Main Analysis of manuscript – Per-pathogen Virulence of HIV-1 subtypes A, C and D

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Setup

Setup R and read open data file.

Analyses

Calculate disease progression from the decline and initial values after primary infection.

Create Figure 2

Compare the CD4 cell decline (calculated with the mixed linear model), the CD4 level at the start of the chronic infection (calculated with the mixed linear model), the setpoint viral load and the disease progression between the subtypes.

Create Supplementary Figure 1

Country-wise comparison.

Results for Table 2

Next, we model the relationship between disease progression (gamma) and the setpoint viral load, to find the per-pathogen virulence.

Suplementary Figure 2

Figure 3