Table S1

PCR primers and thermocycling conditions used in this study.

| **Target region** | **Primers** | **PCR conditions** | **Amplicon size (base pairs)** | **Reference** |
|---|---|---|---|---|
| 16S for ticks | Forward: 16S+1 (5'-CTGCTCAATGATTTTTTAAATTGCTGTGG-3')<br>Reverse: 16S-1 (5'-CCGGTCTGAACTCAGATCAAGT-3') | Initial denaturation: 95 °C, 4min<br>35 cycles of<br>Denaturation: 95 °C, 1min<br>Annealing: 50 °C, 1min<br>Extension: 68 °C, 1min<br>Final extension:68 °C, 10min | 460 | [25] |
| *cox*1 for ticks | Forward: LCO1490 (5'- GGTCAACAAATCATAAAGATATTGG-3')<br>Reverse: HCO2198 (5'-TAAACTTCAGGGTGACCAAAAAATCA-3') | Initial denaturation: 95 °C, 5min<br>40 cycles of<br>Denaturation: 95 °C, 45sec<br>Annealing 50 °C, 45sec<br>Extension: 72 °C, 1min<br>Final extension: 72 °C, 5min | 710 | [40] |
| ITS-2 for ticks | Forward: RIB-8 (5'-GTCGTAGTCCGCCGTC-3')<br>Reverse: RIB-11 (5'-GAGTACGACGCCCTACC-3') | Initial denaturation: 94 °C, 5min<br>35 cycles of<br>Denaturation: 94 °C, 30sec<br>Annealing: 62 °C, 15sec<br>Extension: 72 °C, 15sec<br>Final extension: 72 °C, 5min | 280 | [41] |
| 18S for piroplasms | Forward: (5'-GAGGTAGTGACAAGAAATAACAATA-3')<br>Reverse: (5'-TCTTCGATCCCCTAACTTTC-3') | Initial denaturation: 95 °C, 5min<br>35 cycles of<br>Denaturation: 95 °C, 30sec<br>Annealing: 57 °C, 20 sec<br>Extension: 72 °C, 1 min<br>Final extension: 72 °C, 5min | 500 | [42] |

Table S2

List of primers and probes used in this study for identification of microorganisms and ticks.

| **Species** | **Target** | **Name** | **Sequence** | **Length (base pair)** |
|---|---|---|---|---|
| *Anaplasma marginale* | *msp1* | An_ma_msp1_F | CAGGCTTCAAGCGTACAGTG | 85 |
| | | An_ma_msp1_R | GATATCTGTGCCTGGCCTTC | |
| | | An_ma_msp1_P | ATGAAAGCCTGGAGATGTTAGACCGAG | |
| *Anaplasma platys* | *groEL* | An_pla_groEL_F | TTCTGCCGATCCTTGAAAACG | 75 |
| | | An_pla_groEL_R | CTTCTCCTTCTACATCCTCAG | |
| | | An_pla_groEL_P | TTGCTAGATCCGGCAGGCCTCTGC | |
| *Anaplasma ovis* | *msp4* | An_ov_msp4_F | TCATTCGACATGCGTGAGTCA | 92 |
| | | An_ov_msp4_R | TTTGCTGGCGCACTCACATC | |
| | | An_ov_msp4_P | AGCAGAGAGACCTCGTATGTTAGAGGC | |
| *Anaplasma centrale* | *groEL* | An_cen_groEL_F | AGCTGCCCTGCTATACACG | 79 |
| | | An_cen_groEL_R | GATGTTGATGCCCAATTGCTC | |
| | | An_cen_groEL_P | CTTGCATCTCTAGACGAGGTAAAGGGG | |
| *Anaplasma phagocytophilum* | *msp2* | An_ph_msp2_F | GCTATGGAAGGCAGTGTTGG | 77 |
| | | An_ph_msp2_R | GTCTTGAAGCGCTCGTAACC | |
| | | An_ph_msp2_P | AATCTCAAGCTCAACCCTGGCACCAC | |
| *Anaplasma bovis* | groEL | An_bo_groEL_F | CTGATAGCTACAGTTAAGCCC | 73 |
| | | An_bo_groEL_R | AGGTGCTGTTGGATGTACTGCTGGACC | |
| | | An_bo_groEL_P | TCATTCGACATGCGTGAGTCA | |
| *Anaplasma* spp. | 16S rRNA | Ana_spp_16S_F | CTTAGGGTTGTAAAACTCTTTCAG | 160 |
| | | Ana_spp_16S_R | CTTTAACTTACCAAACCGCCTAC | |
| | | Ana_spp_16S_P | ATGCCCTTTACGCCCAATAATTCCGAACA | |
| Apicomplexa | 18S rRNA | Apic_18S_F | TGAACGAGGAATGCCTAGTATG | 104 |
| | | Apic_18S_R | CACCGGATCACTCGATCGG | |
| | | Apic_18S_S | TAGGAGCGACGGGCGGTGTGTAC | |
| *Babesia divergens* | *hsp70* | Bab_di_hsp70_F | CTCATTGGTGACGCCGCTA | 83 |
| | | Bab_di_hsp70_R | CTCCTCCCGATAAGCCTCTT | |
| | | Bab_di_hsp70_P | AGAACCAGGAGGCCCGTAACCCAGA | |

| | | | | |
|---|---|---|---|---|
| *Babesia caballi* | *Rap1* | Ba_cab_rap1_F | GTTGTTCGGCTGGGGCATC | 94 |
| | | Ba_cab_rap1_R | CAGGCGACTGACGCTGTGT | |
| | | Ba_cab_rap1_P | TCTGTCCCGATGTCAAGGGGCAGGT | |
| *Babesia canis* | 18S rRNA | Ba_ca_RNA18S_F | TGGCCGTTCTTAGTTGGTGG | 104 |
| | | Ba_ca_RNA18S_R | AGAAGCAACCGGAAACTCAAATA | |
| | | Ba_ca_RNA18S_P | ACCGGCACTAGTTAGCAGGTTAAGGTC | |
| *Babesia microti* | *CCTeta* | Bab_mi_CCTeta_F | ACAATGGATTTTCCCCAGCAAAA | 145 |
| | | Bab_mi_CCTeta_R | GCGACATTTCGGCAACTTATATA | |
| | | Bab_mi_CCTeta_P | TACTCTGGTGCAATGAGCGTATGGGTA | |
| *Babesia bovis* | *CCTeta* | Ba_bo_CCTeta_F | GCCAAGTAGTGGTAGACTGTA | 100 |
| | | Ba_bo_CCTeta_R | GCTCCGTCATTGGTTATGGTA | |
| | | Ba_bo_CCTeta_P | TAAAGACAACACTGGGTCCGCGTGG | |
| *Babesia bigemina* | 18S rRNA | Ba_big_RNA18S_F | ATTCCGTTAACGAACGAGACC | 99 |
| | | Ba_big_RNA18S_R | TTCCCCCACGCTTGAAGCA | |
| | | Ba_big_RNA18S_P | CAGGAGTCCCTCTAAGAAGCAAACGAG | |
| *Babesia ovis* | 18S rRNA | Ba_ov_RNA18S_F | TCTGTGATGCCCTTAGATGTC | 92 |
| | | Ba_ov_RNA18S_R | GCTGGTTACCCGCGCCTT | |
| | | Ba_ov_RNA18S_P | TCGGAGCGGGGTCAACTCGATGCAT | |
| *Babesia vulpes* | *COX1* | Bab_vulpes_F | ACT TCC AGT GTT AAC AGC AGC | 129 |
| | | Bab_vulpes_R | GGA TGT CCG AAG ACC CAG AA | |
| | | Bab_vulpes_P | CTT CTG CAT GTT GCT GGC TGA TAG GCA | |
| *Bartonella henselae* | *pap31* | Bar_he_pap31_F | CCGCTGATCGCATTATGCCT | 107 |
| | | Bar_he_pap31_R | AGCGATTTCTGCATCATCTGCT | |
| | | Bar_he_pap31_P | ATGTTGCTGGTGGTGTTTCCTATGCAC | |
| *Bartonella* spp. | ssrA | Bart_spp_ssrA_F | CGTTATCGGGCTAAATGAGTAG | 118 |
| | | Bart_spp_ssrA_R | ACCCCGCTTAAACCTGCGA | |
| | | Bart_spp_ssrA_P | TTGCAAATGACAACTATGCGGAAGCACGTC | |
| *Borrelia burgdorferi* sensu stricto | *rpoB* | Bo_bu_rpoB_F | GCTTACTCACAAAAGGCGTCTT | 83 |
| | | Bo_bu_rpoB_R | GCACATCTCTTACTTCAAATCCT | |
| | | Bo_bu_rpoB_P | AATGCTCTTGGACCAGGAGGACTTTCA | |
| *Borrelia garinii* | *rpoB* | Bo_ga_rpoB_F | TGGCCGAACTTACCCACAAAA | 88 |
| | | Bo_ga_rpoB_R | ACATCTCTTACTTCAAATCCTGC | |
| | | Bo_ga_rpoB_P | TCTATCTCTTGAAAGTCCCCCTGGTCC | |

| | | | | |
|---|---|---|---|---|
| *Borrelia afzelii* | *f/a* | Bo_af_fla_F | GGAGCAAATCAAGATGAAGCAAT | 116 |
| | | Bo_af_fla_R | TGAGCACCCTCTTGAACAGG | |
| | | Bo_af_fla_P | TGCAGCCTGAGCAGCTTGAGCTCC | |
| *Borrelia valaisiana* | *ospA* | Bo_va_ospA_F | ACTCACAAATGACAGATGCTGAA | 135 |
| | | Bo_va_ospA_R | GCTTGCTTAAAGTAACAGTACCT | |
| | | Bo_va_ospA_P | TCCGCCTACAAGATTTCCTGGAAGCTT | |
| *Borrelia miyamotoi* | *glpQ* | B_miya_glpQ_F | CACGACCCAGAAATTGACACA | 94 |
| | | B_miya_glpQ_R | GTGTGAAGTCAGTGGCGTAAT | |
| | | B_miya_glpQ_P | TCGTCCGTTTTCTCTAGCTCGATTGGG | |
| *Borrelia spielmanii* | *f/a* | Bo_spi_fla_F | ATCTATTTTCTGGTGAGGGAGC | 71 |
| | | Bo_spi_fla_R | TCCTTCTTGTTGAGCACCTTC | |
| | | Bo_spi_fla_P | TTGAACAGGCGCAGTCTGAGCAGCTT | |
| *Borrelia lusitaniae* | *rpoB* | Bo_lus_rpoB_F | CGAACTTACTCATAAAAGGCGTC | 87 |
| | | Bo_lus_rpoB_R | TGGACGTCTCTTACTTCAAATCC | |
| | | Bo_lus_rpoB_P | TTAATGCTCTCGGGCCTGGGGGACT | |
| *Borrelia bissettii* | *rpoB* | Bo_bi_rpoB_F | GCAACCAGTCAGCTTTCACAG | 118 |
| | | Bo_bi_rpoB_R | CAAATCCTGCCCTATCCCTTG | |
| | | Bo_bi_rpoB_P | AAAGTCCTCCCGGCCCAAGAGCATTAA | |
| *Borrelia bavariensis* | *pyrG* | Bo_bavar_pyrG_F | GTC TTT GGT TCA TGT TGG AGC | 141 |
| | | Bo_bavar_pyrG_R | CCC TCA TAT CCT TTG CCT CC | |
| | | Bo_bavar_pyrG_P | AAA GCC TCC GGG AAC AAT AAT GCC GTC AA | |
| *Borrelia mayonii* | *fla* | Bo_mayo_fla_F | ACA CAC CAT CAT CAC TTT CAG G | 173 |
| | | Bo_mayo_fla_R | TTG AGC ACC TTC TTG AAC AGG | |
| | | Bo_mayo_fla_P | CGC AAC CTG AGC AGT TTG AGT TCC CT | |
| *Borrelia* spp. | 23S rRNA | Bo_bu_sl_23S_F | GAGTCTTAAAAGGGCGATTTAGT | 73 |
| | | Bo_bu_sl_23S_R | CTTCAGCCTGGCCATAAATAG | |
| | | Bo_bu_sl_23S_P | AGATGTGGTAGACCCGAAGCCGAGT | |
| *Candidatus* Neoehrlichia mikurensis | *groEL* | Neo_mik_groEL_F | AGAGACATCATTCGCATTTTGGA | 96 |
| | | Neo_mik_groEL_R | TTCCGGTGTACCATAAGGCTT | |
| | | Neo_mik_groEL_P | AGATGCTGTTGGATGTACTGCTGGACC | |
| *Coxiella burnetii* | *idc* | Co_bu_icd_F | AGGCCCGTCCGTTATTTTACG | 74 |
| | | Co_bu_icd_R | CGGAAAATCACCATATTCACCTT | |
| | | Co_bu_icd_P | TTCAGGCGTTTTGACCGGGCTTGGC | |

|  |  |  |  |  |
|---|---|---|---|---|
|  | IS*1111* | Co_bu_IS111_F | TGGAGGAGCGAACCATTGGT | 86 |
|  |  | Co_bu_IS111_R | CATACGGTTTGACGTGCTGC |  |
|  |  | Co_bu_IS111_P | ATCGGACGTTTATGGGGATGGGTATCC |  |
| *Ehrlichia canis* | *dsb* | Eh_ca_dsb_F | AATACTTGGTGAGTCTTCACTCA | 110 |
|  |  | Eh_ca_dsb_R | GTTGCTTGTAATGTAGTGCTGC |  |
|  |  | Eh_ca_dsb_P | AAGTTGCCCAAGCAGCACTAGCTGTAC |  |
| *Ehrlichia* spp. | 16S rRNA | Neo_mik_16S_R | GCAACGCGAAAAACCTTACCA | 98 |
|  |  | Neo_mik_16S_R | AGCCATGCAGCACCTGTGT |  |
|  |  | Neo_mik_16S_P | AAGGTCCAGCCAAACTGACTCTTCCG |  |
| *Francisella tularensis* | *tul4* | Fr_tu_tul4_F | ACCCACAAGGAAGTGTAAGATTA | 76 |
|  |  | Fr_tu_tul4_R | GTAATTGGGAAGCTTGTATCATG |  |
|  |  | Fr_tu_tul4_P | AATGGCAGGCTCCAGAAGGTTCTAAGT |  |
|  | *fopA* | Fr_tu_fopA_F | GGCAAATCTAGCAGGTCAAGC | 91 |
|  |  | Fr_tu_fopA_R | CAACACTTGCTTGAACATTTCTAG |  |
|  |  | Fr_tu_fopA_P | AACAGGTGCTTGGGATGTGGGTGGTG |  |
| *Hepatozoon* spp. | 18S rRNA | Hepa_spp_18S_F | ATTGGCTTACCGTGGCAGTG | 175 |
|  |  | Hepa_spp_18S_R | AAAGCATTTTAACTGCCTTGTATTG |  |
|  |  | Hepa_spp_18S_S | ACGGTTAACGGGGGATTAGGGTTCGAT |  |
| *Rickettsia conorii* | 23S-5S ITS | Ri_co_ITS_F | CTCACAAAGTTATCAGGTTAAATAG | 118 |
|  |  | Ri_co_ITS_R | CGATACTCAGCAAAATAATTCTCG |  |
|  |  | Ri_co_ITS_P | CTGGATATCGTGGCAGGGCTACAGTAT |  |
| *Rickettsia slovaca* | 23S-5S ITS | Ri_slo_ITS_F | GTATCTACTCACAAAGTTATCAGG | 138 |
|  |  | Ri_slo_ITS_R | CTTAACTTTTACTACAATACTCAGC |  |
|  |  | Ri_slo_ITS_P | TAATTTTCGCTGGATATCGTGGCAGGG |  |
| *Rickettsia massiliae* | 23S-5S ITS | Ri_ma_ITS_F | GTTATTGCATCACTAATGTTATACTG | 128 |
|  |  | Ri_ma_ITS_R | GTTAATGTTGTTGCACGACTCAA |  |
|  |  | Ri_ma_ITS_P | TAGCCCCGCCACGATATCTAGCAAAAA |  |
| *Rickettsia helvetica* | 23S-5S ITS | Ri_he_ITS_F | AGAACCGTAGCGTACACTTAG | 79 |
|  |  | Ri_he_ITS_R | GAAAACCCTACTTCTAGGGGT |  |
|  |  | Ri_he_ITS_P | TACGTGAGGATTTGAGTACCGGATCGA |  |
| *Rickettsia felis* | orfB | Ri_fel_orfB_F | ACCCTTTTCGTAACGCTTTGC | 163 |
|  |  | Ri_fel_orfB_R | TATACTTAATGCTGGGCTAAACC |  |
|  |  | Ri_fel_orfB_P | AGGGAAACCTGGACTCCATATTCAAAAGAG |  |
| *Rickettsia aeschlimannii* | ITS | Rick_aesch_ITS_F | CTCACAAAGTTATCAGGTTAAATAG | 134 |

| | | | | |
|---|---|---|---|---|
| | | Rick_aesch_ITS_R | CTTAACTTTTACTACGATACTTAGCA | |
| | | Rick_aesch_ITS_P | TAATTTTTGCTGGATATCGTGGCGGGG | |
| *Rickettsia* spp. | gltA | Rick_spp_gltA_F | GTCGCAAATGTTCACGGTACTT | 78 |
| | | Rick_spp_gltA_R | TCTTCGTGCATTTCTTTCCATTG | |
| | | Rick_spp_gltA_P | TGCAATAGCAAGAACCGTAGGCTGGAT | |
| *Theileria* spp. | 18S rRNA | Th_an_18S_F | GCGGTAATTCCAGCTCCAATA | 126 |
| | | Th_an_18S_R | AAACTCCGTCCGAAAAAAGCC | |
| | | Th_an_18S_P | ACATGCACAGACCCCAGAGGGACAC | |
| *Escherichia coli* | *eae* | eae-F2 | CATTGATCAGGATTTTTCTGGTGATA | 102 |
| | | eae-R | CTCATGCGGAAATAGCCGTTA | |
| | | eae-P | ATAGTCTCGCCAGTATTCGCCACCAATACC | |
| *Rhipicephalus sanguineus* sensu lato | ITS-2 | Rhi_san_ITS2_F | TTGAACGCTACGGCAAAGCG | 110 |
| | | Rhi_san_ITS2_R | CCATCACCTCGGTGCAGTC | |
| | | Rhi_san_ITS2_P | ACAAGGGCCGCTCGAAAGGCGAGA | |
| Tick spp. | 16S rRNA | Tick_spp_16S_F | AAATACTCTAGGGATAACAGCGT | 99 |
| | | Tick_spp_16S_R | TCTTCATCAAACAAGTATCCTAATC | |
| | | Tick_spp_16S_P | CAACATCGAGGTCGCAAACCATTTTGTCTA | |

Table S3

Pairwise comparison of 16S nucleotide sequences (aligned over 429 bp) of ticks determined herein. Nucleotide similarity and percentage differences are given above and below the diagonal, respectively.

| Tick species | Sequence ID (GenBank accession no.) | 191 | 187 | 290 | 355 | 192 | 30 | 116 | 302 | 357 | 298 | 7 | 225 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Haemaphysalis punctata* | 191 (MT799944) | - | 0.884 | 0.882 | 0.884 | 0.887 | 0.818 | 0.829 | 0.829 | 0.831 | 0.801 | 0.801 | 0.806 |
| *Hs. sulcata* | 187 (MT799946) | 11.6 | - | 0.985 | 0.988 | 0.99 | 0.818 | 0.828 | 0.828 | 0.83 | 0.819 | 0.822 | 0.826 |
| *Hs. sulcata* | 290 (MT799948) | 11.8 | 1.5 | - | 0.992 | 0.995 | 0.811 | 0.823 | 0.823 | 0.826 | 0.814 | 0.81 | 0.814 |
| *Hs. sulcata* | 355 (MT799949) | 11.6 | 1.2 | 0.8 | - | 0.997 | 0.813 | 0.826 | 0.826 | 0.828 | 0.817 | 0.812 | 0.817 |
| *Hs. sulcata* | 192 (MT799947) | 11.3 | 1 | 0.5 | 0.3 | - | 0.816 | 0.828 | 0.828 | 0.83 | 0.819 | 0.814 | 0.819 |
| *Hyalomma anatolicum* | 30 (MT799950) | 18.2 | 18.2 | 18.9 | 18.7 | 18.4 | - | 0.861 | 0.861 | 0.863 | 0.847 | 0.849 | 0.852 |
| *Rhipicephalus microplus* | 116 (MT799951) | 17.1 | 17.2 | 17.7 | 17.4 | 17.2 | 13.9 | - | 0.995 | 0.997 | 0.901 | 0.884 | 0.887 |
| *Rh. microplus* | 302 (MT799952) | 17.1 | 17.2 | 17.7 | 17.4 | 17.2 | 13.9 | 0.5 | - | 0.997 | 0.898 | 0.882 | 0.884 |
| *Rh. microplus* | 357 (MT799953) | 16.9 | 17 | 17.4 | 17.2 | 17 | 13.7 | 0.3 | 0.3 | - | 0.901 | 0.884 | 0.887 |
| *Rh. haemaphysaloides* | 298 (MT799956) | 19.9 | 18.1 | 18.6 | 18.3 | 18.1 | 15.3 | 9.9 | 10.2 | 9.9 | - | 0.931 | 0.933 |
| *Rh. turanicus* | 7 (MT799954) | 19.9 | 17.8 | 19 | 18.8 | 18.6 | 15.1 | 11.6 | 11.8 | 11.6 | 6.9 | - | 0.992 |
| *Rh. turanicus* | 225 (MT799955) | 19.4 | 17.4 | 18.6 | 18.3 | 18.1 | 14.8 | 11.3 | 11.6 | 11.3 | 6.7 | 0.8 | - |

Table S4

Pairwise comparison of *cox1* nucleotide sequences (aligned over 673 bp) of ticks determined herein. Nucleotide similarity and percentage differences are given above and below the diagonal, respectively.

| **Tick species** | **Sequence ID (GenBank accession no.)** | **30** | **116** | **302** | **7** | **225** | **18** | **298** | **230** | **340** | **191** | **187** | **192** | **355** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Hyalomma anatolicum* | 30 (MT80311) | - | 0.823 | 0.821 | 0.815 | 0.826 | 0.82 | 0.82 | 0.824 | 0.826 | 0.802 | 0.808 | 0.806 | 0.811 |
| *Rhipicephalus microplus* | 116 (MT800322) | 17.7 |  | 0.998 | 0.861 | 0.87 | 0.864 | 0.86 | 0.855 | 0.857 | 0.817 | 0.818 | 0.817 | 0.82 |
| *Rh. microplus* | 302 (MT800323) | 17.9 | 0.2 | - | 0.86 | 0.869 | 0.863 | 0.858 | 0.854 | 0.855 | 0.818 | 0.82 | 0.818 | 0.821 |
| *Rh. turanicus* | 7 (MT800312) | 18.5 | 13.9 | 14 | - | 0.982 | 0.986 | 0.893 | 0.878 | 0.879 | 0.829 | 0.823 | 0.818 | 0.818 |
| *Rh. turanicus* | 225 (MT800313) | 17.4 | 13 | 13.1 | 1.8 | - | 0.992 | 0.895 | 0.887 | 0.888 | 0.841 | 0.83 | 0.829 | 0.826 |
| *Rh. turanicus* | 18 (MT800314) | 18 | 13.6 | 13.7 | 1.4 | 0.8 | - | 0.888 | 0.879 | 0.881 | 0.835 | 0.824 | 0.823 | 0.82 |
| *Rh. haemaphysaloides* | 298 (MT800315) | 18 | 14 | 14.2 | 10.7 | 10.5 | 11.2 | - | 0.924 | 0.925 | 0.827 | 0.833 | 0.833 | 0.832 |
| *Rh. haemaphysaloides* | 230 (MT800316) | 17.6 | 14.5 | 14.6 | 12.2 | 11.3 | 12.1 | 7.6 | - | 0.998 | 0.835 | 0.827 | 0.827 | 0.829 |
| *Rh. haemaphysaloides* | 340 (MT800317) | 17.4 | 14.3 | 14.5 | 12.1 | 11.2 | 11.9 | 7.5 | 0.2 | - | 0.836 | 0.829 | 0.829 | 0.83 |
| *Haemaphysalis punctata* | 191 (MT800318) | 19.8 | 18.3 | 18.2 | 17.1 | 15.9 | 16.5 | 17.3 | 16.5 | 16.4 | - | 0.851 | 0.848 | 0.848 |
| *Hs. sulcata* | 187 (MT800319) | 19.2 | 18.2 | 18 | 17.7 | 17 | 17.6 | 16.7 | 17.3 | 17.1 | 14.9 | - | 0.989 | 0.988 |
| *Hs. sulcata* | 192 (MT800320) | 19.4 | 18.3 | 18.2 | 18.2 | 17.1 | 17.7 | 16.7 | 17.3 | 17.1 | 15.2 | 1.1 | - | 0.992 |
| *Hs. sulcata* | 355 (MT800321) | 18.9 | 18 | 17.9 | 18.2 | 17.4 | 18 | 16.8 | 17.1 | 17 | 15.2 | 1.2 | 0.8 | - |

Table S5

Pairwise comparison of ITS-2 nucleotide sequences (aligned over 273 bp) of ticks belonging to *Rhipicephalus* and *Hyalomma* genera determined herein. Nucleotide similarity and percentage differences are given above and below the diagonal, respectively.

| **Tick species** | **Sequence ID (GenBank accession no.)** | **7** | **298** | **302** | **30** |
|---|---|---|---|---|---|
| *Rhipicephalus turanicus* | 7 (MT818226) | - | 0.972 | 0.913 | 0.734 |
| *Rh. haemaphysaloides* | 298 (MT818227) | 2.8 | - | 9.8 | 0.752 |
| *Rh. microplus* | 302 (MT818223) | 8.7 | 0.902 | - | 0.72 |
| *Hyalomma anatolicum* | 30 (MT818222) | 26.6 | 24.8 | 28 | - |