

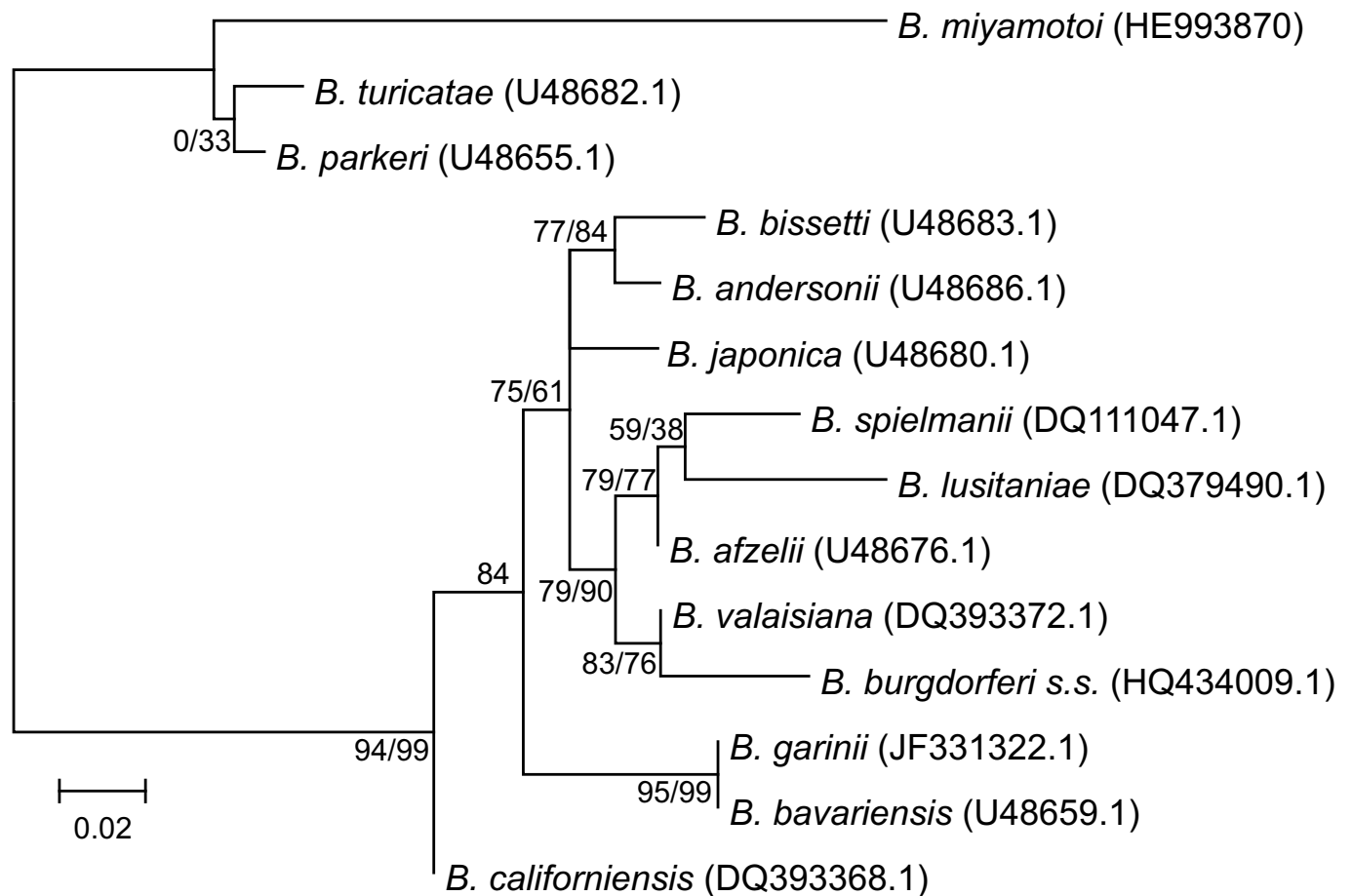


Figure S1 Phylogenetic tree of *Borrelia* spp. sequences for *hbb* gene. The 105 bp sequence used for *B. miyamotoi* is from the present study and was deposited in the EBI database with accession number [HE993870]. Sequences were aligned using ClustalX2. The optimal nucleotide acid substitution model was determined using jModeltest 0.1 before the maximum likelihood tree was calculated with Phyml 3.01 using the TPM3uf substitution model. Statistical support for individual branches is displayed with results of the Shimodaira-Hasegawa modification of the approximate likelihood ratio test before and of the bayesian transformation of the approximate likelihood ratio test after the slash. The bar represents 0.02 substitutions per site. Accession numbers from Genbank® are given in brackets.