

Additional file 16. Phylogeny of annelids inferred using 174 annelid mitogenomes and the Maximum Likelihood method implemented in IQ-TREE. The phylogram was inferred using a dataset comprising concatenated 10 PCGs (atp8, nad3 and nad4L removed). The figure shows (from left to right): a tree with bootstrap values < 100% shown at nodes, species names, taxonomy (class, order and family, respectively), and GC skews represented by bars

