

Supplementary Material

Supplementary Figures

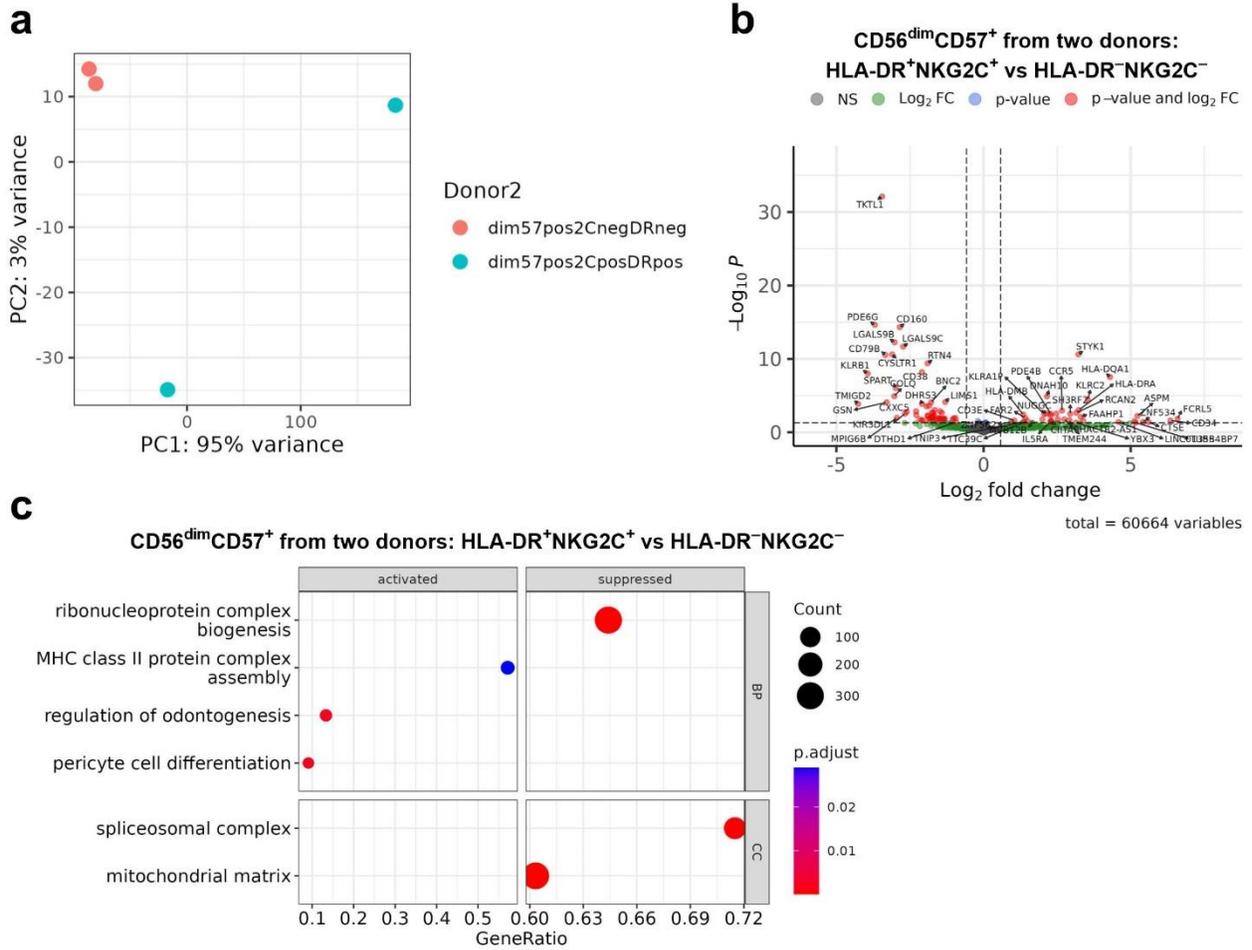


Figure S1. Transcriptome analysis of CD56^{dim}CD57⁺ samples (a) Principal component analysis of normalized count of CD56^{dim}CD57⁺ samples of donor 2; (b) Volcano plot comparing HLA-DR⁺NKG2C⁺ vs HLA-DR⁻NKG2C⁻ CD56^{dim}CD57⁺ NK cells from two donors, part of significant up-regulated and down-regulated genes are labeled. (c) Dotplot of GeneOntology gene set enrichment analysis of HLA-DR⁺NKG2C⁺ vs HLA-DR⁻NKG2C⁻ CD56^{dim}CD57⁺ NK cells of two donors, where y-axis represents GO molecular pathways (Biological Processes (BP) Cellular Component (CC)), separated by sign and x-axis gene ratio. The greater the size of a circle the greater the number of genes involved in a pathway the circles are colored based on p-adjusted value.