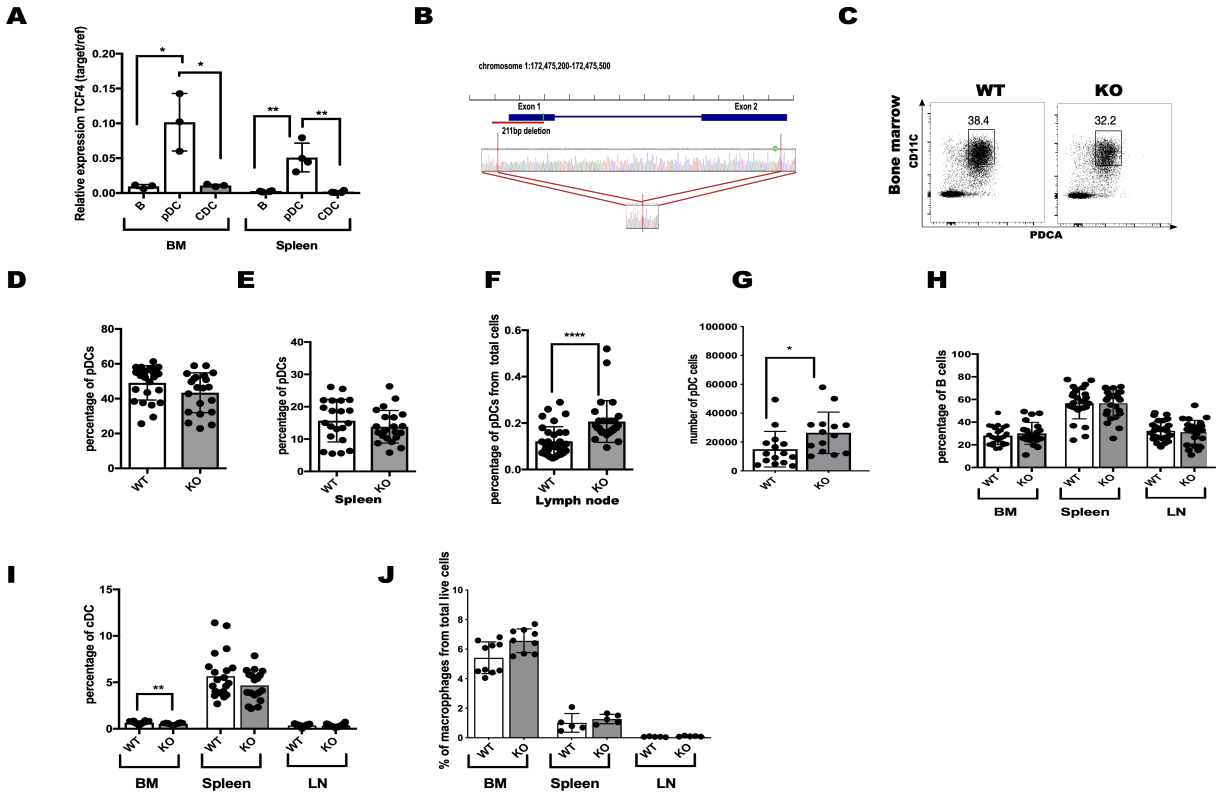


Fig S1- phenotypic characterization of splenic and BM pDCs in SLAMF9 -/- mice and illustration of deleted sequence in SLAMF9-/- mice.

(A) Sorted pDCs (CD19-CD11C^{inter}B220+PDCA+), B cells (CD19+ B220+) and cDCs (CD19-B220-CD11B+CD11C^{high}) were analyzed for the mRNA levels of TCF-4 by qRT-PCR. Graphs show relative expression of target gene/reference gene (L32); n=3 mice. **(B)** Schematic illustration of 211 bp deletion on chromosome one within the genomic region of the SLAMF9 gene. The blue bars indicate exon1 and exon2. Green vertical line within exon1 indicates the location of the initiator methionine. The deleted sequence is indicated between the inner red diagonal line. **(C-D)** Analysis of BM pDCs (CD19-CD11C^{inter}B220+PDCA+) in WT and SLAMF9-/- mice shown in a representative dot plot and a graphical view. **(E)** Graph shows the percent of pDCs in the spleen. Results are a summary of 6 independent experiments. n= 22 mice. **(F-G)** Analysis of lymph node WT and SLAMF9 -/- pDCs. Graph shows the percent of LN pDCs from total live cells (F) and absolute numbers of pDCs in the iLNs (G). Results are a summary of at least three independent experiments. n= 12-22 mice. **(H-J)** Analysis of LN B cells (CD19+ B220+) (H) and LN cDCs (CD19-B220-CD11B+CD11C ^{high}) (I) and macrophages (CD19-B220-CD11C-CD11B+Ly6G- F480+) (J) in WT or SLAMF9-/- mice.

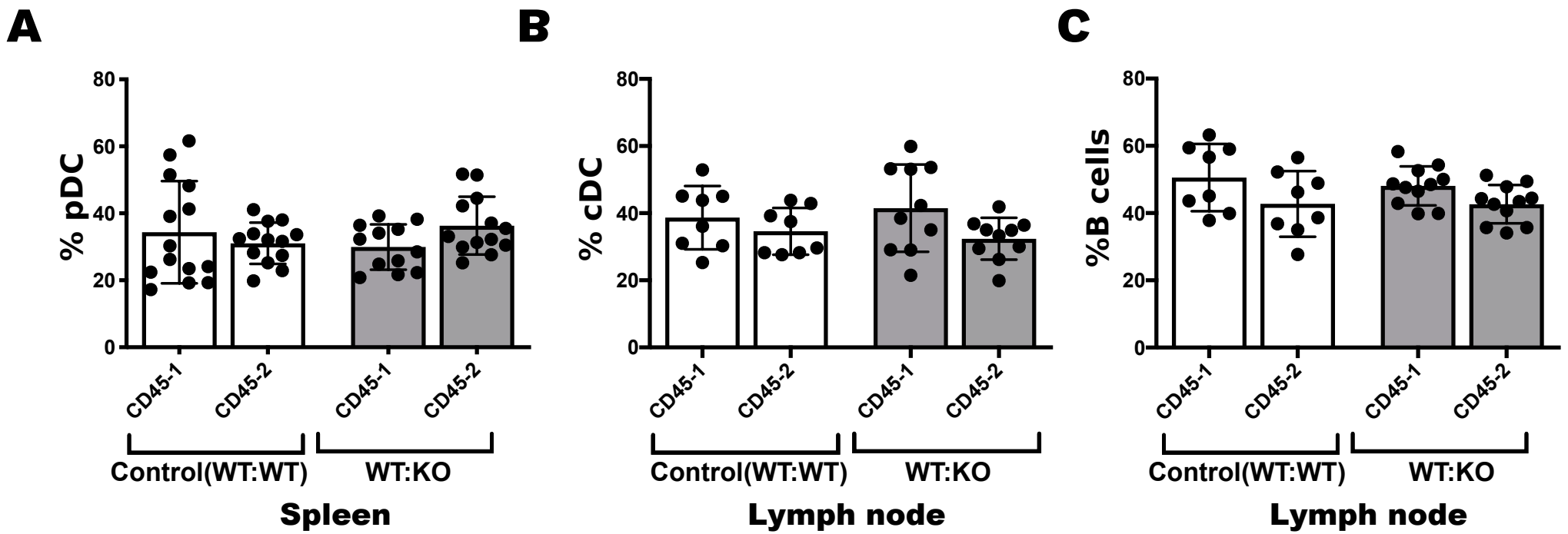


Fig S2 -B cell and CDC frequencies in chimeric mice

Lethally irradiated CD45.1 mice were transplanted with a total of $2x10^6$ BM cells from CD45.1 (WT) and CD45.2 (WT) mice, or from CD45.1 (WT) and CD45.2 (KO: SLAMF9-/-) mice at a 1:1 ratio. Mice were harvested 8 weeks post-transplant and splenic pDCs and cDC and B cell populations in the lymph node were analyzed. **(A)** Graph shows the percentage of pDCs in the spleen derived from CD45.1 and CD45.2 lineages in chimeric mice. **(B-C)** Graph shows the percentage of cDCs (B), or B cells (C) derived from CD45.1 and CD45.2 lineages in chimeric mice. Results are representative of experiments from three independent chimera. n=11-13 mice.

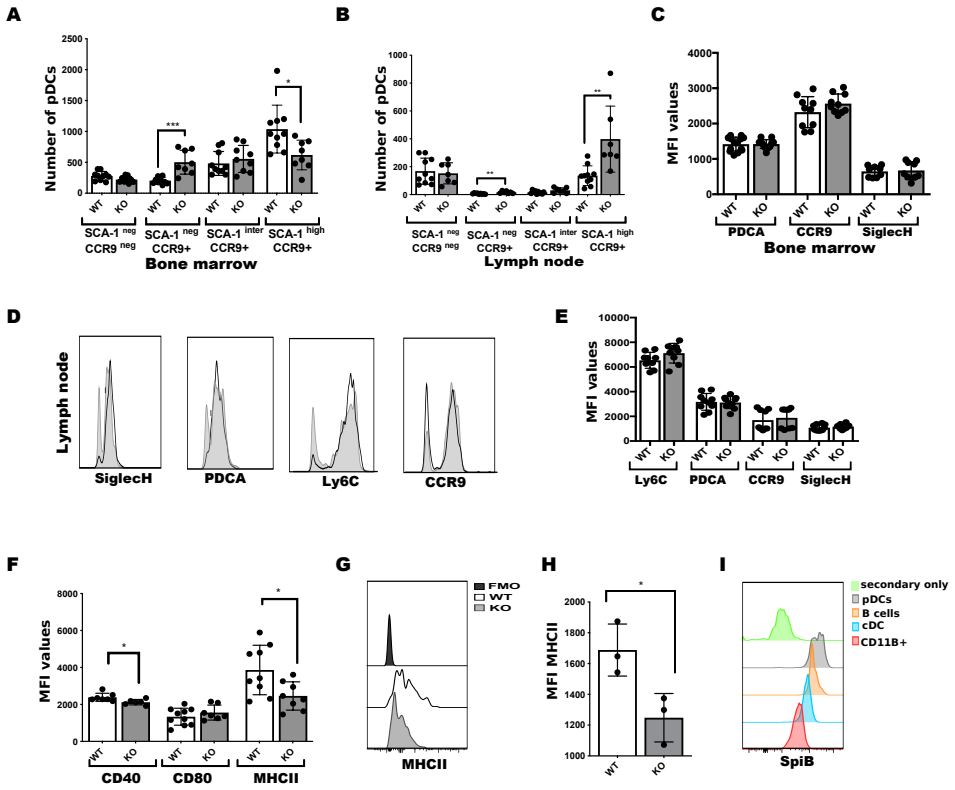
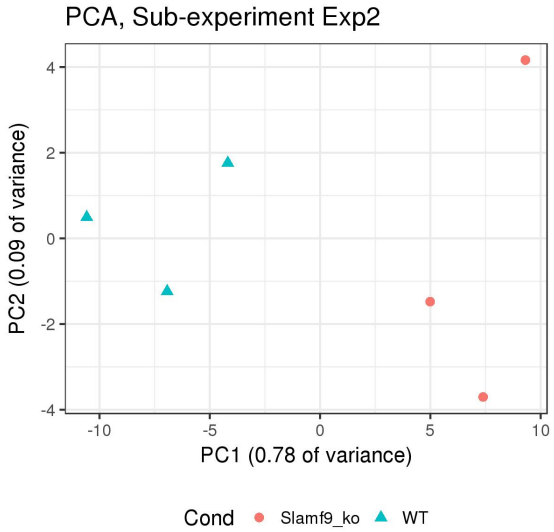


Fig S3- SLAMF9 -/- LN pDCs have similar activation markers

(A-B) pDCs were harvested from the BM and LN of WT and SLAMF9 -/- mice (KO). Graph shows the absolute numbers of pDCs subsets per 300,000 cells in the BM (A) and in the iLNs (B). **(C)** Graph shows the MFI values of pDC markers in the BM. **(D-F)** pDCs were harvested from the LN of WT and SLAMF9 -/- mice (KO). Representative histograms of staining and MFI values for pDC markers in LN of WT and SLAMF9 -/- pDCs (D-E) and MFI values of co-stimulatory markers in LN pDCs (CD19- CD11C^{inter}B220+PDCA+)(F). Results are a summary of three independent experiments. n=8-11 mice. **(G-H)** Analysis of MHC class II expression in pDCs from the LN (CD19-CD11C^{inter} B220+CCR9+SCA-1+CD11B-). Representative histogram of staining for MHC class II in WT and SLAMF9-/- pDCs compared with fluorescence minus one (FMO) control (G) and MFI values of MHC class II of WT and SLAMF9-/- pDCs (H).**(I)** Analysis of SPIB expression in immune cell population in the LN. Representative histogram of staining in B cells, cDC cells, pDCs and CD11B cells compared with negative control (only secondary).

A



B

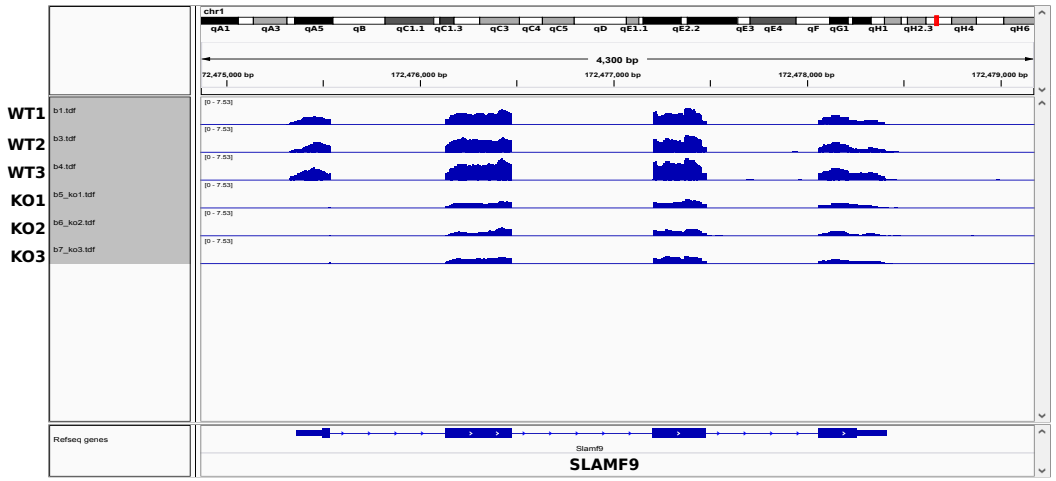


Fig S4-RNA- seq PCA analysis and IGV plots

BM pDCs (CD19-CD11B-CD11C ^{inter} B220+PDCA+) were sorted from WT and SLAMF9 -/- mice (KO). RNA was extracted and subjected to sequencing. Differentially expressed genes were identified by p value< 0.05 and fold change greater or equal to 1.5. **(A)** Principal component analysis (PCA) demonstrating distinct clusters for pDC samples obtained from WT and SLAMF9 -/- mice. **(B)** IGV image demonstrating deleted exon1 region in knockout samples after normalization of the coverage to the library size.

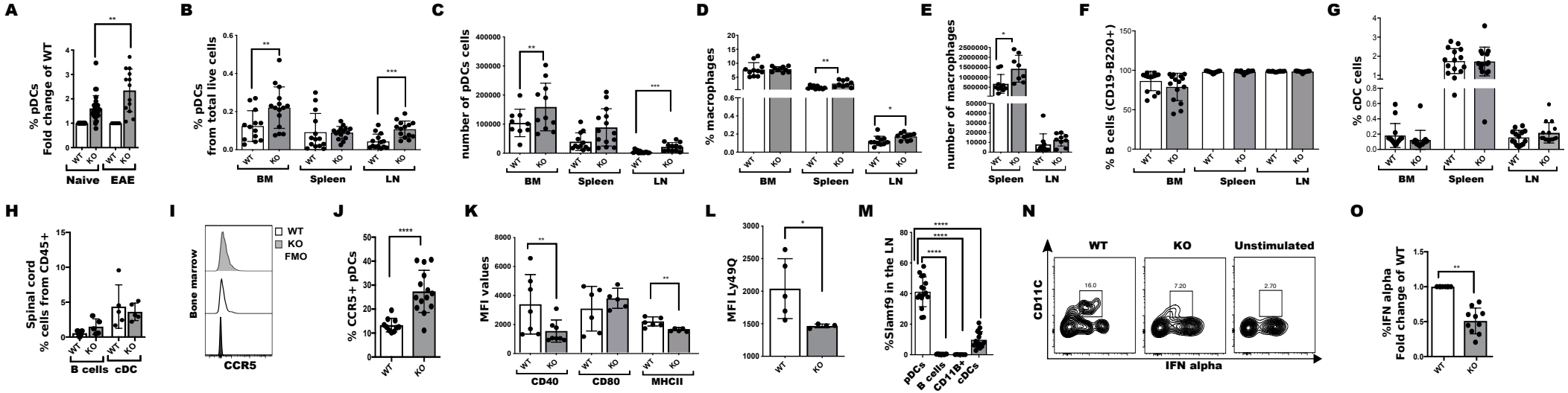


Fig S5-Analysis of cells following 14 days of EAE induction

EAE was induced in C57BL/6 WT and SLAMF9 -/- mice by subcutaneous injection of MOG33-55 peptide in complete Freund's adjuvant and further intraperitoneal injection of Pertussis toxin on days 0 and 2. **(A)** Graph shows the increase in SLAMF9 -/- pDCs (KO) compared to WT cells in healthy animals, and during EAE. **(B-C)** Analysis of pDCs in SLAMF9 -/- compared with WT mice in EAE. Graph shows the percent of pDCs (CD19- $CD11C^{inter}$ B220+PDCA+ CD11B-) from total live cells (B) and absolute numbers in the iLNs (C). **(D-E)** Analysis of macrophages in SLAMF9 -/- compared with WT mice. Graph shows the absolute numbers of macrophages in the spleen and lymph nodes (D) and the percent of macrophages (CD19-B220-CD11C-CD11B+Ly6G-F480) from total live cells (E) **(F-G)** Graph shows the percentages B cells (CD45+B220+CD11B-) and the percent of cDC (CD19-B220-CD11B+$CD11C^{high}$) (G). **(H)** Graph shows the percentages of cDC (CD45+$CD11C^{high}$ CD11B+) and B cells (CD45+B220+CD11B-) in the spinal cord, 16 days after EAE induction. Results are representative of two independent experiments; each dot represents two mice.
(I-J) Analysis of CCR5 levels in BM pDCs following 14 days of EAE induction. Representative histograms of CCR5 on WT and SLAMF9(-/-) pDCs compared with fluorescence minus one (FMO) control)(I) Graph shows the percent of CCR5+ pDCs in the BM (J). Results are representative of two independent experiments; n=10-14 mice; p****<0.0001. **(K-L)** Analysis of MFI values in WT and SLAMF9-/- pDCs in the LN.Graph shows MFI values of co-stimulatory markers in LN pDCs (K) and MFI values for Ly49Q (L). **(M)** SLAMF9 protein levels were analyzed in following 14 days post EAE induction in the LN. Graph shows protein expression in pDCs (CD19- $CD11C^{inter}$ B220+PDCA+ CD11B-), B cells (CD19+ B220+), cDCs (CD19-B220-CD11B+$CD11C^{high}$) and in macrophages (CD11B+$CD11C^{neg}$ CD19-SSC^{low}). **(N-O)** pDCs were freshly isolated at day 16 following EAE induction and stimulated for 18h with 1 µM of ODN1585. (N) Representative plot of IFNa levels on WT and SLAMF9(-/-) pDCs compared with unstimulated control. (O) Graph shows the fold of change in IFNa percent from WT following TLR9 stimulation. Results are representative of two independent experiments n=8-10 ;p****<0.0001.