**Supplementary Table S11. GO terms and pathways identified by GSEA as enriched with genes down-regulated in high-hypoxia tumors**

|  |  |  |  |
| --- | --- | --- | --- |
| NAME | NES | NOM p-val | FDR q-val |
| GO terms | | | |
| GO\_HUMORAL\_IMMUNE\_RESPONSE\_MEDIATED\_BY\_CIRCULATING\_IMMUNOGLOBULIN | -2.204378 | 0 | 0 |
| GO\_RESPONSE\_TO\_TYPE\_I\_INTERFERON | -2.1841977 | 0 | 0 |
| GO\_POSITIVE\_REGULATION\_OF\_T\_CELL\_PROLIFERATION | -2.1557412 | 0 | 0 |
| GO\_ACTIVATION\_OF\_IMMUNE\_RESPONSE | -2.032956 | 0 | 0.001475233 |
| GO\_REGULATION\_OF\_T\_CELL\_PROLIFERATION | -2.0156875 | 0 | 0.001531538 |
| GO\_REGULATION\_OF\_HUMORAL\_IMMUNE\_RESPONSE | -2.0038564 | 0 | 0.001885471 |
| GO\_REGULATION\_OF\_ACTIVATED\_T\_CELL\_PROLIFERATION | -1.9923016 | 0 | 0.001720825 |
| GO\_ADAPTIVE\_IMMUNE\_RESPONSE | -1.9857382 | 0 | 0.001799748 |
| GO\_REGULATION\_OF\_MACROPHAGE\_DERIVED\_FOAM\_CELL\_DIFFERENTIATION | -1.9800603 | 0 | 0.001979961 |
| GO\_NEGATIVE\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE | -1.9785959 | 0 | 0.001929544 |
| GO\_POSITIVE\_REGULATION\_OF\_IMMUNE\_RESPONSE | -1.9646024 | 0 | 0.001938514 |
| GO\_B\_CELL\_MEDIATED\_IMMUNITY | -1.9517437 | 0 | 0.002330195 |
| GO\_LYMPHOCYTE\_MEDIATED\_IMMUNITY | -1.9430013 | 0 | 0.002683156 |
| GO\_ADAPTIVE\_IMMUNE\_RESPONSE\_BASED\_ON\_SOMATIC\_RECOMBINATION\_OF\_IMMUNE\_RECEPTORS\_BUILT\_FROM\_IMMUNOGLOBULIN\_SUPERFAMILY\_DOMAINS | -1.9261609 | 0 | 0.003884297 |
| GO\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE | -1.9255036 | 0 | 0.003854737 |
| GO\_REGULATION\_OF\_CD4\_POSITIVE\_ALPHA\_BETA\_T\_CELL\_ACTIVATION | -1.9117045 | 0 | 0.004805666 |
| GO\_REGULATION\_OF\_INNATE\_IMMUNE\_RESPONSE | -1.8989525 | 0 | 0.005302365 |
| GO\_IMMUNE\_EFFECTOR\_PROCESS | -1.8866003 | 0 | 0.006399169 |
| GO\_INNATE\_IMMUNE\_RESPONSE | -1.8839512 | 0 | 0.006552783 |
| GO\_POSITIVE\_REGULATION\_OF\_INTERFERON\_GAMMA\_PRODUCTION | -1.88315 | 0 | 0.006519649 |
| GO\_REGULATION\_OF\_INTERFERON\_GAMMA\_PRODUCTION | -1.8618282 | 0 | 0.009339782 |
| GO\_POSITIVE\_REGULATION\_OF\_ACTIVATED\_T\_CELL\_PROLIFERATION | -1.8582528 | 0 | 0.009704702 |
| Pathways | | | |
| BROWNE\_INTERFERON\_RESPONSIVE\_GENES | -2.312647 | 0 | 0 |
| SANA\_RESPONSE\_TO\_IFNG\_UP | -2.2968733 | 0 | 0 |
| HECKER\_IFNB1\_TARGETS | -2.2220864 | 0 | 0 |
| PICCALUGA\_ANGIOIMMUNOBLASTIC\_LYMPHOMA\_UP | -2.2196724 | 0 | 0 |
| MOSERLE\_IFNA\_RESPONSE | -2.1919088 | 0 | 0 |
| LEE\_DIFFERENTIATING\_T\_LYMPHOCYTE | -2.1860816 | 0 | 0 |
| FULCHER\_INFLAMMATORY\_RESPONSE\_LECTIN\_VS\_LPS\_DN | -2.1796148 | 0 | 0 |
| RADAEVA\_RESPONSE\_TO\_IFNA1\_UP | -2.1763792 | 0 | 0 |
| BOSCO\_INTERFERON\_INDUCED\_ANTIVIRAL\_MODULE | -2.1699483 | 0 | 0 |
| REACTOME\_INTERFERON\_ALPHA\_BETA\_SIGNALING | -2.1273773 | 0 | 0 |
| REACTOME\_INNATE\_IMMUNE\_SYSTEM | -1.9704398 | 0 | 5.13E-04 |
| ZHANG\_INTERFERON\_RESPONSE | -1.9241569 | 0 | 0.00171187 |
| REACTOME\_IMMUNOREGULATORY\_INTERACTIONS\_BETWEEN\_A\_LYMPHOID\_AND\_A\_NON\_LYMPHOID\_CELL | -1.8427926 | 0 | 0.005805555 |
| REACTOME\_INTERFERON\_SIGNALING | -1.8420798 | 0 | 0.005753698 |
| EINAV\_INTERFERON\_SIGNATURE\_IN\_CANCER | -1.8150855 | 0.001862197 | 0.007985849 |
| REACTOME\_ANTIGEN\_ACTIVATES\_B\_CELL\_RECEPTOR\_LEADING\_TO\_GENERATION\_OF\_SECOND\_MESSENGERS | -1.8134301 | 0 | 0.007971176 |
| REACTOME\_CYTOKINE\_SIGNALING\_IN\_IMMUNE\_SYSTEM | -1.8057749 | 0 | 0.008678869 |
| HOFFMANN\_IMMATURE\_TO\_MATURE\_B\_LYMPHOCYTE\_UP | -1.7950966 | 0.001855288 | 0.009655289 |
| NES: normalized enrichment score; NOM p-val: nominal P value; FDR q-val: false discovery rate corrected P value | | | |