Fig. 1. Dated phylogenetic tree of insect relationships. The tree was inferred through a maximum-likelihood analysis of 413,459 amino acid sites divided into 479 metapartitions. Branch lengths were optimized and node ages estimated from 1,050,000 trees sampled from trees separately generated for 105 partitions that included all taxa (5). All nodes up to orders are labeled with numbers (gray circles). Colored circles indicate bootstrap support (5) (left key). The time line at the bottom of the tree relates the geological origin of insect clades to major geological and biological events. CONDYLO, Condylognatha; PAL, Palaeoptera.
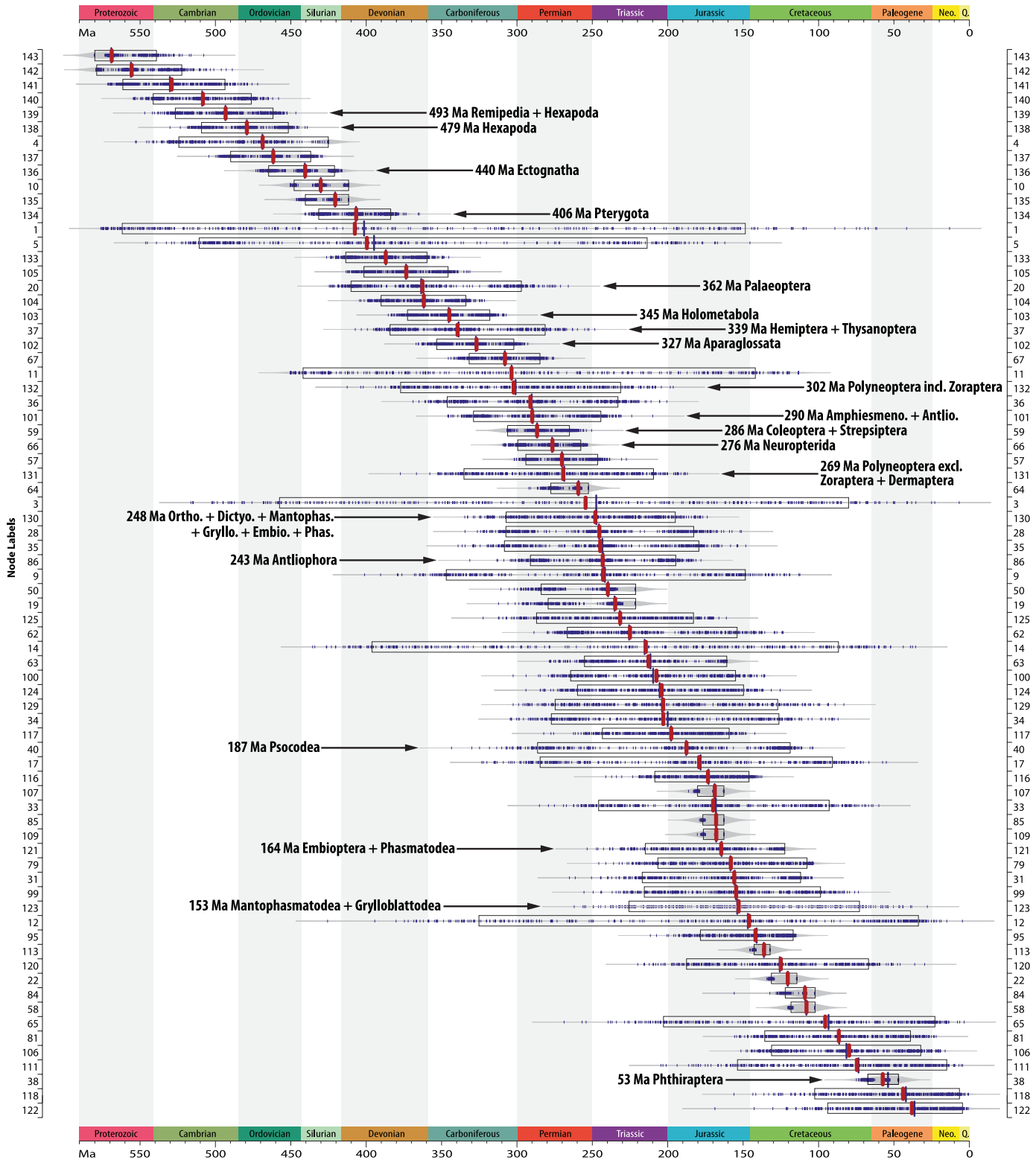
Fig. 2. Sorted ordinal and interordinal node age estimates. For each labeled node (numbers on the left and right of the figure correspond to the node labels in the tree of Fig. 1), the median (red bar), and the range of the upper and lower confidence interval (black rectangle) of age estimates are illustrated. These medians and upper and lower confidence intervals are derived from uniformly sampled trees over all 105 metapartitions (*5*). Additionally, we present medians of age estimates separately derived from each metapartition. Within the bean plot (gray scale), blue bars indicate the distribution of median age estimates, large blue bars indicate the inferred median of medians. All node age estimates refer to the estimated common origin of included species. Stem-lineage representatives can, of course, be older. The maximum root age of the tree was set to 580 Ma to coincide with the oldest Ediacaran fossils (*5*).