

Table S1. Primers for ticks and tick-borne pathogens detection.

Organism	Gene name	PCR method	Primer name	Cycle	Primer sequence 5' to 3'	Approximate amplicon /bp	Reference
Ticks	COI	PCR	TickCOI-F	1	GGTCAACAAATCATAAAGATATTGG	700	[19]
			TickCOI-R	1	TAAACTTCAGGGTGACCAAAAAATCA		
	16S rRNA	PCR	Tick16S-F	1	CCGGTCTGAACTCAGATCAAGT	400	[20]
			Tick16S-R	1	CTGCTCAATGATTTTTTAAATTGCTGTG G		
<i>Rickettsia</i>	16S rRNA	Semi-Nested PCR	Ric-16SF1	1, 2	GTACGGAATAACTTTTAGAAAT	900	[21]
			Ric-16SR1	1	CATGATGACTTGACRTCCT		
			Ric-16SR2	2	CATCTCACGACACGAGCTG		
	<i>gltA</i>	Semi-Nested PCR	R-gltA-F1	1	CCGGGYTTTATGTCTACTGC	900	[21]
			R-gltA-F2	2	CTTTATGTCTACTGCKTCTTG		
			R-gltA-R	1, 2	AGCTGTCTWGGTCTGCTGATT		
	<i>groEL</i>	Nested PCR	Ric-ESL-F1	1	CCATTACATGATAGAATTGCAAT	1100	[21]
			Ric-ESL-F2	2	GAATTGCAATAAAGCCTATCG		
Anaplasmataceae	16S rRNA	Nested PCR	Ric-ESL-R	1, 2	CCATCATTGCTTTTCTTCTATC		[22]
			A&E-rrs-F1	1	GAACGAACGCTGGCGGCAAGC	500	
			A&E-rrs-R1	1	AGTA(T/C)CG(A/G)ACCAGATAGCCGC		
			A&E-rrs-F2	2	TGCATAGGAATCTACCTAGTAG		
<i>Anaplasma bovis</i>	<i>gltA</i>	Semi-Nested PCR	A&E-rrs-R2	2	CTAGGAATTCCGCTATCCTCT		[23]
			A.b-gltA-F1	1	TACATCWACWGTAAGAATGG	400	
			A.b-gltA-R1	1, 2	CCRGCAAGTDCGTCCCAGTGC		
	<i>groEL</i>	Semi-Nested PCR	A.b-gltA-F2	2	ACWGTAAGAATGGTKGGCTC		[23]
			A.b-groEL-F1	1	GTATGCARTTTGATCGYGGAT	800	
			A.b-groEL-F2	2	GAAGTTGGAAGRGAYGGDGT		
<i>Anaplasma capra</i>	<i>gltA</i>	Semi-Nested	A.b-groEL-R	1, 2	GCCTTWACAGCDGCAACTTG		[24]
			AC-CS-F1	1	ATGATCCGGGGTTCTCTGTC	1000	

	<i>groEL</i>	PCR	AC-CS -R	1, 2	TACAATACCGGAGTAAAAGT	1100	[25]
			AC-CS-F2	2	TGCAGGTCTGAGATAACCT		
		Nested PCR	Ac gro-ELF1	1	GCGAGGCGTTAGACAAGTCCATT		
			Ac gro-ELR1	1	TCCAGAGATGCGAGCGTGTATAG		
			Ac gro-ELF2	2	TGCACTGCTGGTCCAAAGGGGCT		
<i>Ehrlichia</i> spp.	<i>groEL</i>		Ac gro-ELR2	2	CAACTTCGCTAGAGCCGCCAACC	1100	[1]
		Semi-Nested	EhgroEL-F1	1	TGGGCTGGYAATGAAATTGA		
		PCR	EhgroEL-R1	1, 2	TCAACAGCAGCTCTAGTTG		
			EhgroEL-F2	2	AACATGGCAAATGTAGTTGT		
		<i>Coxiella</i> spp.	<i>IS1111</i>	Nested PCR	Q-IS1111-F1		
	Q-IS1111-R1			1	CCGTTTCATCCGCGGTG		
	Q-IS1111-F2			2	GTAAAGTGATCTACACGA		
	Q-IS1111-R2			2	TTAACAGCGCTTGAACGT		
<i>Borrelia</i> spp.	<i>ospA</i>			Nested PCR	Bo. OspA F1	1	GGGAATAGGTCTAATATTAGCC
			Bo. OspA R1	1	CACTAATTGTTAAAGTGGAAGT		
			Bo. OspA F2	2	GCAAAATGTTAGCAGCCTTGAT		
			Bo. OspA R2	2	CTGTGTATTCAAGTCTGGC		
			Intergene 5S-23S rRNA	Nested PCR	Bo. rRNA F1	1	CGACCTTCTTCGCCTTAAAGC
	Bo. rRNA R1			1	TAAGCTGACTAATACTAATTACCC		
	Bo. rRNA F2			2	TCCTAGGCATTACCCATA		
	Bo. rRNA R2			2	GAGTTCGCGGGAGA		
<i>Babesia– Theileria-Hepato zoon</i>	18S rRNA			nested PCR	BTH18S-F1	1	GTGAAACTGCGAATGGCTCATTAC
			BTH18S-R1	1	AAGTGATAAGGTTACAAAACCTTCCC		
			BTH18S-F2	2	GGCTCATTACAACAGTTATAGTTTATTT G		
			BTH18S-R2	2	CGGTCCGAATAATTCACCGGAT		

Table S2. Tick prevalence in Chengkou, Chongqing, China.

Tick species	Host (ticks No.)	Geographical distribution (ticks No.)	Total prevalence%
<i>Ixodes acutitarsus</i>	goat (3)	Dongan (3)	0.50% (3/601)
<i>Ixodes ovatus</i>	dog (10)	Dongan (10)	1.66% (10/601)
<i>Haemaphysalis flava</i>	dog (62)	Dongan (39), Pingba (23)	10.32% (62/601)
<i>Haemaphysalis hystrix</i>	dog (59)	Gaoyan (2), Pingba (57)	9.82% (59/601)
<i>Haemaphysalis longicornis</i>	cattle (78), goat (386), dog (3)	Miaoba (256), Gaoyan (141), Bashan (70)	77.70% (467/601)

Table S3. List of nucleotide sequence accession number and identity with BLAST.

Organism	Gene name	Sequence in this study	Closest BLAST		Identity
		Accession No.	Descriptions (Accession No.)	Source (geo.)	
Tick	COI	PQ219422-PQ219423	<i>Ixodes ovatus</i> (NC_062061)	Hog-badger (Wuhan, China)	99.42%
		PQ219424-PQ219431	<i>Ixodes ovatus</i> (MH319666)	Tick (Yunnan, China)	90.02%-90.79%
		PQ219432-PQ219434	<i>Ixodes acutitarsus</i> (HM193896)	Tick (Zhangmu, Tibet, China)	99.49%-100.00%
		PQ219435-PQ219438	<i>Haemaphysalis flava</i> (OR975892)	(Japan)	100.00%
		PQ219439-PQ219443	<i>Haemaphysalis flava</i> (KY021805)	(China)	94.52%-97.51%
		PQ219444-PQ219453	<i>Haemaphysalis hystrix</i> (OQ135148)	(Jinzhai county Anhui province in China)	99.84%-100.00%
		PQ219454-PQ219459	<i>Haemaphysalis longicornis</i> (MT465132)	Tick (Hanzhong, China)	99.68%-100.00%
	16S rRNA	PQ512796-PQ512797	<i>Ixodes ovatus</i> (NC_062061)	Hog-badger (Wuhan, China)	99.51%
		PQ512798-PQ512801	<i>Ixodes ovatus</i> (MH319616)	goat (Yunnan, China)	96.15%
		PQ512802-PQ512805	<i>Ixodes ovatus</i> (MH319598)	goat (Yunnan, China)	96.19%-96.65%
	16S rRNA	PQ203952-PQ203960	Uncultured <i>Rickettsia</i> sp. (ON016521)	<i>Haemaphysalis flava</i> (Jiangsu, China)	99.92%

<i>Ehrlichia</i>	<i>gltA</i>	PQ203972	<i>Rickettsia japonica</i> (CP047359)	Human (Zhejiang, China)	100.00%
		PQ249177	<i>Rickettsia japonica</i> (CP047359)	Human (Zhejiang, China)	100.00%
		PQ249178-PQ249186	<i>Candidatus Rickettsia principis</i> (ON600642)	<i>Haemaphysalis flava</i> (Jiangsu, China)	100.00%
		PQ249175-PQ249176	<i>Rickettsia raoultii</i> (MK304547)	<i>Dermacentor reticulatus</i> (Russia)	100.00%
	<i>groEL</i>	PQ249190-PQ249198	<i>Candidatus Rickettsia principis</i> (PP791919)	Tick collected from vegetation (Rissua)	99.89%
		PQ249187-PQ249188	<i>Rickettsia raoultii</i> (CP010969)	Human (Inner Mongolia, China)	100.00%
		PQ249189	<i>Rickettsia japonica</i> (KX987373)	<i>Haemaphysalis hystricis</i> (Wuhan, China)	100.00%
	16S rRNA	PQ205311	<i>Ehrlichia</i> sp. (KJ410252)	<i>Dermacentor nuttalli</i> (Xinjiang, China)	100.00%
		PQ205309	<i>Candidatus Ehrlichia shimanensis</i> (AB074459)	(USA)	100.00%
	<i>groEL</i>	PQ205310	Uncultured <i>Ehrlichia</i> sp. (FJ966350)	<i>Haemaphysalis japonica</i> (Russia)	100.00%
		PQ205312-PQ205314	<i>Ehrlichia chaffeensis</i> (NR_074500)	(USA)	99.53%,100.00%, 99.53%
		PQ205315	<i>Candidatus Ehrlichia hainanensis</i> (MT875365)	<i>Niviventer fulvescens</i> (Hainan, China)	100.00%
		PQ249204	<i>Ehrlichia chaffeensis</i> (CP000236)	(USA)	94.42%
		PQ249203	<i>Ehrlichia</i> sp. (KJ410295)	Tick (Xinjiang, China)	99.12%
		PQ249199	Uncultured <i>Ehrlichia</i> sp. (FJ966349)	<i>Haemaphysalis japonica</i> (Russia)	99.41%
		PQ249200-PQ249201	<i>Ehrlichia</i> sp. (OQ185236)	<i>Haemaphysalis hystricis</i> (Anhui, China)	100.00%
		PQ249202	<i>Candidatus Ehrlichia zunyiensis</i> (OM920706)	<i>Berylmys bowersi</i> (Guizhou, China)	100.00%
		PQ249205	<i>Candidatus Ehrlichia shimanensis</i> (AB074462)	Tick	94.71%
		PQ206196-PQ206198	<i>Anaplasma bovis</i> (KY548389)	Raccoon dog (South Korea)	100.00%
<i>Anaplasma</i>	16S rRNA				

<i>Babesia</i>	<i>gltA</i>	PQ206199-PQ206201	<i>Anaplasma capra</i> (LC432114)	<i>Hydropotes inermis argyropus</i> from Korean Water Deer (South Korea)	100.00%
		PQ249206-PQ249211	<i>Anaplasma bovis</i> (MH255921)	Goat (Shaanxi, China)	100.00%
		PQ249212-PQ249213	<i>Anaplasma capra</i> (OQ185246)	<i>Haemaphysalis longicornis</i> (Anhui, China)	100.00%
		PQ249217-PQ249219	<i>Anaplasma bovis</i> (MW122329)	Cattle blood (South Korea)	99.86%
		PQ249214-PQ249216	<i>Anaplasma bovis</i> (OQ702283)	<i>Haemaphysalis longicornis</i> (Hebei, China)	100.00%
	18S rRNA	PQ249220-PQ249221	<i>Anaplasma capra</i> (OP974583)	Goat blood (China)	100.00%
		PQ207054	<i>Babesia</i> sp. (AB935167)	(Japan)	100.00%
		PQ207055	<i>Theileria capreoli</i> (JX134577)	White-lipped deer blood (China)	99.93%
		PQ207056-PQ207061	<i>Theileria luwenshuni</i> (MH208628)	<i>Rhipicephalus microplus</i> (Yunnan, China)	100.00%
		PQ207062	<i>Theileria orientalis</i> (MH208641)	<i>Rhipicephalus microplus</i> (Yunnan, China)	100.00%
<i>Coxiella</i>	IS1111	PQ249222-PQ249228	<i>Coxiella burnetii</i> (KX852471)	<i>Hyalomma asiaticum</i> (Xinjiang, China)	100.00%
		PQ249229-PQ249232	<i>Coxiella burnetii</i> (KX852467)	<i>Hyalomma asiaticum</i> (Xinjiang, China)	100.00%

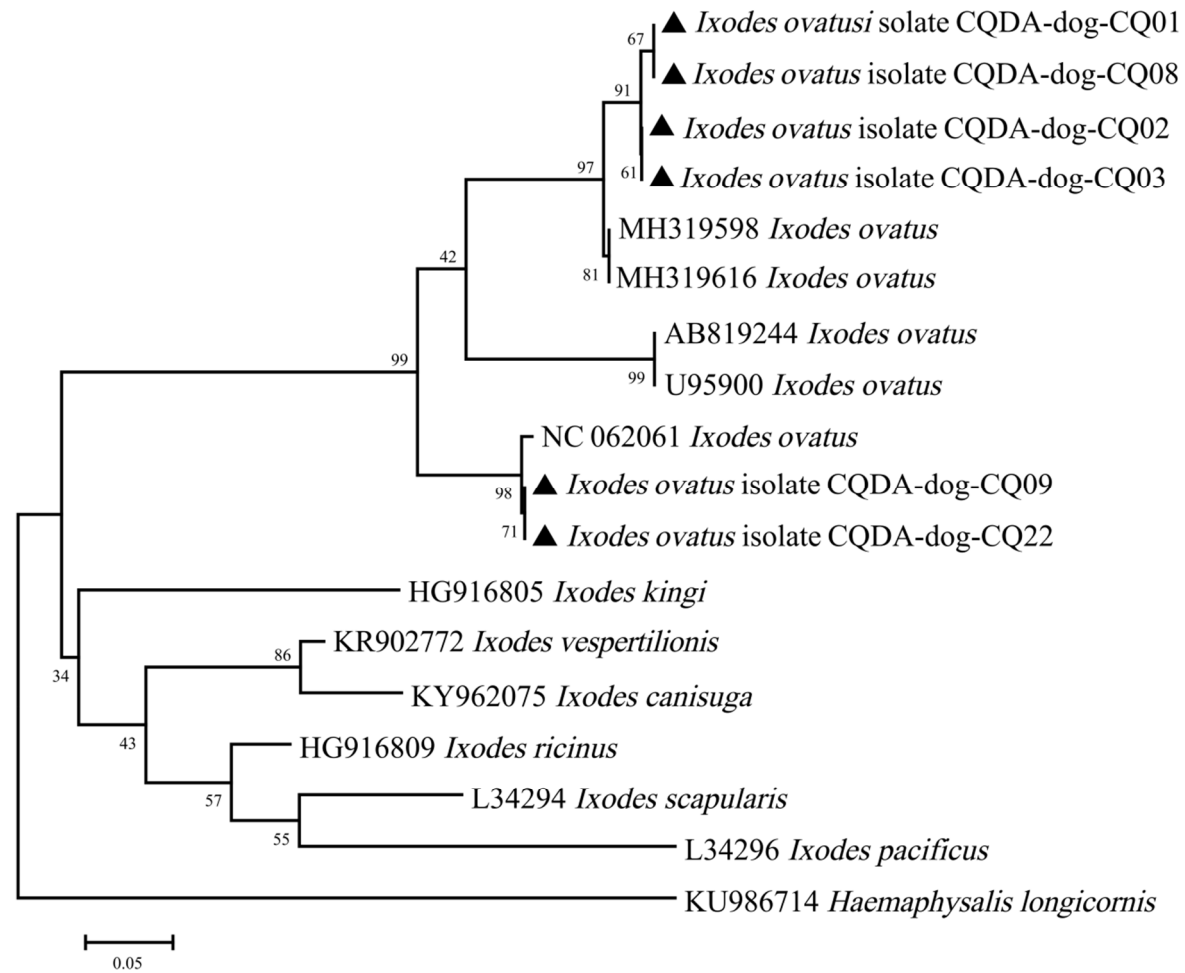


Figure S1. Phylogenetic analysis of ticks based on the nucleotide sequences of 16S rRNA. Sequences obtained in this study were marked with black triangles before their names.