Supplementary File S2A.

Supplementary file S2A contains a control set of 1753 *env/asp* overlapping regions. They are delimited, in the reverse frame, by a *start* codon (ATG) at canonical nucleotide positions (triplet CAT at the end of the sequence) and a *stop* codon at canonical nucleotide positions (triplet CTA at the beginning of the sequence). All overlaps, however, have lost the ability to encode a full-length overlapping ASP protein, because of the presence of internal stop codons. The number of internal stop codons is added at the end of to the accession number after two dots. In detail, 1231 *env* sequences have an *asp* ORF interrupted by 1 internal stop codon (e.g. MH705158..1), 403 env sequences have an *asp* ORF interrupted by 2 internal stop codons (e.g. FM165645..2), 102 env sequences have an *asp* ORF interrupted by 3 internal stop codons (e.g. AF457086..3), 11 env sequences have an *asp* ORF interrupted by 4 internal stop codons (e.g. KT022381..4), and 6 env sequences have an *asp* ORF interrupted by 5 internal stop codons (e.g. KP411836..5). All sequences belong to the group M of HIV-1. Each nucleotide sequence is reported both in the alignment format with gaps and in the format without gaps.

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