**Supplementary material**

Supplementary Table 1. GSEA of high expression group and low expression group in gene prognostic model.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Description | ES | NES | adj.*p* | q value |
| KEGG\_ASCORBATE\_AND\_ALDARATE\_METABOLISM | 0.677704 | 2.101451 | 0.006118 | 0.004941 |
| KEGG\_BASE\_EXCISION\_REPAIR | 0.59795 | 2.028979 | 0.007176 | 0.005796 |
| KEGG\_CARDIAC\_MUSCLE\_CONTRACTION | −0.71244 | −2.06647 | 4.84 × 10−5 | 3.91 × 10−5 |
| KEGG\_CELL\_CYCLE | 0.501311 | 2.156967 | 1.74 × 10−6 | 1.4 × 10−6 |
| KEGG\_PENTOSE\_AND\_GLUCURONATE\_INTERCONVERSIONS | 0.62936 | 2.021268 | 0.01107 | 0.008941 |
| KEGG\_PORPHYRIN\_AND\_CHLOROPHYLL\_METABOLISM | 0.5795 | 2.012498 | 0.004075 | 0.003292 |
| KEGG\_RIBOSOME | 0.600904 | 2.359278 | 1.06 × 10−7 | 8.58 × 10−8 |
| KEGG\_SPLICEOSOME | 0.494495 | 2.130111 | 8.6 × 10−7 | 6.94 × 10−7 |
| PID\_ATR\_PATHWAY | 0.678687 | 2.349332 | 7.53 × 10−5 | 6.08 × 10−5 |
| PID\_AURORA\_A\_PATHWAY | 0.607491 | 2.00372 | 0.018696 | 0.015101 |
| PID\_AURORA\_B\_PATHWAY | 0.671319 | 2.323828 | 0.000107 | 8.66 × 10−5 |
| PID\_FANCONI\_PATHWAY | 0.594145 | 2.139591 | 0.000629 | 0.000508 |
| PID\_PLK1\_PATHWAY | 0.761714 | 2.723417 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_ACTIVATION\_OF\_ATR\_IN\_RESPONSE\_TO\_REPLICATION\_STRESS | 0.709681 | 2.42549 | 3.64 × 10−5 | 2.94 × 10−5 |
| REACTOME\_ACTIVATION\_OF\_THE\_MRNA\_UPON\_BINDING\_OF\_THE\_CAP\_BINDING\_COMPLEX\_AND\_EIFS\_AND\_SUBSEQUENT\_BINDING\_TO\_43S | 0.611878 | 2.309515 | 3.6 × 10−5 | 2.9 × 10−5 |
| REACTOME\_ACTIVATION\_OF\_THE\_PRE\_REPLICATIVE\_COMPLEX | 0.664357 | 2.195379 | 0.000498 | 0.000402 |
| REACTOME\_ANTIGEN\_ACTIVATES\_B\_CELL\_RECEPTOR\_BCR\_LEADING\_TO\_GENERATION\_OF\_SECOND\_MESSENGERS | −0.72398 | −2.14222 | 9.19 × 10−7 | 7.42 × 10−7 |
| REACTOME\_ANTIMICROBIAL\_PEPTIDES | −0.67531 | −2.00233 | 3.99 × 10−5 | 3.22 × 10−5 |
| REACTOME\_APC\_CDC20\_MEDIATED\_DEGRADATION\_OF\_NEK2A | 0.675033 | 2.139675 | 0.00351 | 0.002835 |
| REACTOME\_AURKA\_ACTIVATION\_BY\_TPX2 | 0.525523 | 2.000298 | 0.000642 | 0.000518 |
| REACTOME\_BINDING\_AND\_UPTAKE\_OF\_LIGANDS\_BY\_SCAVENGER\_RECEPTORS | −0.71872 | −2.14411 | 1.45 × 10−7 | 1.18 × 10−7 |
| REACTOME\_CD22\_MEDIATED\_BCR\_REGULATION | −0.77011 | −2.17371 | 8.68 × 10−7 | 7.01 × 10−7 |
| REACTOME\_COMPLEMENT\_CASCADE | −0.69216 | −2.07855 | 7.19 × 10−8 | 5.81 × 10−8 |
| REACTOME\_CONDENSATION\_OF\_PROMETAPHASE\_CHROMOSOMES | 0.803683 | 2.018001 | 0.014727 | 0.011895 |
| REACTOME\_CREATION\_OF\_C4\_AND\_C2\_ACTIVATORS | −0.74475 | −2.14973 | 5.41 × 10−6 | 4.37 × 10−6 |
| REACTOME\_CYCLIN\_A\_B1\_B2\_ASSOCIATED\_EVENTS\_DURING\_G2\_M\_TRANSITION | 0.669465 | 2.075902 | 0.008222 | 0.006641 |
| REACTOME\_CYTOSOLIC\_TRNA\_AMINOACYLATION | 0.647234 | 2.006404 | 0.015215 | 0.012289 |
| REACTOME\_DISEASES\_OF\_DNA\_REPAIR | 0.615586 | 2.247567 | 5.19 × 10−5 | 4.19 × 10−5 |
| REACTOME\_EUKARYOTIC\_TRANSLATION\_ELONGATION | 0.562599 | 2.250273 | 8.68 × 10−7 | 7.01 × 10−7 |
| REACTOME\_EUKARYOTIC\_TRANSLATION\_INITIATION | 0.558061 | 2.355589 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_FCERI\_MEDIATED\_MAPK\_ACTIVATION | −0.69226 | −2.04465 | 1.54 × 10−5 | 1.24 × 10−5 |
| REACTOME\_FCGR\_ACTIVATION | −0.72877 | −2.10048 | 1.74 × 10−5 | 1.41 × 10−5 |
| REACTOME\_FCGR3A\_MEDIATED\_IL10\_SYNTHESIS | −0.68227 | −2.03078 | 5.49 × 10−6 | 4.43 × 10−6 |
| REACTOME\_G0\_AND\_EARLY\_G1 | 0.709483 | 2.289797 | 0.000358 | 0.000289 |
| REACTOME\_G1\_S\_SPECIFIC\_TRANSCRIPTION | 0.696067 | 2.224411 | 0.000293 | 0.000236 |
| REACTOME\_HDR\_THROUGH\_HOMOLOGOUS\_RECOMBINATION\_HRR | 0.600124 | 2.265265 | 3.29 × 10−6 | 2.66 × 10−6 |
| REACTOME\_HDR\_THROUGH\_SINGLE\_STRAND\_ANNEALING\_SSA | 0.601357 | 2.055268 | 0.006297 | 0.005086 |
| REACTOME\_HOMOLOGOUS\_DNA\_PAIRING\_AND\_STRAND\_EXCHANGE | 0.63705 | 2.253046 | 0.000125 | 0.000101 |
| REACTOME\_INFLUENZA\_INFECTION | 0.461903 | 2.052514 | 1.6 × 10−6 | 1.29 × 10−6 |
| REACTOME\_INHIBITION\_OF\_THE\_PROTEOLYTIC\_ACTIVITY\_OF\_APC\_C\_REQUIRED\_FOR\_THE\_ONSET\_OF\_ANAPHASE\_BY\_MITOTIC\_SPINDLE\_CHECKPOINT\_COMPONENTS | 0.7132 | 2.113624 | 0.00631 | 0.005096 |
| REACTOME\_INITIAL\_TRIGGERING\_OF\_COMPLEMENT | −0.73323 | −2.14684 | 1.6 × 10−6 | 1.29 × 10−6 |
| REACTOME\_INTERACTIONS\_OF\_REV\_WITH\_HOST\_CELLULAR\_PROTEINS | 0.597284 | 2.041351 | 0.007084 | 0.005721 |
| REACTOME\_KINESINS | 0.539553 | 2.041186 | 0.000758 | 0.000612 |
| REACTOME\_MITOTIC\_G1\_PHASE\_AND\_G1\_S\_TRANSITION | 0.55331 | 2.408511 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_MITOTIC\_METAPHASE\_AND\_ANAPHASE | 0.47997 | 2.166579 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_MITOTIC\_PROMETAPHASE | 0.535571 | 2.373085 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_MITOTIC\_SPINDLE\_CHECKPOINT | 0.628683 | 2.590894 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_MRNA\_SPLICING | 0.540969 | 2.336766 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_NONSENSE\_MEDIATED\_DECAY\_NMD | 0.561542 | 2.378136 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_NUCLEAR\_PORE\_COMPLEX\_NPC\_DISASSEMBLY | 0.593154 | 2.006283 | 0.012651 | 0.010218 |
| REACTOME\_PHOSPHORYLATION\_OF\_THE\_APC\_C | 0.678585 | 2.002942 | 0.010013 | 0.008088 |
| REACTOME\_POLO\_LIKE\_KINASE\_MEDIATED\_EVENTS | 0.795109 | 2.244383 | 0.001527 | 0.001233 |
| REACTOME\_PROCESSING\_OF\_CAPPED\_INTRON\_CONTAINING\_PRE\_MRNA | 0.551577 | 2.525203 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_RESOLUTION\_OF\_ABASIC\_SITES\_AP\_SITES | 0.597144 | 2.041662 | 0.002685 | 0.002169 |
| REACTOME\_RESOLUTION\_OF\_D\_LOOP\_STRUCTURES | 0.674984 | 2.290373 | 0.000294 | 0.000237 |
| REACTOME\_RESOLUTION\_OF\_D\_LOOP\_STRUCTURES\_THROUGH\_SYNTHESIS\_DEPENDENT\_STRAND\_ANNEALING\_SDSA | 0.715047 | 2.307755 | 0.000279 | 0.000225 |
| REACTOME\_RESOLUTION\_OF\_SISTER\_CHROMATID\_COHESION | 0.57468 | 2.473758 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_RESPONSE\_OF\_EIF2AK4\_GCN2\_TO\_AMINO\_ACID\_DEFICIENCY | 0.525141 | 2.144134 | 7.78 × 10−6 | 6.28 × 10−6 |
| REACTOME\_RHO\_GTPASES\_ACTIVATE\_FORMINS | 0.531083 | 2.302861 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_RNA\_POLYMERASE\_II\_TRANSCRIPTION\_TERMINATION | 0.607358 | 2.276908 | 6.13 × 10−6 | 4.95 × 10−6 |
| REACTOME\_ROLE\_OF\_LAT2\_NTAL\_LAB\_ON\_CALCIUM\_MOBILIZATION | −0.70536 | −2.03603 | 0.000196 | 0.000158 |
| REACTOME\_ROLE\_OF\_PHOSPHOLIPIDS\_IN\_PHAGOCYTOSIS | −0.71055 | −2.08447 | 1.06 × 10−5 | 8.58 × 10−6 |
| REACTOME\_RRNA\_MODIFICATION\_IN\_THE\_NUCLEUS\_AND\_CYTOSOL | 0.620754 | 2.337576 | 1.31 × 10−5 | 1.06 × 10−5 |
| REACTOME\_RRNA\_PROCESSING | 0.59708 | 2.646403 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_S\_PHASE | 0.48666 | 2.157084 | 3.65 × 10−8 | 2.95 × 10−8 |
| REACTOME\_SARS\_COV\_2\_MODULATES\_HOST\_TRANSLATION\_MACHINERY | 0.64732 | 2.363428 | 8.93 × 10−6 | 7.21 × 10−6 |
| REACTOME\_SCAVENGING\_OF\_HEME\_FROM\_PLASMA | −0.75324 | −2.17099 | 1.47 × 10−6 | 1.19 × 10−6 |
| REACTOME\_SEPARATION\_OF\_SISTER\_CHROMATIDS | 0.489018 | 2.138581 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_SNRNP\_ASSEMBLY | 0.570912 | 2.095714 | 0.001124 | 0.000908 |
| REACTOME\_SRP\_DEPENDENT\_COTRANSLATIONAL\_PROTEIN\_TARGETING\_TO\_MEMBRANE | 0.487489 | 2.037408 | 1.24 × 10−5 | 1.00 × 10−5 |
| REACTOME\_STRIATED\_MUSCLE\_CONTRACTION | −0.82722 | −2.18887 | 5.41 × 10−6 | 4.37 × 10−6 |
| REACTOME\_SUMOYLATION\_OF\_DNA\_REPLICATION\_PROTEINS | 0.650339 | 2.325209 | 6.07 × 10−5 | 4.90 × 10−5 |
| REACTOME\_SUMOYLATION\_OF\_RNA\_BINDING\_PROTEINS | 0.562141 | 2.024343 | 0.002375 | 0.001918 |
| REACTOME\_SYNTHESIS\_OF\_DNA | 0.478835 | 2.030394 | 1.45 × 10−5 | 1.17 × 10−5 |
| REACTOME\_TRANSCRIPTION\_OF\_E2F\_TARGETS\_UNDER\_NEGATIVE\_CONTROL\_BY\_P107\_RBL1\_AND\_P130\_RBL2\_IN\_COMPLEX\_WITH\_HDAC1 | 0.712711 | 2.011793 | 0.02349 | 0.018973 |
| REACTOME\_TRANSCRIPTIONAL\_REGULATION\_BY\_E2F6 | 0.598411 | 2.007436 | 0.013717 | 0.011079 |
| REACTOME\_TRANSPORT\_OF\_MATURE\_MRNAS\_DERIVED\_FROM\_INTRONLESS\_TRANSCRIPTS | 0.594865 | 2.103852 | 0.000843 | 0.000681 |
| REACTOME\_TRANSPORT\_OF\_MATURE\_TRANSCRIPT\_TO\_CYTOPLASM | 0.59162 | 2.294238 | 1.60 × 10−6 | 1.29 × 10−6 |
| REACTOME\_TRANSPORT\_OF\_THE\_SLBP\_DEPENDANT\_MATURE\_MRNA | 0.598399 | 2.024022 | 0.010166 | 0.008211 |
| REACTOME\_TRNA\_AMINOACYLATION | 0.590805 | 2.087276 | 0.002476 | 0.002 |
| REACTOME\_TRNA\_MODIFICATION\_IN\_THE\_NUCLEUS\_AND\_CYTOSOL | 0.648314 | 2.292883 | 7.49 × 10−5 | 6.05 × 10−5 |
| REACTOME\_TRNA\_PROCESSING | 0.597573 | 2.428924 | 1.68 × 10−8 | 1.35 × 10−8 |
| REACTOME\_TRNA\_PROCESSING\_IN\_THE\_NUCLEUS | 0.563566 | 2.116258 | 0.000738 | 0.000596 |
| REACTOME\_VLDLR\_INTERNALISATION\_AND\_DEGRADATION | 0.764751 | 2.15869 | 0.004757 | 0.003842 |
| WP\_CELL\_CYCLE | 0.490863 | 2.071942 | 3.85 × 10−6 | 3.11 × 10−6 |
| WP\_COHESIN\_COMPLEX\_CORNELIA\_DE\_LANGE\_SYNDROME | 0.608698 | 2.041944 | 0.009547 | 0.007711 |
| WP\_CYTOPLASMIC\_RIBOSOMAL\_PROTEINS | 0.599655 | 2.354372 | 1.15 × 10−7 | 9.30 × 10−8 |
| WP\_DNA\_IRDAMAGE\_AND\_CELLULAR\_RESPONSE\_VIA\_ATR | 0.60107 | 2.319697 | 4.7 × 10−7 | 3.80 × 10−7 |
| WP\_DNA\_MISMATCH\_REPAIR | 0.666608 | 2.027597 | 0.010013 | 0.008088 |
| WP\_DNA\_REPAIR\_PATHWAYS\_FULL\_NETWORK | 0.509843 | 2.152058 | 8.68 × 10−7 | 7.01 × 10−7 |
| WP\_DNA\_REPLICATION | 0.628186 | 2.219341 | 0.000358 | 0.000289 |
| WP\_GASTRIC\_CANCER\_NETWORK\_1 | 0.693898 | 2.239499 | 0.000843 | 0.000681 |
| WP\_MIRNAS\_INVOLVED\_IN\_DNA\_DAMAGE\_RESPONSE | 0.623496 | 2.163593 | 0.000585 | 0.000472 |
| WP\_MRNA\_PROCESSING | 0.53611 | 2.306696 | 9.23 × 10−8 | 7.46 × 10−8 |
| WP\_REGULATION\_OF\_SISTER\_CHROMATID\_SEPARATION\_AT\_THE\_METAPHASEANAPHASE\_TRANSITION | 0.748763 | 2.051003 | 0.017092 | 0.013805 |
| WP\_RETINOBLASTOMA\_GENE\_IN\_CANCER | 0.616629 | 2.418653 | 2.92 × 10−8 | 2.36 × 10−8 |
| WP\_STRIATED\_MUSCLE\_CONTRACTION\_PATHWAY | −0.80318 | −2.13735 | 0.000153 | 0.000124 |