

## **Supplementary Figures**

**Supplementary Figure 1 | Phylogenetic distribution of fossil calibrations.** Calibration nodes numbered following Table S4 and labeled (red circles). Species included solely for calibration purposes colored red.

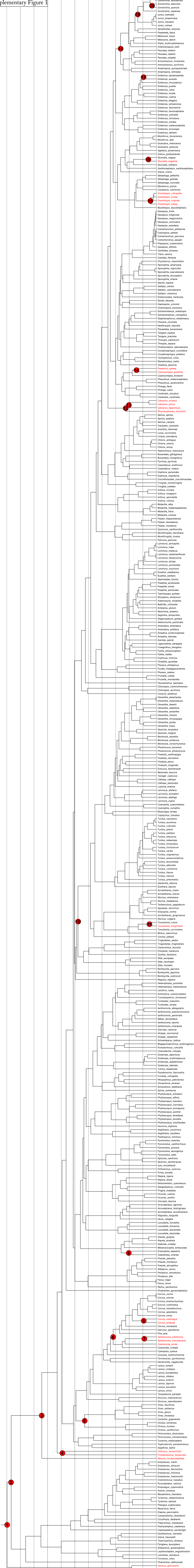
**Supplementary Figure 2 | Pericentric inversion fixation rate variation across passerine birds.** The phylogenetic relationships between the 411 karyotyped species in this study are presented in a time-dated maximum clade credibility tree. Branches are color-coded according to the inferred rate of pericentric inversion fixation using the R package ggtree. Rates are partitioned according to the Jenks natural breaks method where variance within bins is minimized, while variance between bins is maximized.

**Supplementary Figure 3 | Phylogeny used in phylogenetic generalized least squares for clade level analysis.** Branch lengths are proportional to time, and subtend the root node for each clade, and were used to compute the expected error covariance matrix between clades for phylogenetic generalized least-squares. Species identity for the 285 taxa assigned to clades is given in Table S1. Clade information (inversions, branch length, range size, range overlap, ecology, etc.) are given in Table S4.

**Supplementary Figure 4 | Number of inversion differences between sister taxa against sister pair age.**

**Supplementary Figure 5 | Sample size for karyotyped species.** The average number of individuals karyotyped are indicated by arrows for all species (black arrow, 4.8 individuals) and species where structural variants were observed (red arrow, 9.9 individuals) after removing the three species where sampling effort was designed to study inversion polymorphism (Supplementary Tables 1 and 2).

Supplementary Figure 1



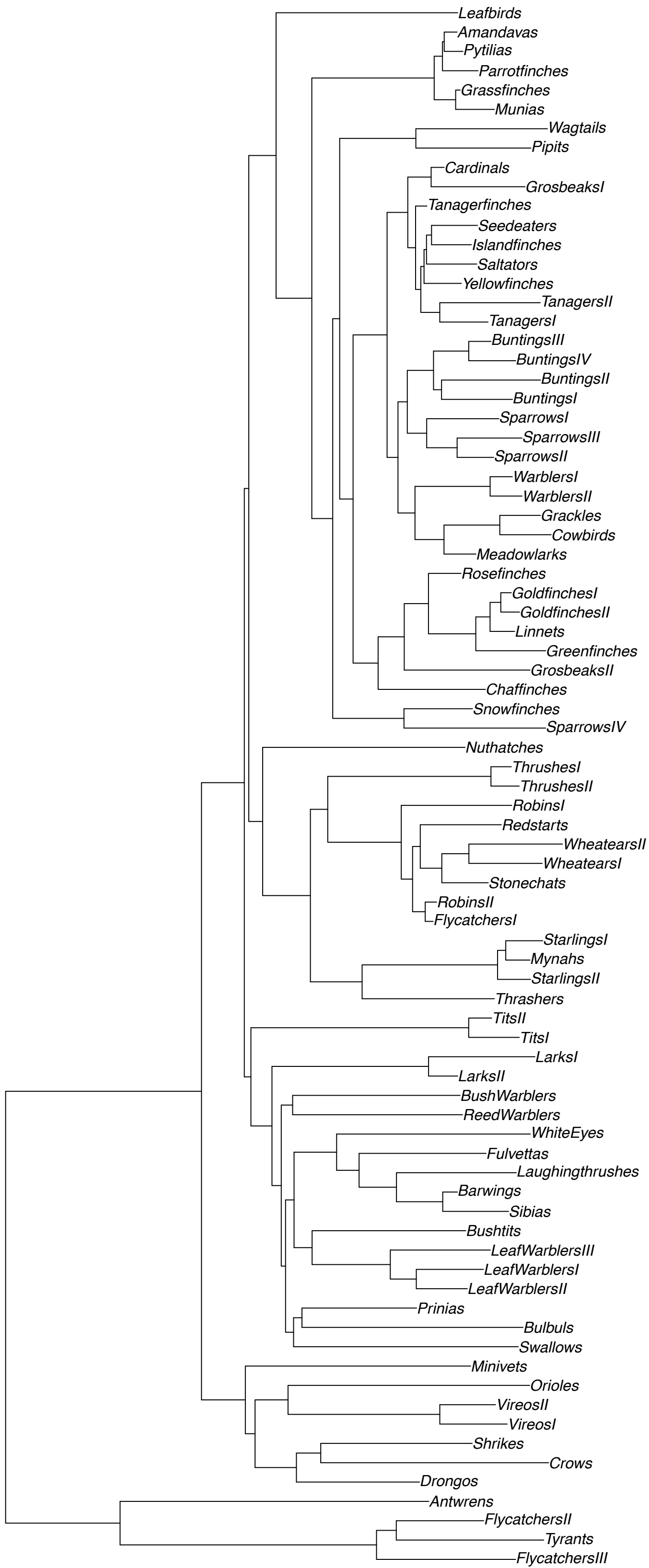
50.0 40.0 30.0 20.0 10.0

Eocene Oligocene Miocene Pliocene Pleistocene

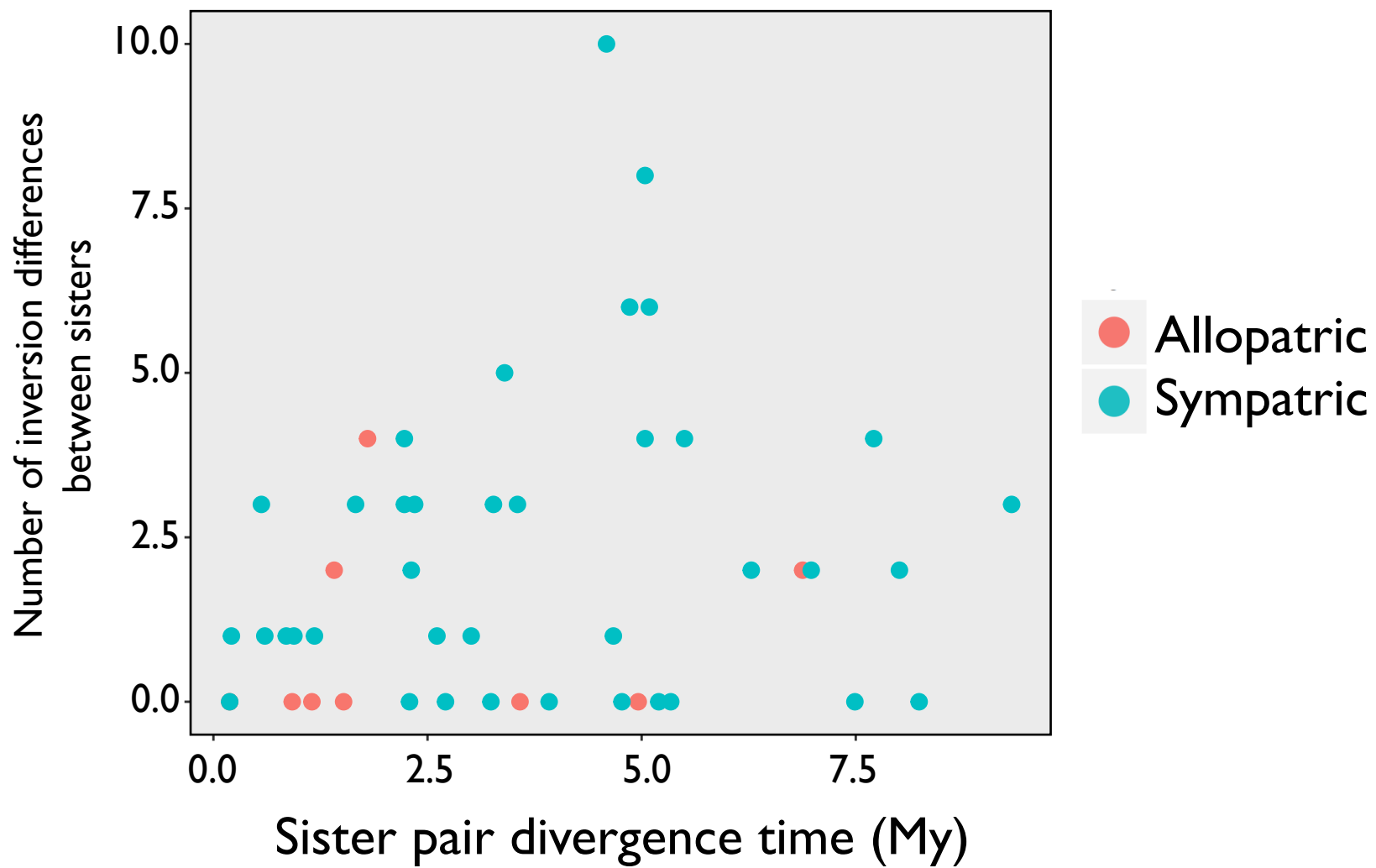




Supplementary Figure 3



Supplementary Figure 4



Supplementary Figure 5

