**SUPPLEMENTARY MATERIAL FIGURE CAPTIONS**

**Figure** **S1.** Phylogeny of the tribe Aspidiotini (Aspidiotinae), whose relationship to the other tribes of Aspidiotinae is shown in Fig. 3. Four clades represented by triangular placeholders are shown in detail in a subsequent figure: *Melanaspis* sensu lato + *Lindingaspis* (Fig. S2), *Chrysomphalus* sensu lato (Fig. S3), *Hemiberlesia* (Fig. S4), and *Diaspidiotus* sensu lato (Fig. S5). To save space, 5 other triangular placeholders are used to represent well-sampled species or species complexes: *Rhizaspidiotus donacis* (Leonardi), *Aspidiotus nerii* Bouché complex, *Selenaspidus articulatus* (Morgan), *Melissoaspis fisheri* Ben-Dov, and *Morganella conspicua* (Brain). UG3995 is an undescribed genus. **Figures 1**–**15 and S1**–**S5** represent the results of the Bayesian analysis of all 4 loci. Taxon names consist of the species name, the type of identification, the name or initials of the identifier, the country of origin, and the prep number. Identifiers are listed in Table 1. ID = identification based on morphological examination of that specimen itself on a microscope slide; lotID = identification based on morphological examination of one or more other specimens of the same series on a microscope slide; fieldID = identification in the field. Values given for internodes are posterior probabilities. Posterior probabilities under 0.5 and most of those within species have been omitted to reduce clutter. Species names are given as the combinations used prior to this study; for species transferred to new genera (Table 9), the new generic assignment is given at the end of the species name. Undescribed species are designated as "ud" followed by a number.

**Figure** **S2.** Phylogeny of *Melanaspis* and allies (Aspidiotinae: Aspidiotini). This figure shows the phylogeny of the clade labeled "*Melanaspis* sensu lato + *Lindingaspis*" in Fig. S1. For further explanation of the analysis and notation, see the caption to Fig. S1.

**Figure** **S3.** Phylogeny of *Chrysomphalus* Ashmead and allies (Aspidiotinae: Aspidiotini). This figure shows the phylogeny of the clade labeled "*Chrysomphalus* sensu lato" in S1. To save space, a triangular placeholder is used to represent 21 individuals of *Aonidiella aurantii* (Maskell). For further explanation of the analysis and notation, see the caption to Fig. S1.

**Figure** **S4.** Phylogeny of *Hemiberlesia* Cockerell (Aspidiotinae: Aspidiotini), whose relationship to its closest relatives is shown in Fig. S1. For further explanation of the analysis and notation, see the caption to Fig. S1.

**Figure** **S5.** Phylogeny of *Diaspidiotus* Berlese and allies (Aspidiotinae: Aspidiotini). This figure shows the phylogeny of the clade labeled "*Diaspidiotus* sensu lato" in Fig. S1.

**Figure S6.** Comparison of branch support across loci.The topology shown here is the one recovered in the Bayesian analysis of all 4 loci concatenated (shown in detail in Figs. 1–15 and S1–S5), pruned to include only the 279 individuals for which all 4 loci were sequenced. To assess support from each locus for each node, this core set of 279 taxa was analyzed separately for each locus, using the same parameters that were applied to that locus in the full dataset. The 4 pie charts along each branch represent the 4 loci: *Uzinura diaspidicola* 16S (orange), diaspidid nuclear 28S (green) and elongation factor 1-alpha (red), and diaspidid mitochondrial cytochrome oxidase I and II (blue). Each pie chart shows the posterior probability of that branch when the phylogeny is inferred using that locus alone.