

1 **Analysis of mRNA processing at whole transcriptome level, transcriptomic profile**
 2 **and genome sequence refinement of *Trypanosoma cruzi*.**

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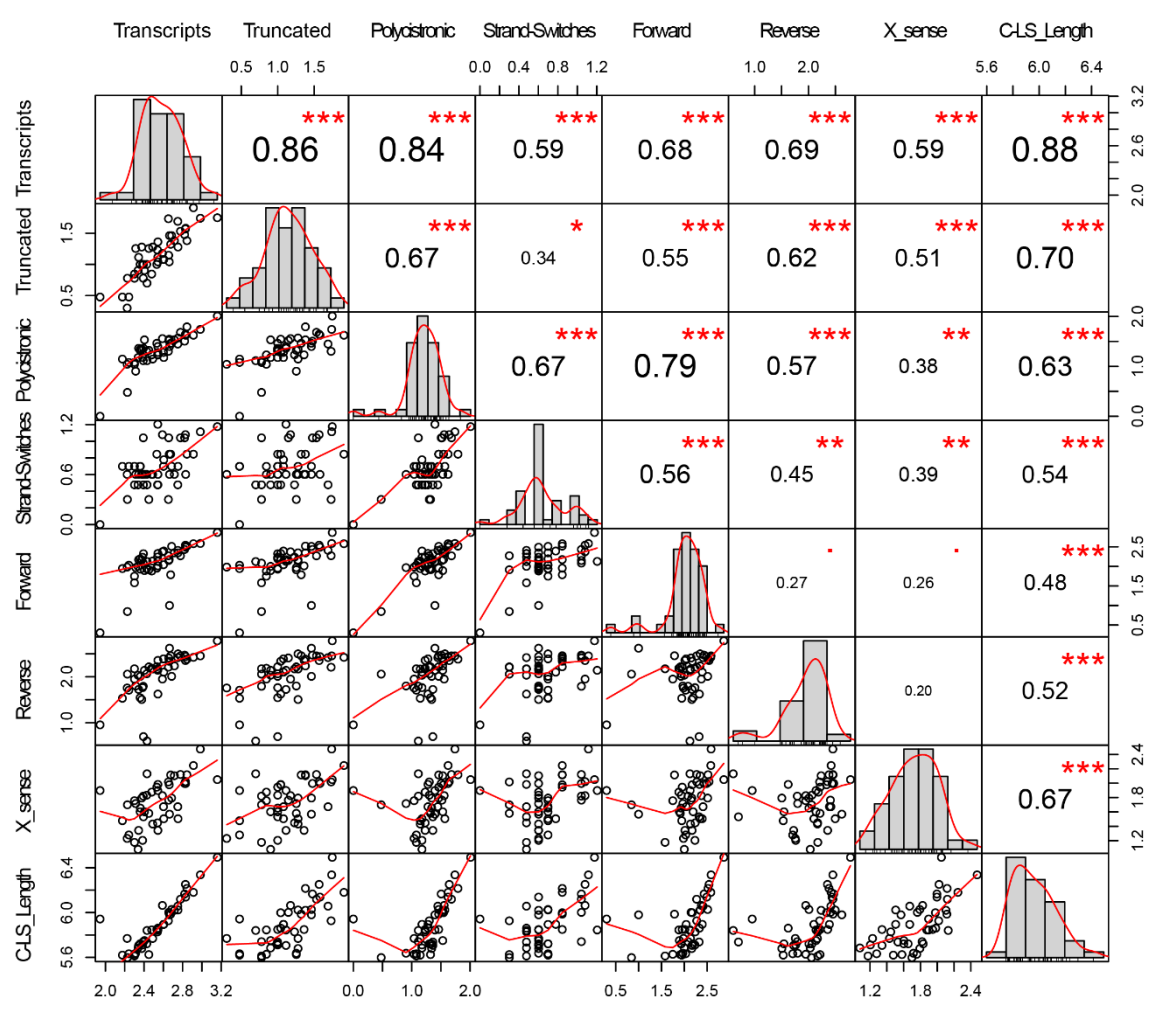
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11 **Supplementary Information**

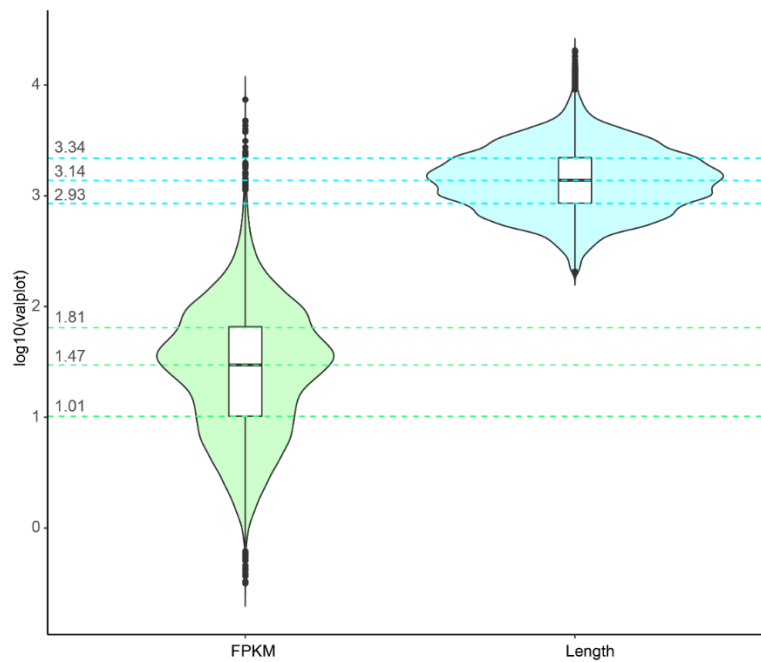


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13 **Supplementary Figure 1.** Spearman correlation of Sylvio X10 transcriptome
 14 annotations. Spearman correlation between the annotated features of Sylvio X10

15 transcriptome, “transcripts”, correspond to total transcripts, the number of polycistronic
16 and truncated transcripts per chromosome are labelled as “polycistronic” and
17 “truncated”, respectively, “Forward”, “Reverse” and “X_sense” refers to the transcript
18 sense, “Strand-switches” to the SSR identified and finally “C-LS_length” corresponds to
19 the chromosomal length. Data distribution is shown in diagonal histograms and density
20 lines, lower matrix contains the bivariate scatter plots with a fitted line and the correlation
21 value is shown in the upper matrix. P-values of the correlation are shown as red stars (\leq
22 to 0, 0.001, 0.01 corresponds to “***”, “**”, “*”, respectively).

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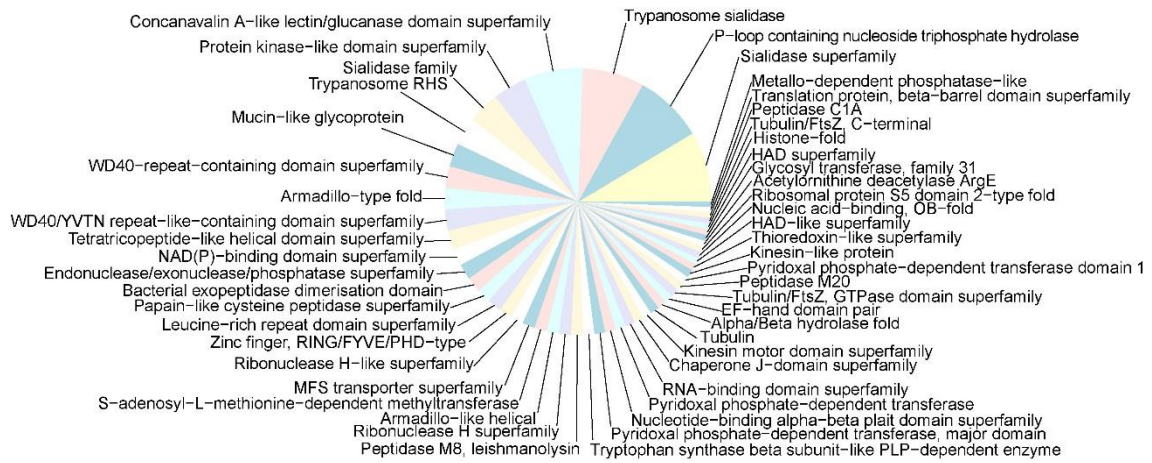


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25 **Supplementary Figure 2.** FPKM values and length distribution of the complete
26 transcriptome. Quartiles Q1, mean and Q3 are represented by dashed lines.

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30 **Supplementary Figure 3.** More abundant transcripts in Sylvio X10 transcriptome.

31 Multicopy gene families more abundant copy-number based in *T. cruzi* tripomastigotes.