Supplementary Figure Legends

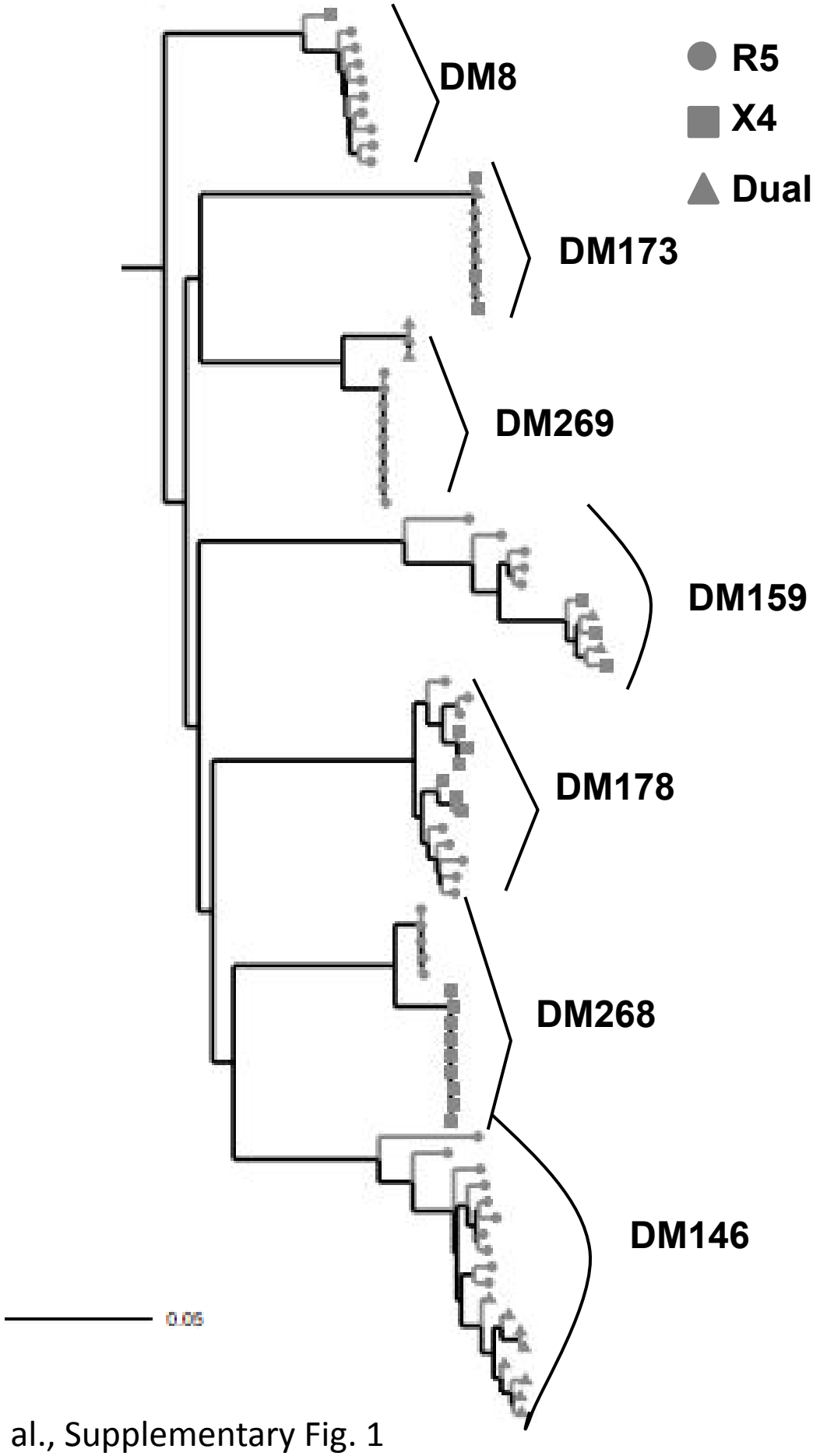
Supplementary Figure 1. Env variants with different co-receptor phenotype are interrelated among the individual subjects. Full-length env sequences from different subjects were aligned with reference sequence HXB2 from the Los Alamos database using Clustal X and manually edited using BioEdit (version 7.1.3). DiveIn (http://indra.mullins.microbiol.washington.edu/DIVEIN) was used to generate the maximum likelihood tree using GTR model. Subject IDs and HXB2 reference outgroup node are noted. Envs phenotyped as R5, dual, and X4 are noted as circles, triangles and boxes respectively. The tree was generated using a web tool at http://www.hiv.lanl.gov/content/sequence/RAINBOWTREE/rainbowtree.html.

Supplementary Figure 2. Single genome amplified HIV-1B X4 as compared to co-circulating R5 envs are more neutralization resistant to autologous contemporaneous plasma. Neutralization IC_{50}s for R5 (circles), dual-tropic (triangles), and X4 (boxes) viruses against autologous contemporaneous plasma. Symbols represent one of the 8 independent single genome amplified envelopes from a subject infected with HIV-1B. Y-axis shows the IC_{50} against autologous contemporaneous plasma as reciprocal dilution. The long line represents the median of the dot plot, and the whiskers show the interquartile range. Star indicates statistically significant difference ($p = 0.01$). The dashed line shows the highest tested plasma dilution (1:50). Symbols below the dotted lines are envs that were not neutralized by at least 50% at the highest tested plasma dilution (1:50). For statistical comparisons, these envs were assigned a midpoint value between 0 and 50.

Supplementary Figure 3. DM8 X4 variant is equivalent susceptible to neutralization by a late plasma sample. Graphs shows neutralization IC_{50}s against autologous plasma (reciprocal dilution) for DM8 R5 (circle) and X4 (box) variants. Graph a shows neutralization with a plasma sample collected around 6 months after the plasma from which the envs were isolated. The long line represents the median of the dot plot, and the whiskers show the interquartile range.

The dashed line shows the highest tested plasma dilution (1:50). Graph b shows the comparisons of the IC_{50}s between the contemporaneous versus late plasma sample. Star indicates statistically significant difference ($p = 0.008$).

Supplementary Figure 4. Passaged viruses show minimal env sequence changes compared to the input stock. The label at the left identifies the amino acid sequence of the env prior to passage (DM268-input), the env recovered from both U87 – CXCR4 and U87 – CCR5 culture supernatants after cells were exposed to day 75 plasma passaged virus stock (DM268+plasma), and env recovered from U87 – CCR5 culture supernatants after cells were exposed to day 75 virus passaged in the absence of plasma (DM268-plasma). Sequences from the beginning of env to the end of the ecto-domain are shown in single-letter amino acid code. The first box highlights the asparagine (N) change in DM268+plasma and the predicted N – linked glycosylation site. The second box shows the V3 loop sequence. Figure also shows the sites with mixture of amino acids in DM268-plasma. Nucleotide sequences were generated after RNA isolation from culture supernatants and direct sequencing of a bulk RT-PCR product. Amino acid sequence was generated using Bioedit (version 7.1.3).



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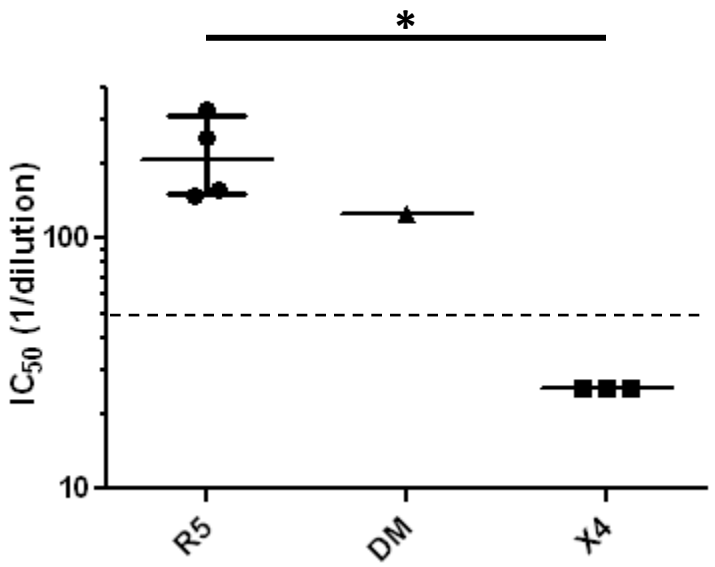
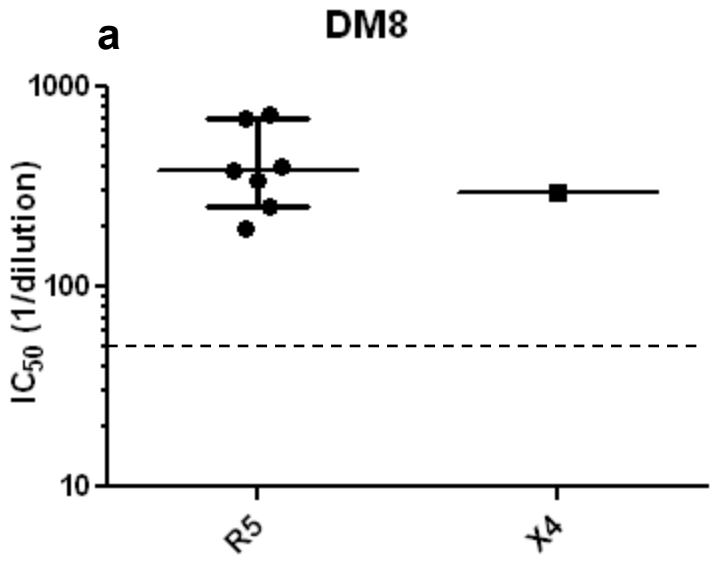
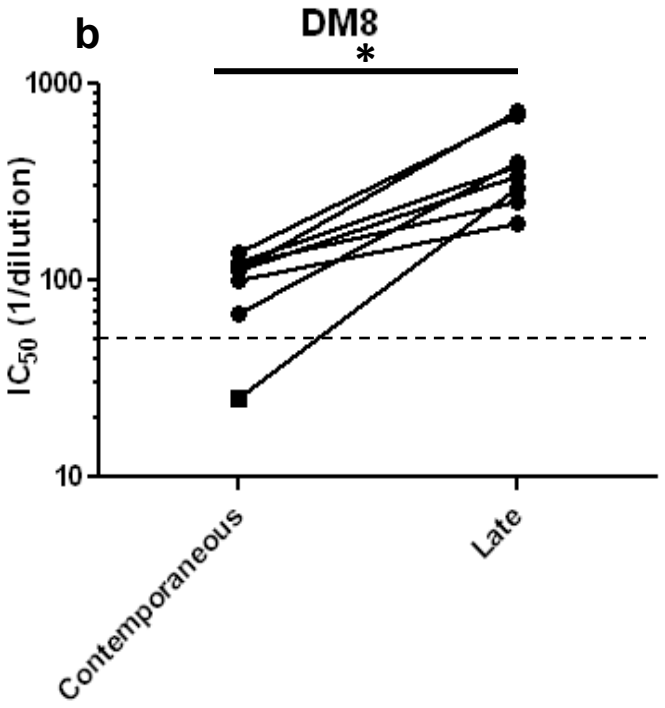


Lin et. al. Supplementary Fig. 2





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Lin et. al. Supplementary Fig. 4