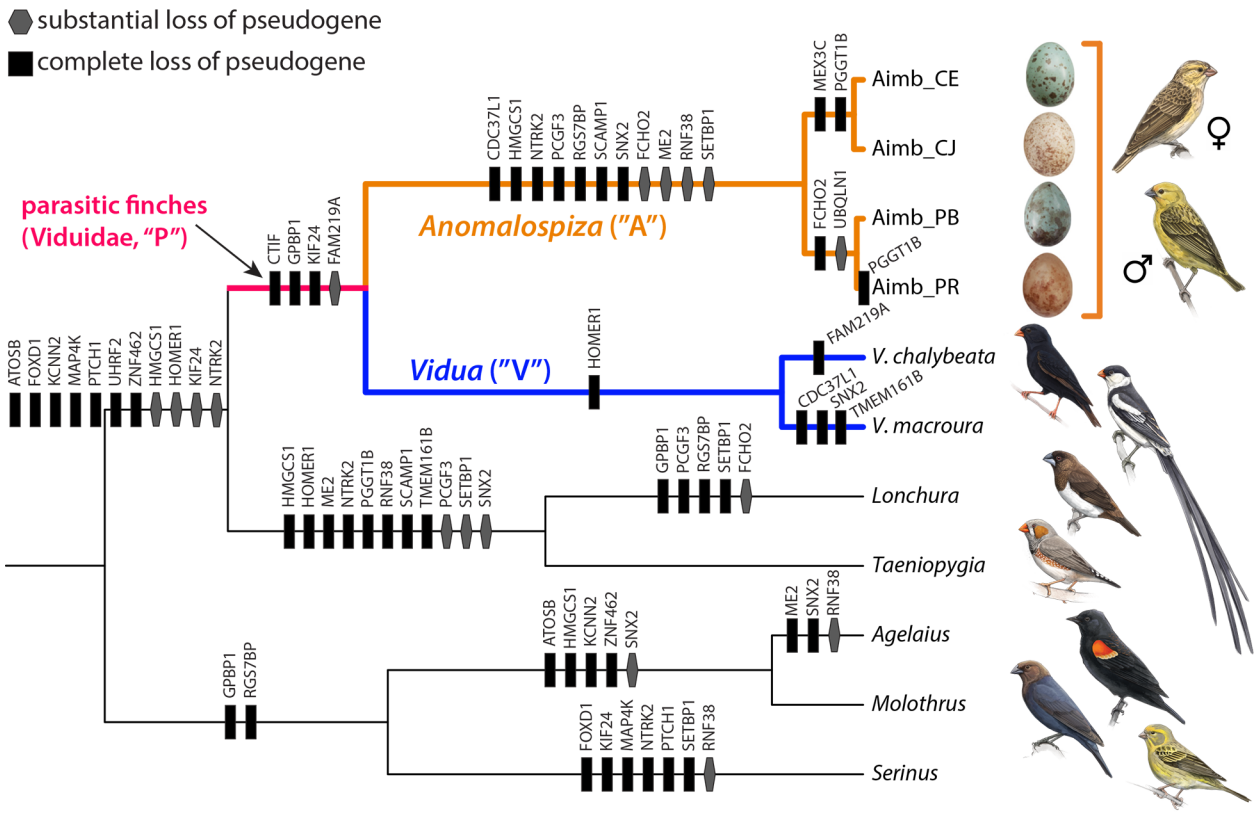
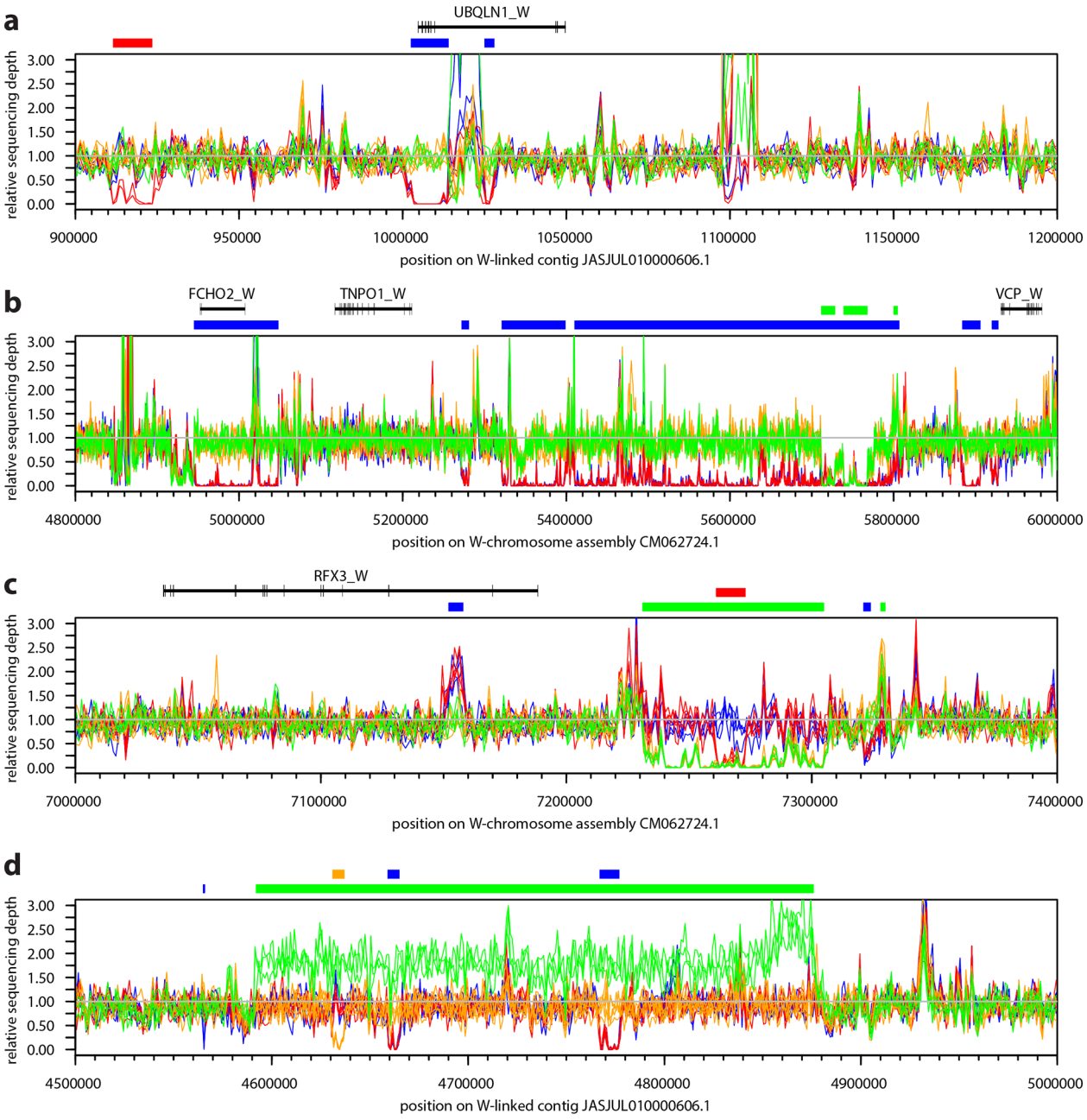
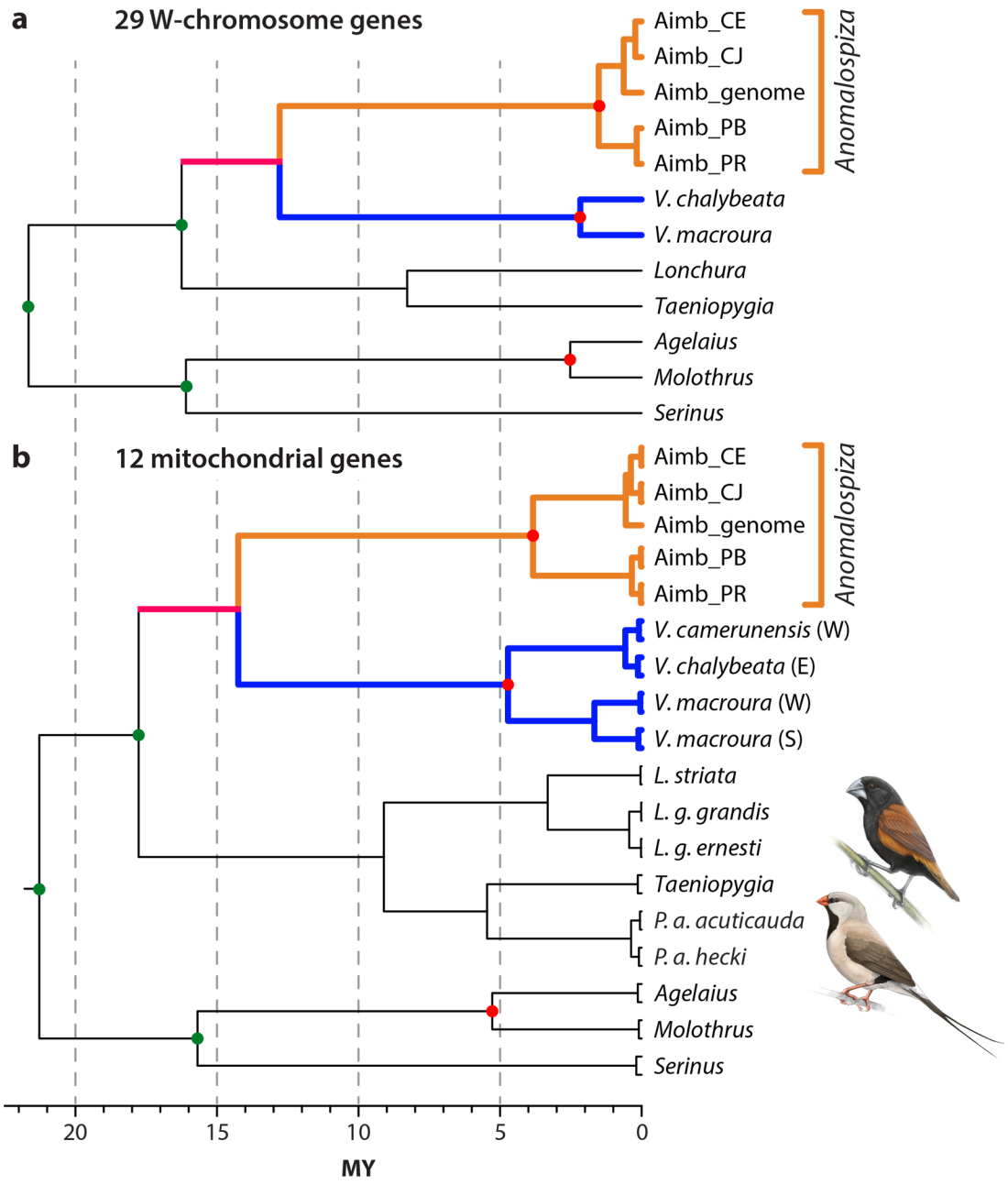


Extended Data Fig. 1 | Dollo parsimony reconstruction of losses (substantial or complete) of pseudogenes that lost function in an earlier ancestor. Reconstructed losses of pseudogenes are indicated on branches with relevant gene names. Detectable pseudogenes with less than 35% of the original coding regions remaining are scored as "substantially lost." From top, the taxa include: four cuckoo finch maternal lineages ("CE" = lineage parasitizing *Cisticola erythrops*; "CJ" = lineage parasitizing *C. juncidis*; "PB" and "PR" = lineages parasitizing *Prinia subflava* and laying eggs with blue and red background color, respectively; two parasitic finches with no evidence of maternally inherited, host-specific adaptations (village indigobird *Vidua chalybeata*; pin-tailed whydah *Vidua macroura*); two estrildid finches (white-rumped munia *Lonchura striata*; zebra finch *Taeniopygia guttata*); red-winged blackbird *Agelaius phoeniceus*; brown-headed cowbird *Molothrus ater*, a host generalist brood parasite; and the canary *Serinus canaria*. The underlying phylogeny is based on a BEAST v. 2.7.6[84,85] analysis of the concatenated coding regions of 29 W-linked genes present in all taxa. Images of male and female cuckoo finch along with males of the remaining species by Javier Lazaro.



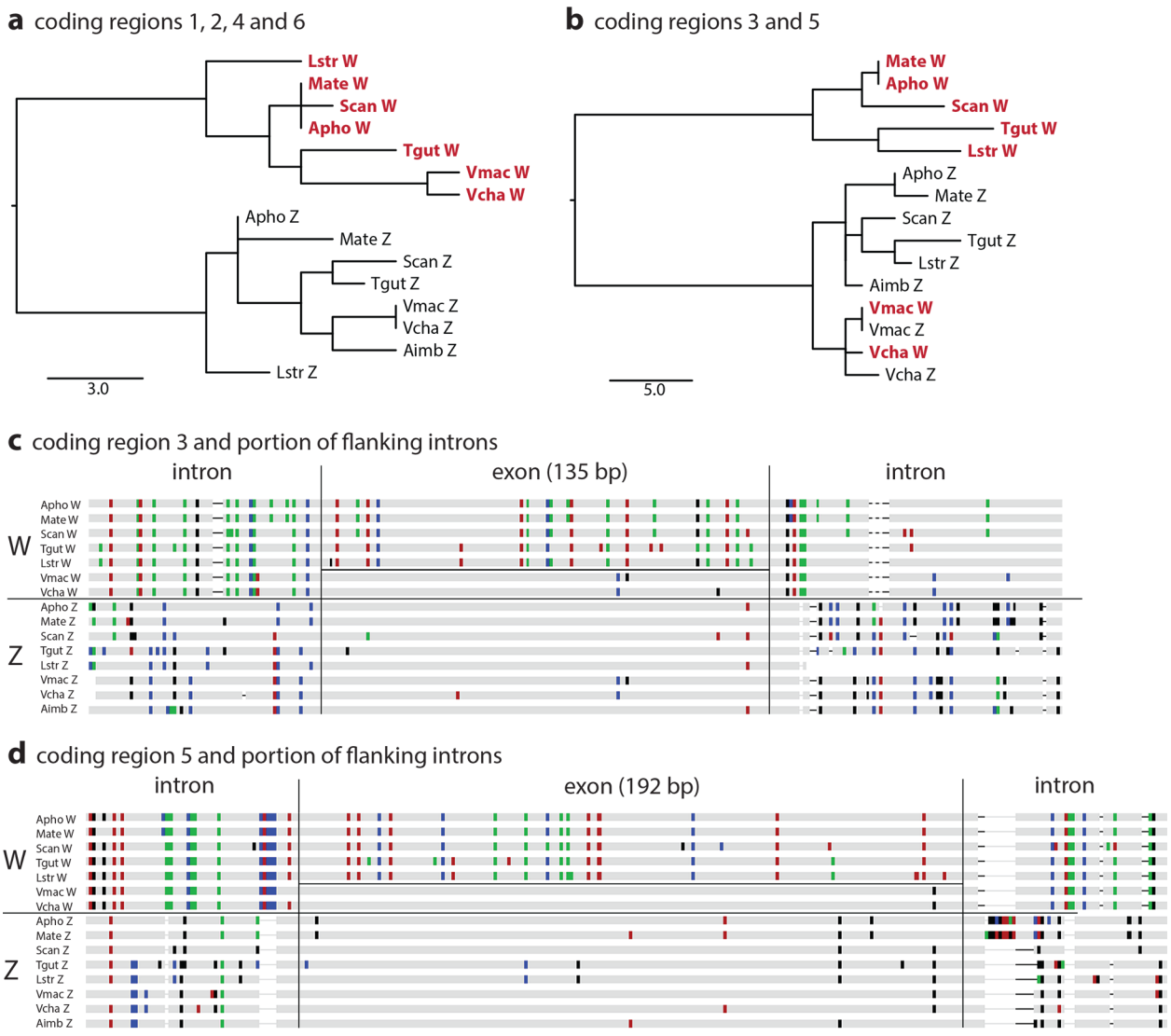
Extended Data Fig. 2 | Examples of W-chromosome deletions and an apparent duplication. All panels plot relative sequencing depth for individual cuckoo finch females across selected portions of the W-chromosome. Sequencing depth scaled to the mean Z-chromosome depth for each sample is plotted for 1-kb intervals. Cuckoo finch matrilines are color-coded as follows: green = parasitizing *Cisticola erythrops*; orange = parasitizing *C. juncidis*; blue and red = parasitizing *Prinia subflava* and laying blue and red eggs, respectively. Protein-coding genes are indicated in black. **a**, A deletion of ~22 kb in the "Prinia" cuckoo finch lineage (red and blue) eliminates six of the remaining exons from UBQLN-W, which was already a pseudogene, having lost two exons in the ancestral cuckoo finch lineage. **b**, A region with multiple deletions in the "Prinia" lineage (red and blue) ranging from ~10 to ~240-kb, with smaller deletions in the

“Cisticola” lineage (green and orange). The former includes an ~100-kb deletion resulting in complete loss of FCHO2-W, which was already a remnant pseudogene. TNPO-W and VCP-W are intact and putatively functional in all lineages. **c**, An ~70-kb deletion in the “Cisticola” lineage with a smaller ~15-kb deletion in the “Prinia-red” lineage in the same region. **d**, An apparent duplication of ~285-kb in the “C. erythrops” lineage (green) with smaller deletions in other lineages (orange, blue/red) in the same region.

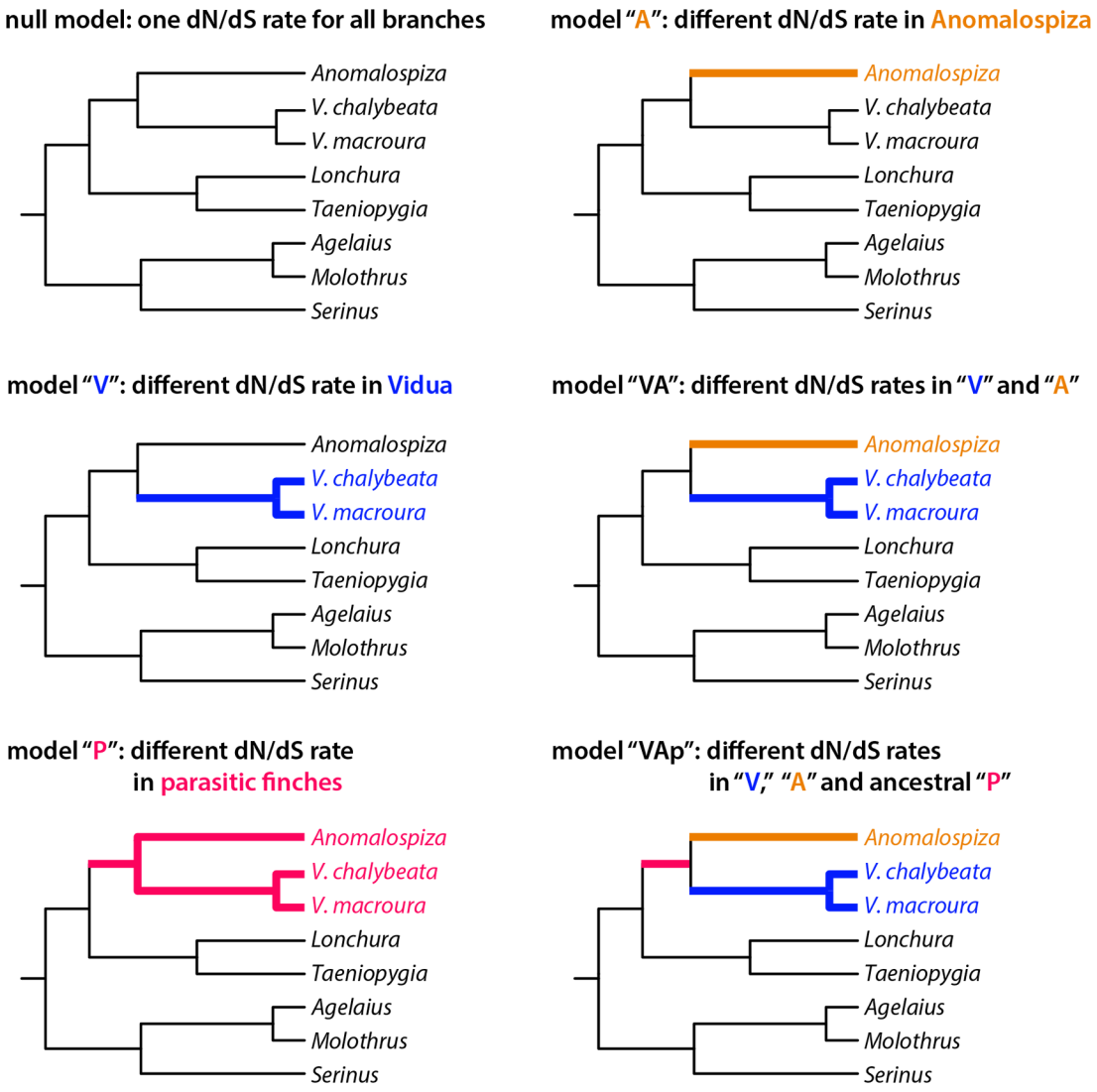


Extended Data Fig. 3 | Sampling and phylogeny of maternal lineages based on W-chromosome and mtDNA data. Results of model-averaged analyses in BEAST v. 2.7.6[84,85] for: **a**, 29 full-length, putatively functional, W-linked genes present in all taxa. **b**, 12 light-strand-encoded mitochondrial protein-coding genes. For both analyses, we partitioned the data by codon position and set divergence time priors for three basal nodes (green dots), reflecting the estimates and 95% HPD intervals from Oliveros *et al.*[86]. The two trees are identical in topology and all nodes had posterior probabilities of 1 but recent divergence time estimates (e.g., red dots) are substantially greater in the mtDNA analysis, likely reflecting the overestimation of recent divergence times (see ref. 104). For the mtDNA analyses in this paper, we analyzed two samples per species/lineage and added samples for *Lonchura grandis* and *Poephila acuticauda* to make the diversity of sampled estrildid finch lineages comparable to that for parasitic finches. Note

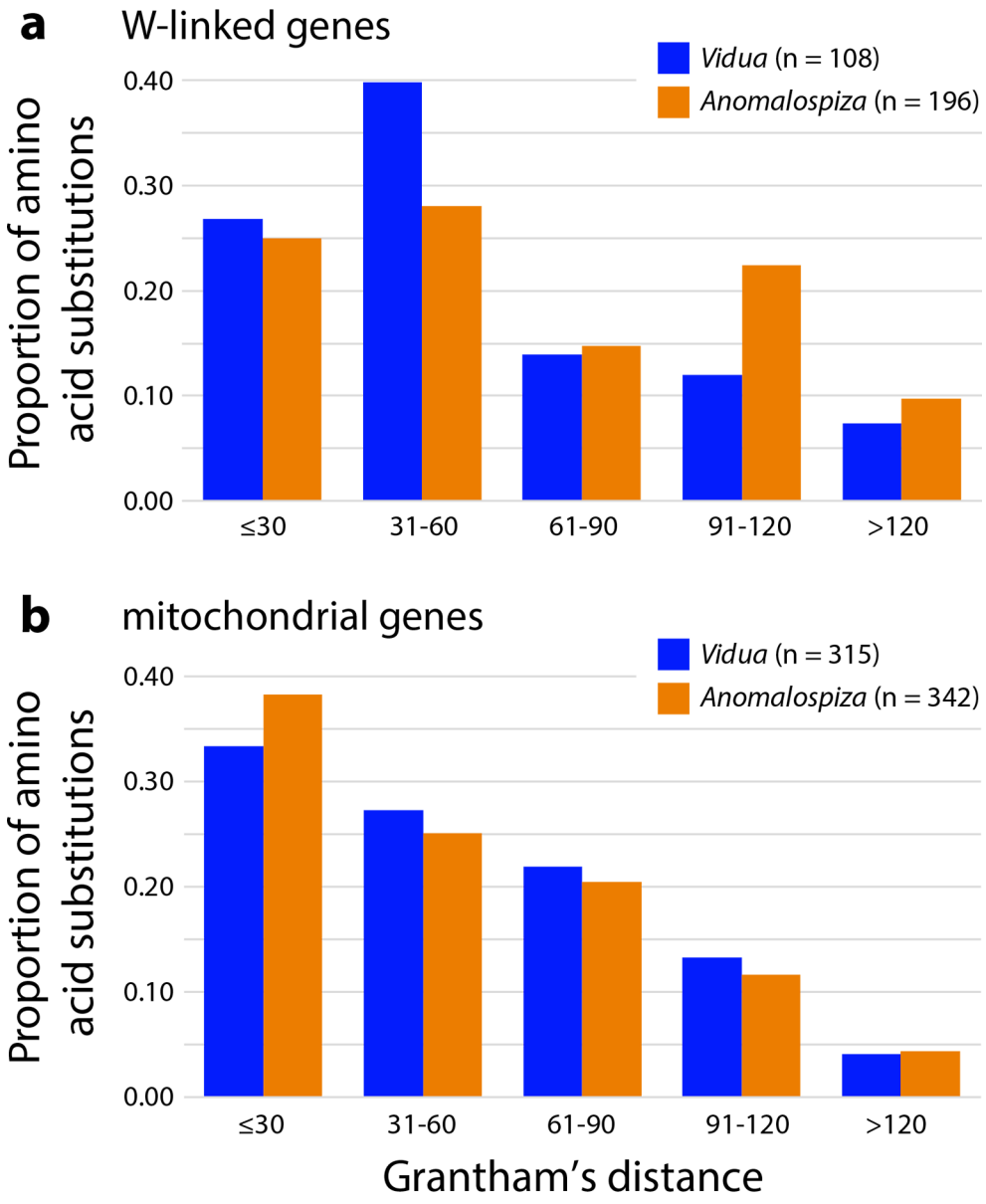
also that the cuckoo finch sample used to generate the reference genome sequence is from a lineage ("Aimb_genome") closely related to but distinct from the "Cisticola erythrops" (CE) and "Cisticola juncidis" (CJ) lineages for which we generated whole genome re-sequencing data.



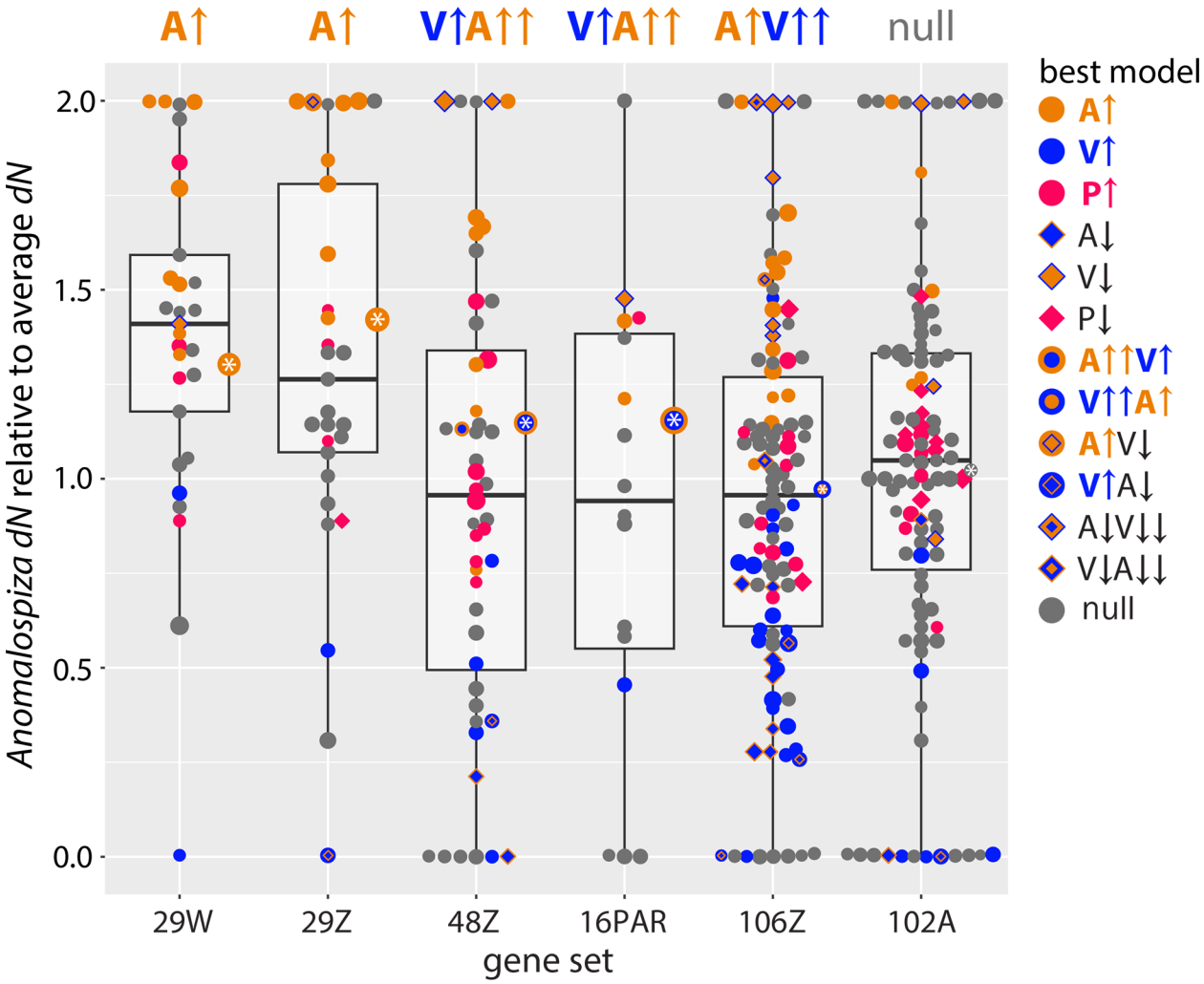
Extended Data Fig. 4 | Apparent case of chromosome Z to W gene conversion in the Vidua lineage. a, Parsimony tree for concatenation of four coding regions in the RPL17-W and RPL17-Z genes showing the expected grouping of W- and Z-linked gametologs, respectively. A similar grouping of W- and Z-linked gene sequences was observed for all other Z-W gametologs we examined. **b**, Parsimony tree for concatenation of the remaining two coding regions in the RPL17 gene showing evidence of Z to W gene conversion in the *Vidua* lineage ("Vcha_W", "Vmac_W"). **c**, Sequence alignment (with bases mismatching the consensus shown in color) for coding region 3 showing that gene conversion was limited to the exon; immediately flanking intron sequences retain their similarity to the W- and Z-linked sequences, respectively, of other taxa. **d**, Sequence alignment for coding region 5, in which a similar pattern is observed. Note that the W-chromosome copy of RPL17 was lost in the cuckoo finch lineage ("Aimb").



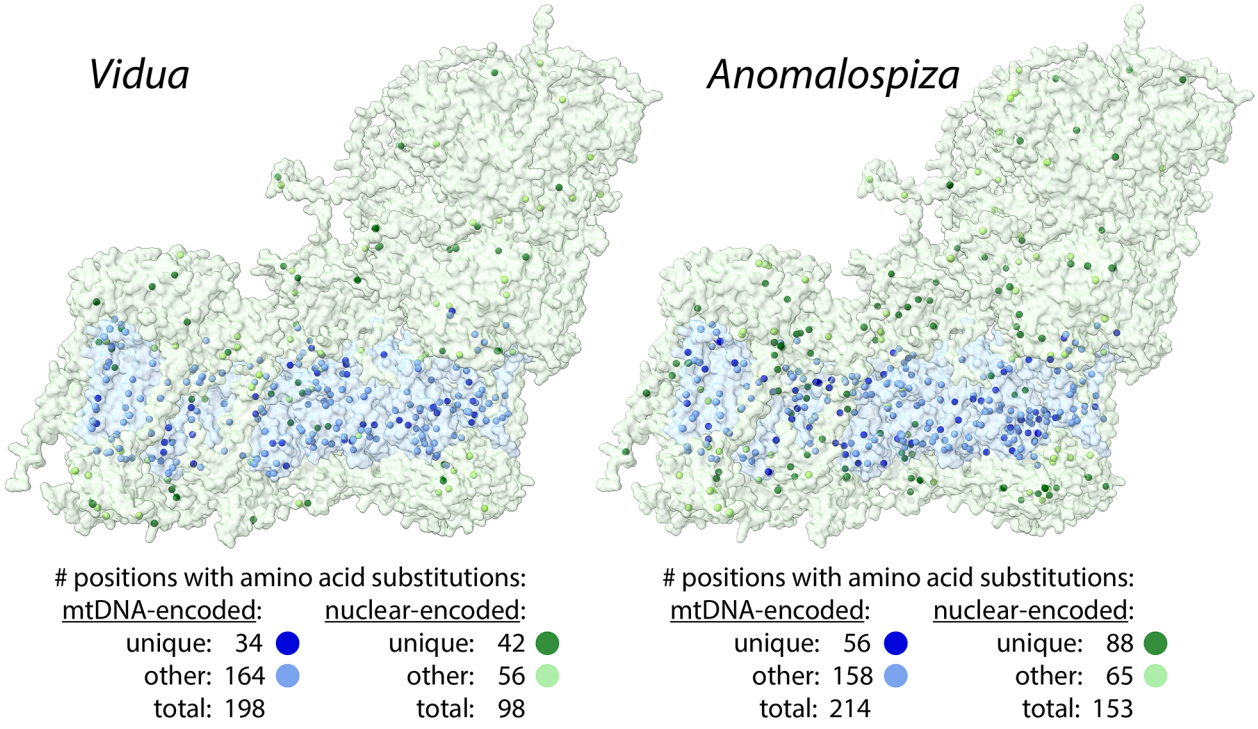
Extended Data Fig. 5 | Graphic summary of alternative branch models tested in PAML. For each gene or set of genes, we calculated the likelihood of the data and estimated d*N*/*dS* values for each of the six models above, in which differently colored branches specify the estimation of different *dN*/*dS* ratios. For each gene or set of genes, we identified the best fit model as having the lowest AICc value. In a few cases, model "VAp," which includes an extra *dN*/*dS* parameter for the ancestral parasitic finch branch, provided a better fit than model "VA," though both models include a difference in rate between *Anomalospiza* and *Vidua*. When either model "VA" or "VAp" provided the best fit, we summarize the results similarly, indicating whether *Anomalospiza* and *Vidua* has a higher rate and how their rates compare to the outgroup rate estimated for the remaining black branches.



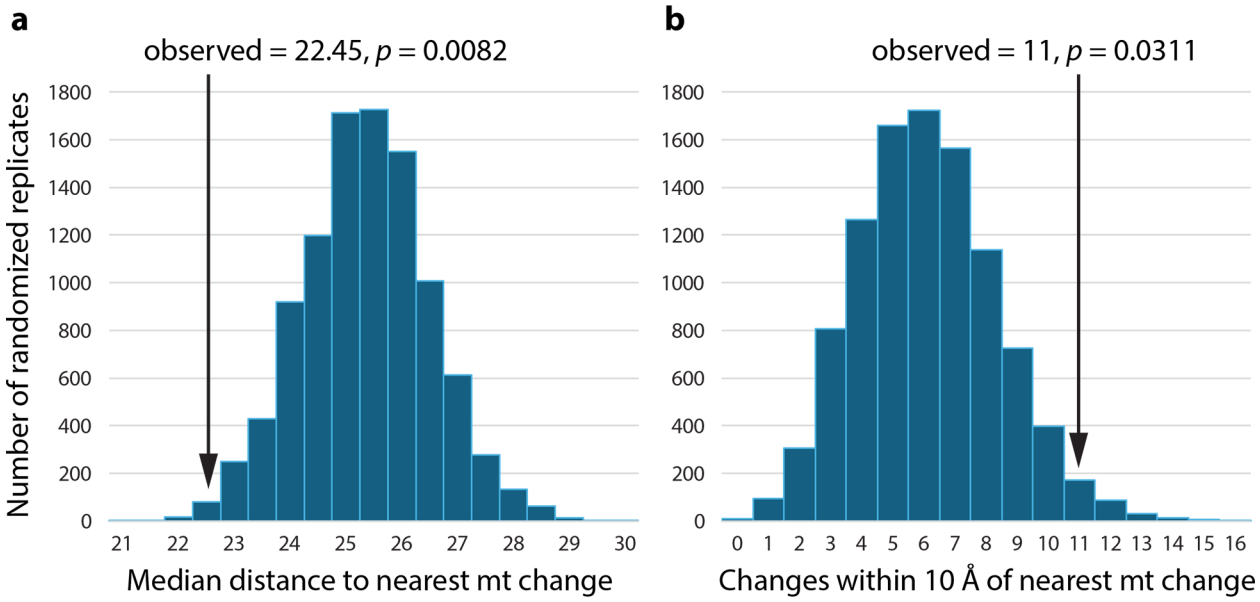
Extended Data Fig. 6 | Distributions of Grantham's distance values for W-linked and mitochondrial amino acid substitutions in the *Vidua* and cuckoo finch lineages. a, Results for 29 W-linked genes present in all taxa analyzed; the distributions differ significantly (two-tailed Kolmogorov-Smirnov test, $D = 0.174$, $p = 0.0149$), due to a relatively higher proportion of substitutions in the cuckoo finch lineage involving changes between amino acids with more divergent chemical properties. **b**, Results for 13 mtDNA protein-coding genes based on "DELTRAN" reconstruction of amino acid substitutions; no significant difference between *Vidua* and *Anomalospiza* ($D = 0.083$, $p = 0.12$).



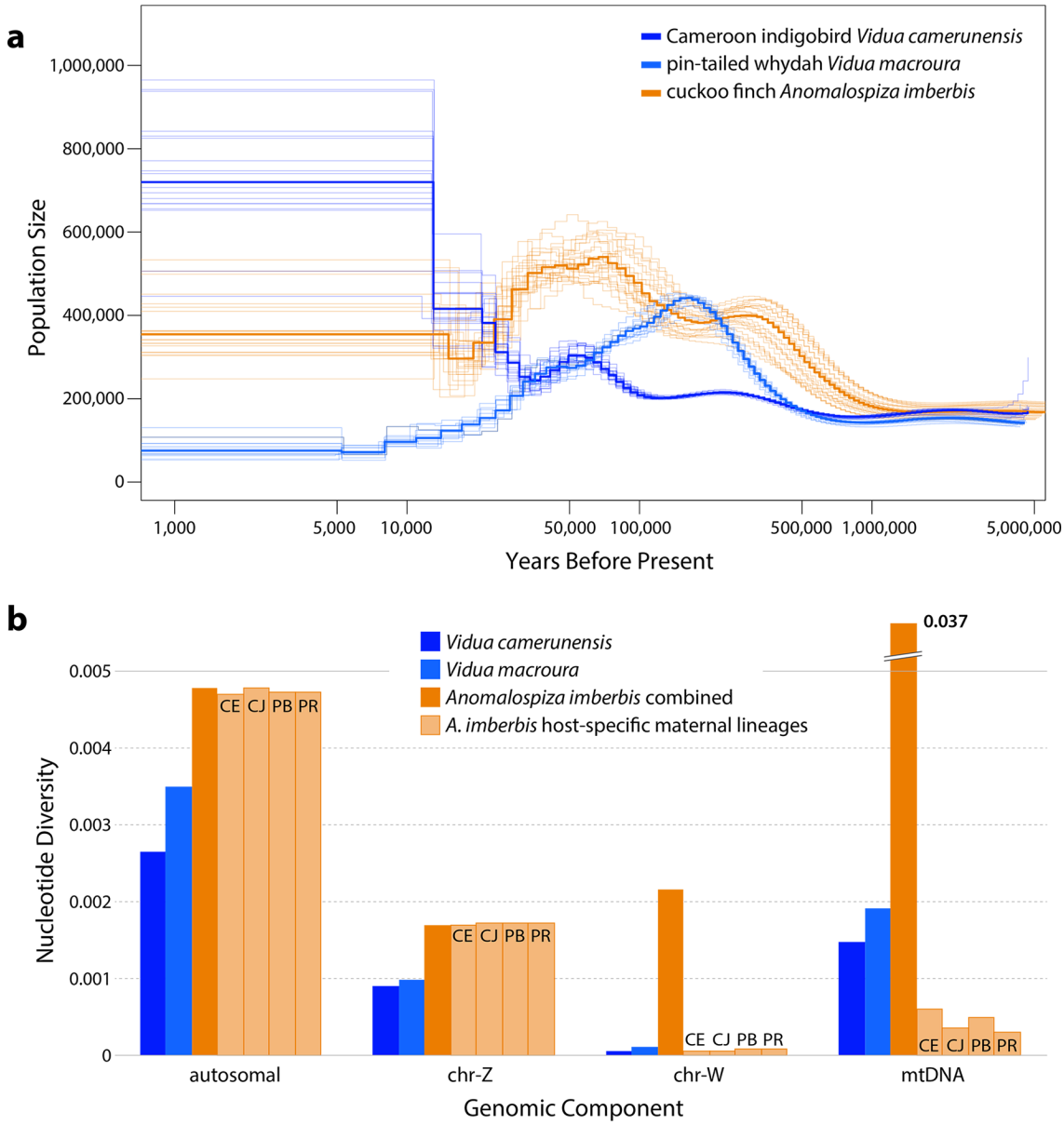
Extended Data Fig. 7 | Rate of non-synonymous change in *Anomalospiza* relative to the average rate in *Anomalospiza* and *Vidua* ($dN_A/((dN_A+dN_V)/2)$) for six sets of genes. The six gene sets include: 1) 29W: 29 W-linked genes for which all species we analyzed retain a putatively functional copy; 2) 29Z: the 29 Z-linked gametologs of the 29 intact W-linked genes; 3) 48Z: 48 Z-linked genes which have W-linked gametologs in a subset of the species we analyzed or in other, more distantly related songbirds; 4) 16PAR: 16 genes in the pseudoautosomal region; 5) 106Z: a control set of 106 Z-linked genes not known to have a W-linked gametolog in any passeriform; and 6) 102A: a control set of 102 autosomal genes. Each gene is represented by a data point; the best model for *dN*/*dS* ratios for each gene based on analyses in PAML is indicated by color and shape according to the legend at right; the top six categories correspond to genes for which the best model had a higher or lower *dN*/*dS* in *Anomalospiza* (A), *Vidua* (V) or in parasitic finches generally (P = the clade comprising *Anomalospiza* plus *Vidua*). The bottom six categories correspond to genes for which the best model had different *dN*/*dS* rates in *Anomalospiza*, *Vidua* and the outgroup, respectively, with arrows indicating the rates for "A" and "V" relative to the outgroup. Results for analyses of all genes within each set combined are indicated at the right edge of each boxplot and denoted with an asterisk; these latter points were not included in calculation of the boxplots.



Extended Data Fig. 8 | Comparison of Complex I amino acid substitutions in *Vidua* and *Anomalospiza*. Structural model of Complex I, NADH dehydrogenase, based on sequences from the cuckoo finch reference genome. Nuclear- and mtDNA-encoded proteins are shown in shades of green and blue, respectively. Positions with amino acid changes are highlighted, with darker green and blue indicating unique changes (i.e., occurring at positions conserved in all other species in our analysis); lighter green and blue indicate positions that also have a change in at least one other species and/or that differ between the two *Vidua* species or between cuckoo finch matrilines (the latter relevant only for mtDNA-encoded proteins). *Anomalospiza* has a larger number of unique mtDNA substitutions and much larger number of unique nuclear-encoded substitutions, with a greater density of changes in proximity to the mtDNA-encoded proteins (see Fig. 4c).



Extended Data Fig. 9 | Proximity of nuclear- and mtDNA-encoded amino acid substitutions in respiratory Complex I (NADH dehydrogenase) of the cuckoo finch. In the context of a structural model for Complex I (see Fig. 4a), this analysis considers the minimum distance between each of 140 amino acid substitutions in the cuckoo finch lineage in nuclear-encoded Complex I genes and the nearest "unique" cuckoo finch substitution in a mtDNA-encoded Complex I gene. "Unique" is defined here as occurring at a site with a single change in the ancestral cuckoo finch lineage (i.e., the substitution is shared by all cuckoo finch matrilines and the site is conserved in the other seven taxa we analyzed), reasoning that such changes are the ones most likely to have selected for nuclear compensation. The observed values for two measures of proximity, **a**, median distance to the nearest unique mtDNA-encoded substitution and **b**, the number of nuclear substitutions (out of 140) within 10 Å of a unique mtDNA-encoded substitution, were compared to results obtained when the positions of the nuclear-encoded substitutions were randomized (n = 10,000 replicates) within each nuclear gene (i.e., the randomization maintained the same number of substitutions within each gene as in the observed data). The analysis excludes seven nuclear genes (NDUFA2, NDUFA5, NDUFS1, NDUFS4, NDUFS6, NDUFV1, NDUFV2) that lack close contact with any mtDNA-encoded residue (all distances > 20 Å).



Extended Data Fig. 10 | Estimates of demographic history and nucleotide diversity for cuckoo finches and two *Vidua* species. a, Results based on the pairwise sequentially Markovian coalescent (PSMC)[35] are shown for individual samples from each of the three parasitic finch species, with bold lines showing the median result for each time interval. **b**, Estimates of nucleotide diversity from ANGSD[103] for females of two *Vidua* species and for all cuckoo finch females combined, along with estimates for four cuckoo finch maternal lineages ("CE" = lineage parasitizing *Cisticola erythrops*; "CJ" = lineage parasitizing *Cisticola juncidis*; "PB" and "PR" = lineages parasitizing *Prinia subflava* and laying eggs with blue and red background color, respectively). Note that diversity for maternally inherited genome components (W-chromosome and mtDNA) is ~20 times greater in cuckoo finch than in *Vidua* due to the divergent, host-specific maternal lineages maintained within the cuckoo finch population, whereas diversity within cuckoo finch maternal lineages is substantially lower for mtDNA and roughly comparable to *Vidua* for the W-chromosome.