

Table S1. Markers used to assess *T. cruzi* diversity.

Marker Name	Accession No.	Size (bp)
18s	AY785564	2260
24s	AY367115	118
HP1	XM_804213.1	1206
HP2	XM_804586.1	1170
Ferric Reductase Transmembrane Protein	XM_806472.1	723
HP4	XM_806040.1	1455
HP5	XM_812200.1	1368
Endomembrane Protein	XM_801081.1	1797
Beta-adaptin	XM_815241.1	2898
HP8	XM_809640.1	954
HP9	XM_816825.1	1359
HP10	XM_811962.1	1935
Protein kinase	XM_811220.1	834
HP12	XM_803751.1	1047
HP14	XM_803821.1	1218
HP15	XM_810049.1	924
Thiol-dependent reductase 1	XM_802287.1	1338
Flagellum-adhesion glycoprotein	XM_800084.1	1746
HP18	XM_810193	708
HP19	XM_816163.1	1365
HP20	XM_802518.1	954
HP21	XM_804543.1	1644
HP22	XM_800573.1	1368
HP23	XM_802177.1	795
HP24	XM_815790.1	1908
HP25	XM_816871.1	2112

HP26	XM_808681.1	552
HP27	XM_810645.1	795
HSP70	KC959991.1	1380
MSH2	AY092834.1	829
SAT	HQ859509.1	805
TcSD5D	XM_799062	837

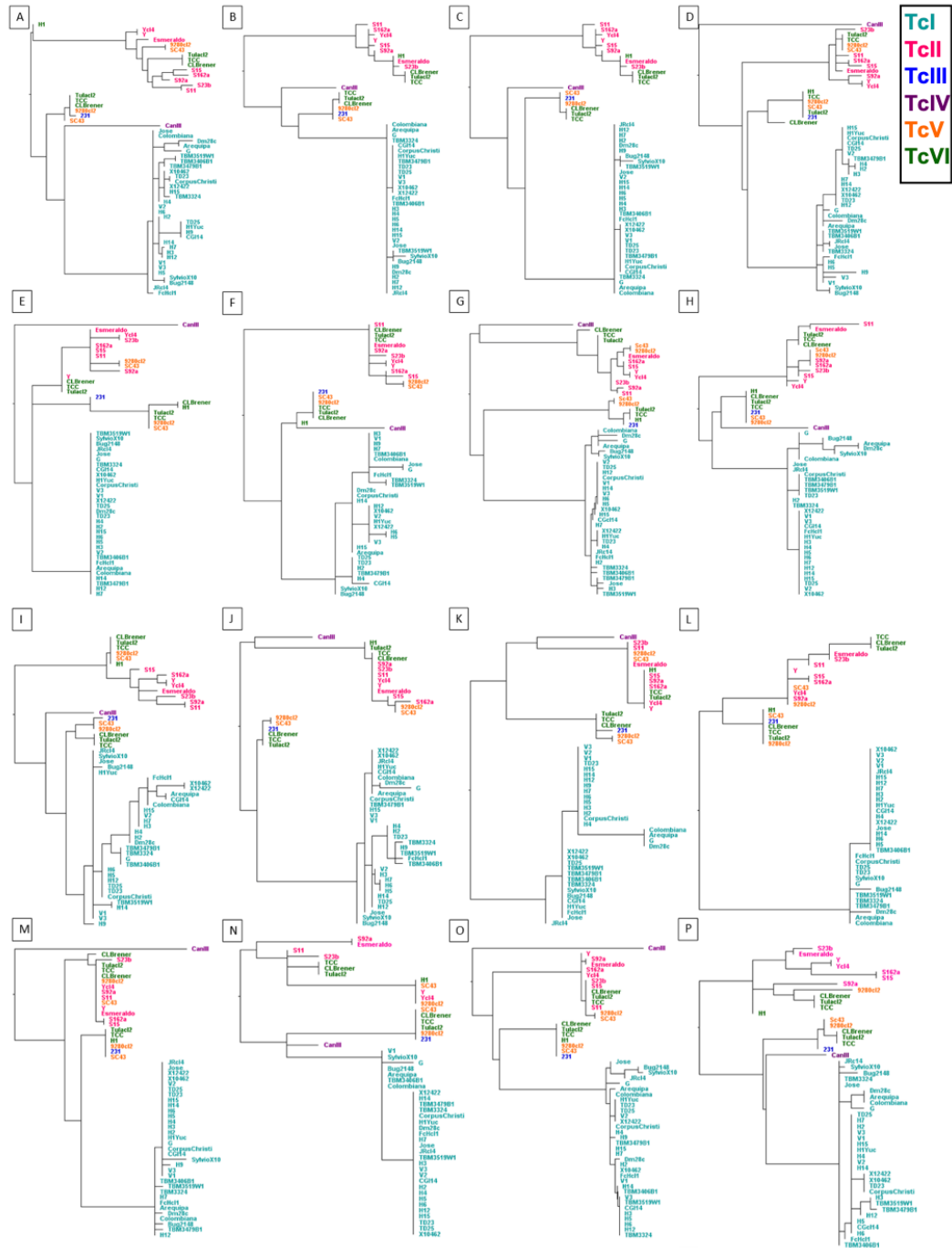
Accession numbers correspond to marker sequence in the CL-Brener genome, except for SAT, HSP70, and 18s, which correspond to marker sequence in the Esmeraldo genome and 24s, which corresponds to marker sequence in the CanIII genome. HP: hypothetical protein

Table S2. Mini-exon copy number in *T. cruzi* genomes

Strain Name - DTU	# of Sequences*
231 - TcIII	4
Arequipa - TcI	636
CanIII - TcIV	13
CGI14 - TcI	150
CLBrener - TcVI	295
Colombiana - TcI	653
Corpus Christi - TcI	286
Esmeraldo - TcII	20
FcHcI1 - TcI	217
H1 Panama -TcVI	154
H2 - TcI	151
H3 - TcI	142
H5 --TcI	122
H6 - TcI	122
H7 - TcI	123
H9 - TcI	104
H12 - TcI	136
H14 - TcI	125
H15 - TcI	128
Jose - TcI	424
JRc14 - TcI	52
M6241 - TcIII	13
TBM3479B1 - TcI	26
TBM3519W1 - TcI	122
Bug2148 - TcI	173
TD23 - TcI	167
TD25 - TcI	151
TMB3406B1 - TcI	148

Tula cI2 - TcVI	21
V1 - TcI	169
V2 -TcI	126
V3 - TcI	167
X10462 - TcI	170
X12422 - TcI	131
Y - TcII	233
G - TcI	1
S11 - TcII	4
S15 - TcII	7
TCC - TcVI	225
Ycl4 - TcII	1
9280cI2 - TcV	214
H4 -TcI	160
s154a - TcI	2
H1Yuc - TcI	133
Dm28c - TcI	746
S162a - TcII	6
S23b - TcII	7
S44 - TcII	4
S92a - TcII	4

*Low copy number was frequently corresponding to incomplete mini-exon sequences.



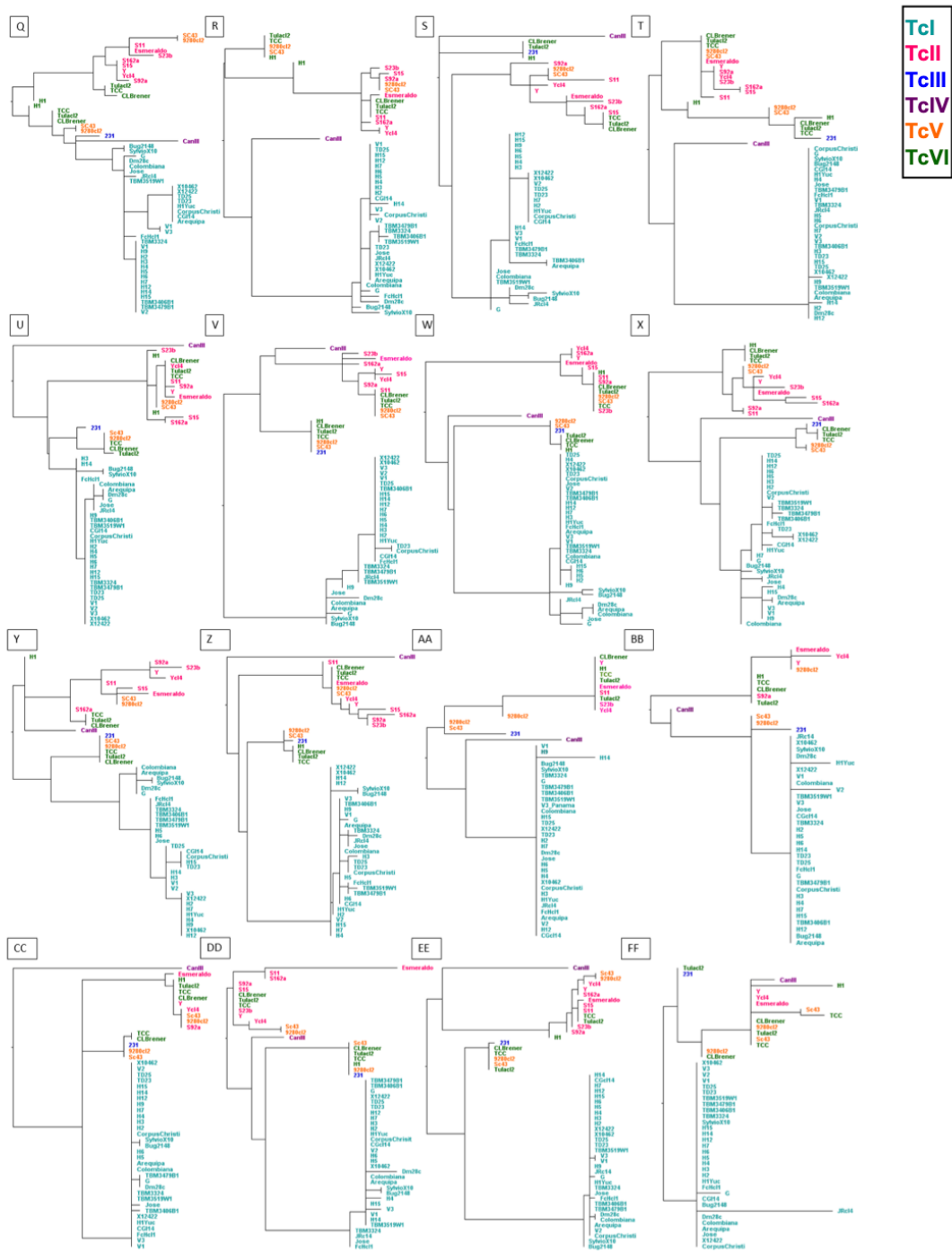


Figure S1. Phylogenetic trees constructed for individual markers.

(A) HP1, (B) HP2, (C) Ferric Reductase Transmembrane Protein, (D) Hypothetical protein HP4, (E) HP5, (F) Endomembrane Protein, (G) Beta-adaptin, (H) HP8, (I) HP9, (J) HP10, (K) Protein kinase, (L) HP12, (M) HP14, (N) HP15, (O) Thiol-dependent reductase 1, (P) Flagellum-adhesion glycoprotein, (Q) HP18, (R) HP19, (S) HP20, (T) HP21, (U) HP22, (V) HP23, (W) HP24, (X) HP25, (Y) HP26, (Z) HP27, (AA) 18S RNA, (BB) 24S RNA, (CC) SAT, (DD) MSH2, (EE) TcSD5D, (FF) HSP70.

