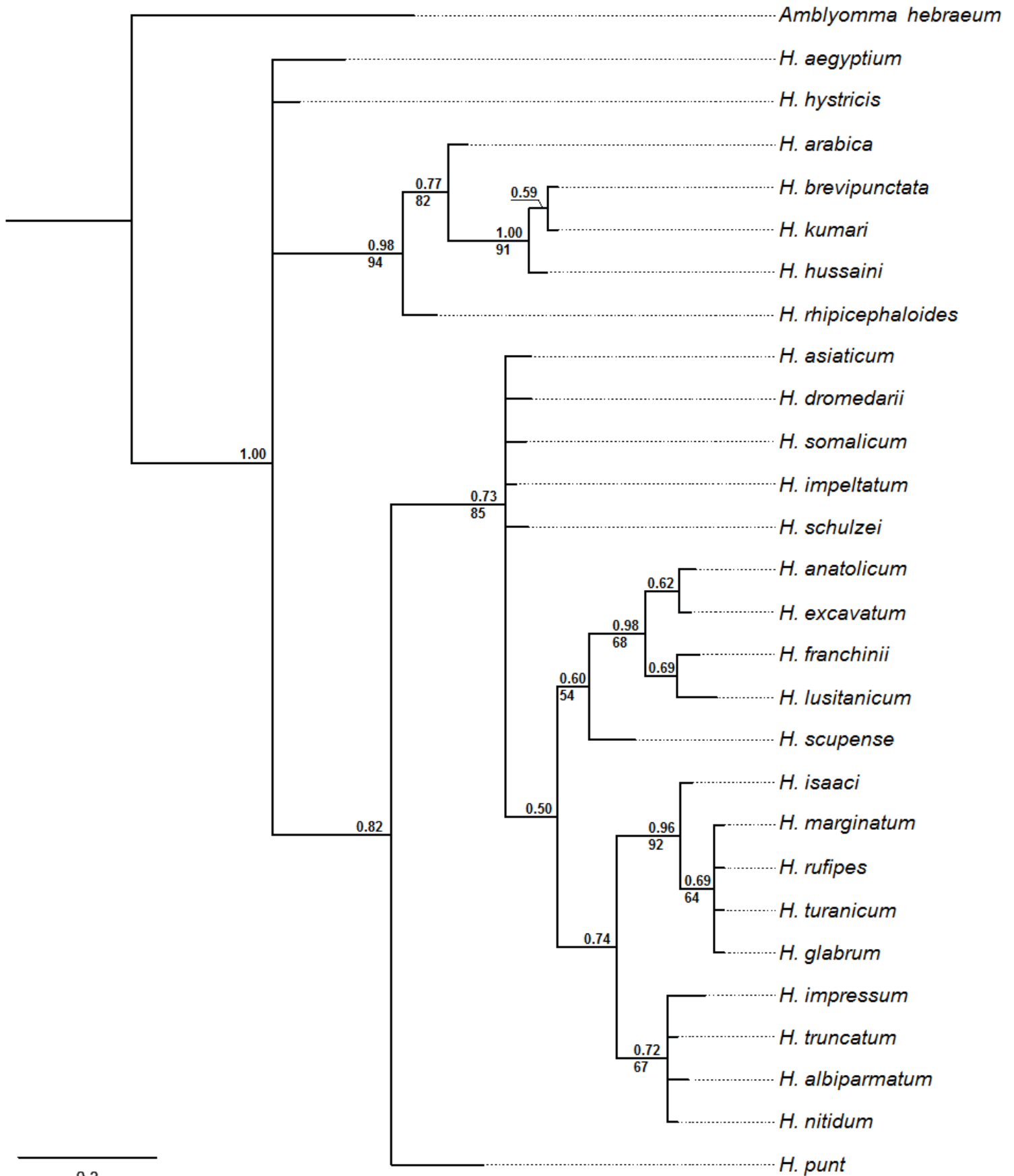# Appendix B
Figures

Effects of tectonics and large scale climatic changes on the evolutionary history of *Hyalomma* ticks

Appendix Fig. B.1: *Hyalomma* mtDNA Bayesian tree based on a supermatrix of COI and 16S gene regions (Outgroup taxa from top to bottom: *Amblyomma variegatum* and *Nosomma monstrosum*). Maximum parsimony bootstrap values are indicated below and Bayesian posterior- probabilities are above branches. Branch lengths represent the number of base-pair changes.

Appendix Fig. B.2: *Hyalomma* Bayesian tree based on 47 morphological characters (Outgroup taxa: *Amblyomma hebraeum*). Maximum parsimony bootstrap values are indicated below and Bayesian posterior- probabilities are above branches. Branch lengths represent the number of base-pair changes.
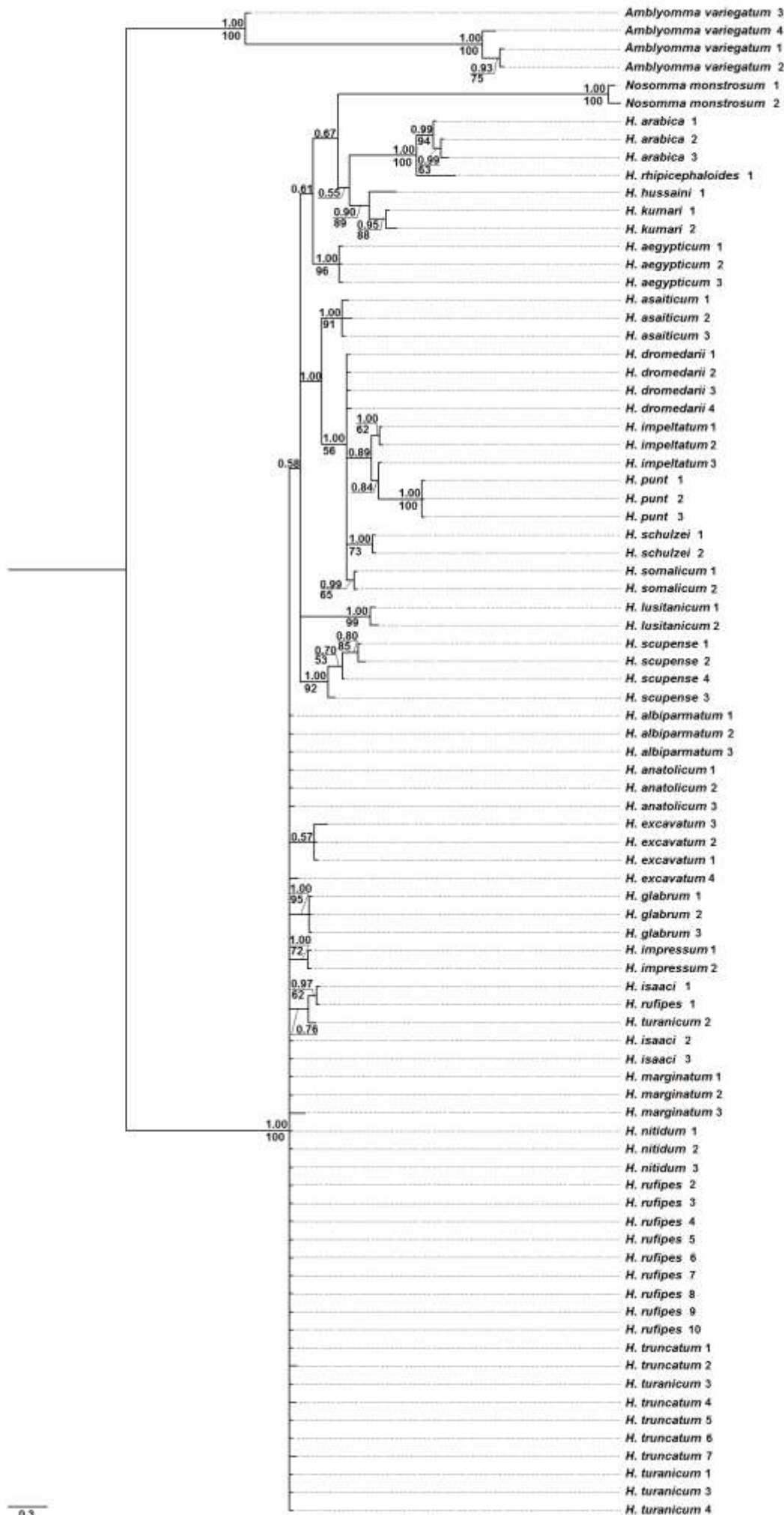
Appendix Fig. B.3: *Hyalomma* nDNA Bayesian tree based on a supermatrix of 28S, ITS II and H3 gene regions (Outgroup taxa from top to bottom: *Amblyomma variegatum* and *Nosomma monstrosum*). Maximum parsimony bootstrap values are indicated below and Bayesian posterior- probabilities are above branches. Branch lengths represent the number of base-pair changes.