

Additional File 1

Table S0. Synthetic positive controls.

Target organism	Accession number used to generate the synthetic positive control	Reference
<i>Anaplasma centrale</i>	AF414867	¹ Decaro <i>et al.</i> , 2008
<i>Anaplasma marginale</i>	M59845	¹ Decaro <i>et al.</i> , 2008
<i>Babesia bigemina</i>	AY603402	² Kim <i>et al.</i> , 2007
<i>Babesia bovis</i>	AY603398	² Kim <i>et al.</i> , 2007
<i>Ehrlichia ruminantium</i>	AY236058	³ Steyn <i>et al.</i> , 2007
<i>Theileria parva</i>	L02366	⁴ Papli <i>et al.</i> , 2011

References

¹ Duplex real-time polymerase chain reaction for simultaneous detection and quantification of *Anaplasma marginale* and *Anaplasma centrale*. J Vet Diagn Invest. 2008;20:606-11.

² Kim C, Iseki H, Herbas MS, Yokoyama N, Suzuki H, Xuan X, et al. Development of TaqMan-based real-time PCR assays for diagnostic detection of *Babesia bovis* and *Babesia bigemina*. Am J Trop Med Hyg. 2007;77:837-41.

³ Steyn HC, Pretorius A, McCrindle CME, Steinmann CML, Van Kleef M. A quantitative real-time PCR assay for *Ehrlichia ruminantium* using pCS20. Vet Microbiol. 2008;131:258-65.

⁴ Papli N, Landt O, Fleischer C, Koekemoer JO, Mans BJ, Pienaar R, et al. Evaluation of a TaqMan real-time PCR for the detection of *Theileria parva* in buffalo and cattle. Vet Parasitol. 2011;175:356-9.

Table S1. Vector-competent ticks for the four tick-borne pathogens covered in the ecological analysis.

	<i>Anaplasma marginale</i>	<i>Ehrlichia ruminantium</i>	<i>Babesia bigemina</i>	<i>Babesia bovis</i>
Tick species				
<i>Amblyomma gemma</i>		X		
<i>Amblyomma variegatum</i>		X		
<i>Hyalomma rufipes</i>	X			
<i>Rhipicephalus decoloratus</i>	X		X	
<i>Rhipicephalus pulchellus</i>	X			
<i>Rhipicephalus microplus</i>	X		X	X
<i>Rhipicephalus evertsi evertsi</i>	X			
<i>Rhipicephalus annulatus</i>	X		X	X
<i>Rhipicephalus geigy</i>				
<i>Rhipicephalus appendiculatus</i>				
<i>Hyalomma truncatum</i>				
<i>Rhipicephalus lunulatus</i>				
<i>Rhipicephalus praetextatus</i>				

Note:

X: considered to be vector-competent.

‘’: other tick species frequently collected, and tested for potential associations with pathogen prevalence (see ‘Statistical Analysis’)

Table S2. Distribution of (co-)infections in cattle individuals.

Co-infection	Overall	Burkina Faso	Benin	Ethiopia	Ghana	Nigeria	Tanzania	Uganda
<i>A. marginale</i>	60.77	86.45	46.76	59.60	62.93	52.05	56.39	74.80
<i>A. marginale</i> × <i>B. bigemina</i>	11.19	1.08	16.41	6.78	17.41	9.36	14.81	2.56
<i>B. bigemina</i>	8.46	0.86	7.70	14.55	0.53	23.59	9.51	6.10
<i>A. marginale</i> × <i>E. ruminantium</i>	4.98	2.37	8.71	6.36	7.37	2.34	2.45	0.79
<i>A. marginale</i> × <i>B. bovis</i>	2.98	1.29	2.57	0.00	7.05	0.78	5.03	1.18
<i>A. marginale</i> × <i>A. centrale</i>	2.27	0.65	2.01	3.67	0.11	5.46	3.80	0.79
<i>A. marginale</i> × <i>B. bigemina</i> × <i>E. ruminantium</i>	1.74	0.00	4.24	0.85	2.24	0.78	1.77	0.20
<i>E. ruminantium</i>	1.68	4.09	1.56	3.11	0.11	2.14	0.14	2.36
<i>B. bigemina</i> × <i>E. ruminantium</i>	1.28	0.00	2.68	3.11	0.00	1.95	0.54	0.20
<i>B. bovis</i>	1.11	2.37	1.23	0.00	0.32	0.00	0.68	4.53
<i>A. marginale</i> × <i>B. bigemina</i> × <i>B. bovis</i>	0.78	0.00	1.56	0.00	0.85	0.00	2.04	0.00
<i>A. marginale</i> × <i>B. bovis</i> × <i>E. ruminantium</i>	0.50	0.22	1.23	0.00	0.85	0.00	0.41	0.20
<i>A. marginale</i> × <i>A. centrale</i> × <i>B. bigemina</i>	0.48	0.00	1.23	0.71	0.00	0.78	0.41	0.00
<i>T. parva</i>	0.46	0.00	0.00	0.00	0.00	0.00	0.00	4.33
<i>B. bigemina</i> × <i>B. bovis</i>	0.27	0.00	0.22	0.00	0.11	0.19	1.09	0.20
<i>A. marginale</i> × <i>A. centrale</i> × <i>E. ruminantium</i>	0.23	0.00	0.11	0.99	0.00	0.39	0.00	0.20
<i>A. centrale</i>	0.21	0.43	0.11	0.28	0.00	0.19	0.27	0.39
<i>A. marginale</i> × <i>B. bigemina</i> × <i>B. bovis</i> × <i>E. ruminantium</i>	0.21	0.00	0.56	0.00	0.11	0.00	0.54	0.00
<i>A. marginale</i> × <i>A. centrale</i> × <i>B. bigemina</i> × <i>E. ruminantium</i>	0.08	0.00	0.45	0.00	0.00	0.00	0.00	0.00
<i>B. bigemina</i> × <i>B. bovis</i> × <i>E. ruminantium</i>	0.06	0.00	0.22	0.00	0.00	0.00	0.14	0.00
<i>B. bovis</i> × <i>E. ruminantium</i>	0.04	0.22	0.11	0.00	0.00	0.00	0.00	0.00
<i>B. bigemina</i> × <i>T. parva</i>	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.39
<i>A. marginale</i> × <i>T. parva</i>	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.39
<i>A. marginale</i> × <i>A. centrale</i> × <i>B. bovis</i>	0.04	0.00	0.22	0.00	0.00	0.00	0.00	0.00
<i>E. ruminantium</i> × <i>T. parva</i>	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.20
<i>A. marginale</i> × <i>B. bovis</i> × <i>T. parva</i>	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.20
<i>A. marginale</i> × <i>A. centrale</i> × <i>B. bigemina</i> × <i>B. bovis</i>	0.02	0.00	0.11	0.00	0.00	0.00	0.00	0.00
Co-infected cows (%)	27.27	5.83	42.64	22.47	36.1	22.03	33.03	7.5
Infected individuals	4762	465	896	708	936	513	736	508

Note: Prevalences refer to the number of host individuals with one or more tick-borne pathogens. From top to bottom: most to least frequently observed (combinations of) infections. (Percentages sum to 100% for each).

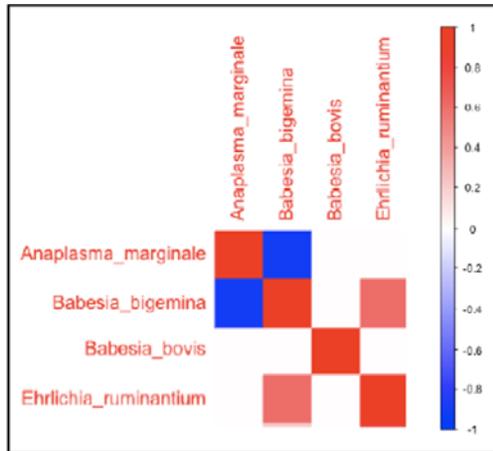


Fig. S1. Heatmap of TBHPs species-to-species associations (co-infections) based on the HMSC model with the cattle individual's identity as a sampling unit, after controlling for covariates (including locations where the blood sample was taken). Blue and red colours show parameters that are estimated to be positive and negative, respectively, with at least 0.95 posterior probability.