We modeled each viral property using a Bayesian hierarchical regression model ([[Gelman et al. 2003]]) in order to account for 1) nested measurements within a transmission pair, 2) multiple transmissions from a single donor, 3) heteroscedasticity between groups and 4) censored data where we only know that a measurement is less than a given value. These models assumed observations within a single patient-fluid-treatment were normally distributed with mean and variance drawn from population-level distributions and are described further in [[supplementary XXX]]. The posterior probability distributions for the parameters were estimated using Markov chain Monte Carlo sampling implemented in Stan v2.12.0 ([[Carpenter et al., In Press]]) and R v3.3.1 ([[R Core Team, 2016]]). [[We could move until end of paragraph into Supplement]] Parameters were included to estimate the change in the log-transformed, or logit-transformed for proportional data, observations between donor plasma and donor genital fluid or recipient plasma viruses along with the effects of HIV subtype and IFNα2- and IFNβ-selection. Reported fold change estimates were based on the estimated posterior mean and probability values were calculated from the estimated cumulative posterior probability for an fold change less than 1 (or above 1 in the case of a posterior mean <1) for the population-level parameters of interest.

Principal component and receiver operating characteristic analysis ([[Robin et al. 2011]]) and plotting were performed using R v3.3.1. Code and data are archived on Zenodo doi:[[XXX.YYY]].

[[REFS

Gelman et al. 2003:

https://www.crcpress.com/Bayesian-Data-Analysis-Second-Edition/Gelman-Carlin-Stern-Rubin/p/book/9781584883883

R Core Team:

R Core Team (2016). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.

Carpenter et al. In Press: <http://www.stat.columbia.edu/~gelman/research/published/stan-paper-revision-feb2015.pdf>

Robin et al. 2011:

http://bmcbioinformatics.biomedcentral.com/articles/10.1186/1471-2105-12-77

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[[We can make a permanent archive of my code (after a bit of cleanup) and potentially your big data summary .csv on Zenodo (hosted by CERN (the Large Hadron Collider guys)):

https://guides.github.com/activities/citable-code/

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