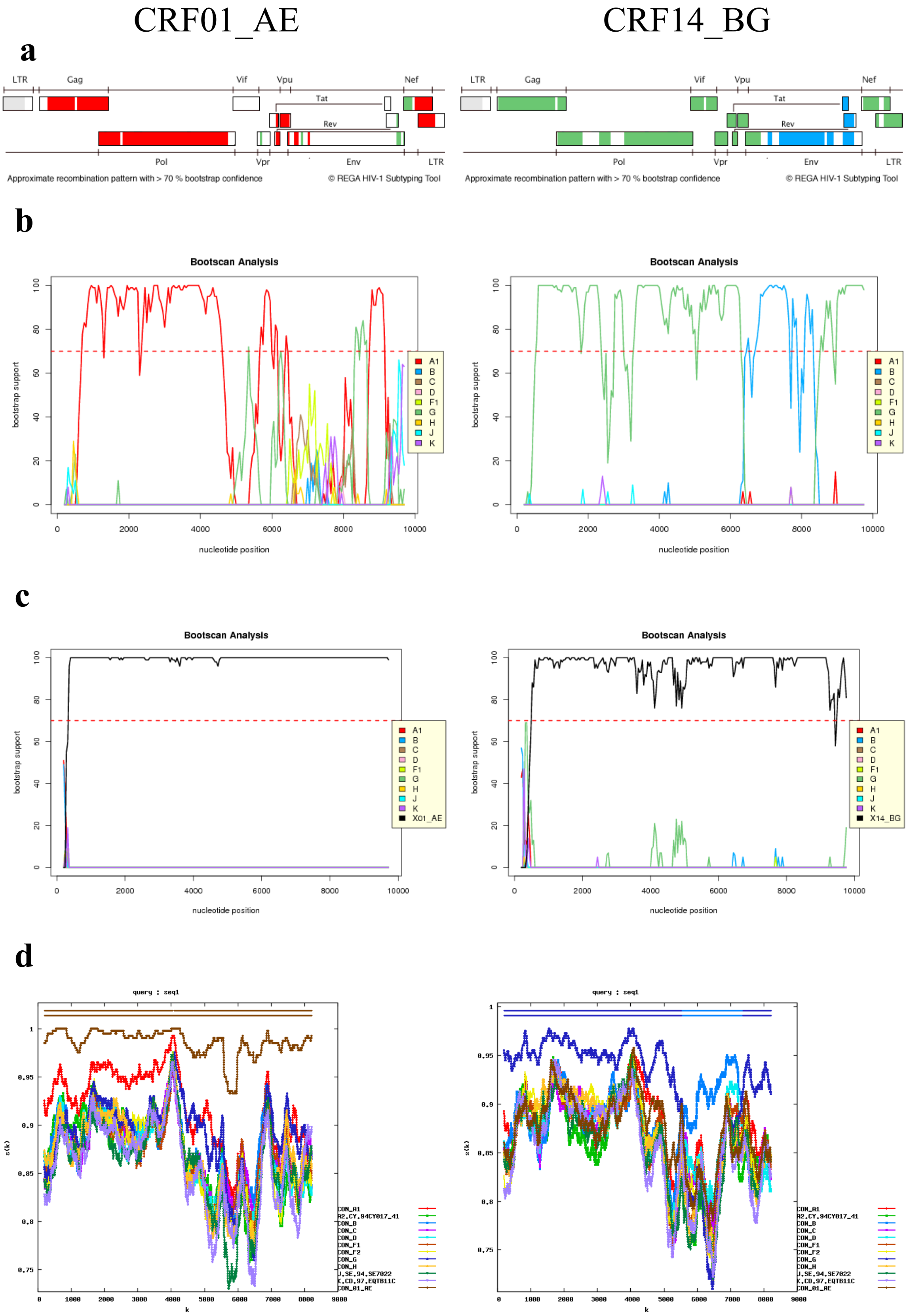
CRF01_AE
CRF14_BG
a
LTR
Gag
Vif
Vpu
Nef
Tat
Rev
Pol
Vpr
Env
LTR
Approximate recombination pattern with > 70 % bootstrap confidence
© REGA HIV-1 Subtyping Tool
b
Bootscan Analysis
bootstrap support
nucleotide position
0
20
40
60
80
100
0
2000
4000
6000
8000
10000
A1
B
C
D
F1
G
H
J
K
c
Bootscan Analysis
X01_AE
X14_BG
d
query : seq1
s(k)
k
0.75
0.8
0.85
0.9
0.95
1
0
1000
2000
3000
4000
5000
6000
7000
8000
9000
CON_A1
A2.CY.94CY017_41
CON_B
CON_C
CON_D
CON_F1
CON_F2
CON_G
CON_H
J.SE.94.SE7022
K.CD.97.EQTB11C
CON_01_AE

FIG S4 Detection of recombination in HIV-1 genomes sequenced in this study. Two CRFs, CRF01_AE (left) and CRF14_BG (right) were sequenced and analysed with **(a-c)** the Rega HIV-1 Subtyping Tool version 2.0 and **(d)** the Recombinant Identification Program version 3.0.

a Genome view of the CRFs. Regions with bootstrap confidence of > 70% are coloured according to the subtype, with the same colour scheme as in **b** and **c.**

b & c Bootscan analysis along the genome. A sliding window of 400 nucleotides was used. For each window, the bootstrap support for the different subtypes and the appropriate CRF is plotted.

d Similarity to different subtypes and CRF01_AE of the HIV-1 subtype consensus alignment. A sliding window of 400 nucleotides was used.