Supplement Table 4. Enriched gene sets.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MSigDB collection | Gene set name | NES | NOM p-val | FDR q-val |
| c2.cp.kegg.v7.2.symbols.gmt |  |  |  |
| CELE10A high expression | KEGG\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION | 2.224 | 0 | 2.15×10-4 |
|  | KEGG\_B\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 2.559 | 0 | 0 |
|  | KEGG\_FC\_EPSILON\_RI\_SIGNALING\_PATHWAY | 2.536 | 0 | 0 |
|  | KEGG\_FC\_GAMMA\_R\_MEDIATED\_PHAGOCYTOSIS | 2.535 | 0 | 0 |
|  | KEGG\_HEMATOPOIETIC\_CELL\_LINEAGE | 2.544 | 0 | 0 |
|  | KEGG\_LEUKOCYTE\_TRANSENDOTHELIAL\_MIGRATION | 2.553 | 0 | 0 |
|  | KEGG\_NATURAL\_KILLER\_CELL\_MEDIATED\_CYTOTOXICITY | 2.587 | 0 | 0 |
|  | KEGG\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 2.625 | 0 | 0 |
| CELE10A low expression | KEGG\_GLYCOSYLPHOSPHATIDYLINOSITOL\_GPI\_ANCHOR\_BIOSYNTHESIS | -2.143 | 0 | 0.008 |
| c7.all.v7.2.symbols.gmt |  |  |  |  |
| CELE10A high expression | GSE3039\_CD4\_TCELL\_VS\_ALPHABETA\_CD8\_TCELL\_UP | 0.740 | 0 | 0 |
|  | GSE4590\_SMALL\_VS\_LARGE\_PRE\_BCELL\_UP | 2.742 | 0 | 0 |
|  | GSE19888\_ADENOSINE\_A3R\_INH\_VS\_ACT\_IN\_MAST\_CELL\_DN | 2.775 | 0 | 0 |
|  | GSE21380\_NON\_TFH\_VS\_TFH\_CD4\_TCELL\_UP | 2.726 | 0 | 0 |
|  | GSE23925\_LIGHT\_ZONE\_VS\_NAIVE\_BCELL\_UP | 2.791 | 0 | 0 |
|  | GSE24142\_EARLY\_THYMIC\_PROGENITOR\_VS\_DN3\_THYMOCYTE\_DN | 2.822 | 0 | 0 |
|  | GSE40274\_CTRL\_VS\_FOXP3\_AND\_LEF1\_TRANSDUCED\_ACTIVATED\_CD4\_TCELL\_UP | 2.727 | 0 | 0 |
|  | GSE43863\_LY6C\_INT\_CXCR5POS\_VS\_LY6C\_LOW\_CXCR5NEG\_EFFECTOR\_CD4\_TCELL\_DN | 2.789 | 0 | 0 |
|  | KAECH\_NAIVE\_VS\_MEMORY\_CD8\_TCELL\_DN | 2.726 | 0 | 0 |
| CELE10A low expression | - | - | - | - |

NES: normalized enrichment score; NOM: nominal p-value; FDR: false discovery rate. Gene sets with NOM p-value less than 0.05 and FDR q-value less than 0.05 were considered as statistical significance. Only several leading sets enriched in CELE10A high expression both in c2.cp.kegg and C7 were listed here due to the large number of enriched gene sets.