

**Table S1.** Tick species identification based on the mitochondrial 16S rDNA gene.

| Tick 16S rDNA Sequence |             |                 |              | Blastn Match     |                                |
|------------------------|-------------|-----------------|--------------|------------------|--------------------------------|
| Accession Number       | Length (bp) | Query Cover (%) | Identity (%) | Accession Number | Tick Species                   |
| OL347853               | 452         | 100             | 99.78        | KT391060         | <i>Hyalomma marginatum</i>     |
| OL347856               | 450         | 100             | 99.33        | KR870972         | <i>Hyalomma excavatum</i>      |
| OL347855               | 448         | 100             | 100          | MK829042         | <i>Hyalomma anatolicum</i>     |
| OL347857               | 453         | 89              | 99.50        | MT229195         | <i>Rhipicephalus turanicus</i> |
| OL347854               | 450         | 100             | 99.78        | MT302761         | <i>Rhipicephalus bursa</i>     |

**Table S2.** Primer sets used for the detection of tick-borne pathogens.

| Pathogen Target gene                   | Type of PCR  | Oligonucleotide Sequences (5'→3')                                | Amplicon Size | Reference |
|--|--------------|--|---------------|-----------|
| Tick 16S rDNA                          | Conventional | F - GCTCAATGATTTTTTAAATTGCTGT<br>R - CCGGTCTGAACTCAGATCAAGT      | 460           | [44]      |
| <i>Theileria/Babesia</i> 18S rRNA (V4) | Conventional | F - GACACAGGGAGGTAGTGACAAG<br>R - CTAAGAATTTACCTCTGACAGT         | 403           | [45]      |
| <i>Theileria orientalis</i> MPSP       | Conventional | F - CTTTGCTAGGATACTTCCT<br>R - ACGGCAAGTGGTGAGAACT               | 776           | [49]      |
| <i>Theileria annulata</i> Tams-1       | Nested       | F1 - GTAACCTTTAAAAACGT<br>R1 - GTTACGAACATGGGTTT                 | 721           | [50]      |
|  |              | F2 - CACCTCAACATAACCCC<br>R2 - TGACCCACTTATCGTCC                 | 453           |           |
|  |              | F1 - AGTTGTTGGAGGAGGCTAAT<br>R1 - TCCTTCTCGGCGTCCTTTTC           | 907           |           |
| <i>Babesia bovis</i> sbp4              | Nested       | F2 - GAAATCCCTGTTCCAGAG<br>R2 - TCGTTGATAACACTGCAA               | 503           | [48]      |
|  |              | F1 - GAGTCTGCCAAATCCTTAC<br>R1 - TCCTCTACAGCTGCTTCG              | 879           |           |
|  |              | F2 - AGCTTGCTTTCACAACTCGCC<br>R2 - TTGGTGCTTTGACCGACGACA         | 412           |           |
| <i>Anaplasma/Ehrlichia</i> 16S rRNA    | Conventional | F - GGTACCTACAGAAGAAGTCC<br>R - TAGCACTCATCGTTTACAGC             | 345           | [46]      |
| <i>Anaplasma marginale</i> msp4        | Conventional | F - CTGAAGGGGGAGTAATGGG<br>R - GTAATAGCTGCCAGAGATTCC             | 344           | [51]      |
| <i>Ehrlichia ruminantium</i> pCS20     | Nested       | F1 - ACTAGTAGAAATTGCACAATCYAT<br>R1 - RCTDGCWGCTTTYTGTTTCAGCTAK  | 279           | [52]      |
|  |              | F2 - TGATAACTTGGWGCRRGDARTCCTT<br>R2 - RCTDGCWGCTTTYTGTTTCAGCTAK |               |           |
|  |              | F - ATTGAAGAGTTTGATTCTGG<br>R - CGGCTTCCCGAAGGTTAG               |               |           |
| <i>Coxiella burnetii</i> 16S rRNA      | Conventional | F - AACGTCATTATCTTCCTTGC<br>R - AGAGTTTGATCCTGGCTCAG             | 1457          | [53]      |
| <i>Rickettsia</i> spp. 16S rRNA        | Conventional | F - GCAAGTATCGGTGAGGATGTAAT<br>R - GCTTCCTTAAATTCATAAATCAG-      | 426           | [47]      |
| <i>Rickettsia</i> spp. gltA            | Conventional | GAT  | 401           | [54]      |
| <i>Rickettsia</i> spp. ompA            | Conventional | F - GCTTTATTACACCTCAAC<br>R - TRATCACCACCGTAAGTAAAT              | 212           | [55]      |