SUPPLEMENTAL MATERIAL

Satpathy et al., http://www.jem.org/cgi/content/full/jem.20120030/DC1

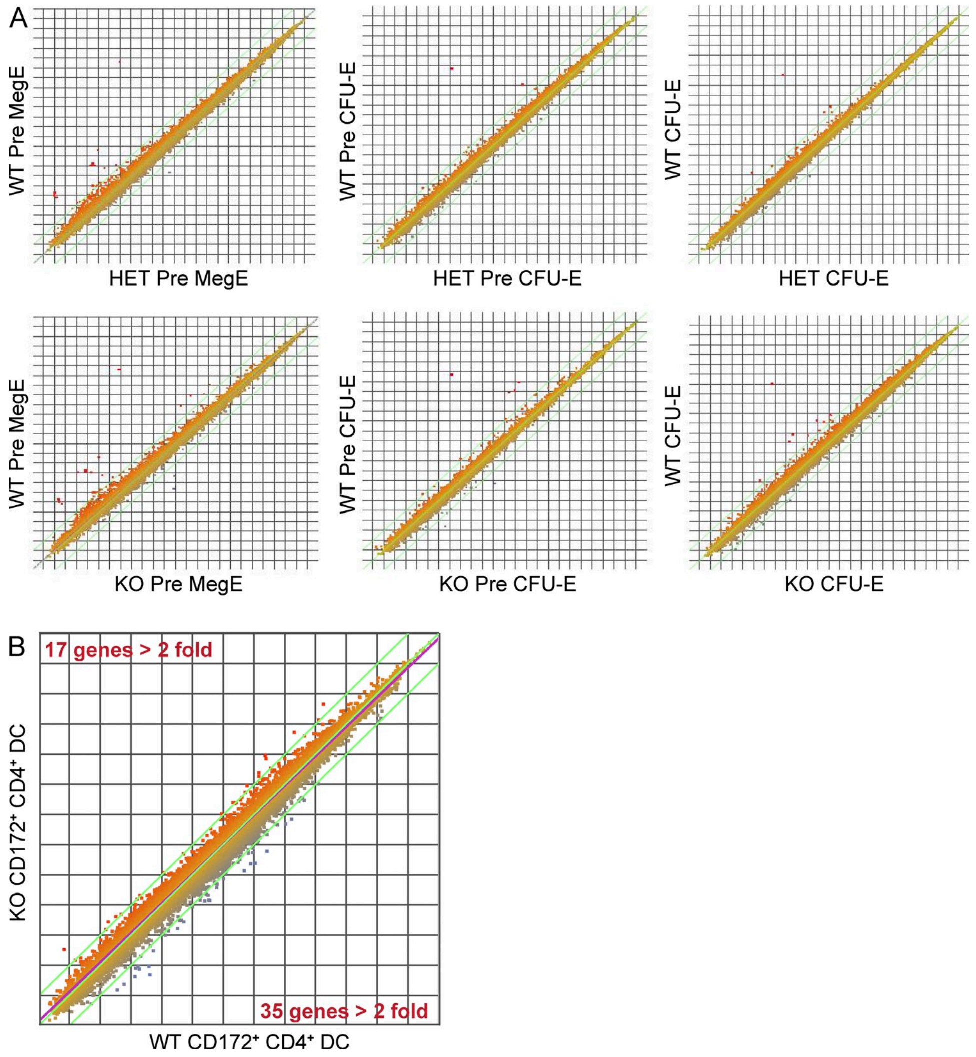

Figure S1. Microarray analysis of erythroid progenitors and CD4$^+$ DCs in *Zbtb46$^{gfp/gfp}$* mice. (A) *Zbtb46* does not impact the transcriptional profile of erythroid precursors. BM precursors from *Zbtb46$^{+/+}$* (WT), *Zbtb46$^{gfp/+}$* (HET), and *Zbtb46$^{gfp/gfp}$* (KO) mice were sorted into populations of pre-MegE, pre–CFU-E, and CFU-E (Pronk et al., 2007), and microarray analysis was performed. Shown are the M plots comparing WT samples with HET (top) or with KO samples (bottom) for the indicated cell type generated using ArrayStar software. Data represent analysis of cells harvested from three individual mice that were pooled for one array replicate per cell type. (B) Sorted steady-state splenic CD172$^+$CD4$^+$ cDCs from *Zbtb46$^{+/+}$* (WT) and *Zbtb46$^{gfp/gfp}$* (KO) mice were purified, and microarray analysis was performed. Shown is the M plot for all genes generated using ArrayStar software. Data represent analysis of cells harvested from three individual mice that were pooled for one array replicate per cell type. Green lines indicate equivalent expression between samples (center lines) or twofold change thresholds (outer lines).

REFERENCE

Pronk, C.J., D.J. Rossi, R. Månsson, J.L. Attema, G.L. Norddahl, C.K. Chan, M. Sigvardsson, I.L. Weissman, and D. Bryder. 2007. Elucidation of the phenotypic, functional, and molecular topography of a myeloerythroid progenitor cell hierarchy. *Cell Stem Cell*. 1:428–442. http://dx.doi.org/10.1016/j.stem.2007.07.005

S2 *Zbtb46* identifies the cDC lineage | Satpathy et al.