**Table S6.** Enriched pathways with key genes.

|  |  |  |  |
| --- | --- | --- | --- |
| Pathways | *p*-values | | |
| BRCA | COAD | GBM |
| TCR signaling in -ve CD4+ T cells(N) | 1.11x10-16 | 3.09x10–08 | 1.83x10–06 |
| Neutrophil degranulation(R) | - | 1.83x10–11 | 8.72x10–10 |
| Osteoclast differentiation(K) | - | 5.67x10–10 | 5.02x10–09 |
| Staphylococcus aureus infection(K) | - | 2.76x10–07 | 7.65x10–07 |
| Natural killer cell mediated cytotoxicity(K) | - | 4.10x10–05 | 5.97x10–09 |
| Fc gamma R-mediated phagocytosis(K) | - | 7.77x10–05 | 1.18x10–08 |
| T cell receptor signaling pathway(K) | 9.29x10–11 | 1.37x10–04 | - |

\*The letters in parenthesis corresponds to the sources of pathways; C: CellMap, R: Reactome, K: KEGG (Kyoto Encyclopedia of Gene and Genomes), N: NCI PID (National Cancer Institute Pathway Interaction Database), P: Panther, and B: Biocarta.