



Figure 1. Study Design, Read Statistics, and Phylogenetic Distribution

(A) Immunosuppression reduces the risk of rejection in transplantation but increases the risk of infection.

(B) Design of study: 656 plasma samples were collected, cell-free DNA was purified and sequenced to an average depth of 1.25 Gbp per sample.

(C) Number of samples collected as function of time for the different patient groups part of the study.

(D) Treatment protocol for patients in the study cohort, all patients are treated with maintenance immunosuppression (tacrolimus-based [TAC] for adult heart at lung transplant recipients and cyclosporine [CYC] for pediatric patients). CMV positive (donor or recipient, CMV+) transplant cases are treated with anti-CMV prophylaxis, valganciclovir (VAL). Mean level of tacrolimus measured in blood of transplant recipients treated with a TAC-based protocol (dashed line actual, solid line window average filter).

(E) Fraction of reads that remain after filtering of lower quality and duplicate reads (mean 86%, left) and after removal of human and low-complexity reads (mean 2%, right).

(F) Relative genomic abundance at different levels of taxonomic classification after removal of human reads (average over all samples from all organ transplant recipients ($n = 656$)). The central pie chart shows the composition at the superkingdom level of classification. Lower levels of classification are shown in donut charts with progressively larger radius.

See also Figure S1.