Supplementary File S5.

Sample set of 124 *env* sequences assembled by selecting the coding region of *env* from multiple primate lentiviruses that is homologous to the *env/asp* overlap in the reference genome sequence HIV-1 (ac. number K03455, nucleotides 7371-7943; see Materials and Methods section *2.6 Assembly of a dataset of env sequences covering a wide phylogenetic range of primate lentiviruses*). The dataset was assembled by selecting the coding region of *env* from multiple primate lentiviruses that covers a wide range of primate lentiviruses, including the four subgroups of HIV-1 (M, N,O, and P), HIV-2, and several SIV species infecting African apes and Old-World monkeys.

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