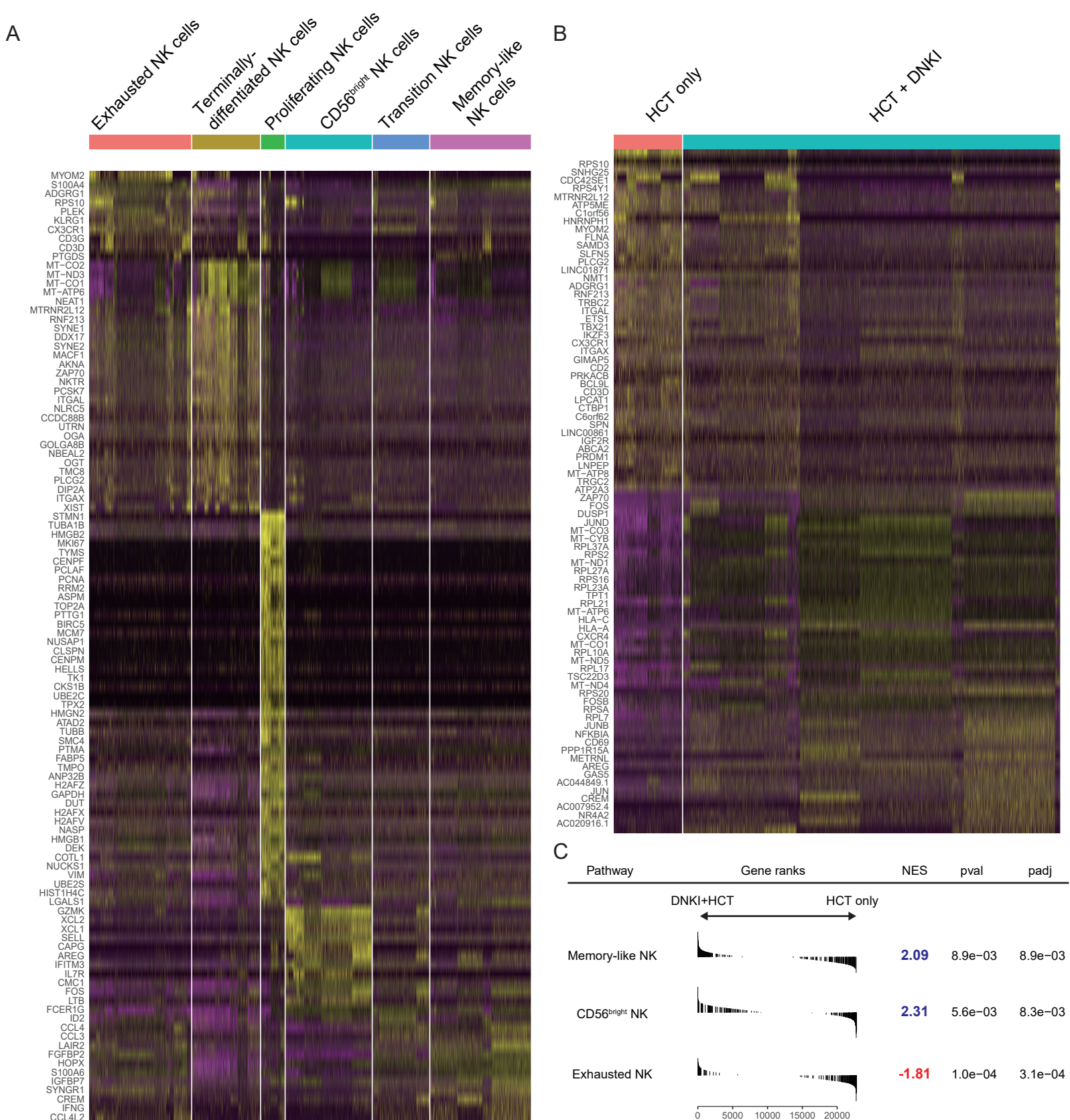




Supplementary Figure S3. Gene expression variations according to the NK cell subcluster and treatment group.

The heatmaps showing (A) the top 20 differentially expressed genes (DEGs) among exhausted, terminally-differentiated, proliferating, CD56^{bright}, transient, and memory-like NK cells and (B) the top 40 DEGs between treatments of HCT only vs HCT plus DNKI. (C) The gene set enrichment analysis (GSEA) showing the normalized enrichment score of NK cell subtype signatures (memory-like, CD56^{bright}, and exhausted NK cells) based on RNA sequencing.