

Phylogenetic clustering of Env167 and Env792

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Supplementary information for:

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

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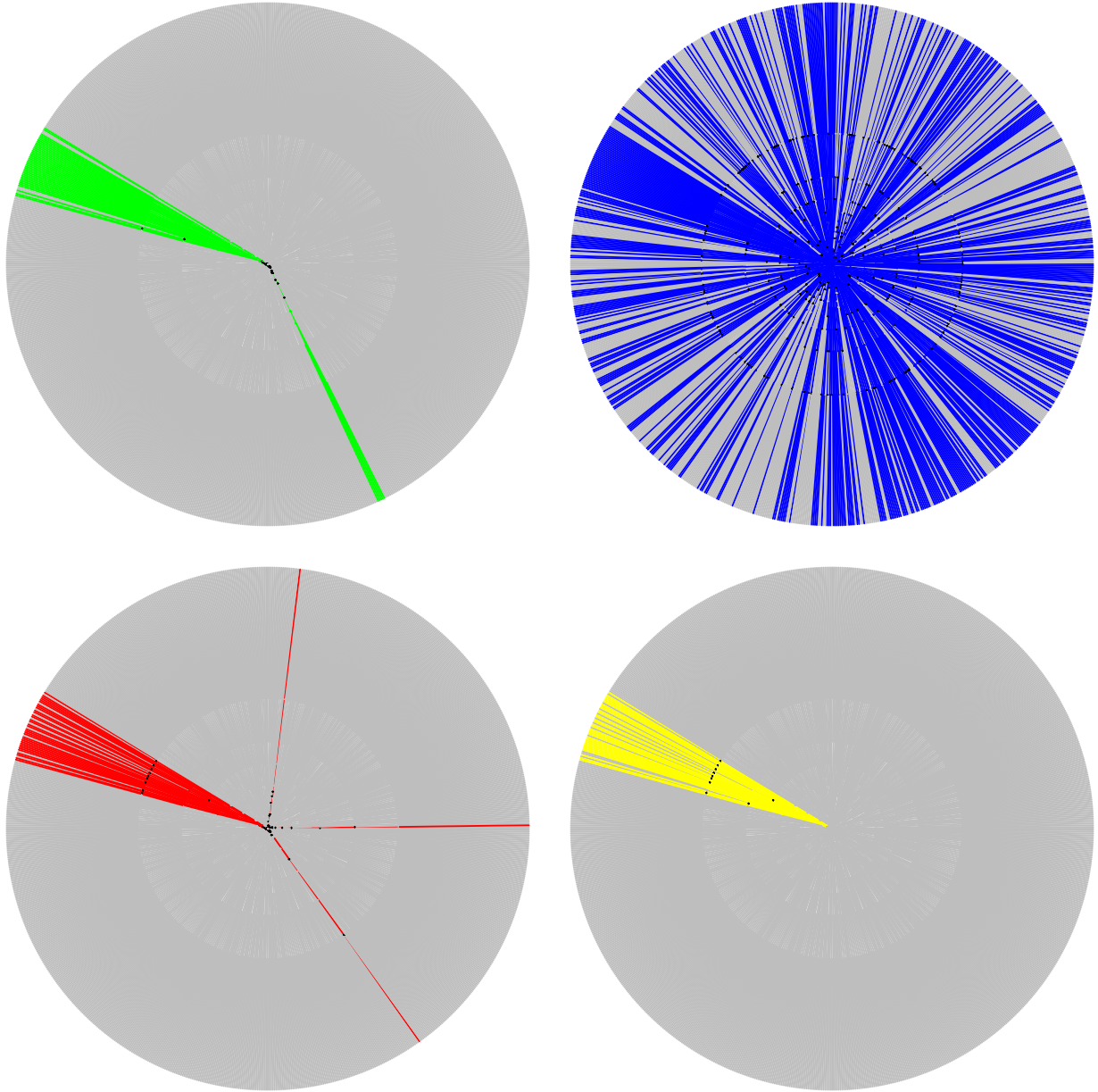


Figure 1: Phylogenetic clustering of Env positions corresponding to HXB2 Env positions 167 and 792. The underlying fan tree is the same described in the main manuscript. Top left (green): branches of subtype B samples from China. Top right (blue): branches matching pattern Env792 = A. Bottom left (red): branches matching Env167 = T. Bottom right (yellow): branches matching Env167 = T AND Env792 = A. The comparison between top left and bottom right shows that pattern Env167 = T AND Env792 = A is a good marker for Chinese sequences.