

Table S1. Trypanosomes band sizes expected and primers sequences.

PCR sequence target	DNA	Primer sequence (5'-3')	Trypanosomes species and band sizes	References
ITS1 PCR, target non-coding DNA between 18S and 5.8S rRNA genes	ITS1 CF: ITS1 BR:	5'-CCGGAAGTTCACCGATATTG-3' 5'-TTGCTGCGTTCTTCAACGAA-3'	<i>T.vi</i> (250bp); <i>T.br</i> (480bp); <i>T.cs</i> (700bp); <i>T.cf</i> (710bp); <i>T.s</i> (400bp); <i>T.s.t</i> (370bp); <i>T.th</i> (273bp)	[11]
Nested ITS PCR target partial 18S, ITS1, 5.8S, ITS2 and partial 28S rRNA genes	ITS1: ITS2: ITS3: ITS4:	5'-GATTACGTCCCTGCCATTTG-3' 5'-TTGTTTCGCTATCGGTCTTCC-3' 5'-GGAAGCAAAAGTCGTAACAAGG-3' 5'-TGTTTTCTTTTCCTCCGCTG-3'	<i>T.vi</i> (620bp); <i>T.br</i> (1215bp); <i>T.cs</i> (1408-1501bp); <i>T.cf</i> (1408-1501bp); <i>T.s</i> (847bp); <i>T.s.t</i> (951bp); <i>T.th</i> (998bp)	[19]
Nested PCR target Glycosomal glyceraldehyde-3- phosphate dehydrogenase gene (gGAPDH)	G3: G5: G1: GAGAT-3' G4a: G4b: Gs:	5'-TTYGCCGYATYGGYCGCATGG-3' 5'-ACMAGRTCCACCACRCGGTG-3' 5'-CGCGGATCCASGGYCTYMTCCGGBAMK GAGAT-3' 5'-GTTYTGCAAGSGTCGCCTTGG-3' 5'-CCAMGASACVAYCTTGAAGAA-3' 5'-GCSTAY CAG ATG AAG TACGAC-3'	<i>T.vi</i> (620bp); <i>T.br</i> (1215bp); <i>T.cs</i> (1408-1501bp); <i>T.cf</i> (1408-1501bp); <i>T.s</i> (847bp); <i>T.s.t</i> (951bp); <i>T.th</i> (998bp)	[20]

PCR: Polymerase chain reaction; ITS: Internal Transcribed Space; DNA: Desoxyribo Nucleic Acid.

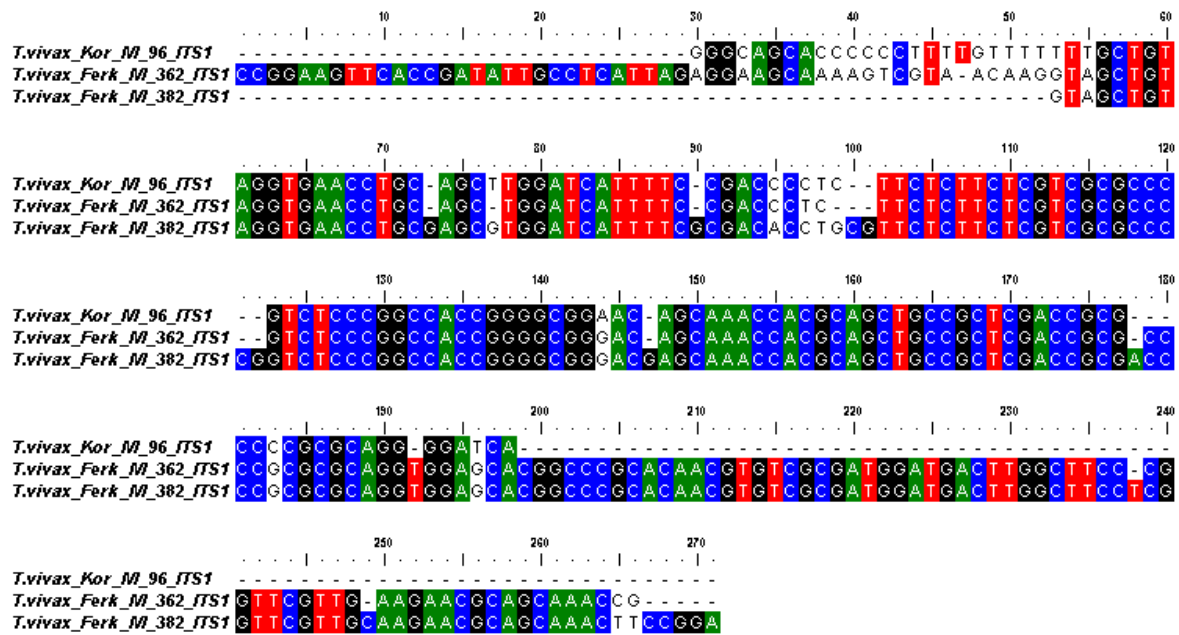


Figure S1. Cluster W alignment of *T. vivax* strain based on Internal Transcribed Spacer 1 (ITS1).

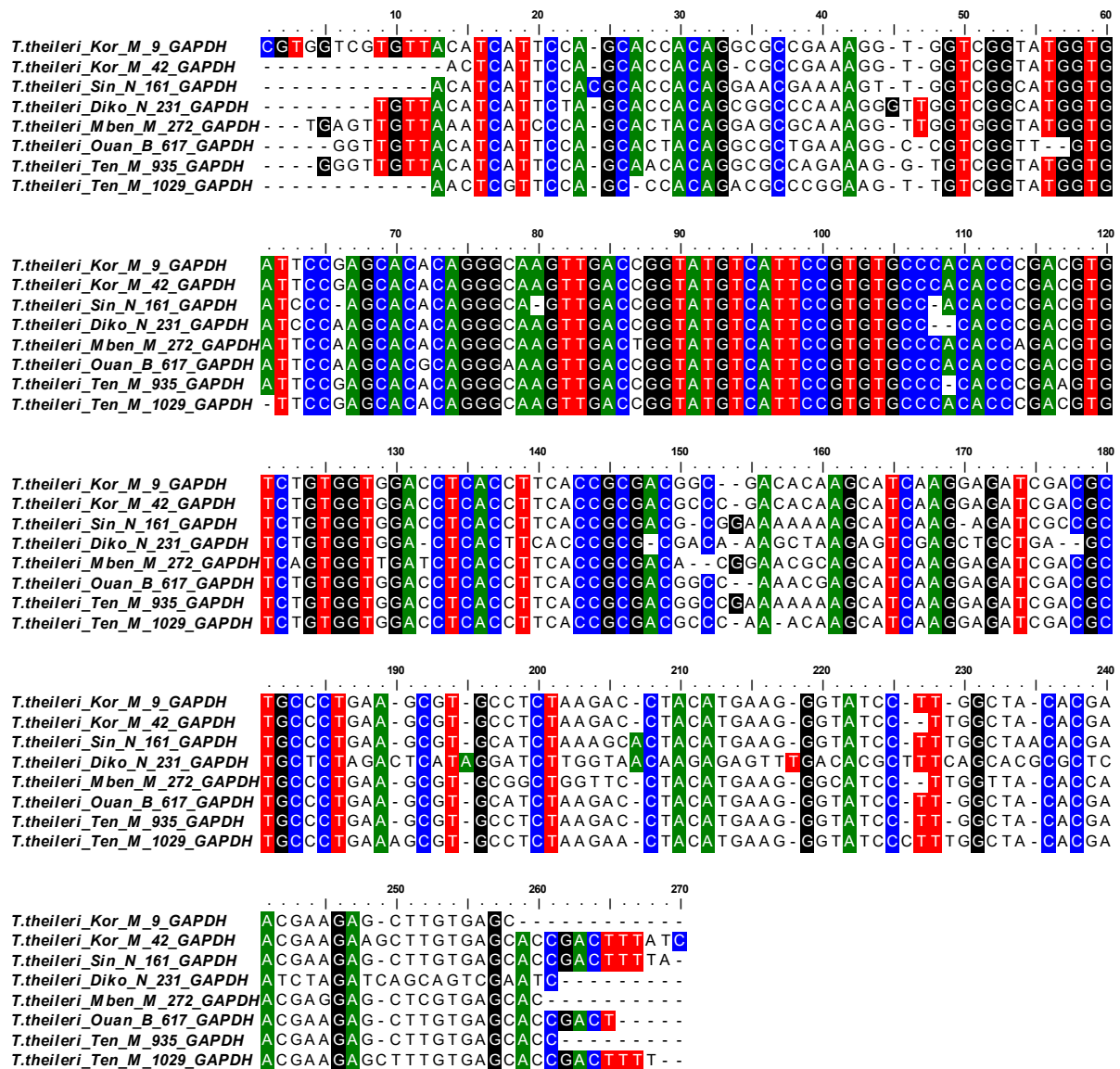


Figure S2. Cluster W alignment of *T. theileri* strain according to the Glycosomal glyceraldehyde-3-phosphate dehydrogenase gene (gGAPDH).

