**Supplemental Digital Content 1. Methods used for linkage analysis.**

The genetic linkage status was determined for index-partner pairs using methods described in a previous report (Eshleman, et al. J Infect Dis. 2011; 204:1918-1926). The classification of “linked” indicates that the HIV sequences from an index participant and the corresponding partner are closely related; in these cases, the index was the likely source of the partner’s infection. The methods used to assess linkage status are summarized below.

First, *pol* region sequences (HIV protease and reverse transcriptase) were obtained using the ViroSeq HIV-1 Genotyping System (Celera, Alameda, CA). Phylogenetic analysis was performed using sequences from index-partner pairs, unrelated index participants (local controls), and reference sequences. Whenever possible, the analysis was performed using two samples from each individual (index and partner), collected on different dates. Sequences were aligned using MegAlign v5.07 (Clustal W method). PHYLIP (Neighbor-Joining and Consense) was used to generate phylogenetic trees and bootstrap values. Index-partner pairs were provisionally classified as linked if all of the sequences from the two individuals clustered together on a single branch of the tree with a high bootstrap value.

Next, genetic similarity values were calculated for the *pol* region sequences from index-partner pairs and local controls. These data were analyzed using Bayesian methods to determine the probability of linkage between different individuals. Index-partner pairs were provisionally characterized as linked by Bayesian analysis if the linkage probability was ≥0.5 for all pairs of sequences from the two individuals. Index-partner pairs were classified as linked (final status) if they were characterized as linked by both of these methods (phylogenetic and Bayesian analysis of *pol* region sequences); no further analysis was performed for these cases.

For the remaining cases, next generation sequencing was performed for a region of gp41 (HXB2 coordinates: 7691-8374) using a Roche 454 instrument (Roche, Branford, CT). Index-partner pairs were classified as linked (final status) if multiple consensus sequences from the index and the partner clustered together on a branch with a high bootstrap value.

Additional information describing the algorithm used for linkage analysis and the results obtained at each phase of testing for partner infections in HPTN 052 is presented elsewhere (Cohen, et al. New Eng J Med. 2016; 375:830-839).