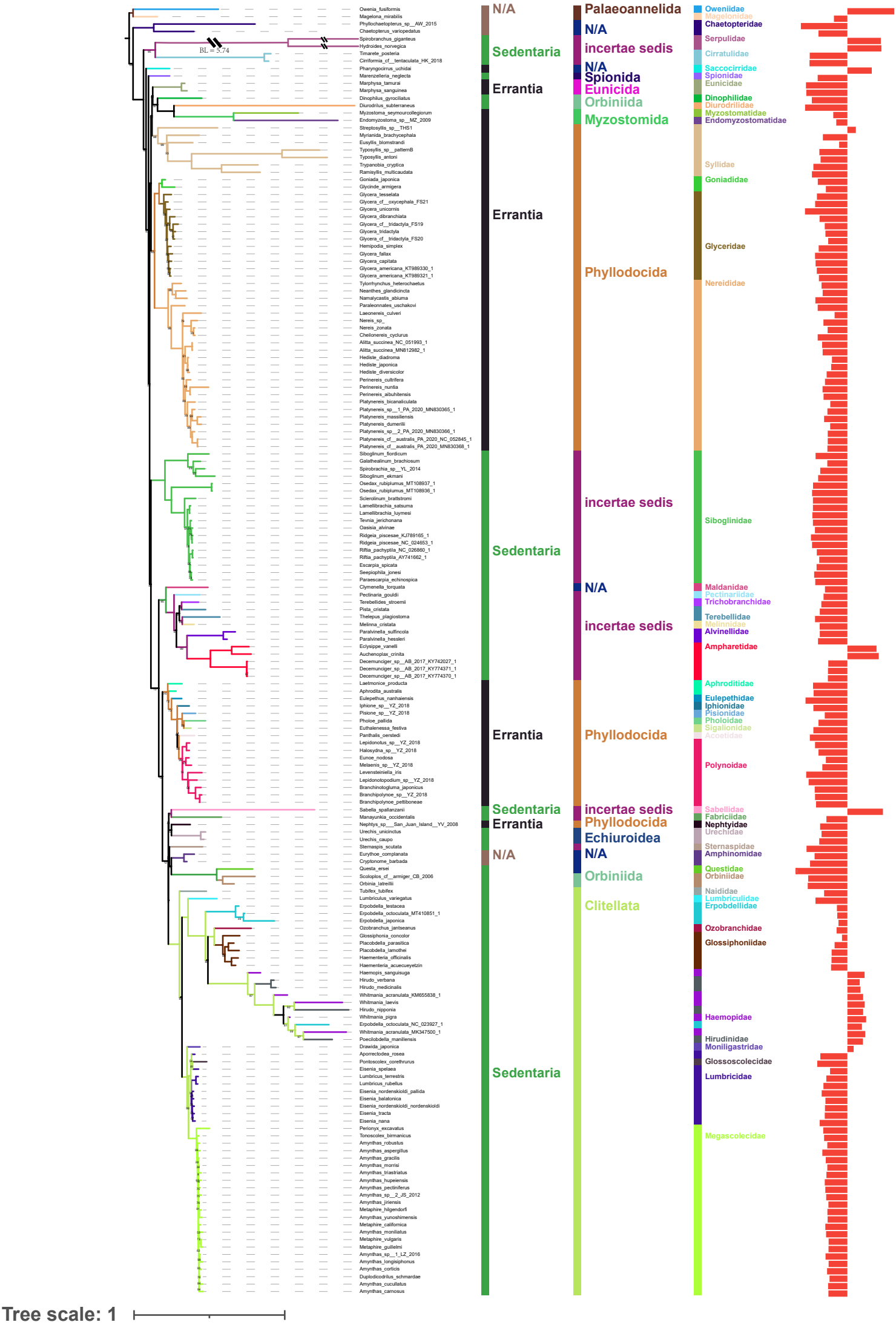Additional file 7. DPCGs_2rRNAs dataset. Phylogeny of annelids inferred using 174 annelid mitogenomes. The phylogram was inferred using DELTRAN concatenated 13 PCGs and 2rRNAs and the Maximum Likelihood methodology implemented in IQ-TREE. The figure shows (from left to right): a tree with bootstrap values < 100% shown at nodes, species names (identical species are shown with GenBank accession numbers), taxonomy (class, order and family, respectively), GC skews represented by bars