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| **Cell type** | **Definition genes** | ***P*-value** |
| NK CD56dim cells  | *IL21R**KIR3DL2**KIR3DL1* (discarded)*KIR\_Inhibiting\_Subgroup\_2* (discarded) | 0.63  |
| Cytotoxic cells  | *GZMB**PRF1**KLRK1**GZMH**KLRB1**KLRD1**GNLY**GZMA**CTSW* | 0  |
| Dendritic cells  | *CD209**HSD11B1**CCL13* | 0.04 |
| Regulatory T cells | *FOXP3* | NA |
| CD45+ cells | *PTPRC* | NA |
| Macrophages  | *CD163**CD68**CD84* (discarded) | 0.40  |
| T cells  | *CD3G**SH2D1A**CD6**CD3D**CD3E* | 0  |
| Mast cells  | *TPSAB1**MS4A2* | 0.29  |
| Neutrophils  | *CSF3R**S100A12* | 0.02  |
| Natural killer cells  | *XCL2**NCR1* | 0.50  |
| Exhausted CD8+ cells  | *CD244**EOMES**LAG3* (discarded) | 0.60  |
| B cells  | *BLK**CD19**MS4A1**TNFRSF17* (discarded) | 0.02  |
| Th1 cells | *TBX21* | NA |
| CD8+ T cells | *CD8A**CD8B* | 0.01 |

The *P*-value is calculated as the proportion (out of 1000 random gene sets) of gene sets that shows a better correlation than the gene sets defined by NanoString.