

**Table S1 Identity comparisons of nucleotide sequence of *Bartonella* *ssrA* gene (301 bp) from small mammals in this study**

	HQ35	HQ4	HQ9	HQ18	HQ25	HQ32	HQ34	HQ38	HQ55	HQ66	HQ73	HQ72	HQ77	HQ80	HQ92	HQ96	HQ76	HQ99	GS183	GS97	GS43	GS60	GS164	GS40	GS39	GS29	GS35	GS37	GS55	GS167	1	2	3	4	5	6	7	8	9	10	11	12								
HQ35	100.0																																																	
HQ4	98.9	100.0																																																
HQ9	93.1	92.1	100.0																																															
HQ18	96.2	95.2	91.5	100.0																																														
HQ25	100.0	98.9	93.1	96.2	100.0																																													
HQ32	99.5	98.4	92.6	95.7	99.5	100.0																																												
HQ34	100.0	98.9	93.1	96.2	100.0	99.5	100.0																																											
HQ38	38.2	38.2	37.1	38.2	38.2	38.2	38.2	100.0																																										
HQ55	95.2	94.1	90.5	97.9	95.2	94.6	95.2	38.2	100.0																																									
HQ66	39.8	40.3	39.7	41.4	39.8	39.8	39.8	88.3	41.4	100.0																																								
HQ73	38.2	38.2	37.1	38.2	38.2	38.2	38.2	100.0	38.2	88.3	100.0																																							
HQ72	38.2	38.2	37.1	38.2	38.2	38.2	38.2	100.0	38.2	88.3	100.0	100.0																																						
HQ77	38.2	38.2	37.1	38.2	38.2	38.2	38.2	99.5	38.2	87.8	99.5	99.5	100.0																																					
HQ80	100.0	98.9	93.1	96.2	100.0	99.5	100.0	38.2	95.2	39.8	38.2	38.2	38.2	100.0																																				
HQ92	39.8	40.3	39.7	41.4	39.8	39.8	39.8	88.8	41.4	99.5	88.8	88.8	88.3	39.8	100.0																																			
HQ96	38.2	38.2	37.1	38.2	38.2	38.2	38.2	100.0	38.2	88.3	100.0	100.0	99.5	38.2	88.8	100.0																																		
HQ76	38.2	38.2	37.1	38.2	38.2	38.2	38.2	100.0	38.2	88.3	100.0	100.0	99.5	38.2	88.8	100.0	100.0																																	
HQ99	38.2	38.2	37.1	38.2	38.2	38.2	38.2	100.0	38.2	88.3	100.0	100.0	99.5	38.2	88.8	100.0	100.0	100.0																																
GS183	90.9	89.8	88.4	88.2	90.9	90.3	90.9	37.7	87.6	39.8	37.7	37.7	37.7	90.9	39.8	37.7	37.7	37.7	100.0																															
GS97	86.8	85.7	83.9	86.8	86.8	86.2	86.8	35.4	85.7	39.6	35.4	35.4	35.4	86.8	39.6	35.4	35.4	35.4	84.7	100.0																														
GS43	86.8	85.7	83.9	86.8	86.8	86.2	86.8	35.4	85.7	39.6	35.4	35.4	35.4	86.8	39.6	35.4	35.4	35.4	84.7	100.0	100.0																													
GS60	92.5	91.4	87.8	93.0	92.5	91.9	92.5	37.6	92.5	39.2	37.6	37.6	37.6	92.5	39.2	37.6	37.6	37.6	88.2	83.6	83.6	100.0																												
GS164	95.7	94.6	94.2	94.1	95.7	95.2	95.7	38.7	93.0	39.8	38.7	38.7	38.7	95.7	39.8	38.7	38.7	38.7	89.8	85.2	85.2	90.3	100.0																											
GS40	86.8	85.7	83.9	86.8	86.8	86.2	86.8	35.4	85.7	39.6	35.4	35.4	35.4	86.8	39.6	35.4	35.4	35.4	84.7	100.0	100.0	83.6	85.2	100.0																										
GS39	86.8	85.7	83.9	86.8	86.8	86.2	86.8	35.4	85.7	39.6	35.4	35.4	35.4	86.8	39.6	35.4	35.4	35.4	84.7	100.0	100.0	83.6	85.2	100.0	100.0																									
GS29	97.9	96.8	92.1	98.4	97.9	97.3	97.9	39.3	97.3	40.8	39.3	39.3	39.3	97.9	40.8	39.3	39.3	39.3	89.3	86.8	86.8	94.1	94.6	86.8	86.8	100.0																								
GS35	97.9	96.8	92.1	98.4	97.9	97.3	97.9	39.3	97.3	40.8	39.3	39.3	39.3	97.9	40.8	39.3	39.3	39.3	89.3	86.8	86.8	94.1	94.6	86.8	86.8	100.0	100.0																							
GS37	97.9	96.8	92.1	98.4	97.9	97.3	97.9	39.3	97.3	40.8	39.3	39.3	39.3	97.9	40.8	39.3	39.3	39.3	89.3	86.8	86.8	94.1	94.6	86.8	86.8	100.0	100.0	100.0																						
GS55	91.4	90.3	87.8	88.2	91.4	90.9	91.4	37.7	87.6	39.3	37.7	37.7	37.7	91.4	39.3	37.7	37.7	37.7	95.7	83.6	83.6	88.2	89.3	83.6	83.6	89.8	89.8	89.8	100.0																					
GS167	89.3	88.2	86.8	87.1	89.3	88.7	89.3	38.2	86.6	39.8	38.2	38.2	38.2	89.3	39.8	38.2	38.2	38.2	95.2	84.1	84.1	87.6	88.2	84.1	84.1	88.7	88.7	88.7	95.2	100.0																				
1	37.7	37.7	36.6	37.7	37.7	37.7	37.7	99.5	37.7	88.8	99.5	99.5	98.9	37.7	89.4	99.5	99.5	99.5	99.5	37.2	34.9	34.9	37.0	38.2	34.9	34.9	38.7	38.7	38.7	37.2	37.7	100.0																		
2	86.8	85.7	83.9	86.2	86.8	86.2	86.8	33.9	85.2	38.0	33.9	33.9	33.9	86.8	38.0	33.9	33.9	33.9	85.2	96.8	96.8	83.6	85.2	96.8	96.8	86.2	86.2	86.2	85.2	84.7	33.3	100.0																		
3	86.2	85.2	83.3	85.7	86.2	85.7	86.2	34.4	84.7	38.5	34.4	34.4	34.4	86.2	38.5	34.4	34.4	34.4	85.2	95.8	95.8	83.1	84.7	95.8	95.8	85.7	85.7	85.7	85.7	84.7	33.9	98.9	100.0																	
4	38.7	38.7	37.6	38.7	38.7	38.7	38.7	94.7	38.7	87.2	94.7	94.7	94.2	38.7	87.8	94.7	94.7	94.7	37.7	35.4	35.4	37.6	38.2	35.4	35.4	39.8	39.8	39.8	37.7	38.2	95.2	33.9	34.4	100.0																
5	85.6	84.6	84.8	84.0	85.6	85.1	85.6	31.9	83.0	35.6	31.9	31.9	31.9	85.6	35.6	31.9	31.9	31.9	85.1	88.4	88.4	82.5	85.1	88.4	88.4	85.1	85.1	85.1	85.6	87.2	31.4	88.9	88.4	31.9	100.0															
6	86.2	85.2	83.3	86.2	86.2	85.7	86.2	34.9	85.2	39.1	34.9	34.9	34.9	86.2	39.1	34.9	34.9	34.9	84.1	99.5	99.5	83.1	84.7	99.5	99.5	86.2	86.2	86.2	84.1	84.7	34.4	97.4	96.3	34.9	88.9	100.0														
7	37.2	37.2	36.1	37.2	37.2	37.2	37.2	98.4	37.2	87.8	98.4	98.4	97.9	37.2	88.3	98.4	98.4	98.4	36.7	34.4	34.4	36.5	37.7	34.4	34.4	38.2	38.2	38.2	37.7	37.2	98.9	32.8	33.3	94.2	30.9	33.9	100.0													
8	86.7	85.6	83.8	86.2	86.7	86.2	86.7	34.6	85.1	38.7	34.6	34.6	34.6	86.7	38.7	34.6	34.6	34.6	85.1	94.7	94.7	83.0	85.1	94.7	94.7	86.2	86.2	86.2	85.1	84.6	34.0	97.9	96.8	34.6	88.8	95.2	33.5	100.0												
9	96.2	95.2	93.7	95.7	96.2	95.7	96.2	37.2	94.6	39.8	37.2	37.2	37.2	96.2	39.8	37.2	37.2	37.2	90.3	86.8	86.8	92.5	96.2	86.8	86.8	96.2	96.2	96.2	89.3	88.2	36.7	86.8	86.2	37.7	84.6	86.2	36.1	86.7	100.0											
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