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**Table S4. Sequence diversity summary statistics**

Locus	Group	N <sup>a</sup>	L <sup>b</sup>	S <sup>c</sup>	k <sup>d</sup>	h <sup>e</sup>	Hd <sup>f</sup>	Hd SD	$\pi$ <sup>g</sup>	$\pi$ SD	
<i>GPI</i>	<i>T. cruzi</i>	172		1038	58	10.502	34	0.918	0.009	0.0101	0.0005
	TcI	58		1038	13	1.969	17	0.840	0.039	0.0019	0.0002
	TcII	18		1038	1	0.471	2	0.471	0.082	0.0005	0.0001
	TcIII	50		1038	9	1.441	9	0.691	0.048	0.0014	0.0001
	TcIV	14		1038	15	6.209	5	0.758	0.084	0.0060	0.0012
	TcV	16		1038	17	9.067	2	0.533	0.046	0.0087	0.0008
	TcVI	16		1038	18	9.6	2	0.533	0.046	0.0093	0.0008
<i>COII-ND1</i>	<i>T. cruzi</i>	102 <sup>h</sup>	1117 (1094)	195	51.788	38	0.957	0.007	0.0473	0.0023	
	TcI	42	1114 (1109)	112	20.129	15	0.900	0.026	0.0182	0.0045	
	TcII	10 <sup>h</sup>	1116 (1114)	7	1.556	4	0.533	0.180	0.0014	0.0006	
	TcIII	18	1115 (1100)	26	6.948	9	0.856	0.062	0.0063	0.0009	
	TcIV	9	1114 (1109)	45	15.444	6	0.833	0.127	0.0139	0.0037	
	TcV	12	1114	3	0.5	4	0.029	0.170	0.0005	0.0002	
	TcVI	11	1114	1	0.182	2	0.182	0.144	0.0002	0.0001	

<sup>a</sup> Number of sequences; 2 per sample for *GPI* (diploid), 1 per sample for *COII-ND1* (haploid)

<sup>b</sup> Length of sequence (excluding sites with alignment gaps)

<sup>c</sup> Number of variable sites

<sup>d</sup> Mean number of pairwise nucleotide differences

<sup>e</sup> Number of haplotypes

<sup>f</sup> Haplotype diversity

<sup>g</sup> Per site nucleotide diversity

<sup>h</sup> Three samples (haplotype 26) excluded due to large deletion