

**Supplementary Figure S1:** Alignment of the 18S rRNA V4 hypervariable region of *Theileria* sp. (bold) and *Theileria luwenshuni* genotypes. Nucleotide changes are indicated on a black box.

| Primers                   | Sequence (5'-3')                   | References |
|---------------------------|------------------------------------|------------|
| Nbab-1F                   | AAGCCATGCATGTCTAAGTATAAGCTTTT      | [25]       |
| Nbab-1R                   | CTTCTCCTTCCTTTAAGTGATAAGGTTTCAC    |            |
| RLB-F2                    | GACACAGGGAGGTAGTGACAAG             | [26]       |
| RLB-R2                    | biotin-CTAAGAATTTCACCTCTGACAGT     |            |
| <b>Probs</b>              |                                    |            |
| Catchall                  | AmMC6-TAATGGTTAATAGGA(AG)C(AG)GTTG | [19]       |
| <i>Theileria</i> spp.     | AmMC6-TGATGGGAATTTAAACC(CT)CTTCCA  | [19]       |
| <i>T. ovis</i>            | AmMC6-TTTTGCTCCTTTACGAGTCTTTGC     | [19]       |
| <i>T. separate</i>        | AmMC6- TCGGATGATACTTGTATTATC       | [54]       |
| <i>T. lestoquardi</i>     | AmMC6-ATTGCTTGTGTCCCTCCG           | [54]       |
| <i>T. uilenbergi</i>      | AmMC6-TGCATTTTCCGAGTGTTACT         | [54]       |
| <i>T. luwenshuni</i>      | AmMC6-TCGGATGATACTTGTATTATC        | [53]       |
| <i>Theileria</i> sp. OT1  | AmMC6-ATCTTCTTTTTGATGAGTTGGTGT     | [19]       |
| <i>Theileria</i> sp. OT3  | AmMC6-ATTTTCTCTTTTATATGAGTTTT      | [19]       |
| <i>Theileria</i> sp. MK   | AmMC6-CATTGTTTCTTCTCATGTC          | [20]       |
| <i>Babesia</i> Catchall 1 | AmMC6 -ATTAGAGTGTTTCAAGCAGAC       | [55]       |
| <i>Babesia</i> Catchall 2 | AmMC6 -ACTAGAGTGTTTCAAACAGGC       | [55]       |
| <i>B. ovis</i>            | AmMC6-GCGCGCGGCCTTTGCGTTTACT       | [19]       |
| <i>B. motasi</i>          | AmMC6-ATTGGAGTATTGCGCTTGCTTTTT     | [19]       |
| <i>B. crassa</i>          | AmMC6-TTATGGCCCGTTGGCTTAT          | [19]       |
| <i>Babesia</i> sp.        | AmMC6-TGCCGTGAATCGACATTCGTC        | [23]       |

AmMC6: Amino group

**Supplementary Table S2:** Pairwise distance matrix comparing of the 18S rRNA V4 hypervariable region (~400 bp) of *Theileria* sp. (bold) to *Theileria luwenshuni* genotypes was created by Clustal2.1. Data represent % identity (p-distance).

[illegible]