159.96	not significant
4137	ZNF558	-1.01	5.34E-01	7.59E-01	161.22	not significant
4138	METTL10	-1.01	6.63E-01	8.41E-01	808.95	not significant
4139	FEM1C	-1.01	6.32E-01	8.22E-01	984.08	not significant
4140	ZNF708	-1.01	6.63E-01	8.41E-01	802.00	not significant
4141	ACBD5	-1.01	6.63E-01	8.41E-01	1106.77	not significant
4142	RAD54B	-1.01	6.60E-01	8.39E-01	1434.51	not significant
4143	SCRIB	-1.01	6.46E-01	8.31E-01	2578.05	not significant
4144	NOTCH1	-1.01	6.47E-01	8.32E-01	11277.72	not significant
4145	FGD5-AS1	-1.01	6.20E-01	8.15E-01	5916.61	not significant
4146	MTHFD1	-1.01	5.70E-01	7.83E-01	11341.17	not significant
4147	FGD2	-1.01	4.94E-01	7.33E-01	102.40	not significant
4148	C16orf91	-1.01	6.49E-01	8.33E-01	547.30	not significant
4149	AHI1	-1.01	6.24E-01	8.16E-01	305.47	not significant
4150	PALD1	-1.01	6.55E-01	8.37E-01	461.02	not significant
4151	MED17	-1.01	6.64E-01	8.42E-01	1361.52	not significant
4152	GPR180	-1.01	6.59E-01	8.39E-01	1699.09	not significant
4153	ANKAR	-1.01	3.49E-01	NA	47.37	not significant
4154	SUSD2	-1.01	1.80E-01	NA	23.15	not significant
4155	PTGDR2	-1.01	3.79E-01	NA	54.83	not significant
4156	RCE1	-1.01	6.63E-01	8.41E-01	895.20	not significant
4157	NDUFAF5	-1.01	6.51E-01	8.34E-01	689.11	not significant
4158	TEX261	-1.01	6.34E-01	8.23E-01	422.66	not significant
4159	DNAAF2	-1.01	6.58E-01	8.39E-01	513.91	not significant
4160	PXN	-1.01	6.43E-01	8.30E-01	458.93	not significant
4161	PPP4C	-1.01	6.53E-01	8.36E-01	4843.34	not significant
4162	RAP2C	-1.01	6.75E-01	8.47E-01	1681.71	not significant
4163	TANGO6	-1.01	6.66E-01	8.43E-01	953.72	not significant
4164	USP19	-1.01	6.52E-01	8.35E-01	3026.06	not significant
4165	CREB3L2	-1.01	6.64E-01	8.42E-01	2845.29	not significant
4166	SATB1	-1.01	6.62E-01	8.41E-01	1898.26	not significant
4167	CTBP1-AS	-1.01	2.57E-01	NA	36.21	not significant
4168	ASPRV1	-1.01	4.37E-01	NA	75.61	not significant
4169	VCAN	-1.01	4.90E-01	7.29E-01	103.40	not significant
4170	CHEK2	-1.01	6.71E-01	8.46E-01	786.00	not significant
4171	PARP16	-1.01	6.71E-01	8.46E-01	849.42	not significant
4172	ARPC1A	-1.01	6.67E-01	8.43E-01	2494.02	not significant
4173	RBM34	-1.01	6.70E-01	8.45E-01	1308.42	not significant
4174	RIOK3	-1.01	6.60E-01	8.39E-01	1931.81	not significant
4175	PHF10	-1.01	6.57E-01	8.38E-01	2180.60	not significant
4176	ERCC6L	-1.01	6.69E-01	8.44E-01	1832.78	not significant
4177	ZBED4	-1.01	6.49E-01	8.33E-01	5315.72	not significant
4178	TTC3	-1.01	6.22E-01	8.15E-01	6295.88	not significant
4179	LINC00852	-1.01	3.32E-01	NA	43.39	not significant
4180	CYTIP	-1.01	1.47E-01	NA	19.16	not significant
4181	SDK2	-1.01	3.08E-01	NA	38.11	not significant
4182	LOC100506100	-1.01	4.98E-01	7.35E-01	100.91	not significant
4183	COQ2	-1.01	5.82E-01	7.90E-01	194.66	not significant
4184	NR1H3	-1.01	5.67E-01	7.81E-01	160.68	not significant
4185	PLEKHA8P1	-1.01	5.94E-01	7.99E-01	224.26	not significant
4186	MNAT1	-1.01	6.70E-01	8.45E-01	971.20	not significant
4187	MAPKAPK2	-1.01	6.47E-01	8.32E-01	659.38	not significant
4188	UAP1	-1.01	6.73E-01	8.47E-01	1354.66	not significant
4189	NECAP2	-1.01	6.72E-01	8.46E-01	2369.53	not significant
4190	WDR45B	-1.01	6.63E-01	8.41E-01	2362.03	not significant
4191	PRKY	-1.01	6.72E-01	8.47E-01	803.95	not significant
4192	SLC38A1	-1.01	6.47E-01	8.32E-01	21081.91	not significant
4193	TBK1	-1.01	7.65E-01	8.95E-01	1569.59	not significant
4194	MBNL1-AS1	-1.01	1.85E-01	NA	21.79	not significant
4195	LIMD1-AS1	-1.01	3.28E-01	NA	47.18	not significant
4196	IL11RA	-1.01	5.06E-01	7.40E-01	110.99	not significant
4197	C16orf46	-1.01	4.38E-01	NA	71.92	not significant
4198	FTX	-1.01	2.87E-01	NA	33.49	not significant
4199	TSEN34	-1.01	5.65E-01	7.80E-01	149.74	not significant
4200	WDR35	-1.01	5.75E-01	7.86E-01	162.11	not significant
4201	OCRL	-1.01	5.79E-01	7.88E-01	181.21	not significant
4202	MIR4697HG	-1.01	5.98E-01	8.02E-01	221.87	not significant
4203	MICALL1	-1.01	6.49E-01	8.32E-01	384.11	not significant
4204	SLBP	-1.01	6.16E-01	8.13E-01	7859.74	not significant
4205	SMARCD1	-1.01	5.88E-01	7.95E-01	9483.14	not significant
4206	NCAPG2	-1.01	6.21E-01	8.15E-01	6025.79	not significant
4207	WDHD1	-1.01	6.60E-01	8.40E-01	3875.30	not significant
4208	OSBP2	-1.01	3.66E-01	NA	47.93	not significant
4209	POU6F1	-1.01	3.53E-01	NA	45.91	not significant
4210	IFI44L	-1.01	2.00E-01	NA	22.58	not significant
4211	UBA52	-1.01	6.75E-01	8.47E-01	15916.74	not significant

4212	IFI6	-1.01	6.81E-01	8.50E-01	1332.81	not significant
4213	TOP1MT	-1.01	6.77E-01	8.49E-01	1759.41	not significant
4214	THNSL1	-1.01	6.67E-01	8.43E-01	714.11	not significant
4215	ICE2	-1.01	6.61E-01	8.40E-01	3033.32	not significant
4216	LRRC39	-1.01	1.66E-01	NA	21.41	not significant
4217	ITGA10	-1.01	1.15E-01	NA	16.42	not significant
4218	PFN2	-1.01	5.46E-01	7.66E-01	125.66	not significant
4219	MDK	-1.01	5.22E-01	7.51E-01	114.15	not significant
4220	MTFMT	-1.01	6.63E-01	8.41E-01	458.77	not significant
4221	AMZ2	-1.01	6.79E-01	8.50E-01	760.55	not significant
4222	SFXN5	-1.01	6.55E-01	8.37E-01	377.71	not significant
4223	BNIP3	-1.01	7.02E-01	8.59E-01	739.34	not significant
4224	PPP2R3C	-1.01	6.69E-01	8.44E-01	1222.34	not significant
4225	PPP1R14B	-1.01	6.82E-01	8.50E-01	2838.78	not significant
4226	SLC39A7	-1.01	6.79E-01	8.50E-01	777.54	not significant
4227	MKS1	-1.01	6.79E-01	8.50E-01	851.39	not significant
4228	AXIN1	-1.01	6.79E-01	8.50E-01	1297.77	not significant
4229	ORMDL3	-1.01	6.14E-01	8.10E-01	5928.23	not significant
4230	SHC4	-1.01	1.97E-01	NA	21.44	not significant
4231	UBE2V1	-1.01	3.75E-01	NA	50.40	not significant
4232	RNPEP	-1.01	6.62E-01	8.41E-01	443.38	not significant
4233	GALE	-1.01	6.65E-01	8.42E-01	678.06	not significant
4234	IPCEF1	-1.01	6.76E-01	8.48E-01	589.11	not significant
4235	GPALPP1	-1.01	6.83E-01	8.51E-01	942.08	not significant
4236	HERC4	-1.01	6.80E-01	8.50E-01	1491.77	not significant
4237	ZNF430	-1.01	6.81E-01	8.50E-01	1307.00	not significant
4238	SNX6	-1.01	6.77E-01	8.48E-01	2033.79	not significant
4239	WDR36	-1.01	6.73E-01	8.47E-01	4074.65	not significant
4240	ZMYND11	-1.01	6.73E-01	8.47E-01	2540.55	not significant
4241	RMND5A	-1.01	6.47E-01	8.32E-01	4951.80	not significant
4242	MMS22L	-1.01	6.85E-01	8.52E-01	3420.28	not significant
4243	ACTA2-AS1	-1.01	2.06E-01	NA	23.01	not significant
4244	AMOTL2	-1.01	3.52E-01	NA	43.75	not significant
4245	ZNF565	-1.01	3.66E-01	NA	48.76	not significant
4246	ZDHHC11	-1.01	3.49E-01	NA	41.61	not significant
4247	RCOR2	-1.01	4.71E-01	NA	78.07	not significant
4248	CFAP44	-1.01	6.04E-01	8.04E-01	246.58	not significant
4249	BOD1L1	-1.01	6.62E-01	8.41E-01	2955.73	not significant
4250	ZNF180	-1.01	6.65E-01	8.42E-01	527.43	not significant
4251	PHF8	-1.01	6.78E-01	8.49E-01	582.78	not significant
4252	KIAA2013	-1.01	6.81E-01	8.50E-01	1799.35	not significant
4253	AHCYL2	-1.01	6.84E-01	8.52E-01	1275.77	not significant
4254	ABHD2	-1.01	6.78E-01	8.49E-01	2951.98	not significant
4255	SORT1	-1.01	6.76E-01	8.48E-01	3277.42	not significant
4256	GUF1	-1.01	6.81E-01	8.50E-01	2348.72	not significant
4257	SPG20	-1.01	1.71E-01	NA	19.21	not significant
4258	PLD6	-1.01	3.34E-01	NA	42.17	not significant
4259	FAM227B	-1.01	3.14E-01	NA	35.15	not significant
4260	ROPN1L	-1.01	2.93E-01	NA	31.16	not significant
4261	SDHAP1	-1.01	5.92E-01	7.98E-01	183.78	not significant
4262	ZNF492	-1.01	5.85E-01	7.93E-01	176.39	not significant
4263	MYL6B	-1.01	6.77E-01	8.49E-01	3068.59	not significant
4264	MON1B	-1.01	6.83E-01	8.51E-01	1740.79	not significant
4265	DTD1	-1.01	7.93E-02	NA	12.18	not significant
4266	LOC100507557	-1.01	1.72E-01	NA	19.63	not significant
4267	PSMD6-AS2	-1.01	2.58E-01	NA	26.34	not significant
4268	RFX2	-1.01	4.52E-01	NA	71.57	not significant
4269	NFAT5	-1.01	6.43E-01	8.30E-01	1503.08	not significant
4270	SDCCAG8	-1.01	6.50E-01	8.33E-01	399.91	not significant
4271	MRPL40	-1.01	6.81E-01	8.50E-01	578.40	not significant
4272	C9orf40	-1.01	6.89E-01	8.54E-01	909.65	not significant
4273	NPM3	-1.01	6.68E-01	8.44E-01	2182.37	not significant
4274	ATE1	-1.01	6.89E-01	8.54E-01	1503.49	not significant
4275	SECISBP2L	-1.01	6.87E-01	8.53E-01	1950.46	not significant
4276	PAX8-AS1	-1.01	6.89E-01	8.54E-01	1082.80	not significant
4277	MAP9	-1.01	6.80E-01	8.50E-01	569.83	not significant
4278	NEIL3	-1.01	6.83E-01	8.51E-01	1856.73	not significant
4279	SELT	-1.01	6.81E-01	8.50E-01	3325.70	not significant
4280	TCF25	-1.01	6.73E-01	8.47E-01	2567.47	not significant
4281	CEP120	-1.01	6.91E-01	8.54E-01	1229.41	not significant
4282	CASP2	-1.01	6.59E-01	8.39E-01	6963.73	not significant
4283	AGGF1	-1.01	6.66E-01	8.42E-01	3171.95	not significant
4284	NRIP3	-1.01	1.52E-01	NA	17.52	not significant
4285	KCNA6	-1.01	1.64E-01	NA	18.71	not significant
4286	SLC38A6	-1.01	6.07E-01	8.06E-01	186.78	not significant
4287	CD109	-1.01	5.98E-01	8.02E-01	172.11	not significant
4288	PRR3	-1.01	6.50E-01	8.33E-01	309.79	not significant
4289	IDS	-1.01	6.79E-01	8.49E-01	507.29	not significant
4290	ARHGAP18	-1.01	6.89E-01	8.54E-01	569.11	not significant
4291	GLDC	-1.01	6.92E-01	8.55E-01	828.01	not significant
4292	PDE10A	-1.01	4.04E-01	NA	63.38	not significant
4293	ATP1A3	-1.01	6.68E-01	8.44E-01	354.00	not significant
4294	SNRPG	-1.01	6.95E-01	8.57E-01	2345.62	not significant
4295	INVS	-1.01	6.68E-01	8.44E-01	569.71	not significant
4296	ATG16L1	-1.01	6.96E-01	8.58E-01	981.73	not significant
4297	CAPZB	-1.01	6.35E-01	8.23E-01	7053.21	not significant
4298	CHID1	-1.01	6.91E-01	8.54E-01	1886.07	not significant
4299	RPL4	-1.01	6.60E-01	8.39E-01	29158.47	not significant

4300	SMC6	-1.01	6.85E-01	8.52E-01	2572.69	not significant
4301	MAP4K5	-1.01	6.94E-01	8.57E-01	1692.79	not significant
4302	LHFPL2	-1.01	1.56E-01	NA	16.60	not significant
4303	TOR4A	-1.01	2.31E-01	NA	24.04	not significant
4304	REEP6	-1.01	2.75E-01	NA	28.79	not significant
4305	FLJ44635	-1.01	4.19E-01	NA	56.81	not significant
4306	ERP27	-1.01	4.90E-01	NA	78.04	not significant
4307	NUGGC	-1.01	6.28E-01	8.19E-01	202.27	not significant
4308	UQCC3	-1.01	6.73E-01	8.47E-01	452.91	not significant
4309	HEMK1	-1.01	6.95E-01	8.57E-01	2413.75	not significant
4310	NUDT19	-1.01	6.89E-01	8.54E-01	602.37	not significant
4311	MAP2K1	-1.01	6.81E-01	8.50E-01	2742.95	not significant
4312	DDX39A	-1.01	6.64E-01	8.42E-01	9479.66	not significant
4313	TRAPPC9	-1.01	6.89E-01	8.54E-01	2252.01	not significant
4314	MLLT6	-1.01	6.67E-01	8.43E-01	7567.47	not significant
4315	LASP1	-1.01	6.20E-01	8.14E-01	8781.86	not significant
4316	MFHAS1	-1.01	6.61E-01	8.40E-01	5232.88	not significant
4317	LOC100288842	-1.01	1.78E-01	NA	19.41	not significant
4318	ZNF432	-1.01	6.36E-01	8.24E-01	272.48	not significant
4319	EFNB1	-1.01	6.61E-01	8.41E-01	307.91	not significant
4320	ZCCHC10	-1.01	7.01E-01	8.59E-01	1117.88	not significant
4321	SALL2	-1.01	6.83E-01	8.51E-01	471.86	not significant
4322	PIGX	-1.01	6.90E-01	8.54E-01	2526.39	not significant
4323	MBD3	-1.01	6.83E-01	8.51E-01	6180.50	not significant
4324	SNRK	-1.01	6.99E-01	8.59E-01	1442.11	not significant
4325	MAP3K5	-1.01	3.32E-01	NA	38.22	not significant
4326	LINC00176	-1.01	4.12E-01	NA	50.60	not significant
4327	AK1	-1.01	4.51E-01	NA	63.73	not significant
4328	SLC25A5-AS1	-1.01	2.10E-01	4.74E-01	565.94	not significant
4329	SOCS2-AS1	-1.01	4.39E-01	NA	55.80	not significant
4330	ANKRD22	-1.01	4.40E-01	NA	55.63	not significant
4331	LINC00630	-1.01	5.58E-01	7.76E-01	113.70	not significant
4332	CBX8	-1.01	6.91E-01	8.54E-01	545.51	not significant
4333	ACTR5	-1.01	7.02E-01	8.59E-01	774.16	not significant
4334	GTF2E1	-1.01	7.01E-01	8.59E-01	913.34	not significant
4335	ARMC10	-1.01	7.01E-01	8.59E-01	1456.73	not significant
4336	DCTN2	-1.01	6.89E-01	8.54E-01	4336.51	not significant
4337	NR2C2	-1.01	6.97E-01	8.59E-01	3142.41	not significant
4338	USP32	-1.01	6.84E-01	8.52E-01	3511.62	not significant
4339	PHACTR4	-1.01	7.00E-01	8.59E-01	2126.73	not significant
4340	ATP8B2	-1.01	6.89E-01	8.54E-01	3305.40	not significant
4341	GSTM2	-1.01	4.84E-01	NA	67.81	not significant
4342	ZNF684	-1.01	6.43E-01	8.29E-01	220.63	not significant
4343	COMMD5	-1.01	6.67E-01	8.43E-01	434.10	not significant
4344	CRAT	-1.01	6.23E-01	8.16E-01	178.76	not significant
4345	ATP11A	-1.01	6.67E-01	8.43E-01	2438.68	not significant
4346	KRT10	-1.01	7.01E-01	8.59E-01	1040.95	not significant
4347	KMT2E	-1.01	6.75E-01	8.47E-01	4862.58	not significant
4348	HUS1	-1.01	7.07E-01	8.62E-01	985.27	not significant
4349	PUF60	-1.01	6.98E-01	8.59E-01	2494.74	not significant
4350	MORF4L1	-1.01	6.74E-01	8.47E-01	4858.72	not significant
4351	PWP1	-1.01	6.84E-01	8.52E-01	2819.14	not significant
4352	NFRKB	-1.01	7.02E-01	8.59E-01	1991.52	not significant
4353	ARFGAP2	-1.01	6.86E-01	8.53E-01	3023.35	not significant
4354	SMARCC1	-1.01	6.47E-01	8.32E-01	13101.73	not significant
4355	ZNF233	-1.01	3.14E-01	NA	34.94	not significant
4356	LOC101927795	-1.01	1.69E-01	NA	18.87	not significant
4357	NBPF8	-1.01	1.25E-01	NA	15.02	not significant
4358	DOK2	-1.01	4.97E-01	NA	75.89	not significant
4359	DBIL5P	-1.01	3.57E-01	NA	36.67	not significant
4360	PRX	-1.01	5.04E-01	NA	78.58	not significant
4361	IFIT1	-1.01	3.41E-01	NA	35.31	not significant
4362	SURF2	-1.01	6.27E-01	8.18E-01	200.39	not significant
4363	QRICH2	-1.01	6.39E-01	8.26E-01	265.14	not significant
4364	NUBP1	-1.01	6.98E-01	8.59E-01	571.16	not significant
4365	ENY2	-1.01	7.01E-01	8.59E-01	3362.13	not significant
4366	SMS	-1.01	7.03E-01	8.60E-01	3469.71	not significant
4367	STAU2	-1.01	6.74E-01	8.47E-01	4014.88	not significant
4368	DIXDC1	-1.01	2.07E-01	NA	21.76	not significant
4369	SNX22	-1.01	2.84E-01	5.54E-01	177.58	not significant
4370	C11orf94	-1.01	8.37E-02	NA	10.06	not significant
4371	LOC439994	-1.01	4.35E-01	NA	57.99	not significant
4372	TMEM182	-1.01	6.23E-01	8.16E-01	178.87	not significant
4373	ELAC1	-1.01	6.26E-01	8.18E-01	188.55	not significant
4374	ZCWPW1	-1.01	4.57E-01	NA	60.31	not significant
4375	SRGAP2	-1.01	6.41E-01	8.28E-01	244.54	not significant
4376	DHODH	-1.01	7.08E-01	8.63E-01	603.93	not significant
4377	TRMU	-1.01	7.09E-01	8.64E-01	1072.16	not significant
4378	APOBEC3F	-1.01	6.98E-01	8.59E-01	563.95	not significant
4379	LOC100130899	-1.01	2.35E-01	NA	22.81	not significant
4380	ARMC12	-1.01	2.03E-01	NA	18.21	not significant
4381	THRIL	-1.01	1.16E-01	NA	52.16	not significant
4382	SLC23A1	-1.01	4.76E-01	NA	64.58	not significant
4383	TMEM62	-1.01	5.42E-01	NA	93.36	not significant
4384	UIMC1	-1.01	7.13E-01	8.67E-01	1147.23	not significant
4385	TAF5	-1.01	7.13E-01	8.66E-01	967.31	not significant
4386	PSMB8	-1.01	7.11E-01	8.65E-01	1726.99	not significant
4387	GABPA	-1.01	7.12E-01	8.65E-01	1921.47	not significant

4388	KIAA0232	-1.01	7.10E-01	8.65E-01	2520.72	not significant
4389	ADAMTSL1	-1.01	9.46E-02	NA	10.88	not significant
4390	HP09053	-1.01	1.23E-01	NA	13.49	not significant
4391	IDI2-AS1	-1.01	1.17E-01	NA	12.75	not significant
4392	APBB1	-1.01	4.96E-01	NA	65.42	not significant
4393	IGF2BP3	-1.01	2.40E-01	NA	20.68	not significant
4394	POLR3GL	-1.01	6.61E-01	8.40E-01	270.51	not significant
4395	MRPS18B	-1.01	7.09E-01	8.64E-01	652.15	not significant
4396	ADCK1	-1.01	6.80E-01	8.50E-01	325.55	not significant
4397	KIZ	-1.01	6.98E-01	8.59E-01	445.31	not significant
4398	TRAF3IP3	-1.01	6.92E-01	8.55E-01	3173.96	not significant
4399	FAM133B	-1.01	4.00E-01	NA	41.35	not significant
4400	ZNF16	-1.01	6.75E-01	8.47E-01	303.26	not significant
4401	CENPW	-1.01	6.48E-01	8.32E-01	937.03	not significant
4402	DNAJC19	-1.01	7.19E-01	8.71E-01	886.42	not significant
4403	MIS18A	-1.01	7.19E-01	8.70E-01	1625.03	not significant
4404	LYRM2	-1.01	7.13E-01	8.66E-01	1690.40	not significant
4405	RNF114	-1.01	6.88E-01	8.54E-01	4008.20	not significant
4406	SH3GLB1	-1.01	6.91E-01	8.54E-01	3179.85	not significant
4407	PPP3R1	-1.01	6.75E-01	8.47E-01	6039.57	not significant
4408	HIPK1	-1.01	7.10E-01	8.64E-01	4682.27	not significant
4409	DEK	-1.01	6.48E-01	8.32E-01	14636.38	not significant
4410	LOC101928020	-1.01	1.49E-01	NA	13.91	not significant
4411	FAM149A	-1.01	5.30E-01	NA	78.75	not significant
4412	SYCP3	-1.01	1.76E-01	NA	16.01	not significant
4413	MGAT3	-1.01	2.90E-01	NA	30.20	not significant
4414	ELL3	-1.01	3.43E-01	NA	31.04	not significant
4415	ZC3H13	-1.01	6.99E-01	8.59E-01	3889.16	not significant
4416	VPS72	-1.01	7.21E-01	8.71E-01	1280.73	not significant
4417	PRKAG1	-1.01	7.19E-01	8.70E-01	1855.58	not significant
4418	PIBF1	-1.01	7.19E-01	8.70E-01	610.87	not significant
4419	ZNF3	-1.01	6.76E-01	8.48E-01	2571.69	not significant
4420	ZC3HAV1	-1.01	7.00E-01	8.59E-01	7623.94	not significant
4421	IL22	-1.01	1.19E-01	NA	11.70	not significant
4422	ACSL1	-1.01	7.01E-01	8.59E-01	390.21	not significant
4423	DOK1	-1.01	7.04E-01	8.61E-01	413.52	not significant
4424	MAGI3	-1.01	6.66E-01	8.43E-01	230.32	not significant
4425	NPAS2	-1.01	7.21E-01	8.71E-01	748.47	not significant
4426	IRGQ	-1.01	7.21E-01	8.71E-01	783.94	not significant
4427	CORO1B	-1.01	7.24E-01	8.73E-01	2181.57	not significant
4428	NUDT15	-1.01	7.21E-01	8.71E-01	1618.17	not significant
4429	TEX10	-1.01	7.21E-01	8.71E-01	1066.83	not significant
4430	GIT2	-1.01	7.02E-01	8.59E-01	3372.79	not significant
4431	KMO	-1.01	8.49E-02	NA	10.95	not significant
4432	PFKFB1	-1.01	1.93E-01	NA	17.92	not significant
4433	DTX2P1-UPK3BP1-	-1.01	5.24E-01	NA	72.93	not significant
4434	TLN2	-1.01	4.73E-01	NA	74.78	not significant
4435	HSD17B8	-1.01	6.31E-01	8.21E-01	176.17	not significant
4436	PCDH10	-1.01	4.82E-01	NA	61.06	not significant
4437	SCML1	-1.01	7.11E-01	8.65E-01	488.26	not significant
4438	TADA1	-1.01	7.24E-01	8.73E-01	884.39	not significant
4439	DHRS4	-1.01	7.17E-01	8.69E-01	532.89	not significant
4440	PLD3	-1.01	7.24E-01	8.73E-01	953.76	not significant
4441	NABP1	-1.01	7.24E-01	8.73E-01	719.73	not significant
4442	YIPF6	-1.01	7.24E-01	8.73E-01	835.78	not significant
4443	KANSL1	-1.01	7.27E-01	8.74E-01	994.77	not significant
4444	TPGS2	-1.01	6.93E-01	8.56E-01	4486.40	not significant
4445	SLC20A2	-1.01	7.23E-01	8.73E-01	1738.11	not significant
4446	RTF1	-1.01	7.01E-01	8.59E-01	3896.43	not significant
4447	NXPE3	-1.01	7.21E-01	8.71E-01	2032.17	not significant
4448	SEC23IP	-1.01	7.05E-01	8.61E-01	2588.13	not significant
4449	LOC100507462	-1.01	3.18E-01	NA	26.93	not significant
4450	LOC401010	-1.01	1.20E-01	NA	10.80	not significant
4451	BET1L	-1.01	7.28E-01	8.75E-01	1658.14	not significant
4452	TOPORS	-1.01	7.26E-01	8.74E-01	1503.67	not significant
4453	RPS19BP1	-1.01	7.21E-01	8.71E-01	3608.99	not significant
4454	PBX2	-1.01	7.29E-01	8.75E-01	859.50	not significant
4455	FASTKD2	-1.01	6.60E-01	8.40E-01	1600.85	not significant
4456	GNPDA1	-1.01	7.07E-01	8.63E-01	3278.99	not significant
4457	PARP1	-1.01	6.50E-01	8.33E-01	10609.78	not significant
4458	VAV3	-1.01	7.27E-01	8.75E-01	1603.51	not significant
4459	RNF38	-1.01	7.43E-01	8.84E-01	1655.58	not significant
4460	SLC35A2	-1.01	5.26E-01	NA	79.45	not significant
4461	SMIM17	-1.01	3.04E-01	NA	24.88	not significant
4462	C17orf67	-1.01	6.25E-01	8.17E-01	143.02	not significant
4463	THAP2	-1.01	6.48E-01	8.32E-01	177.37	not significant
4464	FHIT	-1.01	7.23E-01	8.72E-01	588.95	not significant
4465	ZNF213	-1.01	7.19E-01	8.70E-01	436.98	not significant
4466	PPP1R12B	-1.01	7.12E-01	8.66E-01	673.45	not significant
4467	SCAMP2	-1.01	7.29E-01	8.76E-01	1516.91	not significant
4468	GMFB	-1.01	7.14E-01	8.67E-01	2570.45	not significant
4469	FOXK1	-1.01	7.26E-01	8.74E-01	2611.71	not significant
4470	GAK	-1.01	7.12E-01	8.65E-01	3765.49	not significant
4471	C1orf56	-1.01	2.87E-01	NA	23.45	not significant
4472	MB	-1.01	2.33E-01	NA	19.84	not significant
4473	APOM	-1.01	3.00E-01	NA	27.44	not significant
4474	DUSP19	-1.01	6.10E-01	8.08E-01	133.98	not significant
4475	CBR4	-1.01	7.30E-01	8.76E-01	727.62	not significant

4476	TRAF2	-1.01	7.34E-01	8.78E-01	1225.27	not significant
4477	TMEM14B	-1.01	7.30E-01	8.76E-01	1773.55	not significant
4478	TXN	-1.01	7.15E-01	8.68E-01	5190.87	not significant
4479	ABCF3	-1.01	7.31E-01	8.77E-01	1249.14	not significant
4480	RAN	-1.01	7.03E-01	8.60E-01	29519.84	not significant
4481	LMNB1	-1.01	6.45E-01	8.31E-01	18306.05	not significant
4482	RAB22A	-1.01	7.28E-01	8.75E-01	1643.36	not significant
4483	U2AF2	-1.01	6.89E-01	8.54E-01	20094.68	not significant
4484	C5orf51	-1.01	7.32E-01	8.77E-01	1939.14	not significant
4485	PLXNA2	-1.01	1.71E-01	NA	13.63	not significant
4486	C6orf52	-1.01	3.72E-01	NA	32.78	not significant
4487	SPR	-1.01	5.08E-01	NA	61.16	not significant
4488	OASL	-1.01	5.63E-01	7.79E-01	126.16	not significant
4489	GKAP1	-1.01	5.37E-01	NA	71.87	not significant
4490	THAP5	-1.01	7.49E-01	8.86E-01	1669.70	not significant
4491	IL7R	-1.01	7.08E-01	8.63E-01	419.52	not significant
4492	MCCC1	-1.01	7.37E-01	8.80E-01	807.16	not significant
4493	C14orf166	-1.01	7.19E-01	8.70E-01	5590.54	not significant
4494	CAT	-1.01	7.21E-01	8.71E-01	2879.72	not significant
4495	ASH1L	-1.01	7.35E-01	8.79E-01	1792.63	not significant
4496	BCL2L11	-1.01	7.37E-01	8.80E-01	809.11	not significant
4497	ZC2HC1C	-1.01	7.16E-02	NA	8.24	not significant
4498	LINC00473	-1.01	2.84E-01	NA	23.28	not significant
4499	HEYL	-1.01	4.50E-01	NA	45.28	not significant
4500	PLXNC1	-1.01	5.27E-01	NA	64.06	not significant
4501	ANKFN1	-1.01	6.00E-01	8.02E-01	426.91	not significant
4502	WASH1	-1.01	6.01E-01	8.02E-01	104.00	not significant
4503	STARD10	-1.01	6.24E-01	8.16E-01	135.77	not significant
4504	ITGAV	-1.01	6.55E-01	8.37E-01	161.99	not significant
4505	TXNRD2	-1.01	7.02E-01	8.59E-01	319.62	not significant
4506	PAK4	-1.01	7.38E-01	8.80E-01	818.93	not significant
4507	DCTPP1	-1.01	7.28E-01	8.75E-01	4377.23	not significant
4508	DCAF17	-1.01	6.51E-01	8.34E-01	1587.19	not significant
4509	VEZF1	-1.01	7.21E-01	8.71E-01	3417.45	not significant
4510	ZKSCAN2	-1.01	7.37E-01	8.80E-01	928.85	not significant
4511	SAMD4B	-1.01	7.35E-01	8.79E-01	1840.13	not significant
4512	PPP6C	-1.01	7.10E-01	8.64E-01	3389.73	not significant
4513	EMILIN1	-1.01	4.96E-01	NA	58.68	not significant
4514	TCEB3-AS1	-1.01	5.35E-01	NA	67.81	not significant
4515	TRIM3	-1.01	4.90E-01	NA	53.08	not significant
4516	LOC727896	-1.01	3.11E-01	NA	22.23	not significant
4517	CNR2	-1.01	5.14E-01	NA	59.09	not significant
4518	FGGY	-1.01	6.71E-01	8.46E-01	195.03	not significant
4519	KIAA0895	-1.01	6.92E-01	8.55E-01	243.74	not significant
4520	LINC00294	-1.01	7.24E-01	8.73E-01	497.48	not significant
4521	PER1	-1.01	7.40E-01	8.82E-01	1102.63	not significant
4522	CNPPD1	-1.01	7.32E-01	8.77E-01	2176.69	not significant
4523	POPDC2	-1.01	2.57E-01	NA	18.88	not significant
4524	UACA	-1.01	2.26E-01	NA	16.40	not significant
4525	C5orf30	-1.01	4.66E-01	NA	47.19	not significant
4526	LOC101927919	-1.01	3.19E-01	NA	25.31	not significant
4527	GJC2	-1.01	3.80E-01	NA	29.77	not significant
4528	SCN3A	-1.01	5.93E-01	NA	96.13	not significant
4529	TTC8	-1.01	6.69E-01	8.44E-01	148.80	not significant
4530	ZNF341	-1.01	6.70E-01	8.45E-01	211.34	not significant
4531	FANCF	-1.01	7.42E-01	8.83E-01	1196.38	not significant
4532	KLF6	-1.01	7.20E-01	8.71E-01	2852.52	not significant
4533	CAPN1	-1.01	7.36E-01	8.79E-01	4398.99	not significant
4534	ZNF655	-1.01	7.45E-01	8.84E-01	3363.03	not significant
4535	NSMAF	-1.01	7.18E-01	8.70E-01	3820.94	not significant
4536	UBE2Q2P1	-1.01	4.06E-01	NA	35.53	not significant
4537	AKAP6	-1.01	4.81E-01	NA	47.90	not significant
4538	RBM47	-1.01	2.34E-01	NA	17.49	not significant
4539	AK9	-1.01	5.93E-01	NA	96.90	not significant
4540	RABL2A	-1.01	5.35E-01	NA	70.26	not significant
4541	TDRD7	-1.01	6.85E-01	8.52E-01	211.87	not significant
4542	SLC30A4	-1.01	6.78E-01	8.49E-01	150.58	not significant
4543	GGNBP2	-1.01	7.44E-01	8.84E-01	734.12	not significant
4544	ZFP1	-1.01	7.43E-01	8.84E-01	1490.00	not significant
4545	CSTF3	-1.01	7.45E-01	8.84E-01	1814.26	not significant
4546	RAPGEF2	-1.01	7.47E-01	8.85E-01	1176.57	not significant
4547	LEPROTL1	-1.01	7.24E-01	8.73E-01	3533.61	not significant
4548	SLC31A1	-1.01	7.47E-01	8.85E-01	1426.87	not significant
4549	THAP7-AS1	-1.01	3.34E-01	NA	23.94	not significant
4550	HIST1H4E	-1.01	4.37E-01	NA	38.49	not significant
4551	AMICA1	-1.01	2.26E-01	NA	15.50	not significant
4552	LOC101928766	-1.01	6.52E-01	8.35E-01	145.40	not significant
4553	TYRO3	-1.01	6.92E-01	8.55E-01	441.17	not significant
4554	GUSBP1	-1.01	6.99E-01	8.59E-01	262.12	not significant
4555	ORC5	-1.01	7.49E-01	8.86E-01	1238.15	not significant
4556	STXBP5	-1.01	7.31E-01	8.77E-01	503.87	not significant
4557	ZMAT2	-1.01	7.30E-01	8.76E-01	3074.36	not significant
4558	MED6	-1.01	7.49E-01	8.86E-01	1340.39	not significant
4559	ZNF326	-1.01	7.36E-01	8.79E-01	2622.32	not significant
4560	POLR2M	-1.01	5.63E-01	NA	77.20	not significant
4561	NUTM2A	-1.01	2.03E-01	NA	16.05	not significant
4562	LINC00467	-1.01	5.20E-01	NA	58.01	not significant
4563	TRIM44	-1.01	5.11E-01	NA	50.87	not significant

4564	TNF	-1.01	4.86E-01	NA	50.22	not significant
4565	KCNN3	-1.01	4.21E-01	NA	34.60	not significant
4566	EXOSC1	-1.01	7.49E-01	8.86E-01	835.48	not significant
4567	ARL15	-1.01	7.00E-01	8.59E-01	225.91	not significant
4568	C12orf10	-1.01	7.45E-01	8.85E-01	1538.63	not significant
4569	ATP10D	-1.01	7.46E-01	8.85E-01	583.75	not significant
4570	TERF2IP	-1.01	7.36E-01	8.79E-01	4341.34	not significant
4571	MAPK1IP1L	-1.01	7.46E-01	8.85E-01	5645.87	not significant
4572	DROSHA	-1.01	7.32E-01	8.77E-01	3391.57	not significant
4573	TNFRSF10A	-1.01	2.33E-01	NA	14.78	not significant
4574	C15orf62	-1.01	2.88E-01	NA	18.91	not significant
4575	PON1	-1.01	3.91E-01	NA	28.86	not significant
4576	ZNF19	-1.01	4.00E-01	NA	33.62	not significant
4577	LST1	-1.01	6.25E-01	8.17E-01	103.96	not significant
4578	FAM179A	-1.01	6.91E-01	8.54E-01	190.33	not significant
4579	ZNF14	-1.01	7.29E-01	8.76E-01	353.15	not significant
4580	NDUFB2	-1.01	7.56E-01	8.90E-01	1725.50	not significant
4581	KDM4C	-1.01	7.55E-01	8.90E-01	1119.37	not significant
4582	FAM115A	-1.01	7.52E-01	8.88E-01	888.09	not significant
4583	DCAF16	-1.01	7.54E-01	8.89E-01	2147.08	not significant
4584	GOLPH3	-1.01	7.37E-01	8.80E-01	3433.50	not significant
4585	SETD5	-1.01	7.36E-01	8.79E-01	5045.20	not significant
4586	ZEB1	-1.01	7.41E-01	8.82E-01	3369.48	not significant
4587	CCDC11	-1.01	1.76E-01	NA	11.77	not significant
4588	GPC3	-1.01	3.99E-01	NA	29.61	not significant
4589	LIPT2	-1.01	5.50E-01	NA	67.26	not significant
4590	CRIPAK	-1.01	6.60E-01	8.39E-01	161.71	not significant
4591	GRK4	-1.01	5.70E-01	NA	76.67	not significant
4592	FAM131A	-1.01	6.56E-01	8.37E-01	131.78	not significant
4593	BMI1	-1.01	7.08E-01	8.63E-01	233.38	not significant
4594	METAP1D	-1.01	6.96E-01	8.58E-01	216.99	not significant
4595	NMNAT1	-1.01	7.24E-01	8.73E-01	303.32	not significant
4596	SLC35G2	-1.01	7.39E-01	8.80E-01	366.16	not significant
4597	TUSC5	-1.01	7.54E-01	8.89E-01	571.16	not significant
4598	EMILIN2	-1.01	7.57E-01	8.91E-01	1004.62	not significant
4599	CIZ1	-1.01	7.46E-01	8.85E-01	2384.54	not significant
4600	MTMR12	-1.01	7.54E-01	8.89E-01	1667.85	not significant
4601	KLF13	-1.01	7.23E-01	8.72E-01	4473.53	not significant
4602	COLGALT1	-1.01	7.44E-01	8.84E-01	4298.82	not significant
4603	B9D1	-1.01	5.34E-01	NA	60.52	not significant
4604	FBXW4P1	-1.01	3.63E-01	NA	26.49	not significant
4605	FBXO48	-1.01	6.20E-01	8.15E-01	125.89	not significant
4606	MCM3AP-AS1	-1.01	5.88E-01	NA	93.14	not significant
4607	CDIP1	-1.01	7.03E-01	8.59E-01	285.59	not significant
4608	SNPH	-1.01	6.74E-01	8.47E-01	148.05	not significant
4609	PNRC2	-1.01	7.47E-01	8.85E-01	521.87	not significant
4610	ATG14	-1.01	7.40E-01	8.81E-01	388.41	not significant
4611	DNAJB2	-1.01	7.61E-01	8.93E-01	1083.65	not significant
4612	CDK5R1	-1.01	7.16E-01	8.69E-01	260.88	not significant
4613	PRKRA	-1.01	7.61E-01	8.93E-01	956.19	not significant
4614	SMARCAL1	-1.01	7.58E-01	8.91E-01	1040.51	not significant
4615	ITPK1	-1.01	7.47E-01	8.85E-01	2498.85	not significant
4616	PTCD3	-1.01	7.33E-01	8.77E-01	4759.74	not significant
4617	NUCB2	-1.01	6.87E-01	8.53E-01	20162.43	not significant
4618	KCND1	-1.01	1.60E-01	NA	10.86	not significant
4619	TLR5	-1.01	3.87E-01	NA	30.92	not significant
4620	ACSL6	-1.01	5.30E-01	NA	58.98	not significant
4621	ZBTB8OS	-1.01	7.44E-01	8.84E-01	450.47	not significant
4622	LOC101927045	-1.01	5.44E-01	NA	69.88	not significant
4623	SERPINF1	-1.01	7.44E-01	8.84E-01	369.56	not significant
4624	ZNF527	-1.01	7.57E-01	8.91E-01	491.34	not significant
4625	EMC7	-1.01	7.62E-01	8.94E-01	1118.15	not significant
4626	LANCL2	-1.01	7.63E-01	8.94E-01	869.18	not significant
4627	GBAS	-1.01	7.50E-01	8.87E-01	2328.57	not significant
4628	C10orf76	-1.01	7.61E-01	8.93E-01	1363.01	not significant
4629	MORC3	-1.01	7.52E-01	8.88E-01	2331.62	not significant
4630	CCNT1	-1.01	7.48E-01	8.85E-01	4448.25	not significant
4631	INTS2	-1.01	7.49E-01	8.86E-01	3933.91	not significant
4632	TMEM43	-1.01	7.48E-01	8.86E-01	2515.16	not significant
4633	KIF9-AS1	-1.01	3.39E-01	NA	22.15	not significant
4634	YBX2	-1.01	2.06E-01	NA	11.94	not significant
4635	GSTM4	-1.01	5.82E-01	NA	78.24	not significant
4636	HYAL2	-1.01	5.93E-01	NA	74.53	not significant
4637	ARMC9	-1.01	6.49E-01	8.32E-01	120.60	not significant
4638	CBLB	-1.01	7.21E-01	8.71E-01	261.00	not significant
4639	EOMES	-1.01	7.38E-01	8.80E-01	325.96	not significant
4640	C14orf2	-1.01	7.60E-01	8.93E-01	3122.62	not significant
4641	TMEM201	-1.01	7.58E-01	8.91E-01	2241.55	not significant
4642	ADCY10P1	-1.01	5.42E-01	NA	55.09	not significant
4643	SHF	-1.01	4.92E-01	NA	42.86	not significant
4644	SLC25A43	-1.01	6.12E-01	NA	93.87	not significant
4645	CYTH3	-1.01	6.10E-01	NA	82.17	not significant
4646	CKMT2-AS1	-1.01	6.73E-01	8.47E-01	138.89	not significant
4647	CPTP	-1.01	7.51E-01	8.88E-01	430.22	not significant
4648	LSM14A	-1.01	6.71E-01	8.46E-01	1585.18	not significant
4649	ENSA	-1.01	7.54E-01	8.89E-01	6371.93	not significant
4650	PHF6	-1.01	7.52E-01	8.88E-01	4332.21	not significant
4651	TXNDC12	-1.01	7.49E-01	8.86E-01	3170.24	not significant

4652	BMP2K	-1.01	7.63E-01	8.94E-01	1628.29	not significant
4653	TSPAN10	-1.01	1.73E-01	NA	10.67	not significant
4654	TMEM184A	-1.01	2.37E-01	NA	19.47	not significant
4655	VPREB1	-1.01	2.24E-01	NA	13.00	not significant
4656	RNF219-AS1	-1.01	2.80E-01	NA	20.52	not significant
4657	EBLN2	-1.01	5.70E-01	NA	61.69	not significant
4658	LOC399815	-1.01	6.69E-01	8.44E-01	129.03	not significant
4659	CUBN	-1.01	5.78E-01	NA	64.52	not significant
4660	TIMP2	-1.01	6.87E-01	8.53E-01	162.30	not significant
4661	PRDX4	-1.01	7.70E-01	8.98E-01	1429.49	not significant
4662	FAM114A2	-1.01	7.66E-01	8.96E-01	734.02	not significant
4663	PGAP1	-1.01	7.62E-01	8.94E-01	909.84	not significant
4664	RHNO1	-1.01	7.66E-01	8.96E-01	2431.96	not significant
4665	UBE2I	-1.01	7.55E-01	8.90E-01	7315.19	not significant
4666	THUMPD1	-1.01	7.52E-01	8.88E-01	3369.61	not significant
4667	GNPTAB	-1.01	7.49E-01	8.86E-01	8286.93	not significant
4668	FOXD4	-1.01	1.72E-01	NA	10.38	not significant
4669	DNAH11	-1.01	2.83E-01	NA	18.03	not significant
4670	SPEF1	-1.01	2.79E-01	NA	15.42	not significant
4671	RNF208	-1.01	2.61E-01	NA	14.60	not significant
4672	POU4F1	-1.01	4.38E-01	NA	31.35	not significant
4673	LOC100132077	-1.01	4.63E-01	NA	34.95	not significant
4674	ZNF688	-1.01	6.84E-01	8.52E-01	170.07	not significant
4675	FUT11	-1.01	5.39E-01	NA	49.91	not significant
4676	RNF181	-1.01	7.63E-01	8.94E-01	876.39	not significant
4677	MOCS3	-1.01	7.66E-01	8.96E-01	425.04	not significant
4678	METTL14	-1.01	7.73E-01	9.00E-01	1042.46	not significant
4679	ATAD3B	-1.01	7.73E-01	9.00E-01	1292.09	not significant
4680	JAM3	-1.01	7.57E-01	8.91E-01	3219.22	not significant
4681	PFKP	-1.01	7.37E-01	8.80E-01	5426.04	not significant
4682	ITGB5	-1.01	2.35E-01	NA	13.53	not significant
4683	DUSP5	-1.01	3.43E-01	NA	19.70	not significant
4684	LPCAT2	-1.01	4.84E-01	NA	42.87	not significant
4685	POLR2L	-1.01	7.45E-01	8.85E-01	3175.39	not significant
4686	ZNF772	-1.01	7.16E-01	8.68E-01	658.24	not significant
4687	OSGEPL1	-1.01	7.69E-01	8.97E-01	463.04	not significant
4688	ASNA1	-1.01	7.77E-01	9.02E-01	2220.57	not significant
4689	COG6	-1.01	7.74E-01	9.00E-01	769.78	not significant
4690	RPIA	-1.01	7.58E-01	8.91E-01	3482.89	not significant
4691	ANKLE1	-1.01	7.72E-01	8.99E-01	1759.84	not significant
4692	EXOC1	-1.01	7.75E-01	9.01E-01	848.06	not significant
4693	SLC25A23	-1.01	7.76E-01	9.01E-01	1041.36	not significant
4694	FZD6	-1.01	7.67E-01	8.97E-01	2991.50	not significant
4695	LRRC17	-1.01	2.24E-01	NA	11.80	not significant
4696	PLAU	-1.01	3.63E-01	NA	22.46	not significant
4697	ZNF287	-1.01	7.42E-01	8.83E-01	277.65	not significant
4698	CENPK	-1.01	7.96E-01	9.12E-01	1555.43	not significant
4699	FAM96B	-1.01	7.78E-01	9.03E-01	2466.59	not significant
4700	ANXA4	-1.01	7.74E-01	9.00E-01	575.63	not significant
4701	PGM3	-1.01	7.64E-01	8.95E-01	469.35	not significant
4702	IST1	-1.01	7.59E-01	8.92E-01	3778.22	not significant
4703	SMAD2	-1.01	7.60E-01	8.93E-01	3633.33	not significant
4704	CD82	-1.01	7.26E-01	8.74E-01	7929.16	not significant
4705	MBNL3	-1.01	7.74E-01	9.00E-01	4771.80	not significant
4706	GAS5-AS1	-1.01	3.25E-01	NA	18.54	not significant
4707	EFCAB13	-1.01	6.63E-01	8.41E-01	123.26	not significant
4708	CYP19A1	-1.01	5.86E-01	NA	62.39	not significant
4709	IFT20	-1.01	6.77E-01	8.49E-01	117.73	not significant
4710	TNRC6C-AS1	-1.01	7.21E-01	8.71E-01	184.62	not significant
4711	SKA1	-1.01	7.46E-01	8.85E-01	275.29	not significant
4712	SH3YL1	-1.01	7.68E-01	8.97E-01	481.11	not significant
4713	WBP4	-1.01	7.82E-01	9.05E-01	1141.14	not significant
4714	KLHL28	-1.01	7.79E-01	9.03E-01	786.13	not significant
4715	C7orf49	-1.01	7.74E-01	9.00E-01	2140.20	not significant
4716	GINS1	-1.01	7.59E-01	8.92E-01	4011.40	not significant
4717	SLC25A38	-1.01	8.17E-01	9.24E-01	3249.75	not significant
4718	HS2ST1	-1.01	9.32E-01	9.75E-01	3329.14	not significant
4719	MCMDC2	-1.01	2.56E-01	NA	15.17	not significant
4720	CDH26	-1.01	2.35E-01	NA	14.44	not significant
4721	POU2F2	-1.01	6.57E-01	8.38E-01	104.27	not significant
4722	CHST15	-1.01	4.43E-01	NA	29.12	not significant
4723	ENOX1	-1.01	6.00E-01	NA	62.77	not significant
4724	HIST1H2AM	-1.01	5.06E-01	NA	38.06	not significant
4725	ZNF720	-1.01	7.53E-01	8.89E-01	311.99	not significant
4726	MTX2	-1.01	7.84E-01	9.07E-01	973.82	not significant
4727	CYB5R4	-1.01	7.84E-01	9.07E-01	1048.47	not significant
4728	FAM73A	-1.01	7.82E-01	9.05E-01	631.61	not significant
4729	EDRF1	-1.01	7.36E-01	8.79E-01	1594.98	not significant
4730	DDX26B	-1.01	7.30E-01	8.76E-01	229.08	not significant
4731	SUMO1	-1.01	7.67E-01	8.96E-01	4114.45	not significant
4732	BRD7	-1.01	7.69E-01	8.98E-01	3004.20	not significant
4733	ZNF681	-1.01	7.82E-01	9.05E-01	817.22	not significant
4734	THEMIS2	-1.01	3.72E-01	NA	20.34	not significant
4735	SLC14A2	-1.01	3.57E-01	NA	18.97	not significant
4736	LOC257396	-1.01	5.51E-01	NA	57.87	not significant
4737	TNFSF9	-1.01	6.70E-01	8.45E-01	105.88	not significant
4738	IL17RE	-1.01	7.33E-01	8.77E-01	214.99	not significant
4739	DGUOK-AS1	-1.01	5.07E-01	NA	37.21	not significant

4740	WDR18	-1.01	7.85E-01	9.07E-01	2148.44	not significant
4741	VWA9	-1.01	7.83E-01	9.06E-01	1738.76	not significant
4742	PSMA3	-1.01	7.72E-01	8.99E-01	5766.42	not significant
4743	ST3GAL4	-1.01	7.88E-01	9.09E-01	1174.63	not significant
4744	SP140L	-1.01	7.86E-01	9.07E-01	1210.52	not significant
4745	LRP8	-1.01	7.79E-01	9.03E-01	3059.31	not significant
4746	MLX	-1.01	8.01E-01	9.14E-01	2951.69	not significant
4747	CKAP2	-1.01	7.68E-01	8.97E-01	3623.62	not significant
4748	PML	-1.01	7.78E-01	9.03E-01	2367.14	not significant
4749	EPRS	-1.01	8.01E-01	9.14E-01	7389.70	not significant
4750	GPT	-1.01	1.99E-01	NA	9.65	not significant
4751	SHROOM1	-1.01	5.39E-01	NA	43.20	not significant
4752	METTL12	-1.01	6.59E-01	NA	96.99	not significant
4753	LOC101928103	-1.01	6.13E-01	NA	64.21	not significant
4754	BOLA3-AS1	-1.01	3.23E-01	NA	16.42	not significant
4755	EPHA1	-1.01	6.46E-01	NA	88.76	not significant
4756	ZNF461	-1.01	7.46E-01	8.85E-01	234.87	not significant
4757	UQCRHL	-1.01	7.68E-01	8.97E-01	417.45	not significant
4758	NDUFC1	-1.01	7.31E-01	8.77E-01	944.55	not significant
4759	CROT	-1.01	7.85E-01	9.07E-01	603.94	not significant
4760	WDR55	-1.01	7.90E-01	9.09E-01	1197.80	not significant
4761	EIF3K	-1.01	7.75E-01	9.01E-01	5056.63	not significant
4762	GGH	-1.01	7.89E-01	9.09E-01	1408.40	not significant
4763	ZNF816	-1.01	7.72E-01	8.99E-01	449.87	not significant
4764	RNASEH2B-AS1	-1.01	2.07E-01	NA	9.72	not significant
4765	KLHL31	-1.01	2.58E-01	NA	11.86	not significant
4766	SLC7A7	-1.01	1.79E-01	NA	8.96	not significant
4767	SCRN1	-1.01	5.97E-01	NA	66.36	not significant
4768	HIST1H2AJ	-1.01	3.93E-01	NA	21.69	not significant
4769	TLR7	-1.01	3.06E-01	NA	14.77	not significant
4770	SLC27A3	-1.01	2.52E-01	NA	12.93	not significant
4771	TMPRSS13	-1.01	5.84E-01	NA	54.52	not significant
4772	VAMP8	-1.01	7.76E-01	9.01E-01	461.27	not significant
4773	FLJ42627	-1.01	6.70E-01	8.45E-01	123.07	not significant
4774	RHBDF2	-1.01	7.18E-01	8.70E-01	167.75	not significant
4775	MPI	-1.01	7.88E-01	9.09E-01	637.69	not significant
4776	TMCO6	-1.01	7.87E-01	9.08E-01	667.18	not significant
4777	ABI3	-1.01	7.95E-01	9.12E-01	1655.38	not significant
4778	NAA35	-1.01	7.88E-01	9.09E-01	1076.65	not significant
4779	DHFR	-1.01	7.83E-01	9.06E-01	2997.72	not significant
4780	STAT4	-1.01	7.88E-01	9.09E-01	1599.58	not significant
4781	CBX3	-1.01	7.58E-01	8.91E-01	13987.91	not significant
4782	POLR3E	-1.01	7.83E-01	9.06E-01	2204.81	not significant
4783	TRPM2	-1.01	7.94E-01	9.11E-01	1640.53	not significant
4784	INCA1	-1.01	3.67E-01	NA	18.84	not significant
4785	SPAG5-AS1	-1.01	2.88E-01	NA	14.02	not significant
4786	RAD21-AS1	-1.01	3.54E-01	NA	19.06	not significant
4787	BEND3	-1.01	3.22E-01	NA	15.26	not significant
4788	LOC100130691	-1.01	2.76E-01	NA	14.01	not significant
4789	TAPT1-AS1	-1.01	5.29E-01	NA	45.83	not significant
4790	ACOT11	-1.01	6.24E-01	NA	72.00	not significant
4791	CYFIP1	-1.01	6.85E-01	8.52E-01	155.31	not significant
4792	CAMKMT	-1.01	7.48E-01	8.86E-01	207.31	not significant
4793	SMIM15	-1.01	7.49E-01	8.86E-01	272.04	not significant
4794	ISOC2	-1.01	7.96E-01	9.12E-01	1660.44	not significant
4795	VPS28	-1.01	8.02E-01	9.15E-01	1080.13	not significant
4796	TRAPPC6B	-1.01	7.95E-01	9.12E-01	1324.77	not significant
4797	NUDT22	-1.01	7.90E-01	9.09E-01	773.10	not significant
4798	SSX2IP	-1.01	7.96E-01	9.12E-01	1230.06	not significant
4799	PRDM15	-1.01	7.88E-01	9.09E-01	619.55	not significant
4800	TM9SF2	-1.01	7.67E-01	8.96E-01	7094.03	not significant
4801	CHTOP	-1.01	9.58E-01	9.85E-01	3289.80	not significant
4802	CRYM-AS1	-1.01	3.69E-01	NA	18.62	not significant
4803	RAET1E	-1.01	4.98E-01	NA	32.81	not significant
4804	GPR89B	-1.01	2.36E-01	NA	10.28	not significant
4805	ZNF878	-1.01	5.41E-01	NA	41.34	not significant
4806	TNFAIP8L2	-1.01	4.94E-01	NA	34.40	not significant
4807	TNNT1	-1.01	6.31E-01	NA	67.71	not significant
4808	C2orf69	-1.01	7.95E-01	9.12E-01	752.85	not significant
4809	PSMB6	-1.01	7.97E-01	9.12E-01	3573.06	not significant
4810	MAGED1	-1.01	7.97E-01	9.12E-01	1046.97	not significant
4811	ASB1	-1.01	7.95E-01	9.12E-01	1223.09	not significant
4812	TMEM127	-1.01	7.96E-01	9.12E-01	1939.84	not significant
4813	NFYA	-1.01	7.68E-01	8.97E-01	4810.71	not significant
4814	PRKAR1A	-1.01	7.58E-01	8.91E-01	9341.71	not significant
4815	CTDSPL2	-1.01	7.91E-01	9.10E-01	3823.57	not significant
4816	ZMYM3	-1.01	8.98E-01	9.62E-01	2985.37	not significant
4817	IL2RA	-1.01	5.28E-01	NA	36.35	not significant
4818	KLHL41	-1.01	2.27E-01	NA	10.84	not significant
4819	ID1	-1.01	3.05E-01	NA	13.37	not significant
4820	FADS3	-1.01	6.49E-01	NA	80.25	not significant
4821	MBD5	-1.01	7.66E-01	8.96E-01	256.33	not significant
4822	PCBD1	-1.01	7.65E-01	8.95E-01	301.75	not significant
4823	GPR176	-1.01	7.41E-01	8.82E-01	194.89	not significant
4824	MED19	-1.01	7.89E-01	9.09E-01	530.20	not significant
4825	NR1D1	-1.01	7.91E-01	9.10E-01	497.58	not significant
4826	ARSK	-1.01	7.86E-01	9.08E-01	403.81	not significant
4827	ZNF766	-1.01	7.99E-01	9.13E-01	1026.66	not significant

4828	SRRM1	-1.01	7.67E-01	8.97E-01	5467.12	not significant
4829	PCDHGB3	-1.00	1.67E-01	NA	7.97	not significant
4830	IL13	-1.00	1.88E-01	NA	8.30	not significant
4831	PATL2	-1.00	2.23E-01	NA	9.49	not significant
4832	GRHL1	-1.00	5.23E-01	NA	39.28	not significant
4833	TINCR	-1.00	4.72E-01	NA	27.97	not significant
4834	LAMB2P1	-1.00	3.24E-01	NA	14.52	not significant
4835	TMEM200B	-1.00	3.40E-01	NA	15.88	not significant
4836	LRP1	-1.00	3.86E-01	NA	19.23	not significant
4837	LOC101926943	-1.00	3.52E-01	NA	19.73	not significant
4838	STARD4-AS1	-1.00	5.04E-01	NA	33.90	not significant
4839	MSANTD3	-1.00	7.42E-01	8.83E-01	188.59	not significant
4840	FLJ38122	-1.00	6.98E-01	8.59E-01	108.00	not significant
4841	GLI1	-1.00	5.68E-01	NA	47.23	not significant
4842	WDPCP	-1.00	7.27E-01	8.74E-01	164.08	not significant
4843	AJUBA	-1.00	7.85E-01	9.07E-01	367.62	not significant
4844	ELL	-1.00	8.01E-01	9.14E-01	1077.37	not significant
4845	LOC102723885	-1.00	1.77E-01	NA	8.60	not significant
4846	EPB41L4B	-1.00	3.38E-01	NA	15.71	not significant
4847	FAM71E1	-1.00	4.06E-01	NA	19.37	not significant
4848	MAML2	-1.00	5.08E-01	NA	30.18	not significant
4849	CIDEB	-1.00	3.48E-01	NA	15.17	not significant
4850	GPR135	-1.00	3.01E-01	NA	14.24	not significant
4851	FAM63A	-1.00	4.89E-01	NA	33.02	not significant
4852	PRR34-AS1	-1.00	7.33E-01	8.77E-01	120.47	not significant
4853	ABHD6	-1.00	7.68E-01	8.97E-01	255.92	not significant
4854	DSTYK	-1.00	7.60E-01	8.93E-01	231.40	not significant
4855	LOC101927151	-1.00	8.06E-01	9.17E-01	549.86	not significant
4856	CHCHD1	-1.00	8.06E-01	9.17E-01	1002.69	not significant
4857	SEC61G	-1.00	8.59E-01	9.43E-01	1792.16	not significant
4858	LAMTOR3	-1.00	8.05E-01	9.16E-01	1399.69	not significant
4859	CEP63	-1.00	8.07E-01	9.17E-01	1329.45	not significant
4860	RPL6	-1.00	7.94E-01	9.11E-01	16507.15	not significant
4861	PGGT1B	-1.00	8.05E-01	9.17E-01	803.18	not significant
4862	STAMBPL1	-1.00	8.18E-01	9.24E-01	1736.01	not significant
4863	USP33	-1.00	8.00E-01	9.14E-01	2229.52	not significant
4864	CHEK1	-1.00	7.79E-01	9.03E-01	5747.22	not significant
4865	FBXL19	-1.00	8.01E-01	9.14E-01	3632.33	not significant
4866	CANT1	-1.00	7.83E-01	9.06E-01	4954.35	not significant
4867	LOC341056	-1.00	4.19E-01	NA	19.51	not significant
4868	SDCBP2-AS1	-1.00	6.22E-01	NA	55.80	not significant
4869	RNU6-2	-1.00	3.39E-01	NA	14.03	not significant
4870	KLHL7-AS1	-1.00	5.26E-01	NA	34.37	not significant
4871	BPHL	-1.00	7.63E-01	8.94E-01	212.33	not significant
4872	MDN1	-1.00	7.78E-01	9.03E-01	5278.09	not significant
4873	CDC34	-1.00	8.08E-01	9.18E-01	1044.29	not significant
4874	FLOT2	-1.00	7.98E-01	9.13E-01	535.60	not significant
4875	MRPL37	-1.00	7.93E-01	9.11E-01	5316.42	not significant
4876	MCRS1	-1.00	7.96E-01	9.12E-01	3618.86	not significant
4877	RRAGA	-1.00	8.06E-01	9.17E-01	1114.91	not significant
4878	ZNF865	-1.00	8.06E-01	9.17E-01	755.82	not significant
4879	DHX36	-1.00	8.00E-01	9.14E-01	2685.37	not significant
4880	SLC9A7	-1.00	7.81E-01	9.05E-01	340.92	not significant
4881	FAM53B	-1.00	8.01E-01	9.14E-01	2165.88	not significant
4882	KIAA1551	-1.00	8.03E-01	9.15E-01	3430.67	not significant
4883	HSD11B1L	-1.00	4.82E-01	NA	25.64	not significant
4884	SLAMF8	-1.00	3.20E-01	NA	12.60	not significant
4885	BNIPL	-1.00	4.13E-01	NA	22.12	not significant
4886	HIF1A-AS2	-1.00	2.71E-01	NA	11.86	not significant
4887	ZNF157	-1.00	5.07E-01	NA	28.52	not significant
4888	DRICH1	-1.00	2.77E-01	NA	10.85	not significant
4889	PYGM	-1.00	5.69E-01	NA	51.21	not significant
4890	EFCAB12	-1.00	3.94E-01	NA	19.36	not significant
4891	CAMSAP2	-1.00	4.58E-01	NA	25.28	not significant
4892	NR5A1	-1.00	4.27E-01	NA	21.50	not significant
4893	PHLDA1	-1.00	6.62E-01	NA	71.20	not significant
4894	MIR497HG	-1.00	3.65E-01	NA	17.52	not significant
4895	ZNF597	-1.00	6.99E-01	8.59E-01	110.59	not significant
4896	LOC100507217	-1.00	8.01E-01	9.14E-01	673.38	not significant
4897	PPFIA3	-1.00	7.80E-01	9.04E-01	264.03	not significant
4898	CTNS	-1.00	8.00E-01	9.14E-01	661.82	not significant
4899	F11R	-1.00	8.00E-01	9.14E-01	443.96	not significant
4900	TRMT112	-1.00	8.10E-01	9.19E-01	3287.01	not significant
4901	METTL8	-1.00	8.10E-01	9.19E-01	874.82	not significant
4902	DNAJC21	-1.00	8.09E-01	9.18E-01	1927.71	not significant
4903	ZNF589	-1.00	8.02E-01	9.15E-01	681.19	not significant
4904	AP3M2	-1.00	8.09E-01	9.18E-01	1505.60	not significant
4905	FOXK2	-1.00	7.67E-01	8.97E-01	7265.76	not significant
4906	MMRN1	-1.00	2.77E-01	NA	10.31	not significant
4907	FOXN3-AS1	-1.00	5.10E-01	NA	30.83	not significant
4908	NPM2	-1.00	3.67E-01	NA	14.82	not significant
4909	TANC1	-1.00	2.84E-01	NA	11.65	not significant
4910	ARMCX3	-1.00	7.18E-01	8.70E-01	118.14	not significant
4911	MAP2K6	-1.00	8.07E-01	9.17E-01	466.32	not significant
4912	PPIE	-1.00	8.13E-01	9.21E-01	1588.15	not significant
4913	FAM83G	-1.00	7.63E-01	8.94E-01	206.89	not significant
4914	CLTB	-1.00	8.14E-01	9.21E-01	1336.18	not significant
4915	RPS6KA1	-1.00	7.82E-01	9.05E-01	4495.16	not significant

4916	CMIP	-1.00	7.97E-01	9.12E-01	3395.47	not significant
4917	ATP1A1	-1.00	7.76E-01	9.02E-01	24640.30	not significant
4918	ATP1B2	-1.00	2.36E-01	NA	9.04	not significant
4919	MPP7	-1.00	4.89E-01	NA	24.63	not significant
4920	PRSS57	-1.00	5.68E-01	NA	39.69	not significant
4921	ARHGEF11	-1.00	6.49E-01	NA	66.41	not significant
4922	CAPS2	-1.00	7.03E-01	8.59E-01	101.92	not significant
4923	ARPP21	-1.00	7.98E-01	9.12E-01	352.08	not significant
4924	PDE1B	-1.00	7.98E-01	9.13E-01	461.34	not significant
4925	FTSJ1	-1.00	8.14E-01	9.22E-01	760.95	not significant
4926	TAF1A	-1.00	8.10E-01	9.19E-01	641.50	not significant
4927	CES2	-1.00	8.17E-01	9.24E-01	1347.60	not significant
4928	FRMD8	-1.00	8.13E-01	9.21E-01	1742.44	not significant
4929	OSBP	-1.00	8.05E-01	9.16E-01	3340.93	not significant
4930	SMKR1	-1.00	4.70E-01	NA	21.84	not significant
4931	NCR3	-1.00	3.52E-01	NA	13.65	not significant
4932	AP1S3	-1.00	4.15E-01	NA	18.96	not significant
4933	C15orf54	-1.00	4.44E-01	NA	19.24	not significant
4934	SOCS3	-1.00	6.48E-01	NA	57.16	not significant
4935	KLF5	-1.00	7.56E-01	8.90E-01	154.93	not significant
4936	MRPS33	-1.00	8.20E-01	9.25E-01	1303.84	not significant
4937	TFE3	-1.00	7.77E-01	9.02E-01	213.92	not significant
4938	SAAL1	-1.00	8.17E-01	9.23E-01	1699.70	not significant
4939	GRK6	-1.00	8.41E-01	9.32E-01	3448.39	not significant
4940	MAP1LC3B	-1.00	8.14E-01	9.22E-01	2018.27	not significant
4941	FAM76A	-1.00	8.32E-01	9.29E-01	640.59	not significant
4942	LAX1	-1.00	8.20E-01	9.25E-01	1142.83	not significant
4943	GMCL1	-1.00	8.14E-01	9.21E-01	1886.36	not significant
4944	ARHGAP12	-1.00	8.06E-01	9.17E-01	405.34	not significant
4945	RANBP9	-1.00	8.25E-01	9.27E-01	3055.93	not significant
4946	NSUN4	-1.00	8.22E-01	9.26E-01	1602.43	not significant
4947	MAML1	-1.00	8.13E-01	9.21E-01	3376.86	not significant
4948	PLA2G4A	-1.00	2.98E-01	NA	11.25	not significant
4949	SYNC	-1.00	3.67E-01	NA	75.26	not significant
4950	NPB	-1.00	2.80E-01	NA	9.66	not significant
4951	LHFPL1	-1.00	5.79E-01	NA	35.28	not significant
4952	KMT2A	-1.00	7.33E-01	8.78E-01	678.12	not significant
4953	KATNAL2	-1.00	6.82E-01	NA	73.73	not significant
4954	NDUFV3	-1.00	7.89E-01	9.09E-01	336.96	not significant
4955	TNRC6B	-1.00	7.75E-01	9.01E-01	1921.88	not significant
4956	FAM173B	-1.00	8.14E-01	9.22E-01	456.63	not significant
4957	SLC35E3	-1.00	8.00E-01	9.14E-01	322.30	not significant
4958	FAM86DP	-1.00	7.74E-01	9.00E-01	258.72	not significant
4959	NDUFB8	-1.00	8.05E-01	9.16E-01	4672.42	not significant
4960	RTFDC1	-1.00	8.12E-01	9.21E-01	2935.69	not significant
4961	HADHA	-1.00	7.87E-01	9.08E-01	6468.43	not significant
4962	FLYWCH1	-1.00	8.22E-01	9.26E-01	1078.18	not significant
4963	GTF2IRD1P1	-1.00	3.05E-01	NA	11.32	not significant
4964	TENC1	-1.00	3.88E-01	NA	14.74	not significant
4965	PRKXP1	-1.00	6.18E-01	8.14E-01	249.63	not significant
4966	GPR158	-1.00	5.41E-01	NA	28.96	not significant
4967	GRAMD2	-1.00	3.08E-01	NA	10.34	not significant
4968	CASS4	-1.00	6.25E-01	NA	49.24	not significant
4969	RAB38	-1.00	6.53E-01	NA	56.45	not significant
4970	ACOT2	-1.00	7.84E-01	9.06E-01	213.76	not significant
4971	NLGN4Y	-1.00	7.94E-01	9.11E-01	298.86	not significant
4972	RRP8	-1.00	8.24E-01	9.27E-01	909.36	not significant
4973	CDK11B	-1.00	8.23E-01	9.27E-01	847.68	not significant
4974	CACNB3	-1.00	8.24E-01	9.27E-01	1128.82	not significant
4975	UBE2A	-1.00	8.07E-01	9.17E-01	4361.75	not significant
4976	ELMOD3	-1.00	8.15E-01	9.22E-01	528.43	not significant
4977	RAB18	-1.00	8.18E-01	9.24E-01	2023.97	not significant
4978	TNKS1BP1	-1.00	8.23E-01	9.26E-01	581.47	not significant
4979	ELF2	-1.00	8.24E-01	9.27E-01	1270.97	not significant
4980	SIGLEC8	-1.00	3.35E-01	NA	11.28	not significant
4981	SCARNA9	-1.00	3.91E-01	NA	13.89	not significant
4982	CATSPER3	-1.00	4.52E-01	NA	18.28	not significant
4983	CCDC74B	-1.00	5.39E-01	NA	28.84	not significant
4984	PTAFR	-1.00	3.94E-01	NA	14.47	not significant
4985	LPAR4	-1.00	5.45E-01	NA	30.71	not significant
4986	LRRC23	-1.00	5.87E-01	NA	36.09	not significant
4987	CDC42EP2	-1.00	5.95E-01	NA	38.47	not significant
4988	ATG10	-1.00	8.07E-01	9.17E-01	353.02	not significant
4989	SERGEF	-1.00	8.19E-01	9.24E-01	394.68	not significant
4990	GLRX	-1.00	8.26E-01	9.28E-01	1219.17	not significant
4991	MTM1	-1.00	7.87E-01	9.08E-01	225.31	not significant
4992	ENTPD5	-1.00	7.59E-01	8.92E-01	168.48	not significant
4993	ISG15	-1.00	8.26E-01	9.28E-01	1256.63	not significant
4994	SUV39H1	-1.00	7.85E-01	9.07E-01	231.56	not significant
4995	FAM188A	-1.00	8.19E-01	9.24E-01	531.96	not significant
4996	TRIM11	-1.00	8.26E-01	9.28E-01	1493.82	not significant
4997	FGFRL1	-1.00	8.16E-01	9.23E-01	525.13	not significant
4998	TBC1D24	-1.00	8.27E-01	9.28E-01	1005.34	not significant
4999	INPP4B	-1.00	8.18E-01	9.24E-01	582.10	not significant
5000	RBM33	-1.00	8.25E-01	9.27E-01	3902.30	not significant
5001	MAPK6	-1.00	8.13E-01	9.21E-01	3909.96	not significant
5002	ITLN1	-1.00	4.24E-01	NA	16.13	not significant
5003	VAV2	-1.00	3.28E-01	NA	10.91	not significant

5004	BTN1A1	-1.00	4.78E-01	NA	20.52	not significant
5005	LOC100507437	-1.00	2.41E-01	NA	7.80	not significant
5006	RAP1GAP2	-1.00	6.48E-01	NA	52.00	not significant
5007	HSPA1A	-1.00	4.80E-01	NA	20.65	not significant
5008	RUSC1-AS1	-1.00	4.64E-01	NA	22.49	not significant
5009	C1orf74	-1.00	7.65E-01	8.95E-01	164.26	not significant
5010	WNK4	-1.00	7.22E-01	NA	91.10	not significant
5011	SNAPC5	-1.00	7.89E-01	9.09E-01	231.74	not significant
5012	TXNDC9	-1.00	8.28E-01	9.28E-01	869.28	not significant
5013	TDRKH	-1.00	8.27E-01	9.28E-01	602.47	not significant
5014	MED20	-1.00	8.31E-01	9.29E-01	1353.25	not significant
5015	RBM18	-1.00	8.30E-01	9.29E-01	1142.80	not significant
5016	YTHDC1	-1.00	8.31E-01	9.29E-01	1012.53	not significant
5017	ZNF607	-1.00	8.20E-01	9.25E-01	549.15	not significant
5018	BBS7	-1.00	8.30E-01	9.29E-01	764.57	not significant
5019	NUB1	-1.00	8.12E-01	9.21E-01	4103.01	not significant
5020	TRIP11	-1.00	8.30E-01	9.29E-01	1241.68	not significant
5021	NSG1	-1.00	3.60E-01	NA	14.22	not significant
5022	LOC100507053	-1.00	4.47E-01	NA	17.09	not significant
5023	KIAA1257	-1.00	2.77E-01	NA	9.09	not significant
5024	NTNG2	-1.00	5.02E-01	NA	21.81	not significant
5025	ACTRT3	-1.00	3.05E-01	NA	9.57	not significant
5026	TINAGL1	-1.00	5.00E-01	NA	22.11	not significant
5027	OR2AG2	-1.00	3.95E-01	NA	13.63	not significant
5028	GNA11	-1.00	5.50E-01	NA	28.56	not significant
5029	CXorf40A	-1.00	6.53E-01	NA	50.79	not significant
5030	DNAH10	-1.00	6.38E-01	NA	47.01	not significant
5031	C20orf203	-1.00	6.42E-01	NA	47.97	not significant
5032	ARL3	-1.00	8.26E-01	9.28E-01	401.61	not significant
5033	GMPPA	-1.00	8.31E-01	9.29E-01	877.89	not significant
5034	ZNF639	-1.00	8.29E-01	9.28E-01	2024.51	not significant
5035	LRRC40	-1.00	8.30E-01	9.29E-01	1657.29	not significant
5036	TIAL1	-1.00	8.02E-01	9.14E-01	5880.44	not significant
5037	GPATCH11	-1.00	8.34E-01	9.30E-01	1666.86	not significant
5038	DIAPH3	-1.00	8.29E-01	9.28E-01	1667.29	not significant
5039	PRR34	-1.00	3.61E-01	NA	11.43	not significant
5040	NDRG2	-1.00	4.53E-01	NA	17.24	not significant
5041	RAPGEF4	-1.00	4.59E-01	NA	17.93	not significant
5042	LPAR1	-1.00	4.97E-01	NA	24.77	not significant
5043	TGFB3	-1.00	5.71E-01	NA	31.21	not significant
5044	TLR6	-1.00	4.45E-01	NA	16.56	not significant
5045	LOC283922	-1.00	7.42E-01	8.83E-01	118.42	not significant
5046	TSPAN17	-1.00	8.35E-01	9.31E-01	1058.42	not significant
5047	UCKL1	-1.00	8.36E-01	9.31E-01	1093.98	not significant
5048	SETDB2	-1.00	8.30E-01	9.29E-01	751.48	not significant
5049	LRRC37BP1	-1.00	8.34E-01	9.30E-01	602.01	not significant
5050	TDP1	-1.00	8.31E-01	9.29E-01	2260.51	not significant
5051	FBXW11	-1.00	8.35E-01	9.31E-01	1498.43	not significant
5052	ACO2	-1.00	8.03E-01	9.15E-01	6303.56	not significant
5053	DDX31	-1.00	8.35E-01	9.31E-01	963.53	not significant
5054	SCNM1	-1.00	4.08E-01	NA	13.49	not significant
5055	CHRNA6	-1.00	7.51E-01	8.88E-01	115.44	not significant
5056	ITIH4	-1.00	7.67E-01	8.96E-01	133.02	not significant
5057	C11orf45	-1.00	8.05E-01	9.16E-01	284.92	not significant
5058	YES1	-1.00	8.38E-01	9.31E-01	951.16	not significant
5059	CNOT4	-1.00	8.36E-01	9.31E-01	998.76	not significant
5060	DCUN1D4	-1.00	8.34E-01	9.31E-01	730.38	not significant
5061	ATP6V1A	-1.00	8.30E-01	9.29E-01	2254.78	not significant
5062	ADAMTS17	-1.00	4.48E-01	NA	15.47	not significant
5063	LOC100129697	-1.00	5.67E-01	NA	27.62	not significant
5064	LRRIQ4	-1.00	3.61E-01	NA	11.22	not significant
5065	HIST1H2AE	-1.00	5.94E-01	NA	34.11	not significant
5066	HSPA6	-1.00	4.04E-01	NA	13.69	not significant
5067	LINC01355	-1.00	7.12E-01	NA	76.35	not significant
5068	OTUD7B	-1.00	6.64E-01	NA	47.26	not significant
5069	HAVCR2	-1.00	6.33E-01	NA	40.10	not significant
5070	CNIH3	-1.00	6.17E-01	NA	37.58	not significant
5071	C4orf48	-1.00	7.67E-01	8.96E-01	624.69	not significant
5072	NEK8	-1.00	7.22E-01	NA	79.75	not significant
5073	GTF2H5	-1.00	8.28E-01	9.28E-01	469.91	not significant
5074	TLE4	-1.00	7.97E-01	9.12E-01	189.07	not significant
5075	SLCO3A1	-1.00	7.50E-01	8.86E-01	110.01	not significant
5076	ZNF831	-1.00	7.73E-01	9.00E-01	149.03	not significant
5077	SAV1	-1.00	8.34E-01	9.31E-01	556.61	not significant
5078	GDPGP1	-1.00	6.24E-01	NA	40.70	not significant
5079	TRRAP	-1.00	7.65E-01	8.95E-01	8031.12	not significant
5080	FOXO4	-1.00	8.25E-01	9.27E-01	358.95	not significant
5081	ZNF276	-1.00	8.34E-01	9.30E-01	2362.77	not significant
5082	ACVR1B	-1.00	8.36E-01	9.31E-01	1916.77	not significant
5083	ZCCHC14	-1.00	8.35E-01	9.31E-01	637.76	not significant
5084	USP13	-1.00	8.41E-01	9.32E-01	1334.46	not significant
5085	MAPT	-1.00	4.58E-01	NA	17.33	not significant
5086	ADAM8	-1.00	6.50E-01	NA	50.69	not significant
5087	TRAM2-AS1	-1.00	6.82E-01	NA	54.70	not significant
5088	FTH1P3	-1.00	6.29E-01	NA	39.35	not significant
5089	CHRNA10	-1.00	5.88E-01	NA	35.08	not significant
5090	FBLN7	-1.00	6.75E-01	NA	50.17	not significant
5091	C11orf1	-1.00	7.52E-01	8.88E-01	105.81	not significant

5092	HYLS1	-1.00	8.00E-01	9.14E-01	209.41	not significant
5093	GPR19	-1.00	8.03E-01	9.15E-01	185.89	not significant
5094	PPM1L	-1.00	7.64E-01	8.95E-01	135.00	not significant
5095	FAM219A	-1.00	8.42E-01	9.33E-01	717.59	not significant
5096	C1QTNF3	-1.00	7.93E-01	9.11E-01	178.43	not significant
5097	MAP2K3	-1.00	8.40E-01	9.32E-01	1547.33	not significant
5098	RNF157	-1.00	8.39E-01	9.31E-01	2479.64	not significant
5099	RAB11FIP4	-1.00	5.38E-01	NA	22.91	not significant
5100	ELK3	-1.00	5.44E-01	NA	23.26	not significant
5101	STX1A	-1.00	3.83E-01	NA	10.68	not significant
5102	NUDT13	-1.00	5.03E-01	NA	17.72	not significant
5103	BCL6B	-1.00	4.80E-01	NA	16.74	not significant
5104	SLC6A19	-1.00	5.73E-01	NA	26.42	not significant
5105	APITD1	-1.00	7.79E-01	9.03E-01	132.13	not significant
5106	TRIP6	-1.00	6.47E-01	NA	41.38	not significant
5107	ZNF737	-1.00	6.60E-01	NA	47.74	not significant
5108	PTS	-1.00	8.42E-01	9.32E-01	662.66	not significant
5109	SMARCAD1	-1.00	8.31E-01	9.29E-01	4308.74	not significant
5110	ZBTB21	-1.00	8.70E-01	9.48E-01	1273.67	not significant
5111	WIZ	-1.00	8.94E-01	9.60E-01	2538.72	not significant
5112	ECI1	-1.00	5.42E-01	NA	24.03	not significant
5113	HIST1H2AC	-1.00	4.62E-01	NA	14.36	not significant
5114	FAM135B	-1.00	4.63E-01	NA	14.76	not significant
5115	HIST1H4I	-1.00	5.17E-01	NA	18.25	not significant
5116	KLHDC1	-1.00	5.86E-01	NA	26.93	not significant
5117	ACTR3C	-1.00	5.61E-01	NA	23.34	not significant
5118	ALMS1-IT1	-1.00	6.23E-01	NA	34.14	not significant
5119	SAMHD1	-1.00	5.66E-01	NA	25.12	not significant
5120	ETV5	-1.00	7.39E-01	NA	88.38	not significant
5121	SYNPO2	-1.00	6.45E-01	NA	37.55	not significant
5122	RHPN1-AS1	-1.00	7.77E-01	9.02E-01	125.00	not significant
5123	RNPC3	-1.00	8.35E-01	9.31E-01	356.10	not significant
5124	DANCR	-1.00	8.49E-01	9.36E-01	1961.37	not significant
5125	DNAJC16	-1.00	8.47E-01	9.36E-01	864.15	not significant
5126	ZNF354C	-1.00	8.38E-01	9.31E-01	431.80	not significant
5127	RASA1	-1.00	8.48E-01	9.36E-01	712.06	not significant
5128	JAK2	-1.00	8.48E-01	9.36E-01	911.18	not significant
5129	CMPK1	-1.00	8.28E-01	9.28E-01	5075.50	not significant
5130	TMEM181	-1.00	8.48E-01	9.36E-01	1775.31	not significant
5131	ANAPC2	-1.00	8.50E-01	9.37E-01	1095.71	not significant
5132	NIM1K	-1.00	3.51E-01	NA	9.65	not significant
5133	LOC100129534	-1.00	3.96E-01	NA	11.79	not significant
5134	NLRP11	-1.00	3.76E-01	NA	10.12	not significant
5135	MYH7B	-1.00	4.10E-01	NA	11.22	not significant
5136	TPH1	-1.00	3.81E-01	NA	9.85	not significant
5137	SAMD12	-1.00	6.87E-01	NA	53.29	not significant
5138	CHN1	-1.00	6.38E-01	NA	41.51	not significant
5139	NMNAT3	-1.00	3.65E-01	NA	10.14	not significant
5140	GHRLOS	-1.00	7.14E-01	NA	59.70	not significant
5141	SCOC-AS1	-1.00	6.41E-01	NA	37.74	not significant
5142	WDR17	-1.00	7.91E-01	9.10E-01	145.23	not significant
5143	DNAJC17	-1.00	8.33E-01	9.30E-01	349.40	not significant
5144	DAXX	-1.00	8.45E-01	9.35E-01	624.52	not significant
5145	SPC25	-1.00	8.51E-01	9.37E-01	755.92	not significant
5146	C9orf69	-1.00	8.49E-01	9.36E-01	1870.82	not significant
5147	C12orf75	-1.00	8.27E-01	9.28E-01	4773.48	not significant
5148	CDKN1A	-1.00	8.49E-01	9.37E-01	1679.85	not significant
5149	H2AFV	-1.00	8.22E-01	9.26E-01	8688.26	not significant
5150	TAB3	-1.00	8.50E-01	9.37E-01	1677.34	not significant
5151	LATS2	-1.00	5.73E-01	NA	23.09	not significant
5152	GATA3-AS1	-1.00	4.92E-01	NA	16.05	not significant
5153	DSCAML1	-1.00	5.37E-01	NA	20.89	not significant
5154	LOC100506124	-1.00	6.10E-01	NA	27.86	not significant
5155	LOC644961	-1.00	7.23E-01	NA	61.73	not significant
5156	AURKAPS1	-1.00	5.49E-01	NA	22.97	not significant
5157	PDCL3P4	-1.00	6.21E-01	NA	31.60	not significant
5158	BVES	-1.00	7.02E-01	NA	56.14	not significant
5159	LINC01120	-1.00	8.24E-01	9.27E-01	277.40	not significant
5160	RAD54L2	-1.00	8.01E-01	9.14E-01	986.14	not significant
5161	DKFZP434I0714	-1.00	8.20E-01	9.25E-01	211.18	not significant
5162	LOC728613	-1.00	7.69E-01	8.97E-01	100.73	not significant
5163	PDLIM7	-1.00	8.28E-01	9.28E-01	307.16	not significant
5164	MAP3K10	-1.00	8.45E-01	9.35E-01	537.02	not significant
5165	TANC2	-1.00	8.16E-01	9.22E-01	297.01	not significant
5166	METTL6	-1.00	8.54E-01	9.40E-01	760.37	not significant
5167	SRP9	-1.00	8.40E-01	9.32E-01	6972.48	not significant
5168	LRPAP1	-1.00	8.44E-01	9.35E-01	2597.92	not significant
5169	FAM102A	-1.00	8.53E-01	9.39E-01	1111.57	not significant
5170	RANBP3	-1.00	8.45E-01	9.35E-01	2780.23	not significant
5171	PEAK1	-1.00	8.53E-01	9.40E-01	1049.45	not significant
5172	ITSN2	-1.00	8.53E-01	9.39E-01	2098.46	not significant
5173	TMPO	-1.00	8.20E-01	9.25E-01	31912.30	not significant
5174	WDR59	-1.00	8.49E-01	9.36E-01	2104.77	not significant
5175	GAL3ST4	-1.00	8.40E-01	9.32E-01	320.31	not significant
5176	ZACN	-1.00	3.41E-01	NA	34.99	not significant
5177	CACTIN-AS1	-1.00	4.93E-01	NA	15.67	not significant
5178	IL17D	-1.00	5.09E-01	NA	16.92	not significant
5179	OSCP1	-1.00	6.40E-01	NA	33.89	not significant

5180	MT1HL1	-1.00	5.31E-01	NA	17.36	not significant
5181	SCARNA17	-1.00	6.47E-01	NA	33.61	not significant
5182	ZNRD1-AS1	-1.00	4.98E-01	NA	16.19	not significant
5183	RBKS	-1.00	7.60E-01	NA	88.12	not significant
5184	CCND2	-1.00	7.09E-01	NA	55.37	not significant
5185	DNM3	-1.00	6.37E-01	NA	31.62	not significant
5186	HLF	-1.00	6.74E-01	NA	39.26	not significant
5187	GLB1L3	-1.00	6.06E-01	NA	26.37	not significant
5188	PMFBP1	-1.00	6.94E-01	NA	51.62	not significant
5189	CBWD5	-1.00	6.78E-01	NA	40.52	not significant
5190	GEMIN7	-1.00	8.48E-01	9.36E-01	506.51	not significant
5191	LSM3	-1.00	8.58E-01	9.42E-01	2557.91	not significant
5192	ZNF439	-1.00	8.37E-01	9.31E-01	327.77	not significant
5193	MANBAL	-1.00	8.58E-01	9.43E-01	547.86	not significant
5194	ERMARD	-1.00	8.35E-01	9.31E-01	378.22	not significant
5195	GPX7	-1.00	8.56E-01	9.41E-01	1010.37	not significant
5196	MLXIP	-1.00	8.56E-01	9.42E-01	4294.65	not significant
5197	OVGP1	-1.00	6.66E-01	NA	41.71	not significant
5198	TRIM67	-1.00	4.67E-01	NA	13.01	not significant
5199	DMBT1	-1.00	4.83E-01	NA	14.44	not significant
5200	GPR97	-1.00	5.74E-01	NA	21.79	not significant
5201	FLG-AS1	-1.00	4.46E-01	NA	12.42	not significant
5202	EDA2R	-1.00	5.90E-01	NA	23.88	not significant
5203	CIRBP-AS1	-1.00	5.53E-01	NA	20.80	not significant
5204	IL4	-1.00	7.31E-01	NA	64.32	not significant
5205	LOC100499484	-1.00	5.50E-01	NA	18.94	not significant
5206	PPIL3	-1.00	8.60E-01	9.43E-01	1125.89	not significant
5207	MAP4K3	-1.00	8.58E-01	9.43E-01	751.87	not significant
5208	ATG4D	-1.00	8.60E-01	9.43E-01	1399.27	not significant
5209	OBFC1	-1.00	8.60E-01	9.43E-01	1222.32	not significant
5210	JOSD1	-1.00	8.53E-01	9.39E-01	2279.40	not significant
5211	TENM1	-1.00	8.57E-01	9.42E-01	607.94	not significant
5212	PLCH2	-1.00	5.25E-01	NA	16.44	not significant
5213	DIP2C	-1.00	4.52E-01	NA	12.74	not significant
5214	KCNQ1OT1	-1.00	5.30E-01	NA	18.23	not significant
5215	LOC730202	-1.00	5.62E-01	NA	19.62	not significant
5216	PAIP2B	-1.00	6.03E-01	NA	24.89	not significant
5217	GUSBP4	-1.00	8.19E-01	9.24E-01	203.65	not significant
5218	CEP83-AS1	-1.00	6.25E-01	NA	28.10	not significant
5219	TTC28-AS1	-1.00	8.53E-01	9.39E-01	639.14	not significant
5220	COMMD7	-1.00	8.61E-01	9.43E-01	2468.87	not significant
5221	TOMM20	-1.00	8.35E-01	9.31E-01	6724.56	not significant
5222	DDX23	-1.00	8.24E-01	9.27E-01	10580.70	not significant
5223	PHB2	-1.00	8.97E-01	9.61E-01	5452.08	not significant
5224	GRIK5	-1.00	4.66E-01	NA	11.79	not significant
5225	RPS4Y2	-1.00	4.99E-01	NA	13.96	not significant
5226	ANXA1	-1.00	8.11E-01	9.20E-01	162.05	not significant
5227	DRAM1	-1.00	7.22E-01	NA	55.22	not significant
5228	SCN2A	-1.00	7.00E-01	NA	47.34	not significant
5229	SIRPG	-1.00	8.00E-01	9.14E-01	127.52	not significant
5230	PHYH	-1.00	8.28E-01	9.28E-01	207.04	not significant
5231	SLC43A2	-1.00	8.32E-01	9.29E-01	219.48	not significant
5232	CENPBD1	-1.00	8.42E-01	9.33E-01	269.60	not significant
5233	PGAP2	-1.00	8.65E-01	9.45E-01	910.20	not significant
5234	CHRNA5	-1.00	8.62E-01	9.44E-01	659.70	not significant
5235	ASB14	-1.00	5.05E-01	NA	15.49	not significant
5236	LOC101060498	-1.00	4.08E-01	NA	10.05	not significant
5237	RAET1E-AS1	-1.00	4.82E-01	NA	12.78	not significant
5238	FRMPD2	-1.00	5.56E-01	NA	19.25	not significant
5239	CLDND2	-1.00	5.66E-01	NA	19.20	not significant
5240	POMK	-1.00	8.29E-01	9.29E-01	196.88	not significant
5241	IRS1	-1.00	8.74E-01	9.50E-01	261.85	not significant
5242	UBE2T	-1.00	8.65E-01	9.45E-01	2325.18	not significant
5243	HECTD1	-1.00	8.74E-01	9.50E-01	3249.61	not significant
5244	PFN1	-1.00	8.59E-01	9.43E-01	50077.37	not significant
5245	RHOF	-1.00	8.61E-01	9.43E-01	2490.68	not significant
5246	RHBDL1	-1.00	8.26E-01	9.28E-01	177.10	not significant
5247	POGK	-1.00	8.56E-01	9.42E-01	3840.41	not significant
5248	RAD17	-1.00	8.66E-01	9.45E-01	902.96	not significant
5249	MTA1	-1.00	8.63E-01	9.44E-01	2153.30	not significant
5250	ATN1	-1.00	8.60E-01	9.43E-01	409.48	not significant
5251	ENTPD1	-1.00	3.35E-01	NA	30.10	not significant
5252	UXT-AS1	-1.00	5.07E-01	NA	13.38	not significant
5253	PRKCZ	-1.00	4.83E-01	NA	14.20	not significant
5254	C22orf24	-1.00	6.53E-01	NA	29.22	not significant
5255	DHRS2	-1.00	6.36E-01	NA	26.56	not significant
5256	XYLT1	-1.00	5.45E-01	NA	15.60	not significant
5257	TCAP	-1.00	6.70E-01	NA	32.43	not significant
5258	JAKMIP3	-1.00	7.61E-01	NA	68.16	not significant
5259	XRCC6BP1	-1.00	8.38E-01	9.31E-01	219.12	not significant
5260	CCNT2-AS1	-1.00	7.90E-01	NA	94.85	not significant
5261	ZNF749	-1.00	8.63E-01	9.44E-01	521.94	not significant
5262	PHTF2	-1.00	8.71E-01	9.49E-01	1592.48	not significant
5263	RALGPS1	-1.00	8.69E-01	9.47E-01	797.05	not significant
5264	PURB	-1.00	8.69E-01	9.48E-01	5010.03	not significant
5265	SNX4	-1.00	8.80E-01	9.53E-01	1616.40	not significant
5266	PAGE5	-1.00	6.80E-01	NA	31.96	not significant
5267	TMEM72	-1.00	7.51E-01	NA	36.18	not significant

5268	KCNIP2	-1.00	6.40E-01	NA	27.02	not significant
5269	LINC00861	-1.00	8.25E-01	9.27E-01	154.47	not significant
5270	PGBD4	-1.00	8.24E-01	9.27E-01	148.02	not significant
5271	ICAM1	-1.00	8.29E-01	9.28E-01	165.51	not significant
5272	TCEA2	-1.00	8.60E-01	9.43E-01	331.34	not significant
5273	CD1D	-1.00	8.66E-01	9.46E-01	368.65	not significant
5274	ASXL2	-1.00	8.41E-01	9.32E-01	2220.19	not significant
5275	FBXO44	-1.00	8.75E-01	9.52E-01	1193.94	not significant
5276	FIZ1	-1.00	8.70E-01	9.48E-01	827.05	not significant
5277	SGTB	-1.00	8.72E-01	9.49E-01	614.27	not significant
5278	PAXIP1	-1.00	8.68E-01	9.47E-01	2819.65	not significant
5279	RBM8A	-1.00	9.82E-01	9.96E-01	2085.90	not significant
5280	KIAA1033	-1.00	9.00E-01	9.62E-01	2890.68	not significant
5281	MUC1	-1.00	5.42E-01	NA	13.80	not significant
5282	LOC100506606	-1.00	6.63E-01	NA	26.71	not significant
5283	ZNF197-AS1	-1.00	4.92E-01	NA	11.28	not significant
5284	KIF26B	-1.00	5.91E-01	NA	20.03	not significant
5285	CRTAM	-1.00	5.21E-01	NA	13.36	not significant
5286	TLCD1	-1.00	4.68E-01	NA	10.19	not significant
5287	HORMAD2	-1.00	6.08E-01	NA	20.04	not significant
5288	UBAP1L	-1.00	6.27E-01	NA	22.14	not significant
5289	TMEM8B	-1.00	8.36E-01	9.31E-01	183.47	not significant
5290	GLB1L2	-1.00	8.74E-01	9.51E-01	168.94	not significant
5291	TTC13	-1.00	8.70E-01	9.48E-01	636.41	not significant
5292	TMEM79	-1.00	8.53E-01	9.40E-01	260.29	not significant
5293	MRPL9	-1.00	8.72E-01	9.50E-01	2906.07	not significant
5294	WDR53	-1.00	8.76E-01	9.52E-01	482.55	not significant
5295	RBM19	-1.00	8.65E-01	9.45E-01	3133.29	not significant
5296	MKL2	-1.00	8.76E-01	9.52E-01	1626.46	not significant
5297	GUSBP2	-1.00	6.18E-01	NA	21.38	not significant
5298	CCDC116	-1.00	6.64E-01	NA	26.57	not significant
5299	C2orf27A	-1.00	7.60E-01	NA	74.82	not significant
5300	ARHGAP39	-1.00	5.81E-01	NA	17.97	not significant
5301	ACTA2	-1.00	6.19E-01	NA	19.83	not significant
5302	MGC16142	-1.00	6.86E-01	NA	33.14	not significant
5303	RIN1	-1.00	6.93E-01	NA	32.09	not significant
5304	DNAL4	-1.00	7.92E-01	9.11E-01	330.43	not significant
5305	LYG1	-1.00	7.51E-01	NA	55.10	not significant
5306	ITFG3	-1.00	8.78E-01	9.52E-01	775.92	not significant
5307	ZNF331	-1.00	8.68E-01	9.47E-01	1034.99	not significant
5308	TMEM143	-1.00	8.59E-01	9.43E-01	257.11	not significant
5309	FLII	-1.00	8.56E-01	9.42E-01	5846.44	not significant
5310	FRMD4A	-1.00	8.56E-01	9.42E-01	1034.30	not significant
5311	POLQ	-1.00	8.79E-01	9.52E-01	2247.14	not significant
5312	LIMA1	-1.00	8.78E-01	9.52E-01	1284.20	not significant
5313	MEGF9	-1.00	8.79E-01	9.52E-01	1722.14	not significant
5314	GALNT10	-1.00	8.80E-01	9.53E-01	1408.83	not significant
5315	LRRC63	-1.00	6.61E-01	NA	25.47	not significant
5316	LOC100507634	-1.00	4.59E-01	NA	9.86	not significant
5317	MYL4	-1.00	5.21E-01	NA	12.86	not significant
5318	PLEKHH1	-1.00	5.60E-01	NA	13.93	not significant
5319	PROCA1	-1.00	7.98E-01	NA	84.64	not significant
5320	NHLRC2	-1.00	8.41E-01	9.32E-01	830.75	not significant
5321	MED7	-1.00	8.68E-01	9.47E-01	322.47	not significant
5322	ZNF709	-1.00	8.53E-01	9.40E-01	221.16	not significant
5323	ZNF557	-1.00	8.83E-01	9.55E-01	588.07	not significant
5324	CLHC1	-1.00	8.58E-01	9.42E-01	240.51	not significant
5325	ACAD10	-1.00	8.77E-01	9.52E-01	700.26	not significant
5326	PRPS1	-1.00	8.77E-01	9.52E-01	3043.64	not significant
5327	CCNH	-1.00	8.79E-01	9.52E-01	864.55	not significant
5328	TCEA3	-1.00	6.72E-01	NA	25.31	not significant
5329	TNFSF12	-1.00	6.14E-01	NA	18.07	not significant
5330	RNF138P1	-1.00	5.52E-01	NA	13.30	not significant
5331	HIST1H2BF	-1.00	6.62E-01	NA	26.11	not significant
5332	F3	-1.00	6.00E-01	NA	16.66	not significant
5333	LOC100129931	-1.00	5.96E-01	NA	23.74	not significant
5334	PTPN12	-1.00	6.95E-01	NA	28.55	not significant
5335	POLN	-1.00	6.39E-01	NA	22.19	not significant
5336	MUSTN1	-1.00	5.80E-01	NA	15.86	not significant
5337	SAMD3	-1.00	5.54E-01	NA	13.58	not significant
5338	ZNF232	-1.00	8.83E-01	9.55E-01	758.11	not significant
5339	MFSD2A	-1.00	8.60E-01	9.43E-01	282.30	not significant
5340	RPS11	-1.00	8.91E-01	9.59E-01	22773.36	not significant
5341	FAM122A	-1.00	8.74E-01	9.51E-01	679.03	not significant
5342	BTBD2	-1.00	8.76E-01	9.52E-01	3593.14	not significant
5343	GNAS	-1.00	8.59E-01	9.43E-01	20214.91	not significant
5344	SEC61A1	-1.00	8.64E-01	9.45E-01	13710.07	not significant
5345	SRP72	-1.00	8.57E-01	9.42E-01	7465.19	not significant
5346	PDZD8	-1.00	8.85E-01	9.56E-01	1256.11	not significant
5347	SLC4A5	-1.00	6.36E-01	NA	19.83	not significant
5348	KIAA0513	-1.00	7.11E-01	NA	33.30	not significant
5349	KIAA0825	-1.00	6.84E-01	NA	27.80	not significant
5350	TRIM2	-1.00	6.94E-01	NA	28.15	not significant
5351	BACE1-AS	-1.00	7.11E-01	NA	33.33	not significant
5352	IL10	-1.00	6.34E-01	NA	20.94	not significant
5353	LOC100287098	-1.00	5.77E-01	NA	13.69	not significant
5354	VCL	-1.00	7.04E-01	NA	36.32	not significant
5355	LOC101928068	-1.00	6.08E-01	NA	17.18	not significant

5356	LOC100507250	-1.00	6.71E-01	NA	24.66	not significant
5357	SKIDA1	-1.00	6.46E-01	NA	21.62	not significant
5358	PRDM11	-1.00	7.92E-01	NA	70.65	not significant
5359	LOC389906	-1.00	8.59E-01	9.43E-01	220.77	not significant
5360	KDM4A-AS1	-1.00	7.78E-01	NA	67.50	not significant
5361	BIRC2	-1.00	8.87E-01	9.57E-01	1372.56	not significant
5362	ZNF18	-1.00	8.76E-01	9.52E-01	359.14	not significant
5363	VHL	-1.00	8.67E-01	9.47E-01	5261.69	not significant
5364	PDE4D	-1.00	8.87E-01	9.57E-01	1243.71	not significant
5365	MGAT5	-1.00	9.23E-01	9.71E-01	3106.02	not significant
5366	EGFL7	-1.00	5.16E-01	NA	10.17	not significant
5367	CXCR5	-1.00	5.97E-01	NA	15.11	not significant
5368	IRF5	-1.00	7.22E-01	NA	34.25	not significant
5369	PTPRVP	-1.00	6.67E-01	NA	17.91	not significant
5370	LNP1	-1.00	7.97E-01	NA	66.29	not significant
5371	RIMKLA	-1.00	6.98E-01	NA	30.26	not significant
5372	BUD31	-1.00	9.13E-01	9.67E-01	3210.61	not significant
5373	MAP3K8	-1.00	8.18E-01	NA	97.46	not significant
5374	ADI1	-1.00	8.87E-01	9.57E-01	2311.18	not significant
5375	HIBADH	-1.00	8.90E-01	9.58E-01	717.85	not significant
5376	PTPDC1	-1.00	8.78E-01	9.52E-01	355.85	not significant
5377	STAM2	-1.00	8.85E-01	9.56E-01	836.20	not significant
5378	DOCK5	-1.00	8.84E-01	9.56E-01	847.35	not significant
5379	RASSF2	-1.00	8.86E-01	9.56E-01	2686.44	not significant
5380	MAPRE2	-1.00	8.97E-01	9.61E-01	4492.76	not significant
5381	GALNT13	-1.00	5.41E-01	NA	10.92	not significant
5382	SHB	-1.00	6.14E-01	NA	17.10	not significant
5383	LAMA2	-1.00	5.84E-01	NA	14.40	not significant
5384	LINC00996	-1.00	6.26E-01	NA	18.44	not significant
5385	PLEKHA1	-1.00	7.83E-01	NA	57.85	not significant
5386	CDIPT-AS1	-1.00	5.82E-01	NA	13.05	not significant
5387	BHLHE23	-1.00	6.34E-01	NA	17.58	not significant
5388	EPCAM	-1.00	7.15E-01	NA	30.11	not significant
5389	IFITM10	-1.00	7.22E-01	NA	32.50	not significant
5390	SCAMP5	-1.00	8.87E-01	9.57E-01	410.73	not significant
5391	ZNF549	-1.00	8.79E-01	9.52E-01	584.83	not significant
5392	GID8	-1.00	8.86E-01	9.56E-01	3333.70	not significant
5393	CEP41	-1.00	8.85E-01	9.56E-01	405.42	not significant
5394	MBTPS2	-1.00	8.88E-01	9.57E-01	746.42	not significant
5395	RAB35	-1.00	8.85E-01	9.56E-01	3528.87	not significant
5396	HIST1H3J	-1.00	5.83E-01	NA	12.47	not significant
5397	C7orf55	-1.00	8.02E-01	NA	68.68	not significant
5398	RAB39B	-1.00	7.21E-01	NA	30.02	not significant
5399	MORF4L2-AS1	-1.00	7.47E-01	NA	38.29	not significant
5400	HIP1	-1.00	5.71E-01	NA	12.82	not significant
5401	FXYD2	-1.00	7.85E-01	NA	74.40	not significant
5402	HSD3B7	-1.00	7.65E-01	NA	49.87	not significant
5403	TOP1P1	-1.00	7.77E-01	NA	48.98	not significant
5404	CMTM4	-1.00	7.80E-01	NA	61.33	not significant
5405	TSPY26P	-1.00	8.24E-01	NA	87.03	not significant
5406	RAB3A	-1.00	7.84E-01	NA	56.61	not significant
5407	METTL1	-1.00	8.95E-01	9.61E-01	978.98	not significant
5408	SMUG1	-1.00	8.90E-01	9.59E-01	564.41	not significant
5409	C9orf142	-1.00	8.95E-01	9.61E-01	1221.47	not significant
5410	DCTD	-1.00	8.88E-01	9.57E-01	3257.57	not significant
5411	NAGA	-1.00	8.93E-01	9.60E-01	721.23	not significant
5412	RER1	-1.00	9.04E-01	9.63E-01	4122.76	not significant
5413	ZNF24	-1.00	8.86E-01	9.56E-01	4923.80	not significant
5414	CTSW	-1.00	6.64E-01	NA	20.25	not significant
5415	C10orf91	-1.00	6.73E-01	NA	19.94	not significant
5416	MID1IP1-AS1	-1.00	5.77E-01	NA	11.26	not significant
5417	C1QTNF3-AMACR	-1.00	5.21E-01	NA	9.02	not significant
5418	CEL	-1.00	8.05E-01	NA	68.49	not significant
5419	DNM1P46	-1.00	5.81E-01	NA	12.51	not significant
5420	CDKL2	-1.00	6.17E-01	NA	14.85	not significant
5421	ARHGAP44	-1.00	7.17E-01	NA	29.09	not significant
5422	FLVCR2	-1.00	6.54E-01	NA	16.80	not significant
5423	S100Z	-1.00	8.39E-01	9.31E-01	105.28	not significant
5424	TCF20	-1.00	7.97E-01	9.12E-01	135.48	not significant
5425	C1orf123	-1.00	8.99E-01	9.62E-01	795.62	not significant
5426	ZNF497	-1.00	8.48E-01	9.36E-01	120.18	not significant
5427	TRIM46	-1.00	8.71E-01	9.49E-01	204.87	not significant
5428	DUS2	-1.00	8.91E-01	9.59E-01	492.27	not significant
5429	TUFM	-1.00	8.47E-01	9.36E-01	9983.65	not significant
5430	CTDSPL	-1.00	8.97E-01	9.61E-01	1095.55	not significant
5431	ZNF250	-1.00	7.91E-01	9.10E-01	303.90	not significant
5432	TAF1A-AS1	-1.00	5.63E-01	NA	10.97	not significant
5433	GBP1P1	-1.00	7.60E-01	NA	39.60	not significant
5434	HIST1H4L	-1.00	5.55E-01	NA	11.21	not significant
5435	KIAA1211L	-1.00	5.59E-01	NA	10.07	not significant
5436	SV2B	-1.00	6.64E-01	NA	18.94	not significant
5437	CAB39L	-1.00	8.45E-01	9.35E-01	100.90	not significant
5438	AVEN	-1.00	8.96E-01	9.61E-01	593.11	not significant
5439	CD151	-1.00	8.90E-01	9.58E-01	289.88	not significant
5440	GPR160	-1.00	8.81E-01	9.54E-01	228.73	not significant
5441	GPR137B	-1.00	8.79E-01	9.53E-01	245.67	not significant
5442	COX7A2	-1.00	8.98E-01	9.62E-01	4261.97	not significant
5443	CRELD2	-1.00	9.02E-01	9.63E-01	1185.17	not significant

5444	LOC652276	-1.00	8.43E-01	9.33E-01	124.46	not significant
5445	C1orf35	-1.00	9.02E-01	9.63E-01	1013.32	not significant
5446	ZNF702P	-1.00	8.77E-01	9.52E-01	213.08	not significant
5447	NUDCD2	-1.00	9.02E-01	9.63E-01	1142.40	not significant
5448	ARMCX5	-1.00	9.00E-01	9.62E-01	817.79	not significant
5449	FHL1	-1.00	9.01E-01	9.63E-01	1525.18	not significant
5450	EIF4EBP2	-1.00	8.65E-01	9.45E-01	10784.53	not significant
5451	CASK	-1.00	8.96E-01	9.61E-01	780.04	not significant
5452	ZBTB2	-1.00	9.00E-01	9.63E-01	1793.67	not significant
5453	JMJD1C	-1.00	8.99E-01	9.62E-01	3162.52	not significant
5454	SLC35F6	-1.00	9.02E-01	9.63E-01	1329.27	not significant
5455	ADAM22	-1.00	9.01E-01	9.63E-01	1600.45	not significant
5456	MYO9A	-1.00	8.86E-01	9.56E-01	954.54	not significant
5457	CCDC73	-1.00	4.40E-01	NA	44.63	not significant
5458	HIST1H2BI	-1.00	6.31E-01	NA	16.52	not significant
5459	LCA5L	-1.00	5.49E-01	NA	9.47	not significant
5460	PRKAB2	-1.00	7.51E-01	NA	36.59	not significant
5461	LOC102288414	-1.00	4.98E-01	NA	7.91	not significant
5462	F8	-1.00	7.05E-01	NA	24.74	not significant
5463	RPL23A	-1.00	9.00E-01	9.62E-01	7706.59	not significant
5464	CSRP2BP	-1.00	9.03E-01	9.63E-01	1152.40	not significant
5465	ARFRP1	-1.00	9.03E-01	9.63E-01	1147.22	not significant
5466	F2RL2	-1.00	8.93E-01	9.60E-01	342.41	not significant
5467	TMEM2	-1.00	8.92E-01	9.60E-01	1015.70	not significant
5468	PRRG2	-1.00	5.92E-01	NA	11.07	not significant
5469	HIST1H2BL	-1.00	6.94E-01	NA	19.95	not significant
5470	CD8B	-1.00	6.70E-01	NA	16.89	not significant
5471	CASC14	-1.00	7.54E-01	NA	34.47	not significant
5472	GPR3	-1.00	8.23E-01	NA	64.66	not significant
5473	LINC00936	-1.00	7.11E-01	NA	22.52	not significant
5474	RORB	-1.00	8.29E-01	NA	53.96	not significant
5475	PPM1E	-1.00	8.32E-01	NA	74.86	not significant
5476	LOC100289511	-1.00	6.90E-01	NA	20.13	not significant
5477	PRSS27	-1.00	5.79E-01	NA	10.22	not significant
5478	RP9	-1.00	9.06E-01	9.64E-01	534.91	not significant
5479	LRP5L	-1.00	8.78E-01	9.52E-01	205.05	not significant
5480	PODXL	-1.00	8.54E-01	9.40E-01	208.52	not significant
5481	FKBP8	-1.00	8.94E-01	9.60E-01	5431.34	not significant
5482	RPL7A	-1.00	8.87E-01	9.57E-01	14178.78	not significant
5483	RNF144A-AS1	-1.00	9.06E-01	9.64E-01	405.54	not significant
5484	ZNF570	-1.00	8.83E-01	9.55E-01	212.69	not significant
5485	MED24	-1.00	8.92E-01	9.60E-01	4386.17	not significant
5486	RBM17	-1.00	9.00E-01	9.62E-01	5528.58	not significant
5487	EEF2K	-1.00	9.06E-01	9.64E-01	2062.08	not significant
5488	CCDC134	-1.00	8.94E-01	9.60E-01	345.72	not significant
5489	ITPRIPL1	-1.00	9.08E-01	9.64E-01	1234.64	not significant
5490	ATP6V1C2	-1.00	4.80E-01	NA	74.02	not significant
5491	LOC100128568	-1.00	6.34E-01	NA	11.98	not significant
5492	HIST1H1B	-1.00	6.73E-01	NA	55.64	not significant
5493	PTGER3	-1.00	7.66E-01	NA	32.62	not significant
5494	CNTNAP1	-1.00	5.71E-01	NA	9.53	not significant
5495	OAZ3	-1.00	6.75E-01	NA	15.30	not significant
5496	LOC100862671	-1.00	8.92E-01	9.60E-01	269.78	not significant
5497	LOC653712	-1.00	6.72E-01	NA	16.57	not significant
5498	GS1-259H13.2	-1.00	8.43E-01	NA	78.91	not significant
5499	DHRS4L1	-1.00	8.15E-01	NA	55.61	not significant
5500	ZNF84	-1.00	8.56E-01	NA	98.81	not significant
5501	MDP1	-1.00	7.44E-01	NA	29.06	not significant
5502	CFL1P1	-1.00	6.07E-01	NA	12.30	not significant
5503	NFIL3	-1.00	8.08E-01	NA	48.02	not significant
5504	MED31	-1.00	9.01E-01	9.63E-01	295.22	not significant
5505	CHAT	-1.00	8.67E-01	9.47E-01	123.46	not significant
5506	NAIF1	-1.00	9.05E-01	9.64E-01	421.19	not significant
5507	TNFSF4	-1.00	9.09E-01	9.65E-01	401.24	not significant
5508	SCYL1	-1.00	9.07E-01	9.64E-01	2246.96	not significant
5509	FAM179B	-1.00	8.65E-01	9.45E-01	155.10	not significant
5510	EPS8L2	-1.00	6.04E-01	NA	10.45	not significant
5511	NEK11	-1.00	6.37E-01	NA	11.66	not significant
5512	LOC101929099	-1.00	6.79E-01	NA	14.95	not significant
5513	BCDIN3D-AS1	-1.00	6.36E-01	NA	12.16	not significant
5514	LOC100130093	-1.00	6.35E-01	NA	13.35	not significant
5515	PKIG	-1.00	8.59E-01	NA	90.90	not significant
5516	HIST1H2AI	-1.00	6.55E-01	NA	12.97	not significant
5517	ADPRHL1	-1.00	7.68E-01	NA	30.62	not significant
5518	FDXACB1	-1.00	7.77E-01	NA	35.97	not significant
5519	CSRP2	-1.00	7.17E-01	NA	21.45	not significant
5520	LXN	-1.00	8.50E-01	NA	82.70	not significant
5521	TNS4	-1.00	8.71E-01	9.49E-01	142.73	not significant
5522	DPF1	-1.00	8.84E-01	9.56E-01	160.94	not significant
5523	PFDN5	-1.00	9.16E-01	9.68E-01	4092.36	not significant
5524	MLST8	-1.00	9.13E-01	9.67E-01	2188.95	not significant
5525	PRR14	-1.00	9.89E-01	9.97E-01	1559.84	not significant
5526	RASGRP1	-1.00	9.11E-01	9.66E-01	2246.47	not significant
5527	MBOAT7	-1.00	9.07E-01	9.64E-01	670.43	not significant
5528	FNTB	-1.00	7.95E-01	NA	39.85	not significant
5529	FAM195A	-1.00	7.19E-01	NA	20.46	not significant
5530	TAF7L	-1.00	5.97E-01	NA	8.74	not significant
5531	LEAP2	-1.00	7.58E-01	NA	29.26	not significant

5532	SH3PXD2A-AS1	-1.00	7.11E-01	NA	17.35	not significant
5533	LRP2BP	-1.00	7.46E-01	NA	24.56	not significant
5534	PHKA1	-1.00	7.92E-01	NA	39.17	not significant
5535	PANO	-1.00	8.45E-01	NA	71.91	not significant
5536	CTNNAL1	-1.00	9.14E-01	9.67E-01	950.88	not significant
5537	ZNF44	-1.00	9.13E-01	9.67E-01	431.17	not significant
5538	ST3GAL5	-1.00	9.05E-01	9.64E-01	529.85	not significant
5539	TDRD3	-1.00	9.12E-01	9.66E-01	503.52	not significant
5540	MGC57346	-1.00	9.27E-01	9.73E-01	223.30	not significant
5541	MAX	-1.00	9.17E-01	9.68E-01	5084.44	not significant
5542	RNF187	-1.00	9.15E-01	9.68E-01	5206.38	not significant
5543	EBPL	-1.00	9.16E-01	9.68E-01	1139.45	not significant
5544	CPSF3	-1.00	9.11E-01	9.66E-01	2727.74	not significant
5545	KATNB1	-1.00	9.16E-01	9.68E-01	1455.58	not significant
5546	SCML2	-1.00	9.12E-01	9.66E-01	2026.24	not significant
5547	EPHB4	-1.00	8.91E-01	9.60E-01	212.72	not significant
5548	SLC17A9	-1.00	6.19E-01	NA	9.39	not significant
5549	SOX7	-1.00	7.58E-01	NA	24.27	not significant
5550	PNLDC1	-1.00	7.24E-01	NA	18.17	not significant
5551	IQCD	-1.00	6.37E-01	NA	10.32	not significant
5552	LOC101927178	-1.00	5.81E-01	NA	9.63	not significant
5553	CD4	-1.00	6.72E-01	NA	12.79	not significant
5554	DST	-1.00	7.67E-01	NA	26.87	not significant
5555	TIMP1	-1.00	8.91E-01	9.59E-01	171.88	not significant
5556	FAM86EP	-1.00	8.63E-01	NA	100.09	not significant
5557	NSMCE1	-1.00	9.16E-01	9.68E-01	1541.54	not significant
5558	REXO4	-1.00	9.15E-01	9.67E-01	398.49	not significant
5559	C10orf25	-1.00	9.07E-01	9.64E-01	277.74	not significant
5560	ICA1L	-1.00	8.96E-01	9.61E-01	280.08	not significant
5561	COL11A2	-1.00	6.70E-01	NA	12.54	not significant
5562	CFP	-1.00	6.87E-01	NA	13.64	not significant
5563	PDE6G	-1.00	7.79E-01	NA	27.84	not significant
5564	LOC100130705	-1.00	7.78E-01	NA	31.15	not significant
5565	ZNF879	-1.00	7.88E-01	NA	33.42	not significant
5566	FAHD2CP	-1.00	8.04E-01	NA	39.62	not significant
5567	DHX58	-1.00	8.82E-01	9.54E-01	130.31	not significant
5568	ZNF815P	-1.00	8.09E-01	NA	38.82	not significant
5569	SNTG2	-1.00	8.96E-01	9.61E-01	200.79	not significant
5570	LRFN1	-1.00	9.06E-01	9.64E-01	235.07	not significant
5571	MYT1L	-1.00	9.12E-01	9.66E-01	374.91	not significant
5572	CWF19L2	-1.00	9.18E-01	9.69E-01	655.96	not significant
5573	MYL6	-1.00	9.18E-01	9.69E-01	10205.77	not significant
5574	VAC14	-1.00	9.19E-01	9.69E-01	1712.61	not significant
5575	RMI1	-1.00	9.18E-01	9.69E-01	1999.18	not significant
5576	VPS4B	-1.00	8.95E-01	9.61E-01	3780.85	not significant
5577	NCEH1	-1.00	9.16E-01	9.68E-01	511.58	not significant
5578	SEL1L3	-1.00	6.50E-01	NA	10.56	not significant
5579	ASGR1	-1.00	6.93E-01	NA	12.89	not significant
5580	ARHGAP5-AS1	-1.00	7.73E-01	NA	24.88	not significant
5581	SEMA3G	-1.00	7.00E-01	NA	14.03	not significant
5582	C7orf61	-1.00	7.30E-01	NA	16.19	not significant
5583	LOC728392	-1.00	8.21E-01	NA	40.27	not significant
5584	LOC730183	-1.00	7.08E-01	NA	15.35	not significant
5585	RAG2	-1.00	6.64E-01	NA	10.69	not significant
5586	PPP4R1L	-1.00	7.72E-01	NA	26.50	not significant
5587	RASSF8-AS1	-1.00	7.94E-01	NA	28.91	not significant
5588	ZNF225	-1.00	9.10E-01	9.65E-01	278.29	not significant
5589	GRB10	-1.00	8.51E-01	NA	57.72	not significant
5590	RND2	-1.00	8.40E-01	NA	50.88	not significant
5591	LRRC27	-1.00	8.86E-01	9.56E-01	129.32	not significant
5592	HSP90B2P	-1.00	8.52E-01	NA	66.63	not significant
5593	IL22RA1	-1.00	8.70E-01	NA	84.65	not significant
5594	ATP5D	-1.00	9.24E-01	9.72E-01	2205.12	not significant
5595	TTC9	-1.00	9.22E-01	9.70E-01	465.10	not significant
5596	MRPL32	-1.00	9.25E-01	9.72E-01	1448.23	not significant
5597	NCOR2	-1.00	9.18E-01	9.68E-01	6137.57	not significant
5598	DPF2	-1.00	9.19E-01	9.69E-01	2876.51	not significant
5599	GALNT8	-1.00	7.82E-01	NA	24.37	not significant
5600	RASA4	-1.00	7.50E-01	NA	18.28	not significant
5601	ISYNA1	-1.00	8.11E-01	NA	33.48	not significant
5602	SAMD4A	-1.00	7.23E-01	NA	14.22	not significant
5603	LOC100506023	-1.00	7.74E-01	NA	26.72	not significant
5604	ARRDC3-AS1	-1.00	6.77E-01	NA	11.39	not significant
5605	SRRM5	-1.00	7.29E-01	NA	17.05	not significant
5606	MOK	-1.00	7.61E-01	NA	22.18	not significant
5607	RNFT2	-1.00	9.16E-01	9.68E-01	288.72	not significant
5608	ZNF555	-1.00	8.85E-01	9.56E-01	108.30	not significant
5609	ZNF324B	-1.00	8.86E-01	9.56E-01	258.75	not significant
5610	ZNF410	-1.00	9.27E-01	9.73E-01	1863.63	not significant
5611	ZNF48	-1.00	9.25E-01	9.72E-01	912.76	not significant
5612	ZFX	-1.00	9.28E-01	9.73E-01	1428.34	not significant
5613	NSUN6	-1.00	9.21E-01	9.70E-01	517.04	not significant
5614	FAM120B	-1.00	9.26E-01	9.72E-01	1493.53	not significant
5615	NECAP1	-1.00	9.21E-01	9.70E-01	982.36	not significant
5616	POTEF	-1.00	6.63E-01	NA	9.42	not significant
5617	NUP62CL	-1.00	7.66E-01	NA	19.20	not significant
5618	SMPD3	-1.00	7.32E-01	NA	15.22	not significant
5619	ZP3	-1.00	7.22E-01	NA	13.49	not significant

5620	PILRB	-1.00	8.11E-01	NA	31.99	not significant
5621	ZBTB20	-1.00	8.20E-01	NA	34.93	not significant
5622	SLC2A6	-1.00	7.46E-01	NA	15.85	not significant
5623	SMG1P2	-1.00	8.74E-01	NA	73.89	not significant
5624	IL20RB	-1.00	8.30E-01	NA	38.56	not significant
5625	EVI5L	-1.00	9.29E-01	9.73E-01	640.32	not significant
5626	IGFBP2	-1.00	9.29E-01	9.74E-01	6749.34	not significant
5627	KIAA0586	-1.00	9.30E-01	9.74E-01	1032.57	not significant
5628	RPLP0	-1.00	8.07E-01	9.17E-01	47654.10	not significant
5629	RNF5P1	-1.00	6.99E-01	NA	11.23	not significant
5630	HYMAI	-1.00	7.13E-01	NA	11.47	not significant
5631	SLC22A4	-1.00	7.32E-01	NA	13.81	not significant
5632	KIAA1683	-1.00	6.70E-01	NA	9.45	not significant
5633	PRG2	-1.00	8.11E-01	NA	29.36	not significant
5634	SUMO1P3	-1.00	8.09E-01	NA	26.53	not significant
5635	TSNAXIP1	-1.00	8.37E-01	NA	41.21	not significant
5636	TNFRSF1B	-1.00	7.11E-01	NA	11.33	not significant
5637	HUWE1	-1.00	8.77E-01	9.52E-01	5106.06	not significant
5638	PYCRL	-1.00	9.40E-01	9.78E-01	555.96	not significant
5639	C6orf136	-1.00	9.10E-01	9.65E-01	166.80	not significant
5640	CEP76	-1.00	9.28E-01	9.73E-01	559.55	not significant
5641	KANK2	-1.00	8.77E-01	NA	78.14	not significant
5642	AFG3L2	-1.00	9.28E-01	9.73E-01	2840.79	not significant
5643	MAGT1	-1.00	9.32E-01	9.75E-01	625.40	not significant
5644	GPR89A	-1.00	8.02E-01	NA	29.44	not significant
5645	MYT1	-1.00	7.68E-01	NA	20.16	not significant
5646	TEFM	-1.00	9.29E-01	9.74E-01	238.42	not significant
5647	FAM46C	-1.00	8.27E-01	NA	30.29	not significant
5648	ZNF222	-1.00	9.12E-01	9.66E-01	174.04	not significant
5649	LOC101928063	-1.00	8.16E-01	NA	28.88	not significant
5650	KRCC1	-1.00	9.37E-01	9.77E-01	591.47	not significant
5651	XRCC4	-1.00	9.26E-01	9.72E-01	438.65	not significant
5652	MED18	-1.00	9.33E-01	9.75E-01	690.25	not significant
5653	NDUFS3	-1.00	9.35E-01	9.75E-01	3032.44	not significant
5654	RPL22	-1.00	9.33E-01	9.75E-01	4148.71	not significant
5655	RPL35	-1.00	9.32E-01	9.75E-01	13365.44	not significant
5656	FAM115C	-1.00	9.03E-01	9.63E-01	141.63	not significant
5657	KLC1	-1.00	9.28E-01	9.73E-01	2598.24	not significant
5658	EPAS1	-1.00	9.10E-01	9.65E-01	8626.90	not significant
5659	TARSL2	-1.00	9.22E-01	9.70E-01	282.03	not significant
5660	LOC101928069	-1.00	8.19E-01	NA	24.75	not significant
5661	ABCB9	-1.00	8.71E-01	NA	53.88	not significant
5662	DDTL	-1.00	6.80E-01	NA	8.88	not significant
5663	SETSIP	-1.00	8.19E-01	NA	28.37	not significant
5664	ZBED5-AS1	-1.00	8.84E-01	NA	69.66	not significant
5665	PTCRA	-1.00	7.18E-01	NA	11.03	not significant
5666	CCDC74A	-1.00	9.02E-01	NA	96.97	not significant
5667	ENTPD1-AS1	-1.00	8.74E-01	NA	57.04	not significant
5668	ALKBH2	-1.00	9.38E-01	9.77E-01	984.51	not significant
5669	NTAN1	-1.00	9.37E-01	9.77E-01	1017.35	not significant
5670	MKX	-1.00	8.68E-01	NA	50.19	not significant
5671	KRTCAP2	-1.00	9.33E-01	9.75E-01	1408.61	not significant
5672	ABI1	-1.00	9.30E-01	9.74E-01	2150.49	not significant
5673	TOLLIP	-1.00	9.39E-01	9.78E-01	1589.45	not significant
5674	MANEAL	-1.00	9.36E-01	9.76E-01	943.82	not significant
5675	VAV1	-1.00	9.28E-01	9.73E-01	5005.60	not significant
5676	SLX4IP	-1.00	9.20E-01	9.69E-01	194.00	not significant
5677	UGP2	-1.00	9.42E-01	9.79E-01	10589.69	not significant
5678	ZNF43	-1.00	9.43E-01	9.79E-01	588.20	not significant
5679	SNX19	-1.00	9.37E-01	9.77E-01	3509.17	not significant
5680	CHML	-1.00	9.37E-01	9.77E-01	2400.12	not significant
5681	LINC00539	-1.00	8.38E-01	NA	29.11	not significant
5682	THBS1	-1.00	6.94E-01	NA	9.07	not significant
5683	LAMC3	-1.00	7.57E-01	NA	13.99	not significant
5684	NKX3-2	-1.00	7.75E-01	NA	15.95	not significant
5685	LOC100133985	-1.00	7.47E-01	NA	11.80	not significant
5686	TMEM150A	-1.00	7.63E-01	NA	14.20	not significant
5687	LOC401320	-1.00	9.07E-01	9.64E-01	114.92	not significant
5688	LOC100506321	-1.00	8.12E-01	NA	24.68	not significant
5689	ARG2	-1.00	8.72E-01	NA	48.11	not significant
5690	ZNHIT2	-1.00	9.27E-01	9.73E-01	248.47	not significant
5691	FRA10AC1	-1.00	9.40E-01	9.78E-01	618.30	not significant
5692	SLC7A5P2	-1.00	8.86E-01	NA	67.70	not significant
5693	C1orf213	-1.00	8.52E-01	NA	44.10	not significant
5694	UBA3	-1.00	9.41E-01	9.78E-01	1559.60	not significant
5695	TTC37	-1.00	9.09E-01	9.65E-01	3031.59	not significant
5696	SLC12A2	-1.00	9.33E-01	9.75E-01	1103.09	not significant
5697	IK	-1.00	9.47E-01	9.79E-01	3908.59	not significant
5698	CXorf23	-1.00	9.25E-01	9.72E-01	199.32	not significant
5699	RFX8	-1.00	9.15E-01	9.68E-01	151.24	not significant
5700	C9orf163	-1.00	7.36E-01	NA	9.70	not significant
5701	DGCR6	-1.00	8.00E-01	NA	16.80	not significant
5702	LINC01176	-1.00	7.73E-01	NA	14.85	not significant
5703	HIST1H4B	-1.00	7.37E-01	NA	10.06	not significant
5704	TMEM9B-AS1	-1.00	8.77E-01	NA	40.94	not significant
5705	RAB19	-1.00	8.64E-01	NA	40.76	not significant
5706	SRP14-AS1	-1.00	8.08E-01	NA	19.54	not significant
5707	PROZ	-1.00	9.12E-01	9.66E-01	132.33	not significant

5708	SIRT4	-1.00	7.86E-01	NA	14.80	not significant
5709	C2orf42	-1.00	9.40E-01	9.78E-01	407.53	not significant
5710	CCDC43	-1.00	9.42E-01	9.79E-01	1418.62	not significant
5711	HVCN1	-1.00	9.42E-01	9.79E-01	827.39	not significant
5712	ZNF677	-1.00	8.88E-01	NA	67.24	not significant
5713	ZNF764	-1.00	9.44E-01	9.79E-01	665.96	not significant
5714	ENOX2	-1.00	9.38E-01	9.77E-01	693.49	not significant
5715	C14orf119	-1.00	9.43E-01	9.79E-01	1489.70	not significant
5716	ARL1	-1.00	9.41E-01	9.78E-01	2185.35	not significant
5717	FAU	-1.00	9.40E-01	9.78E-01	7997.09	not significant
5718	TMCC1	-1.00	9.46E-01	9.79E-01	531.55	not significant
5719	ZNF813	-1.00	9.45E-01	9.79E-01	598.01	not significant
5720	CSNK2B	-1.00	9.65E-01	9.89E-01	2754.26	not significant
5721	GPD2	-1.00	9.32E-01	9.75E-01	289.48	not significant
5722	SELO	-1.00	9.42E-01	9.79E-01	845.81	not significant
5723	PCNX	-1.00	9.31E-01	9.74E-01	1981.32	not significant
5724	CHMP3	-1.00	8.13E-01	NA	22.02	not significant
5725	C3orf67	-1.00	7.63E-01	NA	11.20	not significant
5726	PRAME	-1.00	8.13E-01	NA	17.52	not significant
5727	PMP22	-1.00	8.84E-01	NA	57.15	not significant
5728	DCAF13P3	-1.00	7.30E-01	NA	9.60	not significant
5729	GNN	-1.00	7.96E-01	NA	15.95	not significant
5730	LOC100506325	-1.00	8.61E-01	NA	32.56	not significant
5731	ACTN2	-1.00	7.73E-01	NA	12.29	not significant
5732	DYRK3	-1.00	8.81E-01	NA	47.07	not significant
5733	MOSPD2	-1.00	9.43E-01	9.79E-01	485.26	not significant
5734	LOC102606465	-1.00	9.29E-01	9.73E-01	188.91	not significant
5735	KIAA1804	-1.00	9.05E-01	NA	78.50	not significant
5736	C20orf24	-1.00	9.45E-01	9.79E-01	1583.03	not significant
5737	NUP54	-1.00	9.43E-01	9.79E-01	2534.98	not significant
5738	AURKAIP1	-1.00	9.43E-01	9.79E-01	2909.26	not significant
5739	TRMT10A	-1.00	9.37E-01	9.77E-01	337.48	not significant
5740	SEC24B	-1.00	9.44E-01	9.79E-01	2016.14	not significant
5741	TTL	-1.00	9.46E-01	9.79E-01	1797.92	not significant
5742	LOC100507316	-1.00	9.03E-01	NA	86.96	not significant
5743	LOC101927166	-1.00	8.47E-01	NA	25.37	not significant
5744	LINC01144	-1.00	8.55E-01	NA	27.18	not significant
5745	CLK2P	-1.00	7.89E-01	NA	12.15	not significant
5746	SPATS2L	-1.00	7.59E-01	NA	9.60	not significant
5747	FAM71F2	-1.00	7.51E-01	NA	9.44	not significant
5748	IL4I1	-1.00	7.86E-01	NA	14.77	not significant
5749	IPO9-AS1	-1.00	8.22E-01	NA	18.03	not significant
5750	FAM13A-AS1	-1.00	7.80E-01	NA	12.05	not significant
5751	HMGCL	-1.00	9.49E-01	9.80E-01	338.94	not significant
5752	THAP8	-1.00	9.38E-01	9.77E-01	250.11	not significant
5753	BLVRA	-1.00	9.47E-01	9.80E-01	846.10	not significant
5754	P4HTM	-1.00	8.98E-01	NA	57.99	not significant
5755	ECE2	-1.00	9.46E-01	9.79E-01	457.87	not significant
5756	EIF2D	-1.00	9.47E-01	9.80E-01	1114.25	not significant
5757	ZNF550	-1.00	9.43E-01	9.79E-01	802.94	not significant
5758	KLHDC4	-1.00	9.45E-01	9.79E-01	1542.63	not significant
5759	WDR81	-1.00	9.50E-01	9.81E-01	1046.17	not significant
5760	TSC2	-1.00	9.94E-01	9.99E-01	2546.54	not significant
5761	SH3GL1P1	-1.00	8.17E-01	NA	14.46	not significant
5762	CYTH4	-1.00	8.39E-01	NA	18.71	not significant
5763	PGPEP1L	-1.00	8.29E-01	NA	18.13	not significant
5764	ZNF491	-1.00	9.17E-01	NA	89.61	not significant
5765	ZSWIM5	-1.00	9.24E-01	9.72E-01	102.50	not significant
5766	EVA1B	-1.00	7.58E-01	NA	9.29	not significant
5767	ZNF100	-1.00	9.15E-01	NA	76.75	not significant
5768	CFAP20	-1.00	9.81E-01	9.95E-01	3154.63	not significant
5769	C11orf57	-1.00	9.50E-01	9.81E-01	2068.97	not significant
5770	EZR-AS1	-1.00	7.67E-01	NA	8.63	not significant
5771	C19orf71	-1.00	8.26E-01	NA	15.21	not significant
5772	AVIL	-1.00	8.67E-01	NA	25.08	not significant
5773	AOAH	-1.00	8.32E-01	NA	16.58	not significant
5774	ZNF275	-1.00	8.77E-01	NA	32.95	not significant
5775	SH2D7	-1.00	7.80E-01	NA	10.41	not significant
5776	N4BP2L2-IT2	-1.00	8.98E-01	NA	46.22	not significant
5777	LOC101929698	-1.00	7.71E-01	NA	9.25	not significant
5778	GUCY1B2	-1.00	8.25E-01	NA	17.61	not significant
5779	FSIP1	-1.00	8.56E-01	NA	23.26	not significant
5780	CHMP4A	-1.00	9.55E-01	9.83E-01	1330.48	not significant
5781	LINC00954	-1.00	8.30E-01	NA	17.24	not significant
5782	TXNDC17	-1.00	9.54E-01	9.83E-01	1088.31	not significant
5783	DEXI	-1.00	9.55E-01	9.83E-01	613.56	not significant
5784	DEF6	-1.00	9.43E-01	9.79E-01	4063.87	not significant
5785	STK38	-1.00	9.98E-01	1.00E+00	2683.23	not significant
5786	UFSP1	-1.00	8.66E-01	NA	21.71	not significant
5787	NDUFA6-AS1	-1.00	7.92E-01	NA	9.36	not significant
5788	MYLK2	-1.00	6.28E-01	NA	29.13	not significant
5789	TGM5	-1.00	7.89E-01	NA	9.13	not significant
5790	RNF157-AS1	-1.00	8.24E-01	NA	11.97	not significant
5791	BDNF-AS	-1.00	8.15E-01	NA	11.24	not significant
5792	FAM151B	-1.00	8.25E-01	NA	12.70	not significant
5793	LINC01237	-1.00	8.81E-01	NA	28.14	not significant
5794	KANK1	-1.00	9.17E-01	NA	56.96	not significant
5795	NEO1	-1.00	8.38E-01	NA	15.50	not significant

5796	L3HYPDH	-1.00	9.31E-01	NA	98.67	not significant
5797	PTRHD1	-1.00	9.53E-01	9.82E-01	453.85	not significant
5798	MRPS34	-1.00	9.52E-01	9.82E-01	3718.96	not significant
5799	ETV4	-1.00	8.50E-01	NA	18.43	not significant
5800	SLC35G1	-1.00	9.40E-01	9.78E-01	148.46	not significant
5801	PTCH1	-1.00	9.29E-01	NA	82.04	not significant
5802	DND1	-1.00	8.96E-01	NA	39.05	not significant
5803	AFMID	-1.00	9.51E-01	9.82E-01	331.42	not significant
5804	CASC3	-1.00	9.49E-01	9.81E-01	4647.36	not significant
5805	CCAR2	-1.00	9.47E-01	9.79E-01	10734.63	not significant
5806	PDLIM4	-1.00	8.25E-01	NA	11.38	not significant
5807	LOC643072	-1.00	8.18E-01	NA	10.15	not significant
5808	LINC00310	-1.00	8.08E-01	NA	9.34	not significant
5809	ARHGAP22	-1.00	8.48E-01	NA	14.64	not significant
5810	HIST1H1D	-1.00	9.08E-01	NA	44.86	not significant
5811	SIRPB1	-1.00	7.99E-01	NA	8.07	not significant
5812	PWARSN	-1.00	9.09E-01	NA	47.77	not significant
5813	TRIM9	-1.00	8.92E-01	NA	33.29	not significant
5814	APOBEC3H	-1.00	9.54E-01	9.83E-01	169.13	not significant
5815	CDKL5	-1.00	8.39E-01	NA	13.25	not significant
5816	RTCA-AS1	-1.00	7.95E-01	NA	8.70	not significant
5817	CDC26	-1.00	9.46E-01	9.79E-01	142.16	not significant
5818	FICD	-1.00	9.44E-01	9.79E-01	138.07	not significant
5819	TOE1	-1.00	9.59E-01	9.86E-01	1772.57	not significant
5820	MTFR2	-1.00	9.57E-01	9.84E-01	763.46	not significant
5821	PDIA3	-1.00	9.04E-01	9.63E-01	9934.01	not significant
5822	ZNF200	-1.00	9.59E-01	9.86E-01	1070.22	not significant
5823	MGAT1	-1.00	9.57E-01	9.84E-01	3950.56	not significant
5824	NUP205	-1.00	9.54E-01	9.83E-01	8065.51	not significant
5825	SWAP70	-1.00	9.30E-01	9.74E-01	2453.81	not significant
5826	MCM9	-1.00	9.50E-01	9.81E-01	1012.29	not significant
5827	B4GALNT3	-1.00	8.87E-01	NA	24.28	not significant
5828	CDK20	-1.00	9.24E-01	NA	57.88	not significant
5829	ANP32AP1	-1.00	8.62E-01	NA	16.69	not significant
5830	PINLYP	-1.00	9.59E-01	9.86E-01	397.78	not significant
5831	CNIH2	-1.00	8.96E-01	NA	36.12	not significant
5832	HR	-1.00	8.89E-01	NA	25.71	not significant
5833	ALDH4A1	-1.00	9.55E-01	9.83E-01	246.45	not significant
5834	C17orf89	-1.00	9.54E-01	9.83E-01	2520.83	not significant
5835	BMP4	-1.00	9.66E-01	9.89E-01	399.53	not significant
5836	NRN1	-1.00	9.61E-01	9.87E-01	3289.92	not significant
5837	PGP	-1.00	9.61E-01	9.87E-01	1713.84	not significant
5838	TBCB	-1.00	9.62E-01	9.88E-01	2910.43	not significant
5839	BRAT1	-1.00	9.84E-01	9.96E-01	2868.62	not significant
5840	OPA1	-1.00	9.56E-01	9.84E-01	4801.62	not significant
5841	LINC01252	-1.00	8.34E-01	NA	10.57	not significant
5842	C9orf3	-1.00	9.42E-01	9.79E-01	104.62	not significant
5843	HIST1H4A	-1.00	9.08E-01	NA	28.20	not significant
5844	UBTD1	-1.00	9.00E-01	NA	26.89	not significant
5845	LOC101929374	-1.00	9.08E-01	NA	30.66	not significant
5846	C3orf20	-1.00	8.05E-01	NA	7.50	not significant
5847	TRIM39	-1.00	8.25E-01	NA	9.36	not significant
5848	DHRS12	-1.00	9.15E-01	NA	37.97	not significant
5849	ZNHIT3	-1.00	9.67E-01	9.90E-01	314.20	not significant
5850	FAM66D	-1.00	8.60E-01	NA	12.94	not significant
5851	LOC643733	-1.00	9.25E-01	NA	32.66	not significant
5852	SLC27A5	-1.00	9.55E-01	9.83E-01	228.87	not significant
5853	PRPF31	-1.00	9.63E-01	9.88E-01	1529.24	not significant
5854	TSSC1	-1.00	9.67E-01	9.90E-01	1906.41	not significant
5855	ZFP41	-1.00	9.61E-01	9.87E-01	519.07	not significant
5856	LPCAT1	-1.00	9.60E-01	9.87E-01	6667.25	not significant
5857	ACAP2	-1.00	9.65E-01	9.89E-01	5007.20	not significant
5858	TRIM56	-1.00	1.00E+00	1.00E+00	1681.21	not significant
5859	FBXL13	-1.00	9.18E-01	NA	37.47	not significant
5860	F12	-1.00	8.74E-01	NA	14.97	not significant
5861	EOGT	-1.00	9.46E-01	NA	90.62	not significant
5862	GPHN	-1.00	9.03E-01	NA	21.55	not significant
5863	P2RX1	-1.00	9.09E-01	NA	31.71	not significant
5864	COL9A2	-1.00	9.27E-01	NA	39.78	not significant
5865	SLC4A10	-1.00	8.40E-01	9.32E-01	172.01	not significant
5866	KCTD6	-1.00	9.52E-01	9.82E-01	149.89	not significant
5867	FLJ37035	-1.00	8.70E-01	NA	12.55	not significant
5868	LRRC37A	-1.00	8.99E-01	NA	14.18	not significant
5869	POMZP3	-1.00	9.52E-01	9.82E-01	108.71	not significant
5870	GDF9	-1.00	9.04E-01	NA	25.87	not significant
5871	PTPRE	-1.00	9.62E-01	9.88E-01	667.78	not significant
5872	MRPL43	-1.00	9.69E-01	9.91E-01	1531.70	not significant
5873	RPS5	-1.00	9.78E-01	9.94E-01	23449.13	not significant
5874	ACO1	-1.00	9.69E-01	9.91E-01	1304.54	not significant
5875	UBR5	-1.00	9.57E-01	9.84E-01	6948.38	not significant
5876	KDM7A	-1.00	9.67E-01	9.90E-01	597.56	not significant
5877	SMG1P1	-1.00	9.30E-01	NA	63.09	not significant
5878	ACTA1	-1.00	8.62E-01	NA	10.66	not significant
5879	TIPARP-AS1	-1.00	8.50E-01	NA	8.96	not significant
5880	C19orf73	-1.00	8.85E-01	NA	12.98	not significant
5881	MCF2L	-1.00	9.17E-01	NA	23.25	not significant
5882	TMEM232	-1.00	8.75E-01	NA	12.85	not significant
5883	TMLHE	-1.00	9.39E-01	NA	62.77	not significant

5884	KLRAP1	-1.00	9.55E-01	9.83E-01	156.45	not significant
5885	RBM44	-1.00	9.32E-01	NA	41.52	not significant
5886	UPF3A	-1.00	9.69E-01	9.91E-01	719.80	not significant
5887	RBM48	-1.00	9.76E-01	9.94E-01	608.69	not significant
5888	NOP10	-1.00	9.72E-01	9.92E-01	2413.79	not significant
5889	RAB5A	-1.00	9.71E-01	9.92E-01	1806.27	not significant
5890	GLUL	-1.00	9.57E-01	9.84E-01	23702.72	not significant
5891	PCNXL3	-1.00	9.69E-01	9.91E-01	4247.29	not significant
5892	C11orf95	-1.00	9.73E-01	9.92E-01	1350.22	not significant
5893	CHST10	-1.00	9.72E-01	9.92E-01	1307.59	not significant
5894	PHLDB2	-1.00	9.68E-01	9.90E-01	369.23	not significant
5895	DQX1	-1.00	8.79E-01	NA	11.74	not significant
5896	TCN2	-1.00	9.00E-01	NA	16.14	not significant
5897	PIN4P1	-1.00	8.44E-01	NA	8.98	not significant
5898	DBH	-1.00	9.11E-01	NA	17.91	not significant
5899	SMG1P5	-1.00	9.15E-01	NA	20.88	not significant
5900	CLCA1	-1.00	8.76E-01	NA	11.42	not significant
5901	FLJ27354	-1.00	8.76E-01	NA	9.82	not significant
5902	DISP2	-1.00	8.70E-01	NA	9.19	not significant
5903	HIST1H2BO	-1.00	9.19E-01	NA	22.96	not significant
5904	CNKSR1	-1.00	8.83E-01	NA	10.99	not significant
5905	RP1L1	-1.00	8.66E-01	NA	8.81	not significant
5906	RAD51B	-1.00	9.72E-01	9.92E-01	350.32	not significant
5907	CCS	-1.00	9.78E-01	9.95E-01	324.44	not significant
5908	AMACR	-1.00	9.33E-01	NA	34.38	not significant
5909	SSNA1	-1.00	9.73E-01	9.92E-01	2143.11	not significant
5910	TRNAU1AP	-1.00	9.71E-01	9.92E-01	739.01	not significant
5911	CLTA	-1.00	9.71E-01	9.92E-01	4442.78	not significant
5912	PNN	-1.00	9.64E-01	9.88E-01	7854.71	not significant
5913	LINC00926	-1.00	9.25E-01	NA	27.67	not significant
5914	RFFL	-1.00	9.32E-01	NA	34.50	not significant
5915	KIAA0922	-1.00	9.76E-01	9.94E-01	3556.54	not significant
5916	SLC45A3	-1.00	9.26E-01	NA	31.98	not significant
5917	TBC1D25	-1.00	9.50E-01	NA	58.23	not significant
5918	PGM2L1	-1.00	9.71E-01	9.92E-01	1118.79	not significant
5919	SCAF4	-1.00	9.97E-01	1.00E+00	4794.01	not significant
5920	MYCBP2	-1.00	9.79E-01	9.95E-01	6156.32	not significant
5921	SLC25A35	-1.00	9.63E-01	9.88E-01	119.46	not significant
5922	OTOF	-1.00	9.07E-01	NA	11.39	not significant
5923	JUP	-1.00	8.99E-01	NA	10.39	not significant
5924	SCARF1	-1.00	9.08E-01	NA	14.59	not significant
5925	ROGDI	-1.00	9.14E-01	NA	100.06	not significant
5926	CASC10	-1.00	9.28E-01	NA	21.04	not significant
5927	ZNF81	-1.00	9.04E-01	NA	14.00	not significant
5928	GAB3	-1.00	9.66E-01	9.90E-01	132.68	not significant
5929	TSTD3	-1.00	9.09E-01	NA	15.58	not significant
5930	ZNF718	-1.00	9.54E-01	NA	53.57	not significant
5931	MRPS28	-1.00	9.77E-01	9.94E-01	1453.47	not significant
5932	COMT	-1.00	9.65E-01	9.89E-01	2747.35	not significant
5933	SPATA24	-1.00	9.48E-01	NA	42.32	not significant
5934	GLUD2	-1.00	9.63E-01	9.88E-01	120.26	not significant
5935	GABRR2	-1.00	8.92E-01	NA	11.55	not significant
5936	ABL1	-1.00	9.73E-01	9.92E-01	3373.49	not significant
5937	SLC26A4	-1.00	8.93E-01	NA	28.69	not significant
5938	HAL	-1.00	8.87E-01	NA	8.18	not significant
5939	KMT2C	-1.00	6.86E-01	8.53E-01	4131.29	not significant
5940	MID1	-1.00	9.22E-01	NA	14.62	not significant
5941	KIF4B	-1.00	9.07E-01	NA	11.33	not significant
5942	TAGLN	-1.00	9.36E-01	NA	23.79	not significant
5943	HPGDS	-1.00	9.01E-01	NA	9.53	not significant
5944	CKAP4	-1.00	9.10E-01	NA	9.75	not significant
5945	TIMM8A	-1.00	8.99E-01	NA	9.89	not significant
5946	GLIPR1L2	-1.00	8.94E-01	NA	9.14	not significant
5947	WTIP	-1.00	9.64E-01	NA	77.00	not significant
5948	GPR142	-1.00	9.19E-01	NA	11.83	not significant
5949	DLX4	-1.00	9.09E-01	NA	9.64	not significant
5950	GALNT4	-1.00	9.15E-01	NA	12.27	not significant
5951	TRMT10B	-1.00	9.72E-01	9.92E-01	361.71	not significant
5952	HOXB-AS1	-1.00	5.85E-02	2.18E-01	128.71	not significant
5953	PRPS2	-1.00	9.79E-01	9.95E-01	3513.44	not significant
5954	TM7SF3	-1.00	9.80E-01	9.95E-01	8254.10	not significant
5955	ITM2C	-1.00	9.79E-01	9.95E-01	5417.74	not significant
5956	SMARCA4	-1.00	9.74E-01	9.92E-01	12837.79	not significant
5957	AGPAT5	-1.00	9.76E-01	9.94E-01	5776.89	not significant
5958	TAF6L	-1.00	9.72E-01	9.92E-01	1004.91	not significant
5959	ARID4A	-1.00	9.81E-01	9.95E-01	1253.35	not significant
5960	TREML2	-1.00	9.80E-01	9.95E-01	1508.56	not significant
5961	LOC100133331	-1.00	9.48E-01	NA	39.07	not significant
5962	SPRED1	-1.00	9.80E-01	9.95E-01	403.75	not significant
5963	FBLN2	-1.00	9.75E-01	9.93E-01	192.95	not significant
5964	NPIPB5	-1.00	9.74E-01	9.92E-01	125.30	not significant
5965	NDRG4	-1.00	9.55E-01	NA	62.10	not significant
5966	CERKL	-1.00	8.77E-01	NA	64.83	not significant
5967	GMDS-AS1	-1.00	9.54E-01	NA	32.05	not significant
5968	CDK14	-1.00	9.07E-01	NA	10.51	not significant
5969	CPEB2	-1.00	9.10E-01	NA	9.55	not significant
5970	SPARC	-1.00	9.31E-01	NA	14.09	not significant
5971	TMEM26-AS1	-1.00	2.06E-01	4.71E-01	532.72	not significant

5972	LINC00337	-1.00	9.15E-01	NA	10.35	not significant
5973	CDH2	-1.00	9.26E-01	NA	13.19	not significant
5974	RARS2	-1.00	9.88E-01	9.97E-01	787.00	not significant
5975	ZNF891	-1.00	9.76E-01	9.94E-01	194.80	not significant
5976	MYO1F	-1.00	9.73E-01	NA	100.01	not significant
5977	SLC35B1	-1.00	9.82E-01	9.96E-01	1509.17	not significant
5978	VEGFC	-1.00	9.81E-01	9.95E-01	182.66	not significant
5979	C5orf28	-1.00	9.81E-01	9.95E-01	494.92	not significant
5980	ENPP3	-1.00	9.45E-01	NA	20.71	not significant
5981	RNF126	-1.00	9.82E-01	9.96E-01	2648.85	not significant
5982	PARD6B	-1.00	9.76E-01	9.94E-01	134.71	not significant
5983	DRP2	-1.00	9.56E-01	NA	69.59	not significant
5984	MSRB1	-1.00	9.86E-01	9.97E-01	378.65	not significant
5985	NPAS1	-1.00	9.58E-01	NA	24.55	not significant
5986	KDELC1	-1.00	9.49E-01	NA	13.82	not significant
5987	ANTXRLP1	-1.00	9.31E-01	NA	9.43	not significant
5988	SMARCA2	-1.00	9.87E-01	9.97E-01	215.48	not significant
5989	ARID1A	-1.00	9.00E-01	9.62E-01	11078.59	not significant
5990	TCEAL3	-1.00	9.72E-01	NA	47.16	not significant
5991	TATDN1	-1.00	9.99E-01	1.00E+00	587.27	not significant
5992	LOC339803	-1.00	9.79E-01	9.95E-01	194.68	not significant
5993	PDAP1	-1.00	9.84E-01	9.96E-01	5451.25	not significant
5994	IPPK	-1.00	9.84E-01	9.96E-01	402.87	not significant
5995	SYNGR2	-1.00	9.84E-01	9.96E-01	2544.12	not significant
5996	AHCY	-1.00	9.83E-01	9.96E-01	13710.44	not significant
5997	CEP128	-1.00	9.78E-01	9.95E-01	943.38	not significant
5998	TBC1D32	-1.00	9.84E-01	9.96E-01	249.36	not significant
5999	NEK10	-1.00	9.56E-01	NA	25.23	not significant
6000	USP35	-1.00	9.83E-01	9.96E-01	288.38	not significant
6001	ZNF252P-AS1	-1.00	9.50E-01	NA	10.32	not significant
6002	ZNF322	-1.00	9.75E-01	NA	42.39	not significant
6003	ZNF467	-1.00	9.57E-01	NA	14.40	not significant
6004	FAM212A	-1.00	9.82E-01	NA	100.34	not significant
6005	METTL20	-1.00	9.51E-01	NA	10.55	not significant
6006	HIST1H4H	-1.00	9.71E-01	NA	42.68	not significant
6007	MEA1	-1.00	9.89E-01	9.97E-01	4047.06	not significant
6008	TRAPPC3	-1.00	9.90E-01	9.97E-01	1775.54	not significant
6009	MAP1S	-1.00	9.89E-01	9.97E-01	1713.41	not significant
6010	PROCR	-1.00	9.41E-01	NA	9.78	not significant
6011	FBXO21	-1.00	9.88E-01	9.97E-01	2301.10	not significant
6012	EP400NL	-1.00	9.86E-01	9.97E-01	290.60	not significant
6013	ABLIM2	-1.00	9.41E-01	NA	9.69	not significant
6014	FNDC3A	-1.00	9.87E-01	9.97E-01	2832.72	not significant
6015	HCST	-1.00	9.90E-01	9.97E-01	302.34	not significant
6016	PNPLA7	-1.00	9.79E-01	NA	39.38	not significant
6017	GPD1	-1.00	9.59E-01	NA	11.53	not significant
6018	PDE9A	-1.00	9.90E-01	9.97E-01	224.25	not significant
6019	REG4	-1.00	9.53E-01	NA	9.91	not significant
6020	MRPL27	-1.00	9.90E-01	9.98E-01	988.68	not significant
6021	NDUFB7	-1.00	9.96E-01	1.00E+00	1941.45	not significant
6022	HS3ST3B1	-1.00	9.39E-01	NA	13.19	not significant
6023	CLTCL1	-1.00	9.86E-01	NA	52.65	not significant
6024	THUMPD2	-1.00	9.92E-01	9.98E-01	712.36	not significant
6025	FAM193A	-1.00	9.92E-01	9.98E-01	1700.13	not significant
6026	FCHO1	-1.00	9.90E-01	9.98E-01	1479.75	not significant
6027	MIAT	-1.00	9.88E-01	9.97E-01	173.83	not significant
6028	PCOLCE	-1.00	8.63E-01	NA	31.63	not significant
6029	WDR66	-1.00	9.74E-01	NA	15.37	not significant
6030	LINC00963	-1.00	9.81E-01	NA	16.08	not significant
6031	DOC2A	-1.00	9.88E-01	NA	83.62	not significant
6032	UNC93B1	-1.00	9.76E-01	NA	21.07	not significant
6033	LOC102723703	-1.00	9.47E-01	NA	11.93	not significant
6034	WFIKKN1	-1.00	9.86E-01	NA	26.88	not significant
6035	GNMT	-1.00	9.75E-01	NA	15.96	not significant
6036	MCEMP1	-1.00	9.76E-01	NA	8.54	not significant
6037	LINC00342	-1.00	9.79E-01	9.95E-01	178.44	not significant
6038	GPKOW	-1.00	9.94E-01	1.00E+00	292.90	not significant
6039	FAM195B	-1.00	9.93E-01	9.99E-01	2060.28	not significant
6040	TC2N	-1.00	9.86E-01	9.97E-01	745.07	not significant
6041	LINC00173	-1.00	9.83E-01	NA	21.97	not significant
6042	DFNA5	-1.00	9.65E-01	NA	22.00	not significant
6043	BNIP1	-1.00	9.90E-01	9.98E-01	515.48	not significant
6044	BLOC1S6	-1.00	9.98E-01	1.00E+00	2960.70	not significant
6045	XPO7	-1.00	9.94E-01	9.99E-01	4177.96	not significant
6046	DYNC1LI2	-1.00	9.94E-01	9.99E-01	2180.71	not significant
6047	SLC35A3	-1.00	9.94E-01	1.00E+00	1293.15	not significant
6048	ANKH	-1.00	9.94E-01	9.99E-01	2269.11	not significant
6049	ALDH8A1	-1.00	9.83E-01	NA	20.34	not significant
6050	ZHX1-C8orf76	-1.00	9.93E-01	NA	26.28	not significant
6051	ZNF771	-1.00	9.96E-01	1.00E+00	154.11	not significant
6052	LAMA3	-1.00	9.86E-01	NA	16.37	not significant
6053	HIST1H4C	-1.00	9.88E-01	NA	23.63	not significant
6054	ZNF793	-1.00	9.79E-01	NA	8.58	not significant
6055	C8orf58	-1.00	9.95E-01	1.00E+00	106.53	not significant
6056	RABGGTA	-1.00	9.98E-01	1.00E+00	689.77	not significant
6057	RDX	-1.00	9.93E-01	NA	56.27	not significant
6058	KTN1-AS1	-1.00	9.91E-01	NA	42.35	not significant
6059	ANKRD31	-1.00	9.90E-01	NA	14.68	not significant

6060	FAM104B	-1.00	1.00E+00	1.00E+00	459.27	not significant
6061	LINC00471	-1.00	9.86E-01	NA	17.29	not significant
6062	GCAT	-1.00	9.83E-01	9.96E-01	226.90	not significant
6063	ETV2	-1.00	9.92E-01	NA	20.52	not significant
6064	HAS3	-1.00	9.93E-01	NA	84.01	not significant
6065	CHRNA3	-1.00	9.91E-01	NA	24.17	not significant
6066	PTPRF	-1.00	9.92E-01	NA	37.95	not significant
6067	ZNF844	-1.00	9.76E-01	NA	9.80	not significant
6068	MRGBP	-1.00	9.96E-01	1.00E+00	1200.64	not significant
6069	ZNF234	-1.00	9.95E-01	1.00E+00	699.11	not significant
6070	BOP1	-1.00	9.99E-01	1.00E+00	633.33	not significant
6071	IARS2	-1.00	9.77E-01	9.94E-01	4371.44	not significant
6072	DGKH	-1.00	9.92E-01	9.98E-01	1323.14	not significant
6073	RANBP10	-1.00	9.96E-01	1.00E+00	1845.18	not significant
6074	STAP2	-1.00	9.80E-01	NA	8.68	not significant
6075	IL21R	-1.00	9.97E-01	1.00E+00	290.03	not significant
6076	ZNF773	-1.00	9.94E-01	9.99E-01	251.86	not significant
6077	ZFP30	-1.00	9.95E-01	1.00E+00	761.70	not significant
6078	GTSE1-AS1	1.00	1.00E+00	NA	11.30	not significant
6079	CTTN	1.00	9.97E-01	NA	62.29	not significant
6080	LOC100506123	1.00	9.98E-01	NA	22.08	not significant
6081	CYP4F35P	1.00	9.99E-01	NA	12.90	not significant
6082	FAM109A	1.00	9.98E-01	1.00E+00	189.39	not significant
6083	NFKBIL1	1.00	9.99E-01	NA	60.35	not significant
6084	LOC100506548	1.00	9.88E-01	9.97E-01	913.39	not significant
6085	TRIM23	1.00	9.92E-01	9.98E-01	482.13	not significant
6086	EMR1	1.00	9.98E-01	NA	15.23	not significant
6087	DRAXIN	1.00	1.00E+00	1.00E+00	313.27	not significant
6088	ATXN1	1.00	9.99E-01	1.00E+00	188.96	not significant
6089	SLC10A3	1.00	9.95E-01	NA	19.54	not significant
6090	BRPF1	1.00	9.95E-01	1.00E+00	2921.33	not significant
6091	STK36	1.00	9.98E-01	1.00E+00	276.74	not significant
6092	NNT-AS1	1.00	9.97E-01	1.00E+00	572.97	not significant
6093	ANKRD39	1.00	1.00E+00	1.00E+00	464.85	not significant
6094	ZFPM2	1.00	9.98E-01	NA	58.71	not significant
6095	KRTCAP3	1.00	9.98E-01	NA	14.27	not significant
6096	PDZD4	1.00	9.99E-01	NA	18.06	not significant
6097	CITED4	1.00	9.98E-01	NA	19.71	not significant
6098	LMBRD2	1.00	9.99E-01	1.00E+00	680.57	not significant
6099	TECPR2	1.00	9.98E-01	1.00E+00	658.36	not significant
6100	C1orf145	1.00	1.00E+00	NA	13.22	not significant
6101	TRIM69	1.00	9.95E-01	NA	17.42	not significant
6102	TIRAP	1.00	9.93E-01	NA	16.70	not significant
6103	LOC100506746	1.00	9.91E-01	NA	18.21	not significant
6104	MORN1	1.00	9.96E-01	NA	53.88	not significant
6105	LCORL	1.00	1.00E+00	1.00E+00	691.71	not significant
6106	CCDC81	1.00	9.97E-01	NA	25.78	not significant
6107	MRPL44	1.00	1.00E+00	1.00E+00	991.93	not significant
6108	ZBTB3	1.00	9.97E-01	1.00E+00	162.84	not significant
6109	MYL12B	1.00	9.98E-01	1.00E+00	8003.48	not significant
6110	UBTD2	1.00	9.99E-01	1.00E+00	1099.70	not significant
6111	FAM69B	1.00	9.99E-01	1.00E+00	227.83	not significant
6112	ASPH	1.00	9.98E-01	1.00E+00	351.52	not significant
6113	SLC52A2	1.00	9.96E-01	1.00E+00	268.56	not significant
6114	HERC1	1.00	9.98E-01	1.00E+00	2162.76	not significant
6115	GALNT2	1.00	9.98E-01	1.00E+00	9627.38	not significant
6116	ABLIM1	1.00	9.99E-01	1.00E+00	3805.63	not significant
6117	SLC12A9	1.00	1.00E+00	1.00E+00	768.77	not significant
6118	ZRANB2-AS1	1.00	9.91E-01	NA	21.29	not significant
6119	C4orf29	1.00	9.84E-01	9.96E-01	634.54	not significant
6120	NRXN2	1.00	9.96E-01	1.00E+00	617.95	not significant
6121	REP15	1.00	9.90E-01	NA	13.20	not significant
6122	NAPSA	1.00	9.95E-01	NA	14.96	not significant
6123	ZNF528	1.00	9.98E-01	1.00E+00	125.06	not significant
6124	SGSH	1.00	9.80E-01	NA	16.10	not significant
6125	HIC1	1.00	9.88E-01	NA	69.47	not significant
6126	FERMT2	1.00	9.85E-01	NA	69.54	not significant
6127	MGC12916	1.00	9.76E-01	NA	14.14	not significant
6128	GSKIP	1.00	9.94E-01	9.99E-01	1144.14	not significant
6129	CHST1	1.00	9.91E-01	NA	65.82	not significant
6130	IQCH-AS1	1.00	9.94E-01	9.99E-01	185.49	not significant
6131	AQP11	1.00	9.81E-01	NA	15.36	not significant
6132	ISCA1	1.00	9.96E-01	1.00E+00	771.65	not significant
6133	PRDX2	1.00	9.98E-01	1.00E+00	4034.87	not significant
6134	SLC16A3	1.00	9.89E-01	9.97E-01	392.42	not significant
6135	NELFB	1.00	9.95E-01	1.00E+00	2195.19	not significant
6136	CNOT6	1.00	9.82E-01	9.96E-01	10464.27	not significant
6137	VAMP3	1.00	9.97E-01	1.00E+00	924.86	not significant
6138	RMDN3	1.00	9.96E-01	1.00E+00	1480.37	not significant
6139	ATAD5	1.00	9.95E-01	1.00E+00	2989.12	not significant
6140	LRIG2	1.00	9.96E-01	1.00E+00	678.69	not significant
6141	REV1	1.00	9.96E-01	1.00E+00	1230.91	not significant
6142	LINC00910	1.00	9.85E-01	NA	23.66	not significant
6143	PTCH2	1.00	9.83E-01	NA	12.70	not significant
6144	ZNF510	1.00	9.88E-01	9.97E-01	597.82	not significant
6145	LOC100130992	1.00	9.84E-01	NA	25.92	not significant
6146	PTPRG	1.00	9.91E-01	NA	83.69	not significant
6147	CYP4F29P	1.00	5.06E-01	NA	21.87	not significant

6148	ZNF561-AS1	1.00	9.85E-01	9.96E-01	102.23	not significant
6149	KIAA1644	1.00	9.64E-01	NA	11.05	not significant
6150	PIGZ	1.00	9.80E-01	NA	32.14	not significant
6151	ABHD8	1.00	9.89E-01	9.97E-01	313.71	not significant
6152	SDCCAG3	1.00	9.92E-01	9.98E-01	1176.87	not significant
6153	GUK1	1.00	9.89E-01	9.97E-01	6184.00	not significant
6154	CCDC102B	1.00	9.83E-01	NA	55.09	not significant
6155	MAN1B1-AS1	1.00	9.75E-01	NA	28.02	not significant
6156	FARS2	1.00	9.92E-01	9.98E-01	441.69	not significant
6157	PTGER2	1.00	9.89E-01	9.97E-01	295.99	not significant
6158	GUCY1A3	1.00	9.99E-01	1.00E+00	788.05	not significant
6159	GAS2L1	1.00	9.90E-01	9.98E-01	430.75	not significant
6160	FHDC1	1.00	9.56E-01	NA	19.23	not significant
6161	SLC26A2	1.00	9.92E-01	9.98E-01	1162.79	not significant
6162	NBPF10	1.00	9.79E-01	NA	46.91	not significant
6163	TECTA	1.00	9.70E-01	NA	13.15	not significant
6164	ORAI1	1.00	9.97E-01	NA	100.53	not significant
6165	LOC100507530	1.00	9.68E-01	NA	23.85	not significant
6166	ASB12	1.00	9.66E-01	NA	19.61	not significant
6167	SUOX	1.00	9.64E-01	NA	24.43	not significant
6168	TOMM40L	1.00	9.89E-01	9.97E-01	1136.62	not significant
6169	CREG1	1.00	9.89E-01	9.97E-01	1072.59	not significant
6170	WTAP	1.00	9.89E-01	9.97E-01	4134.84	not significant
6171	SCAND2P	1.00	9.88E-01	9.97E-01	156.98	not significant
6172	MOCS1	1.00	9.90E-01	9.97E-01	1080.98	not significant
6173	SETD9	1.00	9.82E-01	9.96E-01	110.05	not significant
6174	TFIP11	1.00	9.90E-01	9.98E-01	2024.77	not significant
6175	PPP2R1A	1.00	9.65E-01	9.89E-01	7515.37	not significant
6176	COQ10A	1.00	9.88E-01	9.97E-01	465.02	not significant
6177	RAB9A	1.00	9.88E-01	9.97E-01	356.81	not significant
6178	COPB1	1.00	1.00E+00	1.00E+00	6908.24	not significant
6179	SMG5	1.00	9.87E-01	9.97E-01	6381.56	not significant
6180	PUS10	1.00	9.87E-01	9.97E-01	422.93	not significant
6181	TMEM248	1.00	9.84E-01	9.96E-01	5906.73	not significant
6182	ZC3H12A	1.00	9.91E-01	9.98E-01	258.40	not significant
6183	RPRD2	1.00	9.97E-01	1.00E+00	2243.89	not significant
6184	WASH7P	1.00	9.67E-01	NA	29.83	not significant
6185	SPSB2	1.00	9.52E-01	NA	15.04	not significant
6186	TREML1	1.00	9.73E-01	NA	49.93	not significant
6187	ARHGEF39	1.00	9.86E-01	9.97E-01	269.15	not significant
6188	NUDCD3	1.00	9.85E-01	9.97E-01	2534.44	not significant
6189	FOXRED1	1.00	9.86E-01	9.97E-01	1448.75	not significant
6190	RASSF3	1.00	9.86E-01	9.97E-01	1804.11	not significant
6191	GAS8	1.00	9.63E-01	NA	27.44	not significant
6192	FAM210A	1.00	9.86E-01	9.97E-01	1310.35	not significant
6193	LOC100506804	1.00	9.44E-01	NA	12.14	not significant
6194	CFH	1.00	9.84E-01	9.96E-01	395.52	not significant
6195	CYBRD1	1.00	9.84E-01	9.96E-01	438.70	not significant
6196	ST7L	1.00	9.83E-01	9.96E-01	381.97	not significant
6197	CCDC53	1.00	9.81E-01	9.95E-01	577.55	not significant
6198	TIGD1	1.00	9.67E-01	9.90E-01	251.21	not significant
6199	FREM1	1.00	9.51E-01	NA	22.05	not significant
6200	TMEM128	1.00	9.77E-01	9.94E-01	569.69	not significant
6201	NCF2	1.00	9.49E-01	NA	24.03	not significant
6202	GNPAT	1.00	9.85E-01	9.96E-01	2322.18	not significant
6203	ELP6	1.00	9.83E-01	9.96E-01	1691.53	not significant
6204	PIGU	1.00	9.83E-01	9.96E-01	1843.33	not significant
6205	FAM122B	1.00	9.81E-01	9.95E-01	4477.41	not significant
6206	LOC101927365	1.00	9.75E-01	NA	92.74	not significant
6207	CHPF	1.00	9.76E-01	9.94E-01	121.58	not significant
6208	DZIP1	1.00	9.85E-01	9.96E-01	446.19	not significant
6209	MIS18BP1	1.00	9.82E-01	9.96E-01	1861.54	not significant
6210	SSSCA1-AS1	1.00	9.34E-01	NA	14.62	not significant
6211	USP46-AS1	1.00	9.32E-01	NA	13.26	not significant
6212	CDCP1	1.00	9.23E-01	NA	12.55	not significant
6213	ALOX15P1	1.00	9.41E-01	NA	17.19	not significant
6214	CREB3L1	1.00	9.65E-01	NA	61.39	not significant
6215	PRMT5-AS1	1.00	9.11E-01	NA	10.39	not significant
6216	CERS6-AS1	1.00	9.03E-01	NA	41.72	not significant
6217	AURKC	1.00	9.21E-01	NA	14.23	not significant
6218	LRRC38	1.00	9.32E-01	NA	15.47	not significant
6219	LFNG	1.00	9.91E-01	9.98E-01	269.46	not significant
6220	C9orf43	1.00	9.21E-01	NA	11.98	not significant
6221	ACSS2	1.00	9.70E-01	9.92E-01	280.19	not significant
6222	HIST1H2BB	1.00	9.12E-01	NA	11.69	not significant
6223	GEMIN8P4	1.00	9.69E-01	NA	90.41	not significant
6224	GPN2	1.00	9.87E-01	9.97E-01	779.25	not significant
6225	ATP6AP2	1.00	9.92E-01	9.98E-01	2624.59	not significant
6226	ZNF282	1.00	9.82E-01	9.96E-01	2003.82	not significant
6227	RB1CC1	1.00	9.80E-01	9.95E-01	2618.53	not significant
6228	CLASP1	1.00	9.81E-01	9.95E-01	3141.29	not significant
6229	KCNH1	1.00	9.29E-01	NA	16.42	not significant
6230	SEMA4B	1.00	9.80E-01	9.95E-01	335.72	not significant
6231	DIS3L2	1.00	9.81E-01	9.95E-01	1273.52	not significant
6232	RAB40B	1.00	9.46E-01	NA	26.95	not significant
6233	ZNF2	1.00	9.73E-01	9.92E-01	251.12	not significant
6234	ITGA7	1.00	9.50E-01	NA	30.72	not significant
6235	ADAMTSL5	1.00	9.52E-01	NA	36.42	not significant

6236	CCDC30	1.00	9.00E-01	NA	9.11	not significant
6237	ADAMTS7P1	1.00	8.97E-01	NA	8.77	not significant
6238	RPL19P12	1.00	9.65E-01	NA	88.65	not significant
6239	C21orf67	1.00	9.67E-01	9.90E-01	141.58	not significant
6240	CCDC13	1.00	9.19E-01	NA	14.67	not significant
6241	FAM167A	1.00	9.37E-01	NA	25.74	not significant
6242	DICER1-AS1	1.00	9.28E-01	NA	19.40	not significant
6243	LOC654342	1.00	9.64E-01	NA	92.36	not significant
6244	MND1	1.00	9.71E-01	9.92E-01	856.36	not significant
6245	MFAP2	1.00	9.11E-01	NA	11.54	not significant
6246	BLVRB	1.00	9.61E-01	NA	85.14	not significant
6247	R3HCC1	1.00	9.77E-01	9.94E-01	1597.55	not significant
6248	PIFO	1.00	9.22E-01	NA	17.16	not significant
6249	PIWIL4	1.00	9.59E-01	NA	65.83	not significant
6250	PCNP	1.00	9.73E-01	9.92E-01	5699.94	not significant
6251	EID2	1.00	9.79E-01	9.95E-01	715.24	not significant
6252	STARD5	1.00	9.63E-01	NA	77.07	not significant
6253	FXR1	1.00	9.73E-01	9.92E-01	4434.51	not significant
6254	TARP	1.00	9.83E-01	9.96E-01	734.50	not significant
6255	AMPD3	1.00	9.78E-01	9.95E-01	1724.37	not significant
6256	IFI30	1.00	9.77E-01	9.94E-01	1157.84	not significant
6257	SAMD13	1.00	9.56E-01	NA	60.68	not significant
6258	MST1P2	1.00	9.09E-01	NA	13.81	not significant
6259	ZXDB	1.00	9.84E-01	9.96E-01	375.27	not significant
6260	ITGB7	1.00	9.72E-01	9.92E-01	309.30	not significant
6261	USP43	1.00	9.41E-01	NA	29.41	not significant
6262	MST1R	1.00	9.56E-01	NA	53.28	not significant
6263	SPATA20	1.00	9.51E-01	NA	44.51	not significant
6264	ZNF620	1.00	8.92E-01	NA	19.62	not significant
6265	TMEM44-AS1	1.00	9.29E-01	NA	28.21	not significant
6266	IFITM2	1.00	9.19E-01	NA	20.18	not significant
6267	TFPT	1.00	9.73E-01	9.92E-01	329.35	not significant
6268	KIFC3	1.00	9.64E-01	NA	46.37	not significant
6269	SSBP2	1.00	9.74E-01	9.93E-01	1185.86	not significant
6270	ADO	1.00	9.76E-01	9.93E-01	1639.51	not significant
6271	RTKN	1.00	8.73E-01	NA	8.53	not significant
6272	STT3A	1.00	9.73E-01	9.92E-01	7055.13	not significant
6273	KIAA0930	1.00	9.95E-01	1.00E+00	2729.04	not significant
6274	CLEC4A	1.00	9.06E-01	NA	13.83	not significant
6275	VIM-AS1	1.00	9.59E-01	9.86E-01	366.90	not significant
6276	RPL23AP82	1.00	9.31E-01	NA	32.82	not significant
6277	SLC6A16	1.00	9.32E-01	NA	29.45	not significant
6278	FKBP1B	1.00	8.81E-01	NA	9.66	not significant
6279	AUH	1.00	9.65E-01	9.89E-01	224.14	not significant
6280	LOC100507501	1.00	9.38E-01	NA	36.30	not significant
6281	FBXO6	1.00	9.65E-01	9.89E-01	232.40	not significant
6282	DYNLT1	1.00	9.67E-01	9.90E-01	389.44	not significant
6283	PRICKLE4	1.00	9.49E-01	NA	83.85	not significant
6284	TNIP2	1.00	9.72E-01	9.92E-01	1311.15	not significant
6285	PLAA	1.00	9.72E-01	9.92E-01	2239.21	not significant
6286	MOSPD3	1.00	9.69E-01	9.91E-01	393.37	not significant
6287	DUS1L	1.00	9.89E-01	9.97E-01	5558.68	not significant
6288	FAM213B	1.00	9.71E-01	9.92E-01	1295.43	not significant
6289	FAM45B	1.00	9.63E-01	9.88E-01	188.78	not significant
6290	CLPTM1L	1.00	9.73E-01	9.92E-01	7185.01	not significant
6291	NLRP14	1.00	9.43E-01	NA	62.03	not significant
6292	MMP14	1.00	9.36E-01	NA	42.11	not significant
6293	CEP95	1.00	9.75E-01	9.93E-01	956.39	not significant
6294	LOC728323	1.00	9.72E-01	NA	30.76	not significant
6295	REEP5	1.00	9.49E-01	9.80E-01	1707.36	not significant
6296	CCZ1	1.00	9.53E-01	9.82E-01	109.19	not significant
6297	KIAA0226	1.00	9.73E-01	9.92E-01	1459.36	not significant
6298	DPF3	1.00	9.76E-01	9.94E-01	992.69	not significant
6299	JADE1	1.00	9.72E-01	9.92E-01	2382.29	not significant
6300	PDE3B	1.00	9.38E-01	NA	49.77	not significant
6301	AGPAT1	1.00	9.65E-01	9.89E-01	274.80	not significant
6302	GALNT3	1.00	9.11E-01	NA	25.07	not significant
6303	ROM1	1.00	8.80E-01	NA	14.99	not significant
6304	FAM132B	1.00	9.02E-01	NA	20.63	not significant
6305	EAF2	1.00	9.50E-01	NA	90.40	not significant
6306	MIF	1.00	9.90E-01	9.98E-01	19406.24	not significant
6307	C14orf169	1.00	9.71E-01	9.92E-01	1315.25	not significant
6308	FAM118A	1.00	9.69E-01	9.91E-01	843.11	not significant
6309	EXOSC2	1.00	9.70E-01	9.91E-01	1643.20	not significant
6310	DENND1B	1.00	9.71E-01	9.92E-01	3519.01	not significant
6311	C17orf85	1.00	9.80E-01	9.95E-01	3867.32	not significant
6312	RAB31	1.00	9.00E-01	NA	20.17	not significant
6313	PYROXD1	1.00	9.52E-01	9.82E-01	493.02	not significant
6314	FAM66C	1.00	8.60E-01	NA	10.75	not significant
6315	ZNF425	1.00	9.45E-01	NA	81.71	not significant
6316	GGT1	1.00	9.53E-01	9.82E-01	484.70	not significant
6317	HSF2BP	1.00	8.95E-01	NA	23.96	not significant
6318	DUS3L	1.00	9.74E-01	9.92E-01	2539.39	not significant
6319	ARPC5	1.00	9.63E-01	9.88E-01	6954.91	not significant
6320	JADE2	1.00	9.63E-01	9.88E-01	4128.93	not significant
6321	PCDHGB2	1.00	9.08E-01	NA	32.30	not significant
6322	USP25	1.00	9.66E-01	9.90E-01	2262.17	not significant
6323	FYB	1.00	9.66E-01	9.89E-01	2845.02	not significant

6324	PLAG1	1.00	9.18E-01	NA	36.40	not significant
6325	LZTS3	1.00	8.31E-01	NA	9.62	not significant
6326	PPP1R2P3	1.00	8.79E-01	NA	17.23	not significant
6327	MIR503HG	1.00	8.56E-01	NA	13.48	not significant
6328	DLX1	1.00	8.94E-01	NA	19.44	not significant
6329	PAXBP1-AS1	1.00	8.80E-01	NA	16.14	not significant
6330	CATSPER2P1	1.00	8.70E-01	NA	13.62	not significant
6331	AKR7A3	1.00	8.58E-01	NA	12.10	not significant
6332	CTH	1.00	8.51E-01	NA	11.72	not significant
6333	ADM	1.00	8.37E-01	NA	9.97	not significant
6334	ZFAND2A	1.00	9.50E-01	9.81E-01	265.36	not significant
6335	MCAT	1.00	9.64E-01	9.88E-01	744.67	not significant
6336	PSMB9	1.00	9.64E-01	9.89E-01	932.76	not significant
6337	DGCR6L	1.00	9.63E-01	9.88E-01	743.03	not significant
6338	RGS19	1.00	9.63E-01	9.88E-01	1391.52	not significant
6339	CETN4P	1.00	8.25E-01	NA	10.61	not significant
6340	FBXO33	1.00	9.62E-01	9.88E-01	1482.83	not significant
6341	SRP68	1.00	9.57E-01	9.84E-01	6435.72	not significant
6342	RAC3	1.00	9.58E-01	9.85E-01	305.86	not significant
6343	ZSCAN31	1.00	9.16E-01	NA	39.29	not significant
6344	LINC00672	1.00	9.09E-01	NA	34.57	not significant
6345	C1orf27	1.00	9.69E-01	9.91E-01	892.74	not significant
6346	DNAJB14	1.00	9.63E-01	9.88E-01	2694.08	not significant
6347	GPR35	1.00	8.82E-01	NA	24.41	not significant
6348	C1orf53	1.00	9.16E-01	NA	45.01	not significant
6349	GTF2H2	1.00	9.31E-01	NA	68.89	not significant
6350	GEMIN2	1.00	9.62E-01	9.88E-01	528.56	not significant
6351	TCTEX1D2	1.00	9.44E-01	9.79E-01	167.30	not significant
6352	ACY1	1.00	8.57E-01	NA	17.52	not significant
6353	BCL2L14	1.00	9.06E-01	NA	39.02	not significant
6354	FGFR1	1.00	9.45E-01	9.79E-01	136.36	not significant
6355	LOC102724297	1.00	8.29E-01	NA	11.52	not significant
6356	GLIS2	1.00	8.57E-01	NA	19.81	not significant
6357	DNAJB4	1.00	9.65E-01	9.89E-01	236.18	not significant
6358	VTI1B	1.00	9.61E-01	9.87E-01	1990.27	not significant
6359	MYSM1	1.00	9.62E-01	9.88E-01	1718.05	not significant
6360	PBLD	1.00	9.13E-01	NA	46.76	not significant
6361	H2AFY2	1.00	8.46E-01	NA	14.40	not significant
6362	HYKK	1.00	8.64E-01	NA	20.40	not significant
6363	NRSN2-AS1	1.00	8.75E-01	NA	21.62	not significant
6364	NBPF15	1.00	8.60E-01	NA	18.46	not significant
6365	CLIP2	1.00	8.95E-01	NA	28.10	not significant
6366	ATP13A4	1.00	8.60E-01	NA	17.40	not significant
6367	APP	1.00	9.10E-01	NA	43.28	not significant
6368	43532_13639	1.00	9.43E-01	9.79E-01	145.69	not significant
6369	HIST1H4D	1.00	7.96E-01	NA	10.19	not significant
6370	HIST1H2BE	1.00	9.90E-01	NA	31.14	not significant
6371	ZNF833P	1.00	8.96E-01	NA	35.77	not significant
6372	C20orf197	1.00	9.43E-01	9.79E-01	163.87	not significant
6373	C1orf101	1.00	8.22E-01	NA	12.06	not significant
6374	LOC729970	1.00	8.23E-01	NA	11.01	not significant
6375	IMMP1L	1.00	9.42E-01	9.79E-01	559.27	not significant
6376	BRF1	1.00	9.58E-01	9.85E-01	1485.66	not significant
6377	RCC2	1.00	9.50E-01	9.81E-01	15394.01	not significant
6378	PTOV1-AS1	1.00	7.91E-01	NA	9.80	not significant
6379	FAM161A	1.00	9.54E-01	9.83E-01	426.22	not significant
6380	ISY1	1.00	9.60E-01	9.87E-01	952.39	not significant
6381	AASDH	1.00	9.54E-01	9.83E-01	481.87	not significant
6382	C3orf35	1.00	7.89E-01	NA	9.34	not significant
6383	ABHD13	1.00	9.57E-01	9.85E-01	1512.82	not significant
6384	ZNF35	1.00	8.52E-01	NA	16.49	not significant
6385	FAM129C	1.00	9.29E-01	NA	80.76	not significant
6386	STX18-AS1	1.00	8.71E-01	NA	88.53	not significant
6387	BRAF	1.00	9.81E-01	9.95E-01	366.22	not significant
6388	RP2	1.00	9.31E-01	NA	92.29	not significant
6389	PI16	1.00	9.02E-01	NA	40.59	not significant
6390	C8orf44	1.00	9.06E-01	NA	46.03	not significant
6391	PSPN	1.00	8.27E-01	NA	13.15	not significant
6392	RAB3B	1.00	8.44E-01	NA	17.66	not significant
6393	TRIM47	1.00	9.12E-01	NA	50.92	not significant
6394	SERHL	1.00	8.08E-01	NA	12.14	not significant
6395	COQ10B	1.00	9.57E-01	9.84E-01	815.57	not significant
6396	SSR1	1.00	9.49E-01	9.80E-01	9230.09	not significant
6397	DYNC1H1	1.00	9.43E-01	9.79E-01	11183.34	not significant
6398	LIMK2	1.00	9.34E-01	9.75E-01	1763.78	not significant
6399	SHPRH	1.00	9.81E-01	9.95E-01	2543.51	not significant
6400	ZNF652	1.00	9.73E-01	9.92E-01	346.00	not significant
6401	UVSSA	1.00	9.53E-01	9.82E-01	485.26	not significant
6402	LOC100130987	1.00	8.25E-01	NA	15.00	not significant
6403	APOE	1.00	8.08E-01	NA	12.35	not significant
6404	LOC100506127	1.00	9.24E-01	NA	85.60	not significant
6405	YTHDF3-AS1	1.00	8.41E-01	NA	17.18	not significant
6406	NPEPL1	1.00	7.69E-01	NA	8.52	not significant
6407	SGK223	1.00	9.19E-01	NA	62.92	not significant
6408	STAG3L1	1.00	9.15E-01	NA	49.89	not significant
6409	HGH1	1.00	8.92E-01	NA	46.82	not significant
6410	XCL1	1.00	7.87E-01	NA	9.81	not significant
6411	PLEKHG5	1.00	8.94E-01	NA	46.30	not significant

6412	TUT1	1.00	9.52E-01	9.82E-01	744.56	not significant
6413	C17orf100	1.00	8.67E-01	NA	28.16	not significant
6414	C18orf54	1.00	9.34E-01	9.75E-01	557.94	not significant
6415	PSD	1.00	8.56E-01	NA	24.58	not significant
6416	TMEM222	1.00	9.52E-01	9.82E-01	1196.29	not significant
6417	MTBP	1.00	9.69E-01	9.91E-01	1067.76	not significant
6418	SLC26A11	1.00	7.92E-01	NA	11.08	not significant
6419	WDR62	1.00	9.88E-01	9.97E-01	3554.88	not significant
6420	ESCO2	1.00	9.52E-01	9.82E-01	2328.89	not significant
6421	CBFA2T3	1.00	9.39E-01	9.78E-01	8520.25	not significant
6422	C22orf46	1.00	9.53E-01	9.82E-01	681.69	not significant
6423	PATL1	1.00	9.47E-01	9.79E-01	3646.81	not significant
6424	OSER1-AS1	1.00	8.58E-01	NA	22.42	not significant
6425	LRRIQ3	1.00	8.43E-01	NA	18.99	not significant
6426	RNF115	1.00	9.48E-01	9.80E-01	396.83	not significant
6427	NOP14-AS1	1.00	9.43E-01	9.79E-01	214.42	not significant
6428	LRRC24	1.00	8.94E-01	NA	50.61	not significant
6429	C15orf52	1.00	7.78E-01	NA	11.00	not significant
6430	RNF150	1.00	9.40E-01	9.78E-01	285.93	not significant
6431	TMEM63C	1.00	7.84E-01	NA	10.40	not significant
6432	SCLY	1.00	7.45E-01	NA	8.85	not significant
6433	OSGIN1	1.00	8.25E-01	NA	15.22	not significant
6434	STXBP5L	1.00	8.73E-01	NA	34.19	not significant
6435	TMEM25	1.00	8.36E-01	NA	20.66	not significant
6436	LOC101928784	1.00	7.88E-01	NA	11.87	not significant
6437	USE1	1.00	9.44E-01	9.79E-01	406.60	not significant
6438	MTFP1	1.00	9.48E-01	9.80E-01	2777.82	not significant
6439	C1orf216	1.00	9.58E-01	9.85E-01	719.22	not significant
6440	PTGES3L	1.00	8.03E-01	NA	14.55	not significant
6441	DLG1	1.00	9.50E-01	9.81E-01	2966.98	not significant
6442	MAPK14	1.00	9.44E-01	9.79E-01	4022.13	not significant
6443	PXK	1.00	9.45E-01	9.79E-01	3085.99	not significant
6444	PPP1CB	1.00	9.20E-01	9.69E-01	7180.74	not significant
6445	ACVR2B-AS1	1.00	7.87E-01	NA	12.88	not significant
6446	ZGLP1	1.00	9.07E-01	NA	73.24	not significant
6447	EP400	1.00	9.35E-01	9.75E-01	6282.40	not significant
6448	ALPK1	1.00	9.40E-01	9.78E-01	229.66	not significant
6449	BLZF1	1.00	9.30E-01	9.74E-01	537.31	not significant
6450	ASIC3	1.00	8.86E-01	NA	40.84	not significant
6451	PCDH9	1.00	8.93E-01	NA	50.47	not significant
6452	ZNF576	1.00	9.49E-01	9.80E-01	461.77	not significant
6453	NBPF12	1.00	8.50E-01	NA	29.01	not significant
6454	CMYA5	1.00	8.81E-01	NA	41.26	not significant
6455	EFCAB7	1.00	9.44E-01	9.79E-01	361.13	not significant
6456	UBAC2-AS1	1.00	8.57E-01	NA	32.62	not significant
6457	TTC23	1.00	8.71E-01	NA	36.69	not significant
6458	ENGASE	1.00	8.16E-01	NA	17.45	not significant
6459	LRRC29	1.00	7.98E-01	NA	13.10	not significant
6460	FAM86JP	1.00	8.88E-01	NA	50.43	not significant
6461	SLC25A11	1.00	9.49E-01	9.80E-01	2220.99	not significant
6462	SUCLG2	1.00	9.47E-01	9.79E-01	1312.25	not significant
6463	APOLD1	1.00	9.02E-01	NA	71.59	not significant
6464	SH3BP2	1.00	9.25E-01	9.72E-01	1810.14	not significant
6465	ICOS	1.00	9.42E-01	9.79E-01	6396.73	not significant
6466	PSMA8	1.00	9.35E-01	9.75E-01	330.75	not significant
6467	PLEC	1.00	9.30E-01	9.74E-01	209.50	not significant
6468	DHFRL1	1.00	9.49E-01	9.80E-01	836.82	not significant
6469	YIPF5	1.00	9.47E-01	9.79E-01	1350.53	not significant
6470	ANKRD50	1.00	9.48E-01	9.80E-01	1265.10	not significant
6471	LRRC8B	1.00	9.21E-01	9.70E-01	514.03	not significant
6472	LRIT3	1.00	7.99E-01	NA	15.09	not significant
6473	AGAP5	1.00	8.96E-01	NA	61.73	not significant
6474	DOCK9-AS2	1.00	7.65E-01	NA	12.03	not significant
6475	PLXNB2	1.00	8.21E-01	NA	18.17	not significant
6476	GUCY2D	1.00	7.38E-01	NA	10.30	not significant
6477	MAP1LC3B2	1.00	7.76E-01	NA	13.05	not significant
6478	PDE6B	1.00	9.33E-01	9.75E-01	327.39	not significant
6479	ETFB	1.00	9.42E-01	9.79E-01	814.62	not significant
6480	SDF2	1.00	9.52E-01	9.82E-01	1018.66	not significant
6481	MTHFSD	1.00	9.35E-01	9.75E-01	554.27	not significant
6482	ADIPOR1	1.00	9.37E-01	9.77E-01	3802.55	not significant
6483	PDIK1L	1.00	9.44E-01	9.79E-01	1543.39	not significant
6484	HIST1H2AL	1.00	8.05E-01	NA	18.71	not significant
6485	SMG1	1.00	9.47E-01	9.79E-01	7345.44	not significant
6486	NLRP3	1.00	8.29E-01	NA	22.22	not significant
6487	CXorf21	1.00	8.50E-01	NA	32.42	not significant
6488	PVRL3	1.00	9.45E-01	9.79E-01	1151.02	not significant
6489	HIST1H3C	1.00	8.47E-01	NA	34.06	not significant
6490	PARP11	1.00	9.52E-01	9.82E-01	925.38	not significant
6491	FAM86C1	1.00	9.31E-01	9.74E-01	171.32	not significant
6492	HOXC4	1.00	9.33E-01	9.75E-01	251.58	not significant
6493	LPAR2	1.00	9.31E-01	9.75E-01	211.71	not significant
6494	ITGB4	1.00	8.60E-01	NA	37.30	not significant
6495	GPR83	1.00	7.77E-01	NA	14.20	not significant
6496	JHDM1D-AS1	1.00	8.96E-01	NA	84.24	not significant
6497	FER	1.00	8.64E-01	9.45E-01	244.02	not significant
6498	SPIN2B	1.00	8.95E-01	NA	78.58	not significant
6499	SNAI3-AS1	1.00	5.11E-01	NA	39.11	not significant

6500	B9D2	1.00	9.20E-01	9.69E-01	157.77	not significant
6501	ID3	1.00	9.38E-01	9.77E-01	747.19	not significant
6502	TUBE1	1.00	9.35E-01	9.75E-01	242.95	not significant
6503	RPL36AL	1.00	9.47E-01	9.80E-01	3890.09	not significant
6504	TIMM10B	1.00	9.44E-01	9.79E-01	2121.17	not significant
6505	LOC493754	1.00	9.27E-01	9.73E-01	496.64	not significant
6506	ATP5A1	1.00	9.48E-01	9.80E-01	18145.64	not significant
6507	LAMTOR5	1.00	8.48E-01	9.36E-01	2192.73	not significant
6508	UBR7	1.00	9.22E-01	9.70E-01	6699.48	not significant
6509	POMGNT1	1.00	9.37E-01	9.77E-01	2562.84	not significant
6510	CNDP2	1.00	9.09E-01	9.65E-01	6764.72	not significant
6511	POLB	1.00	9.42E-01	9.79E-01	1226.62	not significant
6512	MDM4	1.00	9.41E-01	9.78E-01	1536.84	not significant
6513	PDS5B	1.00	9.40E-01	9.78E-01	3804.44	not significant
6514	NOP9	1.00	9.38E-01	9.77E-01	2999.35	not significant
6515	KHDRBS3	1.00	8.87E-01	NA	63.68	not significant
6516	LOC284454	1.00	7.85E-01	NA	20.02	not significant
6517	AFAP1L2	1.00	7.59E-01	NA	12.65	not significant
6518	RSPH3	1.00	8.99E-01	NA	82.01	not significant
6519	S100A4	1.00	8.04E-01	NA	20.37	not significant
6520	H3F3C	1.00	8.71E-01	NA	48.07	not significant
6521	RNF144B	1.00	7.71E-01	NA	15.03	not significant
6522	SMCO4	1.00	8.59E-01	NA	39.70	not significant
6523	SEC24B-AS1	1.00	8.15E-01	NA	24.07	not significant
6524	TSC22D1-AS1	1.00	6.95E-01	NA	9.25	not significant
6525	CTU1	1.00	9.35E-01	9.75E-01	384.49	not significant
6526	ADORA2B	1.00	9.47E-01	9.80E-01	465.82	not significant
6527	TRIM21	1.00	9.45E-01	9.79E-01	730.60	not significant
6528	ATF7IP2	1.00	9.35E-01	9.75E-01	614.57	not significant
6529	RASSF8	1.00	9.32E-01	9.75E-01	409.62	not significant
6530	RAD21	1.00	9.04E-01	9.63E-01	29984.46	not significant
6531	SIVA1	1.00	9.45E-01	9.79E-01	4147.65	not significant
6532	UNC119B	1.00	9.32E-01	9.75E-01	3950.91	not significant
6533	RUNDC1	1.00	9.38E-01	9.77E-01	910.50	not significant
6534	HIST1H2AH	1.00	8.27E-01	NA	26.73	not significant
6535	KIAA0754	1.00	9.17E-01	9.68E-01	1693.59	not significant
6536	ATP6V0A1	1.00	8.72E-01	NA	48.93	not significant
6537	PSTPIP1	1.00	9.23E-01	9.71E-01	479.49	not significant
6538	ADAMTS19	1.00	7.32E-01	NA	10.92	not significant
6539	CERCAM	1.00	7.58E-01	NA	13.91	not significant
6540	ZNF836	1.00	9.21E-01	9.70E-01	237.71	not significant
6541	BTBD8	1.00	7.95E-01	NA	19.07	not significant
6542	PRUNE2	1.00	9.34E-01	9.75E-01	574.86	not significant
6543	PLXNA3	1.00	8.56E-01	9.41E-01	390.86	not significant
6544	BMF	1.00	8.23E-01	NA	25.46	not significant
6545	LINC01296	1.00	6.84E-01	NA	8.40	not significant
6546	LOC344967	1.00	7.18E-01	NA	10.27	not significant
6547	MDFI	1.00	9.36E-01	9.76E-01	1329.92	not significant
6548	C3orf38	1.00	9.37E-01	9.77E-01	1317.95	not significant
6549	DAP	1.00	9.33E-01	9.75E-01	3066.71	not significant
6550	RALB	1.00	9.34E-01	9.75E-01	662.51	not significant
6551	APEX2	1.00	9.37E-01	9.77E-01	1733.19	not significant
6552	MPDU1	1.00	9.35E-01	9.75E-01	2018.68	not significant
6553	DNASE1L1	1.00	8.24E-01	NA	30.37	not significant
6554	PPM1A	1.00	9.30E-01	9.74E-01	3962.49	not significant
6555	CUL4A	1.00	9.24E-01	9.72E-01	6548.13	not significant
6556	GFPT2	1.00	8.08E-01	NA	27.11	not significant
6557	ICAM4	1.00	8.20E-01	NA	27.47	not significant
6558	LOC101927415	1.00	7.93E-01	NA	20.60	not significant
6559	BSPRY	1.00	8.74E-01	NA	64.58	not significant
6560	CD72	1.00	7.58E-01	NA	14.95	not significant
6561	CD79A	1.00	8.94E-01	9.60E-01	193.19	not significant
6562	LIPC	1.00	8.43E-01	NA	42.25	not significant
6563	TGM1	1.00	8.44E-01	NA	38.80	not significant
6564	PHTF1	1.00	8.97E-01	9.61E-01	122.83	not significant
6565	CCDC135	1.00	7.33E-01	NA	11.78	not significant
6566	TAF1L	1.00	6.78E-01	NA	8.93	not significant
6567	ZNF846	1.00	8.57E-01	NA	60.16	not significant
6568	AMN	1.00	9.11E-01	9.66E-01	219.00	not significant
6569	COX6A1	1.00	9.30E-01	9.74E-01	3859.49	not significant
6570	CCDC17	1.00	8.17E-01	NA	33.70	not significant
6571	NAPA	1.00	9.31E-01	9.74E-01	2462.10	not significant
6572	GDPD3	1.00	8.86E-01	NA	80.93	not significant
6573	EIF2AK1	1.00	9.03E-01	9.63E-01	8817.19	not significant
6574	MYL5	1.00	8.41E-01	NA	41.11	not significant
6575	MSTO1	1.00	9.02E-01	9.63E-01	118.23	not significant
6576	C21orf91	1.00	9.40E-01	9.78E-01	2159.45	not significant
6577	ANKRD9	1.00	8.04E-01	NA	26.11	not significant
6578	EXT1	1.00	9.09E-01	9.65E-01	499.08	not significant
6579	GOPC	1.00	9.03E-01	9.63E-01	2665.83	not significant
6580	P2RY10	1.00	9.00E-01	9.62E-01	354.37	not significant
6581	ZNF623	1.00	9.32E-01	9.75E-01	908.22	not significant
6582	HLA-J	1.00	7.00E-01	NA	10.77	not significant
6583	CXorf40B	1.00	9.14E-01	9.67E-01	125.55	not significant
6584	RPL15	1.00	5.65E-01	7.80E-01	13484.54	not significant
6585	LOC102723701	1.00	7.98E-01	NA	23.50	not significant
6586	ABCA4	1.00	8.32E-01	NA	35.39	not significant
6587	C4BPB	1.00	6.83E-01	NA	10.37	not significant

6588	SMG1P3	1.00	9.23E-01	NA	89.89	not significant
6589	ARHGAP29	1.00	7.31E-01	NA	13.70	not significant
6590	GALK2	1.00	9.25E-01	9.72E-01	425.96	not significant
6591	PIAS1	1.00	8.40E-01	9.32E-01	953.65	not significant
6592	PAXBP1	1.00	9.56E-01	9.84E-01	2548.73	not significant
6593	EXOC2	1.00	9.35E-01	9.75E-01	2253.94	not significant
6594	FOXD2	1.00	7.66E-01	NA	19.29	not significant
6595	ZNF160	1.00	9.45E-01	9.79E-01	998.44	not significant
6596	CRYZL1	1.00	9.27E-01	9.73E-01	665.48	not significant
6597	BCOR	1.00	9.33E-01	9.75E-01	3486.25	not significant
6598	FBXO22	1.00	9.22E-01	9.70E-01	392.76	not significant
6599	POLK	1.00	9.33E-01	9.75E-01	1476.66	not significant
6600	ARRDC4	1.00	8.36E-01	NA	36.90	not significant
6601	TRPV3	1.00	7.32E-01	NA	14.64	not significant
6602	CYP4F3	1.00	6.45E-01	NA	9.21	not significant
6603	LOC101929057	1.00	8.06E-01	NA	27.20	not significant
6604	LTBP1	1.00	8.62E-01	NA	57.83	not significant
6605	KLKB1	1.00	6.63E-01	NA	9.70	not significant
6606	STK32C	1.00	7.29E-01	NA	14.66	not significant
6607	MIF4GD	1.00	2.61E-01	5.30E-01	524.65	not significant
6608	LOC100506990	1.00	8.96E-01	9.61E-01	143.92	not significant
6609	SOCS1	1.00	9.30E-01	9.74E-01	4935.74	not significant
6610	ZNF790	1.00	9.14E-01	9.67E-01	234.24	not significant
6611	ALG5	1.00	9.27E-01	9.73E-01	1450.43	not significant
6612	LOC101928767	1.00	8.47E-01	NA	49.45	not significant
6613	MGAT2	1.00	9.25E-01	9.72E-01	2348.13	not significant
6614	GPR65	1.00	9.14E-01	9.67E-01	557.21	not significant
6615	SGCB	1.00	9.27E-01	9.73E-01	1230.04	not significant
6616	PTGR2	1.00	9.11E-01	9.66E-01	270.33	not significant
6617	MYOM1	1.00	6.88E-01	NA	11.90	not significant
6618	NPAT	1.00	9.28E-01	9.73E-01	2290.55	not significant
6619	BAG2	1.00	9.26E-01	9.73E-01	605.22	not significant
6620	C9orf47	1.00	6.63E-01	NA	9.97	not significant
6621	MAP3K9	1.00	9.27E-01	9.73E-01	792.28	not significant
6622	RTN4R	1.00	9.22E-01	9.70E-01	404.26	not significant
6623	ACRC	1.00	8.49E-01	NA	52.04	not significant
6624	IGSF9B	1.00	9.06E-01	9.64E-01	240.67	not significant
6625	GCNT4	1.00	8.29E-01	NA	41.75	not significant
6626	LINC01278	1.00	6.86E-01	NA	11.46	not significant
6627	HTATSF1P2	1.00	8.93E-01	9.60E-01	121.71	not significant
6628	ARHGAP19-SLIT1	1.00	7.82E-01	NA	25.22	not significant
6629	GOLM1	1.00	6.21E-01	NA	9.11	not significant
6630	NIF3L1	1.00	9.25E-01	9.72E-01	1341.24	not significant
6631	POLR2I	1.00	9.24E-01	9.72E-01	1223.49	not significant
6632	SFXN4	1.00	9.22E-01	9.70E-01	1593.54	not significant
6633	SNRPB	1.00	9.07E-01	9.64E-01	14344.39	not significant
6634	GJA3	1.00	7.98E-01	NA	30.74	not significant
6635	TMEM185A	1.00	8.48E-01	NA	60.56	not significant
6636	WAC-AS1	1.00	9.16E-01	9.68E-01	300.53	not significant
6637	P2RX5-TAX1BP3	1.00	8.99E-01	9.62E-01	161.22	not significant
6638	ETV7	1.00	6.47E-01	NA	9.67	not significant
6639	SCARF2	1.00	7.26E-01	NA	15.77	not significant
6640	VWA7	1.00	6.84E-01	NA	12.95	not significant
6641	DPEP2	1.00	6.90E-01	NA	12.79	not significant
6642	ZCWPW2	1.00	6.50E-01	NA	10.63	not significant
6643	RPAIN	1.00	9.20E-01	9.70E-01	1607.72	not significant
6644	IER5	1.00	9.20E-01	9.69E-01	2549.27	not significant
6645	XPNPEP2	1.00	9.22E-01	9.70E-01	1464.72	not significant
6646	ORMDL1	1.00	9.21E-01	9.70E-01	3123.62	not significant
6647	CYB5B	1.00	9.06E-01	9.64E-01	6431.39	not significant
6648	GSTP1	1.00	9.02E-01	9.63E-01	12266.16	not significant
6649	MAFK	1.00	9.18E-01	9.69E-01	2484.43	not significant
6650	PIP4K2A	1.00	9.17E-01	9.68E-01	4756.62	not significant
6651	GIGYF2	1.00	9.45E-01	9.79E-01	3318.32	not significant
6652	TP53BP2	1.00	9.20E-01	9.69E-01	2697.81	not significant
6653	WBSCR16	1.00	9.14E-01	9.67E-01	398.00	not significant
6654	CAMK1D	1.00	9.07E-01	9.64E-01	308.84	not significant
6655	BCAS3	1.00	9.09E-01	9.65E-01	273.86	not significant
6656	CTC-338M12.4	1.00	2.85E-03	2.71E-02	1507.27	not significant
6657	HIST1H3I	1.00	7.64E-01	NA	24.72	not significant
6658	FANCB	1.00	8.73E-01	9.50E-01	438.90	not significant
6659	LRRN1	1.00	7.83E-01	NA	32.88	not significant
6660	C1QL1	1.00	7.29E-01	NA	16.71	not significant
6661	RAD9B	1.00	7.49E-01	NA	21.60	not significant
6662	NOXO1	1.00	6.33E-01	NA	10.46	not significant
6663	APOL4	1.00	7.58E-01	NA	22.97	not significant
6664	CDKN2B-AS1	1.00	7.44E-01	NA	23.45	not significant
6665	PCDHGA10	1.00	6.96E-01	NA	14.10	not significant
6666	CD70	1.00	9.01E-01	9.63E-01	225.90	not significant
6667	LOC100506474	1.00	9.32E-01	9.75E-01	140.92	not significant
6668	SYAP1	1.00	9.77E-01	9.94E-01	875.34	not significant
6669	POC1A	1.00	9.19E-01	9.69E-01	1491.14	not significant
6670	P2RX5	1.00	9.25E-01	9.72E-01	2992.70	not significant
6671	ATP5J	1.00	8.47E-01	9.36E-01	3354.04	not significant
6672	STK38L	1.00	9.17E-01	9.68E-01	1736.35	not significant
6673	TPR	1.00	9.16E-01	9.68E-01	9245.77	not significant
6674	RPS18P9	1.00	8.12E-01	NA	44.30	not significant
6675	ZDHHC7	1.00	9.18E-01	9.69E-01	1706.76	not significant

6676	XYLB	1.00	9.06E-01	9.64E-01	657.46	not significant
6677	KIF21A	1.00	9.05E-01	9.64E-01	288.67	not significant
6678	ANKRD37	1.00	8.42E-01	NA	61.78	not significant
6679	MMP15	1.00	7.77E-01	NA	29.84	not significant
6680	MSTO2P	1.00	8.98E-01	9.61E-01	228.08	not significant
6681	GBP2	1.00	7.02E-01	NA	17.93	not significant
6682	EFNA1	1.00	8.71E-01	9.49E-01	105.69	not significant
6683	KAZALD1	1.00	6.92E-01	NA	15.14	not significant
6684	PCDHGA5	1.00	6.64E-01	NA	12.63	not significant
6685	INO80B	1.00	6.61E-01	NA	12.21	not significant
6686	CLMN	1.00	6.66E-01	NA	12.88	not significant
6687	TMEM81	1.00	8.63E-01	NA	89.23	not significant
6688	GPC6	1.00	8.54E-01	NA	74.32	not significant
6689	CCL28	1.00	7.26E-01	NA	19.61	not significant
6690	SLC9A9	1.00	8.32E-01	NA	55.51	not significant
6691	NDUFB1	1.00	9.17E-01	9.68E-01	863.19	not significant
6692	MTHFS	1.00	7.52E-01	NA	27.08	not significant
6693	HSD17B4	1.00	9.12E-01	9.66E-01	2681.94	not significant
6694	PTPN23	1.00	9.17E-01	9.68E-01	2219.78	not significant
6695	NHP2	1.00	9.11E-01	9.66E-01	5367.80	not significant
6696	RSPRY1	1.00	9.16E-01	9.68E-01	1398.51	not significant
6697	KIAA0247	1.00	9.03E-01	9.63E-01	2588.69	not significant
6698	ZNF181	1.00	9.08E-01	9.65E-01	329.40	not significant
6699	ZNF782	1.00	8.75E-01	9.51E-01	154.67	not significant
6700	43719_6028	1.00	9.14E-01	9.67E-01	523.13	not significant
6701	ZDBF2	1.00	7.74E-01	NA	29.09	not significant
6702	SAMD15	1.00	6.74E-01	NA	14.00	not significant
6703	GPANK1	1.00	8.72E-01	NA	92.60	not significant
6704	AKR7L	1.00	7.00E-01	NA	16.89	not significant
6705	SKOR1	1.00	7.06E-01	NA	18.17	not significant
6706	PLEK	1.00	6.55E-01	NA	12.85	not significant
6707	FAM132A	1.00	5.73E-01	NA	8.37	not significant
6708	MRPL55	1.00	9.12E-01	9.66E-01	855.00	not significant
6709	FBXL5	1.00	9.14E-01	9.67E-01	1437.38	not significant
6710	KEAP1	1.00	9.24E-01	9.72E-01	3018.85	not significant
6711	MCL1	1.00	8.60E-01	9.43E-01	5911.77	not significant
6712	MIR4435-1HG	1.00	8.84E-01	9.56E-01	172.55	not significant
6713	LIN7B	1.00	8.32E-01	NA	65.25	not significant
6714	BMPR2	1.00	9.12E-01	9.66E-01	630.04	not significant
6715	TTC24	1.00	9.05E-01	9.64E-01	403.80	not significant
6716	MYOZ3	1.00	7.55E-01	NA	28.87	not significant
6717	PRRT3	1.00	8.24E-01	NA	53.66	not significant
6718	MSS51	1.00	7.91E-01	NA	38.50	not significant
6719	AVPI1	1.00	6.93E-01	NA	16.35	not significant
6720	TTC3P1	1.00	6.43E-01	NA	13.60	not significant
6721	HSD17B6	1.00	8.78E-01	9.52E-01	174.11	not significant
6722	UNC50	1.00	9.20E-01	9.69E-01	1058.68	not significant
6723	STK16	1.00	8.96E-01	9.61E-01	588.96	not significant
6724	ATOX1	1.00	9.09E-01	9.65E-01	528.34	not significant
6725	UBL4A	1.00	8.83E-01	9.55E-01	502.11	not significant
6726	WDR24	1.00	9.13E-01	9.66E-01	1136.39	not significant
6727	IFT52	1.00	9.29E-01	9.73E-01	1085.07	not significant
6728	EIF3M	1.00	9.03E-01	9.63E-01	10479.94	not significant
6729	ZNF76	1.00	9.16E-01	9.68E-01	1532.82	not significant
6730	CCDC82	1.00	9.09E-01	9.65E-01	1423.09	not significant
6731	LZTS1	1.00	8.99E-01	9.62E-01	6001.32	not significant
6732	OIP5-AS1	1.00	9.09E-01	9.65E-01	2038.37	not significant
6733	THEMIS	1.00	9.16E-01	9.68E-01	2150.66	not significant
6734	ZNRD1	1.00	8.96E-01	9.61E-01	338.62	not significant
6735	RORA	1.00	9.09E-01	9.65E-01	863.55	not significant
6736	GPR107	1.00	9.05E-01	9.64E-01	574.56	not significant
6737	PCBP3	1.00	8.92E-01	9.60E-01	467.33	not significant
6738	CDON	1.00	9.05E-01	9.63E-01	477.14	not significant
6739	RNF139-AS1	1.00	7.48E-01	NA	31.33	not significant
6740	PELI3	1.00	8.08E-01	NA	48.48	not significant
6741	ZNF518A	1.00	8.40E-01	NA	77.74	not significant
6742	LOC100506713	1.00	7.53E-01	NA	30.80	not significant
6743	LOXL1	1.00	7.53E-01	NA	27.37	not significant
6744	NUDT9P1	1.00	6.94E-01	NA	18.15	not significant
6745	MICALCL	1.00	6.61E-01	NA	15.24	not significant
6746	LY86	1.00	5.23E-01	NA	8.34	not significant
6747	CHPT1	1.00	9.01E-01	9.63E-01	750.45	not significant
6748	SMC3	1.00	8.96E-01	9.61E-01	6462.53	not significant
6749	REEP4	1.00	9.05E-01	9.63E-01	1579.57	not significant
6750	LRFN4	1.00	9.05E-01	9.64E-01	1985.96	not significant
6751	SNRPD2	1.00	8.89E-01	9.58E-01	6195.76	not significant
6752	SLC2A1	1.00	9.13E-01	9.66E-01	1537.73	not significant
6753	FUT4	1.00	9.07E-01	9.64E-01	1880.46	not significant
6754	DIS3L	1.00	9.08E-01	9.65E-01	1471.65	not significant
6755	DVL1	1.00	9.09E-01	9.65E-01	1495.18	not significant
6756	RAB3IP	1.00	9.09E-01	9.65E-01	1418.61	not significant
6757	AGBL3	1.00	7.53E-01	NA	34.49	not significant
6758	HECTD2	1.00	8.19E-01	NA	57.19	not significant
6759	BCO2	1.00	7.03E-01	NA	21.06	not significant
6760	HRH2	1.00	6.36E-01	NA	14.21	not significant
6761	LOC100131347	1.00	5.71E-01	NA	9.72	not significant
6762	SLC16A4	1.00	5.46E-01	NA	8.30	not significant
6763	BOD1	1.00	9.02E-01	9.63E-01	853.79	not significant

6764	ARFGEF2	1.00	8.89E-01	9.58E-01	4109.92	not significant
6765	HEATR5B	1.00	9.06E-01	9.64E-01	1225.46	not significant
6766	QDPR	1.00	9.26E-01	9.72E-01	1089.42	not significant
6767	LRP11	1.00	9.01E-01	9.63E-01	2304.69	not significant
6768	LIPE	1.00	8.92E-01	9.60E-01	302.05	not significant
6769	ZSCAN29	1.00	9.05E-01	9.63E-01	1362.28	not significant
6770	ATAD2B	1.00	9.06E-01	9.64E-01	1636.43	not significant
6771	ZNF333	1.00	8.73E-01	9.50E-01	178.59	not significant
6772	C22orf15	1.00	6.88E-01	NA	19.66	not significant
6773	ARHGAP23	1.00	8.76E-01	9.52E-01	198.31	not significant
6774	MEI1	1.00	7.96E-01	NA	48.72	not significant
6775	ZNF853	1.00	6.79E-01	NA	18.93	not significant
6776	KCTD21-AS1	1.00	6.21E-01	NA	13.73	not significant
6777	SNX21	1.00	6.21E-01	NA	15.09	not significant
6778	FLT3	1.00	6.02E-01	NA	11.46	not significant
6779	MARK4	1.00	9.68E-01	9.90E-01	1571.94	not significant
6780	ITPA	1.00	9.03E-01	9.63E-01	1690.84	not significant
6781	SCO2	1.00	8.92E-01	9.60E-01	395.89	not significant
6782	PAPOLG	1.00	9.03E-01	9.63E-01	1385.61	not significant
6783	STIM1	1.00	8.86E-01	9.56E-01	4776.54	not significant
6784	MAMSTR	1.00	7.03E-01	NA	22.97	not significant
6785	TSC1	1.00	9.04E-01	9.63E-01	961.02	not significant
6786	CCDC146	1.00	8.93E-01	9.60E-01	329.74	not significant
6787	OPN3	1.00	9.02E-01	9.63E-01	910.58	not significant
6788	PPM1D	1.00	9.00E-01	9.63E-01	1719.85	not significant
6789	SNAPC4	1.00	9.04E-01	9.63E-01	844.79	not significant
6790	CTD-2201I18.1	1.00	6.40E-01	NA	15.32	not significant
6791	ZNF624	1.00	8.73E-01	9.50E-01	235.23	not significant
6792	EID2B	1.00	8.35E-01	NA	91.49	not significant
6793	TOLLIP-AS1	1.00	6.24E-01	NA	13.79	not significant
6794	LRRC16A	1.00	6.40E-01	NA	15.55	not significant
6795	CDKN2B	1.00	5.91E-01	NA	12.72	not significant
6796	NPFF	1.00	7.12E-01	NA	27.25	not significant
6797	GDI1	1.00	8.98E-01	9.62E-01	797.98	not significant
6798	FAM207A	1.00	9.03E-01	9.63E-01	755.28	not significant
6799	PTPN9	1.00	8.98E-01	9.61E-01	2010.66	not significant
6800	ZNF789	1.00	8.79E-01	9.52E-01	200.11	not significant
6801	GPN3	1.00	8.97E-01	9.61E-01	1901.50	not significant
6802	DLG5	1.00	8.99E-01	9.62E-01	1126.53	not significant
6803	ENPP4	1.00	9.02E-01	9.63E-01	945.14	not significant
6804	ZNF320	1.00	8.98E-01	9.62E-01	1558.39	not significant
6805	NBPF3	1.00	8.71E-01	9.49E-01	350.02	not significant
6806	C12orf60	1.00	7.39E-01	NA	33.63	not significant
6807	ARHGEF17	1.00	7.42E-01	NA	34.10	not significant
6808	CAPN10-AS1	1.00	8.27E-01	NA	94.32	not significant
6809	CACNB4	1.00	6.43E-01	NA	17.60	not significant
6810	ALDH3B2	1.00	7.44E-01	NA	32.45	not significant
6811	TTC4	1.00	6.96E-01	NA	23.61	not significant
6812	LOC101929655	1.00	4.91E-01	NA	8.13	not significant
6813	PLSCR1	1.00	8.96E-01	9.61E-01	1528.16	not significant
6814	UBE2D2	1.00	8.97E-01	9.61E-01	6501.12	not significant
6815	E2F6	1.00	9.17E-01	9.68E-01	1109.78	not significant
6816	UBE2H	1.00	8.95E-01	9.61E-01	1642.32	not significant
6817	DCP1B	1.00	8.93E-01	9.60E-01	479.23	not significant
6818	SLC33A1	1.00	9.00E-01	9.62E-01	1113.36	not significant
6819	ZC3H3	1.00	8.97E-01	9.61E-01	1244.67	not significant
6820	ELMO3	1.00	8.77E-01	9.52E-01	220.81	not significant
6821	SSFA2	1.00	8.94E-01	9.60E-01	703.92	not significant
6822	DPH7	1.00	8.96E-01	9.61E-01	832.04	not significant
6823	FOXJ2	1.00	8.98E-01	9.62E-01	1322.83	not significant
6824	WBP1	1.00	7.74E-01	NA	47.49	not significant
6825	EP300-AS1	1.00	7.01E-01	NA	25.08	not significant
6826	PRAM1	1.00	5.31E-01	NA	9.76	not significant
6827	PHOSPHO2	1.00	8.00E-01	NA	63.15	not significant
6828	LOC646214	1.00	7.08E-01	NA	28.74	not significant
6829	UAP1L1	1.00	7.04E-01	NA	25.93	not significant
6830	LOC400685	1.00	6.16E-01	NA	18.62	not significant
6831	ANK2	1.00	5.32E-01	NA	11.34	not significant
6832	AGAP2-AS1	1.00	6.37E-01	NA	18.61	not significant
6833	USP11	1.00	9.22E-01	9.70E-01	4139.24	not significant
6834	EFNA3	1.00	7.91E-01	NA	63.30	not significant
6835	TCF3	1.00	8.70E-01	9.48E-01	10477.61	not significant
6836	MGEA5	1.00	9.04E-01	9.63E-01	4107.50	not significant
6837	NOL9	1.00	8.93E-01	9.60E-01	1431.37	not significant
6838	CAPN15	1.00	8.97E-01	9.61E-01	2982.89	not significant
6839	IGIP	1.00	8.18E-01	NA	78.08	not significant
6840	RTN4RL1	1.00	6.38E-01	NA	18.98	not significant
6841	GFM2	1.00	8.88E-01	9.58E-01	1692.01	not significant
6842	NDUFB10	1.00	8.94E-01	9.61E-01	2418.79	not significant
6843	PIH1D1	1.00	8.46E-01	9.36E-01	1784.85	not significant
6844	CCDC71	1.00	8.89E-01	9.58E-01	706.39	not significant
6845	AKT2	1.00	8.68E-01	9.47E-01	5504.79	not significant
6846	C3orf17	1.00	8.94E-01	9.61E-01	1736.04	not significant
6847	CRLF3	1.00	8.87E-01	9.57E-01	2252.51	not significant
6848	ZNF767P	1.00	8.86E-01	9.56E-01	626.08	not significant
6849	EFTUD1	1.00	8.97E-01	9.61E-01	1097.10	not significant
6850	ITFG2	1.00	8.96E-01	9.61E-01	1071.21	not significant
6851	UBL5	1.00	8.81E-01	9.54E-01	3415.71	not significant

6852	OGFRP1	1.00	7.27E-01	NA	32.59	not significant
6853	CEBPB-AS1	1.00	7.28E-01	NA	34.68	not significant
6854	LOC401127	1.00	5.75E-01	NA	13.39	not significant
6855	LCMT1-AS1	1.00	6.62E-01	NA	21.95	not significant
6856	GPR137C	1.00	7.38E-01	NA	39.23	not significant
6857	STC2	1.00	6.85E-01	NA	24.72	not significant
6858	LSM2	1.00	8.84E-01	9.56E-01	999.39	not significant
6859	FDX1	1.00	8.48E-01	9.36E-01	710.06	not significant
6860	CCDC109B	1.00	8.90E-01	9.59E-01	2266.99	not significant
6861	CEP250	1.00	8.86E-01	9.56E-01	4046.51	not significant
6862	FGF14-AS2	1.00	7.69E-01	NA	59.61	not significant
6863	MTMR6	1.00	8.80E-01	9.53E-01	2739.26	not significant
6864	NFX1	1.00	8.86E-01	9.56E-01	2508.45	not significant
6865	DNAJB5	1.00	8.76E-01	9.52E-01	322.96	not significant
6866	FMO4	1.00	7.29E-01	NA	37.14	not significant
6867	KLHL3	1.00	8.64E-01	9.45E-01	570.55	not significant
6868	FBXO43	1.00	8.59E-01	9.43E-01	188.01	not significant
6869	ZDHHC14	1.00	8.16E-01	NA	93.71	not significant
6870	HIST1H3F	1.00	6.54E-01	NA	24.04	not significant
6871	GYS2	1.00	4.87E-01	NA	10.48	not significant
6872	UBE2MP1	1.00	7.49E-01	NA	43.38	not significant
6873	PARP15	1.00	8.08E-01	9.18E-01	107.00	not significant
6874	CARNS1	1.00	7.29E-01	NA	38.59	not significant
6875	CNTD1	1.00	5.36E-01	NA	13.36	not significant
6876	PPP1R32	1.00	6.26E-01	NA	21.61	not significant
6877	TRPC3	1.00	7.89E-01	NA	69.34	not significant
6878	EXOC4	1.00	8.78E-01	9.52E-01	2574.89	not significant
6879	MEF2A	1.00	8.88E-01	9.58E-01	2572.46	not significant
6880	RAB15	1.00	8.64E-01	9.45E-01	1726.52	not significant
6881	ZNF678	1.00	8.85E-01	9.56E-01	872.23	not significant
6882	ITGB3	1.00	7.28E-01	NA	38.30	not significant
6883	ECM1	1.00	6.57E-01	NA	26.00	not significant
6884	NINJ2	1.00	8.13E-01	9.21E-01	103.29	not significant
6885	CCDC125	1.00	8.27E-01	9.28E-01	118.88	not significant
6886	DISP1	1.00	8.42E-01	9.33E-01	168.13	not significant
6887	NXN	1.00	7.21E-01	NA	34.95	not significant
6888	ASPDH	1.00	7.93E-01	NA	73.42	not significant
6889	HAR1A	1.00	8.09E-01	NA	70.44	not significant
6890	MAP3K15	1.00	7.07E-01	NA	33.58	not significant
6891	FGFR4	1.00	6.25E-01	NA	20.27	not significant
6892	LOC101929125	1.00	5.18E-01	NA	12.12	not significant
6893	FRMD3	1.00	5.47E-01	NA	13.46	not significant
6894	PDCD6	1.00	8.80E-01	9.53E-01	2338.49	not significant
6895	CREB3	1.00	8.83E-01	9.55E-01	977.45	not significant
6896	IFT43	1.00	8.33E-01	9.30E-01	134.75	not significant
6897	BTG3	1.00	8.82E-01	9.54E-01	1372.22	not significant
6898	PDXDC1	1.00	8.77E-01	9.52E-01	2632.74	not significant
6899	FAF2	1.00	8.74E-01	9.50E-01	2935.65	not significant
6900	FAAH2	1.00	8.09E-01	NA	95.93	not significant
6901	CLCN5	1.00	6.89E-01	NA	29.30	not significant
6902	MAST1	1.00	6.90E-01	NA	36.55	not significant
6903	LOC100507577	1.00	7.52E-01	NA	61.21	not significant
6904	CCDC159	1.00	7.25E-01	NA	42.01	not significant
6905	AUTS2	1.00	7.68E-01	NA	63.34	not significant
6906	AMY2B	1.00	7.52E-01	NA	50.65	not significant
6907	TTTY14	1.00	6.47E-01	NA	25.06	not significant
6908	HIST1H3H	1.00	5.78E-01	NA	17.37	not significant
6909	ACOT1	1.00	6.33E-01	NA	20.15	not significant
6910	PTCD1	1.00	5.07E-01	NA	10.85	not significant
6911	HIST1H2BN	1.00	3.17E-01	NA	17.97	not significant
6912	SLC25A10	1.00	8.80E-01	9.53E-01	1876.49	not significant
6913	ATP5H	1.00	8.73E-01	9.50E-01	3894.57	not significant
6914	CRYBB2P1	1.00	8.79E-01	9.52E-01	944.74	not significant
6915	LSM14B	1.00	8.79E-01	9.52E-01	1736.14	not significant
6916	ZNF653	1.00	8.59E-01	9.43E-01	253.06	not significant
6917	POMGNT2	1.00	8.82E-01	9.55E-01	912.80	not significant
6918	ANTXR2	1.00	8.23E-01	9.27E-01	121.33	not significant
6919	GPR124	1.00	8.84E-01	9.56E-01	2279.95	not significant
6920	FAIM	1.00	8.36E-01	9.31E-01	167.28	not significant
6921	BSCL2	1.00	7.94E-01	NA	81.04	not significant
6922	HIST1H2BD	1.00	7.57E-01	NA	58.35	not significant
6923	PLCB3	1.00	8.74E-01	9.50E-01	484.13	not significant
6924	S100A13	1.00	7.60E-01	NA	58.17	not significant
6925	LINC01012	1.00	6.08E-01	NA	20.54	not significant
6926	MCOLN2	1.00	6.52E-01	NA	25.70	not significant
6927	FBXW9	1.00	8.47E-01	9.36E-01	197.34	not significant
6928	MRPS6	1.00	8.75E-01	9.51E-01	2789.57	not significant
6929	ENDOV	1.00	8.31E-01	9.29E-01	157.19	not significant
6930	TRMT2A	1.00	8.97E-01	9.61E-01	2559.07	not significant
6931	DBR1	1.00	8.77E-01	9.52E-01	1374.04	not significant
6932	RETSAT	1.00	8.78E-01	9.52E-01	764.19	not significant
6933	FAM50A	1.00	8.78E-01	9.52E-01	757.27	not significant
6934	RMND5B	1.00	8.18E-01	9.24E-01	412.11	not significant
6935	ZDHHC15	1.00	8.33E-01	9.30E-01	157.05	not significant
6936	LTBP4	1.00	8.58E-01	9.43E-01	328.51	not significant
6937	TDRD9	1.00	6.13E-01	NA	21.28	not significant
6938	PXN-AS1	1.00	8.37E-01	9.31E-01	176.37	not significant
6939	EIF4E3	1.00	8.69E-01	9.47E-01	418.70	not significant

6940	C1orf21	1.00	7.94E-01	NA	84.97	not significant
6941	RPL32P3	1.00	8.42E-01	9.33E-01	201.49	not significant
6942	GPR126	1.00	6.53E-01	NA	26.99	not significant
6943	MNS1	1.00	7.46E-01	NA	52.60	not significant
6944	AQP4-AS1	1.00	5.44E-01	NA	14.58	not significant
6945	PCDHGB1	1.00	5.93E-01	NA	18.12	not significant
6946	SPAG4	1.00	6.58E-01	NA	27.11	not significant
6947	LRRC46	1.00	6.73E-01	NA	30.07	not significant
6948	DSCR3	1.00	9.96E-01	1.00E+00	3010.46	not significant
6949	C9orf85	1.00	8.63E-01	9.44E-01	384.81	not significant
6950	NUP107	1.00	8.58E-01	9.43E-01	5424.15	not significant
6951	ING3	1.00	8.78E-01	9.52E-01	973.02	not significant
6952	KLHL5	1.00	8.78E-01	9.52E-01	918.71	not significant
6953	THRA	1.00	8.61E-01	9.43E-01	512.82	not significant
6954	TTLL7	1.00	7.33E-01	NA	61.18	not significant
6955	SLC41A2	1.00	7.93E-01	9.11E-01	162.62	not significant
6956	IDH1-AS1	1.00	4.68E-01	NA	10.50	not significant
6957	GPRIN1	1.00	4.75E-01	NA	11.34	not significant
6958	CCDC121	1.00	4.97E-01	NA	12.12	not significant
6959	PRMT6	1.00	8.73E-01	9.50E-01	1340.70	not significant
6960	ASF1A	1.00	8.67E-01	9.47E-01	2827.04	not significant
6961	RBMS1	1.00	8.65E-01	9.45E-01	2713.69	not significant
6962	KLHL25	1.00	8.63E-01	9.44E-01	434.80	not significant
6963	COQ4	1.00	8.73E-01	9.50E-01	724.83	not significant
6964	ZBTB43	1.00	8.69E-01	9.47E-01	721.69	not significant
6965	PI4KAP2	1.00	7.94E-01	9.11E-01	159.00	not significant
6966	HMX3	1.00	7.57E-01	NA	67.43	not significant
6967	HOMEZ	1.00	8.38E-01	9.31E-01	337.46	not significant
6968	FMR1	1.00	8.64E-01	9.45E-01	438.06	not significant
6969	LRRC37A2	1.00	6.78E-01	NA	35.06	not significant
6970	C11orf96	1.00	8.20E-01	9.25E-01	141.62	not significant
6971	LMF1	1.00	8.44E-01	9.34E-01	267.27	not significant
6972	LOC100129550	1.00	7.55E-01	NA	65.22	not significant
6973	C6orf203	1.00	7.63E-01	NA	85.14	not significant
6974	RHOV	1.00	5.12E-01	NA	13.25	not significant
6975	PIGW	1.00	6.60E-01	NA	34.51	not significant
6976	GPR157	1.00	6.71E-01	NA	40.75	not significant
6977	TMOD1	1.00	5.99E-01	NA	20.36	not significant
6978	BRICD5	1.00	6.82E-01	8.50E-01	114.32	not significant
6979	EPHA5	1.00	6.22E-01	NA	24.34	not significant
6980	ABHD17C	1.00	3.99E-01	NA	8.46	not significant
6981	PRC1-AS1	1.00	3.99E-01	NA	10.52	not significant
6982	POT1-AS1	1.00	4.11E-01	NA	8.87	not significant
6983	MVB12A	1.00	8.63E-01	9.44E-01	458.13	not significant
6984	LRRC42	1.00	8.68E-01	9.47E-01	1231.65	not significant
6985	PCBP2	1.00	8.38E-01	9.31E-01	20497.99	not significant
6986	DNAJC10	1.00	8.76E-01	9.52E-01	3853.15	not significant
6987	LOC100506688	1.00	8.68E-01	9.47E-01	822.58	not significant
6988	CCDC107	1.00	8.29E-01	9.29E-01	248.51	not significant
6989	TSLP	1.00	7.71E-01	NA	71.13	not significant
6990	TTC7B	1.00	7.07E-01	NA	42.42	not significant
6991	DLGAP1-AS2	1.00	5.18E-01	NA	13.94	not significant
6992	IZUMO1	1.00	4.80E-01	NA	12.17	not significant
6993	CAPN5	1.00	6.87E-01	NA	35.91	not significant
6994	RGS18	1.00	6.86E-01	NA	43.96	not significant
6995	AGBL2	1.00	7.53E-01	NA	63.98	not significant
6996	HRH1	1.00	4.38E-01	NA	10.93	not significant
6997	TRAPPC2P1	1.00	8.05E-01	9.17E-01	127.86	not significant
6998	SLC7A5P1	1.00	7.72E-01	NA	97.58	not significant
6999	NOTCH2NL	1.00	7.97E-01	9.12E-01	108.15	not significant
7000	MAPK13	1.00	6.87E-01	NA	40.34	not significant
7001	SCG5	1.00	4.11E-01	NA	9.76	not significant
7002	LOC100132352	1.00	6.26E-01	NA	25.78	not significant
7003	SPOCK2	1.00	7.71E-01	NA	82.34	not significant
7004	ZNF192P1	1.00	4.48E-01	NA	10.88	not significant
7005	NTN5	1.00	4.47E-01	NA	10.66	not significant
7006	PPP1R3D	1.00	7.68E-01	NA	82.69	not significant
7007	RARRES3	1.00	8.78E-01	9.52E-01	718.62	not significant
7008	CENPM	1.00	8.66E-01	9.46E-01	2338.98	not significant
7009	LARP7	1.00	8.65E-01	9.45E-01	1803.67	not significant
7010	THAP1	1.00	8.61E-01	9.43E-01	749.56	not significant
7011	PIK3CD	1.00	8.40E-01	9.32E-01	5246.11	not significant
7012	TBC1D9B	1.00	8.32E-01	9.30E-01	3270.63	not significant
7013	ITGA5	1.00	8.66E-01	9.45E-01	3243.18	not significant
7014	SCRN3	1.00	8.27E-01	9.28E-01	457.50	not significant
7015	ZFAT	1.00	8.60E-01	9.43E-01	452.20	not significant
7016	ATG9B	1.00	7.03E-01	NA	52.09	not significant
7017	CA13	1.00	6.67E-01	NA	33.02	not significant
7018	SENCR	1.00	4.40E-01	NA	11.58	not significant
7019	ZNF573	1.00	7.77E-01	9.02E-01	102.73	not significant
7020	GRIN2D	1.00	4.20E-01	NA	10.41	not significant
7021	VGF	1.00	4.99E-01	NA	13.67	not significant
7022	STAG3L5P	1.00	9.86E-01	NA	23.35	not significant
7023	TALDO1	1.00	8.57E-01	9.42E-01	4712.11	not significant
7024	LOC101927181	1.00	8.37E-01	9.31E-01	285.95	not significant
7025	CDC16	1.00	8.64E-01	9.45E-01	2096.62	not significant
7026	KIAA0753	1.00	8.62E-01	9.44E-01	844.75	not significant
7027	PNPLA6	1.00	8.63E-01	9.45E-01	2422.44	not significant

7028	MFSD6	1.00	8.57E-01	9.42E-01	3612.73	not significant
7029	MTSS1L	1.00	8.65E-01	9.45E-01	945.94	not significant
7030	CYSTM1	1.00	8.00E-01	9.14E-01	199.52	not significant
7031	TSPYL2	1.00	7.94E-01	9.11E-01	105.62	not significant
7032	PIK3C2B	1.00	8.64E-01	9.45E-01	1659.31	not significant
7033	LRBA	1.00	8.64E-01	9.45E-01	2895.33	not significant
7034	RCN3	1.00	7.34E-01	NA	63.34	not significant
7035	SAT2	1.00	7.44E-01	NA	65.64	not significant
7036	ABHD11	1.00	7.59E-01	NA	75.62	not significant
7037	RAB30-AS1	1.00	7.61E-01	NA	80.23	not significant
7038	LINC00959	1.00	7.56E-01	NA	82.49	not significant
7039	PLXNB3	1.00	5.40E-01	NA	17.22	not significant
7040	KHDC1	1.00	7.89E-01	9.09E-01	118.19	not significant
7041	HBEGF	1.00	5.73E-01	NA	21.67	not significant
7042	LLGL2	1.00	6.95E-01	NA	44.08	not significant
7043	CPB2-AS1	1.00	5.89E-01	NA	23.31	not significant
7044	ZNF85	1.00	6.78E-01	NA	44.22	not significant
7045	C11orf65	1.00	3.59E-01	NA	8.30	not significant
7046	LY6G5B	1.00	4.60E-01	NA	12.47	not significant
7047	ZNF26	1.00	7.23E-01	NA	56.31	not significant
7048	TMEM214	1.00	8.56E-01	9.41E-01	1909.15	not significant
7049	TBC1D31	1.00	8.64E-01	9.45E-01	958.15	not significant
7050	SOS2	1.00	8.60E-01	9.43E-01	1360.54	not significant
7051	SBNO2	1.00	8.38E-01	9.31E-01	1731.81	not significant
7052	ANKFY1	1.00	8.57E-01	9.42E-01	3687.22	not significant
7053	FAN1	1.00	8.60E-01	9.43E-01	1565.49	not significant
7054	LIPT1	1.00	8.25E-01	9.27E-01	207.44	not significant
7055	ZNF513	1.00	8.65E-01	9.45E-01	340.61	not significant
7056	ZBED8	1.00	7.87E-01	9.08E-01	111.61	not significant
7057	MICB	1.00	8.27E-01	9.28E-01	210.15	not significant
7058	PCBP1-AS1	1.00	8.40E-01	9.32E-01	266.77	not significant
7059	TMX4	1.00	8.20E-01	9.25E-01	168.50	not significant
7060	NME2	1.00	7.65E-01	NA	98.12	not significant
7061	ASB2	1.00	6.83E-01	NA	42.44	not significant
7062	TEN1-CDK3	1.00	6.81E-01	NA	44.24	not significant
7063	BSN	1.00	6.56E-01	NA	34.58	not significant
7064	LEPR	1.00	7.02E-01	NA	50.94	not significant
7065	DARS-AS1	1.00	1.14E-01	3.34E-01	2222.59	not significant
7066	FBXO32	1.00	8.01E-01	9.14E-01	132.59	not significant
7067	ST7	1.00	5.14E-01	NA	15.55	not significant
7068	CYP4F22	1.00	4.26E-01	NA	14.05	not significant
7069	PER3	1.00	4.34E-01	NA	11.93	not significant
7070	C11orf84	1.00	8.52E-01	9.39E-01	3167.12	not significant
7071	UNG	1.00	8.37E-01	9.31E-01	8199.47	not significant
7072	ARRDC2	1.00	8.48E-01	9.36E-01	589.19	not significant
7073	KDM4B	1.00	8.59E-01	9.43E-01	1332.80	not significant
7074	FAM103A1	1.00	8.44E-01	9.34E-01	422.76	not significant
7075	LYRM9	1.00	5.58E-01	NA	22.46	not significant
7076	MYLK4	1.00	4.13E-01	NA	32.33	not significant
7077	BCL2L15	1.00	5.52E-01	NA	20.10	not significant
7078	TRIM66	1.00	7.29E-01	8.76E-01	313.76	not significant
7079	LINC00239	1.00	3.71E-01	NA	9.73	not significant
7080	NUTM2D	1.00	5.89E-01	NA	24.16	not significant
7081	ALG1L2	1.00	3.93E-01	NA	11.10	not significant
7082	TRIB1	1.00	5.11E-01	NA	17.79	not significant
7083	C7orf73	1.00	8.65E-01	9.45E-01	2329.85	not significant
7084	VASP	1.00	8.59E-01	9.43E-01	2185.99	not significant
7085	TRIM33	1.00	8.49E-01	9.36E-01	3757.39	not significant
7086	ABT1	1.00	8.37E-01	9.31E-01	317.08	not significant
7087	NPIPA1	1.00	7.39E-01	NA	72.85	not significant
7088	C2CD2	1.00	8.13E-01	9.21E-01	193.04	not significant
7089	CPT2	1.00	8.48E-01	9.36E-01	621.27	not significant
7090	ZNF34	1.00	7.62E-01	NA	95.09	not significant
7091	LOC389705	1.00	5.37E-01	NA	19.82	not significant
7092	SYNE4	1.00	5.97E-01	NA	27.30	not significant
7093	MC1R	1.00	5.24E-01	NA	17.59	not significant
7094	LOC440028	1.00	5.56E-01	NA	22.51	not significant
7095	LCP1	1.00	8.28E-01	9.28E-01	36579.71	not significant
7096	EXOSC6	1.00	8.55E-01	9.41E-01	1061.77	not significant
7097	FLYWCH2	1.00	8.49E-01	9.37E-01	662.07	not significant
7098	DNAJC13	1.00	8.46E-01	9.35E-01	3038.53	not significant
7099	PEX6	1.00	8.35E-01	9.31E-01	440.86	not significant
7100	MINPP1	1.00	8.54E-01	9.40E-01	1216.13	not significant
7101	POMT2	1.00	8.37E-01	9.31E-01	629.38	not significant
7102	KIAA1586	1.00	8.19E-01	9.24E-01	565.01	not significant
7103	ZMYM5	1.00	8.48E-01	9.36E-01	687.81	not significant
7104	FAM189A1	1.00	5.59E-01	NA	24.09	not significant
7105	LOC102724467	1.00	5.34E-01	NA	19.95	not significant
7106	DGCR11	1.00	5.53E-01	NA	21.53	not significant
7107	ZFP2	1.00	7.12E-01	NA	60.39	not significant
7108	AVL9	1.00	8.46E-01	9.36E-01	676.77	not significant
7109	ZNF182	1.00	6.59E-01	NA	39.79	not significant
7110	LDLRAP1	1.00	5.71E-01	NA	24.01	not significant
7111	GP5	1.00	5.40E-01	NA	20.74	not significant
7112	TMEFF1	1.00	5.49E-01	NA	20.52	not significant
7113	SARNP	1.00	8.52E-01	9.38E-01	2378.44	not significant
7114	C9orf89	1.00	8.28E-01	9.28E-01	338.03	not significant
7115	MED13L	1.00	8.47E-01	9.36E-01	6045.02	not significant

7116	ORC2	1.00	8.48E-01	9.36E-01	2067.46	not significant
7117	TMED7	1.00	8.45E-01	9.35E-01	1903.02	not significant
7118	PSTPIP2	1.00	8.25E-01	9.27E-01	277.06	not significant
7119	PDF	1.00	8.16E-01	9.22E-01	247.27	not significant
7120	NEK6	1.00	8.36E-01	9.31E-01	402.33	not significant
7121	SERPINH1	1.00	7.95E-01	9.12E-01	159.99	not significant
7122	VANGL2	1.00	7.86E-01	9.08E-01	147.09	not significant
7123	MCF2	1.00	6.72E-01	NA	44.65	not significant
7124	FRMD6	1.00	6.80E-01	NA	48.65	not significant
7125	ERI3-IT1	1.00	4.54E-01	NA	13.70	not significant
7126	IER5L	1.00	5.86E-01	NA	28.39	not significant
7127	CHKB	1.00	4.12E-01	NA	12.17	not significant
7128	ALDH9A1	1.00	8.51E-01	9.37E-01	2207.07	not significant
7129	SIRT7	1.00	8.48E-01	9.36E-01	979.14	not significant
7130	STRADA	1.00	8.51E-01	9.38E-01	1809.30	not significant
7131	MINOS1	1.00	8.51E-01	9.37E-01	1001.03	not significant
7132	VPS4A	1.00	8.37E-01	9.31E-01	3292.61	not significant
7133	ATP11B	1.00	8.43E-01	9.33E-01	6749.07	not significant
7134	PTPN22	1.00	8.35E-01	9.31E-01	816.08	not significant
7135	LOC100133315	1.00	7.36E-01	NA	79.10	not significant
7136	PEX11B	1.00	7.49E-01	NA	94.47	not significant
7137	HPGD	1.00	7.58E-01	8.91E-01	101.50	not significant
7138	RYR2	1.00	7.00E-01	NA	56.73	not significant
7139	SUGT1P1	1.00	6.48E-01	NA	38.95	not significant
7140	FKBP1AP1	1.00	6.57E-01	NA	43.14	not significant
7141	ERICH6-AS1	1.00	5.27E-01	NA	20.54	not significant
7142	DPEP1	1.00	5.13E-01	NA	20.45	not significant
7143	HEPACAM	1.00	6.20E-01	NA	36.47	not significant
7144	MED8	1.00	8.46E-01	9.35E-01	1160.98	not significant
7145	C7orf26	1.00	8.39E-01	9.32E-01	1932.69	not significant
7146	TBC1D7	1.00	8.19E-01	9.24E-01	553.75	not significant
7147	TP53RK	1.00	8.28E-01	9.28E-01	1791.64	not significant
7148	SRPR	1.00	7.81E-01	9.05E-01	7405.31	not significant
7149	PI4K2A	1.00	8.41E-01	9.32E-01	1186.77	not significant
7150	CBL	1.00	8.39E-01	9.31E-01	4858.14	not significant
7151	FAM185A	1.00	7.92E-01	9.11E-01	166.19	not significant
7152	ZC3H12B	1.00	7.92E-01	9.11E-01	155.11	not significant
7153	ZNF418	1.00	8.08E-01	9.18E-01	220.75	not significant
7154	POLG2	1.00	7.43E-01	8.84E-01	172.65	not significant
7155	TNFSF8	1.00	7.74E-01	9.00E-01	127.18	not significant
7156	TUSC2	1.00	7.94E-01	9.11E-01	189.81	not significant
7157	FMNL2	1.00	7.91E-01	9.10E-01	165.10	not significant
7158	DUSP28	1.00	7.74E-01	9.00E-01	129.04	not significant
7159	C2orf15	1.00	5.50E-01	NA	23.04	not significant
7160	LINC01222	1.00	4.14E-01	NA	13.55	not significant
7161	AP2S1	1.00	8.37E-01	9.31E-01	3247.13	not significant
7162	ICT1	1.00	8.39E-01	9.32E-01	1259.69	not significant
7163	C12orf73	1.00	8.35E-01	9.31E-01	629.33	not significant
7164	NHLRC3	1.00	8.40E-01	9.32E-01	1058.64	not significant
7165	TNK2	1.00	8.38E-01	9.31E-01	1526.28	not significant
7166	ERLIN1	1.00	8.40E-01	9.32E-01	1745.25	not significant
7167	GALM	1.00	8.40E-01	9.32E-01	948.97	not significant
7168	UGCG	1.00	8.12E-01	9.20E-01	526.34	not significant
7169	PDGFA	1.00	6.40E-01	NA	45.19	not significant
7170	KIAA1467	1.00	8.06E-01	9.17E-01	220.78	not significant
7171	CD99L2	1.00	7.98E-01	9.12E-01	205.84	not significant
7172	TCEANC	1.00	7.46E-01	8.85E-01	102.66	not significant
7173	DNAJC27	1.00	8.09E-01	9.18E-01	290.94	not significant
7174	LOC100506136	1.00	4.44E-01	NA	14.98	not significant
7175	NUDT7	1.00	6.61E-01	NA	48.46	not significant
7176	ZNF70	1.00	7.94E-01	9.11E-01	224.84	not significant
7177	HAGHL	1.00	5.04E-01	NA	19.35	not significant
7178	SYCE1L	1.00	4.71E-01	NA	16.65	not significant
7179	TIGD3	1.00	6.23E-01	NA	37.59	not significant
7180	NR1H2	1.00	8.37E-01	9.31E-01	2082.47	not significant
7181	PHKG2	1.00	8.47E-01	9.36E-01	1053.75	not significant
7182	YIF1A	1.00	8.41E-01	9.32E-01	1522.25	not significant
7183	ZNF680	1.00	8.36E-01	9.31E-01	866.60	not significant
7184	GIN1	1.00	6.51E-01	NA	49.08	not significant
7185	NUTM2B-AS1	1.00	8.21E-01	9.25E-01	340.75	not significant
7186	LOC100131655	1.00	6.18E-01	NA	36.97	not significant
7187	APBB3	1.00	8.11E-01	9.20E-01	323.26	not significant
7188	TSPAN2	1.00	7.20E-01	NA	77.84	not significant
7189	LOC101929767	1.00	7.00E-01	NA	70.25	not significant
7190	ZNF540	1.00	6.79E-01	NA	74.11	not significant
7191	RTP5	1.00	4.66E-01	NA	21.27	not significant
7192	SPON2	1.00	6.34E-01	NA	41.83	not significant
7193	VSIG10L	1.00	6.24E-01	NA	39.18	not significant
7194	LINC01337	1.00	2.74E-01	NA	8.57	not significant
7195	TCP11L2	1.00	3.81E-01	NA	11.67	not significant
7196	SEPT7-AS1	1.00	2.90E-01	NA	8.26	not significant
7197	CD81-AS1	1.00	2.29E-01	NA	7.59	not significant
7198	ACIN1	1.00	8.89E-01	9.58E-01	10222.21	not significant
7199	LAPTM5	1.00	8.10E-01	9.19E-01	14245.18	not significant
7200	NUDT9	1.00	8.39E-01	9.31E-01	967.34	not significant
7201	MCEE	1.00	7.85E-01	9.07E-01	118.83	not significant
7202	RPS14	1.00	8.34E-01	9.30E-01	12666.99	not significant
7203	SCAI	1.00	8.37E-01	9.31E-01	1291.32	not significant

7204	HIST1H2BG	1.00	5.33E-01	NA	23.78	not significant
7205	SH3D21	1.00	5.45E-01	NA	25.55	not significant
7206	TNFAIP1	1.00	7.48E-01	8.85E-01	110.47	not significant
7207	C22orf34	1.00	7.84E-01	9.07E-01	182.85	not significant
7208	F2RL1	1.00	6.64E-01	NA	56.00	not significant
7209	DYNLT3	1.00	5.55E-01	NA	27.22	not significant
7210	LOC100049716	1.00	4.80E-01	NA	18.13	not significant
7211	SLC35D2	1.00	4.19E-01	NA	15.00	not significant
7212	TMED10P1	1.00	4.76E-01	NA	18.76	not significant
7213	DAK	1.00	8.34E-01	9.30E-01	431.19	not significant
7214	MMADHC	1.00	8.39E-01	9.31E-01	2265.51	not significant
7215	TMA16	1.00	8.31E-01	9.29E-01	1513.07	not significant
7216	SEC23B	1.00	8.37E-01	9.31E-01	3519.29	not significant
7217	ZCCHC11	1.00	8.25E-01	9.27E-01	3859.41	not significant
7218	LPIN1	1.00	8.15E-01	9.22E-01	4782.01	not significant
7219	CORO2A	1.00	8.37E-01	9.31E-01	1073.18	not significant
7220	TMEM116	1.00	7.92E-01	9.11E-01	230.21	not significant
7221	VPS33B	1.00	8.28E-01	9.28E-01	511.80	not significant
7222	SHPK	1.00	8.27E-01	9.28E-01	777.02	not significant
7223	RGS9	1.00	7.33E-01	NA	94.22	not significant
7224	PTENP1	1.00	6.82E-01	NA	61.42	not significant
7225	SWT1	1.00	7.50E-01	8.87E-01	124.18	not significant
7226	C2orf81	1.00	6.45E-01	NA	50.83	not significant
7227	KLHL36	1.00	7.69E-01	8.98E-01	170.55	not significant
7228	LOC644656	1.00	6.58E-01	NA	51.34	not significant
7229	SKP1P2	1.00	2.91E-01	NA	10.30	not significant
7230	TMEM56-RWDD3	1.00	2.78E-01	NA	8.56	not significant
7231	MATN4	1.00	2.61E-01	NA	8.06	not significant
7232	RPSAP9	1.00	4.48E-01	NA	18.51	not significant
7233	SELP	1.00	4.26E-01	NA	16.80	not significant
7234	PTPN2	1.00	8.30E-01	9.29E-01	2158.35	not significant
7235	SNAPIN	1.00	8.28E-01	9.28E-01	1030.35	not significant
7236	SHC1	1.00	8.38E-01	9.31E-01	2244.82	not significant
7237	TOP3A	1.00	8.30E-01	9.29E-01	3325.12	not significant
7238	ARNTL2	1.00	8.06E-01	9.17E-01	1703.61	not significant
7239	KDM5C	1.00	8.30E-01	9.29E-01	1557.36	not significant
7240	CPT1B	1.00	6.69E-01	NA	57.37	not significant
7241	SSH1	1.00	7.52E-01	8.88E-01	2133.55	not significant
7242	CELF5	1.00	4.09E-01	NA	14.93	not significant
7243	LINC00476	1.00	7.57E-01	8.91E-01	138.67	not significant
7244	HCG18	1.00	6.62E-01	NA	54.24	not significant
7245	HIST1H2BJ	1.00	4.69E-01	NA	19.26	not significant
7246	C14orf79	1.00	5.00E-01	NA	22.49	not significant
7247	MFSD4	1.00	4.35E-01	NA	17.01	not significant
7248	LGALS4	1.00	1.89E-01	NA	7.26	not significant
7249	CDC37	1.00	7.95E-01	9.12E-01	8780.71	not significant
7250	ETV6	1.00	8.20E-01	9.25E-01	2383.45	not significant
7251	ERLIN2	1.00	8.29E-01	9.28E-01	1736.59	not significant
7252	PI4KA	1.00	8.21E-01	9.25E-01	5116.99	not significant
7253	BBS10	1.00	8.24E-01	9.27E-01	628.76	not significant
7254	FSTL3	1.00	7.65E-01	8.95E-01	155.16	not significant
7255	BCDIN3D	1.00	7.93E-01	9.11E-01	254.46	not significant
7256	HIST1H1E	1.00	6.81E-01	NA	82.31	not significant
7257	PAN3-AS1	1.00	6.96E-01	NA	70.46	not significant
7258	SPIB	1.00	5.99E-01	NA	38.50	not significant
7259	ZNF213-AS1	1.00	7.03E-01	NA	78.39	not significant
7260	EXPH5	1.00	5.99E-01	NA	40.35	not significant
7261	RNASEK	1.00	5.71E-01	NA	31.23	not significant
7262	PDK3	1.00	9.47E-01	9.80E-01	1275.18	not significant
7263	SRGN	1.00	8.06E-01	9.17E-01	410.66	not significant
7264	MKL1	1.00	8.21E-01	9.25E-01	2069.50	not significant
7265	RFT1	1.00	8.24E-01	9.27E-01	1650.07	not significant
7266	CNEP1R1	1.00	8.17E-01	9.24E-01	803.29	not significant
7267	ZRANB3	1.00	8.08E-01	9.18E-01	328.67	not significant
7268	WHAMM	1.00	8.11E-01	9.20E-01	400.30	not significant
7269	SLC9A5	1.00	4.99E-01	NA	22.95	not significant
7270	LAMP3	1.00	8.14E-01	9.21E-01	270.12	not significant
7271	RAET1K	1.00	7.47E-01	8.85E-01	137.32	not significant
7272	ASH1L-AS1	1.00	5.89E-01	NA	37.80	not significant
7273	RRAS	1.00	6.66E-01	NA	63.51	not significant
7274	NFIB	1.00	3.06E-01	NA	11.14	not significant
7275	COL9A3	1.00	5.72E-01	NA	33.70	not significant
7276	ZBTB18	1.00	8.32E-01	9.30E-01	1506.01	not significant
7277	ATP9B	1.00	7.53E-01	8.89E-01	751.66	not significant
7278	VPS13A	1.00	7.87E-01	9.08E-01	3451.66	not significant
7279	ANKRD18DP	1.00	6.48E-01	NA	59.43	not significant
7280	LOC100133091	1.00	6.90E-01	8.54E-01	106.01	not significant
7281	ZNF724P	1.00	6.71E-01	NA	70.50	not significant
7282	DEPDC4	1.00	5.27E-01	NA	28.14	not significant
7283	TSGA10	1.00	6.62E-01	NA	64.03	not significant
7284	STON1	1.00	3.78E-01	NA	15.18	not significant
7285	LRRC43	1.00	2.20E-01	NA	7.80	not significant
7286	AMDHD1	1.00	3.58E-01	NA	13.32	not significant
7287	CCDC28B	1.00	8.19E-01	9.24E-01	674.49	not significant
7288	COX5B	1.00	8.14E-01	9.22E-01	3272.09	not significant
7289	SLC35A1	1.00	7.86E-01	9.08E-01	542.47	not significant
7290	POT1	1.00	8.19E-01	9.24E-01	2100.66	not significant
7291	EAPP	1.00	8.23E-01	9.27E-01	1041.69	not significant

7292	SARS2	1.00	8.18E-01	9.24E-01	858.64	not significant
7293	CBFA2T2	1.00	8.19E-01	9.24E-01	1735.27	not significant
7294	SLX4	1.00	8.16E-01	9.22E-01	797.72	not significant
7295	ITSN1	1.00	8.16E-01	9.22E-01	713.12	not significant
7296	FBXO36	1.00	6.42E-01	NA	58.40	not significant
7297	HABP4	1.00	7.00E-01	NA	94.20	not significant
7298	YY2	1.00	7.38E-01	8.80E-01	125.83	not significant
7299	NKIRAS2	1.00	7.56E-01	8.90E-01	231.59	not significant
7300	TBC1D3P1-DHX40F	1.00	5.27E-01	NA	28.13	not significant
7301	NRSN2	1.00	5.86E-01	NA	40.20	not significant
7302	MURC	1.00	5.91E-01	NA	39.94	not significant
7303	FAM228B	1.00	5.91E-01	NA	45.89	not significant
7304	SCARNA2	1.00	2.68E-01	NA	10.41	not significant
7305	LOC101927051	1.00	2.77E-01	NA	10.28	not significant
7306	ADHFE1	1.00	3.72E-01	NA	14.33	not significant
7307	LINC00260	1.00	3.55E-01	NA	13.58	not significant
7308	LKAAEAR1	1.00	2.21E-01	NA	8.70	not significant
7309	ZMYND19	1.00	8.19E-01	9.24E-01	1052.87	not significant
7310	MRFAP1L1	1.00	8.15E-01	9.22E-01	2195.95	not significant
7311	TFG	1.00	8.12E-01	9.21E-01	2400.98	not significant
7312	ANAPC4	1.00	8.19E-01	9.24E-01	1296.10	not significant
7313	GPS2	1.00	8.23E-01	9.27E-01	2244.19	not significant
7314	ATF2	1.00	7.95E-01	9.12E-01	4181.85	not significant
7315	UBE2D4	1.00	7.74E-01	9.00E-01	539.05	not significant
7316	WDR44	1.00	8.07E-01	9.17E-01	982.27	not significant
7317	RCAN3	1.00	8.12E-01	9.21E-01	723.82	not significant
7318	THAP9	1.00	7.89E-01	9.09E-01	276.77	not significant
7319	GABBR1	1.00	6.49E-01	NA	65.17	not significant
7320	GRAMD1C	1.00	6.82E-01	NA	76.74	not significant
7321	BEND6	1.00	2.88E-01	NA	10.86	not significant
7322	MANEA-AS1	1.00	5.31E-01	NA	32.25	not significant
7323	MIR210HG	1.00	6.08E-01	NA	47.31	not significant
7324	OCLM	1.00	4.23E-01	NA	19.47	not significant
7325	S100B	1.00	1.98E-01	NA	7.95	not significant
7326	RND1	1.00	3.38E-01	NA	34.11	not significant
7327	RNF130	1.00	8.06E-01	9.17E-01	1933.62	not significant
7328	NDUFS7	1.00	8.63E-01	9.44E-01	1638.63	not significant
7329	STK11	1.00	8.29E-01	9.28E-01	2462.40	not significant
7330	ZNF25	1.00	7.36E-01	8.79E-01	218.02	not significant
7331	CARKD	1.00	8.13E-01	9.21E-01	1286.51	not significant
7332	ARHGEF19	1.00	7.70E-01	8.98E-01	232.94	not significant
7333	MFSD12	1.00	8.30E-01	9.29E-01	1188.13	not significant
7334	FUNDC1	1.00	7.82E-01	9.05E-01	554.32	not significant
7335	TMIGD2	1.00	7.34E-01	8.78E-01	137.42	not significant
7336	TESK2	1.00	7.52E-01	8.88E-01	164.45	not significant
7337	LOC642236	1.00	5.06E-01	NA	30.51	not significant
7338	ZSCAN4	1.00	2.41E-01	NA	8.95	not significant
7339	ARIH2OS	1.00	5.87E-01	NA	42.71	not significant
7340	ARTN	1.00	3.67E-01	NA	14.76	not significant
7341	RNF213	1.00	8.31E-01	9.29E-01	26434.06	not significant
7342	CLPTM1	1.00	8.04E-01	9.16E-01	3727.60	not significant
7343	HAUS6	1.00	8.31E-01	9.29E-01	3732.69	not significant
7344	IFNAR2	1.00	7.90E-01	9.09E-01	1942.77	not significant
7345	SLFN12	1.00	8.05E-01	9.17E-01	618.90	not significant
7346	STX4	1.00	8.07E-01	9.17E-01	848.18	not significant
7347	MDGA1	1.00	6.65E-01	NA	70.89	not significant
7348	RPL17	1.00	7.52E-01	8.88E-01	229.46	not significant
7349	BIVM	1.00	7.36E-01	8.79E-01	156.70	not significant
7350	ADAMTS10	1.00	7.92E-01	9.11E-01	331.98	not significant
7351	KIF9	1.00	7.56E-01	8.90E-01	188.52	not significant
7352	CASP9	1.00	7.32E-01	8.77E-01	143.58	not significant
7353	LOC256880	1.00	4.07E-01	NA	17.68	not significant
7354	DAB2IP	1.00	4.02E-01	NA	18.04	not significant
7355	ST8SIA1	1.00	6.36E-01	NA	59.39	not significant
7356	ESR2	1.00	2.75E-01	NA	11.00	not significant
7357	UCN	1.00	4.91E-01	NA	27.19	not significant
7358	CRNKL1	1.00	8.05E-01	9.17E-01	1826.84	not significant
7359	GCA	1.00	7.85E-01	9.07E-01	327.62	not significant
7360	HECTD4	1.00	7.38E-01	8.80E-01	3144.33	not significant
7361	HMX2	1.00	5.98E-01	NA	49.64	not significant
7362	FAM21A	1.00	7.05E-01	NA	92.19	not significant
7363	RALY-AS1	1.00	4.62E-01	NA	23.85	not significant
7364	RAG1	1.00	5.76E-01	NA	41.45	not significant
7365	ANKDD1A	1.00	4.85E-01	NA	29.42	not significant
7366	SNAPC1	1.00	7.99E-01	9.13E-01	671.95	not significant
7367	DUSP12	1.00	8.02E-01	9.15E-01	797.77	not significant
7368	COX4I1	1.00	7.93E-01	9.11E-01	7433.13	not significant
7369	UQCRC1	1.00	7.98E-01	9.12E-01	4795.09	not significant
7370	CD247	1.00	7.83E-01	9.06E-01	7873.03	not significant
7371	RAB5B	1.00	7.73E-01	9.00E-01	4215.85	not significant
7372	POLR1E	1.00	8.06E-01	9.17E-01	1603.95	not significant
7373	TM9SF3	1.00	7.79E-01	9.03E-01	7159.94	not significant
7374	CCDC132	1.00	8.10E-01	9.19E-01	1031.17	not significant
7375	UNC119	1.00	7.97E-01	9.12E-01	749.33	not significant
7376	TVP23B	1.00	7.83E-01	9.06E-01	308.03	not significant
7377	TMEM50B	1.00	7.87E-01	9.08E-01	378.70	not significant
7378	REL	1.00	7.44E-01	8.84E-01	1390.37	not significant
7379	HOXB7	1.00	9.39E-01	NA	27.51	not significant

7380	FES	1.00	6.08E-01	NA	56.66	not significant
7381	GAS6-AS1	1.00	5.00E-01	NA	30.41	not significant
7382	LOC100335030	1.00	4.14E-01	NA	20.31	not significant
7383	PLXDC1	1.00	3.47E-01	NA	17.08	not significant
7384	EXOC7	1.00	7.78E-01	9.03E-01	9481.33	not significant
7385	ERGIC1	1.00	7.57E-01	8.91E-01	10291.80	not significant
7386	PXDN	1.00	7.81E-01	9.05E-01	3313.36	not significant
7387	ZNF559	1.00	7.93E-01	9.11E-01	440.91	not significant
7388	LEF1-AS1	1.00	7.45E-01	8.85E-01	180.76	not significant
7389	CTSK	1.00	6.24E-01	NA	60.88	not significant
7390	SLC44A1	1.00	7.55E-01	8.90E-01	489.62	not significant
7391	COL18A1	1.00	6.69E-01	NA	87.43	not significant
7392	HLA-DMA	1.00	4.38E-01	NA	22.14	not significant
7393	NACA2	1.00	4.94E-01	NA	28.80	not significant
7394	LOC400863	1.00	5.23E-01	NA	34.18	not significant
7395	SARM1	1.00	6.54E-01	NA	89.32	not significant
7396	KIAA2022	1.00	5.70E-01	NA	42.38	not significant
7397	CEACAM21	1.00	4.48E-01	NA	23.55	not significant
7398	SEMA6A-AS1	1.00	2.95E-01	NA	13.04	not significant
7399	LOC100652758	1.00	4.56E-01	NA	25.26	not significant
7400	MID1IP1	1.01	8.28E-01	9.28E-01	3448.47	not significant
7401	APEH	1.01	7.71E-01	8.99E-01	4124.33	not significant
7402	RBX1	1.01	8.07E-01	9.17E-01	2071.69	not significant
7403	UBE2M	1.01	7.97E-01	9.12E-01	4411.19	not significant
7404	TIA1	1.01	7.37E-01	8.80E-01	5773.73	not significant
7405	KIAA0100	1.01	7.84E-01	9.06E-01	9148.72	not significant
7406	ZNF700	1.01	7.94E-01	9.11E-01	525.78	not significant
7407	ZNF292	1.01	8.14E-01	9.21E-01	2844.68	not significant
7408	NADK2	1.01	7.99E-01	9.14E-01	1453.21	not significant
7409	CRHR1-IT1	1.01	4.42E-01	NA	24.18	not significant
7410	GK5	1.01	7.95E-01	9.12E-01	1085.72	not significant
7411	WDR60	1.01	7.74E-01	9.00E-01	597.23	not significant
7412	EPHX1	1.01	6.99E-01	8.59E-01	113.90	not significant
7413	LPP-AS2	1.01	6.23E-01	NA	65.63	not significant
7414	ISPD	1.01	7.12E-01	8.66E-01	139.61	not significant
7415	ARMCX2	1.01	3.03E-01	NA	14.12	not significant
7416	PPFIA4	1.01	4.01E-01	NA	19.17	not significant
7417	C1orf61	1.01	3.97E-01	NA	19.29	not significant
7418	ABCD2	1.01	5.72E-01	NA	46.72	not significant
7419	OTUD1	1.01	4.70E-01	NA	26.98	not significant
7420	RASGRF1	1.01	3.44E-01	NA	16.54	not significant
7421	GPR171	1.01	2.90E-01	NA	12.11	not significant
7422	NR4A3	1.01	4.14E-01	NA	22.86	not significant
7423	LSM8	1.01	7.91E-01	9.10E-01	2807.96	not significant
7424	MAP3K14	1.01	7.71E-01	8.99E-01	588.22	not significant
7425	C6orf211	1.01	7.97E-01	9.12E-01	1488.28	not significant
7426	RNASE6	1.01	5.44E-01	NA	45.98	not significant
7427	TROVE2	1.01	7.96E-01	9.12E-01	1156.92	not significant
7428	WDR64	1.01	2.99E-01	NA	13.03	not significant
7429	TPTE2P5	1.01	4.03E-01	NA	20.39	not significant
7430	SNHG10	1.01	7.43E-01	8.84E-01	231.15	not significant
7431	NDOR1	1.01	7.89E-01	9.09E-01	2861.80	not significant
7432	PNMA2	1.01	7.85E-01	9.07E-01	2362.42	not significant
7433	STAG3	1.01	7.78E-01	9.03E-01	403.31	not significant
7434	UQCR11	1.01	7.83E-01	9.06E-01	3203.08	not significant
7435	ZNF69	1.01	6.70E-01	8.45E-01	101.65	not significant
7436	POLR2J4	1.01	7.53E-01	8.89E-01	244.25	not significant
7437	MX1	1.01	7.02E-01	8.59E-01	124.14	not significant
7438	PCGF2	1.01	7.47E-01	8.85E-01	235.03	not significant
7439	KIAA1328	1.01	7.38E-01	8.80E-01	230.17	not significant
7440	LOC728024	1.01	5.43E-01	NA	43.33	not significant
7441	SDHAP3	1.01	6.92E-01	8.54E-01	111.49	not significant
7442	ANKRD20A5P	1.01	6.20E-01	NA	74.28	not significant
7443	C3AR1	1.01	5.01E-01	NA	33.79	not significant
7444	LOC101929140	1.01	3.79E-01	NA	20.15	not significant
7445	BCL2L2	1.01	4.01E-01	NA	21.27	not significant
7446	FAM66B	1.01	5.06E-01	NA	34.25	not significant
7447	TLL1	1.01	4.73E-01	NA	31.06	not significant
7448	MAPK8IP2	1.01	2.98E-01	NA	15.14	not significant
7449	INO80C	1.01	7.82E-01	9.05E-01	487.54	not significant
7450	TRAPPC1	1.01	7.57E-01	8.91E-01	2951.81	not significant
7451	DAD1	1.01	8.05E-01	9.17E-01	2386.84	not significant
7452	MPHOSPH6	1.01	7.31E-01	8.77E-01	2061.45	not significant
7453	STRN4	1.01	7.84E-01	9.06E-01	3193.60	not significant
7454	TAF1D	1.01	7.91E-01	9.10E-01	1509.01	not significant
7455	HELLS	1.01	7.98E-01	9.12E-01	2411.90	not significant
7456	EPN2	1.01	7.47E-01	8.85E-01	531.06	not significant
7457	PAIP1	1.01	8.16E-01	9.23E-01	1200.72	not significant
7458	SLC35E1	1.01	7.42E-01	8.83E-01	2716.13	not significant
7459	TMEM86B	1.01	7.59E-01	8.92E-01	300.74	not significant
7460	LOC100129034	1.01	7.71E-01	8.99E-01	531.89	not significant
7461	SYNE3	1.01	7.28E-01	8.75E-01	181.44	not significant
7462	LOXL1-AS1	1.01	6.17E-01	NA	65.30	not significant
7463	SLC12A5	1.01	4.05E-01	NA	22.81	not significant
7464	FAM192A	1.01	7.72E-01	8.99E-01	3774.86	not significant
7465	PRKD3	1.01	7.77E-01	9.03E-01	2850.45	not significant
7466	RPS3A	1.01	8.01E-01	9.14E-01	11588.68	not significant
7467	SLC30A7	1.01	7.94E-01	9.11E-01	2020.49	not significant

7468	TMEM120A	1.01	7.23E-01	8.72E-01	170.29	not significant
7469	CGRRF1	1.01	7.49E-01	8.86E-01	278.48	not significant
7470	PITPNM3	1.01	4.51E-01	NA	26.88	not significant
7471	C16orf95	1.01	6.70E-01	NA	100.19	not significant
7472	LOC101927572	1.01	5.31E-01	NA	41.58	not significant
7473	ERICH5	1.01	3.69E-01	NA	19.13	not significant
7474	SATB1-AS1	1.01	3.54E-01	NA	19.74	not significant
7475	PTPMT1	1.01	7.87E-01	9.08E-01	1413.07	not significant
7476	RNF216	1.01	7.80E-01	9.04E-01	3485.68	not significant
7477	POLR2J3	1.01	7.50E-01	8.86E-01	278.22	not significant
7478	NBPF1	1.01	7.88E-01	9.09E-01	926.27	not significant
7479	RPL27A	1.01	7.55E-01	8.90E-01	15147.14	not significant
7480	HCN2	1.01	4.95E-01	NA	39.19	not significant
7481	SPATA2L	1.01	7.05E-01	8.61E-01	141.50	not significant
7482	LACE1	1.01	6.63E-01	8.41E-01	100.67	not significant
7483	SRGAP3	1.01	5.98E-01	NA	78.46	not significant
7484	FGFBP3	1.01	6.57E-01	8.38E-01	103.46	not significant
7485	C17orf58	1.01	4.02E-01	NA	23.67	not significant
7486	LOC100130357	1.01	3.56E-01	NA	19.19	not significant
7487	SKA2	1.01	7.61E-01	8.93E-01	4159.27	not significant
7488	ATP13A1	1.01	7.94E-01	9.11E-01	3499.26	not significant
7489	MIS12	1.01	7.94E-01	9.11E-01	2361.73	not significant
7490	BRF2	1.01	7.80E-01	9.04E-01	956.48	not significant
7491	ZNF273	1.01	8.02E-01	9.14E-01	1433.74	not significant
7492	UQCRQ	1.01	7.66E-01	8.96E-01	3013.24	not significant
7493	RDH5	1.01	4.17E-01	NA	26.70	not significant
7494	LOC102724814	1.01	6.61E-01	8.40E-01	124.82	not significant
7495	C4orf32	1.01	7.00E-01	8.59E-01	151.27	not significant
7496	C21orf128	1.01	2.78E-01	NA	14.22	not significant
7497	ABCA2	1.01	4.82E-01	NA	33.75	not significant
7498	VSX1	1.01	2.68E-01	NA	13.71	not significant
7499	CHKB-AS1	1.01	3.95E-01	NA	24.91	not significant
7500	DNAJC15	1.01	7.69E-01	8.98E-01	456.03	not significant
7501	NFE2L1	1.01	7.62E-01	8.94E-01	4895.37	not significant
7502	PABPC4L	1.01	7.79E-01	9.03E-01	660.80	not significant
7503	STXBP1	1.01	7.72E-01	8.99E-01	455.69	not significant
7504	SNX25	1.01	7.91E-01	9.10E-01	781.98	not significant
7505	APH1B	1.01	7.01E-01	8.59E-01	158.86	not significant
7506	ZNF594	1.01	7.15E-01	8.68E-01	181.31	not significant
7507	NPR2	1.01	6.61E-01	8.40E-01	103.23	not significant
7508	FABP5	1.01	7.19E-01	8.71E-01	1008.50	not significant
7509	ALDH3A2	1.01	3.04E-01	NA	15.50	not significant
7510	AGER	1.01	6.11E-01	NA	71.43	not significant
7511	ADARB2	1.01	4.19E-01	NA	26.55	not significant
7512	SLC23A3	1.01	4.13E-01	NA	25.15	not significant
7513	PARK7	1.01	7.67E-01	8.96E-01	4811.61	not significant
7514	C16orf13	1.01	7.11E-01	8.65E-01	2077.30	not significant
7515	USP22	1.01	7.27E-01	8.75E-01	10176.73	not significant
7516	FLOT1	1.01	7.79E-01	9.03E-01	1355.72	not significant
7517	TM9SF4	1.01	7.98E-01	9.12E-01	3493.24	not significant
7518	ABCG1	1.01	7.29E-01	8.76E-01	225.34	not significant
7519	TOP3B	1.01	7.75E-01	9.01E-01	1051.25	not significant
7520	TCAIM	1.01	7.70E-01	8.98E-01	1058.91	not significant
7521	NID2	1.01	7.02E-01	8.59E-01	156.51	not significant
7522	SMPD1	1.01	6.40E-01	NA	87.09	not significant
7523	TMEM169	1.01	1.60E-01	NA	9.63	not significant
7524	C11orf48	1.01	6.28E-01	NA	80.52	not significant
7525	UCP3	1.01	6.16E-01	NA	72.99	not significant
7526	LOC115110	1.01	5.28E-01	NA	44.15	not significant
7527	LINC00892	1.01	4.02E-01	NA	24.62	not significant
7528	MDH1	1.01	7.46E-01	8.85E-01	6158.96	not significant
7529	NUP85	1.01	7.52E-01	8.88E-01	4283.46	not significant
7530	NELFE	1.01	7.77E-01	9.02E-01	1635.22	not significant
7531	IMPA1	1.01	7.14E-01	8.67E-01	2048.39	not significant
7532	ASAH1	1.01	7.95E-01	9.12E-01	1190.07	not significant
7533	SEC23A	1.01	7.74E-01	9.00E-01	1599.50	not significant
7534	LINC01000	1.01	8.23E-01	9.26E-01	1476.34	not significant
7535	ICK	1.01	7.59E-01	8.92E-01	426.90	not significant
7536	STAC3	1.01	7.19E-01	8.71E-01	199.01	not significant
7537	SYNGAP1	1.01	7.22E-01	8.71E-01	250.85	not significant
7538	NSUN3	1.01	7.41E-01	8.82E-01	276.63	not significant
7539	CCDC7	1.01	6.56E-01	NA	97.78	not significant
7540	CACFD1	1.01	2.76E-01	NA	14.67	not significant
7541	RNF165	1.01	3.30E-01	NA	22.19	not significant
7542	SLC37A2	1.01	5.03E-01	NA	42.33	not significant
7543	GTF2B	1.01	8.01E-01	9.14E-01	1529.87	not significant
7544	THOC2	1.01	7.39E-01	8.80E-01	4651.78	not significant
7545	ANKRD11	1.01	7.63E-01	8.94E-01	5897.23	not significant
7546	SNTB1	1.01	6.85E-01	8.52E-01	148.65	not significant
7547	MRPS31P5	1.01	7.51E-01	8.88E-01	372.34	not significant
7548	NKTR	1.01	7.44E-01	8.84E-01	4649.28	not significant
7549	MIR600HG	1.01	6.89E-01	8.54E-01	190.40	not significant
7550	CALML4	1.01	7.22E-01	8.72E-01	224.81	not significant
7551	TMSB4Y	1.01	5.91E-01	NA	75.85	not significant
7552	NCLN	1.01	7.36E-01	8.79E-01	5061.47	not significant
7553	MAP2K5	1.01	7.62E-01	8.94E-01	862.23	not significant
7554	PNMA1	1.01	7.72E-01	8.99E-01	1409.37	not significant
7555	ZNF71	1.01	7.54E-01	8.89E-01	788.91	not significant

7556	KIAA1211	1.01	7.08E-01	8.63E-01	216.11	not significant
7557	TMA7	1.01	7.37E-01	8.80E-01	2566.01	not significant
7558	SEC61A2	1.01	7.34E-01	8.78E-01	268.84	not significant
7559	PHKG1	1.01	5.55E-01	NA	56.57	not significant
7560	NCK1-AS1	1.01	5.71E-01	NA	60.25	not significant
7561	C18orf32	1.01	4.10E-01	NA	30.67	not significant
7562	SPHK1	1.01	6.45E-01	NA	99.88	not significant
7563	KCNMB3	1.01	2.02E-01	NA	12.18	not significant
7564	LOC100128288	1.01	4.40E-01	NA	31.84	not significant
7565	LOC654841	1.01	2.66E-01	NA	15.48	not significant
7566	XRCC3	1.01	7.56E-01	8.90E-01	2360.05	not significant
7567	TM2D3	1.01	7.61E-01	8.93E-01	978.75	not significant
7568	VIMP	1.01	7.71E-01	8.99E-01	1114.43	not significant
7569	TMEM234	1.01	6.31E-01	NA	94.08	not significant
7570	TMEM140	1.01	6.24E-01	8.16E-01	101.92	not significant
7571	WDR25	1.01	6.88E-01	8.54E-01	153.74	not significant
7572	LOC653160	1.01	4.18E-01	NA	28.34	not significant
7573	RSG1	1.01	6.12E-01	NA	81.94	not significant
7574	CEBPE	1.01	5.71E-01	NA	67.28	not significant
7575	MAP3K14-AS1	1.01	6.56E-01	8.38E-01	118.70	not significant
7576	WFS1	1.01	5.58E-01	NA	65.00	not significant
7577	LYPD5	1.01	3.09E-01	NA	17.96	not significant
7578	C1orf162	1.01	3.06E-01	NA	18.73	not significant
7579	CENPB	1.01	7.51E-01	8.87E-01	4761.06	not significant
7580	FAM89B	1.01	7.64E-01	8.95E-01	978.56	not significant
7581	TMCO1	1.01	7.22E-01	8.72E-01	5983.61	not significant
7582	UBE2L6	1.01	7.03E-01	8.60E-01	5416.94	not significant
7583	C9orf64	1.01	7.68E-01	8.97E-01	857.56	not significant
7584	THRAP3	1.01	7.08E-01	8.63E-01	12065.51	not significant
7585	MVB12B	1.01	7.65E-01	8.95E-01	1286.50	not significant
7586	CNOT3	1.01	7.69E-01	8.98E-01	1117.11	not significant
7587	RIMS3	1.01	7.63E-01	8.94E-01	1590.58	not significant
7588	MAU2	1.01	7.72E-01	9.00E-01	2662.83	not significant
7589	RPS6KA4	1.01	7.19E-01	8.70E-01	1975.50	not significant
7590	MYNN	1.01	7.54E-01	8.89E-01	968.24	not significant
7591	ZFP37	1.01	6.78E-01	8.49E-01	146.15	not significant
7592	ZNF274	1.01	7.44E-01	8.84E-01	378.16	not significant
7593	EPOR	1.01	6.35E-01	8.23E-01	102.09	not significant
7594	RPL23AP7	1.01	6.07E-01	NA	82.03	not significant
7595	ITGA9-AS1	1.01	2.69E-01	NA	16.65	not significant
7596	JMJD7	1.01	6.23E-01	NA	91.32	not significant
7597	CECR7	1.01	4.96E-01	NA	42.84	not significant
7598	LOC101927599	1.01	5.71E-01	NA	69.04	not significant
7599	PTPRD	1.01	4.27E-01	NA	33.06	not significant
7600	FUT8	1.01	7.61E-01	8.93E-01	3203.58	not significant
7601	RBM3	1.01	7.17E-01	8.70E-01	1956.43	not significant
7602	SLC8A1	1.01	7.12E-01	8.65E-01	148.02	not significant
7603	NUMBL	1.01	7.27E-01	8.74E-01	280.75	not significant
7604	SIRT3	1.01	7.39E-01	8.81E-01	348.49	not significant
7605	HERC2P9	1.01	6.91E-01	8.54E-01	181.25	not significant
7606	PAQR7	1.01	4.76E-01	NA	43.69	not significant
7607	HHLA3	1.01	5.28E-01	NA	70.23	not significant
7608	LOC101927391	1.01	1.83E-01	NA	11.02	not significant
7609	HIST1H3G	1.01	2.08E-01	NA	13.83	not significant
7610	GPR85	1.01	1.38E-01	NA	9.78	not significant
7611	LYSMD2	1.01	7.57E-01	8.91E-01	746.88	not significant
7612	RB1	1.01	7.10E-01	8.64E-01	13251.74	not significant
7613	PRRT4	1.01	4.09E-01	NA	29.38	not significant
7614	ZNF696	1.01	7.51E-01	8.87E-01	694.71	not significant
7615	ZNF613	1.01	7.27E-01	8.74E-01	296.78	not significant
7616	MRPS14	1.01	7.46E-01	8.85E-01	890.29	not significant
7617	SNHG20	1.01	7.40E-01	8.81E-01	386.92	not significant
7618	QSOX2	1.01	7.62E-01	8.94E-01	1087.29	not significant
7619	KIAA1656	1.01	5.70E-01	NA	67.78	not significant
7620	TXK	1.01	5.31E-01	NA	52.99	not significant
7621	CHDH	1.01	3.50E-01	NA	23.20	not significant
7622	CARS	1.01	7.12E-01	8.66E-01	2557.77	not significant
7623	HIF1A	1.01	7.38E-01	8.80E-01	3977.63	not significant
7624	MTMR3	1.01	7.56E-01	8.90E-01	1632.49	not significant
7625	FBXO10	1.01	7.25E-01	8.74E-01	305.01	not significant
7626	PRPF40B	1.01	6.71E-01	8.46E-01	155.94	not significant
7627	GLT1D1	1.01	7.36E-01	8.79E-01	354.66	not significant
7628	COX14	1.01	6.87E-01	8.53E-01	787.17	not significant
7629	SLC4A8	1.01	6.90E-01	8.54E-01	196.97	not significant
7630	NMRK1	1.01	6.36E-01	8.24E-01	114.11	not significant
7631	IFITM3	1.01	3.80E-01	NA	27.86	not significant
7632	EGR3	1.01	3.06E-01	NA	19.16	not significant
7633	ESYT3	1.01	3.52E-01	NA	25.01	not significant
7634	BBS12	1.01	5.85E-01	NA	78.80	not significant
7635	CRYGS	1.01	3.51E-01	NA	24.25	not significant
7636	MYO1A	1.01	4.52E-01	NA	37.88	not significant
7637	LOC101926928	1.01	2.21E-01	NA	14.25	not significant
7638	GMDS	1.01	9.20E-01	9.69E-01	1493.23	not significant
7639	RPL29	1.01	7.64E-01	8.94E-01	12178.13	not significant
7640	GDI2	1.01	7.12E-01	8.66E-01	12593.53	not significant
7641	H2AFX	1.01	7.47E-01	8.85E-01	6475.39	not significant
7642	SMIM13	1.01	7.63E-01	8.94E-01	1206.21	not significant
7643	LOC100506083	1.01	3.87E-01	NA	29.08	not significant

7644	TMSB15A	1.01	6.15E-01	8.12E-01	105.14	not significant
7645	PRICKLE3	1.01	4.32E-01	NA	34.92	not significant
7646	LOC642361	1.01	4.72E-01	NA	42.28	not significant
7647	CYP2D7P	1.01	2.76E-01	NA	17.68	not significant
7648	CMC4	1.01	3.11E-01	NA	21.90	not significant
7649	ADAP1	1.01	4.27E-01	NA	33.72	not significant
7650	FXR2	1.01	7.46E-01	8.85E-01	2064.01	not significant
7651	MELK	1.01	7.39E-01	8.80E-01	2963.67	not significant
7652	SNHG11	1.01	7.02E-01	8.59E-01	508.44	not significant
7653	NT5DC1	1.01	7.26E-01	8.74E-01	526.97	not significant
7654	PIAS4	1.01	7.47E-01	8.85E-01	992.51	not significant
7655	MST1	1.01	5.54E-01	NA	66.34	not significant
7656	SYTL3	1.01	2.84E-01	NA	18.77	not significant
7657	BHLHB9	1.01	7.00E-01	8.59E-01	248.52	not significant
7658	DPY19L1	1.01	6.09E-01	NA	93.74	not significant
7659	C5orf55	1.01	5.13E-01	NA	54.20	not significant
7660	MTMR8	1.01	6.57E-01	8.38E-01	126.76	not significant
7661	SLC25A34	1.01	4.06E-01	NA	31.54	not significant
7662	KRBA2	1.01	5.35E-01	NA	68.58	not significant
7663	CAPS	1.01	5.18E-01	NA	57.07	not significant
7664	MYLK-AS1	1.01	8.93E-01	NA	36.18	not significant
7665	IMPA2	1.01	1.87E-01	NA	12.63	not significant
7666	SNHG15	1.01	7.47E-01	8.85E-01	1793.60	not significant
7667	ACTN4	1.01	6.91E-01	8.54E-01	6731.80	not significant
7668	MAMDC4	1.01	6.77E-01	8.49E-01	206.22	not significant
7669	ITPRIP	1.01	7.25E-01	8.74E-01	812.40	not significant
7670	DGCR14	1.01	7.43E-01	8.84E-01	1029.79	not significant
7671	STOX1	1.01	6.91E-01	8.54E-01	209.38	not significant
7672	PPP1R18	1.01	7.26E-01	8.74E-01	351.90	not significant
7673	GLIPR1	1.01	7.05E-01	8.61E-01	389.90	not significant
7674	LINC00174	1.01	6.42E-01	8.29E-01	130.00	not significant
7675	LOC100288798	1.01	5.76E-01	NA	79.22	not significant
7676	CAPN14	1.01	5.05E-01	NA	55.64	not significant
7677	HLA-F	1.01	3.18E-01	NA	22.29	not significant
7678	VWA5A	1.01	3.86E-01	NA	30.62	not significant
7679	HOMER3	1.01	3.18E-01	NA	23.30	not significant
7680	GRAP2	1.01	7.01E-01	8.59E-01	7537.19	not significant
7681	COMMD8	1.01	7.58E-01	8.91E-01	1199.69	not significant
7682	CACNB1	1.01	7.06E-01	8.61E-01	551.20	not significant
7683	NDUFS6	1.01	7.32E-01	8.77E-01	3425.04	not significant
7684	ABCC5	1.01	7.28E-01	8.75E-01	798.21	not significant
7685	C3orf33	1.01	6.20E-01	8.15E-01	112.99	not significant
7686	FAM214B	1.01	6.12E-01	8.10E-01	107.24	not significant
7687	KCNK6	1.01	6.20E-01	8.15E-01	107.19	not significant
7688	ZNF568	1.01	6.86E-01	8.52E-01	218.94	not significant
7689	TRAM1L1	1.01	4.50E-01	NA	39.59	not significant
7690	KLHL32	1.01	2.26E-01	NA	15.14	not significant
7691	RAD51-AS1	1.01	5.20E-04	7.89E-03	1851.90	not significant
7692	NDUFS8	1.01	7.61E-01	8.93E-01	2283.50	not significant
7693	DHX38	1.01	7.17E-01	8.69E-01	3502.83	not significant
7694	LMAN1	1.01	7.32E-01	8.77E-01	10167.77	not significant
7695	PTGER4	1.01	7.14E-01	8.67E-01	6435.84	not significant
7696	ZNF354A	1.01	7.36E-01	8.79E-01	396.93	not significant
7697	LONRF1	1.01	7.26E-01	8.74E-01	712.21	not significant
7698	FOXO3	1.01	7.42E-01	8.83E-01	710.52	not significant
7699	SLC25A4	1.01	6.63E-01	8.41E-01	179.87	not significant
7700	AMH	1.01	7.38E-01	8.80E-01	611.29	not significant
7701	ATP6V0B	1.01	7.20E-01	8.71E-01	4150.81	not significant
7702	DHRS11	1.01	3.54E-01	NA	26.79	not significant
7703	TPO	1.01	5.77E-01	7.87E-01	113.83	not significant
7704	IL1RAP	1.01	5.13E-01	NA	58.87	not significant
7705	NDUFV1	1.01	7.15E-01	8.68E-01	5767.39	not significant
7706	FGFR1OP2	1.01	7.29E-01	8.76E-01	2495.61	not significant
7707	CCDC23	1.01	7.09E-01	8.64E-01	335.92	not significant
7708	USP6NL	1.01	7.35E-01	8.79E-01	1343.20	not significant
7709	PTCHD2	1.01	7.35E-01	8.79E-01	703.88	not significant
7710	PRNP	1.01	7.21E-01	8.71E-01	427.85	not significant
7711	AKAP9	1.01	7.08E-01	8.63E-01	2934.65	not significant
7712	PLTP	1.01	4.44E-01	NA	40.40	not significant
7713	PLEKHA4	1.01	3.66E-01	NA	31.55	not significant
7714	NDUFB6	1.01	7.64E-01	8.95E-01	1623.64	not significant
7715	NDUFA4	1.01	7.18E-01	8.70E-01	4964.73	not significant
7716	DDX5	1.01	6.63E-01	8.41E-01	15017.47	not significant
7717	FASTK	1.01	7.36E-01	8.79E-01	2172.58	not significant
7718	MRPS36	1.01	7.08E-01	8.63E-01	346.93	not significant
7719	PHKB	1.01	7.26E-01	8.74E-01	2520.52	not significant
7720	RNF146	1.01	7.19E-01	8.71E-01	583.04	not significant
7721	NR2C2AP	1.01	7.64E-01	8.95E-01	1231.51	not significant
7722	HDC	1.01	6.82E-01	8.50E-01	218.13	not significant
7723	KLHL20	1.01	7.11E-01	8.65E-01	570.90	not significant
7724	KIAA2026	1.01	7.33E-01	8.78E-01	806.14	not significant
7725	C16orf52	1.01	7.06E-01	8.62E-01	323.81	not significant
7726	LINC00888	1.01	6.75E-01	8.47E-01	210.62	not significant
7727	CACNA1I	1.01	2.42E-01	NA	18.40	not significant
7728	ANAPC11	1.01	7.38E-01	8.80E-01	1695.02	not significant
7729	GSE1	1.01	7.05E-01	8.61E-01	4452.80	not significant
7730	GATAD2B	1.01	7.24E-01	8.73E-01	434.49	not significant
7731	PIGV	1.01	7.12E-01	8.66E-01	361.84	not significant

7732	LYST	1.01	6.98E-01	8.59E-01	385.53	not significant
7733	CUEDC1	1.01	5.72E-01	NA	85.53	not significant
7734	AMT	1.01	5.35E-01	NA	76.09	not significant
7735	LOC729296	1.01	5.20E-01	NA	62.83	not significant
7736	RAB11B-AS1	1.01	5.41E-01	NA	71.88	not significant
7737	LOC100630918	1.01	4.96E-01	NA	56.67	not significant
7738	LINC00638	1.01	4.85E-01	NA	55.77	not significant
7739	ST13	1.01	6.98E-01	8.59E-01	8185.05	not significant
7740	NOC4L	1.01	7.33E-01	8.78E-01	1607.43	not significant
7741	KHNYN	1.01	7.25E-01	8.73E-01	2704.70	not significant
7742	SMURF1	1.01	7.17E-01	8.69E-01	858.89	not significant
7743	TMEM177	1.01	6.91E-01	8.54E-01	266.10	not significant
7744	AKAP5	1.01	7.00E-01	8.59E-01	309.43	not significant
7745	C16orf93	1.01	5.25E-01	NA	75.13	not significant
7746	C1RL-AS1	1.01	6.81E-01	8.50E-01	274.39	not significant
7747	NEURL1B	1.01	5.25E-01	NA	66.50	not significant
7748	ITPKA	1.01	4.10E-01	NA	38.07	not significant
7749	MRPL45P2	1.01	3.80E-01	NA	38.76	not significant
7750	RIPK4	1.01	3.62E-01	NA	33.52	not significant
7751	MAF1	1.01	7.20E-01	8.71E-01	4499.94	not significant
7752	SKAP1	1.01	7.32E-01	8.77E-01	1343.73	not significant
7753	CDKN2D	1.01	7.24E-01	8.73E-01	912.56	not significant
7754	KCNK5	1.01	7.32E-01	8.77E-01	2207.47	not significant
7755	CCDC93	1.01	7.29E-01	8.76E-01	2183.17	not significant
7756	SNX18	1.01	6.97E-01	8.59E-01	424.00	not significant
7757	FAM161B	1.01	6.36E-01	8.24E-01	182.47	not significant
7758	SYDE2	1.01	6.31E-01	8.21E-01	168.35	not significant
7759	LOC100129917	1.01	5.88E-01	7.95E-01	103.56	not significant
7760	ADAM21	1.01	1.69E-01	NA	13.32	not significant
7761	PWAR5	1.01	5.72E-01	7.83E-01	125.14	not significant
7762	HOOK2	1.01	5.61E-01	NA	83.53	not significant
7763	PHEX	1.01	2.21E-01	NA	17.64	not significant
7764	LSMEM1	1.01	3.96E-01	NA	38.16	not significant
7765	FBXO25	1.01	8.30E-01	9.29E-01	1886.59	not significant
7766	WIPF1	1.01	6.94E-01	8.56E-01	9859.24	not significant
7767	COPG1	1.01	7.00E-01	8.59E-01	4397.01	not significant
7768	EHMT1	1.01	7.34E-01	8.78E-01	2455.15	not significant
7769	CTNNB1	1.01	6.96E-01	8.58E-01	4398.64	not significant
7770	EME1	1.01	7.25E-01	8.74E-01	701.15	not significant
7771	DAPK3	1.01	7.02E-01	8.59E-01	899.81	not significant
7772	CLK4	1.01	7.13E-01	8.66E-01	462.10	not significant
7773	KAT6B	1.01	7.33E-01	8.77E-01	2315.27	not significant
7774	ABHD4	1.01	6.07E-01	8.06E-01	119.05	not significant
7775	TIMM17B	1.01	7.06E-01	8.61E-01	444.48	not significant
7776	USP9Y	1.01	7.05E-01	8.61E-01	2088.87	not significant
7777	KDM8	1.01	6.74E-01	8.47E-01	245.15	not significant
7778	RGS5	1.01	5.18E-01	NA	66.99	not significant
7779	THBS3	1.01	5.27E-01	NA	68.98	not significant
7780	RILPL1	1.01	5.66E-01	NA	89.81	not significant
7781	AKAP2	1.01	2.67E-01	NA	21.84	not significant
7782	SYNE2	1.01	3.88E-01	6.49E-01	5686.90	not significant
7783	PLXNA4	1.01	3.75E-01	NA	34.41	not significant
7784	DBH-AS1	1.01	4.15E-01	NA	46.26	not significant
7785	RAD23A	1.01	6.98E-01	8.59E-01	5063.43	not significant
7786	SRSF2	1.01	6.35E-01	8.23E-01	24725.99	not significant
7787	CDC5L	1.01	6.97E-01	8.59E-01	4141.52	not significant
7788	DPAGT1	1.01	7.03E-01	8.60E-01	1880.67	not significant
7789	BTN2A1	1.01	7.26E-01	8.74E-01	1483.98	not significant
7790	C1orf50	1.01	7.00E-01	8.59E-01	350.01	not significant
7791	KDM6A	1.01	7.39E-01	8.80E-01	1197.90	not significant
7792	IPO5P1	1.01	6.99E-01	8.59E-01	933.27	not significant
7793	EFNB2	1.01	6.33E-01	8.22E-01	190.86	not significant
7794	PRR19	1.01	5.31E-01	NA	75.26	not significant
7795	AGRN	1.01	4.69E-01	NA	56.42	not significant
7796	TSC22D3	1.01	2.74E-01	NA	18.14	not significant
7797	ZNF774	1.01	3.28E-01	NA	29.17	not significant
7798	HSPA2	1.01	2.22E-01	NA	19.76	not significant
7799	DUSP5P1	1.01	1.65E-01	NA	14.95	not significant
7800	SRRM2-AS1	1.01	1.59E-01	NA	13.51	not significant
7801	ZNF141	1.01	1.15E-01	NA	10.79	not significant
7802	CDKN2AIP	1.01	7.20E-01	8.71E-01	1690.85	not significant
7803	ETV3	1.01	7.02E-01	8.59E-01	466.49	not significant
7804	ZNF730	1.01	6.69E-01	8.44E-01	273.84	not significant
7805	MPZ	1.01	4.26E-01	NA	44.43	not significant
7806	DDX11L2	1.01	2.59E-01	NA	20.85	not significant
7807	FLJ22447	1.01	2.24E-01	NA	19.98	not significant
7808	CRYGN	1.01	1.83E-01	NA	15.93	not significant
7809	PIN1	1.01	7.19E-01	8.71E-01	2625.39	not significant
7810	TEX30	1.01	7.28E-01	8.75E-01	1100.95	not significant
7811	SIRT6	1.01	6.97E-01	8.59E-01	934.37	not significant
7812	DCAKD	1.01	6.90E-01	8.54E-01	888.38	not significant
7813	AKAP11	1.01	6.66E-01	8.43E-01	1857.67	not significant
7814	FBXW8	1.01	6.94E-01	8.56E-01	1025.97	not significant
7815	TXNDC16	1.01	7.06E-01	8.62E-01	634.13	not significant
7816	HSPBAP1	1.01	6.66E-01	8.42E-01	260.36	not significant
7817	PPARA	1.01	6.34E-01	8.23E-01	174.39	not significant
7818	CCDC126	1.01	6.55E-01	8.37E-01	214.44	not significant
7819	MT1F	1.01	4.97E-01	NA	69.41	not significant

7820	PRSS36	1.01	1.31E-01	NA	12.40	not significant
7821	MICA	1.01	4.25E-01	NA	44.49	not significant
7822	ADRM1	1.01	7.06E-01	8.61E-01	4030.04	not significant
7823	PIGP	1.01	6.91E-01	8.54E-01	397.61	not significant
7824	RAI1	1.01	6.02E-01	8.03E-01	2719.01	not significant
7825	SRD5A3	1.01	6.87E-01	8.53E-01	328.88	not significant
7826	C14orf93	1.01	5.63E-01	NA	97.80	not significant
7827	VPS37C	1.01	6.38E-01	8.25E-01	174.20	not significant
7828	SLC14A1	1.01	3.23E-01	NA	28.75	not significant
7829	FGFR3	1.01	5.61E-01	NA	100.66	not significant
7830	KLF7	1.01	2.93E-01	NA	25.65	not significant
7831	KIAA1407	1.01	3.83E-01	NA	37.40	not significant
7832	HSD17B14	1.01	3.38E-01	NA	33.26	not significant
7833	IRF3	1.01	7.05E-01	8.61E-01	1791.73	not significant
7834	KPTN	1.01	6.88E-01	8.54E-01	375.12	not significant
7835	NADSYN1	1.01	7.16E-01	8.69E-01	1400.68	not significant
7836	POC1B	1.01	7.15E-01	8.68E-01	1458.05	not significant
7837	LINC01215	1.01	6.97E-01	8.59E-01	1004.05	not significant
7838	LPAR5	1.01	7.01E-01	8.59E-01	1091.60	not significant
7839	DNHD1	1.01	6.63E-01	8.41E-01	308.15	not significant
7840	MAP3K7CL	1.01	6.26E-01	8.17E-01	161.76	not significant
7841	OGN	1.01	6.78E-01	8.49E-01	256.57	not significant
7842	HCK	1.01	2.65E-01	NA	23.70	not significant
7843	MIR4674HG	1.01	2.81E-01	NA	25.60	not significant
7844	BCAR3	1.01	1.42E-01	NA	13.88	not significant
7845	TERC	1.01	7.64E-02	NA	9.74	not significant
7846	LINC00618	1.01	9.99E-02	NA	11.92	not significant
7847	RPL27	1.01	7.03E-01	8.60E-01	13517.99	not significant
7848	WBSCR22	1.01	7.16E-01	8.69E-01	1737.04	not significant
7849	ACOX1	1.01	6.97E-01	8.59E-01	2940.63	not significant
7850	DUSP14	1.01	7.11E-01	8.65E-01	725.22	not significant
7851	ATAD1	1.01	6.93E-01	8.56E-01	4578.35	not significant
7852	HOXB4	1.01	6.87E-01	NA	90.20	not significant
7853	ULBP1	1.01	7.09E-01	8.64E-01	641.46	not significant
7854	PORCN	1.01	4.35E-01	NA	51.14	not significant
7855	B3GNT9	1.01	4.94E-01	NA	69.86	not significant
7856	LOC100270804	1.01	3.59E-01	NA	36.59	not significant
7857	C16orf86	1.01	1.15E-01	NA	12.20	not significant
7858	LINC00324	1.01	3.29E-01	NA	31.09	not significant
7859	PSME1	1.01	6.98E-01	8.59E-01	10166.53	not significant
7860	SMIM8	1.01	6.73E-01	8.47E-01	328.26	not significant
7861	DOCK10	1.01	7.06E-01	8.62E-01	3659.25	not significant
7862	COG5	1.01	7.09E-01	8.64E-01	1743.52	not significant
7863	N6AMT1	1.01	6.59E-01	8.39E-01	252.02	not significant
7864	FAM21C	1.01	6.45E-01	8.31E-01	210.81	not significant
7865	ZNF77	1.01	6.47E-01	8.32E-01	217.47	not significant
7866	SARDH	1.01	5.99E-01	8.02E-01	136.79	not significant
7867	AGPAT4	1.01	5.32E-01	NA	86.30	not significant
7868	DDX11-AS1	1.01	1.74E-01	NA	16.54	not significant
7869	LUCAT1	1.01	5.19E-01	NA	84.73	not significant
7870	FN3K	1.01	3.60E-01	NA	31.71	not significant
7871	WDR31	1.01	1.22E-01	NA	13.41	not significant
7872	HARS2	1.01	7.00E-01	8.59E-01	1118.75	not significant
7873	CMAHP	1.01	7.09E-01	8.64E-01	2396.60	not significant
7874	STK10	1.01	7.05E-01	8.61E-01	2933.81	not significant
7875	TRIM65	1.01	7.00E-01	8.59E-01	1956.78	not significant
7876	NTPCR	1.01	6.81E-01	8.50E-01	940.94	not significant
7877	ZNF682	1.01	6.73E-01	8.47E-01	287.50	not significant
7878	KIAA0355	1.01	6.83E-01	8.51E-01	372.22	not significant
7879	INAFM2	1.01	6.81E-01	8.50E-01	372.56	not significant
7880	PACSIN1	1.01	6.31E-01	8.21E-01	186.33	not significant
7881	ACYP2	1.01	5.66E-01	7.81E-01	109.56	not significant
7882	PAPLN	1.01	3.82E-01	NA	42.13	not significant
7883	CACNA1C-AS1	1.01	2.10E-01	NA	19.94	not significant
7884	DUSP10	1.01	4.21E-01	NA	53.04	not significant
7885	ZBTB7C	1.01	3.38E-01	NA	33.95	not significant
7886	RRP7B	1.01	6.76E-01	8.48E-01	786.23	not significant
7887	LETM2	1.01	6.37E-01	8.24E-01	230.36	not significant
7888	ZDHHC23	1.01	6.73E-01	8.47E-01	370.01	not significant
7889	ZKSCAN4	1.01	6.64E-01	8.42E-01	304.28	not significant
7890	TMEM254-AS1	1.01	2.45E-01	NA	23.13	not significant
7891	SLC16A6	1.01	4.01E-01	NA	46.81	not significant
7892	PLCD1	1.01	3.94E-01	NA	43.85	not significant
7893	RAB1B	1.01	6.90E-01	8.54E-01	5985.50	not significant
7894	GET4	1.01	7.02E-01	8.59E-01	2738.96	not significant
7895	LIG3	1.01	7.27E-01	8.74E-01	2460.60	not significant
7896	MIER3	1.01	7.04E-01	8.61E-01	1352.26	not significant
7897	SAMD10	1.01	6.82E-01	8.51E-01	387.18	not significant
7898	CD68	1.01	4.92E-01	NA	75.08	not significant
7899	KANSL1L	1.01	5.60E-01	7.77E-01	130.61	not significant
7900	FLVCR1-AS1	1.01	2.92E-01	NA	29.03	not significant
7901	EVI5	1.01	5.41E-01	7.63E-01	110.37	not significant
7902	RNLS	1.01	6.81E-01	8.50E-01	3178.63	not significant
7903	STK40	1.01	6.70E-01	8.45E-01	3501.60	not significant
7904	OGFOD2	1.01	6.87E-01	8.53E-01	1049.25	not significant
7905	GTF3C1	1.01	6.80E-01	8.50E-01	5011.10	not significant
7906	TMEM245	1.01	6.95E-01	8.57E-01	3265.28	not significant
7907	C6orf120	1.01	7.00E-01	8.59E-01	1387.61	not significant

7908	EXTL3	1.01	6.90E-01	8.54E-01	2686.64	not significant
7909	ATP2B1	1.01	6.82E-01	8.50E-01	2793.93	not significant
7910	GNB5	1.01	6.73E-01	8.47E-01	786.08	not significant
7911	STX12	1.01	6.79E-01	8.49E-01	747.52	not significant
7912	TMCC1-AS1	1.01	5.25E-01	NA	98.37	not significant
7913	ADAT1	1.01	6.96E-01	8.58E-01	813.14	not significant
7914	AKAP7	1.01	6.60E-01	8.39E-01	343.58	not significant
7915	LINC00884	1.01	2.80E-01	NA	26.58	not significant
7916	TBX19	1.01	4.74E-01	NA	70.70	not significant
7917	CCDC90B	1.01	6.98E-01	8.59E-01	1208.97	not significant
7918	LPXN	1.01	6.80E-01	8.50E-01	3032.79	not significant
7919	BLOC1S1	1.01	6.81E-01	8.50E-01	464.10	not significant
7920	DPM1	1.01	7.02E-01	8.59E-01	2103.48	not significant
7921	WHSC1L1	1.01	6.83E-01	8.51E-01	4772.92	not significant
7922	GSG2	1.01	6.99E-01	8.59E-01	1544.65	not significant
7923	ARRDC1	1.01	6.73E-01	8.47E-01	561.13	not significant
7924	PXMP4	1.01	6.94E-01	8.57E-01	697.37	not significant
7925	GMPPB	1.01	6.59E-01	8.39E-01	892.13	not significant
7926	BZRAP1	1.01	5.82E-01	7.90E-01	1445.06	not significant
7927	SLC31A2	1.01	6.46E-01	8.31E-01	266.94	not significant
7928	JPX	1.01	4.97E-01	NA	97.06	not significant
7929	DLL3	1.01	3.70E-01	NA	45.03	not significant
7930	PDCD1	1.01	5.47E-01	7.67E-01	110.06	not significant
7931	FAM57B	1.01	3.85E-01	NA	46.72	not significant
7932	HSBP1	1.01	7.50E-01	8.87E-01	1895.20	not significant
7933	C11orf73	1.01	7.32E-01	8.77E-01	1086.05	not significant
7934	DOCK8	1.01	6.41E-01	8.28E-01	13489.66	not significant
7935	MSL2	1.01	6.31E-01	8.21E-01	6025.73	not significant
7936	CEP135	1.01	6.94E-01	8.56E-01	1533.12	not significant
7937	XPA	1.01	6.81E-01	8.50E-01	474.18	not significant
7938	CST7	1.01	5.87E-01	7.94E-01	226.66	not significant
7939	CRTC1	1.01	6.79E-01	8.50E-01	452.01	not significant
7940	CYP2E1	1.01	3.57E-01	NA	42.49	not significant
7941	CBX7	1.01	5.21E-01	NA	93.27	not significant
7942	TNFRSF10B	1.01	3.67E-01	NA	48.07	not significant
7943	MIOX	1.01	1.23E-01	NA	14.11	not significant
7944	DAP3	1.01	6.54E-01	8.36E-01	3941.26	not significant
7945	SLC8B1	1.01	7.01E-01	8.59E-01	1170.25	not significant
7946	TTC16	1.01	6.56E-01	8.38E-01	557.76	not significant
7947	AIDA	1.01	6.78E-01	8.49E-01	594.02	not significant
7948	PLEKHB1	1.01	6.12E-01	8.10E-01	212.12	not significant
7949	PLEKHM3	1.01	6.65E-01	8.42E-01	573.90	not significant
7950	RFESD	1.01	6.11E-01	8.09E-01	195.80	not significant
7951	SLC25A25-AS1	1.01	6.30E-01	8.21E-01	244.86	not significant
7952	KMT2E-AS1	1.01	5.19E-01	NA	92.66	not significant
7953	PSTK	1.01	5.89E-01	7.96E-01	153.56	not significant
7954	ZBTB11-AS1	1.01	5.59E-01	7.77E-01	134.60	not significant
7955	S1PR2	1.01	4.32E-01	NA	59.07	not significant
7956	NPTN-IT1	1.01	3.15E-01	NA	39.03	not significant
7957	C5	1.01	3.50E-01	NA	38.40	not significant
7958	SUB1	1.01	6.78E-01	8.49E-01	8842.27	not significant
7959	TCHP	1.01	6.89E-01	8.54E-01	1673.01	not significant
7960	C1orf122	1.01	6.89E-01	8.54E-01	962.28	not significant
7961	C5orf24	1.01	6.90E-01	8.54E-01	1734.96	not significant
7962	AGA	1.01	6.73E-01	8.47E-01	580.75	not significant
7963	ELMSAN1	1.01	6.87E-01	8.53E-01	2374.46	not significant
7964	TCEANC2	1.01	6.65E-01	8.42E-01	724.29	not significant
7965	TRMT1L	1.01	6.84E-01	8.51E-01	1159.84	not significant
7966	GLCCI1	1.01	6.57E-01	8.38E-01	848.21	not significant
7967	ADAM9	1.01	6.88E-01	8.53E-01	952.86	not significant
7968	MSANTD2	1.01	6.50E-01	8.33E-01	283.27	not significant
7969	LOC100506639	1.01	5.82E-01	7.90E-01	157.42	not significant
7970	SRI	1.01	6.90E-01	8.54E-01	2701.10	not significant
7971	MCM7	1.01	6.05E-01	8.05E-01	22452.07	not significant
7972	COA5	1.01	7.30E-01	8.76E-01	732.35	not significant
7973	FKBP2	1.01	6.87E-01	8.53E-01	934.60	not significant
7974	ST3GAL2	1.01	6.95E-01	8.57E-01	1800.38	not significant
7975	ATP2C1	1.01	6.62E-01	8.41E-01	3799.22	not significant
7976	MTRF1	1.01	6.69E-01	8.45E-01	446.98	not significant
7977	HIVEP2	1.01	6.89E-01	8.54E-01	2445.00	not significant
7978	NDUFA13	1.01	7.02E-01	8.59E-01	4090.83	not significant
7979	CARD16	1.01	6.00E-01	8.02E-01	202.15	not significant
7980	WDR73	1.01	6.81E-01	8.50E-01	604.71	not significant
7981	CELSR2	1.01	6.87E-01	8.53E-01	766.26	not significant
7982	BACH2	1.01	6.56E-01	8.38E-01	400.79	not significant
7983	CMTM1	1.01	6.03E-01	8.03E-01	200.75	not significant
7984	LRRC16B	1.01	5.99E-01	8.02E-01	185.62	not significant
7985	TBXAS1	1.01	4.74E-01	NA	74.69	not significant
7986	RTN4RL2	1.01	4.07E-01	NA	50.54	not significant
7987	SLC37A4	1.01	5.65E-01	7.80E-01	150.89	not significant
7988	CHCHD5	1.01	5.29E-01	7.56E-01	116.87	not significant
7989	PDCD6IPP2	1.01	4.01E-01	NA	66.31	not significant
7990	PSMB8-AS1	1.01	2.47E-01	NA	26.77	not significant
7991	RALGAPA1	1.01	4.31E-01	NA	60.52	not significant
7992	SPOCD1	1.01	3.61E-01	NA	46.94	not significant
7993	TMEM109	1.01	6.46E-01	8.31E-01	5645.63	not significant
7994	DTNBP1	1.01	6.78E-01	8.49E-01	657.63	not significant
7995	UBE2Q2	1.01	6.81E-01	8.50E-01	1527.32	not significant

7996	ARID4B	1.01	6.84E-01	8.52E-01	2165.04	not significant
7997	ALG14	1.01	6.28E-01	8.19E-01	276.43	not significant
7998	MTHFD2L	1.01	6.19E-01	8.14E-01	214.35	not significant
7999	OSR2	1.01	4.84E-01	NA	85.89	not significant
8000	GRINA	1.01	6.19E-01	8.14E-01	226.24	not significant
8001	SSC4D	1.01	2.01E-01	NA	22.17	not significant
8002	FAM86HP	1.01	2.74E-01	NA	31.30	not significant
8003	ZNF781	1.01	3.76E-01	NA	47.90	not significant
8004	SLC22A18	1.01	4.64E-01	NA	76.35	not significant
8005	NONO	1.01	6.24E-01	8.16E-01	27132.74	not significant
8006	DOCK7	1.01	6.95E-01	8.58E-01	1246.03	not significant
8007	RNF2	1.01	6.82E-01	8.51E-01	1298.81	not significant
8008	NISCH	1.01	6.31E-01	8.21E-01	4807.94	not significant
8009	ZNF354B	1.01	6.62E-01	8.41E-01	438.68	not significant
8010	PLXND1	1.01	6.77E-01	8.48E-01	680.70	not significant
8011	C15orf41	1.01	6.45E-01	8.31E-01	395.64	not significant
8012	LOC728752	1.01	4.45E-01	NA	72.60	not significant
8013	MYCBPAP	1.01	2.70E-01	NA	31.84	not significant
8014	ADNP-AS1	1.01	5.35E-01	7.60E-01	2506.87	not significant
8015	CERS2	1.01	6.34E-01	8.23E-01	7502.75	not significant
8016	RIF1	1.01	6.62E-01	8.41E-01	6556.17	not significant
8017	CSNK2A2	1.01	6.78E-01	8.49E-01	1550.10	not significant
8018	ETFDH	1.01	6.75E-01	8.47E-01	613.83	not significant
8019	TRPV1	1.01	6.18E-01	8.14E-01	241.23	not significant
8020	TBCEL	1.01	6.55E-01	8.37E-01	423.37	not significant
8021	LINC00563	1.01	4.70E-01	NA	70.84	not significant
8022	LINC01137	1.01	1.60E-01	NA	19.53	not significant
8023	ABCC2	1.01	5.20E-01	7.50E-01	107.05	not significant
8024	EFEMP2	1.01	2.96E-01	NA	34.27	not significant
8025	TMEM91	1.01	2.35E-01	NA	25.64	not significant
8026	LOC728730	1.01	2.86E-01	NA	32.66	not significant
8027	LIN54	1.01	6.69E-01	8.45E-01	2108.15	not significant
8028	SIN3B	1.01	6.76E-01	8.48E-01	1691.93	not significant
8029	TCEAL1	1.01	5.15E-01	7.46E-01	119.39	not significant
8030	SERTAD3	1.01	5.50E-01	7.70E-01	107.41	not significant
8031	ZNF169	1.01	4.21E-01	NA	60.75	not significant
8032	ZNF487	1.01	2.83E-01	NA	33.16	not significant
8033	SEPSECS-AS1	1.01	2.23E-01	NA	25.07	not significant
8034	ZNF93	1.01	6.53E-01	8.36E-01	827.34	not significant
8035	LOC101927021	1.01	5.68E-01	7.82E-01	152.53	not significant
8036	GAREML	1.01	6.08E-01	8.07E-01	218.13	not significant
8037	GIMAP5	1.01	2.66E-01	NA	36.16	not significant
8038	DFNB59	1.01	2.30E-01	NA	26.29	not significant
8039	PPP1R13B	1.01	4.09E-01	NA	57.30	not significant
8040	EGR2	1.01	1.38E-01	NA	19.99	not significant
8041	LIN52	1.01	6.69E-01	8.45E-01	693.21	not significant
8042	SDR39U1	1.01	6.87E-01	8.53E-01	1243.10	not significant
8043	ZYX	1.01	6.44E-01	8.30E-01	535.16	not significant
8044	PHF12	1.01	6.71E-01	8.46E-01	2176.20	not significant
8045	SYNJ1	1.01	6.85E-01	8.52E-01	1033.19	not significant
8046	ZNF571	1.01	5.25E-01	7.54E-01	115.53	not significant
8047	PRORSD1P	1.01	2.48E-01	NA	29.21	not significant
8048	LOC101927621	1.01	3.56E-01	NA	50.38	not significant
8049	TMEM30A	1.01	6.35E-01	8.23E-01	4989.50	not significant
8050	BANP	1.01	6.57E-01	8.39E-01	625.86	not significant
8051	TSHR	1.01	6.72E-01	8.46E-01	1192.47	not significant
8052	LINC00094	1.01	6.68E-01	8.44E-01	677.89	not significant
8053	IKBKE	1.01	6.46E-01	8.32E-01	415.50	not significant
8054	RNASEH1-AS1	1.01	6.08E-01	8.07E-01	372.70	not significant
8055	CCR2	1.01	1.62E-01	NA	20.51	not significant
8056	PACSIN3	1.01	5.23E-01	7.52E-01	113.52	not significant
8057	LOC729603	1.01	3.88E-01	NA	67.00	not significant
8058	PLCG2	1.01	3.95E-01	NA	56.93	not significant
8059	RGPD1	1.01	4.77E-01	NA	92.36	not significant
8060	LINC01011	1.01	9.62E-02	NA	14.38	not significant
8061	SLC9B1	1.01	1.39E-01	NA	19.70	not significant
8062	TMTC2	1.01	1.48E-01	NA	19.55	not significant
8063	PMAIP1	1.01	6.43E-01	8.30E-01	4185.81	not significant
8064	PEX26	1.01	6.45E-01	8.31E-01	2677.76	not significant
8065	RPL19	1.01	6.14E-01	8.11E-01	39980.31	not significant
8066	TTC21B	1.01	6.56E-01	8.38E-01	1200.23	not significant
8067	BIN3	1.01	6.40E-01	8.27E-01	1081.90	not significant
8068	SPHK2	1.01	6.85E-01	8.52E-01	1242.11	not significant
8069	TNKS	1.01	6.64E-01	8.41E-01	2177.21	not significant
8070	SETD4	1.01	6.53E-01	8.36E-01	495.54	not significant
8071	LOC100287042	1.01	5.50E-01	7.70E-01	143.44	not significant
8072	WASL	1.01	6.45E-01	8.31E-01	466.03	not significant
8073	ATP2B4	1.01	4.63E-01	7.09E-01	8137.39	not significant
8074	TCTN1	1.01	5.65E-01	7.80E-01	168.52	not significant
8075	LINC00664	1.01	5.13E-01	7.45E-01	117.36	not significant
8076	GPLD1	1.01	4.42E-01	NA	81.92	not significant
8077	DAB1	1.01	1.65E-01	NA	20.53	not significant
8078	PLEKHH2	1.01	2.11E-01	NA	26.00	not significant
8079	GGA1	1.01	6.65E-01	8.42E-01	1557.37	not significant
8080	STK24	1.01	6.04E-01	8.04E-01	5995.50	not significant
8081	DCAF11	1.01	6.35E-01	8.23E-01	3297.39	not significant
8082	PITPNC1	1.01	6.59E-01	8.39E-01	2188.38	not significant
8083	USP4	1.01	6.16E-01	8.12E-01	2525.44	not significant

8084	EDEM3	1.01	6.59E-01	8.39E-01	3825.21	not significant
8085	FAM117B	1.01	6.33E-01	8.22E-01	1073.85	not significant
8086	DUSP2	1.01	6.38E-01	8.25E-01	771.81	not significant
8087	RPL23AP53	1.01	6.65E-01	8.42E-01	845.14	not significant
8088	IFT172	1.01	6.22E-01	8.15E-01	307.97	not significant
8089	TMEM198B	1.01	6.31E-01	8.21E-01	354.93	not significant
8090	ITGA2	1.01	6.21E-01	8.15E-01	327.91	not significant
8091	IL15RA	1.01	6.10E-01	8.08E-01	285.01	not significant
8092	SNX24	1.01	3.86E-01	NA	58.76	not significant
8093	LOC100506472	1.01	3.78E-01	NA	56.09	not significant
8094	LINC00663	1.01	2.18E-01	NA	25.74	not significant
8095	SNHG5	1.01	7.09E-01	8.64E-01	794.00	not significant
8096	HENMT1	1.01	6.59E-01	8.39E-01	1526.15	not significant
8097	SPTAN1	1.01	6.54E-01	8.37E-01	12764.16	not significant
8098	NCAPD3	1.01	6.18E-01	8.14E-01	7917.74	not significant
8099	UBLCP1	1.01	6.60E-01	8.40E-01	1711.71	not significant
8100	CCDC174	1.01	6.63E-01	8.41E-01	889.34	not significant
8101	SLC39A11	1.01	6.35E-01	8.23E-01	1044.23	not significant
8102	ZNF615	1.01	6.48E-01	8.32E-01	466.17	not significant
8103	ZBTB41	1.01	6.24E-01	8.16E-01	1026.70	not significant
8104	FAHD1	1.01	6.27E-01	8.19E-01	552.99	not significant
8105	FAM86A	1.01	6.28E-01	8.19E-01	341.43	not significant
8106	GUCY1A2	1.01	3.60E-01	NA	54.51	not significant
8107	CCDC85B	1.01	5.91E-01	7.97E-01	1179.17	not significant
8108	LCAT	1.01	4.77E-01	7.18E-01	107.26	not significant
8109	ADSSL1	1.01	2.31E-01	NA	29.37	not significant
8110	TOB1-AS1	1.01	8.24E-02	NA	13.60	not significant
8111	TMSB15B	1.01	3.85E-01	NA	61.01	not significant
8112	HIST1H2AG	1.01	2.16E-01	NA	33.23	not significant
8113	PMS2P4	1.01	3.52E-01	NA	49.36	not significant
8114	MFI2-AS1	1.01	2.56E-01	NA	31.79	not significant
8115	NRADDP	1.01	5.46E-02	NA	12.71	not significant
8116	H2AFZ	1.01	6.23E-01	8.16E-01	16359.25	not significant
8117	CYP20A1	1.01	6.62E-01	8.41E-01	1199.35	not significant
8118	KATNBL1	1.01	6.30E-01	8.21E-01	768.04	not significant
8119	SLC35F5	1.01	4.90E-01	7.29E-01	702.43	not significant
8120	GS1-24F4.2	1.01	3.80E-01	NA	58.00	not significant
8121	NPIPA5	1.01	5.18E-01	7.48E-01	136.25	not significant
8122	LINC01481	1.01	4.53E-01	NA	83.68	not significant
8123	E4F1	1.01	6.73E-01	8.47E-01	1244.69	not significant
8124	CCDC12	1.01	6.58E-01	8.39E-01	1258.49	not significant
8125	GM2A	1.01	6.49E-01	8.32E-01	1658.86	not significant
8126	REST	1.01	5.90E-01	7.96E-01	3137.44	not significant
8127	ZNF669	1.01	6.38E-01	8.25E-01	555.50	not significant
8128	FAM220A	1.01	6.48E-01	8.32E-01	634.44	not significant
8129	CD55	1.01	6.11E-01	8.09E-01	310.28	not significant
8130	SLC16A1-AS1	1.01	5.26E-01	7.54E-01	322.96	not significant
8131	DLEU2L	1.01	1.23E-01	NA	18.21	not significant
8132	ACAD11	1.01	3.27E-01	NA	45.24	not significant
8133	NDUFB4	1.01	6.60E-01	8.39E-01	2560.37	not significant
8134	PAPSS1	1.01	6.54E-01	8.36E-01	2394.66	not significant
8135	PRKD2	1.01	6.21E-01	8.15E-01	3768.93	not significant
8136	MRPS18A	1.01	6.53E-01	8.35E-01	1188.21	not significant
8137	NXT1	1.01	6.40E-01	8.27E-01	1469.04	not significant
8138	PARP4	1.01	6.31E-01	8.21E-01	4094.60	not significant
8139	SMIM7	1.01	6.66E-01	8.43E-01	1413.31	not significant
8140	KIAA0319L	1.01	6.48E-01	8.32E-01	1208.26	not significant
8141	GFOD1	1.01	5.97E-01	8.02E-01	217.73	not significant
8142	ZNF215	1.01	6.44E-01	8.30E-01	506.53	not significant
8143	ZBTB45	1.01	6.31E-01	8.21E-01	394.81	not significant
8144	CCDC142	1.01	6.37E-01	8.24E-01	404.33	not significant
8145	CYB5D2	1.01	5.78E-01	7.88E-01	201.58	not significant
8146	SLC16A7	1.01	5.98E-01	8.02E-01	2146.39	not significant
8147	NLRP1	1.01	6.06E-01	8.06E-01	335.54	not significant
8148	IGFLR1	1.01	5.17E-01	7.47E-01	126.53	not significant
8149	ROMO1	1.01	5.75E-01	7.85E-01	1256.61	not significant
8150	PROX1	1.01	3.99E-01	NA	64.77	not significant
8151	RILP	1.01	2.27E-01	NA	29.32	not significant
8152	TADA3	1.01	7.13E-01	8.67E-01	1905.08	not significant
8153	SLC39A3	1.01	6.54E-01	8.37E-01	1690.37	not significant
8154	RFTN1	1.01	6.49E-01	8.32E-01	1807.41	not significant
8155	MARK2	1.01	6.43E-01	8.30E-01	3036.39	not significant
8156	ACTR10	1.01	6.32E-01	8.22E-01	1160.73	not significant
8157	JPH1	1.01	6.56E-01	8.37E-01	1522.76	not significant
8158	CEP104	1.01	6.28E-01	8.19E-01	1929.86	not significant
8159	PLEKHA3	1.01	6.34E-01	8.23E-01	731.97	not significant
8160	ISCA2	1.01	6.23E-01	8.16E-01	798.28	not significant
8161	NCOA3	1.01	6.56E-01	8.37E-01	1743.59	not significant
8162	LINC00634	1.01	2.53E-01	NA	33.23	not significant
8163	RPPH1	1.01	1.57E-01	NA	29.23	not significant
8164	MGMT	1.01	6.40E-01	8.27E-01	859.60	not significant
8165	CIC	1.01	6.35E-01	8.23E-01	3157.20	not significant
8166	PHF13	1.01	6.51E-01	8.34E-01	1358.37	not significant
8167	LIN9	1.01	6.36E-01	8.24E-01	989.32	not significant
8168	NBAS	1.01	6.47E-01	8.32E-01	1713.99	not significant
8169	FAHD2A	1.01	6.48E-01	8.32E-01	711.60	not significant
8170	RBM45	1.01	6.34E-01	8.23E-01	487.50	not significant
8171	FAM83F	1.01	4.31E-01	NA	86.81	not significant

8172	NDUFA4L2	1.01	1.92E-01	NA	27.19	not significant
8173	LEF1	1.01	5.39E-01	7.62E-01	19810.41	not significant
8174	GAA	1.01	6.14E-01	8.11E-01	1068.44	not significant
8175	ZNF419	1.01	6.04E-01	8.04E-01	325.15	not significant
8176	ARL11	1.01	6.07E-01	8.07E-01	334.73	not significant
8177	KCNRG	1.01	2.77E-01	NA	37.69	not significant
8178	KIF27	1.01	5.10E-01	7.44E-01	130.91	not significant
8179	CYP2R1	1.01	4.13E-01	NA	71.51	not significant
8180	CAMK2N2	1.01	2.68E-01	NA	39.59	not significant
8181	NR3C1	1.01	6.33E-01	8.22E-01	1962.92	not significant
8182	GALK1	1.01	6.47E-01	8.32E-01	1358.32	not significant
8183	DMTF1	1.01	6.44E-01	8.30E-01	2738.59	not significant
8184	NDUFA11	1.01	6.13E-01	8.10E-01	3040.27	not significant
8185	PMS2P5	1.01	4.86E-01	7.26E-01	118.94	not significant
8186	CPEB3	1.01	5.23E-01	7.52E-01	144.60	not significant
8187	YBEY	1.01	5.36E-01	7.61E-01	157.63	not significant
8188	SYCE2	1.01	3.80E-01	NA	64.54	not significant
8189	CD274	1.01	2.04E-03	2.14E-02	318.50	not significant
8190	CACNA1A	1.01	6.45E-02	NA	13.63	not significant
8191	PLEKHA7	1.01	4.19E-01	NA	78.66	not significant
8192	MERTK	1.01	3.46E-01	NA	54.24	not significant
8193	CACNA2D4	1.01	2.49E-01	NA	34.54	not significant
8194	ANXA7	1.01	6.21E-01	8.15E-01	3208.63	not significant
8195	HAX1	1.01	6.32E-01	8.22E-01	3196.51	not significant
8196	THYN1	1.01	6.32E-01	8.22E-01	1960.68	not significant
8197	ZMYND8	1.01	6.03E-01	8.04E-01	1051.56	not significant
8198	CPNE2	1.01	5.75E-01	7.86E-01	231.89	not significant
8199	HNRNPA1L2	1.01	6.31E-01	8.21E-01	476.20	not significant
8200	KSR1	1.01	5.29E-01	7.56E-01	160.09	not significant
8201	SEPN1	1.01	3.81E-01	NA	66.20	not significant
8202	ZCCHC5	1.01	1.53E-01	NA	27.02	not significant
8203	LOC100131289	1.01	2.10E-01	NA	30.09	not significant
8204	ORAI2	1.01	6.09E-01	8.08E-01	3445.31	not significant
8205	BCL7A	1.01	6.31E-01	8.21E-01	3131.55	not significant
8206	THADA	1.01	6.33E-01	8.22E-01	2173.94	not significant
8207	TPRG1L	1.01	6.39E-01	8.26E-01	767.66	not significant
8208	GOLGA2	1.01	6.41E-01	8.28E-01	1704.11	not significant
8209	METTL18	1.01	6.24E-01	8.16E-01	469.47	not significant
8210	PPP1R21	1.01	6.18E-01	8.14E-01	563.99	not significant
8211	SLC25A42	1.01	6.19E-01	8.14E-01	533.83	not significant
8212	PDK2	1.01	5.67E-01	7.81E-01	227.22	not significant
8213	LHPP	1.01	5.95E-01	7.99E-01	289.66	not significant
8214	PHLPP1	1.01	5.29E-01	7.56E-01	154.29	not significant
8215	EMC6	1.01	5.58E-01	7.76E-01	1406.70	not significant
8216	EFCAB5	1.01	3.46E-01	NA	61.64	not significant
8217	LOC440311	1.01	2.39E-01	NA	34.32	not significant
8218	ARF5	1.01	6.31E-01	8.21E-01	3151.79	not significant
8219	CABLES2	1.01	6.03E-01	8.03E-01	1071.71	not significant
8220	GXYLT1	1.01	6.38E-01	8.25E-01	2097.72	not significant
8221	IFT74	1.01	5.89E-01	7.96E-01	306.60	not significant
8222	SPAG1	1.01	6.21E-01	8.15E-01	470.54	not significant
8223	LINC00659	1.01	4.98E-01	7.35E-01	135.72	not significant
8224	PTHLH	1.01	1.26E-01	NA	20.37	not significant
8225	ANP32C	1.01	1.87E-01	NA	28.48	not significant
8226	KCMF1	1.01	6.91E-01	8.54E-01	1840.38	not significant
8227	POLR2G	1.01	6.22E-01	8.15E-01	3061.90	not significant
8228	C21orf33	1.01	6.33E-01	8.22E-01	1190.45	not significant
8229	OSTF1	1.01	6.41E-01	8.28E-01	1791.06	not significant
8230	ABI2	1.01	5.60E-01	7.77E-01	6363.72	not significant
8231	PALM	1.01	2.16E-01	NA	33.47	not significant
8232	HERC2P3	1.01	8.82E-02	NA	17.23	not significant
8233	CCDC24	1.01	1.03E-01	NA	18.61	not significant
8234	IMMT	1.01	5.92E-01	7.98E-01	5766.73	not significant
8235	HSPA8	1.01	5.34E-01	7.59E-01	130805.42	not significant
8236	USP15	1.01	5.97E-01	8.02E-01	4204.47	not significant
8237	UBA6	1.01	6.11E-01	8.09E-01	3391.53	not significant
8238	ALG13	1.01	6.30E-01	8.21E-01	1213.71	not significant
8239	VOPP1	1.01	6.29E-01	8.20E-01	628.56	not significant
8240	MKRN3	1.01	5.84E-01	7.92E-01	323.84	not significant
8241	PON2	1.01	5.50E-01	7.70E-01	212.77	not significant
8242	GGACT	1.01	2.37E-01	NA	36.76	not significant
8243	NHLRC4	1.01	1.42E-01	NA	22.31	not significant
8244	TUFT1	1.01	1.01E-01	NA	19.58	not significant
8245	ACP1	1.01	5.99E-01	8.02E-01	5575.53	not significant
8246	SIPA1L3	1.01	6.32E-01	8.22E-01	1526.36	not significant
8247	RAB9B	1.01	6.00E-01	8.02E-01	364.45	not significant
8248	GUSBP11	1.01	6.13E-01	8.10E-01	769.54	not significant
8249	FAM24B	1.01	5.04E-01	7.39E-01	176.86	not significant
8250	AMOTL1	1.01	5.61E-01	7.78E-01	219.57	not significant
8251	GADD45GIP1	1.01	5.54E-01	7.72E-01	2313.78	not significant
8252	EPS8L1	1.01	4.74E-01	7.17E-01	124.58	not significant
8253	PMS2P3	1.01	4.58E-01	7.05E-01	114.59	not significant
8254	HIST1H2BK	1.01	4.57E-01	7.05E-01	125.25	not significant
8255	FAM53A	1.01	1.98E-01	NA	33.73	not significant
8256	HSD17B1	1.01	6.51E-02	NA	15.01	not significant
8257	TCF7	1.01	5.26E-01	7.54E-01	20912.83	not significant
8258	ELP3	1.01	6.29E-01	8.20E-01	1896.78	not significant
8259	PPT1	1.01	5.71E-01	7.83E-01	7329.03	not significant

8260	LDB1	1.01	6.19E-01	8.14E-01	3503.21	not significant
8261	NUMB	1.01	6.18E-01	8.14E-01	2991.32	not significant
8262	TACO1	1.01	6.27E-01	8.19E-01	1354.15	not significant
8263	DTD2	1.01	6.22E-01	8.15E-01	681.15	not significant
8264	PPP2R5B	1.01	6.06E-01	8.06E-01	409.05	not significant
8265	NBEA	1.01	5.42E-01	7.64E-01	245.55	not significant
8266	HPDL	1.01	5.00E-01	7.36E-01	169.74	not significant
8267	NRM	1.01	4.65E-01	7.11E-01	123.13	not significant
8268	CCT6P3	1.01	4.65E-01	7.11E-01	123.62	not significant
8269	LINC00051	1.01	2.30E-01	NA	36.20	not significant
8270	PLEKHH3	1.01	2.82E-02	NA	11.12	not significant
8271	TGOLN2	1.01	7.30E-01	8.76E-01	9187.07	not significant
8272	VRK1	1.01	6.09E-01	8.07E-01	3072.50	not significant
8273	URM1	1.01	6.22E-01	8.15E-01	2560.75	not significant
8274	VPS39	1.01	6.34E-01	8.23E-01	1767.83	not significant
8275	MTR	1.01	6.69E-01	8.44E-01	2072.13	not significant
8276	GOLPH3L	1.01	6.17E-01	8.13E-01	1147.60	not significant
8277	FLCN	1.01	6.28E-01	8.19E-01	1144.68	not significant
8278	ZNF830	1.01	6.22E-01	8.15E-01	650.17	not significant
8279	PCYOX1L	1.01	5.98E-01	8.02E-01	457.26	not significant
8280	LINC01232	1.01	3.01E-01	NA	50.63	not significant
8281	SRY	1.01	1.76E-01	NA	29.89	not significant
8282	LOC100130950	1.01	3.26E-02	NA	11.08	not significant
8283	GUSBP3	1.01	2.89E-01	NA	55.69	not significant
8284	PROB1	1.01	2.76E-01	NA	45.67	not significant
8285	PIK3IP1	1.01	1.83E-01	NA	33.15	not significant
8286	H2AFY	1.01	5.77E-01	7.87E-01	18257.78	not significant
8287	SUMO3	1.01	5.97E-01	8.02E-01	3973.44	not significant
8288	RPS18	1.01	7.30E-01	8.76E-01	19196.03	not significant
8289	MYEOV2	1.01	5.69E-01	7.83E-01	1581.91	not significant
8290	KIAA1161	1.01	5.49E-01	7.69E-01	262.10	not significant
8291	ULK4	1.01	5.24E-01	7.52E-01	187.24	not significant
8292	NRL	1.01	4.18E-01	NA	85.88	not significant
8293	MBLAC1	1.01	4.07E-01	NA	81.92	not significant
8294	MX2	1.01	2.40E-01	NA	37.67	not significant
8295	MRFAP1	1.01	6.00E-01	8.02E-01	4281.14	not significant
8296	RCBTB2	1.01	5.36E-01	7.61E-01	21475.33	not significant
8297	NDNL2	1.01	6.13E-01	8.10E-01	851.87	not significant
8298	SKIV2L	1.01	6.23E-01	8.15E-01	762.62	not significant
8299	KCTD7	1.01	5.97E-01	8.02E-01	714.55	not significant
8300	DFFB	1.01	5.73E-01	7.84E-01	310.19	not significant
8301	TYMSOS	1.01	3.83E-01	NA	77.58	not significant
8302	LRRC37A3	1.01	2.02E-01	NA	37.83	not significant
8303	RSAD1	1.01	6.93E-01	8.55E-01	1830.04	not significant
8304	HMGB2	1.01	5.64E-01	7.79E-01	19110.93	not significant
8305	PGRMC1	1.01	6.01E-01	8.02E-01	2461.80	not significant
8306	USP9X	1.01	6.05E-01	8.05E-01	4543.06	not significant
8307	MTFR1	1.01	6.09E-01	8.08E-01	629.00	not significant
8308	PKN2	1.01	6.53E-01	8.35E-01	1715.34	not significant
8309	MORC4	1.01	6.11E-01	8.09E-01	649.93	not significant
8310	TMEM180	1.01	6.00E-01	8.02E-01	590.23	not significant
8311	SVIL	1.01	6.20E-01	8.15E-01	850.02	not significant
8312	IL15	1.01	5.22E-01	7.51E-01	220.92	not significant
8313	SERPINI1	1.01	1.32E-01	NA	24.12	not significant
8314	UQCR10	1.01	6.11E-01	8.09E-01	2735.54	not significant
8315	TPRKB	1.01	6.06E-01	8.06E-01	1181.61	not significant
8316	BCL11B	1.01	5.93E-01	7.98E-01	8407.58	not significant
8317	DEDD2	1.01	5.96E-01	8.01E-01	794.63	not significant
8318	MSL3	1.01	6.18E-01	8.14E-01	1003.98	not significant
8319	IRF2BPL	1.01	6.13E-01	8.10E-01	1611.31	not significant
8320	ZNF687	1.01	6.12E-01	8.09E-01	1212.34	not significant
8321	C7orf25	1.01	5.57E-01	7.75E-01	292.93	not significant
8322	ZNF337	1.01	6.14E-01	8.10E-01	813.98	not significant
8323	MAFG-AS1	1.01	4.58E-01	7.06E-01	126.07	not significant
8324	SH3BGR	1.01	3.95E-01	NA	84.55	not significant
8325	ARHGEF25	1.01	2.80E-01	NA	47.16	not significant
8326	MIR181A1HG	1.01	1.45E-01	NA	25.10	not significant
8327	RPS15	1.01	5.99E-01	8.02E-01	10233.64	not significant
8328	SF3B1	1.01	4.93E-01	7.31E-01	17392.87	not significant
8329	MBTPS1	1.01	5.83E-01	7.91E-01	4771.34	not significant
8330	YTHDC2	1.01	6.12E-01	8.09E-01	2333.74	not significant
8331	HPS6	1.01	6.00E-01	8.02E-01	720.87	not significant
8332	RNF214	1.01	6.10E-01	8.09E-01	641.53	not significant
8333	ZNF668	1.01	6.13E-01	8.10E-01	899.10	not significant
8334	FRS3	1.01	4.94E-01	7.32E-01	165.94	not significant
8335	PLEKHA5	1.01	5.93E-01	7.98E-01	487.92	not significant
8336	MUC4	1.01	5.72E-01	7.83E-01	336.58	not significant
8337	C15orf37	1.01	3.90E-01	NA	86.96	not significant
8338	BBC3	1.01	4.25E-01	6.79E-01	108.20	not significant
8339	ZFP3	1.01	3.10E-01	NA	58.21	not significant
8340	FRMD4B	1.01	4.05E-01	NA	89.39	not significant
8341	SLC15A2	1.01	2.14E-01	NA	45.04	not significant
8342	PPP1R12C	1.01	5.88E-01	7.95E-01	2960.77	not significant
8343	DDX60L	1.01	5.99E-01	8.02E-01	1672.65	not significant
8344	SAP30BP	1.01	6.02E-01	8.03E-01	2566.81	not significant
8345	PANK2	1.01	6.09E-01	8.08E-01	1535.28	not significant
8346	ERF	1.01	6.07E-01	8.06E-01	1592.69	not significant
8347	OSBPL9	1.01	6.09E-01	8.07E-01	1663.05	not significant

8348	CPNE7	1.01	6.03E-01	8.03E-01	455.74	not significant
8349	LOC101927204	1.01	5.46E-01	7.67E-01	289.21	not significant
8350	PTRH1	1.01	5.62E-01	7.78E-01	324.96	not significant
8351	DUSP16	1.01	4.03E-01	NA	94.41	not significant
8352	SLC25A39	1.01	5.84E-01	7.92E-01	4032.03	not significant
8353	PMPCA	1.01	6.75E-01	8.48E-01	1721.33	not significant
8354	AMBRA1	1.01	6.02E-01	8.03E-01	1877.77	not significant
8355	FANCC	1.01	5.98E-01	8.02E-01	915.18	not significant
8356	ZFY	1.01	5.71E-01	7.83E-01	1195.50	not significant
8357	TP53I3	1.01	3.94E-01	NA	92.21	not significant
8358	TMEM161B-AS1	1.01	3.45E-01	NA	65.89	not significant
8359	ZNF707	1.01	2.91E-01	NA	53.56	not significant
8360	TMPRSS5	1.01	8.93E-02	NA	19.00	not significant
8361	ACADM	1.01	5.79E-01	7.88E-01	3923.36	not significant
8362	FAM204A	1.01	6.08E-01	8.07E-01	1306.83	not significant
8363	CARD11	1.01	5.92E-01	7.98E-01	3022.36	not significant
8364	ACN9	1.01	6.11E-01	8.09E-01	971.77	not significant
8365	ARHGEF18	1.01	5.94E-01	7.99E-01	2849.04	not significant
8366	ITGAL	1.01	5.97E-01	8.02E-01	2424.45	not significant
8367	SOCS5	1.01	6.00E-01	8.02E-01	638.02	not significant
8368	GATS	1.01	5.85E-01	7.93E-01	751.90	not significant
8369	MAP3K1	1.01	5.67E-01	7.81E-01	340.22	not significant
8370	ATAT1	1.01	5.52E-01	7.71E-01	262.44	not significant
8371	PRF1	1.01	4.60E-01	7.07E-01	127.15	not significant
8372	GSTA4	1.01	3.87E-01	NA	85.60	not significant
8373	CADM4	1.01	2.20E-01	NA	39.97	not significant
8374	LRRC75A	1.01	2.35E-01	NA	42.64	not significant
8375	TMED9	1.01	5.62E-01	7.78E-01	3471.40	not significant
8376	ENO2	1.01	5.98E-01	8.02E-01	644.91	not significant
8377	ARHGAP25	1.01	5.95E-01	8.00E-01	1213.61	not significant
8378	CYB561A3	1.01	5.76E-01	7.86E-01	1877.42	not significant
8379	ITGB1BP2	1.01	3.57E-01	NA	86.01	not significant
8380	RICTOR	1.01	5.35E-01	7.60E-01	1631.80	not significant
8381	CECR6	1.01	2.41E-01	NA	48.60	not significant
8382	ACKR3	1.01	4.69E-01	7.13E-01	152.03	not significant
8383	NFYC-AS1	1.01	4.15E-01	6.72E-01	110.82	not significant
8384	CBX3P2	1.01	8.45E-02	NA	19.11	not significant
8385	DIRC2	1.01	4.39E-01	6.91E-01	124.53	not significant
8386	ZNF511	1.01	6.03E-01	8.03E-01	849.55	not significant
8387	PRRG4	1.01	5.55E-01	7.74E-01	318.92	not significant
8388	ANO8	1.01	5.02E-01	7.38E-01	218.90	not significant
8389	BAD	1.01	5.94E-01	7.99E-01	1183.55	not significant
8390	TRIM24	1.01	5.59E-01	7.76E-01	4115.49	not significant
8391	SNRNP27	1.01	5.88E-01	7.95E-01	1786.74	not significant
8392	ZSCAN18	1.01	6.04E-01	8.04E-01	1121.56	not significant
8393	RRAGD	1.01	6.05E-01	8.05E-01	1179.88	not significant
8394	TOR1B	1.01	5.92E-01	7.98E-01	1193.60	not significant
8395	EIF2AK3	1.01	6.00E-01	8.02E-01	1588.64	not significant
8396	IGHMBP2	1.01	6.03E-01	8.03E-01	872.70	not significant
8397	ARID3A	1.01	5.92E-01	7.98E-01	658.29	not significant
8398	LTB4R	1.01	5.70E-01	7.83E-01	406.22	not significant
8399	SOGA3	1.01	5.66E-01	7.81E-01	701.45	not significant
8400	MIRLET7BHG	1.01	8.58E-02	NA	20.10	not significant
8401	ZNF442	1.01	2.99E-01	NA	61.50	not significant
8402	TSG101	1.01	5.98E-01	8.02E-01	1379.12	not significant
8403	WHSC1	1.01	5.37E-01	7.61E-01	12939.24	not significant
8404	EXO1	1.01	5.62E-01	7.78E-01	3329.17	not significant
8405	ZNF574	1.01	5.74E-01	7.84E-01	919.58	not significant
8406	TBL1X	1.01	5.89E-01	7.96E-01	2076.48	not significant
8407	C16orf87	1.01	5.84E-01	7.92E-01	482.15	not significant
8408	MT1H	1.01	5.77E-01	7.87E-01	7060.60	not significant
8409	LOC100996579	1.01	5.62E-01	7.78E-01	371.74	not significant
8410	TTC30B	1.01	4.28E-01	6.82E-01	113.30	not significant
8411	C14orf39	1.01	2.45E-01	NA	46.17	not significant
8412	ZNF572	1.01	1.54E-01	NA	29.65	not significant
8413	ZNF706	1.01	6.87E-01	8.53E-01	1928.07	not significant
8414	DAZAP1	1.01	5.48E-01	7.68E-01	8871.52	not significant
8415	HIRIP3	1.01	5.87E-01	7.94E-01	2377.91	not significant
8416	UBASH3A	1.01	5.98E-01	8.02E-01	1006.68	not significant
8417	BCL2L13	1.01	5.87E-01	7.95E-01	2006.77	not significant
8418	ZNF302	1.01	5.99E-01	8.02E-01	951.64	not significant
8419	AKAP13	1.01	5.72E-01	7.84E-01	2862.67	not significant
8420	HAUS7	1.01	5.68E-01	7.82E-01	363.19	not significant
8421	LOC389765	1.01	3.06E-01	NA	67.87	not significant
8422	ATP1B1	1.01	4.18E-01	6.74E-01	117.94	not significant
8423	DNAJB12	1.01	6.87E-01	8.53E-01	1581.33	not significant
8424	RPS19	1.01	7.77E-01	9.03E-01	15045.35	not significant
8425	SBF1	1.01	5.36E-01	7.61E-01	7666.78	not significant
8426	RNMTL1	1.01	5.88E-01	7.95E-01	760.27	not significant
8427	GMEB2	1.01	5.97E-01	8.02E-01	1075.31	not significant
8428	C19orf70	1.01	5.85E-01	7.93E-01	998.73	not significant
8429	ZNF780A	1.01	5.70E-01	7.83E-01	573.77	not significant
8430	COLQ	1.01	1.92E-01	NA	35.44	not significant
8431	LTBP3	1.01	3.06E-01	NA	76.19	not significant
8432	ZNF517	1.01	3.44E-01	NA	79.84	not significant
8433	LOC155060	1.01	4.86E-01	7.26E-01	216.69	not significant
8434	RPS10P7	1.01	2.68E-01	NA	51.97	not significant
8435	FAM20C	1.01	6.00E-02	NA	17.22	not significant

8436	TXN2	1.01	5.77E-01	7.87E-01	2699.41	not significant
8437	CD244	1.01	5.66E-01	7.81E-01	2721.84	not significant
8438	SEC11A	1.01	5.81E-01	7.90E-01	1994.91	not significant
8439	TFAP4	1.01	5.93E-01	7.98E-01	957.80	not significant
8440	VCPIP1	1.01	6.45E-01	8.31E-01	1814.37	not significant
8441	ATG4C	1.01	5.72E-01	7.83E-01	724.77	not significant
8442	ACAA1	1.01	5.79E-01	7.88E-01	2282.19	not significant
8443	CPT1A	1.01	5.60E-01	7.77E-01	3320.64	not significant
8444	ENTPD6	1.01	5.74E-01	7.85E-01	2049.02	not significant
8445	ZFPL1	1.01	5.80E-01	7.88E-01	570.87	not significant
8446	VIPR2	1.01	5.81E-01	7.90E-01	2026.91	not significant
8447	MTIF3	1.01	5.70E-01	7.83E-01	568.99	not significant
8448	NUDT3	1.01	4.84E-01	7.24E-01	211.29	not significant
8449	DDR1	1.01	3.21E-01	NA	69.03	not significant
8450	SLFNL1-AS1	1.01	2.84E-01	NA	57.37	not significant
8451	LOC100240735	1.01	1.88E-01	NA	38.88	not significant
8452	FAM229A	1.01	1.56E-01	NA	32.89	not significant
8453	SEC14L1P1	1.01	2.10E-01	NA	40.03	not significant
8454	BOLA1	1.01	4.74E-02	NA	16.20	not significant
8455	FASN	1.01	5.29E-01	7.56E-01	30051.74	not significant
8456	NDUFA2	1.01	5.88E-01	7.95E-01	1676.43	not significant
8457	ZNF444	1.01	6.03E-01	8.03E-01	1352.47	not significant
8458	CMAS	1.01	5.81E-01	7.90E-01	1515.62	not significant
8459	PSMD5-AS1	1.01	5.94E-01	7.99E-01	1264.93	not significant
8460	RNF13	1.01	5.88E-01	7.95E-01	1039.92	not significant
8461	ZBTB8A	1.01	5.82E-01	7.90E-01	739.65	not significant
8462	SMG1P7	1.01	4.14E-01	6.71E-01	115.07	not significant
8463	STX11	1.01	2.92E-01	NA	64.45	not significant
8464	CCDC96	1.01	1.53E-01	NA	30.44	not significant
8465	RPA1	1.01	4.71E-01	7.15E-01	11220.23	not significant
8466	SMYD2	1.01	5.80E-01	7.89E-01	1627.41	not significant
8467	IDH1	1.01	5.74E-01	7.84E-01	1500.75	not significant
8468	WAS	1.01	5.77E-01	7.87E-01	1232.48	not significant
8469	YARS2	1.01	5.71E-01	7.83E-01	873.10	not significant
8470	IRF9	1.01	5.40E-01	7.63E-01	336.17	not significant
8471	AFF2	1.01	5.32E-01	7.58E-01	320.78	not significant
8472	SLC27A1	1.01	3.51E-01	NA	83.40	not significant
8473	ZMAT1	1.01	2.36E-01	NA	50.67	not significant
8474	UPP1	1.01	2.26E-01	NA	46.51	not significant
8475	TMEM53	1.01	2.13E-01	NA	40.86	not significant
8476	UHRF1BP1L	1.01	9.07E-01	9.64E-01	1234.03	not significant
8477	PPM1G	1.01	5.06E-01	7.41E-01	9182.20	not significant
8478	TTI2	1.01	6.00E-01	8.02E-01	1298.89	not significant
8479	NAA20	1.01	5.51E-01	7.71E-01	2502.62	not significant
8480	STXBP2	1.01	5.82E-01	7.90E-01	1413.93	not significant
8481	FAM169A	1.01	5.79E-01	7.88E-01	2254.61	not significant
8482	OMA1	1.01	5.67E-01	7.81E-01	595.23	not significant
8483	CA11	1.01	5.15E-01	7.46E-01	247.53	not significant
8484	SOAT2	1.01	4.75E-01	7.18E-01	186.44	not significant
8485	TBC1D2	1.01	7.73E-02	NA	21.89	not significant
8486	LOC90834	1.01	2.55E-01	NA	53.75	not significant
8487	WNT8B	1.01	3.56E-02	NA	15.67	not significant
8488	RASIP1	1.01	1.22E-01	NA	30.96	not significant
8489	PSMB5	1.01	5.91E-01	7.97E-01	1665.91	not significant
8490	TMEM63B	1.01	5.28E-01	7.55E-01	306.44	not significant
8491	KLHL23	1.01	1.97E-01	NA	40.44	not significant
8492	BMS1P4	1.01	4.28E-01	6.82E-01	137.39	not significant
8493	RGS1	1.01	1.17E-01	NA	27.21	not significant
8494	CNOT10	1.01	6.01E-01	8.03E-01	1803.10	not significant
8495	CCDC34	1.01	5.69E-01	7.83E-01	1234.22	not significant
8496	DOCK9	1.01	5.78E-01	7.88E-01	887.44	not significant
8497	TBCC	1.01	5.67E-01	7.81E-01	504.31	not significant
8498	AKT1S1	1.01	5.50E-01	7.70E-01	560.78	not significant
8499	FBN1	1.01	5.30E-01	7.56E-01	274.06	not significant
8500	TNFRSF13C	1.01	1.40E-01	NA	29.95	not significant
8501	HAR1B	1.01	4.01E-02	NA	15.56	not significant
8502	COPS3	1.01	5.33E-01	7.58E-01	4946.19	not significant
8503	TRAPPC11	1.01	5.74E-01	7.84E-01	1696.61	not significant
8504	ZFYVE27	1.01	5.92E-01	7.98E-01	1316.91	not significant
8505	GPR125	1.01	5.75E-01	7.86E-01	1578.71	not significant
8506	PPCDC	1.01	5.37E-01	7.61E-01	382.32	not significant
8507	KCTD18	1.01	5.69E-01	7.82E-01	683.05	not significant
8508	MAST3	1.01	5.67E-01	7.81E-01	626.62	not significant
8509	SLC16A10	1.01	2.40E-01	5.08E-01	299.38	not significant
8510	DYNC2LI1	1.01	3.67E-01	NA	97.68	not significant
8511	BTD	1.01	4.05E-01	6.63E-01	127.16	not significant
8512	LINC00921	1.01	1.21E-01	NA	31.15	not significant
8513	CCDC183-AS1	1.01	1.58E-01	NA	33.69	not significant
8514	MAP3K7	1.01	5.58E-01	7.76E-01	2891.64	not significant
8515	PFDN6	1.01	5.72E-01	7.83E-01	842.33	not significant
8516	SLC36A4	1.01	5.74E-01	7.85E-01	791.34	not significant
8517	CCDC77	1.01	5.59E-01	7.77E-01	715.26	not significant
8518	ZNF775	1.01	5.56E-01	7.75E-01	487.34	not significant
8519	HACL1	1.01	5.44E-01	7.65E-01	407.69	not significant
8520	DAG1	1.01	5.70E-01	7.83E-01	989.60	not significant
8521	PEX13	1.01	5.56E-01	7.74E-01	564.91	not significant
8522	HESX1	1.01	6.85E-02	NA	21.20	not significant
8523	NAPA-AS1	1.01	2.17E-01	NA	54.64	not significant

8524	LOC100652768	1.01	2.11E-02	NA	13.54	not significant
8525	RPN1	1.01	4.96E-01	7.33E-01	10056.37	not significant
8526	ARFIP1	1.01	5.40E-01	7.63E-01	1141.87	not significant
8527	AKR7A2	1.01	5.68E-01	7.82E-01	1710.43	not significant
8528	ALG6	1.01	5.76E-01	7.86E-01	1425.38	not significant
8529	TAF1B	1.01	5.71E-01	7.83E-01	795.91	not significant
8530	ANGPTL6	1.01	3.88E-01	6.50E-01	122.81	not significant
8531	TOMM7	1.01	5.70E-01	7.83E-01	1908.63	not significant
8532	SREK1	1.01	5.19E-01	7.49E-01	4313.39	not significant
8533	KDM5A	1.01	5.25E-01	7.54E-01	4307.90	not significant
8534	LAMTOR2	1.01	5.70E-01	7.83E-01	820.69	not significant
8535	MOCS2	1.01	5.41E-01	7.63E-01	1893.84	not significant
8536	PPAP2A	1.01	5.44E-01	7.65E-01	411.94	not significant
8537	ZER1	1.01	5.69E-01	7.83E-01	819.47	not significant
8538	CD79B	1.01	5.17E-01	7.47E-01	500.33	not significant
8539	ZNF226	1.01	5.54E-01	7.73E-01	528.53	not significant
8540	GSC	1.01	4.35E-01	6.88E-01	149.80	not significant
8541	ANKHD1	1.01	4.87E-01	7.27E-01	222.85	not significant
8542	SMOX	1.01	4.46E-01	6.96E-01	158.39	not significant
8543	BRSK1	1.01	4.50E-01	6.99E-01	162.66	not significant
8544	ABCC8	1.01	3.61E-01	6.26E-01	100.98	not significant
8545	AHCYL1	1.01	5.14E-01	7.46E-01	3900.56	not significant
8546	CYP4F2	1.01	7.35E-01	NA	80.24	not significant
8547	SLC30A9	1.01	5.36E-01	7.61E-01	1899.96	not significant
8548	TM2D2	1.01	5.69E-01	7.83E-01	1067.07	not significant
8549	RAB3GAP1	1.01	5.34E-01	7.60E-01	1191.66	not significant
8550	RNFT1	1.01	5.29E-01	7.56E-01	368.27	not significant
8551	GVINP1	1.01	5.64E-01	7.80E-01	754.69	not significant
8552	HES1	1.01	4.35E-01	6.88E-01	168.08	not significant
8553	ZNF599	1.01	4.12E-01	6.70E-01	134.72	not significant
8554	FAM13A	1.01	2.32E-01	NA	51.82	not significant
8555	IQCK	1.01	2.31E-01	NA	55.88	not significant
8556	RNASEH2B	1.01	5.05E-01	7.40E-01	4487.83	not significant
8557	RPL37	1.01	5.57E-01	7.75E-01	12810.29	not significant
8558	RBM28	1.01	5.59E-01	7.77E-01	1668.30	not significant
8559	PALLD	1.01	5.63E-01	7.79E-01	1258.67	not significant
8560	SCAPER	1.01	5.52E-01	7.71E-01	773.91	not significant
8561	SHANK3	1.01	5.17E-01	7.47E-01	311.14	not significant
8562	BAIAP2L2	1.01	9.31E-02	NA	25.65	not significant
8563	TSPAN7	1.01	5.09E-01	7.43E-01	5316.51	not significant
8564	GTF3C3	1.01	5.38E-01	7.61E-01	2617.18	not significant
8565	GBF1	1.01	5.53E-01	7.71E-01	3782.99	not significant
8566	ZMYM2	1.01	5.05E-01	7.39E-01	3687.34	not significant
8567	EXOC3	1.01	5.58E-01	7.76E-01	1696.48	not significant
8568	PCTP	1.01	5.43E-01	7.65E-01	475.51	not significant
8569	IRX5	1.01	5.32E-01	7.58E-01	459.30	not significant
8570	SURF1	1.01	5.39E-01	7.62E-01	429.50	not significant
8571	ORAOV1	1.01	5.39E-01	7.62E-01	696.62	not significant
8572	ZNF582	1.01	4.73E-01	7.16E-01	221.24	not significant
8573	C8orf37	1.01	4.65E-01	7.11E-01	203.51	not significant
8574	FCHSD1	1.01	4.16E-01	6.72E-01	137.77	not significant
8575	TXLNB	1.01	3.07E-01	NA	83.63	not significant
8576	NFKBIZ	1.01	1.53E-01	NA	41.89	not significant
8577	HIST1H3D	1.01	8.04E-02	NA	24.44	not significant
8578	MED25	1.01	5.37E-01	7.61E-01	1356.45	not significant
8579	DDX59	1.01	5.58E-01	7.76E-01	832.08	not significant
8580	RAP2B	1.01	5.49E-01	7.68E-01	1300.73	not significant
8581	GOLGA2P5	1.01	5.54E-01	7.72E-01	701.44	not significant
8582	SMARCD3	1.01	5.37E-02	NA	19.21	not significant
8583	GLOD4	1.01	5.46E-01	7.66E-01	2417.44	not significant
8584	TMSB4X	1.01	5.24E-01	7.52E-01	34255.60	not significant
8585	C11orf49	1.01	5.60E-01	7.77E-01	894.84	not significant
8586	SMAD6	1.01	5.60E-01	7.77E-01	1084.77	not significant
8587	DAGLB	1.01	5.31E-01	7.58E-01	722.39	not significant
8588	DTNB	1.01	5.31E-01	7.57E-01	395.14	not significant
8589	S1PR3	1.01	4.19E-01	6.75E-01	695.79	not significant
8590	RENBP	1.01	2.72E-01	NA	69.92	not significant
8591	ARPC3	1.01	5.25E-01	7.54E-01	9927.74	not significant
8592	TRIM41	1.01	5.37E-01	7.61E-01	2140.92	not significant
8593	ATP6V0A4	1.01	5.59E-01	7.76E-01	892.63	not significant
8594	MED12L	1.01	5.50E-01	7.70E-01	963.54	not significant
8595	DAPP1	1.01	4.19E-01	6.75E-01	159.55	not significant
8596	PCED1B	1.01	3.49E-01	6.16E-01	107.02	not significant
8597	ADAMTS6	1.01	3.32E-01	NA	88.63	not significant
8598	IL2RG	1.01	4.55E-01	7.04E-01	13428.99	not significant
8599	RAVER1	1.01	4.92E-01	7.31E-01	9343.08	not significant
8600	NOB1	1.01	5.36E-01	7.61E-01	3282.82	not significant
8601	TRAPPC10	1.01	5.37E-01	7.61E-01	2244.26	not significant
8602	PLEKHM2	1.01	5.40E-01	7.63E-01	2257.46	not significant
8603	DGCR2	1.01	5.36E-01	7.61E-01	2351.76	not significant
8604	DOPEY2	1.01	5.40E-01	7.63E-01	1410.36	not significant
8605	LINC00528	1.01	4.86E-01	7.26E-01	249.01	not significant
8606	BCL6	1.01	3.60E-01	6.25E-01	116.85	not significant
8607	EIF3J-AS1	1.01	2.42E-01	NA	57.47	not significant
8608	OVCA2	1.01	2.68E-01	NA	69.36	not significant
8609	MAFF	1.01	1.36E-01	NA	37.65	not significant
8610	CPVL	1.01	5.37E-01	7.61E-01	2313.01	not significant
8611	JAK1	1.01	5.14E-01	7.46E-01	4758.15	not significant

8612	PIKFYVE	1.01	5.42E-01	7.64E-01	5249.21	not significant
8613	CMTR2	1.01	5.47E-01	7.67E-01	1359.18	not significant
8614	LIN37	1.01	4.45E-01	6.96E-01	187.49	not significant
8615	AGAP3	1.01	5.28E-01	7.55E-01	440.09	not significant
8616	SGK1	1.01	2.83E-01	NA	74.98	not significant
8617	GLA	1.01	4.64E-01	7.11E-01	238.71	not significant
8618	ISCU	1.01	5.35E-01	7.60E-01	2522.27	not significant
8619	KAT5	1.01	5.44E-01	7.65E-01	1599.13	not significant
8620	FAM217B	1.01	5.09E-01	7.43E-01	3643.38	not significant
8621	XPC	1.01	5.51E-01	7.71E-01	972.37	not significant
8622	PHF7	1.01	5.27E-01	7.55E-01	423.22	not significant
8623	43526_22646	1.01	3.46E-01	6.13E-01	109.33	not significant
8624	LRRC56	1.01	1.04E-01	NA	31.20	not significant
8625	TIMM13	1.01	5.43E-01	7.64E-01	3211.13	not significant
8626	MPZL1	1.01	5.17E-01	7.47E-01	3482.63	not significant
8627	PHF3	1.01	5.38E-01	7.61E-01	3919.46	not significant
8628	USP12	1.01	5.36E-01	7.61E-01	1984.63	not significant
8629	CPD	1.01	5.08E-01	7.42E-01	2933.72	not significant
8630	MED11	1.01	4.82E-01	7.23E-01	323.29	not significant
8631	PRIMPOL	1.01	5.17E-01	7.47E-01	485.72	not significant
8632	GYG1	1.01	4.66E-01	7.11E-01	229.00	not significant
8633	LOC100128398	1.01	3.59E-01	6.24E-01	120.96	not significant
8634	FIBP	1.01	5.22E-01	7.51E-01	2963.13	not significant
8635	AUP1	1.01	5.02E-01	7.38E-01	4915.98	not significant
8636	CMPK2	1.01	5.14E-01	7.46E-01	3504.47	not significant
8637	SLC39A8	1.01	4.81E-01	7.22E-01	5442.52	not significant
8638	POLE2	1.01	5.48E-01	7.68E-01	971.35	not significant
8639	PPP3CA	1.01	5.39E-01	7.62E-01	1432.26	not significant
8640	PHAX	1.01	5.41E-01	7.63E-01	1496.39	not significant
8641	SLC25A24	1.01	5.25E-01	7.54E-01	1728.71	not significant
8642	SUPT3H	1.01	5.39E-01	7.62E-01	697.31	not significant
8643	ANO5	1.01	4.77E-01	7.19E-01	269.89	not significant
8644	PDPR	1.01	4.72E-01	7.15E-01	3935.12	not significant
8645	ASTN2	1.01	3.43E-01	6.10E-01	105.58	not significant
8646	MYRF	1.01	1.84E-01	NA	47.05	not significant
8647	MTL5	1.01	1.39E-01	NA	37.51	not significant
8648	GYPC	1.01	5.41E-01	7.63E-01	1851.40	not significant
8649	GAMT	1.01	5.42E-01	7.64E-01	2172.58	not significant
8650	BAG1	1.01	5.38E-01	7.61E-01	1678.11	not significant
8651	DEPDC5	1.01	5.46E-01	7.67E-01	938.85	not significant
8652	TMEM200A	1.01	4.48E-01	6.98E-01	207.57	not significant
8653	OXTR	1.01	3.76E-01	6.40E-01	129.95	not significant
8654	ZNF514	1.01	3.62E-01	6.26E-01	129.85	not significant
8655	LOC729218	1.01	3.89E-01	6.51E-01	685.67	not significant
8656	ADORA3	1.01	1.29E-01	NA	33.41	not significant
8657	RPS13	1.01	5.13E-01	7.45E-01	11857.53	not significant
8658	SEC24D	1.01	5.28E-01	7.55E-01	1962.67	not significant
8659	CASP4	1.01	5.42E-01	7.64E-01	1062.70	not significant
8660	AFF1	1.01	5.34E-01	7.59E-01	4438.20	not significant
8661	TMEM223	1.01	4.98E-01	7.35E-01	491.01	not significant
8662	ZNF691	1.01	5.00E-01	7.36E-01	330.56	not significant
8663	GORASP1	1.01	4.88E-01	7.28E-01	310.45	not significant
8664	ST6GALNAC4	1.01	3.23E-01	NA	97.31	not significant
8665	KIAA1279	1.01	5.57E-01	7.75E-01	748.39	not significant
8666	KIF7	1.01	5.32E-01	7.58E-01	658.70	not significant
8667	RBM4B	1.01	5.11E-01	7.44E-01	388.11	not significant
8668	SMIM20	1.01	5.17E-01	7.47E-01	529.03	not significant
8669	MEF2BNB	1.01	4.20E-01	6.75E-01	192.48	not significant
8670	UBALD1	1.01	4.73E-01	7.16E-01	226.62	not significant
8671	PLOD3	1.01	4.65E-01	7.11E-01	265.74	not significant
8672	SIX3-AS1	1.01	2.07E-01	NA	52.54	not significant
8673	ATXN7L3B	1.01	4.52E-01	7.01E-01	8252.09	not significant
8674	MAD2L1	1.01	4.96E-01	7.33E-01	3924.71	not significant
8675	PHC2	1.01	5.16E-01	7.47E-01	3292.08	not significant
8676	IL32	1.01	5.31E-01	7.57E-01	3668.45	not significant
8677	PRRC1	1.01	4.96E-01	7.33E-01	3077.66	not significant
8678	DPYD	1.01	5.09E-01	7.43E-01	2619.54	not significant
8679	TASP1	1.01	5.36E-01	7.61E-01	774.07	not significant
8680	AIF1	1.01	4.46E-01	6.96E-01	1765.48	not significant
8681	LENG1	1.01	3.12E-01	NA	89.87	not significant
8682	TIGD2	1.01	3.70E-01	6.34E-01	130.07	not significant
8683	L3MBTL1	1.01	3.06E-01	5.78E-01	103.14	not significant
8684	RABL2B	1.01	1.57E-01	NA	42.39	not significant
8685	BST1	1.01	2.60E-01	NA	68.46	not significant
8686	C6orf132	1.01	1.90E-01	NA	50.29	not significant
8687	ALDH2	1.01	1.01E-01	NA	30.35	not significant
8688	IPO5	1.01	4.36E-01	6.89E-01	15516.18	not significant
8689	ECH1	1.01	5.31E-01	7.58E-01	2510.10	not significant
8690	TET2	1.01	5.62E-01	7.78E-01	1157.82	not significant
8691	ZNF133	1.01	4.76E-01	7.18E-01	291.00	not significant
8692	BMP1	1.01	5.05E-01	7.40E-01	480.78	not significant
8693	MOB3C	1.01	3.48E-01	6.15E-01	109.40	not significant
8694	PILRA	1.01	2.86E-01	NA	84.77	not significant
8695	CDKL3	1.01	2.05E-01	NA	53.39	not significant
8696	SEMA6C	1.01	2.42E-01	NA	64.86	not significant
8697	ZNF763	1.01	1.62E-01	NA	44.67	not significant
8698	AES	1.01	4.89E-01	7.28E-01	12178.37	not significant
8699	GID4	1.01	5.30E-01	7.57E-01	913.61	not significant

8700	RPL18A	1.01	5.14E-01	7.46E-01	12831.77	not significant
8701	STRIP1	1.01	5.24E-01	7.52E-01	1733.28	not significant
8702	TRAPPC12	1.01	5.33E-01	7.58E-01	1242.67	not significant
8703	IBA57	1.01	5.13E-01	7.45E-01	529.22	not significant
8704	TTBK2	1.01	4.94E-01	7.33E-01	406.03	not significant
8705	FBXO3	1.01	4.80E-01	7.21E-01	335.87	not significant
8706	ALDH1A2	1.01	4.22E-01	6.76E-01	188.60	not significant
8707	LOC101928736	1.01	2.92E-01	NA	78.42	not significant
8708	CD164	1.01	4.62E-01	7.09E-01	15716.75	not significant
8709	SLC7A1	1.01	5.06E-01	7.40E-01	12412.15	not significant
8710	NXF1	1.01	5.00E-01	7.36E-01	3936.07	not significant
8711	SH3GL1	1.01	5.11E-01	7.44E-01	1482.28	not significant
8712	SLC25A28	1.01	5.24E-01	7.52E-01	714.78	not significant
8713	SNRNP35	1.01	5.01E-01	7.37E-01	406.58	not significant
8714	TICAM1	1.01	5.10E-01	7.44E-01	449.06	not significant
8715	NLGN2	1.01	5.05E-01	7.40E-01	457.13	not significant
8716	LY75	1.01	4.95E-01	7.33E-01	416.19	not significant
8717	CTXN1	1.01	3.44E-01	6.10E-01	113.11	not significant
8718	MTCL1	1.01	3.16E-01	NA	100.13	not significant
8719	GPA33	1.01	3.60E-01	6.25E-01	129.70	not significant
8720	PBX4	1.01	3.37E-01	6.05E-01	128.63	not significant
8721	OCEL1	1.01	2.83E-01	NA	79.58	not significant
8722	PCDHGA11	1.01	1.71E-01	NA	47.13	not significant
8723	NUP37	1.01	5.43E-01	7.64E-01	1927.39	not significant
8724	CDCA5	1.01	4.52E-01	7.01E-01	6891.67	not significant
8725	GSTO1	1.01	5.29E-01	7.56E-01	2600.26	not significant
8726	RABL6	1.01	4.95E-01	7.33E-01	3146.38	not significant
8727	GSDMB	1.01	5.09E-01	7.43E-01	565.88	not significant
8728	RABGAP1L	1.01	5.24E-01	7.52E-01	800.60	not significant
8729	ATP5S	1.01	4.51E-01	7.00E-01	241.99	not significant
8730	CDH23	1.01	2.31E-01	NA	65.92	not significant
8731	FLJ20021	1.01	9.01E-02	NA	31.00	not significant
8732	CROCCP3	1.01	2.17E-01	NA	57.24	not significant
8733	LOC100132356	1.01	6.62E-02	NA	25.60	not significant
8734	LOC93622	1.01	5.00E-01	7.36E-01	948.20	not significant
8735	TMBIM1	1.01	5.13E-01	7.45E-01	468.36	not significant
8736	ALG9	1.01	5.08E-01	7.42E-01	582.64	not significant
8737	ERV3-1	1.01	4.54E-01	7.03E-01	313.44	not significant
8738	PJA1	1.01	4.69E-01	7.14E-01	297.29	not significant
8739	PQLC2	1.01	3.25E-01	5.94E-01	111.29	not significant
8740	CACNA1D	1.01	3.86E-01	6.48E-01	145.81	not significant
8741	DDX50	1.01	4.77E-01	7.19E-01	2824.84	not significant
8742	FAM111B	1.01	5.00E-01	7.36E-01	1221.43	not significant
8743	DMXL2	1.01	5.14E-01	7.46E-01	1494.48	not significant
8744	CAMTA2	1.01	5.17E-01	7.47E-01	1280.50	not significant
8745	TRIM8	1.01	5.13E-01	7.45E-01	915.09	not significant
8746	NICN1	1.01	5.11E-01	7.44E-01	518.64	not significant
8747	NCKAP1	1.01	5.12E-01	7.45E-01	465.50	not significant
8748	IFI27L1	1.01	4.61E-01	7.08E-01	274.52	not significant
8749	AARD	1.01	4.37E-01	6.90E-01	216.59	not significant
8750	LINC00263	1.01	3.43E-01	6.10E-01	120.66	not significant
8751	ZNF582-AS1	1.01	2.74E-01	NA	84.52	not significant
8752	TRIM16L	1.01	1.74E-01	NA	48.15	not significant
8753	CSTF3-AS1	1.01	1.55E-01	NA	51.78	not significant
8754	ZNF135	1.01	1.10E-01	NA	37.46	not significant
8755	DCP2	1.01	4.52E-01	7.01E-01	5984.75	not significant
8756	AFG3L1P	1.01	5.21E-01	7.51E-01	905.06	not significant
8757	NFU1	1.01	5.09E-01	7.43E-01	680.87	not significant
8758	ARNT	1.01	4.99E-01	7.36E-01	1319.81	not significant
8759	RPS16	1.01	4.93E-01	7.32E-01	17059.28	not significant
8760	ENOSF1	1.01	4.63E-01	7.09E-01	1174.18	not significant
8761	ZNF382	1.01	4.89E-01	7.28E-01	395.90	not significant
8762	FAM171A2	1.01	3.56E-01	6.22E-01	138.96	not significant
8763	KIAA1875	1.01	1.37E-01	NA	40.87	not significant
8764	IZUMO4	1.01	1.24E-01	NA	39.60	not significant
8765	TMED10	1.01	4.17E-01	6.73E-01	14219.09	not significant
8766	SMYD4	1.01	5.29E-01	7.56E-01	1432.18	not significant
8767	TMF1	1.01	5.13E-01	7.45E-01	1698.13	not significant
8768	GHDC	1.01	5.18E-01	7.48E-01	790.15	not significant
8769	COG1	1.01	4.87E-01	7.27E-01	1391.96	not significant
8770	HMBOX1	1.01	4.99E-01	7.36E-01	644.69	not significant
8771	RDM1	1.01	7.55E-02	NA	28.64	not significant
8772	PRSS53	1.01	3.83E-01	6.46E-01	160.60	not significant
8773	IFNGR2	1.01	4.19E-01	6.75E-01	239.42	not significant
8774	SMIM4	1.01	3.62E-01	6.26E-01	144.27	not significant
8775	CEACAM1	1.01	2.41E-01	NA	73.67	not significant
8776	ZFHX2	1.01	3.18E-01	5.88E-01	121.79	not significant
8777	EIF4B	1.01	4.20E-01	6.75E-01	14632.09	not significant
8778	TANGO2	1.01	5.19E-01	7.49E-01	792.36	not significant
8779	VPS52	1.01	5.11E-01	7.44E-01	602.72	not significant
8780	AKTIP	1.01	4.74E-01	7.17E-01	325.78	not significant
8781	ZNF280C	1.01	4.86E-01	7.26E-01	430.77	not significant
8782	PLEKHM1P	1.01	4.68E-01	7.13E-01	395.29	not significant
8783	TMEM163	1.01	4.42E-01	6.93E-01	288.68	not significant
8784	RETN	1.01	4.08E-01	6.66E-01	187.14	not significant
8785	SPSB4	1.01	2.91E-01	NA	92.43	not significant
8786	CBR3	1.01	1.81E-01	NA	63.72	not significant
8787	ANXA5	1.01	4.89E-01	7.28E-01	3481.83	not significant

8788	UQCRB	1.01	5.10E-01	7.44E-01	3898.17	not significant
8789	ECE1	1.01	4.95E-01	7.33E-01	2292.27	not significant
8790	TP53I11	1.01	4.97E-01	7.34E-01	1510.19	not significant
8791	SAP30	1.01	5.03E-01	7.39E-01	754.88	not significant
8792	C10orf35	1.01	4.38E-01	6.90E-01	233.54	not significant
8793	MACF1	1.01	4.67E-01	7.12E-01	9333.22	not significant
8794	TERT	1.01	3.45E-01	6.12E-01	127.78	not significant
8795	LINC00920	1.01	2.92E-01	NA	97.75	not significant
8796	LOC100507373	1.01	2.80E-01	NA	86.79	not significant
8797	CHURC1	1.01	5.04E-01	7.39E-01	1260.73	not significant
8798	MZT2B	1.01	5.17E-01	7.47E-01	2964.84	not significant
8799	SNX13	1.01	5.13E-01	7.45E-01	1231.14	not significant
8800	TMEM55A	1.01	4.66E-01	7.12E-01	376.74	not significant
8801	VMAC	1.01	2.69E-01	NA	96.38	not significant
8802	RBBP8	1.01	4.67E-01	7.12E-01	4357.62	not significant
8803	RNF113A	1.01	5.04E-01	7.39E-01	704.06	not significant
8804	ZCCHC8	1.01	4.35E-01	6.88E-01	1835.32	not significant
8805	RPL31	1.01	4.59E-01	7.06E-01	12655.61	not significant
8806	ZBTB49	1.01	4.57E-01	7.05E-01	297.95	not significant
8807	GABPB1-AS1	1.01	3.93E-01	6.54E-01	188.89	not significant
8808	RWDD2A	1.01	2.45E-01	NA	76.75	not significant
8809	LINC00969	1.01	6.66E-02	NA	31.93	not significant
8810	BCL2A1	1.01	1.22E-01	NA	39.40	not significant
8811	HCN3	1.01	1.95E-02	NA	16.68	not significant
8812	CDC6	1.01	4.50E-01	6.99E-01	4397.52	not significant
8813	RPL39L	1.01	5.79E-01	7.88E-01	895.27	not significant
8814	BCAP29	1.01	4.86E-01	7.26E-01	2115.20	not significant
8815	RMDN1	1.01	5.11E-01	7.44E-01	1327.35	not significant
8816	ITFG1	1.01	5.12E-01	7.44E-01	1358.76	not significant
8817	TRO	1.01	4.93E-01	7.32E-01	555.67	not significant
8818	BTN2A3P	1.01	2.55E-01	NA	84.20	not significant
8819	CHD5	1.01	2.79E-01	NA	97.11	not significant
8820	LOC100499489	1.01	2.54E-01	NA	87.33	not significant
8821	CARD8	1.01	5.04E-01	7.39E-01	1661.85	not significant
8822	NOL3	1.01	2.44E-01	NA	76.91	not significant
8823	TTC7A	1.01	4.66E-01	7.11E-01	5589.51	not significant
8824	FBXO7	1.01	4.68E-01	7.12E-01	3294.65	not significant
8825	TRNT1	1.01	5.17E-01	7.47E-01	1349.39	not significant
8826	KDM3B	1.01	4.68E-01	7.12E-01	3849.03	not significant
8827	BRD9	1.01	4.82E-01	7.23E-01	2283.11	not significant
8828	CASZ1	1.01	4.82E-01	7.23E-01	548.60	not significant
8829	CBR1	1.01	4.93E-01	7.32E-01	589.08	not significant
8830	ZNF780B	1.01	4.90E-01	7.29E-01	685.88	not significant
8831	NDN	1.01	4.84E-01	7.24E-01	468.05	not significant
8832	WDR13	1.01	3.89E-01	6.50E-01	191.29	not significant
8833	LOC554206	1.01	3.85E-02	NA	21.36	not significant
8834	LOC101928865	1.01	1.77E-01	NA	53.67	not significant
8835	CXorf65	1.01	1.97E-01	NA	67.00	not significant
8836	OAZ1	1.01	6.15E-01	8.11E-01	23145.99	not significant
8837	ELOVL1	1.01	4.81E-01	7.22E-01	2174.37	not significant
8838	PSMG3	1.01	5.10E-01	7.44E-01	1740.71	not significant
8839	WIBG	1.01	4.87E-01	7.27E-01	699.18	not significant
8840	TRAF3IP2-AS1	1.01	4.80E-01	7.22E-01	446.45	not significant
8841	KCNK12	1.01	3.22E-02	NA	20.43	not significant
8842	TMC6	1.01	4.72E-01	7.15E-01	2897.46	not significant
8843	ABHD10	1.01	4.57E-01	7.05E-01	1907.25	not significant
8844	CAMK2D	1.01	5.04E-01	7.39E-01	927.26	not significant
8845	ATP8B3	1.01	4.96E-01	7.33E-01	785.79	not significant
8846	LIAS	1.01	5.03E-01	7.38E-01	610.09	not significant
8847	PAX8	1.01	3.95E-01	6.54E-01	194.82	not significant
8848	GNRH1	1.01	2.46E-01	NA	84.45	not significant
8849	ASB3	1.01	1.73E-01	NA	58.41	not significant
8850	TXNDC5	1.01	1.43E-01	NA	49.17	not significant
8851	IQGAP1	1.01	4.79E-01	7.21E-01	12727.64	not significant
8852	SELK	1.01	5.00E-01	7.36E-01	1093.88	not significant
8853	UCK1	1.01	4.66E-01	7.11E-01	1245.64	not significant
8854	GRHPR	1.01	5.00E-01	7.36E-01	1295.73	not significant
8855	NDST3	1.01	4.97E-01	7.35E-01	1467.61	not significant
8856	TMEM134	1.01	4.80E-01	7.22E-01	597.72	not significant
8857	N4BP3	1.01	1.15E-01	NA	38.89	not significant
8858	LINC00998	1.01	4.99E-01	7.36E-01	1071.99	not significant
8859	NDUFA3	1.01	4.92E-01	7.31E-01	753.02	not significant
8860	RPL36	1.01	4.55E-01	7.04E-01	13651.03	not significant
8861	ASPHD2	1.01	4.19E-01	6.75E-01	242.63	not significant
8862	HIVEP1	1.01	3.95E-01	6.55E-01	219.92	not significant
8863	NEURL2	1.01	6.21E-02	NA	30.93	not significant
8864	CD2BP2	1.01	4.76E-01	7.18E-01	3309.89	not significant
8865	HIP1R	1.01	4.44E-01	6.95E-01	3400.63	not significant
8866	KCTD17	1.01	4.58E-01	7.05E-01	523.93	not significant
8867	ESYT1	1.01	4.21E-01	6.76E-01	12651.24	not significant
8868	GGA3	1.01	4.49E-01	6.99E-01	4155.15	not significant
8869	NUP160	1.01	4.35E-01	6.88E-01	6242.87	not significant
8870	SYNRG	1.01	4.50E-01	6.99E-01	3377.05	not significant
8871	KDM2B	1.01	4.94E-01	7.32E-01	1070.17	not significant
8872	GPR63	1.01	4.91E-01	7.30E-01	824.30	not significant
8873	TBC1D8	1.01	4.66E-01	7.12E-01	475.42	not significant
8874	GZMB	1.01	4.22E-01	6.77E-01	245.42	not significant
8875	ERCC5	1.01	2.31E-01	NA	76.57	not significant

8876	PABPC4	1.01	3.94E-01	6.54E-01	8032.95	not significant
8877	HTATSF1	1.01	4.34E-01	6.88E-01	5191.95	not significant
8878	TMSB10	1.01	6.18E-01	8.14E-01	16707.29	not significant
8879	PRIM2	1.01	4.68E-01	7.12E-01	1240.16	not significant
8880	B3GALTL	1.01	4.91E-01	7.30E-01	1164.77	not significant
8881	ARL13B	1.01	4.84E-01	7.25E-01	640.82	not significant
8882	IKZF1	1.01	4.71E-01	7.15E-01	11846.15	not significant
8883	WDR26	1.01	4.38E-01	6.90E-01	4768.97	not significant
8884	VPS18	1.01	4.90E-01	7.29E-01	928.18	not significant
8885	ZNF841	1.01	4.67E-01	7.12E-01	437.46	not significant
8886	RHBDD2	1.01	4.26E-01	6.80E-01	303.06	not significant
8887	LITAF	1.01	3.22E-01	5.92E-01	581.88	not significant
8888	COL6A4P1	1.01	3.39E-02	NA	22.33	not significant
8889	ZAP70	1.01	3.77E-01	6.42E-01	9759.23	not significant
8890	NEK7	1.01	4.23E-01	6.78E-01	5308.33	not significant
8891	AP2A1	1.01	4.47E-01	6.97E-01	3273.33	not significant
8892	LRRC75A-AS1	1.01	4.42E-01	6.93E-01	17251.08	not significant
8893	MAN1A1	1.01	4.48E-01	6.98E-01	5154.01	not significant
8894	CLDND1	1.01	5.33E-01	7.59E-01	1743.59	not significant
8895	KIF24	1.01	4.78E-01	7.20E-01	827.33	not significant
8896	STX3	1.01	8.39E-02	NA	33.91	not significant
8897	LOC100129518	1.01	7.62E-02	NA	33.78	not significant
8898	HAPLN3	1.01	7.87E-02	NA	40.16	not significant
8899	AARS	1.01	3.73E-01	6.38E-01	9302.39	not significant
8900	CXXC1	1.01	4.54E-01	7.03E-01	2861.39	not significant
8901	TAF10	1.01	4.85E-01	7.26E-01	2062.61	not significant
8902	INSIG2	1.01	4.76E-01	7.18E-01	628.62	not significant
8903	DLG4	1.01	4.72E-01	7.15E-01	740.18	not significant
8904	RPL32	1.01	4.47E-01	6.97E-01	16534.04	not significant
8905	LOC284023	1.01	4.08E-01	6.66E-01	242.69	not significant
8906	B3GNT1	1.01	4.26E-01	6.80E-01	293.33	not significant
8907	LINC00999	1.01	2.25E-01	NA	79.54	not significant
8908	SLC25A25	1.01	4.86E-01	7.26E-01	1009.62	not significant
8909	PIP4K2C	1.01	4.79E-01	7.21E-01	1133.00	not significant
8910	ZNF777	1.01	4.82E-01	7.22E-01	679.47	not significant
8911	CERS4	1.01	2.81E-01	5.52E-01	103.11	not significant
8912	ZFYVE20	1.01	4.59E-01	7.06E-01	473.54	not significant
8913	HIST1H3B	1.01	6.66E-02	NA	34.53	not significant
8914	OLFM2	1.01	1.27E-01	NA	51.05	not significant
8915	ATP6V0D1	1.01	4.73E-01	7.16E-01	1586.45	not significant
8916	CASKIN2	1.01	4.81E-01	7.22E-01	1505.14	not significant
8917	CCDC101	1.01	3.81E-01	6.45E-01	802.02	not significant
8918	C19orf52	1.01	4.80E-01	7.22E-01	616.48	not significant
8919	ZNF610	1.01	3.56E-01	6.21E-01	185.37	not significant
8920	MCM2	1.01	3.85E-01	6.47E-01	17554.91	not significant
8921	SLC43A3	1.01	3.93E-01	6.54E-01	10683.92	not significant
8922	SDCBP	1.01	4.56E-01	7.05E-01	2612.85	not significant
8923	NQO2	1.01	4.92E-01	7.30E-01	632.55	not significant
8924	FAM171A1	1.01	3.25E-01	5.93E-01	139.12	not significant
8925	CNNM2	1.01	3.14E-01	5.85E-01	128.85	not significant
8926	PDE7A	1.01	3.91E-01	6.52E-01	5796.38	not significant
8927	CGGBP1	1.01	3.69E-01	6.33E-01	7690.19	not significant
8928	XPNPEP1	1.01	4.28E-01	6.82E-01	3350.77	not significant
8929	CMTR1	1.01	4.36E-01	6.88E-01	3842.83	not significant
8930	ORC3	1.01	4.58E-01	7.05E-01	1261.47	not significant
8931	MED23	1.01	4.49E-01	6.99E-01	1943.81	not significant
8932	LOC728554	1.01	4.03E-01	6.62E-01	264.46	not significant
8933	TAPBP	1.01	4.70E-01	7.14E-01	870.99	not significant
8934	ZNF521	1.01	4.90E-02	NA	28.16	not significant
8935	MRPL53	1.01	4.62E-01	7.09E-01	718.90	not significant
8936	TMEM168	1.01	4.58E-01	7.05E-01	914.89	not significant
8937	RPL39	1.01	4.74E-01	7.17E-01	500.29	not significant
8938	ANKS3	1.01	4.17E-01	6.73E-01	299.10	not significant
8939	ZNF75D	1.01	8.45E-02	NA	38.53	not significant
8940	UPF3B	1.01	4.56E-01	7.05E-01	1312.58	not significant
8941	TAL1	1.01	4.40E-01	6.92E-01	361.76	not significant
8942	ZNF818P	1.01	3.96E-01	6.56E-01	261.99	not significant
8943	CFL2	1.01	4.14E-01	6.72E-01	289.62	not significant
8944	LOC100130476	1.01	1.89E-01	NA	68.59	not significant
8945	OST4	1.01	4.25E-01	6.79E-01	2887.74	not significant
8946	ETAA1	1.01	4.72E-01	7.15E-01	967.81	not significant
8947	CCDC115	1.01	4.65E-01	7.11E-01	873.37	not significant
8948	FAM110C	1.01	3.74E-01	6.39E-01	222.44	not significant
8949	STK17B	1.01	3.85E-01	6.47E-01	9725.63	not significant
8950	FBXW5	1.01	4.61E-01	7.08E-01	1661.78	not significant
8951	PRUNE	1.01	4.70E-01	7.14E-01	1067.02	not significant
8952	DEAF1	1.01	4.69E-01	7.14E-01	1092.84	not significant
8953	AP4E1	1.01	4.71E-01	7.15E-01	959.12	not significant
8954	SMAGP	1.01	4.29E-01	6.82E-01	365.08	not significant
8955	KATNAL1	1.01	4.71E-01	7.14E-01	853.48	not significant
8956	IGSF3	1.01	4.55E-01	7.04E-01	524.67	not significant
8957	NAPRT	1.01	4.41E-01	6.92E-01	453.47	not significant
8958	PTCD2	1.01	4.11E-01	6.69E-01	327.34	not significant
8959	BCORP1	1.01	3.85E-01	6.47E-01	242.28	not significant
8960	APCDD1	1.01	1.01E-01	NA	42.19	not significant
8961	FBXL8	1.01	2.02E-01	NA	75.81	not significant
8962	TMBIM6	1.01	3.20E-01	5.89E-01	32306.96	not significant
8963	BCL10	1.01	4.70E-01	7.14E-01	789.21	not significant

8964	TPTEP1	1.01	4.59E-01	7.06E-01	656.15	not significant
8965	CA5B	1.01	3.23E-01	5.93E-01	161.27	not significant
8966	LTB4R2	1.01	2.46E-01	NA	98.32	not significant
8967	DUT	1.02	4.80E-01	7.22E-01	5803.60	not significant
8968	PDIA6	1.02	3.28E-01	5.96E-01	13288.61	not significant
8969	BCL7B	1.02	4.50E-01	6.99E-01	682.95	not significant
8970	CRAMP1L	1.02	4.64E-01	7.11E-01	1636.66	not significant
8971	S100A10	1.02	4.08E-01	6.66E-01	350.82	not significant
8972	CLN5	1.02	3.56E-01	6.21E-01	555.55	not significant
8973	SPRYD4	1.02	4.06E-01	6.65E-01	296.14	not significant
8974	KIAA1841	1.02	3.81E-01	6.45E-01	211.40	not significant
8975	RAB43	1.02	1.69E-01	NA	63.52	not significant
8976	CELF6	1.02	2.60E-01	5.29E-01	124.30	not significant
8977	TIGD6	1.02	3.02E-01	5.72E-01	130.02	not significant
8978	DNASE1L2	1.02	2.26E-01	NA	89.72	not significant
8979	NPHP3-ACAD11	1.02	8.06E-02	NA	39.05	not significant
8980	ATP6V0E1	1.02	4.31E-01	6.84E-01	2518.07	not significant
8981	ERP44	1.02	4.56E-01	7.04E-01	2222.13	not significant
8982	POF1B	1.02	4.44E-01	6.95E-01	556.88	not significant
8983	SUMF1	1.02	3.62E-01	6.26E-01	196.27	not significant
8984	WASH2P	1.02	2.47E-01	5.15E-01	100.76	not significant
8985	COX7B	1.02	4.61E-01	7.08E-01	1846.62	not significant
8986	RPS6KB2	1.02	4.00E-01	6.60E-01	2172.03	not significant
8987	MOGS	1.02	4.60E-01	7.07E-01	1949.09	not significant
8988	CASP6	1.02	4.63E-01	7.09E-01	1004.31	not significant
8989	MBOAT2	1.02	4.36E-01	6.89E-01	1257.27	not significant
8990	IFIT5	1.02	4.59E-01	7.06E-01	737.24	not significant
8991	C15orf57	1.02	4.21E-01	6.76E-01	310.18	not significant
8992	CLDN15	1.02	4.52E-01	7.01E-01	649.64	not significant
8993	MPPE1	1.02	4.37E-01	6.90E-01	483.38	not significant
8994	DSTN	1.02	4.47E-01	6.97E-01	2477.65	not significant
8995	LSM7	1.02	4.62E-01	7.09E-01	2056.98	not significant
8996	SAMD9	1.02	4.20E-01	6.75E-01	2605.93	not significant
8997	RUNX2	1.02	4.11E-01	6.69E-01	1762.68	not significant
8998	TRMT11	1.02	4.57E-01	7.05E-01	835.67	not significant
8999	KAT2B	1.02	3.77E-01	6.42E-01	263.48	not significant
9000	CLYBL	1.02	2.43E-01	NA	100.36	not significant
9001	COX7C	1.02	4.40E-01	6.92E-01	5277.46	not significant
9002	COPE	1.02	4.15E-01	6.72E-01	4899.57	not significant
9003	NIT2	1.02	4.58E-01	7.05E-01	1145.61	not significant
9004	MRI1	1.02	4.46E-01	6.96E-01	1377.27	not significant
9005	CPOX	1.02	4.40E-01	6.92E-01	1476.83	not significant
9006	C20orf196	1.02	4.34E-01	6.88E-01	323.03	not significant
9007	TUG1	1.02	4.27E-01	6.81E-01	8601.37	not significant
9008	A1BG-AS1	1.02	4.11E-01	6.69E-01	308.83	not significant
9009	ATP2A1	1.02	3.89E-01	6.50E-01	283.61	not significant
9010	RPL41	1.02	2.45E-01	5.13E-01	3270.91	not significant
9011	CENPH	1.02	4.58E-01	7.05E-01	1876.14	not significant
9012	VPS8	1.02	4.58E-01	7.05E-01	787.60	not significant
9013	LAGE3	1.02	4.12E-01	6.70E-01	447.24	not significant
9014	SAYSD1	1.02	4.36E-01	6.89E-01	596.85	not significant
9015	USP20	1.02	3.57E-01	6.22E-01	7041.92	not significant
9016	SLC39A6	1.02	4.03E-01	6.62E-01	4394.14	not significant
9017	CENPV	1.02	4.19E-01	6.75E-01	2588.57	not significant
9018	DHX35	1.02	4.67E-01	7.12E-01	1563.26	not significant
9019	CHPF2	1.02	4.50E-01	6.99E-01	1639.31	not significant
9020	IL27RA	1.02	4.25E-01	6.79E-01	2350.79	not significant
9021	ZIC2	1.02	7.68E-02	NA	39.28	not significant
9022	IRF2BP2	1.02	4.08E-01	6.66E-01	3559.48	not significant
9023	STMN3	1.02	4.23E-01	6.78E-01	2353.43	not significant
9024	LAMTOR1	1.02	4.42E-01	6.93E-01	2302.18	not significant
9025	ARID1B	1.02	4.50E-01	6.99E-01	3951.12	not significant
9026	BACH1	1.02	4.40E-01	6.92E-01	1430.30	not significant
9027	PPCS	1.02	4.39E-01	6.91E-01	671.36	not significant
9028	MON2	1.02	3.86E-01	6.48E-01	2247.80	not significant
9029	C18orf21	1.02	4.34E-01	6.88E-01	695.20	not significant
9030	SRRM2	1.02	4.25E-01	6.79E-01	27895.03	not significant
9031	FBXL15	1.02	3.82E-01	6.45E-01	262.71	not significant
9032	SLC38A7	1.02	4.20E-01	6.75E-01	522.28	not significant
9033	SZT2	1.02	2.60E-01	5.30E-01	1754.95	not significant
9034	VLDLR-AS1	1.02	3.64E-02	NA	29.33	not significant
9035	ANXA11	1.02	4.22E-01	6.77E-01	3052.78	not significant
9036	ABCD3	1.02	3.98E-01	6.58E-01	3974.00	not significant
9037	DHX40	1.02	4.21E-01	6.76E-01	2123.08	not significant
9038	B3GALT6	1.02	4.41E-01	6.93E-01	1384.16	not significant
9039	RPA3OS	1.02	4.50E-01	6.99E-01	789.79	not significant
9040	KBTBD7	1.02	4.19E-01	6.75E-01	557.99	not significant
9041	NPIPB3	1.02	3.37E-01	6.05E-01	196.26	not significant
9042	GNAO1	1.02	3.03E-01	5.75E-01	151.97	not significant
9043	TIGD7	1.02	1.32E-01	NA	54.10	not significant
9044	ACRBP	1.02	1.97E-02	NA	22.65	not significant
9045	RHOA	1.02	4.97E-01	7.35E-01	19092.74	not significant
9046	ECT2	1.02	4.05E-01	6.64E-01	3043.35	not significant
9047	PSMA7	1.02	4.08E-01	6.66E-01	7185.53	not significant
9048	ZNF598	1.02	4.05E-01	6.63E-01	2946.99	not significant
9049	ELP2	1.02	4.47E-01	6.97E-01	1469.46	not significant
9050	BRI3BP	1.02	4.42E-01	6.93E-01	1634.23	not significant
9051	RNF24	1.02	4.48E-01	6.98E-01	1679.91	not significant

9052	ATPAF2	1.02	4.22E-01	6.76E-01	458.92	not significant
9053	ZNF284	1.02	3.07E-01	5.78E-01	156.52	not significant
9054	LOC153684	1.02	1.55E-01	NA	65.42	not significant
9055	TMPPE	1.02	2.57E-01	5.25E-01	152.89	not significant
9056	DLGAP1-AS1	1.02	1.13E-01	NA	57.46	not significant
9057	EIF2S3	1.02	3.30E-01	5.98E-01	7986.09	not significant
9058	RPL3	1.02	3.80E-01	6.44E-01	38612.96	not significant
9059	DNMT3A	1.02	3.93E-01	6.53E-01	3849.65	not significant
9060	TRAPPC2L	1.02	4.46E-01	6.96E-01	969.12	not significant
9061	EPN1	1.02	4.10E-01	6.68E-01	2547.89	not significant
9062	ZNF346	1.02	4.48E-01	6.98E-01	1070.41	not significant
9063	HGSNAT	1.02	4.45E-01	6.96E-01	1377.28	not significant
9064	THOC3	1.02	4.19E-01	6.75E-01	427.24	not significant
9065	DGAT2	1.02	3.40E-01	6.08E-01	201.05	not significant
9066	PECR	1.02	1.35E-01	NA	59.81	not significant
9067	RPA2	1.02	4.07E-01	6.65E-01	4988.62	not significant
9068	ZC3H7A	1.02	4.11E-01	6.69E-01	2733.34	not significant
9069	CHD2	1.02	3.95E-01	6.55E-01	2719.87	not significant
9070	PANX1	1.02	4.43E-01	6.93E-01	1550.13	not significant
9071	POMT1	1.02	3.25E-01	5.94E-01	584.31	not significant
9072	RBBP7	1.02	3.25E-01	5.93E-01	8726.58	not significant
9073	XRN2	1.02	3.24E-01	5.93E-01	8040.10	not significant
9074	MAGED2	1.02	4.95E-01	7.33E-01	2051.48	not significant
9075	MIEN1	1.02	4.72E-01	7.15E-01	1599.70	not significant
9076	FNTA	1.02	4.25E-01	6.79E-01	2116.12	not significant
9077	MBD6	1.02	3.97E-01	6.56E-01	2055.24	not significant
9078	INTS4	1.02	4.42E-01	6.93E-01	1173.63	not significant
9079	TRAIP	1.02	4.24E-01	6.78E-01	897.39	not significant
9080	ZNF414	1.02	4.15E-01	6.72E-01	502.37	not significant
9081	DHRS7B	1.02	3.65E-01	6.29E-01	240.99	not significant
9082	VCPKMT	1.02	2.53E-01	5.21E-01	575.38	not significant
9083	ZNF441	1.02	3.38E-01	6.06E-01	197.25	not significant
9084	NEDD4L	1.02	2.78E-01	5.48E-01	141.80	not significant
9085	TMEM19	1.02	5.02E-01	7.38E-01	1732.80	not significant
9086	PLEKHO1	1.02	4.45E-01	6.96E-01	1012.91	not significant
9087	GORAB	1.02	4.22E-01	6.77E-01	489.79	not significant
9088	PCDH12	1.02	2.13E-01	NA	93.05	not significant
9089	MTA3	1.02	4.08E-01	6.66E-01	2428.99	not significant
9090	UFD1L	1.02	4.18E-01	6.73E-01	2883.05	not significant
9091	ZZEF1	1.02	4.23E-01	6.77E-01	3500.58	not significant
9092	APOBEC3C	1.02	4.28E-01	6.82E-01	1829.49	not significant
9093	KRI1	1.02	4.11E-01	6.69E-01	2172.91	not significant
9094	RPL24	1.02	4.07E-01	6.65E-01	10559.59	not significant
9095	KLRG1	1.02	1.06E-01	NA	51.71	not significant
9096	CHAF1A	1.02	3.80E-01	6.45E-01	5239.24	not significant
9097	RFC2	1.02	4.17E-01	6.73E-01	2009.86	not significant
9098	KLHL7	1.02	4.37E-01	6.90E-01	1436.91	not significant
9099	RUSC1	1.02	4.00E-01	6.59E-01	1245.07	not significant
9100	RELT	1.02	4.38E-01	6.90E-01	1017.09	not significant
9101	TRIM4	1.02	4.01E-01	6.60E-01	1263.63	not significant
9102	LOC648987	1.02	4.05E-01	6.63E-01	531.67	not significant
9103	LRRC37A4P	1.02	3.41E-01	6.08E-01	1890.58	not significant
9104	ZXDA	1.02	3.07E-01	5.78E-01	177.82	not significant
9105	PTOV1	1.02	4.02E-01	6.61E-01	3619.87	not significant
9106	TMEM26	1.02	4.37E-01	6.89E-01	949.33	not significant
9107	ABCB6	1.02	4.15E-01	6.72E-01	451.98	not significant
9108	FAM184A	1.02	3.73E-01	6.38E-01	300.34	not significant
9109	PET100	1.02	2.73E-01	5.43E-01	594.28	not significant
9110	ZKSCAN7	1.02	2.77E-01	5.47E-01	156.81	not significant
9111	DIAPH1	1.02	3.62E-01	6.26E-01	17916.97	not significant
9112	ZDHHC2	1.02	4.09E-01	6.67E-01	2062.21	not significant
9113	CIR1	1.02	4.36E-01	6.89E-01	904.18	not significant
9114	ATXN7	1.02	5.10E-01	7.44E-01	1267.04	not significant
9115	EEPD1	1.02	4.35E-01	6.88E-01	1146.97	not significant
9116	HSD17B7	1.02	4.02E-01	6.61E-01	403.37	not significant
9117	C5orf34	1.02	3.85E-01	6.47E-01	335.06	not significant
9118	SMIM14	1.02	2.31E-01	4.99E-01	103.23	not significant
9119	EPS15	1.02	4.01E-01	6.60E-01	2775.52	not significant
9120	RTCA	1.02	4.24E-01	6.78E-01	1470.23	not significant
9121	PITPNM2	1.02	4.24E-01	6.79E-01	3256.26	not significant
9122	TMEM120B	1.02	5.20E-01	7.50E-01	1449.60	not significant
9123	KIAA1731	1.02	4.32E-01	6.86E-01	1488.66	not significant
9124	LOC101927027	1.02	4.17E-01	6.73E-01	544.45	not significant
9125	IFT88	1.02	3.78E-01	6.43E-01	342.98	not significant
9126	TAZ	1.02	3.57E-01	6.22E-01	276.54	not significant
9127	ZNF821	1.02	2.49E-02	NA	25.46	not significant
9128	PLCL1	1.02	7.26E-02	NA	41.40	not significant
9129	UBE2R2	1.02	3.65E-01	6.29E-01	4696.92	not significant
9130	ACTL6A	1.02	3.68E-01	6.32E-01	3197.92	not significant
9131	CISD2	1.02	4.31E-01	6.85E-01	1014.69	not significant
9132	NAA16	1.02	4.42E-01	6.93E-01	1667.61	not significant
9133	CES3	1.02	4.21E-01	6.76E-01	583.49	not significant
9134	SH2D3A	1.02	1.49E-01	NA	65.97	not significant
9135	ZKSCAN1	1.02	4.00E-01	6.59E-01	4487.10	not significant
9136	PPP1R16A	1.02	4.28E-01	6.82E-01	791.00	not significant
9137	TSKS	1.02	3.06E-01	5.78E-01	177.26	not significant
9138	KCNG3	1.02	2.52E-01	5.21E-01	125.37	not significant
9139	LOC100289230	1.02	6.10E-02	NA	38.16	not significant

9140	RPUSD4	1.02	4.72E-01	7.15E-01	1354.15	not significant
9141	HNRNPDL	1.02	3.10E-01	5.81E-01	15934.21	not significant
9142	COX15	1.02	4.75E-01	7.17E-01	1898.78	not significant
9143	PAGR1	1.02	4.17E-01	6.73E-01	2290.92	not significant
9144	PSMB10	1.02	4.24E-01	6.78E-01	2409.13	not significant
9145	NDUFB5	1.02	3.77E-01	6.42E-01	2133.42	not significant
9146	NMI	1.02	3.97E-01	6.57E-01	2786.15	not significant
9147	ATP6V1F	1.02	3.84E-01	6.47E-01	2640.50	not significant
9148	HMGXB4	1.02	3.98E-01	6.58E-01	2424.35	not significant
9149	CMC1	1.02	4.26E-01	6.80E-01	883.65	not significant
9150	DCAF8	1.02	3.81E-01	6.45E-01	2661.64	not significant
9151	BMPR1A	1.02	4.02E-01	6.61E-01	415.11	not significant
9152	CCRL2	1.02	3.40E-01	6.07E-01	249.62	not significant
9153	CKB	1.02	2.32E-01	5.00E-01	117.35	not significant
9154	APLF	1.02	2.41E-01	5.10E-01	130.89	not significant
9155	MCF2L2	1.02	1.31E-01	NA	63.91	not significant
9156	KIAA1147	1.02	9.93E-02	NA	37.40	not significant
9157	AARS2	1.02	4.23E-01	6.78E-01	1791.29	not significant
9158	G6PC3	1.02	3.51E-01	6.18E-01	269.84	not significant
9159	FAM174A	1.02	2.90E-01	5.62E-01	158.17	not significant
9160	SLC22A23	1.02	3.41E-01	6.08E-01	248.61	not significant
9161	ATP5E	1.02	1.82E-01	4.39E-01	102.52	not significant
9162	BTF3L4	1.02	3.82E-01	6.46E-01	2410.18	not significant
9163	SPIN1	1.02	3.75E-01	6.39E-01	4284.80	not significant
9164	SYNE1	1.02	4.74E-01	7.17E-01	1245.15	not significant
9165	WRB	1.02	4.15E-01	6.72E-01	921.39	not significant
9166	ZNF319	1.02	4.06E-01	6.65E-01	636.90	not significant
9167	CCDC57	1.02	4.15E-01	6.72E-01	722.77	not significant
9168	SLC7A5	1.02	3.01E-01	5.71E-01	38763.06	not significant
9169	LOC728743	1.02	4.18E-01	6.74E-01	1431.64	not significant
9170	PIGC	1.02	4.21E-01	6.76E-01	1118.71	not significant
9171	TRMT2B	1.02	4.06E-01	6.65E-01	1519.26	not significant
9172	RABEP2	1.02	4.16E-01	6.72E-01	697.53	not significant
9173	SMIM19	1.02	3.72E-01	6.37E-01	363.82	not significant
9174	EMP3	1.02	3.64E-01	6.28E-01	330.38	not significant
9175	SETBP1	1.02	2.70E-01	5.41E-01	144.25	not significant
9176	CD3D	1.02	4.24E-01	6.79E-01	16495.38	not significant
9177	POLR2H	1.02	3.94E-01	6.54E-01	2253.42	not significant
9178	RPS9	1.02	4.03E-01	6.62E-01	6430.65	not significant
9179	GLCE	1.02	1.24E-01	NA	65.16	not significant
9180	PIK3CA	1.02	4.76E-01	7.18E-01	1179.66	not significant
9181	ATG9A	1.02	4.18E-01	6.73E-01	1252.51	not significant
9182	ABTB2	1.02	3.73E-01	6.38E-01	323.63	not significant
9183	CPPED1	1.02	4.13E-01	6.71E-01	1421.25	not significant
9184	LSM6	1.02	4.21E-01	6.76E-01	1588.25	not significant
9185	ZBTB26	1.02	3.73E-01	6.38E-01	333.05	not significant
9186	SP140	1.02	4.16E-01	6.72E-01	653.15	not significant
9187	ZNF175	1.02	4.11E-01	6.69E-01	879.63	not significant
9188	ST3GAL3	1.02	3.63E-01	6.27E-01	317.82	not significant
9189	PHC1	1.02	3.82E-01	6.45E-01	378.46	not significant
9190	PPP2R2D	1.02	3.41E-01	6.08E-01	259.44	not significant
9191	GALC	1.02	3.20E-01	5.89E-01	217.21	not significant
9192	NANOS1	1.02	2.18E-01	4.84E-01	113.59	not significant
9193	RGPD4	1.02	2.44E-02	NA	27.22	not significant
9194	DNAJC9	1.02	3.65E-01	6.30E-01	4971.28	not significant
9195	RAB8B	1.02	3.68E-01	6.33E-01	3952.65	not significant
9196	OXCT1	1.02	3.60E-01	6.25E-01	3838.93	not significant
9197	BABAM1	1.02	3.83E-01	6.46E-01	2283.66	not significant
9198	NAB1	1.02	4.08E-01	6.66E-01	1764.93	not significant
9199	CHD3	1.02	3.85E-01	6.47E-01	3174.78	not significant
9200	FBXW4	1.02	4.17E-01	6.73E-01	956.46	not significant
9201	DDX58	1.02	3.95E-01	6.54E-01	1318.46	not significant
9202	HAUS8	1.02	3.93E-01	6.54E-01	812.12	not significant
9203	SNX16	1.02	3.87E-01	6.48E-01	390.67	not significant
9204	LSAMP	1.02	3.76E-01	6.40E-01	427.66	not significant
9205	MALAT1	1.02	2.04E-01	4.69E-01	7215.43	not significant
9206	MPC2	1.02	3.83E-01	6.46E-01	2550.83	not significant
9207	MIB1	1.02	3.67E-01	6.31E-01	2632.03	not significant
9208	LOC101926963	1.02	2.17E-01	4.83E-01	117.90	not significant
9209	ZFHX3	1.02	3.16E-01	5.86E-01	243.86	not significant
9210	PAFAH1B3	1.02	4.25E-01	6.79E-01	2043.40	not significant
9211	ZFAS1	1.02	4.02E-01	6.61E-01	3701.15	not significant
9212	IFNAR1	1.02	3.79E-01	6.44E-01	3298.24	not significant
9213	IL16	1.02	3.77E-01	6.42E-01	2319.05	not significant
9214	MTHFR	1.02	4.13E-01	6.70E-01	1061.09	not significant
9215	PANK1	1.02	4.11E-01	6.69E-01	868.43	not significant
9216	PTBP2	1.02	4.11E-01	6.69E-01	735.61	not significant
9217	IMMP2L	1.02	3.12E-01	5.83E-01	211.87	not significant
9218	IQGAP2	1.02	3.59E-01	6.24E-01	4644.37	not significant
9219	LRP5	1.02	4.01E-01	6.60E-01	650.04	not significant
9220	RPS6KA5	1.02	3.82E-01	6.45E-01	413.48	not significant
9221	SNHG21	1.02	2.31E-01	4.99E-01	122.02	not significant
9222	ILVBL	1.02	4.38E-01	6.90E-01	1325.82	not significant
9223	CDADC1	1.02	3.80E-01	6.44E-01	556.66	not significant
9224	TRIM45	1.02	1.19E-01	NA	63.74	not significant
9225	KLHDC3	1.02	3.43E-01	6.09E-01	4204.94	not significant
9226	KIAA0391	1.02	3.86E-01	6.48E-01	1760.00	not significant
9227	GPX4	1.02	3.60E-01	6.25E-01	4549.94	not significant

9228	UBXN11	1.02	3.74E-01	6.38E-01	428.92	not significant
9229	SLC17A5	1.02	3.29E-01	5.97E-01	244.79	not significant
9230	CTNNA1	1.02	3.75E-01	6.40E-01	3559.84	not significant
9231	MTMR14	1.02	4.63E-01	7.10E-01	1263.68	not significant
9232	PRPF39	1.02	3.85E-01	6.47E-01	2014.81	not significant
9233	LRCH1	1.02	4.04E-01	6.63E-01	1414.27	not significant
9234	MSH3	1.02	3.70E-01	6.35E-01	1280.92	not significant
9235	DNLZ	1.02	3.94E-01	6.54E-01	691.75	not significant
9236	SLC2A13	1.02	3.56E-01	6.21E-01	379.05	not significant
9237	OTX1	1.02	2.63E-01	5.34E-01	150.37	not significant
9238	PLEKHM1	1.02	3.87E-01	6.49E-01	1408.96	not significant
9239	ARNTL	1.02	3.79E-01	6.44E-01	432.13	not significant
9240	RGCC	1.02	3.50E-01	6.17E-01	510.24	not significant
9241	KIAA0226L	1.02	3.91E-01	6.52E-01	556.94	not significant
9242	C1RL	1.02	2.71E-01	5.42E-01	162.74	not significant
9243	ISL2	1.02	2.95E-01	5.66E-01	201.18	not significant
9244	USP30-AS1	1.02	1.93E-01	4.54E-01	111.32	not significant
9245	SF3B5	1.02	3.92E-01	6.53E-01	3868.33	not significant
9246	DERA	1.02	3.98E-01	6.58E-01	855.51	not significant
9247	PTPRN2	1.02	3.98E-01	6.58E-01	852.43	not significant
9248	ILDR2	1.02	3.91E-01	6.52E-01	661.40	not significant
9249	GPR153	1.02	3.44E-01	6.10E-01	280.93	not significant
9250	FUK	1.02	3.72E-01	6.37E-01	390.78	not significant
9251	SCNN1D	1.02	2.00E-01	4.64E-01	104.61	not significant
9252	IFITM1	1.02	3.35E-01	6.04E-01	5028.07	not significant
9253	NENF	1.02	3.94E-01	6.54E-01	889.12	not significant
9254	DPY19L3	1.02	3.95E-01	6.55E-01	1122.53	not significant
9255	CPNE5	1.02	3.54E-01	6.19E-01	343.51	not significant
9256	RGL2	1.02	3.18E-01	5.87E-01	250.17	not significant
9257	KIAA1109	1.02	3.40E-01	6.08E-01	2291.94	not significant
9258	PRKCQ	1.02	3.53E-01	6.19E-01	1915.01	not significant
9259	EHMT2	1.02	3.62E-01	6.26E-01	2255.36	not significant
9260	SLC15A4	1.02	3.99E-01	6.58E-01	1042.98	not significant
9261	XYLT2	1.02	3.98E-01	6.58E-01	1057.94	not significant
9262	LOC100506469	1.02	2.56E-01	5.25E-01	165.72	not significant
9263	ZNF827	1.02	2.43E-01	5.11E-01	147.59	not significant
9264	DET1	1.02	2.10E-01	4.74E-01	129.54	not significant
9265	MESP1	1.02	6.07E-02	NA	45.57	not significant
9266	KDELR2	1.02	3.54E-01	6.19E-01	3893.97	not significant
9267	FBRSL1	1.02	3.35E-01	6.04E-01	3378.90	not significant
9268	LRRC20	1.02	3.96E-01	6.55E-01	1307.67	not significant
9269	RBBP9	1.02	3.96E-01	6.56E-01	1158.40	not significant
9270	ADAM17	1.02	3.92E-01	6.53E-01	1466.54	not significant
9271	HSDL2	1.02	4.00E-01	6.59E-01	1035.10	not significant
9272	ARL6	1.02	2.09E-01	4.74E-01	120.05	not significant
9273	YPEL3	1.02	9.42E-02	NA	55.51	not significant
9274	NDRG1	1.02	3.54E-01	6.19E-01	2474.39	not significant
9275	RANBP6	1.02	3.58E-01	6.23E-01	2329.26	not significant
9276	KLHL9	1.02	3.85E-01	6.47E-01	2201.73	not significant
9277	TMEM14A	1.02	3.96E-01	6.55E-01	691.49	not significant
9278	SNAPC2	1.02	3.83E-01	6.46E-01	617.59	not significant
9279	GK	1.02	3.20E-01	5.90E-01	308.02	not significant
9280	ADPRM	1.02	2.34E-01	5.01E-01	139.61	not significant
9281	ZNF695	1.02	2.05E-01	4.70E-01	125.17	not significant
9282	DNAJC12	1.02	5.37E-02	NA	43.13	not significant
9283	BCL2	1.02	3.45E-01	6.12E-01	4880.37	not significant
9284	MKKS	1.02	3.84E-01	6.47E-01	1750.34	not significant
9285	LOC101927497	1.02	3.91E-01	6.52E-01	1025.68	not significant
9286	STAG3L5P-PVRIG2	1.02	3.89E-01	6.51E-01	1025.77	not significant
9287	GATAD1	1.02	3.91E-01	6.52E-01	764.08	not significant
9288	LINC00662	1.02	2.30E-01	4.97E-01	129.41	not significant
9289	PTPN6	1.02	3.79E-01	6.44E-01	1834.50	not significant
9290	SCAMP1	1.02	3.84E-01	6.47E-01	1533.57	not significant
9291	APOL1	1.02	3.92E-01	6.53E-01	923.72	not significant
9292	PACS1	1.02	3.94E-01	6.54E-01	950.05	not significant
9293	FBXL12	1.02	3.35E-01	6.04E-01	637.19	not significant
9294	RAB44	1.02	3.09E-01	5.81E-01	322.35	not significant
9295	PCBP1	1.02	2.80E-01	5.51E-01	13232.06	not significant
9296	DLST	1.02	3.34E-01	6.03E-01	3752.67	not significant
9297	ADA	1.02	3.26E-01	5.94E-01	21008.54	not significant
9298	STAT1	1.02	2.85E-01	5.56E-01	6563.20	not significant
9299	LBR	1.02	2.83E-01	5.53E-01	14864.67	not significant
9300	ATP6AP1	1.02	4.04E-01	6.63E-01	661.08	not significant
9301	FAM3A	1.02	2.94E-01	5.65E-01	205.43	not significant
9302	PCYT1B	1.02	3.04E-01	5.76E-01	193.53	not significant
9303	LIG4	1.02	3.50E-01	6.17E-01	2361.70	not significant
9304	LRRC14	1.02	3.79E-01	6.44E-01	1852.15	not significant
9305	POLR2K	1.02	3.87E-01	6.48E-01	2388.93	not significant
9306	TELO2	1.02	3.52E-01	6.19E-01	2313.70	not significant
9307	PDCD10	1.02	3.74E-01	6.38E-01	2257.41	not significant
9308	LCMT1	1.02	3.89E-01	6.51E-01	922.72	not significant
9309	SUCO	1.02	3.82E-01	6.45E-01	2027.91	not significant
9310	FIG4	1.02	2.52E-01	5.21E-01	543.98	not significant
9311	TESC	1.02	3.52E-01	6.19E-01	4969.65	not significant
9312	ARL14EP	1.02	3.87E-01	6.49E-01	885.26	not significant
9313	FUT8-AS1	1.02	8.59E-02	NA	60.09	not significant
9314	CPSF7	1.02	3.00E-01	5.71E-01	6937.50	not significant
9315	PATZ1	1.02	3.52E-01	6.19E-01	2973.32	not significant

9316	NNT	1.02	3.18E-01	5.87E-01	5353.30	not significant
9317	NAT9	1.02	3.87E-01	6.48E-01	995.72	not significant
9318	KMT2B	1.02	3.42E-01	6.09E-01	3546.08	not significant
9319	TMCO3	1.02	3.87E-01	6.48E-01	1117.53	not significant
9320	VPS13D	1.02	3.83E-01	6.46E-01	2189.89	not significant
9321	RUFY2	1.02	3.15E-01	5.86E-01	338.17	not significant
9322	ADRBK1	1.02	2.71E-01	5.41E-01	14045.78	not significant
9323	BSG	1.02	3.18E-01	5.88E-01	10116.67	not significant
9324	TTC39C	1.02	3.84E-01	6.47E-01	872.83	not significant
9325	SIK2	1.02	3.81E-01	6.45E-01	1173.08	not significant
9326	LOC101928710	1.02	2.39E-01	5.07E-01	156.17	not significant
9327	GOLGB1	1.02	3.43E-01	6.10E-01	1996.97	not significant
9328	SAMD1	1.02	3.52E-01	6.19E-01	1345.16	not significant
9329	LACTB2	1.02	3.25E-01	5.93E-01	309.34	not significant
9330	RPS27A	1.02	2.97E-01	5.68E-01	11518.39	not significant
9331	TNK1	1.02	1.17E-01	NA	78.30	not significant
9332	WDR83OS	1.02	3.78E-01	6.43E-01	1481.33	not significant
9333	PAN3	1.02	3.45E-01	6.11E-01	2548.99	not significant
9334	KAT2A	1.02	3.64E-01	6.28E-01	1864.48	not significant
9335	NEDD4	1.02	3.81E-01	6.45E-01	1463.17	not significant
9336	CCHCR1	1.02	3.78E-01	6.43E-01	752.14	not significant
9337	GPATCH2	1.02	3.74E-01	6.38E-01	676.15	not significant
9338	LHX4-AS1	1.02	2.28E-01	4.95E-01	159.23	not significant
9339	C6orf226	1.02	1.74E-01	NA	100.42	not significant
9340	ARHGEF9	1.02	1.91E-01	4.51E-01	115.84	not significant
9341	HAUS1	1.02	3.73E-01	6.38E-01	1921.40	not significant
9342	CWC25	1.02	3.57E-01	6.22E-01	1489.52	not significant
9343	SRBD1	1.02	3.81E-01	6.45E-01	1448.45	not significant
9344	ERG	1.02	3.69E-01	6.34E-01	1363.30	not significant
9345	TYSND1	1.02	3.81E-01	6.45E-01	1022.80	not significant
9346	FAM129A	1.02	3.69E-01	6.33E-01	655.56	not significant
9347	PLP2	1.02	2.67E-01	5.38E-01	559.67	not significant
9348	HSCB	1.02	3.15E-01	5.86E-01	313.80	not significant
9349	C8orf76	1.02	1.97E-01	4.61E-01	115.38	not significant
9350	MTURN	1.02	1.64E-01	NA	97.33	not significant
9351	HCLS1	1.02	3.28E-01	5.96E-01	5100.12	not significant
9352	METAP1	1.02	3.23E-01	5.93E-01	3591.81	not significant
9353	BAG6	1.02	2.98E-01	5.68E-01	4531.05	not significant
9354	GGCT	1.02	3.37E-01	6.05E-01	2396.90	not significant
9355	OTUB1	1.02	3.61E-01	6.26E-01	3043.39	not significant
9356	CDK5	1.02	3.76E-01	6.40E-01	1016.78	not significant
9357	WRAP53	1.02	3.80E-01	6.44E-01	1094.47	not significant
9358	ARL2	1.02	3.13E-01	5.84E-01	409.15	not significant
9359	CLCN2	1.02	2.87E-01	5.58E-01	214.01	not significant
9360	PKD1P1	1.02	3.04E-01	5.76E-01	249.91	not significant
9361	PPP1R11	1.02	2.43E-01	5.11E-01	155.81	not significant
9362	FAM19A2	1.02	2.30E-01	4.98E-01	152.27	not significant
9363	RAB3D	1.02	9.56E-02	NA	61.62	not significant
9364	TVP23C	1.02	1.47E-01	NA	92.64	not significant
9365	HMGN1	1.02	2.93E-01	5.64E-01	11026.82	not significant
9366	USF1	1.02	3.41E-01	6.08E-01	2741.21	not significant
9367	COTL1	1.02	3.43E-01	6.10E-01	7897.23	not significant
9368	DUSP11	1.02	3.78E-01	6.43E-01	915.12	not significant
9369	RNF19A	1.02	3.68E-01	6.33E-01	1527.67	not significant
9370	REEP3	1.02	3.74E-01	6.39E-01	1146.28	not significant
9371	C2CD2L	1.02	3.78E-01	6.43E-01	1048.55	not significant
9372	SLAMF1	1.02	3.53E-01	6.19E-01	429.79	not significant
9373	TK2	1.02	3.13E-01	5.85E-01	273.39	not significant
9374	TMEM238	1.02	2.93E-02	NA	35.42	not significant
9375	TEC	1.02	9.43E-02	NA	62.31	not significant
9376	C1orf112	1.02	3.74E-01	6.38E-01	1373.58	not significant
9377	JAKMIP2	1.02	3.44E-01	6.10E-01	412.18	not significant
9378	NUDT18	1.02	2.91E-01	5.62E-01	245.30	not significant
9379	SPATA7	1.02	2.15E-01	4.81E-01	139.42	not significant
9380	VSIG10	1.02	1.72E-01	4.26E-01	101.83	not significant
9381	CLEC11A	1.02	4.06E-02	NA	38.34	not significant
9382	THOC7	1.02	3.60E-01	6.25E-01	2411.43	not significant
9383	ACSL5	1.02	3.20E-01	5.90E-01	3613.74	not significant
9384	SMCHD1	1.02	3.17E-01	5.87E-01	7698.36	not significant
9385	KIAA1143	1.02	3.64E-01	6.29E-01	1861.79	not significant
9386	PCED1B-AS1	1.02	3.13E-01	5.84E-01	317.24	not significant
9387	VNN2	1.02	2.39E-01	5.07E-01	156.68	not significant
9388	PDCD4-AS1	1.02	1.15E-01	NA	75.56	not significant
9389	IFI16	1.02	2.54E-01	5.23E-01	10351.03	not significant
9390	HNRNPF	1.02	2.24E-01	4.91E-01	20652.23	not significant
9391	FAM208A	1.02	3.17E-01	5.86E-01	4694.09	not significant
9392	AGPAT6	1.02	3.37E-01	6.05E-01	3106.64	not significant
9393	ADCY7	1.02	3.43E-01	6.10E-01	2855.91	not significant
9394	HOXB3	1.02	6.98E-01	8.59E-01	884.52	not significant
9395	FZD2	1.02	1.72E-01	4.26E-01	101.89	not significant
9396	STK19	1.02	1.01E-01	NA	65.56	not significant
9397	GINS3	1.02	4.14E-01	6.71E-01	1415.06	not significant
9398	DBI	1.02	3.27E-01	5.95E-01	4902.95	not significant
9399	RPL30	1.02	3.37E-01	6.05E-01	19829.57	not significant
9400	WBP1L	1.02	3.56E-01	6.21E-01	1754.24	not significant
9401	PMF1	1.02	3.45E-01	6.12E-01	532.06	not significant
9402	RPLP2	1.02	3.53E-01	6.19E-01	19998.72	not significant
9403	LINC00883	1.02	2.23E-01	4.90E-01	151.06	not significant

9404	HLTF	1.02	3.12E-01	5.83E-01	3650.77	not significant
9405	SLC5A3	1.02	3.61E-01	6.26E-01	4986.14	not significant
9406	AZI2	1.02	3.30E-01	5.97E-01	2261.38	not significant
9407	CYB5R1	1.02	3.44E-01	6.11E-01	430.35	not significant
9408	CCR8	1.02	3.31E-01	5.99E-01	523.48	not significant
9409	CA8	1.02	2.59E-01	5.28E-01	223.15	not significant
9410	ZNF823	1.02	3.03E-01	5.75E-01	303.62	not significant
9411	PCID2	1.02	3.26E-01	5.94E-01	3267.85	not significant
9412	MRPS27	1.02	3.23E-01	5.93E-01	3283.50	not significant
9413	YIF1B	1.02	3.53E-01	6.19E-01	1825.56	not significant
9414	RAB28	1.02	3.66E-01	6.30E-01	960.54	not significant
9415	C9orf91	1.02	3.66E-01	6.30E-01	1121.45	not significant
9416	RPL18	1.02	4.58E-01	7.05E-01	17116.00	not significant
9417	LAMTOR4	1.02	3.62E-01	6.26E-01	1058.31	not significant
9418	CCDC120	1.02	1.13E-01	NA	82.26	not significant
9419	BIK	1.02	3.56E-01	6.22E-01	486.50	not significant
9420	COQ7	1.02	2.73E-01	5.44E-01	526.18	not significant
9421	DCBLD2	1.02	3.16E-01	5.86E-01	612.89	not significant
9422	YAE1D1	1.02	2.91E-01	5.62E-01	265.92	not significant
9423	NFKB1	1.02	3.12E-01	5.84E-01	3088.63	not significant
9424	ZMIZ2	1.02	3.23E-01	5.93E-01	3043.97	not significant
9425	DPM2	1.02	3.63E-01	6.27E-01	1162.68	not significant
9426	TMEM135	1.02	3.63E-01	6.27E-01	1792.26	not significant
9427	ZBTB4	1.02	3.69E-01	6.33E-01	1034.12	not significant
9428	GPSM3	1.02	2.74E-01	5.45E-01	218.70	not significant
9429	CLCC1	1.02	3.16E-01	5.86E-01	333.01	not significant
9430	SEC22A	1.02	3.25E-01	5.94E-01	442.95	not significant
9431	CHST7	1.02	2.80E-01	5.51E-01	228.17	not significant
9432	SLC29A4	1.02	1.51E-01	NA	100.20	not significant
9433	TMEM50A	1.02	3.02E-01	5.72E-01	3580.65	not significant
9434	ATP6V1G1	1.02	3.16E-01	5.86E-01	2363.88	not significant
9435	SLC9A8	1.02	3.62E-01	6.26E-01	960.10	not significant
9436	TUBGCP5	1.02	3.60E-01	6.25E-01	741.41	not significant
9437	FAT1	1.02	2.90E-01	5.61E-01	5956.57	not significant
9438	ATP5SL	1.02	2.45E-01	5.12E-01	180.03	not significant
9439	DDX54	1.02	2.50E-01	5.18E-01	6486.67	not significant
9440	CD8A	1.02	2.96E-01	5.67E-01	3779.47	not significant
9441	ZFAND6	1.02	3.64E-01	6.28E-01	1127.28	not significant
9442	ELF4	1.02	3.47E-01	6.14E-01	1786.79	not significant
9443	RPS28	1.02	3.60E-01	6.25E-01	9175.87	not significant
9444	TRIM52	1.02	3.22E-01	5.92E-01	365.64	not significant
9445	SYT11	1.02	1.83E-01	4.41E-01	120.05	not significant
9446	GANC	1.02	3.07E-01	5.78E-01	304.59	not significant
9447	LYRM5	1.02	2.55E-01	5.24E-01	220.55	not significant
9448	ZNF726	1.02	2.44E-01	5.12E-01	185.13	not significant
9449	INTS6-AS1	1.02	9.49E-03	NA	24.84	not significant
9450	ARF6	1.02	2.51E-01	5.19E-01	6645.47	not significant
9451	TSR3	1.02	3.58E-01	6.23E-01	1294.05	not significant
9452	MEF2D	1.02	3.52E-01	6.19E-01	1612.08	not significant
9453	RPS27	1.02	4.51E-01	7.00E-01	11531.12	not significant
9454	EZH2	1.02	2.50E-01	5.19E-01	6487.23	not significant
9455	WARS2	1.02	3.45E-01	6.12E-01	727.38	not significant
9456	GAB1	1.02	4.86E-02	NA	49.47	not significant
9457	RBM39	1.02	2.27E-01	4.95E-01	13539.44	not significant
9458	FOXP4	1.02	3.26E-01	5.94E-01	2866.06	not significant
9459	TRIM68	1.02	3.53E-01	6.19E-01	614.55	not significant
9460	ZNF251	1.02	3.23E-01	5.93E-01	470.56	not significant
9461	TGIF1	1.02	2.87E-01	5.58E-01	263.57	not significant
9462	AGAP6	1.02	1.16E-01	NA	83.62	not significant
9463	MRPS16	1.02	3.02E-01	5.72E-01	4104.14	not significant
9464	NUF2	1.02	3.40E-01	6.08E-01	1930.97	not significant
9465	PAK1	1.02	3.23E-01	5.92E-01	2276.74	not significant
9466	LOC101928378	1.02	2.04E-01	4.69E-01	208.47	not significant
9467	RPN2	1.02	2.27E-01	4.95E-01	17732.82	not significant
9468	LAMP2	1.02	3.15E-01	5.86E-01	3594.15	not significant
9469	RBMX2	1.02	3.39E-01	6.07E-01	1219.96	not significant
9470	RRM2B	1.02	3.49E-01	6.16E-01	780.92	not significant
9471	TMEM42	1.02	2.28E-01	4.95E-01	185.15	not significant
9472	CCDC94	1.02	3.50E-01	6.17E-01	1002.21	not significant
9473	C14orf80	1.02	2.70E-01	5.40E-01	241.05	not significant
9474	PRPF4B	1.02	2.88E-01	5.59E-01	5981.98	not significant
9475	PDE6D	1.02	3.47E-01	6.14E-01	1302.48	not significant
9476	CNPY2	1.02	3.18E-01	5.88E-01	2612.19	not significant
9477	CD81	1.02	3.06E-01	5.78E-01	4662.94	not significant
9478	CCDC167	1.02	3.49E-01	6.16E-01	1438.05	not significant
9479	UBE3B	1.02	3.83E-01	6.46E-01	1666.82	not significant
9480	TEX19	1.02	3.31E-01	5.99E-01	934.44	not significant
9481	TICRR	1.02	3.46E-01	6.12E-01	1883.83	not significant
9482	CENPQ	1.02	2.72E-01	5.42E-01	782.21	not significant
9483	CHAMP1	1.02	1.63E-01	4.14E-01	104.46	not significant
9484	RPL34	1.02	3.30E-01	5.97E-01	6634.45	not significant
9485	ULK1	1.02	2.94E-01	5.65E-01	3602.90	not significant
9486	CDC37L1	1.02	2.47E-01	5.15E-01	212.72	not significant
9487	DBNL	1.02	2.89E-01	5.61E-01	7142.76	not significant
9488	RAB2A	1.02	3.08E-01	5.79E-01	2269.76	not significant
9489	RIN3	1.02	2.95E-01	5.66E-01	2407.31	not significant
9490	CIT	1.02	3.14E-01	5.85E-01	4031.28	not significant
9491	ZNF580	1.02	3.25E-01	5.93E-01	494.94	not significant

9492	EFCAB2	1.02	3.23E-01	5.93E-01	488.38	not significant
9493	RPSA	1.02	3.38E-01	6.06E-01	21963.84	not significant
9494	SLC16A5	1.02	1.19E-01	NA	82.84	not significant
9495	H1FX-AS1	1.02	3.84E-02	NA	43.29	not significant
9496	CPSF4	1.02	3.06E-01	5.78E-01	2176.06	not significant
9497	BLCAP	1.02	3.30E-01	5.98E-01	1751.47	not significant
9498	RAB27A	1.02	3.22E-01	5.92E-01	1377.91	not significant
9499	PIK3R5	1.02	3.45E-01	6.12E-01	1413.12	not significant
9500	POLR3C	1.02	3.09E-01	5.80E-01	586.76	not significant
9501	RMND1	1.02	3.18E-01	5.87E-01	417.85	not significant
9502	OXLD1	1.02	2.99E-01	5.70E-01	329.58	not significant
9503	GUSBP9	1.02	1.18E-02	NA	31.23	not significant
9504	IDNK	1.02	3.54E-02	NA	41.88	not significant
9505	UBE4B	1.02	3.17E-01	5.87E-01	2631.55	not significant
9506	STX5	1.02	3.38E-01	6.06E-01	939.59	not significant
9507	MTERF4	1.02	3.43E-01	6.10E-01	1062.22	not significant
9508	C19orf25	1.02	3.41E-01	6.08E-01	871.40	not significant
9509	SMIM3	1.02	3.52E-01	6.19E-01	531.20	not significant
9510	MFSD11	1.02	3.56E-01	6.22E-01	1053.20	not significant
9511	CCDC22	1.02	2.96E-01	5.67E-01	358.28	not significant
9512	LINC00669	1.02	9.31E-02	NA	69.90	not significant
9513	LOC100289092	1.02	1.18E-01	NA	89.89	not significant
9514	PLD2	1.02	4.55E-02	NA	47.91	not significant
9515	MRPL16	1.02	2.93E-01	5.65E-01	2536.42	not significant
9516	BDH1	1.02	3.41E-01	6.08E-01	1168.73	not significant
9517	PTAR1	1.02	3.79E-01	6.44E-01	2222.52	not significant
9518	BCKDK	1.02	3.41E-01	6.08E-01	1002.53	not significant
9519	RPS10	1.02	2.06E-01	4.71E-01	181.02	not significant
9520	CMTM6	1.02	2.35E-01	5.02E-01	8507.72	not significant
9521	CSTB	1.02	3.80E-01	6.44E-01	2138.86	not significant
9522	HGS	1.02	2.78E-01	5.48E-01	3708.40	not significant
9523	PDK1	1.02	3.42E-01	6.09E-01	1062.21	not significant
9524	LOC150776	1.02	3.27E-01	5.95E-01	539.43	not significant
9525	UNK	1.02	2.88E-01	5.59E-01	3454.02	not significant
9526	ADAM10	1.02	2.92E-01	5.63E-01	4425.35	not significant
9527	TMEM206	1.02	3.32E-01	6.00E-01	1500.87	not significant
9528	WRN	1.02	3.16E-01	5.86E-01	2115.68	not significant
9529	EIF1B	1.02	3.21E-01	5.91E-01	1391.99	not significant
9530	TTF1	1.02	3.15E-01	5.86E-01	2051.18	not significant
9531	WDR37	1.02	3.37E-01	6.05E-01	987.74	not significant
9532	LINC00152	1.02	2.42E-01	5.10E-01	213.47	not significant
9533	ZNF57	1.02	2.50E-01	5.18E-01	229.13	not significant
9534	C6orf57	1.02	2.00E-01	4.64E-01	161.98	not significant
9535	AIM1	1.02	3.53E-01	6.19E-01	4112.86	not significant
9536	TBC1D10C	1.02	2.95E-01	5.66E-01	3805.97	not significant
9537	SLCO4A1	1.02	2.94E-01	5.65E-01	2278.06	not significant
9538	MDM1	1.02	3.29E-01	5.96E-01	1601.95	not significant
9539	WWOX	1.02	3.57E-01	6.23E-01	582.82	not significant
9540	ATG2B	1.02	3.39E-01	6.07E-01	1723.11	not significant
9541	RPSAP58	1.02	2.89E-01	5.61E-01	376.95	not significant
9542	STAG3L4	1.02	2.50E-01	5.18E-01	241.79	not significant
9543	CSAD	1.02	1.88E-01	4.47E-01	143.55	not significant
9544	HDGFRP2	1.02	2.98E-01	5.69E-01	2821.75	not significant
9545	SEC61B	1.02	3.22E-01	5.92E-01	2713.21	not significant
9546	DYM	1.02	3.11E-01	5.83E-01	1944.90	not significant
9547	JMJD4	1.02	3.35E-01	6.04E-01	831.73	not significant
9548	KIAA1958	1.02	3.25E-01	5.94E-01	626.33	not significant
9549	RELL1	1.02	2.99E-01	5.70E-01	412.77	not significant
9550	C11orf80	1.02	3.06E-01	5.78E-01	470.19	not significant
9551	ITPR3	1.02	3.06E-01	5.78E-01	4757.99	not significant
9552	UBL7-AS1	1.02	2.11E-01	4.75E-01	183.37	not significant
9553	FAM134B	1.02	3.27E-01	5.95E-01	1408.28	not significant
9554	DCUN1D1	1.02	3.24E-01	5.93E-01	1468.99	not significant
9555	ELOVL4	1.02	3.33E-01	6.01E-01	1184.85	not significant
9556	RPL28	1.02	3.42E-01	6.09E-01	14747.30	not significant
9557	SOCS6	1.02	2.48E-01	5.16E-01	234.20	not significant
9558	RPS23	1.02	3.16E-01	5.86E-01	10649.91	not significant
9559	LYRM1	1.02	3.28E-01	5.96E-01	705.85	not significant
9560	TESK1	1.02	3.32E-01	6.00E-01	1069.08	not significant
9561	TMEM170A	1.02	3.35E-01	6.04E-01	539.67	not significant
9562	ERVK13-1	1.02	2.57E-01	5.26E-01	252.76	not significant
9563	SNAP47	1.02	3.23E-01	5.93E-01	813.37	not significant
9564	PARP3	1.02	3.21E-01	5.91E-01	742.95	not significant
9565	CXXC5	1.02	3.23E-01	5.92E-01	727.64	not significant
9566	RPS12	1.02	3.02E-01	5.73E-01	22374.60	not significant
9567	SLC35B3	1.02	2.80E-01	5.51E-01	330.18	not significant
9568	ZBED3	1.02	2.54E-01	5.23E-01	288.58	not significant
9569	UHRF1	1.02	2.24E-01	4.92E-01	9858.67	not significant
9570	ANAPC16	1.02	3.19E-01	5.88E-01	2738.96	not significant
9571	AP4B1	1.02	3.26E-01	5.94E-01	914.40	not significant
9572	NCBP2-AS2	1.02	3.18E-01	5.87E-01	788.11	not significant
9573	AMN1	1.02	2.35E-01	5.02E-01	232.02	not significant
9574	MCTS1	1.02	3.12E-01	5.83E-01	1772.96	not significant
9575	ZFP36	1.02	3.70E-01	6.35E-01	588.15	not significant
9576	HRAS	1.02	3.29E-01	5.96E-01	766.70	not significant
9577	CDK7	1.02	3.82E-01	6.46E-01	473.71	not significant
9578	C19orf57	1.02	2.70E-01	5.41E-01	288.70	not significant
9579	TSPAN13	1.02	2.76E-01	5.47E-01	299.43	not significant

9580	CDC25C	1.02	2.74E-01	5.44E-01	310.68	not significant
9581	TTC32	1.02	1.49E-01	3.96E-01	176.79	not significant
9582	USP48	1.02	3.00E-01	5.70E-01	2705.73	not significant
9583	FAM117A	1.02	3.08E-01	5.79E-01	1462.25	not significant
9584	ZNRF1	1.02	2.39E-01	5.08E-01	5163.53	not significant
9585	TOR1A	1.02	2.73E-01	5.43E-01	2674.33	not significant
9586	WDSUB1	1.02	2.63E-01	5.33E-01	280.02	not significant
9587	EFHC1	1.02	2.27E-01	4.95E-01	220.53	not significant
9588	RPLP1	1.02	2.43E-01	5.11E-01	21163.56	not significant
9589	GNB2L1	1.02	2.33E-01	5.00E-01	25345.18	not significant
9590	MEAF6	1.02	2.79E-01	5.50E-01	2714.95	not significant
9591	GBP1	1.02	2.97E-01	5.68E-01	1936.80	not significant
9592	CRBN	1.02	3.22E-01	5.91E-01	1167.80	not significant
9593	ZNF83	1.02	3.23E-01	5.93E-01	970.23	not significant
9594	RNASEL	1.02	2.82E-01	5.53E-01	350.37	not significant
9595	PSIP1	1.02	2.26E-01	4.94E-01	7911.30	not significant
9596	NMD3	1.02	2.77E-01	5.47E-01	2233.55	not significant
9597	TMEM194A	1.02	2.82E-01	5.53E-01	7509.20	not significant
9598	ULK3	1.02	3.11E-01	5.82E-01	1574.38	not significant
9599	ZNF394	1.02	3.29E-01	5.96E-01	626.68	not significant
9600	SMARCB1	1.02	3.45E-01	6.11E-01	3333.75	not significant
9601	CLNS1A	1.02	2.81E-01	5.51E-01	3950.78	not significant
9602	RSRC2	1.02	2.67E-01	5.38E-01	4018.35	not significant
9603	CHMP2B	1.02	3.08E-01	5.80E-01	1708.66	not significant
9604	SYNJ2	1.02	2.88E-01	5.59E-01	3357.49	not significant
9605	BAZ2B	1.02	3.10E-01	5.82E-01	756.13	not significant
9606	KIAA1549	1.02	2.31E-01	4.99E-01	223.72	not significant
9607	ADAT3	1.02	1.86E-01	4.44E-01	161.09	not significant
9608	PPIB	1.02	1.78E-01	4.34E-01	10170.96	not significant
9609	NUMA1	1.02	2.30E-01	4.98E-01	9066.75	not significant
9610	ARGLU1	1.02	2.97E-01	5.67E-01	4440.61	not significant
9611	TTC33	1.02	3.16E-01	5.86E-01	935.22	not significant
9612	LINC01521	1.02	2.92E-01	5.63E-01	425.40	not significant
9613	SLC29A2	1.02	7.27E-02	NA	74.09	not significant
9614	MRPL15	1.02	2.83E-01	5.54E-01	2615.38	not significant
9615	WDR34	1.02	2.99E-01	5.70E-01	2502.08	not significant
9616	IBTK	1.02	2.72E-01	5.43E-01	3024.03	not significant
9617	TMUB1	1.02	3.10E-01	5.81E-01	2069.32	not significant
9618	NAGK	1.02	3.08E-01	5.80E-01	812.43	not significant
9619	TSNARE1	1.02	2.45E-01	5.13E-01	255.20	not significant
9620	PYROXD2	1.02	1.52E-01	3.99E-01	121.67	not significant
9621	P2RX7	1.02	2.62E-01	5.31E-01	290.98	not significant
9622	ST20	1.02	2.27E-01	4.95E-01	206.80	not significant
9623	MCM6	1.02	1.67E-01	4.20E-01	16942.98	not significant
9624	RPS4X	1.02	2.63E-01	5.33E-01	22338.07	not significant
9625	SYPL1	1.02	2.16E-01	4.82E-01	7455.47	not significant
9626	GANAB	1.02	2.21E-01	4.87E-01	13850.92	not significant
9627	C16orf62	1.02	2.89E-01	5.60E-01	1959.85	not significant
9628	DENND6A	1.02	2.85E-01	5.56E-01	1395.64	not significant
9629	TSPAN5	1.02	2.88E-01	5.59E-01	1481.78	not significant
9630	FAM73B	1.02	3.18E-01	5.87E-01	1104.49	not significant
9631	ANKRD13B	1.02	3.14E-01	5.85E-01	913.43	not significant
9632	RBM43	1.02	2.34E-01	5.01E-01	240.14	not significant
9633	C20orf96	1.02	4.01E-01	6.60E-01	445.99	not significant
9634	DPY19L4	1.02	3.15E-01	5.86E-01	1244.80	not significant
9635	HSH2D	1.02	1.67E-01	4.19E-01	140.84	not significant
9636	POLRMT	1.02	2.86E-01	5.57E-01	2719.41	not significant
9637	RASA3	1.02	2.99E-01	5.70E-01	1788.75	not significant
9638	CASP1	1.02	3.06E-01	5.78E-01	679.77	not significant
9639	ZBTB14	1.02	3.10E-01	5.81E-01	1138.03	not significant
9640	MYO19	1.02	3.16E-01	5.86E-01	1003.69	not significant
9641	EPM2A	1.02	3.27E-01	5.95E-01	661.32	not significant
9642	TSSK6	1.02	2.11E-01	4.75E-01	198.95	not significant
9643	RRBP1	1.02	3.09E-01	5.80E-01	1194.98	not significant
9644	NLK	1.02	2.84E-01	5.54E-01	1468.41	not significant
9645	CDKN2A	1.02	3.12E-01	5.83E-01	725.12	not significant
9646	LMO4	1.02	2.17E-01	4.83E-01	223.78	not significant
9647	XKR5	1.02	3.08E-02	NA	47.27	not significant
9648	CEP57L1	1.02	3.04E-01	5.76E-01	817.62	not significant
9649	NBR2	1.02	3.71E-02	NA	49.62	not significant
9650	LOC100506159	1.02	4.47E-02	NA	55.25	not significant
9651	HP1BP3	1.02	2.17E-01	4.83E-01	9999.39	not significant
9652	ARHGEF1	1.02	2.64E-01	5.35E-01	3625.71	not significant
9653	DSCC1	1.02	2.96E-01	5.67E-01	1998.04	not significant
9654	SPCS1	1.02	2.93E-01	5.64E-01	3711.18	not significant
9655	PLEKHG4	1.02	2.61E-01	5.31E-01	4136.77	not significant
9656	FBXO34	1.02	3.04E-01	5.76E-01	1219.20	not significant
9657	ALG10	1.02	2.82E-01	5.53E-01	455.84	not significant
9658	PTPLA	1.02	2.07E-01	4.71E-01	192.69	not significant
9659	FBXL6	1.02	2.22E-01	4.89E-01	208.44	not significant
9660	C11orf71	1.02	1.77E-01	4.33E-01	154.60	not significant
9661	GEMIN8	1.02	4.70E-01	7.14E-01	520.70	not significant
9662	DOT1L	1.02	2.33E-01	5.00E-01	5205.85	not significant
9663	AP5S1	1.02	3.09E-01	5.80E-01	773.23	not significant
9664	CNTLN	1.02	3.07E-01	5.78E-01	862.94	not significant
9665	TMEM115	1.02	2.96E-01	5.66E-01	924.59	not significant
9666	CTAGE5	1.02	3.05E-01	5.77E-01	971.71	not significant
9667	LINC00339	1.02	2.18E-01	4.85E-01	164.51	not significant

9668	KDM3A	1.02	2.48E-01	5.16E-01	3567.52	not significant
9669	TRPV2	1.02	2.96E-01	5.66E-01	1653.53	not significant
9670	SPRED2	1.02	3.05E-01	5.77E-01	1389.93	not significant
9671	SCYL3	1.02	2.80E-01	5.51E-01	454.05	not significant
9672	PEX12	1.02	2.55E-01	5.24E-01	312.95	not significant
9673	CD59	1.02	2.99E-01	5.70E-01	1518.46	not significant
9674	CC2D1A	1.02	2.92E-01	5.64E-01	1669.40	not significant
9675	PEX1	1.02	2.95E-01	5.66E-01	1474.49	not significant
9676	PSMG4	1.02	2.95E-01	5.66E-01	618.40	not significant
9677	ZCCHC6	1.02	3.01E-01	5.72E-01	1022.45	not significant
9678	RRN3P1	1.02	2.64E-01	5.34E-01	331.55	not significant
9679	TTLL3	1.02	1.43E-01	3.85E-01	125.70	not significant
9680	EML6	1.02	1.87E-01	4.45E-01	268.32	not significant
9681	RALY	1.02	2.31E-01	4.99E-01	17343.27	not significant
9682	OSTM1	1.02	2.84E-01	5.54E-01	1764.40	not significant
9683	FAM78A	1.02	2.76E-01	5.47E-01	1396.01	not significant
9684	MRPS21	1.02	2.19E-01	4.86E-01	214.52	not significant
9685	CCDC106	1.02	2.27E-01	4.95E-01	254.52	not significant
9686	ENDOG	1.02	2.09E-01	4.74E-01	237.43	not significant
9687	RTEL1	1.02	6.92E-02	NA	68.73	not significant
9688	LINC00526	1.02	6.80E-02	NA	71.21	not significant
9689	MCM3	1.02	1.57E-01	4.05E-01	23496.15	not significant
9690	UBAC2	1.02	2.59E-01	5.28E-01	2970.63	not significant
9691	SEC63	1.02	2.64E-01	5.34E-01	4661.16	not significant
9692	PTK7	1.02	2.98E-01	5.69E-01	1821.45	not significant
9693	KAT7	1.02	2.77E-01	5.47E-01	2100.15	not significant
9694	NUTM2A-AS1	1.02	2.98E-01	5.68E-01	659.16	not significant
9695	ASF1B	1.02	2.29E-01	4.97E-01	4894.34	not significant
9696	RPL14	1.02	2.32E-01	4.99E-01	12843.43	not significant
9697	STAG2	1.02	2.05E-01	4.70E-01	10686.19	not significant
9698	C7orf60	1.02	2.94E-01	5.65E-01	779.17	not significant
9699	RAD51D	1.02	3.01E-01	5.72E-01	829.61	not significant
9700	DENND3	1.02	2.94E-01	5.66E-01	652.01	not significant
9701	HEXIM2	1.02	1.65E-01	4.17E-01	150.47	not significant
9702	PSMB1	1.02	2.82E-01	5.52E-01	4833.61	not significant
9703	PGM1	1.02	2.49E-01	5.17E-01	2466.90	not significant
9704	NOS3	1.02	1.83E-01	4.40E-01	183.34	not significant
9705	FEN1	1.02	2.34E-01	5.01E-01	7769.59	not significant
9706	PHACTR3	1.02	2.99E-01	5.69E-01	1904.46	not significant
9707	BRIP1	1.02	2.49E-01	5.17E-01	3623.89	not significant
9708	TAOK2	1.02	2.69E-01	5.40E-01	3112.97	not significant
9709	GALNT7	1.02	2.78E-01	5.48E-01	2578.19	not significant
9710	APBA2	1.02	2.98E-01	5.68E-01	1149.31	not significant
9711	MVP	1.02	2.78E-01	5.48E-01	471.15	not significant
9712	ZNF606	1.02	2.65E-01	5.35E-01	355.12	not significant
9713	MICALL2	1.02	1.09E-01	3.26E-01	102.44	not significant
9714	HDAC11	1.02	9.43E-02	NA	93.25	not significant
9715	NPHP3	1.02	7.69E-02	NA	79.20	not significant
9716	ITPKB	1.02	2.87E-01	5.58E-01	925.48	not significant
9717	IGFBP6	1.02	1.75E-01	4.31E-01	173.53	not significant
9718	LINC01115	1.02	7.36E-02	NA	75.67	not significant
9719	ASB9	1.02	2.79E-01	5.49E-01	495.76	not significant
9720	IFI35	1.02	2.47E-01	5.15E-01	361.36	not significant
9721	EEF1G	1.02	2.21E-01	4.88E-01	12406.60	not significant
9722	MAD1L1	1.02	2.79E-01	5.50E-01	1755.90	not significant
9723	WWC3	1.02	2.91E-01	5.62E-01	1335.25	not significant
9724	GBAP1	1.02	9.70E-02	NA	87.39	not significant
9725	ESYT2	1.02	2.42E-01	5.11E-01	12067.82	not significant
9726	TMED3	1.02	2.83E-01	5.53E-01	1507.41	not significant
9727	TRIB3	1.02	2.83E-01	5.53E-01	1588.56	not significant
9728	ACVR1	1.02	2.27E-01	4.95E-01	274.59	not significant
9729	DPH6	1.02	1.85E-01	4.44E-01	179.09	not significant
9730	ERO1LB	1.02	1.60E-01	4.10E-01	145.26	not significant
9731	TAB1	1.02	2.94E-01	5.65E-01	1129.93	not significant
9732	MRPL52	1.02	2.92E-01	5.63E-01	1534.40	not significant
9733	SLC16A13	1.02	4.85E-01	7.26E-01	103.07	not significant
9734	LOC642852	1.02	2.27E-01	4.95E-01	310.50	not significant
9735	SMAD4	1.02	2.45E-01	5.13E-01	2766.10	not significant
9736	CCM2	1.02	2.65E-01	5.36E-01	2483.34	not significant
9737	GDAP1	1.02	2.89E-01	5.60E-01	946.75	not significant
9738	SLC37A3	1.02	2.76E-01	5.46E-01	1796.31	not significant
9739	VKORC1	1.02	2.85E-01	5.56E-01	1390.13	not significant
9740	METTL25	1.02	2.55E-01	5.23E-01	355.87	not significant
9741	BTG2	1.02	2.26E-01	4.94E-01	271.78	not significant
9742	SEC22B	1.02	2.70E-01	5.41E-01	476.12	not significant
9743	TOR3A	1.02	2.37E-01	5.05E-01	2925.37	not significant
9744	PTPN18	1.02	2.85E-01	5.55E-01	1344.65	not significant
9745	ZNF230	1.02	2.47E-01	5.15E-01	314.01	not significant
9746	RRAGB	1.02	1.81E-01	4.39E-01	167.58	not significant
9747	ASL	1.02	1.13E-01	3.32E-01	113.09	not significant
9748	ZNF704	1.02	7.92E-02	NA	88.92	not significant
9749	LOC102723927	1.02	2.12E-02	NA	52.59	not significant
9750	HDGFRP3	1.02	2.55E-01	5.24E-01	1980.79	not significant
9751	SLC41A3	1.02	2.90E-01	5.62E-01	1038.18	not significant
9752	CD1A	1.02	2.86E-01	5.56E-01	829.18	not significant
9753	RPS25	1.02	2.95E-01	5.66E-01	5201.36	not significant
9754	GBA	1.02	2.33E-01	5.00E-01	296.66	not significant
9755	GABRA5	1.02	2.06E-01	4.71E-01	259.67	not significant

9756	TRAK1	1.02	2.05E-01	4.70E-01	225.57	not significant
9757	TP53INP2	1.02	1.69E-01	4.22E-01	166.86	not significant
9758	C9orf9	1.02	1.49E-01	3.96E-01	136.97	not significant
9759	HMGN2	1.02	2.56E-01	5.25E-01	11615.48	not significant
9760	HNRNPA1	1.02	2.78E-01	5.48E-01	1690.49	not significant
9761	CRTC3	1.02	2.76E-01	5.47E-01	1572.83	not significant
9762	HDDC3	1.02	2.38E-01	5.06E-01	311.77	not significant
9763	RELL2	1.02	1.89E-01	4.49E-01	204.53	not significant
9764	CDAN1	1.02	2.79E-01	5.49E-01	1297.87	not significant
9765	MEX3D	1.02	2.76E-01	5.46E-01	1539.97	not significant
9766	FTL	1.02	3.85E-01	6.47E-01	13180.65	not significant
9767	STIM2	1.02	2.82E-01	5.53E-01	1029.01	not significant
9768	COX17	1.02	2.74E-01	5.44E-01	940.91	not significant
9769	SDHAP2	1.02	7.34E-02	NA	90.34	not significant
9770	FMNL1	1.02	1.56E-01	4.05E-01	9135.10	not significant
9771	RPL11	1.02	2.72E-01	5.43E-01	17617.55	not significant
9772	HPRT1	1.02	2.21E-01	4.88E-01	3393.05	not significant
9773	PCGF1	1.02	2.51E-01	5.19E-01	390.26	not significant
9774	ACADS	1.02	2.59E-01	5.28E-01	565.12	not significant
9775	TBC1D16	1.02	2.25E-01	4.93E-01	272.74	not significant
9776	ZFPM1	1.02	1.60E-01	4.09E-01	164.61	not significant
9777	VGLL4	1.02	2.34E-01	5.01E-01	2299.77	not significant
9778	CCDC171	1.02	1.69E-01	4.23E-01	184.77	not significant
9779	COMMD3	1.02	2.81E-01	5.52E-01	697.91	not significant
9780	TMEM64	1.02	2.41E-01	5.09E-01	335.52	not significant
9781	ADCK5	1.02	1.53E-01	4.01E-01	164.29	not significant
9782	MIATNB	1.02	9.06E-02	2.88E-01	101.75	not significant
9783	NDUFS2	1.02	2.50E-01	5.19E-01	1975.35	not significant
9784	TMEM219	1.02	2.81E-01	5.52E-01	916.07	not significant
9785	CCDC130	1.02	2.76E-01	5.47E-01	848.10	not significant
9786	NDUFA6	1.02	2.77E-01	5.47E-01	679.88	not significant
9787	IFT81	1.02	2.54E-01	5.23E-01	406.70	not significant
9788	MACROD1	1.02	2.11E-01	4.75E-01	284.93	not significant
9789	GLB1L	1.02	4.27E-02	NA	64.29	not significant
9790	KDM4A	1.02	2.53E-01	5.21E-01	2014.70	not significant
9791	FRG1	1.02	3.41E-01	6.08E-01	1036.17	not significant
9792	HPS1	1.02	2.78E-01	5.48E-01	1190.97	not significant
9793	APOA1BP	1.02	2.57E-01	5.25E-01	2047.96	not significant
9794	SEC62	1.02	2.20E-01	4.87E-01	3664.75	not significant
9795	VPS16	1.02	2.68E-01	5.38E-01	1542.89	not significant
9796	AIG1	1.02	2.33E-01	5.00E-01	335.11	not significant
9797	SNTA1	1.02	2.16E-01	4.82E-01	310.16	not significant
9798	SCN8A	1.02	2.59E-01	5.28E-01	579.76	not significant
9799	SLC24A1	1.02	1.83E-01	4.41E-01	212.47	not significant
9800	GPR113	1.02	1.48E-01	3.93E-01	161.68	not significant
9801	HIST1H1C	1.02	9.20E-02	NA	97.72	not significant
9802	FAM127A	1.02	1.49E-01	3.95E-01	180.99	not significant
9803	TPM4	1.02	1.44E-01	3.88E-01	9478.61	not significant
9804	CUL4B	1.02	2.42E-01	5.10E-01	2489.14	not significant
9805	RHBDD1	1.02	2.68E-01	5.38E-01	1435.11	not significant
9806	CLDN12	1.02	2.68E-01	5.39E-01	675.44	not significant
9807	SNHG12	1.02	2.67E-01	5.38E-01	568.82	not significant
9808	TMEM80	1.02	1.85E-01	4.44E-01	199.35	not significant
9809	ACTR6	1.02	2.77E-01	5.47E-01	1108.53	not significant
9810	SLC12A7	1.02	2.66E-01	5.37E-01	1627.46	not significant
9811	C19orf68	1.02	2.49E-01	5.17E-01	416.11	not significant
9812	CRYL1	1.02	1.24E-01	3.52E-01	120.91	not significant
9813	CCT6P1	1.02	1.07E-01	3.21E-01	106.89	not significant
9814	GFER	1.02	2.67E-01	5.38E-01	808.74	not significant
9815	HSPB11	1.02	2.50E-01	5.18E-01	1495.16	not significant
9816	UXS1	1.02	2.64E-01	5.35E-01	1574.70	not significant
9817	C14orf142	1.02	2.70E-01	5.41E-01	861.06	not significant
9818	MAP4K2	1.02	2.73E-01	5.43E-01	1098.17	not significant
9819	TIAM2	1.02	2.13E-01	4.78E-01	274.92	not significant
9820	LMO2	1.02	1.58E-01	4.06E-01	7709.05	not significant
9821	ADPGK	1.02	2.96E-01	5.66E-01	1651.92	not significant
9822	EBLN3	1.02	2.30E-01	4.97E-01	3253.39	not significant
9823	MSRB2	1.02	2.24E-01	4.91E-01	307.41	not significant
9824	ZNF524	1.02	1.30E-01	3.62E-01	119.22	not significant
9825	TIMM10	1.02	2.69E-01	5.40E-01	1242.94	not significant
9826	ZFP62	1.02	2.72E-01	5.43E-01	1011.71	not significant
9827	ZNF548	1.02	2.67E-01	5.38E-01	707.70	not significant
9828	TMEM63A	1.02	2.41E-01	5.10E-01	463.31	not significant
9829	LNPEP	1.02	2.03E-01	4.67E-01	1742.16	not significant
9830	MARVELD1	1.02	1.57E-01	4.05E-01	171.13	not significant
9831	PHRF1	1.02	1.95E-01	4.57E-01	4428.95	not significant
9832	ARFIP2	1.02	2.56E-01	5.24E-01	1573.51	not significant
9833	TMEM55B	1.02	2.67E-01	5.38E-01	1025.31	not significant
9834	SLC10A7	1.02	2.67E-01	5.38E-01	915.86	not significant
9835	ERMP1	1.02	2.30E-01	4.97E-01	333.55	not significant
9836	TP53TG1	1.02	1.55E-01	4.03E-01	160.05	not significant
9837	SULT1A1	1.02	1.64E-01	4.15E-01	174.18	not significant
9838	POLA2	1.02	2.10E-01	4.74E-01	3112.50	not significant
9839	TPST2	1.02	2.28E-01	4.95E-01	2121.77	not significant
9840	RBL1	1.02	2.27E-01	4.95E-01	4065.94	not significant
9841	CC2D1B	1.02	2.64E-01	5.34E-01	1499.53	not significant
9842	NME4	1.02	2.68E-01	5.39E-01	1262.91	not significant
9843	GTF2H4	1.02	2.63E-01	5.34E-01	784.68	not significant

9844	FUNDC2	1.02	2.40E-01	5.08E-01	596.39	not significant
9845	SPPL3	1.02	2.08E-01	4.73E-01	3155.35	not significant
9846	ZDHHC4	1.02	2.65E-01	5.36E-01	1294.78	not significant
9847	CCDC42B	1.02	7.53E-02	NA	86.04	not significant
9848	GPC1	1.02	8.18E-02	NA	89.87	not significant
9849	AP5Z1	1.02	2.45E-01	5.12E-01	1922.23	not significant
9850	LY96	1.02	1.15E-01	3.36E-01	124.08	not significant
9851	ARL16	1.02	2.58E-01	5.26E-01	1536.80	not significant
9852	ATPIF1	1.02	2.37E-01	5.04E-01	2194.32	not significant
9853	EHBP1L1	1.02	2.19E-01	4.86E-01	2236.93	not significant
9854	CETN2	1.02	1.22E-01	3.50E-01	131.38	not significant
9855	SV2A	1.02	2.42E-01	5.10E-01	460.80	not significant
9856	PSAP	1.02	1.34E-01	3.69E-01	23674.72	not significant
9857	DAZAP2	1.02	1.63E-01	4.14E-01	10798.01	not significant
9858	SLC50A1	1.02	2.66E-01	5.37E-01	1077.74	not significant
9859	BTBD6	1.02	2.59E-01	5.28E-01	1291.39	not significant
9860	ANKRD10	1.02	2.28E-01	4.95E-01	2078.78	not significant
9861	RALGPS2	1.02	2.65E-01	5.36E-01	1005.74	not significant
9862	DXO	1.02	9.04E-02	NA	97.11	not significant
9863	HEMGN	1.02	9.83E-02	3.05E-01	106.90	not significant
9864	HNRNPA0	1.02	1.79E-01	4.36E-01	15335.51	not significant
9865	C19orf66	1.02	2.62E-01	5.32E-01	1058.04	not significant
9866	TCAM1P	1.02	1.40E-02	NA	44.15	not significant
9867	SARS	1.02	1.78E-01	4.34E-01	5439.39	not significant
9868	ZNF280D	1.02	2.62E-01	5.32E-01	827.81	not significant
9869	MEX3A	1.02	2.59E-01	5.28E-01	930.05	not significant
9870	MRPL45	1.02	2.19E-01	4.86E-01	354.85	not significant
9871	UBR4	1.02	2.80E-01	5.51E-01	6678.13	not significant
9872	PACSIN2	1.02	2.15E-01	4.81E-01	2674.17	not significant
9873	PPP1R35	1.02	2.50E-01	5.19E-01	1494.65	not significant
9874	IRF2BP1	1.02	2.46E-01	5.14E-01	1861.08	not significant
9875	MGRN1	1.02	2.36E-01	5.03E-01	2131.18	not significant
9876	ATP10A	1.02	2.59E-01	5.28E-01	874.95	not significant
9877	EVPL	1.02	2.56E-01	5.25E-01	633.65	not significant
9878	PPP6R2	1.02	2.06E-01	4.71E-01	2365.73	not significant
9879	PSKH1	1.02	2.61E-01	5.31E-01	1156.18	not significant
9880	SBF2-AS1	1.02	1.82E-01	4.39E-01	222.45	not significant
9881	PITX1	1.02	1.61E-01	4.11E-01	194.71	not significant
9882	SIX5	1.02	1.26E-01	3.56E-01	151.86	not significant
9883	ARL17A	1.02	1.12E-01	3.31E-01	124.57	not significant
9884	PDIA4	1.02	1.58E-01	4.07E-01	9854.43	not significant
9885	TSPAN14	1.02	2.43E-01	5.11E-01	1813.10	not significant
9886	OSBPL2	1.02	2.61E-01	5.31E-01	952.63	not significant
9887	FAM92A1	1.02	2.33E-01	5.01E-01	436.84	not significant
9888	RNF125	1.02	1.46E-01	3.90E-01	172.44	not significant
9889	CLSTN1	1.02	1.70E-01	4.23E-01	9136.68	not significant
9890	GSS	1.02	2.04E-01	4.69E-01	2818.04	not significant
9891	DYNC1I2	1.02	2.23E-01	4.90E-01	2021.26	not significant
9892	ZC3H6	1.02	1.97E-01	4.61E-01	280.15	not significant
9893	SFT2D2	1.02	2.10E-01	4.74E-01	325.22	not significant
9894	CHD6	1.02	2.04E-01	4.69E-01	3358.69	not significant
9895	RDH11	1.02	1.95E-01	4.57E-01	4253.95	not significant
9896	CPSF3L	1.02	2.16E-01	4.82E-01	2545.69	not significant
9897	PTDSS2	1.02	2.48E-01	5.15E-01	1342.32	not significant
9898	TMEM69	1.02	2.55E-01	5.24E-01	990.49	not significant
9899	RPS3	1.02	2.78E-01	5.48E-01	29820.86	not significant
9900	LRFN3	1.02	2.57E-01	5.26E-01	644.51	not significant
9901	LINC01096	1.02	1.13E-02	NA	40.97	not significant
9902	ZNF473	1.02	2.57E-01	5.26E-01	1035.12	not significant
9903	SNIP1	1.02	2.55E-01	5.23E-01	928.31	not significant
9904	STK11IP	1.02	2.55E-01	5.23E-01	867.06	not significant
9905	KIF3C	1.02	2.43E-01	5.11E-01	858.85	not significant
9906	SLC25A26	1.02	2.40E-01	5.08E-01	466.28	not significant
9907	SMDT1	1.02	1.79E-01	4.36E-01	227.21	not significant
9908	RHOBTB1	1.02	1.91E-01	4.51E-01	261.05	not significant
9909	DOLK	1.02	1.82E-01	4.39E-01	235.76	not significant
9910	FAM210B	1.02	9.98E-02	3.08E-01	116.80	not significant
9911	SUSD3	1.02	8.47E-02	NA	98.26	not significant
9912	RDH14	1.02	4.04E-02	NA	66.99	not significant
9913	CLIC1	1.02	2.44E-01	5.12E-01	2683.02	not significant
9914	TMEM209	1.02	2.10E-01	4.74E-01	3969.05	not significant
9915	NCKAP5L	1.02	2.33E-01	5.01E-01	1633.25	not significant
9916	ZBTB6	1.02	2.52E-01	5.21E-01	654.54	not significant
9917	BLOC1S4	1.02	2.42E-01	5.10E-01	535.14	not significant
9918	NUP50-AS1	1.02	1.82E-01	4.40E-01	232.50	not significant
9919	ACACB	1.02	2.20E-01	4.87E-01	422.24	not significant
9920	TOPORS-AS1	1.02	2.45E-02	NA	52.75	not significant
9921	MAP2K2	1.03	1.97E-01	4.60E-01	4482.45	not significant
9922	VAMP5	1.03	2.79E-01	5.50E-01	1019.33	not significant
9923	CDK17	1.03	2.07E-01	4.71E-01	2176.24	not significant
9924	TAF11	1.03	2.36E-01	5.03E-01	1399.50	not significant
9925	OSER1	1.03	2.55E-01	5.23E-01	857.17	not significant
9926	CBX5	1.03	2.07E-01	4.72E-01	14588.95	not significant
9927	HINT2	1.03	2.53E-01	5.22E-01	753.24	not significant
9928	GPR174	1.03	2.47E-01	5.15E-01	891.45	not significant
9929	NT5C3B	1.03	2.48E-01	5.16E-01	663.66	not significant
9930	WDR19	1.03	2.31E-01	4.99E-01	560.93	not significant
9931	RPL10A	1.03	2.05E-01	4.70E-01	13014.31	not significant

9932	ERO1L	1.03	2.19E-01	4.86E-01	3974.88	not significant
9933	ZFYVE26	1.03	2.40E-01	5.08E-01	1319.14	not significant
9934	GUCY1B3	1.03	2.52E-01	5.20E-01	1051.28	not significant
9935	LAIR1	1.03	2.45E-01	5.13E-01	969.36	not significant
9936	LEPROT	1.03	2.46E-01	5.14E-01	743.85	not significant
9937	CEP68	1.03	2.28E-01	4.96E-01	428.68	not significant
9938	COIL	1.03	2.44E-01	5.12E-01	1177.26	not significant
9939	ZNF184	1.03	2.46E-01	5.14E-01	1237.50	not significant
9940	AGTPBP1	1.03	2.46E-01	5.14E-01	944.54	not significant
9941	ACOT8	1.03	2.40E-01	5.08E-01	694.82	not significant
9942	ZNF506	1.03	2.49E-01	5.17E-01	934.91	not significant
9943	CNPY4	1.03	2.41E-01	5.10E-01	516.24	not significant
9944	LTN1	1.03	2.43E-01	5.11E-01	1772.66	not significant
9945	RFXAP	1.03	2.45E-01	5.13E-01	654.58	not significant
9946	GCC2	1.03	2.48E-01	5.15E-01	1277.77	not significant
9947	PAX9	1.03	2.35E-01	5.01E-01	470.28	not significant
9948	PSMA1	1.03	1.52E-01	3.99E-01	7701.30	not significant
9949	SH2D1A	1.03	1.53E-01	4.01E-01	7727.35	not significant
9950	SPICE1	1.03	2.43E-01	5.11E-01	700.01	not significant
9951	BET1	1.03	2.41E-01	5.09E-01	782.75	not significant
9952	KLHL2	1.03	2.26E-01	4.94E-01	388.47	not significant
9953	C1R	1.03	1.85E-01	4.44E-01	261.73	not significant
9954	GADD45A	1.03	1.12E-01	3.31E-01	134.60	not significant
9955	ANP32B	1.03	1.90E-01	4.49E-01	13661.29	not significant
9956	TMEM8A	1.03	2.21E-01	4.87E-01	1777.58	not significant
9957	ATXN2	1.03	2.36E-01	5.03E-01	1618.10	not significant
9958	SDHAF1	1.03	2.25E-01	4.92E-01	545.31	not significant
9959	TMEM156	1.03	1.75E-01	4.31E-01	256.66	not significant
9960	HSD17B12	1.03	1.73E-01	4.27E-01	3690.76	not significant
9961	NELFA	1.03	2.44E-01	5.12E-01	1656.66	not significant
9962	C15orf40	1.03	2.10E-01	4.74E-01	339.76	not significant
9963	RNF103	1.03	2.15E-01	4.81E-01	429.26	not significant
9964	WDR45	1.03	1.57E-01	4.05E-01	205.95	not significant
9965	TKT	1.03	1.55E-01	4.03E-01	8655.86	not significant
9966	EDF1	1.03	2.11E-01	4.75E-01	3209.54	not significant
9967	CLK1	1.03	2.06E-01	4.71E-01	1721.26	not significant
9968	MCOLN1	1.03	2.36E-01	5.03E-01	519.36	not significant
9969	VPS29	1.03	2.00E-01	4.64E-01	2143.84	not significant
9970	EIF3F	1.03	1.76E-01	4.32E-01	4014.98	not significant
9971	TNFRSF1A	1.03	2.09E-01	4.74E-01	2402.28	not significant
9972	SLC40A1	1.03	2.26E-01	4.94E-01	1739.37	not significant
9973	ZFP14	1.03	2.29E-01	4.96E-01	514.25	not significant
9974	43709_19983	1.03	1.59E-01	4.09E-01	7400.61	not significant
9975	ATAD2	1.03	1.39E-01	3.79E-01	11345.88	not significant
9976	INTS1	1.03	1.57E-01	4.05E-01	6094.40	not significant
9977	DMAP1	1.03	2.32E-01	4.99E-01	861.38	not significant
9978	EXOC6	1.03	2.38E-01	5.06E-01	983.41	not significant
9979	SFR1	1.03	1.86E-01	4.44E-01	302.87	not significant
9980	QSOX1	1.03	2.42E-01	5.10E-01	1057.50	not significant
9981	ABHD14B	1.03	2.39E-01	5.07E-01	854.45	not significant
9982	TRAF6	1.03	2.37E-01	5.05E-01	808.28	not significant
9983	LOC81691	1.03	2.19E-01	4.86E-01	425.91	not significant
9984	CCDC127	1.03	2.33E-01	5.00E-01	531.42	not significant
9985	B4GALT7	1.03	2.14E-01	4.79E-01	363.40	not significant
9986	ATP13A2	1.03	2.15E-01	4.81E-01	1889.03	not significant
9987	ADCK2	1.03	2.33E-01	5.00E-01	1644.31	not significant
9988	CRTC2	1.03	2.32E-01	4.99E-01	1323.84	not significant
9989	ARID5B	1.03	2.39E-01	5.07E-01	949.01	not significant
9990	BIN1	1.03	2.25E-01	4.92E-01	525.32	not significant
9991	ZKSCAN3	1.03	1.78E-01	4.34E-01	253.41	not significant
9992	MAT2B	1.03	1.99E-01	4.64E-01	3528.95	not significant
9993	ANKRD13D	1.03	2.14E-01	4.79E-01	1784.83	not significant
9994	FCHSD2	1.03	2.08E-01	4.73E-01	2720.06	not significant
9995	EPC1	1.03	2.23E-01	4.91E-01	1533.33	not significant
9996	ABCB8	1.03	2.23E-01	4.91E-01	1691.77	not significant
9997	PROSER3	1.03	2.21E-01	4.88E-01	489.33	not significant
9998	RPL13	1.03	1.84E-01	4.42E-01	27121.48	not significant
9999	LOC101927815	1.03	3.69E-02	NA	66.62	not significant
10000	FBRS	1.03	1.91E-01	4.51E-01	3010.71	not significant
10001	C19orf10	1.03	2.22E-01	4.89E-01	2200.62	not significant
10002	KIFAP3	1.03	2.37E-01	5.04E-01	996.70	not significant
10003	HLCS	1.03	2.35E-01	5.02E-01	803.13	not significant
10004	RNF170	1.03	2.26E-01	4.94E-01	554.42	not significant
10005	MGAT4A	1.03	1.80E-01	4.37E-01	5787.26	not significant
10006	S100PBP	1.03	2.15E-01	4.80E-01	1879.68	not significant
10007	CDK9	1.03	2.05E-01	4.70E-01	1936.94	not significant
10008	TRIM13	1.03	2.20E-01	4.87E-01	1476.74	not significant
10009	SIL1	1.03	2.14E-01	4.79E-01	405.90	not significant
10010	TRAF3IP2	1.03	2.25E-01	4.93E-01	510.31	not significant
10011	CACNB2	1.03	1.75E-01	4.31E-01	262.40	not significant
10012	PCCB	1.03	1.82E-01	4.40E-01	2366.69	not significant
10013	FHOD1	1.03	2.02E-01	4.67E-01	2008.63	not significant
10014	ANKMY1	1.03	2.07E-01	4.71E-01	381.07	not significant
10015	LINC00657	1.03	1.10E-01	3.27E-01	11194.70	not significant
10016	ZMIZ1	1.03	2.29E-01	4.96E-01	6133.83	not significant
10017	INPP5K	1.03	2.31E-01	4.99E-01	1267.79	not significant
10018	CD52	1.03	2.34E-01	5.01E-01	716.93	not significant
10019	FNIP1	1.03	2.34E-01	5.01E-01	1125.06	not significant

10020	CRIP1	1.03	2.01E-01	4.65E-01	390.10	not significant
10021	SIMC1	1.03	2.07E-01	4.71E-01	394.67	not significant
10022	CTDNEP1	1.03	1.41E-01	3.82E-01	5727.97	not significant
10023	PEX14	1.03	2.33E-01	5.00E-01	1045.75	not significant
10024	ARAP2	1.03	2.30E-01	4.98E-01	1312.37	not significant
10025	OFD1	1.03	2.25E-01	4.92E-01	862.98	not significant
10026	PI4KAP1	1.03	4.70E-02	NA	83.80	not significant
10027	ZBTB5	1.03	2.21E-01	4.88E-01	1388.35	not significant
10028	CCDC15	1.03	2.09E-01	4.73E-01	418.97	not significant
10029	STAG3L2	1.03	1.42E-01	3.83E-01	195.00	not significant
10030	ZNF554	1.03	7.34E-02	2.53E-01	100.77	not significant
10031	OS9	1.03	1.63E-01	4.14E-01	4179.54	not significant
10032	NUDT2	1.03	2.27E-01	4.95E-01	739.16	not significant
10033	EFCAB11	1.03	1.87E-01	4.46E-01	219.74	not significant
10034	EME2	1.03	7.56E-02	2.57E-01	139.93	not significant
10035	GPBP1L1	1.03	1.30E-01	3.62E-01	5314.25	not significant
10036	NDUFAF3	1.03	2.29E-01	4.96E-01	1478.75	not significant
10037	PSENEN	1.03	2.29E-01	4.97E-01	911.23	not significant
10038	USP40	1.03	2.28E-01	4.95E-01	752.27	not significant
10039	ERCC6	1.03	1.89E-01	4.48E-01	371.65	not significant
10040	NR1D2	1.03	2.00E-01	4.64E-01	369.31	not significant
10041	C5orf42	1.03	1.51E-01	3.99E-01	1440.18	not significant
10042	SUSD1	1.03	1.40E-01	3.81E-01	185.77	not significant
10043	TMEM242	1.03	7.57E-02	2.57E-01	119.75	not significant
10044	CHN2	1.03	1.79E-01	4.36E-01	2830.96	not significant
10045	GTPBP1	1.03	1.90E-01	4.49E-01	2232.84	not significant
10046	TMEM170B	1.03	2.27E-01	4.95E-01	1054.95	not significant
10047	MBTD1	1.03	2.09E-01	4.74E-01	1490.66	not significant
10048	HCFC1R1	1.03	1.86E-01	4.44E-01	411.54	not significant
10049	MZT2A	1.03	2.26E-01	4.94E-01	1858.27	not significant
10050	SPN	1.03	1.40E-01	3.81E-01	22640.05	not significant
10051	MED15	1.03	1.92E-01	4.52E-01	2002.43	not significant
10052	TUBGCP3	1.03	1.87E-01	4.46E-01	2437.87	not significant
10053	SNN	1.03	2.17E-01	4.83E-01	1358.01	not significant
10054	NAA38	1.03	2.19E-01	4.86E-01	760.94	not significant
10055	DTX2	1.03	2.22E-01	4.89E-01	609.78	not significant
10056	ZSWIM4	1.03	1.92E-01	4.53E-01	334.53	not significant
10057	NME3	1.03	9.37E-02	2.95E-01	148.43	not significant
10058	IPO9	1.03	1.67E-01	4.20E-01	4765.83	not significant
10059	BTN2A2	1.03	2.13E-01	4.78E-01	478.81	not significant
10060	PIGB	1.03	1.65E-01	4.16E-01	237.14	not significant
10061	DNMT1	1.03	9.67E-02	3.02E-01	16986.46	not significant
10062	TK1	1.03	2.22E-01	4.89E-01	1102.99	not significant
10063	COG4	1.03	2.22E-01	4.89E-01	998.83	not significant
10064	SMIM11	1.03	2.17E-01	4.83E-01	708.40	not significant
10065	TRIM52-AS1	1.03	1.89E-01	4.48E-01	339.40	not significant
10066	PICK1	1.03	1.71E-01	4.25E-01	255.45	not significant
10067	MYL12A	1.03	1.54E-01	4.02E-01	5360.29	not significant
10068	SOAT1	1.03	1.77E-01	4.34E-01	3714.45	not significant
10069	ARHGAP1	1.03	1.99E-01	4.63E-01	1826.15	not significant
10070	PLCL2	1.03	2.13E-01	4.78E-01	1401.99	not significant
10071	COMMD6	1.03	2.19E-01	4.86E-01	1205.08	not significant
10072	TSHZ1	1.03	2.19E-01	4.86E-01	1250.60	not significant
10073	HLA-H	1.03	1.20E-01	3.45E-01	156.31	not significant
10074	DPP4	1.03	1.31E-01	3.64E-01	6858.71	not significant
10075	KIF21B	1.03	1.73E-01	4.27E-01	8645.06	not significant
10076	MRPS26	1.03	2.17E-01	4.83E-01	2391.66	not significant
10077	PANK4	1.03	2.21E-01	4.88E-01	1035.22	not significant
10078	IFNGR1	1.03	2.12E-01	4.76E-01	873.15	not significant
10079	MUL1	1.03	2.02E-01	4.67E-01	790.68	not significant
10080	LOC440434	1.03	1.30E-02	NA	48.85	not significant
10081	ORMDL2	1.03	2.22E-01	4.89E-01	830.73	not significant
10082	TSEN54	1.03	1.86E-01	4.44E-01	2589.28	not significant
10083	RPL5	1.03	1.53E-01	4.00E-01	23537.97	not significant
10084	TMEM106B	1.03	1.94E-01	4.55E-01	2082.68	not significant
10085	TMEM260	1.03	3.68E-02	1.60E-01	1490.75	not significant
10086	SNRPA	1.03	1.57E-01	4.05E-01	5197.34	not significant
10087	SPG21	1.03	1.85E-01	4.44E-01	2011.32	not significant
10088	PRMT2	1.03	2.08E-01	4.73E-01	1296.33	not significant
10089	NMT2	1.03	1.92E-01	4.52E-01	749.17	not significant
10090	FAM175A	1.03	1.88E-01	4.48E-01	358.31	not significant
10091	PTPLAD1	1.03	1.24E-01	3.52E-01	6644.50	not significant
10092	JAGN1	1.03	2.05E-01	4.70E-01	1235.24	not significant
10093	CTBP1	1.03	1.42E-01	3.84E-01	7364.46	not significant
10094	ATP6V0C	1.03	1.82E-01	4.40E-01	3937.18	not significant
10095	ATRAID	1.03	2.04E-01	4.69E-01	2061.77	not significant
10096	NIFK-AS1	1.03	1.55E-01	4.04E-01	271.34	not significant
10097	RPL9	1.03	1.75E-01	4.31E-01	15159.78	not significant
10098	TMEM9B	1.03	2.04E-01	4.70E-01	1004.64	not significant
10099	ARSG	1.03	1.99E-01	4.63E-01	424.83	not significant
10100	RXRB	1.03	1.84E-01	4.42E-01	331.28	not significant
10101	MROH1	1.03	1.13E-01	3.32E-01	162.24	not significant
10102	GABARAP	1.03	1.92E-01	4.52E-01	2430.22	not significant
10103	STK25	1.03	1.68E-01	4.21E-01	2646.24	not significant
10104	RNF144A	1.03	1.56E-01	4.05E-01	3567.66	not significant
10105	CEPT1	1.03	1.68E-01	4.22E-01	2147.15	not significant
10106	IL6ST	1.03	2.13E-01	4.78E-01	714.55	not significant
10107	CYP4V2	1.03	2.03E-01	4.69E-01	619.08	not significant

10108	NAAA	1.03	1.56E-01	4.04E-01	262.82	not significant
10109	HADH	1.03	1.79E-01	4.36E-01	3558.30	not significant
10110	CUEDC2	1.03	2.06E-01	4.71E-01	2116.84	not significant
10111	FBXL17	1.03	2.06E-01	4.71E-01	1356.75	not significant
10112	GSTZ1	1.03	1.37E-01	3.75E-01	279.65	not significant
10113	PAQR6	1.03	1.37E-01	3.75E-01	201.87	not significant
10114	ARHGAP21	1.03	2.23E-01	4.89E-01	2112.94	not significant
10115	GOLGA5	1.03	2.09E-01	4.73E-01	826.27	not significant
10116	FSTL1	1.03	1.95E-01	4.57E-01	464.56	not significant
10117	SPAG16	1.03	1.83E-01	4.40E-01	334.75	not significant
10118	PEX2	1.03	1.79E-01	4.36E-01	2330.60	not significant
10119	PLEKHF2	1.03	2.05E-01	4.70E-01	1113.63	not significant
10120	SIAH1	1.03	2.09E-01	4.73E-01	653.75	not significant
10121	NDUFA1	1.03	2.06E-01	4.71E-01	1933.95	not significant
10122	C5orf56	1.03	1.91E-01	4.51E-01	1012.98	not significant
10123	LINS	1.03	1.89E-01	4.49E-01	407.93	not significant
10124	PLXNB1	1.03	8.20E-02	2.71E-01	125.13	not significant
10125	WHAMMP1	1.03	3.82E-02	NA	77.67	not significant
10126	FOXB1	1.03	1.05E-02	NA	48.33	not significant
10127	JARID2	1.03	1.46E-01	3.90E-01	4920.94	not significant
10128	AGBL5	1.03	2.06E-01	4.71E-01	1286.38	not significant
10129	NBEAL2	1.03	1.95E-01	4.57E-01	7920.26	not significant
10130	DENND1C	1.03	1.56E-01	4.04E-01	3098.35	not significant
10131	PEX5L	1.03	1.86E-01	4.44E-01	3169.61	not significant
10132	PPP1R2	1.03	2.04E-01	4.69E-01	1228.37	not significant
10133	RPS8	1.03	1.84E-01	4.42E-01	26346.55	not significant
10134	GLTSCR1	1.03	2.05E-01	4.70E-01	596.85	not significant
10135	TMEM256	1.03	1.59E-01	4.09E-01	260.22	not significant
10136	LEMD3	1.03	1.71E-01	4.25E-01	2256.58	not significant
10137	MIDN	1.03	1.65E-01	4.16E-01	2910.28	not significant
10138	DEGS1	1.03	1.70E-01	4.24E-01	2264.12	not significant
10139	PARP6	1.03	2.05E-01	4.70E-01	1042.70	not significant
10140	RIT1	1.03	2.09E-01	4.74E-01	886.60	not significant
10141	GLIPR2	1.03	1.45E-01	3.89E-01	227.33	not significant
10142	IER3IP1	1.03	1.89E-01	4.48E-01	2028.68	not significant
10143	DPYSL2	1.03	1.36E-01	3.73E-01	3366.72	not significant
10144	TWF2	1.03	1.83E-01	4.40E-01	3251.54	not significant
10145	WRAP73	1.03	1.98E-01	4.62E-01	1234.63	not significant
10146	SLC19A1	1.03	1.94E-01	4.55E-01	2020.50	not significant
10147	MMD	1.03	1.81E-01	4.39E-01	1845.18	not significant
10148	YIPF1	1.03	2.01E-01	4.65E-01	836.34	not significant
10149	KIAA1468	1.03	2.35E-01	5.02E-01	1026.75	not significant
10150	PAAF1	1.03	2.03E-01	4.67E-01	621.51	not significant
10151	ZNF519	1.03	1.66E-01	4.19E-01	406.52	not significant
10152	FBXL19-AS1	1.03	3.87E-02	NA	99.89	not significant
10153	GDPD5	1.03	2.02E-01	4.67E-01	1192.92	not significant
10154	RBM5	1.03	1.53E-01	4.01E-01	3106.01	not significant
10155	STIL	1.03	1.80E-01	4.37E-01	2694.95	not significant
10156	IFIT3	1.03	1.94E-01	4.56E-01	490.31	not significant
10157	PWWP2B	1.03	1.95E-01	4.57E-01	503.19	not significant
10158	IFT140	1.03	1.83E-01	4.40E-01	492.04	not significant
10159	UGT3A2	1.03	5.29E-02	NA	99.73	not significant
10160	SSR4	1.03	1.73E-01	4.28E-01	3012.14	not significant
10161	PPP3CC	1.03	2.01E-01	4.65E-01	822.66	not significant
10162	KCTD1	1.03	1.94E-01	4.55E-01	745.26	not significant
10163	TGFBR2	1.03	2.01E-01	4.65E-01	861.10	not significant
10164	ZBTB42	1.03	1.52E-01	3.99E-01	251.65	not significant
10165	SWSAP1	1.03	9.40E-02	2.96E-01	144.90	not significant
10166	TNRC18	1.03	1.39E-01	3.79E-01	5917.41	not significant
10167	ALG1	1.03	1.96E-01	4.59E-01	1446.73	not significant
10168	CENPT	1.03	1.97E-01	4.60E-01	1589.78	not significant
10169	GOLGA1	1.03	1.93E-01	4.54E-01	515.27	not significant
10170	ZNF862	1.03	1.82E-01	4.39E-01	476.87	not significant
10171	ZNF628	1.03	1.69E-01	4.22E-01	337.66	not significant
10172	CTNNBIP1	1.03	2.01E-01	4.65E-01	709.70	not significant
10173	ZNF345	1.03	1.01E-01	3.09E-01	157.39	not significant
10174	MCM8	1.03	1.47E-01	3.91E-01	4067.04	not significant
10175	BRD1	1.03	1.69E-01	4.23E-01	2868.67	not significant
10176	ACP2	1.03	2.01E-01	4.65E-01	750.50	not significant
10177	ARHGEF2	1.03	1.28E-01	3.59E-01	3452.64	not significant
10178	ATP11C	1.03	1.95E-01	4.57E-01	1577.28	not significant
10179	MIA3	1.03	1.71E-01	4.25E-01	2480.69	not significant
10180	LRRC1	1.03	1.85E-01	4.44E-01	457.80	not significant
10181	COPG2	1.03	1.82E-01	4.40E-01	428.31	not significant
10182	FLJ37453	1.03	9.07E-02	2.88E-01	140.54	not significant
10183	PRDX5	1.03	1.62E-01	4.13E-01	4521.16	not significant
10184	LMO7	1.03	1.60E-01	4.09E-01	350.53	not significant
10185	CSNK1G2	1.03	1.00E-01	3.09E-01	5603.79	not significant
10186	PRKAB1	1.03	1.42E-01	3.84E-01	3012.09	not significant
10187	PCYT2	1.03	1.65E-01	4.17E-01	2119.11	not significant
10188	FAM134C	1.03	1.82E-01	4.40E-01	1440.87	not significant
10189	LOC145783	1.03	1.17E-01	3.39E-01	189.36	not significant
10190	LINC01061	1.03	6.27E-02	2.28E-01	110.47	not significant
10191	OCIAD1	1.03	1.17E-01	3.39E-01	4494.19	not significant
10192	HNRNPLL	1.03	1.42E-01	3.83E-01	2898.55	not significant
10193	AGPAT2	1.03	1.77E-01	4.33E-01	428.62	not significant
10194	MXRA7	1.03	1.23E-01	3.51E-01	201.51	not significant
10195	MGAT4B	1.03	1.87E-01	4.46E-01	1203.13	not significant

10196	PHIP	1.03	1.70E-01	4.25E-01	4089.90	not significant
10197	PDCL	1.03	1.88E-01	4.48E-01	943.80	not significant
10198	GLUD1P3	1.03	3.08E-02	NA	78.61	not significant
10199	GINS4	1.03	1.44E-01	3.88E-01	2499.96	not significant
10200	ANAPC13	1.03	1.81E-01	4.39E-01	1585.24	not significant
10201	ATG2A	1.03	1.90E-01	4.49E-01	1051.81	not significant
10202	LOC100505549	1.03	1.55E-01	4.03E-01	298.44	not significant
10203	NDUFB9	1.03	1.42E-01	3.84E-01	4395.81	not significant
10204	XAB2	1.03	1.40E-01	3.81E-01	2535.75	not significant
10205	MITD1	1.03	1.84E-01	4.42E-01	860.61	not significant
10206	C22orf29	1.03	1.47E-01	3.92E-01	2578.82	not significant
10207	UBE2B	1.03	1.80E-01	4.37E-01	1778.91	not significant
10208	ZNF738	1.03	1.76E-01	4.31E-01	1304.94	not significant
10209	UBXN4	1.03	8.72E-02	2.82E-01	7338.26	not significant
10210	LGALS3BP	1.03	8.87E-02	2.85E-01	10597.73	not significant
10211	HEXB	1.03	1.65E-01	4.16E-01	1662.35	not significant
10212	SCAMP4	1.03	1.70E-01	4.24E-01	1967.84	not significant
10213	NRDE2	1.03	1.79E-01	4.36E-01	624.80	not significant
10214	LINC00667	1.03	1.86E-01	4.44E-01	710.61	not significant
10215	PRKAR1B	1.03	1.62E-01	4.12E-01	3735.23	not significant
10216	TSC22D4	1.03	1.41E-01	3.83E-01	2732.77	not significant
10217	LLGL1	1.03	1.57E-01	4.05E-01	2073.54	not significant
10218	ZSWIM7	1.03	1.84E-01	4.42E-01	558.38	not significant
10219	RERE	1.03	1.82E-01	4.39E-01	1413.42	not significant
10220	LPGAT1	1.03	1.68E-01	4.21E-01	978.76	not significant
10221	C14orf28	1.03	4.62E-02	NA	94.24	not significant
10222	PDHB	1.03	1.44E-01	3.88E-01	2583.99	not significant
10223	SNHG8	1.03	1.81E-01	4.38E-01	2125.60	not significant
10224	GLG1	1.03	1.60E-01	4.09E-01	3104.03	not significant
10225	HAUS3	1.03	1.73E-01	4.27E-01	1349.44	not significant
10226	RBM12B	1.03	1.75E-01	4.30E-01	1633.56	not significant
10227	SDF4	1.03	1.57E-01	4.05E-01	3467.68	not significant
10228	ALKBH6	1.03	1.72E-01	4.26E-01	482.62	not significant
10229	RPL35A	1.03	1.47E-01	3.92E-01	9336.61	not significant
10230	TBC1D1	1.03	1.20E-01	3.45E-01	3583.86	not significant
10231	PIGS	1.03	1.74E-01	4.28E-01	1623.28	not significant
10232	UBR2	1.03	1.76E-01	4.31E-01	2205.25	not significant
10233	FUZ	1.03	1.80E-01	4.36E-01	811.32	not significant
10234	DOPEY1	1.03	1.80E-01	4.37E-01	900.53	not significant
10235	MAML3	1.03	1.79E-01	4.36E-01	586.80	not significant
10236	ORC6	1.03	1.45E-01	3.90E-01	2182.68	not significant
10237	BRCA1	1.03	1.46E-01	3.90E-01	3955.72	not significant
10238	CRY1	1.03	1.52E-01	4.00E-01	2077.50	not significant
10239	FBF1	1.03	1.78E-01	4.35E-01	932.23	not significant
10240	CCDC136	1.03	1.66E-01	4.18E-01	628.38	not significant
10241	KCTD19	1.03	4.15E-02	NA	89.97	not significant
10242	RLTPR	1.03	6.62E-02	2.36E-01	9148.05	not significant
10243	RNF123	1.03	1.67E-01	4.20E-01	1392.49	not significant
10244	FIS1	1.03	1.77E-01	4.33E-01	1817.45	not significant
10245	RPS20	1.03	1.36E-01	3.73E-01	15205.75	not significant
10246	BAX	1.03	1.33E-01	3.68E-01	3126.48	not significant
10247	LIPA	1.03	1.32E-01	3.67E-01	2575.17	not significant
10248	KCNA3	1.03	1.63E-01	4.14E-01	2629.22	not significant
10249	FBXO11	1.03	1.38E-01	3.76E-01	2129.04	not significant
10250	KIAA0368	1.03	1.52E-01	3.99E-01	3073.25	not significant
10251	DRAM2	1.03	1.76E-01	4.31E-01	849.37	not significant
10252	RASSF7	1.03	1.46E-01	3.91E-01	358.65	not significant
10253	CHRAC1	1.03	1.26E-01	3.56E-01	3336.93	not significant
10254	HMG20B	1.03	1.71E-01	4.25E-01	1599.34	not significant
10255	TBCK	1.03	1.75E-01	4.31E-01	800.50	not significant
10256	C3orf58	1.03	1.75E-01	4.31E-01	660.40	not significant
10257	AKT1	1.03	7.17E-02	2.49E-01	8610.25	not significant
10258	BRI3	1.03	1.61E-01	4.11E-01	635.36	not significant
10259	TRAPPC6A	1.03	1.20E-01	3.45E-01	254.27	not significant
10260	HMHA1	1.03	6.30E-02	2.28E-01	8561.53	not significant
10261	NEDD9	1.03	1.73E-01	4.27E-01	884.98	not significant
10262	HMGN4	1.03	1.16E-01	3.38E-01	4250.12	not significant
10263	BARD1	1.03	1.54E-01	4.02E-01	1710.35	not significant
10264	RPS6	1.03	1.96E-01	4.59E-01	48098.96	not significant
10265	NCK2	1.03	1.71E-01	4.25E-01	951.03	not significant
10266	TM2D1	1.03	1.68E-01	4.21E-01	455.66	not significant
10267	STOML1	1.03	1.33E-01	3.68E-01	274.59	not significant
10268	CHFR	1.03	9.05E-02	2.88E-01	4531.80	not significant
10269	MRPL34	1.03	1.70E-01	4.23E-01	1858.36	not significant
10270	UROD	1.03	1.76E-01	4.32E-01	1008.38	not significant
10271	TMEM205	1.03	1.71E-01	4.25E-01	805.38	not significant
10272	DNTT	1.03	1.76E-01	4.32E-01	838.65	not significant
10273	C21orf2	1.03	1.57E-01	4.05E-01	442.69	not significant
10274	FBXL20	1.03	1.71E-01	4.25E-01	596.06	not significant
10275	LOC374443	1.03	6.30E-02	2.28E-01	121.44	not significant
10276	43723_1041	1.03	1.00E-01	3.09E-01	6782.44	not significant
10277	ZNF33A	1.03	1.54E-01	4.02E-01	1970.99	not significant
10278	C19orf43	1.03	1.26E-01	3.56E-01	5744.44	not significant
10279	USO1	1.03	1.22E-01	3.49E-01	2851.28	not significant
10280	FLT4	1.03	1.61E-01	4.11E-01	1403.77	not significant
10281	B4GALT3	1.03	1.67E-01	4.20E-01	1223.79	not significant
10282	PLA2G12A	1.03	1.58E-01	4.06E-01	429.51	not significant
10283	ADCY3	1.03	1.39E-01	3.78E-01	2133.90	not significant

10284	MAN1B1	1.03	1.65E-01	4.16E-01	771.54	not significant
10285	CHRNB1	1.03	1.51E-01	3.98E-01	383.52	not significant
10286	C1orf159	1.03	1.67E-01	4.20E-01	527.52	not significant
10287	TMEM67	1.03	1.11E-01	3.28E-01	373.57	not significant
10288	RGS10	1.03	1.51E-01	3.99E-01	2677.40	not significant
10289	RAD51	1.03	1.84E-01	4.42E-01	1519.85	not significant
10290	PEX10	1.03	1.56E-01	4.04E-01	576.67	not significant
10291	TGFB1	1.03	1.40E-01	3.81E-01	3068.24	not significant
10292	BRD8	1.03	1.41E-01	3.82E-01	2261.58	not significant
10293	PIK3R6	1.03	1.86E-01	4.44E-01	417.53	not significant
10294	ECSIT	1.03	1.71E-01	4.25E-01	983.20	not significant
10295	TMEM132D	1.03	1.50E-01	3.97E-01	387.31	not significant
10296	BBS1	1.03	1.33E-01	3.68E-01	319.07	not significant
10297	MESDC1	1.03	1.27E-01	3.58E-01	3062.80	not significant
10298	ZNF131	1.03	1.26E-01	3.55E-01	2120.01	not significant
10299	GLB1	1.03	1.61E-01	4.11E-01	1324.64	not significant
10300	HILPDA	1.03	1.70E-01	4.24E-01	891.90	not significant
10301	EFNA4	1.03	4.52E-02	NA	99.45	not significant
10302	FAM96A	1.03	1.63E-01	4.14E-01	1355.36	not significant
10303	PEMT	1.03	1.66E-01	4.19E-01	815.88	not significant
10304	ELMO1	1.03	6.03E-02	2.22E-01	10461.96	not significant
10305	TMEM9	1.03	1.70E-01	4.23E-01	835.77	not significant
10306	TBC1D19	1.03	1.25E-01	3.54E-01	265.26	not significant
10307	FAM98C	1.03	9.32E-02	2.94E-01	176.25	not significant
10308	SUPT7L	1.03	1.44E-01	3.86E-01	1877.28	not significant
10309	MASTL	1.03	1.49E-01	3.95E-01	1793.15	not significant
10310	COX18	1.03	1.66E-01	4.18E-01	654.47	not significant
10311	ZNF622	1.03	1.62E-01	4.13E-01	1033.84	not significant
10312	NUP210	1.03	1.84E-01	4.42E-01	20016.98	not significant
10313	ZDHHC8	1.03	1.46E-01	3.91E-01	1951.68	not significant
10314	KAT8	1.03	1.55E-01	4.03E-01	1280.05	not significant
10315	ALCAM	1.03	1.63E-01	4.13E-01	971.25	not significant
10316	FAM135A	1.03	1.84E-01	4.42E-01	437.65	not significant
10317	AKIP1	1.03	1.53E-01	4.01E-01	538.05	not significant
10318	PRAF2	1.03	1.17E-01	3.40E-01	240.11	not significant
10319	IL23A	1.03	4.66E-02	1.87E-01	105.59	not significant
10320	GOLGA8A	1.03	5.72E-02	2.15E-01	639.59	not significant
10321	D2HGDH	1.03	1.62E-01	4.12E-01	520.01	not significant
10322	RNF220	1.03	1.10E-01	3.27E-01	2841.88	not significant
10323	ZNF384	1.03	1.31E-01	3.64E-01	2771.27	not significant
10324	HINFP	1.03	1.62E-01	4.13E-01	653.88	not significant
10325	PPIEL	1.03	7.76E-02	2.61E-01	167.61	not significant
10326	SLC30A5	1.03	9.96E-02	3.08E-01	3467.30	not significant
10327	NOL4L	1.03	1.57E-01	4.05E-01	1940.97	not significant
10328	PPIL4	1.03	1.54E-01	4.02E-01	831.99	not significant
10329	MSH6	1.03	8.05E-02	2.68E-01	5348.83	not significant
10330	HIATL1	1.03	1.06E-01	3.20E-01	3447.49	not significant
10331	STUB1	1.03	1.50E-01	3.97E-01	2171.60	not significant
10332	ZGPAT	1.03	1.57E-01	4.05E-01	1167.76	not significant
10333	PIP5K1C	1.03	1.55E-01	4.03E-01	1078.66	not significant
10334	TBC1D10B	1.03	1.09E-01	3.26E-01	2938.79	not significant
10335	POGZ	1.03	1.26E-01	3.56E-01	3542.79	not significant
10336	VAMP1	1.03	1.59E-01	4.07E-01	991.25	not significant
10337	PPP1R9B	1.03	1.10E-01	3.27E-01	2553.72	not significant
10338	CAMK2G	1.03	1.29E-01	3.62E-01	1971.25	not significant
10339	TXLNGY	1.03	1.13E-01	3.32E-01	4685.56	not significant
10340	ATR	1.03	1.38E-01	3.77E-01	1961.13	not significant
10341	HOXB2	1.03	3.43E-01	6.09E-01	447.80	not significant
10342	NLRC5	1.03	1.40E-01	3.81E-01	1761.56	not significant
10343	CBS	1.03	1.54E-01	4.03E-01	1207.60	not significant
10344	B4GALT1	1.03	1.49E-01	3.95E-01	1269.28	not significant
10345	CRELD1	1.03	1.14E-01	3.35E-01	286.85	not significant
10346	STX16	1.03	1.28E-01	3.60E-01	2733.87	not significant
10347	SPTLC2	1.03	1.34E-01	3.69E-01	2952.97	not significant
10348	TMEM87A	1.03	1.20E-01	3.45E-01	2104.73	not significant
10349	LRCH4	1.03	9.96E-02	3.08E-01	3238.44	not significant
10350	DRAP1	1.03	1.33E-01	3.67E-01	3366.58	not significant
10351	CDKN2C	1.03	1.43E-01	3.85E-01	1689.96	not significant
10352	CCDC88C	1.03	1.04E-01	3.15E-01	4669.66	not significant
10353	SVIP	1.03	1.54E-01	4.02E-01	1026.43	not significant
10354	KIAA1715	1.03	1.24E-01	3.53E-01	2294.03	not significant
10355	ZSCAN16-AS1	1.03	5.41E-02	2.08E-01	131.57	not significant
10356	S100P	1.03	1.14E-02	NA	61.33	not significant
10357	RNF168	1.03	1.18E-01	3.40E-01	2505.48	not significant
10358	POLE	1.03	1.92E-01	4.52E-01	11151.14	not significant
10359	TMEM87B	1.03	1.50E-01	3.97E-01	1103.83	not significant
10360	PCGF6	1.03	1.45E-01	3.90E-01	513.88	not significant
10361	ELOVL6	1.03	1.54E-01	4.02E-01	1069.79	not significant
10362	BCL11A	1.03	1.52E-01	3.99E-01	718.63	not significant
10363	TXNDC15	1.03	1.38E-01	3.78E-01	1392.15	not significant
10364	CEP290	1.03	1.51E-01	3.98E-01	1052.77	not significant
10365	PPP1R37	1.03	1.51E-01	3.99E-01	889.82	not significant
10366	AGAP2	1.03	8.93E-02	2.86E-01	4309.02	not significant
10367	LUC7L3	1.03	9.51E-02	2.98E-01	4911.21	not significant
10368	POLD3	1.03	1.12E-01	3.31E-01	2425.75	not significant
10369	ZNF217	1.03	1.22E-01	3.50E-01	2716.06	not significant
10370	VPS13C	1.03	1.20E-01	3.45E-01	4079.73	not significant
10371	EID1	1.03	9.29E-02	2.93E-01	4244.07	not significant

10372	SYVN1	1.03	1.38E-01	3.77E-01	2039.01	not significant
10373	PHLDB3	1.03	8.76E-02	2.83E-01	187.15	not significant
10374	HHAT	1.03	2.95E-02	NA	86.47	not significant
10375	SPIDR	1.03	1.30E-01	3.62E-01	1747.09	not significant
10376	EMB	1.03	1.10E-01	3.27E-01	3533.71	not significant
10377	NOD1	1.03	1.48E-01	3.94E-01	930.45	not significant
10378	MRPL54	1.03	1.54E-01	4.02E-01	901.19	not significant
10379	RNF215	1.03	7.10E-02	2.47E-01	150.77	not significant
10380	DONSON	1.03	1.36E-01	3.74E-01	1536.60	not significant
10381	QTRT1	1.03	1.45E-01	3.89E-01	1347.22	not significant
10382	LUC7L2	1.03	1.51E-01	3.98E-01	733.47	not significant
10383	AEBP1	1.03	6.08E-02	2.23E-01	32837.74	not significant
10384	FPGS	1.03	1.30E-01	3.62E-01	1758.26	not significant
10385	IL18BP	1.03	1.50E-01	3.97E-01	662.17	not significant
10386	PAWR	1.03	1.49E-01	3.96E-01	686.49	not significant
10387	ASH2L	1.03	9.71E-02	3.02E-01	3064.45	not significant
10388	TBC1D10A	1.03	1.45E-01	3.89E-01	1484.28	not significant
10389	TMEM161B	1.03	1.50E-01	3.97E-01	879.86	not significant
10390	EMID1	1.03	1.50E-01	3.97E-01	929.11	not significant
10391	MED12	1.03	1.25E-01	3.54E-01	3135.66	not significant
10392	USP30	1.03	1.49E-01	3.96E-01	754.18	not significant
10393	PGPEP1	1.03	1.46E-01	3.91E-01	1031.80	not significant
10394	SMAD3	1.03	1.40E-01	3.81E-01	549.40	not significant
10395	ERN1	1.03	1.14E-01	3.34E-01	1521.46	not significant
10396	SIN3A	1.03	9.36E-02	2.95E-01	4287.09	not significant
10397	ASB13	1.03	1.45E-01	3.90E-01	502.17	not significant
10398	APLN	1.03	1.28E-01	3.59E-01	1770.80	not significant
10399	ARAF	1.03	1.15E-01	3.36E-01	2057.62	not significant
10400	SHARPIN	1.03	1.42E-01	3.84E-01	1105.08	not significant
10401	OSGIN2	1.03	1.37E-01	3.75E-01	1370.28	not significant
10402	JRKL	1.03	1.49E-01	3.95E-01	850.46	not significant
10403	UQCC2	1.03	1.48E-01	3.95E-01	1061.31	not significant
10404	GPR137	1.03	1.38E-01	3.77E-01	866.62	not significant
10405	WNT3	1.03	1.20E-01	3.45E-01	314.83	not significant
10406	TRPC4AP	1.03	8.89E-02	2.85E-01	4492.32	not significant
10407	ZNF395	1.03	9.75E-02	3.03E-01	2584.47	not significant
10408	OXR1	1.03	1.26E-01	3.56E-01	1486.00	not significant
10409	HES4	1.03	1.46E-01	3.90E-01	720.31	not significant
10410	STX7	1.03	1.46E-01	3.90E-01	626.78	not significant
10411	PACRGL	1.03	1.31E-01	3.65E-01	388.78	not significant
10412	VMP1	1.03	9.07E-02	2.88E-01	3539.81	not significant
10413	YEATS2	1.03	8.78E-02	2.83E-01	4564.13	not significant
10414	C6orf1	1.03	1.35E-01	3.71E-01	406.11	not significant
10415	NS3BP	1.03	6.84E-03	NA	53.48	not significant
10416	CDC42SE2	1.03	4.47E-02	1.83E-01	8990.95	not significant
10417	E2F2	1.03	7.80E-02	2.62E-01	3788.36	not significant
10418	CDK16	1.03	1.25E-01	3.54E-01	1918.01	not significant
10419	PACS2	1.03	1.26E-01	3.56E-01	380.51	not significant
10420	RPL10	1.03	1.06E-01	3.20E-01	8520.13	not significant
10421	MYO9B	1.03	7.35E-02	2.53E-01	6808.19	not significant
10422	PIGL	1.03	1.01E-01	3.09E-01	254.03	not significant
10423	CCNI	1.03	6.70E-02	2.38E-01	9010.84	not significant
10424	ATP1B3	1.03	5.92E-02	2.20E-01	5359.63	not significant
10425	ATP2A3	1.03	5.15E-02	2.01E-01	12573.74	not significant
10426	STARD3NL	1.03	1.00E-01	3.09E-01	2457.27	not significant
10427	MAPK3	1.03	1.03E-01	3.13E-01	2190.12	not significant
10428	PDXP	1.03	1.03E-01	3.14E-01	2523.54	not significant
10429	MADD	1.03	9.83E-02	3.05E-01	2635.59	not significant
10430	BEX4	1.03	1.20E-01	3.45E-01	1743.94	not significant
10431	SPCS2	1.03	1.29E-01	3.60E-01	1541.05	not significant
10432	CYTH1	1.03	4.90E-02	1.94E-01	6712.71	not significant
10433	SORBS3	1.03	1.35E-01	3.72E-01	1454.15	not significant
10434	RPS24	1.03	1.64E-01	4.16E-01	13143.91	not significant
10435	ATL3	1.03	5.86E-02	2.18E-01	5059.61	not significant
10436	RAB33B	1.03	1.39E-01	3.79E-01	513.29	not significant
10437	TOR1AIP1	1.03	7.72E-02	2.60E-01	3729.60	not significant
10438	CERS5	1.03	1.03E-01	3.14E-01	1931.95	not significant
10439	MXD1	1.03	1.07E-01	3.21E-01	267.85	not significant
10440	HES6	1.03	7.13E-02	2.48E-01	197.47	not significant
10441	LINC01436	1.03	1.85E-02	NA	79.43	not significant
10442	PRPSAP1	1.03	1.14E-01	3.34E-01	1928.04	not significant
10443	PDCD7	1.03	1.07E-01	3.21E-01	2415.53	not significant
10444	ARL6IP5	1.03	9.97E-02	3.08E-01	2091.72	not significant
10445	ZNF787	1.03	1.35E-01	3.71E-01	1123.44	not significant
10446	PDE8A	1.03	1.23E-01	3.52E-01	398.85	not significant
10447	ENKD1	1.03	1.11E-01	3.29E-01	296.30	not significant
10448	SPTA1	1.03	1.12E-01	3.31E-01	312.11	not significant
10449	FLJ31306	1.03	1.29E-01	3.62E-01	1327.25	not significant
10450	MFN1	1.03	1.25E-01	3.54E-01	800.96	not significant
10451	TMEM230	1.04	7.41E-02	2.53E-01	3969.50	not significant
10452	MUTYH	1.04	1.34E-01	3.69E-01	1296.78	not significant
10453	PLXNA1	1.04	1.19E-01	3.44E-01	2329.69	not significant
10454	PHPT1	1.04	1.35E-01	3.71E-01	1157.26	not significant
10455	SCOC	1.04	1.03E-01	3.14E-01	2523.06	not significant
10456	PSEN1	1.04	1.21E-01	3.47E-01	1859.23	not significant
10457	B3GNTL1	1.04	1.28E-01	3.59E-01	450.95	not significant
10458	COMMD4	1.04	1.40E-01	3.81E-01	942.96	not significant
10459	IRF7	1.04	9.06E-02	2.88E-01	249.99	not significant

10460	LOC202181	1.04	7.46E-02	2.55E-01	202.55	not significant
10461	TMEM263	1.04	9.19E-01	NA	11.72	not significant
10462	ZCCHC7	1.04	1.34E-01	3.70E-01	833.66	not significant
10463	C1orf86	1.04	1.36E-01	3.74E-01	1436.32	not significant
10464	B4GALT4	1.04	1.30E-01	3.62E-01	509.97	not significant
10465	RTP4	1.04	8.71E-02	2.82E-01	233.40	not significant
10466	SELPLG	1.04	6.09E-02	2.23E-01	5133.66	not significant
10467	RCN1	1.04	1.32E-01	3.67E-01	1334.34	not significant
10468	PHKA2	1.04	1.31E-01	3.65E-01	1438.91	not significant
10469	LRP12	1.04	1.33E-01	3.67E-01	1107.22	not significant
10470	PDE4A	1.04	5.41E-02	2.08E-01	137.86	not significant
10471	GIMAP8	1.04	1.01E-01	3.09E-01	2232.58	not significant
10472	TRABD	1.04	7.29E-02	2.51E-01	3478.74	not significant
10473	CHST11	1.04	7.46E-02	2.54E-01	17064.36	not significant
10474	PMS1	1.04	1.17E-01	3.38E-01	1541.75	not significant
10475	DDX60	1.04	1.30E-01	3.62E-01	1126.95	not significant
10476	GTPBP3	1.04	1.22E-01	3.50E-01	1503.78	not significant
10477	ATXN7L2	1.04	1.52E-01	3.99E-01	440.44	not significant
10478	NFATC2IP	1.04	1.08E-01	3.23E-01	3090.27	not significant
10479	RHEB	1.04	1.23E-01	3.52E-01	1751.94	not significant
10480	ZNF443	1.04	1.27E-01	3.58E-01	442.68	not significant
10481	CD84	1.04	1.18E-01	3.40E-01	3413.27	not significant
10482	SPNS1	1.04	1.12E-01	3.31E-01	1695.45	not significant
10483	RAB40C	1.04	1.32E-01	3.66E-01	530.09	not significant
10484	SLC25A36	1.04	8.15E-02	2.70E-01	3294.96	not significant
10485	OSBPL5	1.04	1.08E-01	3.24E-01	1699.17	not significant
10486	GOLT1B	1.04	1.10E-01	3.27E-01	1651.47	not significant
10487	GPATCH3	1.04	1.33E-01	3.68E-01	569.25	not significant
10488	ARHGAP32	1.04	1.27E-01	3.56E-01	1724.97	not significant
10489	METTL21A	1.04	1.28E-01	3.59E-01	734.19	not significant
10490	CDS2	1.04	7.29E-02	2.51E-01	3485.30	not significant
10491	ACD	1.04	1.24E-01	3.52E-01	1203.40	not significant
10492	MAP3K12	1.04	1.30E-01	3.63E-01	692.80	not significant
10493	NT5M	1.04	8.97E-02	2.87E-01	264.39	not significant
10494	WDFY2	1.04	1.30E-01	3.62E-01	624.94	not significant
10495	ZNF428	1.04	1.21E-01	3.48E-01	1607.08	not significant
10496	ABHD17B	1.04	1.05E-01	3.17E-01	1974.48	not significant
10497	FOXN3	1.04	1.15E-01	3.35E-01	2896.61	not significant
10498	SHKBP1	1.04	8.09E-02	2.69E-01	2667.07	not significant
10499	ZBTB10	1.04	1.18E-01	3.42E-01	1058.26	not significant
10500	PRKCQ-AS1	1.04	1.25E-01	3.54E-01	979.69	not significant
10501	COL7A1	1.04	1.02E-01	3.11E-01	290.41	not significant
10502	NCKAP1L	1.04	7.63E-02	2.58E-01	6065.50	not significant
10503	TSPYL1	1.04	1.01E-01	3.09E-01	2017.82	not significant
10504	SURF4	1.04	1.16E-01	3.37E-01	1042.51	not significant
10505	LOH12CR1	1.04	9.87E-02	3.06E-01	257.54	not significant
10506	RBM7	1.04	1.16E-01	3.38E-01	1177.87	not significant
10507	TJAP1	1.04	1.15E-01	3.36E-01	1297.33	not significant
10508	TSPAN33	1.04	1.28E-01	3.60E-01	736.06	not significant
10509	DALRD3	1.04	1.16E-01	3.37E-01	364.91	not significant
10510	TMEM173	1.04	1.21E-01	3.47E-01	1175.02	not significant
10511	MAN2A1	1.04	1.10E-01	3.27E-01	2314.20	not significant
10512	S1PR1	1.04	1.23E-01	3.52E-01	1257.75	not significant
10513	SNX5	1.04	6.57E-02	2.35E-01	5038.74	not significant
10514	COX5A	1.04	1.01E-01	3.09E-01	3166.21	not significant
10515	MAL	1.04	1.01E-01	3.10E-01	6831.10	not significant
10516	DHRS1	1.04	6.20E-02	2.26E-01	163.69	not significant
10517	YIPF2	1.04	1.27E-01	3.57E-01	683.80	not significant
10518	STAM	1.04	1.25E-01	3.55E-01	791.57	not significant
10519	NAPEPLD	1.04	1.27E-01	3.56E-01	654.81	not significant
10520	CCND3	1.04	4.32E-02	1.79E-01	20931.37	not significant
10521	EVL	1.04	2.29E-02	1.18E-01	16781.16	not significant
10522	MMS19	1.04	9.01E-02	2.87E-01	2448.57	not significant
10523	UBL7	1.04	1.14E-01	3.34E-01	1328.13	not significant
10524	TYK2	1.04	7.70E-02	2.60E-01	3582.49	not significant
10525	DNMBP	1.04	1.24E-01	3.53E-01	634.98	not significant
10526	TMEM208	1.04	1.24E-01	3.52E-01	1268.06	not significant
10527	RPS29	1.04	1.46E-01	3.90E-01	6027.64	not significant
10528	DDX42	1.04	5.72E-02	2.15E-01	6965.04	not significant
10529	PRKAA1	1.04	6.99E-02	2.45E-01	3256.53	not significant
10530	SIGLEC6	1.04	7.84E-02	2.63E-01	3971.90	not significant
10531	ABHD3	1.04	8.24E-02	2.72E-01	2317.73	not significant
10532	DIP2A	1.04	1.12E-01	3.31E-01	1060.90	not significant
10533	FZD1	1.04	8.10E-02	2.69E-01	239.28	not significant
10534	RUFY1	1.04	1.05E-01	3.17E-01	1551.26	not significant
10535	ZNF211	1.04	1.16E-01	3.38E-01	578.50	not significant
10536	TWSG1	1.04	1.18E-01	3.41E-01	1232.97	not significant
10537	FAM122C	1.04	4.04E-02	1.70E-01	121.99	not significant
10538	ARL2BP	1.04	1.01E-01	3.09E-01	2032.53	not significant
10539	UNC5CL	1.04	3.02E-02	1.41E-01	111.89	not significant
10540	TSEN15	1.04	8.42E-02	2.76E-01	2691.07	not significant
10541	SQRDL	1.04	1.22E-01	3.50E-01	738.35	not significant
10542	ATP5G2	1.04	8.42E-02	2.76E-01	8821.37	not significant
10543	RRM2	1.04	2.35E-02	1.20E-01	18482.48	not significant
10544	JAKMIP1	1.04	9.66E-02	3.02E-01	1876.43	not significant
10545	RCN2	1.04	9.21E-02	2.92E-01	2728.81	not significant
10546	LSM4	1.04	8.70E-02	2.82E-01	7595.69	not significant
10547	ZFC3H1	1.04	9.11E-02	2.89E-01	3145.38	not significant

10548	GPR56	1.04	8.36E-02	2.75E-01	2398.29	not significant
10549	SFXN2	1.04	1.08E-01	3.23E-01	1057.95	not significant
10550	CDC45	1.04	5.50E-02	2.10E-01	4136.43	not significant
10551	RBM6	1.04	7.28E-02	2.51E-01	4460.39	not significant
10552	ZNF740	1.04	8.64E-02	2.81E-01	2062.32	not significant
10553	CREBL2	1.04	1.16E-01	3.38E-01	791.68	not significant
10554	ZNF500	1.04	9.82E-02	3.05E-01	337.86	not significant
10555	LYRM4	1.04	1.18E-01	3.42E-01	951.76	not significant
10556	MFAP4	1.04	1.07E-01	3.22E-01	1521.19	not significant
10557	XKR8	1.04	1.01E-01	3.09E-01	352.62	not significant
10558	SLC2A4RG	1.04	1.02E-01	3.11E-01	351.36	not significant
10559	APEX1	1.04	4.53E-02	1.85E-01	8986.81	not significant
10560	INPP5B	1.04	1.11E-01	3.28E-01	1167.83	not significant
10561	PRCP	1.04	1.18E-01	3.41E-01	619.88	not significant
10562	KLHL26	1.04	1.10E-01	3.27E-01	419.27	not significant
10563	GPR161	1.04	6.07E-02	2.23E-01	175.20	not significant
10564	ZNF445	1.04	9.97E-02	3.08E-01	2612.36	not significant
10565	DLGAP4	1.04	1.08E-01	3.23E-01	1115.72	not significant
10566	ASCC1	1.04	1.09E-01	3.25E-01	1029.90	not significant
10567	KLHL6	1.04	8.27E-02	2.73E-01	2275.70	not significant
10568	PCSK7	1.04	9.52E-02	2.98E-01	1729.44	not significant
10569	FRAT1	1.04	2.72E-02	1.32E-01	114.17	not significant
10570	SND1	1.04	1.93E-02	1.04E-01	11572.25	not significant
10571	CTSC	1.04	4.66E-02	1.87E-01	5298.47	not significant
10572	PIGO	1.04	1.09E-01	3.25E-01	1154.70	not significant
10573	RINL	1.04	1.15E-01	3.36E-01	607.98	not significant
10574	LMAN2	1.04	4.17E-02	1.74E-01	6035.92	not significant
10575	OBSCN	1.04	1.13E-01	3.33E-01	1406.26	not significant
10576	PITPNA-AS1	1.04	6.65E-02	2.37E-01	211.68	not significant
10577	RPS7	1.04	7.31E-02	2.52E-01	13557.71	not significant
10578	TMEM14C	1.04	1.02E-01	3.12E-01	1569.57	not significant
10579	MLH1	1.04	8.03E-02	2.68E-01	2618.52	not significant
10580	LOC642846	1.04	1.14E-01	3.35E-01	754.63	not significant
10581	ANKLE2	1.04	3.62E-02	1.59E-01	5712.06	not significant
10582	PTPRK	1.04	1.02E-01	3.12E-01	1765.96	not significant
10583	ZNF784	1.04	2.46E-02	NA	97.64	not significant
10584	LINC01004	1.04	1.86E-02	NA	89.20	not significant
10585	RHOT2	1.04	6.22E-02	2.27E-01	3041.91	not significant
10586	RAP1GAP	1.04	7.71E-02	2.60E-01	3719.52	not significant
10587	CITED2	1.04	1.13E-01	3.33E-01	641.05	not significant
10588	A1BG	1.04	8.77E-02	2.83E-01	311.79	not significant
10589	MFSD10	1.04	1.07E-01	3.21E-01	931.14	not significant
10590	MAP2K7	1.04	8.00E-02	2.67E-01	2237.85	not significant
10591	DUS4L	1.04	1.12E-01	3.31E-01	574.80	not significant
10592	CDPF1	1.04	6.46E-02	2.32E-01	200.56	not significant
10593	NIPSNAP1	1.04	7.99E-02	2.67E-01	2511.86	not significant
10594	TRAPPC2	1.04	1.12E-01	3.31E-01	708.02	not significant
10595	SYS1	1.04	9.82E-02	3.05E-01	1339.44	not significant
10596	ABHD16A	1.04	1.06E-01	3.20E-01	994.66	not significant
10597	MR1	1.04	1.09E-01	3.26E-01	657.16	not significant
10598	PKN1	1.04	3.43E-02	1.53E-01	6493.85	not significant
10599	BCR	1.04	5.70E-02	2.15E-01	3202.51	not significant
10600	USP21	1.04	9.70E-02	3.02E-01	1267.30	not significant
10601	PCNT	1.04	8.69E-02	2.82E-01	2317.75	not significant
10602	LRRC8A	1.04	1.02E-01	3.12E-01	1199.02	not significant
10603	GABRB3	1.04	1.05E-01	3.17E-01	910.31	not significant
10604	SLC38A9	1.04	1.03E-01	3.13E-01	1068.01	not significant
10605	CROCC	1.04	1.09E-01	3.25E-01	833.94	not significant
10606	DHRS13	1.04	1.10E-01	3.27E-01	590.19	not significant
10607	RWDD3	1.04	4.88E-02	1.94E-01	221.92	not significant
10608	NFE2L3	1.04	7.51E-02	2.55E-01	247.06	not significant
10609	PGBD2	1.04	7.65E-02	2.59E-01	220.19	not significant
10610	LTA4H	1.04	5.03E-02	1.98E-01	3337.35	not significant
10611	CROCCP2	1.04	1.07E-01	3.21E-01	504.88	not significant
10612	FZD5	1.04	5.48E-02	2.09E-01	150.91	not significant
10613	SUMO2	1.04	5.90E-02	2.19E-01	6977.77	not significant
10614	GIMAP6	1.04	3.64E-02	1.59E-01	4718.22	not significant
10615	WDTC1	1.04	7.44E-02	2.54E-01	2089.66	not significant
10616	ACYP1	1.04	1.01E-01	3.09E-01	546.28	not significant
10617	ZBTB1	1.04	6.73E-02	2.39E-01	2762.78	not significant
10618	CD248	1.04	1.07E-01	3.22E-01	610.48	not significant
10619	ZSCAN26	1.04	8.47E-02	2.76E-01	282.44	not significant
10620	C9orf72	1.04	8.07E-02	2.68E-01	252.21	not significant
10621	NDFIP1	1.04	3.54E-02	1.57E-01	5303.34	not significant
10622	AKR1A1	1.04	6.86E-02	2.42E-01	2878.31	not significant
10623	PRRC2B	1.04	6.57E-02	2.35E-01	6602.31	not significant
10624	TSC22D1	1.04	7.51E-02	2.55E-01	1959.55	not significant
10625	SMARCC2	1.04	4.50E-02	1.84E-01	8659.52	not significant
10626	PELO	1.04	8.11E-02	2.69E-01	1793.33	not significant
10627	POFUT2	1.04	1.00E-01	3.09E-01	442.43	not significant
10628	SFT2D1	1.04	7.97E-02	2.66E-01	1822.33	not significant
10629	SSR3	1.04	2.68E-02	1.30E-01	6644.58	not significant
10630	TSNAX	1.04	8.99E-02	2.87E-01	1643.05	not significant
10631	MAPK7	1.04	9.99E-02	3.08E-01	956.80	not significant
10632	TRIQK	1.04	1.00E-01	3.09E-01	429.30	not significant
10633	NUBP2	1.04	8.79E-02	2.84E-01	2423.95	not significant
10634	TMEM218	1.04	1.05E-01	3.18E-01	538.05	not significant
10635	RFC4	1.04	6.03E-02	2.22E-01	3200.93	not significant

10636	PNISR	1.04	6.50E-02	2.33E-01	3903.12	not significant
10637	BCKDHA	1.04	1.04E-01	3.17E-01	660.56	not significant
10638	RFC5	1.04	3.49E-02	1.56E-01	4827.28	not significant
10639	RTN3	1.04	2.70E-02	1.31E-01	6617.95	not significant
10640	REPIN1	1.04	3.55E-02	1.57E-01	4746.66	not significant
10641	TBC1D9	1.04	1.04E-01	3.16E-01	496.03	not significant
10642	PLAUR	1.04	9.56E-02	2.99E-01	350.05	not significant
10643	GATSL3	1.04	9.27E-02	2.93E-01	1287.18	not significant
10644	BDH2	1.04	1.06E-01	3.19E-01	852.02	not significant
10645	SORL1	1.04	8.75E-02	2.83E-01	2896.57	not significant
10646	TCTN3	1.04	9.42E-02	2.96E-01	1208.02	not significant
10647	BAHCC1	1.04	9.73E-02	3.03E-01	1756.84	not significant
10648	ALKBH4	1.04	9.92E-02	3.07E-01	583.48	not significant
10649	ZNF747	1.04	1.05E-01	3.18E-01	772.36	not significant
10650	CAST	1.04	1.03E-01	3.13E-01	612.66	not significant
10651	CLCN3	1.04	6.36E-02	2.30E-01	4434.99	not significant
10652	TYMS	1.04	2.82E-02	1.35E-01	24436.59	not significant
10653	NMRAL1	1.04	6.32E-02	2.29E-01	2945.90	not significant
10654	C18orf8	1.04	8.47E-02	2.76E-01	1365.46	not significant
10655	OSTC	1.04	5.76E-02	2.16E-01	4024.45	not significant
10656	SLIT1	1.04	5.10E-02	2.00E-01	7237.40	not significant
10657	TATDN3	1.04	9.68E-02	3.02E-01	877.61	not significant
10658	WDR70	1.04	1.05E-01	3.18E-01	698.86	not significant
10659	XRCC2	1.04	1.01E-01	3.10E-01	1654.36	not significant
10660	PPM1B	1.04	7.93E-02	2.65E-01	1962.98	not significant
10661	PLOD1	1.04	8.74E-02	2.83E-01	1328.01	not significant
10662	ITK	1.04	2.86E-02	1.36E-01	7246.15	not significant
10663	DERL2	1.04	9.24E-02	2.92E-01	1075.91	not significant
10664	CCDC64	1.04	9.51E-02	2.98E-01	1005.23	not significant
10665	ZNF154	1.04	9.87E-02	3.06E-01	1101.99	not significant
10666	ZNF10	1.04	1.01E-01	3.09E-01	524.60	not significant
10667	WDYHV1	1.04	9.95E-02	3.08E-01	895.79	not significant
10668	RNF149	1.04	7.86E-02	2.63E-01	1510.83	not significant
10669	POLE4	1.04	1.06E-01	3.19E-01	873.06	not significant
10670	ABHD17A	1.04	9.75E-02	3.03E-01	982.49	not significant
10671	C2orf48	1.04	1.43E-02	NA	82.46	not significant
10672	RBCK1	1.04	3.81E-02	1.64E-01	3917.45	not significant
10673	FIGNL2	1.04	1.28E-02	NA	81.63	not significant
10674	ERAP2	1.04	3.30E-02	1.49E-01	11532.81	not significant
10675	DNA2	1.04	5.20E-02	2.02E-01	2913.64	not significant
10676	NUDT8	1.04	7.38E-02	2.53E-01	278.41	not significant
10677	RSRP1	1.04	8.99E-02	2.87E-01	990.61	not significant
10678	FAM89A	1.04	6.33E-02	2.29E-01	210.17	not significant
10679	STMN1	1.04	2.70E-02	1.31E-01	37240.95	not significant
10680	POLM	1.04	5.64E-02	2.13E-01	3324.62	not significant
10681	CDH4	1.04	8.31E-02	2.73E-01	1278.74	not significant
10682	ZNF692	1.04	9.22E-02	2.92E-01	896.22	not significant
10683	CD5	1.04	2.57E-02	1.27E-01	6042.29	not significant
10684	APMAP	1.04	4.46E-02	1.83E-01	3590.78	not significant
10685	RBBP4	1.04	1.13E-02	7.22E-02	15299.06	not significant
10686	C5orf15	1.04	7.04E-02	2.46E-01	1940.65	not significant
10687	SLC4A4	1.04	9.49E-02	2.97E-01	1104.25	not significant
10688	WDR83	1.04	9.21E-02	2.92E-01	470.85	not significant
10689	FGL2	1.04	8.71E-02	2.82E-01	378.30	not significant
10690	RASA4CP	1.04	5.36E-02	2.06E-01	191.47	not significant
10691	EXT2	1.04	7.87E-02	2.64E-01	1466.86	not significant
10692	SLC11A2	1.04	7.06E-02	2.46E-01	1904.91	not significant
10693	IMPDH2	1.04	3.34E-02	1.50E-01	10384.33	not significant
10694	MCM5	1.04	2.64E-02	1.29E-01	12312.74	not significant
10695	RPL26	1.04	6.21E-02	2.26E-01	8520.59	not significant
10696	MBD4	1.04	5.78E-02	2.16E-01	2259.98	not significant
10697	GGT7	1.04	8.87E-02	2.85E-01	978.07	not significant
10698	LOC399491	1.04	7.63E-02	2.58E-01	312.18	not significant
10699	ACAP3	1.04	6.64E-02	2.36E-01	1863.18	not significant
10700	DUSP22	1.04	8.89E-02	2.85E-01	865.91	not significant
10701	VEGFB	1.04	9.28E-02	2.93E-01	1131.51	not significant
10702	C1D	1.04	9.41E-02	2.96E-01	579.79	not significant
10703	SLC18B1	1.04	9.40E-02	2.96E-01	492.41	not significant
10704	ZFYVE1	1.04	9.36E-02	2.95E-01	766.30	not significant
10705	CPSF1	1.04	3.99E-02	1.70E-01	4377.55	not significant
10706	ZNF674-AS1	1.04	4.64E-02	1.87E-01	162.67	not significant
10707	KIAA1107	1.04	1.87E-02	NA	99.46	not significant
10708	MOB2	1.04	9.62E-02	3.01E-01	449.75	not significant
10709	SCD	1.04	3.26E-02	1.48E-01	35041.20	not significant
10710	ZFAND1	1.04	9.41E-02	2.96E-01	834.90	not significant
10711	ARHGAP27	1.04	9.83E-02	3.05E-01	836.26	not significant
10712	SPG7	1.04	6.57E-02	2.35E-01	1791.04	not significant
10713	SASS6	1.04	7.82E-02	2.63E-01	1549.46	not significant
10714	ACVR2B	1.04	8.90E-02	2.85E-01	1201.27	not significant
10715	EXOSC9	1.04	5.12E-02	2.00E-01	2662.74	not significant
10716	MICU2	1.04	7.48E-02	2.55E-01	1384.97	not significant
10717	PSPH	1.04	6.82E-02	2.41E-01	2062.70	not significant
10718	ZFP36L1	1.04	7.79E-02	2.62E-01	1207.39	not significant
10719	IFT80	1.04	9.08E-02	2.89E-01	735.20	not significant
10720	HLA-C	1.04	4.48E-02	1.83E-01	8291.46	not significant
10721	PHF2	1.04	4.18E-02	1.75E-01	3018.95	not significant
10722	SLC38A10	1.04	5.22E-02	2.02E-01	3062.74	not significant
10723	THEM6	1.04	8.74E-02	2.83E-01	967.17	not significant

10724	GCHFR	1.04	7.67E-02	2.59E-01	159.79	not significant
10725	YJEFN3	1.04	1.50E-02	NA	88.70	not significant
10726	NAP1L1	1.04	1.23E-02	7.66E-02	34582.38	not significant
10727	RNPEPL1	1.04	6.35E-02	2.29E-01	1939.75	not significant
10728	KHK	1.04	6.66E-02	2.37E-01	268.91	not significant
10729	TP53	1.04	2.95E-02	1.39E-01	5016.96	not significant
10730	WDR48	1.04	6.61E-02	2.36E-01	1523.71	not significant
10731	SEC11C	1.04	7.99E-02	2.67E-01	1596.66	not significant
10732	IAH1	1.04	8.91E-02	2.85E-01	961.48	not significant
10733	SCCPDH	1.04	4.32E-02	1.79E-01	3548.68	not significant
10734	PNKD	1.04	8.85E-02	2.85E-01	824.39	not significant
10735	RAP2A	1.04	6.34E-02	2.29E-01	1747.81	not significant
10736	CDC42BPG	1.04	5.94E-02	2.20E-01	219.71	not significant
10737	ZC3H10	1.04	8.49E-02	2.77E-01	437.13	not significant
10738	WDR91	1.04	8.88E-02	2.85E-01	485.83	not significant
10739	LEPRE1	1.04	7.03E-02	2.46E-01	1344.39	not significant
10740	MIB2	1.04	8.15E-02	2.70E-01	1024.71	not significant
10741	SLC48A1	1.04	1.89E-02	NA	98.77	not significant
10742	COX7A2L	1.04	5.53E-02	2.10E-01	4281.71	not significant
10743	C6orf89	1.04	3.07E-02	1.42E-01	4262.45	not significant
10744	RASAL3	1.04	4.60E-02	1.86E-01	2406.50	not significant
10745	RIMKLB	1.04	8.71E-02	2.82E-01	794.38	not significant
10746	TSPAN31	1.04	7.64E-02	2.59E-01	327.80	not significant
10747	L3MBTL3	1.04	8.35E-02	2.74E-01	946.21	not significant
10748	ZNF212	1.04	8.69E-02	2.82E-01	697.08	not significant
10749	MAP10	1.04	8.70E-02	2.82E-01	551.36	not significant
10750	CDK19	1.04	7.40E-02	2.53E-01	1333.18	not significant
10751	FGD3	1.04	7.95E-02	2.66E-01	974.26	not significant
10752	DNAJC25	1.04	5.83E-02	2.18E-01	227.42	not significant
10753	DHCR24	1.04	3.39E-02	1.51E-01	6654.49	not significant
10754	HPS5	1.04	7.81E-02	2.63E-01	1006.58	not significant
10755	CLK3	1.04	6.63E-02	2.36E-01	1432.55	not significant
10756	SLC45A4	1.04	5.49E-02	2.09E-01	2339.80	not significant
10757	LIME1	1.04	8.53E-02	2.78E-01	738.72	not significant
10758	TRAT1	1.04	6.96E-02	2.44E-01	1552.09	not significant
10759	ANKRD32	1.04	6.82E-02	2.41E-01	1388.54	not significant
10760	LINC01366	1.04	4.19E-02	1.75E-01	158.18	not significant
10761	TMC8	1.04	2.69E-02	1.30E-01	6959.57	not significant
10762	ATP8A1	1.04	8.60E-02	2.80E-01	635.94	not significant
10763	RECQL	1.04	3.69E-02	1.60E-01	3136.54	not significant
10764	RNF31	1.04	4.50E-02	1.84E-01	2552.96	not significant
10765	VAMP2	1.04	8.05E-02	2.68E-01	861.37	not significant
10766	PEX16	1.04	8.32E-02	2.74E-01	792.80	not significant
10767	DERL3	1.04	3.03E-02	1.41E-01	126.29	not significant
10768	TNIP1	1.04	4.94E-02	1.95E-01	3147.79	not significant
10769	WDR76	1.04	5.71E-02	2.15E-01	2294.65	not significant
10770	SETD1B	1.04	5.81E-02	2.17E-01	3182.73	not significant
10771	PCNXL2	1.04	8.83E-02	2.84E-01	711.79	not significant
10772	NRROS	1.04	1.87E-02	1.02E-01	6363.85	not significant
10773	CDIPT	1.04	4.54E-02	1.85E-01	2253.46	not significant
10774	UTRN	1.04	6.36E-02	2.30E-01	3373.35	not significant
10775	PMS2P1	1.04	7.46E-02	2.54E-01	1003.04	not significant
10776	TMEM154	1.04	8.78E-02	2.83E-01	800.29	not significant
10777	RPS21	1.04	1.04E-01	3.17E-01	9615.72	not significant
10778	QARS	1.04	2.59E-02	1.28E-01	4502.39	not significant
10779	GCH1	1.04	4.33E-02	1.79E-01	3054.36	not significant
10780	STARD4	1.04	4.79E-02	1.91E-01	2105.84	not significant
10781	TMEM179B	1.04	8.29E-02	2.73E-01	718.92	not significant
10782	COA3	1.04	8.39E-02	2.75E-01	572.01	not significant
10783	KLC4	1.04	7.51E-02	2.56E-01	370.88	not significant
10784	SLC25A16	1.04	7.82E-02	2.63E-01	389.52	not significant
10785	RSL24D1	1.04	4.92E-02	1.95E-01	3965.07	not significant
10786	RFX3	1.04	7.18E-02	2.49E-01	434.46	not significant
10787	NASP	1.04	2.24E-02	1.16E-01	11130.67	not significant
10788	ZNF672	1.04	4.53E-02	1.85E-01	2261.36	not significant
10789	WDR11	1.04	6.23E-02	2.27E-01	1424.08	not significant
10790	SNHG1	1.04	1.88E-02	1.03E-01	6136.54	not significant
10791	HIAT1	1.04	3.01E-02	1.41E-01	3363.37	not significant
10792	PLA2G15	1.04	8.34E-02	2.74E-01	291.79	not significant
10793	HS1BP3	1.04	5.88E-02	2.19E-01	230.95	not significant
10794	STARD9	1.04	7.41E-02	2.53E-01	391.52	not significant
10795	LY6E	1.04	6.86E-02	2.42E-01	1622.43	not significant
10796	TCTN2	1.04	4.06E-02	1.71E-01	172.61	not significant
10797	CEP72	1.04	8.12E-02	2.69E-01	543.24	not significant
10798	MTCH1	1.04	1.91E-02	1.04E-01	7269.37	not significant
10799	ODF2L	1.04	7.94E-02	2.65E-01	731.22	not significant
10800	FOXO6	1.04	8.28E-02	2.73E-01	452.99	not significant
10801	TMEM106C	1.04	3.66E-02	1.59E-01	7287.29	not significant
10802	LRRC57	1.05	8.02E-02	2.67E-01	504.85	not significant
10803	NFATC2	1.05	4.40E-02	1.81E-01	2178.26	not significant
10804	LOC100507419	1.05	3.17E-02	1.45E-01	138.60	not significant
10805	VPS51	1.05	4.39E-02	1.81E-01	3018.91	not significant
10806	GTPBP8	1.05	7.70E-02	2.60E-01	729.88	not significant
10807	C2CD5	1.05	4.72E-02	1.89E-01	2412.33	not significant
10808	NARF	1.05	3.91E-02	1.67E-01	2921.10	not significant
10809	KBTBD4	1.05	8.01E-02	2.67E-01	838.66	not significant
10810	CCDC71L	1.05	7.78E-02	2.62E-01	721.70	not significant
10811	DVL3	1.05	2.49E-02	1.24E-01	3918.96	not significant

10812	PKN3	1.05	5.85E-02	2.18E-01	246.96	not significant
10813	ARL6IP6	1.05	5.26E-02	2.03E-01	1948.57	not significant
10814	HEIH	1.05	7.19E-02	2.49E-01	710.35	not significant
10815	HCAR1	1.05	8.13E-02	2.70E-01	495.93	not significant
10816	RFC1	1.05	1.79E-02	9.94E-02	6431.77	not significant
10817	SLC23A2	1.05	5.35E-02	2.06E-01	2757.38	not significant
10818	FLT1	1.05	6.55E-02	2.35E-01	1574.25	not significant
10819	CSNK1E	1.05	4.03E-02	1.70E-01	2134.51	not significant
10820	ZNF792	1.05	6.00E-02	2.21E-01	255.74	not significant
10821	TRG-AS1	1.05	2.73E-02	1.32E-01	3839.18	not significant
10822	TMEM123	1.05	8.57E-03	5.97E-02	18499.45	not significant
10823	TOM1L2	1.05	7.05E-02	2.46E-01	342.97	not significant
10824	WDR54	1.05	7.56E-02	2.57E-01	640.61	not significant
10825	DIDO1	1.05	3.28E-02	1.48E-01	4250.03	not significant
10826	SENP7	1.05	6.86E-02	2.42E-01	1095.67	not significant
10827	STYXL1	1.05	6.55E-02	2.35E-01	286.51	not significant
10828	VEZT	1.05	2.37E-02	1.20E-01	3799.43	not significant
10829	ZNF646	1.05	5.95E-02	2.21E-01	1710.82	not significant
10830	HDHD3	1.05	6.83E-02	2.41E-01	301.18	not significant
10831	PLK4	1.05	3.65E-02	1.59E-01	3432.48	not significant
10832	MAN2B2	1.05	5.34E-02	2.06E-01	1683.64	not significant
10833	RTTN	1.05	6.74E-02	2.39E-01	1436.40	not significant
10834	C17orf53	1.05	7.79E-02	2.62E-01	506.05	not significant
10835	UNKL	1.05	7.30E-02	2.51E-01	787.18	not significant
10836	SLC2A11	1.05	2.60E-02	1.28E-01	122.82	not significant
10837	PGLS	1.05	5.47E-02	2.09E-01	2092.56	not significant
10838	TMEM243	1.05	7.09E-02	2.47E-01	903.07	not significant
10839	WDR5B	1.05	6.63E-02	2.36E-01	323.26	not significant
10840	EPHX2	1.05	6.11E-02	2.24E-01	321.81	not significant
10841	PFDN4	1.05	7.28E-02	2.51E-01	542.65	not significant
10842	SLC39A4	1.05	1.53E-02	9.03E-02	104.89	not significant
10843	DENND2D	1.05	1.01E-02	6.70E-02	7771.48	not significant
10844	SEMA4D	1.05	1.63E-02	9.37E-02	9669.04	not significant
10845	MTG1	1.05	5.23E-02	2.03E-01	1481.51	not significant
10846	EIF2A	1.05	2.17E-02	1.13E-01	3649.48	not significant
10847	PJA2	1.05	2.48E-02	1.24E-01	3567.74	not significant
10848	C16orf58	1.05	4.58E-02	1.86E-01	1814.95	not significant
10849	SFMBT1	1.05	5.58E-02	2.12E-01	1761.40	not significant
10850	FANCD2	1.05	3.18E-02	1.45E-01	3896.15	not significant
10851	QPCTL	1.05	6.39E-02	2.30E-01	303.76	not significant
10852	CLUAP1	1.05	7.41E-02	2.53E-01	557.96	not significant
10853	PREX1	1.05	2.80E-02	1.34E-01	3085.71	not significant
10854	CD200R1	1.05	7.03E-02	2.46E-01	307.10	not significant
10855	JUNB	1.05	3.72E-02	1.61E-01	3082.18	not significant
10856	AKAP8L	1.05	3.83E-02	1.65E-01	2126.26	not significant
10857	CRIPT	1.05	7.49E-02	2.55E-01	419.88	not significant
10858	IPO7	1.05	6.13E-03	4.72E-02	15092.16	not significant
10859	SLC6A6	1.05	4.24E-02	1.77E-01	2817.11	not significant
10860	CEP83	1.05	6.04E-02	2.22E-01	1076.14	not significant
10861	ABHD15	1.05	7.21E-02	2.50E-01	476.22	not significant
10862	BSDC1	1.05	4.98E-02	1.96E-01	1617.83	not significant
10863	PLEKHJ1	1.05	5.08E-02	1.99E-01	2619.58	not significant
10864	IRX3	1.05	7.46E-02	2.54E-01	771.35	not significant
10865	DPY19L2P2	1.05	6.89E-02	2.42E-01	717.62	not significant
10866	SAMD9L	1.05	7.27E-02	2.51E-01	873.95	not significant
10867	NIN	1.05	3.89E-02	1.66E-01	3369.07	not significant
10868	ATXN2L	1.05	1.44E-02	8.62E-02	14531.48	not significant
10869	MAD2L2	1.05	4.55E-02	1.85E-01	5223.67	not significant
10870	TTC9C	1.05	6.83E-02	2.41E-01	863.15	not significant
10871	MZT1	1.05	4.56E-02	1.86E-01	2845.54	not significant
10872	GINS2	1.05	4.16E-02	1.74E-01	3276.43	not significant
10873	EEF1A1	1.05	1.92E-02	1.04E-01	98678.03	not significant
10874	GRAMD4	1.05	1.93E-02	1.04E-01	5064.95	not significant
10875	EML3	1.05	4.52E-02	1.85E-01	1750.92	not significant
10876	TUBG2	1.05	6.19E-02	2.26E-01	281.91	not significant
10877	NAA40	1.05	4.46E-02	1.83E-01	1948.20	not significant
10878	TEP1	1.05	5.28E-02	2.04E-01	1604.09	not significant
10879	VEGFA	1.05	6.39E-02	2.30E-01	1085.95	not significant
10880	APBA3	1.05	7.17E-02	2.49E-01	813.33	not significant
10881	IQGAP3	1.05	7.28E-02	2.51E-01	813.53	not significant
10882	TCTA	1.05	6.80E-02	2.41E-01	692.10	not significant
10883	UBXN8	1.05	7.26E-02	2.51E-01	628.28	not significant
10884	SCD5	1.05	4.57E-02	1.86E-01	1712.89	not significant
10885	JKAMP	1.05	6.04E-02	2.22E-01	1110.21	not significant
10886	ALG10B	1.05	6.70E-02	2.38E-01	1253.85	not significant
10887	CHIC2	1.05	5.86E-02	2.18E-01	266.60	not significant
10888	SRPK2	1.05	1.20E-02	7.54E-02	5539.25	not significant
10889	ASXL1	1.05	2.15E-02	1.13E-01	5582.67	not significant
10890	TPRA1	1.05	6.12E-02	2.24E-01	979.79	not significant
10891	DNAJC18	1.05	7.04E-02	2.46E-01	448.63	not significant
10892	STX2	1.05	5.54E-02	2.11E-01	1239.47	not significant
10893	PTGES2	1.05	6.23E-02	2.27E-01	952.11	not significant
10894	FBXO9	1.05	3.53E-02	1.56E-01	2102.20	not significant
10895	RASA2	1.05	5.51E-02	2.10E-01	1419.20	not significant
10896	GCNT1	1.05	6.42E-02	2.31E-01	338.50	not significant
10897	COA1	1.05	3.07E-02	1.42E-01	3266.51	not significant
10898	USP28	1.05	6.58E-02	2.35E-01	862.00	not significant
10899	MBLAC2	1.05	6.87E-02	2.42E-01	562.91	not significant

10900	BBIP1	1.05	6.28E-02	2.28E-01	342.08	not significant
10901	UXT	1.05	5.89E-02	2.19E-01	1438.51	not significant
10902	MYPOP	1.05	6.85E-02	2.41E-01	447.25	not significant
10903	SAC3D1	1.05	6.34E-02	2.29E-01	1086.13	not significant
10904	PKD2	1.05	6.81E-02	2.41E-01	684.51	not significant
10905	SF3A2	1.05	1.08E-02	7.03E-02	6583.81	not significant
10906	IFI27L2	1.05	5.32E-02	2.05E-01	263.11	not significant
10907	PTDSS1	1.05	1.19E-02	7.53E-02	5153.11	not significant
10908	TMEM161A	1.05	5.40E-02	2.08E-01	1229.40	not significant
10909	SH3GLB2	1.05	5.07E-02	1.99E-01	1540.96	not significant
10910	R3HDM2	1.05	4.38E-02	1.81E-01	1766.95	not significant
10911	B2M	1.05	4.76E-03	3.91E-02	26571.96	not significant
10912	METTL3	1.05	6.04E-02	2.22E-01	1361.87	not significant
10913	LYSMD1	1.05	6.78E-02	2.40E-01	496.29	not significant
10914	TLR3	1.05	5.62E-02	2.13E-01	356.28	not significant
10915	PABPC1	1.05	2.32E-03	2.38E-02	52464.32	not significant
10916	43529_13977	1.05	4.21E-02	1.75E-01	1850.34	not significant
10917	MGC72080	1.05	6.25E-02	2.27E-01	372.93	not significant
10918	SIGMAR1	1.05	2.54E-02	1.26E-01	3260.53	not significant
10919	SLFN11	1.05	9.58E-03	6.46E-02	6831.92	not significant
10920	CASD1	1.05	3.93E-02	1.67E-01	2245.45	not significant
10921	METTL23	1.05	6.00E-02	2.21E-01	902.13	not significant
10922	TRADD	1.05	5.86E-02	2.18E-01	351.35	not significant
10923	ITGB1	1.05	1.53E-02	9.01E-02	5542.58	not significant
10924	EPHB6	1.05	2.29E-02	1.18E-01	2947.08	not significant
10925	ZFAND2B	1.05	6.18E-02	2.26E-01	866.51	not significant
10926	TAPBPL	1.05	5.72E-02	2.15E-01	943.67	not significant
10927	CTBP1-AS2	1.05	6.47E-02	2.32E-01	656.91	not significant
10928	DDX12P	1.05	6.42E-02	2.31E-01	949.37	not significant
10929	ANKRA2	1.05	6.32E-02	2.29E-01	367.59	not significant
10930	INPP5E	1.05	6.21E-02	2.26E-01	767.18	not significant
10931	RFX1	1.05	6.17E-02	2.26E-01	808.62	not significant
10932	LOC100505812	1.05	5.66E-02	2.13E-01	297.45	not significant
10933	PDDC1	1.05	3.63E-02	1.59E-01	1885.45	not significant
10934	LOC148413	1.05	6.14E-02	2.25E-01	766.88	not significant
10935	ZNF627	1.05	6.36E-02	2.30E-01	381.31	not significant
10936	AMIGO2	1.05	3.90E-02	1.67E-01	203.98	not significant
10937	SPCS3	1.05	4.74E-03	3.89E-02	10066.43	not significant
10938	CXCR4	1.05	1.27E-02	7.86E-02	5235.71	not significant
10939	DDOST	1.05	6.61E-03	4.99E-02	7519.84	not significant
10940	C1orf43	1.05	1.91E-02	1.04E-01	7392.73	not significant
10941	CEP192	1.05	4.01E-02	1.70E-01	2683.32	not significant
10942	PUSL1	1.05	5.99E-02	2.21E-01	880.20	not significant
10943	FBXL4	1.05	6.46E-02	2.32E-01	624.14	not significant
10944	GCDH	1.05	5.12E-02	2.00E-01	1329.39	not significant
10945	PQLC3	1.05	6.30E-02	2.28E-01	562.41	not significant
10946	KIAA0430	1.05	3.90E-02	1.67E-01	2718.14	not significant
10947	PPOX	1.05	6.25E-02	2.27E-01	434.91	not significant
10948	CD44	1.05	6.32E-02	2.29E-01	683.46	not significant
10949	MPND	1.05	6.43E-02	2.31E-01	609.93	not significant
10950	RNF167	1.05	1.90E-02	1.03E-01	4072.16	not significant
10951	BFAR	1.05	2.87E-02	1.36E-01	2374.67	not significant
10952	GMPR2	1.05	4.64E-02	1.87E-01	1453.18	not significant
10953	CEP44	1.05	5.84E-02	2.18E-01	845.28	not significant
10954	GLTSCR1L	1.05	6.00E-02	2.21E-01	1019.36	not significant
10955	RNF7	1.05	5.20E-02	2.02E-01	1401.73	not significant
10956	SIGIRR	1.05	4.76E-02	1.90E-01	1310.64	not significant
10957	NSUN5P2	1.05	1.56E-02	9.12E-02	108.65	not significant
10958	TMEM101	1.05	6.18E-02	2.26E-01	467.48	not significant
10959	ITM2A	1.05	1.61E-02	9.29E-02	10577.37	not significant
10960	C16orf59	1.05	5.22E-02	2.02E-01	990.66	not significant
10961	CCNT2	1.05	2.88E-02	1.36E-01	2314.42	not significant
10962	SCN9A	1.05	4.69E-02	1.89E-01	2702.90	not significant
10963	GMNN	1.05	1.88E-02	1.03E-01	4060.33	not significant
10964	HM13	1.05	1.09E-02	7.07E-02	5381.00	not significant
10965	PNPLA2	1.05	5.27E-02	2.04E-01	1200.78	not significant
10966	OXA1L	1.05	2.22E-02	1.15E-01	2850.53	not significant
10967	ZNF768	1.05	6.07E-02	2.23E-01	406.41	not significant
10968	ST3GAL1	1.05	3.06E-02	1.42E-01	2420.48	not significant
10969	ACADVL	1.05	9.27E-03	6.30E-02	5215.10	not significant
10970	EEF2	1.05	7.20E-03	5.30E-02	77450.90	not significant
10971	MED30	1.05	4.87E-02	1.93E-01	1153.53	not significant
10972	TPP1	1.05	3.79E-02	1.64E-01	2718.17	not significant
10973	BANF1	1.05	4.00E-02	1.70E-01	3158.45	not significant
10974	ANKRD36B	1.05	3.38E-02	1.51E-01	225.00	not significant
10975	METTL17	1.05	2.90E-02	1.37E-01	2514.90	not significant
10976	HDAC10	1.05	4.81E-02	1.92E-01	1123.64	not significant
10977	RRN3P3	1.05	3.21E-02	1.46E-01	185.77	not significant
10978	PXMP2	1.05	5.14E-02	2.00E-01	1318.08	not significant
10979	TCF19	1.05	5.23E-02	2.03E-01	903.61	not significant
10980	ANKRD13A	1.05	1.17E-02	7.43E-02	4260.46	not significant
10981	PIEZO1	1.05	2.56E-02	1.27E-01	11081.59	not significant
10982	SLC12A6	1.05	4.42E-02	1.82E-01	2866.21	not significant
10983	NUDT16L1	1.05	5.46E-02	2.09E-01	984.61	not significant
10984	MFSD8	1.05	6.03E-02	2.22E-01	612.26	not significant
10985	ACAP1	1.05	1.34E-02	8.17E-02	5058.15	not significant
10986	TRMT1	1.05	2.94E-02	1.38E-01	2740.58	not significant
10987	CR2	1.05	5.91E-02	2.20E-01	520.14	not significant

10988	COX6C	1.05	3.41E-02	1.52E-01	3941.98	not significant
10989	ALDH16A1	1.05	4.35E-02	1.80E-01	1411.20	not significant
10990	IDH3G	1.05	4.94E-02	1.95E-01	1078.14	not significant
10991	CYLD	1.05	5.12E-02	2.00E-01	977.31	not significant
10992	TNKS2	1.05	2.06E-02	1.09E-01	3503.30	not significant
10993	PPP1R16B	1.05	3.03E-02	1.41E-01	3171.41	not significant
10994	LPIN2	1.05	2.69E-02	1.30E-01	2342.52	not significant
10995	ANKRD26	1.05	5.75E-02	2.16E-01	812.82	not significant
10996	PGAP3	1.05	5.61E-02	2.12E-01	364.61	not significant
10997	BUD13	1.05	3.64E-02	1.59E-01	1695.37	not significant
10998	FAM160B2	1.05	3.91E-02	1.67E-01	1524.76	not significant
10999	NPC1	1.05	5.05E-02	1.99E-01	1161.72	not significant
11000	C8orf88	1.05	4.90E-02	1.94E-01	959.94	not significant
11001	APLP2	1.05	8.96E-03	6.16E-02	4912.17	not significant
11002	VILL	1.05	5.19E-02	2.02E-01	852.47	not significant
11003	TOM1	1.05	5.76E-02	2.16E-01	687.84	not significant
11004	ARMCX6	1.05	2.83E-02	1.35E-01	156.23	not significant
11005	GINM1	1.05	5.97E-02	2.21E-01	590.45	not significant
11006	MRPL57	1.05	4.48E-02	1.83E-01	2176.60	not significant
11007	ZNF837	1.05	2.35E-02	1.20E-01	142.91	not significant
11008	BCAP31	1.05	2.28E-02	1.18E-01	2583.10	not significant
11009	CTSA	1.05	2.81E-02	1.34E-01	2178.58	not significant
11010	TRAPPC5	1.05	5.44E-02	2.08E-01	818.90	not significant
11011	CLCN6	1.05	5.42E-02	2.08E-01	735.16	not significant
11012	CCBL1	1.05	4.64E-02	1.87E-01	260.40	not significant
11013	SNX14	1.05	4.64E-02	1.87E-01	989.49	not significant
11014	ARL4C	1.05	2.63E-03	2.58E-02	11919.76	not significant
11015	ELF1	1.05	1.35E-02	8.19E-02	4927.48	not significant
11016	ZNF451	1.05	3.00E-02	1.40E-01	1954.25	not significant
11017	FAM110A	1.05	5.20E-02	2.02E-01	722.22	not significant
11018	TRIP10	1.05	3.21E-02	1.46E-01	168.28	not significant
11019	C11orf31	1.05	3.65E-02	1.59E-01	3363.59	not significant
11020	CHMP5	1.05	4.29E-02	1.78E-01	1277.79	not significant
11021	MVK	1.05	5.60E-02	2.12E-01	702.51	not significant
11022	DENND4C	1.05	3.24E-02	1.47E-01	2298.23	not significant
11023	EDEM2	1.05	3.80E-02	1.64E-01	1434.91	not significant
11024	TOR2A	1.05	5.31E-02	2.05E-01	747.37	not significant
11025	ZNF581	1.05	5.74E-02	2.16E-01	553.24	not significant
11026	SECISBP2	1.05	3.76E-02	1.63E-01	1658.07	not significant
11027	IRF2	1.05	3.75E-02	1.63E-01	1472.07	not significant
11028	CNNM3	1.05	3.29E-02	1.48E-01	2139.73	not significant
11029	HSPB1	1.05	4.31E-02	1.79E-01	2123.06	not significant
11030	PYHIN1	1.05	4.40E-02	1.81E-01	1022.45	not significant
11031	PABPN1	1.05	5.58E-02	2.12E-01	598.65	not significant
11032	MESDC2	1.05	2.01E-02	1.07E-01	2416.80	not significant
11033	SUN2	1.05	2.33E-02	1.19E-01	2584.89	not significant
11034	MRPL10	1.05	4.49E-02	1.84E-01	1273.89	not significant
11035	SPECC1L	1.05	4.17E-02	1.74E-01	1235.57	not significant
11036	PYGO2	1.05	2.53E-02	1.26E-01	2026.82	not significant
11037	INF2	1.05	2.61E-02	1.28E-01	2822.27	not significant
11038	HSD17B7P2	1.05	1.69E-02	9.60E-02	136.24	not significant
11039	POLD4	1.05	5.34E-02	2.06E-01	424.19	not significant
11040	PP7080	1.05	4.94E-02	1.95E-01	701.91	not significant
11041	LAPTM4A	1.05	3.83E-02	1.65E-01	1326.22	not significant
11042	KDSR	1.05	3.78E-02	1.63E-01	1501.94	not significant
11043	GNE	1.05	3.35E-02	1.50E-01	1406.63	not significant
11044	LMBR1L	1.05	4.55E-02	1.85E-01	861.67	not significant
11045	CAMK4	1.05	4.73E-02	1.89E-01	1006.62	not significant
11046	HINT1	1.05	1.90E-02	1.03E-01	10722.84	not significant
11047	RRM1	1.05	1.95E-03	2.07E-02	12052.51	not significant
11048	EEF1D	1.05	1.60E-02	9.26E-02	13490.60	not significant
11049	TM9SF1	1.05	3.60E-02	1.58E-01	1288.69	not significant
11050	MFSD1	1.05	4.21E-02	1.75E-01	982.37	not significant
11051	AMOT	1.05	4.99E-02	1.97E-01	803.78	not significant
11052	MFI2	1.05	4.08E-02	1.72E-01	260.68	not significant
11053	LEMD2	1.05	1.95E-02	1.05E-01	2419.37	not significant
11054	TNFSF10	1.05	1.50E-03	1.72E-02	11663.60	not significant
11055	TRIOBP	1.05	3.26E-02	1.47E-01	1398.99	not significant
11056	DPH1	1.05	5.14E-02	2.00E-01	425.97	not significant
11057	TMEM261	1.05	8.29E-02	2.73E-01	2790.39	not significant
11058	BLM	1.05	2.21E-02	1.15E-01	2611.24	not significant
11059	ACTG1	1.05	5.10E-03	4.11E-02	18848.48	not significant
11060	PQLC1	1.05	3.22E-02	1.46E-01	1371.50	not significant
11061	UFL1	1.05	2.79E-02	1.34E-01	2191.94	not significant
11062	LINC00265	1.05	5.04E-02	1.98E-01	466.88	not significant
11063	THG1L	1.05	5.06E-02	1.99E-01	484.13	not significant
11064	UBXN6	1.05	2.66E-02	1.29E-01	1855.27	not significant
11065	FAM65B	1.05	2.58E-02	1.27E-01	1856.41	not significant
11066	RECK	1.05	4.80E-02	1.91E-01	690.08	not significant
11067	IKBKB	1.05	1.62E-02	9.34E-02	2631.31	not significant
11068	CKLF	1.05	4.39E-02	1.81E-01	979.09	not significant
11069	NT5C3A	1.05	4.03E-02	1.70E-01	1040.81	not significant
11070	RAB32	1.05	4.96E-02	1.96E-01	705.47	not significant
11071	CUTA	1.06	3.51E-02	1.56E-01	1321.77	not significant
11072	TTYH3	1.06	1.60E-02	9.29E-02	3014.37	not significant
11073	IGF2R	1.06	2.09E-02	1.10E-01	6631.22	not significant
11074	P4HA1	1.06	2.89E-02	1.37E-01	1517.47	not significant
11075	UTY	1.06	3.87E-02	1.66E-01	1014.65	not significant

11076	RAB33A	1.06	4.37E-02	1.81E-01	286.45	not significant
11077	SNRNP70	1.06	6.16E-03	4.73E-02	8767.49	not significant
11078	C4orf46	1.06	1.92E-02	1.04E-01	2703.59	not significant
11079	PASK	1.06	3.47E-02	1.55E-01	1464.18	not significant
11080	RING1	1.06	4.89E-02	1.94E-01	425.25	not significant
11081	ULBP2	1.06	2.26E-02	1.17E-01	154.87	not significant
11082	CNIH1	1.06	2.24E-02	1.16E-01	3094.12	not significant
11083	KCTD13	1.06	4.86E-02	1.93E-01	519.10	not significant
11084	MRPL33	1.06	4.03E-02	1.70E-01	1127.34	not significant
11085	MYADM	1.06	3.43E-02	1.53E-01	1420.14	not significant
11086	TPCN2	1.06	4.83E-02	1.92E-01	514.78	not significant
11087	MARCKSL1	1.06	3.06E-03	2.87E-02	10069.97	not significant
11088	MNT	1.06	4.65E-02	1.87E-01	716.20	not significant
11089	HERC5	1.06	2.24E-02	1.16E-01	1924.46	not significant
11090	ZNF219	1.06	4.58E-02	1.86E-01	727.27	not significant
11091	CUL9	1.06	3.14E-02	1.44E-01	1712.01	not significant
11092	ANO6	1.06	1.95E-02	1.05E-01	3838.03	not significant
11093	C12orf57	1.06	4.70E-02	1.89E-01	403.06	not significant
11094	TMX3	1.06	2.02E-02	1.07E-01	3434.24	not significant
11095	FRAT2	1.06	4.30E-02	1.79E-01	298.69	not significant
11096	CALCOCO2	1.06	6.79E-03	5.08E-02	3994.23	not significant
11097	MPLKIP	1.06	3.97E-02	1.69E-01	981.27	not significant
11098	HTRA2	1.06	3.12E-02	1.44E-01	1427.79	not significant
11099	PCBP4	1.06	4.33E-02	1.79E-01	320.79	not significant
11100	SYCP2	1.06	2.55E-02	1.26E-01	2642.36	not significant
11101	KDM5D	1.06	1.52E-02	8.97E-02	3113.63	not significant
11102	APAF1	1.06	2.35E-02	1.20E-01	1688.98	not significant
11103	UBE2J1	1.06	1.95E-02	1.05E-01	1875.59	not significant
11104	USF2	1.06	1.39E-02	8.40E-02	3031.83	not significant
11105	PCGF3	1.06	1.73E-02	9.69E-02	2132.35	not significant
11106	PRTFDC1	1.06	3.86E-02	1.66E-01	859.15	not significant
11107	ADD3	1.06	3.39E-03	3.05E-02	6219.69	not significant
11108	GMFG	1.06	2.55E-02	1.26E-01	2781.33	not significant
11109	GNS	1.06	1.33E-02	8.12E-02	3622.23	not significant
11110	GLI4	1.06	4.56E-02	1.85E-01	522.26	not significant
11111	EIF3L	1.06	4.29E-03	3.64E-02	9752.78	not significant
11112	MMAB	1.06	3.03E-02	1.41E-01	1441.58	not significant
11113	GSTK1	1.06	2.44E-02	1.23E-01	1635.16	not significant
11114	N4BP2L2	1.06	2.31E-02	1.19E-01	1853.71	not significant
11115	VIPAS39	1.06	3.67E-02	1.60E-01	884.55	not significant
11116	FAS	1.06	4.10E-02	1.72E-01	928.79	not significant
11117	ETS1	1.06	3.89E-03	3.37E-02	15177.88	not significant
11118	FURIN	1.06	2.97E-02	1.39E-01	1240.07	not significant
11119	PHYKPL	1.06	3.86E-02	1.66E-01	784.66	not significant
11120	TMEM254	1.06	4.61E-02	1.87E-01	535.81	not significant
11121	ABCC10	1.06	4.18E-02	1.75E-01	825.46	not significant
11122	UHRF2	1.06	1.40E-02	8.42E-02	2363.19	not significant
11123	BCKDHB	1.06	3.64E-02	1.59E-01	883.86	not significant
11124	RCSD1	1.06	4.32E-03	3.65E-02	4559.90	not significant
11125	TBCA	1.06	2.60E-02	1.28E-01	3377.73	not significant
11126	NFIC	1.06	3.19E-02	1.46E-01	1022.37	not significant
11127	C8orf82	1.06	4.36E-02	1.80E-01	634.08	not significant
11128	GIMAP1	1.06	7.03E-03	5.23E-02	3584.51	not significant
11129	PLCG1	1.06	2.84E-03	2.71E-02	10576.61	not significant
11130	PRR12	1.06	1.11E-02	7.17E-02	3031.29	not significant
11131	CLUHP3	1.06	3.75E-02	1.63E-01	313.03	not significant
11132	PARP2	1.06	2.18E-02	1.14E-01	1606.76	not significant
11133	BAI2	1.06	3.70E-02	1.61E-01	892.08	not significant
11134	LDLR	1.06	1.55E-02	9.10E-02	2870.29	not significant
11135	UBXN1	1.06	3.05E-02	1.41E-01	2228.16	not significant
11136	NIT1	1.06	3.60E-02	1.58E-01	825.98	not significant
11137	CKS1B	1.06	3.79E-02	1.64E-01	1273.25	not significant
11138	ZNF32	1.06	3.95E-02	1.68E-01	819.64	not significant
11139	RNF44	1.06	6.51E-03	4.92E-02	3928.29	not significant
11140	OARD1	1.06	3.60E-02	1.58E-01	893.34	not significant
11141	ALDH6A1	1.06	4.32E-02	1.79E-01	477.41	not significant
11142	GCSAM	1.06	4.29E-02	1.78E-01	577.68	not significant
11143	HERPUD2	1.06	3.40E-02	1.52E-01	1027.93	not significant
11144	MEGF8	1.06	3.59E-02	1.58E-01	891.27	not significant
11145	RAD52	1.06	3.96E-02	1.69E-01	744.53	not significant
11146	CHAF1B	1.06	1.36E-02	8.26E-02	2224.92	not significant
11147	USP49	1.06	1.54E-02	9.07E-02	3045.63	not significant
11148	MUM1	1.06	3.04E-02	1.41E-01	1167.44	not significant
11149	ZNF512	1.06	1.06E-02	6.92E-02	2551.28	not significant
11150	DTX3	1.06	1.87E-02	1.02E-01	1644.36	not significant
11151	SLC25A5	1.06	7.87E-03	5.66E-02	17168.10	not significant
11152	DENND5A	1.06	1.05E-02	6.88E-02	2905.88	not significant
11153	RPL13A	1.06	1.42E-02	8.50E-02	4552.05	not significant
11154	GPR108	1.06	2.29E-02	1.18E-01	1523.09	not significant
11155	HPCAL1	1.06	2.67E-02	1.30E-01	1154.78	not significant
11156	RPS15A	1.06	7.86E-03	5.66E-02	10764.88	not significant
11157	GBP3	1.06	3.86E-02	1.65E-01	663.65	not significant
11158	CTBS	1.06	4.02E-02	1.70E-01	542.61	not significant
11159	FLJ32255	1.06	3.92E-02	1.67E-01	597.03	not significant
11160	LINC00649	1.06	4.06E-02	1.71E-01	519.57	not significant
11161	ALOX5AP	1.06	1.68E-02	9.55E-02	1828.57	not significant
11162	CD47	1.06	1.39E-03	1.63E-02	8991.74	not significant
11163	WDR6	1.06	1.25E-03	1.49E-02	8092.90	not significant

11164	PIK3C3	1.06	3.24E-02	1.47E-01	855.64	not significant
11165	CENPU	1.06	8.94E-03	6.16E-02	3775.33	not significant
11166	TRAM1	1.06	1.45E-03	1.67E-02	16569.00	not significant
11167	CNOT6L	1.06	1.73E-02	9.72E-02	1706.33	not significant
11168	NPHP4	1.06	2.40E-02	1.21E-01	1214.67	not significant
11169	POLI	1.06	3.52E-02	1.56E-01	287.63	not significant
11170	E2F7	1.06	2.30E-02	1.18E-01	2160.38	not significant
11171	REC8	1.06	3.63E-02	1.59E-01	640.70	not significant
11172	KBTBD2	1.06	1.74E-02	9.75E-02	2014.25	not significant
11173	SPTBN1	1.06	5.20E-02	2.02E-01	17731.68	not significant
11174	SUN1	1.06	1.45E-02	8.64E-02	2415.52	not significant
11175	FANCE	1.06	3.51E-02	1.56E-01	657.91	not significant
11176	HERC2	1.06	1.89E-02	1.03E-01	2164.66	not significant
11177	PRSS21	1.06	3.33E-02	1.50E-01	732.93	not significant
11178	ZNF37BP	1.06	3.50E-02	1.56E-01	1184.96	not significant
11179	TOX	1.06	1.03E-03	1.30E-02	7153.24	not significant
11180	MOAP1	1.06	2.42E-02	1.22E-01	1132.48	not significant
11181	TUSC3	1.06	1.18E-02	7.48E-02	2036.36	not significant
11182	SEPSECS	1.06	3.22E-02	1.46E-01	750.16	not significant
11183	TMX1	1.06	5.20E-03	4.16E-02	4778.17	not significant
11184	PLCB2	1.06	2.67E-02	1.30E-01	1518.15	not significant
11185	MXD4	1.06	3.83E-02	1.65E-01	362.89	not significant
11186	TREX1	1.06	3.80E-02	1.64E-01	378.54	not significant
11187	NFKBIA	1.06	2.47E-02	1.24E-01	1168.21	not significant
11188	DDT	1.06	3.85E-02	1.65E-01	514.53	not significant
11189	C19orf48	1.06	3.76E-03	3.28E-02	5214.49	not significant
11190	RAD54L	1.06	3.71E-03	3.26E-02	4097.25	not significant
11191	TRIB2	1.06	1.21E-03	1.46E-02	6873.13	not significant
11192	DENND4B	1.06	6.99E-03	5.21E-02	4555.61	not significant
11193	RNASEH2A	1.06	2.08E-02	1.10E-01	2381.96	not significant
11194	CENPJ	1.06	2.59E-02	1.28E-01	1131.37	not significant
11195	RUFY3	1.06	1.81E-02	1.00E-01	1805.12	not significant
11196	SNAPC3	1.06	1.96E-02	1.05E-01	1441.97	not significant
11197	CCBL2	1.06	3.32E-02	1.49E-01	664.13	not significant
11198	CCDC14	1.06	8.55E-03	5.96E-02	3001.16	not significant
11199	COX8A	1.06	1.31E-02	8.04E-02	5110.82	not significant
11200	IL12RB1	1.06	2.10E-02	1.11E-01	1249.55	not significant
11201	CYB561D2	1.06	3.61E-02	1.59E-01	642.27	not significant
11202	STAT3	1.06	8.41E-04	1.12E-02	10114.25	not significant
11203	ERGIC3	1.06	5.09E-03	4.10E-02	3739.27	not significant
11204	ARL6IP4	1.06	1.08E-02	7.01E-02	4537.38	not significant
11205	PCNXL4	1.06	8.99E-03	6.18E-02	3800.46	not significant
11206	NAGLU	1.06	2.77E-02	1.33E-01	228.46	not significant
11207	PIK3CG	1.06	1.42E-02	8.53E-02	2293.99	not significant
11208	MAFG	1.06	1.08E-02	7.05E-02	2072.97	not significant
11209	STRIP2	1.06	3.56E-02	1.57E-01	417.91	not significant
11210	CDCA7L	1.06	1.14E-03	1.40E-02	5972.59	not significant
11211	CLEC2B	1.06	3.64E-02	1.59E-01	432.26	not significant
11212	PSMG2	1.06	1.60E-02	9.26E-02	2020.14	not significant
11213	IPO8	1.06	1.27E-02	7.84E-02	2228.62	not significant
11214	ATF3	1.06	2.38E-02	1.21E-01	998.85	not significant
11215	TFAP2C	1.06	3.60E-02	1.58E-01	545.73	not significant
11216	LAMP1	1.06	3.17E-03	2.94E-02	5541.58	not significant
11217	HDHD2	1.06	1.41E-02	8.48E-02	1856.64	not significant
11218	KIAA0195	1.06	4.16E-03	3.55E-02	4269.91	not significant
11219	ZSCAN2	1.06	3.59E-02	1.58E-01	443.41	not significant
11220	RFX5	1.06	7.32E-03	5.37E-02	2923.38	not significant
11221	SIX3	1.06	2.98E-02	1.40E-01	738.94	not significant
11222	ZRSR2	1.06	3.34E-02	1.50E-01	283.67	not significant
11223	FKBP11	1.06	2.96E-02	1.39E-01	840.69	not significant
11224	WIPI1	1.06	3.56E-02	1.57E-01	424.13	not significant
11225	TMEM18	1.06	2.34E-02	1.20E-01	1521.43	not significant
11226	MYO18A	1.06	5.06E-03	4.09E-02	2958.75	not significant
11227	PLEKHG2	1.06	1.77E-02	9.86E-02	2586.35	not significant
11228	EIF4A2	1.06	5.42E-04	8.11E-03	10757.94	not significant
11229	RBM4	1.06	2.87E-02	1.36E-01	781.08	not significant
11230	MYB	1.06	3.02E-04	5.25E-03	14197.44	not significant
11231	PGD	1.06	1.31E-03	1.55E-02	10113.34	not significant
11232	RHOH	1.06	5.22E-03	4.18E-02	3596.74	not significant
11233	HAGH	1.06	3.29E-02	1.48E-01	901.57	not significant
11234	CAPRIN2	1.06	3.16E-02	1.45E-01	311.06	not significant
11235	EMC10	1.06	6.00E-03	4.64E-02	3637.28	not significant
11236	ST6GAL1	1.06	9.10E-03	6.21E-02	3656.18	not significant
11237	SYF2	1.06	1.40E-02	8.41E-02	1552.10	not significant
11238	MAP3K3	1.06	9.61E-03	6.48E-02	2127.92	not significant
11239	CTDSP2	1.06	5.34E-04	8.07E-03	9105.38	not significant
11240	ANKZF1	1.06	2.23E-02	1.16E-01	994.81	not significant
11241	TECR	1.06	5.08E-03	4.10E-02	2993.74	not significant
11242	DCAF15	1.06	5.38E-03	4.27E-02	2869.79	not significant
11243	GJC1	1.06	8.63E-03	6.01E-02	2226.52	not significant
11244	43531_3536	1.06	2.63E-03	2.58E-02	4389.65	not significant
11245	VAMP4	1.06	3.08E-02	1.42E-01	653.17	not significant
11246	ZFYVE16	1.06	2.74E-02	1.32E-01	824.99	not significant
11247	FLI1	1.06	5.51E-03	4.36E-02	2638.44	not significant
11248	CD97	1.06	1.67E-02	9.52E-02	1303.50	not significant
11249	TUBB	1.06	8.16E-04	1.10E-02	8262.83	not significant
11250	AIP	1.06	1.52E-02	8.99E-02	3648.73	not significant
11251	SRSF5	1.06	8.28E-04	1.11E-02	6745.22	not significant

11252	NDFIP2	1.07	2.66E-03	2.60E-02	3712.89	not significant
11253	N4BP2	1.07	9.25E-03	6.29E-02	4204.18	not significant
11254	PAN2	1.07	1.97E-02	1.05E-01	1842.94	not significant
11255	SH2B1	1.07	1.21E-02	7.58E-02	2004.19	not significant
11256	ALG12	1.07	2.64E-02	1.29E-01	919.38	not significant
11257	LOC146880	1.07	2.80E-02	1.34E-01	884.95	not significant
11258	STARD3	1.07	5.80E-03	4.53E-02	2888.58	not significant
11259	NIPAL3	1.07	3.03E-02	1.41E-01	703.83	not significant
11260	MEN1	1.07	5.98E-03	4.63E-02	3544.25	not significant
11261	CAPN10	1.07	2.33E-02	1.19E-01	907.94	not significant
11262	SMPD2	1.07	3.31E-02	1.49E-01	449.73	not significant
11263	PPM1K	1.07	1.36E-02	8.24E-02	1543.35	not significant
11264	ATP6V0A2	1.07	9.38E-03	6.35E-02	3147.43	not significant
11265	LIG1	1.07	1.02E-03	1.30E-02	5299.80	not significant
11266	PKD1	1.07	1.01E-02	6.67E-02	2604.31	not significant
11267	TMED4	1.07	1.30E-02	8.01E-02	1931.21	not significant
11268	ATP6V1H	1.07	1.39E-02	8.40E-02	1669.75	not significant
11269	DDX17	1.07	4.35E-03	3.67E-02	17150.50	not significant
11270	HAUS5	1.07	9.05E-03	6.20E-02	2028.97	not significant
11271	CENPC	1.07	1.91E-02	1.04E-01	1133.40	not significant
11272	MAN2B1	1.07	1.74E-02	9.76E-02	1344.45	not significant
11273	CREBRF	1.07	2.05E-02	1.09E-01	153.87	not significant
11274	MRE11A	1.07	7.92E-03	5.67E-02	2272.51	not significant
11275	CLN6	1.07	6.10E-03	4.70E-02	2314.21	not significant
11276	FAM221A	1.07	3.25E-02	1.47E-01	355.86	not significant
11277	BST2	1.07	1.58E-02	9.23E-02	2030.71	not significant
11278	TNFRSF25	1.07	2.95E-02	1.39E-01	593.46	not significant
11279	ENO3	1.07	2.91E-02	1.37E-01	257.36	not significant
11280	C2orf68	1.07	1.18E-02	7.48E-02	1449.36	not significant
11281	C11orf30	1.07	1.58E-02	9.20E-02	1668.58	not significant
11282	ARID5A	1.07	2.39E-02	1.21E-01	775.85	not significant
11283	AP4M1	1.07	3.18E-02	1.45E-01	542.07	not significant
11284	RELB	1.07	3.12E-02	1.44E-01	333.36	not significant
11285	C9orf16	1.07	2.64E-02	1.29E-01	971.12	not significant
11286	ABCB7	1.07	2.43E-02	1.22E-01	774.24	not significant
11287	DGAT1	1.07	2.43E-02	1.22E-01	795.92	not significant
11288	HIGD2A	1.07	1.58E-02	9.23E-02	1927.51	not significant
11289	PHGDH	1.07	1.63E-03	1.83E-02	10316.66	not significant
11290	COMTD1	1.07	2.42E-02	1.22E-01	198.45	not significant
11291	MLLT11	1.07	5.41E-03	4.28E-02	2766.46	not significant
11292	SLC3A2	1.07	7.36E-04	1.02E-02	10741.66	not significant
11293	DDX11	1.07	6.37E-03	4.83E-02	2736.31	not significant
11294	WIPI2	1.07	5.40E-03	4.28E-02	2919.68	not significant
11295	C1GALT1	1.07	7.67E-03	5.58E-02	2538.34	not significant
11296	PHF11	1.07	1.72E-02	9.68E-02	1068.83	not significant
11297	ZNF248	1.07	2.38E-02	1.21E-01	762.17	not significant
11298	SGSM2	1.07	1.13E-02	7.22E-02	2320.34	not significant
11299	TMEM258	1.07	1.23E-02	7.66E-02	1552.97	not significant
11300	SC5D	1.07	1.23E-02	7.68E-02	1764.70	not significant
11301	PVRIG	1.07	8.12E-03	5.76E-02	2314.08	not significant
11302	DCK	1.07	1.02E-03	1.30E-02	6116.56	not significant
11303	SNX10	1.07	1.09E-02	7.07E-02	1512.56	not significant
11304	SLC35A5	1.07	1.17E-02	7.41E-02	1418.35	not significant
11305	BBS2	1.07	2.75E-02	1.32E-01	615.38	not significant
11306	ADCK4	1.07	2.92E-02	1.38E-01	528.63	not significant
11307	DSN1	1.07	4.75E-03	3.90E-02	2435.99	not significant
11308	NLRX1	1.07	2.40E-02	1.21E-01	805.23	not significant
11309	CTDSP1	1.07	1.06E-02	6.95E-02	1847.48	not significant
11310	UBQLN2	1.07	7.82E-03	5.64E-02	2062.92	not significant
11311	CAMSAP1	1.07	1.09E-02	7.07E-02	1866.80	not significant
11312	ERLEC1	1.07	8.01E-03	5.71E-02	1870.24	not significant
11313	NBR1	1.07	7.77E-03	5.62E-02	2083.24	not significant
11314	ABCC1	1.07	4.42E-03	3.71E-02	5587.00	not significant
11315	PCSK4	1.07	1.74E-02	9.74E-02	144.27	not significant
11316	VIM	1.07	5.27E-04	7.99E-03	34125.19	not significant
11317	TINF2	1.07	5.72E-03	4.48E-02	2491.79	not significant
11318	DHTKD1	1.07	9.85E-03	6.57E-02	1464.80	not significant
11319	MGST3	1.07	2.92E-02	1.38E-01	409.65	not significant
11320	SRC	1.07	2.89E-02	1.37E-01	331.20	not significant
11321	C17orf59	1.07	2.95E-02	1.39E-01	378.61	not significant
11322	DPM3	1.07	2.87E-02	1.36E-01	288.87	not significant
11323	SLC26A6	1.07	2.17E-02	1.13E-01	794.61	not significant
11324	SLC12A4	1.07	2.38E-02	1.21E-01	889.51	not significant
11325	TMEM106A	1.07	2.94E-02	1.38E-01	348.37	not significant
11326	FECH	1.07	1.92E-02	1.04E-01	918.03	not significant
11327	C7orf43	1.07	9.96E-03	6.62E-02	1406.21	not significant
11328	UBOX5	1.07	2.58E-02	1.27E-01	607.98	not significant
11329	TAF7	1.07	1.02E-03	1.30E-02	6269.89	not significant
11330	CTHRC1	1.07	2.19E-02	1.14E-01	772.97	not significant
11331	FDPS	1.07	2.63E-03	2.58E-02	5897.00	not significant
11332	CDK10	1.07	9.19E-03	6.26E-02	1533.85	not significant
11333	PAXIP1-AS1	1.07	2.87E-02	1.36E-01	329.82	not significant
11334	MINK1	1.07	1.13E-02	7.23E-02	1434.11	not significant
11335	DMC1	1.07	2.75E-02	1.32E-01	493.18	not significant
11336	CDK2	1.07	8.66E-04	1.15E-02	6127.18	not significant
11337	SHMT2	1.07	6.11E-04	8.82E-03	12811.95	not significant
11338	ZNRF2	1.07	1.20E-02	7.54E-02	1162.24	not significant
11339	ORAI3	1.07	1.95E-02	1.05E-01	161.12	not significant

11340	DDB2	1.07	9.85E-03	6.57E-02	1460.47	not significant
11341	H1FX	1.07	2.52E-02	1.25E-01	8695.65	not significant
11342	GAB2	1.07	2.74E-04	4.86E-03	29656.88	not significant
11343	DLG3	1.07	1.70E-02	9.61E-02	977.18	not significant
11344	P2RX4	1.07	2.34E-02	1.19E-01	619.42	not significant
11345	CD3E	1.07	6.14E-05	1.46E-03	21284.71	not significant
11346	CARHSP1	1.07	3.08E-03	2.87E-02	5289.55	not significant
11347	ST8SIA4	1.07	4.38E-03	3.69E-02	2756.17	not significant
11348	SLC25A3	1.07	3.90E-04	6.34E-03	16727.15	not significant
11349	RCBTB1	1.07	6.17E-03	4.73E-02	1768.70	not significant
11350	CCNL1	1.07	4.29E-03	3.64E-02	3750.85	not significant
11351	GGCX	1.07	2.16E-02	1.13E-01	690.29	not significant
11352	CHD1L	1.07	1.34E-02	8.17E-02	1133.16	not significant
11353	CDCA7	1.07	1.70E-04	3.29E-03	8860.99	not significant
11354	RPL22L1	1.07	6.47E-03	4.89E-02	3464.81	not significant
11355	DTL	1.07	2.50E-04	4.54E-03	6265.08	not significant
11356	CEP97	1.07	1.61E-02	9.29E-02	998.68	not significant
11357	EPG5	1.07	1.99E-02	1.06E-01	1354.25	not significant
11358	HERC3	1.07	2.00E-02	1.06E-01	735.18	not significant
11359	SBK1	1.07	7.50E-03	5.48E-02	1497.76	not significant
11360	BRK1	1.07	4.47E-03	3.74E-02	3683.91	not significant
11361	VASH2	1.07	1.31E-02	8.04E-02	1033.19	not significant
11362	USP51	1.07	2.61E-02	1.28E-01	313.45	not significant
11363	YAF2	1.07	1.78E-02	9.92E-02	812.58	not significant
11364	CHST12	1.07	2.59E-03	2.56E-02	2693.30	not significant
11365	FANCA	1.07	7.07E-03	5.24E-02	2310.95	not significant
11366	NT5C	1.07	1.26E-02	7.81E-02	1089.58	not significant
11367	PIN4	1.07	2.65E-02	1.29E-01	392.48	not significant
11368	ZNF785	1.07	2.63E-02	1.29E-01	314.19	not significant
11369	LINC01089	1.07	2.63E-02	1.29E-01	371.30	not significant
11370	TSPYL4	1.07	3.18E-03	2.94E-02	2549.46	not significant
11371	NCSTN	1.07	6.79E-03	5.08E-02	1892.46	not significant
11372	CDC7	1.07	2.40E-03	2.44E-02	2637.25	not significant
11373	PI4K2B	1.07	3.18E-03	2.94E-02	2153.23	not significant
11374	SLC35B2	1.07	7.92E-03	5.67E-02	1626.15	not significant
11375	BIN2	1.07	7.71E-03	5.59E-02	1607.57	not significant
11376	SLC25A1	1.07	2.48E-02	1.24E-01	622.15	not significant
11377	SPG11	1.07	1.67E-02	9.51E-02	1358.79	not significant
11378	SPTSSA	1.07	1.41E-02	8.45E-02	1074.57	not significant
11379	EPM2AIP1	1.07	1.15E-02	7.31E-02	1934.35	not significant
11380	DHRS3	1.07	2.57E-02	1.27E-01	338.54	not significant
11381	TMEM38B	1.07	2.00E-02	1.07E-01	853.55	not significant
11382	NDST2	1.07	1.58E-02	9.20E-02	1135.82	not significant
11383	KRBA1	1.07	2.22E-02	1.15E-01	577.60	not significant
11384	IDI1	1.07	5.29E-04	8.01E-03	4617.48	not significant
11385	RPA3	1.07	8.66E-03	6.02E-02	1361.91	not significant
11386	SLC4A2	1.07	7.93E-04	1.08E-02	4115.05	not significant
11387	MOV10	1.07	2.08E-03	2.17E-02	3627.86	not significant
11388	SMO	1.07	8.00E-03	5.71E-02	1426.25	not significant
11389	NFATC1	1.07	1.48E-02	8.77E-02	947.45	not significant
11390	TSPAN4	1.07	2.38E-02	1.21E-01	463.03	not significant
11391	EBP	1.08	2.16E-02	1.13E-01	577.96	not significant
11392	CXorf57	1.08	2.35E-02	1.20E-01	485.35	not significant
11393	HLA-B	1.08	1.70E-03	1.88E-02	5830.97	not significant
11394	HEXA	1.08	7.81E-03	5.64E-02	1513.44	not significant
11395	ANXA3	1.08	1.66E-02	9.51E-02	145.36	not significant
11396	ZNF367	1.08	3.23E-03	2.97E-02	2164.96	not significant
11397	LCMT2	1.08	1.68E-02	9.57E-02	740.38	not significant
11398	LMBRD1	1.08	1.56E-02	9.14E-02	913.63	not significant
11399	POU2AF1	1.08	2.43E-02	1.22E-01	397.08	not significant
11400	KRBOX4	1.08	2.40E-02	1.21E-01	458.17	not significant
11401	DVL2	1.08	1.03E-03	1.30E-02	3176.67	not significant
11402	GUSB	1.08	3.41E-03	3.07E-02	2598.56	not significant
11403	ERMAP	1.08	1.85E-02	1.02E-01	163.33	not significant
11404	PARP10	1.08	2.07E-02	1.10E-01	564.96	not significant
11405	ZFP90	1.08	1.55E-02	9.09E-02	1081.62	not significant
11406	C19orf54	1.08	1.64E-02	9.40E-02	799.98	not significant
11407	ILF3-AS1	1.08	2.43E-02	1.22E-01	391.04	not significant
11408	TPT1	1.08	1.67E-03	1.86E-02	56512.94	not significant
11409	KDELR1	1.08	1.08E-03	1.34E-02	3188.98	not significant
11410	POLR1D	1.08	2.57E-03	2.54E-02	3858.51	not significant
11411	CD53	1.08	2.95E-04	5.16E-03	4636.42	not significant
11412	FAM213A	1.08	1.07E-02	6.98E-02	1214.07	not significant
11413	CLN3	1.08	6.71E-03	5.04E-02	1386.94	not significant
11414	IL4R	1.08	2.20E-03	2.27E-02	2264.09	not significant
11415	CD1E	1.08	3.82E-05	9.87E-04	11451.30	not significant
11416	OPTN	1.08	7.55E-03	5.50E-02	1545.92	not significant
11417	SH2D3C	1.08	9.70E-03	6.52E-02	1225.51	not significant
11418	NECAB3	1.08	1.69E-02	9.58E-02	742.84	not significant
11419	ZNF316	1.08	3.05E-03	2.86E-02	2036.18	not significant
11420	ACAD8	1.08	1.23E-02	7.67E-02	910.41	not significant
11421	C4orf3	1.08	6.86E-03	5.12E-02	1584.66	not significant
11422	SLC1A4	1.08	1.12E-04	2.37E-03	9967.86	not significant
11423	FN3KRP	1.08	2.38E-03	2.43E-02	2424.98	not significant
11424	TMEM160	1.08	1.60E-02	9.27E-02	976.79	not significant
11425	XRN1	1.08	5.11E-03	4.11E-02	2046.36	not significant
11426	ZNF362	1.08	7.57E-03	5.51E-02	1380.53	not significant
11427	EEF1B2	1.08	1.66E-03	1.85E-02	9221.93	not significant

11428	SUGP2	1.08	4.82E-03	3.95E-02	4400.48	not significant
11429	HYI	1.08	2.35E-02	1.20E-01	312.96	not significant
11430	MZB1	1.08	1.14E-03	1.39E-02	4341.18	not significant
11431	ZNF266	1.08	2.70E-03	2.62E-02	2400.19	not significant
11432	PARP8	1.08	4.50E-03	3.75E-02	1603.47	not significant
11433	SELL	1.08	9.65E-05	2.10E-03	7260.83	not significant
11434	CNOT8	1.08	5.81E-04	8.52E-03	3726.28	not significant
11435	ABRACL	1.08	1.07E-03	1.34E-02	5776.27	not significant
11436	LBH	1.08	6.34E-03	4.83E-02	1347.75	not significant
11437	INPPL1	1.08	9.84E-04	1.26E-02	3789.44	not significant
11438	CCDC9	1.08	1.63E-02	9.37E-02	685.36	not significant
11439	MED28	1.08	2.88E-03	2.74E-02	2487.09	not significant
11440	DGKA	1.08	4.06E-04	6.49E-03	5981.59	not significant
11441	SHISA2	1.08	3.86E-04	6.30E-03	5193.06	not significant
11442	NCAPH2	1.08	6.87E-04	9.61E-03	5052.47	not significant
11443	PTK2B	1.08	1.40E-04	2.83E-03	5409.48	not significant
11444	DPP7	1.08	1.40E-03	1.63E-02	2511.00	not significant
11445	MIER2	1.08	1.13E-02	7.22E-02	878.16	not significant
11446	HACE1	1.08	2.78E-03	2.67E-02	1923.75	not significant
11447	DNASE2	1.08	8.27E-03	5.84E-02	1089.18	not significant
11448	METTL9	1.08	7.58E-04	1.04E-02	4125.66	not significant
11449	SAMSN1	1.08	7.32E-03	5.37E-02	1552.22	not significant
11450	PCNA	1.08	3.87E-04	6.31E-03	24237.10	not significant
11451	JMY	1.08	1.76E-02	9.86E-02	644.39	not significant
11452	CCNE2	1.08	1.64E-03	1.84E-02	3413.05	not significant
11453	KLHDC2	1.08	1.26E-02	7.81E-02	874.31	not significant
11454	NEURL4	1.08	3.55E-03	3.17E-02	1989.97	not significant
11455	RBFA	1.08	9.77E-03	6.54E-02	1006.75	not significant
11456	JRK	1.08	2.23E-02	1.16E-01	336.30	not significant
11457	TSPAN3	1.08	1.52E-03	1.73E-02	3485.39	not significant
11458	HSDL1	1.08	9.42E-04	1.22E-02	2819.92	not significant
11459	GRN	1.08	1.71E-02	9.63E-02	607.95	not significant
11460	SLC39A13	1.08	1.77E-02	9.86E-02	556.06	not significant
11461	LRRC34	1.08	1.79E-02	9.94E-02	168.37	not significant
11462	MTHFD2	1.08	9.27E-05	2.04E-03	9663.10	not significant
11463	CLASRP	1.08	3.28E-03	3.00E-02	1842.65	not significant
11464	PCMTD2	1.08	6.33E-03	4.82E-02	1230.84	not significant
11465	P4HB	1.08	1.78E-05	5.52E-04	32773.52	not significant
11466	CECR1	1.08	4.26E-03	3.62E-02	1920.12	not significant
11467	DNAJB9	1.08	1.63E-02	9.37E-02	637.19	not significant
11468	BTG1	1.08	2.52E-04	4.56E-03	5146.89	not significant
11469	GNPTG	1.08	2.03E-02	1.08E-01	504.10	not significant
11470	DERL1	1.08	6.62E-04	9.35E-03	4256.58	not significant
11471	SLC25A14	1.08	1.91E-02	1.04E-01	535.65	not significant
11472	FANCI	1.08	4.63E-04	7.22E-03	5150.55	not significant
11473	SLFN5	1.08	8.43E-03	5.93E-02	1205.96	not significant
11474	DOCK11	1.08	4.03E-03	3.46E-02	1901.71	not significant
11475	SLC4A7	1.08	3.29E-03	3.00E-02	4157.22	not significant
11476	SHMT1	1.08	4.01E-03	3.45E-02	1702.46	not significant
11477	GIMAP4	1.08	1.63E-04	3.19E-03	6504.95	not significant
11478	TRIM5	1.08	4.53E-03	3.77E-02	1486.68	not significant
11479	NSMCE4A	1.08	5.52E-03	4.36E-02	1485.25	not significant
11480	HLA-A	1.08	3.23E-03	2.97E-02	2805.15	not significant
11481	ENTHD2	1.08	1.14E-02	7.25E-02	994.56	not significant
11482	POLD1	1.08	6.02E-04	8.71E-03	5349.81	not significant
11483	KNTC1	1.08	1.68E-03	1.87E-02	6524.08	not significant
11484	MAPK8IP3	1.08	2.93E-03	2.77E-02	1958.76	not significant
11485	SCARB2	1.08	1.89E-02	1.03E-01	487.91	not significant
11486	NDUFB11	1.08	1.38E-02	8.31E-02	747.95	not significant
11487	KLHL22	1.08	1.95E-02	1.05E-01	419.39	not significant
11488	IGSF8	1.08	3.25E-03	2.98E-02	1895.07	not significant
11489	FBXO46	1.08	1.05E-02	6.88E-02	826.37	not significant
11490	CHI3L2	1.08	2.30E-05	6.75E-04	27010.18	not significant
11491	PIDD1	1.08	2.50E-03	2.50E-02	1904.81	not significant
11492	C10orf32	1.08	1.14E-02	7.25E-02	758.17	not significant
11493	GTPBP2	1.08	2.30E-03	2.37E-02	1831.23	not significant
11494	ATM	1.08	4.78E-03	3.91E-02	2918.47	not significant
11495	MFSD3	1.08	2.08E-02	1.10E-01	361.79	not significant
11496	NEU1	1.08	1.88E-02	1.03E-01	194.02	not significant
11497	SLC25A40	1.08	1.40E-03	1.63E-02	2448.84	not significant
11498	BNIP3L	1.08	2.35E-03	2.41E-02	1813.13	not significant
11499	CALHM2	1.08	1.10E-02	7.11E-02	829.97	not significant
11500	CD46	1.08	9.17E-04	1.20E-02	4588.56	not significant
11501	PRKCSH	1.08	7.47E-05	1.71E-03	8171.00	not significant
11502	LRRC37B	1.08	1.66E-02	9.48E-02	523.57	not significant
11503	PPM1M	1.08	1.30E-02	7.99E-02	679.78	not significant
11504	ALAS1	1.08	1.49E-03	1.71E-02	2103.54	not significant
11505	XBP1	1.08	2.78E-04	4.93E-03	3836.72	not significant
11506	TBC1D15	1.08	2.42E-03	2.46E-02	1749.60	not significant
11507	YIPF4	1.08	1.13E-02	7.22E-02	930.16	not significant
11508	RSAD2	1.08	3.38E-03	3.05E-02	1736.39	not significant
11509	SLC1A5	1.08	2.75E-05	7.63E-04	10336.43	not significant
11510	ARRDC1-AS1	1.08	1.95E-02	1.05E-01	349.34	not significant
11511	ORC1	1.08	4.58E-04	7.16E-03	3074.30	not significant
11512	ACBD4	1.08	1.73E-02	9.70E-02	184.14	not significant
11513	NUCB1	1.08	1.03E-04	2.24E-03	4868.38	not significant
11514	SLC35C2	1.08	3.33E-03	3.02E-02	1694.47	not significant
11515	VWCE	1.08	2.00E-02	1.06E-01	306.91	not significant

11516	IGBP1	1.09	6.85E-03	5.12E-02	1129.44	not significant
11517	SYT1	1.09	1.34E-02	8.17E-02	662.06	not significant
11518	FAM160A2	1.09	1.46E-02	8.66E-02	542.93	not significant
11519	C14orf159	1.09	4.71E-03	3.88E-02	1551.18	not significant
11520	DNPH1	1.09	1.87E-02	1.02E-01	381.15	not significant
11521	SNHG6	1.09	1.66E-02	9.51E-02	2168.55	not significant
11522	PHF19	1.09	1.07E-04	2.28E-03	4287.98	not significant
11523	SPPL2A	1.09	6.00E-03	4.64E-02	991.73	not significant
11524	CIRBP	1.09	7.38E-05	1.70E-03	5468.69	not significant
11525	TMEM147	1.09	3.38E-03	3.05E-02	2212.92	not significant
11526	MIR155HG	1.09	1.84E-02	1.01E-01	236.26	not significant
11527	S1PR4	1.09	3.48E-03	3.11E-02	1533.59	not significant
11528	TAPT1	1.09	4.62E-03	3.83E-02	1353.71	not significant
11529	LYSMD4	1.09	1.92E-02	1.04E-01	345.87	not significant
11530	FIGNL1	1.09	1.33E-03	1.57E-02	2915.06	not significant
11531	GMIP	1.09	9.78E-03	6.54E-02	709.00	not significant
11532	KIAA0141	1.09	1.64E-03	1.83E-02	2077.43	not significant
11533	PTPLAD2	1.09	6.37E-03	4.83E-02	1016.15	not significant
11534	TMEM259	1.09	3.37E-05	8.88E-04	6374.31	not significant
11535	LZTR1	1.09	1.98E-03	2.09E-02	1911.19	not significant
11536	PFKL	1.09	1.16E-03	1.41E-02	2023.63	not significant
11537	SETDB1	1.09	1.76E-03	1.93E-02	1706.58	not significant
11538	CD96	1.09	8.07E-04	1.09E-02	5277.32	not significant
11539	CFTR	1.09	1.07E-04	2.29E-03	4207.53	not significant
11540	F2R	1.09	3.74E-03	3.28E-02	1309.21	not significant
11541	ATG13	1.09	9.80E-04	1.26E-02	2019.91	not significant
11542	CSGALNACT2	1.09	1.90E-03	2.04E-02	1806.17	not significant
11543	CYBA	1.09	2.72E-03	2.63E-02	2181.20	not significant
11544	PMM1	1.09	1.25E-02	7.79E-02	622.63	not significant
11545	EHD2	1.09	4.93E-03	4.01E-02	1020.64	not significant
11546	RPUSD3	1.09	6.26E-03	4.79E-02	874.99	not significant
11547	APPL2	1.09	7.07E-03	5.24E-02	831.39	not significant
11548	TTLL1	1.09	1.81E-02	1.00E-01	244.70	not significant
11549	ANKRD36	1.09	1.83E-02	1.01E-01	259.61	not significant
11550	ZDHHC17	1.09	2.20E-03	2.28E-02	1689.66	not significant
11551	PTPRCAP	1.09	1.67E-04	3.25E-03	5777.93	not significant
11552	GTF3C5	1.09	1.29E-04	2.64E-03	5243.16	not significant
11553	ARHGAP9	1.09	1.78E-03	1.94E-02	1729.10	not significant
11554	GABARAPL2	1.09	3.04E-03	2.85E-02	1638.43	not significant
11555	H6PD	1.09	4.51E-03	3.76E-02	1713.57	not significant
11556	FBXO8	1.09	1.59E-02	9.26E-02	379.86	not significant
11557	SIPA1	1.09	1.36E-02	8.26E-02	476.69	not significant
11558	SPTBN2	1.09	1.20E-03	1.45E-02	1759.98	not significant
11559	KCNK1	1.09	1.78E-03	1.94E-02	1648.15	not significant
11560	PELI1	1.09	1.50E-02	8.89E-02	440.89	not significant
11561	GBP4	1.09	5.15E-04	7.84E-03	2494.12	not significant
11562	FANCG	1.09	4.06E-04	6.49E-03	2734.91	not significant
11563	FCGRT	1.09	1.03E-02	6.83E-02	676.41	not significant
11564	GAS5	1.09	6.14E-04	8.82E-03	3241.28	not significant
11565	TAF1C	1.09	6.14E-04	8.82E-03	2701.30	not significant
11566	SDE2	1.09	9.71E-04	1.25E-02	1945.30	not significant
11567	YIPF3	1.09	1.41E-03	1.64E-02	1720.77	not significant
11568	THUMPD3-AS1	1.09	1.71E-02	9.63E-02	372.93	not significant
11569	CASP10	1.09	6.33E-04	9.04E-03	2052.41	not significant
11570	C17orf62	1.09	3.01E-05	8.15E-04	5227.02	not significant
11571	LPCAT4	1.09	3.43E-03	3.09E-02	1158.41	not significant
11572	JAK3	1.09	3.70E-03	3.26E-02	1295.75	not significant
11573	TMED1	1.09	1.70E-02	9.62E-02	330.83	not significant
11574	WSB1	1.09	9.84E-04	1.26E-02	3201.55	not significant
11575	RABAC1	1.09	1.67E-02	9.52E-02	337.53	not significant
11576	ARFGAP3	1.09	3.30E-04	5.54E-03	3350.01	not significant
11577	TMEM60	1.09	1.18E-02	7.44E-02	532.63	not significant
11578	PSMC3IP	1.09	5.27E-03	4.21E-02	1062.39	not significant
11579	CLK2	1.09	6.42E-03	4.86E-02	816.98	not significant
11580	SS18L1	1.09	4.43E-03	3.72E-02	1132.10	not significant
11581	TMEM102	1.09	1.59E-02	9.23E-02	334.04	not significant
11582	ZADH2	1.09	8.83E-03	6.09E-02	840.78	not significant
11583	ZC4H2	1.09	4.66E-03	3.85E-02	952.75	not significant
11584	CCR4	1.09	1.55E-02	9.09E-02	353.47	not significant
11585	TNFAIP8	1.09	1.59E-04	3.14E-03	3051.35	not significant
11586	RHOC	1.09	4.71E-03	3.88E-02	1385.55	not significant
11587	TCEAL8	1.09	2.88E-03	2.74E-02	1455.72	not significant
11588	TMEM41B	1.09	1.93E-03	2.07E-02	1547.37	not significant
11589	FADS2	1.09	3.34E-06	1.36E-04	12825.28	not significant
11590	RECQL5	1.09	2.55E-03	2.53E-02	1207.07	not significant
11591	SAT1	1.09	4.95E-03	4.02E-02	938.17	not significant
11592	SEMA4A	1.09	8.49E-03	5.94E-02	631.07	not significant
11593	FAM134A	1.09	1.59E-04	3.14E-03	2811.48	not significant
11594	CCNDBP1	1.09	7.04E-03	5.23E-02	813.43	not significant
11595	KLHL17	1.09	8.50E-03	5.94E-02	619.11	not significant
11596	SGPP1	1.09	2.19E-03	2.27E-02	1331.71	not significant
11597	TRPT1	1.09	1.30E-02	7.98E-02	495.69	not significant
11598	SERINC1	1.09	5.14E-04	7.84E-03	2599.98	not significant
11599	EML2	1.09	9.33E-03	6.32E-02	561.20	not significant
11600	ETHE1	1.09	1.52E-02	8.95E-02	387.82	not significant
11601	TRAF5	1.09	1.47E-03	1.69E-02	1597.10	not significant
11602	CTC1	1.09	8.34E-01	NA	49.80	not significant
11603	HSF2	1.09	1.22E-03	1.46E-02	1486.71	not significant

11604	NAGPA	1.09	9.92E-03	6.60E-02	537.83	not significant
11605	TEX264	1.09	1.82E-03	1.96E-02	1327.81	not significant
11606	SCN7A	1.10	1.32E-03	1.56E-02	2227.16	not significant
11607	PCBD2	1.10	1.44E-02	8.62E-02	375.76	not significant
11608	NARFL	1.10	4.65E-03	3.85E-02	883.27	not significant
11609	RRNAD1	1.10	1.12E-02	7.19E-02	475.13	not significant
11610	TECPR1	1.10	2.07E-03	2.17E-02	1330.01	not significant
11611	FAM111A	1.10	3.85E-04	6.30E-03	4204.96	not significant
11612	AACS	1.10	2.01E-03	2.12E-02	1219.49	not significant
11613	SLC37A1	1.10	8.25E-03	5.83E-02	578.53	not significant
11614	SSR2	1.10	1.77E-05	5.52E-04	5870.43	not significant
11615	HDAC6	1.10	1.33E-02	8.12E-02	500.58	not significant
11616	CLGN	1.10	2.55E-03	2.53E-02	1156.76	not significant
11617	ZNF224	1.10	9.65E-03	6.50E-02	525.17	not significant
11618	RAD51AP1	1.10	3.38E-01	NA	26.29	not significant
11619	KDELC2	1.10	2.17E-04	4.04E-03	3066.94	not significant
11620	CLIC4	1.10	3.10E-04	5.33E-03	2119.03	not significant
11621	PAIP2	1.10	3.25E-05	8.67E-04	4555.22	not significant
11622	ACSS1	1.10	1.98E-05	6.05E-04	4381.13	not significant
11623	HEXDC	1.10	5.51E-03	4.36E-02	777.20	not significant
11624	TJP2	1.10	1.14E-02	7.27E-02	475.25	not significant
11625	FBXO4	1.10	1.56E-02	9.11E-02	268.99	not significant
11626	CPNE1	1.10	2.66E-05	7.46E-04	4924.19	not significant
11627	ATF6B	1.10	2.96E-03	2.79E-02	1106.67	not significant
11628	NAPB	1.10	1.13E-02	7.22E-02	487.58	not significant
11629	TP53INP1	1.10	6.67E-03	5.03E-02	937.29	not significant
11630	KCNH2	1.10	1.05E-02	6.88E-02	587.79	not significant
11631	CD2	1.10	1.60E-05	5.09E-04	4980.30	not significant
11632	CNN3	1.10	6.12E-04	8.82E-03	1963.86	not significant
11633	SERINC3	1.10	2.65E-04	4.73E-03	3593.86	not significant
11634	BRWD1	1.10	1.51E-03	1.72E-02	1492.92	not significant
11635	TUBGCP6	1.10	1.25E-03	1.49E-02	2616.53	not significant
11636	ITGB2-AS1	1.10	1.28E-02	7.89E-02	151.02	not significant
11637	LGALS9	1.10	8.59E-04	1.14E-02	1609.03	not significant
11638	C6orf48	1.10	5.19E-03	4.16E-02	759.28	not significant
11639	ELOVL5	1.10	6.26E-07	3.28E-05	18225.18	not significant
11640	SEPW1	1.10	5.37E-04	8.09E-03	2359.85	not significant
11641	THAP9-AS1	1.10	3.02E-03	2.84E-02	933.75	not significant
11642	AMFR	1.10	9.18E-05	2.03E-03	2674.87	not significant
11643	PRIM1	1.10	6.13E-04	8.82E-03	1557.22	not significant
11644	U2AF1L4	1.10	1.44E-02	8.62E-02	284.55	not significant
11645	LINC00493	1.10	5.97E-03	4.63E-02	889.45	not significant
11646	CD1C	1.10	2.48E-03	2.48E-02	1166.20	not significant
11647	ZBTB17	1.10	2.10E-03	2.18E-02	1169.61	not significant
11648	RECQL4	1.10	2.94E-05	8.03E-04	3782.12	not significant
11649	CUL7	1.10	2.55E-03	2.53E-02	1087.79	not significant
11650	FAM160B1	1.10	3.22E-04	5.45E-03	2086.08	not significant
11651	SEPT7P2	1.10	1.27E-02	7.84E-02	352.43	not significant
11652	SUV420H2	1.10	4.47E-03	3.74E-02	749.50	not significant
11653	LRRC45	1.10	1.83E-04	3.50E-03	2161.35	not significant
11654	EIF3E	1.10	3.17E-06	1.31E-04	9046.07	not significant
11655	DGKD	1.10	4.15E-04	6.58E-03	2231.75	not significant
11656	GPRASP1	1.10	5.14E-03	4.13E-02	762.73	not significant
11657	ZNF579	1.10	1.15E-02	7.29E-02	364.50	not significant
11658	SARAF	1.10	7.62E-07	3.85E-05	7086.76	not significant
11659	DHPS	1.10	9.02E-04	1.18E-02	2039.51	not significant
11660	GIGYF1	1.10	3.82E-04	6.27E-03	4021.92	not significant
11661	NAT14	1.10	8.18E-03	5.80E-02	510.65	not significant
11662	MXD3	1.10	5.30E-03	4.22E-02	686.38	not significant
11663	GPAA1	1.10	4.36E-03	3.68E-02	845.04	not significant
11664	MUT	1.10	3.08E-03	2.87E-02	915.82	not significant
11665	CTSD	1.10	2.98E-06	1.23E-04	6685.35	not significant
11666	BRD3	1.10	2.47E-04	4.49E-03	2029.66	not significant
11667	GLT8D1	1.10	3.71E-03	3.26E-02	992.08	not significant
11668	ITM2B	1.10	2.00E-07	1.22E-05	12561.04	not significant
11669	PNPLA8	1.10	1.94E-03	2.07E-02	1078.52	not significant
11670	RBL2	1.10	1.45E-05	4.70E-04	4935.36	not significant
11671	TRANK1	1.10	1.58E-03	1.79E-02	1281.91	not significant
11672	RTN4	1.10	5.16E-07	2.79E-05	8416.47	not significant
11673	RNASEH2C	1.10	7.56E-04	1.04E-02	1539.27	not significant
11674	PMPCB	1.10	5.32E-05	1.30E-03	2945.27	not significant
11675	MUS81	1.10	8.72E-04	1.15E-02	1412.41	not significant
11676	ABHD12	1.10	2.61E-04	4.68E-03	1833.16	not significant
11677	LOC220729	1.10	9.11E-03	6.21E-02	445.75	not significant
11678	CD38	1.10	4.85E-04	7.48E-03	1971.74	not significant
11679	IFFO1	1.10	6.89E-03	5.14E-02	529.76	not significant
11680	43530_6595	1.10	6.82E-05	1.60E-03	4976.41	not significant
11681	EPB41L4A-AS1	1.10	8.06E-03	5.73E-02	501.68	not significant
11682	MBOAT1	1.11	4.60E-03	3.82E-02	677.85	not significant
11683	B3GAT3	1.11	2.43E-03	2.46E-02	1006.42	not significant
11684	ASAP2	1.11	1.35E-02	8.19E-02	183.20	not significant
11685	CCNB1IP1	1.11	7.84E-04	1.07E-02	2014.46	not significant
11686	C6orf147	1.11	1.14E-02	7.25E-02	124.87	not significant
11687	ZSWIM8	1.11	2.43E-04	4.44E-03	2229.54	not significant
11688	ZDHHC24	1.11	5.90E-03	4.59E-02	599.82	not significant
11689	GFI1	1.11	1.79E-03	1.95E-02	1131.78	not significant
11690	FXYD5	1.11	3.66E-05	9.54E-04	2806.75	not significant
11691	USP44	1.11	2.09E-03	2.18E-02	1026.54	not significant

11692	CASC15	1.11	4.55E-03	3.78E-02	853.06	not significant
11693	EZH1	1.11	2.25E-03	2.32E-02	922.37	not significant
11694	IKZF2	1.11	5.05E-05	1.25E-03	9011.33	not significant
11695	ALKBH7	1.11	5.34E-03	4.24E-02	728.09	not significant
11696	CCNG1	1.11	3.03E-05	8.20E-04	3241.35	not significant
11697	C14orf1	1.11	6.38E-04	9.09E-03	1520.37	not significant
11698	OGT	1.11	2.25E-05	6.67E-04	8231.64	not significant
11699	FANCL	1.11	1.65E-03	1.85E-02	977.27	not significant
11700	HAUS4	1.11	1.41E-03	1.63E-02	1053.58	not significant
11701	HMGCR	1.11	3.24E-07	1.89E-05	7921.69	not significant
11702	C17orf70	1.11	5.76E-05	1.39E-03	2426.36	not significant
11703	RNASET2	1.11	3.58E-03	3.19E-02	669.34	not significant
11704	ARHGAP4	1.11	6.35E-05	1.50E-03	2369.35	not significant
11705	HSPA13	1.11	3.36E-05	8.87E-04	3596.10	not significant
11706	TRIM22	1.11	1.59E-04	3.14E-03	2051.97	not significant
11707	TNFRSF14	1.11	9.29E-04	1.21E-02	1159.01	not significant
11708	TMEM194B	1.11	1.97E-03	2.09E-02	940.73	not significant
11709	SLC25A29	1.11	1.61E-04	3.16E-03	1958.22	not significant
11710	C22orf39	1.11	8.19E-04	1.10E-02	1286.35	not significant
11711	CRNDE	1.11	8.48E-04	1.13E-02	1227.92	not significant
11712	GRAMD1A	1.11	8.66E-05	1.93E-03	2238.29	not significant
11713	MAPKAPK5-AS1	1.11	3.45E-03	3.09E-02	716.63	not significant
11714	E2F8	1.11	3.14E-04	5.39E-03	1810.02	not significant
11715	PKMYT1	1.11	7.68E-06	2.71E-04	3790.22	not significant
11716	TMUB2	1.11	3.77E-03	3.29E-02	680.39	not significant
11717	PPAPDC2	1.11	8.42E-03	5.93E-02	386.14	not significant
11718	MAN2A2	1.11	5.50E-04	8.18E-03	2320.12	not significant
11719	XRCC1	1.11	4.42E-04	6.94E-03	1316.42	not significant
11720	SEC31B	1.11	1.08E-02	7.05E-02	9352.32	not significant
11721	ZNF512B	1.11	2.00E-05	6.08E-04	2774.29	not significant
11722	ACTR1B	1.11	3.04E-04	5.28E-03	2060.34	not significant
11723	QPRT	1.11	2.19E-03	2.27E-02	894.07	not significant
11724	GBA2	1.11	1.91E-03	2.05E-02	861.42	not significant
11725	CCDC150	1.11	1.15E-02	7.31E-02	290.29	not significant
11726	JUND	1.11	2.28E-05	6.73E-04	6443.63	not significant
11727	DDRGK1	1.11	2.33E-04	4.28E-03	1784.85	not significant
11728	ABCB10	1.11	8.58E-05	1.92E-03	2208.51	not significant
11729	WBP2	1.11	2.29E-05	6.73E-04	3360.74	not significant
11730	CEP152	1.11	3.95E-04	6.38E-03	1674.18	not significant
11731	ZDHHC13	1.11	2.70E-03	2.62E-02	974.87	not significant
11732	LUC7L	1.11	1.15E-04	2.42E-03	2088.93	not significant
11733	LSS	1.11	3.67E-05	9.54E-04	2115.56	not significant
11734	CTSS	1.11	3.30E-03	3.01E-02	669.19	not significant
11735	FOXD2-AS1	1.11	1.09E-02	7.07E-02	251.04	not significant
11736	ITGA1	1.11	3.21E-04	5.44E-03	3730.71	not significant
11737	SCAND1	1.12	1.68E-03	1.87E-02	1330.79	not significant
11738	WDR27	1.12	8.04E-03	5.72E-02	368.50	not significant
11739	ACSF3	1.12	2.53E-05	7.27E-04	2326.53	not significant
11740	DYRK1B	1.12	1.21E-02	7.59E-02	172.10	not significant
11741	ASIC1	1.12	1.41E-03	1.64E-02	1053.23	not significant
11742	MIR17HG	1.12	8.35E-03	5.89E-02	371.24	not significant
11743	CDK18	1.12	5.93E-03	4.60E-02	436.57	not significant
11744	TMEM44	1.12	9.28E-03	6.30E-02	408.63	not significant
11745	GALT	1.12	3.45E-03	3.09E-02	591.19	not significant
11746	RAB11B	1.12	1.67E-05	5.25E-04	3090.37	not significant
11747	CHMP6	1.12	1.18E-03	1.43E-02	998.16	not significant
11748	FAM107B	1.12	6.66E-04	9.38E-03	1427.04	not significant
11749	CNPY3	1.12	1.66E-05	5.24E-04	3474.04	not significant
11750	CASP8	1.12	1.18E-04	2.46E-03	1748.11	not significant
11751	CLIP4	1.12	7.09E-04	9.88E-03	994.00	not significant
11752	DHRS7	1.12	4.70E-04	7.31E-03	1151.09	not significant
11753	TUBA1A	1.12	5.85E-05	1.40E-03	3751.23	not significant
11754	PELI2	1.12	1.29E-04	2.64E-03	1703.92	not significant
11755	FKRP	1.12	9.37E-04	1.22E-02	923.56	not significant
11756	FAAH	1.12	5.82E-03	4.54E-02	443.21	not significant
11757	BTN3A1	1.12	3.29E-04	5.54E-03	1213.41	not significant
11758	ZBED6	1.12	4.17E-03	3.56E-02	564.92	not significant
11759	C21orf58	1.12	4.40E-03	3.70E-02	561.14	not significant
11760	LIMD2	1.12	2.34E-05	6.84E-04	3558.28	not significant
11761	TTC17	1.12	1.14E-04	2.41E-03	2194.63	not significant
11762	RAD9A	1.12	1.36E-04	2.77E-03	1793.49	not significant
11763	EIF4EBP1	1.12	1.49E-04	2.98E-03	3422.34	not significant
11764	PCIF1	1.12	1.49E-05	4.80E-04	2426.10	not significant
11765	IP6K2	1.12	2.16E-05	6.47E-04	2380.56	not significant
11766	IDH2	1.12	1.99E-07	1.22E-05	8984.58	not significant
11767	FUOM	1.12	1.09E-02	7.07E-02	138.52	not significant
11768	STAT2	1.12	6.95E-05	1.62E-03	1939.79	not significant
11769	ACAT2	1.12	3.04E-05	8.20E-04	3898.65	not significant
11770	LRMP	1.12	6.75E-04	9.49E-03	1025.02	not significant
11771	CARF	1.12	7.83E-03	5.64E-02	312.86	not significant
11772	TMEM59	1.12	1.07E-05	3.56E-04	2282.91	not significant
11773	ICAM3	1.12	4.85E-06	1.88E-04	2965.28	not significant
11774	FAIM3	1.12	7.87E-03	5.66E-02	312.99	not significant
11775	CCNL2	1.12	1.98E-05	6.05E-04	2586.25	not significant
11776	BTN3A3	1.12	1.45E-03	1.67E-02	754.78	not significant
11777	INSR	1.12	2.73E-03	2.63E-02	616.05	not significant
11778	LRRC8C	1.12	1.36E-04	2.77E-03	1655.55	not significant
11779	MAGEH1	1.12	2.61E-03	2.57E-02	587.67	not significant

11780	DBN1	1.12	2.57E-05	7.31E-04	2747.89	not significant
11781	AGFG2	1.12	8.86E-04	1.16E-02	868.46	not significant
11782	SCAMP1-AS1	1.12	9.73E-03	6.53E-02	253.11	not significant
11783	SUZ12P1	1.12	5.93E-03	4.60E-02	374.54	not significant
11784	MYO1G	1.12	2.02E-07	1.23E-05	7231.11	not significant
11785	YEATS4	1.12	2.92E-04	5.12E-03	1930.09	not significant
11786	BEND5	1.13	9.68E-03	6.51E-02	235.53	not significant
11787	APH1A	1.13	1.93E-03	2.07E-02	800.34	not significant
11788	TONSL	1.13	1.07E-05	3.57E-04	3174.16	not significant
11789	SMAD1	1.13	3.72E-03	3.27E-02	492.40	not significant
11790	SLC18A2	1.13	1.05E-03	1.31E-02	891.82	not significant
11791	AMZ2P1	1.13	5.75E-03	4.50E-02	371.27	not significant
11792	SYTL1	1.13	2.47E-03	2.48E-02	533.30	not significant
11793	TMEM107	1.13	9.79E-03	6.55E-02	140.23	not significant
11794	CDK5RAP3	1.13	5.95E-06	2.21E-04	5116.87	not significant
11795	MBNL2	1.13	5.98E-04	8.69E-03	939.18	not significant
11796	C19orf60	1.13	1.87E-03	2.02E-02	712.17	not significant
11797	SLAMF6	1.13	1.04E-04	2.25E-03	1292.39	not significant
11798	LOC645513	1.13	8.45E-03	5.94E-02	234.51	not significant
11799	SOX4	1.13	3.64E-11	5.87E-09	16972.81	not significant
11800	RNF122	1.13	5.91E-03	4.60E-02	331.49	not significant
11801	ZNF33B	1.13	6.27E-04	8.99E-03	890.08	not significant
11802	SREBF2	1.13	1.24E-08	1.18E-06	9651.34	not significant
11803	IL10RB	1.13	4.48E-05	1.13E-03	1566.92	not significant
11804	ZGRF1	1.13	2.98E-04	5.20E-03	1771.00	not significant
11805	HECA	1.13	2.49E-05	7.19E-04	2016.42	not significant
11806	WDR90	1.13	1.95E-04	3.68E-03	1730.06	not significant
11807	CCDC28A	1.13	3.17E-03	2.94E-02	484.25	not significant
11808	RPP25L	1.13	4.53E-03	3.77E-02	409.98	not significant
11809	TIMELESS	1.13	1.28E-10	1.97E-08	8684.31	not significant
11810	GRIPAP1	1.13	4.94E-04	7.58E-03	929.05	not significant
11811	N4BP2L1	1.13	3.56E-03	3.18E-02	454.50	not significant
11812	ZNF711	1.13	7.61E-05	1.73E-03	1775.74	not significant
11813	C15orf61	1.13	7.54E-03	5.50E-02	275.34	not significant
11814	CD37	1.13	9.47E-05	2.07E-03	1260.61	not significant
11815	BTN3A2	1.13	7.14E-05	1.66E-03	1377.05	not significant
11816	HDAC9	1.13	4.74E-04	7.37E-03	871.86	not significant
11817	SGSM3	1.13	7.90E-05	1.78E-03	1504.79	not significant
11818	HHIP-AS1	1.13	7.94E-05	1.78E-03	1334.36	not significant
11819	NSUN5P1	1.13	9.68E-03	6.51E-02	132.67	not significant
11820	CCDC61	1.13	6.35E-03	4.83E-02	305.56	not significant
11821	KCNN4	1.13	6.32E-03	4.82E-02	308.39	not significant
11822	SERINC5	1.13	4.53E-07	2.52E-05	7924.65	not significant
11823	NR2C1	1.13	8.58E-05	1.92E-03	1381.38	not significant
11824	AGO4	1.14	8.04E-04	1.09E-02	989.28	not significant
11825	RBM38	1.14	1.87E-03	2.01E-02	528.74	not significant
11826	KIAA0101	1.14	5.93E-07	3.16E-05	3493.25	not significant
11827	BIRC3	1.14	1.23E-03	1.48E-02	631.69	not significant
11828	LOC730101	1.14	1.71E-03	1.88E-02	655.07	not significant
11829	MYO18B	1.14	4.07E-07	2.31E-05	11527.66	not significant
11830	PAQR4	1.14	4.67E-05	1.17E-03	1855.98	not significant
11831	TMEM175	1.14	2.46E-03	2.47E-02	444.21	not significant
11832	MPG	1.14	7.84E-04	1.07E-02	833.24	not significant
11833	TP53I13	1.14	7.41E-05	1.70E-03	1255.77	not significant
11834	ADCK3	1.14	5.37E-04	8.09E-03	732.56	not significant
11835	OSBPL3	1.14	2.92E-06	1.22E-04	2826.21	not significant
11836	GATA3	1.14	3.41E-09	3.87E-07	6028.00	not significant
11837	ICAM2	1.14	6.14E-09	6.20E-07	5350.61	not significant
11838	MVD	1.14	1.74E-04	3.35E-03	1454.85	not significant
11839	TAF8	1.14	2.25E-04	4.15E-03	1031.48	not significant
11840	TMBIM4	1.14	5.00E-05	1.24E-03	1422.37	not significant
11841	SLC35E2B	1.14	2.00E-05	6.08E-04	2401.57	not significant
11842	ITGA4	1.14	1.04E-08	1.01E-06	20253.32	not significant
11843	PPDPF	1.14	5.44E-04	8.11E-03	983.47	not significant
11844	AMDHD2	1.14	2.86E-03	2.72E-02	480.19	not significant
11845	MZF1	1.14	6.61E-03	4.99E-02	268.74	not significant
11846	TMEM129	1.14	1.02E-03	1.30E-02	588.10	not significant
11847	SUMF2	1.14	2.38E-08	2.19E-06	3988.11	not significant
11848	RAB24	1.14	4.84E-04	7.47E-03	792.79	not significant
11849	ASPSCR1	1.14	3.46E-04	5.75E-03	921.39	not significant
11850	EDEM1	1.14	6.08E-08	4.61E-06	7945.34	not significant
11851	DGKQ	1.14	3.80E-05	9.86E-04	1357.41	not significant
11852	TSTD1	1.14	6.32E-03	4.82E-02	244.88	not significant
11853	ERP29	1.14	4.53E-09	4.87E-07	7259.63	not significant
11854	TMEM159	1.14	3.10E-03	2.89E-02	375.68	not significant
11855	ZNF496	1.14	1.11E-04	2.35E-03	1024.94	not significant
11856	NFKBID	1.14	6.66E-03	5.02E-02	242.47	not significant
11857	SVOPL	1.14	4.21E-03	3.59E-02	352.74	not significant
11858	DDAH2	1.14	2.94E-03	2.78E-02	385.06	not significant
11859	CD28	1.14	1.82E-10	2.60E-08	9132.31	not significant
11860	CAMLG	1.14	8.36E-05	1.88E-03	1215.17	not significant
11861	FAM84B	1.14	8.55E-03	5.96E-02	181.31	not significant
11862	STT3B	1.14	2.08E-10	2.94E-08	25627.61	not significant
11863	ERAP1	1.14	1.29E-06	6.17E-05	3304.73	not significant
11864	NOA1	1.14	2.02E-05	6.10E-04	1445.03	not significant
11865	MAN2C1	1.14	4.99E-05	1.24E-03	1149.23	not significant
11866	ANKRD23	1.14	9.00E-03	6.18E-02	130.79	not significant
11867	RCCD1	1.14	4.80E-04	7.42E-03	707.33	not significant

11868	PPP1R3E	1.14	3.47E-03	3.11E-02	356.54	not significant
11869	CD1B	1.15	4.46E-08	3.57E-06	3370.75	not significant
11870	NPC2	1.15	3.36E-04	5.64E-03	750.17	not significant
11871	PIGM	1.15	3.45E-04	5.75E-03	897.62	not significant
11872	GPCPD1	1.15	1.52E-04	3.03E-03	874.72	not significant
11873	IRS2	1.15	8.31E-04	1.11E-02	607.02	not significant
11874	OGFOD3	1.15	3.44E-05	9.04E-04	1215.24	not significant
11875	TBC1D17	1.15	1.18E-03	1.44E-02	505.71	not significant
11876	TTC31	1.15	6.11E-05	1.46E-03	1022.90	not significant
11877	LOC646719	1.15	8.13E-04	1.10E-02	566.23	not significant
11878	LINC01003	1.15	7.05E-03	5.24E-02	191.10	not significant
11879	HNRNPU-AS1	1.15	3.16E-04	5.40E-03	931.37	not significant
11880	CEP57	1.15	5.83E-09	6.10E-07	3297.41	not significant
11881	LINC00938	1.15	1.47E-04	2.95E-03	836.38	not significant
11882	CEBPB	1.15	1.39E-03	1.63E-02	708.00	not significant
11883	LOC285074	1.15	2.39E-03	2.43E-02	371.90	not significant
11884	FLJ10038	1.15	5.77E-03	4.51E-02	234.39	not significant
11885	SPPL2B	1.15	1.11E-05	3.64E-04	1437.80	not significant
11886	SERPINB1	1.15	6.19E-07	3.26E-05	2445.61	not significant
11887	UBALD2	1.15	2.91E-07	1.73E-05	3326.58	not significant
11888	USP3	1.15	5.12E-05	1.26E-03	1004.66	not significant
11889	HSF4	1.15	5.86E-03	4.57E-02	216.70	not significant
11890	PDE4DIP	1.15	3.70E-03	3.26E-02	307.11	not significant
11891	FDFT1	1.15	1.57E-11	3.14E-09	15948.48	not significant
11892	ERBB2	1.15	7.42E-03	5.44E-02	162.20	not significant
11893	MEX3B	1.15	6.17E-03	4.73E-02	206.96	not significant
11894	AK3	1.15	9.41E-06	3.19E-04	1340.69	not significant
11895	DKFZP586I1420	1.15	2.72E-03	2.63E-02	364.92	not significant
11896	MANBA	1.15	5.39E-04	8.09E-03	588.22	not significant
11897	LRIG1	1.16	5.67E-04	8.37E-03	675.99	not significant
11898	LOC100287015	1.16	7.84E-03	5.65E-02	141.43	not significant
11899	EVI2B	1.16	4.00E-04	6.41E-03	715.82	not significant
11900	PCMTD1	1.16	1.52E-04	3.03E-03	841.48	not significant
11901	PITPNM1	1.16	2.55E-08	2.26E-06	2981.65	not significant
11902	TMEM57	1.16	1.88E-06	8.34E-05	1815.52	not significant
11903	NIPSNAP3A	1.16	3.14E-04	5.39E-03	638.06	not significant
11904	DNAJC1	1.16	6.90E-05	1.61E-03	909.74	not significant
11905	SLFN13	1.16	4.45E-05	1.13E-03	1169.66	not significant
11906	ZNF446	1.16	2.90E-03	2.75E-02	299.48	not significant
11907	TTC14	1.16	4.38E-07	2.46E-05	2463.54	not significant
11908	SESTD1	1.16	1.13E-03	1.39E-02	507.34	not significant
11909	SCGB3A1	1.16	3.32E-03	3.02E-02	382.35	not significant
11910	FAM214A	1.16	1.76E-03	1.92E-02	409.92	not significant
11911	LMF2	1.16	2.42E-07	1.46E-05	2697.84	not significant
11912	C11orf68	1.16	6.28E-04	8.99E-03	508.62	not significant
11913	PDCD4	1.16	2.63E-05	7.46E-04	1078.61	not significant
11914	CCNE1	1.16	5.47E-04	8.15E-03	540.94	not significant
11915	ENTPD4	1.16	1.18E-06	5.65E-05	2348.85	not significant
11916	FADS1	1.16	1.13E-10	1.77E-08	7931.75	not significant
11917	UBA7	1.16	4.59E-07	2.52E-05	2142.51	not significant
11918	SAP25	1.16	2.46E-03	2.47E-02	340.44	not significant
11919	STAT5B	1.16	1.09E-13	3.21E-11	7310.16	not significant
11920	SLC44A2	1.16	6.40E-08	4.78E-06	2238.00	not significant
11921	ZDHHC12	1.16	9.12E-05	2.02E-03	1024.55	not significant
11922	PSAT1	1.16	4.15E-12	9.88E-10	7268.14	not significant
11923	NINL	1.16	2.66E-07	1.60E-05	1770.72	not significant
11924	SFI1	1.16	2.07E-06	9.02E-05	1753.21	not significant
11925	VPS11	1.16	2.46E-03	2.47E-02	356.53	not significant
11926	TMEM97	1.16	4.89E-03	3.99E-02	214.22	not significant
11927	AP1G2	1.16	2.95E-07	1.75E-05	2352.09	not significant
11928	PDXDC2P	1.16	2.68E-03	2.61E-02	295.44	not significant
11929	DHCR7	1.16	3.83E-08	3.19E-06	2702.29	not significant
11930	KIAA0895L	1.16	6.77E-06	2.45E-04	1350.43	not significant
11931	SLC29A3	1.16	3.71E-03	3.26E-02	253.80	not significant
11932	CEP131	1.16	3.23E-06	1.32E-04	1353.05	not significant
11933	CHMP1B	1.16	1.45E-06	6.71E-05	1435.00	not significant
11934	TTYH2	1.16	5.27E-03	4.21E-02	211.46	not significant
11935	FAM173A	1.16	7.45E-03	5.45E-02	133.54	not significant
11936	ASB16-AS1	1.16	3.08E-03	2.87E-02	294.40	not significant
11937	CD27-AS1	1.16	4.09E-01	NA	76.89	not significant
11938	PHF1	1.16	2.63E-03	2.58E-02	282.76	not significant
11939	LRP10	1.16	8.13E-06	2.82E-04	1131.98	not significant
11940	DCHS1	1.17	3.22E-03	2.96E-02	1593.80	not significant
11941	IER2	1.17	1.71E-07	1.08E-05	2829.51	not significant
11942	CD83	1.17	4.86E-06	1.88E-04	1452.61	not significant
11943	THTPA	1.17	1.97E-03	2.09E-02	322.68	not significant
11944	LENG8	1.17	1.26E-04	2.59E-03	904.37	not significant
11945	APOBR	1.17	2.37E-05	6.91E-04	927.41	not significant
11946	ABCD4	1.17	6.51E-06	2.37E-04	1163.98	not significant
11947	SPAG7	1.17	5.39E-05	1.32E-03	1091.52	not significant
11948	NSDHL	1.17	2.71E-03	2.63E-02	305.92	not significant
11949	ZBED6CL	1.17	1.52E-04	3.03E-03	641.16	not significant
11950	TMTC4	1.17	1.39E-04	2.82E-03	702.31	not significant
11951	PNKP	1.17	2.42E-05	7.05E-04	855.63	not significant
11952	MGST2	1.17	3.92E-03	3.39E-02	236.95	not significant
11953	INSIG1	1.17	2.30E-16	9.59E-14	16850.18	not significant
11954	CD69	1.17	1.64E-06	7.38E-05	1477.30	not significant
11955	CCDC88B	1.17	1.92E-06	8.46E-05	1307.30	not significant

11956	MDFIC	1.17	3.47E-13	9.38E-11	5400.51	not significant
11957	PYCARD	1.17	4.89E-03	3.99E-02	176.42	not significant
11958	MIEF2	1.17	3.66E-03	3.24E-02	240.97	not significant
11959	PTPRC	1.17	5.74E-10	7.55E-08	7870.40	not significant
11960	PCAT18	1.17	1.75E-03	1.92E-02	338.92	not significant
11961	IFIT2	1.17	2.61E-03	2.57E-02	258.00	not significant
11962	CRTAP	1.17	1.77E-11	3.35E-09	3714.18	not significant
11963	LINC00847	1.18	2.83E-04	4.98E-03	513.91	not significant
11964	MMP24-AS1	1.18	3.91E-04	6.34E-03	485.38	not significant
11965	SLC35E2	1.18	8.12E-04	1.10E-02	386.52	not significant
11966	CD58	1.18	2.45E-08	2.21E-06	2037.91	not significant
11967	CLEC2D	1.18	3.61E-05	9.46E-04	777.83	not significant
11968	SLC25A45	1.18	1.32E-03	1.56E-02	325.06	not significant
11969	CHST14	1.18	3.13E-05	8.38E-04	847.32	not significant
11970	CD48	1.18	1.13E-08	1.08E-06	2586.68	not significant
11971	HSD17B11	1.18	2.09E-05	6.27E-04	824.36	not significant
11972	CYP51A1	1.18	2.22E-06	9.55E-05	1138.77	not significant
11973	IFI44	1.18	1.85E-05	5.73E-04	818.49	not significant
11974	RMI2	1.18	5.53E-05	1.35E-03	725.37	not significant
11975	AZIN2	1.18	2.85E-03	2.71E-02	223.89	not significant
11976	PIGQ	1.18	6.10E-06	2.25E-04	945.94	not significant
11977	ZBED5	1.18	6.09E-07	3.22E-05	1530.78	not significant
11978	GLTSCR2	1.18	3.27E-11	5.54E-09	7349.15	not significant
11979	CCR9	1.18	5.10E-12	1.13E-09	3892.44	not significant
11980	CDKN1B	1.18	9.26E-07	4.52E-05	1298.95	not significant
11981	PPAPDC1B	1.18	1.77E-05	5.52E-04	917.54	not significant
11982	E2F1	1.18	3.15E-13	8.76E-11	4148.90	not significant
11983	CHTF18	1.18	4.03E-08	3.31E-06	2615.43	not significant
11984	CLCN7	1.18	1.25E-07	8.54E-06	1842.32	not significant
11985	SLC46A3	1.18	7.03E-05	1.64E-03	676.17	not significant
11986	SPSB3	1.18	1.27E-04	2.62E-03	727.04	not significant
11987	AGTRAP	1.19	1.53E-03	1.74E-02	272.01	not significant
11988	ARAP1	1.19	2.39E-11	4.43E-09	3812.90	not significant
11989	C5orf45	1.19	3.79E-03	3.30E-02	194.28	not significant
11990	HLA-E	1.19	3.97E-07	2.27E-05	1354.33	not significant
11991	OGDHL	1.19	1.13E-03	1.39E-02	303.87	not significant
11992	C16orf54	1.19	9.75E-08	6.87E-06	1604.61	not significant
11993	SNHG7	1.19	1.37E-07	8.99E-06	1600.59	not significant
11994	ZMYM6NB	1.19	4.35E-04	6.86E-03	467.16	not significant
11995	ACSF2	1.19	7.49E-04	1.03E-02	323.66	not significant
11996	CYTH2	1.19	5.58E-10	7.45E-08	2202.92	not significant
11997	ABCA7	1.19	1.50E-06	6.90E-05	1021.52	not significant
11998	RPARP-AS1	1.19	5.39E-04	8.09E-03	362.33	not significant
11999	SLC6A9	1.19	2.43E-04	4.44E-03	454.15	not significant
12000	FAM219B	1.19	1.41E-05	4.59E-04	876.12	not significant
12001	GSDMD	1.19	1.82E-10	2.60E-08	2454.22	not significant
12002	FAM193B	1.19	2.93E-08	2.50E-06	2392.22	not significant
12003	GIMAP2	1.19	8.81E-10	1.09E-07	2315.68	not significant
12004	CD40LG	1.20	9.74E-09	9.58E-07	1612.54	Increased
12005	JDP2	1.20	5.63E-04	8.34E-03	344.75	Increased
12006	RHEBL1	1.20	5.61E-03	4.41E-02	120.03	Increased
12007	NEAT1	1.20	7.98E-04	1.09E-02	2396.75	Increased
12008	GPT2	1.20	3.05E-08	2.59E-06	1438.15	Increased
12009	PABPC1L	1.20	1.46E-05	4.74E-04	922.42	Increased
12010	MRC2	1.20	4.34E-09	4.73E-07	1624.21	Increased
12011	LOC100131564	1.20	4.50E-03	3.75E-02	155.29	Increased
12012	IVNS1ABP	1.20	3.15E-19	2.25E-16	5738.87	Increased
12013	RFNG	1.21	9.03E-07	4.45E-05	898.55	Increased
12014	SQLE	1.21	1.69E-16	7.71E-14	5734.30	Increased
12015	LOC100130872	1.21	2.54E-05	7.27E-04	561.07	Increased
12016	SFT2D3	1.21	6.09E-05	1.45E-03	489.92	Increased
12017	LOC729683	1.21	6.91E-03	NA	66.50	Increased
12018	SPRY1	1.21	1.94E-04	3.68E-03	394.30	Increased
12019	AHSA2	1.21	5.97E-09	6.10E-07	1880.22	Increased
12020	PPP1R15A	1.22	5.06E-06	1.95E-04	673.28	Increased
12021	GOLGA8B	1.22	1.49E-05	4.80E-04	727.83	Increased
12022	DUSP1	1.22	2.24E-04	4.14E-03	361.91	Increased
12023	TCIRG1	1.22	3.53E-11	5.80E-09	3168.31	Increased
12024	SLC38A2	1.22	1.51E-15	5.61E-13	16561.73	Increased
12025	CALCOCO1	1.22	7.75E-05	1.76E-03	410.22	Increased
12026	CDT1	1.22	1.07E-15	4.28E-13	6187.96	Increased
12027	BCHE	1.22	6.42E-07	3.33E-05	834.97	Increased
12028	TPM2	1.23	3.76E-03	3.28E-02	136.42	Increased
12029	RHPN1	1.23	1.24E-11	2.53E-09	2879.29	Increased
12030	RASGEF1B	1.23	1.02E-03	1.30E-02	218.19	Increased
12031	LETMD1	1.23	4.16E-11	6.60E-09	1702.47	Increased
12032	PLA2G6	1.23	2.09E-07	1.27E-05	812.19	Increased
12033	STAT5A	1.23	2.38E-30	5.95E-27	17679.76	Increased
12034	GPC2	1.23	4.78E-05	1.20E-03	463.42	Increased
12035	ZNF277	1.23	2.29E-06	9.74E-05	647.32	Increased
12036	HERC2P2	1.23	2.47E-05	7.15E-04	585.13	Increased
12037	C1orf228	1.23	4.95E-15	1.71E-12	2800.04	Increased
12038	NFKB2	1.23	4.20E-07	2.37E-05	815.89	Increased
12039	ATHL1	1.24	1.38E-15	5.31E-13	6336.37	Increased
12040	ROBO3	1.24	1.69E-06	7.58E-05	632.12	Increased
12041	ADM2	1.24	1.53E-05	4.89E-04	559.61	Increased
12042	PCED1A	1.24	3.62E-07	2.08E-05	795.84	Increased
12043	MSMO1	1.24	4.35E-15	1.56E-12	2653.06	Increased

12044	DNASE1	1.24	1.18E-04	2.46E-03	352.11	Increased
12045	PRDM8	1.24	9.56E-04	1.24E-02	198.34	Increased
12046	SLC43A1	1.24	9.24E-04	1.20E-02	206.19	Increased
12047	ITGA6	1.24	1.17E-04	2.45E-03	367.82	Increased
12048	SLC7A11	1.24	3.36E-09	3.86E-07	1308.91	Increased
12049	TTC39B	1.25	2.74E-05	7.61E-04	412.57	Increased
12050	SPC24	1.25	5.48E-06	2.08E-04	492.08	Increased
12051	MAGEF1	1.25	2.72E-05	7.60E-04	396.41	Increased
12052	C12orf76	1.25	5.17E-04	7.86E-03	207.11	Increased
12053	KIFC2	1.26	8.40E-08	6.09E-06	767.19	Increased
12054	CREBZF	1.26	1.44E-17	8.02E-15	3371.94	Increased
12055	NATD1	1.26	1.18E-03	1.43E-02	157.57	Increased
12056	METRN	1.26	3.15E-03	2.92E-02	108.01	Increased
12057	HDAC7	1.26	2.09E-26	3.49E-23	5641.88	Increased
12058	TIFA	1.26	5.95E-09	6.10E-07	861.30	Increased
12059	TNFAIP3	1.26	8.23E-14	2.49E-11	2149.82	Increased
12060	ANO9	1.26	5.32E-03	NA	67.95	Increased
12061	HMGCS1	1.26	1.89E-31	6.30E-28	7829.15	Increased
12062	INAFM1	1.26	3.10E-04	5.33E-03	238.88	Increased
12063	KLF2	1.26	4.82E-05	1.20E-03	332.30	Increased
12064	PAQR8	1.27	1.11E-06	5.35E-05	518.51	Increased
12065	TM7SF2	1.27	1.79E-04	3.42E-03	258.06	Increased
12066	MFGE8	1.27	1.26E-09	1.53E-07	889.48	Increased
12067	PCK2	1.27	1.81E-09	2.15E-07	957.99	Increased
12068	FCGBP	1.27	2.57E-04	4.63E-03	213.65	Increased
12069	UCP2	1.27	9.58E-17	4.56E-14	2162.98	Increased
12070	C1orf85	1.27	7.82E-06	2.74E-04	439.86	Increased
12071	C6orf223	1.27	3.14E-11	5.50E-09	1158.41	Increased
12072	EPB41L4A	1.28	1.25E-03	1.49E-02	141.12	Increased
12073	RAB37	1.28	4.09E-14	1.32E-11	1744.98	Increased
12074	ARHGAP33	1.28	3.31E-12	8.10E-10	1162.57	Increased
12075	ASNS	1.28	1.72E-11	3.34E-09	1070.89	Increased
12076	SLC20A1	1.29	1.64E-21	1.64E-18	4143.13	Increased
12077	ISG20	1.29	1.07E-03	1.34E-02	136.30	Increased
12078	HDAC5	1.29	1.61E-07	1.03E-05	593.58	Increased
12079	HBP1	1.29	5.92E-06	2.21E-04	371.45	Increased
12080	ARRDC3	1.29	9.76E-09	9.58E-07	686.59	Increased
12081	GLYCTK	1.29	1.10E-04	2.33E-03	244.42	Increased
12082	CDH24	1.29	2.24E-04	4.14E-03	220.02	Increased
12083	SESN2	1.30	2.99E-11	5.35E-09	947.13	Increased
12084	CREB3L4	1.30	3.85E-04	6.30E-03	169.12	Increased
12085	VLDLR	1.30	1.67E-07	1.06E-05	485.66	Increased
12086	YPEL5	1.30	1.51E-06	6.90E-05	394.34	Increased
12087	LOC100288152	1.30	5.12E-03	NA	55.79	Increased
12088	LY9	1.30	1.24E-04	2.57E-03	220.08	Increased
12089	CTSG	1.31	9.30E-05	2.05E-03	210.10	Increased
12090	SPNS3	1.31	1.51E-10	2.29E-08	873.74	Increased
12091	ZEB1-AS1	1.31	1.31E-05	4.29E-04	280.94	Increased
12092	OSBPL7	1.31	4.78E-07	2.62E-05	460.81	Increased
12093	CLIC5	1.32	1.41E-03	NA	98.41	Increased
12094	PTP4A3	1.32	8.65E-18	5.09E-15	1533.19	Increased
12095	MAPK11	1.32	6.45E-04	9.14E-03	144.53	Increased
12096	CHAC1	1.33	1.44E-06	6.69E-05	375.18	Increased
12097	PBXIP1	1.33	2.19E-16	9.54E-14	1330.03	Increased
12098	IDUA	1.34	6.40E-07	3.33E-05	398.98	Increased
12099	EGR1	1.34	1.13E-29	2.27E-26	2988.34	Increased
12100	ING4	1.35	5.41E-08	4.26E-06	471.70	Increased
12101	MICAL1	1.35	9.35E-19	6.24E-16	2132.51	Increased
12102	LPAR6	1.37	4.16E-22	4.63E-19	1814.68	Increased
12103	SCRN2	1.37	1.25E-07	8.54E-06	377.11	Increased
12104	PNRC1	1.37	9.18E-06	3.13E-04	235.71	Increased
12105	ATG16L2	1.38	1.27E-13	3.63E-11	1083.85	Increased
12106	ARSA	1.39	2.65E-08	2.32E-06	346.62	Increased
12107	TM6SF1	1.40	2.52E-04	4.56E-03	108.60	Increased
12108	ANXA2R	1.43	1.74E-12	4.57E-10	539.87	Increased
12109	KLHL24	1.44	6.71E-08	4.94E-06	300.22	Increased
12110	TPGS1	1.45	1.58E-06	7.20E-05	209.38	Increased
12111	ABTB1	1.46	6.63E-07	3.40E-05	195.65	Increased
12112	EVI2A	1.46	2.44E-08	2.21E-06	265.44	Increased
12113	GPR18	1.48	1.29E-04	NA	91.22	Increased
12114	LRRC70	1.49	3.67E-03	NA	32.03	Increased
12115	SCART1	1.53	1.93E-19	1.49E-16	878.92	Increased
12116	SLC7A3	1.54	2.75E-03	NA	34.53	Increased
12117	YPEL1	1.59	1.77E-14	5.89E-12	374.44	Increased
12118	CCNG2	1.66	1.30E-23	1.63E-20	590.43	Increased
12119	ASS1	1.72	6.62E-07	3.40E-05	102.08	Increased
12120	FOS	1.93	1.64E-05	NA	47.86	Increased
12121	NR4A1	2.16	4.89E-12	1.11E-09	104.29	Increased
12122	BCL3	2.82	3.48E-03	NA	7.29	Increased