Additional file 4. PCGs_2rRNAs dataset. Phylogeny was inferred using 174 annelid mitogenomes, concatenated 13 PCGs and 2rRNAs, 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 (mitogenomes belonging to identical species are shown with GenBank accession numbers), taxonomy (class, order and family, respectively), and GC skews represented by bars.