**Results of Reactome pathways analysis based on GSEA.**

**A**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **PATHWAY** | **SIZE** | **ES** | **NOM p-val** | **FDR q-val** |
| REACTOME\_RNA\_POL\_I\_PROMOTER\_  OPENING | 39 | 0.7571808 | 0 | 0 |
| REACTOME\_INTERFERON\_  ALPHA\_BETA\_SIGNALING | 47 | 0.7390151 | 0 | 0 |
| REACTOME\_PACKAGING\_OF\_  TELOMERE\_ENDS | 30 | 0.7253221 | 0 | 0 |
| REACTOME\_METABOLISM\_OF\_STEROID\_  HORMONES\_AND\_VITAMINS\_A\_AND\_D | 16 | 0.72153693 | 0.001831502 | 0.002075139 |
| REACTOME\_GENERATION\_OF\_  SECOND\_MESSENGER\_MOLECULES | 19 | 0.71909744 | 0 | 0.001035765 |
| REACTOME\_AMYLOIDS | 49 | 0.69897753 | 0 | 0 |
| REACTOME\_CYTOCHROME\_  P450\_ARRANGED\_BY\_SUBSTRATE\_TYPE | 24 | 0.679377 | 0 | 8.54E-04 |
| REACTOME\_AMINE\_COMPOUND\_  SLC\_TRANSPORTERS | 16 | 0.6727143 | 0.001872659 | 0.009288154 |
| REACTOME\_INTERFERON\_  GAMMA\_SIGNALING | 52 | 0.6550511 | 0 | 0 |
| REACTOME\_PHASE1\_FUNCTIONALIZATION\_  OF\_COMPOUNDS | 34 | 0.64593416 | 0 | 1.08E-04 |
| REACTOME\_MEIOTIC\_SYNAPSIS | 50 | 0.60007626 | 0 | 3.19E-04 |
| REACTOME\_DOWNSTREAM\_TCR\_SIGNALING | 30 | 0.582416 | 0 | 0.008053294 |
| REACTOME\_RNA\_POL\_I\_TRANSCRIPTION | 64 | 0.56907827 | 0 | 4.33E-04 |
| REACTOME\_BIOLOGICAL\_OXIDATIONS | 74 | 0.5608006 | 0 | 3.64E-04 |
| REACTOME\_MEIOTIC\_RECOMBINATION | 59 | 0.5248495 | 0 | 0.004610789 |
| REACTOME\_INTERFERON\_SIGNALING | 133 | 0.48589844 | 0 | 9.57E-04 |
| REACTOME\_MEIOSIS | 84 | 0.47009262 | 0 | 0.009622734 |

**Activated REACTOME pathways**

**B**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **PATHWAY** | | **SIZE** | **ES** | **NOM p-val** | **FDR q-val** |
| REACTOME\_G1\_S\_SPECIFIC\_  TRANSCRIPTION | 16 | -0.8642605 | 0 | 0 |
| REACTOME\_DNA\_STRAND\_  ELONGATION | | 30 | -0.8639629 | 0 | 0 |
| REACTOME\_EXTENSION\_OF\_  TELOMERES | | 27 | -0.8303774 | 0 | 0 |
| REACTOME\_LAGGING\_STRAND\_  SYNTHESIS | | 19 | -0.82774264 | 0 | 0 |
| REACTOME\_ACTIVATION\_OF\_THE\_  PRE\_REPLICATIVE\_COMPLEX | | 30 | -0.8141718 | 0 | 0 |
| REACTOME\_PROCESSIVE\_SYNTHESIS\_ON\_THE\_LAGGING\_STRAND | | 15 | -0.80766445 | 0 | 2.89E-05 |
| REACTOME\_ACTIVATION\_OF\_ATR\_IN\_RESPONSE\_TO\_REPLICATION\_STRESS | | 35 | -0.80128485 | 0 | 0 |
| REACTOME\_G2\_M\_CHECKPOINTS | | 41 | -0.7908015 | 0 | 0 |
| REACTOME\_E2F\_MEDIATED\_  REGULATION\_OF\_DNA\_REPLICATION | | 32 | -0.7828214 | 0 | 0 |
| REACTOME\_KINESINS | | 20 | -0.7749984 | 0 | 0 |
| REACTOME\_HOMOLOGOUS\_  RECOMBINATION\_REPAIR\_OF\_  REPLICATION\_INDEPENDENT\_DOUBLE\_STRAND\_BREAKS | | 16 | -0.7529953 | 0 | 7.11E-05 |
| REACTOME\_G0\_AND\_EARLY\_G1 | | 22 | -0.73598343 | 0 | 0 |
| REACTOME\_PEPTIDE\_CHAIN\_  ELONGATION | | 83 | -0.7175654 | 0 | 0 |
| REACTOME\_REGULATION\_OF\_  GLUCOKINASE\_BY\_GLUCOKINASE\_  REGULATORY\_PROTEIN | | 25 | -0.7153815 | 0 | 0 |
| REACTOME\_NEP\_NS2\_INTERACTS\_  WITH\_THE\_CELLULAR\_EXPORT\_  MACHINERY | | 27 | -0.71085745 | 0 | 0 |
| REACTOME\_FORMATION\_OF\_THE\_  TERNARY\_COMPLEX\_AND\_  SUBSEQUENTLY\_THE\_43S\_COMPLEX | | 48 | -0.70507 | 0 | 0 |
| REACTOME\_TRANSPORT\_OF\_  RIBONUCLEOPROTEINS\_INTO\_THE  \_HOST\_NUCLEUS | | 27 | -0.7031889 | 0 | 0 |
| REACTOME\_INFLUENZA\_VIRAL\_RNA\_  TRANSCRIPTION\_AND\_REPLICATION | | 99 | -0.69562536 | 0 | 0 |
| REACTOME\_METABOLISM\_OF\_NON  \_CODING\_RNA | | 48 | -0.69479805 | 0 | 0 |
| REACTOME\_3\_UTR\_MEDIATED\_  TRANSLATIONAL\_REGULATION | | 103 | -0.6944623 | 0 | 0 |
| REACTOME\_INTERACTIONS\_OF\_  VPR\_WITH\_HOST\_CELLULAR\_  PROTEINS | | 32 | -0.69361234 | 0 | 0 |
| REACTOME\_MITOTIC\_  PROMETAPHASE | | 84 | -0.6913364 | 0 | 0 |
| REACTOME\_DNA\_REPLICATION | | 184 | -0.6848482 | 0 | 0 |
| REACTOME\_ACTIVATION\_OF\_THE\_  MRNA\_UPON\_BINDING\_OF\_THE\_CAP\_BINDING\_COMPLEX\_AND\_EIFS\_AND\_  SUBSEQUENT\_BINDING\_TO\_43S | | 56 | -0.6823825 | 0 | 0 |
| REACTOME\_INFLUENZA\_LIFE\_CYCLE | | 133 | -0.67958224 | 0 | 0 |
| REACTOME\_MITOTIC\_M\_  M\_G1\_PHASES | | 165 | -0.6766168 | 0 | 0 |
| REACTOME\_FANCONI\_ANEMIA\_  PATHWAY | | 21 | -0.67199504 | 0 | 4.55E-04 |
| REACTOME\_FORMATION\_OF\_  TUBULIN\_FOLDING\_INTERMEDIATES\_  BY\_CCT\_TRIC | | 20 | -0.6694275 | 0 | 2.81E-04 |
| REACTOME\_NONSENSE\_MEDIATED\_  DECAY\_ENHANCED\_BY\_THE\_EXON\_  JUNCTION\_COMPLEX | | 103 | -0.66857463 | 0 | 0 |
| REACTOME\_GLOBAL\_GENOMIC\_  NER\_GG\_NER | | 33 | -0.6680151 | 0 | 0 |
| REACTOME\_PREFOLDIN\_MEDIATED\_  TRANSFER\_OF\_SUBSTRATE\_TO\_  CCT\_TRIC | | 26 | -0.66648877 | 0 | 4.88E-05 |
| REACTOME\_S\_PHASE | | 104 | -0.6638708 | 0 | 0 |
| REACTOME\_SYNTHESIS\_OF\_DNA | | 88 | -0.6585429 | 0 | 0 |
| REACTOME\_SRP\_DEPENDENT\_  COTRANSLATIONAL\_PROTEIN\_  TARGETING\_TO\_MEMBRANE | | 106 | -0.656066 | 0 | 0 |
| REACTOME\_G1\_S\_TRANSITION | | 105 | -0.65573084 | 0 | 0 |
| REACTOME\_M\_G1\_TRANSITION | | 77 | -0.65304494 | 0 | 0 |
| REACTOME\_TRANSPORT\_OF\_MATURE\_MRNA\_DERIVED\_FROM\_AN\_  INTRONLESS\_TRANSCRIPT | | 32 | -0.6520071 | 0 | 2.95E-05 |
| REACTOME\_MRNA\_SPLICING\_  MINOR\_PATHWAY | | 42 | -0.64506197 | 0 | 0 |
| REACTOME\_RNA\_POL\_III\_  TRANSCRIPTION\_TERMINATION | | 19 | -0.6434694 | 0 | 0.001610112 |
| REACTOME\_DOUBLE\_STRAND\_  BREAK\_REPAIR | | 22 | -0.642346 | 0 | 0.001191476 |
| REACTOME\_CELL\_CYCLE\_MITOTIC | | 304 | -0.6391397 | 0 | 0 |
| REACTOME\_RNA\_POL\_I\_  TRANSCRIPTION\_TERMINATION | | 21 | -0.63748866 | 0 | 0.002091157 |
| REACTOME\_TRANSLATION | | 142 | -0.6370052 | 0 | 0 |
| REACTOME\_MITOTIC\_G1\_G1\_S\_  PHASES | | 129 | -0.63251984 | 0 | 0 |
| REACTOME\_PROCESSING\_OF\_CAPPED\_INTRONLESS\_PRE\_MRNA | | 23 | -0.6243813 | 0 | 0.001055595 |
| REACTOME\_RNA\_POL\_III\_CHAIN\_  ELONGATION | | 17 | -0.623266 | 0.004514673 | 0.007013481 |
| REACTOME\_G\_BETA\_GAMMA\_  SIGNALLING\_THROUGH\_PLC\_BETA | | 16 | -0.61838025 | 0 | 0.005880694 |
| REACTOME\_APC\_CDC20\_MEDIATED\_  DEGRADATION\_OF\_NEK2A | | 21 | -0.61837274 | 0 | 0.001675552 |
| REACTOME\_ASSEMBLY\_OF\_  THE\_PRE\_REPLICATIVE\_COMPLEX | | 62 | -0.6164791 | 0 | 0 |
| REACTOME\_PHOSPHORYLATION\_  OF\_THE\_APC\_C | | 17 | -0.6159139 | 0.004640371 | 0.006144868 |
| REACTOME\_GLUCOSE\_TRANSPORT | | 32 | -0.61584157 | 0 | 1.31E-04 |
| REACTOME\_CELL\_CYCLE\_  CHECKPOINTS | | 110 | -0.6068631 | 0 | 0 |
| REACTOME\_CYTOSOLIC\_TRNA\_  AMINOACYLATION | | 24 | -0.6066835 | 0 | 0.001642803 |
| REACTOME\_RESOLUTION\_OF\_AP\_  SITES\_VIA\_THE\_MULTIPLE\_  NUCLEOTIDE\_PATCH\_  REPLACEMENT\_PATHWAY | | 17 | -0.6065045 | 0.008752735 | 0.008734645 |
| REACTOME\_INHIBITION\_OF\_THE\_  PROTEOLYTIC\_ACTIVITY\_OF\_APC\_C\_  REQUIRED\_FOR\_THE\_ONSET\_OF\_  ANAPHASE\_BY\_MITOTIC\_SPINDLE\_  CHECKPOINT\_COMPONENTS | | 18 | -0.6038739 | 0.00896861 | 0.008679578 |
| REACTOME\_SMOOTH\_MUSCLE\_  CONTRACTION | | 22 | -0.60006946 | 0.002386635 | 0.004187366 |
| REACTOME\_CDT1\_ASSOCIATION\_  WITH\_THE\_CDC6\_ORC\_ORIGIN\_  COMPLEX | | 53 | -0.5979396 | 0 | 0 |
| REACTOME\_TRANSPORT\_OF\_  MATURE\_TRANSCRIPT\_  TO\_CYTOPLASM | | 52 | -0.59595996 | 0 | 2.84E-05 |
| REACTOME\_PROCESSING\_OF\_CAPPED\_INTRON\_CONTAINING\_PRE\_MRNA | | 135 | -0.5951692 | 0 | 0 |
| REACTOME\_MRNA\_SPLICING | | 106 | -0.59391373 | 0 | 0 |
| REACTOME\_MITOCHONDRIAL\_  TRNA\_AMINOACYLATION | | 21 | -0.5911081 | 0.005037783 | 0.00638738 |
| REACTOME\_RNA\_POL\_III\_  TRANSCRIPTION\_INITIATION\_  FROM\_TYPE\_3\_PROMOTER | | 26 | -0.5903188 | 0.002439024 | 0.002414777 |
| REACTOME\_TRNA\_AMINOACYLATION | | 42 | -0.59024864 | 0 | 1.35E-04 |
| REACTOME\_APC\_C\_CDC20\_MEDIATED\_DEGRADATION\_OF\_CYCLIN\_B | | 19 | -0.59001476 | 0.002298851 | 0.008633464 |
| REACTOME\_P53\_INDEPENDENT\_  G1\_S\_DNA\_DAMAGE\_CHECKPOINT | | 47 | -0.58805925 | 0 | 2.64E-05 |
| REACTOME\_CDK\_MEDIATED\_  PHOSPHORYLATION\_AND\_  REMOVAL\_OF\_CDC6 | | 45 | -0.58700734 | 0 | 5.04E-05 |
| REACTOME\_G\_PROTEIN\_BETA\_  GAMMA\_SIGNALLING | | 21 | -0.5868193 | 0.00486618 | 0.006103213 |
| REACTOME\_ORC1\_REMOVAL\_FROM\_  CHROMATIN | | 63 | -0.585339 | 0 | 0 |
| REACTOME\_MITOTIC\_G2\_  G2\_M\_PHASES | | 77 | -0.5811044 | 0 | 0 |
| REACTOME\_VIF\_MEDIATED\_  DEGRADATION\_OF\_APOBEC3G | | 48 | -0.5807526 | 0 | 4.96E-05 |
| REACTOME\_MRNA\_PROCESSING | | 153 | -0.58031523 | 0 | 0 |
| REACTOME\_REGULATION\_OF\_  MITOTIC\_CELL\_CYCLE | | 75 | -0.57908165 | 0 | 0 |
| REACTOME\_TRANSCRIPTION\_  COUPLED\_NER\_TC\_NER | | 44 | -0.5757114 | 0 | 1.37E-04 |
| REACTOME\_FORMATION\_OF\_  THE\_HIV1\_EARLY\_ELONGATION\_COMPLEX | | 29 | -0.5725151 | 0 | 0.001688026 |
| REACTOME\_RNA\_POL\_III\_  TRANSCRIPTION | | 33 | -0.5704762 | 0 | 0.001169088 |
| REACTOME\_REGULATION\_OF\_  ORNITHINE\_DECARBOXYLASE\_ODC | | 47 | -0.5663566 | 0 | 1.33E-04 |
| REACTOME\_APC\_C\_CDC20\_MEDIATED\_  DEGRADATION\_OF\_  MITOTIC\_PROTEINS | | 64 | -0.5619387 | 0 | 2.79E-05 |
| REACTOME\_CYCLIN\_E\_ASSOCIATED\_  EVENTS\_DURING\_G1\_S\_TRANSITION\_ | | 61 | -0.5605064 | 0 | 2.74E-05 |
| REACTOME\_METABOLISM\_OF\_RNA | | 250 | -0.55944085 | 0 | 0 |
| REACTOME\_AUTODEGRADATION\_  OF\_THE\_E3\_UBIQUITIN\_LIGASE\_COP1 | | 46 | -0.55872524 | 0 | 3.16E-04 |
| REACTOME\_APC\_C\_CDH1\_MEDIATED\_DEGRADATION\_OF\_CDC20\_AND\_OTHER\_APC\_C CDH1\_TARGETED\_PROTEINS\_IN\_LATE\_  MITOSIS\_EARLY\_G1 | | 63 | -0.55845815 | 0 | 2.60E-05 |
| REACTOME\_NUCLEOTIDE\_  EXCISION\_REPAIR | | 49 | -0.5555992 | 0 | 3.34E-04 |
| REACTOME\_CLEAVAGE\_OF\_GROWING\_TRANSCRIPT\_IN\_THE\_TERMINATION\_REGION\_ | | 42 | -0.55287915 | 0 | 5.26E-04 |
| REACTOME\_DNA\_REPAIR | | 104 | -0.54827315 | 0 | 0 |
| REACTOME\_SCFSKP2\_MEDIATED\_  DEGRADATION\_OF\_P27\_P21 | | 52 | -0.54439205 | 0 | 2.42E-04 |
| REACTOME\_MRNA\_CAPPING | | 29 | -0.54394615 | 0.002358491 | 0.005664275 |
| REACTOME\_RNA\_POL\_II\_TRANSCRIPTION\_  PRE\_INITIATION\_AND\_PROMOTER\_OPENING | | 40 | -0.53918284 | 0 | 0.001695035 |
| REACTOME\_SCF\_BETA\_TRCP\_  MEDIATED\_DEGRADATION\_OF\_EMI1 | | 48 | -0.5389407 | 0 | 7.54E-04 |
| REACTOME\_CELL\_CYCLE | | 374 | -0.53856295 | 0 | 0 |
| REACTOME\_HIV\_LIFE\_CYCLE | | 107 | -0.5332148 | 0 | 0 |
| REACTOME\_G1\_PHASE | | 35 | -0.5323318 | 0 | 0.004227321 |
| REACTOME\_LOSS\_OF\_NLP\_FROM\_  MITOTIC\_CENTROSOMES | | 56 | -0.52931577 | 0 | 4.00E-04 |
| REACTOME\_FORMATION\_OF\_  RNA\_POL\_II\_ELONGATION\_COMPLEX\_ | | 39 | -0.5285054 | 0 | 0.002454045 |
| REACTOME\_METABOLISM\_OF\_MRNA | | 205 | -0.526802 | 0 | 0 |
| REACTOME\_DESTABILIZATION\_OF\_  MRNA\_BY\_AUF1\_HNRNP\_D0 | | 49 | -0.522038 | 0 | 0.001689183 |
| REACTOME\_AUTODEGRADATION\_OF\_  CDH1\_BY\_CDH1\_APC\_C | | 56 | -0.5180637 | 0 | 0.001030658 |
| REACTOME\_HOST\_INTERACTIONS\_OF\_  HIV\_FACTORS | | 115 | -0.51601005 | 0 | 0 |
| REACTOME\_CROSS\_PRESENTATION\_OF\_  SOLUBLE\_EXOGENOUS\_  ANTIGENS\_ENDOSOMES | | 42 | -0.5155201 | 0 | 0.003121394 |
| REACTOME\_RECRUITMENT\_OF\_  MITOTIC\_CENTROSOME\_PROTEINS\_AND\_  COMPLEXES | | 63 | -0.51546013 | 0 | 3.68E-04 |
| REACTOME\_LATE\_PHASE\_OF\_  HIV\_LIFE\_CYCLE | | 97 | -0.5119963 | 0 | 2.56E-05 |
| REACTOME\_MITOCHONDRIAL\_  PROTEIN\_IMPORT | | 48 | -0.5092736 | 0 | 0.003211276 |
| REACTOME\_METABOLISM\_OF\_  NUCLEOTIDES | | 62 | -0.50759304 | 0 | 7.64E-04 |
| REACTOME\_MUSCLE\_CONTRACTION | | 34 | -0.50743794 | 0.002463054 | 0.007582443 |
| REACTOME\_RNA\_POL\_II\_  TRANSCRIPTION | | 97 | -0.50117356 | 0 | 1.17E-04 |
| REACTOME\_RNA\_POL\_II\_  PRE\_TRANSCRIPTION\_EVENTS | | 55 | -0.49347672 | 0 | 0.003166686 |
| REACTOME\_HIV\_INFECTION | | 182 | -0.49037874 | 0 | 0 |
| REACTOME\_PROTEIN\_FOLDING | | 50 | -0.48529267 | 0 | 0.004177411 |
| REACTOME\_P53\_DEPENDENT\_  G1\_DNA\_DAMAGE\_RESPONSE | | 52 | -0.46014234 | 0 | 0.007203301 |
| REACTOME\_CHROMOSOME\_  MAINTENANCE | | 97 | -0.4364906 | 0 | 0.003316784 |
| REACTOME\_METABOLISM\_OF\_  PROTEINS | | 390 | -0.4287051 | 0 | 2.69E-05 |
| REACTOME\_REGULATION\_OF\_MRNA\_  STABILITY\_BY\_PROTEINS\_THAT\_  BIND\_AU\_RICH\_ELEMENTS | | 80 | -0.42395088 | 0 | 0.008571514 |

**Repressive REACTOME pathways**

The table lists all the results of Reactome pathways analysis based on GSEA. Table A showed the activated REACTOME pathways in CAL27AR cells. Table B showed the repressive REACTOME pathways in CAL27AR cells.