

## Supplementary Figures S1-S2

from Harvey et al., “Habitat predicts population divergence”, *The American Naturalist*

**Figure S1:** Unrooted MrBayes trees of concatenated SNPs from both alleles in each individual after mis-identified, contaminated, and failed samples were removed. In each individual, the rarer allele in the population was generally assigned to the second haplotype. As a result, many individuals are represented by one short and one long terminal branch. Extra-Amazonian samples are colored red.

**Figure S2:** Unrooted BEAST2 trees of whole mitochondrial genomes in each species including extra-Amazonian samples (colored red). Some individuals are missing because insufficient mitochondrial sequence was recovered for analysis.

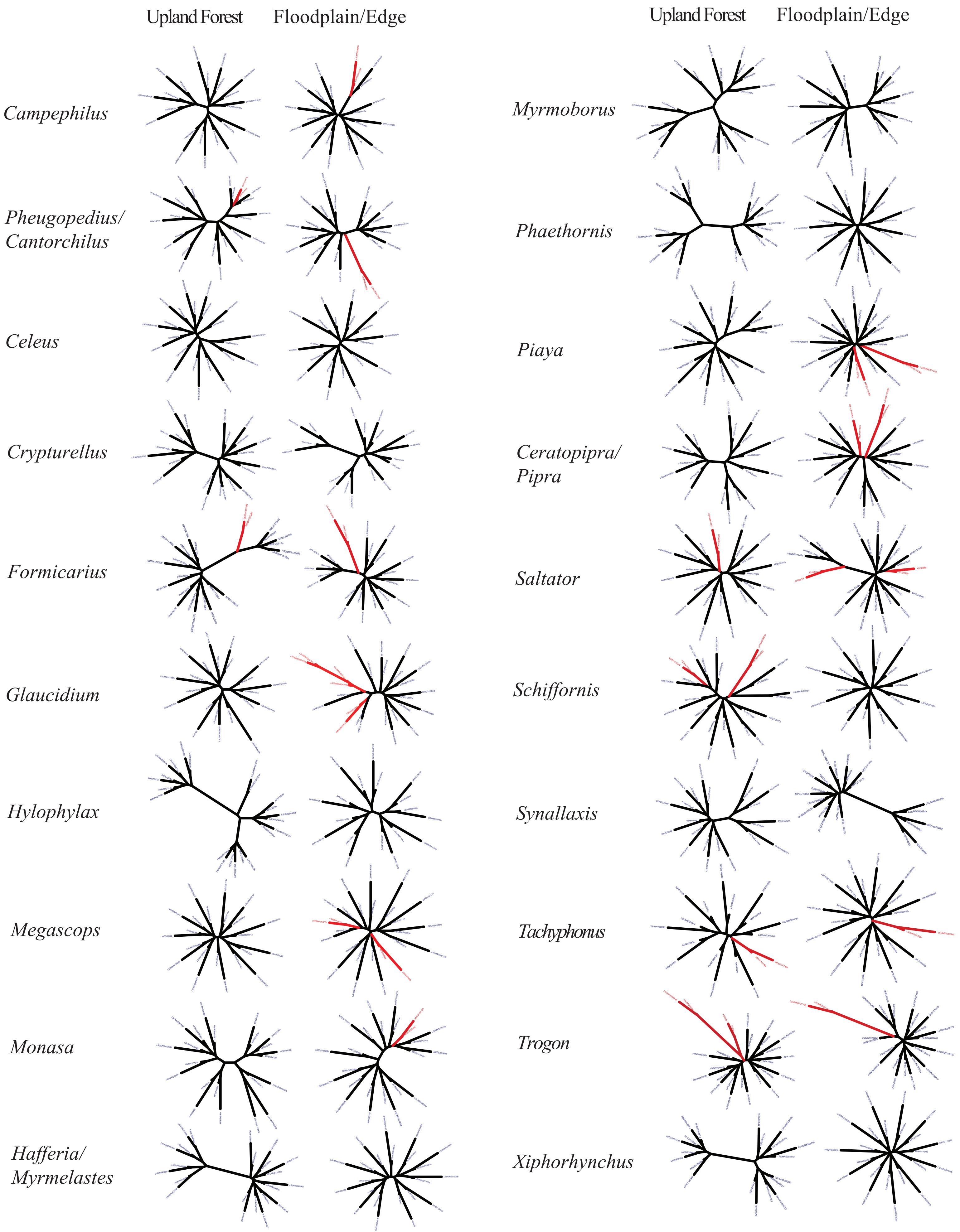
**Figure S3:** Plots of population genetic structure and cluster assignments inferred from Structure, BAPS, and DAPC for all 40 study species. Distinct colors represent different clusters, and the size of bars is proportional to the probability of assignment to a particular cluster. The individuals are in rows.

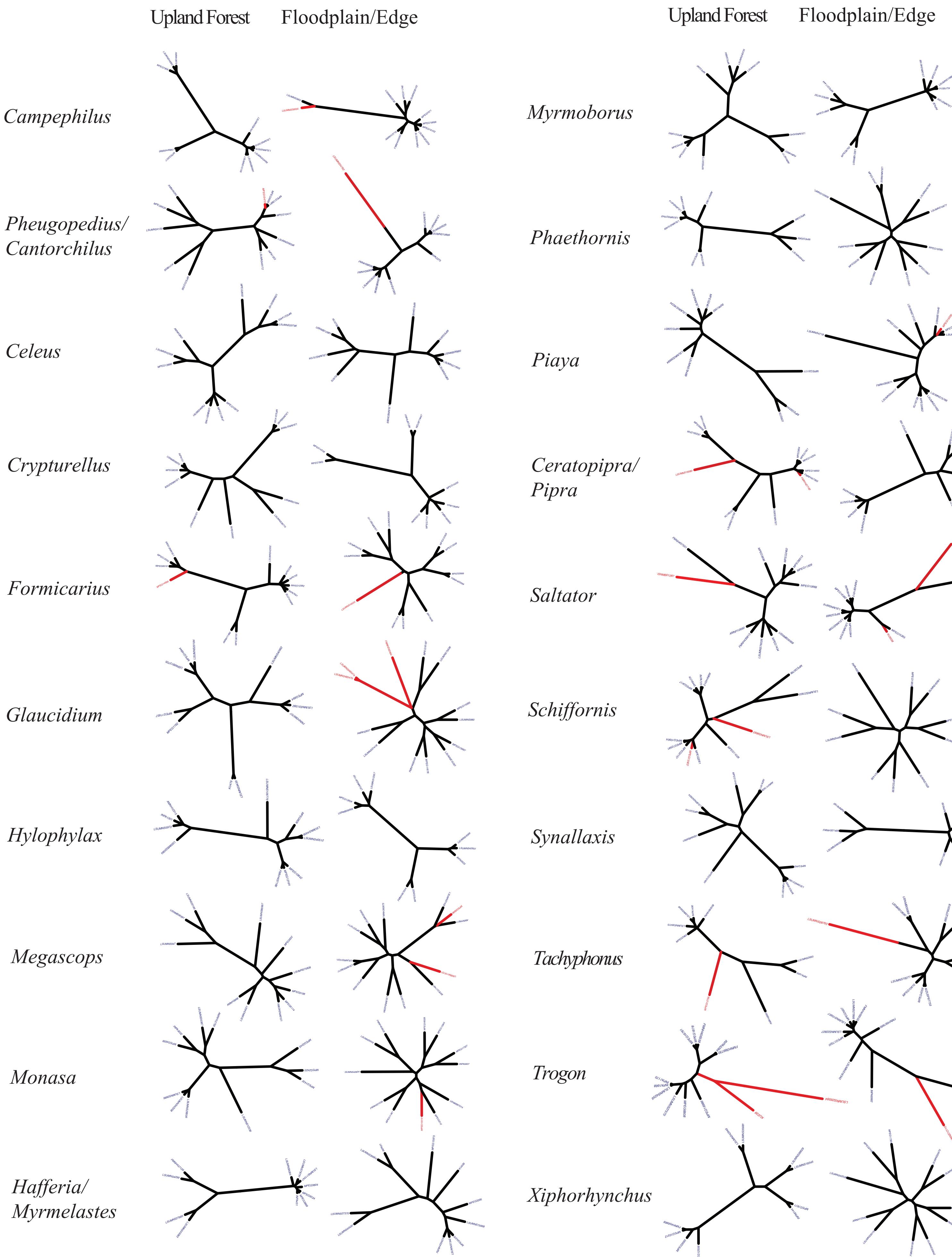
**Figure S4:** Population genetic structure and cluster assignments from BAPS adjoining maps showing the distribution of samples assigned to each cluster across the Amazon Basin.

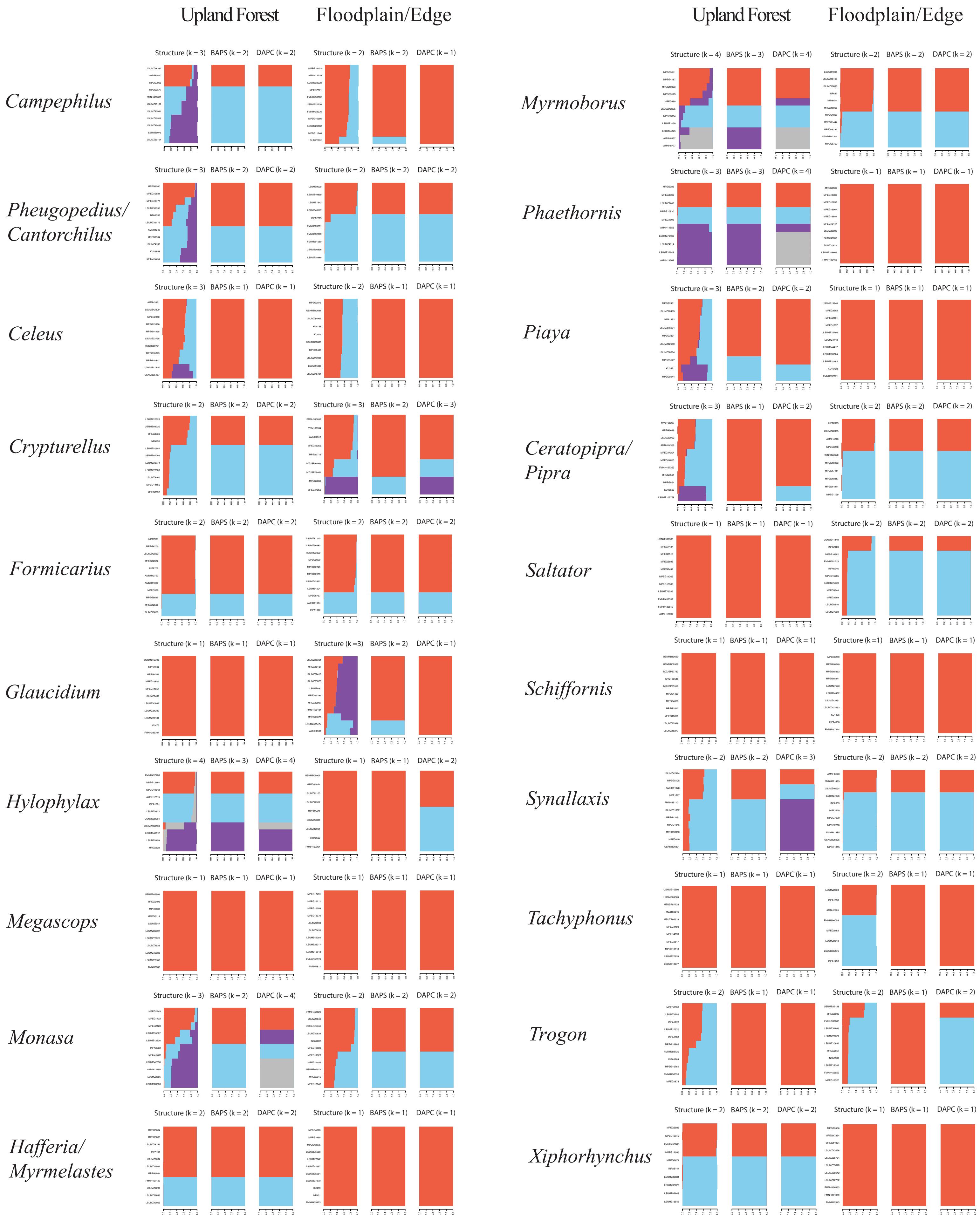
**Figure S5:** Pairwise Spearman’s correlation coefficients between all genetic parameters. The size of circles reflects relative significance levels, and empty cells represent no significant

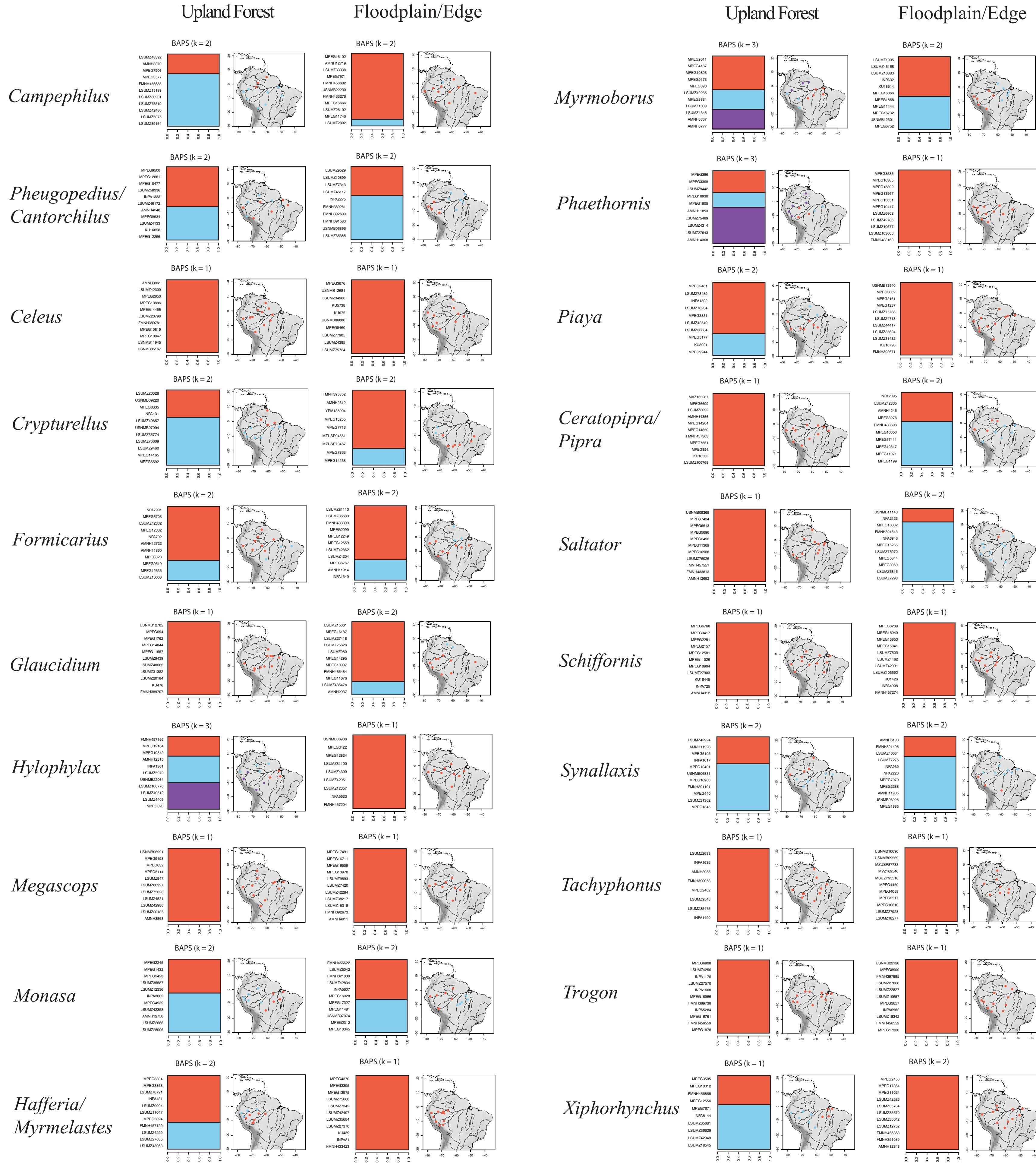
correlation ( $P > 0.05$ ). Black polygons outline the eight groups of highly correlated variables based on ClustOfVar analysis.

**Figure S6:** A plot showing the ratio of nucleotide diversity between loci mapping to the Z chromosome and those mapping to the autosomes versus forest stratum. Points are colored green for upland forest species and orange for floodplain/edge species. The outliers in the understory group represent the two *Crypturellus* tinamous.









Spearman's Correlation Coefficient ( $\rho$ )

