*Following text could be add after the text where we describe Figure 4A.*

…To investigate the relations between PU.1 and enhancer elements marked by H3K4me1, we examined the co-localization of PU.1 peaks and H3K4me1 footprints, which represent enhancer regions. We found an increasing overlap from 20% in MPP to 70% in cDC (Figure SxA), suggesting that PU.1 are more frequently binding to the enhancer elements during the DC specification. However, many enhancer elements seem to be independent from PU.1. To extend our analysis and to identify transcription factors that bind to PU.1 independent enhancer elements, we performed similar analysis based on H3K4me1 footprints (Figure SxB). Many PU.1 co-binding transcription factors identified in Figure 4A were recaptured here, except cDC-specific transcript factors, Rel, Nfkb1. Surprisingly, such analysis only identified two new transcription factors, Cebpa and Bhlhe40 (Figure SxB). Further enrichment analysis restricted on PU.1 independent H3K4me1 footprints identified much less transcription factors. Therefore, we decided to use PU.1 co-binding factors identified in Figure 4A for the following analysis….

*Following text could be added to methods.*

Histone modification footprinting: It was previously demonstrated that transcription factor binding sites are likely to occur between two regions with high levels of active histone marks (Hon, G. et al. 2009). These depletions are termed footprints. We used a modified version of the computational method described in (Gusmao, E.G. et al. 2014) to detect significant footprints in H3K4me1 data. The number of states of the hidden Markov model was reduced to include only background, histone-level and footprint states. Additional transitions were added from the histone-level DOWN state to the FOOTPRINT state and from the FOOTPRINT state to the histone-level UP state. The parameters of the model were estimated using data from H3K4me1 in a genomic region that was not present in further analyses. Given the lower resolution of ChIP-seq data and the nature of the probabilistic model, footprints from H3K4me1 tend to span larger regions than the functional depletion. Consequently, we have further reduced the footprints by considering only 250 bp upstream and downstream of its center.

Hon, G. et al. (2009). Discovery and Annotation of Functional Chromatin Signatures in the Human Genome. PLoS Comput Biol, 5(11), e1000566+.

Gusmao, E.G. et al. (2014). Detection of active transcription factor binding sites with the combination of DNase hypersensitivity and histone modifications. Bioinformatics, 30(22), 3143-3151.

*Figure Legend*

**Figure S. Enrichment of transcription factor motifs for the enhancer elements.**

**(A)** The overlap of PU.1 peaks with H3K4me1 footprints, which represent the enhancer elements, during DC development. **(B)** Heat map depicts the enrichment of transcription factor motifs in MPP, CDP, cDC and pDC based on H3K4me1 footprints. *P* values are plotted and color-coded using a continuous spectrum from gray (*p* value > 0.05) to blue (*p* value < 0.05). The genes were arranged according to their order in Figure 4A, with two newly identified transcription factors at bottom. **(C)** The enrichment analysis of transcription factor motifs based on PU.1-independent H3K4me1 footprints, which identified much less transcription factors.