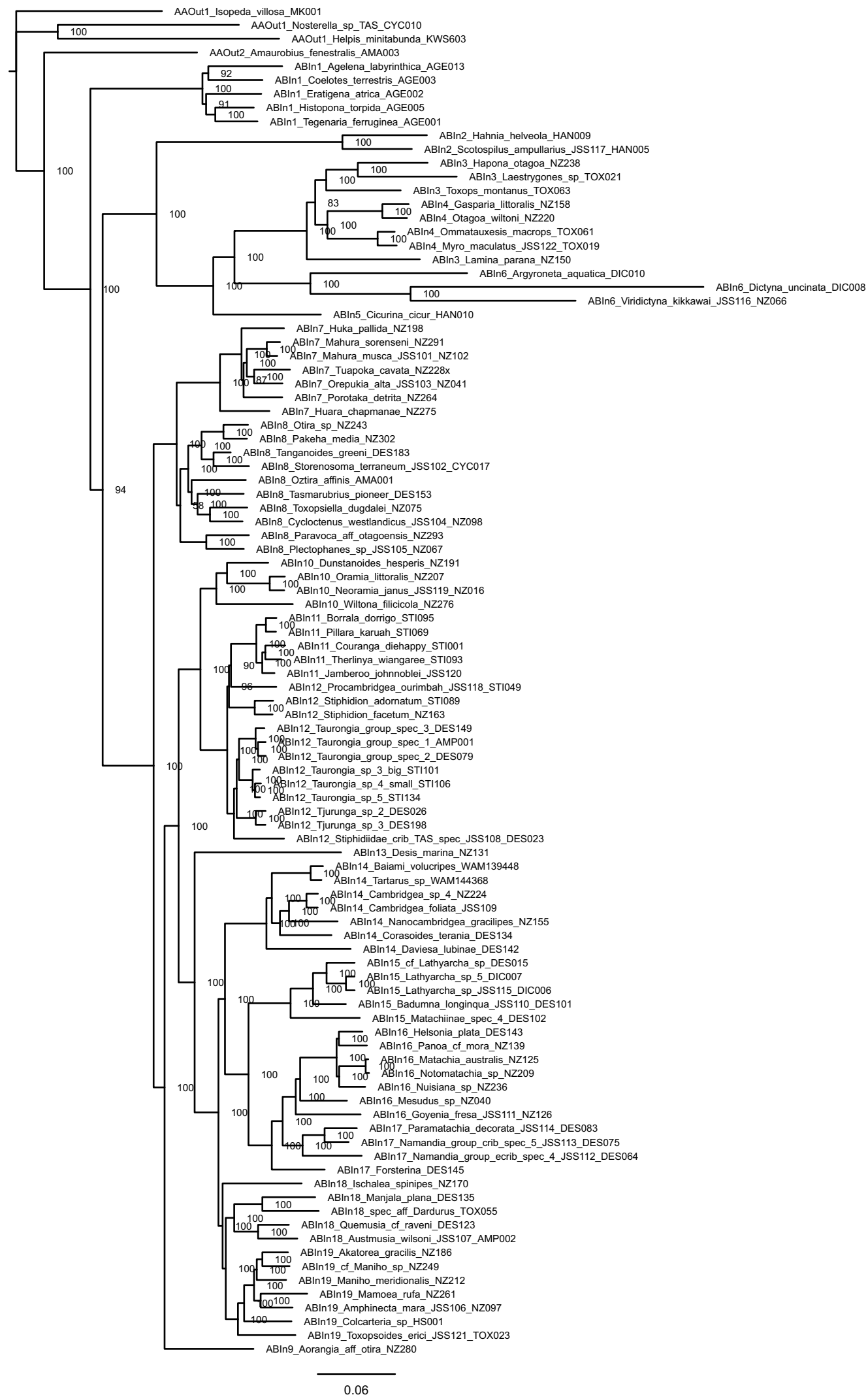
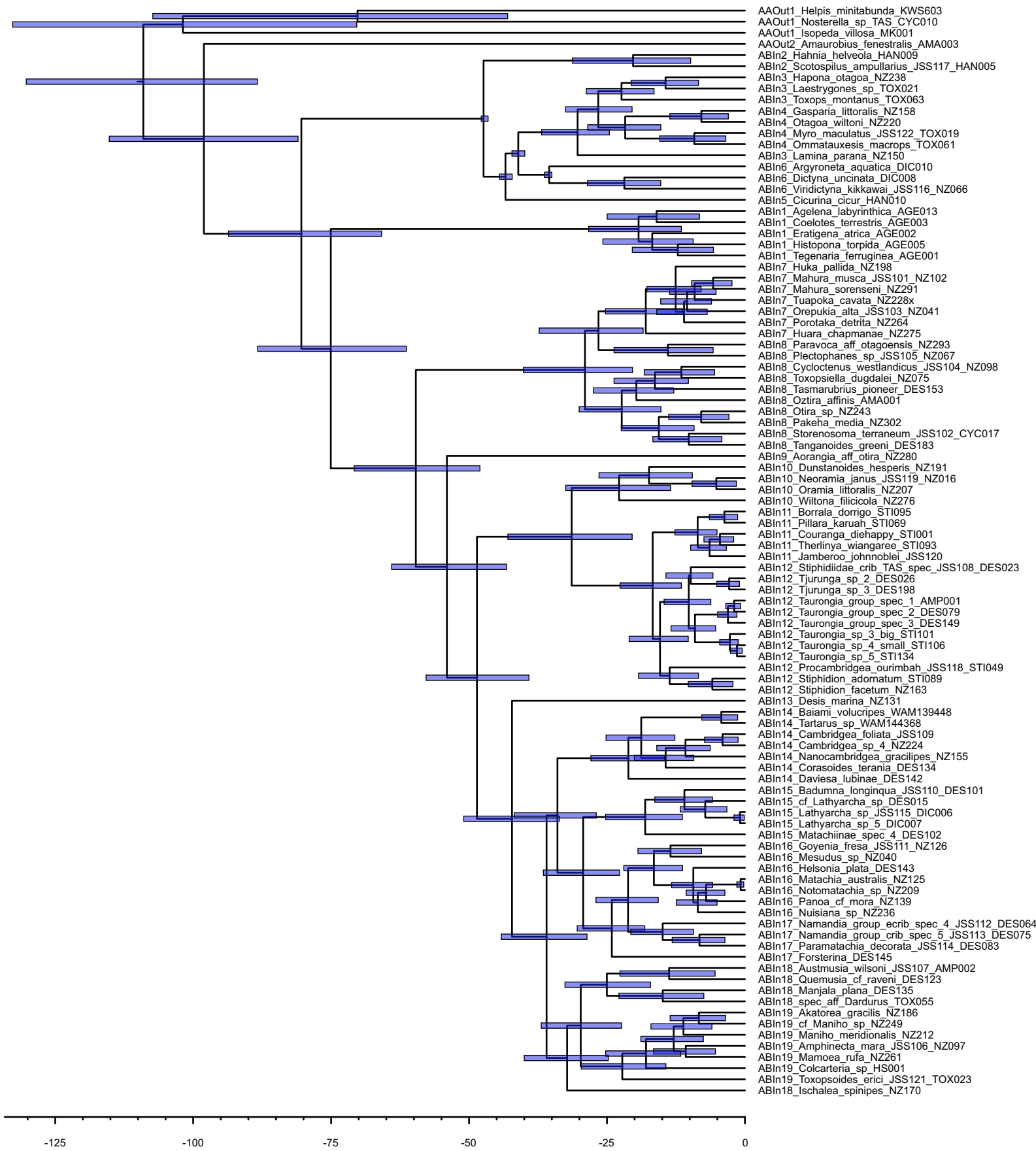


Maximum likelihood phylogeny using the full UCE data set cleaned with medium Gblock settings. Node labels give the ultra-fast bootstrap values (nodes with a ubf-value of over 95 are well supported)

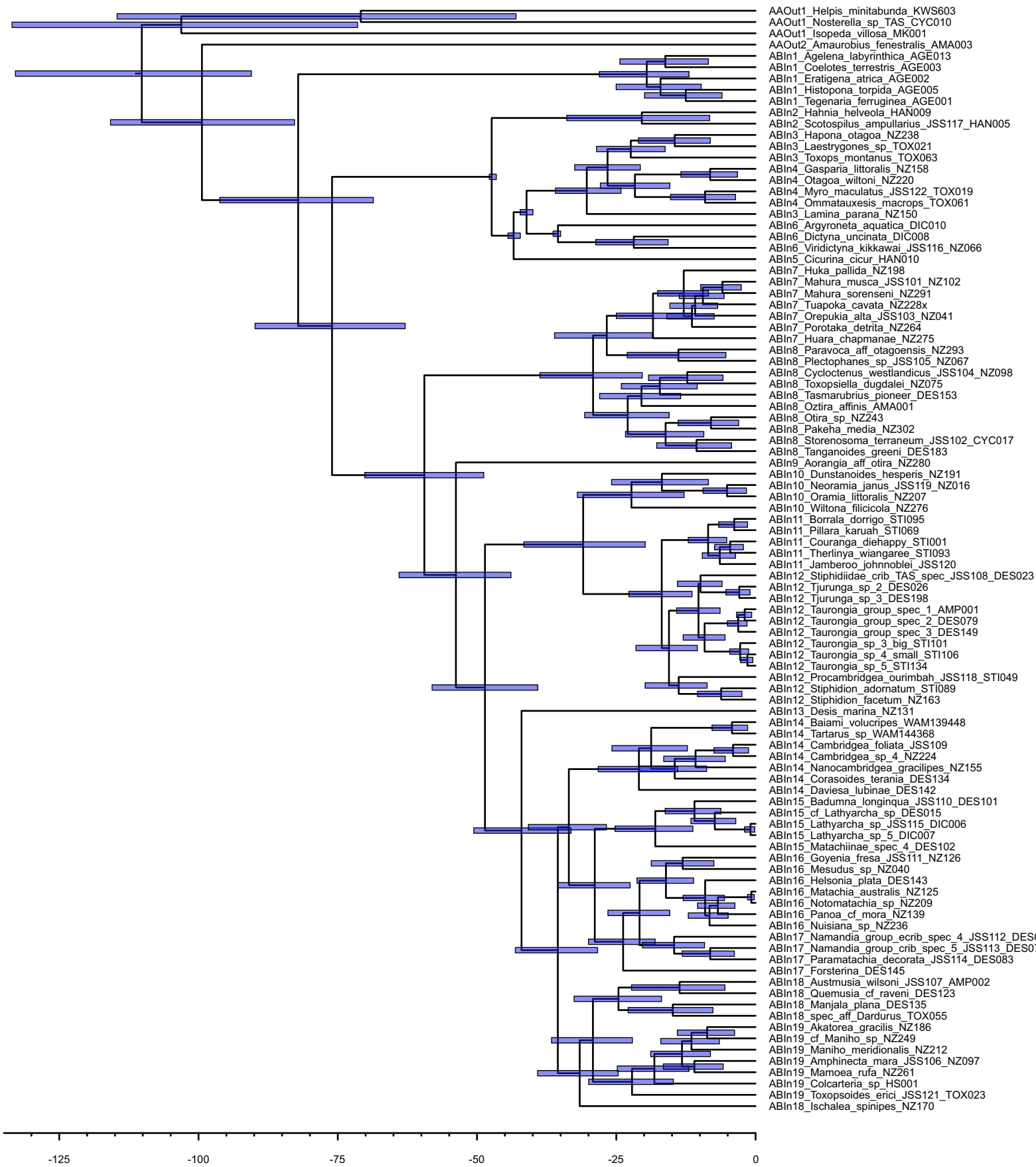


0.06

Maximum likelihood phylogeny using the full UCE data set cleaned with strict Gblock settings. Node labels give the ultra-fast bootstrap values (nodes with a ubf-value of over 95 are well supported)



Bayesian phylogeny using a subsample of 50 phylogenetically most informative loci after cleaning with strict Gblock settings, time-stamped with 2 fossil and 5 secondary calibration points. Node bars show the HPD of divergence time estimates.



Bayesian phylogeny using a subsample of 50 phylogenetically most informative loci after cleaning with strict Gblock settings, time-stamped with 2 fossil and 5 secondary calibration points and a monophyly prior constraining the position of Agelenidae s.s.. Node bars show the HPD of divergence time estimates.