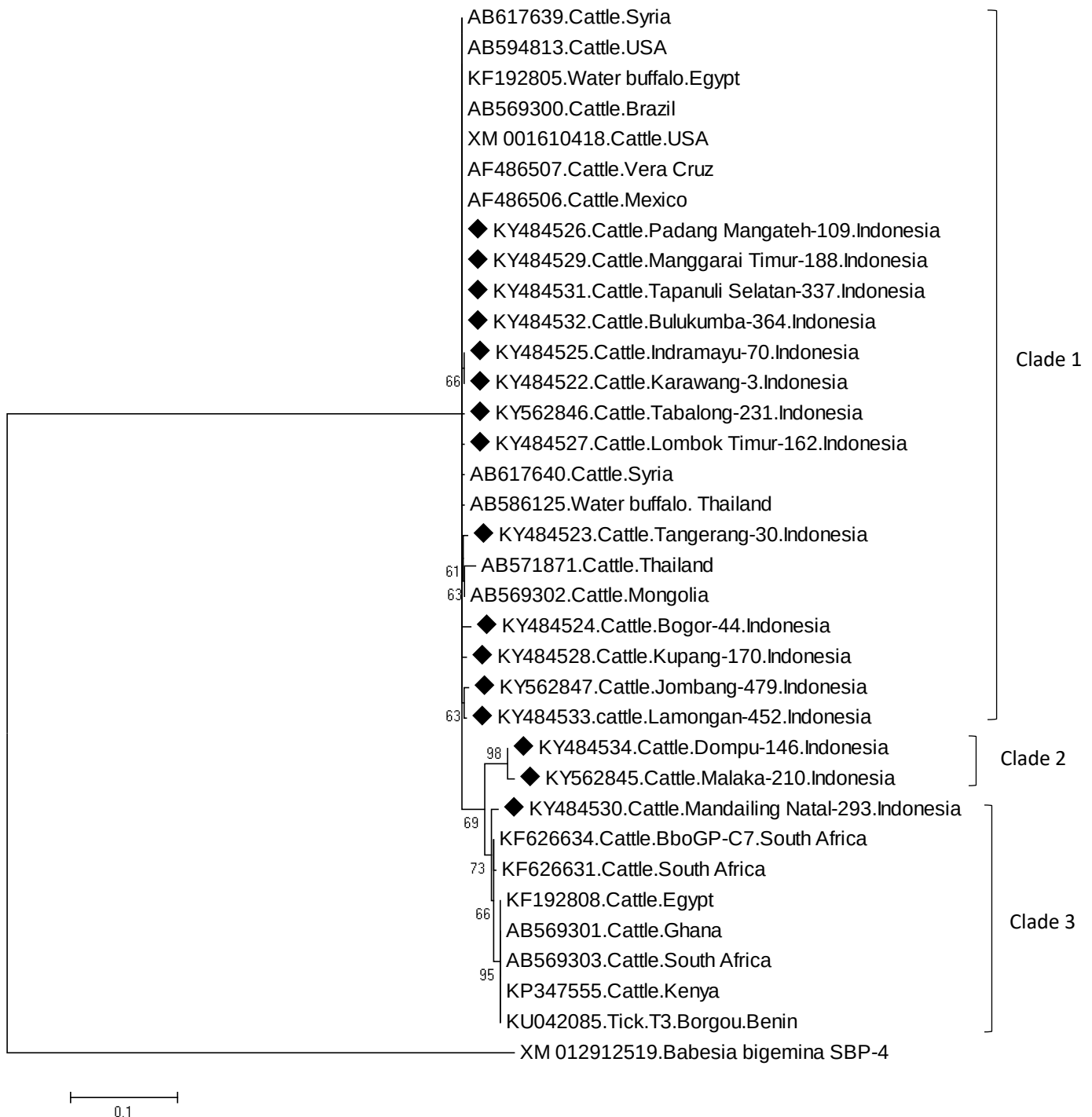


Additional file 4: Figure S1 Phylogenetic tree of *Babesia bovis* sbp4 gene sequences. The maximum likelihood method based on the Kimura 2-parameter model with 1000 bootstrap replicates, available in MEGA ver.7, was used to determine the evolutionary history [30, 40]. All positions containing gaps and missing data were eliminated. Indonesian *B. bovis* sbp4 sequences are indicated by diamonds.



Additional file 4: Figure S2 Phylogenetic analysis of *Babesia bigemina* rap-1a gene sequences. The maximum likelihood method based on the Kimura 2-parameter model with 1000 bootstrap replicates, available in MEGA ver.7, was used to determine the evolutionary history [30, 40]. All positions containing gaps and missing data were eliminated. Indonesian *B. bigemina* rap-1a sequences are indicated by diamonds.

