## Supplementary Materials

**Table S1.** 56 MRE genes shared by at least 8 cancer types.

- ADAMTSL3
- AGPAT4
- AP1S1
- ARHGAP24
- AVPI1
- C16orf74
- CLDN11
- CNTN4
- CORO2B
- CRYAB
- CXCL12
- DBNDD1
- DMD
- FBLN1
- FEZ1
- GPRASP1
- HEPH
- HSPB6
- LEPREL1
- LIMCH1
- MAN1C1
- MCM2
- MRGPRF
- NAALADL1
- NCAM1
- NTRK2
- PALM
- PDZRN3
- PGCP
- RRM2
- SEMA6D
- SMARCD3
- SPG20
- SPON1
- ST6GALNAC3
- SYNPO
- TBXA2R
- UBE2E2
- USP2
- ZCCHC24
- ZFPM2
- ADCY5
- AQP1
- C16orf45
- CELSR3
- DIRAS3
- GYPC
- HSPB7
- JDP2
- LOC399959
- NDRG2
- SPATA18
- TNS1
- ANK2
- SYNPO2
- TGFBR3

**Table S2.** The significance values of the 29 enriched pathways using the 56 MRE genes in Table S1.

| | |
|---|---|
| AXON_GUIDANCE | 0.0023 |
| PROTEIN_AMINO_ACID_N_LINKED_GLYCOSYLATION | 0.0034 |
| NFE2L2.V2 | 0.0049 |
| SYSTEM_PROCESS | 0.0074 |
| REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPORINS | 0.0075 |
| AXONOGENESIS | 0.0075 |
| REACTOME_AQUAPORIN_MEDIATED_TRANSPORT | 0.0084 |
| CELLULAR_MORPHOGENESIS_DURING_DIFFERENTIATION | 0.0094 |
| NEURITE_DEVELOPMENT | 0.0109 |
| GOLGI_MEMBRANE | 0.0131 |
| NEURON_DEVELOPMENT | 0.0155 |
| PID_TAP63PATHWAY | 0.0161 |
| NEURON_DIFFERENTIATION | 0.0194 |
| GLYCOPROTEIN_BIOSYNTHETIC_PROCESS | 0.0207 |
| REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION | 0.0212 |
| GENERATION_OF_NEURONS | 0.0236 |
| CELL_CELL_ADHESION | 0.0274 |
| KEGG_DILATED_CARDIOMYOPATHY | 0.0290 |
| ACTIN_BINDING | 0.0290 |
| NEUROGENESIS | 0.0306 |
| G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY | 0.0306 |
| GLYCOPROTEIN_METABOLIC_PROCESS | 0.0322 |
| CELL_MIGRATION | 0.0331 |
| PROTEINACEOUS_EXTRACELLULAR_MATRIX | 0.0356 |
| EXTRACELLULAR_MATRIX | 0.0365 |
| CAHOY_ASTROCYTIC | 0.0365 |
| EXTRACELLULAR_REGION_PART | 0.0460 |
| RESPONSE_TO_BIOTIC_STIMULUS | 0.0476 |
| REACTOME_G_ALPHA_I_SIGNALLING_EVENTS | 0.0495 |

**Table S3**. Cancer type specific MREs enriched pathways. The significance of enrichment is adjusted for FDR.

| pathways | Adjust *p*-value | cancer |
|---|---|---|
| KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS | 0.0222 | BLCA |
| KEGG_CALCIUM_SIGNALING_PATHWAY | 0.0465 | BLCA |
| KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION | 0.0467 | BLCA |
| KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION | 0.0427 | BLCA |
| KEGG_MELANOGENESIS | 0.0328 | BLCA |
| KEGG_PATHWAYS_IN_CANCER | 0.0080 | BLCA |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 0.0047 | BLCA |
| KEGG_DILATED_CARDIOMYOPATHY | 0.0068 | BLCA |
| PID_SHP2_PATHWAY | 0.0496 | BLCA |
| REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM | 0.0465 | BLCA |
| REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS | 0.0390 | BLCA |
| REACTOME_BIOLOGICAL_OXIDATIONS | 0.0489 | BLCA |
| REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES | 0.0330 | BLCA |
| REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE | 0.0452 | BLCA |
| REACTOME_NEURONAL_SYSTEM | 0.0097 | BLCA |
| REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS | 0.0027 | BLCA |
| REACTOME_SIGNALING_BY_GPCR | 0.0079 | BLCA |
| REACTOME_INTEGRATION_OF_ENERGY_METABOLISM | 0.0064 | BLCA |
| REACTOME_OPIOID_SIGNALLING | 0.0175 | BLCA |
| REACTOME_MUSCLE_CONTRACTION | 0.0061 | BLCA |
| REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADRENALINE | 0.0333 | BLCA |
| REACTOME_GPCR_DOWNSTREAM_SIGNALING | 0.0188 | BLCA |
| REACTOME_G_ALPHA_S_SIGNALLING_EVENTS | 0.0489 | BLCA |
| REACTOME_SMOOTH_MUSCLE_CONTRACTION | 0.0270 | BLCA |
| REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE | 0.0427 | BLCA |
| REACTOME_PLATELET_HOMEOSTASIS | 0.0408 | BLCA |

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|---|---|---|
| REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPORINS | 0.0464 | BLCA |
| REACTOME_HEMOSTASIS | 0.0427 | BLCA |
| MUSCLE_DEVELOPMENT | 0.0201 | BLCA |
| CATION_CHANNEL_ACTIVITY | 0.0489 | BLCA |
| MONOOXYGENASE_ACTIVITY | 0.0222 | BLCA |
| KEGG_MAPK_SIGNALING_PATHWAY | 0.0293 | BRCA |
| KEGG_CALCIUM_SIGNALING_PATHWAY | 0.0017 | BRCA |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 0.0152 | BRCA |
| KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION | 0.0005 | BRCA |
| KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION | 0.0054 | BRCA |
| KEGG_AXON_GUIDANCE | 0.0007 | BRCA |
| KEGG_ECM_RECEPTOR_INTERACTION | 0.0470 | BRCA |
| KEGG_ADHERENS_JUNCTION | 0.0192 | BRCA |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS | 0.0192 | BRCA |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 0.0002 | BRCA |
| KEGG_PATHWAYS_IN_CANCER | 0.0002 | BRCA |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 0.0143 | BRCA |
| BIOCARTA_CBL_PATHWAY | 0.0206 | BRCA |
| PID_IL4_2PATHWAY | 0.0055 | BRCA |
| PID_GLYPICAN_1PATHWAY | 0.0491 | BRCA |
| PID_TCPTP_PATHWAY | 0.0437 | BRCA |
| PID_VEGFR1_2_PATHWAY | 0.0235 | BRCA |
| REACTOME_SIGNALING_BY_RHO_GTPASES | 0.0180 | BRCA |
| REACTOME_DEVELOPMENTAL_BIOLOGY | 0.0196 | BRCA |
| REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK | 0.0308 | BRCA |
| REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS | 0.0055 | BRCA |
| REACTOME_NEURONAL_SYSTEM | 0.0310 | BRCA |
| REACTOME_SIGNALING_BY_GPCR | 0.0000 | BRCA |

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|---|---|---|
| REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS | 0.0028 | BRCA |
| REACTOME_INTEGRIN_ALPHAIIB_BETA3_SIGNALING | 0.0105 | BRCA |
| REACTOME_AXON_GUIDANCE | 0.0112 | BRCA |
| REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS | 0.0173 | BRCA |
| REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT | 0.0215 | BRCA |
| REACTOME_GPCR_DOWNSTREAM_SIGNALING | 0.0001 | BRCA |
| REACTOME_GPCR_LIGAND_BINDING | 0.0013 | BRCA |
| REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE | 0.0273 | BRCA |
| REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION | 0.0074 | BRCA |
| REACTOME_HEMOSTASIS | 0.0002 | BRCA |
| REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION | 0.0188 | BRCA |
| INTRINSIC_TO_PLASMA_MEMBRANE | 0.0000 | BRCA |
| EXTRACELLULAR_REGION | 0.0043 | BRCA |
| INTRINSIC_TO_MEMBRANE | 0.0000 | BRCA |
| MEMBRANE_PART | 0.0000 | BRCA |
| MEMBRANE | 0.0000 | BRCA |
| INTEGRAL_TO_MEMBRANE | 0.0000 | BRCA |
| INTEGRAL_TO_PLASMA_MEMBRANE | 0.0000 | BRCA |
| PLASMA_MEMBRANE_PART | 0.0000 | BRCA |
| PLASMA_MEMBRANE | 0.0000 | BRCA |
| SYSTEM_DEVELOPMENT | 0.0001 | BRCA |
| ESTABLISHMENT_OF_LOCALIZATION | 0.0247 | BRCA |
| SIGNAL_TRANSDUCTION | 0.0000 | BRCA |
| CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166 | 0.0150 | BRCA |
| TISSUE_DEVELOPMENT | 0.0052 | BRCA |
| ACTIN_FILAMENT_BASED_PROCESS | 0.0043 | BRCA |
| MULTICELLULAR_ORGANISMAL_DEVELOPMENT | 0.0000 | BRCA |
| ALCOHOL_METABOLIC_PROCESS | 0.0295 | BRCA |

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|---|---|---|
| ACTIN_POLYMERIZATION_AND_OR_DEPOLYMERIZATION | 0.0202 | BRCA |
| INFLAMMATORY_RESPONSE | 0.0470 | BRCA |
| ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS | 0.0066 | BRCA |
| TRANSPORT | 0.0161 | BRCA |
| EPIDERMIS_DEVELOPMENT | 0.0136 | BRCA |
| CELL_PROLIFERATION_GO_0008283 | 0.0367 | BRCA |
| ANATOMICAL_STRUCTURE_DEVELOPMENT | 0.0001 | BRCA |
| RESPONSE_TO_EXTERNAL_STIMULUS | 0.0364 | BRCA |
| CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS | 0.0076 | BRCA |
| RESPONSE_TO_WOUNDING | 0.0161 | BRCA |
| ORGAN_DEVELOPMENT | 0.0020 | BRCA |
| ECTODERM_DEVELOPMENT | 0.0054 | BRCA |
| TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY | 0.0054 | BRCA |
| GTPASE_REGULATOR_ACTIVITY | 0.0429 | BRCA |
| SUBSTRATE_SPECIFIC_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0350 | BRCA |
| SMALL_GTPASE_REGULATOR_ACTIVITY | 0.0350 | BRCA |
| AMINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0491 | BRCA |
| SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY | 0.0360 | BRCA |
| PROTEIN_TYROSINE_KINASE_ACTIVITY | 0.0196 | BRCA |
| G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY | 0.0169 | BRCA |
| RECEPTOR_ACTIVITY | 0.0001 | BRCA |
| TRANSMEMBRANE_RECEPTOR_ACTIVITY | 0.0020 | BRCA |
| CYTOSKELETAL_PROTEIN_BINDING | 0.0310 | BRCA |
| TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVITY | 0.0046 | BRCA |
| ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0491 | BRCA |
| CARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0491 | BRCA |
| TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0076 | BRCA |
| KEGG_CALCIUM_SIGNALING_PATHWAY | 0.0341 | COAD |

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|---|---|---|
| KEGG_CHEMOKINE_SIGNALING_PATHWAY | 0.0310 | COAD |
| KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION | 0.0263 | COAD |
| KEGG_AXON_GUIDANCE | 0.0039 | COAD |
| KEGG_FOCAL_ADHESION | 0.0095 | COAD |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 0.0012 | COAD |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES | 0.0159 | COAD |
| KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY | 0.0318 | COAD |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS | 0.0117 | COAD |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 0.0290 | COAD |
| KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION | 0.0117 | COAD |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 0.0016 | COAD |
| KEGG_TYPE_I_DIABETES_MELLITUS | 0.0137 | COAD |
| KEGG_PATHWAYS_IN_CANCER | 0.0342 | COAD |
| KEGG_MELANOMA | 0.0160 | COAD |
| KEGG_ASTHMA | 0.0160 | COAD |
| KEGG_AUTOIMMUNE_THYROID_DISEASE | 0.0404 | COAD |
| KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS | 0.0329 | COAD |
| KEGG_ALLOGRAFT_REJECTION | 0.0198 | COAD |
| KEGG_GRAFT_VERSUS_HOST_DISEASE | 0.0404 | COAD |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 0.0208 | COAD |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 0.0102 | COAD |
| KEGG_DILATED_CARDIOMYOPATHY | 0.0196 | COAD |
| KEGG_VIRAL_MYOCARDITIS | 0.0083 | COAD |
| BIOCARTA_COMP_PATHWAY | 0.0062 | COAD |
| BIOCARTA_CXCR4_PATHWAY | 0.0488 | COAD |
| PID_LYSOPHOSPHOLIPID_PATHWAY | 0.0112 | COAD |
| PID_CXCR4_PATHWAY | 0.0012 | COAD |
| PID_THROMBIN_PAR1_PATHWAY | 0.0482 | COAD |

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|---|---|---|
| REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS | 0.0482 | COAD |
| REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS | 0.0207 | COAD |
| REACTOME_SIGNALING_BY_GPCR | 0.0008 | COAD |
| REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS | 0.0192 | COAD |
| REACTOME_GPCR_DOWNSTREAM_SIGNALING | 0.0007 | COAD |
| REACTOME_HEMOSTASIS | 0.0001 | COAD |
| REACTOME_COMPLEMENT_CASCADE | 0.0116 | COAD |
| REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION | 0.0196 | COAD |
| INTRINSIC_TO_PLASMA_MEMBRANE | 0.0007 | COAD |
| CELL_JUNCTION | 0.0378 | COAD |
| INTRINSIC_TO_MEMBRANE | 0.0001 | COAD |
| MEMBRANE_PART | 0.0001 | COAD |
| MEMBRANE | 0.0000 | COAD |
| INTEGRAL_TO_MEMBRANE | 0.0003 | COAD |
| INTEGRAL_TO_PLASMA_MEMBRANE | 0.0019 | COAD |
| PLASMA_MEMBRANE_PART | 0.0000 | COAD |
| PLASMA_MEMBRANE | 0.0000 | COAD |
| MUSCLE_DEVELOPMENT | 0.0005 | COAD |
| AXON_GUIDANCE | 0.0458 | COAD |
| SYSTEM_DEVELOPMENT | 0.0016 | COAD |
| SIGNAL_TRANSDUCTION | 0.0495 | COAD |
| TISSUE_DEVELOPMENT | 0.0380 | COAD |
| ACTIN_FILAMENT_BASED_PROCESS | 0.0371 | COAD |
| MULTICELLULAR_ORGANISMAL_DEVELOPMENT | 0.0016 | COAD |
| ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS | 0.0196 | COAD |
| ANATOMICAL_STRUCTURE_DEVELOPMENT | 0.0023 | COAD |
| ORGAN_DEVELOPMENT | 0.0011 | COAD |
| SULFOTRANSFERASE_ACTIVITY | 0.0314 | COAD |

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| SUBSTRATE_SPECIFIC_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0211 | COAD |
| SUBSTRATE_SPECIFIC_CHANNEL_ACTIVITY | 0.0228 | COAD |
| SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY | 0.0329 | COAD |
| RECEPTOR_ACTIVITY | 0.0376 | COAD |
| CARBOXYLESTERASE_ACTIVITY | 0.0423 | COAD |
| METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0329 | COAD |
| ION_CHANNEL_ACTIVITY | 0.0329 | COAD |
| TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS | 0.0160 | COAD |
| TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0252 | COAD |
| KEGG_HISTIDINE_METABOLISM | 0.0105 | HNSC |
| KEGG_AXON_GUIDANCE | 0.0092 | HNSC |
| KEGG_FOCAL_ADHESION | 0.0002 | HNSC |
| KEGG_ECM_RECEPTOR_INTERACTION | 0.0000 | HNSC |
| KEGG_DILATED_CARDIOMYOPATHY | 0.0223 | HNSC |
| PID_INTEGRIN1_PATHWAY | 0.0000 | HNSC |
| PID_INTEGRIN3_PATHWAY | 0.0046 | HNSC |
| PID_INTEGRIN_A9B1_PATHWAY | 0.0084 | HNSC |
| PID_INTEGRIN4_PATHWAY | 0.0039 | HNSC |
| PID_SYNDECAN_4_PATHWAY | 0.0141 | HNSC |
| PID_UPA_UPAR_PATHWAY | 0.0043 | HNSC |
| PID_A6B1_A6B4_INTEGRIN_PATHWAY | 0.0238 | HNSC |
| PID_HIF1_TFPATHWAY | 0.0432 | HNSC |
| REACTOME_DEVELOPMENTAL_BIOLOGY | 0.0057 | HNSC |
| REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION | 0.0135 | HNSC |
| REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL | 0.0076 | HNSC |
| REACTOME_COLLAGEN_FORMATION | 0.0064 | HNSC |
| REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS | 0.0301 | HNSC |
| REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS | 0.0432 | HNSC |

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|---|---|---|
| REACTOME_AXON_GUIDANCE | 0.0014 | HNSC |
| REACTOME_OTHER_SEMAPHORIN_INTERACTIONS | 0.0052 | HNSC |
| REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING | 0.0229 | HNSC |
| REACTOME_SEMAPHORIN_INTERACTIONS | 0.0030 | HNSC |
| REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CONE_COLLAPSE | 0.0210 | HNSC |
| REACTOME_INTERFERON_ALPHA_BETA_SIGNALING | 0.0013 | HNSC |
| REACTOME_HEMOSTASIS | 0.0064 | HNSC |
| PROTEINACEOUS_EXTRACELLULAR_MATRIX | 0.0398 | HNSC |
| INTRINSIC_TO_PLASMA_MEMBRANE | 0.0154 | HNSC |
| EXTRACELLULAR_REGION | 0.0060 | HNSC |
| EXTRACELLULAR_REGION_PART | 0.0060 | HNSC |
| INTEGRAL_TO_PLASMA_MEMBRANE | 0.0172 | HNSC |
| EXTRACELLULAR_MATRIX | 0.0452 | HNSC |
| PLASMA_MEMBRANE_PART | 0.0040 | HNSC |
| PLASMA_MEMBRANE | 0.0020 | HNSC |
| SYSTEM_DEVELOPMENT | 0.0037 | HNSC |
| SKELETAL_DEVELOPMENT | 0.0229 | HNSC |
| TISSUE_DEVELOPMENT | 0.0432 | HNSC |
| MULTICELLULAR_ORGANISMAL_DEVELOPMENT | 0.0023 | HNSC |
| REGULATION_OF_MITOTIC_CELL_CYCLE | 0.0321 | HNSC |
| ANATOMICAL_STRUCTURE_DEVELOPMENT | 0.0081 | HNSC |
| ORGAN_DEVELOPMENT | 0.0067 | HNSC |
| RECEPTOR_BINDING | 0.0070 | HNSC |
| TRANSMEMBRANE_RECEPTOR_ACTIVITY | 0.0250 | HNSC |
| HEMATOPOIETIN_INTERFERON_CLASSD200_DOMAIN_CYTOKINE_RECEPTOR_ACTIVITY | 0.0210 | HNSC |
| CYTOKINE_BINDING | 0.0359 | HNSC |
| KEGG_CHEMOKINE_SIGNALING_PATHWAY | 0.0459 | KIRP |
| KEGG_ENDOCYTOSIS | 0.0463 | KIRP |

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|---|---|---|
| KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION | 0.0026 | KIRP |
| KEGG_VEGF_SIGNALING_PATHWAY | 0.0125 | KIRP |
| KEGG_FOCAL_ADHESION | 0.0276 | KIRP |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 0.0183 | KIRP |
| KEGG_GAP_JUNCTION | 0.0042 | KIRP |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 0.0363 | KIRP |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 0.0048 | KIRP |
| KEGG_TYPE_II_DIABETES_MELLITUS | 0.0359 | KIRP |
| KEGG_GLIOMA | 0.0392 | KIRP |
| KEGG_PROSTATE_CANCER | 0.0395 | KIRP |
| KEGG_BLADDER_CANCER | 0.0363 | KIRP |
| PID_INTEGRIN_CS_PATHWAY | 0.0438 | KIRP |
| PID_TXA2PATHWAY | 0.0460 | KIRP |
| PID_S1P_S1P1_PATHWAY | 0.0483 | KIRP |
| PID_AVB3_INTEGRIN_PATHWAY | 0.0490 | KIRP |
| REACTOME_SIGNALLING_BY_NGF | 0.0405 | KIRP |
| REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE | 0.0005 | KIRP |
| REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES | 0.0356 | KIRP |
| REACTOME_SIGNALING_BY_PDGF | 0.0063 | KIRP |
| REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION | 0.0122 | KIRP |
| REACTOME_AXON_GUIDANCE | 0.0463 | KIRP |
| REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT | 0.0203 | KIRP |
| REACTOME_OTHER_SEMAPHORIN_INTERACTIONS | 0.0312 | KIRP |
| REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_OLIGOPEPTIDES | 0.0206 | KIRP |
| REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS | 0.0039 | KIRP |
| REACTOME_SMOOTH_MUSCLE_CONTRACTION | 0.0116 | KIRP |
| REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE | 0.0392 | KIRP |

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|---|---:|---|
| REACTOME_HEMOSTASIS | 0.0031 | KIRP |
| INTRINSIC_TO_PLASMA_MEMBRANE | 0.0000 | KIRP |
| INTRINSIC_TO_MEMBRANE | 0.0000 | KIRP |
| MEMBRANE_PART | 0.0000 | KIRP |
| MEMBRANE | 0.0000 | KIRP |
| CELL_FRACTION | 0.0133 | KIRP |
| VOLTAGE_GATED_POTASSIUM_CHANNEL_COMPLEX | 0.0483 | KIRP |
| INTEGRAL_TO_MEMBRANE | 0.0000 | KIRP |
| INTEGRAL_TO_PLASMA_MEMBRANE | 0.0000 | KIRP |
| MEMBRANE_FRACTION | 0.0060 | KIRP |
| INTEGRIN_COMPLEX | 0.0163 | KIRP |
| PLASMA_MEMBRANE_PART | 0.0000 | KIRP |
| PLASMA_MEMBRANE | 0.0000 | KIRP |
| ESTABLISHMENT_OF_LOCALIZATION | 0.0431 | KIRP |
| SIGNAL_TRANSDUCTION | 0.0024 | KIRP |
| CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166 | 0.0010 | KIRP |
| CYTOPLASM_ORGANIZATION_AND_BIOGENESIS | 0.0215 | KIRP |
| ANATOMICAL_STRUCTURE_MORPHOGENESIS | 0.0328 | KIRP |
| INTERCELLULAR_JUNCTION_ASSEMBLY | 0.0026 | KIRP |
| ACTIN_FILAMENT_BASED_PROCESS | 0.0388 | KIRP |
| ANATOMICAL_STRUCTURE_FORMATION | 0.0466 | KIRP |
| INTERCELLULAR_JUNCTION_ASSEMBLY_AND_MAINTENANCE | 0.0083 | KIRP |
| ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS | 0.0398 | KIRP |
| CELL_CELL_ADHESION | 0.0187 | KIRP |
| SECOND_MESSENGER_MEDIATED_SIGNALING | 0.0480 | KIRP |
| ANATOMICAL_STRUCTURE_DEVELOPMENT | 0.0410 | KIRP |
| RESPONSE_TO_EXTERNAL_STIMULUS | 0.0359 | KIRP |
| CATION_TRANSPORT | 0.0497 | KIRP |

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| G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY | 0.0005 | KIRP |
| ION_TRANSPORT | 0.0106 | KIRP |
| SYSTEM_PROCESS | 0.0031 | KIRP |
| CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0465 | KIRP |
| PHOSPHOTRANSFERASE_ACTIVITY_ALCOHOL_GROUP_AS_ACCEPTOR | 0.0343 | KIRP |
| VOLTAGE_GATED_CHANNEL_ACTIVITY | 0.0405 | KIRP |
| GATED_CHANNEL_ACTIVITY | 0.0398 | KIRP |
| SUBSTRATE_SPECIFIC_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0023 | KIRP |
| KINASE_ACTIVITY | 0.0466 | KIRP |
| SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY | 0.0005 | KIRP |
| TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0029 | KIRP |
| ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0125 | KIRP |
| KEGG_LINOLEIC_ACID_METABOLISM | 0.0126 | LIHC |
| KEGG_RETINOL_METABOLISM | 0.0098 | LIHC |
| KEGG_DRUG_METABOLISM_CYTOCHROME_P450 | 0.0329 | LIHC |
| REACTOME_DAG_AND_IP3_SIGNALING | 0.0456 | LIHC |
| REACTOME_BIOLOGICAL_OXIDATIONS | 0.0075 | LIHC |
| REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS | 0.0212 | LIHC |
| REACTOME_OPIOID_SIGNALLING | 0.0480 | LIHC |
| REACTOME_CA_DEPENDENT_EVENTS | 0.0098 | LIHC |
| REACTOME_PLC_BETA_MEDIATED_EVENTS | 0.0030 | LIHC |
| REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE | 0.0232 | LIHC |
| REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINATION | 0.0169 | LIHC |
| INTRINSIC_TO_PLASMA_MEMBRANE | 0.0085 | LIHC |
| EXTRACELLULAR_REGION | 0.0204 | LIHC |
| INTRINSIC_TO_MEMBRANE | 0.0117 | LIHC |
| MEMBRANE | 0.0066 | LIHC |
| EXTRACELLULAR_REGION_PART | 0.0428 | LIHC |

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|---|---|---|
| INTEGRAL_TO_MEMBRANE | 0.0098 | LIHC |
| INTEGRAL_TO_PLASMA_MEMBRANE | 0.0075 | LIHC |
| MEMBRANE_FRACTION | 0.0479 | LIHC |
| PLASMA_MEMBRANE_PART | 0.0446 | LIHC |
| PLASMA_MEMBRANE | 0.0006 | LIHC |
| SYSTEM_DEVELOPMENT | 0.0075 | LIHC |
| LYMPHOCYTE_DIFFERENTIATION | 0.0469 | LIHC |
| TISSUE_DEVELOPMENT | 0.0230 | LIHC |
| ACTIVATION_OF_MAPK_ACTIVITY | 0.0146 | LIHC |
| MULTICELLULAR_ORGANISMAL_DEVELOPMENT | 0.0230 | LIHC |
| POSITIVE_REGULATION_OF_MAP_KINASE_ACTIVITY | 0.0371 | LIHC |
| PROTEIN_KINASE_CASCADE | 0.0422 | LIHC |
| ANATOMICAL_STRUCTURE_DEVELOPMENT | 0.0047 | LIHC |
| MAPKKK_CASCADE_GO_0000165 | 0.0056 | LIHC |
| ORGAN_DEVELOPMENT | 0.0066 | LIHC |
| SYSTEM_PROCESS | 0.0119 | LIHC |
| OXIDOREDUCTASE_ACTIVITY | 0.0092 | LIHC |
| OXYGEN_BINDING | 0.0306 | LIHC |
| KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES | 0.0388 | LUAD |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 0.0438 | LUAD |
| KEGG_WNT_SIGNALING_PATHWAY | 0.0484 | LUAD |
| KEGG_HEDGEHOG_SIGNALING_PATHWAY | 0.0128 | LUAD |
| KEGG_AXON_GUIDANCE | 0.0016 | LUAD |
| KEGG_ECM_RECEPTOR_INTERACTION | 0.0376 | LUAD |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 0.0002 | LUAD |
| KEGG_HEMATOPOIETIC_CELL_LINEAGE | 0.0039 | LUAD |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 0.0215 | LUAD |
| KEGG_PATHWAYS_IN_CANCER | 0.0108 | LUAD |

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| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 0.0093 | LUAD |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 0.0353 | LUAD |
| KEGG_DILATED_CARDIOMYOPATHY | 0.0079 | LUAD |
| BIOCARTA_LAIR_PATHWAY | 0.0235 | LUAD |
| WNT_SIGNALING | 0.0437 | LUAD |
| PID_INTEGRIN_CS_PATHWAY | 0.0044 | LUAD |
| REACTOME_SIGNALING_BY_RHO_GTPASES | 0.0415 | LUAD |
| REACTOME_CELL_CELL_COMMUNICATION | 0.0083 | LUAD |
| REACTOME_SIGNALING_BY_GPCR | 0.0012 | LUAD |
| REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES | 0.0313 | LUAD |
| REACTOME_MUSCLE_CONTRACTION | 0.0320 | LUAD |
| REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS | 0.0111 | LUAD |
| REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT | 0.0221 | LUAD |
| REACTOME_GPCR_DOWNSTREAM_SIGNALING | 0.0062 | LUAD |
| REACTOME_OTHER_SEMAPHORIN_INTERACTIONS | 0.0111 | LUAD |
| REACTOME_SEMAPHORIN_INTERACTIONS | 0.0012 | LUAD |
| REACTOME_CELL_JUNCTION_ORGANIZATION | 0.0246 | LUAD |
| REACTOME_GPCR_LIGAND_BINDING | 0.0045 | LUAD |
| REACTOME_SIGNAL_REGULATORY_PROTEIN_SIRP_FAMILY_INTERACTIONS | 0.0352 | LUAD |
| REACTOME_HEMOSTASIS | 0.0005 | LUAD |
| REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION | 0.0458 | LUAD |
| INTRINSIC_TO_PLASMA_MEMBRANE | 0.0000 | LUAD |
| CELL_JUNCTION | 0.0091 | LUAD |
| EXTRACELLULAR_REGION | 0.0023 | LUAD |
| INTRINSIC_TO_MEMBRANE | 0.0000 | LUAD |
| MEMBRANE_PART | 0.0000 | LUAD |
| INTERCELLULAR_JUNCTION | 0.0014 | LUAD |
| MEMBRANE | 0.0000 | LUAD |

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|---|---|---|
| EXTRACELLULAR_REGION_PART | 0.0363 | LUAD |
| INTEGRAL_TO_MEMBRANE | 0.0000 | LUAD |
| INTEGRAL_TO_PLASMA_MEMBRANE | 0.0000 | LUAD |
| EXTRACELLULAR_SPACE | 0.0462 | LUAD |
| INTEGRIN_COMPLEX | 0.0408 | LUAD |
| PLASMA_MEMBRANE_PART | 0.0000 | LUAD |
| PLASMA_MEMBRANE | 0.0000 | LUAD |
| SYSTEM_DEVELOPMENT | 0.0097 | LUAD |
| SIGNAL_TRANSDUCTION | 0.0016 | LUAD |
| CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166 | 0.0016 | LUAD |
| CELL_CELL_SIGNALING | 0.0371 | LUAD |
| METAL_ION_TRANSPORT | 0.0404 | LUAD |
| CELL_CELL_ADHESION | 0.0443 | LUAD |
| CELL_PROLIFERATION_GO_0008283 | 0.0491 | LUAD |
| ANATOMICAL_STRUCTURE_DEVELOPMENT | 0.0027 | LUAD |
| POTASSIUM_ION_TRANSPORT | 0.0120 | LUAD |
| ORGAN_DEVELOPMENT | 0.0051 | LUAD |
| PHOSPHOTRANSFERASE_ACTIVITY_ALCOHOL_GROUP_AS_ACCEPTOR | 0.0455 | LUAD |
| CATION_CHANNEL_ACTIVITY | 0.0112 | LUAD |
| SUBSTRATE_SPECIFIC_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0062 | LUAD |
| PROTEIN_KINASE_ACTIVITY | 0.0291 | LUAD |
| SUBSTRATE_SPECIFIC_CHANNEL_ACTIVITY | 0.0046 | LUAD |
| ANTIGEN_BINDING | 0.0215 | LUAD |
| KINASE_ACTIVITY | 0.0413 | LUAD |
| SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY | 0.0024 | LUAD |
| POTASSIUM_CHANNEL_ACTIVITY | 0.0133 | LUAD |
| RECEPTOR_ACTIVITY | 0.0000 | LUAD |
| TRANSMEMBRANE_RECEPTOR_ACTIVITY | 0.0001 | LUAD |

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|---|---|---|
| METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0115 | LUAD |
| ION_CHANNEL_ACTIVITY | 0.0079 | LUAD |
| TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0079 | LUAD |
| ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0265 | LUAD |
| KEGG_PURINE_METABOLISM | 0.0471 | LUSC |
| KEGG_ARACHIDONIC_ACID_METABOLISM | 0.0439 | LUSC |
| KEGG_ERBB_SIGNALING_PATHWAY | 0.0169 | LUSC |
| KEGG_CALCIUM_SIGNALING_PATHWAY | 0.0101 | LUSC |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 0.0246 | LUSC |
| KEGG_CHEMOKINE_SIGNALING_PATHWAY | 0.0109 | LUSC |
| KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION | 0.0170 | LUSC |
| KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION | 0.0100 | LUSC |
| KEGG_AXON_GUIDANCE | 0.0023 | LUSC |
| KEGG_VEGF_SIGNALING_PATHWAY | 0.0197 | LUSC |
| KEGG_FOCAL_ADHESION | 0.0086 | LUSC |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 0.0017 | LUSC |
| KEGG_HEMATOPOIETIC_CELL_LINEAGE | 0.0006 | LUSC |
| KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY | 0.0274 | LUSC |
| KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY | 0.0210 | LUSC |
| KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY | 0.0152 | LUSC |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS | 0.0414 | LUSC |
| KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION | 0.0176 | LUSC |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 0.0002 | LUSC |
| KEGG_GNRH_SIGNALING_PATHWAY | 0.0118 | LUSC |
| KEGG_TYPE_I_DIABETES_MELLITUS | 0.0372 | LUSC |
| KEGG_LEISHMANIA_INFECTION | 0.0194 | LUSC |
| KEGG_RENAL_CELL_CARCINOMA | 0.0110 | LUSC |
| KEGG_ALLOGRAFT_REJECTION | 0.0338 | LUSC |

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| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 0.0414 | LUSC |
| KEGG_DILATED_CARDIOMYOPATHY | 0.0082 | LUSC |
| BIOCARTA_EPO_PATHWAY | 0.0390 | LUSC |
| BIOCARTA_ECM_PATHWAY | 0.0414 | LUSC |
| BIOCARTA_NGF_PATHWAY | 0.0390 | LUSC |
| BIOCARTA_PDGF_PATHWAY | 0.0390 | LUSC |
| BIOCARTA_TCR_PATHWAY | 0.0458 | LUSC |
| ST_INTEGRIN_SIGNALING_PATHWAY | 0.0414 | LUSC |
| PID_INTEGRIN_CS_PATHWAY | 0.0070 | LUSC |
| PID_TCPTP_PATHWAY | 0.0248 | LUSC |
| PID_TXA2PATHWAY | 0.0329 | LUSC |
| PID_CXCR4_PATHWAY | 0.0030 | LUSC |
| PID_INTEGRIN2_PATHWAY | 0.0377 | LUSC |
| PID_UPA_UPAR_PATHWAY | 0.0086 | LUSC |
| REACTOME_SIGNALING_BY_RHO_GTPASES | 0.0079 | LUSC |
| REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL | 0.0023 | LUSC |
| REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK | 0.0471 | LUSC |
| REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS | 0.0302 | LUSC |
| REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0442 | LUSC |
| REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS | 0.0210 | LUSC |
| REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE | 0.0377 | LUSC |
| REACTOME_SIGNALING_BY_GPCR | 0.0000 | LUSC |
| REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS | 0.0010 | LUSC |
| REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT | 0.0349 | LUSC |
| REACTOME_GPCR_DOWNSTREAM_SIGNALING | 0.0002 | LUSC |
| REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY | 0.0414 | LUSC |
| REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS | 0.0275 | LUSC |
| REACTOME_GPCR_LIGAND_BINDING | 0.0053 | LUSC |

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| REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE | 0.0414 | LUSC |
| REACTOME_IL_2_SIGNALING | 0.0329 | LUSC |
| REACTOME_METABOLISM_OF_CARBOHYDRATES | 0.0492 | LUSC |
| REACTOME_HEMOSTASIS | 0.0000 | LUSC |
| REACTOME_UNWINDING_OF_DNA | 0.0492 | LUSC |
| REACTOME_IMMUNE_SYSTEM | 0.0275 | LUSC |
| REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION | 0.0036 | LUSC |
| INTRINSIC_TO_PLASMA_MEMBRANE | 0.0000 | LUSC |
| INTRINSIC_TO_MEMBRANE | 0.0000 | LUSC |
| MEMBRANE_PART | 0.0000 | LUSC |
| MEMBRANE | 0.0000 | LUSC |
| INTEGRAL_TO_MEMBRANE | 0.0000 | LUSC |
| INTEGRAL_TO_PLASMA_MEMBRANE | 0.0000 | LUSC |
| PLASMA_MEMBRANE_PART | 0.0000 | LUSC |
| PLASMA_MEMBRANE | 0.0000 | LUSC |
| SOLUBLE_FRACTION | 0.0414 | LUSC |
| SYSTEM_DEVELOPMENT | 0.0224 | LUSC |
| ESTABLISHMENT_OF_LOCALIZATION | 0.0377 | LUSC |
| CELL_ACTIVATION | 0.0492 | LUSC |
| SIGNAL_TRANSDUCTION | 0.0013 | LUSC |
| CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166 | 0.0231 | LUSC |
| CARBOXYLIC_ACID_METABOLIC_PROCESS | 0.0479 | LUSC |
| TISSUE_DEVELOPMENT | 0.0188 | LUSC |
| DEFENSE_RESPONSE | 0.0031 | LUSC |
| ACTIN_FILAMENT_BASED_PROCESS | 0.0414 | LUSC |
| T_CELL_DIFFERENTIATION | 0.0492 | LUSC |
| MULTICELLULAR_ORGANISMAL_DEVELOPMENT | 0.0224 | LUSC |
| LEUKOCYTE_ACTIVATION | 0.0480 | LUSC |

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| INFLAMMATORY_RESPONSE | 0.0414 | LUSC |
| RESPONSE_TO_STRESS | 0.0189 | LUSC |
| IMMUNE_RESPONSE | 0.0089 | LUSC |
| TRANSPORT | 0.0380 | LUSC |
| EPIDERMIS_DEVELOPMENT | 0.0414 | LUSC |
| SECOND_MESSENGER_MEDIATED_SIGNALING | 0.0170 | LUSC |
| CELL_PROLIFERATION_GO_0008283 | 0.0112 | LUSC |
| IMMUNE_SYSTEM_PROCESS | 0.0055 | LUSC |
| ANATOMICAL_STRUCTURE_DEVELOPMENT | 0.0036 | LUSC |
| RESPONSE_TO_EXTERNAL_STIMULUS | 0.0008 | LUSC |
| RESPONSE_TO_WOUNDING | 0.0024 | LUSC |
| G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY | 0.0085 | LUSC |
| ORGAN_DEVELOPMENT | 0.0005 | LUSC |
| ECTODERM_DEVELOPMENT | 0.0414 | LUSC |
| OXIDOREDUCTASE_ACTIVITY | 0.0211 | LUSC |
| G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY | 0.0334 | LUSC |
| RECEPTOR_ACTIVITY | 0.0055 | LUSC |
| TRANSMEMBRANE_RECEPTOR_ACTIVITY | 0.0152 | LUSC |
| ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0414 | LUSC |
| CARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0414 | LUSC |
| KEGG_GLUTATHIONE_METABOLISM | 0.0174 | PRAD |
| KEGG_AXON_GUIDANCE | 0.0296 | PRAD |
| KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION | 0.0472 | PRAD |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 0.0191 | PRAD |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 0.0127 | PRAD |
| KEGG_DILATED_CARDIOMYOPATHY | 0.0052 | PRAD |
| BIOCARTA_MYOSIN_PATHWAY | 0.0466 | PRAD |
| REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS | 0.0251 | PRAD |

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| REACTOME_NEURONAL_SYSTEM | 0.0199 | PRAD |
| REACTOME_PEPTIDE_CHAIN_ELONGATION | 0.0420 | PRAD |
| REACTOME_SIGNALING_BY_GPCR | 0.0258 | PRAD |
| REACTOME_MUSCLE_CONTRACTION | 0.0150 | PRAD |
| REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION | 0.0214 | PRAD |
| REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS | 0.0374 | PRAD |
| REACTOME_GPCR_DOWNSTREAM_SIGNALING | 0.0092 | PRAD |
| REACTOME_SMOOTH_MUSCLE_CONTRACTION | 0.0126 | PRAD |
| REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS | 0.0029 | PRAD |
| REACTOME_POTASSIUM_CHANNELS | 0.0127 | PRAD |
| REACTOME_GAP_JUNCTION_ASSEMBLY | 0.0367 | PRAD |
| INTRINSIC_TO_PLASMA_MEMBRANE | 0.0038 | PRAD |
| INTRINSIC_TO_MEMBRANE | 0.0441 | PRAD |
| INTEGRAL_TO_PLASMA_MEMBRANE | 0.0050 | PRAD |
| PLASMA_MEMBRANE_PART | 0.0038 | PRAD |
| PLASMA_MEMBRANE | 0.0020 | PRAD |
| CELL_CELL_SIGNALING | 0.0442 | PRAD |
| METAL_ION_TRANSPORT | 0.0002 | PRAD |
| SODIUM_ION_TRANSPORT | 0.0251 | PRAD |
| ANATOMICAL_STRUCTURE_DEVELOPMENT | 0.0437 | PRAD |
| CARBOHYDRATE_METABOLIC_PROCESS | 0.0150 | PRAD |
| CATION_TRANSPORT | 0.0001 | PRAD |
| MONOVALENT_INORGANIC_CATION_TRANSPORT | 0.0035 | PRAD |
| ION_TRANSPORT | 0.0004 | PRAD |
| SYSTEM_PROCESS | 0.0466 | PRAD |
| CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0237 | PRAD |
| CATION_CHANNEL_ACTIVITY | 0.0164 | PRAD |
| GATED_CHANNEL_ACTIVITY | 0.0374 | PRAD |

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| SUBSTRATE_SPECIFIC_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0150 | PRAD |
| SUBSTRATE_SPECIFIC_CHANNEL_ACTIVITY | 0.0090 | PRAD |
| SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY | 0.0235 | PRAD |
| VOLTAGE_GATED_CATION_CHANNEL_ACTIVITY | 0.0155 | PRAD |
| STRUCTURAL_MOLECULE_ACTIVITY | 0.0170 | PRAD |
| METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0150 | PRAD |
| ION_CHANNEL_ACTIVITY | 0.0200 | PRAD |
| TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0199 | PRAD |
| ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0097 | PRAD |
| KEGG_PPAR_SIGNALING_PATHWAY | 0.0410 | THCA |
| KEGG_MAPK_SIGNALING_PATHWAY | 0.0206 | THCA |
| KEGG_CALCIUM_SIGNALING_PATHWAY | 0.0227 | THCA |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 0.0002 | THCA |
| KEGG_P53_SIGNALING_PATHWAY | 0.0214 | THCA |
| KEGG_APOPTOSIS | 0.0287 | THCA |
| KEGG_AXON_GUIDANCE | 0.0263 | THCA |
| KEGG_FOCAL_ADHESION | 0.0002 | THCA |
| KEGG_ECM_RECEPTOR_INTERACTION | 0.0001 | THCA |
| KEGG_CIRCADIAN_RHYTHM_MAMMAL | 0.0188 | THCA |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 0.0040 | THCA |
| KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY | 0.0250 | THCA |
| KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS | 0.0273 | THCA |
| KEGG_PATHWAYS_IN_CANCER | 0.0032 | THCA |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 0.0017 | THCA |
| KEGG_DILATED_CARDIOMYOPATHY | 0.0378 | THCA |
| BIOCARTA_ECM_PATHWAY | 0.0113 | THCA |
| BIOCARTA_INTEGRIN_PATHWAY | 0.0236 | THCA |
| BIOCARTA_UCALPAIN_PATHWAY | 0.0384 | THCA |

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| PID_INTEGRIN1_PATHWAY | 0.0003 | THCA |
| PID_INTEGRIN3_PATHWAY | 0.0005 | THCA |
| PID_ARF6_PATHWAY | 0.0188 | THCA |
| PID_INTEGRIN_A9B1_PATHWAY | 0.0041 | THCA |
| PID_CERAMIDE_PATHWAY | 0.0123 | THCA |
| PID_AVB3_INTEGRIN_PATHWAY | 0.0334 | THCA |
| PID_RXR_VDR_PATHWAY | 0.0004 | THCA |
| PID_SYNDECAN_4_PATHWAY | 0.0236 | THCA |
| PID_SYNDECAN_1_PATHWAY | 0.0101 | THCA |
| PID_RETINOIC_ACID_PATHWAY | 0.0439 | THCA |
| PID_INTEGRIN5_PATHWAY | 0.0056 | THCA |
| PID_A6B1_A6B4_INTEGRIN_PATHWAY | 0.0001 | THCA |
| PID_FGF_PATHWAY | 0.0002 | THCA |
| PID_FAK_PATHWAY | 0.0482 | THCA |
| REACTOME_SIGNALING_BY_RHO_GTPASES | 0.0457 | THCA |
| REACTOME_DEVELOPMENTAL_BIOLOGY | 0.0052 | THCA |
| REACTOME_CELL_CELL_COMMUNICATION | 0.0019 | THCA |
| REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM | 0.0447 | THCA |
| REACTOME_GLYCOSAMINOGLYCAN_METABOLISM | 0.0178 | THCA |
| REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS | 0.0260 | THCA |
| REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_ | 0.0178 | THCA |
| REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS | 0.0060 | THCA |
| REACTOME_AXON_GUIDANCE | 0.0009 | THCA |
| REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH | 0.0187 | THCA |
| REACTOME_SEMAPHORIN_INTERACTIONS | 0.0378 | THCA |
| REACTOME_CELL_JUNCTION_ORGANIZATION | 0.0114 | THCA |
| REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION | 0.0272 | THCA |
| PROTEINACEOUS_EXTRACELLULAR_MATRIX | 0.0081 | THCA |

| | | |
|---|---|---|
| INTRINSIC_TO_PLASMA_MEMBRANE | 0.0000 | THCA |
| EXTRACELLULAR_REGION | 0.0000 | THCA |
| INTRINSIC_TO_MEMBRANE | 0.0001 | THCA |
| MEMBRANE_PART | 0.0005 | THCA |
| MEMBRANE | 0.0002 | THCA |
| CELL_FRACTION | 0.0272 | THCA |
| EXTRACELLULAR_REGION_PART | 0.0003 | THCA |
| INTEGRAL_TO_MEMBRANE | 0.0001 | THCA |
| INTEGRAL_TO_PLASMA_MEMBRANE | 0.0000 | THCA |
| EXTRACELLULAR_SPACE | 0.0108 | THCA |
| EXTRACELLULAR_MATRIX | 0.0098 | THCA |
| PLASMA_MEMBRANE_PART | 0.0000 | THCA |
| PLASMA_MEMBRANE | 0.0000 | THCA |
| SYSTEM_DEVELOPMENT | 0.0005 | THCA |
| ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY | 0.0178 | THCA |
| ESTABLISHMENT_OF_LOCALIZATION | 0.0417 | THCA |
| SIGNAL_TRANSDUCTION | 0.0000 | THCA |
| CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166 | 0.0232 | THCA |
| SKELETAL_DEVELOPMENT | 0.0001 | THCA |
| ANATOMICAL_STRUCTURE_MORPHOGENESIS | 0.0143 | THCA |
| TISSUE_DEVELOPMENT | 0.0032 | THCA |
| MULTICELLULAR_ORGANISMAL_DEVELOPMENT | 0.0002 | THCA |
| B_CELL_ACTIVATION | 0.0273 | THCA |
| APOPTOTIC_MITOCHONDRIAL_CHANGES | 0.0391 | THCA |
| BONE_REMODELING | 0.0273 | THCA |
| ANATOMICAL_STRUCTURE_DEVELOPMENT | 0.0001 | THCA |
| POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS | 0.0430 | THCA |
| TISSUE_REMODELING | 0.0273 | THCA |

| | | |
|---|---|---|
| POSITIVE_REGULATION_OF_CELLULAR_PROCESS | 0.0373 | THCA |
| TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY | 0.0148 | THCA |
| ION_TRANSPORT | 0.0440 | THCA |
| ORGAN_DEVELOPMENT | 0.0001 | THCA |
| SYSTEM_PROCESS | 0.0192 | THCA |
| TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY | 0.0495 | THCA |
| PHOSPHOTRANSFERASE_ACTIVITY_ALCOHOL_GROUP_AS_ACCEPTOR | 0.0040 | THCA |
| GTPASE_REGULATOR_ACTIVITY | 0.0320 | THCA |
| ENZYME_ACTIVATOR_ACTIVITY | 0.0217 | THCA |
| PHOSPHOLIPID_BINDING | 0.0447 | THCA |
| LIGAND_DEPENDENT_NUCLEAR_RECEPTOR_ACTIVITY | 0.0439 | THCA |
| SUBSTRATE_SPECIFIC_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0338 | THCA |
| PROTEIN_KINASE_ACTIVITY | 0.0005 | THCA |
| SUBSTRATE_SPECIFIC_CHANNEL_ACTIVITY | 0.0370 | THCA |
| ENZYME_REGULATOR_ACTIVITY | 0.0206 | THCA |
| KINASE_ACTIVITY | 0.0105 | THCA |
| SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY | 0.0040 | THCA |
| PROTEIN_TYROSINE_KINASE_ACTIVITY | 0.0017 | THCA |
| RECEPTOR_BINDING | 0.0063 | THCA |
| RECEPTOR_ACTIVITY | 0.0001 | THCA |
| TRANSMEMBRANE_RECEPTOR_ACTIVITY | 0.0034 | THCA |
| TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVITY | 0.0160 | THCA |
| TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0049 | THCA |
| ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY | 0.0145 | THCA |

**Table S4.** Differential expression analysis of DNA (de)methylation genes. The *p*-values are tests of hypothesis that the gene is up-regulated in normal than tumor. Lower *p*-values indicate that the gene is up-regulated in cancer than normal samples for respective cancer types.

| | TDG | TET1 | TET2 | TET3 | DNMT1 | DNMT3A | DNMT3B |
|---|---|---|---|---|---|---|---|
| BLCA | 3.46E-04 | 1.67E-01 | 6.61E-01 | 1.66E-03 | 8.13E-08 | 1.29E-07 | 1.05E-06 |
| BRCA | 1.50E-19 | 1.00E+00 | 1.00E+00 | 3.19E-16 | 1.94E-35 | 4.22E-42 | 4.09E-43 |
| COAD | 5.52E-04 | 1.21E-01 | 1.00E+00 | 4.97E-01 | 8.94E-17 | 1.09E-07 | 1.33E-28 |
| HNSC | 9.19E-05 | 6.32E-03 | 1.00E+00 | 6.10E-03 | 9.49E-14 | 1.51E-04 | 6.80E-25 |
| KIRP | 2.48E-13 | 1.00E+00 | 1.00E+00 | 2.60E-08 | 8.21E-03 | 1.18E-02 | 2.06E-15 |
| LIHC | 2.21E-03 | 1.48E-09 | 1.00E+00 | 7.69E-10 | 1.76E-24 | 1.08E-30 | 4.88E-21 |
| LUAD | 9.40E-30 | 5.45E-15 | 9.95E-01 | 7.74E-05 | 1.94E-25 | 3.40E-32 | 1.09E-32 |
| LUSC | 9.35E-38 | 5.66E-18 | 5.06E-01 | 5.11E-29 | 1.72E-26 | 9.03E-31 | 7.30E-37 |
| PRAD | 3.16E-04 | 5.67E-01 | 1.00E+00 | 4.97E-10 | 2.91E-01 | 2.56E-12 | 1.12E-05 |
| THCA | 1.00E+00 | 1.00E+00 | 1.00E+00 | 8.28E-14 | 2.95E-10 | 4.85E-04 | 1.00E+00 |

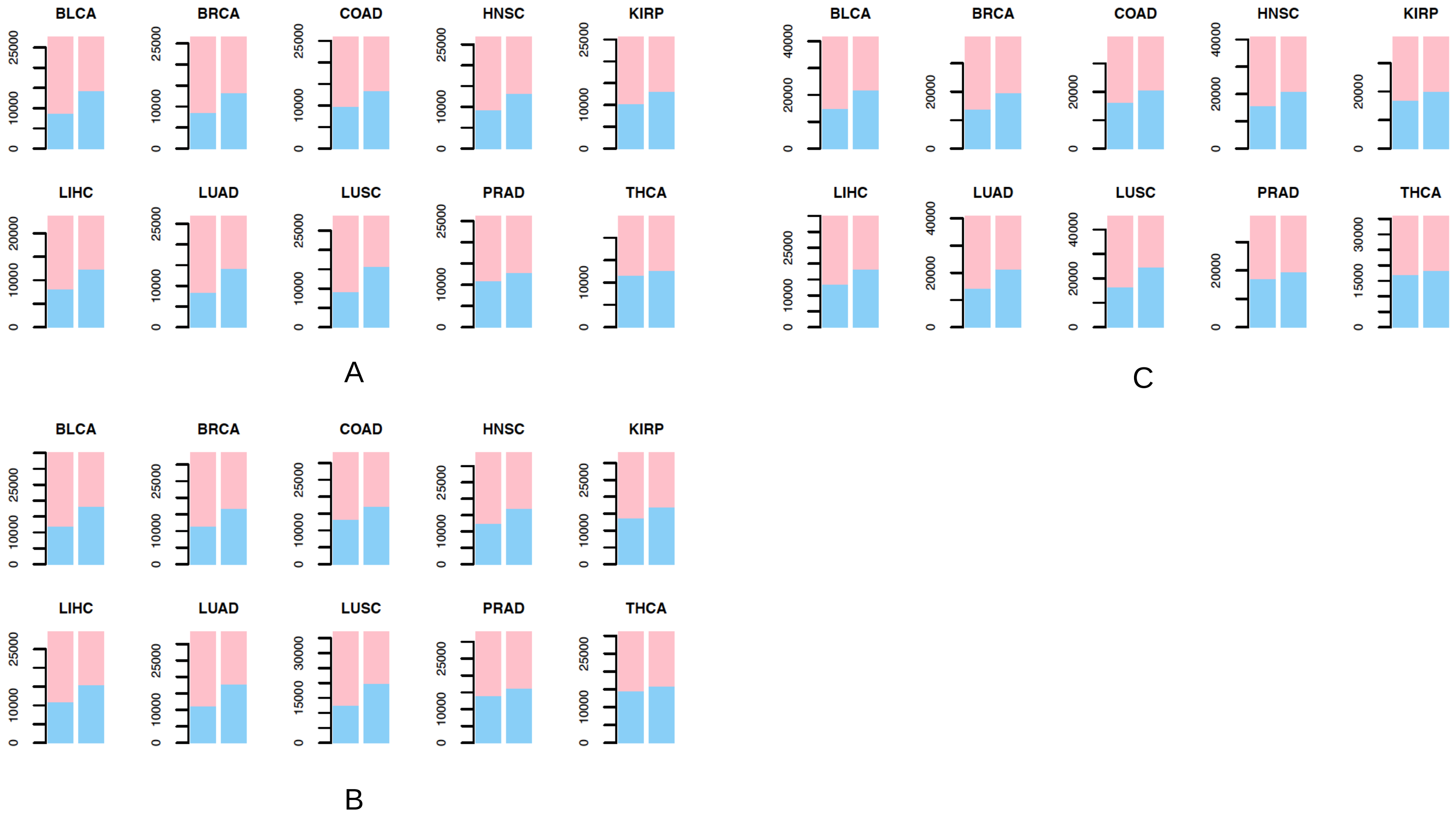

**Figure S1.** The numbers of selected predictors in control (left bar) and cancer (right bar) for each of the 10 cancer types, where the selected CpGs in the proximity of the genes are marked in blue and proximity of genes' TFs in pink, when the number of predictors selected for the linear models are fixed to be three (A), four and (B) five (C).