

Additional file 6. PCGs12_2rRNAs dataset. Phylogeny of annelids inferred using 174 annelid mitogenomes. The phylogram was inferred from concatenated 13 PCGs (from which the third codon site was removed) and 2 rRNAs, and Bayesian Inference methodology implemented in MrBayes. The figure shows (from left to right): a tree with posterior support values < 1.0 shown at nodes, species names (identical species are shown with GenBank accession numbers), taxonomy (class, order and family, respectively), GC skews represented by bars.

