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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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

Run 4

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