Additional file 11. PCGs_2rRNAs_nonORI dataset. Phylogeny of annelids inferred using 156 annelid mitogenomes. The phylogram was inferred using concatenated 13 PCGs and 2rRNAs and the 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