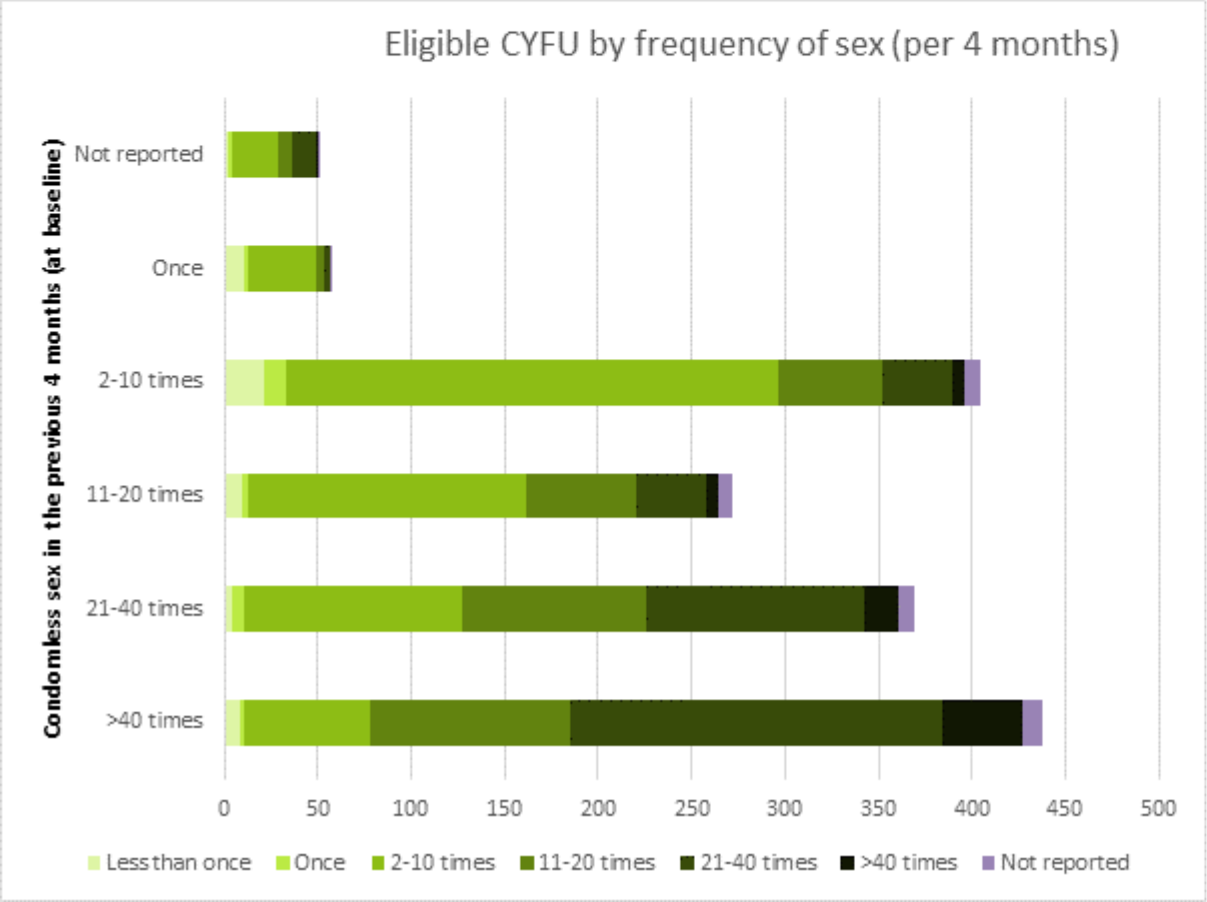
THE LANCET

Supplementary appendix

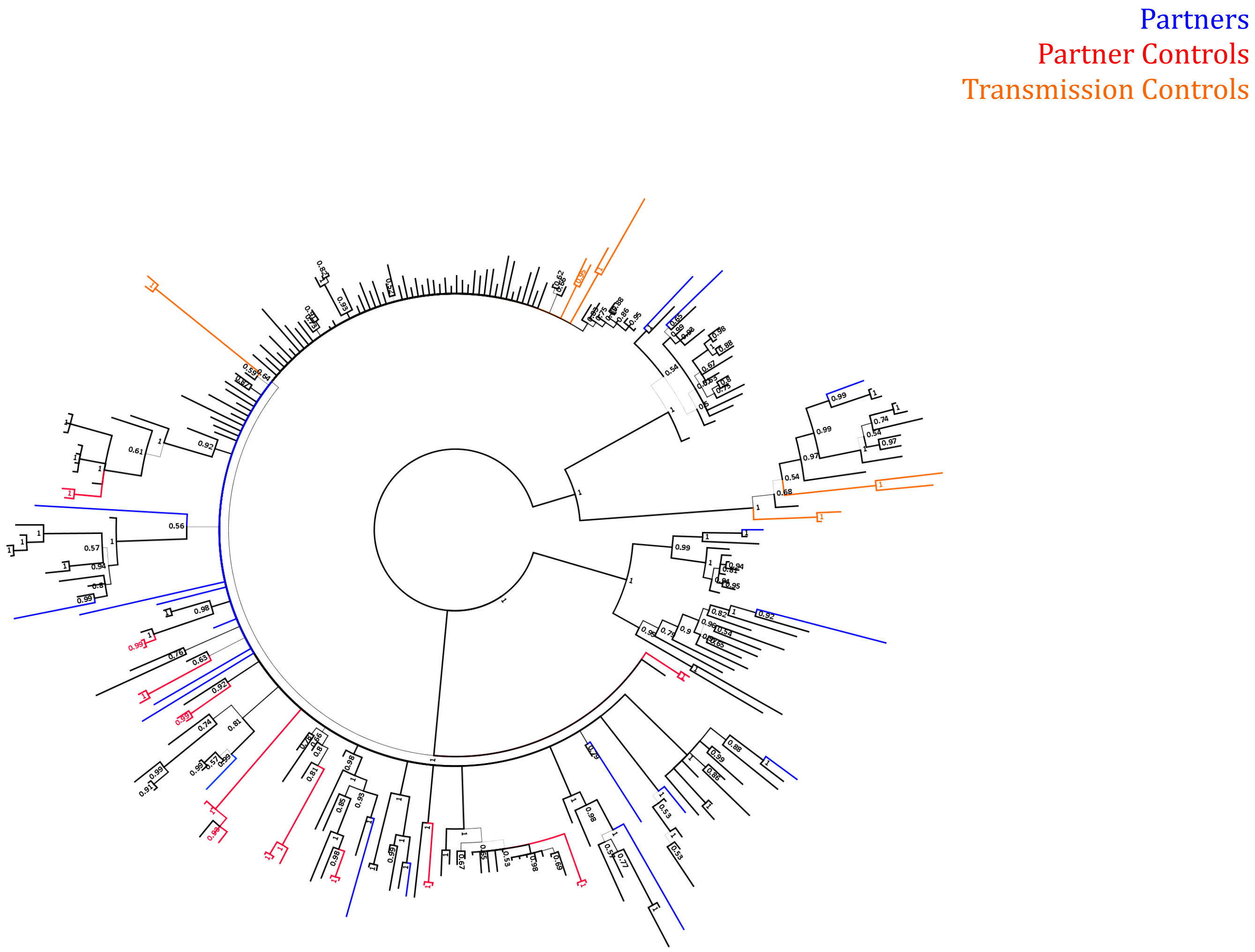
Supplement to: Rodger AJ, Cambiano V, Bruun T, et al. Risk of HIV transmission through condomless sex in serodifferent gay couples with the HIV-positive partner taking suppressive antiretroviral therapy (PARTNER): final results of a multicentre, prospective, observational study. *Lancet* 2019; published online May 2. http://dx.doi.org/10.1016/S0140-6736(19)30418-0.

Suppl. figure 1: Frequency of condomless sex during eligible Couple Years of Follow Up (CYFU)



Suppl. figure 2a: Phylogenetic tree of *pol* sequences from 15 couples, including 6 couples with subtype-discordant infections.

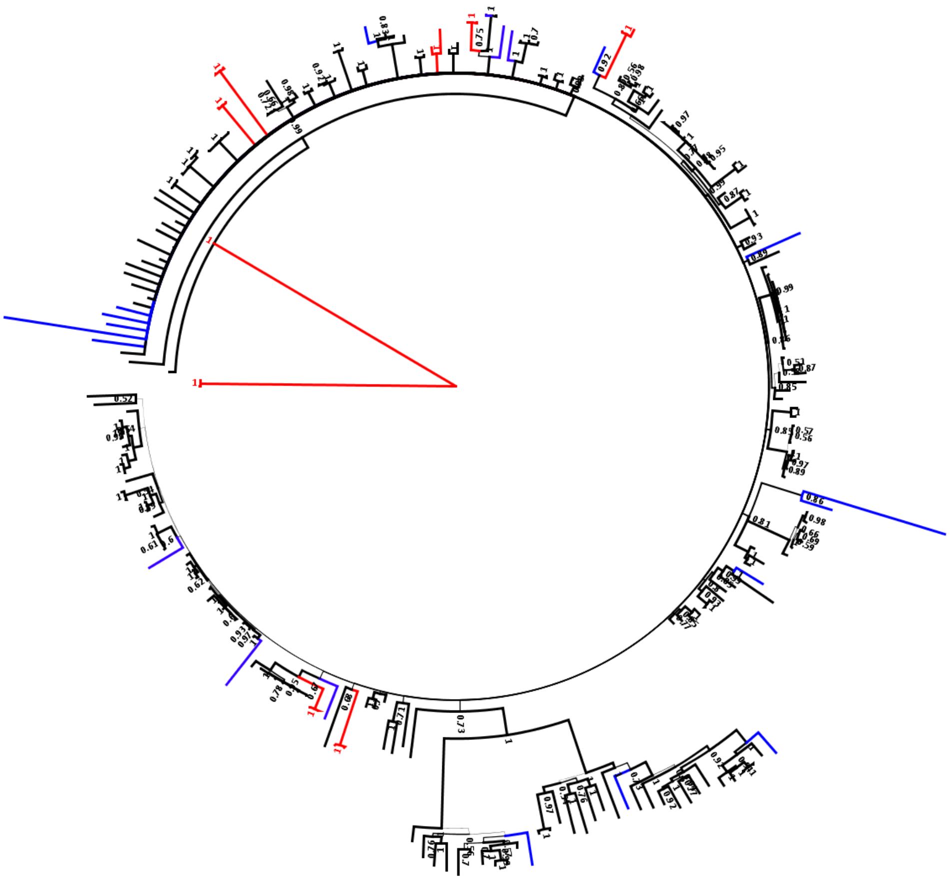
Bayesian Markov Chain Monte-Carlo (MCMC) inference (012212+I+G+F). Branch length is proportional to the genetic distance and line weight is proportional to the posterior probability. Partners' sequences are in blue and are phylogenetically unlinked to viruses recovered from their putative transmitters, with a median pairwise genetic distance 0.068 (0.060, 0.086) and pairwise genetic distances consistently >0.040. Positive control sequences comprised replicate sequences from study partners (in red) and sequences from confirmed transmission pairs obtained in a separate study (in orange)[1]. The positive control sequences shown pairwise genetic distance 0.004 (IQR: < 0.000, 0.007) and always closely linked on monophyletic branches with posterior probabilities >0.95 (red and orange clusters in the phylogenetic tree). Control sequences comprised the 10 closest sequences identified through BLAST searches of GenBank.



Suppl. Figure 2b: Phylogenetic tree of *env* sequences from 15 couples, including 6 couples with subtype-discordant infections.

Bayesian Markov Chain Monte-Carlo (MCMC) inference (012312+I+G+F). Branch length is proportional to the genetic distance and line weight is proportional to the posterior probability Partners' sequences are in blue and found phylogenetically unlinked to viruses recovered from their putative transmitters, with a median pairwise genetic distance 0.171 (0.134, 0.204) and positive control sequences comprised replicate sequences from study partners are in red. The positive control sequences shown pairwise genetic distance 0.001 (<0.001, 0.014) and always clustered on monophyletic branches with posterior probabilities =1.00 (red clusters in the phylogenetic tree). Control sequences comprised the 10 closest sequences identified through BLAST searches of GenBank.

Partners
Partner Controls



Reference

1. Beloukas A, Magiorkinis E, Magiorkinis G, et al. Assessment of phylogenetic sensitivity for reconstructing HIV-1 epidemiological relationships. Virus Res 2012; 166: 54–60.