

Figure S2. Individual gene support and conflict measures for nodes recovered in concatenated maximum likelihood (ML) analysis of the **complete character** data matrix (Figure S1). Each graph shows the support (dark bars above the abscissa), and best supported conflict (light bars below the abscissa) for the corresponding node. The first bar in each plot shows the estimated posterior probability (percent) in a Bayesian species tree analysis of the same data (Figure S3), while bars 2-6 show the ML bootstrap values recovered in single gene analyses of the five genetic loci included in this study. Although not labelled, the ordinate scales range from -100 to 100, with additional ticks at -50, 0, and 50, and dashed lines marking ± 75 (see Figure 2 for a more detailed explanation).

