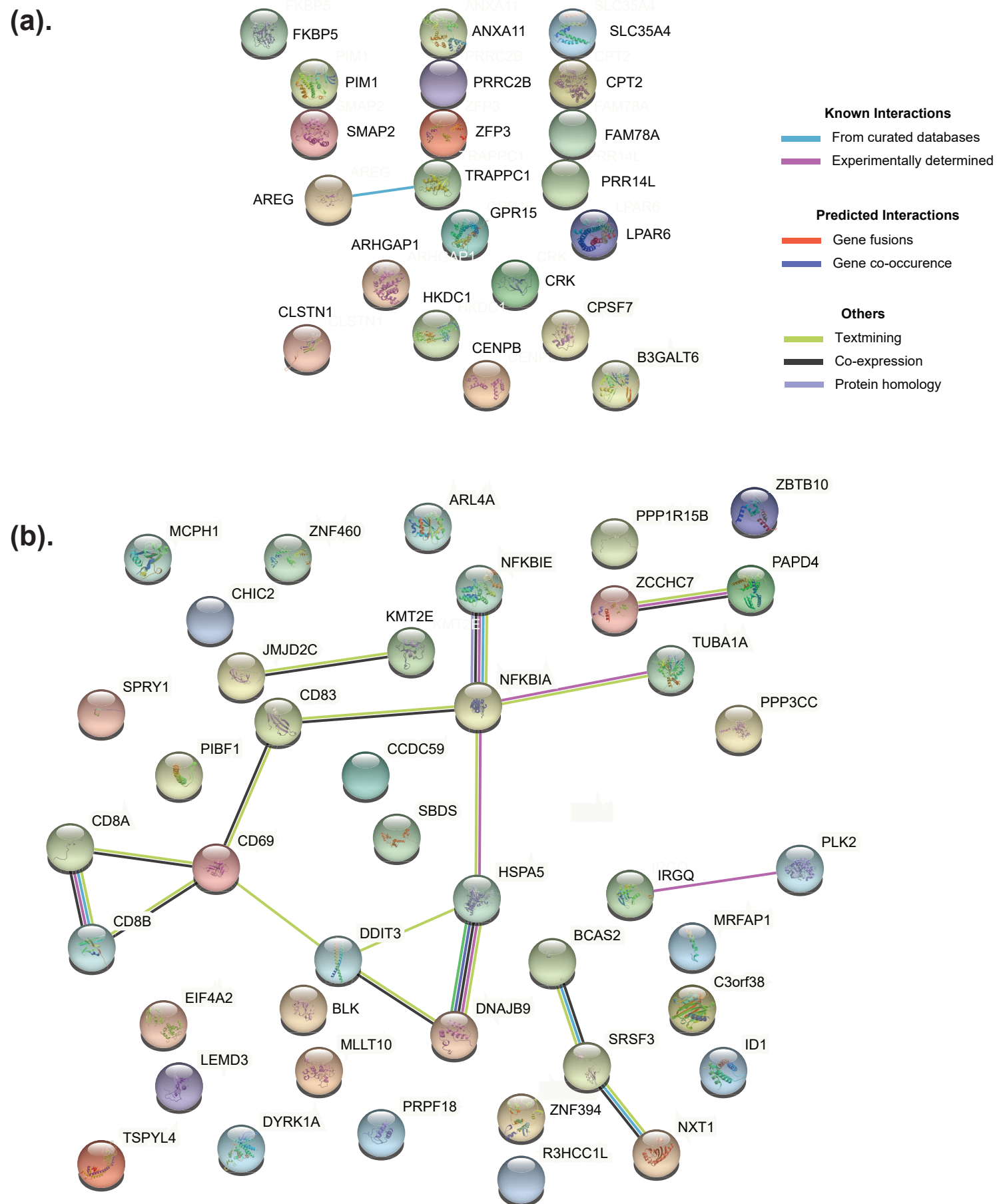
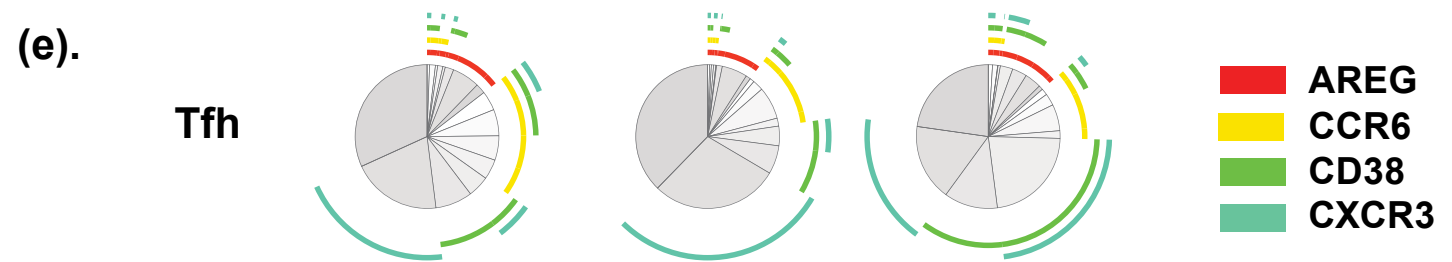
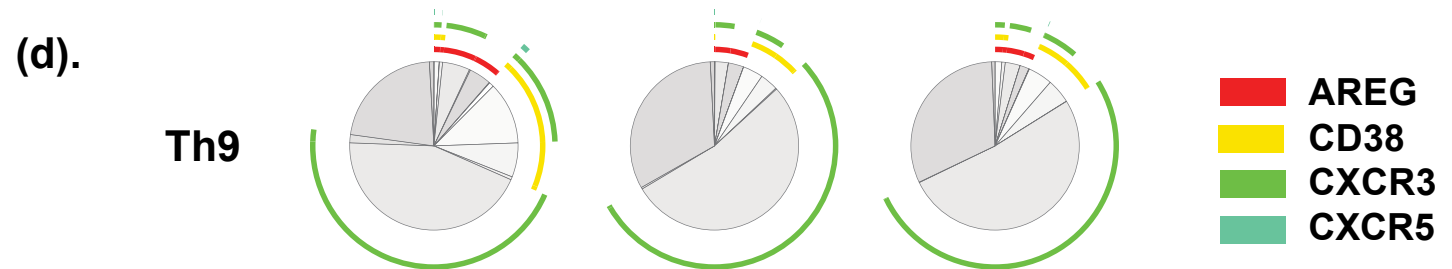
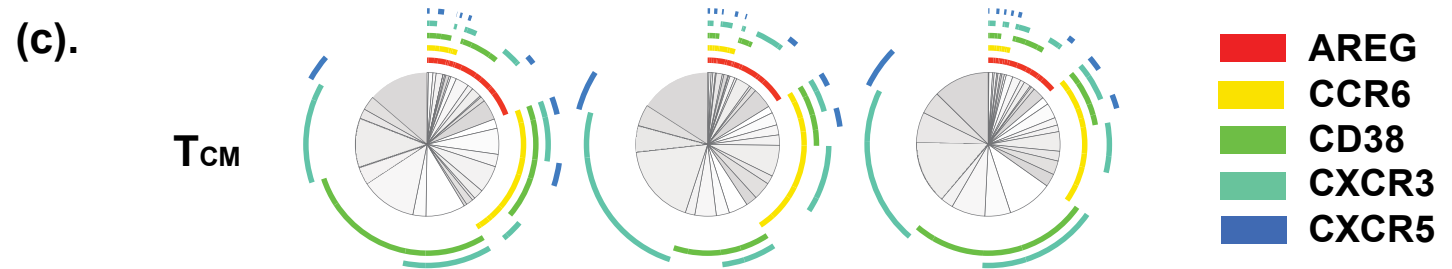
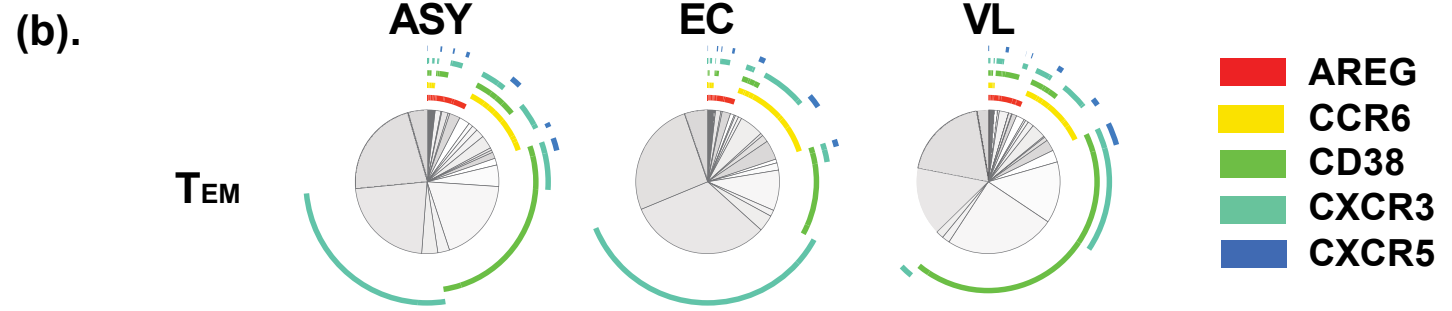
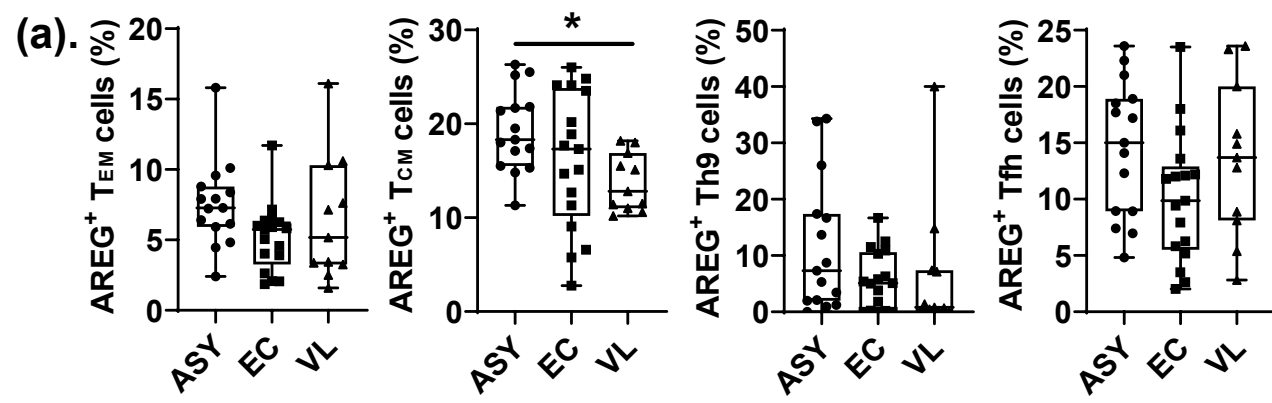


Supplementary figure 1. The STRING networks show the relationships identified amongst up-regulated **(a)** or down-regulated **(b)** genes in CD4<sup>+</sup> T cells from asymptomatic individuals compared to the average of visceral leishmaniasis patients and endemic controls. Filtering of genes was performed based on a false discovery rate cutoff of 0.05 and a log fold-change cutoff of 1.



Supplementary figure 2. The STRING networks show the relationships identified amongst up-regulated **(a)** or down-regulated **(b)** genes in CD4<sup>+</sup> T cells from asymptomatic individuals compared to endemic controls. Filtering of genes was performed based on a false discovery rate cutoff of 0.05 and a log fold-change cutoff of 1.



Supplementary figure 3. AREG expression by CD4<sup>+</sup> T cell subsets. The frequency of AREG<sup>+</sup> CD4<sup>+</sup> T cell subsets was measured by FACS. The box shows the extent of the lower and upper quartiles plus the median, while the whiskers indicate the minimum and maximum data points **(a)**. Simplified presentation of incredibly complex evaluations (SPICE) was used to establish overlap in expression of AREG, CD38 and indicated chemokine receptors by effector memory CD4<sup>+</sup> T (T<sub>EM</sub>) cells **(b)**, central memory CD4<sup>+</sup> T (T<sub>CM</sub>) cells **(c)**, Th9 cells **(d)** and T follicular helper (T<sub>fh</sub>) **(e)** from asymptomatic (ASY; n = 15) individuals, endemic controls (EC; n = 17) and visceral leishmaniasis (VL; n = 11) patients, as indicated. \**P* < 0.05, \*\**P* < 0.01 and \*\*\**P* < 0.001. Significance assessed by One-way ANOVA with Tukey's multiple comparisons test **(a)**.