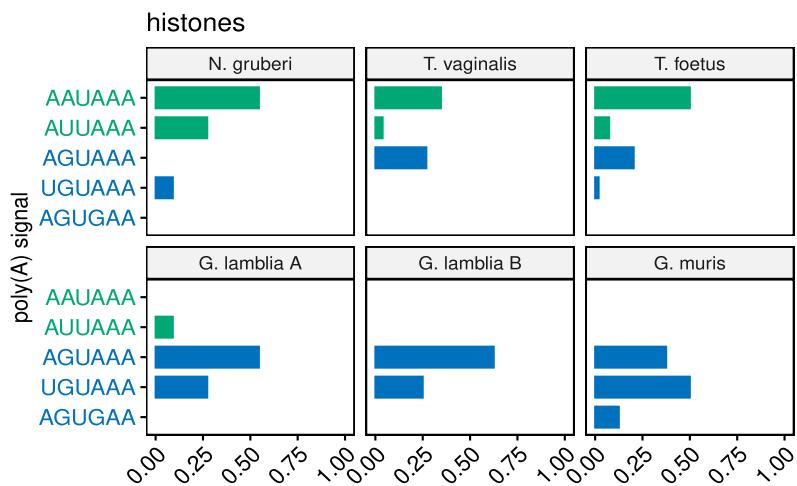
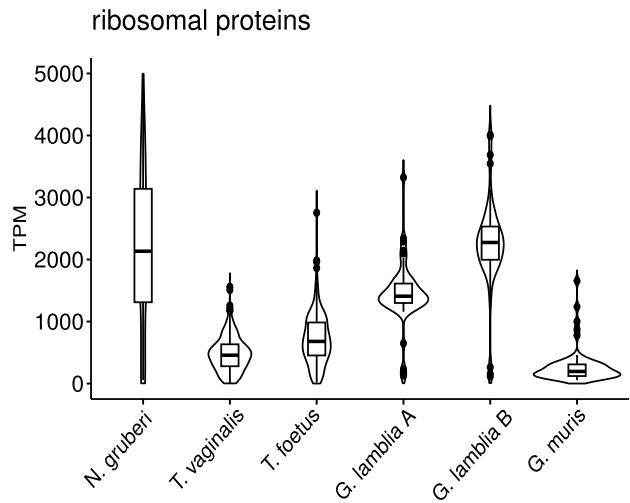


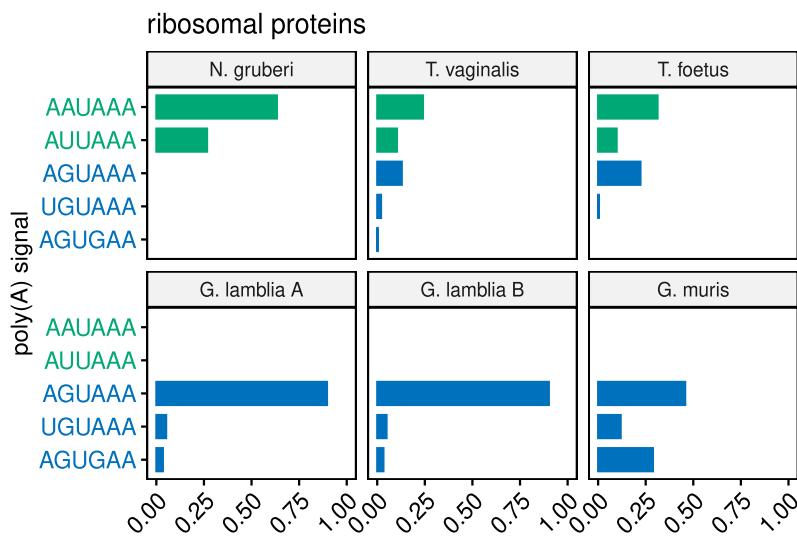
G



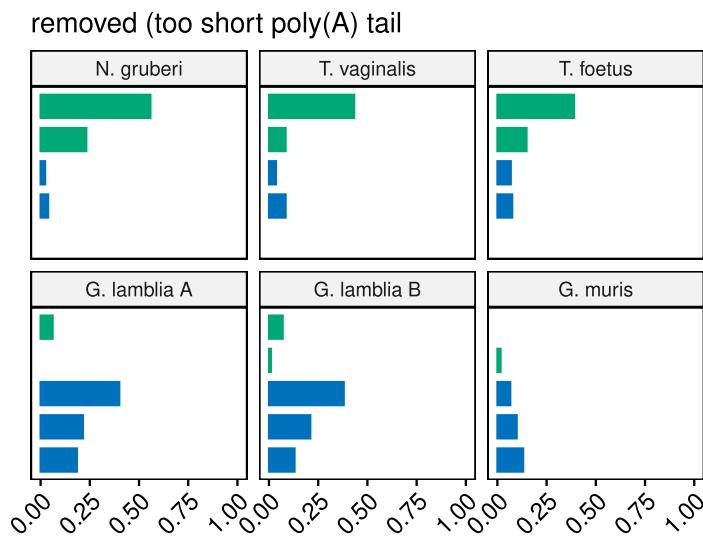
H



I



J



Supplemental Figure S1. Technical characterization of protists ONT sequencing results (related to Figure 1). A. Heatmap of the Spearman correlation of gene expression levels between sequencing replicates. B. Distribution of poly(A) tail lengths in sequenced organisms. Bars highlighted purple indicate reads with poly(A) tails shorter than minimal length threshold for a given organism, that were discarded from the analysis. Vertical dashed lines indicate median lengths. C. Fraction of reads included or discarded from the analysis for each dataset based on poly(A) tail annotation. D. Boxplot of expression of genes included in subsequent analysis vs genes removed because of too short poly(A) tail. E. Barplot of the number of annotated 3'UTRs in protists. F. Violin plot of 3'UTR lengths in protists. Median lengths of the annotated 3'UTRs are showed on top. G. Quantification of poly(A) signal hexamer frequencies in annotated histone genes in the regions 40 nt upstream from the cleavage sites. H. Violin plot of expression of genes encoding ribosomal proteins genes in the regions 40 nt upstream from the cleavage sites. I. Quantification of poly(A) signal hexamer frequencies in annotated ribosomal proteins genes in the regions 40 nt upstream from the cleavage sites. J. Quantification of poly(A) signal hexamer frequencies in genes removed from the analysis because of too short poly(A) tails.