

Figure S1.

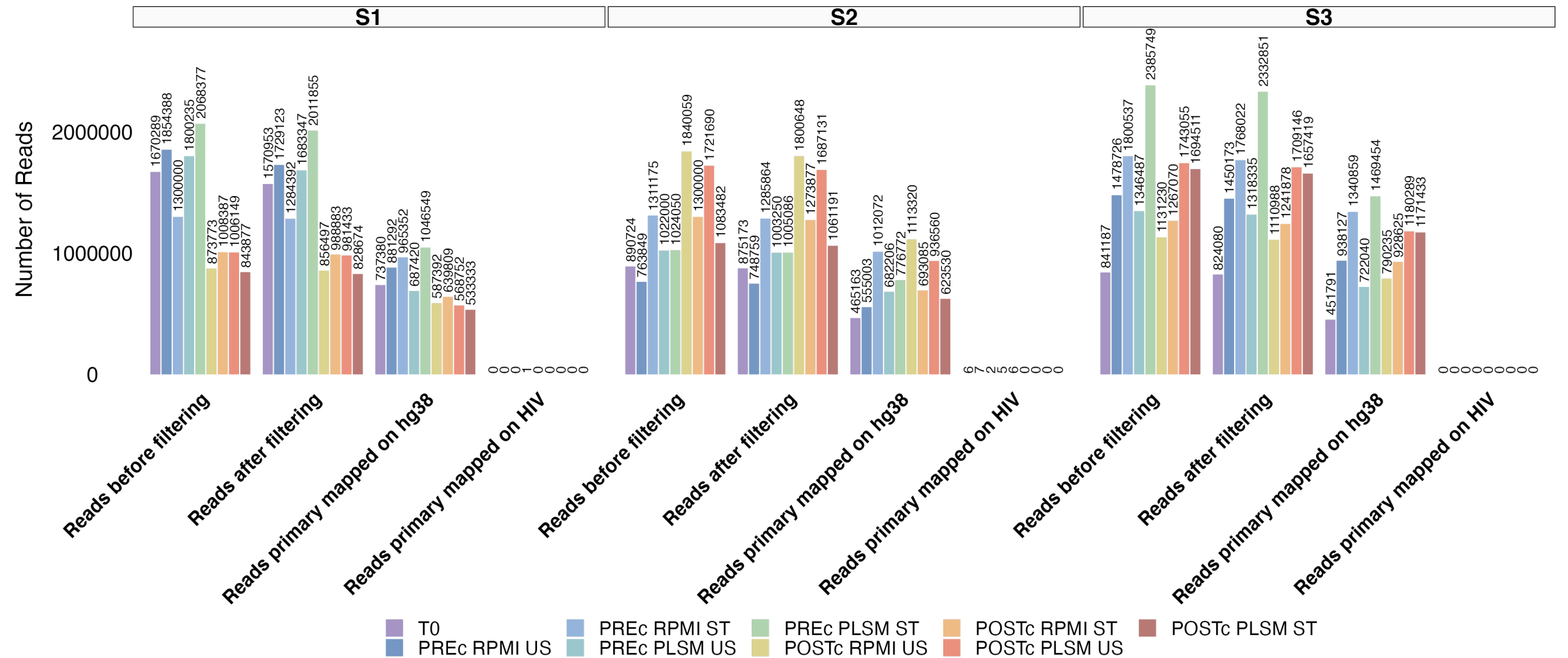


Figure S1. Histogram showing the numbers of total reads sequenced, reads left after filtering (reads with more than 40% of the base with a Phred score of less than 10 were filtered out), 523 reads aligned on the human transcriptome (hg38 Gencode), and reads aligned against the Human 524 immunodeficiency virus type 1 (HXB2) genome sequence.