Figure 2: Phylogenetic tree of LTR sequences from chronically infected patients with and without helminths coinfection (Current isolates are designated by 4 digit numbers and the rest are reference sequences). The two genotypes cocirculating are indicated as C and C’. **Keys:** Sequences with Black Square (■) are from patients with chronic helminths infection and with Black circles (●) are isolates which could not be classified in either one of the two subclusters.