Figure S1. Gene set enrichment analysis of signaling pathways based on The Cancer Genome Atlas - bladder urothelial carcinoma datasets. Enrichment plots for (A) the hallmark epithelial-mesenchymal transition, (B) KEGG-ECM receptor interaction; (C) KEGG focal adhesion, (D) the hallmark apical junction, (E) the hallmark KRAS signaling upregulated and (F) KEGG TGF-beta signaling pathway. KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor.

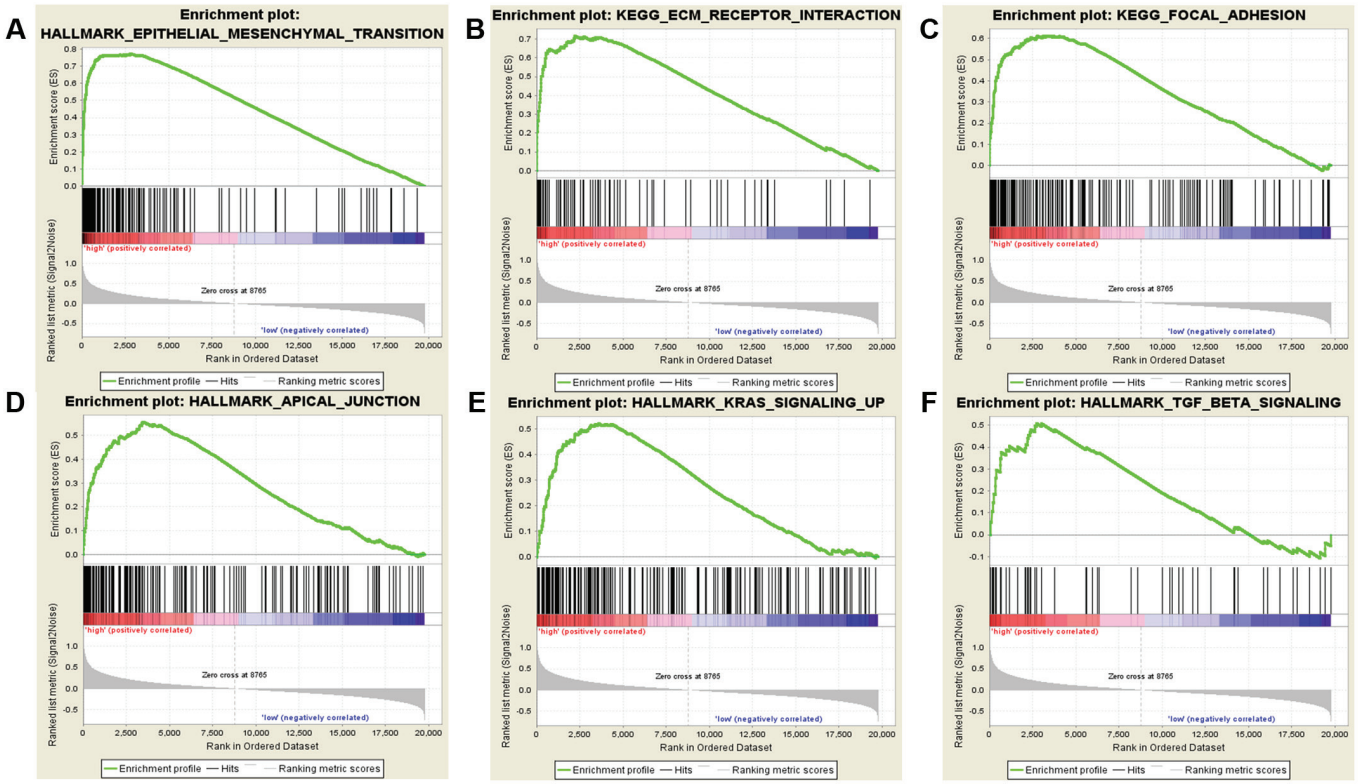


Figure S2. Gene set enrichment analysis of signaling pathways based on The Cancer Genome Atlas - breast invasive carcinoma datasets. Enrichment plots for (A) the hallmark epithelial-mesenchymal transition, (B) KEGG-ECM receptor interaction; (C) KEGG focal adhesion, (D) the hallmark apical junction, (E) the hallmark KRAS signaling upregulated and (F) KEGG TGF-β signaling pathway. KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor.

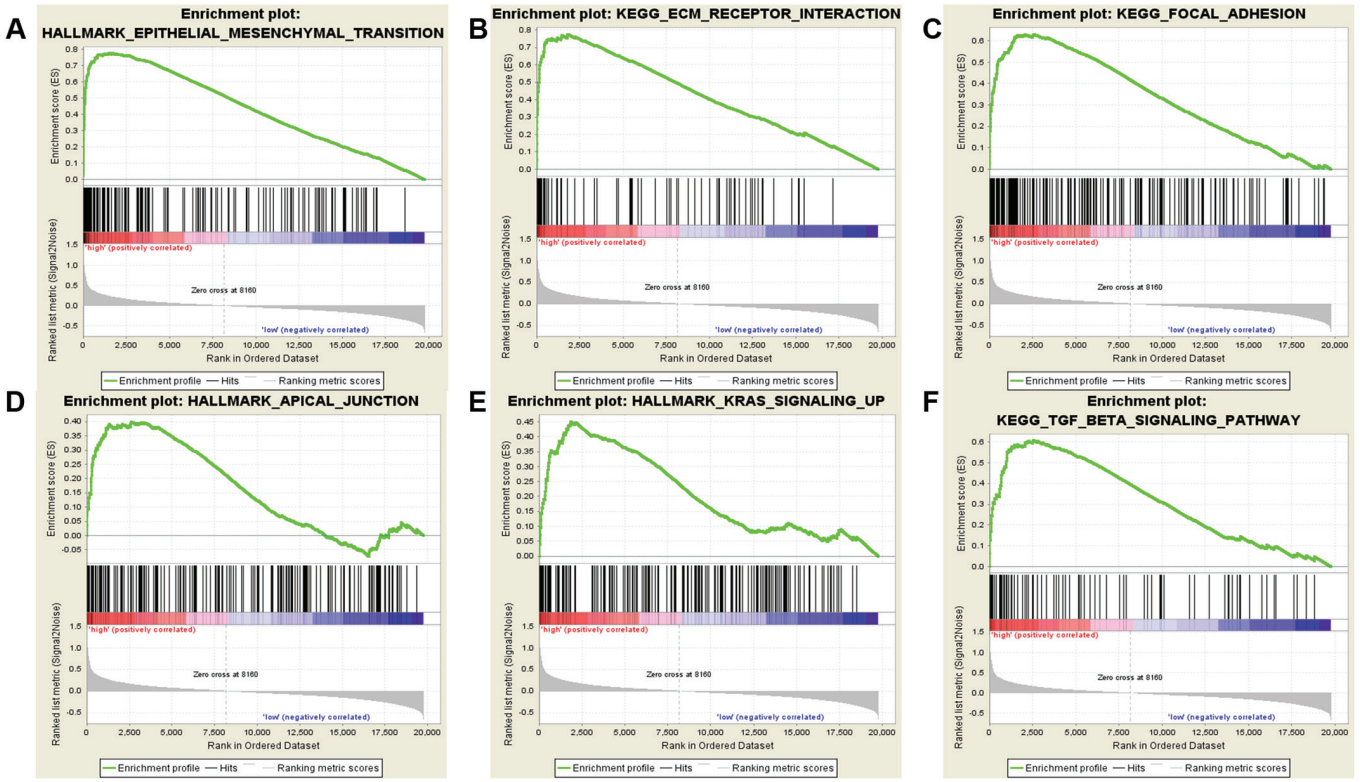


Figure S3. Gene set enrichment analysis of signaling pathways based on The Cancer Genome Atlas - kidney renal clear cell carcinoma datasets. Enrichment plots for (A) the hallmark epithelial-mesenchymal transition, (B) KEGG-ECM receptor interaction; (C) KEGG focal adhesion, (D) the hallmark apical junction, (E) the hallmark KRAS signaling upregulated and (F) KEGG TGF-β signaling pathway. KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor.

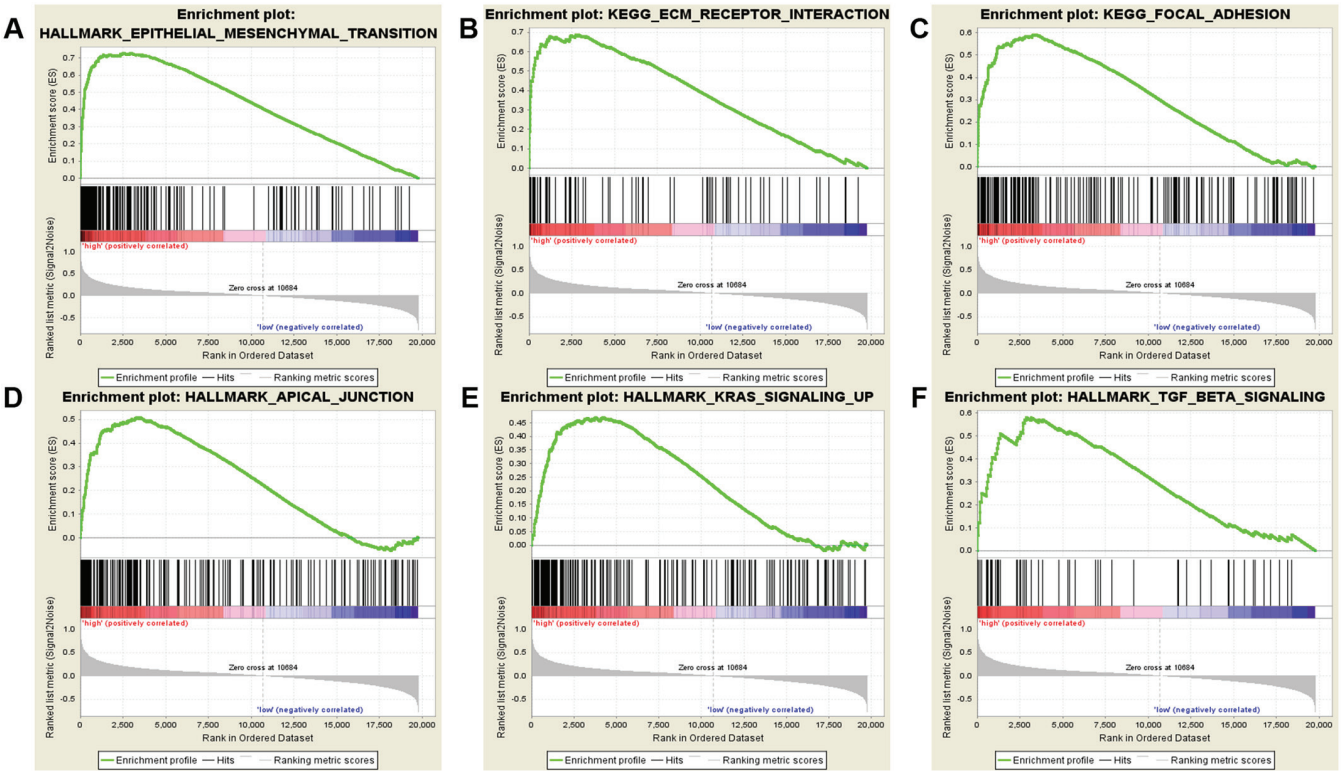


Figure S4. Gene set enrichment analysis of signaling pathways based on The Cancer Genome Atlas - lung adenocarcinoma datasets. Enrichment plots for (A) the hallmark epithelial-mesenchymal transition, (B) KEGG-ECM receptor interaction; (C) KEGG focal adhesion, (D) the hallmark apical junction, (E) the hallmark KRAS signaling upregulated and (F) KEGG TGF-β signaling pathway. KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor.

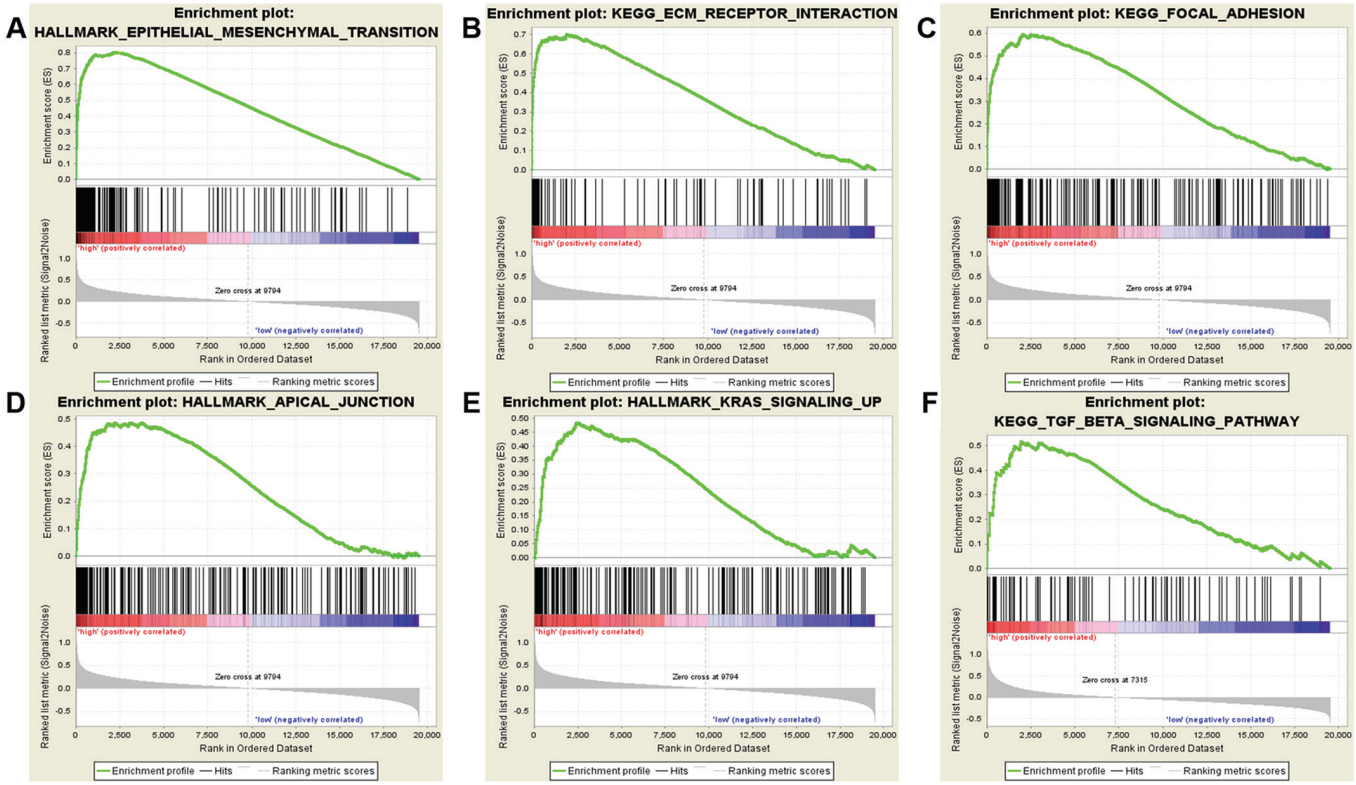


Figure S5. Gene set enrichment analysis of signaling pathways based on The Cancer Genome Atlas - lung squamous cell carcinoma datasets. Enrichment plots for (A) the hallmark epithelial-mesenchymal transition, (B) KEGG-ECM receptor interaction; (C) KEGG focal adhesion, (D) the hallmark apical junction, (E) the hallmark KRAS signaling upregulated and (F) KEGG TGF-β signaling pathway. KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor.

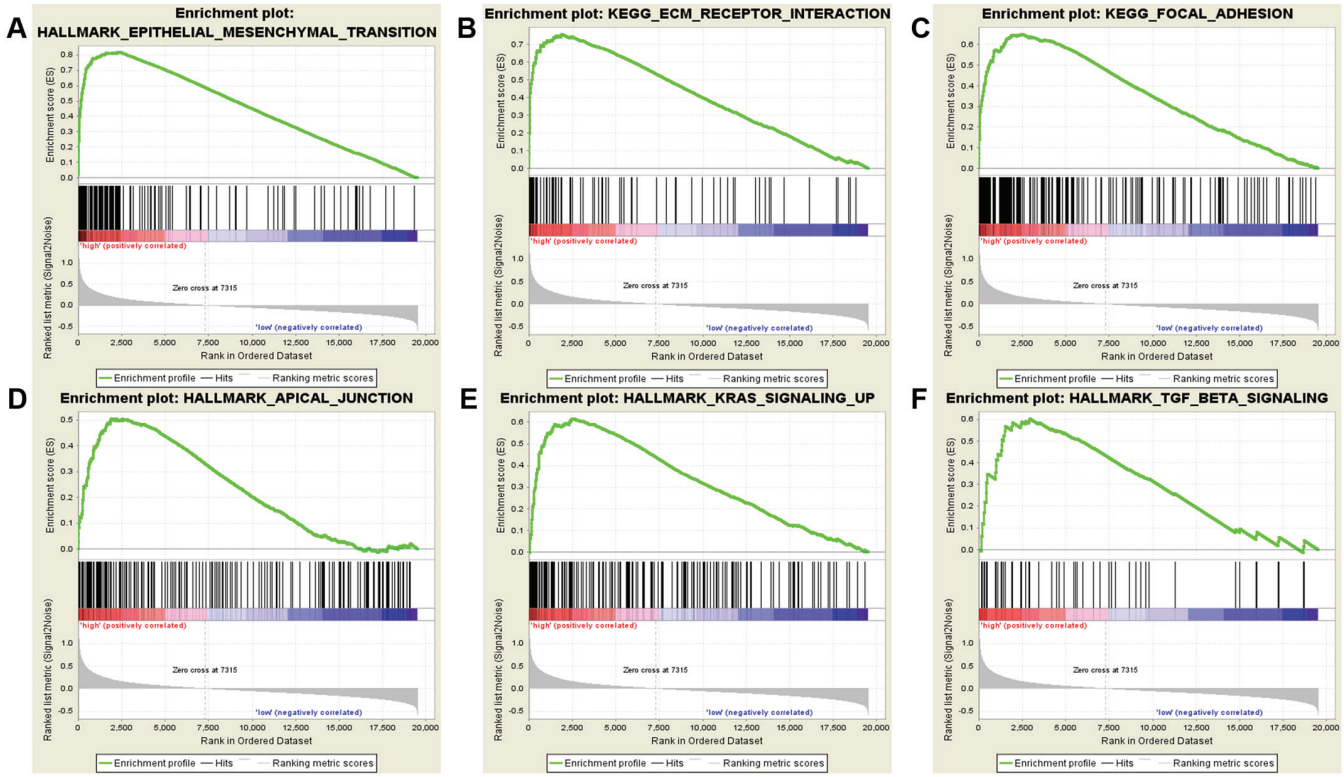


Figure S6. Gene set enrichment analysis of signaling pathways based on The Cancer Genome Atlas - skin cutaneous melanoma datasets. Enrichment plots for (A) the hallmark epithelial-mesenchymal transition, (B) KEGG-ECM receptor interaction; (C) KEGG focal adhesion, (D) the hallmark apical junction, (E) the hallmark KRAS signaling upregulated and (F) KEGG TGF-β signaling pathway. KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor.

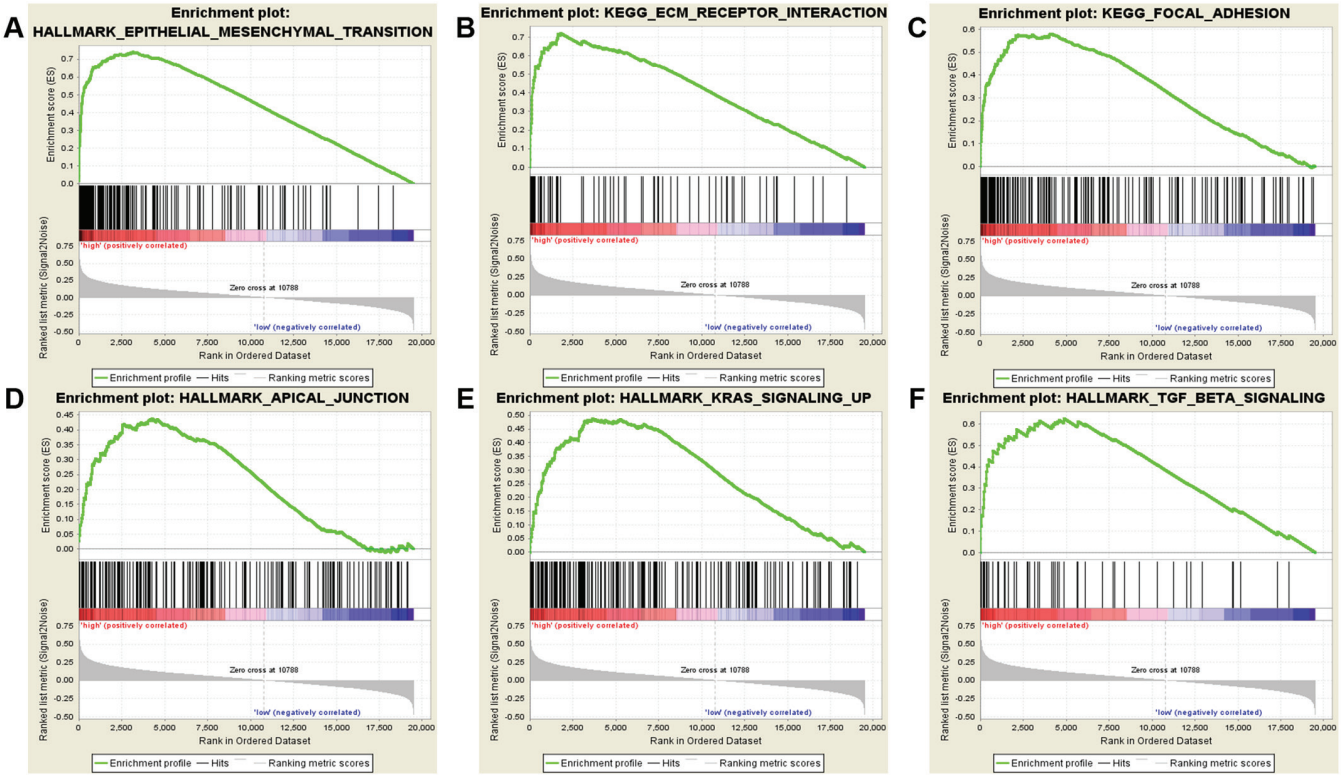


Figure S7. Gene set enrichment analysis of signaling pathways based on The Cancer Genome Atlas - stomach adenocarcinoma datasets. Enrichment plots for (A) the hallmark epithelial-mesenchymal transition, (B) KEGG-ECM receptor interaction; (C) KEGG focal adhesion, (D) the hallmark apical junction, (E) the hallmark KRAS signaling upregulated and (F) KEGG TGF-β signaling pathway. KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor.

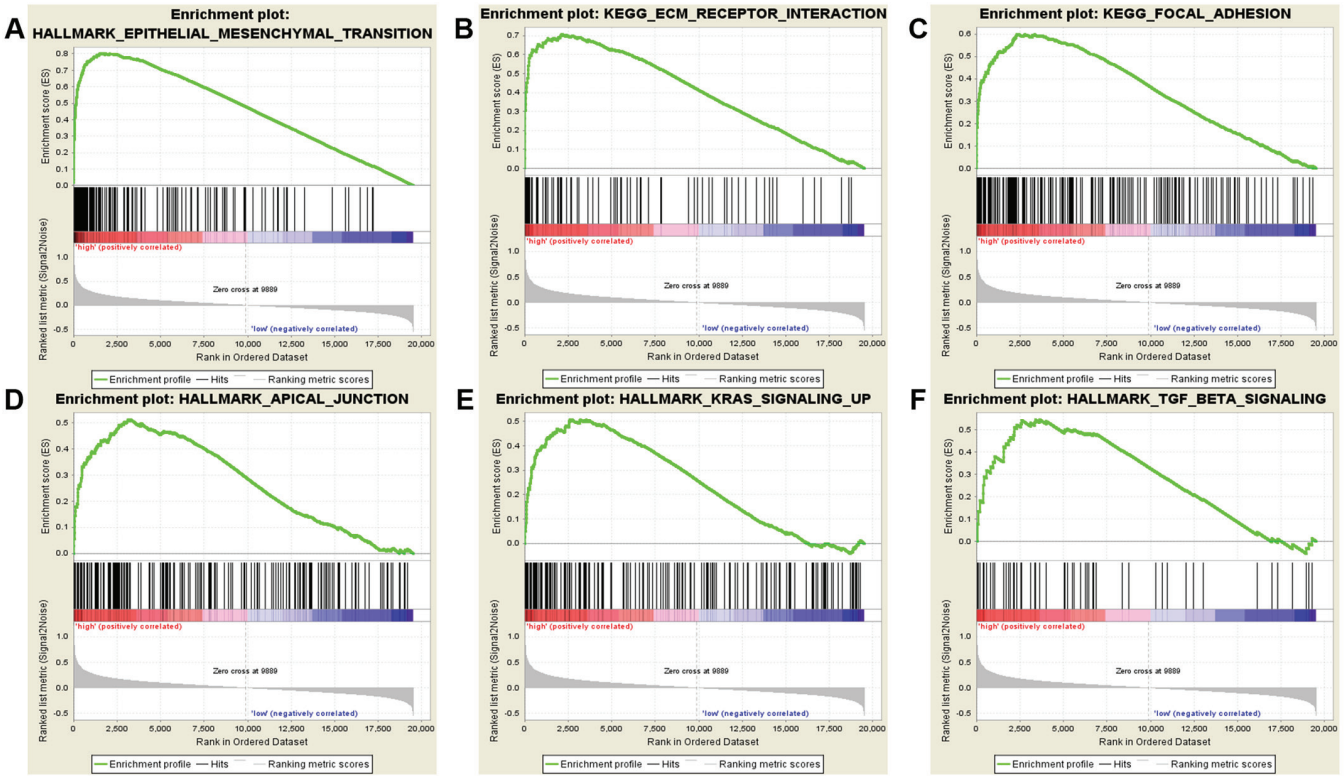


Table SI. Overlapping genesets associated with high long intergenic non-coding RNA 1614 expression in eight datasets.

| Name | BLCA | BRCA | HNSC | KIRC | LUAD | LUSC | SKCM | STAD |
|---|---|---|---|---|---|---|---|---|
| HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION | 2.319977 | 2.421568 | 2.251603 | 2.295864 | 2.354199 | 2.436062 | 2.329045 | 2.42547 |
| KEGG_ECM_RECEPTOR_INTERACTION | 2.228237 | 2.447187 | 2.214272 | 2.339243 | 2.170209 | 2.292903 | 2.416589 | 2.244313 |
| KEGG_FOCAL_ADHESION | 2.245701 | 2.402377 | 2.153617 | 2.322943 | 2.161017 | 2.385017 | 2.303515 | 2.283906 |
| HALLMARK_ANGIOGENESIS | 2.039228 | 2.417417 | 1.993366 | 2.145896 | 2.015657 | 2.16215 | 2.12799 | 2.322704 |
| HALLMARK_KRAS_SIGNALING_UP | 2.076869 | 1.803808 | 1.974417 | 1.941858 | 1.930524 | 2.382318 | 1.904406 | 2.132223 |
| HALLMARK_APICAL_JUNCTION | 2.238599 | 1.626286 | 1.959682 | 2.153307 | 1.919788 | 2.111226 | 1.811451 | 2.094329 |
| HALLMARK_TGF_BETA_SIGNALING | 1.782916 | 2.185035 | 2.07431 | 1.868891 | 1.544537 | 2.111406 | 2.086891 | 1.851744 |
| KEGG_TGF_BETA_SIGNALING_PATHWAY | 1.773944 | 2.237942 | 2.010778 | 1.833763 | 1.643181 | 2.053812 | 1.874222 | 2.018398 |
| KEGG_PATHWAYS_IN_CANCER | 1.801834 | 1.709585 | 1.916503 | 1.839816 | 1.677507 | 1.766175 | 2.016903 | 2.001147 |
| HALLMARK_APOPTOSIS | 1.948465 | 1.472098 | 1.647255 | 1.609501 | 1.968342 | 1.944486 | 1.596243 | 2.420888 |
| KEGG_MELANOMA | 1.957388 | 1.537822 | 1.925128 | 1.32304 | 1.890394 | 1.759874 | 1.779419 | 1.999465 |
| KEGG_GAP_JUNCTION | 1.86225 | 1.758253 | 1.813051 | 1.850384 | 1.844161 | 1.578778 | 1.899272 | 1.476961 |
| KEGG_SMALL_CELL_LUNG_CANCER | 1.576375 | 1.611174 | 1.797904 | 1.773829 | 1.623433 | 1.643442 | 1.763465 | 1.893137 |
| KEGG_RENAL_CELL_CARCINOMA | 1.540688 | 1.469492 | 1.872896 | 1.493913 | 1.789058 | 1.358703 | 1.770554 | 2.08042 |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 2.159269 | 0.796984 | 1.606492 | 1.628884 | 1.53571 | 2.1555 | 1.757237 | 1.67177 |
| KEGG_PANCREATIC_CANCER | 1.493728 | 1.519641 | 1.702961 | 1.609916 | 1.68741 | 1.36677 | 1.838292 | 2.006617 |
| HALLMARK_TNFA_SIGNALING_VIA_NFKB | 1.774 | 0.975652 | 1.319184 | 1.405842 | 1.642565 | 2.060267 | 1.816272 | 1.992929 |
| KEGG_GLIOMA | 1.785677 | 1.141955 | 1.901312 | 1.709631 | 1.681051 | 1.424286 | 1.853801 | 1.472442 |
| KEGG_MAPK_SIGNALING_PATHWAY | 1.640697 | 1.398966 | 1.969788 | 1.56787 | 1.31722 | 1.467678 | 1.737818 | 1.674826 |
| KEGG_PROSTATE_CANCER | 1.543862 | 1.512227 | 1.992295 | 1.175577 | 1.553706 | 1.396537 | 1.753545 | 1.729097 |
| KEGG_CHRONIC_MYELOID_LEUKEMIA | 1.308981 | 1.238759 | 1.845025 | 1.632581 | 1.43094 | 1.288406 | 1.745753 | 1.749182 |
| KEGG_ADHERENS_JUNCTION | 1.54966 | 1.858174 | 1.732766 | 1.557626 | 1.097652 | 1.315099 | 1.46218 | 1.313376 |
| KEGG_WNT_SIGNALING_PATHWAY | 1.442298 | 1.483091 | 2.005016 | 1.638382 | 0.757474 | 1.09438 | 1.64614 | 1.555504 |
| KEGG_BLADDER_CANCER | 1.307758 | 0.988674 | 1.429029 | 1.341178 | 1.538679 | 1.255317 | 1.420665 | 1.801741 |

BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; HNSC, head and neck squamous cell carcinoma; KIRC, kidney renal clear cell carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; SKCM, skin cutaneous melanoma; STAD, stomach adenocarcinoma; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor; TNF, tumor necrosis factor; MAPK, mitogen-activated protein kinase.

Table SII. Genesets associated with high long intergenic non-coding RNA 1614 expression in the BLCA dataset.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION | 196 | 0.771722 | 2.319977 | 0 | 0 |
| HALLMARK_APICAL_JUNCTION | 199 | 0.557594 | 2.238599 | 0 | 0 |
| KEGG_FOCAL_ADHESION | 199 | 0.612775 | 2.245701 | 0 | 0 |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 74 | 0.642188 | 2.23691 | 0 | 0 |
| KEGG_ECM_RECEPTOR_INTERACTION | 84 | 0.717495 | 2.228237 | 0 | 0 |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 116 | 0.580663 | 2.218888 | 0 | 0 |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 212 | 0.531848 | 2.160687 | 0 | 0 |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 131 | 0.637858 | 2.159269 | 0 | 0 |
| KEGG_DILATED_CARDIOMYOPATHY | 90 | 0.600227 | 2.078292 | 0.001946 | 0.001232 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 258 | 0.591364 | 2.078322 | 0 | 0.001408 |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 83 | 0.601616 | 2.060778 | 0 | 0.001589 |
| HALLMARK_COAGULATION | 136 | 0.593564 | 2.140262 | 0 | 0.001605 |
| HALLMARK_MYOGENESIS | 200 | 0.567674 | 2.065345 | 0 | 0.003222 |
| HALLMARK_KRAS_SIGNALING_UP | 199 | 0.521154 | 2.076869 | 0 | 0.00345 |
| HALLMARK_ANGIOGENESIS | 36 | 0.654531 | 2.039228 | 0 | 0.004842 |
| HALLMARK_IL2_STAT5_SIGNALING | 199 | 0.500864 | 2.010231 | 0.001984 | 0.004986 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE | 22 | 0.733296 | 1.994859 | 0 | 0.005377 |
| HALLMARK_INFLAMMATORY_RESPONSE | 198 | 0.608684 | 1.998819 | 0.001972 | 0.005433 |
| HALLMARK_COMPLEMENT | 195 | 0.552992 | 2.010494 | 0.004098 | 0.005699 |
| KEGG_MELANOMA | 71 | 0.552394 | 1.957388 | 0 | 0.007548 |
| KEGG_HEMATOPOIETIC_CELL_LINEAGE | 85 | 0.665358 | 1.961719 | 0.005769 | 0.007695 |
| KEGG_VIRAL_MYOCARDITIS | 68 | 0.62243 | 1.92743 | 0.002016 | 0.008785 |
| HALLMARK_APOPTOSIS | 160 | 0.466135 | 1.948465 | 0 | 0.009306 |
| KEGG_CHEMOKINE_SIGNALING_PATHWAY | 186 | 0.520279 | 1.92985 | 0 | 0.009322 |
| KEGG_LEISHMANIA_INFECTION | 69 | 0.65531 | 1.904899 | 0.006048 | 0.010947 |
| HALLMARK_ALLOGRAFT_REJECTION | 200 | 0.638623 | 1.862985 | 0.007874 | 0.014336 |
| HALLMARK_IL6_JAK_STAT3_SIGNALING | 87 | 0.589208 | 1.864457 | 0.003968 | 0.015057 |
| KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY | 130 | 0.530583 | 1.859268 | 0.003968 | 0.015942 |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES | 69 | 0.605638 | 1.870441 | 0 | 0.016017 |
| HALLMARK_UV_RESPONSE_DN | 144 | 0.482571 | 1.86515 | 0.007937 | 0.016426 |
| KEGG_GAP_JUNCTION | 89 | 0.479607 | 1.86225 | 0.00202 | 0.016521 |
| KEGG_PRION_DISEASES | 35 | 0.586544 | 1.849198 | 0 | 0.016554 |
| KEGG_AUTOIMMUNE_THYROID_DISEASE | 50 | 0.688626 | 1.830436 | 0.014028 | 0.019144 |
| KEGG_PATHWAYS_IN_CANCER | 324 | 0.404299 | 1.801834 | 0 | 0.024294 |
| HALLMARK_TGF_BETA_SIGNALING | 54 | 0.508541 | 1.782916 | 0.018182 | 0.027128 |
| KEGG_GLIOMA | 65 | 0.462753 | 1.785677 | 0.007619 | 0.027259 |
| HALLMARK_TNFA_SIGNALING_VIA_NFKB | 199 | 0.534002 | 1.774 | 0.031683 | 0.027318 |
| KEGG_TGF_BETA_SIGNALING_PATHWAY | 85 | 0.459999 | 1.773944 | 0.005952 | 0.029232 |

Table SII. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_JAK_STAT_SIGNALING_PATHWAY | 151 | 0.461849 | 1.765246 | 0.005929 | 0.030705 |
| KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION | 115 | 0.456768 | 1.736105 | 0.005607 | 0.038678 |
| KEGG_ASTHMA | 28 | 0.678617 | 1.717012 | 0.032064 | 0.044638 |
| HALLMARK_APICAL_SURFACE | 44 | 0.436941 | 1.653417 | 0.003795 | 0.053039 |
| HALLMARK_INTERFERON_GAMMA_RESPONSE | 197 | 0.577285 | 1.665487 | 0.062378 | 0.05405 |
| HALLMARK_HYPOXIA | 198 | 0.415757 | 1.656495 | 0.022449 | 0.054605 |
| KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION | 46 | 0.669884 | 1.674914 | 0.033465 | 0.055274 |
| KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY | 107 | 0.467273 | 1.670957 | 0.030948 | 0.055874 |
| KEGG_MELANOGENESIS | 101 | 0.415063 | 1.681677 | 0.002016 | 0.056271 |
| KEGG_ALLOGRAFT_REJECTION | 35 | 0.728434 | 1.665629 | 0.04008 | 0.056318 |
| KEGG_GRAFT_VERSUS_HOST_DISEASE | 37 | 0.722405 | 1.675724 | 0.030303 | 0.057033 |
| KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION | 79 | 0.585631 | 1.684183 | 0.022774 | 0.057453 |
| KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION | 55 | 0.47341 | 1.639263 | 0.020243 | 0.06472 |
| KEGG_MAPK_SIGNALING_PATHWAY | 265 | 0.366536 | 1.640697 | 0 | 0.066092 |
| KEGG_AXON_GUIDANCE | 128 | 0.389511 | 1.621698 | 0.012121 | 0.071056 |
| KEGG_TYPE_I_DIABETES_MELLITUS | 41 | 0.63753 | 1.617763 | 0.054108 | 0.071226 |
| KEGG_SMALL_CELL_LUNG_CANCER | 84 | 0.402324 | 1.576375 | 0.028958 | 0.091186 |
| KEGG_ADHERENS_JUNCTION | 73 | 0.408986 | 1.54966 | 0.042636 | 0.092675 |
| KEGG_RENAL_CELL_CARCINOMA | 70 | 0.406475 | 1.540688 | 0.017375 | 0.093324 |
| KEGG_PROSTATE_CANCER | 89 | 0.393378 | 1.543862 | 0.017682 | 0.093692 |
| KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY | 74 | 0.486641 | 1.550238 | 0.041667 | 0.094325 |
| KEGG_ACUTE_MYELOID_LEUKEMIA | 57 | 0.413038 | 1.553389 | 0.015717 | 0.094573 |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS | 95 | 0.381462 | 1.534671 | 0.046211 | 0.094719 |
| KEGG_RENIN_ANGIOTENSIN_SYSTEM | 17 | 0.559321 | 1.556632 | 0.029126 | 0.09493 |
| KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION | 270 | 0.392862 | 1.558765 | 0.007952 | 0.096584 |
| KEGG_CALCIUM_SIGNALING_PATHWAY | 176 | 0.393608 | 1.562919 | 0.011788 | 0.097038 |
| KEGG_GLYCOSAMINOGLYCAN_DEGRADATION | 21 | 0.539599 | 1.509912 | 0.07722 | 0.1021 |
| KEGG_PRIMARY_IMMUNODEFICIENCY | 35 | 0.646265 | 1.516436 | 0.096267 | 0.10259 |
| KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY | 101 | 0.412809 | 1.512543 | 0.051335 | 0.102676 |
| HALLMARK_HEDGEHOG_SIGNALING | 36 | 0.455952 | 1.523636 | 0.067308 | 0.103532 |
| KEGG_TIGHT_JUNCTION | 130 | 0.352847 | 1.491581 | 0.030364 | 0.109215 |
| HALLMARK_NOTCH_SIGNALING | 32 | 0.402275 | 1.502247 | 0.018519 | 0.109303 |
| KEGG_PANCREATIC_CANCER | 70 | 0.388892 | 1.493728 | 0.035019 | 0.109965 |
| KEGG_WNT_SIGNALING_PATHWAY | 149 | 0.344003 | 1.442298 | 0.042945 | 0.140015 |
| HALLMARK_ANDROGEN_RESPONSE | 100 | 0.34942 | 1.420357 | 0.068627 | 0.158972 |
| KEGG_COLORECTAL_CANCER | 62 | 0.379921 | 1.41356 | 0.078585 | 0.160465 |
| KEGG_LONG_TERM_POTENTIATION | 69 | 0.365532 | 1.400346 | 0.049524 | 0.168912 |

Table SII. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY | 61 | 0.413089 | 1.388904 | 0.11134 | 0.176187 |
| KEGG_LONG_TERM_DEPRESSION | 70 | 0.350013 | 1.375037 | 0.054159 | 0.181693 |
| KEGG_NEUROTROPHIN_SIGNALING_PATHWAY | 126 | 0.331553 | 1.376742 | 0.068898 | 0.183667 |
| KEGG_ENDOMETRIAL_CANCER | 52 | 0.368594 | 1.353094 | 0.095331 | 0.199642 |
| KEGG_LYSOSOME | 119 | 0.377673 | 1.343491 | 0.166031 | 0.205186 |
| KEGG_BLADDER_CANCER | 41 | 0.362698 | 1.307758 | 0.133462 | 0.222798 |
| KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS | 131 | 0.538203 | 1.321741 | 0.12326 | 0.22299 |
| KEGG_CHRONIC_MYELOID_LEUKEMIA | 73 | 0.335981 | 1.308981 | 0.113725 | 0.225051 |
| KEGG_APOPTOSIS | 86 | 0.337731 | 1.311325 | 0.140625 | 0.226178 |
| KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT | 38 | 0.370855 | 1.31314 | 0.14741 | 0.228042 |
| HALLMARK_INTERFERON_ALPHA_RESPONSE | 94 | 0.514099 | 1.307359 | 0.261122 | 0.249277 |

BLCA, bladder urothelial carcinoma; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor; TNF, tumor necrosis factor; MAPK, mitogen-activated protein kinase; IL, interleukin; STAT, signal transducer and activator of transcription; JAK, Janus kinase; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table SIII. Genesets associated with high long intergenic non-coding RNA 1614 expression in the BRCA dataset.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION | 196 | 0.777813 | 2.421568 | 0 | 0 |
| HALLMARK_ANGIOGENESIS | 36 | 0.766313 | 2.417417 | 0 | 0 |
| KEGG_ECM_RECEPTOR_INTERACTION | 84 | 0.775224 | 2.447187 | 0 | 0 |
| KEGG_FOCAL_ADHESION | 199 | 0.630382 | 2.402377 | 0 | 0 |
| KEGG_TGF_BETA_SIGNALING_PATHWAY | 85 | 0.607786 | 2.237942 | 0 | 0 |
| HALLMARK_TGF_BETA_SIGNALING | 54 | 0.622548 | 2.185035 | 0 | 1.69E-04 |
| HALLMARK_UV_RESPONSE_DN | 144 | 0.58956 | 2.216393 | 0 | 2.25E-04 |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 74 | 0.560801 | 2.054411 | 0 | 0.004028 |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 212 | 0.460189 | 2.021483 | 0 | 0.005988 |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 83 | 0.558046 | 1.951621 | 0 | 0.01116 |
| KEGG_DILATED_CARDIOMYOPATHY | 90 | 0.539931 | 1.963418 | 0 | 0.011651 |
| HALLMARK_COAGULATION | 136 | 0.490598 | 1.899169 | 0.001876 | 0.014068 |
| KEGG_HEDGEHOG_SIGNALING_PATHWAY | 56 | 0.494591 | 1.921715 | 0 | 0.014662 |
| KEGG_ADHERENS_JUNCTION | 73 | 0.500317 | 1.858174 | 0 | 0.027081 |
| HALLMARK_PROTEIN_SECRETION | 96 | 0.526151 | 1.82264 | 0.018443 | 0.027395 |
| HALLMARK_KRAS_SIGNALING_UP | 199 | 0.450507 | 1.803808 | 0.004008 | 0.028826 |
| KEGG_GAP_JUNCTION | 89 | 0.423552 | 1.758253 | 0 | 0.064256 |
| HALLMARK_HEDGEHOG_SIGNALING | 36 | 0.487468 | 1.626071 | 0.024291 | 0.068667 |
| HALLMARK_APICAL_JUNCTION | 199 | 0.399882 | 1.626286 | 0.018219 | 0.076297 |
| HALLMARK_ANDROGEN_RESPONSE | 100 | 0.409681 | 1.636199 | 0.02045 | 0.08193 |
| KEGG_PATHWAYS_IN_CANCER | 324 | 0.366614 | 1.709585 | 0 | 0.087864 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE | 22 | 0.587064 | 1.676773 | 0.036538 | 0.10441 |
| KEGG_AXON_GUIDANCE | 128 | 0.386086 | 1.65506 | 0.009881 | 0.114356 |
| KEGG_SMALL_CELL_LUNG_CANCER | 84 | 0.403775 | 1.611174 | 0.016878 | 0.145501 |
| HALLMARK_APOPTOSIS | 160 | 0.337672 | 1.472098 | 0.039841 | 0.148472 |
| HALLMARK_MITOTIC_SPINDLE | 198 | 0.373894 | 1.437008 | 0.116232 | 0.163153 |
| HALLMARK_COMPLEMENT | 195 | 0.362682 | 1.406026 | 0.107724 | 0.171443 |
| HALLMARK_INFLAMMATORY_RESPONSE | 198 | 0.389757 | 1.367417 | 0.172962 | 0.189631 |
| KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION | 115 | 0.350933 | 1.5078 | 0.023438 | 0.216458 |
| KEGG_MELANOMA | 71 | 0.378529 | 1.537822 | 0.012474 | 0.219302 |
| KEGG_PROSTATE_CANCER | 89 | 0.368793 | 1.512227 | 0.016162 | 0.222711 |
| KEGG_PANCREATIC_CANCER | 70 | 0.376861 | 1.519641 | 0.032587 | 0.226682 |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES | 69 | 0.425283 | 1.460102 | 0.074 | 0.229931 |
| KEGG_O_GLYCAN_BIOSYNTHESIS | 27 | 0.46422 | 1.467664 | 0.071006 | 0.230852 |
| KEGG_WNT_SIGNALING_PATHWAY | 149 | 0.325416 | 1.483091 | 0.018 | 0.235606 |
| KEGG_RENAL_CELL_CARCINOMA | 70 | 0.36972 | 1.469492 | 0.056311 | 0.239651 |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 116 | 0.371786 | 1.43576 | 0.069388 | 0.249022 |

BRCA, breast invasive carcinoma; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor; TNF, tumor necrosis factor; MAPK, mitogen-activated protein kinase; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table SIV. Genesets associated with high long intergenic non-coding RNA 1614 expression in the HNSC dataset.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION | 196 | 0.753639 | 2.251603 | 0 | 0 |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 83 | 0.690327 | 2.200774 | 0.001946 | 0.001528 |
| KEGG_DILATED_CARDIOMYOPATHY | 90 | 0.665728 | 2.169664 | 0.001942 | 0.001554 |
| HALLMARK_TGF_BETA_SIGNALING | 54 | 0.650099 | 2.07431 | 0 | 0.002732 |
| KEGG_ECM_RECEPTOR_INTERACTION | 84 | 0.727786 | 2.214272 | 0 | 0.003057 |
| KEGG_FOCAL_ADHESION | 199 | 0.623859 | 2.153617 | 0 | 0.003336 |
| HALLMARK_UV_RESPONSE_DN | 144 | 0.603493 | 2.042789 | 0 | 0.003971 |
| HALLMARK_COAGULATION | 136 | 0.562083 | 2.074818 | 0 | 0.004098 |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 74 | 0.646619 | 2.109686 | 0.002028 | 0.006504 |
| HALLMARK_ANGIOGENESIS | 36 | 0.677673 | 1.993366 | 0 | 0.007317 |
| HALLMARK_NOTCH_SIGNALING | 32 | 0.587326 | 1.996123 | 0 | 0.0077 |
| HALLMARK_KRAS_SIGNALING_UP | 199 | 0.503581 | 1.974417 | 0 | 0.008271 |
| HALLMARK_APICAL_JUNCTION | 199 | 0.500604 | 1.959682 | 0.001972 | 0.008377 |
| HALLMARK_HEDGEHOG_SIGNALING | 36 | 0.606231 | 1.961273 | 0 | 0.0089 |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 212 | 0.532897 | 2.064222 | 0 | 0.009954 |
| HALLMARK_COMPLEMENT | 195 | 0.496476 | 1.907617 | 0 | 0.014148 |
| KEGG_PROSTATE_CANCER | 89 | 0.548392 | 1.992295 | 0 | 0.014816 |
| KEGG_WNT_SIGNALING_PATHWAY | 149 | 0.510554 | 2.005016 | 0 | 0.014852 |
| KEGG_LYSOSOME | 119 | 0.575871 | 1.967552 | 0.002049 | 0.015509 |
| KEGG_TGF_BETA_SIGNALING_PATHWAY | 85 | 0.562366 | 2.010778 | 0 | 0.015787 |
| KEGG_MAPK_SIGNALING_PATHWAY | 265 | 0.472651 | 1.969788 | 0 | 0.01657 |
| HALLMARK_IL2_STAT5_SIGNALING | 199 | 0.474956 | 1.866001 | 0.001992 | 0.016778 |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 116 | 0.525802 | 1.958277 | 0 | 0.017008 |
| KEGG_GLYCOSAMINOGLYCAN_DEGRADATION | 21 | 0.702583 | 2.011474 | 0.002114 | 0.017379 |
| HALLMARK_MYOGENESIS | 200 | 0.6318 | 1.869159 | 0.023301 | 0.018072 |
| KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION | 115 | 0.505442 | 1.938053 | 0 | 0.020402 |
| KEGG_MELANOMA | 71 | 0.521695 | 1.925128 | 0 | 0.020667 |
| KEGG_AXON_GUIDANCE | 128 | 0.509164 | 1.928918 | 0 | 0.021199 |
| KEGG_PATHWAYS_IN_CANCER | 324 | 0.461868 | 1.916503 | 0 | 0.022992 |
| KEGG_GLIOMA | 65 | 0.53734 | 1.901312 | 0 | 0.025826 |
| KEGG_MELANOGENESIS | 101 | 0.498381 | 1.887427 | 0 | 0.027847 |
| KEGG_RENAL_CELL_CARCINOMA | 70 | 0.525635 | 1.872896 | 0 | 0.030307 |
| HALLMARK_HYPOXIA | 198 | 0.449744 | 1.773137 | 0.014141 | 0.031121 |
| HALLMARK_PROTEIN_SECRETION | 96 | 0.542629 | 1.785888 | 0.007797 | 0.031137 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE | 22 | 0.722735 | 1.863408 | 0.002033 | 0.031588 |
| KEGG_CHRONIC_MYELOID_LEUKEMIA | 73 | 0.537214 | 1.845025 | 0.004073 | 0.035431 |
| KEGG_SMALL_CELL_LUNG_CANCER | 84 | 0.504799 | 1.797904 | 0.002092 | 0.039018 |

Table SIV. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_VIBRIO_CHOLERAE_INFECTION | 53 | 0.514536 | 1.822542 | 0.002096 | 0.039187 |
| KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES | 15 | 0.720682 | 1.827701 | 0.002024 | 0.039295 |
| HALLMARK_INFLAMMATORY_RESPONSE | 198 | 0.49578 | 1.738713 | 0.033268 | 0.03947 |
| KEGG_CALCIUM_SIGNALING_PATHWAY | 176 | 0.4504 | 1.800665 | 0 | 0.039623 |
| KEGG_INSULIN_SIGNALING_PATHWAY | 137 | 0.456133 | 1.789806 | 0.00202 | 0.039827 |
| KEGG_GAP_JUNCTION | 89 | 0.48678 | 1.813051 | 0 | 0.040669 |
| KEGG_COLORECTAL_CANCER | 62 | 0.516512 | 1.801913 | 0.004098 | 0.040862 |
| KEGG_LONG_TERM_POTENTIATION | 69 | 0.484401 | 1.779365 | 0.003922 | 0.041129 |
| KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY | 67 | 0.490182 | 1.78263 | 0.002053 | 0.041507 |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS | 95 | 0.486802 | 1.802938 | 0 | 0.042208 |
| KEGG_TYPE_II_DIABETES_MELLITUS | 46 | 0.495977 | 1.758455 | 0.001898 | 0.044627 |
| HALLMARK_ANDROGEN_RESPONSE | 100 | 0.45954 | 1.713198 | 0.009843 | 0.044905 |
| KEGG_ERBB_SIGNALING_PATHWAY | 87 | 0.48899 | 1.758846 | 0.004264 | 0.045626 |
| KEGG_NEUROTROPHIN_SIGNALING_PATHWAY | 126 | 0.471477 | 1.76202 | 0.004193 | 0.045831 |
| KEGG_ENDOMETRIAL_CANCER | 52 | 0.530646 | 1.748508 | 0.004193 | 0.046904 |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES | 69 | 0.543874 | 1.738868 | 0.023211 | 0.050021 |
| KEGG_ADHERENS_JUNCTION | 73 | 0.525517 | 1.732766 | 0.010504 | 0.051004 |
| KEGG_PRION_DISEASES | 35 | 0.516727 | 1.725 | 0.011952 | 0.05175 |
| KEGG_NOTCH_SIGNALING_PATHWAY | 47 | 0.508702 | 1.725896 | 0.008081 | 0.052387 |
| KEGG_ACUTE_MYELOID_LEUKEMIA | 57 | 0.496206 | 1.708939 | 0.018072 | 0.055858 |
| KEGG_ENDOCYTOSIS | 178 | 0.427705 | 1.710247 | 0.00404 | 0.056652 |
| KEGG_VEGF_SIGNALING_PATHWAY | 75 | 0.431435 | 1.697582 | 0.005882 | 0.056855 |
| KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM | 76 | 0.471864 | 1.693375 | 0.008147 | 0.057516 |
| KEGG_PANCREATIC_CANCER | 70 | 0.474104 | 1.702961 | 0.01222 | 0.057552 |
| KEGG_SPHINGOLIPID_METABOLISM | 39 | 0.498138 | 1.700686 | 0.006186 | 0.057576 |
| KEGG_LONG_TERM_DEPRESSION | 70 | 0.447329 | 1.697811 | 0 | 0.058083 |
| HALLMARK_IL6_JAK_STAT3_SIGNALING | 87 | 0.498139 | 1.667263 | 0.043825 | 0.058404 |
| KEGG_NON_SMALL_CELL_LUNG_CANCER | 54 | 0.48138 | 1.686725 | 0.010183 | 0.059525 |
| KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION | 67 | 0.453594 | 1.67652 | 0.020747 | 0.062813 |
| HALLMARK_APOPTOSIS | 160 | 0.396309 | 1.647255 | 0.015905 | 0.064131 |
| KEGG_HEDGEHOG_SIGNALING_PATHWAY | 56 | 0.479917 | 1.666388 | 0.01875 | 0.06597 |
| KEGG_TIGHT_JUNCTION | 130 | 0.423674 | 1.661361 | 0.008333 | 0.066402 |
| HALLMARK_WNT_BETA_CATENIN_SIGNALING | 42 | 0.479101 | 1.625152 | 0.017682 | 0.070907 |
| KEGG_INOSITOL_PHOSPHATE_METABOLISM | 54 | 0.487308 | 1.645451 | 0.020921 | 0.072522 |
| KEGG_CHEMOKINE_SIGNALING_PATHWAY | 186 | 0.450821 | 1.637972 | 0.036072 | 0.073265 |
| KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM | 44 | 0.474493 | 1.639355 | 0.017822 | 0.074035 |
| KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY | 101 | 0.449768 | 1.625586 | 0.03252 | 0.078167 |
| KEGG_BASAL_CELL_CARCINOMA | 55 | 0.484217 | 1.61916 | 0.028926 | 0.080287 |

Table SIV. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_OTHER_GLYCAN_DEGRADATION | 16 | 0.611878 | 1.615559 | 0.024194 | 0.080622 |
| KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION | 55 | 0.44812 | 1.605065 | 0.020992 | 0.08374 |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 131 | 0.466306 | 1.606492 | 0.072692 | 0.084209 |
| KEGG_RIBOFLAVIN_METABOLISM | 16 | 0.543992 | 1.59376 | 0.02004 | 0.086794 |
| KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION | 44 | 0.444927 | 1.595858 | 0.021696 | 0.087207 |
| KEGG_VIRAL_MYOCARDITIS | 68 | 0.51027 | 1.590791 | 0.069767 | 0.087291 |
| HALLMARK_UNFOLDED_PROTEIN_RESPONSE | 112 | 0.442236 | 1.579656 | 0.038095 | 0.08802 |
| KEGG_GNRH_SIGNALING_PATHWAY | 101 | 0.399729 | 1.580526 | 0.013752 | 0.091365 |
| KEGG_GALACTOSE_METABOLISM | 26 | 0.49801 | 1.573268 | 0.042339 | 0.094155 |
| KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY | 74 | 0.460167 | 1.568908 | 0.044088 | 0.095827 |
| HALLMARK_MITOTIC_SPINDLE | 198 | 0.474409 | 1.551773 | 0.072 | 0.097563 |
| KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS | 133 | 0.429723 | 1.562364 | 0.040254 | 0.098324 |
| KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION | 42 | 0.456865 | 1.558372 | 0.042596 | 0.099622 |
| KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY | 79 | 0.400413 | 1.535337 | 0.032882 | 0.114149 |
| KEGG_REGULATION_OF_AUTOPHAGY | 34 | 0.442792 | 1.525087 | 0.045365 | 0.114633 |
| KEGG_HEMATOPOIETIC_CELL_LINEAGE | 85 | 0.474743 | 1.526783 | 0.105364 | 0.115371 |
| KEGG_MTOR_SIGNALING_PATHWAY | 52 | 0.421719 | 1.528749 | 0.030612 | 0.115471 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE | 26 | 0.512558 | 1.531176 | 0.052743 | 0.115508 |
| KEGG_PURINE_METABOLISM | 155 | 0.378228 | 1.517622 | 0.031621 | 0.117781 |
| KEGG_N_GLYCAN_BIOSYNTHESIS | 46 | 0.48093 | 1.510098 | 0.067347 | 0.120371 |
| HALLMARK_PI3K_AKT_MTOR_SIGNALING | 105 | 0.393328 | 1.496802 | 0.053892 | 0.122289 |
| KEGG_CARDIAC_MUSCLE_CONTRACTION | 73 | 0.451845 | 1.504008 | 0.058 | 0.12349 |
| HALLMARK_HEME_METABOLISM | 193 | 0.352559 | 1.50358 | 0.019646 | 0.124223 |
| KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM | 22 | 0.463712 | 1.492119 | 0.036511 | 0.13014 |
| KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY | 61 | 0.440754 | 1.488486 | 0.084536 | 0.131169 |
| KEGG_GLYCEROPHOSPHOLIPID_METABOLISM | 76 | 0.37403 | 1.478636 | 0.034483 | 0.13673 |
| KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY | 107 | 0.434141 | 1.475976 | 0.087129 | 0.137258 |
| HALLMARK_ALLOGRAFT_REJECTION | 200 | 0.447177 | 1.46098 | 0.156126 | 0.141852 |
| KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION | 85 | 0.3949 | 1.461817 | 0.063008 | 0.145544 |
| KEGG_JAK_STAT_SIGNALING_PATHWAY | 151 | 0.382002 | 1.454262 | 0.050881 | 0.145685 |
| KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION | 23 | 0.464637 | 1.455293 | 0.0625 | 0.146601 |
| KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM | 34 | 0.432195 | 1.457099 | 0.070833 | 0.147139 |
| KEGG_GLYCEROLIPID_METABOLISM | 48 | 0.382059 | 1.434992 | 0.047131 | 0.158881 |
| KEGG_BLADDER_CANCER | 41 | 0.401481 | 1.429029 | 0.056911 | 0.161526 |
| HALLMARK_ESTROGEN_RESPONSE_EARLY | 200 | 0.32885 | 1.423506 | 0.050302 | 0.162486 |
| HALLMARK_GLYCOLYSIS | 199 | 0.340456 | 1.413291 | 0.079051 | 0.162878 |
| KEGG_APOPTOSIS | 86 | 0.387471 | 1.418539 | 0.102161 | 0.164869 |

Table SIV. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 258 | 0.386031 | 1.422019 | 0.118447 | 0.165714 |
| KEGG_RENIN_ANGIOTENSIN_SYSTEM | 17 | 0.536696 | 1.419291 | 0.114723 | 0.166159 |
| KEGG_DORSO_VENTRAL_AXIS_FORMATION | 24 | 0.467091 | 1.402445 | 0.105932 | 0.176194 |
| KEGG_LYSINE_DEGRADATION | 44 | 0.414718 | 1.394978 | 0.132653 | 0.180683 |
| HALLMARK_ADIPOGENESIS | 196 | 0.348521 | 1.378392 | 0.095327 | 0.185088 |
| HALLMARK_XENOBIOTIC_METABOLISM | 198 | 0.316956 | 1.370074 | 0.066277 | 0.18535 |
| KEGG_LEISHMANIA_INFECTION | 69 | 0.455201 | 1.383768 | 0.182353 | 0.186289 |
| KEGG_OOCYTE_MEIOSIS | 111 | 0.371347 | 1.384484 | 0.139721 | 0.187702 |
| KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION | 270 | 0.346582 | 1.37389 | 0.097196 | 0.192959 |
| HALLMARK_PEROXISOME | 103 | 0.325643 | 1.332848 | 0.126654 | 0.201692 |
| HALLMARK_UV_RESPONSE_UP | 156 | 0.31169 | 1.339032 | 0.089147 | 0.204254 |
| KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT | 38 | 0.417489 | 1.356393 | 0.123984 | 0.205689 |
| HALLMARK_TNFA_SIGNALING_VIA_NFKB | 199 | 0.386326 | 1.319184 | 0.18711 | 0.206154 |
| KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY | 130 | 0.38002 | 1.327866 | 0.180556 | 0.222559 |
| KEGG_PROTEIN_EXPORT | 23 | 0.478315 | 1.32851 | 0.168378 | 0.224229 |
| KEGG_HISTIDINE_METABOLISM | 28 | 0.39228 | 1.32977 | 0.0998 | 0.2254 |
| KEGG_ARGININE_AND_PROLINE_METABOLISM | 52 | 0.356231 | 1.331625 | 0.127349 | 0.22577 |
| KEGG_O_GLYCAN_BIOSYNTHESIS | 27 | 0.418689 | 1.315129 | 0.17004 | 0.232517 |
| HALLMARK_BILE_ACID_METABOLISM | 112 | 0.315891 | 1.277261 | 0.131179 | 0.236 |
| KEGG_ABC_TRANSPORTERS | 44 | 0.376058 | 1.306836 | 0.152401 | 0.236137 |
| KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS | 52 | 0.344171 | 1.30782 | 0.126761 | 0.237673 |
| HALLMARK_APICAL_SURFACE | 44 | 0.340052 | 1.259626 | 0.14346 | 0.238327 |
| HALLMARK_MTORC1_SIGNALING | 199 | 0.348648 | 1.261068 | 0.226263 | 0.244074 |

HNSC, head and neck squamous cell carcinoma; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor; TNF, tumor necrosis factor; MAPK, mitogen-activated protein kinase; IL, interleukin; STAT, signal transducer and activator of transcription; JAK, Janus kinase; PI3K, phosphatidylinositol 3-kinase; mTOR, mammalian target of rapamycin; VEGF, vascular endothelial growth factor; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table SV. Genesets associated with high long intergenic non-coding RNA 1614 expression in the KIRC dataset.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_ECM_RECEPTOR_INTERACTION | 84 | 0.687793 | 2.339243 | 0 | 0 |
| KEGG_FOCAL_ADHESION | 199 | 0.591389 | 2.322943 | 0 | 0 |
| HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION | 196 | 0.728483 | 2.295864 | 0 | 0.001699 |
| KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION | 115 | 0.534616 | 2.117786 | 0 | 0.002222 |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 74 | 0.579886 | 2.122662 | 0 | 0.002315 |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 83 | 0.563819 | 2.12971 | 0 | 0.002589 |
| KEGG_DILATED_CARDIOMYOPATHY | 90 | 0.563888 | 2.142032 | 0 | 0.002873 |
| HALLMARK_ANGIOGENESIS | 36 | 0.659956 | 2.145896 | 0 | 0.003762 |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 212 | 0.486166 | 2.076397 | 0 | 0.004307 |
| HALLMARK_APICAL_JUNCTION | 199 | 0.509404 | 2.153307 | 0 | 0.005643 |
| KEGG_AXON_GUIDANCE | 128 | 0.508823 | 2.03674 | 0 | 0.006521 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE | 22 | 0.708254 | 2.019092 | 0 | 0.007914 |
| HALLMARK_INFLAMMATORY_RESPONSE | 198 | 0.540584 | 1.98723 | 0.002053 | 0.012935 |
| HALLMARK_COAGULATION | 136 | 0.494871 | 1.998458 | 0 | 0.013969 |
| HALLMARK_KRAS_SIGNALING_UP | 199 | 0.47025 | 1.941858 | 0.002033 | 0.017098 |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 116 | 0.499517 | 1.942385 | 0.003846 | 0.017334 |
| KEGG_PRION_DISEASES | 35 | 0.555882 | 1.933313 | 0.003922 | 0.017464 |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES | 69 | 0.540894 | 1.947301 | 0.003906 | 0.017726 |
| KEGG_HEMATOPOIETIC_CELL_LINEAGE | 85 | 0.546469 | 1.913223 | 0.006148 | 0.020931 |
| HALLMARK_MYOGENESIS | 200 | 0.427933 | 1.83313 | 0.001965 | 0.023158 |
| HALLMARK_UV_RESPONSE_DN | 144 | 0.512645 | 1.8888 | 0.001866 | 0.023344 |
| HALLMARK_COMPLEMENT | 195 | 0.479702 | 1.863389 | 0.00611 | 0.023406 |
| HALLMARK_TGF_BETA_SIGNALING | 54 | 0.582261 | 1.868891 | 0.003817 | 0.02442 |
| HALLMARK_HEDGEHOG_SIGNALING | 36 | 0.544363 | 1.845035 | 0.007782 | 0.024737 |
| HALLMARK_WNT_BETA_CATENIN_SIGNALING | 42 | 0.559256 | 1.833662 | 0.011236 | 0.025264 |
| HALLMARK_IL6_JAK_STAT3_SIGNALING | 87 | 0.548018 | 1.790087 | 0.023857 | 0.028426 |
| KEGG_TGF_BETA_SIGNALING_PATHWAY | 85 | 0.506392 | 1.833763 | 0.003795 | 0.0363 |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS | 95 | 0.477419 | 1.838665 | 0.003937 | 0.036526 |
| KEGG_GAP_JUNCTION | 89 | 0.455771 | 1.850384 | 0 | 0.038016 |
| KEGG_PATHWAYS_IN_CANCER | 324 | 0.409125 | 1.839816 | 0 | 0.038522 |
| HALLMARK_ALLOGRAFT_REJECTION | 200 | 0.516252 | 1.717329 | 0.072727 | 0.044722 |
| KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION | 55 | 0.515738 | 1.769199 | 0.018595 | 0.054953 |
| KEGG_CALCIUM_SIGNALING_PATHWAY | 176 | 0.417122 | 1.769208 | 0 | 0.057846 |
| KEGG_SMALL_CELL_LUNG_CANCER | 84 | 0.476725 | 1.773829 | 0.003745 | 0.059241 |
| HALLMARK_MITOTIC_SPINDLE | 198 | 0.464454 | 1.641426 | 0.050093 | 0.060953 |
| HALLMARK_NOTCH_SIGNALING | 32 | 0.455481 | 1.630358 | 0.021073 | 0.061113 |
| HALLMARK_IL2_STAT5_SIGNALING | 199 | 0.378822 | 1.643555 | 0.018036 | 0.064309 |

Table SV. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| HALLMARK_APOPTOSIS | 160 | 0.372229 | 1.609501 | 0.014056 | 0.064442 |
| KEGG_GLIOMA | 65 | 0.438999 | 1.709631 | 0.00381 | 0.071318 |
| KEGG_CHEMOKINE_SIGNALING_PATHWAY | 186 | 0.446786 | 1.728051 | 0.037475 | 0.071663 |
| KEGG_JAK_STAT_SIGNALING_PATHWAY | 151 | 0.426231 | 1.700696 | 0.009843 | 0.072515 |
| KEGG_DORSO_VENTRAL_AXIS_FORMATION | 24 | 0.557307 | 1.709945 | 0.007463 | 0.074206 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 258 | 0.419165 | 1.711968 | 0.01848 | 0.076708 |
| KEGG_HEDGEHOG_SIGNALING_PATHWAY | 56 | 0.436249 | 1.677579 | 0.013359 | 0.082446 |
| HALLMARK_G2M_CHECKPOINT | 198 | 0.497956 | 1.534678 | 0.112403 | 0.092172 |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 131 | 0.426179 | 1.628884 | 0.058594 | 0.094242 |
| KEGG_CHRONIC_MYELOID_LEUKEMIA | 73 | 0.44495 | 1.632581 | 0.018727 | 0.094477 |
| KEGG_LONG_TERM_POTENTIATION | 69 | 0.426992 | 1.652398 | 0.009579 | 0.095589 |
| KEGG_LEISHMANIA_INFECTION | 69 | 0.538317 | 1.634601 | 0.074447 | 0.096169 |
| KEGG_WNT_SIGNALING_PATHWAY | 149 | 0.40197 | 1.638382 | 0.011516 | 0.097212 |
| KEGG_NOTCH_SIGNALING_PATHWAY | 47 | 0.482086 | 1.638897 | 0.019964 | 0.100122 |
| KEGG_PANCREATIC_CANCER | 70 | 0.438385 | 1.609916 | 0.028517 | 0.103479 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE | 26 | 0.509583 | 1.602107 | 0.031189 | 0.105023 |
| KEGG_BASAL_CELL_CARCINOMA | 55 | 0.424812 | 1.588806 | 0.035782 | 0.110747 |
| KEGG_MAPK_SIGNALING_PATHWAY | 265 | 0.340961 | 1.56787 | 0.009398 | 0.120503 |
| KEGG_ADHERENS_JUNCTION | 73 | 0.432742 | 1.557626 | 0.045627 | 0.124272 |
| KEGG_VEGF_SIGNALING_PATHWAY | 75 | 0.366635 | 1.545535 | 0.009524 | 0.124376 |
| KEGG_COLORECTAL_CANCER | 62 | 0.434762 | 1.553165 | 0.041509 | 0.124544 |
| KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES | 15 | 0.532853 | 1.548669 | 0.046092 | 0.125026 |
| HALLMARK_HYPOXIA | 198 | 0.349356 | 1.453873 | 0.091816 | 0.127538 |
| HALLMARK_TNFA_SIGNALING_VIA_NFKB | 199 | 0.402981 | 1.405842 | 0.150515 | 0.149612 |
| KEGG_RENAL_CELL_CARCINOMA | 70 | 0.397657 | 1.493913 | 0.068441 | 0.160041 |
| KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION | 270 | 0.389073 | 1.487831 | 0.009804 | 0.161366 |
| HALLMARK_APICAL_SURFACE | 44 | 0.369153 | 1.36612 | 0.113462 | 0.169685 |
| KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY | 74 | 0.416105 | 1.465339 | 0.099029 | 0.176756 |
| KEGG_VIRAL_MYOCARDITIS | 68 | 0.424321 | 1.454452 | 0.135729 | 0.178375 |
| KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY | 61 | 0.418668 | 1.457154 | 0.087824 | 0.18 |
| KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS | 52 | 0.356056 | 1.429777 | 0.061144 | 0.187621 |
| KEGG_P53_SIGNALING_PATHWAY | 67 | 0.384086 | 1.425235 | 0.104126 | 0.187674 |
| KEGG_LONG_TERM_DEPRESSION | 70 | 0.370502 | 1.433249 | 0.051181 | 0.188619 |
| KEGG_NEUROTROPHIN_SIGNALING_PATHWAY | 126 | 0.349752 | 1.433513 | 0.07963 | 0.192541 |
| KEGG_APOPTOSIS | 86 | 0.368989 | 1.409429 | 0.086538 | 0.19785 |
| KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY | 107 | 0.394881 | 1.39944 | 0.133065 | 0.202483 |

Table SV. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_CELL_CYCLE | 124 | 0.397364 | 1.385118 | 0.173653 | 0.211677 |
| HALLMARK_E2F_TARGETS | 199 | 0.431278 | 1.293536 | 0.272016 | 0.215055 |
| KEGG_OOCYTE_MEIOSIS | 111 | 0.341643 | 1.366294 | 0.128655 | 0.220168 |
| KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY | 130 | 0.35934 | 1.368131 | 0.165692 | 0.222706 |
| KEGG_MELANOGENESIS | 101 | 0.316072 | 1.339899 | 0.086304 | 0.232694 |
| HALLMARK_PI3K_AKT_MTOR_SIGNALING | 105 | 0.296255 | 1.261295 | 0.145957 | 0.232778 |
| KEGG_BLADDER_CANCER | 41 | 0.353304 | 1.341178 | 0.103314 | 0.235744 |
| KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION | 85 | 0.341204 | 1.34286 | 0.132554 | 0.238366 |
| KEGG_MELANOMA | 71 | 0.328854 | 1.32304 | 0.095785 | 0.244435 |

KIRC, kidney renal clear cell carcinoma; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor; TNF, tumor necrosis factor; MAPK, mitogen-activated protein kinase; IL, interleukin; STAT, signal transducer and activator of transcription; JAK, Janus kinase; PI3K, phosphatidylinositol 3-kinase; VEGF, vascular endothelial growth factor; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table SVI. Genesets associated with high long intergenic non-coding RNA 1614 expression in the LUAD dataset.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION | 196 | 0.804425 | 2.354199 | 0 | 0 |
| KEGG_FOCAL_ADHESION | 199 | 0.595585 | 2.161017 | 0 | 5.91E-04 |
| HALLMARK_HYPOXIA | 198 | 0.540246 | 2.163296 | 0 | 6.72E-04 |
| KEGG_ECM_RECEPTOR_INTERACTION | 84 | 0.70236 | 2.170209 | 0 | 0.001182 |
| KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION | 55 | 0.614379 | 2.123152 | 0 | 0.003318 |
| HALLMARK_APICAL_JUNCTION | 199 | 0.486371 | 1.919788 | 0 | 0.012013 |
| HALLMARK_KRAS_SIGNALING_UP | 199 | 0.483691 | 1.930524 | 0 | 0.012155 |
| HALLMARK_ALLOGRAFT_REJECTION | 200 | 0.606664 | 1.935449 | 0.005871 | 0.013169 |
| HALLMARK_INFLAMMATORY_RESPONSE | 198 | 0.556193 | 1.947869 | 0.005917 | 0.013409 |
| HALLMARK_ANGIOGENESIS | 36 | 0.652924 | 2.015657 | 0 | 0.014328 |
| HALLMARK_APOPTOSIS | 160 | 0.462895 | 1.968342 | 0 | 0.015195 |
| HALLMARK_IL6_JAK_STAT3_SIGNALING | 87 | 0.568537 | 1.886882 | 0.00578 | 0.015328 |
| HALLMARK_GLYCOLYSIS | 199 | 0.472096 | 1.846806 | 0.002024 | 0.019468 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE | 22 | 0.693739 | 2.024961 | 0.001934 | 0.019639 |
| HALLMARK_COMPLEMENT | 195 | 0.479774 | 1.837009 | 0.001972 | 0.020353 |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 212 | 0.488215 | 2.001637 | 0.001976 | 0.022104 |
| HALLMARK_E2F_TARGETS | 199 | 0.635197 | 1.762218 | 0.024341 | 0.029377 |
| HALLMARK_INTERFERON_GAMMA_RESPONSE | 197 | 0.573223 | 1.768833 | 0.035363 | 0.029918 |
| HALLMARK_MTORC1_SIGNALING | 199 | 0.516408 | 1.77791 | 0.012146 | 0.030582 |
| HALLMARK_APICAL_SURFACE | 44 | 0.488531 | 1.738844 | 0.010204 | 0.032594 |
| HALLMARK_IL2_STAT5_SIGNALING | 199 | 0.411876 | 1.723632 | 0.006024 | 0.034698 |
| HALLMARK_G2M_CHECKPOINT | 198 | 0.58851 | 1.704767 | 0.050209 | 0.03831 |
| HALLMARK_MYOGENESIS | 200 | 0.414307 | 1.674837 | 0.010225 | 0.044387 |
| HALLMARK_TNFA_SIGNALING_VIA_NFKB | 199 | 0.485706 | 1.642565 | 0.048 | 0.052164 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 258 | 0.49533 | 1.865659 | 0.010142 | 0.055737 |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS | 95 | 0.480482 | 1.854158 | 0.007921 | 0.055768 |
| HALLMARK_COAGULATION | 136 | 0.440003 | 1.623912 | 0.021236 | 0.055857 |
| KEGG_GAP_JUNCTION | 89 | 0.475757 | 1.844161 | 0.001949 | 0.056195 |
| KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY | 101 | 0.495236 | 1.87987 | 0.011811 | 0.057118 |
| KEGG_MELANOMA | 71 | 0.501593 | 1.890394 | 0.001949 | 0.059326 |
| HALLMARK_PI3K_AKT_MTOR_SIGNALING | 105 | 0.371507 | 1.571608 | 0.017822 | 0.07326 |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 83 | 0.485532 | 1.788443 | 0.007905 | 0.073998 |
| KEGG_P53_SIGNALING_PATHWAY | 67 | 0.463565 | 1.761046 | 0.006186 | 0.074619 |
| KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY | 61 | 0.516388 | 1.775828 | 0.010246 | 0.075304 |
| KEGG_CELL_CYCLE | 124 | 0.547914 | 1.768399 | 0.017893 | 0.075336 |
| KEGG_RENAL_CELL_CARCINOMA | 70 | 0.467915 | 1.789058 | 0.005758 | 0.080364 |
| HALLMARK_TGF_BETA_SIGNALING | 54 | 0.452388 | 1.544537 | 0.047619 | 0.081999 |
| KEGG_PROTEASOME | 44 | 0.699217 | 1.738337 | 0.022177 | 0.084155 |

Table SVI. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_DNA_REPLICATION | 36 | 0.704108 | 1.712946 | 0.026104 | 0.086292 |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 74 | 0.478601 | 1.704122 | 0.011905 | 0.087778 |
| KEGG_DILATED_CARDIOMYOPATHY | 90 | 0.46763 | 1.718032 | 0.011605 | 0.087831 |
| KEGG_PATHWAYS_IN_CANCER | 324 | 0.387482 | 1.677507 | 0.011742 | 0.089027 |
| KEGG_LEISHMANIA_INFECTION | 69 | 0.550126 | 1.723252 | 0.024096 | 0.089201 |
| KEGG_GLIOMA | 65 | 0.439796 | 1.681051 | 0.024668 | 0.090483 |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 116 | 0.439856 | 1.683296 | 0.013972 | 0.093358 |
| KEGG_PANCREATIC_CANCER | 70 | 0.452111 | 1.68741 | 0.018219 | 0.094266 |
| HALLMARK_UNFOLDED_PROTEIN_RESPONSE | 112 | 0.412877 | 1.501208 | 0.070994 | 0.103055 |
| HALLMARK_MYC_TARGETS_V1 | 199 | 0.523543 | 1.491059 | 0.116424 | 0.104547 |
| KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY | 130 | 0.458695 | 1.638803 | 0.04499 | 0.107147 |
| KEGG_TGF_BETA_SIGNALING_PATHWAY | 85 | 0.429857 | 1.643181 | 0.023121 | 0.108036 |
| KEGG_CHEMOKINE_SIGNALING_PATHWAY | 186 | 0.421545 | 1.619512 | 0.038776 | 0.110665 |
| KEGG_MISMATCH_REPAIR | 23 | 0.643321 | 1.620526 | 0.032064 | 0.113532 |
| KEGG_SMALL_CELL_LUNG_CANCER | 84 | 0.441919 | 1.623433 | 0.034 | 0.115712 |
| HALLMARK_UV_RESPONSE_DN | 144 | 0.379029 | 1.435024 | 0.088115 | 0.131455 |
| KEGG_OOCYTE_MEIOSIS | 111 | 0.401692 | 1.579958 | 0.04175 | 0.139253 |
| KEGG_PROSTATE_CANCER | 89 | 0.39548 | 1.553706 | 0.03125 | 0.159754 |
| KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY | 107 | 0.436829 | 1.5347 | 0.06237 | 0.162528 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE | 26 | 0.475097 | 1.508504 | 0.065385 | 0.166229 |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 131 | 0.429866 | 1.53571 | 0.064854 | 0.166357 |
| KEGG_BLADDER_CANCER | 41 | 0.414404 | 1.538679 | 0.027613 | 0.169295 |
| KEGG_AXON_GUIDANCE | 128 | 0.381985 | 1.508753 | 0.030364 | 0.16996 |
| KEGG_PENTOSE_PHOSPHATE_PATHWAY | 26 | 0.48801 | 1.500208 | 0.078156 | 0.170959 |
| HALLMARK_MITOTIC_SPINDLE | 197 | 0.383715 | 1.367267 | 0.169456 | 0.172533 |
| KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION | 67 | 0.375488 | 1.509304 | 0.036885 | 0.17384 |
| HALLMARK_UV_RESPONSE_UP | 156 | 0.311599 | 1.356 | 0.066253 | 0.17386 |
| KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS | 133 | 0.384118 | 1.513663 | 0.056911 | 0.173953 |
| KEGG_HOMOLOGOUS_RECOMBINATION | 28 | 0.574217 | 1.517171 | 0.086 | 0.175121 |
| KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION | 85 | 0.378123 | 1.475787 | 0.06986 | 0.191391 |
| HALLMARK_PROTEIN_SECRETION | 96 | 0.377907 | 1.322137 | 0.167653 | 0.193467 |
| HALLMARK_NOTCH_SIGNALING | 32 | 0.380309 | 1.299157 | 0.14898 | 0.203905 |
| HALLMARK_INTERFERON_ALPHA_RESPONSE | 94 | 0.46415 | 1.276358 | 0.254941 | 0.216859 |
| HALLMARK_ANDROGEN_RESPONSE | 100 | 0.307068 | 1.249029 | 0.166333 | 0.233318 |
| KEGG_PRION_DISEASES | 35 | 0.423854 | 1.427914 | 0.072125 | 0.233724 |
| KEGG_CHRONIC_MYELOID_LEUKEMIA | 73 | 0.386211 | 1.43094 | 0.094118 | 0.235709 |

LUAD, lung adenocarcinoma; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor; TNF, tumor necrosis factor; MAPK, mitogen-activated protein kinase; IL, Interleukin; STAT, signal transducer and activator of transcription; JAK, Janus kinase; PI3K, phosphatidylinositol 3-kinase; mTOR, mammalian target of rapamycin; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table SVII. Genesets associated with high long intergenic non-coding RNA 1614 expression in the LUSC dataset.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION | 196 | 0.81977 | 2.436062 | 0 | 0 |
| HALLMARK_KRAS_SIGNALING_UP | 199 | 0.616362 | 2.382318 | 0 | 0 |
| HALLMARK_INFLAMMATORY_RESPONSE | 198 | 0.683281 | 2.290595 | 0 | 0 |
| HALLMARK_IL6_JAK_STAT3_SIGNALING | 87 | 0.705588 | 2.27773 | 0 | 0 |
| HALLMARK_COMPLEMENT | 195 | 0.612893 | 2.20804 | 0 | 0 |
| HALLMARK_ANGIOGENESIS | 36 | 0.719328 | 2.16215 | 0 | 0 |
| HALLMARK_IL2_STAT5_SIGNALING | 199 | 0.542285 | 2.153106 | 0 | 0 |
| KEGG_FOCAL_ADHESION | 199 | 0.651105 | 2.385017 | 0 | 0 |
| KEGG_ECM_RECEPTOR_INTERACTION | 84 | 0.757192 | 2.292903 | 0 | 0 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 258 | 0.648507 | 2.239219 | 0 | 0 |
| HALLMARK_MYOGENESIS | 200 | 0.504886 | 2.095983 | 0 | 1.61E-04 |
| HALLMARK_ALLOGRAFT_REJECTION | 200 | 0.693562 | 2.108667 | 0 | 1.76E-04 |
| HALLMARK_APICAL_JUNCTION | 199 | 0.505402 | 2.111226 | 0 | 1.93E-04 |
| HALLMARK_TGF_BETA_SIGNALING | 54 | 0.603209 | 2.111406 | 0 | 2.15E-04 |
| HALLMARK_UV_RESPONSE_DN | 144 | 0.539418 | 2.083071 | 0 | 2.26E-04 |
| HALLMARK_COAGULATION | 136 | 0.644205 | 2.1182 | 0 | 2.42E-04 |
| KEGG_VIRAL_MYOCARDITIS | 68 | 0.69662 | 2.168696 | 0 | 5.03E-04 |
| HALLMARK_TNFA_SIGNALING_VIA_NFKB | 199 | 0.613176 | 2.060267 | 0.002037 | 5.16E-04 |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 83 | 0.593169 | 2.11908 | 0 | 7.89E-04 |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 212 | 0.483998 | 2.127574 | 0 | 8.88E-04 |
| HALLMARK_INTERFERON_GAMMA_RESPONSE | 197 | 0.672825 | 2.011434 | 0 | 9.15E-04 |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 116 | 0.580352 | 2.135101 | 0 | 0.001015 |
| KEGG_DILATED_CARDIOMYOPATHY | 90 | 0.586725 | 2.10482 | 0 | 0.00104 |
| KEGG_LEISHMANIA_INFECTION | 69 | 0.712099 | 2.138804 | 0 | 0.001184 |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 131 | 0.65672 | 2.1555 | 0 | 0.001197 |
| KEGG_JAK_STAT_SIGNALING_PATHWAY | 151 | 0.553552 | 2.092384 | 0 | 0.001471 |
| KEGG_TGF_BETA_SIGNALING_PATHWAY | 85 | 0.5173 | 2.053812 | 0 | 0.002334 |
| HALLMARK_APOPTOSIS | 160 | 0.442634 | 1.944486 | 0 | 0.002483 |
| KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES | 15 | 0.759877 | 2.0248 | 0 | 0.003385 |
| KEGG_CHEMOKINE_SIGNALING_PATHWAY | 186 | 0.538791 | 1.981183 | 0 | 0.004698 |
| KEGG_HEMATOPOIETIC_CELL_LINEAGE | 85 | 0.685401 | 1.960289 | 0 | 0.006301 |
| KEGG_AUTOIMMUNE_THYROID_DISEASE | 50 | 0.739658 | 1.950822 | 0.002092 | 0.006684 |
| KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY | 101 | 0.516116 | 1.943766 | 0.001919 | 0.007035 |
| KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION | 115 | 0.484044 | 1.934105 | 0 | 0.007483 |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 74 | 0.541343 | 1.919742 | 0 | 0.008166 |
| KEGG_LYSOSOME | 119 | 0.530546 | 1.875755 | 0.002075 | 0.013588 |
| KEGG_TYPE_I_DIABETES_MELLITUS | 41 | 0.74178 | 1.868209 | 0.002101 | 0.013796 |
| KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY | 130 | 0.528042 | 1.853047 | 0.004283 | 0.015564 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE | 22 | 0.656085 | 1.844195 | 0.003795 | 0.016804 |

Table SVII. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION | 46 | 0.746425 | 1.83101 | 0.004264 | 0.019301 |
| KEGG_ASTHMA | 28 | 0.749117 | 1.817718 | 0.011976 | 0.021184 |
| HALLMARK_HYPOXIA | 198 | 0.423294 | 1.727097 | 0.012739 | 0.023289 |
| HALLMARK_INTERFERON_ALPHA_RESPONSE | 94 | 0.629756 | 1.68552 | 0.05642 | 0.029634 |
| KEGG_MELANOMA | 71 | 0.463718 | 1.759874 | 0 | 0.032199 |
| KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION | 79 | 0.575004 | 1.750065 | 0.028747 | 0.032835 |
| KEGG_GRAFT_VERSUS_HOST_DISEASE | 37 | 0.779894 | 1.762416 | 0.012526 | 0.032899 |
| KEGG_PATHWAYS_IN_CANCER | 324 | 0.385452 | 1.766175 | 0 | 0.033041 |
| KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION | 55 | 0.442278 | 1.750811 | 0.006303 | 0.033694 |
| HALLMARK_HEDGEHOG_SIGNALING | 36 | 0.504536 | 1.633883 | 0.023715 | 0.038778 |
| KEGG_ALLOGRAFT_REJECTION | 35 | 0.783105 | 1.726251 | 0.010395 | 0.038836 |
| HALLMARK_ANDROGEN_RESPONSE | 100 | 0.388762 | 1.625558 | 0.011696 | 0.038861 |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES | 69 | 0.617656 | 1.720558 | 0.022495 | 0.039641 |
| KEGG_CALCIUM_SIGNALING_PATHWAY | 176 | 0.387315 | 1.689899 | 0.001969 | 0.048943 |
| KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY | 61 | 0.480898 | 1.667282 | 0.030651 | 0.055897 |
| KEGG_AXON_GUIDANCE | 128 | 0.400921 | 1.662739 | 0.003945 | 0.055961 |
| KEGG_SMALL_CELL_LUNG_CANCER | 84 | 0.430991 | 1.643442 | 0.022599 | 0.06131 |
| KEGG_GLYCOSAMINOGLYCAN_DEGRADATION | 21 | 0.581014 | 1.644765 | 0.038306 | 0.062371 |
| KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION | 270 | 0.39517 | 1.63569 | 0.004049 | 0.062957 |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS | 95 | 0.395939 | 1.599879 | 0.028455 | 0.07741 |
| HALLMARK_NOTCH_SIGNALING | 32 | 0.41161 | 1.482521 | 0.03675 | 0.085417 |
| KEGG_GAP_JUNCTION | 89 | 0.385687 | 1.578778 | 0.015873 | 0.086161 |
| KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY | 107 | 0.426449 | 1.5155 | 0.067347 | 0.12452 |
| HALLMARK_APICAL_SURFACE | 44 | 0.366212 | 1.384135 | 0.072266 | 0.134303 |
| KEGG_MAPK_SIGNALING_PATHWAY | 265 | 0.321071 | 1.467678 | 0.011811 | 0.159755 |
| KEGG_RENIN_ANGIOTENSIN_SYSTEM | 17 | 0.518485 | 1.43505 | 0.114458 | 0.176421 |
| KEGG_APOPTOSIS | 86 | 0.373258 | 1.437887 | 0.079457 | 0.177616 |
| HALLMARK_PROTEIN_SECRETION | 96 | 0.337848 | 1.307867 | 0.147239 | 0.178224 |
| KEGG_LONG_TERM_DEPRESSION | 70 | 0.368502 | 1.439387 | 0.035491 | 0.180222 |
| KEGG_GLIOMA | 65 | 0.353994 | 1.424286 | 0.04908 | 0.182081 |
| KEGG_PROSTATE_CANCER | 89 | 0.347384 | 1.396537 | 0.06968 | 0.202446 |
| KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS | 131 | 0.426283 | 1.39727 | 0.135699 | 0.205862 |
| KEGG_SPHINGOLIPID_METABOLISM | 39 | 0.389939 | 1.388227 | 0.093117 | 0.206489 |
| KEGG_PANCREATIC_CANCER | 70 | 0.335472 | 1.36677 | 0.065637 | 0.218755 |
| KEGG_RENAL_CELL_CARCINOMA | 70 | 0.333726 | 1.358703 | 0.094961 | 0.218852 |
| KEGG_OTHER_GLYCAN_DEGRADATION | 16 | 0.510258 | 1.370704 | 0.129817 | 0.219266 |
| KEGG_ENDOCYTOSIS | 178 | 0.301576 | 1.360296 | 0.059961 | 0.221414 |
| KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY | 74 | 0.425023 | 1.342642 | 0.149068 | 0.230858 |

LUSC, lung squamous cell carcinoma; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor; TNF, tumor necrosis factor; MAPK, mitogen-activated protein kinase; IL, Interleukin; STAT, signal transducer and activator of transcription; JAK, Janus kinase; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table SVIII. Genesets associated with high long intergenic non-coding RNA 1614 expression in the SKCM dataset.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION | 196 | 0.740531 | 2.329045 | 0 | 0 |
| KEGG_ECM_RECEPTOR_INTERACTION | 84 | 0.721682 | 2.416589 | 0 | 0 |
| KEGG_FOCAL_ADHESION | 199 | 0.580686 | 2.303515 | 0 | 0 |
| HALLMARK_ANGIOGENESIS | 36 | 0.685793 | 2.12799 | 0 | 0.001028 |
| HALLMARK_TGF_BETA_SIGNALING | 54 | 0.626425 | 2.086891 | 0 | 0.003414 |
| HALLMARK_UV_RESPONSE_DN | 144 | 0.534352 | 2.044105 | 0 | 0.003603 |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 212 | 0.493402 | 2.129453 | 0 | 0.003891 |
| KEGG_PATHWAYS_IN_CANCER | 324 | 0.43948 | 2.016903 | 0 | 0.015809 |
| KEGG_DILATED_CARDIOMYOPATHY | 90 | 0.536302 | 1.982853 | 0 | 0.01904 |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 83 | 0.54621 | 1.987356 | 0 | 0.020746 |
| HALLMARK_INFLAMMATORY_RESPONSE | 198 | 0.564216 | 1.888204 | 0.009921 | 0.021808 |
| HALLMARK_KRAS_SIGNALING_UP | 199 | 0.488698 | 1.904406 | 0 | 0.02438 |
| HALLMARK_APICAL_JUNCTION | 199 | 0.438834 | 1.811451 | 0 | 0.034228 |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 116 | 0.492101 | 1.851333 | 0.006061 | 0.0355 |
| HALLMARK_TNFA_SIGNALING_VIA_NFKB | 199 | 0.522778 | 1.816272 | 0.018182 | 0.037208 |
| KEGG_PANCREATIC_CANCER | 70 | 0.474857 | 1.838292 | 0.002004 | 0.037401 |
| HALLMARK_HYPOXIA | 198 | 0.402189 | 1.756833 | 0.003984 | 0.03838 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE | 22 | 0.619957 | 1.851826 | 0.005976 | 0.038458 |
| HALLMARK_IL6_JAK_STAT3_SIGNALING | 87 | 0.570905 | 1.7636 | 0.01848 | 0.039189 |
| HALLMARK_MYOGENESIS | 200 | 0.432792 | 1.77429 | 0.003745 | 0.040328 |
| KEGG_GLIOMA | 65 | 0.455842 | 1.853801 | 0 | 0.041489 |
| KEGG_GAP_JUNCTION | 89 | 0.464803 | 1.899272 | 0 | 0.042225 |
| KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION | 115 | 0.466356 | 1.859901 | 0 | 0.042968 |
| KEGG_AXON_GUIDANCE | 128 | 0.475227 | 1.865744 | 0 | 0.045652 |
| KEGG_LEISHMANIA_INFECTION | 69 | 0.610087 | 1.806005 | 0.02449 | 0.045851 |
| KEGG_TGF_BETA_SIGNALING_PATHWAY | 85 | 0.523588 | 1.874222 | 0 | 0.047906 |
| KEGG_MAPK_SIGNALING_PATHWAY | 265 | 0.38222 | 1.737818 | 0 | 0.048787 |
| KEGG_CHRONIC_MYELOID_LEUKEMIA | 73 | 0.43764 | 1.745753 | 0.007968 | 0.049804 |
| KEGG_LONG_TERM_POTENTIATION | 69 | 0.436829 | 1.738592 | 0.004115 | 0.050298 |
| KEGG_O_GLYCAN_BIOSYNTHESIS | 27 | 0.530471 | 1.749177 | 0.003992 | 0.050479 |
| KEGG_APOPTOSIS | 86 | 0.448548 | 1.753141 | 0.014028 | 0.050659 |
| KEGG_PROSTATE_CANCER | 89 | 0.421749 | 1.753545 | 0 | 0.053192 |
| KEGG_MELANOMA | 71 | 0.447168 | 1.779419 | 0.001972 | 0.053968 |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 131 | 0.514328 | 1.757237 | 0.023109 | 0.054737 |
| KEGG_RENAL_CELL_CARCINOMA | 70 | 0.453624 | 1.770554 | 0.001931 | 0.055074 |
| KEGG_SMALL_CELL_LUNG_CANCER | 84 | 0.429057 | 1.763465 | 0 | 0.055353 |
| HALLMARK_MITOTIC_SPINDLE | 197 | 0.446692 | 1.680237 | 0.014583 | 0.05728 |

Table SVIII. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| HALLMARK_IL2_STAT5_SIGNALING | 199 | 0.410311 | 1.669356 | 0.020492 | 0.057718 |
| HALLMARK_ANDROGEN_RESPONSE | 100 | 0.418042 | 1.650735 | 0.010288 | 0.060427 |
| HALLMARK_COMPLEMENT | 195 | 0.447367 | 1.680345 | 0.02439 | 0.062053 |
| HALLMARK_COAGULATION | 136 | 0.451629 | 1.593832 | 0.021869 | 0.075567 |
| HALLMARK_APOPTOSIS | 160 | 0.371071 | 1.596243 | 0.017717 | 0.078811 |
| KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY | 101 | 0.465013 | 1.676699 | 0.026585 | 0.079585 |
| KEGG_DORSO_VENTRAL_AXIS_FORMATION | 24 | 0.520205 | 1.670304 | 0.009709 | 0.080653 |
| KEGG_NEUROTROPHIN_SIGNALING_PATHWAY | 126 | 0.374997 | 1.656139 | 0.002004 | 0.085447 |
| KEGG_WNT_SIGNALING_PATHWAY | 149 | 0.393826 | 1.64614 | 0.006148 | 0.088881 |
| KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY | 61 | 0.479885 | 1.625212 | 0.036961 | 0.095586 |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS | 95 | 0.400659 | 1.627581 | 0.017578 | 0.096696 |
| KEGG_LONG_TERM_DEPRESSION | 70 | 0.401422 | 1.612786 | 0.016227 | 0.100841 |
| KEGG_ENDOCYTOSIS | 178 | 0.347828 | 1.598407 | 0.008214 | 0.107284 |
| KEGG_GNRH_SIGNALING_PATHWAY | 101 | 0.352117 | 1.572508 | 0.008282 | 0.116384 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 258 | 0.446268 | 1.573906 | 0.056604 | 0.118511 |
| HALLMARK_HEDGEHOG_SIGNALING | 36 | 0.429915 | 1.499132 | 0.044834 | 0.120756 |
| KEGG_ERBB_SIGNALING_PATHWAY | 87 | 0.380407 | 1.575137 | 0.012146 | 0.120835 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE | 26 | 0.492473 | 1.544906 | 0.059548 | 0.135224 |
| HALLMARK_NOTCH_SIGNALING | 32 | 0.409877 | 1.466115 | 0.045726 | 0.13544 |
| KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION | 55 | 0.396779 | 1.516554 | 0.044231 | 0.144552 |
| KEGG_N_GLYCAN_BIOSYNTHESIS | 46 | 0.43599 | 1.513023 | 0.055102 | 0.144761 |
| KEGG_HEDGEHOG_SIGNALING_PATHWAY | 56 | 0.421539 | 1.517827 | 0.031746 | 0.147066 |
| KEGG_MELANOGENESIS | 101 | 0.356265 | 1.520612 | 0.023857 | 0.148221 |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 74 | 0.414361 | 1.523602 | 0.044807 | 0.149467 |
| HALLMARK_PROTEIN_SECRETION | 96 | 0.420176 | 1.436428 | 0.131959 | 0.150978 |
| KEGG_CHEMOKINE_SIGNALING_PATHWAY | 186 | 0.39693 | 1.484658 | 0.101293 | 0.166862 |
| KEGG_VIRAL_MYOCARDITIS | 68 | 0.438095 | 1.459653 | 0.139293 | 0.178272 |
| KEGG_TYPE_II_DIABETES_MELLITUS | 46 | 0.381985 | 1.460976 | 0.031558 | 0.181039 |
| KEGG_OOCYTE_MEIOSIS | 111 | 0.362185 | 1.444022 | 0.079051 | 0.181569 |
| KEGG_P53_SIGNALING_PATHWAY | 67 | 0.375226 | 1.44706 | 0.060311 | 0.182742 |
| KEGG_ADHERENS_JUNCTION | 73 | 0.389235 | 1.46218 | 0.060078 | 0.183975 |
| KEGG_THYROID_CANCER | 29 | 0.420115 | 1.448488 | 0.085417 | 0.185137 |
| KEGG_CALCIUM_SIGNALING_PATHWAY | 176 | 0.334065 | 1.431952 | 0.047325 | 0.188975 |
| KEGG_BLADDER_CANCER | 41 | 0.389133 | 1.420665 | 0.068359 | 0.195612 |
| HALLMARK_INTERFERON_GAMMA_RESPONSE | 197 | 0.467671 | 1.347925 | 0.226121 | 0.196368 |
| HALLMARK_APICAL_SURFACE | 44 | 0.356402 | 1.352457 | 0.106557 | 0.201292 |

Table SVIII. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_COLORECTAL_CANCER | 62 | 0.383185 | 1.411023 | 0.091816 | 0.201617 |
| HALLMARK_UNFOLDED_PROTEIN_RESPONSE | 112 | 0.35342 | 1.362319 | 0.135903 | 0.20218 |
| HALLMARK_ALLOGRAFT_REJECTION | 200 | 0.427163 | 1.328766 | 0.236434 | 0.206312 |
| KEGG_HEMATOPOIETIC_CELL_LINEAGE | 85 | 0.459345 | 1.370732 | 0.171134 | 0.237921 |
| HALLMARK_PI3K_AKT_MTOR_SIGNALING | 105 | 0.30752 | 1.273122 | 0.165254 | 0.248471 |

SKCM, skin cutaneous melanoma; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor; TNF, tumor necrosis factor; MAPK, mitogen-activated protein kinase; IL, Interleukin; STAT, signal transducer and activator of transcription; JAK, Janus kinase; PI3K, phosphatidylinositol 3-kinase; mTOR, mammalian target of rapamycin; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table SIX. Genesets associated with high long intergenic non-coding RNA 1614 expression in the STAD dataset.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION | 196 | 0.800922 | 2.42547 | 0 | 0 |
| HALLMARK_APOPTOSIS | 160 | 0.582895 | 2.420888 | 0 | 0 |
| KEGG_FOCAL_ADHESION | 199 | 0.59971 | 2.283906 | 0 | 0 |
| HALLMARK_ANGIOGENESIS | 36 | 0.765508 | 2.322704 | 0 | 3.59E-04 |
| HALLMARK_INFLAMMATORY_RESPONSE | 198 | 0.636799 | 2.191135 | 0 | 4.70E-04 |
| KEGG_ECM_RECEPTOR_INTERACTION | 84 | 0.708074 | 2.244313 | 0 | 5.08E-04 |
| HALLMARK_HYPOXIA | 198 | 0.556912 | 2.243256 | 0 | 5.87E-04 |
| HALLMARK_KRAS_SIGNALING_UP | 199 | 0.507577 | 2.132223 | 0 | 0.001722 |
| HALLMARK_COMPLEMENT | 195 | 0.534209 | 2.118863 | 0.002008 | 0.002078 |
| HALLMARK_APICAL_JUNCTION | 199 | 0.512091 | 2.094329 | 0.002012 | 0.002534 |
| HALLMARK_IL6_JAK_STAT3_SIGNALING | 87 | 0.600383 | 2.009541 | 0.007663 | 0.004747 |
| HALLMARK_COAGULATION | 136 | 0.532328 | 2.016236 | 0 | 0.004766 |
| HALLMARK_NOTCH_SIGNALING | 32 | 0.551351 | 1.978243 | 0 | 0.005068 |
| HALLMARK_TNFA_SIGNALING_VIA_NFKB | 199 | 0.596655 | 1.992929 | 0.006048 | 0.005091 |
| HALLMARK_ALLOGRAFT_REJECTION | 200 | 0.616974 | 1.966683 | 0.005882 | 0.005168 |
| KEGG_RENAL_CELL_CARCINOMA | 70 | 0.533836 | 2.08042 | 0 | 0.006738 |
| KEGG_LEISHMANIA_INFECTION | 69 | 0.669993 | 2.064608 | 0 | 0.008244 |
| KEGG_LYSOSOME | 119 | 0.580163 | 2.085535 | 0 | 0.008422 |
| KEGG_MELANOMA | 71 | 0.526277 | 1.999465 | 0 | 0.009315 |
| KEGG_PANCREATIC_CANCER | 70 | 0.530043 | 2.006617 | 0 | 0.00962 |
| KEGG_GLYCOSAMINOGLYCAN_DEGRADATION | 21 | 0.662949 | 2.011158 | 0.001972 | 0.00996 |
| HALLMARK_IL2_STAT5_SIGNALING | 199 | 0.457675 | 1.89677 | 0.002024 | 0.010085 |
| KEGG_PATHWAYS_IN_CANCER | 324 | 0.443584 | 2.001147 | 0 | 0.010142 |
| HALLMARK_INTERFERON_GAMMA_RESPONSE | 197 | 0.650234 | 1.902011 | 0.014113 | 0.010442 |
| KEGG_TGF_BETA_SIGNALING_PATHWAY | 85 | 0.539568 | 2.018398 | 0 | 0.010546 |
| KEGG_PRION_DISEASES | 35 | 0.617579 | 2.087587 | 0 | 0.011229 |
| KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION | 79 | 0.65288 | 1.971985 | 0.002101 | 0.011679 |
| KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY | 101 | 0.540835 | 1.96588 | 0.002041 | 0.011715 |
| HALLMARK_TGF_BETA_SIGNALING | 54 | 0.547003 | 1.851744 | 0.001965 | 0.013793 |
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 212 | 0.440459 | 1.913141 | 0 | 0.020654 |
| KEGG_VIRAL_MYOCARDITIS | 68 | 0.556194 | 1.889841 | 0.007921 | 0.02274 |
| KEGG_SMALL_CELL_LUNG_CANCER | 84 | 0.482346 | 1.893137 | 0 | 0.02353 |
| HALLMARK_INTERFERON_ALPHA_RESPONSE | 94 | 0.666374 | 1.771376 | 0.042065 | 0.02769 |
| HALLMARK_UV_RESPONSE_DN | 144 | 0.480205 | 1.761661 | 0.008097 | 0.028067 |
| KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY | 61 | 0.528181 | 1.863449 | 0.004124 | 0.028425 |
| KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY | 130 | 0.510981 | 1.851916 | 0.011976 | 0.029754 |
| HALLMARK_P53_PATHWAY | 198 | 0.409899 | 1.725601 | 0.015656 | 0.033689 |

Table SIX. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| HALLMARK_PI3K_AKT_MTOR_SIGNALING | 105 | 0.405244 | 1.730067 | 0.005618 | 0.03448 |
| KEGG_GRAFT_VERSUS_HOST_DISEASE | 37 | 0.758865 | 1.81174 | 0.012605 | 0.040232 |
| KEGG_BLADDER_CANCER | 41 | 0.507156 | 1.801741 | 0.002037 | 0.042255 |
| KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION | 55 | 0.483993 | 1.788244 | 0.014583 | 0.045324 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION | 258 | 0.489644 | 1.781059 | 0.006237 | 0.046449 |
| HALLMARK_UV_RESPONSE_UP | 156 | 0.402101 | 1.671196 | 0.005882 | 0.048044 |
| HALLMARK_GLYCOLYSIS | 199 | 0.413717 | 1.650111 | 0.018182 | 0.05279 |
| HALLMARK_MTORC1_SIGNALING | 199 | 0.47041 | 1.641917 | 0.050584 | 0.053266 |
| KEGG_CHRONIC_MYELOID_LEUKEMIA | 73 | 0.460239 | 1.749182 | 0.006135 | 0.057765 |
| KEGG_TYPE_I_DIABETES_MELLITUS | 41 | 0.638709 | 1.726668 | 0.039256 | 0.061817 |
| KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES | 15 | 0.638416 | 1.727656 | 0.01046 | 0.063751 |
| KEGG_AUTOIMMUNE_THYROID_DISEASE | 50 | 0.621969 | 1.717661 | 0.036961 | 0.06459 |
| KEGG_PROSTATE_CANCER | 89 | 0.431509 | 1.729097 | 0.010661 | 0.065167 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE | 22 | 0.615634 | 1.70437 | 0.016293 | 0.06834 |
| HALLMARK_CHOLESTEROL_HOMEOSTASIS | 73 | 0.430945 | 1.592481 | 0.044534 | 0.069336 |
| KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION | 67 | 0.429515 | 1.696024 | 0.006198 | 0.070449 |
| HALLMARK_DNA_REPAIR | 143 | 0.448892 | 1.578454 | 0.05916 | 0.072092 |
| HALLMARK_MYOGENESIS | 200 | 0.440512 | 1.560504 | 0.053678 | 0.07735 |
| KEGG_CELL_ADHESION_MOLECULES_CAMS | 131 | 0.477281 | 1.67177 | 0.02459 | 0.078851 |
| KEGG_MAPK_SIGNALING_PATHWAY | 265 | 0.382175 | 1.674826 | 0.002088 | 0.079691 |
| KEGG_APOPTOSIS | 86 | 0.433212 | 1.650667 | 0.022177 | 0.086522 |
| KEGG_ALLOGRAFT_REJECTION | 35 | 0.684701 | 1.650682 | 0.047817 | 0.089193 |
| KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY | 55 | 0.479514 | 1.63311 | 0.026263 | 0.094652 |
| KEGG_MTOR_SIGNALING_PATHWAY | 52 | 0.428524 | 1.619638 | 0.018557 | 0.097664 |
| KEGG_ASTHMA | 28 | 0.641947 | 1.615063 | 0.06917 | 0.09768 |
| KEGG_AXON_GUIDANCE | 128 | 0.384837 | 1.620185 | 0.00818 | 0.100189 |
| KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM | 44 | 0.476458 | 1.599458 | 0.02621 | 0.105709 |
| HALLMARK_APICAL_SURFACE | 44 | 0.424223 | 1.483631 | 0.044266 | 0.111068 |
| HALLMARK_HEDGEHOG_SIGNALING | 36 | 0.462445 | 1.46466 | 0.08982 | 0.113746 |
| HALLMARK_UNFOLDED_PROTEIN_RESPONSE | 112 | 0.412526 | 1.465115 | 0.103846 | 0.117555 |
| KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS | 133 | 0.394271 | 1.539827 | 0.063918 | 0.120015 |
| KEGG_P53_SIGNALING_PATHWAY | 67 | 0.40971 | 1.564767 | 0.035225 | 0.120153 |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION | 116 | 0.400731 | 1.54902 | 0.036 | 0.120903 |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES | 69 | 0.47501 | 1.545274 | 0.0499 | 0.121283 |
| KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM | 83 | 0.438386 | 1.541578 | 0.045455 | 0.121352 |

Table SIX. Continued.

| Name | Size (gene) | ES | NES | NOM P-value | FDR q-value |
|---|---|---|---|---|---|
| KEGG_HEMATOPOIETIC_CELL_LINEAGE | 85 | 0.505882 | 1.570736 | 0.075665 | 0.121829 |
| KEGG_HEDGEHOG_SIGNALING_PATHWAY | 56 | 0.436457 | 1.55085 | 0.034413 | 0.122031 |
| KEGG_DILATED_CARDIOMYOPATHY | 90 | 0.446459 | 1.566047 | 0.033797 | 0.122122 |
| KEGG_NOTCH_SIGNALING_PATHWAY | 47 | 0.43522 | 1.553772 | 0.053719 | 0.122423 |
| KEGG_WNT_SIGNALING_PATHWAY | 149 | 0.372225 | 1.555504 | 0.016129 | 0.124183 |
| KEGG_JAK_STAT_SIGNALING_PATHWAY | 151 | 0.394867 | 1.49607 | 0.047904 | 0.137151 |
| KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC | 74 | 0.432541 | 1.510445 | 0.057803 | 0.137335 |
| KEGG_VIBRIO_CHOLERAE_INFECTION | 53 | 0.377454 | 1.505653 | 0.033264 | 0.137906 |
| KEGG_PROTEASOME | 44 | 0.553234 | 1.497044 | 0.140873 | 0.138892 |
| KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS | 131 | 0.449492 | 1.497436 | 0.103158 | 0.141292 |
| KEGG_BASAL_CELL_CARCINOMA | 55 | 0.414818 | 1.470052 | 0.060291 | 0.143818 |
| KEGG_GLIOMA | 65 | 0.382051 | 1.472442 | 0.040169 | 0.144413 |
| KEGG_GAP_JUNCTION | 89 | 0.363621 | 1.476961 | 0.030364 | 0.146343 |
| KEGG_COLORECTAL_CANCER | 62 | 0.397546 | 1.472834 | 0.058577 | 0.146713 |
| KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE | 26 | 0.473157 | 1.478812 | 0.056112 | 0.147285 |
| KEGG_CHEMOKINE_SIGNALING_PATHWAY | 186 | 0.374518 | 1.442524 | 0.081301 | 0.160746 |
| KEGG_NEUROTROPHIN_SIGNALING_PATHWAY | 126 | 0.350321 | 1.442706 | 0.056604 | 0.16338 |
| KEGG_PYRIMIDINE_METABOLISM | 96 | 0.38685 | 1.429051 | 0.10625 | 0.166838 |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS | 95 | 0.367741 | 1.430141 | 0.085657 | 0.168608 |
| HALLMARK_ANDROGEN_RESPONSE | 100 | 0.328744 | 1.360671 | 0.09073 | 0.172174 |
| HALLMARK_WNT_BETA_CATENIN_SIGNALING | 42 | 0.429363 | 1.364705 | 0.142315 | 0.175243 |
| KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY | 107 | 0.396786 | 1.406532 | 0.102941 | 0.180136 |
| KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION | 46 | 0.525419 | 1.409133 | 0.167339 | 0.180802 |
| KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION | 85 | 0.355637 | 1.400235 | 0.065934 | 0.182243 |
| KEGG_PURINE_METABOLISM | 155 | 0.312366 | 1.395604 | 0.069038 | 0.182945 |
| KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS | 16 | 0.459522 | 1.354746 | 0.114224 | 0.218516 |
| KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT | 38 | 0.368971 | 1.341828 | 0.109244 | 0.228497 |
| KEGG_RNA_POLYMERASE | 29 | 0.448967 | 1.338335 | 0.170431 | 0.228626 |
| HALLMARK_HEME_METABOLISM | 193 | 0.280022 | 1.278394 | 0.120482 | 0.232493 |
| KEGG_CELL_CYCLE | 124 | 0.39393 | 1.324892 | 0.2173 | 0.239195 |
| KEGG_VEGF_SIGNALING_PATHWAY | 75 | 0.326558 | 1.320334 | 0.079108 | 0.240446 |
| KEGG_ADHERENS_JUNCTION | 73 | 0.344565 | 1.313376 | 0.117769 | 0.244197 |
| HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY | 47 | 0.392636 | 1.255609 | 0.225873 | 0.244983 |
| KEGG_ACUTE_MYELOID_LEUKEMIA | 57 | 0.359146 | 1.308455 | 0.151261 | 0.246318 |
| KEGG_OOCYTE_MEIOSIS | 111 | 0.322947 | 1.301358 | 0.149194 | 0.247019 |
| KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY | 74 | 0.400941 | 1.302846 | 0.201613 | 0.248636 |

STAD, stomach adenocarcinoma; KEGG, Kyoto Encyclopedia of Genes and Genomes; ECM, extracellular matrix; TGF, transforming growth factor; TNF, tumor necrosis factor; MAPK, mitogen-activated protein kinase; IL, interleukin; STAT, signal transducer and activator of transcription; JAK, Janus kinase; PI3K, phosphatidylinositol 3-kinase; mTOR, mammalian target of rapamycin; VEGF, vascular endothelial growth factor; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.