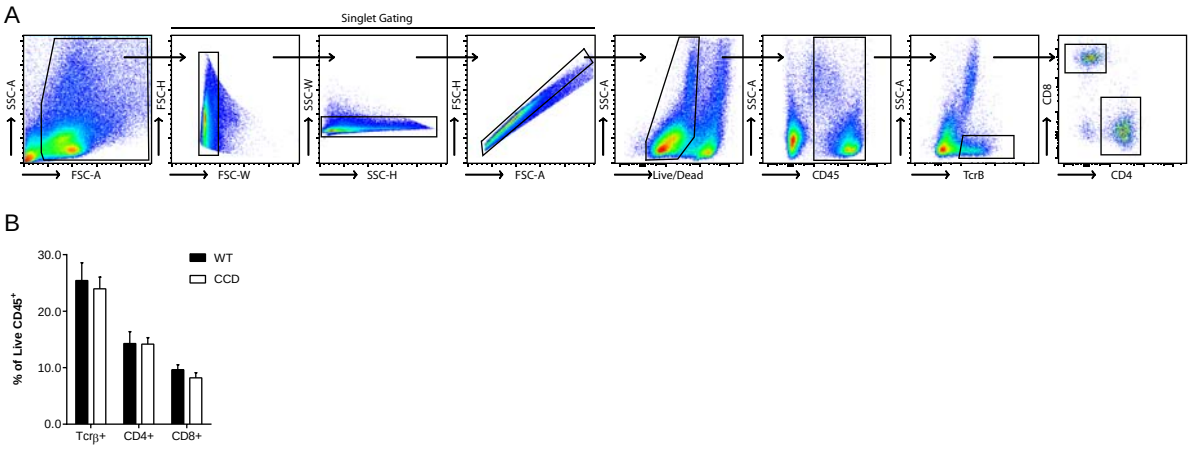

Figure S1. Inhibition of Notch signaling does not significantly alter the percentage of T cells in the lungs during cryptococcal infection. (A) Schematic of gating strategy used to identify Tcrβ$^+$ CD4$^+$ and CD8$^+$ T cells in the perfused lungs of *C. neoformans* infected mice. (B) Percentage (of CD45$^+$) of all Tcrβ$^+$, Tcrβ$^+$ CD4$^+$ and Tcrβ$^+$ CD8$^+$ T cells in the lungs of infected mice at 4 weeks post infection. Data shown are the mean frequencies ± SEM from 1 of 3 independent experiments with n=5-6/group and were not significantly different.

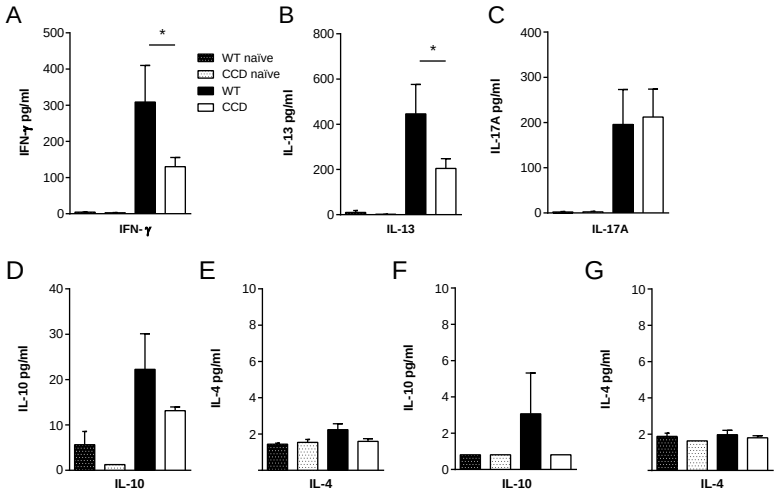

Figure S2. Inhibition of T cell restricted Notch signaling reduces spontaneous Th1 and Th2 cytokine production in the lungs of mice with cryptococcal infection in the absence of exogenous re-stimulation. (A-C) Leukocytes were isolated from perfused naïve and infected lungs at 4 wpi ($5x10^6$/ml) and cultured for 24 hours. Cytokine levels in supernatants were measured by ELISA and cytometric bead assays. Data are the mean ± SEM with n=4-24 mice per group. *$p<0.05$ (D-G) Inhibition of T cell restricted notch signaling does not significantly reduce IL-4 and IL-10 production in the lungs of mice with cryptococcal infection, even following re-stimulation. Leukocytes were isolated from perfused naïve and infected lungs (D-E) and spleens (F-G) at 4 wpi ($5x10^6$/ml) and stimulated with heat-killed *C. neoformans* ($10x10^6$/ml) at a 2:1 ratio for 24 or 48 hours, respectively. Cytokine levels in supernatants were measured by ELISA and cytometric bead assays. Data are the mean ± SEM with n=3-7 mice per group.

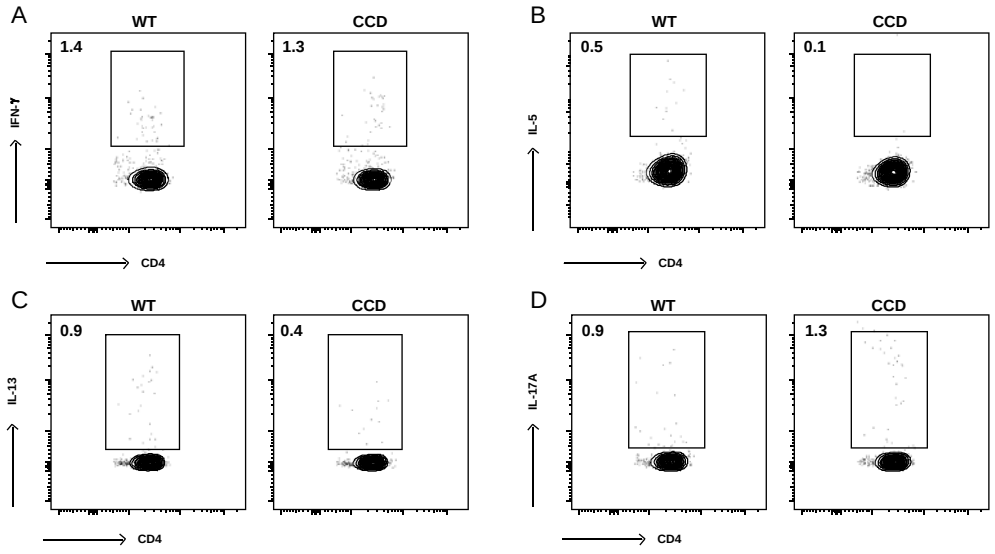

Figure S3. Cytokine production by T cells from the lungs of naïve mice. Lung leukocytes were isolated from perfused naïve CCD and WT mice then stimulated with plate bound anti-CD3 and anti-CD28 antibodies and analyzed for the proportion of cells producing (A) IFN-γ, (B) IL-5, (C) IL-13 and (D) IL-17A by flow cytometry, as described in Figure 5. Representative plots shown are gated on Live, $CD45^+$, $TCR\beta^+$ $CD4^+$ T cells and FMO controls were used to set cytokine gates. The percentages of cells in the positive gate are indicated.

Supplementary Table 1. List of primers used to quantify gene expression by qRT-PCR.

Gene Name	Primer Sequences
Arg1	*5'-CTAAGGACAGGCCAACAGAA-3'* and *5'-CAAACTTCCATCCTCCTCCAATG-3'*
Fizz1	*5'-TTCTTGCCAATCCAGCTAAC-3'* and *5'-GGGTTCTCCACCTCTTCATT-3'*
Foxp3	*5'- CACCCAGGAAAGACAGCAACC-3'* and *5'-GCAAGAGCTCTTGTCCATTGA -3'*
Gapdh	*5'-TATGTCGTGGAGTCTATTGGT-3'* and *5'-GAGTTGTCATATTTCTCGTGG-3'*
Gata3	*5'-AGAACCGGCCCCTTATCAA-3'* and *5'-AGTTCGCGCAGGATGTCC-3'*
Nos2 (iNos)	*5'-GGCAGCCTGTGAGACCTTTG-3'* and *5'-GCATTGGAAGTGAAGCGTTTC-3'*
Rorc	*5'-TGTGGTTGTTGGCATTGTAG-3'* and *5'-CCAGCTACCAGAGGAAGTCA-3'*
Tbx21 (Tbet)	*5'-CAACAACCCCTTTGCCAAAG-3'* and *5'-TCCCCCAAGCAGTTGACAGT-3'*
Chil4 (Ym2)	*5'-CAGAAGAATGGAAGAGTCAG-3'* and *5'-CAGATATGCAGGGAGTCACC-3'*