Supplemental Table 6 : GSEA analysis of genes differentially expressed genes in VillinCre;Imp1fl/fl mice intestinal crypts as compared to controls

NAME	NES	NOM p-val	FDR q-val	FWER p-val
GO_RIBOSOMAL_SUBUNIT	-3.154938	0	0.00E+00	0
GO_RIBOSOME	-3.0670123	0	0.00E+00	0
GO_CYTOSOLIC_RIBOSOME	-2.9051516	0	0.00E+00	0
GO_MITOCHONDRIAL_TRANSLATION	-2.892131	0	0.00E+00	0
GO_TRANSLATIONAL_TERMINATION	-2.888401	0	0.00E+00	0
GO_TRANSLATIONAL_INITIATION	-2.8423738	0	0.00E+00	0
GO_ORGANELLAR_RIBOSOME	-2.784141	0	0.00E+00	0
ZHANG_TLX_TARGETS_60HR_DN	-3.2253294	0	0.00E+00	0
ZHANG_TLX_TARGETS_DN	-3.1786401	0	0.00E+00	0
ZHANG_TLX_TARGETS_36HR_DN	-3.1668155	0	0.00E+00	0
HALLMARK_E2F_TARGETS	-3.1554654	0	0.00E+00	0
GO_LARGE_RIBOSOMAL_SUBUNIT	-2.7557027	0	0.00E+00	0
HALLMARK_MYC_TARGETS_V1	-3.0919576	0	0.00E+00	0
GO_SMALL_RIBOSOMAL_SUBUNIT	-2.7095683	0	0.00E+00	0
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	-3.0447555	0	0.00E+00	0
FEVR_CTNNB1_TARGETS_DN	-2.9432278	0	0.00E+00	0
WONG_EMBRYONIC_STEM_CELL_CORE	-2.9341679	0	0.00E+00	0
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	-2.9078352	0	0.00E+00	0
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	-2.9058435	0	0.00E+00	0
GO_SISTER_CHROMATID_COHESION	-2.6864874	0	0.00E+00	0
PUJANA_CHEK2_PCC_NETWORK	-2.8975575	0	0.00E+00	0
GO_RIBOSOME_BIOGENESIS	-2.6746385	0	0.00E+00	0
REACTOME_TRANSLATION	-2.8910217	0	0.00E+00	0
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	-2.6285388	0	0.00E+00	0
KEGG_RIBOSOME	-2.8790286	0	0.00E+00	0
REACTOME_PEPTIDE_CHAIN_ELONGATION	-2.8541281	0	0.00E+00	0
GO_CONDENSED_CHROMOSOME	-2.5778222	0	0.00E+00	0

REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	-2.8348467	0	0.00E+00	0
KAMMINGA_EZH2_TARGETS	-2.8097804	0	0.00E+00	0
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	-2.7875233	0	0.00E+00	0
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	-2.5516093	0	0.00E+00	0
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	-2.5474973	0	0.00E+00	0
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	-2.743423	0	0.00E+00	0
LEE_EARLY_T_LYMPHOCYTE_UP	-2.736412	0	0.00E+00	0
ISHIDA_E2F_TARGETS	-2.7350755	0	0.00E+00	0
KAUFFMANN_MELANOMA_RELAPSE_UP	-2.7326438	0	0.00E+00	0
PUJANA_XPRSS_INT_NETWORK	-2.7210326	0	0.00E+00	0
PUJANA_BRCA_CENTERED_NETWORK	-2.7155685	0	0.00E+00	0
GO_DNA_RECOMBINATION	-2.544963	0	0.00E+00	0
BENPORATH_PROLIFERATION	-2.7082338	0	0.00E+00	0
CROONQUIST_IL6_DEPRIVATION_DN	-2.7042186	0	0.00E+00	0
WHITEFORD_PEDIATRIC_CANCER_MARKERS	-2.6872954	0	0.00E+00	0
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	-2.5012343	0	0.00E+00	0
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR	-2.6799917	0	0.00E+00	0
GO_RECOMBINATIONAL_REPAIR	-2.4871025	0	0.00E+00	0
WINNEPENNINCKX_MELANOMA_METASTASIS_UP	-2.6388457	0	0.00E+00	0
GO_CONDENSED_CHROMOSOME_CENTROMERIC_REGION	-2.449905	0	0.00E+00	0
MISSIAGLIA_REGULATED_BY_METHYLATION_DN	-2.6203012	0	0.00E+00	0
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR	-2.6132808	0	0.00E+00	0
FARMER_BREAST_CANCER_CLUSTER_2	-2.6011872	0	0.00E+00	0
CROONQUIST_NRAS_SIGNALING_DN	-2.5994081	0	0.00E+00	0
REACTOME_INFLUENZA_LIFE_CYCLE	-2.5720546	0	0.00E+00	0

ZHANG_BREAST_CANCER_PROGENITORS_UP	-2.5698965	0	0.00E+00	0
PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP	-2.5567155	0	0.00E+00	0
HALLMARK_G2M_CHECKPOINT	-2.5393524	0	0.00E+00	0
BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES	-2.5199327	0	0.00E+00	0
ZHAN_MULTIPLE_MYELOMA_PR_UP	-2.5195396	0	0.00E+00	0
HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP	-2.4886186	0	0.00E+00	0
KANG_DOXORUBICIN_RESISTANCE_UP	-2.4658346	0	0.00E+00	0
CHANG_CYCLING_GENES	-2.455247	0	0.00E+00	0
MORI_LARGE_PRE_BII_LYMPHOCYTE_UP	-2.4369445	0	1.48E-05	0.001
GO_RECIPROCAL_DNA_RECOMBINATION	-2.4213686	0	2.81E-05	0.002
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	-2.423429	0	2.85E-05	0.002
GO_MITOCHONDRIAL_RNA_METABOLIC_PROCESS	-2.4249806	0	2.88E-05	0.002
GO_RRNA_METABOLIC_PROCESS	-2.426538	0	2.92E-05	0.002
MORI_IMMATURE_B_LYMPHOCYTE_DN	-2.4026685	0	7.07E-05	0.005
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP	-2.4044044	0	7.15E-05	0.005
LI_WILMS_TUMOR_ANAPLASTIC_UP	-2.3812122	0	1.07E-04	0.008
GO_TRANSLATIONAL_ELONGATION	-2.3865504	0	1.09E-04	0.008
GO_NCRNA_PROCESSING	-2.386837	0	1.10E-04	0.008
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	-2.388242	0	1.11E-04	0.008
GREENBAUM_E2A_TARGETS_UP	-2.3894558	0	1.12E-04	0.008
GO_CENTROMERE_COMPLEX_ASSEMBLY	-2.3770785	0	1.18E-04	0.009
GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN	-2.378077	0	1.20E-04	0.009
GARY_CD5_TARGETS_DN	-2.3567214	0	1.40E-04	0.011
GO_RECIPROCAL_MEIOTIC_RECOMBINATION	-2.3567653	0	1.41E-04	0.011
REACTOME_MITOTIC_PROMETAPHASE	-2.359001	0	1.43E-04	0.011

REACTOME_DNA_REPLICATION	-2.3521676	0	1.73E-04	0.014
REACTOME_MEIOTIC_RECOMBINATION	-2.3529928	0	1.75E-04	0.014
SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM	-2.346571	0	1.80E-04	0.015
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	-2.3472748	0	1.82E-04	0.015
GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	-2.3491597	0	1.84E-04	0.015
EGUCHI_CELL_CYCLE_RB1_TARGETS	-2.3393679	0	2.00E-04	0.017
ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN	-2.3411274	0	2.02E-04	0.017
REN_BOUND_BY_E2F	-2.3274734	0	2.18E-04	0.019
CAIRO_HEPATOBLASTOMA_CLASSES_UP	-2.328137	0	2.20E-04	0.019
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP	-2.3287632	0	2.22E-04	0.019
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	-2.322896	0	2.27E-04	0.02
FERREIRA_EWINGS_SARCOMA_UNSTABLE_VS_STABLE_UP	-2.3099387	0	2.34E-04	0.021
GO_NUCLEAR_CHROMOSOME_SEGREGATION	-2.313504	0	2.36E-04	0.021
GO_DNA_REPLICATION_INDEPENDENT_NUCLEOSOME_ASSEMBLY	-2.2997105	0	2.65E-04	0.024
GO_KINETOCHORE	-2.2935853	0	2.82E-04	0.026
RHODES_CANCER_META_SIGNATURE	-2.293903	0	2.85E-04	0.026
GO_MULTI_ORGANISM_METABOLIC_PROCESS	-2.2902653	0	2.90E-04	0.027
BIDUS_METASTASIS_UP	-2.2818964	0	3.19E-04	0.03
GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	-2.2762191	0	3.35E-04	0.032
REACTOME_MITOTIC_M_M_G1_PHASES	-2.2772303	0	3.38E-04	0.032
BURTON_ADIPOGENESIS_3	-2.2715037	0	3.53E-04	0.034
SONG_TARGETS_OF_IE86_CMV_PROTEIN	-2.270831	0	3.91E-04	0.038

REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	-2.2696426	0	3.98E-04	0.039
KAUFFMANN_DNA_REPAIR_GENES	-2.2675486	0	4.15E-04	0.041
KOBAYASHI_EGFR_SIGNALING_24HR_DN	-2.2656665	0	4.31E-04	0.043
GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT	-2.264162	0	4.37E-04	0.044
GO_RIBOSOME_ASSEMBLY	-2.2608027	0	4.53E-04	0.046
WU_APOPTOSIS_BY_CDKN1A_VIA_TP53	-2.2542005	0	4.88E-04	0.05
GO_CHROMOSOME_SEGREGATION	-2.2461815	0	5.14E-04	0.053
GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	-2.244062	0	5.19E-04	0.054
KONG_E2F3_TARGETS	-2.2380137	0	5.62E-04	0.059
REACTOME_MRNA_SPLICING	-2.2362843	0	5.67E-04	0.06
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	-2.2312508	0	5.76E-04	0.062
CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP	-2.232094	0	5.81E-04	0.062
MANALO_HYPOXIA_DN	-2.2257705	0	6.28E-04	0.068
LY_AGING_OLD_DN	-2.2255225	0	6.32E-04	0.069
GO_DNA_REPLICATION_INDEPENDENT_NUCLEOSOME_ORGANIZATION	-2.2237232	0	6.37E-04	0.07
CHEN_ETV5_TARGETS_TESTIS	-2.2208817	0	6.59E-04	0.073
GO_MITOCHONDRIAL_MATRIX	-2.2191396	0	6.63E-04	0.074
GO_SISTER_CHROMATID_SEGREGATION	-2.2158525	0	7.03E-04	0.079
GO_MITOTIC_RECOMBINATION	-2.2089179	0	7.65E-04	0.088
GO_CHROMOSOME_CENTROMERIC_REGION	-2.2111146	0	7.68E-04	0.087
DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP	-2.2096872	0	7.71E-04	0.088
GO_MITOCHONDRIAL_PROTEIN_COMPLEX	-2.204627	0	8.36E-04	0.096
GO_TRNA_METABOLIC_PROCESS	-2.1990793	0	8.57E-04	0.099
RHODES_UNDIFFERENTIATED_CANCER	-2.1948526	0	8.94E-04	0.104
GO_NCRNA_METABOLIC_PROCESS	-2.191913	0	9.21E-04	0.107
ABRAMSON_INTERACT_WITH_AIRE	-2.1877239	0	9.31E-04	0.109

KEGG_DNA_REPLICATION	-2.1857688	0	9.35E-04	0.111
MARSON_BOUND_BY_E2F4_UNSTIMULATED	-2.1857908	0	9.42E-04	0.111
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	-2.180974	0	9.73E-04	0.118
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	-2.1819098	0	9.80E-04	0.118
DANG_MYC_TARGETS_UP	-2.1824553	0	9.86E-04	0.118
AMUNDSON_GAMMA_RADIATION_RESPONSE	-2.1775804	0	1.03E-03	0.125
FINETTI_BREAST_CANCER_KINOME_RED	-2.1744251	0	1.04E-03	0.129
PUJANA_BRCA2_PCC_NETWORK	-2.17473	0	1.05E-03	0.129
MILI_PSEUDOPODIA_HAPTOTAXIS_UP	-2.1755166	0	1.06E-03	0.129
FUJII_YBX1_TARGETS_DN	-2.1702824	0	1.12E-03	0.138
GO_GLYOXYLATE_METABOLIC_PROCESS	-2.1656415	0	1.18E-03	0.144
HORIUCHI_WTAP_TARGETS_DN	-2.1618683	0	1.19E-03	0.149
REACTOME_METABOLISM_OF_RNA	-2.161958	0	1.19E-03	0.149
RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN	-2.1631062	0	1.19E-03	0.148
REACTOME_CELL_CYCLE_MITOTIC	-2.1636264	0	1.20E-03	0.148
COLLER_MYC_TARGETS_UP	-2.1566684	0	1.22E-03	0.154
SMID_BREAST_CANCER_LUMINAL_A_DN	-2.1583538	0	1.22E-03	0.153
GO_STRAND_DISPLACEMENT	-2.1520903	0	1.26E-03	0.159
MARKEY_RB1_ACUTE_LOF_UP	-2.1405838	0	1.45E-03	0.18
KEGG_HOMOLOGOUS_RECOMBINATION	-2.139822	0	1.46E-03	0.183
GO_DNA_DEPENDENT_DNA_REPLICATION	-2.1400557	0	1.47E-03	0.183
ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN	-2.1358795	0	1.57E-03	0.197
GO_DNA_REPLICATION	-2.1321795	0	1.65E-03	0.207
REACTOME_MRNA_PROCESSING	-2.1322634	0	1.66E-03	0.207
REACTOME_G2_M_CHECKPOINTS	-2.1294022	0	1.66E-03	0.209
GO_SINGLE_STRANDED_DNA_BINDING	-2.1298435	0	1.67E-03	0.209
GO_PRERIBOSOME	-2.125224	0	1.70E-03	0.215
REICHERT_MITOSIS_LIN9_TARGETS	-2.121514	0	1.78E-03	0.226

GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_ASSEMBLY	-2.1171653	0	1.88E-03	0.238
GO_NUCLEOCYTOPLASMIC_TRANSPORTER_ACTIVITY	-2.1165326	0	1.89E-03	0.24
WAKASUGI_HAVE_ZNF143_BINDING_SITES	-2.112256	0	1.99E-03	0.254
GO_SPLICEOSOMAL_COMPLEX_ASSEMBLY	-2.1092677	0	2.01E-03	0.259
LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN	-2.1098447	0	2.02E-03	0.259
REACTOME_METABOLISM_OF_NON_CODING_RNA	-2.1030977	0	2.08E-03	0.271
GO_MATURATION_OF_SSU_RRNA	-2.1022663	0	2.09E-03	0.274
GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_NADH_TO_UBIQUINONE	-2.1048694	0	2.10E-03	0.27
GO_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	-2.1001253	0	2.13E-03	0.279
GO_RNA_PROCESSING	-2.0992224	0	2.14E-03	0.281
GO_DNA_STRAND_ELONGATION	-2.097738	0	2.16E-03	0.285
GO_MEIOSIS_I	-2.0946403	0	2.30E-03	0.301
MUELLER_PLURINET	-2.0934398	0	2.33E-03	0.307
GO_NUCLEOID	-2.0918074	0	2.34E-03	0.313
MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_DN	-2.0920846	0	2.35E-03	0.313
GO_INTRACILIARY_TRANSPORT_PARTICLE	-2.088878	0	2.41E-03	0.322
GO_AMINO_ACID_ACTIVATION	-2.082886	0	2.57E-03	0.341
REACTOME_TELOMERE_MAINTENANCE	-2.0737834	0	2.80E-03	0.362
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	-2.073336	0	2.81E-03	0.363
FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN	-2.0703921	0	2.84E-03	0.372
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	-2.0705433	0	2.85E-03	0.372
GO_TRNA_AMINOACYLATION	-2.0693483	0	2.86E-03	0.377
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-2.070544	0	2.86E-03	0.372
GO_ENDODEOXYRIBONUCLEASE_ACTIVITY	-2.0709417	0	2.87E-03	0.371
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	-2.0630367	0	3.13E-03	0.407
GO_CHROMOSOMAL_REGION	-2.062064	0	3.15E-03	0.41

GO_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY	-2.061382	0	3.15E-03	0.412
GO_DNA_DEPENDENT_ATPASE_ACTIVITY	-2.0565486	0	3.34E-03	0.43
GO_NON_RECOMBINATIONAL_REPAIR	-2.052252	0	3.50E-03	0.444
ODONNELL_TFRC_TARGETS_DN	-2.0457988	0	3.75E-03	0.466
GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	-2.0430572	0	3.76E-03	0.474
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	-2.0437298	0	3.76E-03	0.471
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	-2.0441823	0	3.78E-03	0.471
GO_MEIOTIC_CHROMOSOME_SEGREGATION	-2.0399902	0	3.83E-03	0.486
GO_SOMATIC_CELL_DNA_RECOMBINATION	-2.0400481	0	3.85E-03	0.486
REACTOME_CELL_CYCLE	-2.0364423	0	3.99E-03	0.501
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	-2.033705	0	4.09E-03	0.51
GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX	-2.0327728	0	4.10E-03	0.515
GO_RIBONUCLEASE_ACTIVITY	-2.0330467	0	4.10E-03	0.514
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	-2.0320709	0	4.10E-03	0.519
GO_SPLICEOSOMAL_TRI_SNRNP_COMPLEX	-2.0304146	0	4.15E-03	0.523
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM	-2.0293868	0	4.16E-03	0.525
GO_RESPIRATORY_CHAIN	-2.0282016	0	4.21E-03	0.53
SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN	-2.0229633	0	4.39E-03	0.547
LE_EGR2_TARGETS_UP	-2.0230393	0	4.41E-03	0.547
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	-2.0230582	0	4.43E-03	0.547
GO_RNA_CATABOLIC_PROCESS	-2.0204039	0	4.49E-03	0.561
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	-2.0199234	0	4.50E-03	0.563
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION_	-2.0149858	0	4.68E-03	0.584
MOOTHA_VOXPHOS	-2.0143092	0	4.68E-03	0.584
REACTOME_CHROMOSOME_MAINTENANCE	-2.0103214	0	4.90E-03	0.601

GO_NADH_DEHYDROGENASE_ACTIVITY	-2.003054	0	5.31E-03	0.635
GO_CONDENSED_NUCLEAR_CHROMOSOME	-2.0003564	0	5.44E-03	0.648
REACTOME_TRNA_AMINOACYLATION	-1.9974858	0	5.44E-03	0.658
GO_OXIDATIVE_PHOSPHORYLATION	-1.9978825	0	5.46E-03	0.657
GO_CHROMOSOME_CONDENSATION	-1.9980999	0	5.48E-03	0.657
ZHAN_MULTIPLE_MYELOMA_SUBGROUPS	-1.9984179	0	5.50E-03	0.657
REACTOME_EXTENSION_OF_TELOMERES	-1.9954416	0	5.51E-03	0.663
REACTOME_METABOLISM_OF_MRNA	-1.9958578	0	5.53E-03	0.663
CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN	-1.9887396	0	5.80E-03	0.682
GO_REPLICATION_FORK	-1.9847032	0	5.94E-03	0.69
LEE_BMP2_TARGETS_DN	-1.9842999	0	5.94E-03	0.691
GO_CYTOPLASMIC_TRANSLATION	-1.9848615	0	5.95E-03	0.689
GO_PRECATALYTIC_SPLICEOSOME	-1.983428	0	5.97E-03	0.694
GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	-1.9782245	0	6.16E-03	0.718
GO_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	-1.978804	0	6.17E-03	0.716
GO_TELOMERE_MAINTENANCE_VIA_RECOMBINATION	-1.9791749	0	6.17E-03	0.713
TARTE_PLASMA_CELL_VS_PLASMABLAST_DN	-1.97652	0	6.24E-03	0.725
MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_DN	-1.9750235	0	6.26E-03	0.727
GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS	-1.9752959	0	6.26E-03	0.727
GO_DNA_GEOMETRIC_CHANGE	-1.9721626	0	6.37E-03	0.739
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS	-1.9673762	0	6.65E-03	0.755
GO_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	-1.9665323	0	6.69E-03	0.759
VANTVEER_BREAST_CANCER_METASTASIS_DN	-1.9655198	0	6.73E-03	0.761
GO_CHROMOSOME_ORGANIZATION_INVOLVED_IN_MEIOTIC_CELL_CYCLE	-1.9647412	0	6.77E-03	0.765

SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_DN	-1.9579866	0	7.15E-03	0.782
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	-1.9498342	0	7.63E-03	0.803
TANG_SENESCENCE_TP53_TARGETS_DN	-1.9463059	0	7.81E-03	0.818
REACTOME_DNA_REPAIR	-1.945084	0	7.82E-03	0.819
GO_DNA_CONFORMATION_CHANGE	-1.9454901	0	7.82E-03	0.818
GO_MRNA_METABOLIC_PROCESS	-1.9401791	0	8.18E-03	0.831
WONG_MITOCHONDRIA_GENE_MODULE	-1.9375548	0	8.30E-03	0.841
IRITANI_MAD1_TARGETS_DN	-1.9363651	0	8.36E-03	0.843
MITSIADES_RESPONSE_TO_APLIDIN_DN	-1.9328203	0	8.56E-03	0.855
VERNELL_RETINOBLASTOMA_PATHWAY_UP	-1.9309503	0	8.70E-03	0.864
KEGG_SPLICEOSOME	-1.9230103	0	9.40E-03	0.885
GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS	-1.9221232	0	9.43E-03	0.886
REACTOME_CELL_CYCLE_CHECKPOINTS	-1.9214103	0	9.47E-03	0.891
GO_NUCLEASE_ACTIVITY	-1.9205034	0	9.53E-03	0.893
YU_MYC_TARGETS_UP	-1.9192064	0	9.59E-03	0.896
JOHNSTONE_PARVB_TARGETS_3_DN	-1.9179076	0	9.64E-03	0.9
GO_TRNA_PROCESSING	-1.9169971	0	9.70E-03	0.903
WHITFIELD_CELL_CYCLE_LITERATURE	-1.9157039	0	9.78E-03	0.905
GO_RNA_SPLICING	-1.9147022	0	9.84E-03	0.908
PID_AURORA_B_PATHWAY	-1.9081205	0	1.03E-02	0.919
LEE_METASTASIS_AND_RNA_PROCESSING_UP	-1.9030626	0	1.06E-02	0.925
GO_RAN_GTPASE_BINDING	-1.8992962	0	1.09E-02	0.932
MARIADASON_RESPONSE_TO_BUTYRATE_SULINDAC_4	-1.8970667	0	1.10E-02	0.937
KAUFFMANN_DNA_REPLICATION_GENES	-1.8975507	0	1.10E-02	0.936
GO_MEIOTIC_CELL_CYCLE	-1.8978089	0	1.10E-02	0.936
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	-1.8978766	0	1.10E-02	0.936
GO_MEIOTIC_CELL_CYCLE_PROCESS	-1.8931545	0	1.13E-02	0.943
GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME	-1.8909372	0	1.15E-02	0.945

GO_CATALYTIC_STEP_2_SPLICEOSOME	-1.889588	0	1.15E-02	0.945
GO_DOUBLE_STRAND_BREAK_REPAIR	-1.8871117	0	1.16E-02	0.948
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	-1.8875479	0	1.16E-02	0.948
GO_DNA_PACKAGING	-1.8861384	0	1.17E-02	0.949
GO_SOMATIC_RECOMBINATION_OF_IMMUNOGLOBULIN_GENE_SEGMENTS	-1.8845189	0	1.18E-02	0.952
GO_TRANSLATION_INITIATION_FACTOR_ACTIVITY	-1.883813	0	1.19E-02	0.952
IKEDA_MIR30_TARGETS_DN	-1.8779494	0	1.24E-02	0.952
GO_RIBONUCLEOPROTEIN_COMPLEX	-1.8781248	0	1.24E-02	0.952
REACTOME_MEIOSIS	-1.8713695	0	1.30E-02	0.96
GO_SNRNA_BINDING	-1.8713715	0	1.30E-02	0.96
GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP	-1.8720988	0	1.30E-02	0.96
KEGG_NUCLEOTIDE_EXCISION_REPAIR	-1.8684937	0	1.33E-02	0.964
MODY_HIPPOCAMPUS_PRENATAL	-1.8680393	0	1.33E-02	0.965
GO_DNA_PACKAGING_COMPLEX	-1.8581667	0	1.41E-02	0.974
GO_NADH_DEHYDROGENASE_COMPLEX	-1.8583031	0	1.42E-02	0.974
NELSON_RESPONSE_TO_ANDROGEN_DN	-1.8554463	0	1.45E-02	0.977
BOYAULT_LIVER_CANCER_SUBCLASS_G3_UP	-1.852529	0	1.48E-02	0.979
GO_PROTEIN_COMPLEX_LOCALIZATION	-1.8433392	0	1.58E-02	0.981
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	-1.8405235	0	1.61E-02	0.982
GO_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.8369672	0	1.65E-02	0.983
GO_SMALL_NUCLEAR_RIBONUCLEOPROTEIN_COMPLEX	-1.8371911	0	1.65E-02	0.983
GO_RIBONUCLEOPROTEIN_COMPLEX_LOCALIZATION	-1.8330393	0	1.69E-02	0.983
SCHUHMACHER_MYC_TARGETS_UP	-1.830725	0	1.71E-02	0.984
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC	-1.8283001	0	1.74E-02	0.985
GO_CENTROSOME_CYCLE	-1.8277206	0	1.74E-02	0.985

GO_TRNA_BINDING	-1.8236291	0	1.79E-02	0.986
REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT	-1.8239187	0	1.79E-02	0.986
GO_NEGATIVE_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION	-1.8214928	0	1.82E-02	0.989
GRADE_COLON_AND_RECTAL_CANCER_UP	-1.8079123	0	1.99E-02	0.994
REACTOME_RNA_POL_II_TRANSCRIPTION	-1.8084198	0	2.00E-02	0.994
RUIZ_TNC_TARGETS_DN	-1.8031473	0	2.07E-02	0.997
GO_RRNA_BINDING	-1.802315	0	2.08E-02	0.997
TIEN_INTESTINE_PROBIOTICS_24HR_UP	-1.7997254	0	2.12E-02	0.997
MENSSEN_MYC_TARGETS	-1.7994329	0	2.12E-02	0.997
SANSOM_APC_TARGETS_UP	-1.7966429	0	2.15E-02	0.997
GO_INTRACILIARY_TRANSPORT	-1.7945349	0	2.16E-02	0.997
GO_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	-1.7921681	0	2.19E-02	0.997
GO_MITOCHONDRIAL_MEMBRANE_PART	-1.7890564	0	2.25E-02	0.999
GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS	-1.7808735	0	2.37E-02	1
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	-1.7796048	0	2.39E-02	1
TOYOTA_TARGETS_OF_MIR34B_AND_MIR34C	-1.778119	0	2.40E-02	1
HALLMARK_MYC_TARGETS_V2	-1.7781357	0	2.41E-02	1
LINDGREN_BLADDER_CANCER_CLUSTER_3_UP	-1.7784126	0	2.41E-02	1
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP	-1.7751089	0	2.45E-02	1
MALONEY_RESPONSE_TO_17AAG_DN	-1.7696918	0	2.53E-02	1
GO_CHROMOSOME_TELOMERIC_REGION	-1.7691748	0	2.54E-02	1
MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN	-1.7618749	0	2.66E-02	1
REACTOME_S_PHASE	-1.7587535	0	2.71E-02	1
GO_PROTEIN_PEPTIDYL_PROLYL_ISOMERIZATION	-1.7579278	0	2.72E-02	1
GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	-1.7545375	0	2.77E-02	1
SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP	-1.7545646	0	2.78E-02	1
PAL_PRMT5_TARGETS_UP	-1.7502209	0	2.85E-02	1

BLUM_RESPONSE_TO_SALIRASIB_DN	-1.7498065	0	2.85E-02	1
PYEON_HPV_POSITIVE_TUMORS_UP	-1.7494633	0	2.85E-02	1
VECCHI_GASTRIC_CANCER_EARLY_UP	-1.7459084	0	2.88E-02	1
REACTOME_SYNTHESIS_OF_DNA	-1.7452798	0	2.88E-02	1
GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN	-1.7433413	0	2.91E-02	1
NAKAMURA_CANCER_MICROENVIRONMENT_DN	-1.7429074	0	2.91E-02	1
GO_MITOTIC_SISTER_CHROMATID_SEGREGATION	-1.7343864	0	3.06E-02	1
ZHANG_RESPONSE_TO_CANTHARIDIN_DN	-1.7344747	0	3.06E-02	1
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	-1.7330563	0	3.06E-02	1
REACTOME_HIV_LIFE_CYCLE	-1.7324461	0	3.07E-02	1
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1	-1.729688	0	3.11E-02	1
GO_ATP_DEPENDENT_CHROMATIN_REMODELING	-1.7302943	0	3.11E-02	1
GO_SPLICEOSOMAL_COMPLEX	-1.7262076	0	3.18E-02	1
WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN	-1.7222751	0	3.26E-02	1
GO_DNA_POLYMERASE_ACTIVITY	-1.7202244	0	3.28E-02	1
GO_CELL_RECOGNITION	-1.7165861	0	3.35E-02	1
BURTON_ADIPOGENESIS_PEAK_AT_16HR	-1.7167016	0	3.36E-02	1
FOURNIER_ACINAR_DEVELOPMENT_LATE_2	-1.7141271	0	3.40E-02	1
GO_CYTOSOLIC_PART	-1.7131348	0	3.41E-02	1
GO_CELL_REDOX_HOMEOSTASIS	-1.7120179	0	3.42E-02	1
GO_MRNA_PROCESSING	-1.6991675	0	3.70E-02	1
REACTOME_TRANSCRIPTION	-1.6960592	0	3.77E-02	1
GO_OXIDOREDUCTASE_COMPLEX	-1.6962394	0	3.77E-02	1
GO_PHOTORECEPTOR_CONNECTING_CILIUM	-1.6899316	0	3.94E-02	1
MILI_PSEUDOPODIA_CHEMOTAXIS_UP	-1.6873559	0	3.98E-02	1
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP	-1.6831113	0	4.09E-02	1

SANSOM_APC_TARGETS	-1.6809139	0	4.14E-02	1
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	-1.6788803	0	4.19E-02	1
GO_QUINONE_METABOLIC_PROCESS	-1.6743364	0	4.31E-02	1
PENG_LEUCINE_DEPRIVATION_DN	-1.6705128	0	4.39E-02	1
GO_DNA_METABOLIC_PROCESS	-1.6547999	0	4.83E-02	1
HAMAI_APOPTOSIS_VIA_TRAIL_UP	-1.653433	0	4.85E-02	1
GO_NUCLEOTIDE_EXCISION_REPAIR	-1.6480132	0	5.00E-02	1
GO_DNA_REPAIR	-1.6365308	0	5.39E-02	1
BENPORATH_CYCLING_GENES	-1.6328033	0	5.48E-02	1
CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_UP	-1.6331615	0	5.49E-02	1
GAVIN_FOXP3_TARGETS_CLUSTER_P6	-1.631059	0	5.53E-02	1
LEE_LIVER_CANCER_SURVIVAL_DN	-1.6294492	0	5.58E-02	1
GO_CHROMOSOME	-1.6247091	0	5.73E-02	1
BORCZUK_MALIGNANT_MESOTHELIOMA_UP	-1.6224124	0	5.80E-02	1
GO_PROTEIN_DNA_COMPLEX	-1.6168284	0	5.99E-02	1
GO_HUMORAL_IMMUNE_RESPONSE	-1.6171271	0	5.99E-02	1
IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR	-1.6159132	0	6.00E-02	1
CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN	-1.6116334	0	6.16E-02	1
GO_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	-1.6103646	0	6.18E-02	1
GO_NUCLEAR_CHROMOSOME_TELOMERIC_REGION	-1.6072797	0	6.28E-02	1
MORI_MATURE_B_LYMPHOCYTE_DN	-1.6074524	0	6.28E-02	1
GO_AMIDE_BIOSYNTHETIC_PROCESS	-1.6031382	0	6.38E-02	1
WEI_MYCN_TARGETS_WITH_E_BOX	-1.5997937	0	6.46E-02	1
KEGG_OXIDATIVE_PHOSPHORYLATION	-1.5969752	0	6.55E-02	1
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER_THAN_METHYL_GROUPS	-1.5955685	0	6.57E-02	1

GO_ELECTRON_TRANSPORT_CHAIN	-1.5941863	0	6.59E-02	1
AFFAR_YY1_TARGETS_DN	-1.5910951	0	6.70E-02	1
CHICAS_RB1_TARGETS_GROWING	-1.5885978	0	6.79E-02	1
PENG_GLUTAMINE_DEPRIVATION_DN	-1.5841917	0	6.98E-02	1
GARCIA_TARGETS_OF_FLI1_AND_DAX1_DN	-1.5833141	0	7.01E-02	1
GO_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	-1.5797354	0	7.15E-02	1
GO_NUCLEAR_EXPORT	-1.5755546	0	7.30E-02	1
SHEPARD_CRUSH_AND_BURN_MUTANT_DN	-1.5657848	0	7.63E-02	1
GO_ORGANELLE_FISSION	-1.5538926	0	8.11E-02	1
GO_MACROMOLECULAR_COMPLEX_DISASSEMBLY	-1.5522444	0	8.15E-02	1
VEGF_A_UP.V1_DN	-1.552468	0	8.15E-02	1
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14	-1.5492555	0	8.26E-02	1
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP	-1.5492647	0	8.27E-02	1
GO_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	-1.5472966	0	8.29E-02	1
BENPORATH_ES_1	-1.5241921	0	9.36E-02	1
GO_CENTRIOLE	-1.508479	0	1.01E-01	1
KARLSSON_TGFB1_TARGETS_UP	-1.5035982	0	1.04E-01	1
GCNP_SHH_UP_LATE.V1_UP	-1.5017421	0	1.04E-01	1
GO_MITOTIC_NUCLEAR_DIVISION	-1.5013794	0	1.05E-01	1
GO_HELICASE_ACTIVITY	-1.470066	0	1.22E-01	1
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP	-1.4651562	0	1.24E-01	1
WHITFIELD_CELL_CYCLE_S	-1.4636275	0	1.25E-01	1
HALLMARK_OXIDATIVE_PHOSPHORYLATION	-1.4600822	0	1.27E-01	1
GO_CHROMOSOME_ORGANIZATION	-1.4547433	0	1.30E-01	1
BOYLAN_MULTIPLE_MYELOMA_C_D_UP	-1.4489841	0	1.33E-01	1
RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP	-1.4415766	0	1.38E-01	1
BERENJENO_TRANSFORMED_BY_RHOA_UP	-1.4373509	0	1.40E-01	1
CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN	-1.4379563	0	1.40E-01	1

OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_UP	-1.4305875	0	1.44E-01	1
MOOTHA_HUMAN_MITODB_6_2002	-1.4160346	0	1.55E-01	1
GO_CELLULAR_RESPIRATION	-1.4125538	0	1.58E-01	1
GO_CELLULAR_MACROMOLECULAR_COMPLEX_ASSEMBLY	-1.4103186	0	1.59E-01	1
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	-1.4079702	0	1.61E-01	1
NFE2L2.V2	-1.4070404	0	1.61E-01	1
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP	-1.4029816	0	1.64E-01	1
GO_PEPTIDE_METABOLIC_PROCESS	-1.3991277	0	1.67E-01	1
GO_ISOMERASE_ACTIVITY	-1.3931388	0	1.70E-01	1
CSR_LATE_UP.V1_UP	-1.3820891	0	1.77E-01	1
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	-1.3717731	0	1.84E-01	1
RAMALHO_STEMNESS_UP	-1.3707092	0	1.85E-01	1
GO_NUCLEAR_CHROMOSOME	-1.3687268	0	1.86E-01	1
GO_PRIMARY_CILIUM	-1.3444443	0	2.05E-01	1
GO_PROTEIN_FOLDING	-1.340986	0	2.08E-01	1
MOOTHA_MITOCHONDRIA	-1.3292915	0	2.18E-01	1
BASAKI_YBX1_TARGETS_UP	-1.3187628	0	2.28E-01	1
GO_MITOTIC_CELL_CYCLE	-1.2978681	0	2.47E-01	1
GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	-1.2865189	0	2.58E-01	1
GO_MITOCHONDRIAL_PART	-1.2850395	0	2.58E-01	1
WHITFIELD_CELL_CYCLE_G2_M	-1.2804883	0	2.63E-01	1
REACTOME_METABOLISM_OF_PROTEINS	-1.2745355	0	2.69E-01	1
STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN	-1.2636421	0	2.82E-01	1
MARTENS_TRETINOIN_RESPONSE_DN	-1.2592951	0	2.86E-01	1
SHEN_SMARCA2_TARGETS_UP	-1.248782	0	2.99E-01	1
WEST_ADRENOCORTICAL_TUMOR_UP	-1.2456837	0	3.01E-01	1
GO_NUCLEOLUS	-1.2408242	0	3.07E-01	1
GO_ORGANELLE_INNER_MEMBRANE	-1.2395691	0	3.08E-01	1
GO_CILIUM	-1.2269989	0	3.23E-01	1
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN	-1.1853538	0	3.77E-01	1

GO_PROTEIN_LOCALIZATION_TO_ORGANELLE	-1.1836272	0	3.79E-01	1
SMID_BREAST_CANCER_BASAL_UP	-1.1698909	0	3.98E-01	1
GEORGES_TARGETS_OF_MIR192_AND_MIR215	-1.1522197	0	4.26E-01	1
KIM_WT1_TARGETS_DN	-1.1240956	0	4.72E-01	1
IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR	-1.1205506	0	4.77E-01	1
GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN	-1.0994998	0	5.06E-01	1
GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY_TRANSPOSING_S_S_BONDS	-1.8673164	0.00310559	1.33E-02	0.966
REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	-1.8965714	0.00323625	1.10E-02	0.938
GO_CHROMOSOME_SEPARATION	-1.8188921	0.00324675	1.85E-02	0.991
GO_PHAGOCYTOSIS_RECOGNITION	-1.9632922	0.00341297	6.83E-03	0.766
GO_DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATION	-1.9058698	0.00341297	1.05E-02	0.922
GO_PYRIMIDINE_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	-1.9016821	0.00341297	1.07E-02	0.929
REACTOME_MRNA_3_END_PROCESSING	-1.8886789	0.00344828	1.16E-02	0.946
GO_SPINDLE_CHECKPOINT	-1.7301264	0.00344828	3.11E-02	1
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	-1.7414984	0.00346021	2.93E-02	1
GO_SOMATIC_DIVERSIFICATION_OF_IMMUNOGLOBULINS	-1.794429	0.00347222	2.16E-02	0.997
KEGG_MISMATCH_REPAIR	-1.9749538	0.0034965	6.23E-03	0.727
GO_ENDORIBONUCLEASE_ACTIVITY_PRODUCING_5_PHOSPHOMONOESTERS	-1.8401909	0.0034965	1.61E-02	0.982
GO_SPINAL_CORD_MOTOR_NEURON_DIFFERENTIATION	-1.9039191	0.00352113	1.06E-02	0.924
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	-1.9484867	0.00358423	7.65E-03	0.807
GO_U12_TYPE_SPLICEOSOMAL_COMPLEX	-1.893825	0.00358423	1.12E-02	0.943
REACTOME_DNA_STRAND_ELONGATION	-2.0294516	0.00361011	4.18E-03	0.525
GO_DNA_BINDING_BENDING	-1.7332556	0.00362319	3.07E-02	1
GO_PROTEIN_TRANSPORT_ALONG_MICROTUBULE	-1.8362902	0.00363636	1.65E-02	0.983
GO_U2_TYPE_SPLICEOSOMAL_COMPLEX	-1.6672591	0.00363636	4.48E-02	1

GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_EXONUCLEOLYTIC	-1.6534845	0.00367647	4.86E-02	1
GO_RNA_SECONDARY_STRUCTURE_UNWINDING	-1.8716078	0.00369004	1.31E-02	0.96
JIANG_HYPOXIA_VIA_VHL	-1.795508	0.0037594	2.16E-02	0.997
LY_AGING_MIDDLE_DN	-2.0933025	0.00381679	2.32E-03	0.307
GO_SMALL_SUBUNIT_PROCESSOME	-1.8080784	0.00381679	2.00E-02	0.994
LI_WILMS_TUMOR_VS_FETAL_KIDNEY_2_UP	-1.5699098	0.00384615	7.47E-02	1
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	-1.7474756	0.00395257	2.88E-02	1
VANTVEER_BREAST_CANCER_BRCA1_UP	-1.9495742	0.00396825	7.62E-03	0.803
GO_HOMOLOGOUS_CHROMOSOME_SEGREGATION	-1.796975	0.00406504	2.15E-02	0.997
BURTON_ADIPOGENESIS_PEAK_AT_24HR	-1.7079865	0.00406504	3.50E-02	1
GO_CIS_TRANS_ISOMERASE_ACTIVITY	-1.8232617	0.00408163	1.79E-02	0.987
GO_TRNA_TRANSPORT	-1.6331159	0.00408163	5.48E-02	1
KEGG_BASE_EXCISION_REPAIR	-1.8309333	0.00411523	1.71E-02	0.984
GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	-1.9090523	0.00413223	1.03E-02	0.918
REACTOME_GLOBAL_GENOMIC_NER_GG_NER	-1.5264044	0.0041841	9.25E-02	1
IWANAGA_E2F1_TARGETS_INDUCED_BY_SERUM	-1.8672645	0.00420168	1.33E-02	0.966
GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_GERMLINE_RECOMBINATION_WITHIN_A_SINGLE_LOCUS	-2.104186	0.00438597	2.08E-03	0.27
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	-1.571537	0.00438597	7.43E-02	1
GO_BASE_EXCISION_REPAIR	-1.7657889	0.00442478	2.58E-02	1
GO_TRNA_MODIFICATION	-1.7484667	0.00442478	2.86E-02	1
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	-1.7014955	0.00444445	3.65E-02	1
KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN	-1.6359586	0.00454545	5.40E-02	1
GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	-1.7463595	0.00456621	2.88E-02	1
GO_PROTEIN_TARGETING_TO_MITOCHONDRION	-1.6702343	0.0046083	4.39E-02	1

SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP	-1.8622515	0.00492611	1.38E-02	0.972
GO_DEOXYRIBONUCLEASE_ACTIVITY	-1.722122	0.005	3.26E-02	1
PID_FANCONI_PATHWAY	-1.9185114	0.00507614	9.64E-03	0.898
KEGG_RNA_DEGRADATION	-1.7248378	0.00510204	3.20E-02	1
GO_DNA_HELICASE_ACTIVITY	-1.721625	0.00518135	3.26E-02	1
GO_NUCLEOLAR_PART	-1.6041789	0.0052356	6.37E-02	1
GO_CILIARY_BASAL_BODY	-1.4391246	0.00549451	1.39E-01	1
SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP	-1.547531	0.00564972	8.32E-02	1
MORI_PRE_BI_LYMPHOCYTE_UP	-1.5960205	0.00617284	6.57E-02	1
GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	-1.5240059	0.00628931	9.35E-02	1
REACTOME_M_G1_TRANSITION	-1.6286346	0.00632911	5.61E-02	1
GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT	-1.8798611	0.00636943	1.23E-02	0.952
REACTOME_FANCONI_ANEMIA_PATHWAY	-1.7809943	0.00641026	2.37E-02	1
DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCOCORTICOIDS	-1.9341197	0.00671141	8.48E-03	0.848
MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_UP	-1.4837611	0.00675676	1.14E-01	1
GO_DNA_SECONDARY_STRUCTURE_BINDING	-1.9728744	0.00699301	6.34E-03	0.736
GO_NEGATIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.7687477	0.00704225	2.54E-02	1
REACTOME_G1_S_TRANSITION	-1.6024923	0.0070922	6.38E-02	1
WEST_ADRENOCORTICAL_TUMOR_MARKERS_UP	-1.6866105	0.00714286	3.99E-02	1
HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN	-1.5796355	0.00719425	7.12E-02	1
GO_ENDONUCLEASE_ACTIVITY	-1.8693486	0.00729927	1.32E-02	0.963
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	-1.8590806	0.00743494	1.42E-02	0.973
GO_BINDING_OF_SPERM_TO_ZONA_PELLUCIDA	-1.6487145	0.00757576	4.98E-02	1
GO_RNA_POLYMERASE_COMPLEX	-1.4377512	0.00763359	1.40E-01	1
GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	-1.4568753	0.00775194	1.29E-01	1
MIKKELSEN_ES_HCP_WITH_H3K27ME3	-1.8183779	0.00796813	1.85E-02	0.991

GO_CENTROSOME_DUPLICATION	-1.7329624	0.008	3.06E-02	1
PID_ATM_PATHWAY	-1.7389603	0.00806452	2.98E-02	1
PID_BARD1_PATHWAY	-1.7748884	0.00819672	2.45E-02	1
GO_RNA_CAPPING	-1.6885667	0.00826446	3.95E-02	1
GO_7_METHYLGUANOSINE_RNA_CAPPING	-1.6823592	0.0083682	4.10E-02	1
WHITFIELD_CELL_CYCLE_G1_S	-1.3819922	0.00840336	1.77E-01	1
GO_DNA_REPAIR_COMPLEX	-1.7448764	0.00843882	2.89E-02	1
GO_3_5_EXONUCLEASE_ACTIVITY	-1.727597	0.00843882	3.15E-02	1
DAIRKEE_CANCER_PRONE_RESPONSE_BPA	-1.625986	0.00884956	5.69E-02	1
GO_DNA_BIOSYNTHETIC_PROCESS	-1.4670559	0.00900901	1.23E-01	1
REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	-1.5386645	0.00921659	8.66E-02	1
WILCOX_RESPONSE_TO_PROGESTERONE_UP	-1.591328	0.00934579	6.70E-02	1
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	-1.5579816	0.00934579	7.93E-02	1
GO_B_CELL_RECEPTOR_SIGNALING_PATHWAY	-1.5168726	0.00943396	9.64E-02	1
DELPUECH_FOXO3_TARGETS_DN	-1.5797195	0.00947867	7.13E-02	1
REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_REPLICATION_INDEPENDENT_DOUBLE_STRAND_BREAKS	-1.8584013	0.00949367	1.42E-02	0.974
GO_HISTONE_EXCHANGE	-1.8009359	0.00956938	2.10E-02	0.997
GO_V_D_J_RECOMBINATION	-1.7426318	0.00958466	2.91E-02	1
GO_REGULATION_OF_SYNAPSE_ASSEMBLY	-1.4845363	0.00985222	1.14E-01	1
BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AND_TSC2	-1.4116298	0.00995025	1.58E-01	1
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	-1.7976208	0.00996678	2.14E-02	0.997
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	-1.8882422	0.01027397	1.16E-02	0.946
GO_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING	-1.4559885	0.0106383	1.30E-01	1
GO_MULTIVESICULAR_BODY	-1.6001804	0.01149425	6.46E-02	1
CHICAS_RB1_TARGETS_LOW_SERUM	-1.4341288	0.01156069	1.42E-01	1
BIOCARTA_PROTEASOME_PATHWAY	-1.6891288	0.01162791	3.95E-02	1

GO_SKIN_EPIDERMIS_DEVELOPMENT	-1.5128475	0.01176471	9.86E-02	1
GO_ENDONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCLEIC_ACIDS_AND_PRODUCING_5_PHOSPHOMONOESTERS	-1.6165828	0.01190476	5.98E-02	1
JIANG_AGING_CEREBRAL_CORTEX_UP	-1.606705	0.012	6.29E-02	1
LY_AGING_PREMATURE_DN	-1.6339211	0.01209677	5.47E-02	1
TOMLINS_PROSTATE_CANCER_UP	-1.5971503	0.01209677	6.56E-02	1
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM5	-1.5309055	0.01219512	9.01E-02	1
GCNP_SHH_UP_EARLY.V1_UP	-1.332443	0.01234568	2.15E-01	1
PID_ATR_PATHWAY	-1.7109572	0.01244813	3.44E-02	1
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR	-1.6786853	0.01265823	4.18E-02	1
BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_DN	-1.3391049	0.01265823	2.09E-01	1
REACTOME_PACKAGING_OF_TELOMERE_ENDS	-1.6887952	0.01282051	3.95E-02	1
GO_CENTRIOLE_ASSEMBLY	-1.8513018	0.01290323	1.49E-02	0.979
GO_RNA_3_END_PROCESSING	-1.4574914	0.01324503	1.29E-01	1
GO_PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	-1.4471751	0.01327434	1.34E-01	1
GO_U1_SNRNP	-1.7845634	0.01328904	2.32E-02	1
FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_DN	-1.5230465	0.01342282	9.38E-02	1
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	-1.5359267	0.01363636	8.75E-02	1
GO_NEURON_PROJECTION_GUIDANCE	-1.3092182	0.01369863	2.35E-01	1
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	-1.7150029	0.01374571	3.38E-02	1
GO_HORMONE_ACTIVITY	-1.4687891	0.0137931	1.22E-01	1
GO_CALCIUM_DEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	-1.7117805	0.01423488	3.42E-02	1
GO_SPINAL_CORD_PATTERNING	-1.6716913	0.01433692	4.38E-02	1

GO_MATURATION_OF_5_8S_RRNA	-1.7735958	0.01454546	2.47E-02	1
GO_MEMBRANE_DISASSEMBLY	-1.5473466	0.01463415	8.30E-02	1
GO_PROTEIN_LOCALIZATION_TO_CILIUM	-1.6110787	0.01470588	6.17E-02	1
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	-1.7414663	0.01481482	2.92E-02	1
GO_EXORIBONUCLEASE_ACTIVITY	-1.7107351	0.01503759	3.43E-02	1
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	-1.6346027	0.01503759	5.45E-02	1
SANSOM_APC_TARGETS_REQUIRE_MYC	-1.3088795	0.01515152	2.35E-01	1
SHEPARD_BMYB_TARGETS	-1.5621214	0.01530612	7.78E-02	1
REACTOME_BASE_EXCISION_REPAIR	-1.7465373	0.0154321	2.88E-02	1
CHESLER_BRAIN_HIGHEST_EXPRESSION	-1.602554	0.01568628	6.40E-02	1
VANASSE_BCL2_TARGETS_DN	-1.4763668	0.01595745	1.18E-01	1
GO_DNA_REPLICATION_INITIATION	-1.7659826	0.01612903	2.58E-02	1
GO_REGULATION_OF_TELOMERE_MAINTENANCE	-1.5342103	0.01621622	8.84E-02	1
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	-1.595465	0.01639344	6.56E-02	1
GO_EXONUCLEASE_ACTIVITY	-1.5376558	0.01657459	8.68E-02	1
GO_NUCLEAR_REPLICATION_FORK	-1.6066426	0.01659751	6.28E-02	1
GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_CYTOCHROME_C_TO_OXYGEN	-1.7472405	0.01683502	2.88E-02	1
GO_EXONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCLEIC_ACIDS_AND_PRODUCING_5_PHOSPHOMONOESTERS	-1.571208	0.01731602	7.44E-02	1
GO_MICROTUBULE_ORGANIZING_CENTER_ORGANIZATION	-1.5596461	0.01744186	7.87E-02	1
NADERI_BREAST_CANCER_PROGNOSIS_UP	-1.5698159	0.01762115	7.46E-02	1
GO_NONMOTILE_PRIMARY_CILIUM	-1.3418198	0.01785714	2.07E-01	1
WIERENGA_PML_INTERACTOME	-1.5186665	0.01793722	9.56E-02	1
BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_UP	-1.4931945	0.01801802	1.08E-01	1
GO_DAMAGED_DNA_BINDING	-1.4507017	0.01807229	1.33E-01	1

PID_MYC_ACTIV_PATHWAY	-1.401974	0.01818182	1.65E-01	1
GO_DNA_DAMAGE_RESPONSE_DETECTION_OF_DNA_DAMAGE	-1.6603605	0.01843318	4.68E-02	1
GO_MISMATCH_REPAIR	-1.5473778	0.01879699	8.31E-02	1
CERIBELLI_PROMOTERS_INACTIVE_AND_BOUND_BY_NFY	-1.5398315	0.01879699	8.61E-02	1
GO_RNA_MODIFICATION	-1.4281529	0.01935484	1.46E-01	1
OXFORD_RALA_OR_RALB_TARGETS_UP	-1.4816161	0.01992032	1.15E-01	1
GO_IMMUNOGLOBULIN_PRODUCTION_INVOLVED_IN_IMMUNOGLOBULIN_MEDIATED_IMMUNE_RESPONSE	-1.6715218	0.02	4.37E-02	1
GO_ISOTYPE_SWITCHING	-1.6105287	0.02027027	6.18E-02	1
GO_NEURON_FATE_SPECIFICATION	-1.5085973	0.02027027	1.01E-01	1
REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	-1.5738555	0.02030457	7.36E-02	1
EPPERT_PROGENITOR	-1.5099139	0.02040816	1.00E-01	1
REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY	-1.7368655	0.02047782	3.02E-02	1
GO_MICROTUBULE_ORGANIZING_CENTER_PART	-1.3845533	0.02054795	1.75E-01	1
GO_OLFACTORY_LOBE_DEVELOPMENT	-1.4369361	0.0209205	1.40E-01	1
UDAYAKUMAR_MED1_TARGETS_UP	-1.307864	0.02105263	2.36E-01	1
MARIADASON_RESPONSE_TO_BUTYRATE_SULINDAC_6	-1.4459574	0.02150538	1.35E-01	1
GO_SPERMATID_DIFFERENTIATION	-1.3971882	0.02158273	1.68E-01	1
GO_REGULATION_OF_DNA_RECOMBINATION	-1.4628823	0.02162162	1.26E-01	1
GO_IMMUNOGLOBULIN_PRODUCTION	-1.570048	0.02164502	7.48E-02	1
GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	-1.4242573	0.02173913	1.49E-01	1
GO_REGULATION_OF_ERAD_PATHWAY	-1.6007837	0.02197802	6.45E-02	1
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_DEADENYLATION_DEPENDENT_DECAY	-1.43747	0.02209945	1.40E-01	1
GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	-1.6035368	0.02212389	6.38E-02	1

GO_GLUTATHIONE_DERIVATIVE_METABOLIC_PROCESS	-1.5003326	0.02230483	1.05E-01	1
BIOCARTA_ATRBRCA_PATHWAY	-1.5490835	0.02238806	8.25E-02	1
GO_CAJAL_BODY	-1.4851065	0.02252252	1.14E-01	1
GO_SOMATIC_DIVERSIFICATION_OF_IMMUNOGLOBULINS_INVOLVED_IN_IMMUNE_RESPONSE	-1.6230067	0.02302632	5.78E-02	1
GO_RNA_HELICASE_ACTIVITY	-1.395313	0.02312139	1.69E-01	1
HALLMARK_SPERMATOGENESIS	-1.3694566	0.02325581	1.85E-01	1
GO_NEGATIVE_REGULATION_OF_DNA_REPLICATION	-1.5116819	0.02358491	9.93E-02	1
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE	-1.573075	0.02369668	7.37E-02	1
REACTOME_LAGGING_STRAND_SYNTHESIS	-1.6578051	0.02405498	4.76E-02	1
PENG_RAPAMYCIN_RESPONSE_DN	-1.3464465	0.02439024	2.04E-01	1
GO_CELL_CYCLE_PHASE_TRANSITION	-1.1795657	0.02439024	3.84E-01	1
GO_PRESPLICEOSOME	-1.5732418	0.02473498	7.38E-02	1
GO_90S_PRERIBOSOME	-1.5689874	0.02508961	7.49E-02	1
GO_POSITIVE_REGULATION_OF_B_CELL_ACTIVATION	-1.4414095	0.02515723	1.38E-01	1
PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP	-1.3341932	0.02531646	2.14E-01	1
GO_NUCLEAR_ENVELOPE_DISASSEMBLY	-1.5406373	0.02538071	8.59E-02	1
GO_DNA_DEPENDENT_DNA_REPLICATION_MAINTENANCE_OF_FIDELITY	-1.5583193	0.02545455	7.93E-02	1
GO_ANTIGEN_BINDING	-1.5950246	0.0257732	6.57E-02	1
GO_BASAL_TRANSCRIPTION_MACHINERY_BINDING	-1.6497563	0.02614379	4.96E-02	1
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.5233319	0.02693603	9.38E-02	1
GO_CHROMATIN_REMODELING	-1.3772113	0.02702703	1.80E-01	1
GO_SOMATIC_RECOMBINATION_OF_IMMUNOGLOBULIN_GENES_INVOLVED_IN_IMMUNE_RESPONSE	-1.6198385	0.02711864	5.89E-02	1
BURTON_ADIPOGENESIS_12	-1.6282399	0.02734375	5.61E-02	1
GO_GERM_CELL_NUCLEUS	-1.6519185	0.02749141	4.90E-02	1
SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN	-1.4335731	0.02777778	1.42E-01	1
KLEIN_TARGETS_OF_BCR_ABL1_FUSION	-1.5116177	0.02857143	9.92E-02	1

REACTOME_MITOTIC_G1_G1_S_PHASES	-1.3731928	0.02857143	1.83E-01	1
OLSSON_E2F3_TARGETS_DN	-1.3553704	0.02870813	1.98E-01	1
GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	-1.6577519	0.02903226	4.75E-02	1
GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_HOMOLOGOUS_RECOMBINATION	-1.6570141	0.02922078	4.76E-02	1
GO_VENTRAL_SPINAL_CORD_DEVELOPMENT	-1.5535465	0.02985075	8.12E-02	1
GO_TELOMERE_ORGANIZATION	-1.4035859	0.02985075	1.64E-01	1
GEORGES_CELL_CYCLE_MIR192_TARGETS	-1.4481798	0.02994012	1.34E-01	1
GO_REGULATION_OF_ALTERNATIVE_MRNA_SPLICING_VIA_SPLICEOSOME	-1.5962416	0.03007519	6.57E-02	1
GO_REGULATION_OF_SISTER_CHROMATID_SEGREGATION	-1.5741618	0.03030303	7.36E-02	1
GO_SNRNA_METABOLIC_PROCESS	-1.4396904	0.03144654	1.39E-01	1
GO_RESPONSE_TO_MANGANESE_ION	-1.5362523	0.03180212	8.75E-02	1
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	-1.5082093	0.03212851	1.01E-01	1
GO_EXOSOME_RNASE_COMPLEX_	-1.6631304	0.03215434	4.59E-02	1
GO_REGULATION_OF_BEHAVIOR	-1.3741935	0.03225806	1.83E-01	1
REACTOME_MITOTIC_G2_G2_M_PHASES	-1.4492315	0.03311258	1.33E-01	1
LEE_LIVER_CANCER_MYC_UP	-1.4183037	0.03317536	1.53E-01	1
GO_U4_U6_X_U5_TRI_SNRNP_COMPLEX	-1.5600528	0.03358209	7.87E-02	1
XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN	-1.5023828	0.03374233	1.04E-01	1
PID_PLK1_PATHWAY	-1.4822922	0.03389831	1.15E-01	1
MATZUK_MEIOTIC_AND_DNA_REPAIR	-1.5445474	0.03463204	8.41E-02	1
GO_LUNG_CELL_DIFFERENTIATION	-1.5213184	0.03496504	9.43E-02	1
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	-1.3747956	0.03508772	1.82E-01	1
GO_B_CELL_PROLIFERATION	-1.4923117	0.03636364	1.09E-01	1
REACTOME_MRNA_CAPPING	-1.5426228	0.03663004	8.50E-02	1
KRAS.KIDNEY_UP.V1_UP	-1.2614777	0.03703704	2.84E-01	1

GO_PROTEIN_ACTIVATION_CASCADE	-1.3949065	0.0372093	1.69E-01	1
KEGG_PROTEIN_EXPORT	-1.5827727	0.03745318	7.02E-02	1
SCIBETTA_KDM5B_TARGETS_DN	-1.4144465	0.03773585	1.56E-01	1
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_ENDONUCLEOLYTIC	-1.4708605	0.03862661	1.21E-01	1
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	-1.4770533	0.03883495	1.18E-01	1
GO_U2_SNRNP	-1.5380908	0.03928572	8.67E-02	1
GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	-1.322195	0.03947368	2.25E-01	1
LE_NEURONAL_DIFFERENTIATION_DN	-1.4985704	0.03956835	1.05E-01	1
GO_BRANCHED_CHAIN_AMINO_ACID_METABOLIC_PROCESS	-1.5200753	0.03968254	9.49E-02	1
HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_DN	-1.5495657	0.03971119	8.27E-02	1
GO_REPLISOME	-1.5010208	0.03985507	1.05E-01	1
MORI_PLASMA_CELL_DN	-1.4236596	0.04032258	1.49E-01	1
PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN	-1.2786298	0.04040404	2.64E-01	1
GO_NUCLEOSOMAL_DNA_BINDING	-1.5000571	0.04104478	1.05E-01	1
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	-1.5471061	0.04166667	8.28E-02	1
GO_RNA_POLYMERASE_III_ACTIVITY	-1.5225624	0.04210527	9.39E-02	1
HESS_TARGETS_OF_HOXA9_AND_MEIS1_UP	-1.4385979	0.04210527	1.40E-01	1
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	-1.4673487	0.04225352	1.23E-01	1
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	-1.3901728	0.04255319	1.71E-01	1
GO_NUCLEAR_PORE	-1.378746	0.04301075	1.79E-01	1
GO_HAIR_CYCLE	-1.3189003	0.04320988	2.28E-01	1
GO_SYNAPSIS	-1.5579076	0.04347826	7.92E-02	1
GO_NEURON_RECOGNITION	-1.4955689	0.0438247	1.07E-01	1
GO_METHYLTRANSFERASE_COMPLEX	-1.4193972	0.0448718	1.53E-01	1
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_GAP_FILLING	-1.4772662	0.0449827	1.18E-01	1
RAY_TUMORIGENESIS_BY_ERBB2_CDC25A_UP	-1.3264045	0.04666667	2.21E-01	1

REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	-1.3540207	0.04678363	1.99E-01	1
GO_G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	-1.2594984	0.046875	2.87E-01	1
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13	-1.2854557	0.04705882	2.58E-01	1
MIKKELSEN_IPS_HCP_WITH_H3_UNMETHYLATED	-1.392396	0.04712042	1.70E-01	1
GO_MALE_MEIOSIS	-1.4627385	0.04744526	1.26E-01	1
GO_POSITIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.3106426	0.04761905	2.34E-01	1
BIOCARTA_CYTOKINE_PATHWAY	-1.5217724	0.04823151	9.42E-02	1
ASGHARZADEH_NEUROBLASTOMA_POOR_SURVIVAL_DN	-1.3848034	0.04867257	1.75E-01	1
GO_PROTEIN_MONOUBIQUITINATION	-1.2987188	0.04878049	2.46E-01	1
POOLA_INVASIVE_BREAST_CANCER_UP	-1.1918898	0.04878049	3.69E-01	1
CAHOY_NEURONAL	-1.3465466	0.04964539	2.04E-01	1
NAM_FXYD5_TARGETS_DN	-1.5141219	0.05016723	9.80E-02	1
ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN	-1.342819	0.05063291	2.07E-01	1
GO_DNA_DIRECTED_RNA_POLYMERASE_III_COMPLEX	-1.5006427	0.05102041	1.05E-01	1
PTEN_DN.V1_UP	-1.2630323	0.05154639	2.82E-01	1
GO_GLUTATHIONE_DERIVATIVE_BIOSYNTHETIC_PROCESS	-1.4784817	0.0515873	1.17E-01	1
GO_RNA_LOCALIZATION	-1.2478216	0.05194805	2.99E-01	1
NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON	-1.2801629	0.05263158	2.63E-01	1
GO_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	-1.3865511	0.0531401	1.74E-01	1
SEIDEN_MET_SIGNALING	-1.473615	0.05369128	1.19E-01	1
GO_DETECTION_OF_VISIBLE_LIGHT	-1.4052031	0.05394191	1.63E-01	1
GO_CHROMOSOME_LOCALIZATION	-1.3482525	0.05418719	2.03E-01	1
GO_SPINDLE_MICROTUBULE	-1.3975441	0.05434782	1.68E-01	1
GO_PROTEIN_K11_LINKED_UBIQUITINATION	-1.5622038	0.05439331	7.79E-02	1
GO_PEPTIDYL_PROLINE_MODIFICATION	-1.3666801	0.05445544	1.87E-01	1
SU_TESTIS	-1.2883044	0.05454546	2.56E-01	1
GO_CELLULAR_RESPONSE_TO_DRUG	-1.3408655	0.05464481	2.08E-01	1

VERHAAK_GLIOBLASTOMA_NEURAL	-1.2892107	0.05511811	2.55E-01	1
YANG_BREAST_CANCER_ESR1_LASER_DN	-1.3510641	0.05633803	2.01E-01	1
GO_ENDORIBONUCLEASE_ACTIVITY	-1.397844	0.05645161	1.68E-01	1
GO_NEGATIVE_REGULATION_OF_CELL_DIVISION	-1.3474007	0.05681818	2.03E-01	1
GO_DNA_DIRECTED_DNA_POLYMERASE_ACTIVITY	-1.4977137	0.0569395	1.06E-01	1
GO_ANTIMICROBIAL_HUMORAL_RESPONSE	-1.3910719	0.05701754	1.71E-01	1
WANG_TARGETS_OF_MLL_CBP_FUSION_DN	-1.343607	0.05714286	2.06E-01	1
GO_CELLULAR_KETONE_METABOLIC_PROCESS	-1.3480316	0.05759163	2.03E-01	1
BHATTACHARYA_EMBRYONIC_STEM_CELL	-1.3174825	0.05921053	2.28E-01	1
BROWN_MYELOID_CELL_DEVELOPMENT_DN	-1.2967713	0.05932203	2.47E-01	1
CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_UP	-1.2474384	0.05932203	2.99E-01	1
GO_POSITIVE_REGULATION_OF_SYNAPSE_ASSEMBLY	-1.3834146	0.05940594	1.76E-01	1
BENPORATH_MYC_TARGETS_WITH_EBOX	-1.2012868	0.06	3.56E-01	1
SHIN_B_CELL_LYMPHOMA_CLUSTER_9	-1.4817147	0.06040268	1.15E-01	1
GO_RNA_METHYLATION	-1.3671961	0.0608365	1.87E-01	1
HU_ANGIOGENESIS_DN	-1.4381076	0.06086956	1.40E-01	1
GO_ORGAN_OR_TISSUE_SPECIFIC_IMMUNE_RESPONSE	-1.4104801	0.06101695	1.59E-01	1
GO_MITOTIC_SPINDLE_ORGANIZATION	-1.3281705	0.06122449	2.19E-01	1
GO_PANCREAS_DEVELOPMENT	-1.311245	0.06122449	2.34E-01	1
GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTENTIAL	-1.3597802	0.06153846	1.93E-01	1
GO_DNA_LIGATION	-1.4759152	0.06164384	1.18E-01	1
THILLAINADESAN_ZNF217_TARGETS_UP	-1.3501378	0.0625	2.02E-01	1
GO_HYDROLASE_ACTIVITY_HYDROLYZING_N_GLYCOSYL_COMPOUNDS	-1.518386	0.06382979	9.56E-02	1
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	-1.3419831	0.06467662	2.07E-01	1
GO_MOTILE_CILIUM	-1.2767179	0.06508876	2.66E-01	1

GO_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.1745024	0.06521739	3.92E-01	1
RICKMAN_METASTASIS_UP	-1.2166455	0.06666667	3.37E-01	1
GO_POSITIVE_REGULATION_OF_HISTONE_METHYLATION	-1.3968234	0.06837607	1.68E-01	1
GO_POLYSOME	-1.3773779	0.06844106	1.80E-01	1
GO_CELL_DIFFERENTIATION_IN_SPINAL_CORD	-1.4293485	0.06880734	1.45E-01	1
KIM_MYC_AMPLIFICATION_TARGETS_UP	-1.1896331	0.06896552	3.72E-01	1
DEN_INTERACT_WITH_LCA5	-1.4507197	0.06976745	1.33E-01	1
WATANABE_COLON_CANCER_MSI_VS_MSS_UP	-1.4068868	0.06993007	1.61E-01	1
GO_MRNA_3_END_PROCESSING	-1.3618478	0.07109005	1.92E-01	1
GO_PHOTORECEPTOR_CELL_MAINTENANCE	-1.3927852	0.07142858	1.71E-01	1
KEGG_PARKINSONS_DISEASE	-1.2563382	0.07216495	2.90E-01	1
GO_NEGATIVE_REGULATION_OF_NUCLEAR_DIVISION	-1.386031	0.07228915	1.75E-01	1
GO_NEGATIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	-1.2456104	0.07246377	3.01E-01	1
CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN	-1.4037734	0.07272727	1.64E-01	1
PEART_HDAC_PROLIFERATION_CLUSTER_DN	-1.3154389	0.0738255	2.30E-01	1
GO_BRANCHING_INVOLVED_IN_SALIVARY_GLAND_MORPHOGENESIS	-1.4538124	0.07420494	1.31E-01	1
GO_B_CELL_MEDIATED_IMMUNITY	-1.3171362	0.07453416	2.29E-01	1
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	-1.3451447	0.0746888	2.05E-01	1
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	-1.4500048	0.07490636	1.33E-01	1
GO_PEPTIDYL_GLUTAMIC_ACID_MODIFICATION	-1.4436859	0.07508533	1.37E-01	1
ZHAN_V1_LATE_DIFFERENTIATION_GENES_DN	-1.4523404	0.07615894	1.32E-01	1
GO_POSITIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	-1.3909271	0.07630522	1.71E-01	1
NIKOLSKY_BREAST_CANCER_6P24_P22_AMPLICON	-1.3873389	0.07720588	1.74E-01	1
ZHAN_MULTIPLE_MYELOMA_MF_DN	-1.3801899	0.07786885	1.78E-01	1
LEE_LIVER_CANCER_CIPROFIBRATE_DN	-1.3024135	0.078125	2.43E-01	1

SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_UP	-1.300389	0.07831325	2.44E-01	1
REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	-1.3338022	0.07834102	2.14E-01	1
GO_RIBONUCLEOSIDE_BISPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.418091	0.07911392	1.53E-01	1
GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR	-1.3021743	0.07913669	2.43E-01	1
GO_NEURON_MIGRATION	-1.2433003	0.07913669	3.03E-01	1
GO_AEROBIC_RESPIRATION	-1.3235652	0.07936508	2.24E-01	1
GO_VOLTAGE_GATED_SODIUM_CHANNEL_ACTIVITY	-1.4331435	0.0797546	1.42E-01	1
GO_SENSORY_PERCEPTION_OF_TASTE	-1.3518701	0.08032128	2.01E-01	1
ERB2_UP.V1_DN	-1.2959286	0.08045977	2.48E-01	1
GO_DIENCEPHALON_DEVELOPMENT	-1.2860699	0.08092485	2.58E-01	1
GO_REGULATION_OF_B_CELL_ACTIVATION	-1.2373558	0.08130081	3.11E-01	1
STANELLE_E2F1_TARGETS	-1.3621016	0.08139535	1.92E-01	1
GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	-1.2486005	0.08148148	2.98E-01	1
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	-1.2880859	0.08152174	2.56E-01	1
GO_COENZYME_A_METABOLIC_PROCESS	-1.398796	0.08304498	1.67E-01	1
GO_COMPLEMENT_ACTIVATION	-1.3513943	0.08333334	2.01E-01	1
ZHENG_GLIOBLASTOMA_PLASTICITY_UP	-1.1571931	0.08333334	4.19E-01	1
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	-1.3910216	0.08366534	1.71E-01	1
PARK_HSC_VS_MULTIPOTENT_PROGENITORS_UP	-1.4524789	0.08387097	1.32E-01	1
GO_NUCLEOSIDE_BISPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.3956486	0.08561644	1.69E-01	1
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	-1.3318027	0.08679245	2.16E-01	1
GO_CHROMATIN_DISASSEMBLY	-1.3748493	0.08710802	1.83E-01	1
GO_DNA_REPLICATION_DEPENDENT_NUCLEOSOME_ASSEMBLY	-1.3404833	0.088	2.08E-01	1
GO_NUCLEAR_HETEROCHROMATIN	-1.319102	0.08812261	2.28E-01	1
REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIVATION	-1.3650488	0.08813559	1.89E-01	1

GO_NUCLEOSOME_BINDING	-1.3054857	0.0883721	2.39E-01	1
GO_MOLTING_CYCLE	-1.2853345	0.08854166	2.58E-01	1
CAFFAREL_RESPONSE_TO_THC_24HR_5_UP	-1.3259611	0.09053498	2.21E-01	1
MILI_PSEUDOPODIA	-1.3368745	0.09055118	2.12E-01	1
GO_CELL_CYCLE_G1_S_PHASE_TRANSITION	-1.2462476	0.09090909	3.01E-01	1
SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP	-1.3208766	0.0913242	2.26E-01	1
GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	-1.3955891	0.09174312	1.69E-01	1
HUANG_DASATINIB_RESISTANCE_DN	-1.275171	0.09326425	2.68E-01	1
GO_RNA_METHYLTRANSFERASE_ACTIVITY	-1.4345658	0.09407666	1.41E-01	1
GO_CARBON_OXYGEN_LYASE_ACTIVITY	-1.2594213	0.09433962	2.87E-01	1
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	-1.3714381	0.09507042	1.84E-01	1
GOLDRATH_HOMEOSTATIC_PROLIFERATION	-1.2041252	0.0952381	3.53E-01	1
MATZUK_SPERMATOCYTE	-1.2535042	0.09550562	2.93E-01	1
GO_CILIUM_MOVEMENT	-1.385117	0.09655172	1.75E-01	1
GO_DNA_MODIFICATION	-1.3056432	0.0972973	2.39E-01	1
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	-1.280208	0.09756097	2.63E-01	1
GO_PURINE_NUCLEOSIDE_BISPHOSPHATE_BIOSYNTHETIC_PROCESS	-1.3924593	0.09824561	1.71E-01	1
GO_POSITIVE_REGULATION_OF_DENDRITE_EXTENSION	-1.3735167	0.0990099	1.83E-01	1
GO_DNA_DIRECTED_RNA_POLYMERASE_II_HOLOENZYME	-1.2528152	0.09937888	2.94E-01	1
AIYAR_COBRA1_TARGETS_DN	-1.3198481	0.09964413	2.27E-01	1
GO_MRNA_SPLICE_SITE_SELECTION	-1.3538637	0.09966777	1.99E-01	1
GO_RNA_POLYMERASE_ACTIVITY	-1.3313712	0.10043668	2.16E-01	1
GO_PYRIMIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-1.272888	0.10106383	2.70E-01	1

GO_CALCIUM_INDEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	-1.3609642	0.1013986	1.92E-01	1
GO_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	-1.226695	0.10191083	3.23E-01	1
REACTOME_RNA_POL_I_PROMOTER_OPENING	-1.3179281	0.10212766	2.28E-01	1
GO_METAPHASE_PLATE_CONGRESSION	-1.2995827	0.10222222	2.45E-01	1
GO_DRUG_BINDING	-1.2139888	0.10344828	3.41E-01	1
REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	-1.3738211	0.10365854	1.83E-01	1
KEGG_CELL_CYCLE	-1.2135953	0.10465116	3.41E-01	1
EPPERT_CE_HSC_LSC	-1.2813723	0.10526316	2.62E-01	1
REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	-1.3119848	0.10891089	2.34E-01	1
REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	-1.3345528	0.11042945	2.14E-01	1
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_UP	-1.2548198	0.11059908	2.91E-01	1
PID_LKB1_PATHWAY	-1.2771109	0.1106383	2.66E-01	1
GO_PROTEIN_DNA_COMPLEX_DISASSEMBLY	-1.3704312	0.11111111	1.85E-01	1
GO_GLUTATHIONE_TRANSFERASE_ACTIVITY	-1.3477501	0.11111111	2.03E-01	1
GO_CHROMATIN_ORGANIZATION	-1.0732228	0.11111111	5.46E-01	1
GO_HSP70_PROTEIN_BINDING	-1.3098658	0.11155379	2.35E-01	1
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_INCISION	-1.2905139	0.11160714	2.54E-01	1
FURUKAWA_DUSP6_TARGETS_PCI35_DN	-1.2500829	0.11170213	2.97E-01	1
BRCA1_DN.V1_UP	-1.177504	0.1118421	3.88E-01	1
KEGG_BUTANOATE_METABOLISM	-1.2925092	0.1119403	2.52E-01	1
GO_RESPONSE_TO_TESTOSTERONE	-1.2903711	0.11297071	2.54E-01	1
GO_EMBRYONIC_SKELETAL_SYSTEM_MORPHOGENESIS	-1.1841149	0.11464968	3.78E-01	1
GO_STRUCTURE_SPECIFIC_DNA_BINDING	-1.197035	0.1147541	3.62E-01	1
GO_DNA_CATABOLIC_PROCESS_ENDONUCLEOLYTIC	-1.358289	0.11486486	1.95E-01	1

GO_ENDOTHELIAL_CELL_PROLIFERATION	-1.3180658	0.116	2.28E-01	1
BCAT.100_UP.V1_DN	-1.2971637	0.11740891	2.47E-01	1
LIU_BREAST_CANCER	-1.3471552	0.11787073	2.03E-01	1
GO_CILIARY_PLASM	-1.2202982	0.11864407	3.32E-01	1
REACTOME_HIV_INFECTION	-1.1552583	0.11864407	4.22E-01	1
GO_REGULATION_OF_DENDRITE_EXTENSION	-1.3818034	0.11904762	1.77E-01	1
RAHMAN_TP53_TARGETS_PHOSPHORYLATED	-1.3109118	0.11904762	2.34E-01	1
GO_DNA_REPLICATION_DEPENDENT_NUCLEOSOME_ORGANIZATION	-1.32284	0.11923077	2.25E-01	1
ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_DN	-1.1951374	0.12142857	3.64E-01	1
FOURNIER_ACINAR_DEVELOPMENT_LATE_DN	-1.3801913	0.12195122	1.78E-01	1
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	-1.1084946	0.12195122	4.93E-01	1
GO_PTERIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-1.3154033	0.12292359	2.30E-01	1
GO_NEGATIVE_REGULATION_OF_DNA_RECOMBINATION	-1.3330874	0.12297735	2.15E-01	1
REACTOME_MYOGENESIS	-1.3145155	0.12323944	2.31E-01	1
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	-1.2687683	0.12328767	2.75E-01	1
GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	-1.209075	0.12337662	3.46E-01	1
GO_CELL_DIVISION	-1.1035384	0.125	5.00E-01	1
CUI_TCF21_TARGETS_2_UP	-1.081537	0.125	5.34E-01	1
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	-1.2325534	0.12631579	3.17E-01	1
YEGNASUBRAMANIAN_PROSTATE_CANCER	-1.1836319	0.12804878	3.79E-01	1
GO_CRANIAL_NERVE_MORPHOGENESIS	-1.315363	0.12847222	2.30E-01	1
GO_STRUCTURAL_CONSTITUENT_OF_CYTOSKELETON	-1.1950402	0.12883435	3.64E-01	1
GO_NUCLEOSOME_DISASSEMBLY	-1.3486159	0.13057324	2.03E-01	1
GO_ACETYL_COA_METABOLIC_PROCESS	-1.2824647	0.13284133	2.61E-01	1
GO_METHIONINE_METABOLIC_PROCESS	-1.2718259	0.13356164	2.71E-01	1

REN_ALVEOLAR_RHABDOMYOSARCOMA_UP	-1.1984165	0.13605443	3.60E-01	1
SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_DN	-1.2445546	0.13679245	3.02E-01	1
POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN	-1.2090977	0.13744076	3.47E-01	1
VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_UP	-1.2278167	0.13772455	3.22E-01	1
GO_REGULATION_OF_CENTROSOME_CYCLE	-1.2292689	0.13793103	3.20E-01	1
KEGG_PROPANOATE_METABOLISM	-1.2215664	0.1388889	3.31E-01	1
SANSOM_WNT_PATHWAY_REQUIRE_MYC	-1.2340572	0.13917525	3.15E-01	1
GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	-1.2320992	0.13917525	3.17E-01	1
ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN	-1.1732906	0.1392405	3.93E-01	1
GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	-1.150605	0.13934426	4.28E-01	1
WHITEHURST_PACLITAXEL_SENSITIVITY	-1.241544	0.1402715	3.06E-01	1
GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	-1.2823702	0.14056225	2.61E-01	1
GO_NCRNA_3_END_PROCESSING	-1.301343	0.14067279	2.43E-01	1
GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR	-1.2314726	0.14112903	3.18E-01	1
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	-1.1188602	0.14285715	4.79E-01	1
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	-1.240673	0.1440678	3.06E-01	1
MATZUK_SPERMATID_DIFFERENTIATION	-1.2592034	0.14453125	2.86E-01	1
GO_SINGLE_FERTILIZATION	-1.1878685	0.1452514	3.74E-01	1
STK33_SKM_DN	-1.133802	0.14754099	4.57E-01	1
GO_RIBONUCLEOPROTEIN_COMPLEX_BINDING	-1.172841	0.14814815	3.94E-01	1
GO_CILIARY_TIP	-1.2435888	0.14847161	3.03E-01	1
GO_VENTRICULAR_SYSTEM_DEVELOPMENT	-1.281766	0.15	2.62E-01	1
GO_NEGATIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	-1.1774138	0.15189873	3.87E-01	1

GO_REGULATION_OF_HISTONE_METHYLATION	-1.1892782	0.15350877	3.73E-01	1
GO_REGULATION_OF_MESONEPHROS_DEVELOPMENT	-1.2911941	0.15498155	2.54E-01	1
GO_REGULATION_OF_DNA_REPAIR	-1.2015529	0.1552795	3.56E-01	1
GO_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	-1.2309308	0.1563786	3.18E-01	1
GO_PHOSPHATIDYLETHANOLAMINE_ACYL_CHAIN_REMODELING	-1.249756	0.15646258	2.97E-01	1
REACTOME_FORMATION_OF_TRANSCRIPTION_COUPLED_NER_TC_NER_REPAIR_COMPLEX	-1.1958708	0.15730338	3.63E-01	1
MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN	-1.2975014	0.15789473	2.47E-01	1
GO_CYTOCHROME_COMPLEX	-1.2857426	0.15789473	2.58E-01	1
GO_TELOMERE_CAPPING	-1.2593443	0.15789473	2.87E-01	1
HOFMANN_CELL_LYMPHOMA_UP	-1.176596	0.15789473	3.88E-01	1
REACTOME_RNA_POL_I_TRANSCRIPTION	-1.181465	0.15822785	3.82E-01	1
GO_TELOMERIC_DNA_BINDING	-1.2897192	0.15830116	2.55E-01	1
WANG_CISPLATIN_RESPONSE_AND_XPC_UP	-1.1068401	0.15873016	4.96E-01	1
GO_POSITIVE_REGULATION_OF_BEHAVIOR	-1.2932593	0.15957446	2.51E-01	1
GO_POSITIVE_REGULATION_OF_VASODILATION	-1.2718946	0.15957446	2.71E-01	1
OUILLETTE_CLL_13Q14_DELETION_UP	-1.2095835	0.15957446	3.46E-01	1
GO_SITE_OF_DOUBLE_STRAND_BREAK	-1.2462608	0.16049382	3.01E-01	1
GO_EAR_MORPHOGENESIS	-1.1482973	0.16153847	4.32E-01	1
GO_RETINA_LAYER_FORMATION	-1.2695998	0.1627907	2.74E-01	1
GO_NEUROPEPTIDE_RECEPTOR_BINDING	-1.2519169	0.16376306	2.95E-01	1
PIGF_UP.V1_UP	-1.1245472	0.16393442	4.72E-01	1
GO_ARGININE_METABOLIC_PROCESS	-1.2742388	0.16498317	2.69E-01	1
RB_P107_DN.V1_UP	-1.1158565	0.16504854	4.83E-01	1
GO_B_CELL_ACTIVATION	-1.1138843	0.16528925	4.86E-01	1
GO_ESTROUS_CYCLE	-1.2590401	0.16666667	2.86E-01	1
GO_SODIUM_CHANNEL_ACTIVITY	-1.2299454	0.16666667	3.19E-01	1
GO_HISTONE_MONOUBIQUITINATION	-1.2137693	0.16666667	3.41E-01	1
GO_PURINE_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	-1.2190049	0.16731517	3.34E-01	1
YU_BAP1_TARGETS	-1.2559124	0.16788322	2.90E-01	1

KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	-1.230974	0.16867469	3.18E-01	1
GO_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	-1.2018532	0.16949153	3.56E-01	1
GO_FOREBRAIN_REGIONALIZATION	-1.2756974	0.16955018	2.68E-01	1
GO_MEMBRANE_DEPOLARIZATION_DURING_ACTION_POTENTIAL	-1.1966553	0.16956522	3.62E-01	1
GO_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	-1.2889068	0.17142858	2.55E-01	1
GO_LUNG_EPITHELIUM_DEVELOPMENT	-1.198548	0.17375886	3.61E-01	1
RPS14_DN.V1_DN	-1.1053482	0.175	4.98E-01	1
WANG_METASTASIS_OF_BREAST_CANCER_ESR1_UP	-1.2552948	0.17627119	2.91E-01	1
CHIARETTI_T_ALL_RELAPSE_PROGNOSIS	-1.268843	0.17857143	2.75E-01	1
BIOCARTA_DC_PATHWAY	-1.2243811	0.17880794	3.27E-01	1
GO_CATION_CHANNEL_COMPLEX	-1.1013784	0.17977528	5.04E-01	1
MAYBURD_RESPONSE_TO_L663536_DN	-1.1871194	0.17989418	3.75E-01	1
GO_SULFUR_AMINO_ACID_BIOSYNTHETIC_PROCESS	-1.2360746	0.18037975	3.12E-01	1
GO_PURINE_RIBONUCLEOSIDE_BIOSYNTHETIC_PROCESS	-1.1458124	0.18115942	4.36E-01	1
REACTOME_FORMATION_OF_THE_HIV1_EARLY_ELONGATION_COMPLEX	-1.2382227	0.18181819	3.10E-01	1
GO_POSITIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION	-1.2315824	0.1821192	3.18E-01	1
GO_SPINAL_CORD_DEVELOPMENT	-1.1424718	0.18238993	4.42E-01	1
GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_III_PROMOTER	-1.1722513	0.18502203	3.94E-01	1
KOHOUTEK_CCNT2_TARGETS	-1.1674256	0.18536586	4.01E-01	1
MADAN_DPPA4_TARGETS	-1.1850206	0.18604651	3.78E-01	1
GO_INNER_EAR_MORPHOGENESIS	-1.1246853	0.1861702	4.72E-01	1
GO_CILIARY_PART	-1.0997825	0.18644068	5.06E-01	1
GO_MITOTIC_SPINDLE_ASSEMBLY	-1.2334385	0.1870229	3.16E-01	1
GO_HETEROTRIMERIC_G_PROTEIN_COMPLEX	-1.2111504	0.1875	3.44E-01	1
GO_LRR_DOMAIN_BINDING	-1.2125051	0.18770227	3.42E-01	1

GO_REGULATION_OF_SYNAPSE_ORGANIZATION	-1.1222208	0.18796992	4.75E-01	1
GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	-1.1550453	0.18831168	4.22E-01	1
CAIRO_PML_TARGETS_BOUND_BY_MYC_UP	-1.2191031	0.18867925	3.34E-01	1
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	-1.2069753	0.18930042	3.50E-01	1
GO_CRANIAL_NERVE_DEVELOPMENT	-1.1868885	0.18930042	3.75E-01	1
GO_WNT_PROTEIN_BINDING	-1.1862004	0.19029851	3.76E-01	1
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	-1.2206688	0.1904762	3.32E-01	1
GO_RIBONUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	-1.2179193	0.19087137	3.35E-01	1
GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	-1.1743581	0.19282511	3.92E-01	1
GO_NUCLEAR_NUCLEOSOME	-1.2022755	0.1954023	3.56E-01	1
GO_RNA_DEPENDENT_DNA_BIOSYNTHETIC_PROCESS	-1.2441095	0.19578314	3.03E-01	1
GO_PHOTORECEPTOR_INNER_SEGMENT	-1.179731	0.19767442	3.84E-01	1
GO_AUTONOMIC_NERVOUS_SYSTEM_DEVELOPMENT	-1.2045987	0.1977612	3.53E-01	1
GOLUB_ALL_VS_AML_UP	-1.1886275	0.199262	3.73E-01	1
CAFFAREL_RESPONSE_TO_THC_DN	-1.2177734	0.20068027	3.35E-01	1
GO_REGULATION_OF_HISTONE_H3_K4_METHYLATION	-1.202888	0.2016129	3.55E-01	1
GO_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	-1.1638749	0.20192307	4.07E-01	1
KEGG_ALLOGRAFT_REJECTION	-1.2182664	0.20198676	3.35E-01	1
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	-1.1534017	0.2021858	4.25E-01	1
CHANG_CORE_SERUM_RESPONSE_UP	-1.1099166	0.2037037	4.91E-01	1
GO_POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	-1.1916399	0.20567375	3.69E-01	1
GRABARCZYK_BCL11B_TARGETS_DN	-1.1198645	0.20588236	4.77E-01	1
GO_REGULATION_OF_ALPHA_AMINO_3_HYDROXY_5_METHYL_4_ISOXAZOLE_PROPIONATE_SELECTIVE_GLUTAMATE_RECEPTOR_ACTIVITY	-1.2065399	0.20875421	3.50E-01	1
GO_CHANNEL_REGULATOR_ACTIVITY	-1.1104878	0.20952381	4.90E-01	1

GO_ATP_DEPENDENT_DNA_HELICASE_ACTIVITY	-1.2103047	0.20987654	3.45E-01	1
SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY	-1.1888319	0.21008404	3.73E-01	1
GO_CILIUM_MORPHOGENESIS	-1.119992	0.21052632	4.77E-01	1
GO_NEGATIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	-1.2066935	0.21071428	3.50E-01	1
GO_CELL_DIFFERENTIATION_IN_HINDBRAIN	-1.1831567	0.2147651	3.79E-01	1
DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2	-1.0962802	0.21495327	5.11E-01	1
GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	-1.1516849	0.21518987	4.26E-01	1
JAK2_DN.V1_DN	-1.1283243	0.21568628	4.67E-01	1
PECE_MAMMARY_STEM_CELL_UP	-1.0986737	0.21621622	5.07E-01	1
BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE	-1.1681541	0.21777777	4.00E-01	1
DOANE_BREAST_CANCER_CLASSES_UP	-1.1281173	0.22033899	4.67E-01	1
GO_ASTROCYTE_DEVELOPMENT	-1.1758288	0.22142857	3.90E-01	1
GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION_INVOLVED_IN_MITOSIS	-1.1983503	0.22177419	3.60E-01	1
GO_PYRIMIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-1.1812446	0.224	3.82E-01	1
RIZ_ERYTHROID_DIFFERENTIATION_HBZ	-1.1585736	0.2243346	4.16E-01	1
GO_DETECTION_OF_STIMULUS	-1.0708933	0.22535211	5.48E-01	1
GO_MULTICELLULAR_ORGANISM_AGING	-1.1610988	0.2260274	4.12E-01	1
GO_AROMATIC_AMINO_ACID_FAMILY_CATABOLIC_PROCESS	-1.1945115	0.2265861	3.64E-01	1
REACTOME_SIGNAL_AMPLIFICATION	-1.1597512	0.22705314	4.15E-01	1
GOLDRATH_ANTIGEN_RESPONSE	-1.0559785	0.22727273	5.71E-01	1
GO_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	-1.1727718	0.23046875	3.94E-01	1
GO_SYNAPTONEMAL_COMPLEX	-1.1623802	0.23076923	4.10E-01	1
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	-1.1701728	0.23104693	3.97E-01	1
GO_AXONEME_PART	-1.2020729	0.23225807	3.56E-01	1

KEGG_DRUG_METABOLISM_CYTOCHROME_P450	-1.1481152	0.23255815	4.32E-01	1
KEGG_CITRATE_CYCLE_TCA_CYCLE	-1.1849827	0.23357664	3.77E-01	1
GO_CARBOXY_TERMINAL_DOMAIN_PROTEIN_KINASE_COMPLEX	-1.169567	0.23404256	3.98E-01	1
ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_DN	-1.2023181	0.23426573	3.56E-01	1
GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY	-1.1272378	0.23555556	4.68E-01	1
JUBAN_TARGETS_OF_SPI1_AND_FLI1_DN	-1.109546	0.2361111	4.92E-01	1
REACTOME_ACYL_CHAIN_REMODELLING_OF_PE	-1.1956306	0.23666666	3.64E-01	1
SEIDEN_ONCOGENESIS_BY_MET	-1.1126611	0.23837209	4.87E-01	1
GO_DETECTION_OF_ABIOTIC_STIMULUS	-1.0846115	0.23846154	5.30E-01	1
KEGG_PYRIMIDINE_METABOLISM	-1.0889374	0.23880596	5.22E-01	1
GO_DNA_CATABOLIC_PROCESS	-1.1504444	0.23970038	4.28E-01	1
REACTOME_RNA_POL_III_TRANSCRIPTION	-1.1300142	0.24	4.64E-01	1
GO_EPIDERMIS_MORPHOGENESIS	-1.1440196	0.24025974	4.39E-01	1
GO_PURINE_NTP_DEPENDENT_HELICASE_ACTIVITY	-1.0876482	0.24025974	5.24E-01	1
SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP	-1.1525908	0.24125874	4.25E-01	1
KEGG_TYPE_I_DIABETES_MELLITUS	-1.138089	0.24125874	4.51E-01	1
MCCLUNG_DELTA_FOSB_TARGETS_2WK	-1.1170623	0.2413793	4.81E-01	1
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_10	-1.0950654	0.24277456	5.13E-01	1
REACTOME_G_PROTEIN_ACTIVATION	-1.1555699	0.24295774	4.22E-01	1
SCHMIDT_POR_TARGETS_IN_LIMB_BUD_UP	-1.1533753	0.24542125	4.24E-01	1
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	-1.0914409	0.24615385	5.18E-01	1
DARWICHE_PAPILLOMA_RISK_LOW_UP	-1.0923343	0.24742268	5.17E-01	1
GO_CELL_CELL_SIGNALING_INVOLVED_IN_CARDIAC_CONDUCTION	-1.1703737	0.24809161	3.97E-01	1
GO_NEURON_FATE_COMMITMENT	-1.1312457	0.25	4.62E-01	1

ALCALAY_AML_BY_NPM1_LOCALIZATION_DN	-1.0615913	0.25	5.62E-01	1
GO_CELLULAR_RESPONSE_TO_DNA_DAMAGE_STIMULUS	-1.0322846	0.25	6.13E-01	1
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	-1.1468716	0.2513369	4.34E-01	1
GO_ENDOCRINE_PANCREAS_DEVELOPMENT	-1.1345545	0.25221238	4.57E-01	1
GO_EYE_PHOTORECEPTOR_CELL_DEVELOPMENT	-1.135876	0.25291827	4.55E-01	1
GO_PROTEASOME_ACCESSORY_COMPLEX	-1.1398861	0.25296444	4.47E-01	1
KEGG_PRIMARY_IMMUNODEFICIENCY	-1.1306376	0.25431034	4.63E-01	1
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	-1.1777835	0.25448027	3.87E-01	1
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	-1.1045414	0.25503355	4.99E-01	1
GO_PROTEIN_TARGETING_TO_MEMBRANE	-1.0931817	0.25609756	5.16E-01	1
GO_SPINDLE_ASSEMBLY	-1.1114787	0.25663716	4.89E-01	1
VANTVEER_BREAST_CANCER_POOR_PROGNOSIS	-1.0994632	0.25757575	5.06E-01	1
GO_DORSAL_VENTRAL_PATTERN_FORMATION	-1.120531	0.25882354	4.77E-01	1
GO_PHAGOCYTOSIS_ENGULFMENT	-1.1256069	0.26007327	4.72E-01	1
REACTOME_MEIOTIC_SYNAPSIS	-1.0929002	0.2606383	5.16E-01	1
GO_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	-1.1077926	0.26153848	4.94E-01	1
KEGG_AUTOIMMUNE_THYROID_DISEASE	-1.1657292	0.26262626	4.04E-01	1
KEGG_BASAL_TRANSCRIPTION_FACTORS	-1.1127809	0.26506025	4.87E-01	1
GO_NEGATIVE_REGULATION_OF_NEURON_DEATH	-1.0668917	0.26506025	5.53E-01	1
GO_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLUCOSE_STIMULUS	-1.1204795	0.2652174	4.76E-01	1
PID_TELOMERASE_PATHWAY	-1.1043336	0.2654321	4.99E-01	1
GO_GAMMA_TUBULIN_BINDING	-1.1245176	0.26666668	4.72E-01	1
GO_FOREBRAIN_NEURON_DEVELOPMENT	-1.1157439	0.2682927	4.83E-01	1
GO_POSITIVE_REGULATION_OF_MESONEPHROS_DEVELOPMENT	-1.1341197	0.2689655	4.58E-01	1

KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_DN	-1.1252719	0.2693727	4.72E-01	1
GO_CILIUM_ORGANIZATION	-1.081444	0.26966292	5.34E-01	1
FURUKAWA_DUSP6_TARGETS_PCI35_UP	-1.1254319	0.27027026	4.72E-01	1
CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_UP	-1.1064022	0.2713568	4.96E-01	1
GO_POSITIVE_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	-1.0986385	0.27450982	5.07E-01	1
GO_REGULATION_OF_DNA_REPLICATION	-1.0734365	0.2747253	5.46E-01	1
SCHRAMM_INHBA_TARGETS_DN	-1.1118188	0.27710843	4.89E-01	1
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREEN_UP	-1.1355056	0.27715355	4.56E-01	1
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	-1.1086245	0.28015563	4.93E-01	1
GO_POSITIVE_REGULATION_OF_RNA_SPLICING	-1.1476288	0.28064516	4.33E-01	1
PID_FAS_PATHWAY	-1.1001443	0.2825112	5.06E-01	1
PLASARI_TGFB1_TARGETS_10HR_DN	-1.082687	0.28301886	5.32E-01	1
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE	-1.0979735	0.2832618	5.08E-01	1
GO_REGULATION_OF_RNA_SPLICING	-1.0870955	0.2837838	5.25E-01	1
GO_GTP_METABOLIC_PROCESS	-1.1225789	0.28382838	4.74E-01	1
CLIMENT_BREAST_CANCER_COPY_NUMBER_UP	-1.1212195	0.2847222	4.77E-01	1
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	-1.0934111	0.285	5.16E-01	1
GO_MITOCHONDRION_ORGANIZATION	-1.0377748	0.2857143	6.04E-01	1
GO_SERINE_TYPE_EXOPEPTIDASE_ACTIVITY	-1.122781	0.28673837	4.74E-01	1
BASSO_B_LYMPHOCYTE_NETWORK	-1.0611454	0.28703704	5.62E-01	1
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	-1.1211774	0.28723404	4.76E-01	1
RODWELL_AGING_KIDNEY_DN	-1.0691308	0.288	5.51E-01	1
GO_POSITIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	-1.1338668	0.28903654	4.58E-01	1

GO_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	-1.0855682	0.28968254	5.28E-01	1
REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADRENALINE	-1.1535141	0.2901961	4.25E-01	1
BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_48HR_DN	-1.1082565	0.2901961	4.93E-01	1
RIZ_ERYTHROID_DIFFERENTIATION_6HR	-1.1241846	0.29032257	4.72E-01	1
GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	-1.0669751	0.29100528	5.54E-01	1
FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_UP	-1.07557	0.29166666	5.42E-01	1
GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_OXIDATIVE_STRESS	-1.1186255	0.292	4.79E-01	1
GO_ASPARTATE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	-1.1153512	0.29310346	4.83E-01	1
GO_CELL_CYCLE_G2_M_PHASE_TRANSITION	-1.0796574	0.2952381	5.36E-01	1
GO_PHOTORECEPTOR_CELL_DEVELOPMENT	-1.1002169	0.29535866	5.06E-01	1
KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_DN	-1.1179568	0.29642856	4.80E-01	1
GO_ICOSANOID_BIOSYNTHETIC_PROCESS	-1.0899525	0.29803923	5.20E-01	1
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	-1.0507901	0.2986111	5.80E-01	1
GO_NCRNA_TRANSCRIPTION	-1.0712917	0.2987013	5.48E-01	1
GO_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	-1.0925771	0.2996633	5.16E-01	1
GO_ATRIAL_SEPTUM_DEVELOPMENT	-1.133467	0.30033004	4.58E-01	1
GO_SPERM_EGG_RECOGNITION	-1.1044149	0.30081302	4.99E-01	1
YANAGIHARA_ESX1_TARGETS	-1.0828847	0.30252102	5.32E-01	1
GO_FATTY_ACID_DERIVATIVE_BIOSYNTHETIC_PROCESS	-1.0985897	0.30357143	5.07E-01	1
GO_EPITHELIAL_TUBE_BRANCHING_INVOLVED_IN_LUNG_MORPHOGENESIS	-1.1160494	0.30402932	4.83E-01	1
GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_UP	-1.1110233	0.30491802	4.90E-01	1
SHEPARD_BMYB_MORPHOLINO_DN	-1.0676565	0.30588236	5.53E-01	1
MIKKELSEN_MEF_ICP_WITH_H3K4ME3_AND_H3K27ME3	-1.0836494	0.30597016	5.31E-01	1

ROVERSI_GLIOMA_LOH_REGIONS	-1.0966063	0.3073593	5.10E-01	1
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT5_PROTEIN	-1.1132603	0.30821916	4.87E-01	1
FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_DN	-1.0913008	0.31118882	5.18E-01	1
GO_MODULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	-1.1017275	0.31178707	5.03E-01	1
BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP	-1.0756731	0.31188118	5.42E-01	1
HORTON_SREBF_TARGETS	-1.0891417	0.31226766	5.22E-01	1
GO_OLIGODENDROCYTE_DEVELOPMENT	-1.1149623	0.31300813	4.84E-01	1
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQUOISE_DN	-1.0944521	0.31553397	5.14E-01	1
STEIN_ESRRA_TARGETS_RESPONSIVE_TO_ESTROGEN_DN	-1.088548	0.31627908	5.23E-01	1
ABE_INNER_EAR	-1.0714223	0.31658292	5.48E-01	1
GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_ASSEMBLY	-1.0759345	0.3181818	5.42E-01	1
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_INCISION_3_TO_LESION	-1.0676183	0.3205575	5.52E-01	1
GO_REGULATION_OF_INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	-1.1300055	0.32258064	4.64E-01	1
GALE_APL_WITH_FLT3_MUTATED_UP	-1.0784904	0.32286996	5.39E-01	1
GO_REGULATION_OF_HEART_RATE_BY_CARDIAC_CONDUCTION	-1.0817997	0.32307693	5.34E-01	1
GO_ATPASE_REGULATOR_ACTIVITY	-1.0836791	0.32352942	5.32E-01	1
MIKKELSEN_IPS_ICP_WITH_H3K27ME3	-1.0764242	0.3237705	5.42E-01	1
GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_STABILIZATION	-1.0715976	0.3252595	5.48E-01	1
GO_DOUBLE_STRANDED_RNA_BINDING	-1.0721166	0.3254717	5.48E-01	1
GO_G2_DNA_DAMAGE_CHECKPOINT	-1.082836	0.3269962	5.32E-01	1
GO_HETEROCHROMATIN	-1.0419325	0.32786885	5.97E-01	1
GO_GERM_CELL_DEVELOPMENT	-1.0377698	0.32876712	6.03E-01	1
PAL_PRMT5_TARGETS_DN	-1.080228	0.32936507	5.36E-01	1
PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_6	-1.1026635	0.32962963	5.02E-01	1

MANTOVANI_VIRAL_GPCR_SIGNALING_DN	-1.0679493	0.3304721	5.53E-01	1
GO_CALCIUM_CHANNEL_COMPLEX	-1.0618638	0.33175355	5.63E-01	1
GO_INTERSTRAND_CROSS_LINK_REPAIR	-1.0600208	0.3319672	5.63E-01	1
GO_PYRIMIDINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	-1.0798897	0.3321033	5.36E-01	1
GO_BICARBONATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-1.1023428	0.33333334	5.02E-01	1
GO_SPINDLE	-1.036997	0.33333334	6.05E-01	1
GO_ASTROCYTE_DIFFERENTIATION	-1.0625262	0.33636364	5.62E-01	1
GO_RETINA_HOMEOSTASIS	-1.0779706	0.3377193	5.39E-01	1
GO_PRE_MRNA_BINDING	-1.0617855	0.33870968	5.63E-01	1
GO_BLOOD_COAGULATION_FIBRIN_CLOT_FORMATION	-1.0773128	0.33887044	5.40E-01	1
BIOCARTA_INFLAM_PATHWAY	-1.0796827	0.34074074	5.36E-01	1
NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_UP	-1.033252	0.3409091	6.13E-01	1
RIZ_ERYTHROID_DIFFERENTIATION_HEMGN	-1.0692326	0.34181818	5.51E-01	1
GO_DETECTION_OF_LIGHT_STIMULUS	-1.0859549	0.34313726	5.27E-01	1
REACTOME_ADP_SIGNALLING_THROUGH_P2RY1	-1.0935403	0.34412956	5.16E-01	1
GO_S_ADENOSYLMETHIONINE_METABOLIC_PROCESS	-1.0745722	0.3451613	5.44E-01	1
MAGRANGEAS_MULTIPLE_MYELOMA_IGG_VS_IGA_DN	-1.0615512	0.3456376	5.62E-01	1
AUNG_GASTRIC_CANCER	-1.0545398	0.3472222	5.73E-01	1
GO_EYE_PHOTORECEPTOR_CELL_DIFFERENTIATION	-1.0340751	0.3472222	6.12E-01	1
WATANABE_COLON_CANCER_MSI_VS_MSS_DN	-1.0699055	0.3473054	5.50E-01	1
GO_METALLOCARBOXYPEPTIDASE_ACTIVITY	-1.0697756	0.34732825	5.50E-01	1
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_UP	-1.0348122	0.34751773	6.11E-01	1
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	-1.0730228	0.34962407	5.46E-01	1
DORMOY_ELAVL1_TARGETS	-1.0899981	0.35031846	5.21E-01	1
GO_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	-1.0757227	0.35080644	5.42E-01	1

TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_DN	-1.0479876	0.35211268	5.85E-01	1
SHAFFER_IRF4_TARGETS_IN_ACTIVATED_DENDRITIC_CELL	-1.0419352	0.35403726	5.98E-01	1
GO_POTASSIUM_ION_IMPORT	-1.0742489	0.35433072	5.44E-01	1
REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	-1.0619487	0.3561644	5.63E-01	1
TIEN_INTESTINE_PROBIOTICS_6HR_UP	-1.0677681	0.3568075	5.53E-01	1
GO_REGULATION_OF_TELOMERE_CAPPING	-1.0761278	0.35689047	5.42E-01	1
GO_NEUROMUSCULAR_PROCESS_CONTROLLING_BALANCE	-1.0574732	0.35779816	5.69E-01	1
GO_OVARIAN_FOLLICLE_DEVELOPMENT	-1.0557708	0.36097562	5.71E-01	1
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_UP	-1.0597038	0.36196318	5.63E-01	1
GO_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR	-1.048931	0.36238533	5.83E-01	1
FERRANDO_HOX11_NEIGHBORS	-1.0600986	0.36486486	5.63E-01	1
GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_ACTIVITY	-1.0713751	0.36619717	5.48E-01	1
GO_HAIR_CELL_DIFFERENTIATION	-1.0612056	0.36637932	5.62E-01	1
GO_RESPONSE_TO_LEPTIN	-1.0634279	0.36858973	5.61E-01	1
GO_RESPONSE_TO_MUSCLE_ACTIVITY	-1.061597	0.36949152	5.63E-01	1
GO_PROTEIN_EXPORT_FROM_NUCLEUS	-1.0532556	0.36981133	5.75E-01	1
HOXA9_DN.V1_DN	-1.0256933	0.37037036	6.24E-01	1
GO_NUCLEAR_IMPORT	-1.0218811	0.37078652	6.31E-01	1
GO_DNA_ALKYLATION	-1.0191491	0.37083334	6.34E-01	1
GO_CHAPERONE_MEDIATED_PROTEIN_FOLDING	-1.0307548	0.37155962	6.15E-01	1
GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	-1.0466015	0.37337664	5.88E-01	1
OXFORD_RALA_OR_RALB_TARGETS_DN	-1.0301942	0.37380192	6.16E-01	1
GO_ENDOCRINE_SYSTEM_DEVELOPMENT	-1.0510491	0.37391305	5.80E-01	1
PARK_HSC_AND_MULTIPOTENT_PROGENITORS	-1.0627872	0.3744076	5.62E-01	1
GO_CELL_FATE_SPECIFICATION	-1.0416437	0.375	5.97E-01	1

SANA_RESPONSE_TO_IFNG_DN	-1.0312872	0.375	6.15E-01	1
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_LEADING_TO_GENERATION_OF_SECOND_MESSENGERS	-1.0327904	0.3755274	6.13E-01	1
GO_CEREBELLAR_CORTEX_MORPHOGENESIS	-1.0564822	0.3759124	5.70E-01	1
GO_COENZYME_BIOSYNTHETIC_PROCESS	-1.022167	0.37704918	6.31E-01	1
GO_GLUTAMINE_METABOLIC_PROCESS	-1.0325959	0.37984496	6.13E-01	1
DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_UP	-1.0309615	0.3802817	6.15E-01	1
GO_HISTONE_UBIQUITINATION	-1.0551742	0.38076922	5.72E-01	1
WALLACE_JAK2_TARGETS_UP	-1.0569527	0.38132295	5.69E-01	1
HALLMARK_PANCREAS_BETA_CELLS	-1.0532775	0.38135594	5.75E-01	1
HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP	-1.0609493	0.3815261	5.62E-01	1
GO_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	-1.0380403	0.38222224	6.04E-01	1
GO_MRNA_CLEAVAGE	-1.0479556	0.38263667	5.85E-01	1
GO_SNRNA_PROCESSING	-1.0451235	0.3857143	5.90E-01	1
GO_DEOXYRIBOSE_PHOSPHATE_CATABOLIC_PROCESS	-1.0393164	0.38652483	6.01E-01	1
GO_NEGATIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	-1.039227	0.38666666	6.01E-01	1
GO_GENE_SILENCING_BY_RNA	-1.0169089	0.38709676	6.37E-01	1
GO_SMOOTH_MUSCLE_TISSUE_DEVELOPMENT	-1.0500563	0.3880597	5.81E-01	1
GO_TRANSCRIPTION_FACTOR_TFIID_COMPLEX	-1.0467159	0.38906753	5.88E-01	1
CHOI_ATL_STAGE_PREDICTOR	-1.0270933	0.38938054	6.23E-01	1
GO_NONMOTILE_PRIMARY_CILIUM_ASSEMBLY	-1.0601139	0.39041096	5.64E-01	1
GO_CARDIAC_MUSCLE_CELL_CONTRACTION	-1.043832	0.39163497	5.93E-01	1
GO_SERTOLI_CELL_DEVELOPMENT	-1.0656343	0.39261746	5.56E-01	1
KEGG_ONE_CARBON_POOL_BY_FOLATE	-1.0557576	0.3935484	5.71E-01	1
RODWELL_AGING_KIDNEY_NO_BLOOD_DN	-1.0193869	0.39473686	6.34E-01	1
CHOW_RASSF1_TARGETS_UP	-1.0323476	0.3951049	6.13E-01	1
GO_UNFOLDED_PROTEIN_BINDING	-1.0400974	0.39869282	6.00E-01	1

GO_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	-1.0165642	0.3991228	6.37E-01	1
WALLACE_PROSTATE_CANCER_UP	-1.0411648	0.39937106	5.98E-01	1
GO_CELLULAR_PROCESS_INVOLVED_IN_REPRODUCTION_IN_MULTICELLULAR_ORGANISM	-1.0233421	0.4	6.28E-01	1
GOUYER_TATI_TARGETS_DN	-1.020971	0.4013378	6.33E-01	1
GO_NLS_BEARING_PROTEIN_IMPORT_INTO_NUCLEUS	-1.0204875	0.40140846	6.33E-01	1
GO_PROTEIN_SUMOYLATION	-1.0519251	0.40186915	5.78E-01	1
GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION	-1.0462173	0.40229884	5.88E-01	1
ZAMORA_NOS2_TARGETS_UP	-1.0253145	0.40229884	6.24E-01	1
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	-1.000071	0.4032258	6.66E-01	1
GO_DNA_METHYLATION	-1.0338616	0.40392157	6.12E-01	1
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH2_GROUP_OF_DONORS	-1.0428488	0.4057971	5.96E-01	1
GO_GUANOSINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-1.0235386	0.4059829	6.28E-01	1
PETROVA_PROX1_TARGETS_UP	-1.0059799	0.40625	6.55E-01	1
GO_GLIAL_CELL_DEVELOPMENT	-1.0324262	0.4064171	6.13E-01	1
GO_OXIDOREDUCTASE_ACTIVITY_OXIDIZING_METAL_IONS	-1.0019124	0.40789473	6.64E-01	1
GO_FERTILIZATION	-1.026531	0.40833333	6.23E-01	1
GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY	-1.0402942	0.4085603	6.00E-01	1
GO_NEURAL_TUBE_PATTERNING	-1.0174298	0.40939596	6.36E-01	1
GO_GENE_SILENCING	-1.0266806	0.40983605	6.24E-01	1
YU_MYC_TARGETS_DN	-0.9926533	0.4107143	6.79E-01	1
GO_REGULATION_OF_GLUCONEOGENESIS	-1.0274271	0.41125542	6.23E-01	1
GO_DNA_METHYLATION_OR_DEMETHYLATION	-1.0186614	0.4117647	6.34E-01	1
PARK_HSC_VS_MULTIPOTENT_PROGENITORS_DN	-1.0020101	0.4129693	6.64E-01	1
GO_REGULATION_OF_DNA_METABOLIC_PROCESS	-1.0333827	0.41379312	6.13E-01	1
TAYLOR_METHYLATED_IN_ACUTE_LYMPHOBLASTIC_LEUKEMIA	-1.018932	0.41401273	6.34E-01	1
REACTOME_RNA_POL_I_TRANSCRIPTION_INITIATION	-1.0189105	0.4140625	6.34E-01	1
GO_EXCITATORY_POSTSYNAPTIC_POTENTIAL	-1.0253494	0.41532257	6.25E-01	1

GO_CHAPERONE_BINDING	-1.0032853	0.41566265	6.61E-01	1
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_DN	-1.0263216	0.41638225	6.23E-01	1
GO_CEREBELLAR_CORTEX_FORMATION	-1.0134223	0.41750842	6.42E-01	1
GUTIERREZ_MULTIPLE_MYELOMA_UP	-1.0091307	0.4183267	6.49E-01	1
NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON	-1.0202155	0.41836736	6.33E-01	1
GO_POSITIVE_REGULATION_OF_LIGASE_ACTIVITY	-1.0152643	0.42105263	6.39E-01	1
REACTOME_ADP_SIGNALLING_THROUGH_P2RY12	-1.0203742	0.42142856	6.33E-01	1
KEGG_PYRUVATE_METABOLISM	-0.9808946	0.42173913	7.00E-01	1
GO_MONOCYTE_CHEMOTAXIS	-1.0104028	0.4227941	6.46E-01	1
GO_NEURAL_NUCLEUS_DEVELOPMENT	-1.0118551	0.42364532	6.44E-01	1
GO_COCHLEA_MORPHOGENESIS	-1.0138446	0.4248366	6.42E-01	1
GO_TRICARBOXYLIC_ACID_METABOLIC_PROCESS	-1.0138366	0.42672414	6.42E-01	1
GO_GENETIC_IMPRINTING	-1.0009654	0.42718446	6.65E-01	1
BIOCARTA_TEL_PATHWAY	-1.0160196	0.42767295	6.38E-01	1
GO_EMBRYONIC_CRANIAL_SKELETON_MORPHOGENESIS	-1.0133903	0.43037975	6.42E-01	1
GO_FATTY_ACID_BIOSYNTHETIC_PROCESS	-1.007163	0.43065694	6.53E-01	1
GO_CELLULAR_RESPONSE_TO_GLUCAGON_STIMULUS	-1.0272459	0.43162394	6.23E-01	1
GO_TBP_CLASS_PROTEIN_BINDING	-1.0191054	0.43223444	6.34E-01	1
GO_LEUKOCYTE_HOMEOSTASIS	-1.0113173	0.43406594	6.45E-01	1
GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	-1.0136641	0.436214	6.42E-01	1
GO_REGULATION_OF_DOPAMINE_SECRETION	-1.024474	0.43648207	6.26E-01	1
GO_SNORNA_BINDING	-0.9981803	0.43686005	6.69E-01	1
REACTOME_REGULATION_OF_INSULIN_SECRETION	-1.0154878	0.4397163	6.39E-01	1
GO_ISOPRENOID_BIOSYNTHETIC_PROCESS	-0.9920982	0.4397163	6.80E-01	1
REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINATION	-0.9885166	0.4397163	6.87E-01	1
KORKOLA_YOLK_SAC_TUMOR_UP	-1.0265799	0.43986255	6.23E-01	1
KEGG_HUNTINGTONS_DISEASE	-0.991279	0.44047618	6.81E-01	1

GO_MEMBRANE_DEPOLARIZATION	-1.0108205	0.44131455	6.45E-01	1
GO_CELL_CELL_RECOGNITION	-0.9937139	0.44166666	6.79E-01	1
CROMER_TUMORIGENESIS_DN	-0.998449	0.44298247	6.69E-01	1
GO_CARDIAC_RIGHT_VENTRICLE_MORPHOGENESIS	-0.9957765	0.44642857	6.74E-01	1
PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_UP	-0.9991345	0.44660193	6.68E-01	1
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	-0.9977014	0.4467005	6.70E-01	1
REACTOME_G0_AND_EARLY_G1	-1.0010942	0.44966444	6.65E-01	1
GO_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	-1.0125453	0.45070422	6.43E-01	1
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DEVELOPMENT	-1.0060413	0.4507772	6.55E-01	1
REACTOME_DEADENYLATION_OF_MRNA	-1.0013281	0.45423728	6.65E-01	1
REACTOME_SHC_MEDIATED_CASCADE	-0.9829671	0.45555556	6.97E-01	1
KEGG_RNA_POLYMERASE	-1.0206459	0.4559387	6.33E-01	1
GO_SERTOLI_CELL_DIFFERENTIATION	-0.9789668	0.45918366	7.03E-01	1
XU_HGF_SIGNALING_NOT_VIA_AKT1_48HR_DN	-0.9995171	0.460177	6.67E-01	1
GO_RESPONSE_TO_GLUCAGON	-1.0065343	0.4608295	6.54E-01	1
GO_POSITIVE_REGULATION_OF_AXON_EXTENSION	-1.0009384	0.46090534	6.64E-01	1
GO_ERROR_PRONE_TRANSLESION_SYNTHESIS	-0.9604532	0.46127945	7.31E-01	1
GO_AXONAL_FASCICULATION	-1.008859	0.4620462	6.49E-01	1
CHEN_ETV5_TARGETS_SERTOLI	-0.9873557	0.4636678	6.89E-01	1
GO_REGULATION_OF_RHODOPSIN_MEDIATED_SIGNALING_PATHWAY	-0.9908889	0.46387833	6.81E-01	1
WANG_TUMOR_INVASIVENESS_UP	-0.9844605	0.4642857	6.95E-01	1
GROSS_HYPOXIA_VIA_HIF1A_UP	-1.0054742	0.46551725	6.56E-01	1
GO_HETEROPHILIC_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	-0.9965212	0.46640316	6.73E-01	1
MMS_MOUSE_LYMPH_HIGH_4HRS_UP	-0.9617113	0.46666667	7.28E-01	1
GO_GLUTAMATE_SECRETION	-0.9781913	0.46718147	7.03E-01	1
ONO_AML1_TARGETS_DN	-0.9930119	0.46818182	6.79E-01	1
GO_RNA_POLYADENYLATION	-0.9943934	0.46825397	6.77E-01	1

REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON_LIKE_PEPTIDE1	-0.9735646	0.46887967	7.09E-01	1
GO_MITOTIC_CELL_CYCLE_CHECKPOINT	-1.0170307	0.47058824	6.37E-01	1
GO_ENDOPLASMIC_RETICULUM_SUBCOMPARTMENT	-0.9856129	0.4713376	6.93E-01	1
GO_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	-0.9732058	0.4722222	7.10E-01	1
GO_RETINOIC_ACID_METABOLIC_PROCESS	-0.9519383	0.47315437	7.47E-01	1
WANG_RESPONSE_TO_FORSKOLIN_UP	-0.9795507	0.47349823	7.02E-01	1
GO_POSITIVE_REGULATION_OF_ORGAN_GROWTH	-0.9801597	0.4743083	7.01E-01	1
GO_AROMATIC_AMINO_ACID_FAMILY_METABOLIC_PROCESS	-0.9528071	0.47482014	7.45E-01	1
ZHAN_MULTIPLE_MYELOMA_CD2_UP	-0.9847487	0.475	6.95E-01	1
YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP	-0.9929941	0.47549018	6.79E-01	1
BENPORATH_ES_2	-0.9822339	0.4755245	6.99E-01	1
GO_RESPONSE_TO_IONIZING_RADIATION	-0.9810256	0.47777778	7.01E-01	1
PRAMOONJAGO_SOX4_TARGETS_DN	-0.9937039	0.48095238	6.78E-01	1
GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	-0.9880872	0.4820144	6.88E-01	1
GO_INO80_TYPE_COMPLEX	-0.9686621	0.4820847	7.18E-01	1
REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING	-0.9767249	0.48301888	7.05E-01	1
MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITORS_DN	-0.9730802	0.48464164	7.10E-01	1
GO_GLYCINE_METABOLIC_PROCESS	-0.9743161	0.4847561	7.09E-01	1
GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY_P53_CLASS_MEDIATOR	-0.9666532	0.48514852	7.20E-01	1
GO_RIBOSOME_BINDING	-0.9879875	0.48559672	6.88E-01	1
GO_ESTABLISHMENT_OF_MITOTIC_SPINDLE_LOCALIZATION	-0.9769874	0.4861111	7.05E-01	1
GO_REPRESSING_TRANSCRIPTION_FACTOR_BINDING	-0.9702528	0.49197862	7.16E-01	1
CHANDRAN_METASTASIS_TOP50_UP	-0.9814072	0.49253732	7.00E-01	1

GO_WNT_ACTIVATED_RECEPTOR_ACTIVITY	-0.9920564	0.49295774	6.79E-01	1
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_INTERCONVERSION	-0.954045	0.4944238	7.43E-01	1
JOHANSSON_GLIOMAGENESIS_BY_PDGFB_DN	-0.9623998	0.49454546	7.27E-01	1
PUJANA_BREAST_CANCER_LIT_INT_NETWORK	-0.9787378	0.49635038	7.02E-01	1
GO_HISTONE_MRNA_METABOLIC_PROCESS	-0.9806008	0.49822065	7.01E-01	1
GO_SUPEROXIDE_METABOLIC_PROCESS	-0.9792254	0.49823323	7.02E-01	1
GO_SEXUAL_REPRODUCTION	-1.0120419	0.5	6.44E-01	1
GO_CELLULAR_AMIDE_METABOLIC_PROCESS	-1.011195	0.5	6.45E-01	1
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	-0.9948553	0.5	6.77E-01	1
PID_REG_GR_PATHWAY	-0.9836023	0.5	6.97E-01	1
WHITFIELD_CELL_CYCLE_G2	-0.977194	0.5	7.05E-01	1
GO_CELL_CYCLE_CHECKPOINT	-0.9739093	0.5	7.09E-01	1
TAKAO_RESPONSE_TO_UVB_RADIATION_UP	-0.9665611	0.5	7.20E-01	1
GO_MACROMOLECULE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	-0.9488167	0.5	7.51E-01	1
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_SINGLE_DONORS_WITH_INCORPORATION_OF_MOLECULAR_OXYGEN	-0.9683919	0.5016835	7.18E-01	1
GO_PROTEIN_IMPORT_INTO_NUCLEUS_TRANSLOCATION	-0.9700375	0.5017182	7.15E-01	1
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA	-0.9677457	0.5017668	7.18E-01	1
GO_REGULATION_OF_VASODILATION	-0.9788042	0.50212765	7.02E-01	1
GO_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	-0.9682991	0.50246304	7.17E-01	1
CAFFAREL_RESPONSE_TO_THC_24HR_5_DN	-0.9786024	0.50259066	7.02E-01	1
GO_POSITIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	-0.9517779	0.5035461	7.46E-01	1
GO_ZINC_ION_HOMEOSTASIS	-0.9276285	0.5051546	7.83E-01	1
REACTOME_KINESINS	-0.9361268	0.5055762	7.67E-01	1
GO_MITOTIC_SPINDLE	-0.9754981	0.50660795	7.07E-01	1

GO_TRANSLATION_INITIATION_FACTOR_BINDING	-0.965662	0.5066225	7.21E-01	1
GO_RESPONSE_TO_CAFFEINE	-0.9474779	0.5066225	7.52E-01	1
GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	-0.9740592	0.509434	7.09E-01	1
MASSARWEH_RESPONSE_TO_ESTRADIOL	-0.9479044	0.509901	7.51E-01	1
GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-0.9627448	0.5106383	7.26E-01	1
GO_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	-0.9506409	0.51131225	7.47E-01	1
WOOD_EBV_EBNA1_TARGETS_DN	-0.9690628	0.5126051	7.17E-01	1
WHITFIELD_CELL_CYCLE_M_G1	-0.9725964	0.51376146	7.10E-01	1
GO_SINGLE_STRANDED_RNA_BINDING	-0.9657151	0.51428574	7.22E-01	1
GO_CAMP_METABOLIC_PROCESS	-0.9629692	0.51428574	7.27E-01	1
REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER	-0.9580281	0.5148515	7.37E-01	1
GO_E_BOX_BINDING	-0.9764057	0.5156794	7.05E-01	1
WEBER_METHYLATED_HCP_IN_FIBROBLAST_DN	-0.9670594	0.5162455	7.20E-01	1
GO_OLIGOSACCHARIDE_LIPID_INTERMEDIATE_BIOSYNTHETIC_PROCESS	-0.9455499	0.5182724	7.56E-01	1
RICKMAN_HEAD_AND_NECK_CANCER_D	-0.9523892	0.5185185	7.46E-01	1
GO_HISTONE_DEUBIQUITINATION	-0.9363312	0.5197368	7.68E-01	1
GO_HISTONE_BINDING	-0.9922353	0.52112675	6.80E-01	1
LIANG_SILENCED_BY_METHYLATION_UP	-0.9644994	0.5217391	7.23E-01	1
GO_VIRAL_GENOME_REPLICATION	-0.9570355	0.5221843	7.38E-01	1
KYNG_ENVIRONMENTAL_STRESS_RESPONSE_DN	-0.9743109	0.5229682	7.09E-01	1
GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE	-0.9519175	0.5232975	7.46E-01	1
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_RED_UP	-0.9302616	0.52491695	7.77E-01	1
GO_DOLICHOL_LINKED_OLIGOSACCHARIDE_BIOSYNTHETIC_PROCESS	-0.9249964	0.5264797	7.85E-01	1
BIOCARTA_NKT_PATHWAY	-0.9362929	0.5272727	7.67E-01	1

GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	-0.9395086	0.5283688	7.64E-01	1
GO_DEFINITIVE_HEMOPOIESIS	-0.9326974	0.528481	7.72E-01	1
COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_UP	-0.941627	0.5289256	7.60E-01	1
GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	-0.980038	0.5294118	7.01E-01	1
TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_UP	-0.9575599	0.53038675	7.37E-01	1
GO_ENDORIBONUCLEASE_COMPLEX	-0.9181165	0.53582555	7.96E-01	1
GO_DETECTION_OF_MECHANICAL_STIMULUS	-0.9387642	0.536036	7.66E-01	1
GO_MYOFILAMENT	-0.955622	0.53731346	7.40E-01	1
HU_GENOTOXIC_DAMAGE_4HR	-0.9493073	0.53846157	7.50E-01	1
SESTO_RESPONSE_TO_UV_C7	-0.9701809	0.5388889	7.15E-01	1
MIKKELSEN_ES_HCP_WITH_H3_UNMETHYLATED	-0.9554216	0.5391705	7.40E-01	1
GO_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	-0.9568731	0.5394737	7.38E-01	1
GO_PTERIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-0.9430218	0.54077256	7.60E-01	1
RIZ_ERYTHROID_DIFFERENTIATION	-0.9726731	0.54140127	7.10E-01	1
GO_COFACTOR_BIOSYNTHETIC_PROCESS	-0.960204	0.54347825	7.31E-01	1
GO_SUBPALLIUM_DEVELOPMENT	-0.9326569	0.5438067	7.71E-01	1
HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_DN	-0.9629648	0.5441176	7.26E-01	1
GO_RIBONUCLEOPROTEIN_GRANULE	-0.9743927	0.54545456	7.10E-01	1
GO_METHYLATION	-0.9572044	0.54545456	7.38E-01	1
GO_CELLULAR_ALDEHYDE_METABOLIC_PROCESS	-0.9458067	0.5464481	7.56E-01	1
GO_ORGANIC_ACID_SODIUM_SYMPORTER_ACTIVITY	-0.9214616	0.54681647	7.90E-01	1
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GABAERGIC	-0.9410299	0.5498008	7.61E-01	1
GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	-0.9841303	0.5504587	6.96E-01	1
GO_SEX_DETERMINATION	-0.9131739	0.5520833	8.01E-01	1
GO_CEREBELLAR_CORTEX_DEVELOPMENT	-0.9432135	0.5527426	7.60E-01	1

GO_GLUTAMINE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	-0.9386692	0.5529801	7.65E-01	1
GO_MLL1_2_COMPLEX	-0.9350827	0.5531136	7.69E-01	1
BAKER_HEMATOPOIESIS_STAT3_TARGETS	-0.9182759	0.556338	7.97E-01	1
GO_FK506_BINDING	-0.9176887	0.5601266	7.96E-01	1
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	-0.9479461	0.5605381	7.52E-01	1
DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP	-0.9814136	0.5614035	7.01E-01	1
GO_POSITIVE_REGULATION_OF_TELOMERASE_ACTIVITY	-0.9231305	0.5620438	7.87E-01	1
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHARIDE_LLO_AND_TRANSFER_TO_A_NASCENT_PROTEIN	-0.9369875	0.56302524	7.67E-01	1
GO_NEGATIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	-0.9548745	0.5652174	7.41E-01	1
GO_RNA_POLYMERASE_II_REPRESSING_TRANSCRIPTION_FACTOR_BINDING	-0.9428096	0.56554306	7.60E-01	1
GO_POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	-0.9385735	0.5660377	7.65E-01	1
GO_CYCLIN_DEPENDENT_PROTEIN_KINASE_HOLOENZYME_COMPLEX	-0.9072344	0.5687023	8.09E-01	1
WU_HBX_TARGETS_3_UP	-0.9015243	0.5689655	8.18E-01	1
DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_UP	-0.9371399	0.56914896	7.67E-01	1
GO_REGULATION_OF_TELOMERASE_ACTIVITY	-0.9111086	0.5696721	8.04E-01	1
GO_PEPTIDYL_CYSTEINE_MODIFICATION	-0.911583	0.57042253	8.04E-01	1
REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT	-0.9140905	0.57051283	8.00E-01	1
SMID_BREAST_CANCER_RELAPSE_IN_BONE_UP	-0.9432477	0.5714286	7.61E-01	1
BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN	-0.9454674	0.57261413	7.56E-01	1
NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON	-0.942031	0.5735294	7.60E-01	1
REACTOME_MICRORNA_MIRNA_BIOGENESIS	-0.8942391	0.5755627	8.26E-01	1

IVANOVA_HEMATOPOIESIS_STEM_CELL_SHORT_TERM	-0.9003531	0.5777778	8.19E-01	1
GO_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	-0.8960713	0.5782748	8.24E-01	1
GO_POSITIVE_REGULATION_OF_B_CELL_PROLIFERATION	-0.9239183	0.57847536	7.86E-01	1
GO_MONOAMINE_TRANSPORT	-0.8998234	0.57859534	8.19E-01	1
GO_CORECEPTOR_ACTIVITY	-0.9154176	0.5787402	7.98E-01	1
KIM_TIAL1_TARGETS	-0.9340254	0.5805085	7.70E-01	1
HAHTOLA_SEZARY_SYNDROM_UP	-0.9436597	0.58064514	7.60E-01	1
GO_MUSCLE_HYPERTROPHY	-0.9062333	0.58064514	8.11E-01	1
GO_NEGATIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	-0.9251207	0.581749	7.85E-01	1
PID_FOXM1_PATHWAY	-0.9264619	0.58181816	7.84E-01	1
AKT_UP_MTOR_DN.V1_DN	-0.9685626	0.5822785	7.18E-01	1
GO_GLUTAMINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	-0.9407786	0.5824176	7.61E-01	1
GO_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	-0.9169391	0.5833333	7.97E-01	1
DANG_REGULATED_BY_MYC_UP	-0.9343444	0.58381504	7.69E-01	1
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	-0.9481185	0.5839416	7.52E-01	1
GO_PROTEIN_TRANSMEMBRANE_TRANSPORT	-0.9422803	0.5845411	7.60E-01	1
GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION	-0.9326857	0.58469945	7.72E-01	1
HOSHIDA_LIVER_CANCER_SUBCLASS_S2	-0.950795	0.5849057	7.48E-01	1
MARTINEZ_RESPONSE_TO_TRABECTEDIN_DN	-0.9650493	0.58536583	7.22E-01	1
STREICHER_LSM1_TARGETS_UP	-0.924158	0.58549225	7.86E-01	1
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	-0.9487273	0.5862069	7.51E-01	1
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	-0.9098501	0.58759123	8.06E-01	1
GO_MRNA_BINDING	-0.9832963	0.59090906	6.97E-01	1
BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_DN	-0.9022925	0.59090906	8.17E-01	1
GO_PROTEIN_AUTOUBIQUITINATION	-0.9338926	0.5914894	7.70E-01	1
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	-0.9425296	0.59195405	7.60E-01	1

GO_POSITIVE_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	-0.9067155	0.5925926	8.10E-01	1
GO_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	-0.9161581	0.5932836	7.98E-01	1
RIZ_ERYTHROID_DIFFERENTIATION_CCNE1	-0.9268341	0.59386975	7.84E-01	1
GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN	-0.9048315	0.5951557	8.14E-01	1
ABBUD_LIF_SIGNALING_1_DN	-0.9006256	0.5971223	8.19E-01	1
GO_COP9_SIGNALOSOME	-0.9159586	0.5990991	7.98E-01	1
GO_PURINE_RIBONUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	-0.8960615	0.6026936	8.24E-01	1
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_INVOLVED_IN_CELLULAR_RESPONSE_TO_CHEMICAL_STIMULUS	-0.8917852	0.60273975	8.30E-01	1
GO_ERROR_FREE_TRANSLESION_SYNTHESIS	-0.8951873	0.6028881	8.24E-01	1
TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA	-0.9380159	0.60365856	7.65E-01	1
GO_NEGATIVE_REGULATION_OF_TRANSLATIONAL_INITIATION	-0.9029536	0.6044304	8.17E-01	1
GO_CELLULAR_RESPONSE_TO_TOXIC_SUBSTANCE	-0.9195536	0.6061776	7.94E-01	1
GO_FEAR_RESPONSE	-0.8903962	0.6097561	8.32E-01	1
GO_COMPLEMENT_BINDING	-0.886543	0.61	8.35E-01	1
HOLLEMAN_ASPARAGINASE_RESISTANCE_B_ALL_UP	-0.8874652	0.6102362	8.34E-01	1
GO_REGULATION_OF_PROTEIN_TARGETING_TO_MITOCHONDRION	-0.9419648	0.6111111	7.60E-01	1
MELLMAN_TUT1_TARGETS_UP	-0.8787145	0.61217946	8.46E-01	1
NOUZOVA_TRETINOIN_AND_H4_ACETYLATION	-0.9513226	0.61417323	7.47E-01	1
GO_LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	-0.9424365	0.6142857	7.60E-01	1
REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	-0.9029685	0.61538464	8.17E-01	1
GO_DYNEIN_COMPLEX	-0.9112665	0.6160714	8.04E-01	1
GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION	-0.9291988	0.61764705	7.79E-01	1
WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_UP	-0.9240404	0.62096775	7.86E-01	1

GO_MACROLIDE_BINDING	-0.8935841	0.6215278	8.27E-01	1
GO_RESPONSE_TO_OXYGEN_RADICAL	-0.8959667	0.6221498	8.23E-01	1
GO_LEFT_RIGHT_PATTERN_FORMATION	-0.8615303	0.6223022	8.73E-01	1
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	-0.8871332	0.62357414	8.35E-01	1
GO_ESC_E_Z_COMPLEX	-0.8569711	0.6237288	8.76E-01	1
HUTTMANN_B_CLL_POOR_SURVIVAL_DN	-0.9266721	0.625	7.84E-01	1
RICKMAN_HEAD_AND_NECK_CANCER_F	-0.8882684	0.625	8.33E-01	1
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	-0.8870894	0.625	8.34E-01	1
GO_REGULATION_OF_CELLULAR_SENESCENCE	-0.8902655	0.6294964	8.31E-01	1
GO_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	-0.8774759	0.6305733	8.47E-01	1
BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_DN	-0.9210553	0.63131315	7.90E-01	1
GO_POSITIVE_REGULATION_OF_ORGANELLE_ASSEMBLY	-0.9009711	0.63135594	8.19E-01	1
GO_REGULATION_OF_CHROMATIN_SILENCING	-0.8512085	0.633218	8.82E-01	1
GO_THIOESTER_BIOSYNTHETIC_PROCESS	-0.9078561	0.6334842	8.08E-01	1
GO_MULTI_ORGANISM_TRANSPORT	-0.9081119	0.6335404	8.08E-01	1
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	-0.9178562	0.6344086	7.97E-01	1
ZIRN_TRETINOIN_RESPONSE_WT1_UP	-0.8768739	0.6386861	8.47E-01	1
GO_POTASSIUM_CHANNEL_REGULATOR_ACTIVITY	-0.9096202	0.6388889	8.06E-01	1
GO_PYRIMIDINE_NUCLEOSIDE_METABOLIC_PROCESS	-0.9261383	0.6391304	7.83E-01	1
NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_DN	-0.8663726	0.64026403	8.67E-01	1
GO_NUCLEAR_PERIPHERY	-0.9239067	0.64122134	7.85E-01	1
GO_POSITIVE_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	-0.8742142	0.6421725	8.52E-01	1
GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	-0.8964937	0.64319247	8.24E-01	1

REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	-0.9037187	0.6437247	8.16E-01	1
LOPEZ_TRANSLATION_VIA_FN1_SIGNALING	-0.8972125	0.645	8.23E-01	1
GO_POSITIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	-0.8845465	0.6486486	8.37E-01	1
GO_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	-0.9097192	0.6496815	8.06E-01	1
GO_OOCYTE_DIFFERENTIATION	-0.868057	0.65	8.64E-01	1
MATZUK_SPERMATOZOA	-0.9345946	0.6510067	7.69E-01	1
BIOCARTA_IGF1MTOR_PATHWAY	-0.8591913	0.652027	8.73E-01	1
KEGG_PROTEASOME	-0.8977122	0.6527197	8.22E-01	1
GO_MAST_CELL_MEDIATED_IMMUNITY	-0.8619978	0.65273315	8.72E-01	1
REACTOME_PYRUVATE_METABOLISM	-0.8555554	0.65319866	8.78E-01	1
GO_CENTRIOLAR_SATELLITE	-0.8698509	0.65436244	8.61E-01	1
GO_ONE_CARBON_METABOLIC_PROCESS	-0.8602083	0.65591395	8.74E-01	1
GO_HINDBRAIN_MORPHOGENESIS	-0.8825128	0.65625	8.41E-01	1
GO_ACYL_COA_BIOSYNTHETIC_PROCESS	-0.9082578	0.65800864	8.09E-01	1
VIETOR_IFRD1_TARGETS	-0.8521765	0.65909094	8.83E-01	1
GO_CEREBELLAR_PURKINJE_CELL_LAYER_DEVELOPMENT	-0.8903993	0.65925926	8.32E-01	1
STAEGE_EWING_FAMILY_TUMOR	-0.8458996	0.6594982	8.89E-01	1
GO_REGULATION_OF_CELL_CYCLE_CHECKPOINT	-0.8837112	0.6617647	8.38E-01	1
TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_UP	-0.8893446	0.6625	8.32E-01	1
GO_REGULATION_OF_MICROTUBULE_POLYMERIZATION	-0.8803608	0.66283524	8.44E-01	1
GO_MULTI_ORGANISM_LOCALIZATION	-0.915716	0.6632124	7.98E-01	1
GO_NEUROTRANSMITTER_BINDING	-0.8516565	0.66435987	8.82E-01	1
REACTOME_DESTABILIZATION_OF_MRNA_BY_BRF1	-0.8612702	0.6643836	8.73E-01	1
LEE_LIVER_CANCER_DENA_DN	-0.8991604	0.6647059	8.20E-01	1
CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_UP	-0.8917431	0.66486484	8.29E-01	1
GO_REGULATION_OF_MEMBRANE_REPOLARIZATION	-0.8777909	0.6678201	8.47E-01	1

GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	-0.848786	0.66787004	8.85E-01	1
GO_HISTONE_METHYLTRANSFERASE_COMPLEX	-0.8968192	0.6717949	8.23E-01	1
GO_PHOSPHATIDYLINOSITOL_3_5_BISPHOSPHATE_BINDING	-0.8572098	0.67320263	8.76E-01	1
GO_PITUITARY_GLAND_DEVELOPMENT	-0.8846895	0.6740088	8.38E-01	1
FARMER_BREAST_CANCER_APOCRINE_VS_BASAL	-0.9348842	0.67741936	7.69E-01	1
GO_NEGATIVE_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	-0.8649352	0.67741936	8.67E-01	1
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING	-0.845108	0.67785233	8.88E-01	1
GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION	-0.8732894	0.67980295	8.54E-01	1
SHIN_B_CELL_LYMPHOMA_CLUSTER_5	-0.8424552	0.6807818	8.90E-01	1
GO_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	-0.8799312	0.6818182	8.44E-01	1
ZHAN_VARIABLE_EARLY_DIFFERENTIATION_GENES_DN	-0.8647922	0.6827309	8.67E-01	1
THUM_SYSTOLIC_HEART_FAILURE_DN	-0.9260505	0.6849315	7.83E-01	1
BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP	-0.8891105	0.685446	8.32E-01	1
GO_NEGATIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	-0.8176275	0.6858108	9.13E-01	1
GO_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	-0.8518324	0.6875	8.83E-01	1
GO_ALPHA_AMINO_ACID_METABOLIC_PROCESS	-0.9363107	0.6885246	7.68E-01	1
GO_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	-0.8300414	0.6886447	9.00E-01	1
GENTILE_UV_RESPONSE_CLUSTER_D4	-0.9001144	0.68899524	8.19E-01	1
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	-0.8779171	0.692	8.47E-01	1
GO_CENTROSOME	-0.9383797	0.6923077	7.65E-01	1
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_DN	-0.8150692	0.6923077	9.13E-01	1
GO_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	-0.8335016	0.69520545	8.98E-01	1
DE_YY1_TARGETS_UP	-0.8224233	0.6958042	9.10E-01	1

LOPES_METHYLATED_IN_COLON_CANCER_DN	-0.8467406	0.6977612	8.88E-01	1
REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RECEPTOR	-0.8423749	0.69921875	8.90E-01	1
GO_MIDDLE_EAR_MORPHOGENESIS	-0.8212887	0.6996587	9.10E-01	1
GO_FEMALE_GAMETE_GENERATION	-0.9222843	0.7016575	7.88E-01	1
GO_APOPTOTIC_NUCLEAR_CHANGES	-0.8208653	0.70547944	9.10E-01	1
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	-0.8326329	0.70689654	8.99E-01	1
GO_EXON_EXON_JUNCTION_COMPLEX	-0.8343405	0.7089041	8.98E-01	1
GO_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	-0.8329393	0.71034485	8.99E-01	1
KAMIKUBO_MYELOID_MN1_NETWORK	-0.8436247	0.7104377	8.89E-01	1
GO_RESPONSE_TO_AMINE	-0.8851612	0.7105263	8.37E-01	1
GO_NEGATIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	-0.8842898	0.7112676	8.38E-01	1
SIRNA_EIF4GI_DN	-0.9148965	0.7114094	7.99E-01	1
LIU_PROSTATE_CANCER_UP	-0.897714	0.7133758	8.23E-01	1
GO_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	-0.9547308	0.71428573	7.41E-01	1
BENPORATH_ES_CORE_NINE_CORRELATED	-0.914614	0.71428573	7.99E-01	1
GO_ANAPHASE_PROMOTING_COMPLEX	-0.8306508	0.71480143	8.99E-01	1
WANG_RECURRENT_LIVER_CANCER_UP	-0.8173037	0.7161716	9.13E-01	1
LINDGREN_BLADDER_CANCER_CLUSTER_1_UP	-0.8901352	0.71710527	8.31E-01	1
GO_GLUTATHIONE_PEROXIDASE_ACTIVITY	-0.814165	0.71779144	9.15E-01	1
GO_TRANSFERASE_COMPLEX_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	-0.9130627	0.72	8.01E-01	1
GO_HYDRO_LYASE_ACTIVITY	-0.8295333	0.72	9.00E-01	1
GO_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	-0.8488388	0.7206704	8.85E-01	1
GO_G_PROTEIN_BETA_GAMMA_SUBUNIT_COMPLEX_BINDING	-0.8292369	0.7208481	9.00E-01	1
SIMBULAN_PARP1_TARGETS_DN	-0.8311207	0.7218543	9.00E-01	1

COLLIS_PRKDC_SUBSTRATES	-0.8420414	0.7222222	8.90E-01	1
GO_POSITIVE_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	-0.8255838	0.7227723	9.06E-01	1
GO_HISTONE_KINASE_ACTIVITY	-0.821733	0.7235495	9.11E-01	1
ODONNELL_METASTASIS_DN	-0.8221453	0.7238806	9.10E-01	1
GO_SIN3_TYPE_COMPLEX	-0.7966982	0.724359	9.20E-01	1
LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_DN	-0.8404982	0.72540987	8.92E-01	1
GO_CYTOPLASMIC_MICROTUBULE_ORGANIZATION	-0.8360848	0.7257384	8.96E-01	1
JISON_SICKLE_CELL_DISEASE_DN	-0.9263365	0.72727275	7.84E-01	1
GO_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	-0.8368437	0.72727275	8.95E-01	1
GO_POSITIVE_REGULATION_OF_TOR_SIGNALING	-0.8099793	0.72757477	9.18E-01	1
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	-0.8460109	0.7276596	8.89E-01	1
KEGG_ARGININE_AND_PROLINE_METABOLISM	-0.8710758	0.73134327	8.58E-01	1
GO_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	-0.8386444	0.73134327	8.93E-01	1
GO_DEFENSE_RESPONSE_TO_FUNGUS	-0.8095771	0.7316176	9.17E-01	1
GO_ROUGH_ENDOPLASMIC_RETICULUM_MEMBRANE	-0.8313869	0.73355263	9.00E-01	1
SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_DN	-0.8117413	0.7356688	9.17E-01	1
HASLINGER_B_CLL_WITH_6Q21_DELETION	-0.821668	0.7361111	9.10E-01	1
REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PI3KGAMMA	-0.8516986	0.73630136	8.82E-01	1
GO_BAF_TYPE_COMPLEX	-0.784398	0.73770493	9.28E-01	1
GO_MICROTUBULE_BASED_MOVEMENT	-0.9103096	0.73913044	8.06E-01	1
GO_B_CELL_DIFFERENTIATION	-0.8760171	0.73913044	8.49E-01	1
GO_DENDRITIC_SPINE_DEVELOPMENT	-0.7846935	0.7404844	9.28E-01	1
GO_REGULATION_OF_PROTEIN_IMPORT_INTO_NUCLEUS_TRANSLOCATION	-0.8091721	0.74113476	9.18E-01	1
GO_SPINDLE_POLE	-0.886024	0.7421875	8.36E-01	1

GO_SALIVARY_GLAND_DEVELOPMENT	-0.8529367	0.74319065	8.81E-01	1
GO_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	-0.8308933	0.7434211	9.00E-01	1
GO_BRANCHING_INVOLVED_IN_URETERIC_BUD_MORPHOGENESIS	-0.8449874	0.74407583	8.88E-01	1
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	-0.8440724	0.7440945	8.89E-01	1
REACTOME_PLATELET_SENSITIZATION_BY_LDL	-0.7865008	0.7458194	9.28E-01	1
GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	-0.8237191	0.7468355	9.09E-01	1
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	-0.8794484	0.7473684	8.45E-01	1
GO_RESPONSE_TO_PROTOZOAN	-0.8066885	0.74825174	9.18E-01	1
GO_PROTEIN_TARGETING	-0.8811938	0.75	8.43E-01	1
PID_CONE_PATHWAY	-0.7859141	0.75	9.27E-01	1
KIM_MYCL1_AMPLIFICATION_TARGETS_DN	-0.8127889	0.7507987	9.16E-01	1
GO_RESPONSE_TO_ISCHEMIA	-0.8151467	0.75088966	9.14E-01	1
GO_1_PHOSPHATIDYLINOSITOL_BINDING	-0.793592	0.75185186	9.22E-01	1
KEGG_TASTE_TRANSDUCTION	-0.8183845	0.75298804	9.12E-01	1
HADDAD_B_LYMPHOCYTE_PROGENITOR	-0.9275683	0.754717	7.83E-01	1
BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_UP	-0.811321	0.754717	9.17E-01	1
GO_ASPARTATE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	-0.7988972	0.75609756	9.21E-01	1
GO_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATION	-0.7729634	0.7594502	9.37E-01	1
GO_DNA_INTEGRITY_CHECKPOINT	-0.8651409	0.76086956	8.67E-01	1
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS	-0.8186998	0.76119405	9.13E-01	1
ROSS_AML_WITH_AML1_ETO_FUSION	-0.8809922	0.7615894	8.43E-01	1
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_12	-0.8892199	0.76282054	8.32E-01	1
REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS	-0.8259562	0.7637795	9.06E-01	1
GO_PROTEIN_KINASE_A_BINDING	-0.8376834	0.7644628	8.94E-01	1
TERAMOTO_OPN_TARGETS_CLUSTER_6	-0.7942579	0.76447874	9.22E-01	1

CHIN_BREAST_CANCER_COPY_NUMBER_UP	-0.7868152	0.76512456	9.28E-01	1
GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	-0.805913	0.7664671	9.18E-01	1
ZHAN_MULTIPLE_MYELOMA_HP_UP	-0.8317564	0.7707317	9.00E-01	1
MOOTHA_GLYCOLYSIS	-0.8008851	0.7708333	9.20E-01	1
GO_REGULATION_OF_ATPASE_ACTIVITY	-0.8600767	0.7719298	8.73E-01	1
GO_POSITIVE_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS	-0.8606357	0.7723577	8.74E-01	1
VILIMAS_NOTCH1_TARGETS_DN	-0.7898917	0.7733333	9.24E-01	1
GO_REGULATION_OF_HYDROGEN_PEROXIDE_INDUCED_CELL_DEATH	-0.7737773	0.7733333	9.38E-01	1
GO_POSITIVE_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	-0.7700993	0.7746479	9.40E-01	1
GO_CARDIAC_VENTRICLE_MORPHOGENESIS	-0.8665441	0.77472526	8.67E-01	1
HU_GENOTOXIN_ACTION_DIRECT_VS_INDIRECT_24HR	-0.8436702	0.7751196	8.89E-01	1
GO_CARBOXY_LYASE_ACTIVITY	-0.8086726	0.7762557	9.18E-01	1
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	-0.8595109	0.7763158	8.74E-01	1
GO_POSITIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	-0.7970719	0.77740866	9.21E-01	1
WIKMAN_ASBESTOS_LUNG_CANCER_UP	-0.7733496	0.7788779	9.38E-01	1
FERNANDEZ_BOUND_BY_MYC	-0.913893	0.7794118	8.00E-01	1
BIOCARTA_G2_PATHWAY	-0.8024378	0.7804878	9.18E-01	1
GO_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	-0.8249611	0.78099173	9.07E-01	1
GO_NUCLEAR_OUTER_MEMBRANE	-0.7649796	0.781362	9.41E-01	1
CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN	-0.7806634	0.7820069	9.30E-01	1
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	-0.8046392	0.78305084	9.18E-01	1
CHOI_ATL_CHRONIC_VS_ACUTE_DN	-0.7776275	0.78504676	9.34E-01	1
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	-0.7938229	0.7854406	9.22E-01	1
LANG_MYB_FAMILY_TARGETS	-0.8051737	0.78600824	9.18E-01	1

WANG_RESPONSE_TO_ANDROGEN_UP	-0.8153112	0.7867647	9.14E-01	1
GO_REGULATION_OF_HEART_MORPHOGENESIS	-0.7996212	0.7869416	9.20E-01	1
TOMIDA_METASTASIS_UP	-0.7770119	0.7883212	9.34E-01	1
CROMER_METASTASIS_UP	-0.865523	0.79113925	8.67E-01	1
GO_HISTONE_METHYLTRANSFERASE_ACTIVITY	-0.8184821	0.7916667	9.12E-01	1
MOOTHA_TCA	-0.7241259	0.79288024	9.56E-01	1
GAJATE_RESPONSE_TO_TRABECTEDIN_DN	-0.7524573	0.7937063	9.47E-01	1
GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	-0.8397824	0.7945946	8.92E-01	1
GO_CARDIAC_ATRIUM_DEVELOPMENT	-0.8007734	0.79577464	9.20E-01	1
GO_PROTEIN_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	-0.773277	0.79710144	9.37E-01	1
GO_POSITIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	-0.8499845	0.7987805	8.84E-01	1
GO_1_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	-0.7935411	0.7991453	9.21E-01	1
GO_INTRASPECIES_INTERACTION_BETWEEN_ORGANISMS	-0.7979684	0.8008658	9.21E-01	1
GO_GLUCOSAMINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	-0.7704676	0.8014184	9.40E-01	1
SHIPP_DLBCL_CURED_VS_FATAL_DN	-0.8075364	0.80172414	9.17E-01	1
REACTOME_APOPTOTIC_EXECUTION_PHASE	-0.808225	0.80225986	9.16E-01	1
BREDEMEYER_RAG_SIGNALING_VIA_ATM_NOT_VIA_NFKB_DN	-0.8106121	0.8028674	9.17E-01	1
ZHAN_MULTIPLE_MYELOMA_CD1_AND_CD2_UP	-0.8458896	0.8044693	8.88E-01	1
GO_NEGATIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	-0.7924258	0.80536914	9.22E-01	1
CAFFAREL_RESPONSE_TO_THC_UP	-0.7852768	0.80658436	9.28E-01	1
KEGG_TRYPTOPHAN_METABOLISM	-0.806407	0.8067633	9.18E-01	1
GO_THREONINE_TYPE_PEPTIDASE_ACTIVITY	-0.7638182	0.8074074	9.42E-01	1
IIZUKA_LIVER_CANCER_PROGRESSION_L0_L1_DN	-0.7573868	0.80921054	9.43E-01	1

YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17	-0.9173607	0.8095238	7.97E-01	1
GO_CHROMATIN_SILENCING_AT_RDNA	-0.7969824	0.8106996	9.20E-01	1
GO_PREASSEMBLY_OF_GPI_ANCHOR_IN_ER_MEMBRANE	-0.7492374	0.81333333	9.47E-01	1
GO_NUCLEAR_MATRIX	-0.8544538	0.8148148	8.79E-01	1
GO_POSITIVE_REGULATION_OF_TELOMERE_CAPPING	-0.7257748	0.8149351	9.59E-01	1
YANG_BREAST_CANCER_ESR1_UP	-0.7566019	0.81526107	9.43E-01	1
BOYLAN_MULTIPLE_MYELOMA_D_UP	-0.8346379	0.8154762	8.98E-01	1
GO_SUBSTANTIA_NIGRA_DEVELOPMENT	-0.8124504	0.8161435	9.16E-01	1
GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY_P53_CLASS_MEDIATOR	-0.7574559	0.8167939	9.44E-01	1
DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_DN	-0.8595024	0.81714284	8.73E-01	1
GO_STEROID_CATABOLIC_PROCESS	-0.7670477	0.81877023	9.41E-01	1
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS	-0.8082877	0.8199052	9.17E-01	1
GO_AXONAL_GROWTH_CONE	-0.7502575	0.82274246	9.48E-01	1
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	-0.7659631	0.8228347	9.41E-01	1
POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_DN	-0.8082469	0.8229167	9.17E-01	1
GO_POSITIVE_REGULATION_OF_DNA_BINDING	-0.7904769	0.8240741	9.24E-01	1
GO_MACROMOLECULE_METHYLATION	-0.8921526	0.82417583	8.30E-01	1
GO_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNALING_PATHWAY	-0.7183809	0.8245033	9.59E-01	1
GO_HEPARAN_SULFATE_PROTEOGLYCAN_BIOSYNTHETIC_PROCESS	-0.7618841	0.82481754	9.43E-01	1
HWANG_PROSTATE_CANCER_MARKERS	-0.7523205	0.8262712	9.47E-01	1
GO_PEPTIDYL_ASPARAGINE_MODIFICATION	-0.7962163	0.8262911	9.20E-01	1
GO_PYRIMIDINE_RIBONUCLEOSIDE_METABOLIC_PROCESS	-0.7605095	0.82733816	9.44E-01	1

BILANGES_SERUM_SENSITIVE_VIA_TSC2	-0.787223	0.82758623	9.28E-01	1
GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_I_PROMOTER	-0.8044558	0.8278689	9.18E-01	1
GO_MATING	-0.8042654	0.8286853	9.17E-01	1
GO_SOCIAL_BEHAVIOR	-0.7824577	0.82905984	9.30E-01	1
LU_AGING_BRAIN_DN	-0.8575985	0.82954544	8.75E-01	1
REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT	-0.7402564	0.83157897	9.51E-01	1
GO_2_OXOGLUTARATE_METABOLIC_PROCESS	-0.7604244	0.8333333	9.43E-01	1
GO_GABA_RECEPTOR_ACTIVITY	-0.7431499	0.8333333	9.50E-01	1
LEE_INTRATHYMIC_T_PROGENITOR	-0.7394155	0.8344827	9.51E-01	1
GO_CRANIAL_SKELETAL_SYSTEM_DEVELOPMENT	-0.8037892	0.83516484	9.18E-01	1
GO_NEURON_PROJECTION_MEMBRANE	-0.7616358	0.8367347	9.43E-01	1
GO_NUCLEAR_TRANSPORT	-0.9016092	0.84	8.18E-01	1
BOYAULT_LIVER_CANCER_SUBCLASS_G2	-0.7249384	0.84016395	9.58E-01	1
GO_NUCLEAR_ENVELOPE_ORGANIZATION	-0.8160899	0.8414634	9.14E-01	1
GO_ESTABLISHMENT_OF_MITOTIC_SPINDLE_ORIENTATION	-0.7179192	0.8414634	9.59E-01	1
BIOCARTA_CELLCYCLE_PATHWAY	-0.7663155	0.84210527	9.41E-01	1
PENG_GLUTAMINE_DEPRIVATION_UP	-0.7666885	0.8425926	9.41E-01	1
PARK_HSC_MARKERS	-0.7958894	0.84304935	9.20E-01	1
GO_NEGATIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION	-0.7720817	0.8436214	9.38E-01	1
REACTOME_G1_PHASE	-0.7680176	0.8468468	9.41E-01	1
GO_MEDIATOR_COMPLEX	-0.749785	0.8471761	9.47E-01	1
GO_PIGMENT_GRANULE_ORGANIZATION	-0.7114602	0.84829724	9.58E-01	1
GO_ORGAN_FORMATION	-0.7685899	0.84836066	9.40E-01	1
REACTOME_TIE2_SIGNALING	-0.7172365	0.84876543	9.57E-01	1
DARWICHE_SKIN_TUMOR_PROMOTER_DN	-0.8939577	0.8488372	8.26E-01	1
TERAO_AOX4_TARGETS_SKIN_UP	-0.7811093	0.8495575	9.30E-01	1
GO_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_CELL_DEATH	-0.7943916	0.85	9.22E-01	1

KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	-0.7631417	0.85020244	9.42E-01	1
REACTOME_REGULATORY_RNA_PATHWAYS	-0.7596868	0.8503401	9.43E-01	1
GO_AMINO_ACID_BINDING	-0.8342078	0.8518519	8.97E-01	1
CHEMELLO_SOLEUS_VS_EDL_MYOFIBERS_DN	-0.7079518	0.85303515	9.57E-01	1
GO_MITOCHONDRIAL_GENOME_MAINTENANCE	-0.7318118	0.8556701	9.57E-01	1
ENK_UV_RESPONSE_KERATINOCYTE_DN	-0.9171802	0.85714287	7.97E-01	1
GO_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	-0.8388466	0.85714287	8.93E-01	1
GO_REGULATION_OF_LONG_TERM_NEURONAL_SYNAPTIC_PLASTICITY	-0.7400788	0.85714287	9.51E-01	1
GROSS_ELK3_TARGETS_UP	-0.7426646	0.85877866	9.50E-01	1
GO_SULFUR_COMPOUND_CATABOLIC_PROCESS	-0.7580162	0.8596491	9.44E-01	1
HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_UP	-0.8769974	0.86021507	8.48E-01	1
WONG_PROTEASOME_GENE_MODULE	-0.7756536	0.861244	9.36E-01	1
GO_PROTEIN_K63_LINKED_DEUBIQUITINATION	-0.7175742	0.8615917	9.58E-01	1
GO_GLUTAMINE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	-0.7245157	0.86206895	9.56E-01	1
GO_ESTABLISHMENT_OF_LOCALIZATION_BY_MOVEMENT_ALONG_MICROTUBULE	-0.8193475	0.8652482	9.13E-01	1
GO_SYNAPSE_ASSEMBLY	-0.8057369	0.8652482	9.18E-01	1
GO_REGULATION_OF_CENTROSOME_DUPLICATION	-0.7421605	0.86538464	9.50E-01	1
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	-0.7592138	0.8656126	9.43E-01	1
GO_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	-0.7928028	0.8666667	9.22E-01	1
GO_NEGATIVE_REGULATION_OF_MRNA_METABOLIC_PROCESS	-0.7258114	0.8684211	9.59E-01	1
GO_ENERGY_COUPLED_PROTON_TRANSPORT_DOWN_ELECTROCHEMICAL_GRADIENT	-0.7487481	0.86868685	9.46E-01	1
GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	-0.8096399	0.8689655	9.18E-01	1
BROWNE_HCMV_INFECTION_18HR_UP	-0.8632621	0.8701299	8.70E-01	1

COLLIS_PRKDC_REGULATORS	-0.7127382	0.8703704	9.59E-01	1
REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR	-0.750653	0.87096775	9.48E-01	1
KARAKAS_TGFB1_SIGNALING	-0.6932972	0.87108016	9.62E-01	1
GO_LIVER_REGENERATION	-0.7229449	0.87205386	9.56E-01	1
GO_PROTEIN_K48_LINKED_DEUBIQUITINATION	-0.7097445	0.8731884	9.58E-01	1
BIOCARTA_VEGF_PATHWAY	-0.7158669	0.8736462	9.57E-01	1
GO_ARACHIDONIC_ACID_METABOLIC_PROCESS	-0.7231215	0.8745098	9.56E-01	1
GO_POSITIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	-0.7176077	0.8745387	9.59E-01	1
BILANGES_RAPAMYCIN_SENSITIVE_GENES	-0.7516158	0.875969	9.47E-01	1
ZHAN_EARLY_DIFFERENTIATION_GENES_DN	-0.745842	0.8765432	9.48E-01	1
HONRADO_BREAST_CANCER_BRCA1_VS_BRCA2	-0.7159293	0.8773585	9.57E-01	1
GO_PERICENTRIOLAR_MATERIAL	-0.7116375	0.87741935	9.59E-01	1
LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_DN	-0.7662879	0.8780488	9.41E-01	1
GO_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT	-0.7246986	0.8782288	9.57E-01	1
GO_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATION	-0.7568006	0.87903225	9.43E-01	1
GO_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	-0.8516398	0.88	8.81E-01	1
GO_PHOSPHOTRANSFERASE_ACTIVITY_PHOSPHATE_GROUP_AS_ACCEPTOR	-0.7440329	0.8803419	9.50E-01	1
GO_REGULATION_OF_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	-0.7974263	0.88095236	9.21E-01	1
GO_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	-0.7901519	0.8817734	9.24E-01	1
COLDREN_GEFITINIB_RESISTANCE_UP	-0.7864883	0.88268155	9.27E-01	1
KEGG_OOCYTE_MEIOSIS	-0.8187786	0.8833333	9.13E-01	1
GO_SULFOTRANSFERASE_ACTIVITY	-0.7692697	0.8833333	9.40E-01	1
GO_REGULATION_OF_HEAT_GENERATION	-0.681523	0.8833922	9.67E-01	1

GO_REGULATION_OF_MRNA_METABOLIC_PROCESS	-0.8112024	0.8851351	9.17E-01	1
PROVENZANI_METASTASIS_UP	-0.8530175	0.8875	8.82E-01	1
FERRANDO_LYL1_NEIGHBORS	-0.6536694	0.888535	9.77E-01	1
GO_NCRNA_CATABOLIC_PROCESS	-0.6941038	0.89	9.63E-01	1
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ONE_CARBON_GROUPS	-0.8405846	0.8913044	8.92E-01	1
JEON_SMAD6_TARGETS_DN	-0.657792	0.8913044	9.75E-01	1
GO_NEGATIVE_REGULATION_OF_ANION_TRANSPORT	-0.7305062	0.8921933	9.57E-01	1
GO_REGULATION_OF_SULFUR_METABOLIC_PROCESS	-0.708476	0.8923611	9.58E-01	1
GO_PROTEIN_IMPORT	-0.8380375	0.89361703	8.94E-01	1
HOLLMANN_APOPTOSIS_VIA_CD40_UP	-0.8590542	0.8947368	8.73E-01	1
GO_POSITIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	-0.6748395	0.8947368	9.67E-01	1
GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS	-0.7601572	0.8962264	9.43E-01	1
PID_DNA_PK_PATHWAY	-0.6256448	0.89666665	9.83E-01	1
SYED_ESTRADIOL_RESPONSE	-0.6784751	0.8980263	9.65E-01	1
GO_RESPONSE_TO_LITHIUM_ION	-0.698716	0.900369	9.62E-01	1
GO_POSITIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	-0.7403895	0.90338165	9.52E-01	1
GO_MITOTIC_CYTOKINESIS	-0.7205812	0.90384614	9.57E-01	1
GO_CHROMATIN_SILENCING	-0.7820889	0.9041916	9.30E-01	1
GO_MITOTIC_DNA_INTEGRITY_CHECKPOINT	-0.8006574	0.9044586	9.19E-01	1
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GAMMA_SUBUNITS	-0.6838661	0.90612245	9.67E-01	1
BERNARD_PPAPDC1B_TARGETS_UP	-0.7263894	0.9068826	9.60E-01	1
ONDER_CDH1_TARGETS_1_DN	-0.7987309	0.90697676	9.20E-01	1
GO_POSITIVE_REGULATION_OF_CYTOKINESIS	-0.7136542	0.90816325	9.58E-01	1
GO_REGULATION_OF_COENZYME_METABOLIC_PROCESS	-0.7388401	0.90909094	9.51E-01	1
GO_CYTOKINE_SECRETION	-0.7100778	0.90909094	9.58E-01	1
GO_MODULATION_OF_TRANSCRIPTION_IN_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	-0.6856753	0.9096573	9.66E-01	1
NAKAJIMA_MAST_CELL	-0.7396715	0.9116279	9.51E-01	1

PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_DN	-0.6830887	0.9166667	9.67E-01	1
GO_REGULATION_OF_ORGAN_FORMATION	-0.7093431	0.91698116	9.58E-01	1
GO_DENDRITIC_SPINE_ORGANIZATION	-0.6516417	0.9179811	9.77E-01	1
MARTINEZ_RESPONSE_TO_TRABECTEDIN	-0.7124003	0.9182692	9.58E-01	1
GO_PROTEASOME_CORE_COMPLEX	-0.708509	0.91851854	9.58E-01	1
JOHNSTONE_PARVB_TARGETS_2_DN	-0.9025885	0.9189189	8.17E-01	1
GO_POSITIVE_REGULATION_OF_PROTEIN_ACETYLATION	-0.6987239	0.920354	9.62E-01	1
GO_POSITIVE_REGULATION_OF_COAGULATION	-0.6356559	0.9204152	9.82E-01	1
BIOCARTA_EIF4_PATHWAY	-0.6604916	0.92142856	9.74E-01	1
BROWNE_HCMV_INFECTION_10HR_DN	-0.7251856	0.9230769	9.58E-01	1
GO_HISTONE_H3_K4_METHYLATION	-0.7039411	0.92779785	9.60E-01	1
KAYO_AGING_MUSCLE_DN	-0.81536	0.928	9.15E-01	1
PECE_MAMMARY_STEM_CELL_DN	-0.8085508	0.93043476	9.17E-01	1
GO_PROTEIN_METHYLTRANSFERASE_ACTIVITY	-0.7491784	0.9310345	9.46E-01	1
FORTSCHEGGER_PHF8_TARGETS_UP	-0.8452629	0.9322034	8.89E-01	1
JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER	-0.6954978	0.9328358	9.63E-01	1
GO_NEGATIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	-0.6495369	0.93421054	9.77E-01	1
GO_PROTEIN_HETEROTETRAMERIZATION	-0.6978515	0.9351145	9.62E-01	1
GO_TRANSCRIPTION_ELONGATION_FACTOR_COMPLEX	-0.6918101	0.9391304	9.63E-01	1
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_DN	-0.6872164	0.9402391	9.65E-01	1
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	-0.7527676	0.9402985	9.47E-01	1
GO_ALPHA_AMINO_ACID_BIOSYNTHETIC_PROCESS	-0.7237854	0.94219655	9.56E-01	1
GO_POSITIVE_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	-0.6311166	0.9433333	9.83E-01	1

REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	-0.7254921	0.94358975	9.58E-01	1
GO_SEX_CHROMOSOME	-0.6517413	0.94716984	9.77E-01	1
GO_ORGANELLE_ASSEMBLY	-0.8569128	0.94736844	8.75E-01	1
HALLMARK_MTORC1_SIGNALING	-0.8443888	0.94827586	8.89E-01	1
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_OUTER_MEMBRANE	-0.6472899	0.9498328	9.78E-01	1
GO_CHROMATIN	-0.816376	0.95	9.14E-01	1
GO_NEUROTRANSMITTER_METABOLIC_PROCESS	-0.6238766	0.9501661	9.82E-01	1
LIAO_HAVE_SOX4_BINDING_SITES	-0.690959	0.95022625	9.63E-01	1
REACTOME_SIGNALING_BY_WNT	-0.7502098	0.95027626	9.47E-01	1
GO_REGULATION_OF_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	-0.6268792	0.9506579	9.84E-01	1
NGO_MALIGNANT_GLIOMA_1P_LOH	-0.6171615	0.95076925	9.84E-01	1
WENDT_COHESIN_TARGETS_UP	-0.6803105	0.9513109	9.67E-01	1
JIANG_VHL_TARGETS	-0.717501	0.9516129	9.58E-01	1
PID_E2F_PATHWAY	-0.7310048	0.9520958	9.57E-01	1
RAMASWAMY_METASTASIS_UP	-0.7299231	0.95238096	9.57E-01	1
GO_POSITIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	-0.6423314	0.95289856	9.79E-01	1
MOOTHA_FFA_OXYDATION	-0.5873634	0.9530686	9.88E-01	1
SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX4_DN	-0.6802801	0.95327103	9.66E-01	1
GO_MICROTUBULE_NUCLEATION	-0.5965562	0.9533333	9.87E-01	1
LEE_RECENT_THYMIC_EMIGRANT	-0.781205	0.9558824	9.31E-01	1
HOEBEKE_LYMPHOID_STEM_CELL_DN	-0.7262875	0.9559748	9.59E-01	1
GO_SERINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	-0.6682729	0.95614034	9.71E-01	1
GO_LYASE_ACTIVITY	-0.7970607	0.95789474	9.21E-01	1
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	-0.680288	0.9589041	9.66E-01	1
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	-0.7030925	0.9593023	9.60E-01	1
REACTOME_PKB_MEDIATED_EVENTS	-0.5821237	0.95970696	9.88E-01	1
GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	-0.7996321	0.96	9.20E-01	1

GO_PROTEIN_TRANSPORTER_ACTIVITY	-0.7337873	0.96	9.56E-01	1
GO_CYCLIN_DEPENDENT_PROTEIN_SERINE_THREONINE_KINASE_REGULATOR_ACTIVITY	-0.62626	0.96113074	9.83E-01	1
VANTVEER_BREAST_CANCER_METASTASIS_UP	-0.6997255	0.9622642	9.62E-01	1
WANG_IMMORTALIZED_BY_HOXA9_AND_MEIS1_DN	-0.627444	0.96245736	9.84E-01	1
ZUCCHI_METASTASIS_UP	-0.6448492	0.9626168	9.79E-01	1
GO_NUCLEOBASE_CONTAINING_COMPOUND_KINASE_ACTIVITY	-0.6665353	0.96313363	9.72E-01	1
LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS	-0.6097557	0.9644013	9.84E-01	1
BRIDEAU_IMPRINTED_GENES	-0.7067962	0.96666664	9.58E-01	1
RASHI_RESPONSE_TO_IONIZING_RADIATION_4	-0.6797125	0.96713614	9.66E-01	1
PID_INSULIN_GLUCOSE_PATHWAY	-0.5959137	0.9699248	9.86E-01	1
GO_PHOSPHATIDYLINOSITOL_DEPHOSPHORYLATION	-0.5519799	0.9701987	9.90E-01	1
GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_DN	-0.621331	0.97083336	9.83E-01	1
JAIN_NFKB_SIGNALING	-0.711631	0.97282606	9.58E-01	1
GO_NUCLEOTIDYLTRANSFERASE_ACTIVITY	-0.7248815	0.973913	9.57E-01	1
LI_DCP2_BOUND_MRNA	-0.6792536	0.9747899	9.66E-01	1
GO_LYMPH_VESSEL_DEVELOPMENT	-0.6135831	0.97651005	9.84E-01	1
GO_PHOSPHOLIPID_DEPHOSPHORYLATION	-0.5696701	0.977492	9.89E-01	1
GO_REGULATION_OF_TRANSLATIONAL_INITIATION	-0.682565	0.9777778	9.66E-01	1
GO_N_METHYLTRANSFERASE_ACTIVITY	-0.6239571	0.9798995	9.83E-01	1
GO_ORGANELLE_ENVELOPE_LUMEN	-0.7174613	0.98013246	9.57E-01	1
GO_POSITIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	-0.6007378	0.9855596	9.86E-01	1
HASLINGER_B_CLL_WITH_CHROMOSOME_12_TRISOMY	-0.5722867	0.9858156	9.89E-01	1
GO_NEGATIVE_REGULATION_OF_PROTEIN_ACETYLATION	-0.514703	0.98657715	9.91E-01	1
GO_PEPTIDE_N_ACETYLTRANSFERASE_ACTIVITY	-0.6127154	0.9872881	9.83E-01	1
DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_UP	-0.4943273	0.9880952	9.91E-01	1

GO_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	-0.7478449	0.9882353	9.47E-01	1
GO_POSITIVE_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	-0.5616425	0.9894737	9.90E-01	1
HEDENFALK_BREAST_CANCER_BRCA1_VS_BRCA2	-0.7257185	0.9895833	9.58E-01	1
GO_MANNOSYLTRANSFERASE_ACTIVITY	-0.5574479	0.989899	9.89E-01	1
GO_PIGMENT_GRANULE_LOCALIZATION	-0.4929719	0.99006623	9.91E-01	1
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	-0.5122792	0.990099	9.91E-01	1
BIOCARTA_MTOR_PATHWAY	-0.5157656	0.9919028	9.92E-01	1
GO_ATP_BIOSYNTHETIC_PROCESS	-0.5054529	0.99245286	9.91E-01	1
GO_ENHANCER_BINDING	-0.694755	0.9932432	9.63E-01	1
GO_REGULATION_OF_RESPIRATORY_GASEOUS_EXCHANGE	-0.4735784	0.99352753	9.91E-01	1
REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI	-0.4896782	0.9938462	9.91E-01	1
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	-0.61326	0.9942857	9.84E-01	1
KEGG_N_GLYCAN_BIOSYNTHESIS	-0.5797238	0.9950739	9.88E-01	1
REACTOME_GLUCOSE_TRANSPORT	-0.5589915	0.9955157	9.90E-01	1
GO_RIBONUCLEOTIDE_CATABOLIC_PROCESS	-0.5162023	0.99596775	9.92E-01	1
GO_SAGA_TYPE_COMPLEX	-0.4444679	0.9964158	9.91E-01	1
BENPORATH_MYC_MAX_TARGETS	-0.8998002	1	8.19E-01	1
OSMAN_BLADDER_CANCER_UP	-0.8657439	1	8.67E-01	1
GO_CHROMATIN_MODIFICATION	-0.8601385	1	8.73E-01	1
GO_MITOCHONDRIAL_ENVELOPE	-0.848324	1	8.85E-01	1
GO_GLYCOSYL_COMPOUND_METABOLIC_PROCESS	-0.8412582	1	8.91E-01	1
GRADE_COLON_CANCER_UP	-0.8390588	1	8.93E-01	1
IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR	-0.8347793	1	8.98E-01	1
ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP	-0.8033887	1	9.18E-01	1

GO_POSTTRANSCRIPTIONAL_REGULATION_OF_GENE_EXPRESSION	-0.804615	1	9.18E-01	1
GO_NUCLEOBASE_CONTAINING_COMPOUND_TRANSPORT	-0.8025329	1	9.18E-01	1
ROME_INSULIN_TARGETS_IN_MUSCLE_UP	-0.7655283	1	9.41E-01	1
ALONSO_METASTASIS_UP	-0.7595948	1	9.43E-01	1
GO_NUCLEOPLASM_PART	-0.7495061	1	9.47E-01	1
GO_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	-0.7326033	1	9.56E-01	1
GO_TRANSFERASE_COMPLEX	-0.6935409	1	9.63E-01	1
DAZARD_UV_RESPONSE_CLUSTER_G6	-0.6961657	1	9.63E-01	1
GO_REGULATION_OF_LIGASE_ACTIVITY	-0.6632208	1	9.73E-01	1
PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP	-0.6245539	1	9.83E-01	1
GO_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	-0.6321903	1	9.83E-01	1
GO_S_ADENOSYLMETHIONINE_DEPENDENT_METHYLTRANSFERASE_ACTIVITY	-0.6162726	1	9.84E-01	1
GO_REGULATION_OF_CYTOKINESIS	-0.5955331	1	9.86E-01	1
REACTOME_ER_PHAGOSOME_PATHWAY	-0.5870922	1	9.87E-01	1
GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	-0.5605612	1	9.90E-01	1
GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_I_PROMOTER	-0.3727115	1	9.90E-01	1
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	-0.3881038	1	9.91E-01	1
HALLMARK_DNA_REPAIR	-0.5368891	1	9.91E-01	1
REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS	-0.4113057	1	9.91E-01	1
REACTOME_REGULATION_OF_APOPTOSIS	-0.5380183	1	9.91E-01	1
GO_PROTEASOME_COMPLEX	-0.5216593	1	9.92E-01	1
DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP			1.00E+00	0
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP			1.00E+00	0
DODD_NASOPHARYNGEAL_CARCINOMA_DN			1.00E+00	0

GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN			1.00E+00	0
PUJANA_BRCA1_PCC_NETWORK			1.00E+00	0
PUJANA_ATM_PCC_NETWORK			1.00E+00	0
NUYTTEN_EZH2_TARGETS_DN			1.00E+00	0
BLALOCK_ALZHEIMERS_DISEASE_DN			1.00E+00	0
KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN			1.00E+00	0
DANG_BOUND_BY_MYC			1.00E+00	0
PILON_KLF1_TARGETS_DN			1.00E+00	0
GO_CELL_CYCLE			1.00E+00	0
GO_ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS			1.00E+00	0
GO_CELL_CYCLE_PROCESS			1.00E+00	0
GO_MITOCHONDRION			1.00E+00	0
GO_ENVELOPE			1.00E+00	0
GO_POLY_A_RNA_BINDING			1.00E+00	0
GO_RNA_BINDING			1.00E+00	0