The variances of Sp1 and NF-κB elements correlate with the greater capacity of Chinese HIV-1 B′-LTR for driving gene expression

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Figure legends

Figure S1. Phylogenetic tree of HIV-1 LTR sequences. Phylogenetic analysis was performed based on HIV-1 LTR nucleotide sequences from the HIV database. The phylogenetic tree was performed by the neighbor-joining method with MEGA version 5 software, and the reliabilities indicated at the branch nodes were evaluated using 500 bootstrap replications. Each isolate was specified with HIV database accession number, strain name, isolation place, isolation year, and sub genotype.

Figure S2. Alignment of HIV-1 LTR sequences. Different subtypes of HIV-1 LTR sequences were downloaded from the HIV database (http://www.hiv.lanl.gov/content/index) and aligned in the Mega software. Variations in elements for transcription factor binding were summarized.

Table S1. **The information of HIV-1 subtypes endemic in China**. 300 LTR sequences of circulating HIV-1 strains in China including B′ (54 sequences), CRF07_BC (42 sequences), CRF08_BC (36 sequences) and CRF01_AE (168 sequences) from the HIV database (http://www.hiv.lanl.gov/content/index, on April 21, 2014) were downloaded

Figure S1

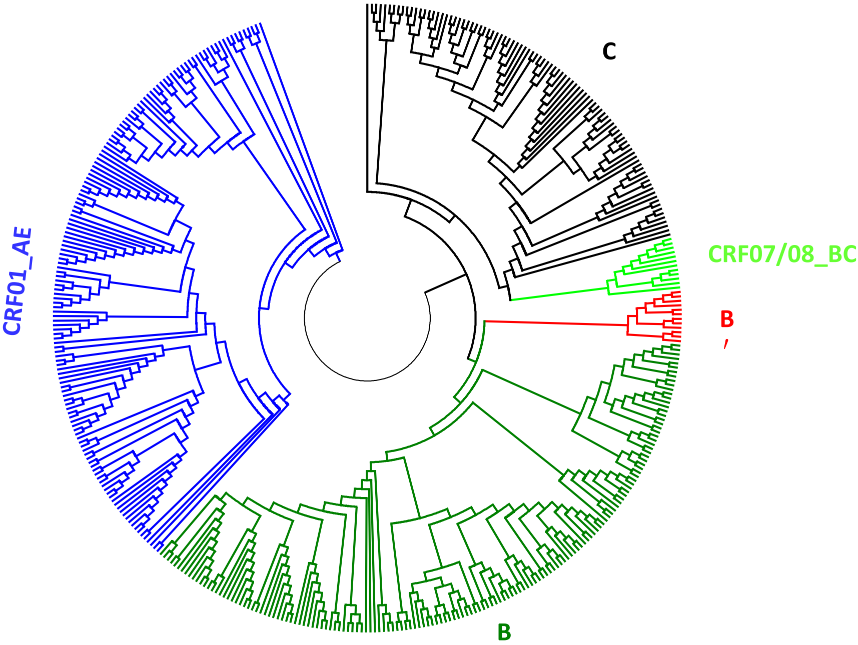
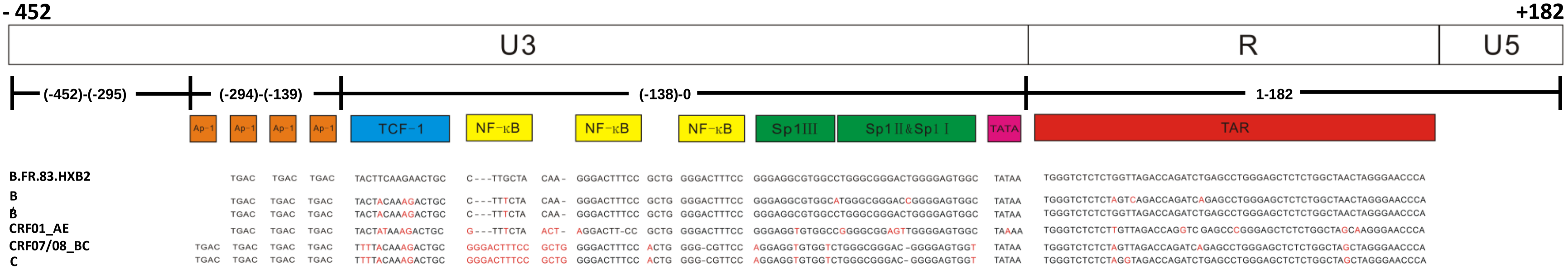


Figure S2


- 452
+182
U3
R
U5
(-452)-(-295)
(-294)-(-139)
(-138)-0
1-182
Ap-1
Ap-1
Ap-1
Ap-1
TCF-1
NF-κB
NF-κB
NF-κB
Sp1Ⅲ
Sp1Ⅱ&Sp1Ⅰ
TATA
TAR
B.FR.83.HXB2 TGAC TGAC TGAC TACTTCAAGAACTGC C---TTGCTA CAA- GGGACTTTCC GCTG GGGACTTTCC GGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGC TATAA TGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCA
B TGAC TGAC TGAC TACTACAAAGACTGC C---TTTCTA CAA- GGGACTTTCC GCTG GGGACTTTCC GGGAGGCGTGGCATGGGCGGGACCGGGGAGTGGC TATAA TGGGTCTCTCTAGTCAGACCAGATCAGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCA
B' TGAC TGAC TGAC TACTACAAAGACTGC C---TTTCTA CAA- GGGACTTTCC GCTG GGGACTTTCC GGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGC TATAA TGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCA
CRF01_AE TGAC TGAC TGAC TACTATAAAGACTGC G---TTTCTA ACT- AGGACTT-CC GCTG GGGACTTTCC GGGAGGTGTGGCCGGGGCGGAGTTGGGGAGTGGC TAAAA TGGGTCTCTCTTGTTAGACCAGGTC GAGCCCGGGAGCTCTCTGGCTAGCAAGGGAACCCA
CRF07/08_BC TGAC TGAC TGAC TGAC TTTTACAAAGACTGC GGGACTTTCC GCTG GGGACTTTCC ACTG GGG-CGTTCC AGGAGGTGTGGTCTGGGCGGGAC -GGGGAGTGGT TATAA TGGGTCTCTCTAGTTAGACCAGATCAGAGCCTGGGAGCTCTCTGGCTAGCTAGGGAACCCA
C TGAC TGAC TGAC TGAC TTTTACAAAGACTGC GGGACTTTCC GCTG GGGACTTTCC ACTG GGG-CGTTCC AGGAGGTGTGGTCTGGGCGGGAC- GGGGAGTGGT TATAA TGGGTCTCTCTAGGTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCTAGCTAGGGAACCCA