Phylogenetic clustering of Env553

Supplementary information for:

A small set of succinct signature patterns distinguishes Chinese and non-Chinese HIV-1 genomes

Yan Wang^{1,2,†}, Reda Rawi^{1,†}, Christoph Wilms¹, Dominik Heider¹, Rongge Yang^{2,*}, Daniel Hoffmann^{1,*}

1 Research Group Bioinformatics, Center for Medical Biology, University of Duisburg-Essen, Essen, Germany; 2 AIDS and HIV Research Group, State key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, P.R.China;* E-mail: ryang@wh.iov.cn, daniel.hoffmann@uni-due.de

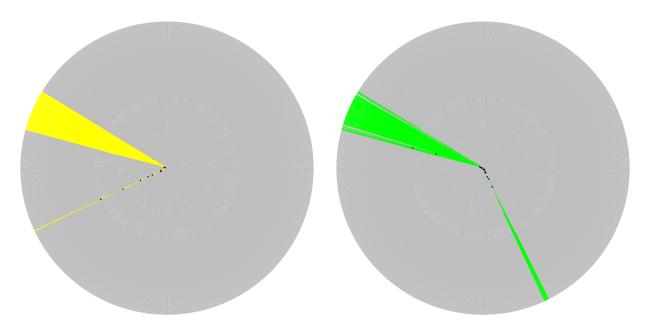


Figure 1: Phylogenetic clustering of the Env position corresponding to HXB2 Env553. The underlying fan tree is the same described in the main manuscript. Left side: branches in agreement with pattern Env553 = R colored yellow. Right side: branches of subtype B samples from China colored green. The comparison shows that Env553 = R is a good marker for Chinese sequences.