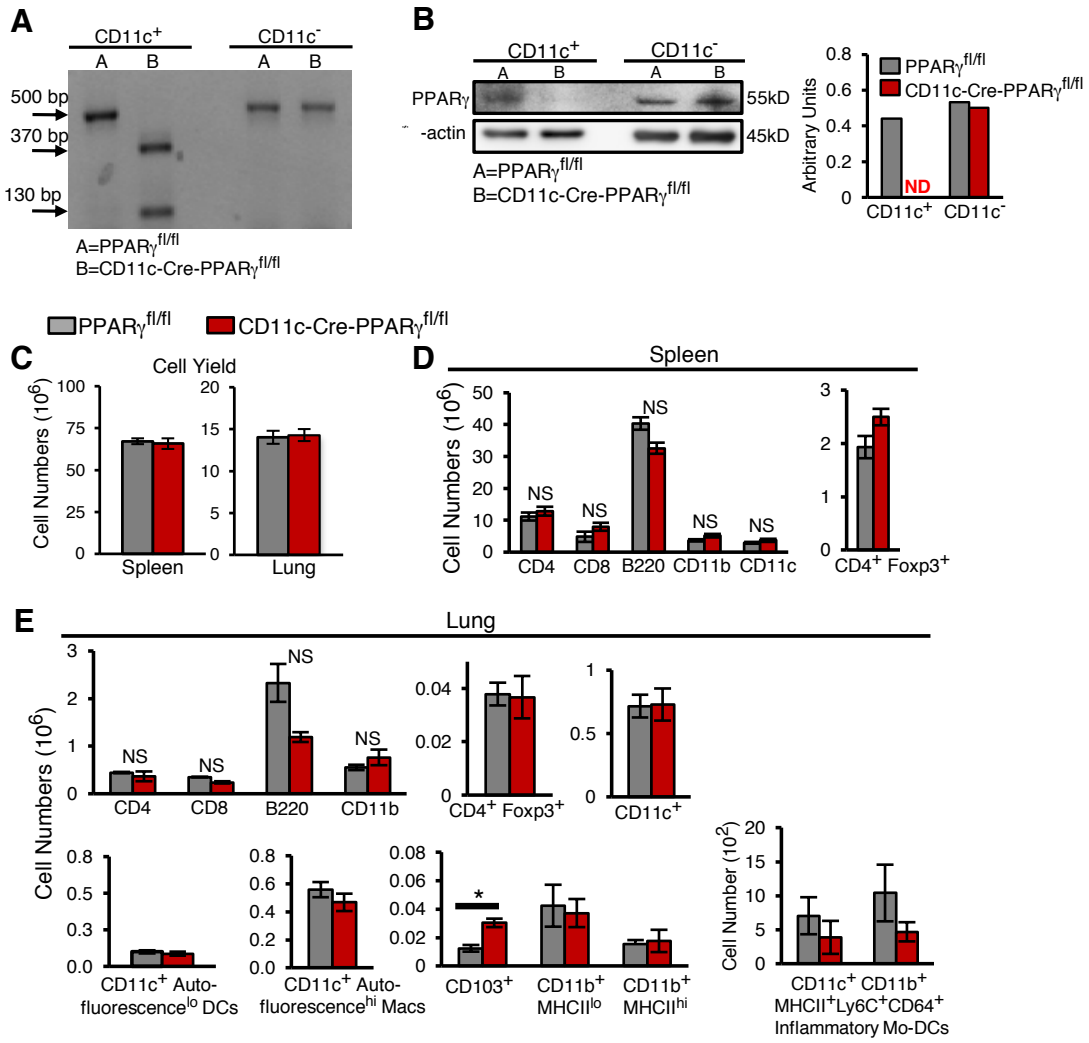
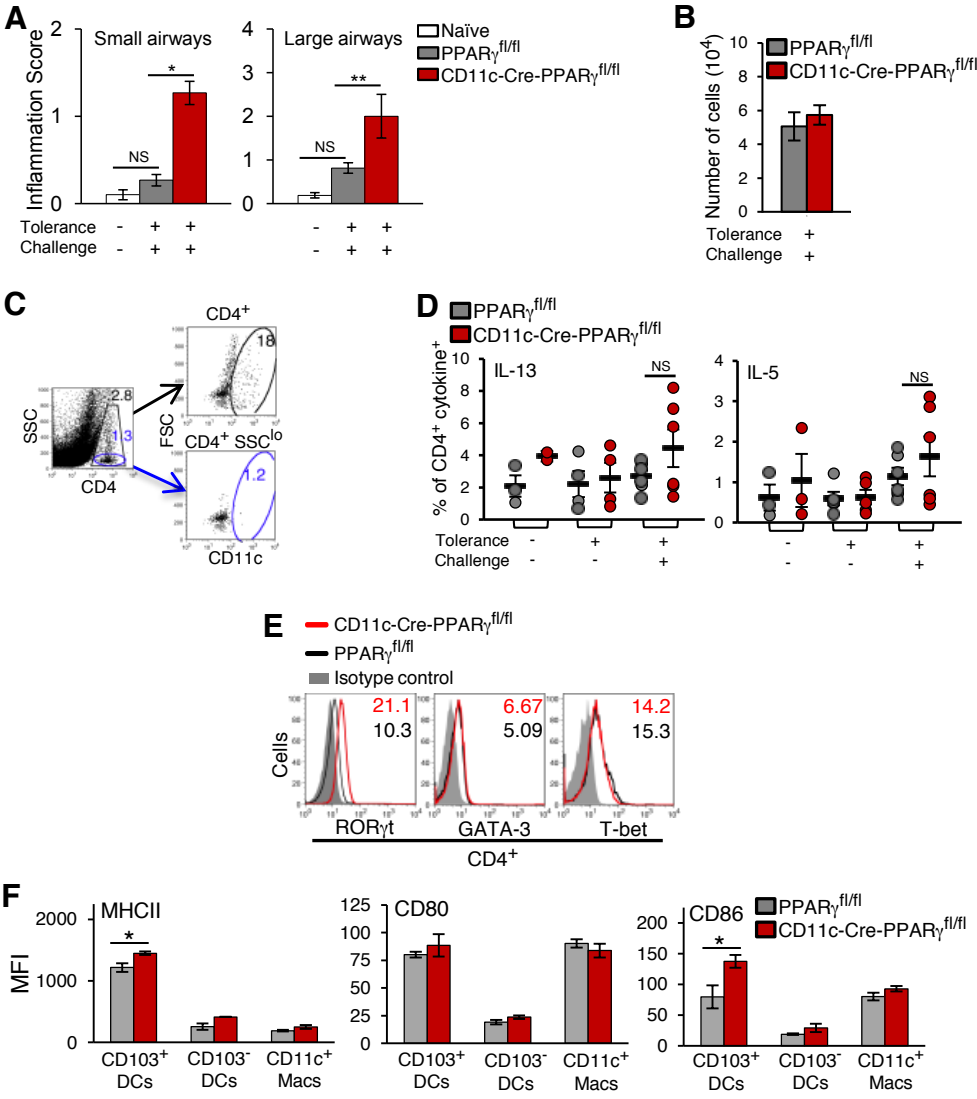


Supplemental Figure 1. Detection of different cell populations in the lungs and spleens of PPARγ$^{fl/fl}$ and CD11c-Cre-PPARγ$^{fl/fl}$ mice.

(**A**) Semi-quantitaitve RT-PCR showing cre-mediated deletion of exons 1 and 2 in the PPARγ gene in CD11c$^+$ cells from PPARγ$^{fl/fl}$ (Lane A) and CD11c-Cre-PPARγ$^{fl/fl}$ (Lane B) mice (primers: forward 5'-AGCGGTGAACCACTGATATTC-3' & reverse 5'-TTCAATCGGATGGTTCTTCGG-3)'. Arrows indicate the full (500 bp) and recombined (370 and 130 bp) RT-PCR products. (**B**) Western blot analysis and associated densitometry of PPARγ protein in sorted lung CD11c$^+$ and CD11c$^-$ cells from PPARγ$^{fl/fl}$ (Lane A) and CD11c-Cre-PPARγ$^{fl/fl}$ (Lane B) mice. (**C**) Total cell yields from spleen and lungs. (**D and E**) Flow cytometry-based identification and enumeration of various lymphoid and myeloid cell populations in the (**D**) spleen and (**E**) lung. All data are representative of two independent experiments and combined as mean ± SD. *P< 0.05, NS= not significant.



Supplemental Figure 2. PPARγ deletion in CD11c$^+$ cells potentiates lung inflammation. (**A**) Inflammation was scored semi-quanitatively in five small and four large airways of PAS stained lung sections of naïve (4), PPARγ$^{fl/fl}$ (4) and CD11c-Cre-PPARγ$^{fl/fl}$ (3) mice from two independent experiments, subjected to indicated conditions. Data shown as mean± SEM. Inflammation scoring criteria (peribronchial): 0=no cellular inflammation, 1=few cells; cuffing, 2=1-5 rings of cells surrounding airway and 3=5 rings of cells surrounding structure. (**B**) BAL cell differential counts for macrophages in CD11c-Cre-PPARγ$^{fl/fl}$ and PPARγ$^{fl/fl}$ mice subjected to the indicated condition. (**C**) Gating strategy for lung CD4$^+$ T cells. Based on the light scatter properties and expression of CD11c and CD4 surface marker, lung CD4$^+$ T cells were identified as CD4$^+$SSC^{lo} cells. (**D**) IL-13 and IL-5 expression in lung CD4$^+$ T cells from mice subjected to the indicated conditions. Data shown are representative of two independent experiments; symbols in the graphs represent data from individual mice (n=3 mice/group), horizontal lines represent mean and error bars denote SEM. (**E**) Expression of transcription factors RORγt, GATA-3 and T-bet in lung CD4+ T cells from PPARγ$^{fl/fl}$ and CD11c-Cre-PPARγ$^{fl/fl}$ mice (n=6) subjected sequentially to tolerance and inflammation models. Numbers shown represent mean fluorescence intensities (MFIs). (**F**) Expression of MHCII, CD80 and CD86 on different CD11c$^+$ subsets shown as mean ± SD of MFIs assessed by flowcytometry. *P< 0.05, **P<0.01, NS=not significant.