

Supplementary file

## Unique Mitochondrial Single Nucleotide Polymorphisms demonstrate resolution potential to discriminate *Theileria parva* Vaccine and Buffalo-Derived Strains

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### Supplementary Materials

**Table S1.** Amplification and sequencing primer sequences.

Reaction.	Primer name	Sequence
Amplification	Tp_mit_F79	5'-GTGTCAGGAAATCATAAAAATTATTGG-3'
	Tp_mit_R5885	5'-TGAGTAAGAATAATGATACTCAAATATATGTCG-3'
Sanger sequencing	Tp_mit_F118	5'-GTGGCTGGCTTATTGGTTCG-3'
	Tp_mit_R965	5'-GCGAGTATCTGCTTCCAAACC-3'
	Tp_mit_F905	5'-GTTAGGTTGTTTGGTTGGGGAC-3'
	Tp_mit_R5610	5'-TTTAGTGAAGGAACCTGACAGGTACA -3'
	Tp_mit_R2080	5'-TTTGAACACACTGCTCGACAC-3'
	Tp_mit_R1379	5'-CAGGATAATCTGGTATTCTTCTTGG-3'
	Tp_mit_F1863	5'-CAAGGTAGTTGACAGTGAACCTGTAGC-3'
	Tp_mit_F3056	5'-CGCTGTTTCGCATTTGACTAC-3'
	Tp_mit_R4186	5'-TTCTTTGCCTTGGATGTCAGTTAG-3'
	Tp_mit_F3659	5'-CAATCCTTATGTATGCTTGAATGCTG-3'

M13-24F- Blue\*                      5'-GTAAAACGACGGCCAGTGAAGCGCG-'3  
M13-24R- Blue\*                      5'-AACAGCTATGACCATGATTACGCC-'3

\* pSC – B – amp/kan PCR cloning vector standard sequencing primers.

**Table S2.** Summary of NGS reads (SRA accession number: DRA000613) mapped to *T. parva* muguga- mitochondrial sequence (AB499089).

Strain	Accession no.	Origin	Total reads downloaded	Mapped reads	Read coverage
Buffalo Z5E5	DRR002446	Zambia	14,821,055	2,627	96.4%
Nyakizu	DRR002443	Rwanda	31,095,446	2,574	98.9%
Buffalo LAWR	DRR002445	Kenya	17,072,361	2,021	95.0%
Entebbe	DRR002442	Uganda	10,171,313	1,826	96.8%
ChitongoZ2	DRR002438	Zambia	14,405,286	1,198	94.4%
MandaliZ22H10	DRR002441	Zambia	16,362,288	591	91.1%
Katumba	DRR002444	Tanzania	35,406,726	463	85.3%
KiambuZ464/C12	DRR002440	Kenya	15,848,448	428	84.1%
KateteB2	DRR002439	Zambia	16,558,766	426	81.1%