

Supplemental Figure S1: SeLOX output of the search for loxP/loxH and rox – like sites (Suppl. File 1) in 8 HIV-LTR sequences (Suppl. File 2). 5 mutations were allowed in the flanking region and 8 mismatches for the symmetry.

Supplemental Figure S2: SeLOX output of the search for three yeast-like recombinases with conserved target sites (Suppl. File 1, bold letters) in 8 HIV-LTR sequences (Suppl. File 2). 5 mutations were allowed in the flanking region and 8 mismatches for the symmetry.