**Table S3.** Reactome pathways down-regulated by Bevacizumab in IGROV-1 and SKOV3 models

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **IGROV-1 model** |  |  |  | |  | |  |
| **Pathway** | **size** | **NES** | | **p-value** | | **FDR q-value** | | |
| REACTOME\_MITOTIC\_M\_M\_G1\_PHASES | 161 | -2.86 | | 0.000 | | 0.000 | | |
| **REACTOME\_DNA\_REPLICATION** | 181 | -2.84 | | 0.000 | | 0.000 | | |
| REACTOME\_MITOTIC\_PROMETAPHASE | 79 | -2.66 | | 0.000 | | 0.000 | | |
| REACTOME\_M\_G1\_TRANSITION | 78 | -2.60 | | 0.000 | | 0.000 | | |
| REACTOME\_DEPOSITION\_OF\_NEW\_CENPA\_CONTAINING\_NUCLEOSOMES.. (REACT\_22186) | 60 | -2.58 | | 0.000 | | 0.000 | | |
| REACTOME\_MEIOTIC\_RECOMBINATION | 80 | -2.50 | | 0.000 | | 0.000 | | |
| REACTOME\_CELL\_CYCLE\_CHECKPOINTS | 111 | -2.49 | | 0.000 | | 0.000 | | |
| REACTOME\_G1\_S\_TRANSITION | 106 | -2.48 | | 0.000 | | 0.000 | | |
| **REACTOME\_SYNTHESIS\_OF\_DNA** | 90 | -2.48 | | 0.000 | | 0.000 | | |
| REACTOME\_CELL\_CYCLE | 391 | -2.44 | | 0.000 | | 0.000 | | |
| REACTOME\_CELL\_CYCLE\_MITOTIC | 300 | -2.43 | | 0.000 | | 0.000 | | |
| REACTOME\_REGULATION\_OF\_MITOTIC\_CELL\_CYCLE | 77 | -2.38 | | 0.000 | | 0.000 | | |
| REACTOME\_S\_PHASE | 106 | -2.38 | | 0.000 | | 0.000 | | |
| REACTOME\_ASSEMBLY\_OF\_THE\_PRE\_REPLICATIVE\_COMPLEX | 63 | -2.38 | | 0.000 | | 0.000 | | |
| REACTOME\_APC\_C\_CDC20\_MEDIATED\_DEGRADATION\_OF\_MITOTIC\_PROTEINS | 65 | -2.37 | | 0.000 | | 0.000 | | |
| REACTOME\_ACTIVATION\_OF\_THE\_PRE\_REPLICATIVE\_COMPLEX | 30 | -2.32 | | 0.000 | | 0.000 | | |
| REACTOME\_RNA\_POL\_I\_PROMOTER\_OPENING | 58 | -2.32 | | 0.000 | | 0.000 | | |
| REACTOME\_MITOTIC\_G1\_G1\_S\_PHASES | 130 | -2.30 | | 0.000 | | 0.000 | | |
| REACTOME\_CDT1\_ASSOCIATION\_WITH\_THE\_CDC6\_ORC\_ORIGIN\_COMPLEX | 54 | -2.29 | | 0.000 | | 0.000 | | |
| REACTOME\_VIF\_MEDIATED\_DEGRADATION\_OF\_APOBEC3G | 47 | -2.26 | | 0.000 | | 0.000 | | |
| REACTOME\_ORC1\_REMOVAL\_FROM\_CHROMATIN | 65 | -2.25 | | 0.000 | | 0.000 | | |
| REACTOME\_CHROMOSOME\_MAINTENANCE | 116 | -2.24 | | 0.000 | | 0.001 | | |
| REACTOME\_CDK\_MEDIATED\_PHOSPHORYLATION\_AND\_REMOVAL\_OF\_CDC6 | 46 | -2.23 | | 0.000 | | 0.000 | | |
| REACTOME\_SCF\_BETA\_TRCP\_MEDIATED\_DEGRADATION\_OF\_EMI1 | 49 | -2.21 | | 0.000 | | 0.001 | | |
| REACTOME\_AMYLOIDS | 78 | -2.20 | | 0.000 | | 0.001 | | |
| **REACTOME\_DNA\_STRAND\_ELONGATION** | 30 | -2.19 | | 0.000 | | 0.001 | | |
| REACTOME\_ACTIVATED\_POINT\_MUTANTS\_OF\_FGFR2 | 16 | -2.18 | | 0.000 | | 0.001 | | |
| REACTOME\_MEIOSIS | 108 | -2.17 | | 0.000 | | 0.001 | | |
| REACTOME\_AUTODEGRADATION\_OF\_CDH1\_BY\_CDH1\_APC\_C | 56 | -2.17 | | 0.000 | | 0.001 | | |
| REACTOME\_ACTIVATION\_OF\_NF\_KAPPAB\_IN\_B\_CELLS | 61 | -2.16 | | 0.000 | | 0.001 | | |
| REACTOME\_APC\_C\_CDH1\_MEDIATED\_DEGRADATION\_OF\_CDC20\_AND.. (REACT\_6761) | 64 | -2.15 | | 0.000 | | 0.001 | | |
| REACTOME\_G2\_M\_CHECKPOINTS | 41 | -2.14 | | 0.000 | | 0.001 | | |
| REACTOME\_ACTIVATION\_OF\_ATR\_IN\_RESPONSE\_TO\_REPLICATION\_STRESS | 35 | -2.13 | | 0.000 | | 0.001 | | |
| REACTOME\_CROSS\_PRESENTATION\_OF\_SOLUBLE\_EXOGENOUS\_ANTIGENS\_ENDOSOMES | 47 | -2.11 | | 0.003 | | 0.002 | | |
| REACTOME\_P53\_INDEPENDENT\_G1\_S\_DNA\_DAMAGE\_CHECKPOINT | 48 | -2.10 | | 0.000 | | 0.002 | | |
| REACTOME\_DESTABILIZATION\_OF\_MRNA\_BY\_AUF1\_HNRNP\_D0 | 50 | -2.09 | | 0.000 | | 0.002 | | |
| REACTOME\_SCFSKP2\_MEDIATED\_DEGRADATION\_OF\_P27\_P21 | 53 | -2.08 | | 0.000 | | 0.002 | | |
| REACTOME\_AUTODEGRADATION\_OF\_THE\_E3\_UBIQUITIN\_LIGASE\_COP1 | 47 | -2.07 | | 0.000 | | 0.002 | | |
| REACTOME\_TELOMERE\_MAINTENANCE | 75 | -2.07 | | 0.000 | | 0.002 | | |
| **REACTOME\_REGULATION\_OF\_APOPTOSIS** | 56 | -2.06 | | 0.000 | | 0.002 | | |
| REACTOME\_SIGNALING\_BY\_WNT | 62 | -2.04 | | 0.000 | | 0.002 | | |
| REACTOME\_P53\_DEPENDENT\_G1\_DNA\_DAMAGE\_RESPONSE | 53 | -2.04 | | 0.000 | | 0.002 | | |
| REACTOME\_RNA\_POL\_I\_TRANSCRIPTION | 81 | -2.03 | | 0.000 | | 0.003 | | |
| REACTOME\_CYCLIN\_E\_ASSOCIATED\_EVENTS\_DURING\_G1\_S\_TRANSITION | 62 | -1.98 | | 0.000 | | 0.005 | | |
| REACTOME\_E2F\_MEDIATED\_REGULATION\_OF\_DNA\_REPLICATION | 33 | -1.96 | | 0.000 | | 0.005 | | |
| REACTOME\_DOUBLE\_STRAND\_BREAK\_REPAIR | 21 | -1.95 | | 0.000 | | 0.006 | | |
| REACTOME\_PACKAGING\_OF\_TELOMERE\_ENDS | 48 | -1.93 | | 0.000 | | 0.007 | | |
| REACTOME\_REGULATION\_OF\_ORNITHINE\_DECARBOXYLASE\_ODC | 48 | -1.93 | | 0.000 | | 0.008 | | |
| REACTOME\_APC\_CDC20\_MEDIATED\_DEGRADATION\_OF\_NEK2A | 21 | -1.92 | | 0.004 | | 0.008 | | |
| REACTOME\_ANTIGEN\_PROCESSING\_CROSS\_PRESENTATION | 72 | -1.90 | | 0.000 | | 0.009 | | |
| REACTOME\_MEIOTIC\_SYNAPSIS | 71 | -1.89 | | 0.000 | | 0.010 | | |
| REACTOME\_FANCONI\_ANEMIA\_PATHWAY | 19 | -1.88 | | 0.005 | | 0.011 | | |
| **REACTOME\_APOPTOSIS** | 142 | -1.88 | | 0.000 | | 0.011 | | |
| REACTOME\_HOMOLOGOUS\_RECOMBINATION\_REPAIR\_OF\_REPLICATION.. (REACT\_1587) | 15 | -1.85 | | 0.009 | | 0.015 | | |
| REACTOME\_METABOLISM\_OF\_NON\_CODING\_RNA | 47 | -1.84 | | 0.000 | | 0.015 | | |
| REACTOME\_TRANSPORT\_TO\_THE\_GOLGI\_AND\_SUBSEQUENT\_MODIFICATION | 33 | -1.83 | | 0.002 | | 0.015 | | |
| REACTOME\_SHC\_MEDIATED\_CASCADE | 28 | -1.83 | | 0.009 | | 0.016 | | |
| REACTOME\_FGFR\_LIGAND\_BINDING\_AND\_ACTIVATION | 22 | -1.82 | | 0.005 | | 0.017 | | |
| REACTOME\_G0\_AND\_EARLY\_G1 | 23 | -1.81 | | 0.002 | | 0.018 | | |
| REACTOME\_CYCLIN\_A\_B1\_ASSOCIATED\_EVENTS\_DURING\_G2\_M\_TRANSITION | 15 | -1.79 | | 0.009 | | 0.022 | | |
| REACTOME\_ER\_PHAGOSOME\_PATHWAY | 58 | -1.77 | | 0.002 | | 0.024 | | |
| REACTOME\_G1\_S\_SPECIFIC\_TRANSCRIPTION | 17 | -1.75 | | 0.004 | | 0.028 | | |
| REACTOME\_INHIBITION\_OF\_THE\_PROTEOLYTIC\_ACTIVITY\_OF\_APC\_C.. (REACT\_1041) | 18 | -1.75 | | 0.007 | | 0.028 | | |
| REACTOME\_ANTIVIRAL\_MECHANISM\_BY\_IFN\_STIMULATED\_GENES | 63 | -1.73 | | 0.000 | | 0.031 | | |
| REACTOME\_HOST\_INTERACTIONS\_OF\_HIV\_FACTORS | 117 | -1.73 | | 0.000 | | 0.031 | | |
| REACTOME\_APC\_C\_CDC20\_MEDIATED\_DEGRADATION\_OF\_CYCLIN\_B | 19 | -1.72 | | 0.009 | | 0.034 | | |
| **REACTOME\_APOPTOTIC\_EXECUTION\_PHASE** | 51 | -1.71 | | 0.000 | | 0.035 | | |
| REACTOME\_DOWNSTREAM\_SIGNALING\_EVENTS\_OF\_B\_CELL\_RECEPTOR\_BCR | 92 | -1.71 | | 0.000 | | 0.034 | | |
| REACTOME\_FRS2\_MEDIATED\_CASCADE | 36 | -1.69 | | 0.014 | | 0.042 | | |
| REACTOME\_LAGGING\_STRAND\_SYNTHESIS | 19 | -1.67 | | 0.017 | | 0.047 | | |
| REACTOME\_ACTIVATION\_OF\_KAINATE\_RECEPTORS\_UPON\_GLUTAMATE\_BINDING | 30 | -1.66 | | 0.019 | | 0.050 | | |
| REACTOME\_G\_PROTEIN\_ACTIVATION | 26 | -1.64 | | 0.019 | | 0.057 | | |
| REACTOME\_RNA\_POL\_I\_RNA\_POL\_III\_AND\_MITOCHONDRIAL\_TRANSCRIPTION | 113 | -1.63 | | 0.000 | | 0.059 | | |
| REACTOME\_EXTENSION\_OF\_TELOMERES | 27 | -1.63 | | 0.016 | | 0.061 | | |
| REACTOME\_REGULATION\_OF\_MRNA\_STABILITY\_BY\_PROTEINS\_THAT\_BIND.. (REACT\_24994) | 81 | -1.60 | | 0.008 | | 0.071 | | |
| REACTOME\_G\_ALPHA\_I\_SIGNALLING\_EVENTS | 186 | -1.59 | | 0.000 | | 0.076 | | |
| REACTOME\_PREFOLDIN\_MEDIATED\_TRANSFER\_OF\_SUBSTRATE\_TO\_CCT\_TRIC | 27 | -1.59 | | 0.019 | | 0.076 | | |
| REACTOME\_SIGNALING\_BY\_THE\_B\_CELL\_RECEPTOR\_BCR | 121 | -1.58 | | 0.000 | | 0.077 | | |
| REACTOME\_METABOLISM\_OF\_RNA | 252 | -1.56 | | 0.000 | | 0.088 | | |
| REACTOME\_HIV\_INFECTION | 184 | -1.54 | | 0.000 | | 0.095 | | |
| REACTOME\_TRANSCRIPTION | 191 | -1.51 | | 0.000 | | 0.108 | | |
| REACTOME\_PEPTIDE\_LIGAND\_BINDING\_RECEPTORS | 174 | -1.49 | | 0.000 | | 0.116 | | |
| **REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT\_ATP\_SYNTHESIS\_BY.. (REACT\_6305)** | 84 | -1.48 | | 0.007 | | 0.120 | | |
| **REACTOME\_DNA\_REPAIR** | 101 | -1.47 | | 0.013 | | 0.128 | | |
| REACTOME\_CLASS\_I\_MHC\_MEDIATED\_ANTIGEN\_PROCESSING\_PRESENTATION | 231 | -1.43 | | 0.000 | | 0.150 | | |
| REACTOME\_CLASS\_A1\_RHODOPSIN\_LIKE\_RECEPTORS | 285 | -1.41 | | 0.003 | | 0.161 | | |
| REACTOME\_GPCR\_LIGAND\_BINDING | 381 | -1.35 | | 0.004 | | 0.208 | | |
|  |  |  | |  | |  | | |
| **SKOV3 model** |  |  | |  | |  | | |
| **pathway** | **size** | **NES** | | **p-value** | | **FDR q-value** | | |
| **REACTOME\_DNA\_REPLICATION** | 181 | -3.60 | | 0.000 | | 0.000 | | |
| REACTOME\_MITOTIC\_M\_M\_G1\_PHASES | 161 | -3.48 | | 0.000 | | 0.000 | | |
| REACTOME\_G1\_S\_TRANSITION | 106 | -3.40 | | 0.000 | | 0.000 | | |
| **REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT\_ATP\_SYNTHESIS\_BY.. (REACT\_6305)** | 84 | -3.37 | | 0.000 | | 0.000 | | |
| **REACTOME\_SYNTHESIS\_OF\_DNA** | 90 | -3.35 | | 0.000 | | 0.000 | | |
| REACTOME\_S\_PHASE | 106 | -3.34 | | 0.000 | | 0.000 | | |
| REACTOME\_TCA\_CYCLE\_AND\_RESPIRATORY\_ELECTRON\_TRANSPORT | 120 | -3.34 | | 0.000 | | 0.000 | | |
| REACTOME\_MITOTIC\_G1\_G1\_S\_PHASES | 130 | -3.31 | | 0.000 | | 0.000 | | |
| REACTOME\_M\_G1\_TRANSITION | 78 | -3.28 | | 0.000 | | 0.000 | | |
| REACTOME\_CELL\_CYCLE\_CHECKPOINTS | 111 | -3.22 | | 0.000 | | 0.000 | | |
| REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT | 67 | -3.19 | | 0.000 | | 0.000 | | |
| REACTOME\_CELL\_CYCLE\_MITOTIC | 300 | -3.18 | | 0.000 | | 0.000 | | |
| REACTOME\_ASSEMBLY\_OF\_THE\_PRE\_REPLICATIVE\_COMPLEX | 63 | -3.15 | | 0.000 | | 0.000 | | |
| REACTOME\_ORC1\_REMOVAL\_FROM\_CHROMATIN | 65 | -3.10 | | 0.000 | | 0.000 | | |
| REACTOME\_CELL\_CYCLE | 391 | -3.07 | | 0.000 | | 0.000 | | |
| REACTOME\_G2\_M\_CHECKPOINTS | 41 | -2.97 | | 0.000 | | 0.000 | | |
| REACTOME\_REGULATION\_OF\_ORNITHINE\_DECARBOXYLASE\_ODC | 48 | -2.93 | | 0.000 | | 0.000 | | |
| REACTOME\_REGULATION\_OF\_MITOTIC\_CELL\_CYCLE | 77 | -2.93 | | 0.000 | | 0.000 | | |
| REACTOME\_E2F\_MEDIATED\_REGULATION\_OF\_DNA\_REPLICATION | 33 | -2.92 | | 0.000 | | 0.000 | | |
| REACTOME\_CDT1\_ASSOCIATION\_WITH\_THE\_CDC6\_ORC\_ORIGIN\_COMPLEX | 54 | -2.89 | | 0.000 | | 0.000 | | |
| REACTOME\_ACTIVATION\_OF\_ATR\_IN\_RESPONSE\_TO\_REPLICATION\_STRESS | 35 | -2.86 | | 0.000 | | 0.000 | | |
| **REACTOME\_DNA\_STRAND\_ELONGATION** | 30 | -2.85 | | 0.000 | | 0.000 | | |
| REACTOME\_APC\_C\_CDH1\_MEDIATED\_DEGRADATION\_OF\_CDC20\_AND.. (REACT\_6761) | 64 | -2.85 | | 0.000 | | 0.000 | | |
| REACTOME\_APC\_C\_CDC20\_MEDIATED\_DEGRADATION\_OF\_MITOTIC\_PROTEINS | 65 | -2.85 | | 0.000 | | 0.000 | | |
| REACTOME\_SCFSKP2\_MEDIATED\_DEGRADATION\_OF\_P27\_P21 | 53 | -2.84 | | 0.000 | | 0.000 | | |
| REACTOME\_CYCLIN\_E\_ASSOCIATED\_EVENTS\_DURING\_G1\_S\_TRANSITION\_ | 62 | -2.84 | | 0.000 | | 0.000 | | |
| REACTOME\_CDK\_MEDIATED\_PHOSPHORYLATION\_AND\_REMOVAL\_OF\_CDC6 | 46 | -2.82 | | 0.000 | | 0.000 | | |
| REACTOME\_MITOTIC\_PROMETAPHASE | 79 | -2.77 | | 0.000 | | 0.000 | | |
| REACTOME\_P53\_INDEPENDENT\_G1\_S\_DNA\_DAMAGE\_CHECKPOINT | 48 | -2.76 | | 0.000 | | 0.000 | | |
| REACTOME\_HIV\_INFECTION | 184 | -2.76 | | 0.000 | | 0.000 | | |
| REACTOME\_MITOCHONDRIAL\_PROTEIN\_IMPORT | 48 | -2.75 | | 0.000 | | 0.000 | | |
| REACTOME\_AUTODEGRADATION\_OF\_CDH1\_BY\_CDH1\_APC\_C | 56 | -2.75 | | 0.000 | | 0.000 | | |
| REACTOME\_HOST\_INTERACTIONS\_OF\_HIV\_FACTORS | 117 | -2.75 | | 0.000 | | 0.000 | | |
| REACTOME\_DESTABILIZATION\_OF\_MRNA\_BY\_AUF1\_HNRNP\_D0 | 50 | -2.73 | | 0.000 | | 0.000 | | |
| REACTOME\_ACTIVATION\_OF\_THE\_PRE\_REPLICATIVE\_COMPLEX | 30 | -2.73 | | 0.000 | | 0.000 | | |
| REACTOME\_G1\_S\_SPECIFIC\_TRANSCRIPTION | 17 | -2.71 | | 0.000 | | 0.000 | | |
| REACTOME\_VIF\_MEDIATED\_DEGRADATION\_OF\_APOBEC3G | 47 | -2.66 | | 0.000 | | 0.000 | | |
| REACTOME\_SCF\_BETA\_TRCP\_MEDIATED\_DEGRADATION\_OF\_EMI1 | 49 | -2.63 | | 0.000 | | 0.000 | | |
| REACTOME\_CROSS\_PRESENTATION\_OF\_SOLUBLE\_EXOGENOUS\_ANTIGENS\_ENDOSOMES | 47 | -2.62 | | 0.000 | | 0.000 | | |
| REACTOME\_P53\_DEPENDENT\_G1\_DNA\_DAMAGE\_RESPONSE | 53 | -2.60 | | 0.000 | | 0.000 | | |
| REACTOME\_AUTODEGRADATION\_OF\_THE\_E3\_UBIQUITIN\_LIGASE\_COP1 | 47 | -2.58 | | 0.000 | | 0.000 | | |
| REACTOME\_MRNA\_SPLICING\_MINOR\_PATHWAY | 40 | -2.57 | | 0.000 | | 0.000 | | |
| REACTOME\_ER\_PHAGOSOME\_PATHWAY | 58 | -2.56 | | 0.000 | | 0.000 | | |
| REACTOME\_METABOLISM\_OF\_AMINO\_ACIDS\_AND\_DERIVATIVES | 189 | -2.51 | | 0.000 | | 0.000 | | |
| REACTOME\_REGULATION\_OF\_MRNA\_STABILITY\_BY\_PROTEINS\_THAT\_BIND.. (REACT\_24994) | 81 | -2.50 | | 0.000 | | 0.000 | | |
| **REACTOME\_REGULATION\_OF\_APOPTOSIS** | 56 | -2.49 | | 0.000 | | 0.000 | | |
| REACTOME\_EXTENSION\_OF\_TELOMERES | 27 | -2.48 | | 0.000 | | 0.000 | | |
| REACTOME\_PROCESSING\_OF\_CAPPED\_INTRON\_CONTAINING\_PRE\_MRNA | 132 | -2.45 | | 0.000 | | 0.000 | | |
| REACTOME\_MRNA\_SPLICING | 104 | -2.45 | | 0.000 | | 0.000 | | |
| REACTOME\_G0\_AND\_EARLY\_G1 | 23 | -2.43 | | 0.000 | | 0.000 | | |
| REACTOME\_MRNA\_PROCESSING | 151 | -2.43 | | 0.000 | | 0.000 | | |
| REACTOME\_ACTIVATION\_OF\_NF\_KAPPAB\_IN\_B\_CELLS | 61 | -2.40 | | 0.000 | | 0.000 | | |
| REACTOME\_LAGGING\_STRAND\_SYNTHESIS | 19 | -2.39 | | 0.000 | | 0.000 | | |
| REACTOME\_CITRIC\_ACID\_CYCLE\_TCA\_CYCLE | 19 | -2.39 | | 0.000 | | 0.000 | | |
| REACTOME\_SIGNALING\_BY\_WNT | 62 | -2.38 | | 0.000 | | 0.000 | | |
| REACTOME\_ANTIGEN\_PROCESSING\_CROSS\_PRESENTATION | 72 | -2.37 | | 0.000 | | 0.000 | | |
| REACTOME\_METABOLISM\_OF\_NON\_CODING\_RNA | 47 | -2.37 | | 0.000 | | 0.000 | | |
| **REACTOME\_DNA\_REPAIR** | 101 | -2.32 | | 0.000 | | 0.000 | | |
| REACTOME\_METABOLISM\_OF\_RNA | 252 | -2.28 | | 0.000 | | 0.000 | | |
| REACTOME\_CYCLIN\_A\_B1\_ASSOCIATED\_EVENTS\_DURING\_G2\_M\_TRANSITION | 15 | -2.28 | | 0.000 | | 0.000 | | |
| REACTOME\_CHROMOSOME\_MAINTENANCE | 116 | -2.23 | | 0.000 | | 0.000 | | |
| REACTOME\_HIV\_LIFE\_CYCLE | 105 | -2.22 | | 0.000 | | 0.000 | | |
| REACTOME\_RNA\_POL\_III\_TRANSCRIPTION\_TERMINATION | 19 | -2.20 | | 0.000 | | 0.000 | | |
| REACTOME\_RNA\_POL\_III\_CHAIN\_ELONGATION | 17 | -2.18 | | 0.000 | | 0.000 | | |
| REACTOME\_KINESINS | 24 | -2.18 | | 0.000 | | 0.000 | | |
| REACTOME\_PYRUVATE\_METABOLISM\_AND\_CITRIC\_ACID\_TCA\_CYCLE | 40 | -2.17 | | 0.000 | | 0.000 | | |
| REACTOME\_METABOLISM\_OF\_VITAMINS\_AND\_COFACTORS | 50 | -2.14 | | 0.000 | | 0.000 | | |
| REACTOME\_BRANCHED\_CHAIN\_AMINO\_ACID\_CATABOLISM | 17 | -2.13 | | 0.000 | | 0.001 | | |
| REACTOME\_METABOLISM\_OF\_NUCLEOTIDES | 69 | -2.13 | | 0.000 | | 0.000 | | |
| REACTOME\_LATE\_PHASE\_OF\_HIV\_LIFE\_CYCLE | 92 | -2.12 | | 0.000 | | 0.001 | | |
| REACTOME\_APC\_CDC20\_MEDIATED\_DEGRADATION\_OF\_NEK2A | 21 | -2.12 | | 0.000 | | 0.001 | | |
| REACTOME\_TELOMERE\_MAINTENANCE | 75 | -2.11 | | 0.000 | | 0.001 | | |
| REACTOME\_RNA\_POL\_II\_PRE\_TRANSCRIPTION\_EVENTS | 51 | -2.10 | | 0.000 | | 0.001 | | |
| REACTOME\_PROCESSIVE\_SYNTHESIS\_ON\_THE\_LAGGING\_STRAND | 15 | -2.10 | | 0.002 | | 0.001 | | |
| REACTOME\_PROCESSING\_OF\_CAPPED\_INTRONLESS\_PRE\_MRNA | 23 | -2.09 | | 0.000 | | 0.001 | | |
| REACTOME\_DOUBLE\_STRAND\_BREAK\_REPAIR | 21 | -2.06 | | 0.000 | | 0.001 | | |
| REACTOME\_METABOLISM\_OF\_PROTEINS | 418 | -2.06 | | 0.000 | | 0.001 | | |
| REACTOME\_APC\_C\_CDC20\_MEDIATED\_DEGRADATION\_OF\_CYCLIN\_B | 19 | -2.06 | | 0.000 | | 0.001 | | |
| REACTOME\_TRANSCRIPTION\_COUPLED\_NER\_TC\_NER | 43 | -2.05 | | 0.000 | | 0.001 | | |
| **REACTOME\_APOPTOSIS** | 142 | -2.04 | | 0.000 | | 0.001 | | |
| REACTOME\_RNA\_POL\_II\_TRANSCRIPTION\_PRE\_INITIATION\_AND\_PROMOTER\_OPENING | 39 | -2.03 | | 0.000 | | 0.001 | | |
| REACTOME\_RNA\_POL\_III\_TRANSCRIPTION\_INITIATION\_FROM\_TYPE\_3\_PROMOTER | 26 | -2.03 | | 0.000 | | 0.001 | | |
| REACTOME\_BIOSYNTHESIS\_OF\_THE\_N\_GLYCAN\_PRECURSOR\_DOLICHOL.. (REACT\_22433) | 28 | -2.02 | | 0.000 | | 0.001 | | |
| REACTOME\_TRNA\_AMINOACYLATION | 42 | -2.02 | | 0.000 | | 0.001 | | |
| REACTOME\_TRANSCRIPTION | 191 | -2.02 | | 0.000 | | 0.001 | | |
| REACTOME\_METABOLISM\_OF\_MRNA | 208 | -2.01 | | 0.000 | | 0.002 | | |
| REACTOME\_RNA\_POL\_II\_TRANSCRIPTION | 93 | -2.00 | | 0.000 | | 0.002 | | |
| REACTOME\_HOMOLOGOUS\_RECOMBINATION\_REPAIR\_OF\_REPLICATION.. (REACT\_1587) | 15 | -2.00 | | 0.002 | | 0.002 | | |
| REACTOME\_INHIBITION\_OF\_THE\_PROTEOLYTIC\_ACTIVITY\_OF\_APC\_C.. (REACT\_1041) | 18 | -1.99 | | 0.002 | | 0.002 | | |
| REACTOME\_ANTIVIRAL\_MECHANISM\_BY\_IFN\_STIMULATED\_GENES | 63 | -1.99 | | 0.000 | | 0.002 | | |
| REACTOME\_RNA\_POL\_III\_TRANSCRIPTION | 33 | -1.99 | | 0.000 | | 0.002 | | |
| REACTOME\_ABORTIVE\_ELONGATION\_OF\_HIV1\_TRANSCRIPT\_IN\_THE\_ABSENCE\_OF\_TAT | 19 | -1.98 | | 0.002 | | 0.002 | | |
| REACTOME\_ASPARAGINE\_N\_LINKED\_GLYCOSYLATION | 80 | -1.97 | | 0.000 | | 0.002 | | |
| REACTOME\_DOWNSTREAM\_SIGNALING\_EVENTS\_OF\_B\_CELL\_RECEPTOR\_BCR | 92 | -1.96 | | 0.000 | | 0.002 | | |
| REACTOME\_FANCONI\_ANEMIA\_PATHWAY | 19 | -1.96 | | 0.000 | | 0.002 | | |
| REACTOME\_ANTIGEN\_PROCESSING\_UBIQUITINATION\_PROTEASOME\_DEGRADATION | 194 | -1.95 | | 0.000 | | 0.003 | | |
| REACTOME\_RNA\_POL\_III\_TRANSCRIPTION\_INITIATION\_FROM\_TYPE\_2\_PROMOTER | 23 | -1.91 | | 0.000 | | 0.004 | | |
| REACTOME\_PHOSPHORYLATION\_OF\_THE\_APC\_C | 17 | -1.91 | | 0.004 | | 0.004 | | |
| REACTOME\_CLASS\_I\_MHC\_MEDIATED\_ANTIGEN\_PROCESSING\_PRESENTATION | 231 | -1.89 | | 0.000 | | 0.004 | | |
| REACTOME\_DEPOSITION\_OF\_NEW\_CENPA\_CONTAINING\_NUCLEOSOMES.. (REACT\_22186) | 60 | -1.86 | | 0.000 | | 0.006 | | |
| REACTOME\_MHC\_CLASS\_II\_ANTIGEN\_PRESENTATION | 89 | -1.84 | | 0.000 | | 0.007 | | |
| REACTOME\_LYSOSOME\_VESICLE\_BIOGENESIS | 23 | -1.83 | | 0.007 | | 0.007 | | |
| REACTOME\_MICRORNA\_MIRNA\_BIOGENESIS | 18 | -1.83 | | 0.004 | | 0.008 | | |
| REACTOME\_MITOCHONDRIAL\_TRNA\_AMINOACYLATION | 21 | -1.82 | | 0.004 | | 0.008 | | |
| REACTOME\_NUCLEOTIDE\_EXCISION\_REPAIR | 48 | -1.81 | | 0.002 | | 0.008 | | |
| REACTOME\_GLUTATHIONE\_CONJUGATION | 22 | -1.81 | | 0.007 | | 0.008 | | |
| REACTOME\_FORMATION\_OF\_RNA\_POL\_II\_ELONGATION\_COMPLEX\_ | 35 | -1.78 | | 0.002 | | 0.011 | | |
| REACTOME\_DEADENYLATION\_DEPENDENT\_MRNA\_DECAY | 42 | -1.78 | | 0.004 | | 0.011 | | |
| REACTOME\_SIGNALING\_BY\_THE\_B\_CELL\_RECEPTOR\_BCR | 121 | -1.77 | | 0.000 | | 0.011 | | |
| REACTOME\_FORMATION\_OF\_THE\_HIV1\_EARLY\_ELONGATION\_COMPLEX | 28 | -1.77 | | 0.005 | | 0.011 | | |
| REACTOME\_ELONGATION\_ARREST\_AND\_RECOVERY | 24 | -1.77 | | 0.011 | | 0.011 | | |
| REACTOME\_SYNTHESIS\_AND\_INTERCONVERSION\_OF\_NUCLEOTIDE\_DI\_AND\_TRIPHOSPHATES | 17 | -1.77 | | 0.004 | | 0.011 | | |
| REACTOME\_RNA\_POL\_I\_RNA\_POL\_III\_AND\_MITOCHONDRIAL\_TRANSCRIPTION | 113 | -1.77 | | 0.000 | | 0.011 | | |
| REACTOME\_MRNA\_CAPPING | 28 | -1.76 | | 0.005 | | 0.012 | | |
| REACTOME\_ASSOCIATION\_OF\_TRIC\_CCT\_WITH\_TARGET\_PROTEINS\_DURING\_BIOSYNTHESIS | 26 | -1.75 | | 0.009 | | 0.013 | | |
| REACTOME\_BASE\_EXCISION\_REPAIR | 19 | -1.72 | | 0.018 | | 0.016 | | |
| REACTOME\_FORMATION\_OF\_THE\_TERNARY\_COMPLEX\_AND\_SUBSEQUENTLY.. (REACT\_1079) | 48 | -1.71 | | 0.000 | | 0.018 | | |
| REACTOME\_CONVERSION\_FROM\_APC\_C\_CDC20\_TO\_APC\_C\_CDH1\_IN\_LATE\_ANAPHASE | 16 | -1.70 | | 0.020 | | 0.018 | | |
| REACTOME\_RESOLUTION\_OF\_AP\_SITES\_VIA\_THE\_MULTIPLE\_NUCLEOTIDE.. ( REACT\_1128) | 17 | -1.70 | | 0.004 | | 0.018 | | |
| REACTOME\_THE\_ROLE\_OF\_NEF\_IN\_HIV1\_REPLICATION\_AND\_DISEASE\_PATHOGENESIS | 27 | -1.69 | | 0.013 | | 0.020 | | |
| REACTOME\_CYTOSOLIC\_TRNA\_AMINOACYLATION | 24 | -1.69 | | 0.018 | | 0.020 | | |
| REACTOME\_NEF\_MEDIATES\_DOWN\_MODULATION\_OF\_CELL\_SURFACE.. (REACT\_11149) | 20 | -1.66 | | 0.013 | | 0.024 | | |
| REACTOME\_PURINE\_METABOLISM | 33 | -1.66 | | 0.013 | | 0.023 | | |
| REACTOME\_RNA\_POL\_I\_TRANSCRIPTION\_INITIATION | 23 | -1.66 | | 0.013 | | 0.024 | | |
| REACTOME\_POST\_TRANSLATIONAL\_PROTEIN\_MODIFICATION | 178 | -1.66 | | 0.000 | | 0.023 | | |
| REACTOME\_NEP\_NS2\_INTERACTS\_WITH\_THE\_CELLULAR\_EXPORT\_MACHINERY | 26 | -1.66 | | 0.019 | | 0.024 | | |
| REACTOME\_TRANSPORT\_OF\_MATURE\_MRNA\_DERIVED\_FROM\_AN\_INTRONLESS\_TRANSCRIPT | 31 | -1.65 | | 0.013 | | 0.026 | | |
| REACTOME\_G1\_PHASE | 35 | -1.64 | | 0.018 | | 0.027 | | |
| REACTOME\_FORMATION\_OF\_TRANSCRIPTION\_COUPLED\_NER\_TC\_NER\_REPAIR\_COMPLEX | 28 | -1.63 | | 0.018 | | 0.028 | | |
| REACTOME\_INTERACTIONS\_OF\_VPR\_WITH\_HOST\_CELLULAR\_PROTEINS | 31 | -1.63 | | 0.014 | | 0.029 | | |
| REACTOME\_ACTIVATION\_OF\_THE\_MRNA\_UPON\_BINDING\_OF\_THE\_CAP.. (REACT\_1258) | 56 | -1.62 | | 0.011 | | 0.029 | | |
| REACTOME\_INTERFERON\_SIGNALING | 152 | -1.62 | | 0.002 | | 0.030 | | |
| REACTOME\_MEIOTIC\_RECOMBINATION | 80 | -1.61 | | 0.004 | | 0.032 | | |
| REACTOME\_INFLUENZA\_LIFE\_CYCLE | 134 | -1.61 | | 0.000 | | 0.032 | | |
| REACTOME\_MITOTIC\_G2\_G2\_M\_PHASES | 77 | -1.57 | | 0.007 | | 0.040 | | |
| REACTOME\_CLEAVAGE\_OF\_GROWING\_TRANSCRIPT\_IN\_THE\_TERMINATION\_REGION | 42 | -1.57 | | 0.016 | | 0.042 | | |
| REACTOME\_PHASE\_II\_CONJUGATION | 61 | -1.55 | | 0.013 | | 0.045 | | |
| REACTOME\_MEIOSIS | 108 | -1.54 | | 0.010 | | 0.049 | | |
| REACTOME\_MEMBRANE\_TRAFFICKING | 124 | -1.53 | | 0.007 | | 0.050 | | |
| REACTOME\_UNFOLDED\_PROTEIN\_RESPONSE | 73 | -1.53 | | 0.007 | | 0.051 | | |
| REACTOME\_TRANSLATION | 144 | -1.51 | | 0.002 | | 0.056 | | |
| REACTOME\_PROTEIN\_FOLDING | 51 | -1.51 | | 0.016 | | 0.056 | | |

Results of gene set enrichment analysis. Size: number of genes in the expression dataset belonging to the pathway; NES: normalized enrichment score; FDR: false discovery rate. Pathways with too long names have been univocally identified posing the corresponding Reactome ID in brackets. Pathways directly cited in the results section are elicited in bold.