

Austin et al., <http://www.jem.org/cgi/content/full/jem.20121061/DC1>

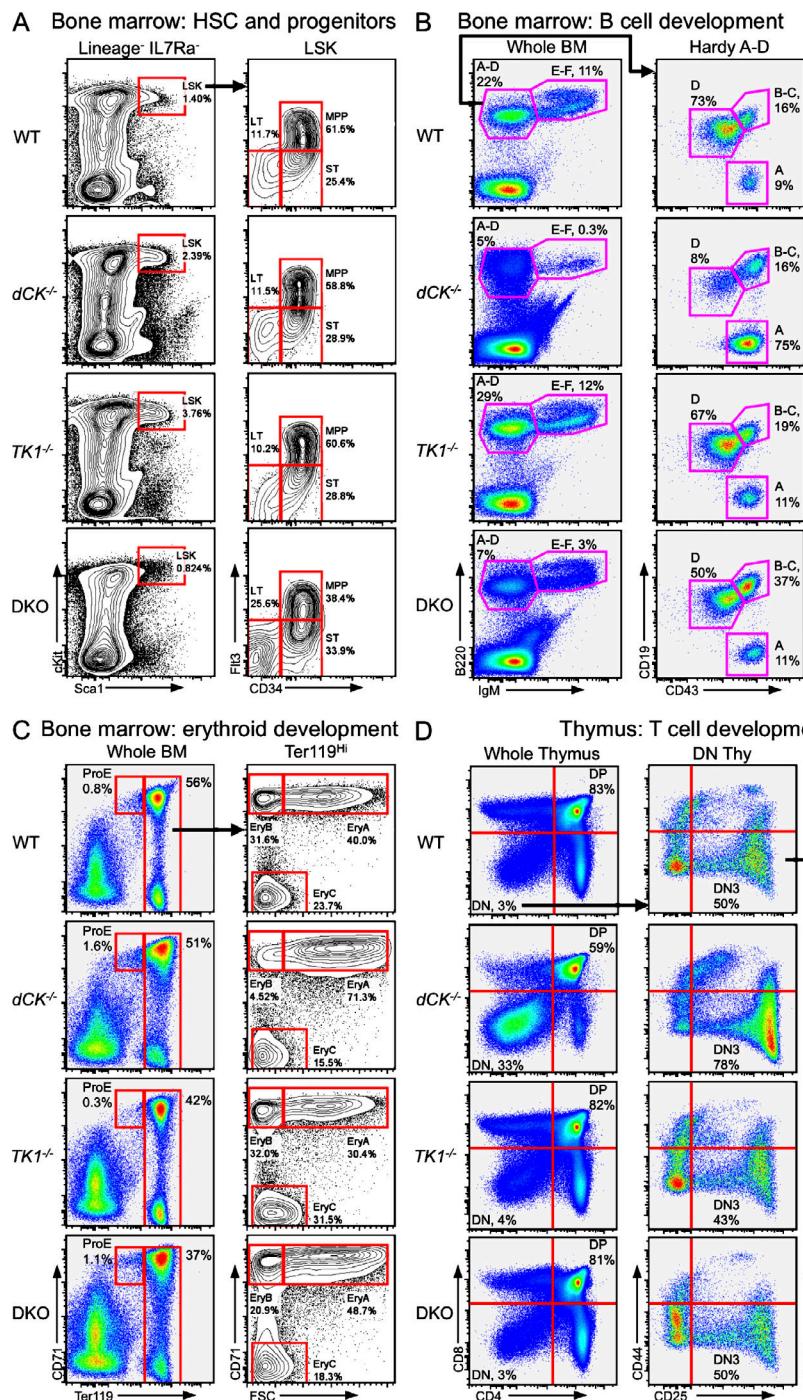


Figure S1. Flow cytometry gating strategies for various hematopoietic populations. (A) HSC and progenitors. Lineage⁻/IL-7Ra⁻ cells were identified from whole BM cells from WT, dCK^{-/-}, TK1^{-/-}, and DKO mice and were co-stained with Sca-1 and c-Kit antibodies to identify Lineage⁻ Sca-1⁺ c-Kit⁺ (LSK) populations. LSK cells were further sub-gated and analyzed for CD34 and Flt3 expression to identify long-term (LT), short-term (ST), and multipotent progenitor (MPP) hematopoietic stem cell populations. Representative plots from two independent stains/genotype. (B) B cell development. Whole BM from WT, dCK^{-/-}, TK1^{-/-}, and DKO mice was stained with B220 and IgM antibodies to identify Hardy fraction A-D and Hardy fraction E-F populations. Hardy fraction A-D cells were further sub-gated and analyzed for CD43 and CD19 expression to identify Hardy fraction A, Hardy fraction B-C, and Hardy fraction D populations. Representative plots from four independent stains/genotype. (C) Erythroid development. Whole BM from WT, dCK^{-/-}, TK1^{-/-}, and DKO mice was stained with Ter119 and CD71 to identify ProE and Ter119^{hi} populations. Ter119^{hi} cells were further sub-gated and analyzed for CD71 expression and forward scatter size (FSC) to identify EryA, EryB, and EryC erythroid populations. Representative plots from three independent stains/genotype. (D) T cell development. Whole thymocytes were stained with CD4 and CD8 to identify double-positive (DP) and double-negative (DN) populations. DN cells were further sub-gated and analyzed for CD25 and CD44 expression to identify the DN3 population. DN3 cells were further sub-gated and analyzed for CD25 and CD27 expression to identify DN3a and DN3b populations. Representative plots from four independent stains/genotype.