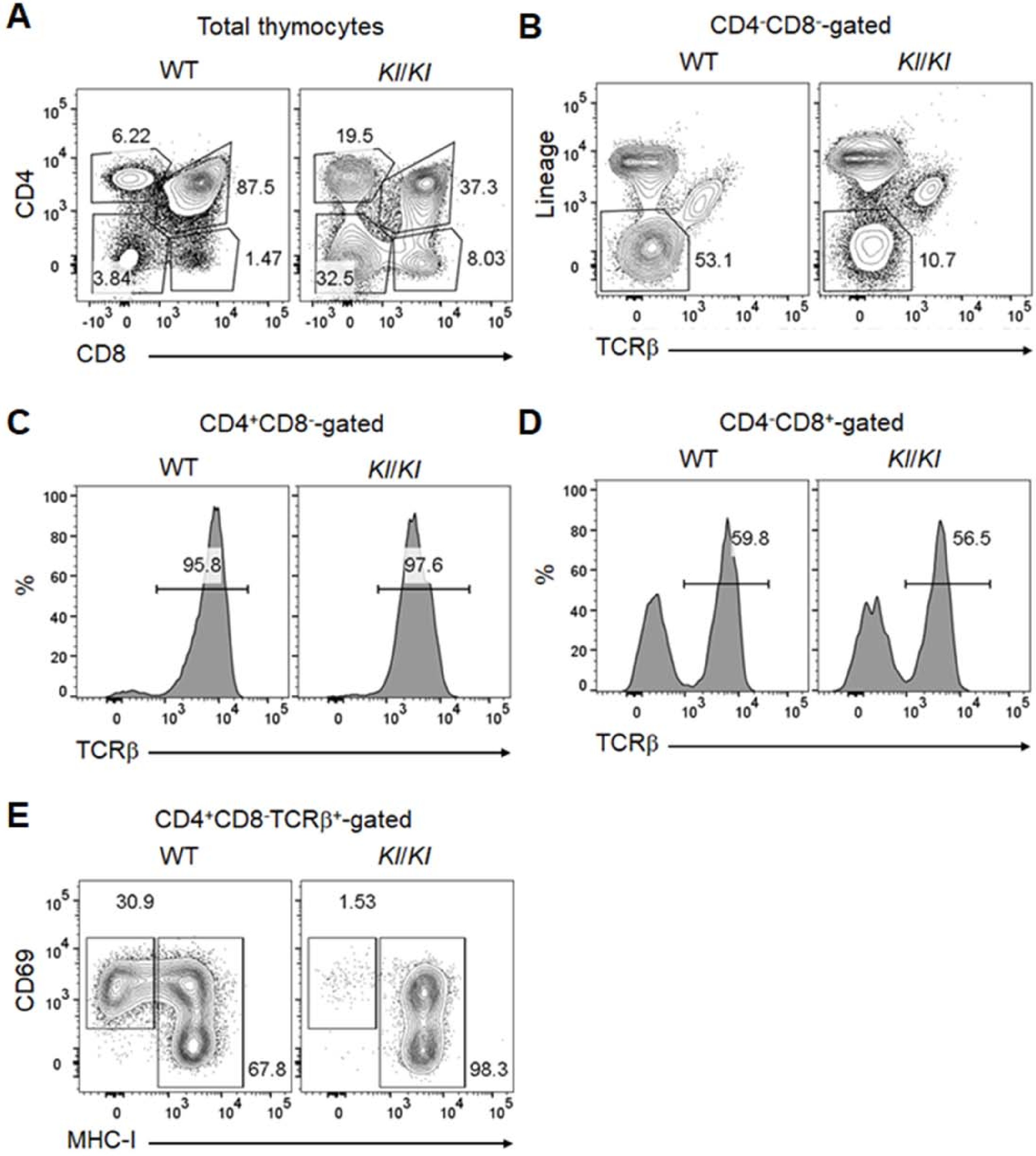
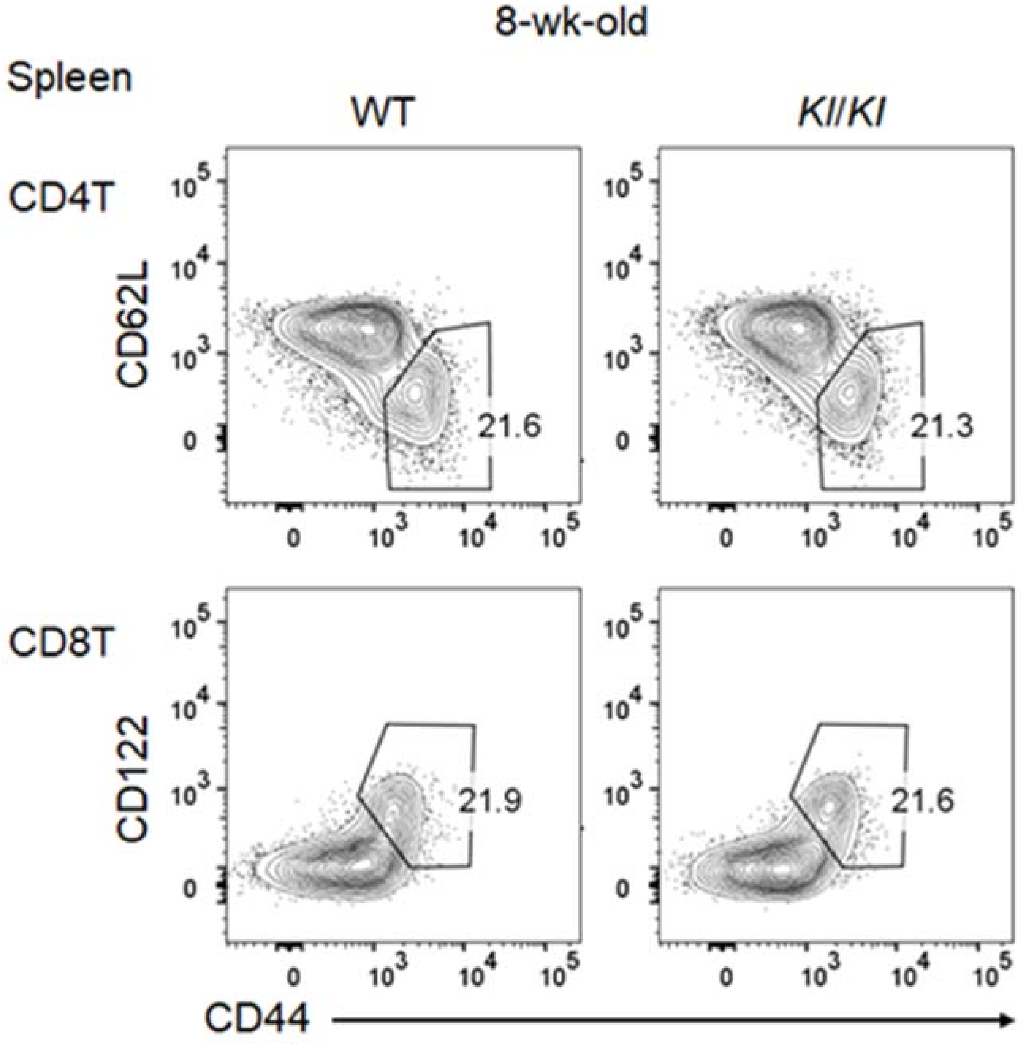
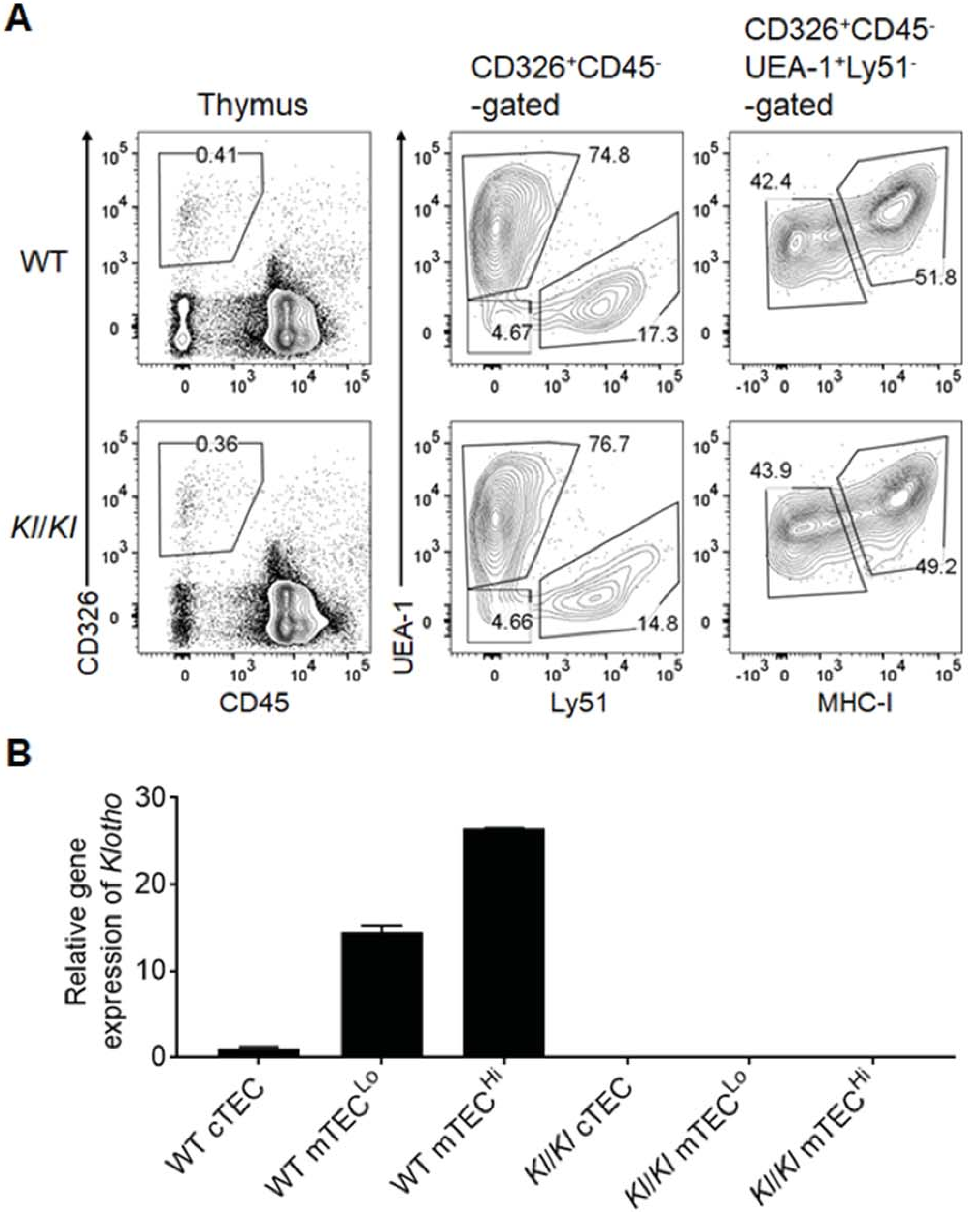


Supplemental Fig. 1. Gate strategy for identifying subpopulations of thymocytes on flow cytometric profiles. (**A**) Total thymocytes were identified by surface expression of CD4 and CD8 by flow cytometry. (**B**) DN population was defined by negative for CD4, CD8 and lineage markers. (**C**) CD4SP and (**D**) CD8SP were gated by TCRβ-positive. (**E**) Semi-mature (CD69^{+}MHC-I^{-}) and mature (CD69$^{+/-}$MHC-I^{+}) populations in CD4SP were identified by flow cytometry.



Supplemental Fig. 2. Gate strategy for identifying CD44^{hi} memory-like subpopulations in CD4T and CD8T cells in the spleen on flow cytometric profiles.



Supplemental Fig. 3. (**A**) Gate strategy for identifying cTEC (CD326^{+}CD45^{-}UEA-1^{-}Ly51^{+}), mTEC^{Lo} (CD326^{+}CD45^{-}UEA-1^{+}Ly51^{-}MHC-I^{Low}) and mTEC^{Hi} (CD326^{+}CD45^{-}UEA-1^{+}Ly51^{-}MHC-I^{High}) subpopulations in the thymus on flow cytometric profiles. (**B**) *Klotho* expression was quantified using real-time RT-PCR in the different populations. RNA was isolated from sorted cTEC, mTEC^{Lo} and mTEC^{Hi} subpopulations of 4-week-old WT and *Kl*/*Kl* mice. Quantitative gene expression data were normalized to the expression levels of a housekeeping gene, Glyceraldehyde-3-phosphate dehydrogenase (*Gapdh*).