

Additional File 3.

Relative abundances of eukaryotic 18S rRNA gene sequences in assembled metagenomic contigs. Predicted 18S rRNA genes > 530 nt were pooled from all assembled contigs and given taxonomic assignments based on closest SILVA database match. Relative abundances were calculated based on assembly coverage depth multiplied by assembled 18S rRNA gene length. Additional details provided in Additional File 4.

