



### Supplementary Figure 1. Computational processing workflow

Sequencing reads first underwent universal quality control, human depletion (via stringent criteria of >20% kmers within the read classifying specifically to human taxid), and deduplication (A). These reads were assembled into contigs, and >600bp contigs were BLASTed to recover strong reference matches for long contigs (B). These were used as a "negative controls" depletion database, after which remaining reads were classified via comprehensive Krakenuniq and Kaiju databases. Viral hits were validated using BLASTn.