

Figure S1. Verification of the differences in subsets of PBMCs in irradiated patients. (A) Heat map of differentially expressed genes in samples from irradiated patient and normal controls. (B) KEGG analysis of pathways involved in upregulated genes and downregulated genes. (C) The t-SNE map shows the different distribution of 6 clusters in Con, Stage 1, and Stage 2. The bars on the right show the number of cells in Con, Stage 1 and Stage 2 for the five cell types. PBMCs, peripheral blood mononuclear cells; KEGG, Kyoto Encyclopedia of Genes and Genomes; t-SNE, t-distributed stochastic neighbor embedding; Con, control.

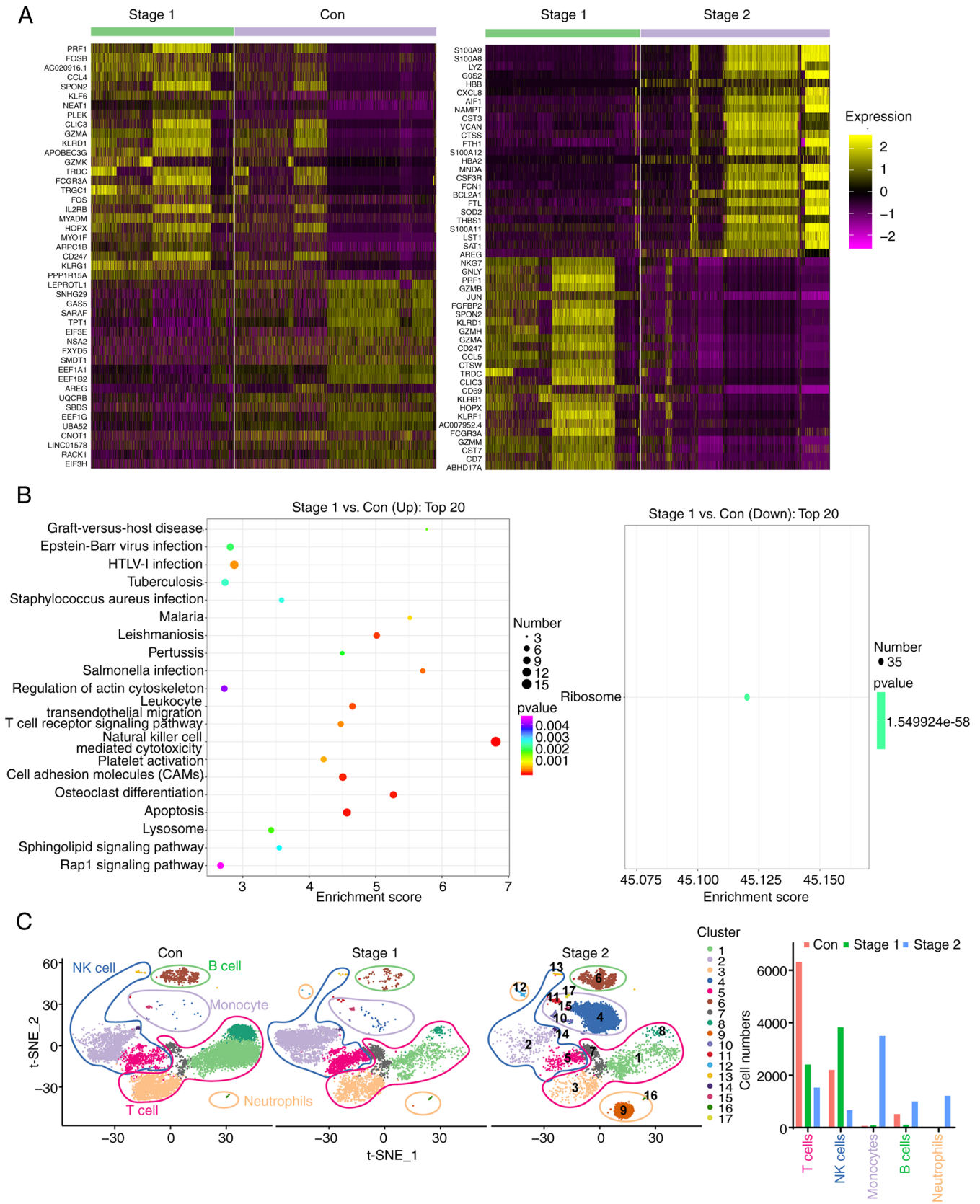




Figure S3. KEGG analysis of differential gene expression. (A) KEGG analysis of differential gene expression in NK cells. (B) KEGG analysis of differential gene expression in B cells. KEGG, Kyoto Encyclopedia of Genes and Genomes; NK, natural killer.

