

Supplementary Table 1A

C2-Canonical Pathway

LC vs HD

| NAME | SIZE | NES | NOM p-val | FDR q-val |
|---|------|--------|-----------|-----------|
| KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM | 37 | 2.087 | 0.000 | 0.004 |
| REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHARIDE_LLO_AND_TRANSFER_TO_A_NASCENT_PROTEIN | 26 | 2.031 | 0.000 | 0.007 |
| REACTOME_PURINE_METABOLISM | 23 | 1.980 | 0.001 | 0.009 |
| REACTOME_METABOLISM_OF_NUCLEOTIDES | 53 | 1.992 | 0.000 | 0.009 |
| REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT | 120 | 1.944 | 0.000 | 0.010 |
| REACTOME_GLUCOSE_METABOLISM | 52 | 1.935 | 0.000 | 0.010 |
| KEGG_PENTOSE_PHOSPHATE_PATHWAY | 21 | 1.951 | 0.000 | 0.010 |
| PID_INTEGRIN3_PATHWAY | 16 | -2.279 | 0.000 | 0.011 |
| REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_ | 88 | 1.955 | 0.000 | 0.012 |
| KEGG_OXIDATIVE_PHOSPHORYLATION | 108 | 1.914 | 0.000 | 0.012 |
| REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES | 120 | 1.903 | 0.000 | 0.014 |
| REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C | 54 | 1.876 | 0.000 | 0.015 |
| KEGG_ALZHEIMERS_DISEASE | 132 | 1.872 | 0.000 | 0.015 |
| KEGG_PEROXISOME | 57 | 1.878 | 0.000 | 0.016 |
| REACTOME_GLUCCONEOGENESIS | 24 | 1.863 | 0.000 | 0.016 |
| REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING | 15 | 1.878 | 0.003 | 0.017 |
| KEGG_PYRIMIDINE_METABOLISM | 79 | 1.857 | 0.000 | 0.017 |
| KEGG_FRUCTOSE_AND_MANNANOSE_METABOLISM | 26 | 1.851 | 0.001 | 0.018 |
| REACTOME_SCSK2_MEDIATED_DEGRADATION_OF_P27_P21 | 49 | 1.846 | 0.000 | 0.018 |
| REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1 | 46 | 1.879 | 0.001 | 0.018 |
| REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION | 114 | 1.841 | 0.000 | 0.019 |
| REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1 | 58 | 1.818 | 0.001 | 0.019 |
| KEGG_PURINE_METABOLISM | 102 | 1.827 | 0.000 | 0.019 |
| REACTOME_DARPP_32_EVENTS | 21 | 1.823 | 0.000 | 0.020 |
| REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE | 50 | 1.819 | 0.000 | 0.020 |
| KEGG_PARKINSONS_DISEASE | 105 | 1.828 | 0.000 | 0.020 |
| REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS | 50 | 1.805 | 0.002 | 0.020 |
| REACTOME_RESPIRATORY_ELECTRON_TRANSPORT | 71 | 1.807 | 0.000 | 0.020 |
| REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT | 44 | 1.829 | 0.001 | 0.021 |
| REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX | 46 | 1.808 | 0.000 | 0.021 |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES | 18 | -2.149 | 0.000 | 0.022 |
| KEGG_N_GLYCAN_BIOSYNTHESIS | 40 | 1.799 | 0.000 | 0.022 |
| KEGG_PROTEASOME | 41 | 1.787 | 0.000 | 0.022 |
| KEGG_HUNTINGTONS_DISEASE | 145 | 1.788 | 0.000 | 0.022 |
| REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT | 46 | 1.790 | 0.000 | 0.023 |
| REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC | 45 | 1.792 | 0.000 | 0.023 |
| REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM | 16 | 1.779 | 0.006 | 0.024 |
| BIOCARTA_ACTINY_PATHWAY | 15 | 1.770 | 0.001 | 0.026 |
| REACTOME_CELL_CYCLE_CHECKPOINTS | 89 | 1.756 | 0.000 | 0.029 |
| REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION | 171 | 1.758 | 0.000 | 0.030 |
| REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES | 43 | 1.756 | 0.001 | 0.030 |
| KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION | 38 | 1.750 | 0.001 | 0.031 |
| REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_ | 57 | 1.746 | 0.001 | 0.031 |
| REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6 | 44 | 1.737 | 0.002 | 0.034 |
| KEGG_GLYCOLYSIS_GLUCCONEOGENESIS | 40 | 1.730 | 0.001 | 0.035 |
| REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G | 48 | 1.731 | 0.001 | 0.035 |
| REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION | 65 | 1.732 | 0.002 | 0.035 |
| REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS | 60 | 1.726 | 0.000 | 0.036 |
| REACTOME_G1_S_TRANSITION | 88 | 1.722 | 0.000 | 0.037 |
| REACTOME_TRNA_AMINOACYLATION | 36 | 1.720 | 0.000 | 0.037 |
| REACTOME_S_PHASE | 86 | 1.723 | 0.000 | 0.037 |
| KEGG_PROPANOATE_METABOLISM | 26 | 1.716 | 0.002 | 0.038 |
| REACTOME_SULFUR_AMINO_ACID_METABOLISM | 17 | 1.710 | 0.007 | 0.040 |
| REACTOME_REGULATION_OF_APOPTOSIS | 51 | 1.706 | 0.003 | 0.041 |
| KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS | 19 | 1.703 | 0.003 | 0.042 |
| REACTOME_MITOTIC_G1_G1_S_PHASES | 107 | 1.698 | 0.000 | 0.044 |
| REACTOME_M_G1_TRANSITION | 67 | 1.689 | 0.000 | 0.048 |
| BIOCARTA_IL2_PATHWAY | 19 | 1.681 | 0.014 | 0.051 |
| REACTOME_SYNTHESIS_OF_DNA | 73 | 1.671 | 0.003 | 0.054 |
| REACTOME_ORC1_REMOVAL_FROM_CHROMATIN | 54 | 1.669 | 0.002 | 0.054 |
| REACTOME_PYRIMIDINE_METABOLISM | 16 | 1.668 | 0.007 | 0.054 |
| REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1 | 48 | 1.671 | 0.001 | 0.055 |
| REACTOME_SIGNALING_BY_WNT | 62 | 1.672 | 0.001 | 0.056 |
| REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION | 203 | 1.664 | 0.000 | 0.056 |

| | | | | |
|---|-----|--------|-------|-------|
| REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_DO | 49 | 1.659 | 0.001 | 0.057 |
| REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE | 67 | 1.654 | 0.002 | 0.058 |
| REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX | 55 | 1.654 | 0.003 | 0.059 |
| BIOCARTA_PGC1A_PATHWAY | 15 | 1.651 | 0.011 | 0.059 |
| KEGG_AMINOACYL_TRNA_BIOSYNTHESIS | 36 | 1.654 | 0.002 | 0.060 |
| BIOCARTA_MPR_PATHWAY | 22 | 1.646 | 0.004 | 0.062 |
| REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS | 20 | 1.642 | 0.009 | 0.063 |
| REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS | 17 | 1.642 | 0.014 | 0.064 |
| REACTOME_GLYCOSPHINGOLIPID_METABOLISM | 22 | 1.626 | 0.011 | 0.072 |
| KEGG_PYRUVATE_METABOLISM | 30 | 1.624 | 0.011 | 0.073 |
| REACTOME_DOUBLE_STRAND_BREAK_REPAIR | 18 | 1.626 | 0.009 | 0.073 |
| REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE | 19 | 1.615 | 0.020 | 0.077 |
| REACTOME_DNA_REPAIR | 90 | 1.616 | 0.002 | 0.078 |
| REACTOME_OLFACTORY_SIGNALING_PATHWAY | 16 | -1.973 | 0.000 | 0.084 |
| KEGG_TYROSINE_METABOLISM | 19 | 1.603 | 0.023 | 0.085 |
| KEGG_CYSTEINE_AND_METHIONINE_METABOLISM | 24 | 1.606 | 0.005 | 0.085 |
| REACTOME_METABOLISM_OF_PROTEINS | 337 | 1.604 | 0.000 | 0.086 |
| REACTOME_OPIOID_SIGNALING | 50 | 1.588 | 0.006 | 0.095 |
| BIOCARTA_BCR_PATHWAY | 30 | 1.589 | 0.010 | 0.096 |
| ST_TUMOR_NECROSIS_FACTOR_PATHWAY | 27 | -1.923 | 0.011 | 0.100 |
| KEGG_GALACTOSE_METABOLISM | 19 | 1.577 | 0.024 | 0.102 |
| REACTOME_LAGGING_STRAND_SYNTHESIS | 17 | 1.577 | 0.022 | 0.103 |
| REACTOME_PHASE_II_CONJUGATION | 28 | 1.578 | 0.011 | 0.104 |
| REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER | 24 | 1.571 | 0.016 | 0.108 |
| REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHOGENESIS | 24 | 1.566 | 0.024 | 0.111 |
| REACTOME_ERK_MAPK_TARGETS | 19 | 1.564 | 0.022 | 0.112 |
| REACTOME_G1_PHASE | 31 | 1.561 | 0.017 | 0.113 |
| KEGG_STARCH_AND_SUCROSE_METABOLISM | 18 | 1.553 | 0.025 | 0.114 |
| REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION | 17 | 1.561 | 0.031 | 0.114 |
| KEGG_GLUTATHIONE_METABOLISM | 31 | 1.558 | 0.015 | 0.114 |
| REACTOME_METABOLISM_OF_CARBOHYDRATES | 148 | 1.552 | 0.001 | 0.115 |
| REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION | 20 | 1.557 | 0.023 | 0.115 |
| BIOCARTA_G1_PATHWAY | 21 | 1.554 | 0.016 | 0.115 |
| PID_PS1_PATHWAY | 34 | 1.555 | 0.018 | 0.115 |
| REACTOME_LYSOSOME_VESICLE_BIOGENESIS | 19 | 1.550 | 0.018 | 0.116 |
| REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS | 21 | 1.544 | 0.025 | 0.121 |
| REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY | 16 | 1.536 | 0.030 | 0.129 |
| REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES | 15 | 1.528 | 0.034 | 0.137 |
| BIOCARTA_NDKDYNAMIN_PATHWAY | 16 | 1.526 | 0.027 | 0.139 |
| KEGG_NOTCH_SIGNALING_PATHWAY | 34 | 1.521 | 0.026 | 0.140 |
| PID_FOXM1_PATHWAY | 24 | 1.521 | 0.030 | 0.142 |
| REACTOME_PEROXISOMAL_LIPID_METABOLISM | 16 | 1.519 | 0.039 | 0.142 |
| PID_ALK1_PATHWAY | 16 | 1.522 | 0.033 | 0.143 |
| REACTOME_INTERFERON_ALPHA_BETA_SIGNALING | 46 | 1.510 | 0.018 | 0.153 |
| KEGG_CITRATE_CYCLE_TCA_CYCLE | 27 | 1.507 | 0.037 | 0.156 |
| REACTOME_BASE_EXCISION_REPAIR | 18 | 1.505 | 0.029 | 0.157 |
| REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_Glutamate_BINDING | 18 | 1.498 | 0.043 | 0.165 |
| NABA_MATRISOME | 285 | -1.761 | 0.000 | 0.166 |
| ST_ADRENERGIC | 20 | -1.774 | 0.010 | 0.174 |
| REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY | 17 | -1.611 | 0.014 | 0.174 |
| PID_INTEGRIN1_PATHWAY | 27 | -1.616 | 0.016 | 0.176 |
| BIOCARTA_CCR3_PATHWAY | 15 | 1.488 | 0.040 | 0.178 |
| NABA_BASEMENT_MEMBRANES | 15 | -1.641 | 0.017 | 0.179 |
| REACTOME_APOPTOTIC_EXECUTION_PHASE | 35 | -1.698 | 0.000 | 0.180 |
| KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM | 20 | 1.483 | 0.049 | 0.184 |
| NABA_CORE_MATRISOME | 71 | -1.626 | 0.000 | 0.185 |
| BIOCARTA_TNFR2_PATHWAY | 16 | -1.616 | 0.041 | 0.186 |
| PID_CD40_PATHWAY | 23 | -1.705 | 0.016 | 0.189 |
| REACTOME_DNA_STRAND_ELONGATION | 25 | 1.478 | 0.048 | 0.190 |
| BIOCARTA_P53HYPOXIA_PATHWAY | 19 | -1.641 | 0.014 | 0.191 |
| KEGG_RNA_DEGRADATION | 52 | 1.476 | 0.032 | 0.191 |
| PID_FRA_PATHWAY | 20 | -1.651 | 0.019 | 0.191 |
| NABA_SECRETED_FACTORS | 88 | -1.718 | 0.000 | 0.193 |
| KEGG_RNA_POLYMERASE | 27 | 1.474 | 0.047 | 0.193 |
| NABA_ECM_AFFILIATED | 56 | -1.780 | 0.000 | 0.196 |
| REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE | 36 | 1.470 | 0.043 | 0.197 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 101 | -1.586 | 0.000 | 0.197 |
| PID_TCTP_PATHWAY | 30 | -1.573 | 0.031 | 0.205 |
| NABA_ECM_GLYCOPROTEINS | 50 | -1.664 | 0.009 | 0.205 |
| REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS | 30 | -1.652 | 0.000 | 0.206 |
| KEGG_ECM_RECEPTOR_INTERACTION | 31 | -1.794 | 0.006 | 0.210 |

| | | | | |
|--|-----|--------|-------|-------|
| BIOCARTA_TID_PATHWAY | 15 | 1.458 | 0.066 | 0.216 |
| REACTOME_RNA_POL_III_TRANSCRIPTION_TERMINATION | 16 | 1.453 | 0.060 | 0.220 |
| BIOCARTA_IL1R_PATHWAY | 26 | -1.551 | 0.018 | 0.222 |
| REACTOME_RNA_POL_III_CHAIN_ELONGATION | 15 | 1.454 | 0.054 | 0.222 |
| BIOCARTA_AT1R_PATHWAY | 26 | 1.453 | 0.041 | 0.222 |
| REACTOME_GLOBAL_GENOMIC_NER_GG_NER | 27 | 1.448 | 0.050 | 0.223 |
| PID_TCR_CALCIIUM_PATHWAY | 20 | 1.449 | 0.049 | 0.224 |
| REACTOME_EXTENSION_OF_TELOMERES | 21 | 1.448 | 0.050 | 0.225 |
| REACTOME_IL_2_SIGNALING | 30 | 1.444 | 0.040 | 0.228 |
| REACTOME_SPHINGOLIPID_METABOLISM | 38 | 1.438 | 0.046 | 0.234 |
| REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA | 19 | 1.439 | 0.058 | 0.235 |
| REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS | 58 | 1.438 | 0.033 | 0.236 |
| NABA_MATRISOME_ASSOCIATED | 214 | -1.531 | 0.000 | 0.241 |
| REACTOME_ER_PHAGOSOME_PATHWAY | 57 | 1.429 | 0.040 | 0.248 |
| REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION | 22 | 1.428 | 0.054 | 0.248 |

HCC vs HD

| NAME | SIZE | NES | NOM p-val | FDR q-val |
|--|------|--------|-----------|-----------|
| KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM | 37 | 2.087 | 0.000 | 0.004 |
| REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHARIDE_ILLO_AND_TRANSFER_TO_A_NASCENT_PROTEIN | 26 | 2.031 | 0.000 | 0.007 |
| REACTOME_PURINE_METABOLISM | 23 | 1.980 | 0.001 | 0.009 |
| REACTOME_METABOLISM_OF_NUCLEOTIDES | 53 | 1.992 | 0.000 | 0.009 |
| REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT | 120 | 1.944 | 0.000 | 0.010 |
| REACTOME_GLUCOSE_METABOLISM | 52 | 1.935 | 0.000 | 0.010 |
| KEGG_PENTOSE_PHOSPHATE_PATHWAY | 21 | 1.951 | 0.000 | 0.010 |
| PID_INTEGRIN3_PATHWAY | 16 | -2.279 | 0.000 | 0.011 |
| REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS | 88 | 1.955 | 0.000 | 0.012 |
| KEGG_OXIDATIVE_PHOSPHORYLATION | 108 | 1.914 | 0.000 | 0.012 |
| REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES | 120 | 1.903 | 0.000 | 0.014 |
| REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C | 54 | 1.876 | 0.000 | 0.015 |
| KEGG_ALZHEIMERS_DISEASE | 132 | 1.872 | 0.000 | 0.015 |
| KEGG_PEROXISOME | 57 | 1.878 | 0.000 | 0.016 |
| REACTOME_GLUCCONEOGENESIS | 24 | 1.863 | 0.000 | 0.016 |
| REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING | 15 | 1.878 | 0.003 | 0.017 |
| KEGG_PYRIMIDINE_METABOLISM | 79 | 1.857 | 0.000 | 0.017 |
| KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM | 26 | 1.851 | 0.001 | 0.018 |
| REACTOME_SCF5KP2_MEDIATED_DEGRADATION_OF_P27_P21 | 49 | 1.846 | 0.000 | 0.018 |
| REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1 | 46 | 1.879 | 0.001 | 0.018 |
| REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION | 114 | 1.841 | 0.000 | 0.019 |
| REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1 | 58 | 1.818 | 0.001 | 0.019 |
| KEGG_PURINE_METABOLISM | 102 | 1.827 | 0.000 | 0.019 |
| REACTOME_DARPP_32_EVENTS | 21 | 1.823 | 0.000 | 0.020 |
| REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE | 50 | 1.819 | 0.000 | 0.020 |
| KEGG_PARKINSONS_DISEASE | 105 | 1.828 | 0.000 | 0.020 |
| REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS | 50 | 1.805 | 0.002 | 0.020 |
| REACTOME_RESPIRATORY_ELECTRON_TRANSPORT | 71 | 1.807 | 0.000 | 0.020 |
| REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT | 44 | 1.829 | 0.001 | 0.021 |
| REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX | 46 | 1.808 | 0.000 | 0.021 |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES | 18 | -2.149 | 0.000 | 0.022 |
| KEGG_N_GLYCAN_BIOSYNTHESIS | 40 | 1.799 | 0.000 | 0.022 |
| KEGG_PROTEASOME | 41 | 1.787 | 0.000 | 0.022 |
| KEGG_HUNTINGTONS_DISEASE | 145 | 1.788 | 0.000 | 0.022 |
| REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT | 46 | 1.790 | 0.000 | 0.023 |
| REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC | 45 | 1.792 | 0.000 | 0.023 |
| REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM | 16 | 1.779 | 0.006 | 0.024 |
| BIOCARTA_ACTINY_PATHWAY | 15 | 1.770 | 0.001 | 0.026 |
| REACTOME_CELL_CYCLE_CHECKPOINTS | 89 | 1.756 | 0.000 | 0.029 |
| REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION | 171 | 1.758 | 0.000 | 0.030 |
| REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES | 43 | 1.756 | 0.001 | 0.030 |
| KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION | 38 | 1.750 | 0.001 | 0.031 |
| REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION | 57 | 1.746 | 0.001 | 0.031 |
| REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6 | 44 | 1.737 | 0.002 | 0.034 |
| KEGG_GLYCOLYSIS_GLUCCONEOGENESIS | 40 | 1.730 | 0.001 | 0.035 |
| REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G | 48 | 1.731 | 0.001 | 0.035 |
| REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION | 65 | 1.732 | 0.002 | 0.035 |
| REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS | 60 | 1.726 | 0.000 | 0.036 |

| | | | | |
|---|-----|--------|-------|-------|
| REACTOME_G1_S_TRANSITION | 88 | 1.722 | 0.000 | 0.037 |
| REACTOME_TRNA_AMINOACYLATION | 36 | 1.720 | 0.000 | 0.037 |
| REACTOME_S_PHASE | 86 | 1.723 | 0.000 | 0.037 |
| KEGG_PROPANOATE_METABOLISM | 26 | 1.716 | 0.002 | 0.038 |
| REACTOME_SULFUR_AMINO_ACID_METABOLISM | 17 | 1.710 | 0.007 | 0.040 |
| REACTOME_REGULATION_OF_APOPTOSIS | 51 | 1.706 | 0.003 | 0.041 |
| KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS | 19 | 1.703 | 0.003 | 0.042 |
| REACTOME_MITOTIC_G1_G1_S_PHASES | 107 | 1.698 | 0.000 | 0.044 |
| REACTOME_M_G1_TRANSITION | 67 | 1.689 | 0.000 | 0.048 |
| BIOCARTA_IL2_PATHWAY | 19 | 1.681 | 0.014 | 0.051 |
| REACTOME_SYNTHESIS_OF_DNA | 73 | 1.671 | 0.003 | 0.054 |
| REACTOME_ORC1_REMOVAL_FROM_CHROMATIN | 54 | 1.669 | 0.002 | 0.054 |
| REACTOME_PYRIMIDINE_METABOLISM | 16 | 1.668 | 0.007 | 0.054 |
| REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1 | 48 | 1.671 | 0.001 | 0.055 |
| REACTOME_SIGNALING_BY_WNT | 62 | 1.672 | 0.001 | 0.056 |
| REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION | 203 | 1.664 | 0.000 | 0.056 |
| REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_DO | 49 | 1.659 | 0.001 | 0.057 |
| REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE | 67 | 1.654 | 0.002 | 0.058 |
| REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX | 55 | 1.654 | 0.003 | 0.059 |
| BIOCARTA_PGC1A_PATHWAY | 15 | 1.651 | 0.011 | 0.059 |
| KEGG_AMINOACYL_TRNA_BIOSYNTHESIS | 36 | 1.654 | 0.002 | 0.060 |
| BIOCARTA_MPR_PATHWAY | 22 | 1.646 | 0.004 | 0.062 |
| REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS | 20 | 1.642 | 0.009 | 0.063 |
| REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_ | 17 | 1.642 | 0.014 | 0.064 |
| RECRUITING_THEM_TO_CLATHRIN_ADAPTERS | | | | |
| REACTOME_GLYCOSPHINGOLIPID_METABOLISM | 22 | 1.626 | 0.011 | 0.072 |
| KEGG_PYRUVATE_METABOLISM | 30 | 1.624 | 0.011 | 0.073 |
| REACTOME_DOUBLE_STRAND_BREAK_REPAIR | 18 | 1.626 | 0.009 | 0.073 |
| REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE | 19 | 1.615 | 0.020 | 0.077 |
| REACTOME_DNA_REPAIR | 90 | 1.616 | 0.002 | 0.078 |
| REACTOME_OLFACTORY_SIGNALING_PATHWAY | 16 | -1.973 | 0.000 | 0.084 |
| KEGG_TYROSINE_METABOLISM | 19 | 1.603 | 0.023 | 0.085 |
| KEGG_CYSTEINE_AND_METHIONINE_METABOLISM | 24 | 1.606 | 0.005 | 0.085 |
| REACTOME_METABOLISM_OF_PROTEINS | 337 | 1.604 | 0.000 | 0.086 |
| REACTOME_OPIOID_SIGNALLING | 50 | 1.588 | 0.006 | 0.095 |
| BIOCARTA_BCR_PATHWAY | 30 | 1.589 | 0.010 | 0.096 |
| ST_TUMOR_NECROSIS_FACTOR_PATHWAY | 27 | -1.923 | 0.011 | 0.100 |
| KEGG_GALACTOSE_METABOLISM | 19 | 1.577 | 0.024 | 0.102 |
| REACTOME_LAGGING_STRAND_SYNTHESIS | 17 | 1.577 | 0.022 | 0.103 |
| REACTOME_PHASE_II_CONJUGATION | 28 | 1.578 | 0.011 | 0.104 |
| REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER | 24 | 1.571 | 0.016 | 0.108 |
| REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHOGENESIS | 24 | 1.566 | 0.024 | 0.111 |
| REACTOME_ERK_MAPK_TARGETS | 19 | 1.564 | 0.022 | 0.112 |
| REACTOME_G1_PHASE | 31 | 1.561 | 0.017 | 0.113 |
| KEGG_STARCH_AND_SUCROSE_METABOLISM | 18 | 1.553 | 0.025 | 0.114 |
| REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION | 17 | 1.561 | 0.031 | 0.114 |
| KEGG_GLUTATHIONE_METABOLISM | 31 | 1.558 | 0.015 | 0.114 |
| REACTOME_METABOLISM_OF_CARBOHYDRATES | 148 | 1.552 | 0.001 | 0.115 |
| REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION | 20 | 1.557 | 0.023 | 0.115 |
| BIOCARTA_G1_PATHWAY | 21 | 1.554 | 0.016 | 0.115 |
| PID_PS1_PATHWAY | 34 | 1.555 | 0.018 | 0.115 |
| REACTOME_LYSOSOME_VESICLE_BIOGENESIS | 19 | 1.550 | 0.018 | 0.116 |
| REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS | 21 | 1.544 | 0.025 | 0.121 |
| REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY | 16 | 1.536 | 0.030 | 0.129 |
| REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES | 15 | 1.528 | 0.034 | 0.137 |
| BIOCARTA_NDKDYNAMIN_PATHWAY | 16 | 1.526 | 0.027 | 0.139 |
| KEGG_NOTCH_SIGNALING_PATHWAY | 34 | 1.521 | 0.026 | 0.140 |
| PID_FOXM1_PATHWAY | 24 | 1.521 | 0.030 | 0.142 |
| REACTOME_PEROXISOMAL_LIPID_METABOLISM | 16 | 1.519 | 0.039 | 0.142 |
| PID_ALK1_PATHWAY | 16 | 1.522 | 0.033 | 0.143 |
| REACTOME_INTERFERON_ALPHA_BETA_SIGNALING | 46 | 1.510 | 0.018 | 0.153 |
| KEGG_CITRATE_CYCLE_TCA_CYCLE | 27 | 1.507 | 0.037 | 0.156 |
| REACTOME_BASE_EXCISION_REPAIR | 18 | 1.505 | 0.029 | 0.157 |
| REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_Glutamate_BINDING | 18 | 1.498 | 0.043 | 0.165 |
| NABA_MATRISOME | 285 | -1.761 | 0.000 | 0.166 |
| ST_ADRENERGIC | 20 | -1.774 | 0.010 | 0.174 |
| REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY | 17 | -1.611 | 0.014 | 0.174 |
| PID_INTEGRIN1_PATHWAY | 27 | -1.616 | 0.016 | 0.176 |
| BIOCARTA_CCR3_PATHWAY | 15 | 1.488 | 0.040 | 0.178 |
| NABA_BASEMENT_MEMBRANES | 15 | -1.641 | 0.017 | 0.179 |
| REACTOME_APOPTOTIC_EXECUTION_PHASE | 35 | -1.698 | 0.000 | 0.180 |
| KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM | 20 | 1.483 | 0.049 | 0.184 |

| | | | | |
|--|-----|--------|-------|-------|
| NABA_CORE_MATRISOME | 71 | -1.626 | 0.000 | 0.185 |
| BIOCARTA_TNFR2_PATHWAY | 16 | -1.616 | 0.041 | 0.186 |
| PID_CD40_PATHWAY | 23 | -1.705 | 0.016 | 0.189 |
| REACTOME_DNA_STRAND_ELONGATION | 25 | 1.478 | 0.048 | 0.190 |
| BIOCARTA_P53HYPOXIA_PATHWAY | 19 | -1.641 | 0.014 | 0.191 |
| KEGG_RNA_DEGRADATION | 52 | 1.476 | 0.032 | 0.191 |
| PID_FRA_PATHWAY | 20 | -1.651 | 0.019 | 0.191 |
| NABA_SECRETED_FACTORS | 88 | -1.718 | 0.000 | 0.193 |
| KEGG_RNA_POLYMERASE | 27 | 1.474 | 0.047 | 0.193 |
| NABA_ECM_AFFILIATED | 56 | -1.780 | 0.000 | 0.196 |
| REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE | 36 | 1.470 | 0.043 | 0.197 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 101 | -1.586 | 0.000 | 0.197 |
| PID_TCPTP_PATHWAY | 30 | -1.573 | 0.031 | 0.205 |
| NABA_ECM_GLYCOPROTEINS | 50 | -1.664 | 0.009 | 0.205 |
| REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS | 30 | -1.652 | 0.000 | 0.206 |
| KEGG_ECM_RECEPTOR_INTERACTION | 31 | -1.794 | 0.006 | 0.210 |
| BIOCARTA_TID_PATHWAY | 15 | 1.458 | 0.066 | 0.216 |
| REACTOME_RNA_POL_III_TRANSCRIPTION_TERMINATION | 16 | 1.453 | 0.060 | 0.220 |
| BIOCARTA_IL1R_PATHWAY | 26 | -1.551 | 0.018 | 0.222 |
| REACTOME_RNA_POL_III_CHAIN_ELONGATION | 15 | 1.454 | 0.054 | 0.222 |
| BIOCARTA_AT1R_PATHWAY | 26 | 1.453 | 0.041 | 0.222 |
| REACTOME_GLOBAL_GENOMIC_NER_GG_NER | 27 | 1.448 | 0.050 | 0.223 |
| PID_TCR_CALCIIUM_PATHWAY | 20 | 1.449 | 0.049 | 0.224 |
| REACTOME_EXTENSION_OF_TELOMERES | 21 | 1.448 | 0.050 | 0.225 |
| REACTOME_IL_2_SIGNALING | 30 | 1.444 | 0.040 | 0.228 |
| REACTOME_SPHINGOLIPID_METABOLISM | 38 | 1.438 | 0.046 | 0.234 |
| REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA | 19 | 1.439 | 0.058 | 0.235 |
| REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS | 58 | 1.438 | 0.033 | 0.236 |
| NABA_MATRISOME_ASSOCIATED | 214 | -1.531 | 0.000 | 0.241 |
| REACTOME_ER_PHAGOSOME_PATHWAY | 57 | 1.429 | 0.040 | 0.248 |
| REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION | 22 | 1.428 | 0.054 | 0.248 |

HCC vs LC

| NAME | SIZE | NES | NOM p-val | FDR q-val |
|---|------|--------|-----------|-----------|
| REACTOME_GENERIC_TRANSCRIPTION_PATHWAY | 217 | 3.281 | 0.000 | 0.000 |
| REACTOME_PEPTIDE_CHAIN_ELONGATION | 81 | -5.219 | 0.000 | 0.000 |
| REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE | 104 | -5.151 | 0.000 | 0.000 |
| KEGG_RIBOSOME | 83 | -5.061 | 0.000 | 0.000 |
| REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION | 96 | -5.015 | 0.000 | 0.000 |
| REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION | 101 | -4.649 | 0.000 | 0.000 |
| REACTOME_TRANSLATION | 141 | -4.632 | 0.000 | 0.000 |
| REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX | 100 | -4.471 | 0.000 | 0.000 |
| REACTOME_METABOLISM_OF_PROTEINS | 337 | -4.187 | 0.000 | 0.000 |
| REACTOME_INFLUENZA_LIFE_CYCLE | 129 | -3.967 | 0.000 | 0.000 |
| REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS | 88 | -3.873 | 0.000 | 0.000 |
| KEGG_OXIDATIVE_PHOSPHORYLATION | 108 | -3.777 | 0.000 | 0.000 |
| REACTOME_METABOLISM_OF_MRNA | 199 | -3.744 | 0.000 | 0.000 |
| KEGG_PARKINSONS_DISEASE | 105 | -3.660 | 0.000 | 0.000 |
| KEGG_HUNTINGTONS_DISEASE | 145 | -3.465 | 0.000 | 0.000 |
| REACTOME_RESPIRATORY_ELECTRON_TRANSPORT | 71 | -3.264 | 0.000 | 0.000 |
| KEGG_ALZHEIMERS_DISEASE | 132 | -3.253 | 0.000 | 0.000 |
| REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT | 120 | -3.100 | 0.000 | 0.000 |
| REACTOME_METABOLISM_OF_RNA | 241 | -3.112 | 0.000 | 0.000 |
| KEGG_FRUCTOSE_AND_MANNANOSE_METABOLISM | 26 | -2.783 | 0.000 | 0.000 |
| REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX | 47 | -2.757 | 0.000 | 0.000 |
| REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING | 15 | -2.610 | 0.000 | 0.002 |
| REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S | 55 | -2.557 | 0.000 | 0.002 |
| REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 26 | -2.482 | 0.000 | 0.004 |
| KEGG_PURINE_METABOLISM | 102 | -2.458 | 0.000 | 0.004 |
| REACTOME_INTEGRATION_OF_ENERGY_METABOLISM | 66 | -2.384 | 0.004 | 0.008 |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 116 | -2.355 | 0.000 | 0.009 |
| REACTOME_GLUCOSE_METABOLISM | 52 | -2.339 | 0.000 | 0.010 |
| REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT | 44 | -2.266 | 0.000 | 0.018 |
| PID_TCR_PATHWAY | 60 | -2.243 | 0.000 | 0.020 |
| REACTOME_GLYCOLYSIS | 23 | -2.232 | 0.002 | 0.021 |
| REACTOME_PURINE_METABOLISM | 23 | -2.199 | 0.002 | 0.026 |
| KEGG_PENTOSE_PHOSPHATE_PATHWAY | 21 | -2.174 | 0.000 | 0.029 |

| | | | | |
|---|-----|--------|-------|-------|
| BIOCARTA_PGC1A_PATHWAY | 15 | -2.160 | 0.000 | 0.031 |
| BIOCARTA_NDKDYNAMIN_PATHWAY | 16 | -2.136 | 0.002 | 0.034 |
| REACTOME_METABOLISM_OF_NUCLEOTIDES | 53 | -2.117 | 0.004 | 0.037 |
| KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM | 37 | -2.104 | 0.000 | 0.037 |
| BIOCARTA_RHO_PATHWAY | 23 | -2.107 | 0.006 | 0.038 |
| KEGG_NEUROTROPHIN_SIGNALING_PATHWAY | 101 | -2.084 | 0.006 | 0.041 |
| REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION | 67 | -2.028 | 0.000 | 0.053 |
| REACTOME_RECYCLING_PATHWAY_OF_L1 | 19 | -2.035 | 0.004 | 0.054 |
| KEGG_CARDIAC_MUSCLE_CONTRACTION | 38 | -2.028 | 0.004 | 0.055 |
| REACTOME_ADAPTIVE_IMMUNE_SYSTEM | 417 | -2.009 | 0.000 | 0.057 |
| REACTOME_GLUCONEOGENESIS | 24 | -2.011 | 0.004 | 0.058 |
| REACTOME_PD1_SIGNALING | 16 | -1.982 | 0.006 | 0.066 |
| PID_FANCONI_PATHWAY | 35 | 2.403 | 0.000 | 0.066 |
| REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS | 16 | -1.962 | 0.010 | 0.072 |
| PID_ECADHERIN_NASCENT_AJ_PATHWAY | 31 | -1.944 | 0.012 | 0.078 |
| KEGG_LONG_TERM_POTENTIATION | 47 | -1.923 | 0.008 | 0.085 |
| BIOCARTA_CSK_PATHWAY | 19 | -1.910 | 0.015 | 0.090 |
| PID_LYSOPHOSPHOLIPID_PATHWAY | 38 | -1.900 | 0.009 | 0.093 |
| BIOCARTA_CHREBP2_PATHWAY | 35 | -1.880 | 0.015 | 0.098 |
| REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1 | 46 | -1.886 | 0.006 | 0.098 |
| REACTOME_REGULATION_OF_INSULIN_SECRETION | 46 | -1.875 | 0.014 | 0.099 |
| REACTOME_SIGNALLING_TO_ERKS | 27 | -1.870 | 0.006 | 0.099 |
| PID_ERBB1_DOWNSTREAM_PATHWAY | 84 | -1.880 | 0.008 | 0.100 |
| REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_Glutamate_BINDING | 18 | -1.862 | 0.018 | 0.102 |
| BIOCARTA_GPCR_PATHWAY | 27 | -1.859 | 0.012 | 0.102 |
| REACTOME_ER_PHAGOSOME_PATHWAY | 57 | -1.854 | 0.006 | 0.103 |
| REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE | 67 | -1.844 | 0.010 | 0.103 |
| REACTOME_AMYLOIDS | 62 | -1.831 | 0.010 | 0.104 |
| KEGG_PYRIMIDINE_METABOLISM | 79 | -1.849 | 0.015 | 0.104 |
| KEGG_PROTEIN_EXPORT | 22 | -1.845 | 0.008 | 0.104 |
| REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS | 17 | -1.832 | 0.025 | 0.105 |
| BIOCARTA_INTEGRIN_PATHWAY | 29 | -1.837 | 0.012 | 0.105 |
| REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G | 48 | -1.833 | 0.016 | 0.106 |
| NABA_ECM_REGULATORS | 70 | -1.817 | 0.018 | 0.110 |
| PID_TRKR_PATHWAY | 44 | -1.819 | 0.022 | 0.110 |
| REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE_PATHOGENESIS | 24 | -1.798 | 0.008 | 0.120 |
| BIOCARTA_CHEMICAL_PATHWAY | 19 | -1.789 | 0.014 | 0.121 |
| PID_IL8_CXCR2_PATHWAY | 26 | -1.793 | 0.010 | 0.122 |
| KEGG_GALACTOSE_METABOLISM | 19 | -1.790 | 0.017 | 0.122 |
| REACTOME_TCR_SIGNALING | 46 | -1.776 | 0.027 | 0.128 |
| REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT | 46 | -1.768 | 0.024 | 0.131 |
| BIOCARTA_MPR_PATHWAY | 22 | -1.750 | 0.043 | 0.140 |
| REACTOME_METABOLISM_OF_CARBOHYDRATES | 148 | -1.751 | 0.027 | 0.141 |
| PID_ERBB2_ERBB3_PATHWAY | 33 | -1.746 | 0.019 | 0.141 |
| REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C | 54 | -1.742 | 0.026 | 0.142 |
| REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION | 66 | -1.734 | 0.022 | 0.146 |
| REACTOME_IL_RECEPTOR_SHC_SIGNALING | 17 | -1.729 | 0.029 | 0.148 |
| KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS | 99 | -1.726 | 0.021 | 0.148 |
| BIOCARTA_CALCINEURIN_PATHWAY | 15 | -1.715 | 0.038 | 0.155 |
| REACTOME_IL_2_SIGNALING | 30 | -1.711 | 0.023 | 0.155 |
| BIOCARTA_CCR3_PATHWAY | 15 | -1.699 | 0.027 | 0.159 |
| REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6 | 44 | -1.704 | 0.027 | 0.160 |
| REACTOME_SIGNALING_BY_WNT | 62 | -1.700 | 0.023 | 0.161 |
| PID_ENDOTHELIN_PATHWAY | 37 | -1.690 | 0.026 | 0.161 |
| REACTOME_SIGNALLING_TO_RAS | 20 | -1.677 | 0.035 | 0.162 |
| REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX | 46 | -1.686 | 0.045 | 0.162 |
| REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS | 15 | -1.690 | 0.028 | 0.162 |
| REACTOME_MUSCLE_CONTRACTION | 20 | -1.681 | 0.025 | 0.163 |
| KEGG_ASTHMA | 16 | -1.692 | 0.034 | 0.163 |
| BIOCARTA_MEF2D_PATHWAY | 16 | -1.677 | 0.028 | 0.163 |
| KEGG_CALCIIUM_SIGNALING_PATHWAY | 78 | -1.682 | 0.038 | 0.164 |
| SIG_BCR_SIGNALING_PATHWAY | 42 | -1.670 | 0.027 | 0.164 |
| REACTOME_HEMOSTASIS | 265 | -1.670 | 0.030 | 0.166 |
| PID_ALPHA_SYNUCLEIN_PATHWAY | 25 | -1.663 | 0.035 | 0.167 |
| REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMBRANE | 103 | -1.657 | 0.036 | 0.171 |
| KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION | 43 | -1.645 | 0.029 | 0.179 |
| REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION | 15 | 2.153 | 0.000 | 0.184 |
| KEGG_LYSOSOME | 94 | -1.636 | 0.040 | 0.185 |
| REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM | 43 | 2.020 | 0.006 | 0.191 |
| BIOCARTA_NFAT_PATHWAY | 35 | -1.615 | 0.047 | 0.192 |
| BIOCARTA_TCR_PATHWAY | 41 | -1.620 | 0.035 | 0.193 |

| | | | | |
|---|-----|--------|-------|-------|
| BIOCARTA_BCR_PATHWAY | 30 | -1.611 | 0.032 | 0.194 |
| REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX | 55 | -1.617 | 0.042 | 0.194 |
| REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS | 60 | -1.615 | 0.046 | 0.194 |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 66 | -1.620 | 0.041 | 0.195 |
| REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC | 45 | -1.602 | 0.062 | 0.197 |
| KEGG_ARACHIDONIC_ACID_METABOLISM | 20 | -1.620 | 0.029 | 0.197 |
| REACTOME_SCFSPK2_MEDIATED_DEGRADATION_OF_P27_P21 | 49 | -1.603 | 0.054 | 0.198 |
| REACTOME_LYSOSOME_VESICLE_BIOGENESIS | 19 | -1.605 | 0.045 | 0.198 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 101 | 2.031 | 0.004 | 0.199 |
| BIOCARTA_ACTININ_PATHWAY | 15 | -1.596 | 0.032 | 0.201 |
| PID_CD8_TCR_PATHWAY | 47 | -1.587 | 0.034 | 0.205 |
| PID_PDGFBRB_PATHWAY | 103 | -1.588 | 0.058 | 0.206 |
| KEGG_MAPK_SIGNALING_PATHWAY | 167 | 1.913 | 0.012 | 0.215 |
| BIOCARTA_PROTEASOME_PATHWAY | 28 | -1.566 | 0.061 | 0.216 |
| REACTOME_MRNA_SPLICING_MINOR_PATHWAY | 35 | -1.572 | 0.067 | 0.216 |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES | 18 | 2.041 | 0.004 | 0.217 |
| REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES | 120 | -1.562 | 0.052 | 0.217 |
| REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1 | 48 | -1.556 | 0.048 | 0.217 |
| REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION | 120 | -1.569 | 0.063 | 0.217 |
| BIOCARTA_HDAC_PATHWAY | 22 | -1.567 | 0.048 | 0.217 |
| REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE_COLLAPSE | 16 | -1.563 | 0.050 | 0.217 |
| PID_CXCR4_PATHWAY | 83 | -1.559 | 0.030 | 0.217 |
| PID_TCR_CALCIIUM_PATHWAY | 20 | -1.572 | 0.036 | 0.217 |
| BIOCARTA_IL2RB_PATHWAY | 36 | -1.556 | 0.050 | 0.218 |
| REACTOME_MEIOTIC_SYNOPSIS | 60 | 2.098 | 0.002 | 0.218 |
| KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION | 27 | -1.548 | 0.063 | 0.220 |
| REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING | 19 | -1.548 | 0.056 | 0.221 |
| KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY | 63 | -1.550 | 0.057 | 0.221 |
| REACTOME_REGULATION_OF_APOPTOSIS | 51 | -1.535 | 0.059 | 0.225 |
| PID_PI3KCI_PATHWAY | 38 | -1.536 | 0.068 | 0.226 |
| REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_II | 58 | -1.539 | 0.066 | 0.226 |
| PID_AR_NONGENOMIC_PATHWAY | 25 | -1.532 | 0.056 | 0.226 |
| PID_TOLL_ENDOGENOUS_PATHWAY | 21 | 1.915 | 0.004 | 0.227 |
| PID_THROMBIN_PAR1_PATHWAY | 33 | -1.537 | 0.055 | 0.227 |
| BIOCARTA_NKT_PATHWAY | 15 | 1.879 | 0.010 | 0.229 |
| REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION | 72 | 1.888 | 0.008 | 0.232 |
| REACTOME_RNA_POL_I_PROMOTER_OPENING | 54 | -1.521 | 0.058 | 0.236 |
| ST_TUMOR_NECROSIS_FACTOR_PATHWAY | 27 | 2.049 | 0.006 | 0.239 |
| PID_INTEGRIN3_PATHWAY | 16 | 2.157 | 0.002 | 0.240 |
| REACTOME_MITOTIC_PROMETAPHASE | 63 | 1.932 | 0.011 | 0.240 |
| PID_INTEGRIN1_PATHWAY | 27 | 1.917 | 0.008 | 0.242 |
| REACTOME_RNA_POL_I_TRANSCRIPTION | 75 | -1.513 | 0.061 | 0.244 |
| PID_FOXM1_PATHWAY | 24 | -1.509 | 0.067 | 0.246 |