

Additional file 5. PCGs12_2rRNAs dataset. Phylogeny of annelids inferred using 174 annelid mitogenomes and the Maximum Likelihood methodology implemented in IQ-TREE. The phylogram was inferred using a dataset comprising concatenated 13 PCGs, from which the third codon site was removed, and 2rRNAs. The figure shows (from left to right): a tree with bootstrap values < 100% shown at nodes, species names (mitogenomes belonging to identical species are shown with GenBank accession numbers), taxonomy (class, order and family, respectively), and GC skews represented by bars.

