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Supplemental Figure S1

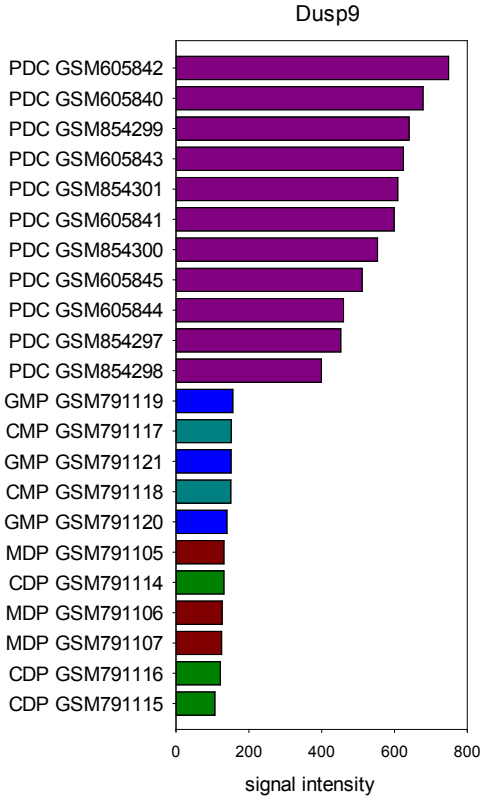

Fig. S1: Signal intensity values for the Dusp9 probeset for pDC and different progenitor cell types from the ImmGen Dataset GSE15907 were ranked.
pDC *(lilac),* GMP *(blue)*, CDP *(green),* CMP *(dark blue),* MDP *(deep red).*

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Supplemental Figure S2

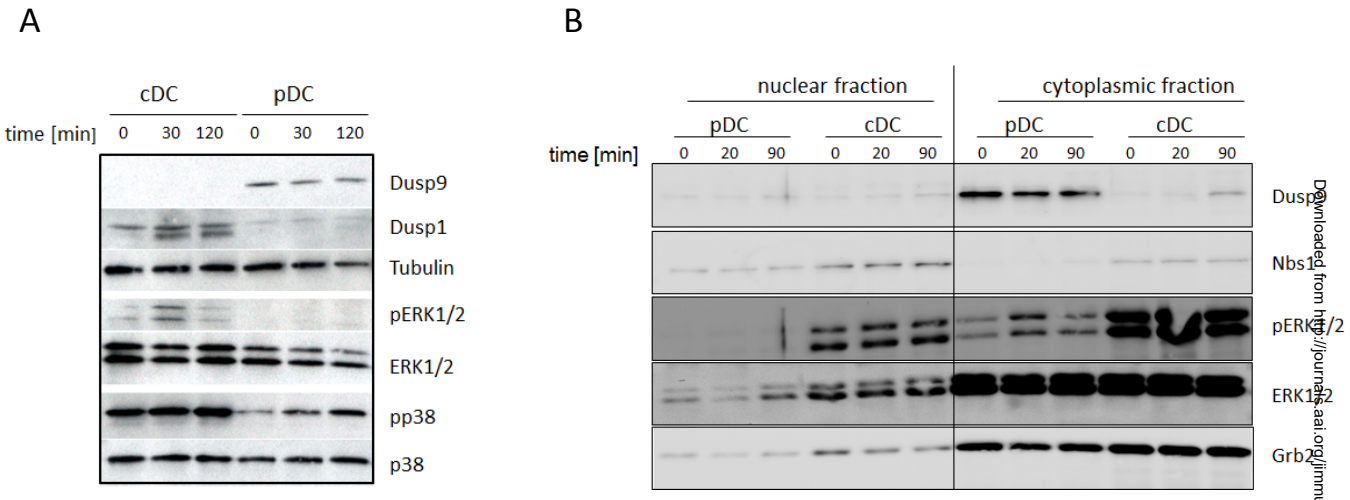

Fig. S2: Reduced phosphorylation of MAPK in pDC is not due to reduced total ERK1/2 or p38 levels. Western blot analysis of FACS-sorted pDC and cDC after stimulation with CpG ODN 1826.

(A) Total cell lysates were analysed with the indicated antibodies. Tubulin was used as control for equal loading.

(B) Nuclear and cytoplasmic fractions from equal numbers of pDC and cDC. Nbs1 and Grb2 were used to demonstrate subcellular fractionation and comparable loading.

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Supplemental Figure S3

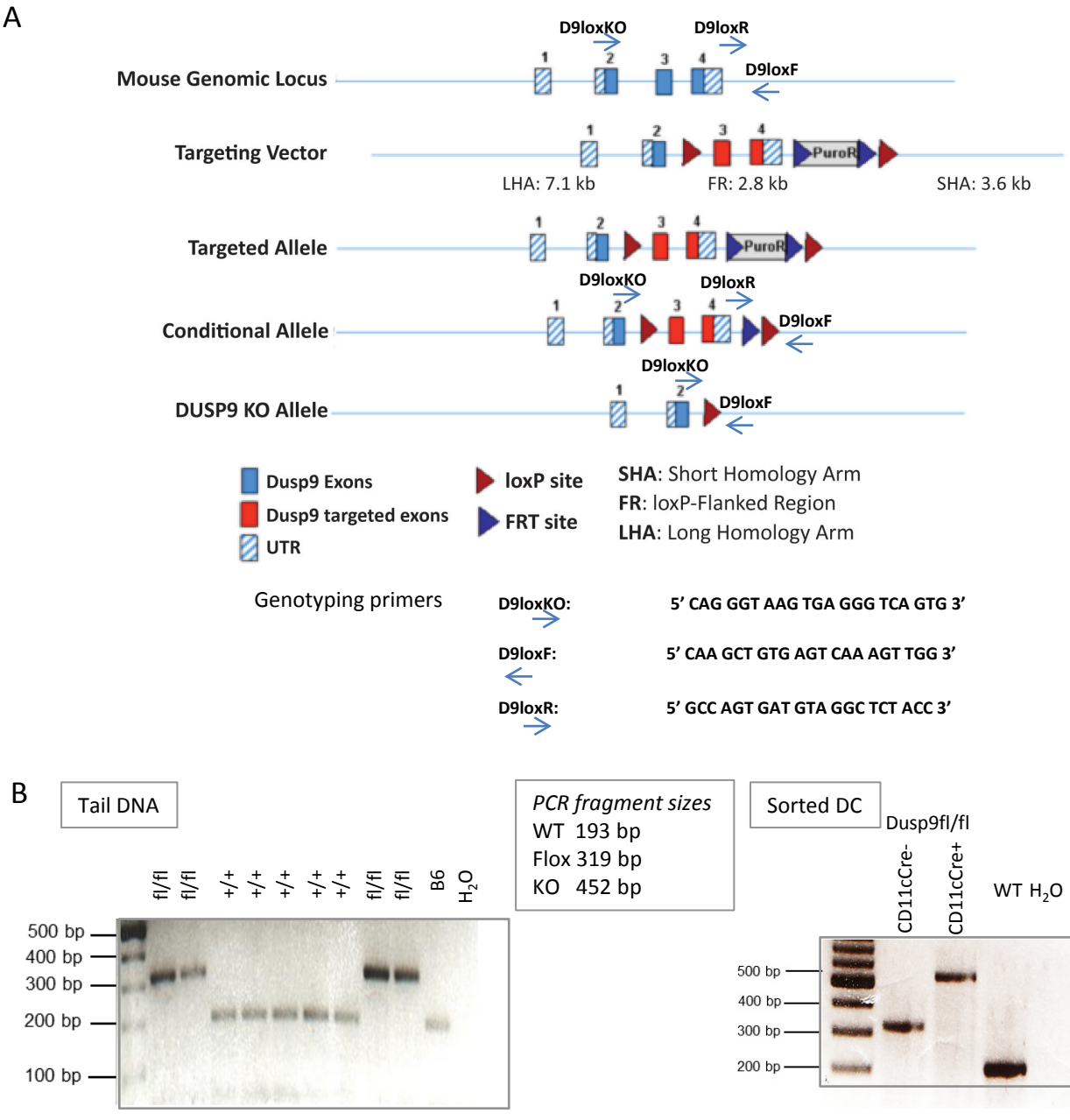

Fig. S3: Generation of mice with conditional deletion of Dusp9 in DC.

(A) Targeting strategy for insertion of *loxP* sites flanking exons 3 and 4 of Dusp9. The position of the primers used for genotyping is indicated.

(B) Results of genotyping PCRs from genomic DNA isolated from mouse tail biopsies (left) or DC (right). Fragment sizes correspond to expected amplification products for WT, the loxP-flanked conditional allele, or the Dusp9KO allele after Cre-mediated deletion in CD11c+ DC.

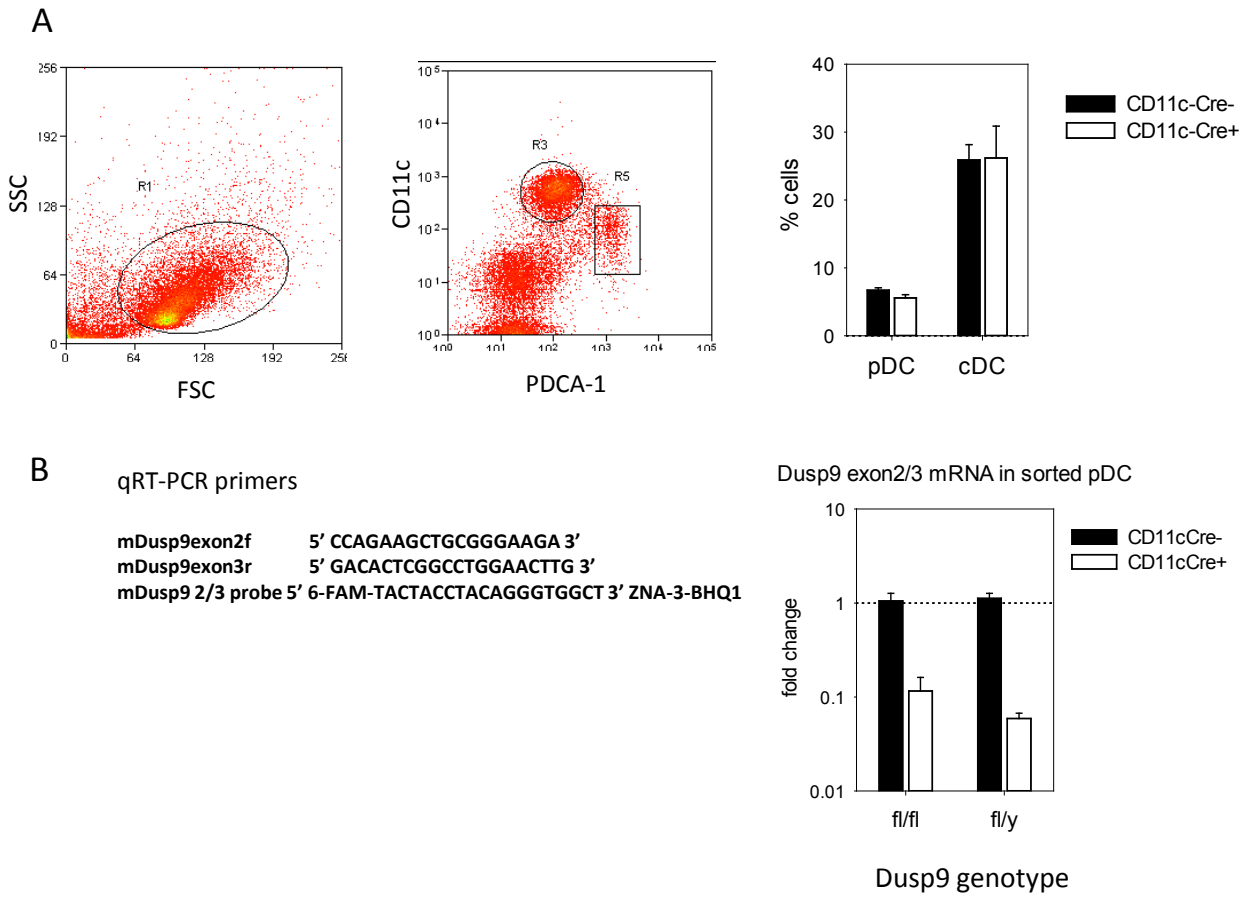

Fig. S4: FACS-sorting of pDC and cDC from conditional Dusp9KO splenocytes.

(A) 10 days after hydrodynamic injection of FL plasmid, splenocytes were stained and gated on cells (FSC/SSC, left), lack of CD11b expression (not shown), and sorted for cDC (R3: CD11c^{hi}, PDCA-1^{lo}) and pDC (R5: CD11c^{int}, PDCA-1^{hi}). Percentages of cDC and pDC among the CD11b- splenocytes comparing WT (CD11cCre-) and Dusp9KO (CD11cCre+) conditional Dusp9 mice. Mean and SEM, n=9 mice per genotype.

(B) Deletion efficiency assessed by Taqman qRT-PCR in sorted pDC. Sequences of primers and Taqman probe for amplification of a exon2/3 fragment not present after Cre-mediated deletion. CT values were normalized to Hprt, followed by calculation of fold change values using the male (fl/y) and female (fl/fl) CD1cCre- WT mouse as calibrator. Geometric mean and SEM. n=5 (males) and n=4 (females).