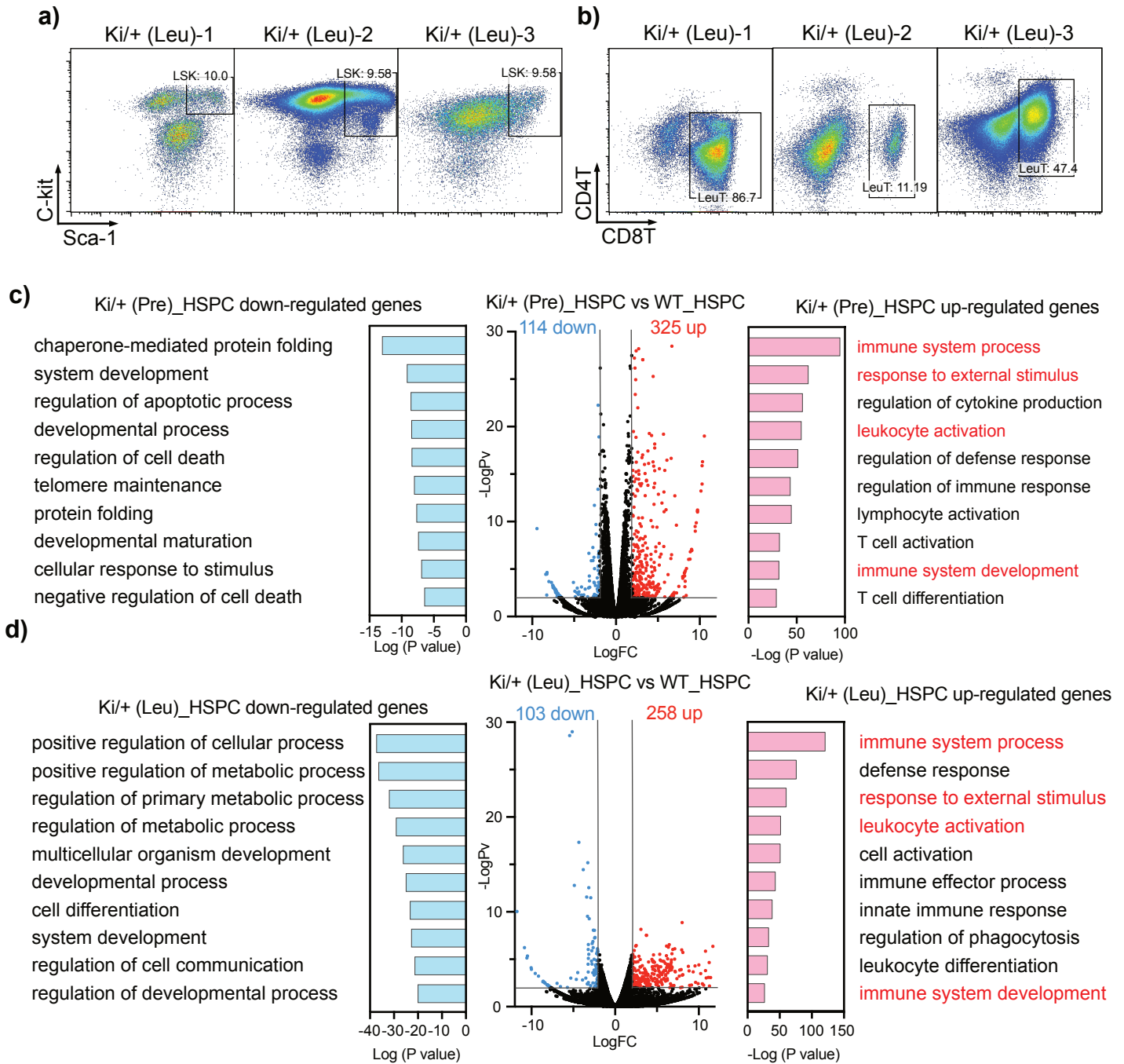


Figure S5: Additional RNA sequencing data for the WT, Ki/+ (Pre), and Ki/+ (Leu).



a,b) Representative FACS plots showing the HSPCs (a) and CD8⁺ T-cells (b) collected for RNA-seq in Ki/+ (Leu) from the recipients of the transplanted bone marrows (BMs).

c, d) Volcano plot showing differentially expressed genes (DEGs) in Ki/+ (Pre)_T cells versus WT_T-cells (c), Ki/+ (Pre)_HSPCs versus WT_HSPCs (d), and Ki/+ (Leu)_HSPCs versus WT_HSPCs (e) ($P < 0.05$ colored dots, WT $n = 2$, Ki/+ (Pre) $n = 2$, Ki/+ (Leu) $n = 3$).

f) Venn diagram showing the overlapping up- and down-regulated genes in Ki/+ (Pre)_HSPC (yellow), Ki/+ (Leu)_HSPC (pink), and Ki/+ (Leu)_T (green) mice compared to the WT. Representative gene clusters (c) and (d) were subjected to GO analysis. Terms commonly elevated in Ki/+(Pre) and Ki/+(Leu) are noted in red text.