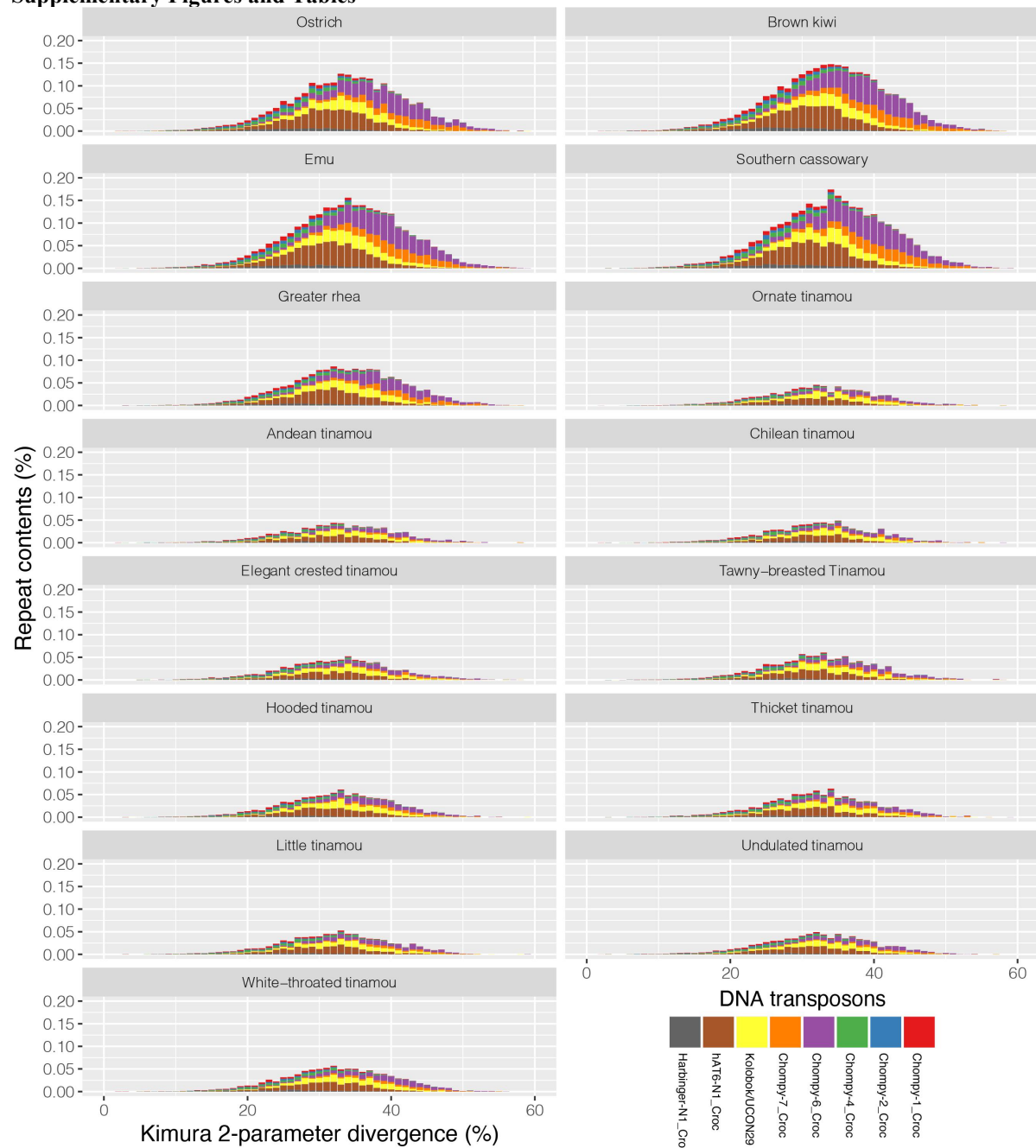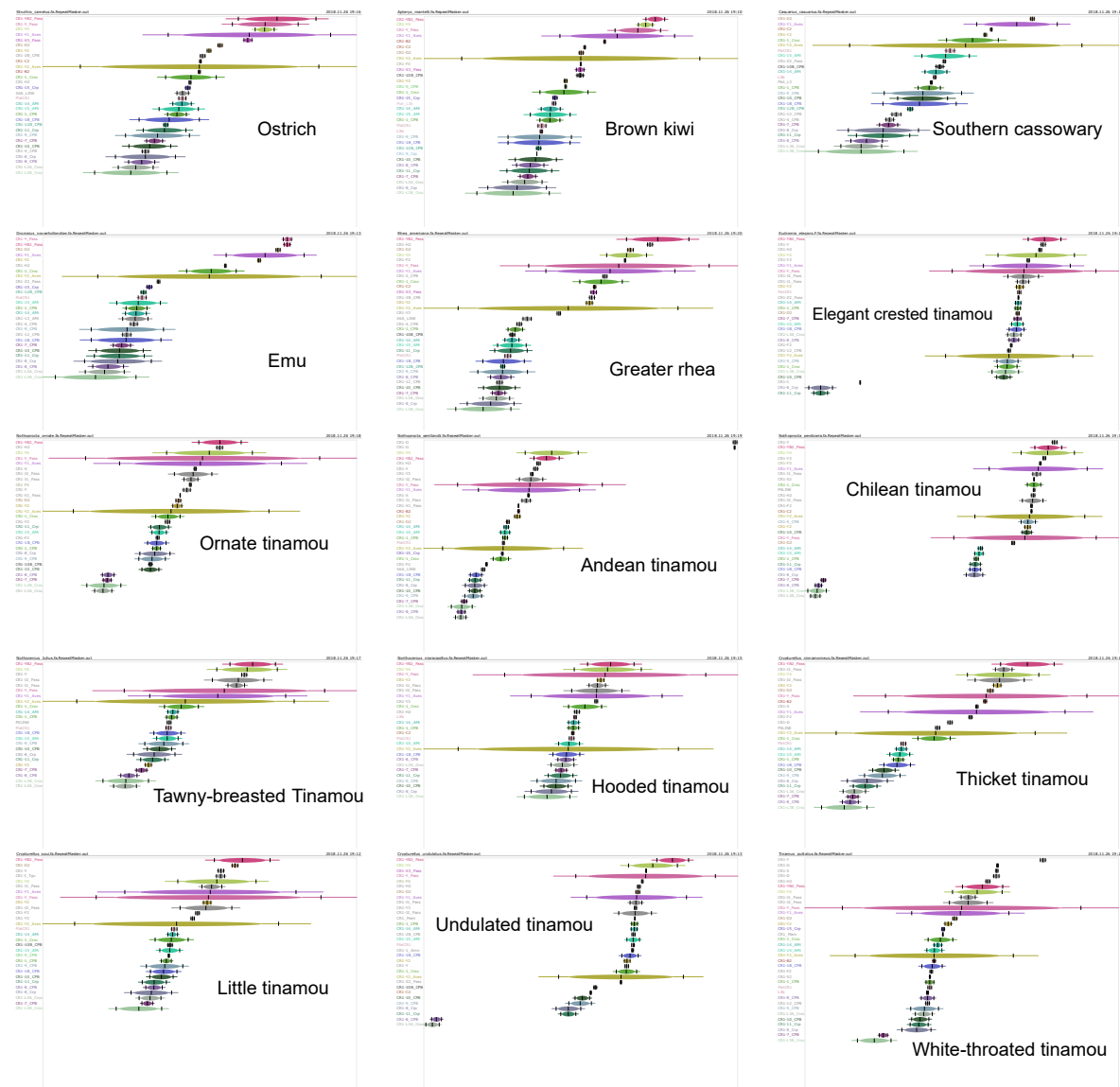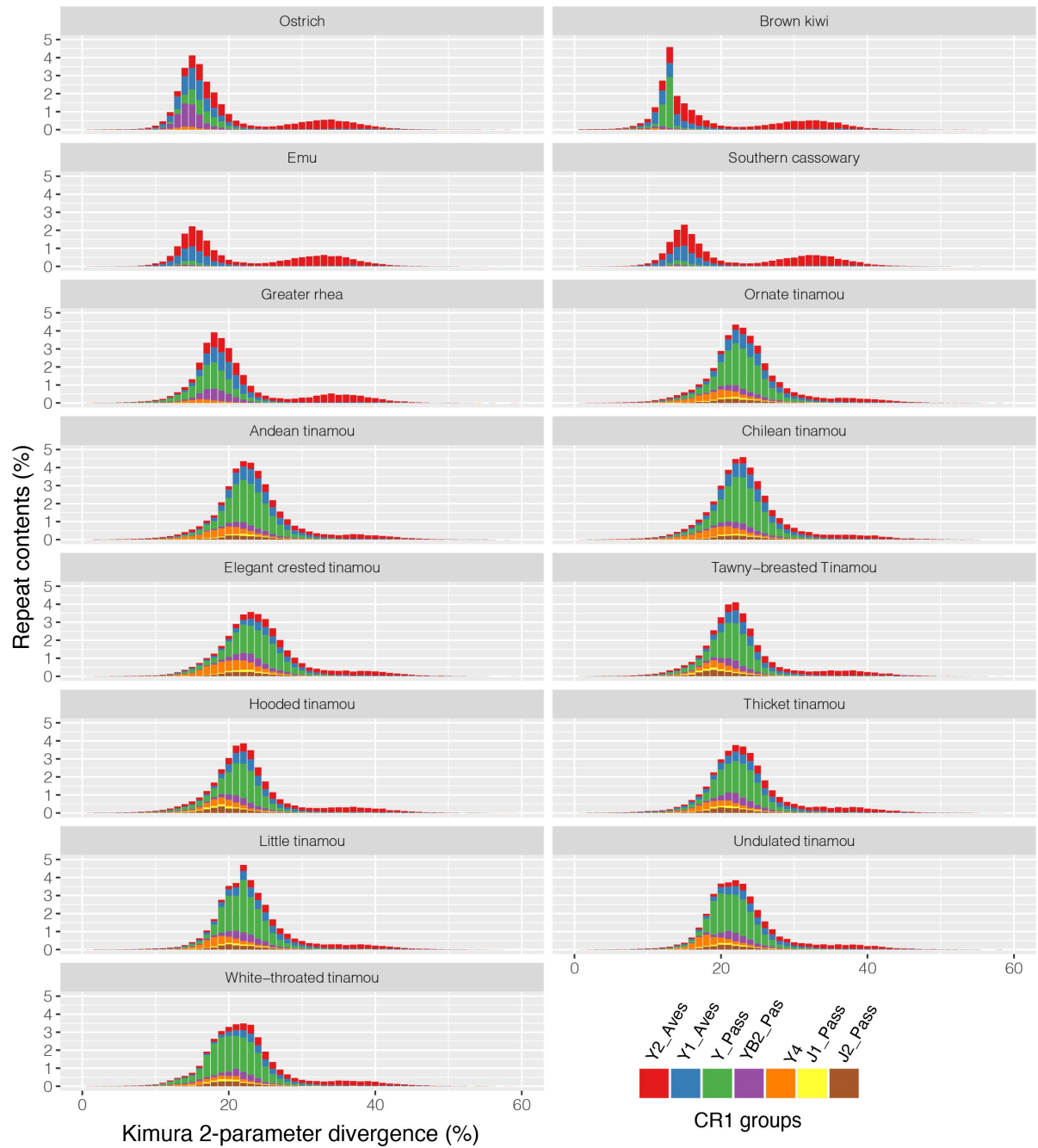Supplementary Figure S1. Distribution of sequence divergence patterns of paleognathous DNA transposons compared to their consensus sequences.
We showed divergence pattern for each subfamily of DNA transposons here, with the fraction of the genome of each family shown on the y-axis, and Kimura 2-Parameter sequence divergence between individual TE copies and consensus references on the x-axis.

Supplementary Figure S2. TinT analyses of different CR1 subfamilies in Palaeognathae. Each oval represents one CR1 subfamily, sorted by peak time of activity (line in the middle of the oval), from top to bottom, from most recent to most ancient time period. Each oval contains 75% (at oval end), 95% (vertical lines), and 99% (ends of each line) of the probable activity period range

Supplementary Figure S3. Distribution of sequence divergence patterns of paleognathous CR1 LINEs compared to their consensus sequences.

We showed divergence pattern for each subfamily of CR1 LINE elements here, with the fraction of the genome of each family shown on the y-axis, and Kimura 2-Parameter sequence divergence between individual TE copies and consensus references on the x-axis.
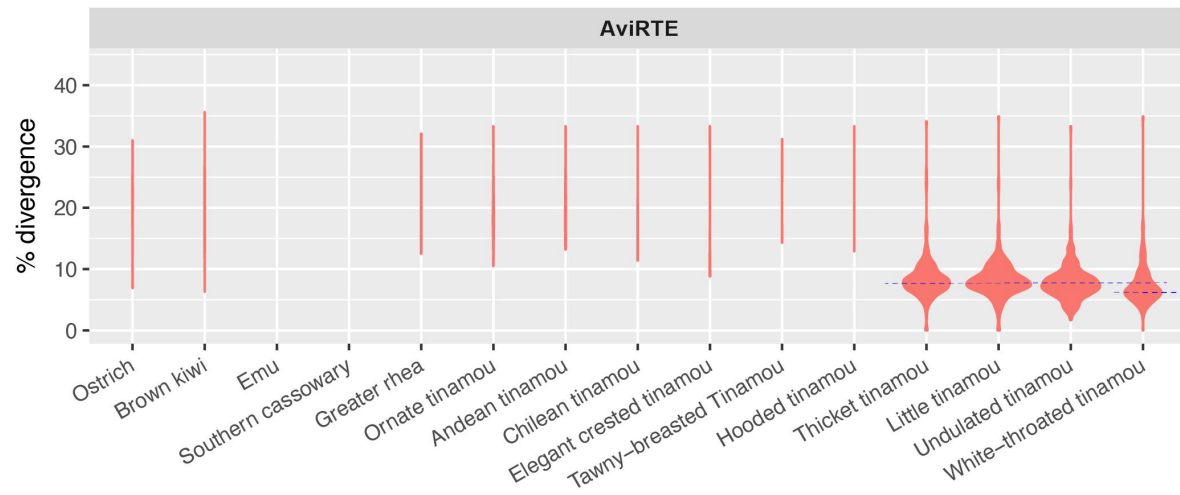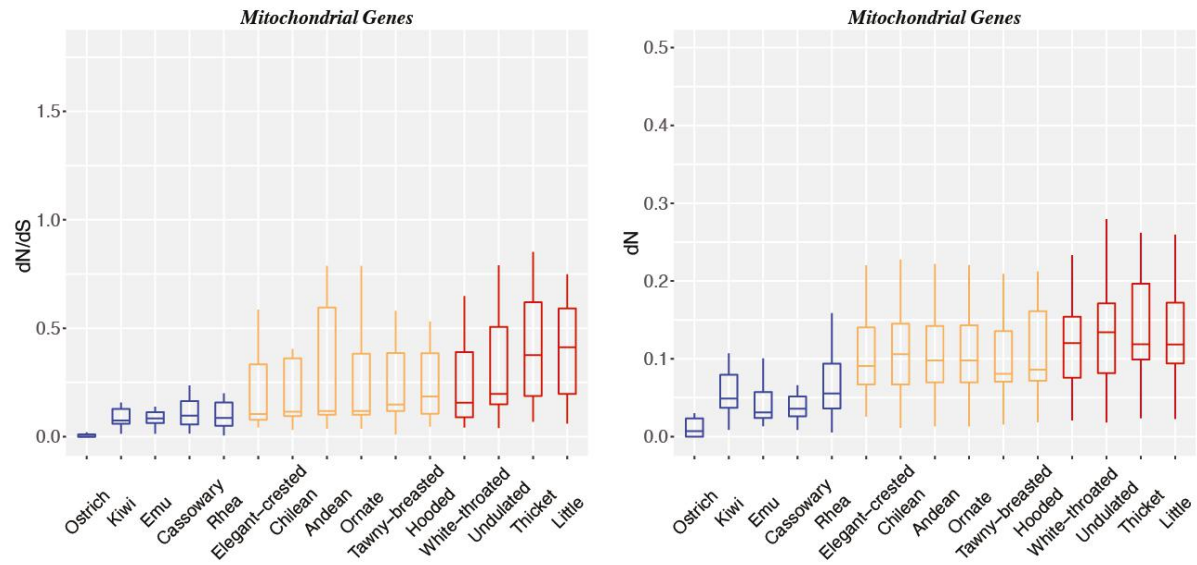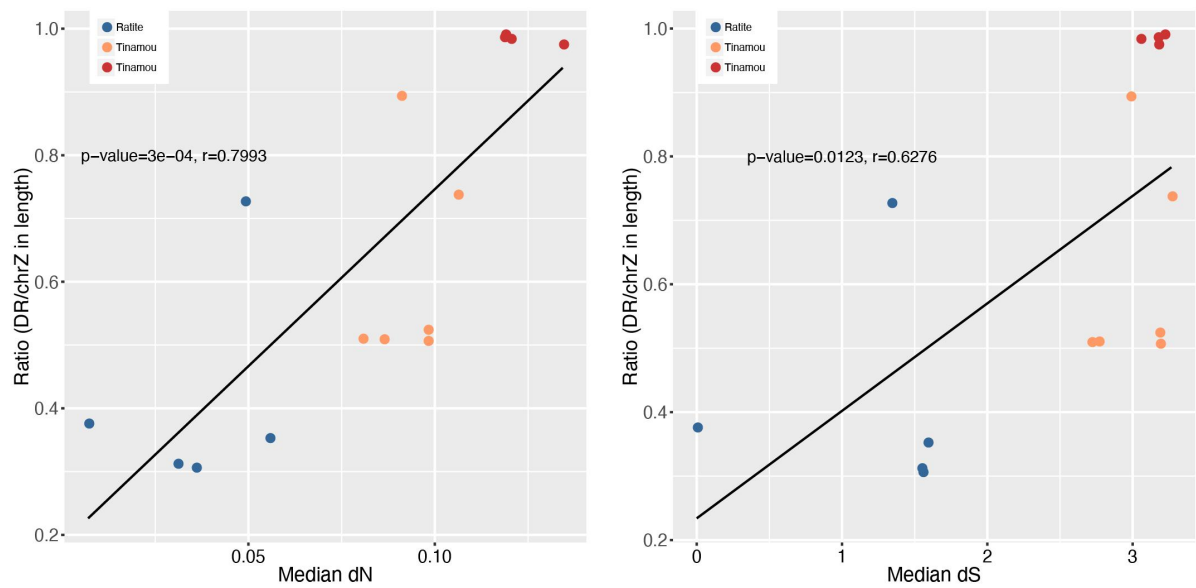
Supplementary Figure S4. Violin plot showing AviRTEs' frequency distribution of sequence divergence level from inferred ancestral consensus sequences. Clustering of TEs with similar divergence levels, manifested as 'bout' of the violin, corresponds to the burst of AviRTE amplification. Blue dashed lines indicate position of burst.

Supplementary Figure S5. Evolutionary patterns of mitochondrial (MT) genes among different groups.

Evolutionary patterns in MT genes (13 genes) at their ratio of non-synonymous over synonymous sequence divergence (dN/dS) [left panel], and their non-synonymous substitutions (dN) [right panel]. Colors refer to ratites (blue), tinamous with moderately degenerated chrW (yellow), and tinamous with highly degenerated chrW (red).

Supplementary Figure S6. Correlation between non-synonymous sites (dN) [left panel] and synonymous sites (dS) [right panel] and ratio of differentiated region (DR) over chrZ in length. Each data point represents a certain bird species. Pearson correlation coefficients (r) are shown for comparison. Colors refer to ratites (blue), tinamous with moderately degenerated chrW (yellow), and tinamous with highly degenerated chrW (red).

Supplementary Tables

Supplementary Table S1. Information on genome assemblies used in this study

Supplementary Table S2. Summary of ecological features in Paleognaths

Supplementary Table S3. Temporal dynamics of avian populations

Supplementary Table S4a. Comparison of assembly contiguity statistics in emus

Supplementary Table S4b. Comparison of repeat content in emus (PacBio emu genome was recently produced in the lab)

Supplementary Table S5. Comparison of repeat content across Palaeognathae

Supplementary Table S6. Statistics of AviRTE in tinamous

Supplementary Table S7. Correlation analysis between mean effective population size and percentage of transposable elements

Supplementary Tables S1-S7 are listed as a separate xlsx file due to their large size.