

Number of sequences

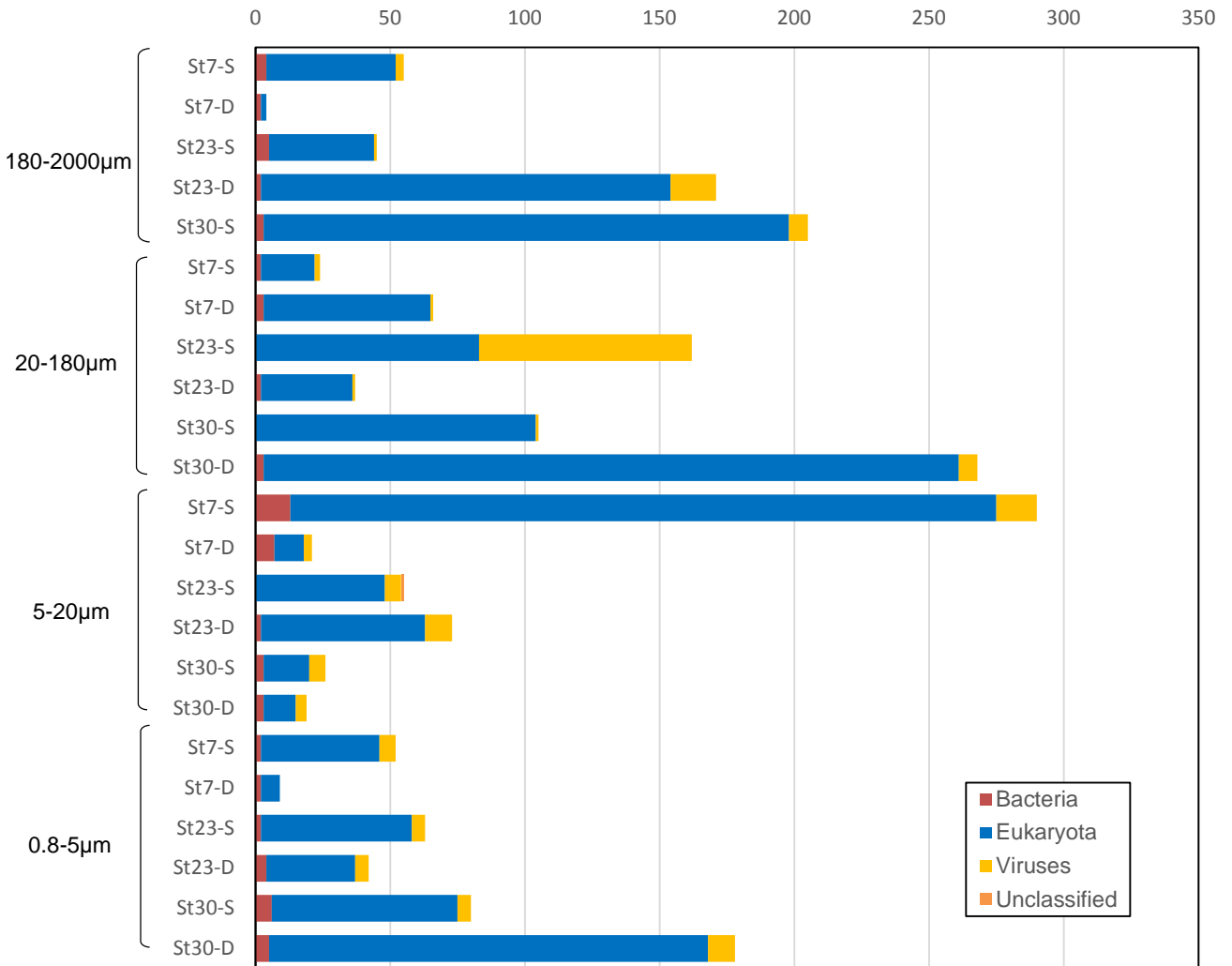


Figure S7. Number of identified RT-like metatranscriptomic sequences and their taxonomic classification. The stringent taxonomy annotation method allowed us to classify 2050 metatranscriptomic sequences.