**Table S2.** Reactome pathways up-regulated by Bevacizumab in IGROV-1 and SKOV3 models

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **IGROV-1 model** |  |  |  |  |
| **Pathway** | **size** | **NES** | **p-value** | **FDR q-value** |
| **REACTOME\_GLYCOLYSIS** | 26 | 2.36 | 0.000 | 0.000 |
| REACTOME\_GENERIC\_TRANSCRIPTION\_PATHWAY | 333 | 2.10 | 0.000 | 0.011 |
| REACTOME\_PRE\_NOTCH\_TRANSCRIPTION\_AND\_TRANSLATION | 23 | 2.00 | 0.002 | 0.028 |
| REACTOME\_SYNTHESIS\_OF\_PIPS\_AT\_THE\_GOLGI\_MEMBRANE | 17 | 1.94 | 0.002 | 0.043 |
| REACTOME\_GLUCOSE\_METABOLISM | 63 | 1.90 | 0.002 | 0.049 |
| **REACTOME\_PHOSPHOLIPID\_METABOLISM** | 189 | 1.89 | 0.000 | 0.047 |
| REACTOME\_PRE\_NOTCH\_EXPRESSION\_AND\_PROCESSING | 38 | 1.87 | 0.000 | 0.046 |
| REACTOME\_GLUCONEOGENESIS | 31 | 1.87 | 0.000 | 0.044 |
| REACTOME\_TRANS\_GOLGI\_NETWORK\_VESICLE\_BUDDING | 57 | 1.80 | 0.002 | 0.075 |
| REACTOME\_INSULIN\_RECEPTOR\_RECYCLING | 23 | 1.79 | 0.005 | 0.073 |
| REACTOME\_PROTEOLYTIC\_CLEAVAGE\_OF\_SNARE\_COMPLEX\_PROTEINS | 16 | 1.75 | 0.017 | 0.098 |
| REACTOME\_ACYL\_CHAIN\_REMODELLING\_OF\_PS | 15 | 1.70 | 0.009 | 0.135 |
| **REACTOME\_SIGNALING\_BY\_NOTCH** | 95 | 1.67 | 0.005 | 0.162 |
| REACTOME\_GOLGI\_ASSOCIATED\_VESICLE\_BIOGENESIS | 50 | 1.66 | 0.003 | 0.154 |
| REACTOME\_GAB1\_SIGNALOSOME | 36 | 1.62 | 0.017 | 0.197 |
| REACTOME\_METABOLISM\_OF\_CARBOHYDRATES | 229 | 1.62 | 0.000 | 0.195 |
| **REACTOME\_GLYCOSPHINGOLIPID\_METABOLISM** | 37 | 1.61 | 0.015 | 0.190 |
| REACTOME\_PI\_METABOLISM | 47 | 1.60 | 0.018 | 0.190 |
| **REACTOME\_GLYCEROPHOSPHOLIPID\_BIOSYNTHESIS** | 79 | 1.60 | 0.008 | 0.186 |
| **REACTOME\_TRIGLYCERIDE\_BIOSYNTHESIS** | 36 | 1.57 | 0.015 | 0.216 |
| **REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS** | 461 | 1.56 | 0.000 | 0.211 |
|  |  |  |  |  |
| **SKOV3 model** |  |  |  |  |
| **Pathway** | **size** | **NES** | **p-value** | **FDR q-value** |
| **REACTOME\_CHONDROITIN\_SULFATE\_BIOSYNTHESIS** | 19 | 2.20 | 0.000 | 0.007 |
| **REACTOME\_CHONDROITIN\_SULFATE\_DERMATAN\_SULFATE\_METABOLISM** | 47 | 2.14 | 0.000 | 0.008 |
| REACTOME\_OLFACTORY\_SIGNALING\_PATHWAY | 305 | 2.08 | 0.000 | 0.014 |
| REACTOME\_CLASS\_B\_2\_SECRETIN\_FAMILY\_RECEPTORS | 82 | 1.88 | 0.000 | 0.100 |
| REACTOME\_NCAM1\_INTERACTIONS | 39 | 1.86 | 0.002 | 0.095 |
| **REACTOME\_GLYCOSAMINOGLYCAN\_METABOLISM** | 106 | 1.84 | 0.000 | 0.093 |
| REACTOME\_PHOSPHORYLATION\_OF\_CD3\_AND\_TCR\_ZETA\_CHAINS | 16 | 1.79 | 0.005 | 0.135 |
| REACTOME\_A\_TETRASACCHARIDE\_LINKER\_SEQUENCE\_IS\_REQUIRED\_FOR\_GAG\_SYNTHESIS | 25 | 1.78 | 0.009 | 0.128 |
| REACTOME\_COMPLEMENT\_CASCADE | 29 | 1.77 | 0.002 | 0.125 |
| REACTOME\_SYNTHESIS\_SECRETION\_AND\_DEACYLATION\_OF\_GHRELIN | 15 | 1.73 | 0.009 | 0.149 |
| REACTOME\_NCAM\_SIGNALING\_FOR\_NEURITE\_OUT\_GROWTH | 64 | 1.73 | 0.002 | 0.138 |
| REACTOME\_CD28\_DEPENDENT\_PI3K\_AKT\_SIGNALING | 21 | 1.72 | 0.013 | 0.140 |
| **REACTOME\_SIGNALING\_BY\_NOTCH** | 95 | 1.71 | 0.002 | 0.141 |
| REACTOME\_NUCLEAR\_SIGNALING\_BY\_ERBB4 | 38 | 1.71 | 0.009 | 0.136 |
| REACTOME\_SIGNALING\_BY\_PDGF | 117 | 1.68 | 0.002 | 0.149 |
| **REACTOME\_SIGNALING\_BY\_NOTCH1** | 67 | 1.65 | 0.009 | 0.168 |
| REACTOME\_G\_ALPHA\_S\_SIGNALLING\_EVENTS | 119 | 1.64 | 0.000 | 0.171 |
| REACTOME\_GPCR\_LIGAND\_BINDING | 381 | 1.63 | 0.000 | 0.177 |
| REACTOME\_KERATAN\_SULFATE\_BIOSYNTHESIS | 25 | 1.61 | 0.018 | 0.193 |
| REACTOME\_CIRCADIAN\_CLOCK | 50 | 1.60 | 0.012 | 0.202 |
| REACTOME\_NEURONAL\_SYSTEM | 275 | 1.59 | 0.000 | 0.206 |
| REACTOME\_TGF\_BETA\_RECEPTOR\_SIGNALING\_ACTIVATES\_SMADS | 24 | 1.59 | 0.016 | 0.199 |
| REACTOME\_HEPARAN\_SULFATE\_HEPARIN\_HS\_GAG\_METABOLISM | 50 | 1.58 | 0.009 | 0.199 |
| REACTOME\_NOTCH1\_INTRACELLULAR\_DOMAIN\_REGULATES\_TRANSCRIPTION | 44 | 1.58 | 0.019 | 0.192 |
| REACTOME\_ION\_CHANNEL\_TRANSPORT | 54 | 1.55 | 0.016 | 0.210 |
| REACTOME\_POTASSIUM\_CHANNELS | 97 | 1.54 | 0.004 | 0.205 |
| REACTOME\_PHASE1\_FUNCTIONALIZATION\_OF\_COMPOUNDS | 68 | 1.54 | 0.014 | 0.204 |
| REACTOME\_EXTRACELLULAR\_MATRIX\_ORGANIZATION | 81 | 1.50 | 0.009 | 0.214 |
| REACTOME\_TRANSMISSION\_ACROSS\_CHEMICAL\_SYNAPSES | 183 | 1.48 | 0.009 | 0.230 |
| REACTOME\_DEVELOPMENTAL\_BIOLOGY | 380 | 1.48 | 0.000 | 0.226 |

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 directly cited in the results section are elicited in bold.