**Figure 1 – Identification of foreign sequences in 3 independent *H. dujardini* assemblies by different methods.**

**(A)**, Foreign genes identified using the HGT index. The percent of all foreign genes in each dataset is shown. Tardigrade datasets are labeled in blue. Rotifer (animals known to contain high levels of foreign genes within their genomes) are shown in brown. Other invertebrates (*C. elegans* and *D. melanogaster*) are labeled in green.

**(B)**, Foreign genes were identified by selecting only those with BLAST hits to prokaryotes, but not eukaryotes (Evalue cutoff 1e-5). Note that this is a significantly more stringent approach for identifying foreign genes than the HGT index and excludes identification of prokaryotic genes with metazoan homologs, non-metazoan eukaryotic genes, or metazoan genes that have been horizontally transferred. The raw number of all foreign genes in each dataset is shown. Tardigrade datasets are labeled in blue. Rotifer (animals known to contain high levels of foreign genes within their genomes) are shown in brown. Other invertebrates (*C. elegans* and *D. melanogaster*) are labeled in green.