

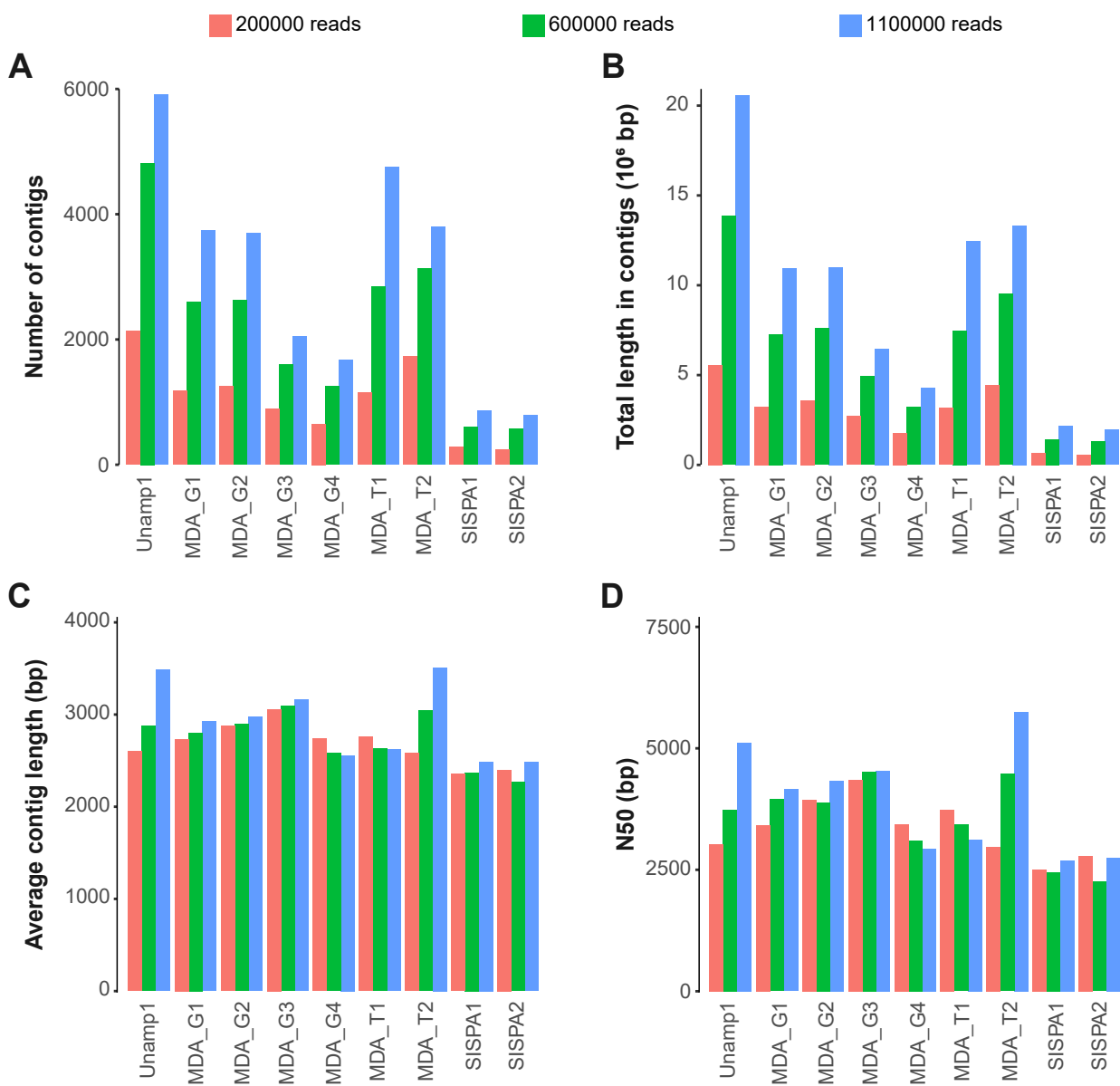


Figure S4. Impact of random amplification and sequencing depth on de novo assembly metrics. (A) Number of contigs, (B) total length in contigs, (C) average contig length and (D) N50, obtained with 200,000, 600,000, and 1,100,000 reads for each virome are shown.