Supplementary Material

# Supplementary Figures and Tables

## Supplementary Figures

**Supplementary Figure S1.** Development of a nomogram based on the metabolism-related signature in the GEO testing cohort. (A) Development of MRGs nomogram. (B-C) Calibration plots for the signature at 3-year and 5-year.



## Supplementary Tables

**Supplementary Table S1.** TheHALLMARK gene pathway enrichment in the high-risk group of patients in the Cancer Genome Atlas database.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **NAME** | **SIZE** | **ES** | **NES** | **NOM p-val** | **FDR q-val** | **FWER p-val** |
| HALLMARK\_OXIDATIVE\_PHOSPHORYLATION | 200 | 0.70143 | 1.80643 | 0.002058 | 0.004643 | 0.003 |
| HALLMARK\_MTORC1\_SIGNALING | 200 | 0.66222 | 1.74344 | 0 | 0.00938 | 0.014 |
| HALLMARK\_E2F\_TARGETS | 200 | 0.72687 | 1.69378 | 0.003992 | 0.02204 | 0.038 |
| HALLMARK\_IL6\_JAK\_STAT3\_SIGNALING | 87 | 0.72077 | 1.64972 | 0.00998 | 0.039023 | 0.069 |
| HALLMARK\_GLYCOLYSIS | 199 | 0.58453 | 1.64223 | 0.00404 | 0.037206 | 0.077 |
| HALLMARK\_G2M\_CHECKPOINT | 200 | 0.67284 | 1.63384 | 0.005929 | 0.033942 | 0.083 |
| HALLMARK\_INFLAMMATORY\_RESPONSE | 200 | 0.63636 | 1.58394 | 0.027559 | 0.059814 | 0.138 |
| HALLMARK\_MYC\_TARGETS\_V1 | 200 | 0.61453 | 1.57601 | 0.028169 | 0.058128 | 0.148 |
| HALLMARK\_MYC\_TARGETS\_V2 | 58 | 0.64179 | 1.56863 | 0.032922 | 0.056689 | 0.158 |
| HALLMARK\_ADIPOGENESIS | 200 | 0.52163 | 1.5654 | 0.009921 | 0.052561 | 0.16 |
| HALLMARK\_PEROXISOME | 104 | 0.54525 | 1.53233 | 0.018367 | 0.069511 | 0.199 |
| HALLMARK\_UV\_RESPONSE\_UP | 158 | 0.50609 | 1.51398 | 0.02004 | 0.075924 | 0.217 |
| HALLMARK\_IL2\_STAT5\_SIGNALING | 199 | 0.54559 | 1.51362 | 0.022312 | 0.070295 | 0.217 |
| HALLMARK\_REACTIVE\_OXYGEN\_SPECIES\_PATHWAY | 49 | 0.61412 | 1.51284 | 0.026477 | 0.065425 | 0.217 |
| HALLMARK\_UNFOLDED\_PROTEIN\_RESPONSE | 113 | 0.56979 | 1.51019 | 0.02988 | 0.062487 | 0.222 |
| HALLMARK\_NOTCH\_SIGNALING | 32 | 0.59773 | 1.50938 | 0.034 | 0.059197 | 0.224 |
| HALLMARK\_COMPLEMENT | 200 | 0.5554 | 1.50881 | 0.051282 | 0.055903 | 0.224 |
| HALLMARK\_ANGIOGENESIS | 36 | 0.60021 | 1.50247 | 0.033473 | 0.055724 | 0.232 |
| HALLMARK\_TNFA\_SIGNALING\_VIA\_NFKB | 200 | 0.57082 | 1.50243 | 0.042596 | 0.052847 | 0.232 |
| HALLMARK\_FATTY\_ACID\_METABOLISM | 158 | 0.50433 | 1.48002 | 0.020161 | 0.061899 | 0.264 |
| HALLMARK\_ESTROGEN\_RESPONSE\_LATE | 199 | 0.47526 | 1.47824 | 0.026052 | 0.059831 | 0.267 |
| HALLMARK\_APOPTOSIS | 161 | 0.52356 | 1.46714 | 0.040733 | 0.063233 | 0.277 |
| HALLMARK\_PI3K\_AKT\_MTOR\_SIGNALING | 105 | 0.51316 | 1.45714 | 0.028169 | 0.066334 | 0.29 |
| HALLMARK\_COAGULATION | 138 | 0.48655 | 1.44114 | 0.045549 | 0.072317 | 0.314 |
| HALLMARK\_EPITHELIAL\_MESENCHYMAL\_TRANSITION | 200 | 0.53541 | 1.43341 | 0.081466 | 0.074166 | 0.332 |
| HALLMARK\_APICAL\_JUNCTION | 200 | 0.48737 | 1.42614 | 0.067073 | 0.075824 | 0.341 |
| HALLMARK\_HYPOXIA | 200 | 0.48892 | 1.42505 | 0.054656 | 0.073858 | 0.344 |
| HALLMARK\_ALLOGRAFT\_REJECTION | 200 | 0.61805 | 1.41336 | 0.13834 | 0.077576 | 0.36 |
| HALLMARK\_MITOTIC\_SPINDLE | 199 | 0.52463 | 1.41101 | 0.073705 | 0.076055 | 0.365 |
| HALLMARK\_PROTEIN\_SECRETION | 96 | 0.58668 | 1.39971 | 0.087302 | 0.080146 | 0.379 |
| HALLMARK\_INTERFERON\_GAMMA\_RESPONSE | 200 | 0.64187 | 1.37633 | 0.155419 | 0.093125 | 0.419 |
| HALLMARK\_KRAS\_SIGNALING\_UP | 200 | 0.51219 | 1.37201 | 0.071869 | 0.093517 | 0.425 |
| HALLMARK\_XENOBIOTIC\_METABOLISM | 200 | 0.44436 | 1.35095 | 0.086066 | 0.105968 | 0.459 |
| HALLMARK\_DNA\_REPAIR | 149 | 0.45034 | 1.34182 | 0.104418 | 0.108885 | 0.469 |
| HALLMARK\_TGF\_BETA\_SIGNALING | 54 | 0.51619 | 1.33276 | 0.136461 | 0.112328 | 0.481 |
| HALLMARK\_P53\_PATHWAY | 199 | 0.43106 | 1.31979 | 0.08125 | 0.117848 | 0.506 |
| HALLMARK\_HEDGEHOG\_SIGNALING | 36 | 0.52545 | 1.2836 | 0.154959 | 0.140037 | 0.55 |
| HALLMARK\_ANDROGEN\_RESPONSE | 100 | 0.48233 | 1.27832 | 0.176238 | 0.140184 | 0.558 |
| HALLMARK\_CHOLESTEROL\_HOMEOSTASIS | 74 | 0.42526 | 1.23843 | 0.167019 | 0.167108 | 0.598 |
| HALLMARK\_PANCREAS\_BETA\_CELLS | 40 | 0.50393 | 1.22105 | 0.195266 | 0.17662 | 0.618 |
| HALLMARK\_UV\_RESPONSE\_DN | 144 | 0.46865 | 1.2208 | 0.216102 | 0.172429 | 0.618 |
| HALLMARK\_SPERMATOGENESIS | 135 | 0.41559 | 1.21828 | 0.166329 | 0.169933 | 0.62 |
| HALLMARK\_APICAL\_SURFACE | 44 | 0.42266 | 1.20467 | 0.190678 | 0.176093 | 0.634 |
| HALLMARK\_ESTROGEN\_RESPONSE\_EARLY | 200 | 0.38942 | 1.17736 | 0.229167 | 0.193337 | 0.665 |
| HALLMARK\_INTERFERON\_ALPHA\_RESPONSE | 97 | 0.58549 | 1.16802 | 0.349693 | 0.197192 | 0.676 |
| HALLMARK\_WNT\_BETA\_CATENIN\_SIGNALING | 42 | 0.41116 | 1.13169 | 0.281059 | 0.226039 | 0.72 |
| HALLMARK\_MYOGENESIS | 200 | 0.37732 | 1.12762 | 0.279261 | 0.224854 | 0.722 |
| HALLMARK\_BILE\_ACID\_METABOLISM | 112 | 0.35776 | 1.10266 | 0.287169 | 0.2436 | 0.743 |
| HALLMARK\_HEME\_METABOLISM | 200 | 0.3391 | 1.01981 | 0.436874 | 0.323563 | 0.793 |
| HALLMARK\_KRAS\_SIGNALING\_DN | 200 | 0.2797 | 0.87167 | 0.713427 | 0.509475 | 0.879 |

**Supplementary Table S2.** The KEGG gene pathway enrichment in the high-risk group of patients in the Cancer Genome Atlas database.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **NAME** | **SIZE** | **ES** | **NES** | **NOM p-val** | **FDR q-val** | **FWER p-val** |
| KEGG\_ALZHEIMERS\_DISEASE | 165 | -0.65875 | -1.87656 | 0 | 0.007477 | 0.004 |
| KEGG\_HUNTINGTONS\_DISEASE | 180 | -0.57819 | -1.77394 | 0 | 0.027235 | 0.033 |
| KEGG\_OXIDATIVE\_PHOSPHORYLATION | 131 | -0.65246 | -1.75634 | 0.006494 | 0.022239 | 0.041 |
| KEGG\_PROTEASOME | 46 | -0.81218 | -1.74682 | 0.002066 | 0.020288 | 0.051 |
| KEGG\_PARKINSONS\_DISEASE | 128 | -0.62563 | -1.73883 | 0.004338 | 0.018576 | 0.057 |
| KEGG\_CITRATE\_CYCLE\_TCA\_CYCLE | 31 | -0.73874 | -1.69745 | 0.005988 | 0.035308 | 0.106 |
| KEGG\_PYRIMIDINE\_METABOLISM | 97 | -0.59707 | -1.68032 | 0 | 0.042814 | 0.14 |
| KEGG\_OOCYTE\_MEIOSIS | 112 | -0.63592 | -1.67293 | 0 | 0.043365 | 0.152 |
| KEGG\_VIBRIO\_CHOLERAE\_INFECTION | 54 | -0.61795 | -1.67179 | 0.004158 | 0.039203 | 0.152 |
| KEGG\_GLYOXYLATE\_AND\_DICARBOXYLATE\_METABOLISM | 16 | -0.70108 | -1.61696 | 0.017928 | 0.113196 | 0.249 |
| KEGG\_N\_GLYCAN\_BIOSYNTHESIS | 46 | -0.62196 | -1.59272 | 0.023346 | 0.136403 | 0.293 |
| KEGG\_AMINO\_SUGAR\_AND\_NUCLEOTIDE\_SUGAR\_METABOLISM | 43 | -0.6357 | -1.59162 | 0.020121 | 0.126502 | 0.293 |
| KEGG\_RNA\_POLYMERASE | 28 | -0.58419 | -1.5811 | 0.012 | 0.131535 | 0.314 |
| KEGG\_APOPTOSIS | 87 | -0.60255 | -1.58004 | 0.011928 | 0.12308 | 0.317 |
| KEGG\_CELL\_CYCLE | 124 | -0.63116 | -1.57705 | 0.003922 | 0.119128 | 0.324 |
| KEGG\_GLUTATHIONE\_METABOLISM | 49 | -0.55534 | -1.56473 | 0.023454 | 0.127622 | 0.348 |
| KEGG\_CYTOSOLIC\_DNA\_SENSING\_PATHWAY | 55 | -0.6364 | -1.53523 | 0.034137 | 0.167207 | 0.412 |
| KEGG\_AMYOTROPHIC\_LATERAL\_SCLEROSIS\_ALS | 53 | -0.61645 | -1.53259 | 0.008147 | 0.166945 | 0.424 |
| KEGG\_GALACTOSE\_METABOLISM | 26 | -0.63343 | -1.52841 | 0.047009 | 0.172724 | 0.432 |
| KEGG\_PURINE\_METABOLISM | 158 | -0.51399 | -1.52088 | 0.008032 | 0.176869 | 0.455 |
| KEGG\_PROTEIN\_EXPORT | 24 | -0.69234 | -1.51306 | 0.015504 | 0.179714 | 0.474 |
| KEGG\_P53\_SIGNALING\_PATHWAY | 68 | -0.54382 | -1.50887 | 0.015564 | 0.177327 | 0.48 |
| KEGG\_NATURAL\_KILLER\_CELL\_MEDIATED\_CYTOTOXICITY | 132 | -0.6124 | -1.48611 | 0.061386 | 0.205657 | 0.529 |
| KEGG\_TOLL\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | 102 | -0.57407 | -1.47689 | 0.067061 | 0.213202 | 0.546 |
| KEGG\_MTOR\_SIGNALING\_PATHWAY | 52 | -0.51344 | -1.4678 | 0.031496 | 0.219003 | 0.565 |
| KEGG\_PRION\_DISEASES | 35 | -0.55964 | -1.46592 | 0.063008 | 0.213638 | 0.568 |
| KEGG\_HOMOLOGOUS\_RECOMBINATION | 28 | -0.66772 | -1.46345 | 0.038384 | 0.210556 | 0.574 |
| KEGG\_DNA\_REPLICATION | 36 | -0.64504 | -1.46099 | 0.07 | 0.210092 | 0.584 |
| KEGG\_ABC\_TRANSPORTERS | 44 | -0.57834 | -1.45179 | 0.037037 | 0.225617 | 0.608 |
| KEGG\_NOTCH\_SIGNALING\_PATHWAY | 47 | -0.52559 | -1.45111 | 0.053254 | 0.218868 | 0.609 |
| KEGG\_REGULATION\_OF\_ACTIN\_CYTOSKELETON | 213 | -0.48196 | -1.44892 | 0.037549 | 0.217278 | 0.617 |
| KEGG\_GLYCOSYLPHOSPHATIDYLINOSITOL\_GPI\_ANCHOR\_BIOSYNTHESIS | 25 | -0.61417 | -1.44864 | 0.071154 | 0.210947 | 0.617 |
| KEGG\_HYPERTROPHIC\_CARDIOMYOPATHY\_HCM | 83 | -0.5737 | -1.44382 | 0.034908 | 0.211708 | 0.626 |
| KEGG\_MATURITY\_ONSET\_DIABETES\_OF\_THE\_YOUNG | 25 | -0.59266 | -1.44286 | 0.069672 | 0.207176 | 0.627 |
| KEGG\_TERPENOID\_BACKBONE\_BIOSYNTHESIS | 15 | -0.61508 | -1.44282 | 0.048193 | 0.201285 | 0.627 |
| KEGG\_BIOSYNTHESIS\_OF\_UNSATURATED\_FATTY\_ACIDS | 22 | -0.5945 | -1.44145 | 0.055102 | 0.197531 | 0.631 |
| KEGG\_SPHINGOLIPID\_METABOLISM | 39 | -0.55174 | -1.43393 | 0.065868 | 0.203114 | 0.641 |
| KEGG\_DRUG\_METABOLISM\_OTHER\_ENZYMES | 51 | -0.46798 | -1.43372 | 0.016913 | 0.198101 | 0.642 |
| KEGG\_GLYCOLYSIS\_GLUCONEOGENESIS | 62 | -0.49747 | -1.43302 | 0.069328 | 0.19384 | 0.642 |
| KEGG\_CYTOKINE\_CYTOKINE\_RECEPTOR\_INTERACTION | 264 | -0.56565 | -1.43296 | 0.083004 | 0.189154 | 0.642 |
| KEGG\_SNARE\_INTERACTIONS\_IN\_VESICULAR\_TRANSPORT | 38 | -0.58109 | -1.42963 | 0.056 | 0.189428 | 0.649 |
| KEGG\_TYPE\_I\_DIABETES\_MELLITUS | 41 | -0.72249 | -1.42843 | 0.086172 | 0.186486 | 0.65 |
| KEGG\_DILATED\_CARDIOMYOPATHY | 90 | -0.57299 | -1.42818 | 0.04499 | 0.182345 | 0.65 |
| KEGG\_PROGESTERONE\_MEDIATED\_OOCYTE\_MATURATION | 85 | -0.50023 | -1.42416 | 0.040856 | 0.183572 | 0.658 |
| KEGG\_STARCH\_AND\_SUCROSE\_METABOLISM | 52 | -0.48926 | -1.42371 | 0.045082 | 0.180011 | 0.658 |
| KEGG\_LEISHMANIA\_INFECTION | 70 | -0.62382 | -1.423 | 0.101796 | 0.177066 | 0.659 |
| KEGG\_PORPHYRIN\_AND\_CHLOROPHYLL\_METABOLISM | 41 | -0.53091 | -1.41644 | 0.067901 | 0.182382 | 0.667 |
| KEGG\_MAPK\_SIGNALING\_PATHWAY | 267 | -0.48403 | -1.41563 | 0.05098 | 0.179556 | 0.667 |
| KEGG\_GRAFT\_VERSUS\_HOST\_DISEASE | 37 | -0.7901 | -1.41239 | 0.078947 | 0.180074 | 0.673 |
| KEGG\_NOD\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | 62 | -0.58128 | -1.41203 | 0.075099 | 0.176989 | 0.674 |
| KEGG\_ADIPOCYTOKINE\_SIGNALING\_PATHWAY | 67 | -0.49711 | -1.41018 | 0.060311 | 0.17632 | 0.679 |
| KEGG\_O\_GLYCAN\_BIOSYNTHESIS | 30 | -0.58996 | -1.40816 | 0.060547 | 0.175359 | 0.686 |
| KEGG\_BLADDER\_CANCER | 42 | -0.50016 | -1.4063 | 0.054 | 0.174093 | 0.686 |
| KEGG\_GLYCEROLIPID\_METABOLISM | 49 | -0.4912 | -1.40471 | 0.033865 | 0.173704 | 0.693 |
| KEGG\_ONE\_CARBON\_POOL\_BY\_FOLATE | 17 | -0.62973 | -1.40462 | 0.086614 | 0.170674 | 0.693 |
| KEGG\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION | 81 | -0.65777 | -1.40049 | 0.115538 | 0.172734 | 0.696 |
| KEGG\_VASCULAR\_SMOOTH\_MUSCLE\_CONTRACTION | 114 | -0.49755 | -1.38842 | 0.06917 | 0.183979 | 0.713 |
| KEGG\_EPITHELIAL\_CELL\_SIGNALING\_IN\_HELICOBACTER\_PYLORI\_INFECTION | 68 | -0.50704 | -1.38804 | 0.06986 | 0.181264 | 0.714 |
| KEGG\_HEMATOPOIETIC\_CELL\_LINEAGE | 85 | -0.60972 | -1.38707 | 0.117647 | 0.179281 | 0.716 |
| KEGG\_VEGF\_SIGNALING\_PATHWAY | 76 | -0.47086 | -1.38422 | 0.065476 | 0.179286 | 0.719 |
| KEGG\_GLYCOSAMINOGLYCAN\_BIOSYNTHESIS\_CHONDROITIN\_SULFATE | 22 | -0.59197 | -1.38302 | 0.094142 | 0.177984 | 0.721 |
| KEGG\_CARDIAC\_MUSCLE\_CONTRACTION | 78 | -0.5533 | -1.37813 | 0.112266 | 0.181493 | 0.735 |
| KEGG\_AMINOACYL\_TRNA\_BIOSYNTHESIS | 41 | -0.5859 | -1.37578 | 0.125749 | 0.181283 | 0.741 |
| KEGG\_PATHWAYS\_IN\_CANCER | 325 | -0.4576 | -1.37453 | 0.082852 | 0.179684 | 0.744 |
| KEGG\_SYSTEMIC\_LUPUS\_ERYTHEMATOSUS | 135 | -0.51643 | -1.37162 | 0.112016 | 0.180209 | 0.75 |
| KEGG\_RENIN\_ANGIOTENSIN\_SYSTEM | 17 | -0.56234 | -1.36678 | 0.070727 | 0.182638 | 0.756 |
| KEGG\_FC\_GAMMA\_R\_MEDIATED\_PHAGOCYTOSIS | 96 | -0.50038 | -1.3657 | 0.112 | 0.181102 | 0.758 |
| KEGG\_CELL\_ADHESION\_MOLECULES\_CAMS | 131 | -0.5575 | -1.35794 | 0.117769 | 0.188565 | 0.768 |
| KEGG\_ENDOCYTOSIS | 181 | -0.47329 | -1.35774 | 0.093496 | 0.186023 | 0.768 |
| KEGG\_RIG\_I\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | 71 | -0.51884 | -1.35271 | 0.122736 | 0.189415 | 0.774 |
| KEGG\_RENAL\_CELL\_CARCINOMA | 70 | -0.49098 | -1.34819 | 0.111969 | 0.191113 | 0.78 |
| KEGG\_MELANOMA | 71 | -0.46044 | -1.34796 | 0.093439 | 0.189442 | 0.781 |
| KEGG\_COMPLEMENT\_AND\_COAGULATION\_CASCADES | 69 | -0.51105 | -1.34665 | 0.108333 | 0.188128 | 0.784 |
| KEGG\_LEUKOCYTE\_TRANSENDOTHELIAL\_MIGRATION | 116 | -0.47671 | -1.34601 | 0.126016 | 0.186373 | 0.785 |
| KEGG\_PANTOTHENATE\_AND\_COA\_BIOSYNTHESIS | 16 | -0.55386 | -1.34354 | 0.117296 | 0.186961 | 0.79 |
| KEGG\_CALCIUM\_SIGNALING\_PATHWAY | 177 | -0.52078 | -1.33799 | 0.103792 | 0.191397 | 0.8 |
| KEGG\_GLIOMA | 65 | -0.48356 | -1.33128 | 0.12549 | 0.196266 | 0.807 |
| KEGG\_FOCAL\_ADHESION | 199 | -0.44597 | -1.32877 | 0.097416 | 0.196491 | 0.815 |
| KEGG\_GLYCOSPHINGOLIPID\_BIOSYNTHESIS\_GANGLIO\_SERIES | 15 | -0.60102 | -1.32535 | 0.137214 | 0.197677 | 0.817 |
| KEGG\_PYRUVATE\_METABOLISM | 40 | -0.48004 | -1.32422 | 0.107071 | 0.196462 | 0.818 |
| KEGG\_ECM\_RECEPTOR\_INTERACTION | 84 | -0.48901 | -1.32141 | 0.117988 | 0.197474 | 0.823 |
| KEGG\_LONG\_TERM\_POTENTIATION | 70 | -0.52792 | -1.31935 | 0.106996 | 0.197344 | 0.825 |
| KEGG\_BASE\_EXCISION\_REPAIR | 35 | -0.48699 | -1.31903 | 0.124514 | 0.195354 | 0.825 |
| KEGG\_PROXIMAL\_TUBULE\_BICARBONATE\_RECLAMATION | 23 | -0.59168 | -1.318 | 0.090164 | 0.194057 | 0.828 |
| KEGG\_SPLICEOSOME | 127 | -0.50416 | -1.30593 | 0.164093 | 0.20569 | 0.843 |
| KEGG\_GLYCINE\_SERINE\_AND\_THREONINE\_METABOLISM | 31 | -0.49616 | -1.30416 | 0.123348 | 0.204716 | 0.846 |
| KEGG\_B\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 75 | -0.50512 | -1.30388 | 0.14902 | 0.202631 | 0.846 |
| KEGG\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 108 | -0.50583 | -1.30159 | 0.178503 | 0.20341 | 0.85 |
| KEGG\_JAK\_STAT\_SIGNALING\_PATHWAY | 155 | -0.48135 | -1.29998 | 0.152642 | 0.202973 | 0.851 |
| KEGG\_CHEMOKINE\_SIGNALING\_PATHWAY | 188 | -0.49583 | -1.29568 | 0.164683 | 0.20573 | 0.854 |
| KEGG\_LYSOSOME | 121 | -0.49232 | -1.29509 | 0.169165 | 0.20394 | 0.856 |
| KEGG\_NEUROTROPHIN\_SIGNALING\_PATHWAY | 126 | -0.44709 | -1.2936 | 0.142578 | 0.203331 | 0.859 |
| KEGG\_FRUCTOSE\_AND\_MANNOSE\_METABOLISM | 33 | -0.47785 | -1.29182 | 0.134694 | 0.202838 | 0.86 |
| KEGG\_PHOSPHATIDYLINOSITOL\_SIGNALING\_SYSTEM | 76 | -0.47141 | -1.28311 | 0.160321 | 0.209795 | 0.869 |
| KEGG\_VIRAL\_MYOCARDITIS | 68 | -0.52221 | -1.28081 | 0.189691 | 0.20986 | 0.869 |
| KEGG\_ALLOGRAFT\_REJECTION | 35 | -0.72027 | -1.28046 | 0.212982 | 0.208105 | 0.87 |
| KEGG\_PATHOGENIC\_ESCHERICHIA\_COLI\_INFECTION | 56 | -0.44971 | -1.27898 | 0.130178 | 0.207565 | 0.873 |
| KEGG\_PANCREATIC\_CANCER | 70 | -0.45661 | -1.27527 | 0.167954 | 0.210856 | 0.878 |
| KEGG\_MISMATCH\_REPAIR | 23 | -0.58896 | -1.27369 | 0.216433 | 0.210434 | 0.88 |
| KEGG\_RNA\_DEGRADATION | 59 | -0.53788 | -1.27352 | 0.20155 | 0.208622 | 0.881 |
| KEGG\_CHRONIC\_MYELOID\_LEUKEMIA | 73 | -0.45588 | -1.27091 | 0.183432 | 0.210253 | 0.883 |
| KEGG\_PEROXISOME | 78 | -0.44891 | -1.26955 | 0.160569 | 0.209465 | 0.884 |
| KEGG\_ARRHYTHMOGENIC\_RIGHT\_VENTRICULAR\_CARDIOMYOPATHY\_ARVC | 74 | -0.49868 | -1.26738 | 0.15748 | 0.209875 | 0.886 |
| KEGG\_AUTOIMMUNE\_THYROID\_DISEASE | 50 | -0.65041 | -1.26554 | 0.245436 | 0.209959 | 0.891 |
| KEGG\_TGF\_BETA\_SIGNALING\_PATHWAY | 85 | -0.46207 | -1.2585 | 0.205993 | 0.215128 | 0.899 |
| KEGG\_SELENOAMINO\_ACID\_METABOLISM | 26 | -0.50515 | -1.25606 | 0.167323 | 0.215771 | 0.904 |
| KEGG\_DORSO\_VENTRAL\_AXIS\_FORMATION | 24 | -0.51927 | -1.2516 | 0.179842 | 0.218224 | 0.907 |
| KEGG\_GNRH\_SIGNALING\_PATHWAY | 101 | -0.43369 | -1.24902 | 0.17126 | 0.219261 | 0.909 |
| KEGG\_FC\_EPSILON\_RI\_SIGNALING\_PATHWAY | 79 | -0.43765 | -1.24188 | 0.192157 | 0.224861 | 0.916 |
| KEGG\_INTESTINAL\_IMMUNE\_NETWORK\_FOR\_IGA\_PRODUCTION | 46 | -0.61275 | -1.2382 | 0.27668 | 0.226482 | 0.917 |
| KEGG\_NUCLEOTIDE\_EXCISION\_REPAIR | 44 | -0.51327 | -1.23089 | 0.215726 | 0.232341 | 0.923 |
| KEGG\_SMALL\_CELL\_LUNG\_CANCER | 84 | -0.43514 | -1.22299 | 0.208413 | 0.238493 | 0.929 |
| KEGG\_ETHER\_LIPID\_METABOLISM | 33 | -0.45015 | -1.20972 | 0.204771 | 0.251534 | 0.931 |
| KEGG\_NICOTINATE\_AND\_NICOTINAMIDE\_METABOLISM | 24 | -0.47092 | -1.20412 | 0.23 | 0.255634 | 0.936 |
| KEGG\_INOSITOL\_PHOSPHATE\_METABOLISM | 54 | -0.43614 | -1.19645 | 0.233663 | 0.263202 | 0.943 |
| KEGG\_GLYCOSAMINOGLYCAN\_DEGRADATION | 21 | -0.48574 | -1.19114 | 0.25 | 0.267255 | 0.944 |
| KEGG\_UBIQUITIN\_MEDIATED\_PROTEOLYSIS | 134 | -0.44241 | -1.18035 | 0.265267 | 0.276956 | 0.947 |
| KEGG\_NEUROACTIVE\_LIGAND\_RECEPTOR\_INTERACTION | 271 | -0.50554 | -1.16964 | 0.264228 | 0.288171 | 0.951 |
| KEGG\_GLYCOSAMINOGLYCAN\_BIOSYNTHESIS\_KERATAN\_SULFATE | 15 | -0.50972 | -1.16832 | 0.269076 | 0.287274 | 0.952 |
| KEGG\_GAP\_JUNCTION | 90 | -0.43672 | -1.16827 | 0.260246 | 0.284923 | 0.952 |
| KEGG\_GLYCEROPHOSPHOLIPID\_METABOLISM | 77 | -0.39464 | -1.16527 | 0.254369 | 0.286235 | 0.952 |
| KEGG\_ADHERENS\_JUNCTION | 73 | -0.42222 | -1.162 | 0.280769 | 0.28757 | 0.952 |
| KEGG\_FATTY\_ACID\_METABOLISM | 42 | -0.43412 | -1.15754 | 0.276892 | 0.289865 | 0.954 |
| KEGG\_HEDGEHOG\_SIGNALING\_PATHWAY | 56 | -0.41054 | -1.15705 | 0.261682 | 0.288186 | 0.955 |
| KEGG\_ALANINE\_ASPARTATE\_AND\_GLUTAMATE\_METABOLISM | 32 | -0.43585 | -1.15667 | 0.231237 | 0.286318 | 0.955 |
| KEGG\_INSULIN\_SIGNALING\_PATHWAY | 137 | -0.36593 | -1.15026 | 0.240777 | 0.292144 | 0.956 |
| KEGG\_PPAR\_SIGNALING\_PATHWAY | 69 | -0.37785 | -1.14394 | 0.23299 | 0.297491 | 0.959 |
| KEGG\_ARGININE\_AND\_PROLINE\_METABOLISM | 54 | -0.42313 | -1.13588 | 0.279749 | 0.305122 | 0.959 |
| KEGG\_TYPE\_II\_DIABETES\_MELLITUS | 47 | -0.43886 | -1.12911 | 0.337374 | 0.310669 | 0.961 |
| KEGG\_ASTHMA | 28 | -0.55048 | -1.11698 | 0.406439 | 0.322885 | 0.965 |
| KEGG\_VASOPRESSIN\_REGULATED\_WATER\_REABSORPTION | 44 | -0.40599 | -1.10256 | 0.338115 | 0.339274 | 0.968 |
| KEGG\_PRIMARY\_IMMUNODEFICIENCY | 35 | -0.55121 | -1.10233 | 0.405088 | 0.337028 | 0.968 |
| KEGG\_PROSTATE\_CANCER | 89 | -0.36981 | -1.09398 | 0.355769 | 0.345128 | 0.969 |
| KEGG\_VALINE\_LEUCINE\_AND\_ISOLEUCINE\_DEGRADATION | 44 | -0.4399 | -1.08705 | 0.369352 | 0.35174 | 0.97 |
| KEGG\_LINOLEIC\_ACID\_METABOLISM | 29 | -0.41984 | -1.08615 | 0.35098 | 0.35037 | 0.97 |
| KEGG\_RETINOL\_METABOLISM | 64 | -0.37046 | -1.08291 | 0.307229 | 0.351967 | 0.971 |
| KEGG\_ALPHA\_LINOLENIC\_ACID\_METABOLISM | 19 | -0.43919 | -1.08082 | 0.337302 | 0.352207 | 0.972 |
| KEGG\_STEROID\_HORMONE\_BIOSYNTHESIS | 55 | -0.34507 | -1.07919 | 0.267308 | 0.351645 | 0.972 |
| KEGG\_ALDOSTERONE\_REGULATED\_SODIUM\_REABSORPTION | 42 | -0.40984 | -1.0733 | 0.359438 | 0.356202 | 0.973 |
| KEGG\_PENTOSE\_PHOSPHATE\_PATHWAY | 27 | -0.38442 | -1.07235 | 0.329293 | 0.354928 | 0.975 |
| KEGG\_MELANOGENESIS | 101 | -0.35921 | -1.06194 | 0.366534 | 0.36589 | 0.979 |
| KEGG\_BUTANOATE\_METABOLISM | 34 | -0.40324 | -1.04791 | 0.405512 | 0.381453 | 0.981 |
| KEGG\_ERBB\_SIGNALING\_PATHWAY | 87 | -0.36803 | -1.04324 | 0.395303 | 0.38471 | 0.981 |
| KEGG\_LONG\_TERM\_DEPRESSION | 70 | -0.41853 | -1.03789 | 0.451346 | 0.388913 | 0.984 |
| KEGG\_BASAL\_TRANSCRIPTION\_FACTORS | 35 | -0.42939 | -1.02931 | 0.477099 | 0.398572 | 0.984 |
| KEGG\_LYSINE\_DEGRADATION | 44 | -0.39834 | -1.02313 | 0.441584 | 0.404108 | 0.984 |
| KEGG\_AXON\_GUIDANCE | 129 | -0.36644 | -1.01882 | 0.434608 | 0.407618 | 0.985 |
| KEGG\_ACUTE\_MYELOID\_LEUKEMIA | 57 | -0.35797 | -0.99927 | 0.455285 | 0.431851 | 0.989 |
| KEGG\_WNT\_SIGNALING\_PATHWAY | 150 | -0.32435 | -0.97283 | 0.485437 | 0.466305 | 0.991 |
| KEGG\_COLORECTAL\_CANCER | 62 | -0.35504 | -0.96442 | 0.514852 | 0.475889 | 0.991 |
| KEGG\_ARACHIDONIC\_ACID\_METABOLISM | 58 | -0.31901 | -0.96284 | 0.484849 | 0.474797 | 0.991 |
| KEGG\_OTHER\_GLYCAN\_DEGRADATION | 16 | -0.39224 | -0.9388 | 0.544355 | 0.510361 | 0.992 |
| KEGG\_TRYPTOPHAN\_METABOLISM | 40 | -0.33927 | -0.93791 | 0.548193 | 0.508093 | 0.992 |
| KEGG\_PENTOSE\_AND\_GLUCURONATE\_INTERCONVERSIONS | 28 | -0.34794 | -0.93273 | 0.529652 | 0.512361 | 0.992 |
| KEGG\_TASTE\_TRANSDUCTION | 51 | -0.38983 | -0.93196 | 0.60835 | 0.510528 | 0.992 |
| KEGG\_METABOLISM\_OF\_XENOBIOTICS\_BY\_CYTOCHROME\_P450 | 69 | -0.29712 | -0.92716 | 0.572301 | 0.514203 | 0.992 |
| KEGG\_NITROGEN\_METABOLISM | 23 | -0.36292 | -0.92029 | 0.59127 | 0.521867 | 0.992 |
| KEGG\_GLYCOSAMINOGLYCAN\_BIOSYNTHESIS\_HEPARAN\_SULFATE | 26 | -0.39915 | -0.90175 | 0.636364 | 0.54796 | 0.993 |
| KEGG\_GLYCOSPHINGOLIPID\_BIOSYNTHESIS\_LACTO\_AND\_NEOLACTO\_SERIES | 26 | -0.35571 | -0.88531 | 0.650407 | 0.571245 | 0.994 |
| KEGG\_REGULATION\_OF\_AUTOPHAGY | 35 | -0.35395 | -0.87958 | 0.625483 | 0.576994 | 0.995 |
| KEGG\_BETA\_ALANINE\_METABOLISM | 22 | -0.34385 | -0.8714 | 0.673511 | 0.586092 | 0.995 |
| KEGG\_NON\_SMALL\_CELL\_LUNG\_CANCER | 54 | -0.30721 | -0.86852 | 0.664032 | 0.586534 | 0.995 |
| KEGG\_BASAL\_CELL\_CARCINOMA | 55 | -0.30544 | -0.86398 | 0.679688 | 0.590057 | 0.996 |
| KEGG\_RIBOFLAVIN\_METABOLISM | 16 | -0.33205 | -0.85912 | 0.69574 | 0.594643 | 0.997 |
| KEGG\_STEROID\_BIOSYNTHESIS | 17 | -0.34863 | -0.83649 | 0.68254 | 0.627435 | 0.998 |
| KEGG\_CYSTEINE\_AND\_METHIONINE\_METABOLISM | 34 | -0.29861 | -0.81209 | 0.760784 | 0.663957 | 0.999 |
| KEGG\_PROPANOATE\_METABOLISM | 33 | -0.30365 | -0.73076 | 0.809237 | 0.796765 | 1 |
| KEGG\_OLFACTORY\_TRANSDUCTION | 385 | -0.21354 | -0.71053 | 0.973896 | 0.826051 | 1 |
| KEGG\_ENDOMETRIAL\_CANCER | 52 | -0.25258 | -0.69877 | 0.876494 | 0.839565 | 1 |

**Supplementary Table S3.** The KEGG gene pathway enrichment in the low-risk group of patients in the Cancer Genome Atlas database.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **NAME** | **SIZE** | **ES** | **NES** | **NOM p-val** | **FDR q-val** | **FWER p-val** |
| KEGG\_RIBOSOME | 88 | 0.76077 | 1.427731 | 0.101449 | 0.401084 | 0.648 |
| KEGG\_HISTIDINE\_METABOLISM | 29 | 0.451921 | 1.200231 | 0.176938 | 0.795731 | 0.917 |
| KEGG\_PRIMARY\_BILE\_ACID\_BIOSYNTHESIS | 16 | 0.420301 | 1.095795 | 0.2818 | 0.81065 | 0.961 |
| KEGG\_TYROSINE\_METABOLISM | 42 | 0.337784 | 0.955989 | 0.500967 | 0.97829 | 0.991 |
| KEGG\_THYROID\_CANCER | 29 | 0.317904 | 0.888053 | 0.629857 | 0.952781 | 0.997 |
| KEGG\_DRUG\_METABOLISM\_CYTOCHROME\_P450 | 71 | 0.283104 | 0.874423 | 0.681905 | 0.826216 | 0.997 |
| KEGG\_TIGHT\_JUNCTION | 132 | 0.288097 | 0.863131 | 0.698225 | 0.730023 | 0.997 |
| KEGG\_ASCORBATE\_AND\_ALDARATE\_METABOLISM | 25 | 0.296462 | 0.772642 | 0.832046 | 0.800272 | 1 |
| KEGG\_PHENYLALANINE\_METABOLISM | 18 | 0.288441 | 0.652885 | 0.890805 | 0.894469 | 1 |