Figure S1

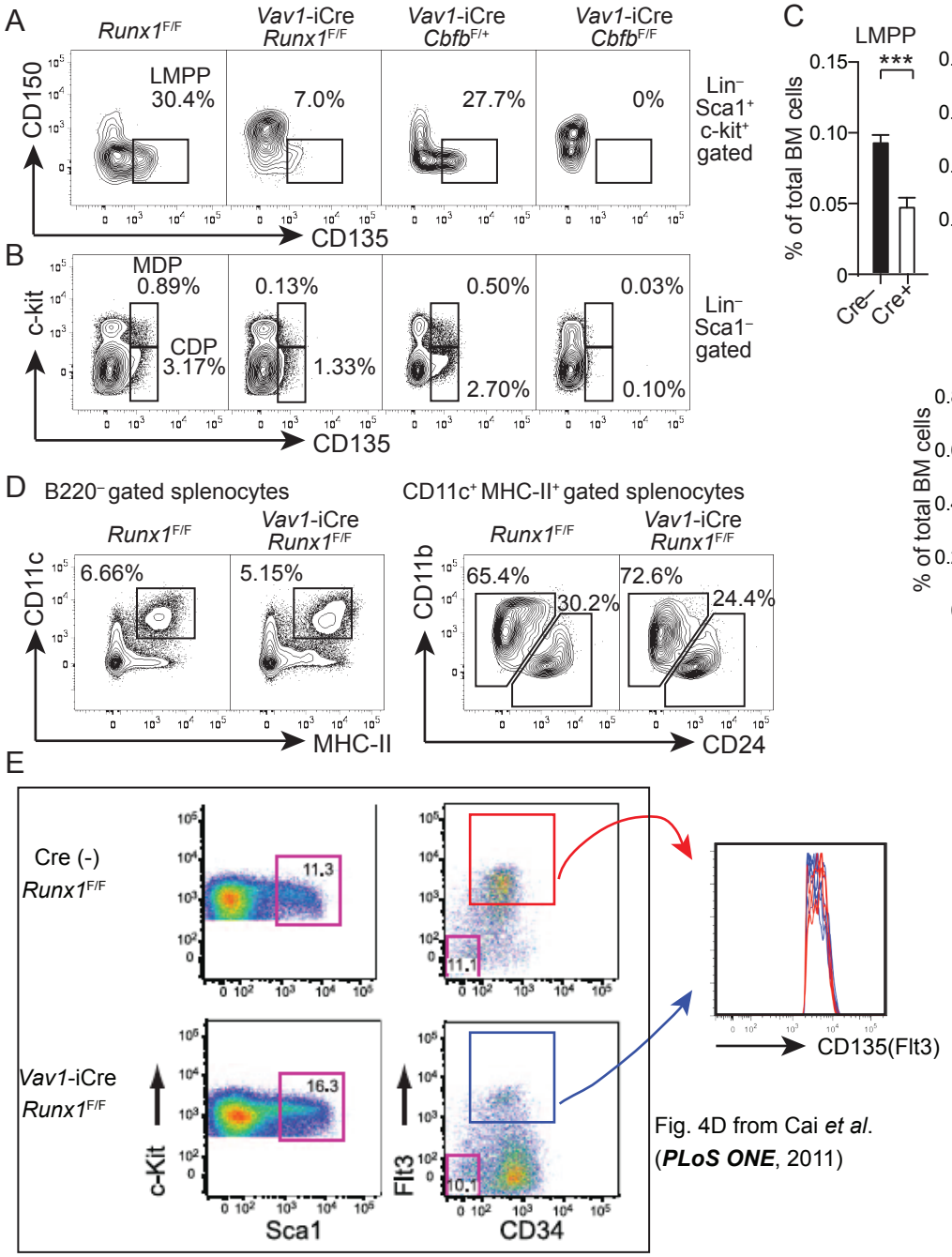

Fig. 4D from Cai *et al.* (***PLoS ONE***, 2011)

Figure S1. *Runx1* is required for the normal development of Flt3$^+$ MDPs but dispensable for mature DC development. (A - C) BM cells from *Runx1*-CKO (*Vav1*-iCre$^+$ *Runx1*$^{F/F}$, Cre$^+$) and control (*Runx1*$^{F/F}$, Cre$^-$) mice were analyzed for expression of lineage markers (B220, CD11b, MHC-II, CD16/32), c-kit, Sca1, CD150, and CD135 (Flt3). Frequencies of Flt3$^+$ Lin$^-$ Sca1$^+$ c-kit$^+$ (LMPP, **A**), Flt3$^+$ Lin$^-$ Sca1$^-$ c-kit$^+$ (MDP/CLP) and Flt3$^+$ Lin$^-$ Sca1$^-$ c-kit$^{lo/-}$ (CDP) populations **(B)** are shown with rectangle gates. Data from *Vav1*-iCre$^+$ *Cbfb*$^{F/+}$ and *Vav1*-iCre$^+$ *Cbfb*$^{F/F}$ mice analyzed at the same time are shown for comparison. Statistical analysis from three mice is shown as mean and standard deviation in (**C**). **(D)** Splenocytes from *Runx1*-CKO (*Vav1*-iCre *Runx1*$^{F/F}$) or control (*Runx1*$^{F/F}$) mice were analyzed for expression of B220, CD11c, MHC-II, CD11b, and CD24. CD11c$^+$MHC-II$^+$ cDCs in B220$^-$ gated splenocytes and CD11b and CD24 expression in cDCs are shown with rectangle gates and percentages. Data represents 6 mice per genotype. **(E)** Flt3 expression in Runx1-deficient LMPPs. A histogram overlay shows CD135 (Flt3) expression in LMPPs (Lin$^-$ Sca1$^+$ c-kit$^+$ Flt3$^+$) from *Vav1*-iCre$^+$ *Runx1*$^{F/F}$ (blue histograms) and control Cre (–) Runx1$^{F/F}$ (red histograms) mice. Data shown in Figure 4D of Cai *et al.* (***PLoS ONE***, 2011;6(12):e28430) were reanalyzed.

Figure S2

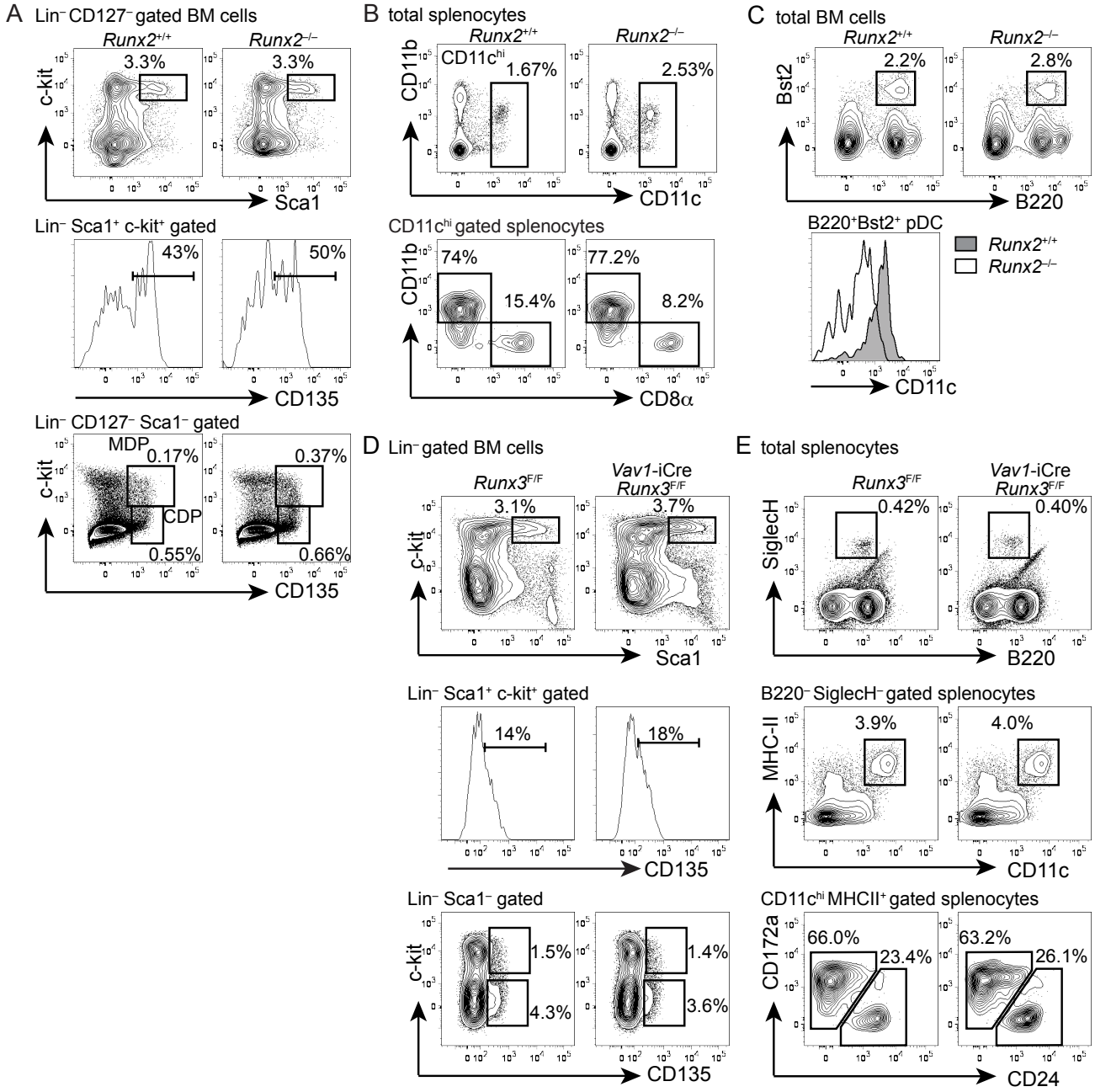

Figure S2. *Runx2* is required for CD11c expression in pDCs, but neither *Runx2* nor *Runx3* are necessary for cDC differentiation. **(A)** Frequencies of MPP, LMPP, Flt3$^+$ MDP, and CDP populations in irradiation chimeric mice reconstituted with *Runx2*$^{+/+}$ and *Runx2*$^{-/-}$ fetal liver cells. Data represent analysis of four recipient mice per genotype. **(B)** Splenocytes from *Runx2*$^{+/+}$ and *Runx2*$^{-/-}$ fetal liver chimeras were analyzed for CD11b, CD11c and CD8α expression. CD11c^{hi} DCs are gated with rectangles in upper panels with percentages of total splenocytes. Bottom panels show CD11b and CD8α expression in CD11c^{hi} cells, and percentages of CD8α$^-$ CD11b$^+$ DCs and CD8α$^+$ CD11b$^-$ DCs are shown. **(C)** BM cells from *Runx2*$^{+/+}$ and *Runx2*$^{-/-}$ fetal liver chimeras were analyzed for B220, Bst2 and CD11c expression. Bst2$^+$ B220$^+$ pDCs are shown with rectangles and their percentages of total BM cells are shown. The histogram depicts CD11c expression in gated pDCs. Data is representative of 4 mice with similar results. **(D)** Frequencies of MPP, LMPP, Flt3$^+$ MDP and CDP populations in *Vav1*-iCre *Runx3*$^{F/F}$ and control Cre(–) *Runx3*$^{F/F}$ mice. **(E)** Splenocytes from *Vav1*-iCre *Runx3*$^{F/F}$ and control Cre(–) *Runx3*$^{F/F}$ mice were analyzed for expression of B220, SiglecH, MHCII, CD11c, CD24 and CD172a expression. B220^{int} SiglecH$^+$ pDCs and B220$^-$ MHCII$^+$ CD11c^{hi} cDCs are gated with rectangles with percentages in total splenocytes shown. Bottom panels show CD24 and CD172a expression in B220$^-$ MHCII$^+$ CD11c^{hi} cells, and percentages of CD172a$^+$ (CD8α$^-$ CD11b$^+$) DCs and CD24$^+$ (CD8α$^+$ CD11b$^-$) DCs are shown. Data represent analysis of four mice per genotype with similar results.

Figure S3

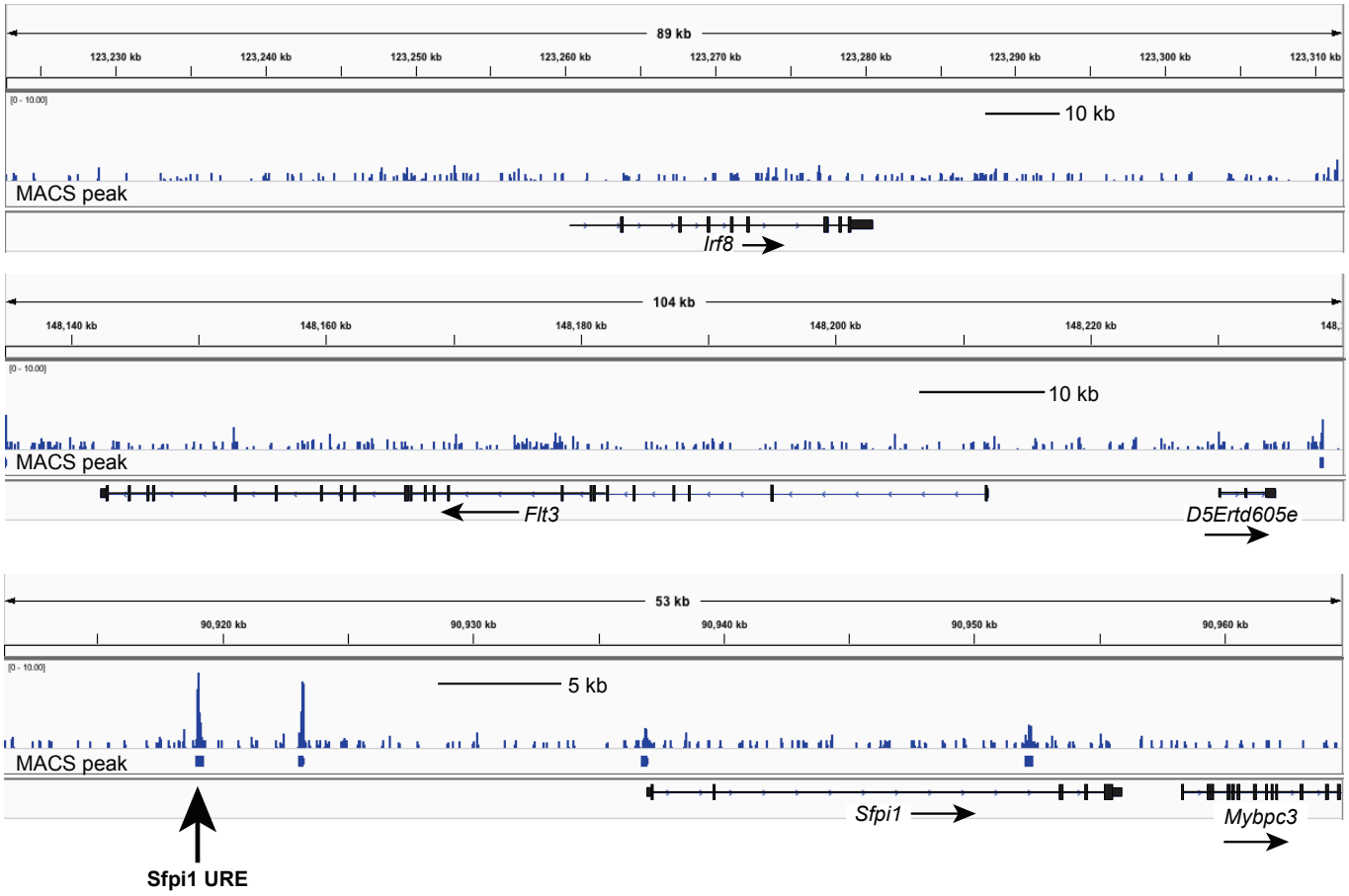

Figure S3. Reanalysis of a published dataset of genome-wide Runx1 binding profiles in a murine hematopoietic progenitor model cell line. Runx1 ChIP sequencing data from GSM552241 were mapped to the mouse genome mm9, and binding peaks were called using bowtie2-2 1.0 with a P-value of 1 x 10^{-6}. Histograms of Runx1-pulled binding tags encompassing *Irf8*, *Flt3* and *Sfpi1* loci are shown.