



**Supplementary Figure 3. *Env* sequences from all patients.** A maximum likelihood phylogenetic tree was constructed from all viral *env* sequences (Q<sup>2</sup>VOA, rebound SGA, and near full-length genome) from all participants. The tree was constructed using RAxML v.8.0.22 with a GTR GAMMA substitution model, with 1000 bootstrap replicates and midpoint rooted. Asterisks indicate nodes with significant bootstrap values (bootstrap support ≥ 90%).