Supplementary Information

Bioinformatic Processing of GBS Sequences:

When demultiplexing samples I allowed for a single sequencing error in the barcodes. After removing the restriction site and barcodes, I removed low quality reads by filtering those with more than five sites with a Phred score of <20 and I retained reads >50 bp. I used a clustering threshold of 88% for within- and across-sample clustering and retained clusters if they had ≥ 6x depth of coverage. One bioinformatic challenge of GBS is the potential for duplicated sequences resulting from overlapping fragments. To account for this issue, I used *pyRAD*'s reverse-complement clustering method (Eaton 2014). To filter potential paralogs, I only retained clusters with heterozygous sites across ≤ 3 samples and with ≤ 3 total heterozygous sites. I retained consensus sequences with ≤ 4 undetermined sites.

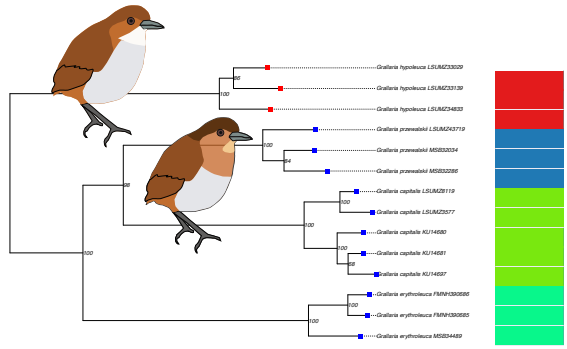
Eaton, D. A. R. 2014. PyRAD: assembly of de novo RADseq loci for phylogenetic analyses. Bioinformatics 30:1844–1849.

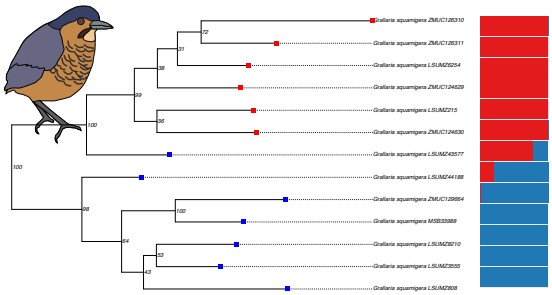
Table S1 (Excel Spreadsheet). Sample information and bioinformatics statistics from *pyRAD*. ANSP = Academy of Natural Sciences of Drexel University; FMNH = Field Museum of Natural History; KU = Kansas University Biodiversity Institute and Natural History Museum; LSUMZ = Louisiana State University Museum of Natural Science; MVZ = University of California Berkeley Museum of Vertebrate Zoology; MSB = University of New Mexico Museum of Southwestern Biology; ZMUC = Zoological Museum University of Copenhagen.

Table S2 (Excel Spreadsheet). The ABBA/BABA tests and their results. "Scheme" indicates the geographic relationships of ((P1,P2)P3) as depicted in Fig. 3 (six lineages had two schemes that could be sampled from the topologies). Columns P1, P2, P3 and O indicate the samples used for each population designation (see Table S1 for locality information). ABBA and BABA are the SNP frequencies of those allele patterns in the population, nloci the total number of loci used in the test, *D* and std.D indicate the *D*-statistic and the standard deviation in 100 bootstrap samples, Z the Z-score from bootstrapping, and p the p-values converted from Z-scores. *f* indicates the proportion of the genome that was introgressed (see equation 2 in text and Fig. 4).

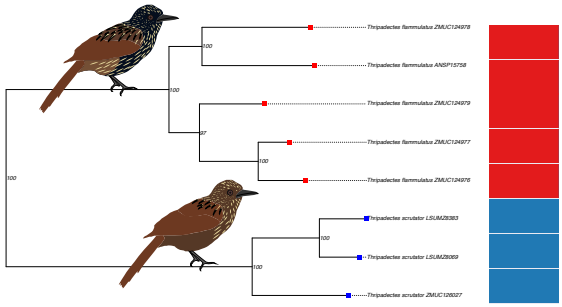
Superspecies

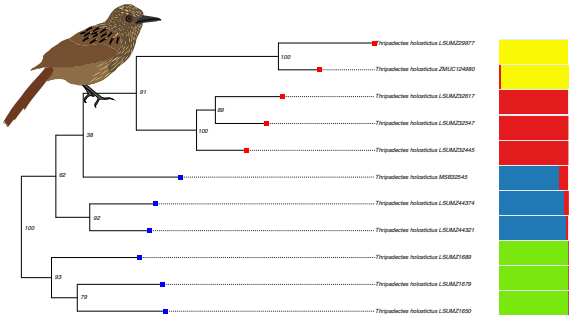
Monotypic Species



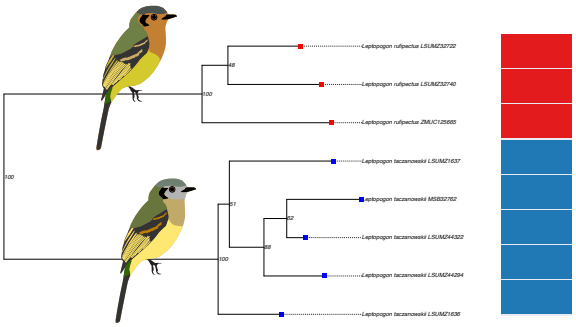


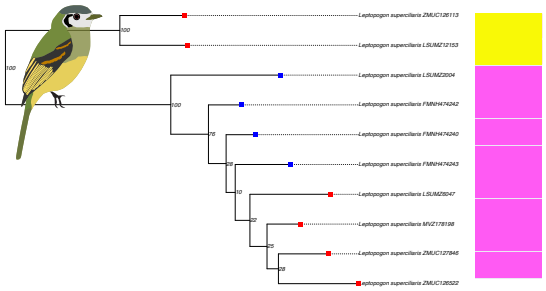
Grallaria



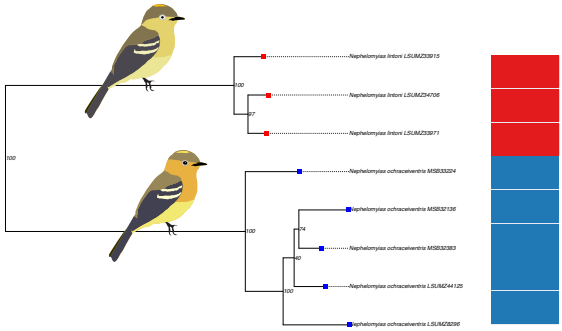


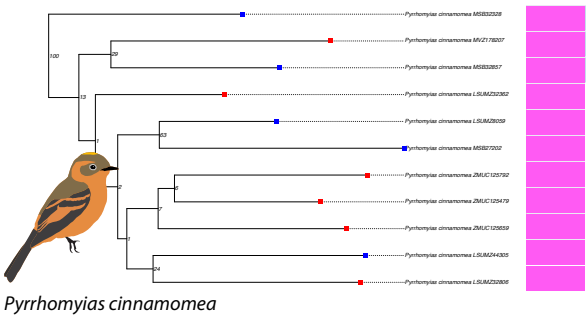
Thripadectes





Leptopogon



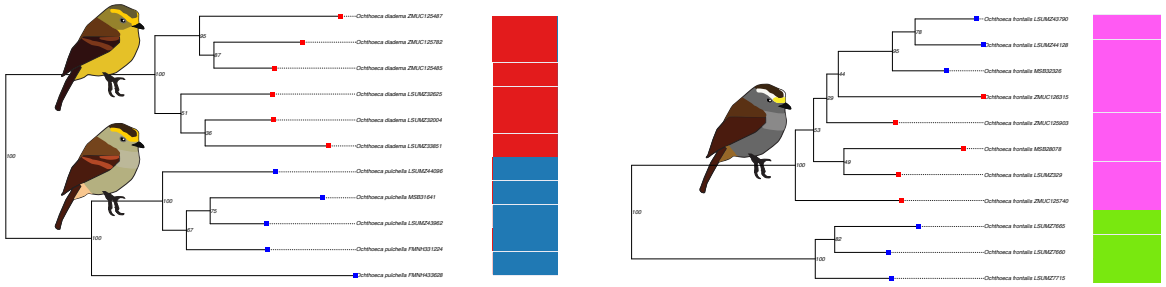


Nephelomyias

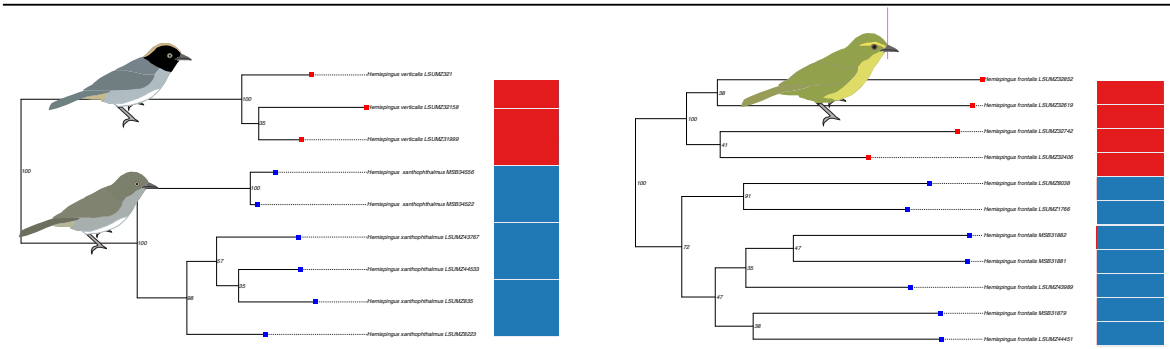
Pyrrhomyias cinnamomea

Superspecies

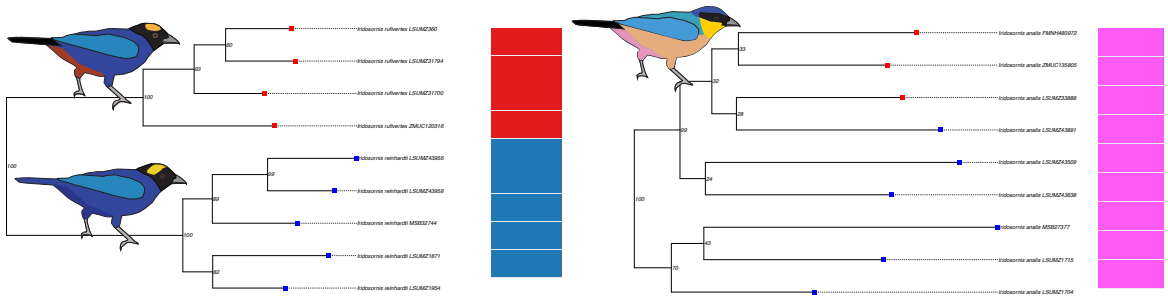
Monotypic Species



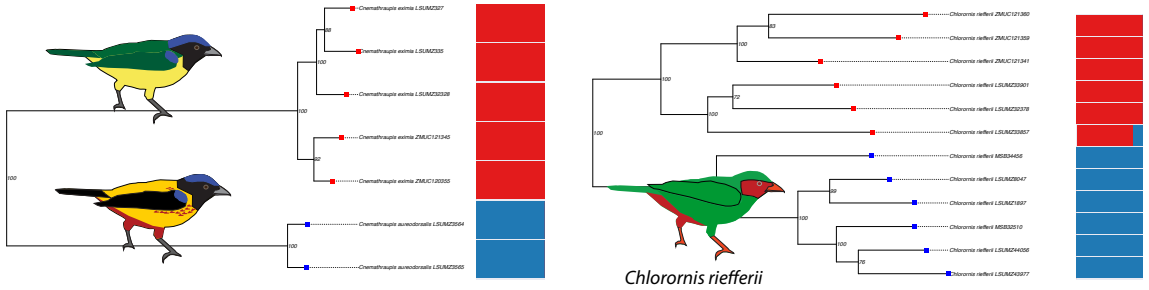
Ochthoeca



Hemispingus



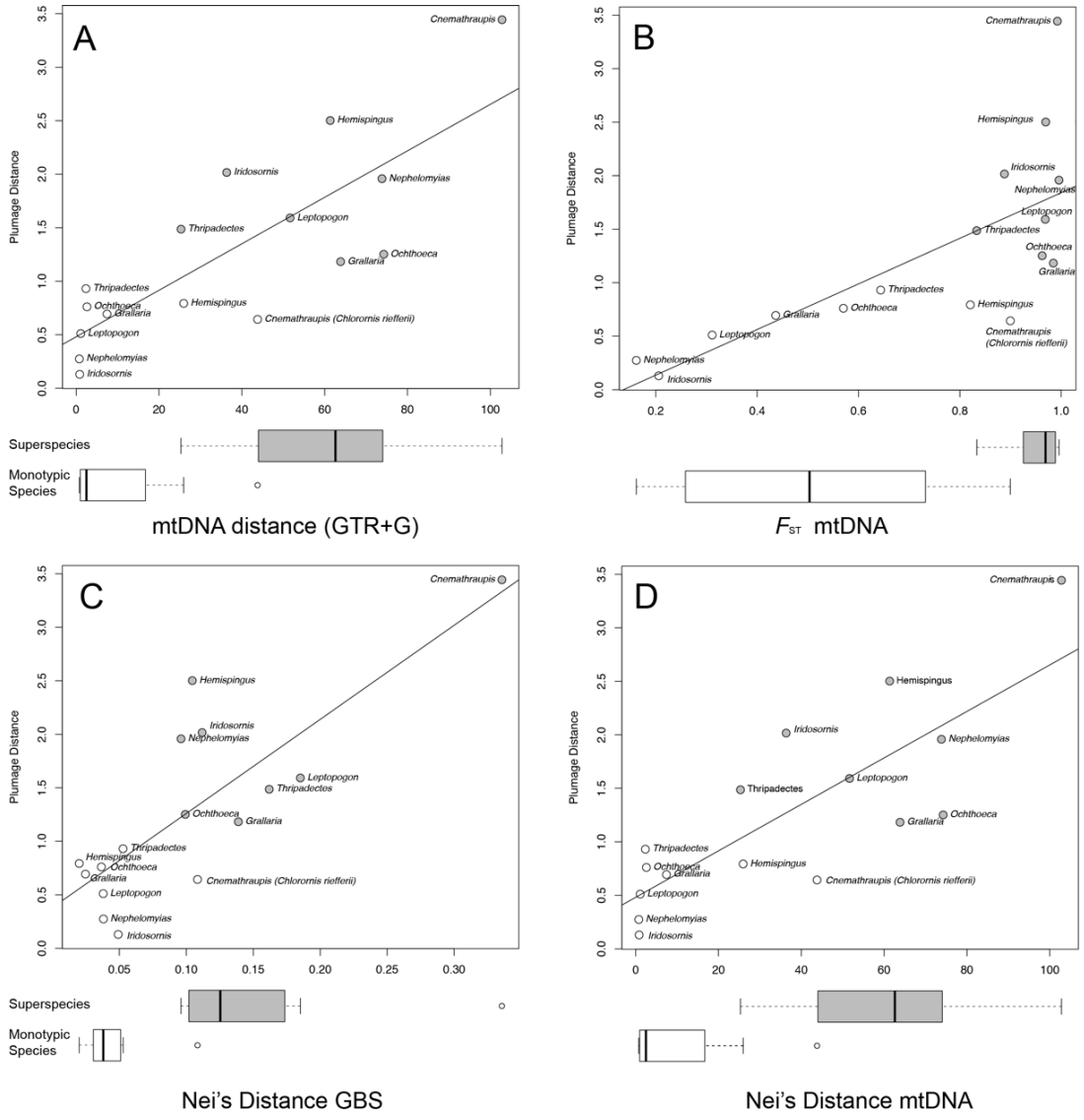
Iridosornis



Chlorornis riefferii

Cnemathraupis

Figure S1 –*ML* phylogenies and *Structure* plots of the superspecies and monotypic species from each of 8 genera (16 lineages total). In each genus, the left phylogeny shows the superspecies (with each member of the allospecies pair illustrated at the corresponding clade) and the right phylogeny the congeneric monotypic species. In the phylogenies, red squares at the tips indicate samples from north of the Marañón, and blue from south of the Marañón, throughout the entire sampling region (Fig. 1). Outgroups, which are described in the text, were pruned for ease of visualization and the phylogenies are drawn at different scales from one another so that shallow nodes are visible. Numbers at the nodes indicate bootstrap support. In the *Structure* plots, the number of colors corresponds to the K value with the highest likelihood. In plots where red and blue are present, the *Structure* runs at the best K value clustered populations north (red) and south (blue) of the Marañón as separate clusters. In plots with pink, *Structure* clustered populations north and south of the Marañón in one cluster. Additional colors indicate clusters that correspond to divergence across other barriers away from the Marañón in the north (yellow; west slope of Andes, Fig. 1) and south (green; south Huallaga Valley, Fig. 1). Plots without green and yellow may still have samples from across these other barriers, but they did not cluster separately in the *Structure* analyses.



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78 **Figure S2.** Trans-Marañón genetic differentiation versus plumage divergence. Plumage distance
79 is the mean Mahalonobis distance of three colorimetric variables across 10 plumage patches
80 from spectrophotometric data (see text). A) GTR-distances, modified with permission from
81 Winger and Bates (2015); B, F_{ST} using mtDNA (ND2), *cf*. Fig. 2 for F_{ST} using GBS; Nei's
82 genetic distance using C) GBS and D) mtDNA datasets.

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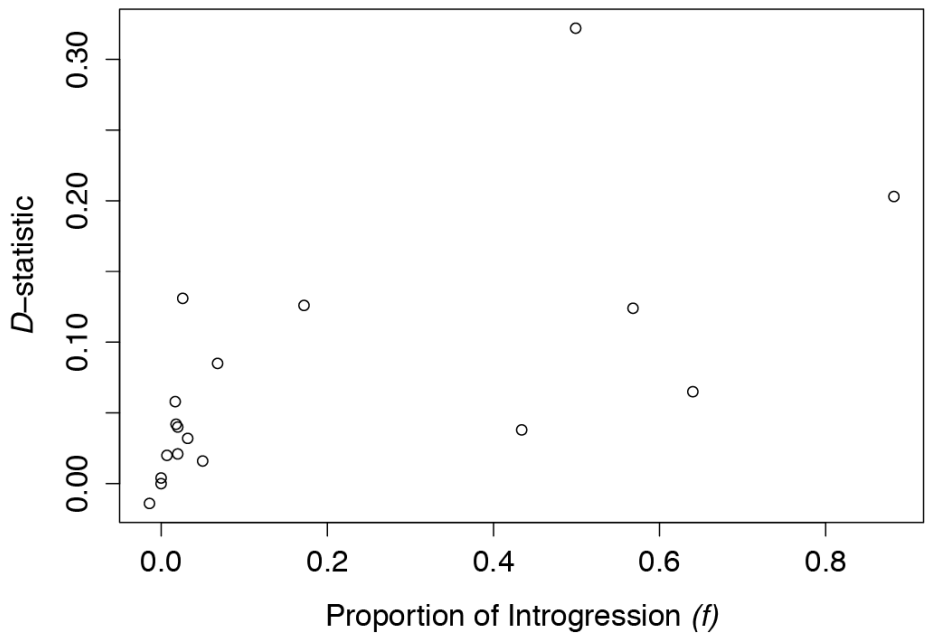

Figure S3. The *D*-statistic versus *f,* the proportion of genomic introgression. See equation 2 and Table S2.