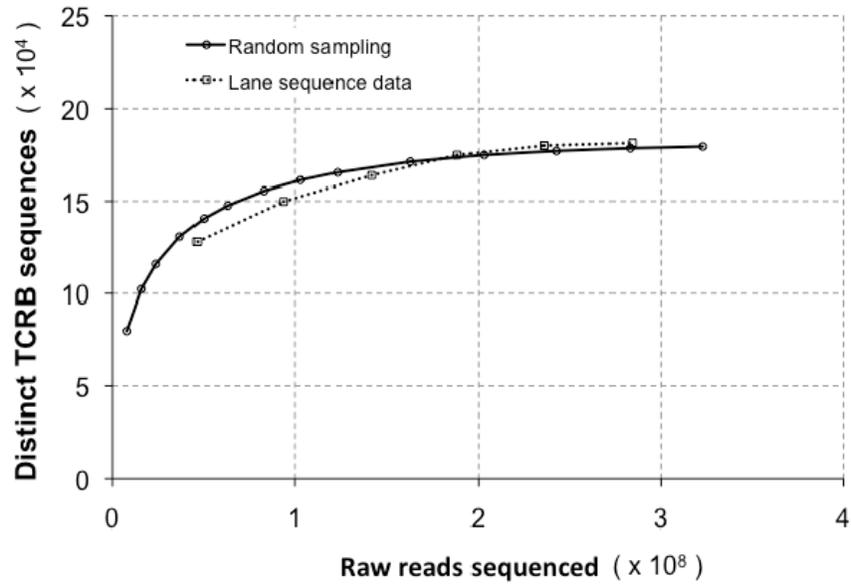


Supplemental online



material

Figure S1. TCRB sequence saturation of library 1 from male subject 1, blood draw 1 by the number of incremental Illumina lanes sequenced (round symbols), or by rarefaction (random re-sampling) of the entire data set (square symbols). For rarefaction, re-sampling was done in triplicate (error bars within symbols). Both approaches show that most of the diversity of this particular library has been captured.

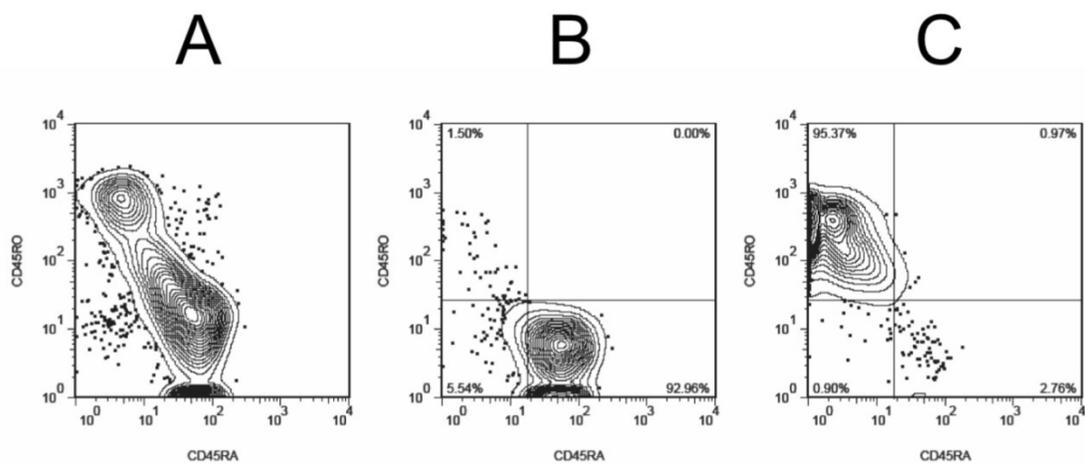


Figure S2. FACS sorting of CD45RA⁺/CD45RO⁻ and CD45RA⁻/CD45RO⁺ cells from Male Donor 1, Day 1. A) Pre-sorted cells. B) CD45RA⁺/CD45RO⁻ sorted cells. C) CD45RA⁻/CD45RO⁺ sorted cells.

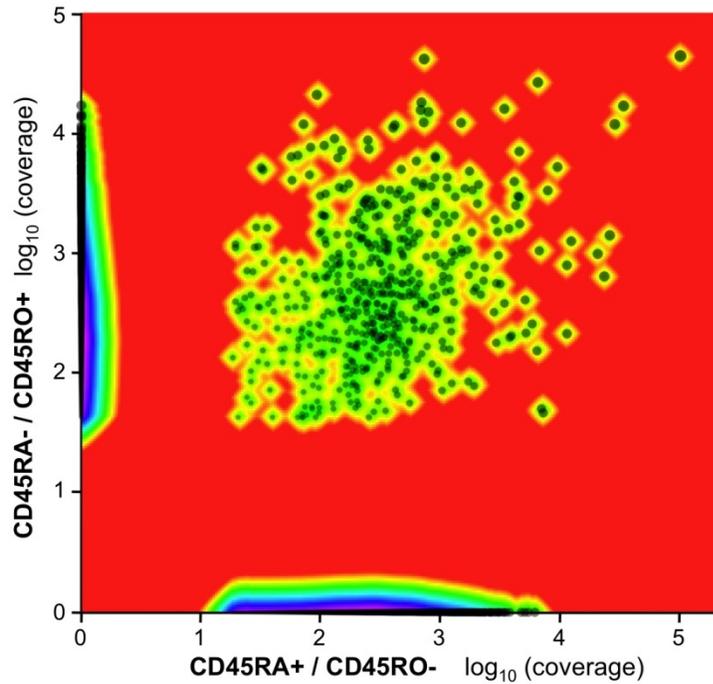


Figure S3. High abundance TCRB sequences from sorted memory and naïve T cells. TCRB sequence abundance in naïve (CD45RA+/CD45RO-) versus memory (CD45RA-/CD45RO+) T-cell subsets, showing high density of subset-specific TCRB sequences as density clouds along axes, plus the 540 TCRB sequences that are present in both subsets. Data point size is proportional to copy number. The color mapping is logarithmically scaled (log power=1) from red (density=0) to magenta (density>10,000).

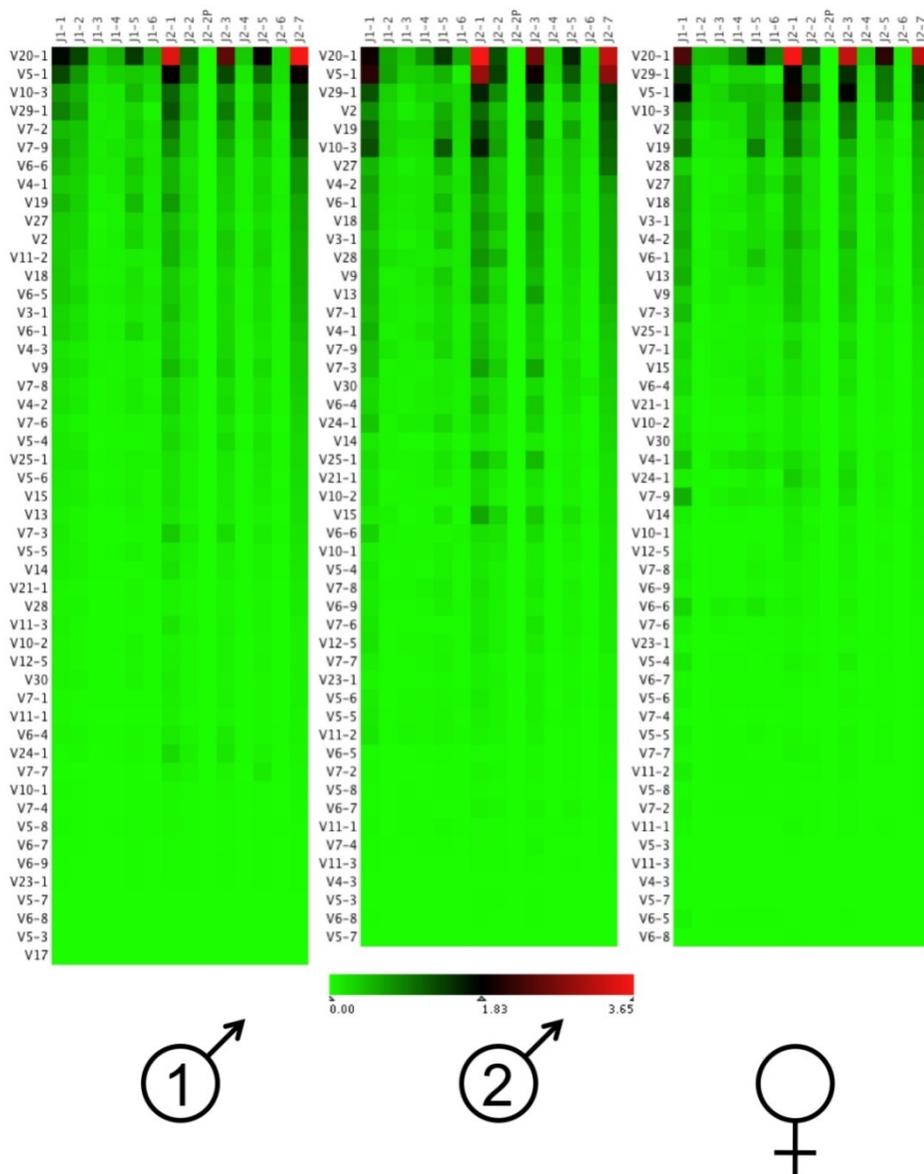


Figure S4. VJ pairing frequencies in 3 healthy individuals. The green to red transition indicates less to more frequent pairing between TRBV and TRBJ segments. The three most frequent pairs include TRBV20-1_TRBJ2-1 (average frequency = 3.28%), TRBV20-1_TRBJ2-7 (average frequency = 3.11%) and TRBV20-1_TRBJ2-3 (average frequency = 2.59%). TRBV12-3, 12-4, 6-2 and 6-3 cannot be differentiated unambiguously and thus are not shown here. Pairings that include TRBV17 are undetected or absent in both male donor 2 and the female, but detected at low frequencies in male donor 1. The unpaired pseudogene TRBJ2-2p is added to show null frequency baseline. VJ pairing frequency is similar for all three individuals (Average Pearson correlation = 0.90 between any two donors).