**Table S7**. Gene Ontology (GO) enrichment analysis of key genes.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | GO Terms | *p*-values | | |
| BRCA | COAD | GBM |
| BP | Immune system process | 2.33x10-20 | 1.54x10-11 | 3.64x10–10 |
| Regulation of immune system process | 9.06x10–20 | 1.49x10–09 | 1.69x10–08 |
| Positive regulation of immune system process | 2.08x10–17 | 8.28x10–11 | 8.93x10–08 |
| T cell activation | 7.71x10–16 | 7.25x10–09 | 6.53x10–09 |
| Lymphocyte activation | 1.36x10–16 | - | 5.66x10–09 |
| Cell activation | 1.16x10–15 | - | 2.60x10–10 |
| Leukocyte activation | 3.24x10–15 | - | 1.40x10–09 |
| Immune response | - | 1.63x10–09 | 5.12x10–08 |
| Activation of immune response | - | 3.88x10–08 | 6.14x10–08 |
| CC | T cell receptor complex | 7.29x10–14 | - | 2.09x10–04 |
| Plasma membrane | 1.39x10–10 | 5.22x10–08 | 8.83x10–07 |
| Plasma membrane part | 2.97x10–09 | 1.58x10–06 | 1.95x10–04 |
| Integral to plasma membrane | 5.73x10–08 | 1.59x10–06 | 7.93x10–04 |
| Intrinsic to plasma membrane | 7.33x10–08 | 2.00x10–06 | 9.00x10–04 |
| Receptor complex | 1.00x10–07 | 5.59x10–04 | 9.28x10–05 |
| Membrane | - | 6.26x10–06 | 1.79x10–04 |
| Cell surface | 3.62x10–07 | 1.14x10–03 | - |
| MF | Molecular transducer activity | 4.80x10–07 | 3.92x10–11 | 3.52x10–04 |
| Signal transducer activity | 4.80x10–07 | 3.92x10–11 | 3.52x10–04 |
| Protein binding | 4.90x10–05 | 3.84x10–04 | 9.00x10–05 |
| GTPase regulator activity | - | 9.26x10–04 | 1.13x10–03 |
| Nucleoside-triphosphatase regulator activity | - | 9.08x10–06 | 1.24x10–03 |
| Receptor activity | 1.41x10–05 | 6.16x10–10 | - |
| Non-membrane spanning protein tyrosine kinase activity | 1.60x10–04 | 3.08x10–04 | - |