Figure S1.  A representative gating strategy to define pDCs in the BM of Mtg16-deficient mice. Note the combination of multiple broad gates that accommodate lower expression levels of some markers (B220, Ly6C, and Bst2); also note that other markers (e.g., CD11c and SiglecH) are unaffected in Mtg16-null pDCs.
Figure S2. Characterization of DC progenitors. (A) Phenotypic definition of Lin− Sca1− Fit3+ progenitors in the BM of WT and Mtg16−/− (KO) mice. MDP, monocyte/DC progenitor. (B) Gating strategy to define subsets of pre-DCs in the BM of WT mice. (C) The progeny of SiglecH+ pre-DC subsets that were sorted and cultured with Flt3L. Note that the SiglecH+ Ccr9+ subset produced exclusively pDCs, whereas the SiglecH+ Ccr9− subset gave rise to pDCs and two cDC subsets.

Dataset S1, included as a separate Excel file, shows genome-wide expression analysis of Mtg16−/− pDCs.

Dataset S2, included as a separate Excel file, shows ChIP-Seq results for MTG16 and E2-2 in CAL-1 cells.