

**Table S1.** Part of pairwise distance matrix based on nucleotide sequences of *Candidatus Mycoplasma haemobos* and *Mycoplasma wenyonii* strains.

No.		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	<i>Ca. M. haemobos</i> BGD29 (This study)																	
2	<i>Ca. M. haemobos</i> BGD49 (This study)	0.000																
3	MT341495 <i>Ca. M. haemobos</i> Cattle blood (Brazil)	0.002	0.002															
4	KT985638 <i>Ca. M. haemobos</i> Cattle blood (Malaysia)	0.002	0.002	0.000														
5	MG948631 <i>Ca. M. haemobos</i> Cattle blood (Cuba)	0.002	0.002	0.000	0.000													
6	KJ883514 <i>Ca. M. haemobos</i> Dog blood (Taiwan)	0.002	0.002	0.000	0.000	0.000												
7	EF616468 <i>Ca. M. haemobos</i> Cattle Blood (Switzerland)	0.002	0.002	0.000	0.000	0.000	0.000											
8	MH388480 <i>Ca. M. haemobos Rhipicephalus microplus</i> (China)	0.004	0.004	0.002	0.002	0.002	0.002	0.002										
9	MW463060 <i>Ca. M. haemobos</i> Dog blood (China)	0.004	0.004	0.002	0.002	0.002	0.002	0.002	0.000									
10	EU367965 <i>Ca. M. haemobos</i> Cattle blood (Japan)	0.004	0.004	0.002	0.002	0.002	0.002	0.002	0.004	0.004								
11	<i>M. Wenyonii</i> HND16 (This study)	1.399	1.399	1.397	1.397	1.397	1.397	1.397	1.394	1.394	1.399							
12	<i>M. Wenyonii</i> BVD39 (This study)	1.399	1.399	1.397	1.397	1.397	1.397	1.397	1.394	1.394	1.399	0.004						
13	MT241311 <i>M. wenyonii</i> Buffalo blood (Philippines)	1.373	1.373	1.370	1.370	1.370	1.370	1.370	1.368	1.368	1.373	0.004	0.004					
14	FN392885 <i>M. wenyonii</i> Cattle blood (Switzerland)	1.339	1.339	1.336	1.336	1.336	1.336	1.336	1.334	1.334	1.339	0.000	0.004	0.004				
15	FJ375309 <i>M. wenyonii</i> Cattle blood (China)	1.505	1.505	1.503	1.503	1.503	1.503	1.503	1.501	1.501	1.505	0.015	0.015	0.010	0.014			
16	MG948626 <i>M. wenyonii</i> Cattle blood (Cuba)	1.373	1.373	1.370	1.370	1.370	1.370	1.370	1.368	1.368	1.373	0.004	0.004	0.000	0.004	0.010		
17	KY328836 <i>M. wenyonii</i> Buffalo blood (Brazil)	1.512	1.512	1.510	1.510	1.510	1.510	1.510	1.507	1.507	1.512	0.004	0.004	0.000	0.004	0.011	0.000	

Pairwise distances calculations were accomplished using MEGA X software.

**Table S2.** Part of pairwise distance matrix based on nucleotide sequences of *Rickettsia* sp. strains.

No.		1	2	3	4	5	6	7	8	9	10	11
1	<i>R. felis</i> Cte <i>felis felis</i> BVD20 (This study)											
2	<i>R. felis</i> Cte <i>felis felis</i> HND16 (This study)	0.000										
3	<i>R. felis</i> Cte <i>felis felis</i> BGD39 (This study)	0.000	0.000									
4	<i>R. felis</i> Cte <i>felis felis</i> VPD59 (This study)	0.000	0.000	0.000								
5	KY417891 <i>R. felis</i> Cte <i>felis felis</i> (Hongkong)	0.000	0.000	0.000	0.000							
6	KP318092 <i>R. felis</i> Homo sapiens (Bangladesh)	0.000	0.000	0.000	0.000	0.000						
7	MT019628 <i>R. felis</i> Dog blood (China)	0.000	0.000	0.000	0.000	0.000	0.000					
8	JN375498 <i>R. felis</i> Cte <i>felis felis</i> (Brazil)	0.000	0.000	0.000	0.000	0.000	0.000	0.000				
9	KP749467 <i>R. felis</i> Cte <i>canis</i> (Czech Republic)	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000			
10	JQ284386 <i>R. felis</i> Dog blood (Australia)	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
11	MH523408 <i>Rickettsia</i> sp. genotype RF2125 Cat blood (Thailand)	0.015	0.015	0.015	0.015	0.015	0.016	0.015	0.015	0.015	0.015	
12	MH523408 <i>Rickettsia</i> sp. genotype RF2125 Cte <i>canis</i> (France)	0.015	0.015	0.015	0.015	0.015	0.016	0.015	0.015	0.015	0.015	0.000

Pairwise distances calculations were accomplished using MEGA X software.