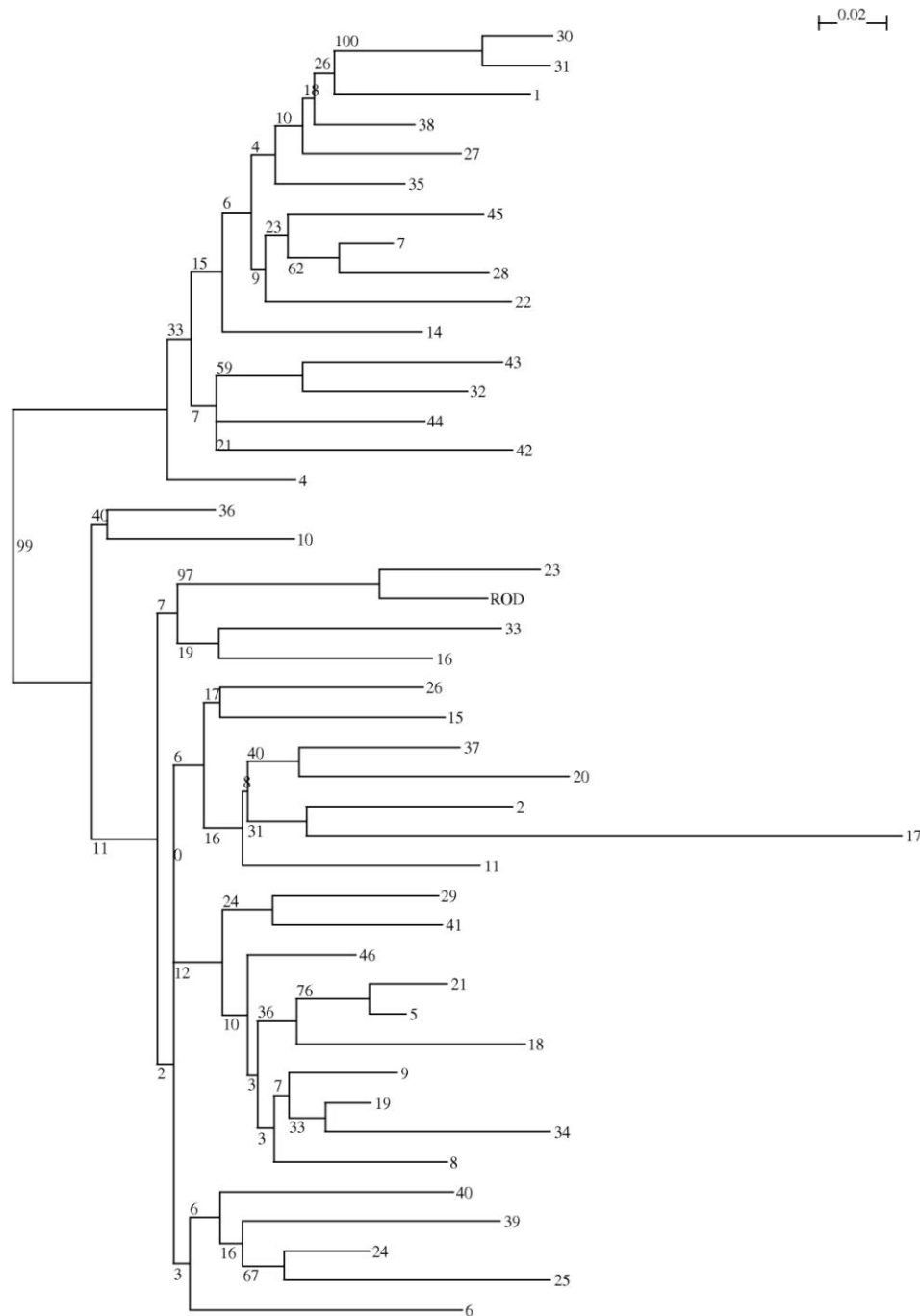**Supplemental Digital Content**

Phylogenetic relationships between group-A HIV-2 *gag* sequences (*n=43*) of viruses taken from patients, and identified using numbers. Phylogenetic trees were inferred using the neighbour-joining method and two Kimura parameters with 100 bootstrap values. Clusters of sequences were confirmed by constructing phylogenetic trees from Gag sequences using the maximum likelihood method with a PhyML algorithm and using a discrete gamma model of nucleotide substitution (HKY85). Robust clusters were identified by high bootstrap values (98%) with 100 re-samplings and a short branch. The HIV-2 group-A ROD reference strain is included in the construction of the phylogenetic tree.

1 to 46: patients, ROD: HIV-2 group-A ROD reference strain.