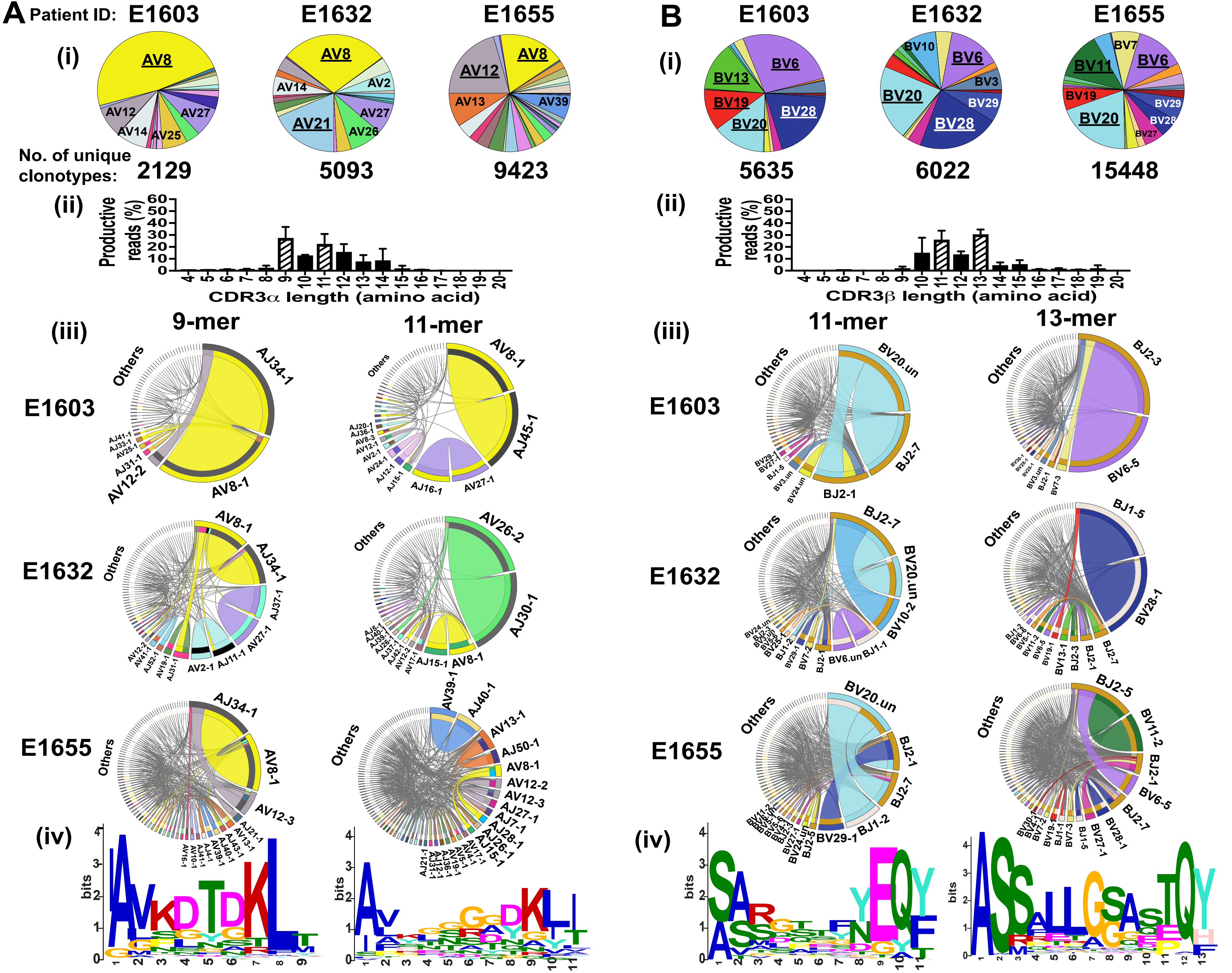

**Figure S1: 9-mer TCR AV8.1-VKDTDK-AJ34 drives the selection of YVL-specific CD8 T-cells in AIM.** The TCR repertoire is deconstructed by analyzing V family usage in pie chart format, CDR3 length analyses, VJ pairing by using circos plot analyses, and CDR3 amino acid motif analyses using Multiple MEME framework(77). (i) YVL-BR-specific TCRVA (A) and TRVB (B) repertoires are analyzed for 3 AIM donors (E1603, E1632, E1655) during AIM. Frequency of each TRAV (A) and TRBV (B) in total YVL-BR-specific TCR-repertoire is shown in pie charts (i). The pie plots are labeled with gene families having a frequency >5%. The total numbers of unique clonotypes in each donor is shown below the pie charts. (ii) CDR3 length distribution along with (iii) circos plots depicting V-J gene pairing and (iiii) CDR3 motif analysis for the clonotypes with the two most dominant CDR3 lengths. Genes are colored by V gene family with a fixed color sequence used throughout the manuscript.