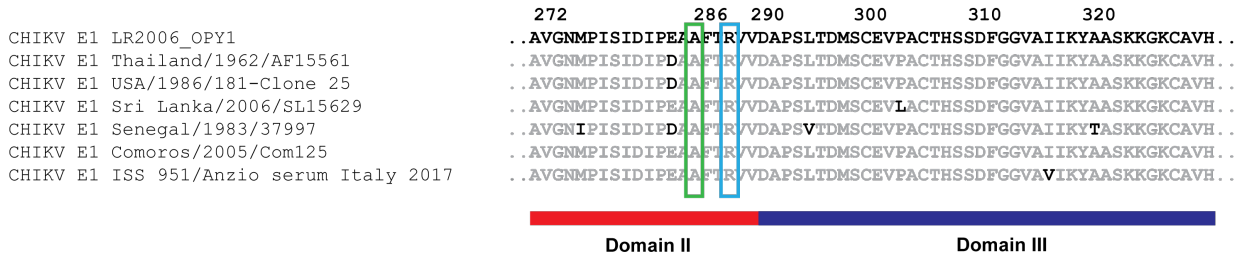

Figure S9. Alignment of CHIKV E1 Sequences Near DIII. The domain boundaries are indicated at the bottom. The two positions at which viral escape mutations were isolated for E1-specific human mAbs (A286 for DC2.315, green, and R289 for DC1.7, cyan) are indicated.