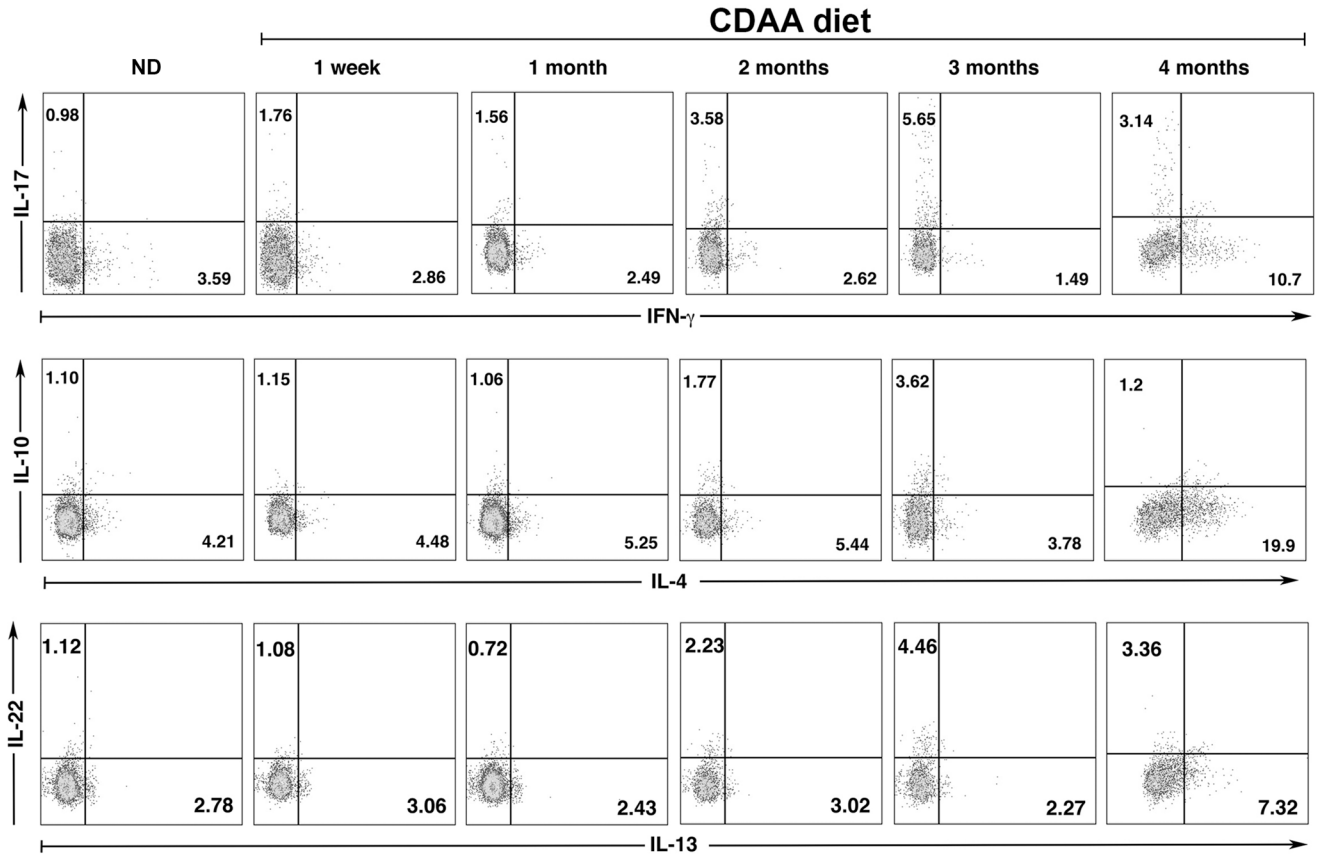
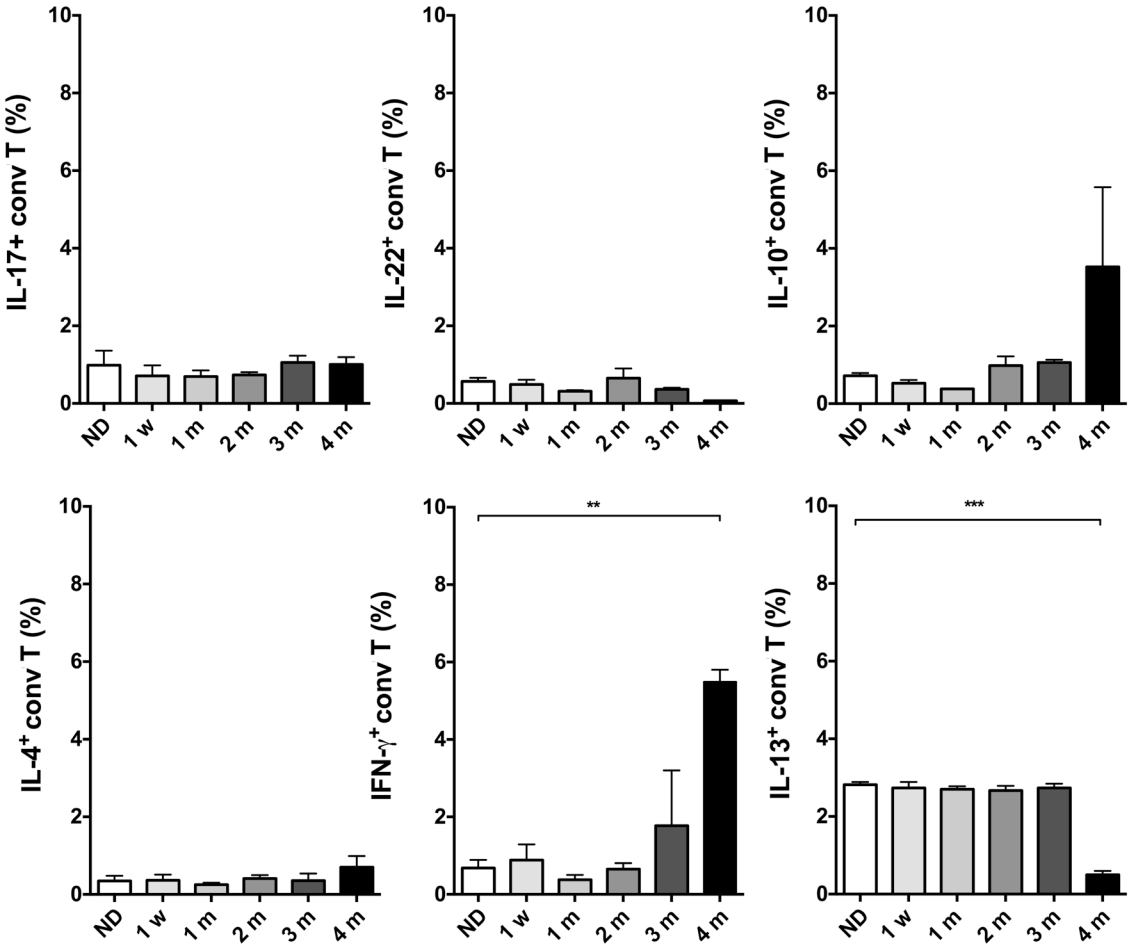
Supplemental Figure 1



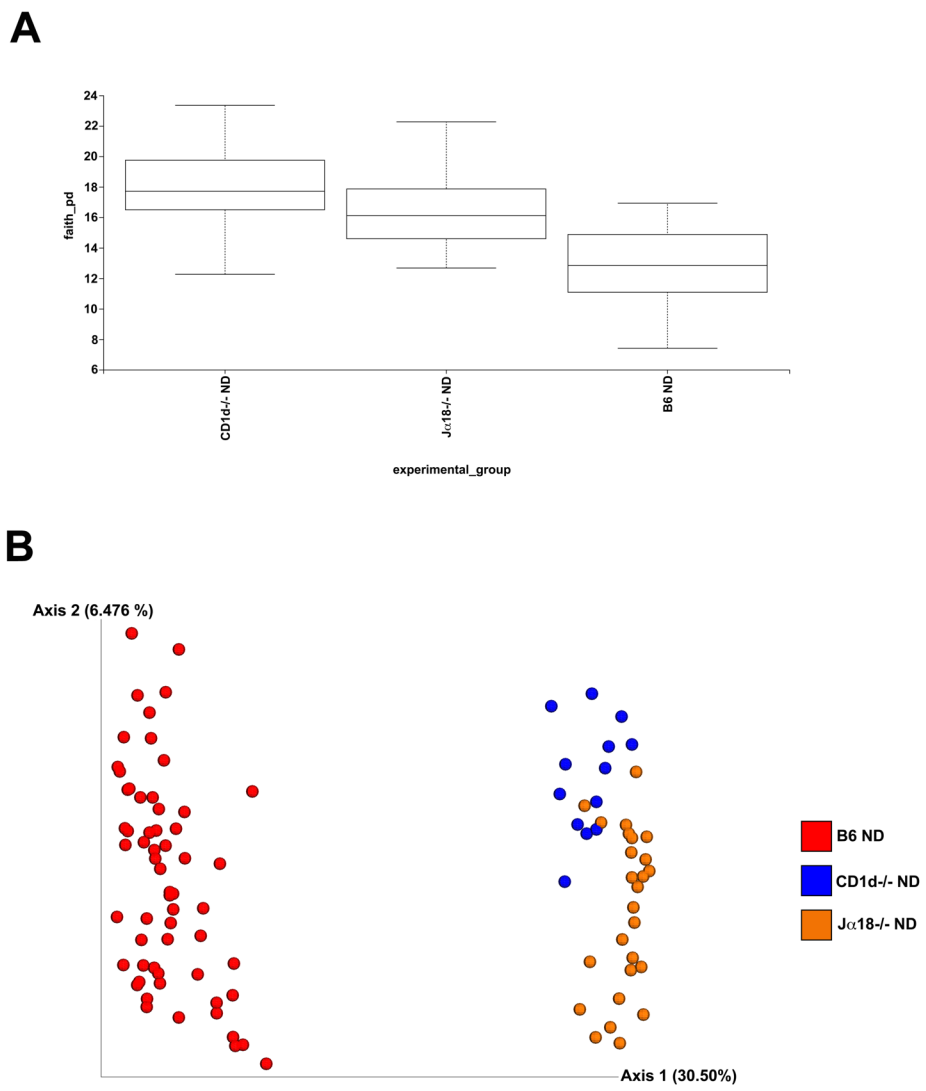
Supplemental Figure 1. Differential Activation and cytokine secretion profiles of iNKT cells in a diet-induced NASH model. Representative dot plot of intracellular production of IFNγ, IL-17, IL-4, IL-10, IL-13 and IL-22 cytokines by iNKT cells in liver of ND-fed B6 mice and B6 mice fed CDAA diet at the indicated time points. Numbers on dot plots indicate the percentage of cytokine positive cells. Each group included three mice. All data presented as mean ± SEM. Data representative of three independent experiments.

Supplemental Figure 2



Supplemental Figure 2. Cytokine production by conventional T cells from CDAA-fed B6 mice. Liver MNCs were stimulated with PMA and ionomycin, and stained for surface TCRβ, NK1.1 and αGalCer/CD1d tetramers as well as intracellular IFNγ, IL-17, IL-4, IL-10, IL-13, and IL-22 cytokines. Conventional T cells were identified as $TCR\beta^{+}$αGalCer/CD1d-$tetramer^{-}$ on the $NK1.1^{-}$ gate. Bar graphs show the percentage of conventional T cells producing IFNγ, IL-17, IL-4, IL-10, IL-13, and IL-22 from liver of B6 mice maintained on ND diet or fed CDAA diet for 1 wk, 1, 2, 3 or 4 months. Three mice per group. All data are presented as mean ± SEM. Data representative of three independent experiments. $^{**}p \leq 0.01$, $^{***}p \leq 0.001$ by unpaired two-sample t-test.

Supplemental Figure 3



Supplemental Figure 3. Differential microbial diversity in mice lacking functional iNKT cells. Jα18-/- (n=26), CD1d-/- (n=13) and B6 (n=60) mice were maintained on ND diet. All groups were housed in separate cages. Genomic bacterial DNA was isolated from fecal samples and the V4 region of 16S rDNA was amplified and sequenced. (**A**) Box-plot of Faith's phylogenetic alpha diversity for each of the experimental groups; bars indicate the interquartile range. (**B**) Discrimination of mice groups based on Principal Coordinates Analysis (PCoA) of UniFrac distance. Red= B6; Blue= CD1d-/-; Orange= Jα18-/-.