#### Analysis of cell-associated DENV RNA by oligo(dT) primed 5' capture scRNAseq

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**Supplemental Figures** 

# 10x Genomics "poly(dT)" primer

Non-Poly(dT)

Poly(dT)VN

Degenerate 3' end

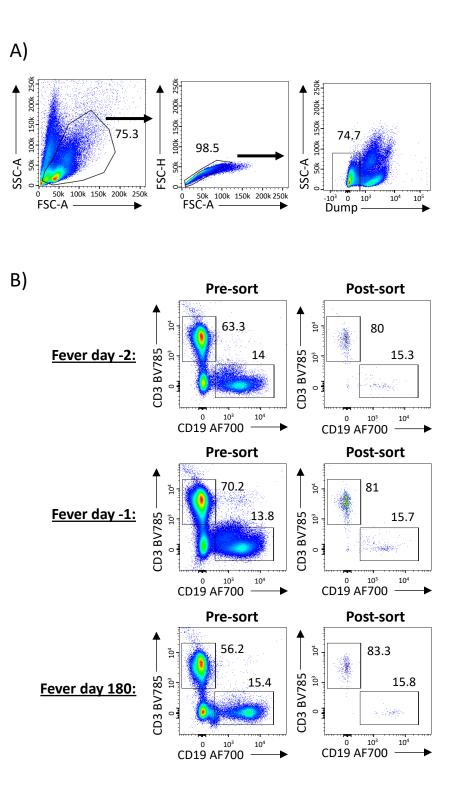
#### **DENV-specific primer**

Non-Poly(dT)

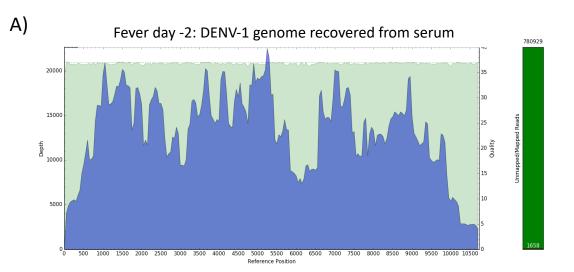
**DENV 3' UTR** 

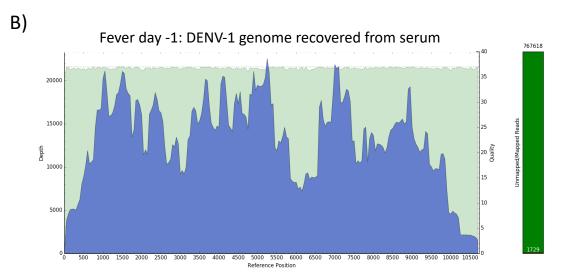
5'-AAGCAGTGGTATCAACGCAGAGTAC-GAACCTGTTGATTCAACAGC-3'

Supplemental Figure 1. Primer sequences utilized in this analysis. V = A, C, G. N = A, T, C, G.

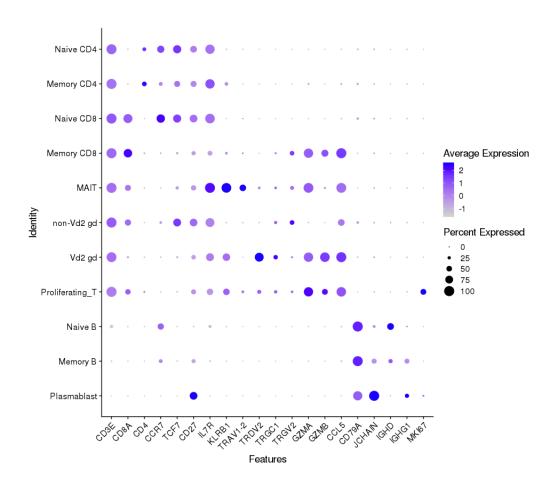


**Supplemental Figure 2.** Gating strategy and post-sort purity of PBMC samples analyzed by flow cytometry. **A)** Gating scheme used to identify and sort viable lymphocytes. **B)** Pre and post sort sample purity of CD3<sup>+</sup> T cells and CD19<sup>+</sup> B cells from all PBMC samples analyzed.

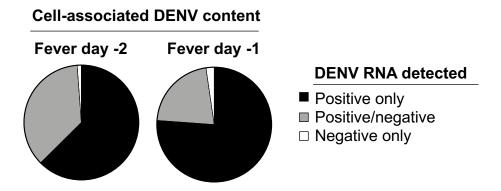




**Supplemental Figure 3.** Sequence coverage and depth of DENV-1 genomic RNA recovered from of serum. **A)** Sequence coverage from fever day -2 **B)** Sequence coverage from fever day -1



**Supplemental Figure 4.** Expression of key linage-defining genes within the annotated populations identified by scRNAseq analysis of sorted CD3<sup>+</sup> T cells and CD19<sup>+</sup> B cells.



**Supplemental Figure 5. Characterization of negative-sense DENV RNA by 5' capture scRNAseq** Fraction of indicated cell populations containing either only positive-sense DENV RNA (black), both positive- and negative-sense DENV RNA (gray), or only negative-sense DENV RNA (white) as quantified by 5' capture scRNAseq.