Supplemental Information

Longitudinal deep sequencing and phylogenetic reconstruction of CXCR4 HIV-1 transmission to an individual homozygous for the CCR5Δ32 mutation

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Supplementary Figure 1

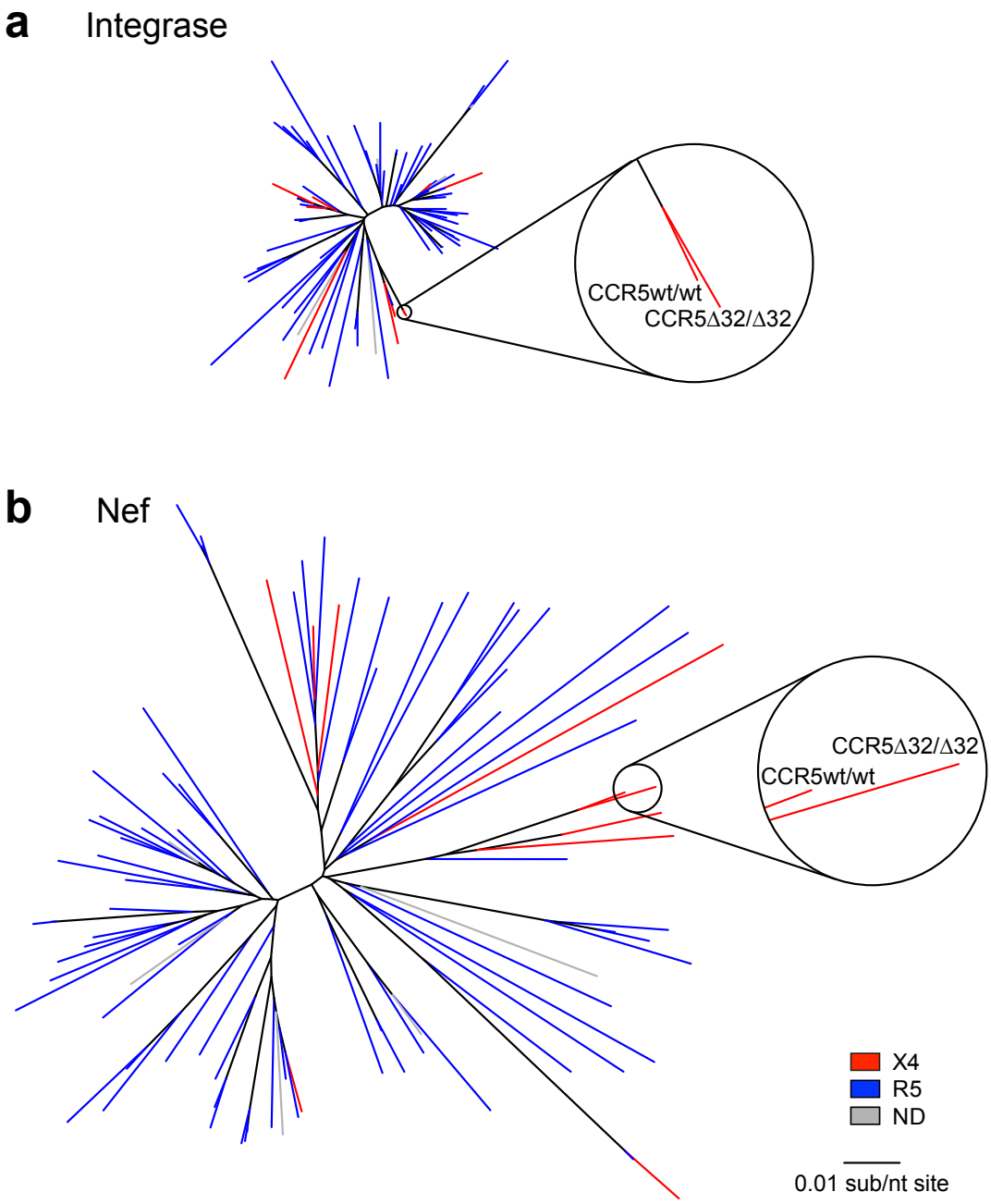

Figure S1: Maximum likelihood phylogenies of bulk HIV-1 Integrase and Nef sequences from VIDUS participants

Maximum likelihood phylogenetic trees were constructed using available bulk Integrase (*panel A*) and Nef (*panel B*) sequences from acute and chronically infected participants of

the Vancouver Injection Drug Users Study. The CCR5wt/wt and CCR5Δ32/Δ32 individuals' sequences are shown in the zoomed-in window. Tree tips are coloured according to coreceptor usage predicted using V3 genotypes: red for X4-using, blue for R5-using sequences and gray for Gag sequences for which no corresponding V3 sequence was available for coreceptor prediction (ND; not determined).

Supplementary Figure 2

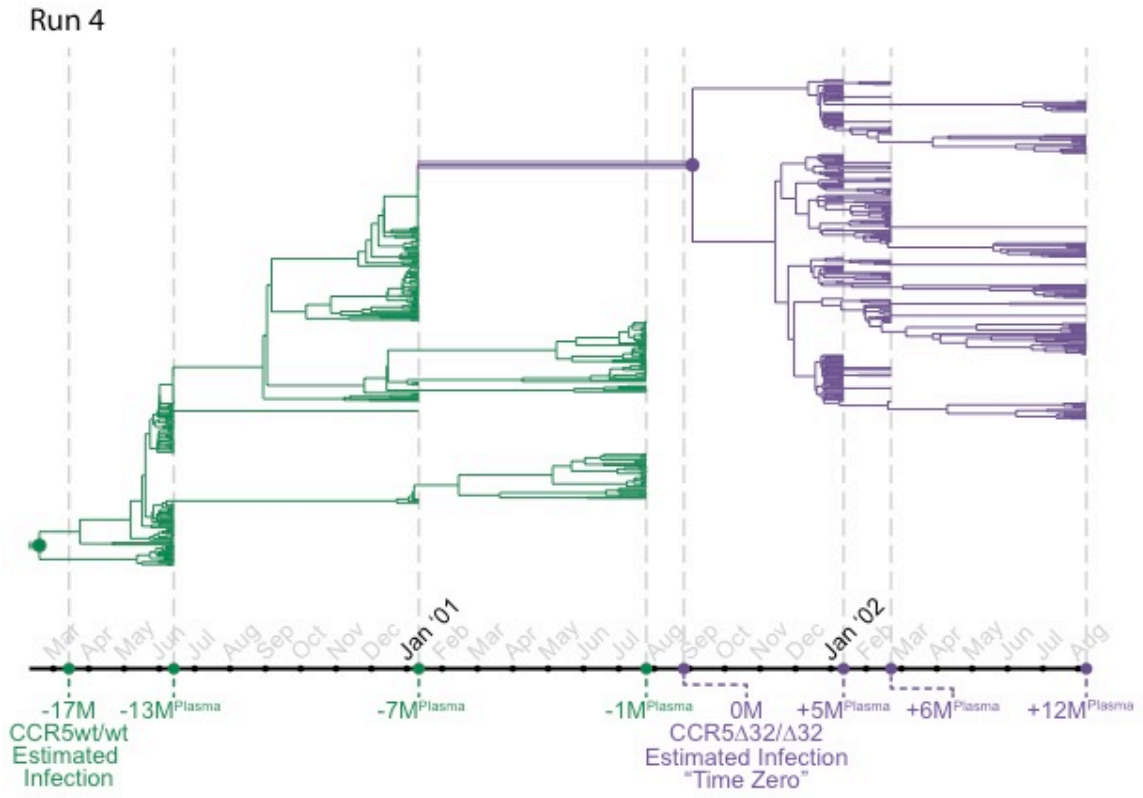

Figure S2: Second representative ancestral phylogenetic reconstruction of HIV-1 V3 transmission/evolution

A total of 10 ancestral phylogenetic reconstructions were performed by sampling 100 plasma HIV RNA-derived ultradeep sequences per timepoint for the three CCR5wt/wt (green) and three CCR5Δ32/Δ32 (purple) timepoints closest to time zero. Shown is a second representative ancestral phylogenetic reconstruction. Again, reconstruction supports that the CCR5wt/wt and CCR5Δ32/Δ32 individuals were productively infected by a single X4 virus, within a time period that coincides with the clinical estimated dates of infection (shaded branches).

Supplementary Figure 3

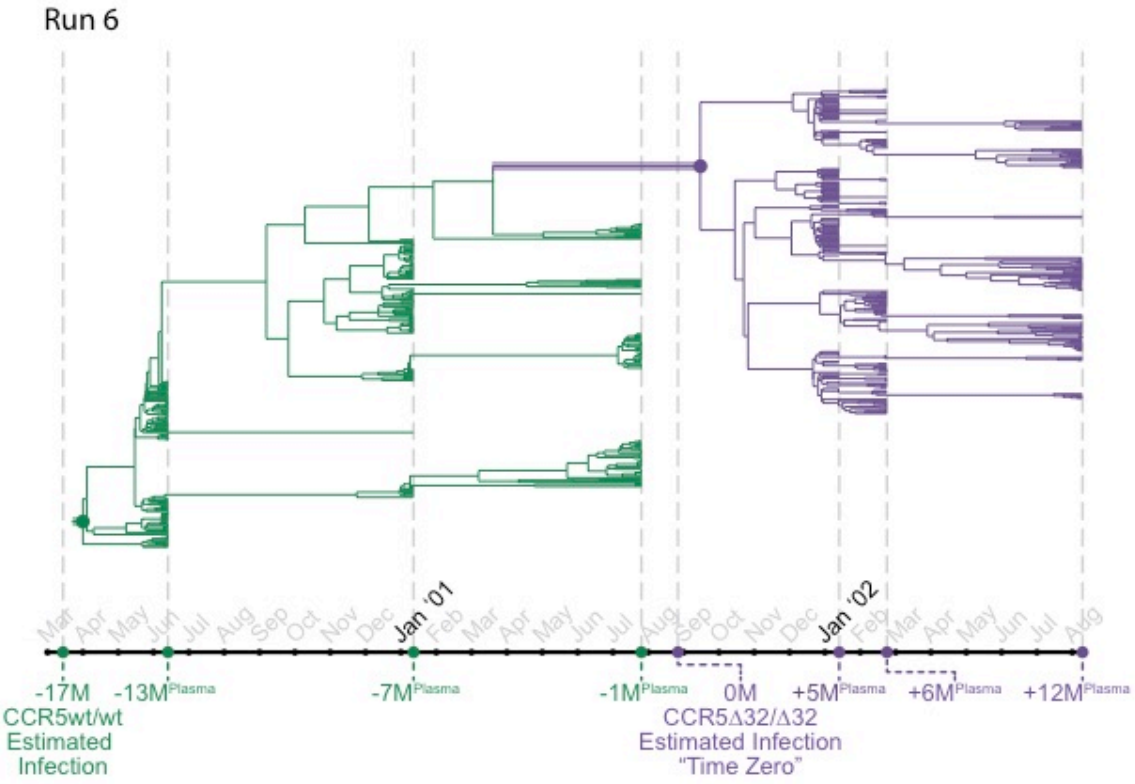

Figure S3: Third representative ancestral phylogenetic reconstruction of HIV-1 V3 transmission/evolution. See legend for Figure S2.