Background
The cytokine/chemokine network in genital secretions reflects the functional status of immune cells in the genital tract, where the key events related to sexual transmission occur.

Objective
To describe differences in cytokine/chemokine levels in semen between men living with HIV who transmitted and men who did not transmit HIV to their male sexual partner.

Cohort and Sampling
- Participants were men with primary HIV infection and their recent male sexual partners (HIV-positive or negative).
- HIV transmission among sero-concordant partnerships was defined as phylogenetic linkage (31.5% genetic distance in pol).
- The HIV-positive partner with the earlier estimated time of infection (EDI) was considered the source.
- Among sero-discordant couples, the HIV-positive partner was considered the (potential) source.
- All analyses were restricted to the source partners.
- Sources with sero-discordant partners were classified as non-transmitters (n=23); those with sero-concordant phylogenetically-linked partners were considered transmitters (n=21).
- For each source partner (transmitter or non-transmitter), semen was collected at a cross-sectional visit.

Data Generated
- The following 33 cytokines/chemokines were measured by Luminescex: IL-10, MIP-3α, GRO-α, Calgranulin, IL-33, IL-21, IL-12, iTAC, IL-18, IL-4, IFN-γ, IL-8, IL-16, IL-2, GM-CSF, M-CSF, IP-10, TNF-α, IL-1α, IL-6, IL-15, RANTES, TGF-β, MIP-1α, MIG, MCP-1, IL-1β, Eotaxin, IL-13, IL-17, IL-22, IL-7, MIP-1β.

Statistical Methods
- Unsupervised principal-components analysis was used to cluster cytokines (Figure 1). Clusters of cytokines were identified that were the most correlated among themselves and least correlated with cytokines in other clusters, by splitting clusters if the second eigenvalue for the cluster was greater than 0.70.
- Within each cluster, we chose the cytokine with the strongest association with transmission using logistic regression as a cluster representative.
- Cytokines with p<0.10 were considered for multiple regression, in the presence of the following covariates from the source partner: ART status, EDI, age, race/ethnicity, CD4+ and CD8+ cells, HIV RNA levels in blood and semen, presence of seminal HSV-2, EBV or CMV DNA.