

Supplementary Material to “Mitochondrial genomes of genus *Atta* (Formicidae: Myrmicinae) reveal high gene organization and giant intergenic spacers”

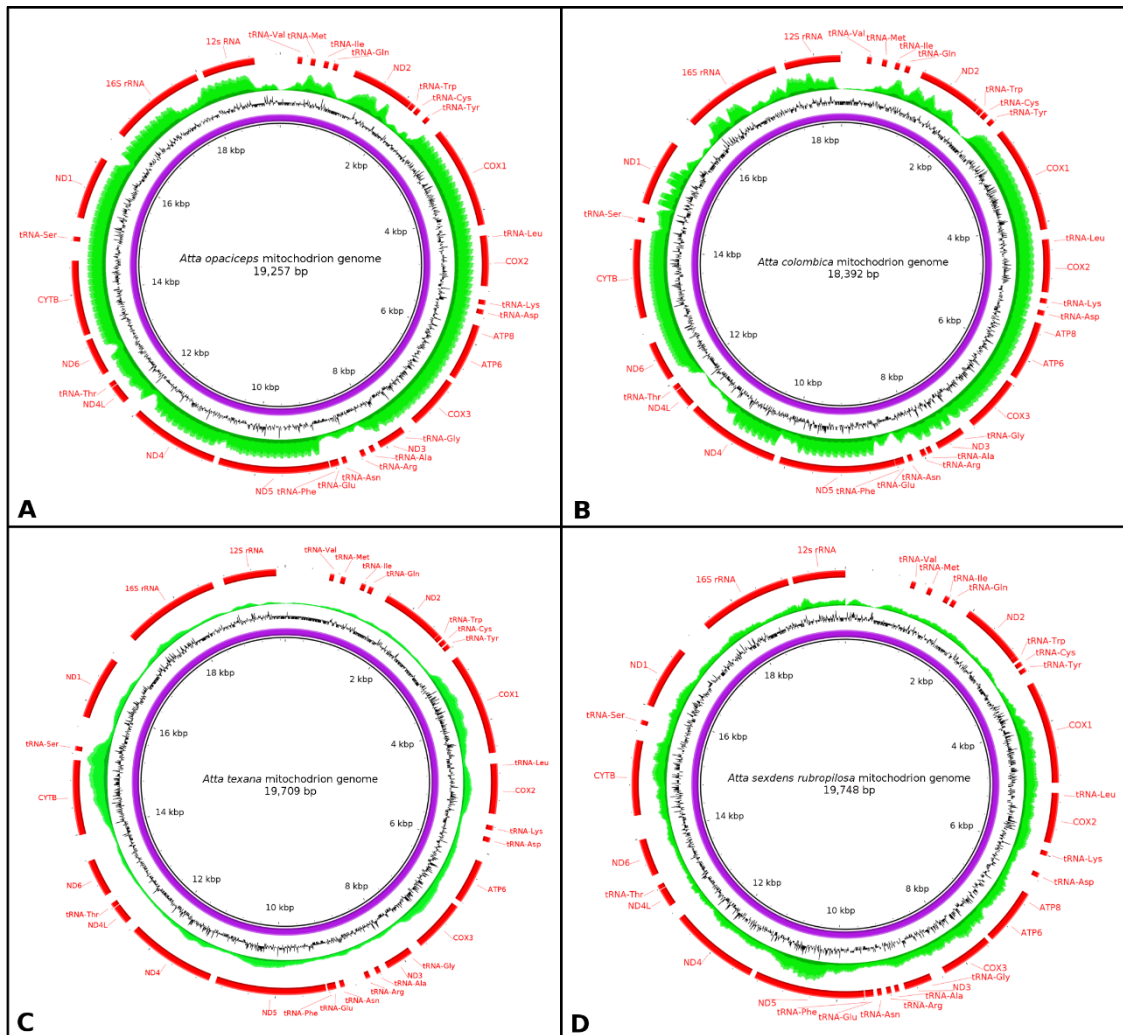


Figure S1 - Coverage of *Atta* genomes after mapping of short reads. The first ring represents the genome, the second represents CG content, and the third indicates coverage of the mapped reads. The annotations in red show the regions used for validation using sequencing following the Sanger method.