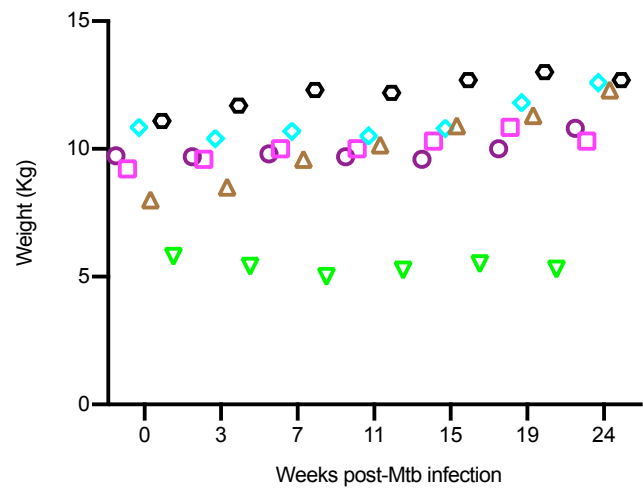
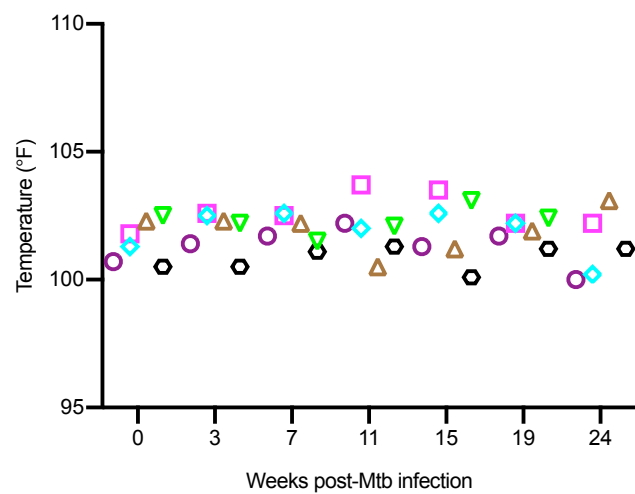


**Supplementary Figure 1:** A) Weight and B) Temperature did not change pre- and post-Mtb infection and until week 24 indicating asymptomatic latent infection in rhesus macaques (n=6).

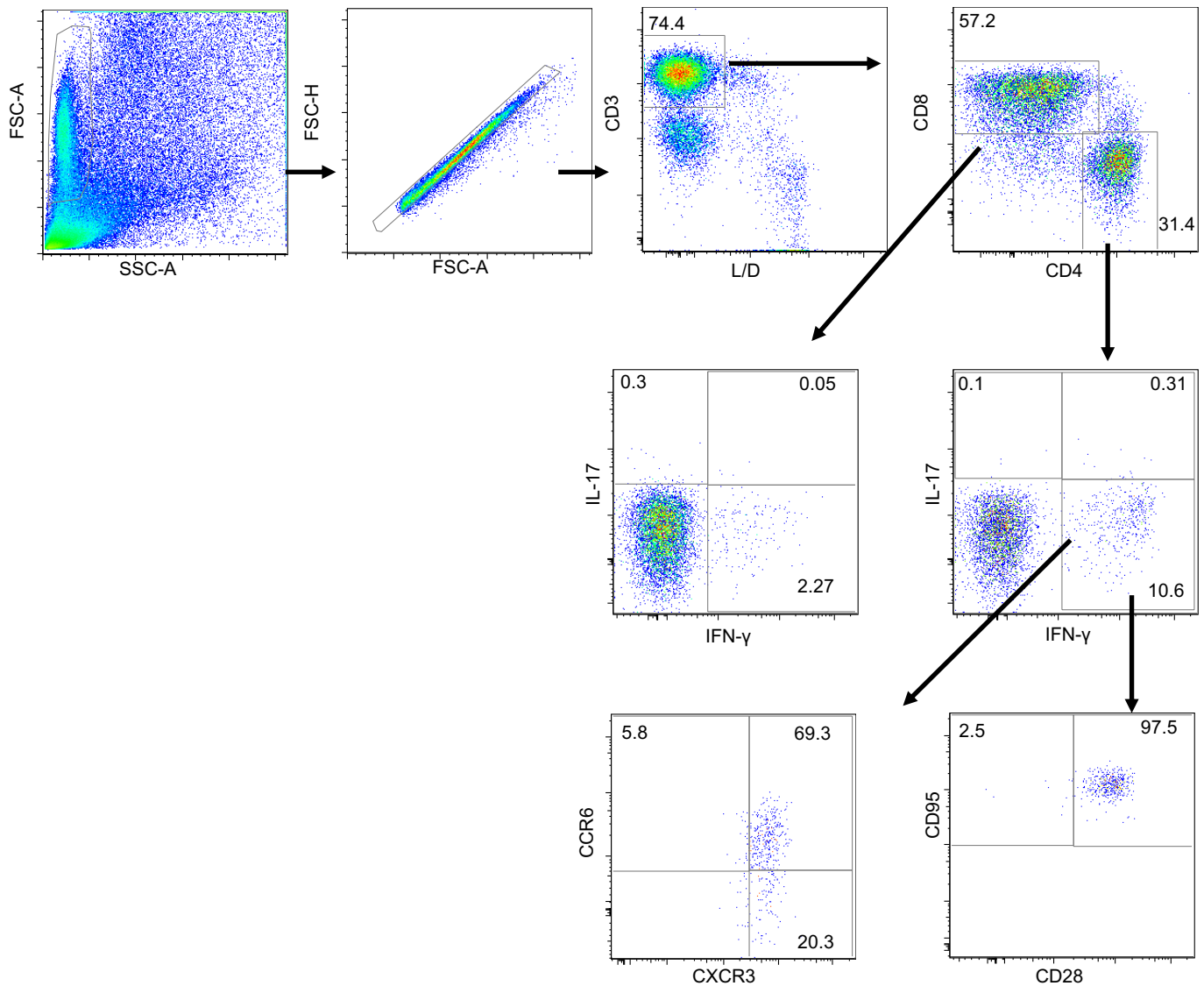
**A**



**B**



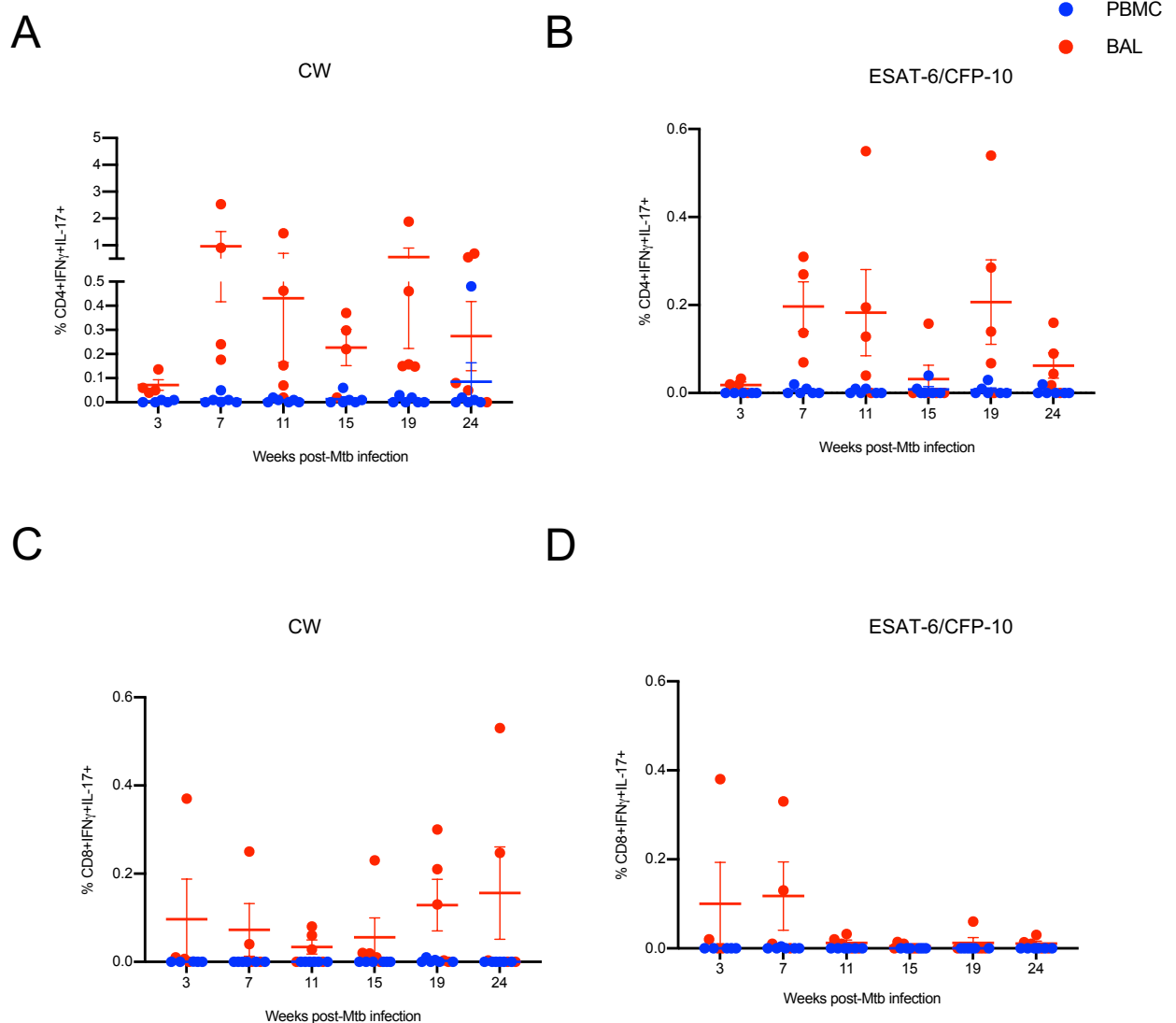
**Supplementary Figure 2: Representative gating strategy used to measure Mtb-specific CD4 and CD8 T cells.** Shown here is representative gating strategy used to measure antigen-specific T cells in BAL stimulated with CW. Lymphocytes were first gated followed by singlets, then live CD3 cells and then for CD4 and CD8 T cells. IFN- $\gamma$  and IL-17 positive CD4 and CD8 T cells were then gated to measure the expression of chemokine (CCR6 and CXCR3) and memory markers (CD28 and CD95).



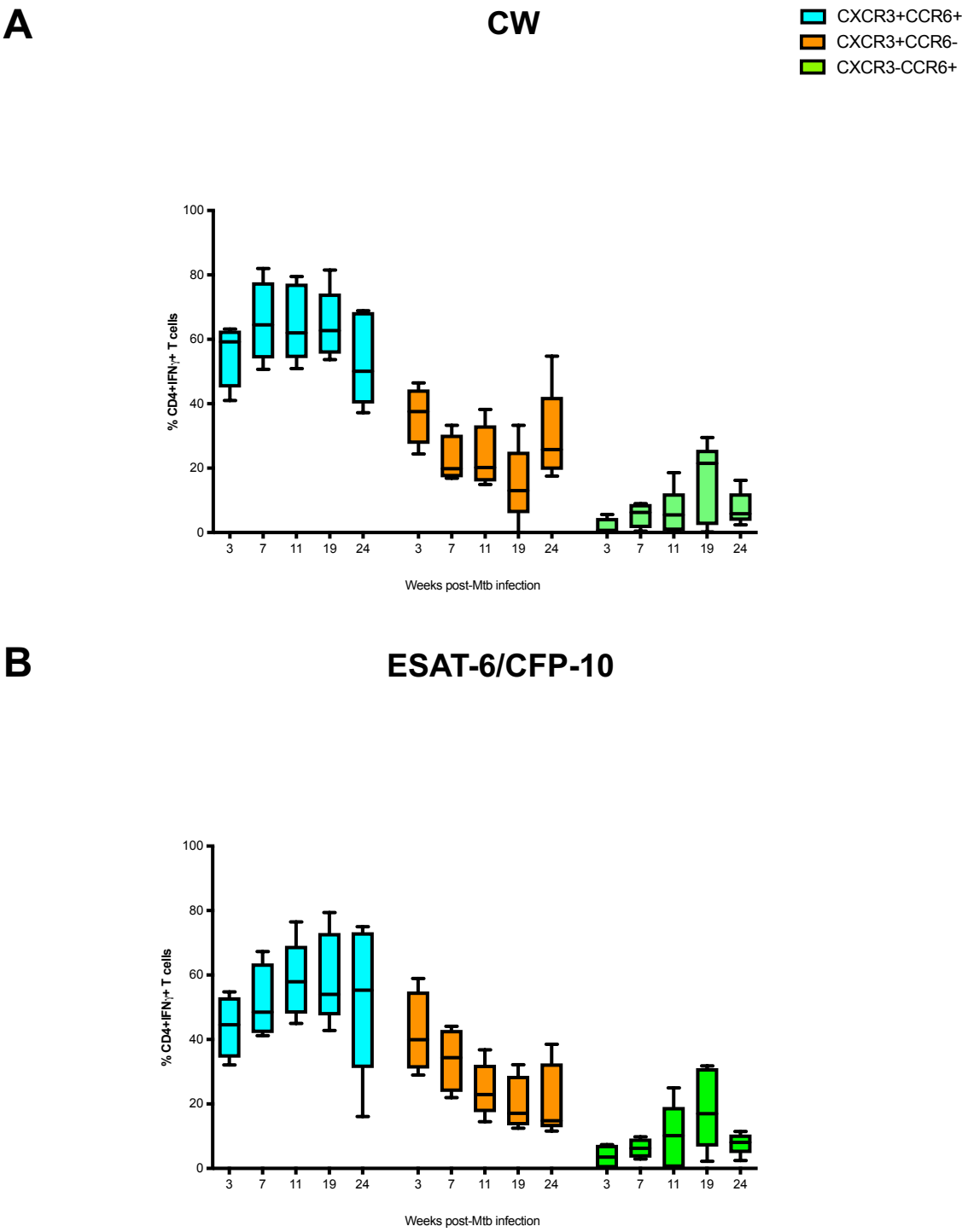
### Supplementary Figure 3: Kinetics of Mtb-specific CD4 and CD8 T cells co-producing IFN- $\gamma$ and IL-17 in PBMC and BAL.

PBMCs (blue circles) and BAL (red circles) samples (n=6) were stimulated with CW (A & C) and ESAT-6/CFP-10 peptide pools (B & D) and IFN- $\gamma$ +IL-17 production by CD4 (A & B) and CD8 (C & D) T cells assessed by ICS and flow cytometry.

Wilcoxon matched-pairs signed rank test was used to compare the frequencies of IL-17 producing CD4 and CD8 T cells between BAL and PBMC. Horizontal lines indicate the mean with SEM.



**Supplementary Figure 4: Frequency of Mtb-specific CD4+ T cells producing IFN- $\gamma$  co-expressing CXCR3 and CCR6.** CW (A) and ESAT-6/CFP-10 (B) specific IFN- $\gamma$ + CD4 T cells in BAL co-expressing CXCR3 and CCR6 (blue) were significantly higher compared to CXCR3+CCR6- (orange) and CXCR3-CCR6+ (green) subsets at all time points. Median line, 25th and 75th percentiles (boundaries of boxes), and 5th and 95th percentiles (whiskers above and below box plots) are indicated in the boxplots. 2-way Anova with Sidak's multiple correction test was used to calculate the statistical difference.



**Supplementary Figure 5: Representative image showing granuloma and non-granuloma region classification:**

Tissue segmentation performed using pattern recognition software (Tissue Classifier, HALO, Indica Labs). A random forest classifier was set at a resolution of 7 $\mu\text{m}/\text{pixel}$  and to detect a minimum object size of 50 $\mu\text{m}^2$ . The classifier was then trained to detect the following tissue classes: granuloma (area in brown and blue) and non-granuloma (area in green). Annotation regions were drawn around each piece of tissue on a slide and tissue segmentation was performed on the entire piece of tissue.

