



S1 Fig. Cytolytic protein and transcription factor expression profiles in MAIT cells. (A) Most of MAIT cell cytolitic proteins expressed at steady state are co-expressed with perforin (Prf). FACS plots representative of data from 20 healthy individuals are shown. (B) PLZF and ROR γ t co-expression in the CD8⁺ T cell population sufficiently identifies the MAIT cell population. Freshly isolated PBMCs from 10 healthy individuals were stained for the transcription factors PLZF and ROR γ t. The co-expression patterns for these transcription factors, PLZF⁺ ROR γ t⁺ (gate no. 1), PLZF⁻ ROR γ t⁺ (gate no. 2), PLZF⁺ ROR γ t⁻ (gate no. 3) were determined in total T cells, CD8⁺ T cells, and CD4⁻ CD8⁻ double-negative (DN) T cells. MAIT cells were identified from these sub-populations by their $V\alpha 7.2$ TCR and high levels of CD161 co-expression. Box and whisker plot shows median, IQR and the 10th to the 90th percentile. Significance across multiple paired samples was determined by the Friedman test followed by Dunn's post-hoc test. Representative FACS plots from a single individual are shown.