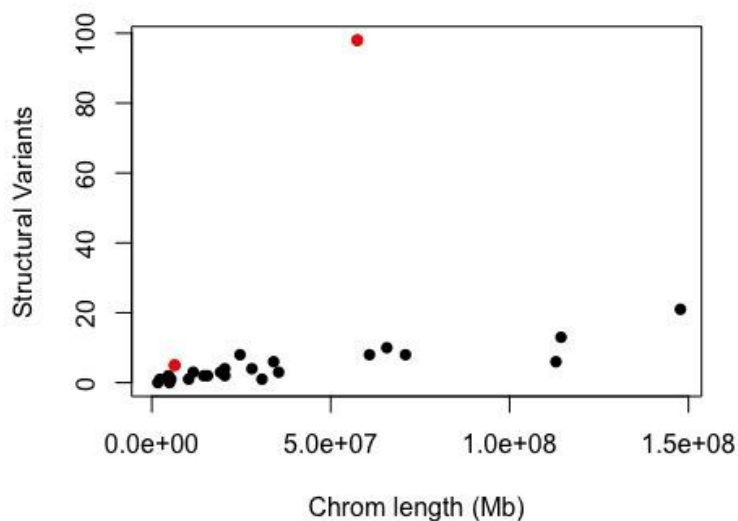
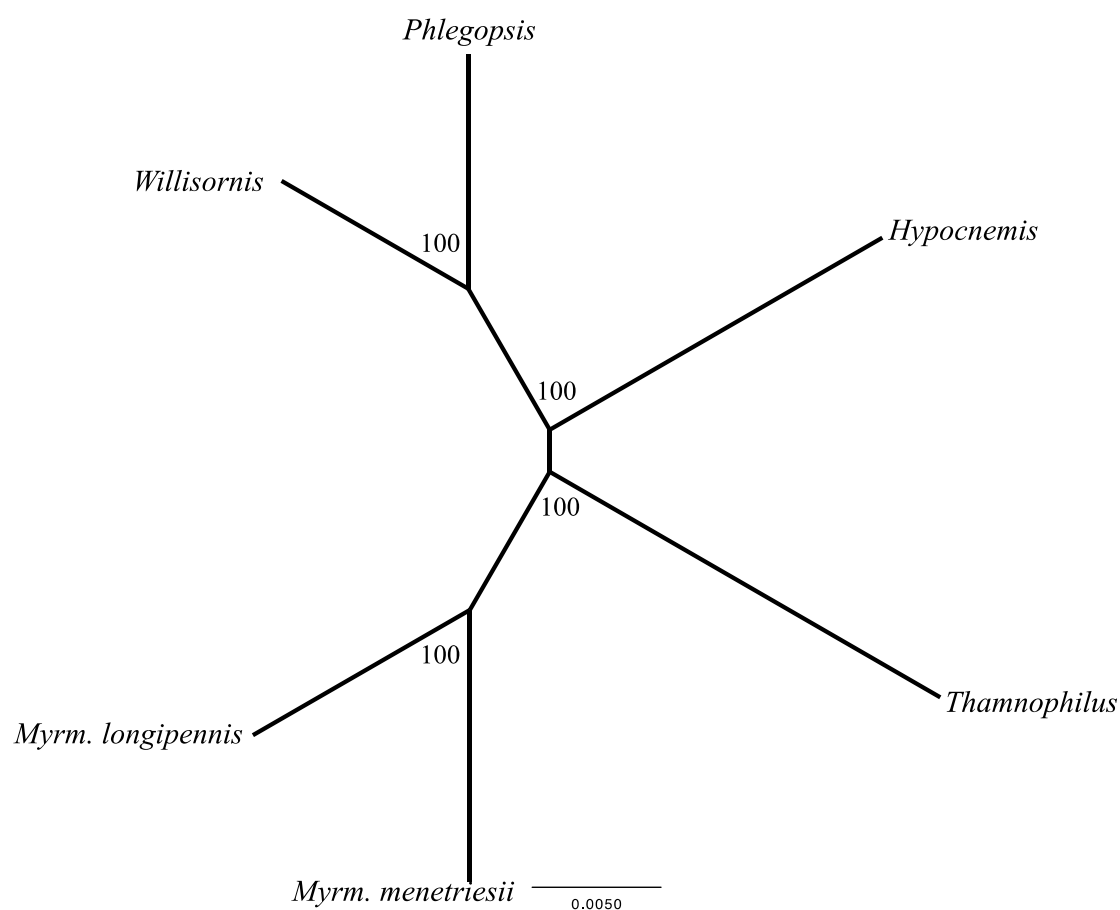


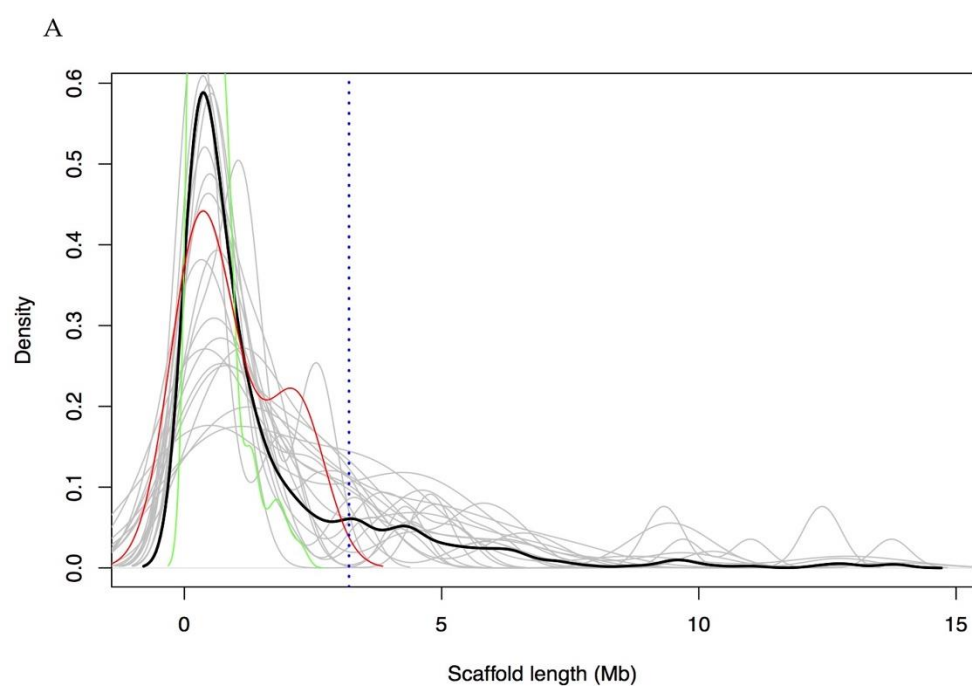
Supplementary Figure1. The phylogeny used to inform the whole-genome alignment. The topology was extracted from [18].



Supplementary Figure2. Number of structural variants (insertions/deletions, duplications, rearrangements) mapped to *Rhegmatorhina melanosticta* chromosomes in relation to chromosome length. The red points represent the sex chromosomes.



Supplementary Figure 3: Phylogenetic relationships for some birds in the family, Thamnophilidae. The topology was inferred using RAxML based on 4,870 GBS loci mapped to the *R. melanosticta* genome. The relationships are consistent with well-accepted phylogenetic hypotheses [34,40].



Supplementary Figure4. Distribution of lengths of scaffolds that form each chromosome (thin lines) in the *Rhegmatorhina melanosticta* genome. The red and green lines correspond to the W and Z

chromosomes, respectively. The bold line corresponds to the length distribution of all scaffolds combined. The blue dashed line represents the scaffold N50 (3.2Mb).