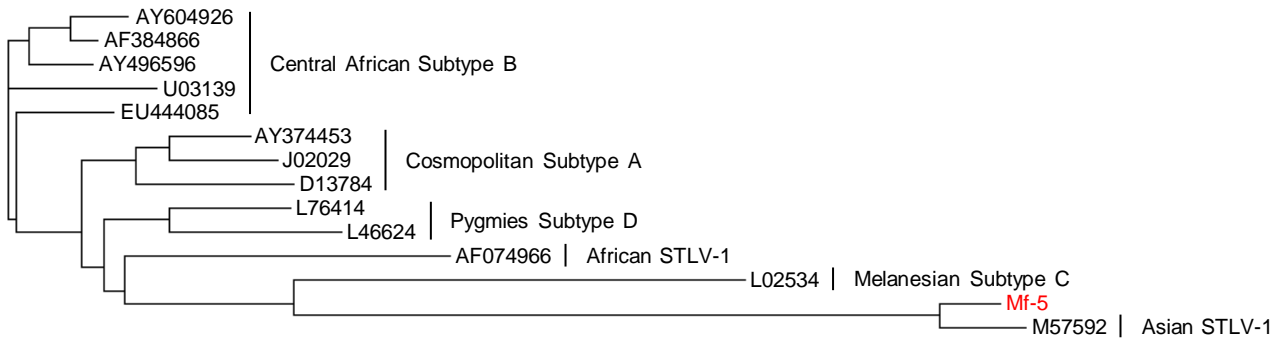**Phylogenetic analyses of HTLV-1 subtypes and Japanese macaque STLV-1**

Supplementary Figure 1. Phylogenetic analyses of HTLV-1, STLV-1 subtypes and Japanese macaque STLV-1.

Japanese macaque STLV-1 env region was aligned with exactly the same region (6069-6590 in J02029) of several HTLV-1 and STLV-1 isolates by clustarW (http://www.genome.jp/tools/clustalw/), with default settings. Then, the alignment was processed to generate phylogenetic tree by neighbor-joining method using ClustalW2-phylogeny (http://www.ebi.ac.uk/Tools/phylogeny/clustalw2_phylogeny/) with default settings. Each leaf represents the accession number of the HTLV-1 or STLV-1 isolate.