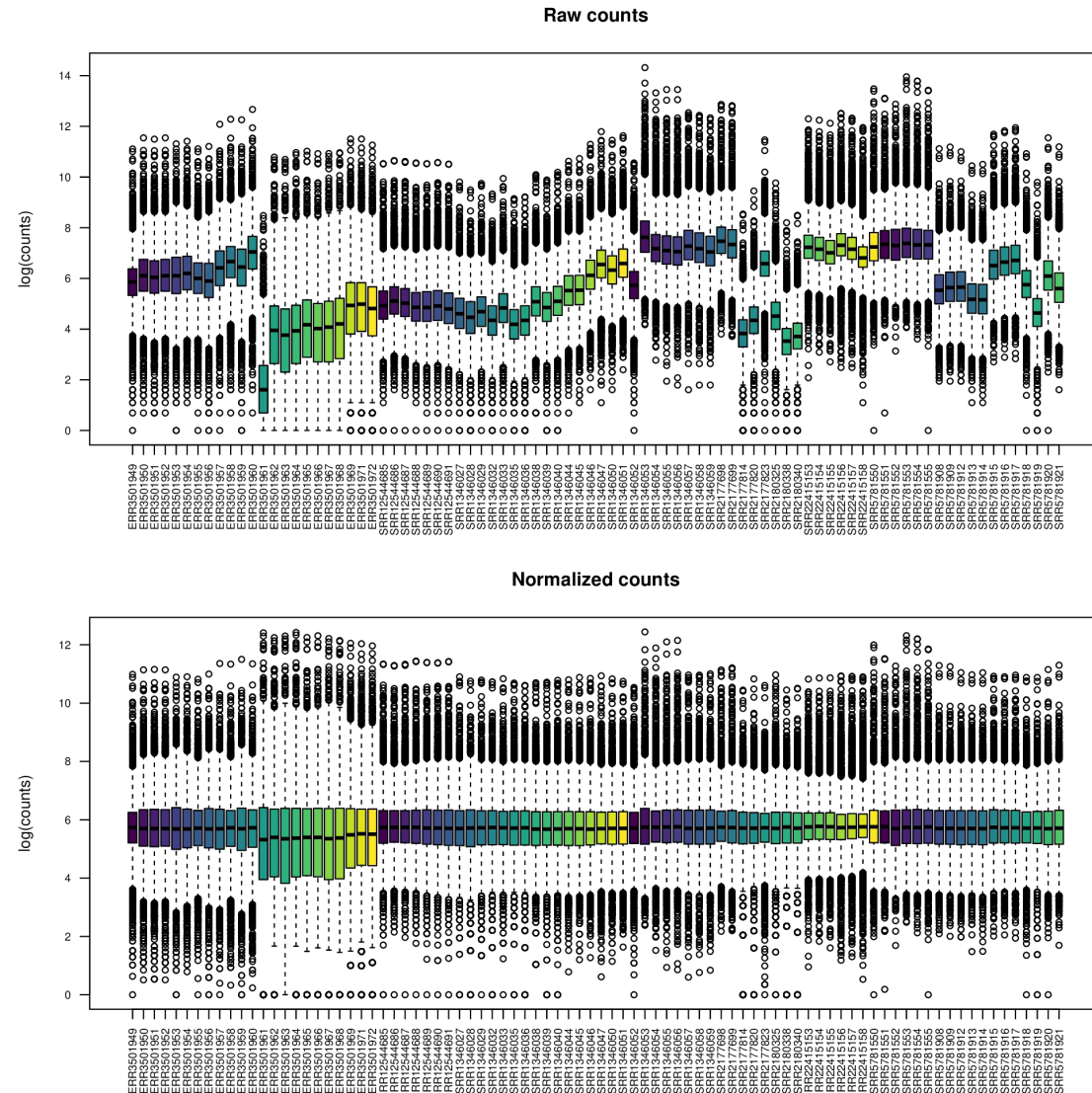


Supplementary Figure S1. The graph shows the dispersion of the counts before and after normalization using median proportions with DESeq2. Box plots were generated from the logarithmically transformed counts ($\log(\text{counts} + 1)$).



Supplementary Figure S2. Expression analysis process used for comparison across *T. cruzi* life cycle forms and strains. A) First, libraries derived from intracellular amastigotes were filtered to remove human reads. B) The human-sequence-free amastigote libraries, along with the libraries corresponding to the other *T. cruzi* life cycle forms, were processed by Seq2Fun for cleaning, mapping, and quantification. Subsequently, differential expression analysis and Gene Ontology (GO)-KEGG term enrichment analysis was performed using Gene Set Enrichment Analysis (GSEA), and orthologous group co-expression network analysis of orthologous group modules. Silhouette images were obtained from phylopic.org.

