

Strain	Gene	Protein, aa	GeneBank ID	T-Aligner mode
Sylvio X/10	ND8	145	OM022896	coverage
Sylvio X/10	ND9	192	OM022897	coverage
Sylvio X/10	ND7	387	OM022895	editing
Sylvio X/10	CO3	288	OM022893	coverage
Sylvio X/10	CYb	370	OM022898	extension
Sylvio X/10	A6	233	OM022892	extension
Sylvio X/10	CR3	89*	not submitted	editing
Sylvio X/10	CO2	210	OM022894	coverage
Sylvio X/10	MURF2	357	OM022899	coverage
Sylvio X/10	CR4	163*	not submitted	coverage
Sylvio X/10	ND3	125*	not submitted	extension
Sylvio X/10	RPS12	95	OM022900	editing
CL Brener	CO3	288	OM022901	coverage
CL Brener	CYb	368	OM022903	coverage
CL Brener	CO2	210	OM022902	coverage
CL Brener	RPS12	95	OM022904	editing
Esmeraldo	CO3	288	OM022905	coverage
Esmeraldo	RPS12	87	OM022906	coverage
* but multiple products present				

Table S1. Length of assembled *Trypanosoma cruzi* mature maxicircle-encoded mRNAs and their most supported full-length open reading frames (ORFs). Sequences were reconstructed from reads using T-Aligner for the three strains indicated, and the accession numbers of NCBI submission provided. The Editing Pattern column indicates whether this maxicircle transcript is not edited (non-edited), edited at a small domain only (minimally edited), or edited throughout an extensive portion of the transcript (pan-edited). The percentage of the likely full-length ORF that was able to be reconstructed with the acquired reads for that strain is shown. The T-Aligner mode indicated in the last column controls the preferable read overlap graph path when the program does ORFs assembly. In ‘coverage’ mode T-Aligner prefers reads with maximal support of editing states, in ‘editing’ mode reads with more edits are preferred, in ‘extension’ mode longest read with best overlap is preferred.