

Figure 1. Maximum-likelihood tree showing the relationships between 18 key amphipod species based on a fully concatenated dataset. Bayesian posterior probabilities and maximum-likelihood bootstrap support are shown on branch nodes. Values less than 50% were not stated or depicted by an asterisk. Families are denoted by brackets and colours

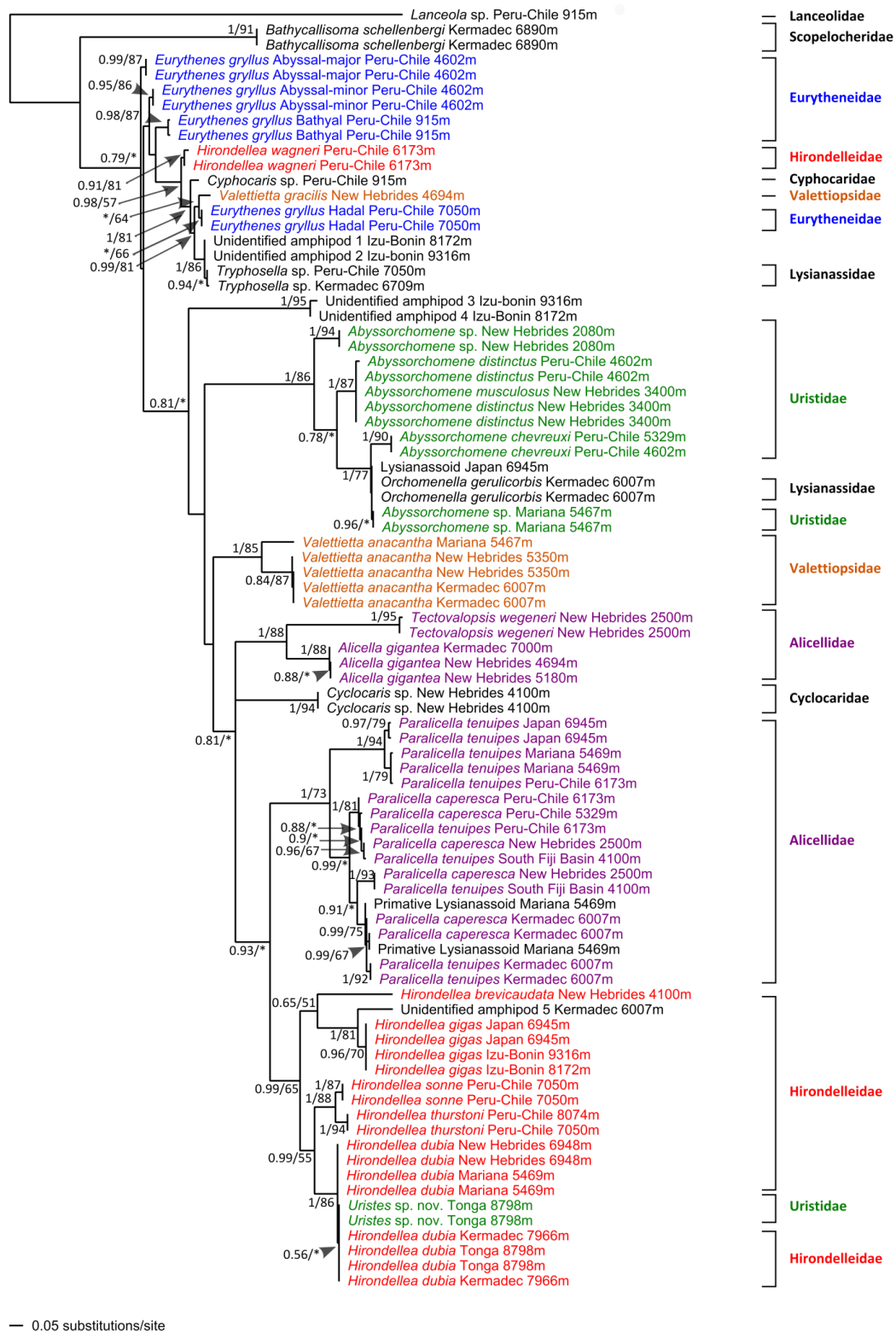


Figure 2. Maximum-likelihood tree showing the relationships between 24 identified amphipod species based on all 16S sequence data, excluding sequences of *Scopelochirus schellenbergi*.

Bayesian posterior probabilities and maximum-likelihood bootstrap support are shown on branch nodes. Values less than 50% were not stated or depicted by an asterisk. Families are denoted by brackets and colours.

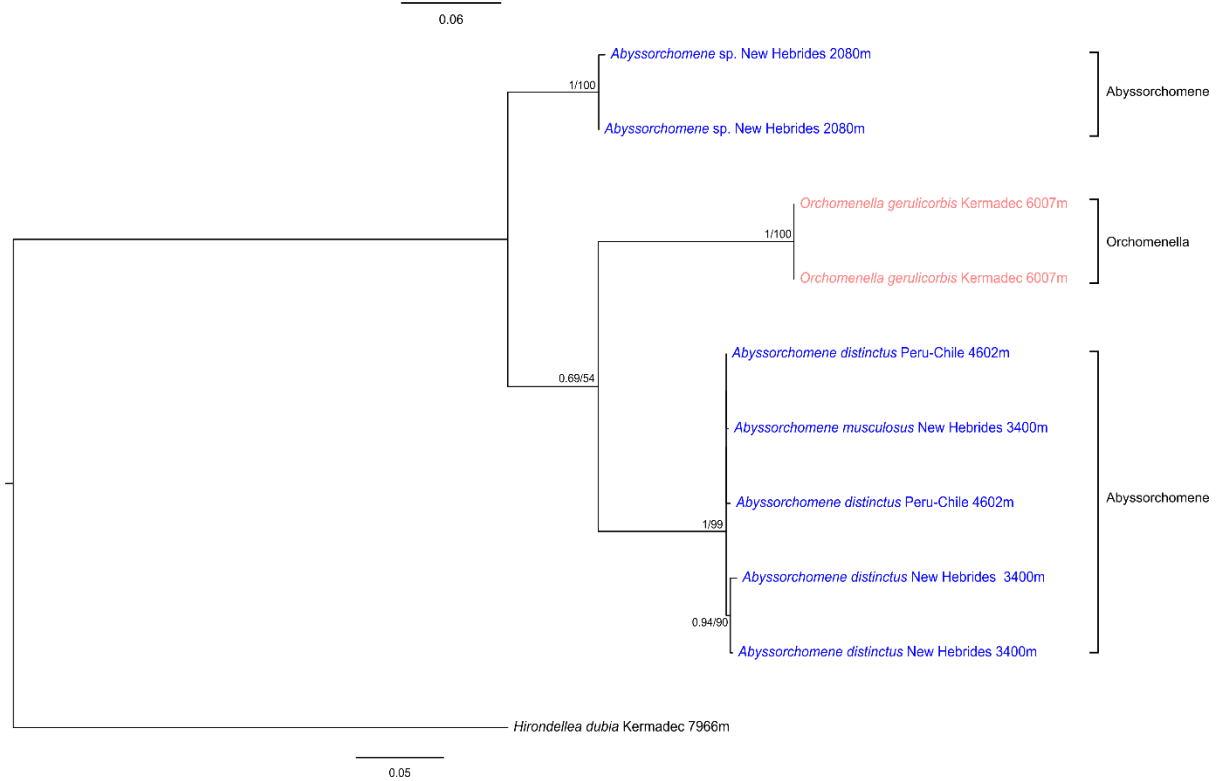
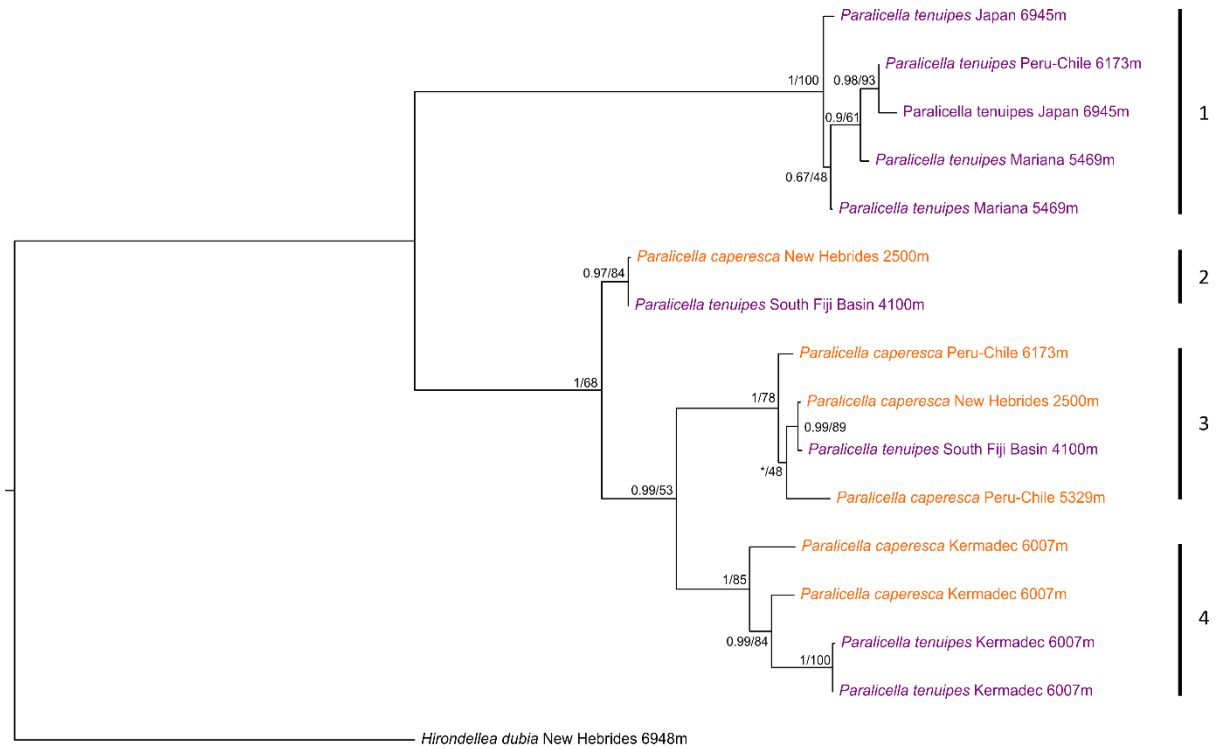
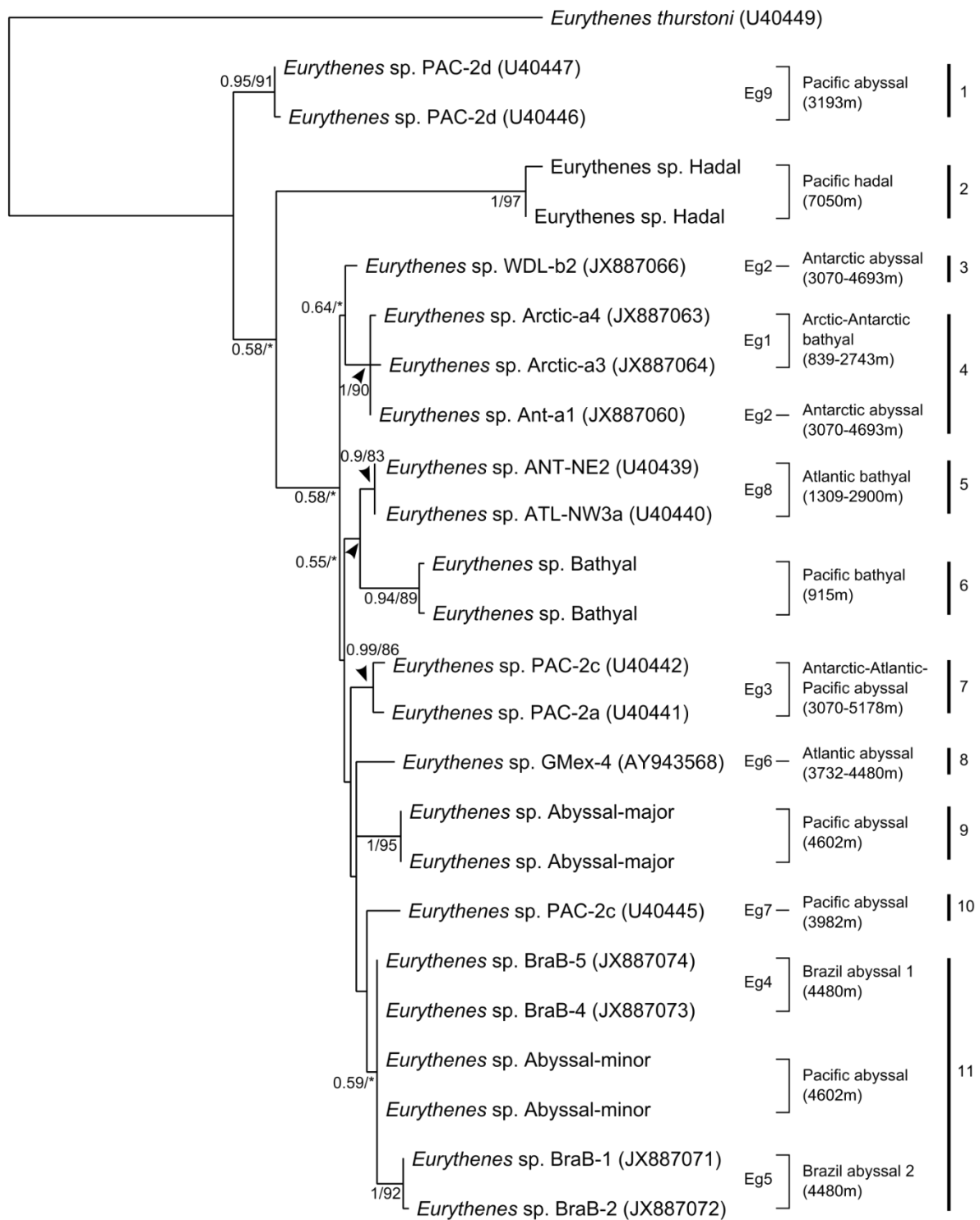


Figure 3. Maximum-likelihood tree showing the relationships of amphipod species based on a concatenated mtDNA dataset for a) the two putative species *Paralicella tenuipes* and *Paralicella caperesca* and b) the two putative genera *Abyssoorchomene* and *Orchomenella*. Trees are rooted using *Hirondellea dubia*. Bayesian posterior probabilities and maximum-likelihood bootstrap support are shown on branch nodes. 3a also shows species groups within *Paralicella* indicated by bPTP analysis.



— 0.05 substitutions/site

Figure 4. Maximum-likelihood tree showing the relationships between 25 *Eurythenes* species based on 16S sequence data used in a previous *Eurythenes* study (Havermans et al., 2013) augmented by

individuals of abyssal and hadal depth from this study (shown with no accession numbers). Bayesian posterior probabilities and maximum-likelihood bootstrap support are shown on branch nodes. Values less than 50% were not stated or depicted by an asterisk if supported by the alternative method. Previously described groups of *Eurythenes* and their sampling locations have been shown by brackets.