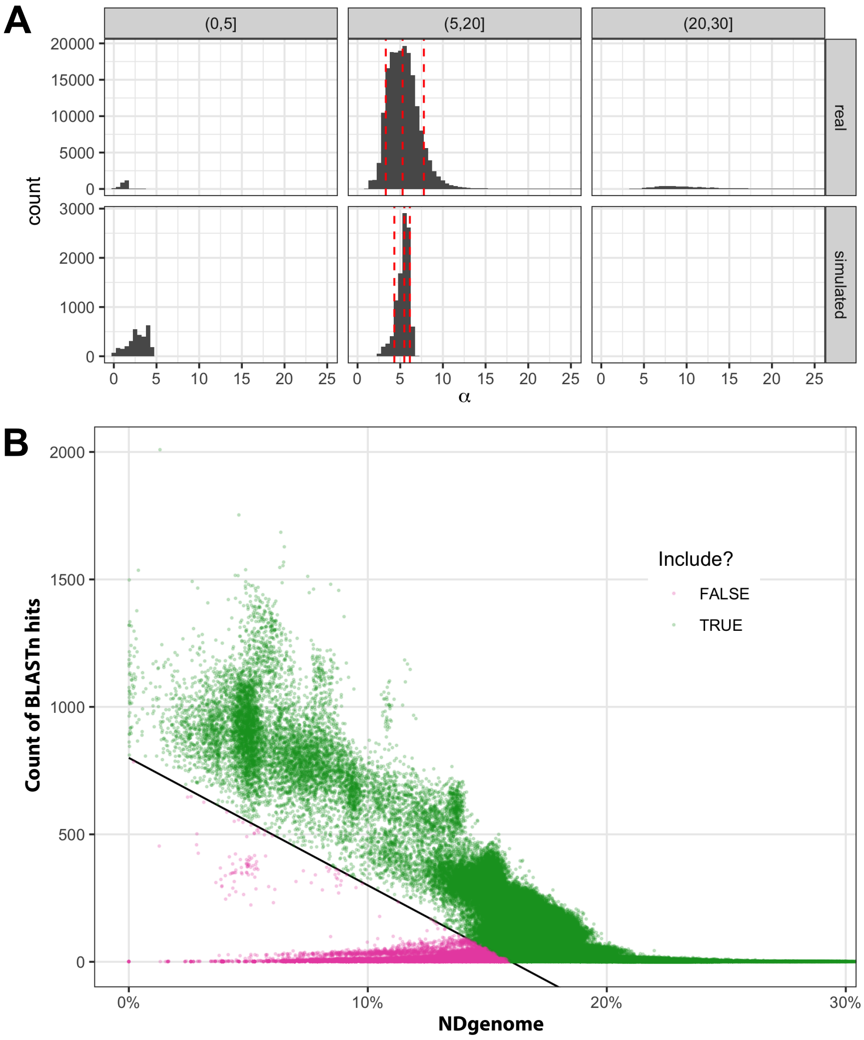

Fig. S3. Determination of the shape parameter α, the inverse of the variance of one-centered substitution rate multipliers across genes. (A) Distribution of α estimated for pairs of genomes in the GORG-Tropics (top) and a simulated, LGT-free dataset (bottom). We divided the set of genome pairs by their estimated NDgenome into three groups (thresholds set at 5% and 20% NDgenome). Genome pairs with <5% or >20% NDgenome had outlier estimates of α and thus were excluded. Quantiles of the distribution in the middle panel (3.31, 5.28, and 7.77) are shown as dotted lines. **(B)** Correlation between the count of BLASTn hits and NDgenome in pairs of GORG-Tropics genomes. Outliers below the shown line were excluded from α estimates.