

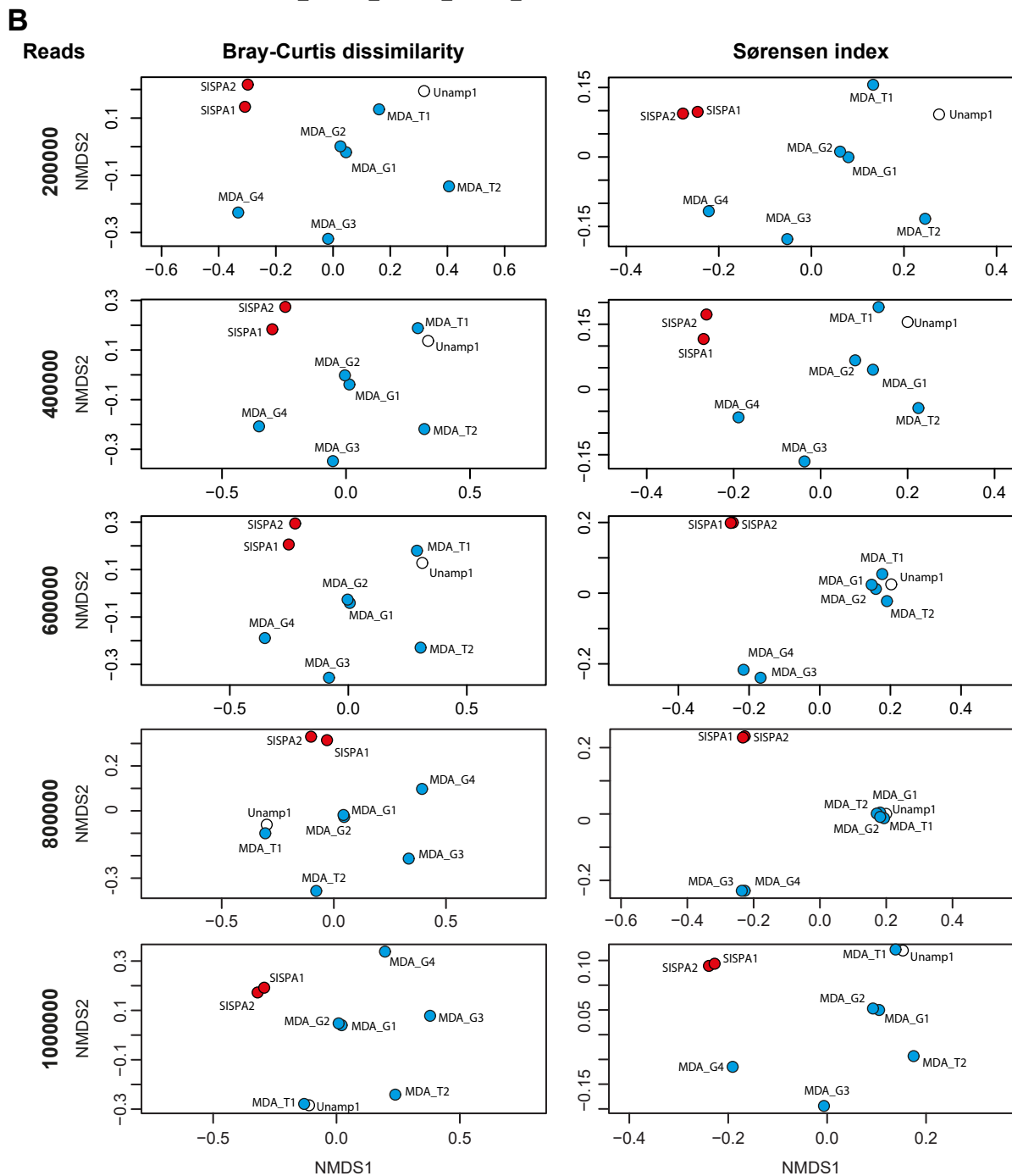
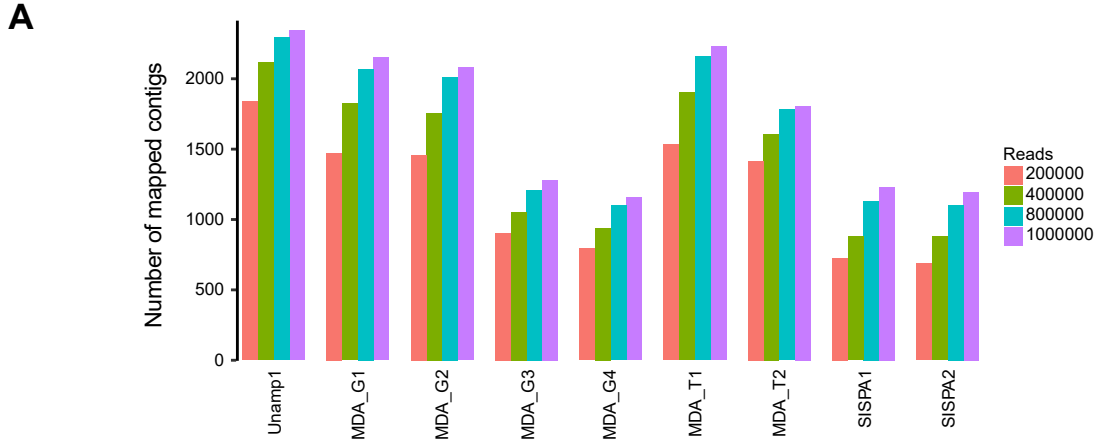


Figure S3. Impact of random amplification on beta diversity studies of saliva viromes at different sequencing depths.

(A) Cross-contigs mapped with 200000, 400000, 800000 and 1000000 reads from unamplified and amplified viromes are shown. **(B)** NMDS ordination plots of Bray-Curtis dissimilarities and Sørensen indexes calculated from normalized (RPKM) cross-contig abundance are shown.