

Supplementary Table S1. Predicted *B. rossi*-specific genes with unassigned orthogroups.

Genomic coordinates (assembly)	Predicted protein sequence	Predicted protein length (aa)	AED	Assembly
Chr2: 1444890-1445513 (R)	(R_chr2_P1) MRSQAVWPRSTTSMAYGG PLVSCHSPKKNSTELTRRST RACVSACQRAAPSRPNTYIP NTMKCHPSCGRTYSWHR	207	0.05	R
Chr4: 60399-60866 (PMB)	(PMB_chr4_P1) MKWLEGIRKPLYEAVYLEC MQGANEDDWFYQGYTYLF AKKEKPENASEYRPITCMS NLYKLTTTRCVTESFVKDVE LRGLLTENQMGTRRRVQGA KEHALTNIVLNHAHQYKLH SSWVDGRKAYDSIDHRYLT HVLSQLNLPPWFMQFVTGI STRN	155	0.43	PMB
Chr1: 2294248-2294475 (PMB)	(PMB_chr1_P1) MRSQAVWPRSTTSMAYGG PLVSCHSPKKNSTELTRRST RACVSACQRAAPSRPNTYIP NTMKCHPSCGRTYSWHR	75	0.20	PMB
Chr2: 2155800-2155948 (R)	(R_chr2_P2) MRILTFRQGIRLSALRARN TSYLRLRTTESVANSN	36	0.47	R
Chr2: 2123982-2124023 (PMB)	MSRKVISGALTSG	13	0.50	PMB, K, R
Chr1: 2545299-2545331 (PMB)	MTLPCNLHRQ	10	0.49	PMB, K, R
Chr1: 35(65348-3565377 (PMB)	MTVSCLEF	9	0.37	PMB, K, R
Chr2: 1717043-1717057 (PMB)	MNNC	4	0.47	PMB, K

Supplementary Table S2. Syntenic inversion breakpoints in genome assemblies of *Babesia rossi* clinical isolates.

Identifier [#]	Chromosome	<i>B. rossi</i> PMB coordinates			# genes (per strand)
		Start	End	Length (bp)	Total (+ / -)
a	Chr1	1401884	1577278	175395	58 (39/19)
b	Chr1	2603464	2752912	149449	64 (43/30)
c	Chr2	2009096	2137630	128535	6 (3/3)
d	Chr2	1061633	1070793	9161	42 (25/17)

[#] Location of breakpoints indicated in Figure 3

Supplementary Table S3. Total polymorphisms in *Babesia rossi* field isolates.

PMB isolate	SNPs		INDELs	
	Isolate K	Isolate R	Isolate K	Isolate R
Chr1	29,134	8,180	2,238	569
Chr2	3,980	10,680	317	755
Chr3	610	1,740	53	107
Chr4	4,806	4,959	282	263
Chr5	2,914	3,726	152	177
Apicoplast	25	16	2	1