



**Supplementary Figure 2. Global transcriptomic analysis on primary CD49a<sup>+</sup> and CD49a<sup>-</sup> NK cells.** (A) Distribution by functional category of up- (red) or down-regulated (blue) genes in CD49a<sup>+</sup> NK cells compared to CD49a<sup>-</sup> NK cells. Genes with greater than a 2-fold difference were included. (B) Overview of functional pathway analysis. Enrichment of functional process pathways defined by Gene Ontology was generated using the BiNGO 3.0.3 plugin with Cytoscape 3.3.0. Red nodes describe processes targeted by up-regulated genes, while green nodes depict processes targeted by down-regulated genes. Number of the genes involved in the functional pathways is represented by the size of the nodes.