Supplementary Figure S2. Heatmap of fpkm for the eDNAs. The figure shows a heatmap of the fpkm of eDNAs. Sequence data from 11 eDNA samples were assigned to NCBI taxonomy IDs that corresponded to 6641 metazoan species using blastn. The read counts were converted to fpkm, and a fpkm matrix with 11 rows and 6641 columns was created. The heatmap was created using the heatmap function in R with the following options: clustering_distance_cols = "correlation", clustering_method = "ward.D2".