Figure S1: Genetic maps of five *Hymenochaetales* mitogenomes in this study. (A) *Phellinus lamaensis,* (B) *Porodaedalea pini,* (C) *Coniferiporia sulphurascens*, (D) *Fomitiporia mediterranea* and (E) *Schizopora paradoxa*. Legends and descriptions refer to fig. 1. A *S. paradoxa* trn(gtg)-rev tRNA is encoded on negative strand but plotted at outer circle for aesthetic reasons.
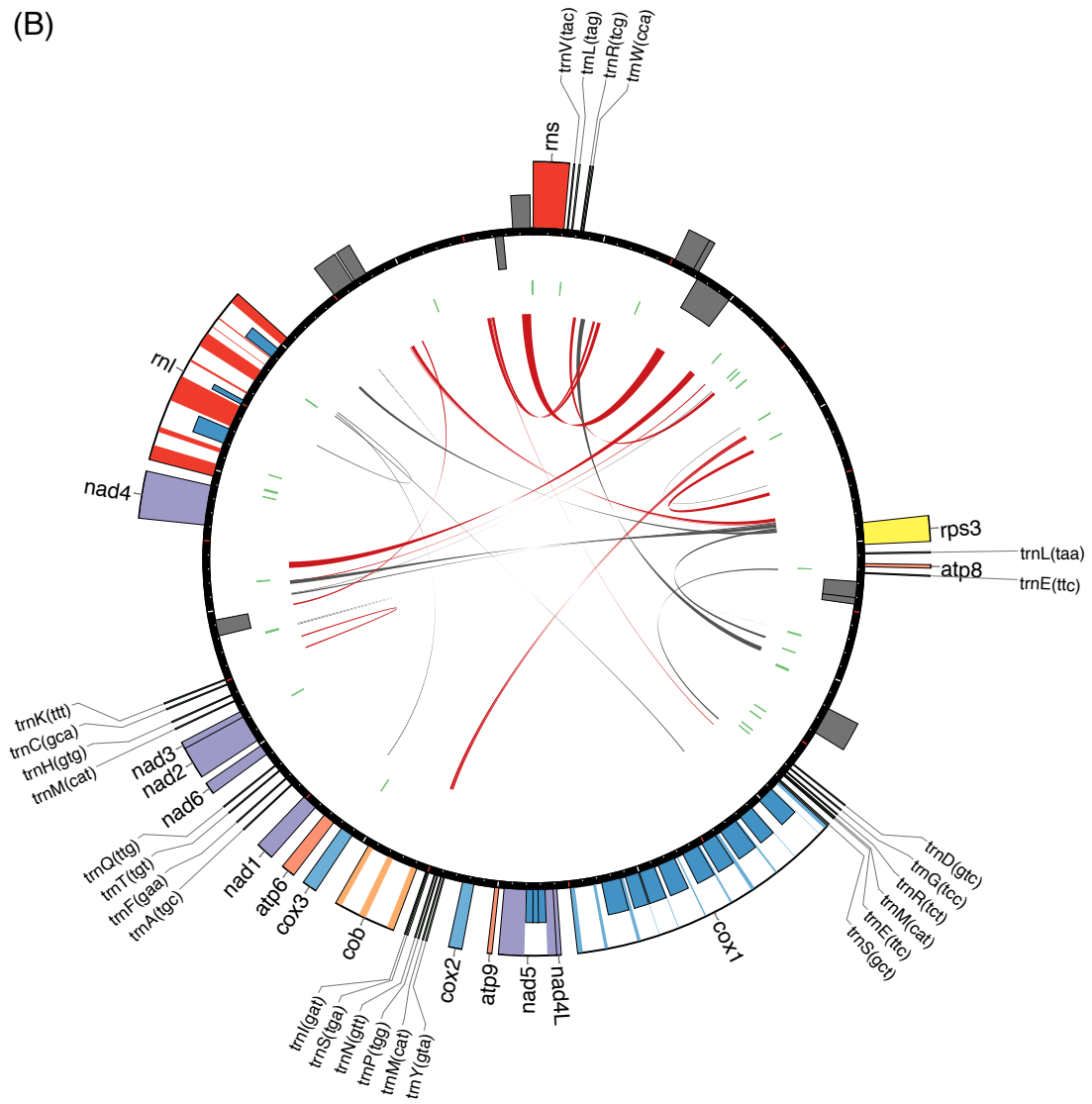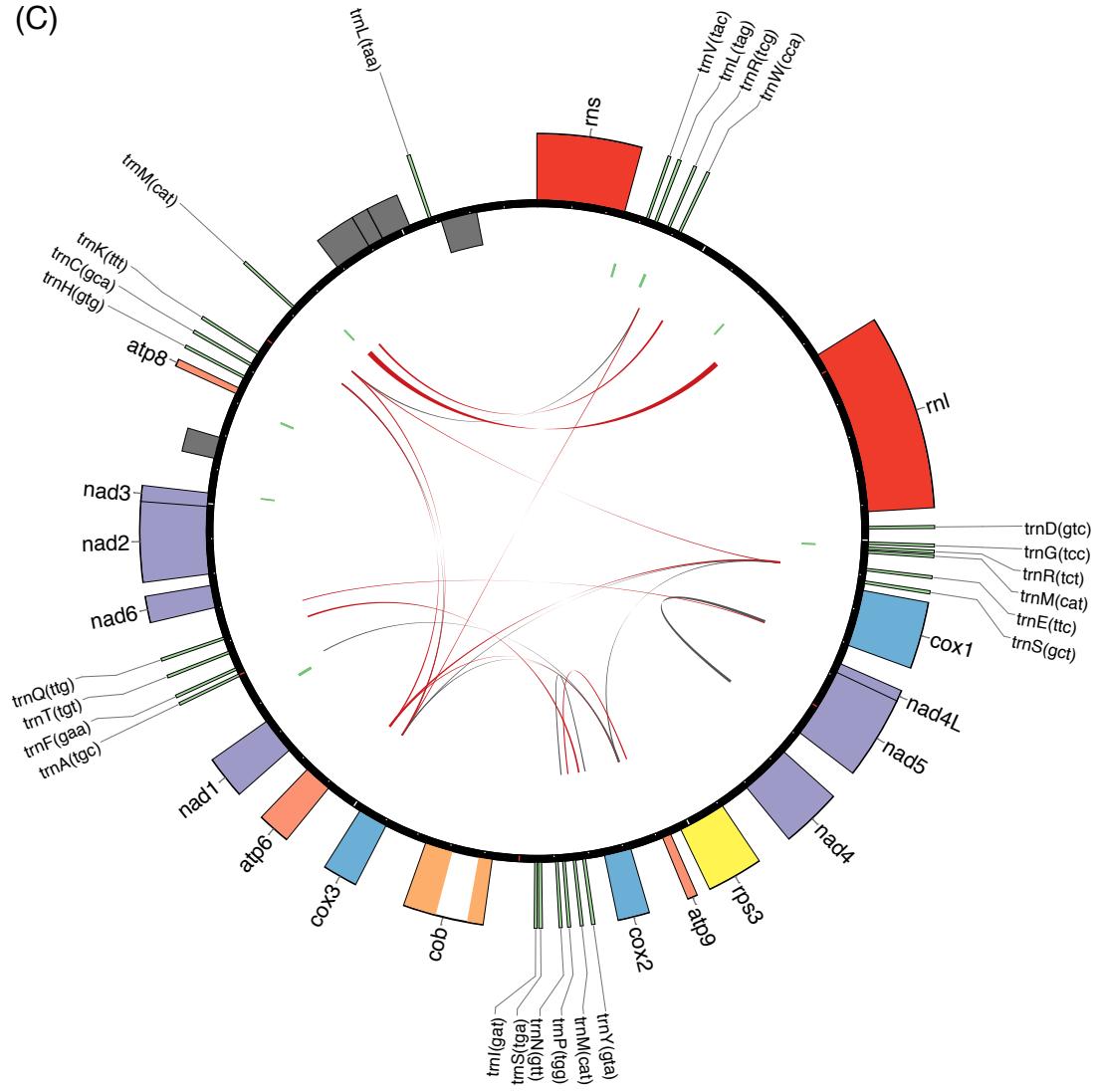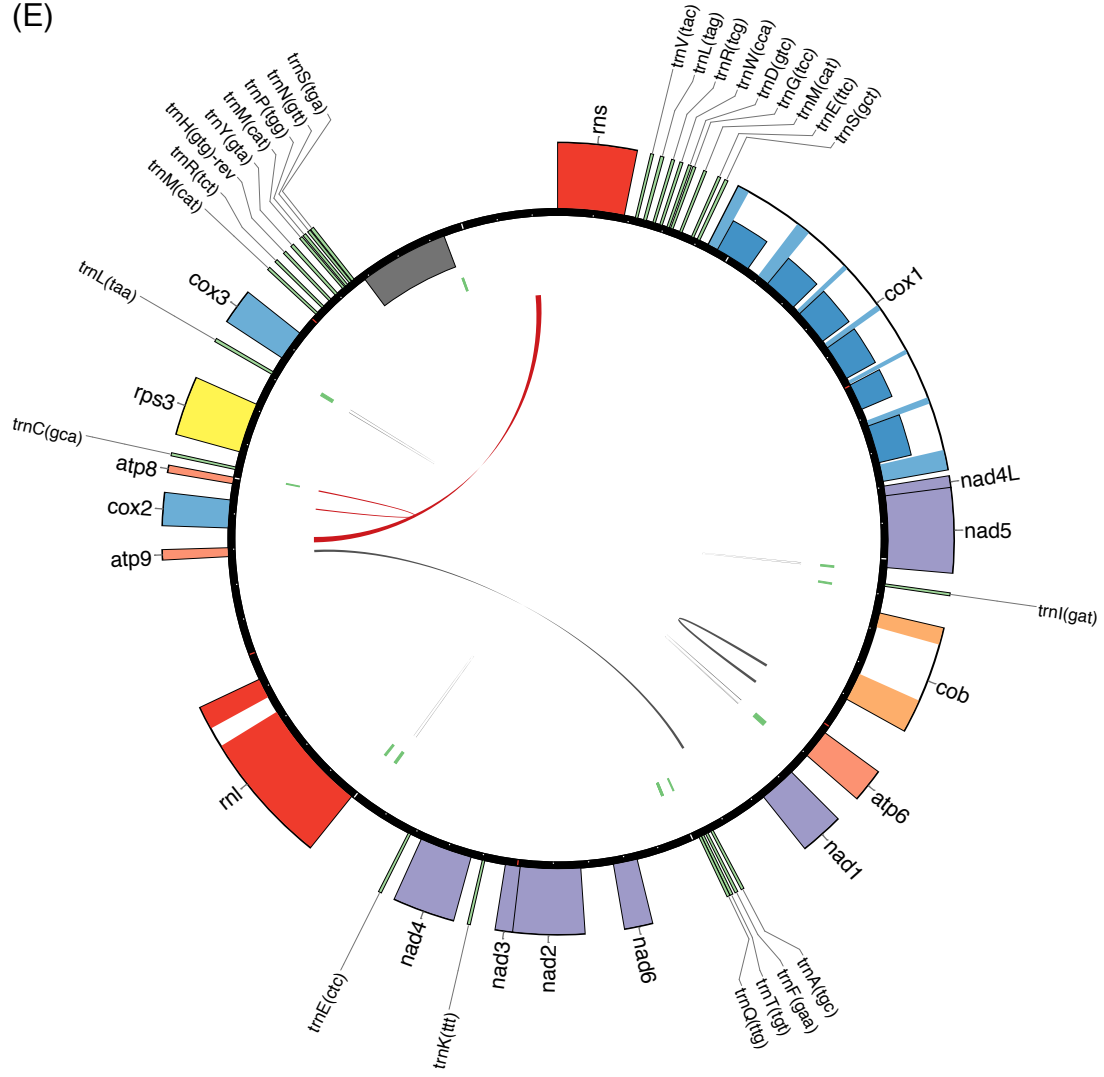
(B)

(C)

(D)

(E)

Figure S2: Scaled plots of mitogenome synteny of (A) six *Hymenochaetales* species and (B) comparation between *Phellinus noxius* and *Phellinus lamaensis.* Red arrows are mitochondrial standard genes and green tiles are tRNA genes. The red links between two mitogenomes are aligned regions with identity > 80 %. The plot was generated with genoplotR package in R.
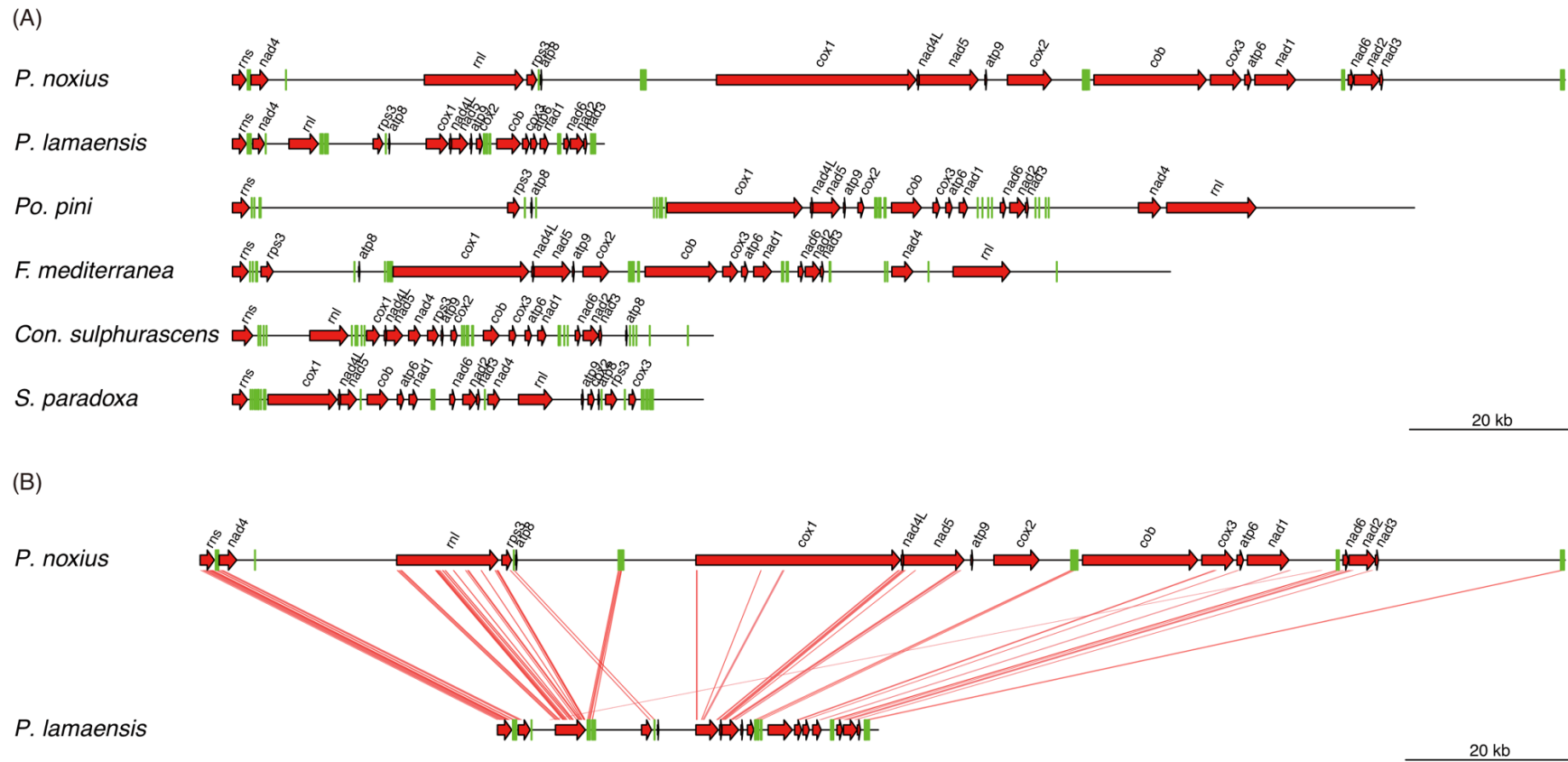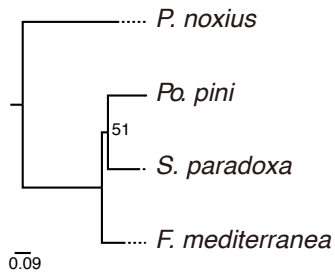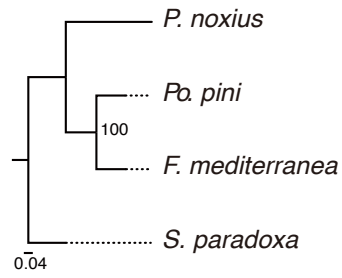
Figure S3: Intron phylogeny of 3 intron sites shared by more than 4 species. The bootstrap values were inferred with 100 replicates.

(A) cob_site5
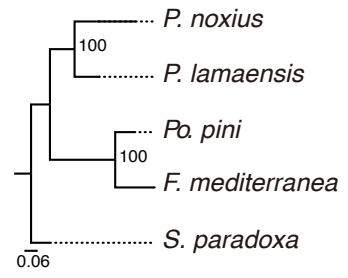
(B) cox_site10

(C) cox_site13

Figure S4: Alleles of amino acid comparing to KPN91. The x labels show gene names and positions in align protein sequences. The texts in plot are amino acid abbreviations.
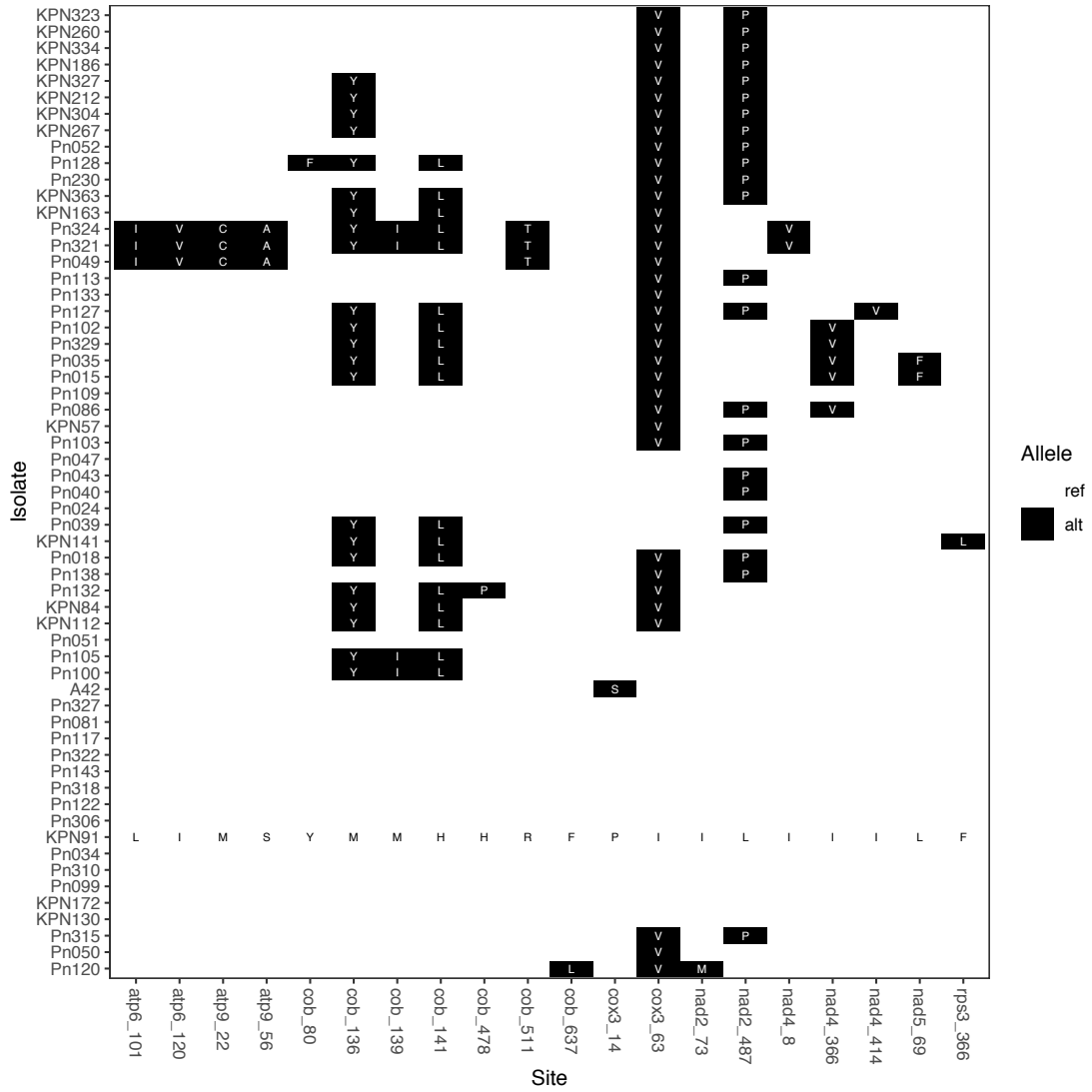
Figure S5: Length of all introns in 59 *Phellinus noxius* isolates. Length is normalized

to KPN91. Blank tiles indicate lack of intron.

Figure S6: Phylogenetic tree of concatenated intron sequences. Red dots represent
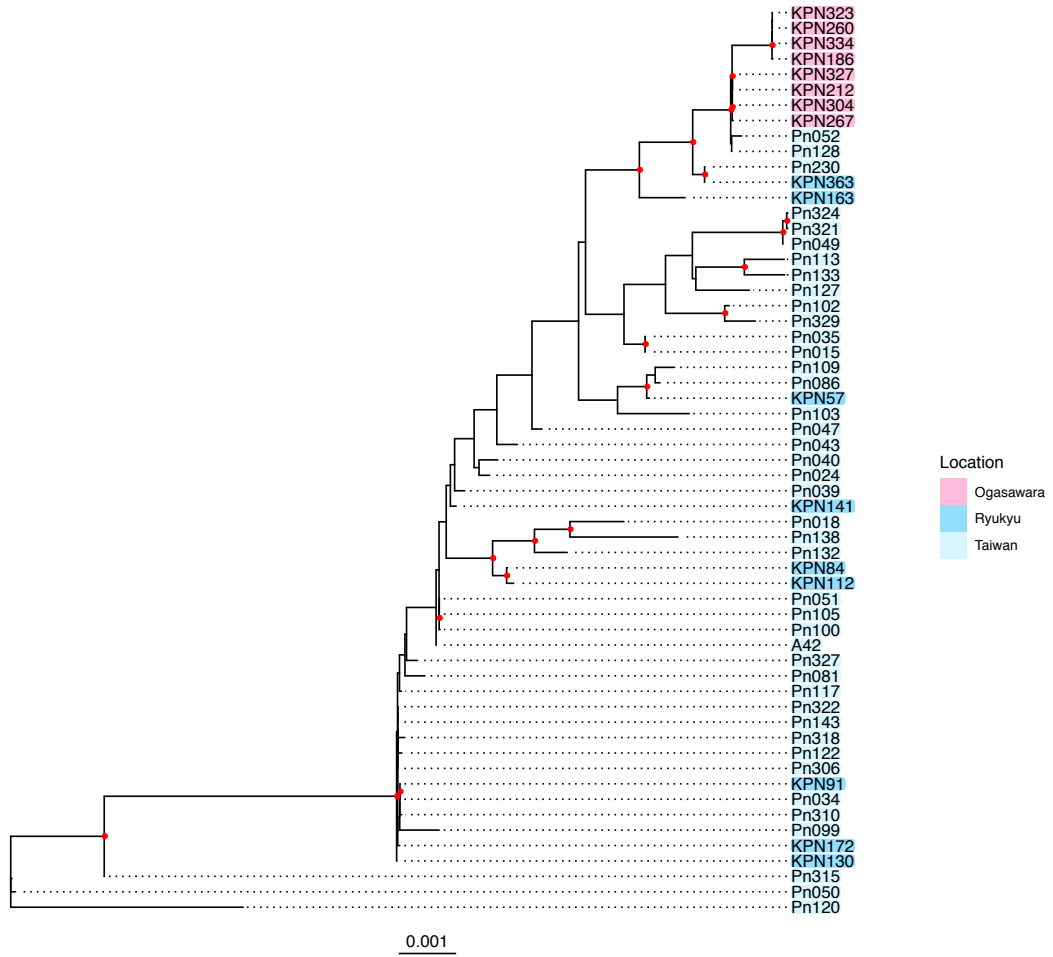
bootstrap value > 80.

Figure S7: PCR validation of intergenic rearrangement events. (A-C) Three selected regions for PCR validation. The red boxes represent the targeted synteny blocks. The small blue arrows are the approximate position of primers. Precise coordinates refer to table S4. (D) The sizes of amplified fragments of different primer combinations.
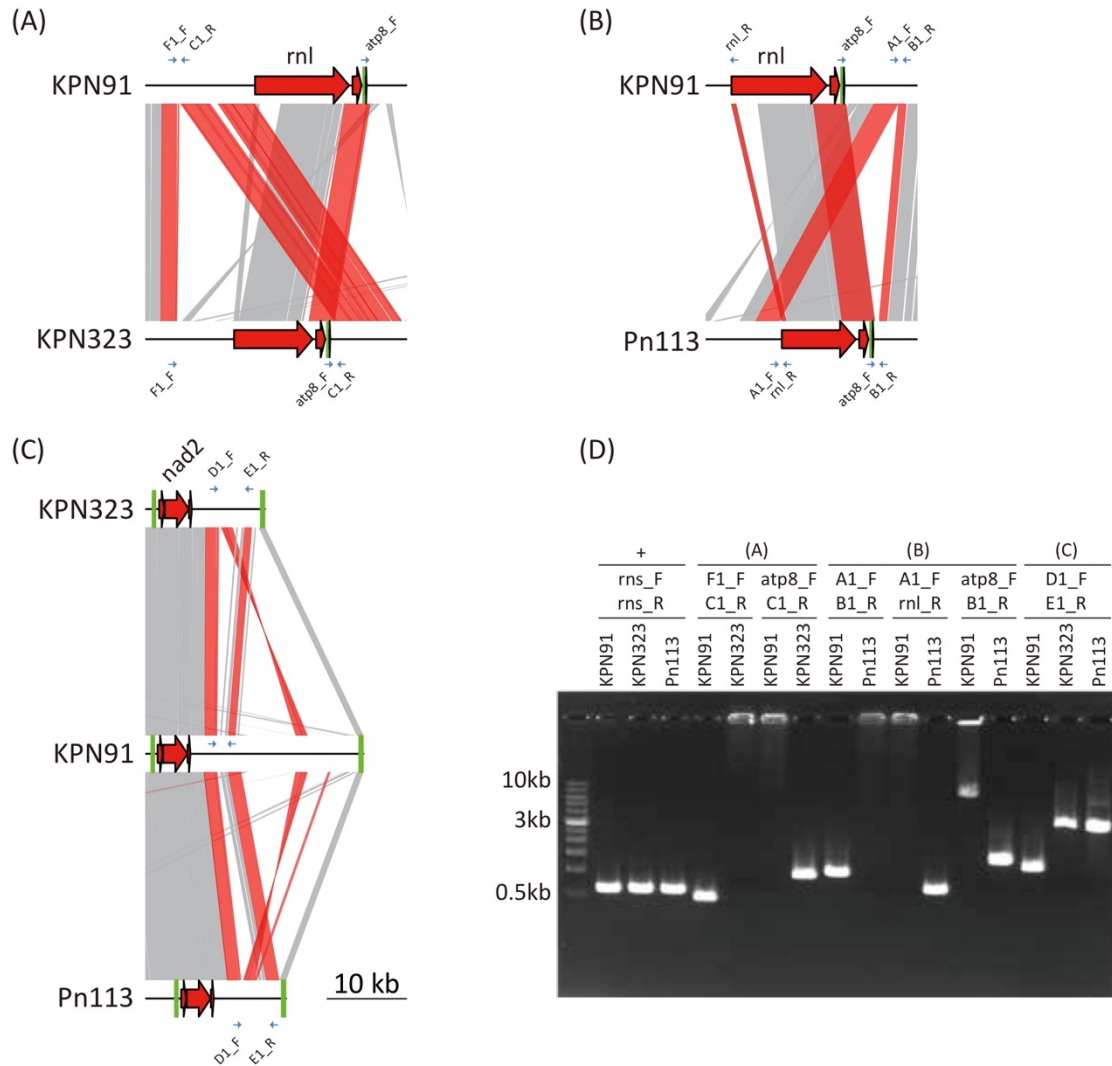
Figure S8: Example mitogenome synteny plots showing the rearrangement events. Legends refer to fig. S2. (A) Intra- and inter-rearrangements in intergenes between KPN91 (Taiwan/Ryukyu lineage) and KPN323 (Ogasawara lineage). (B) No rearrangement between KPN91 (Taiwan/Ryukyu lineage) and KPN130 (Taiwan/Ryukyu lineage). The only gap is an exclusive *rnl* intron in KPN91. (C-D) Rearrangement and indel result in alternation of a free-standing tRNA (black arrow).
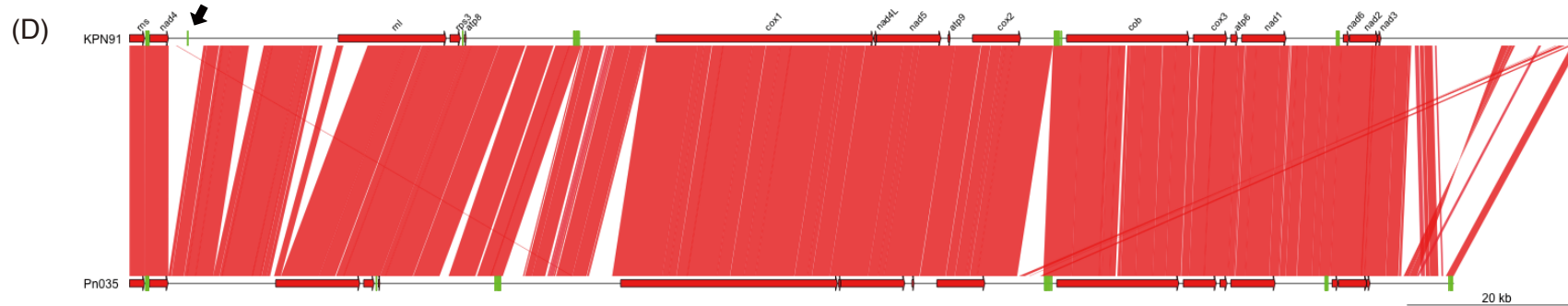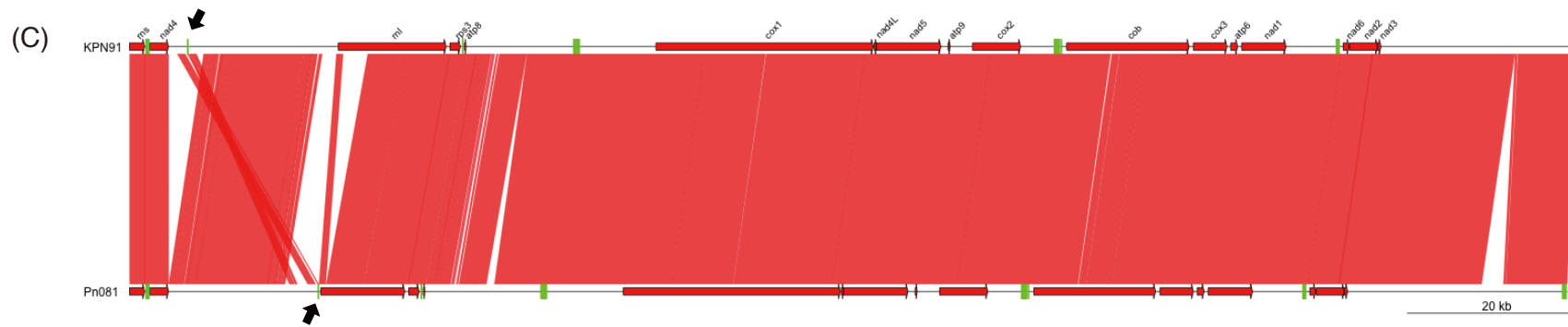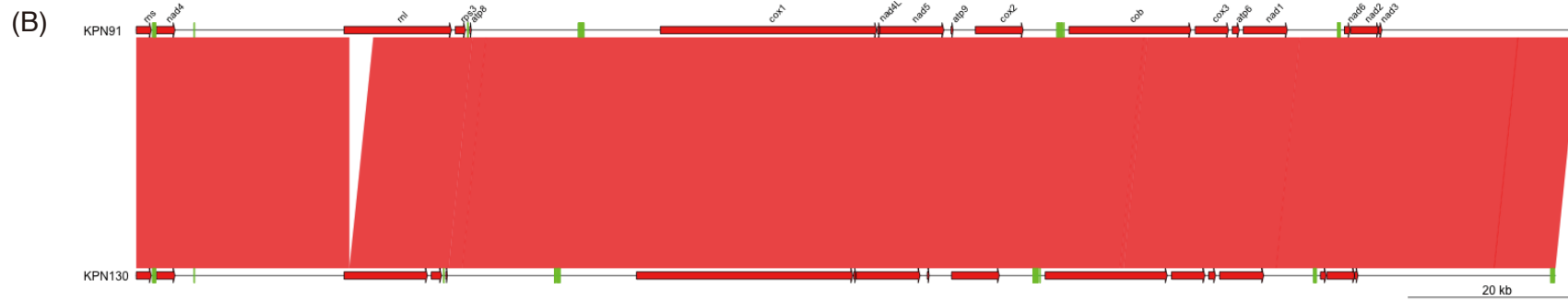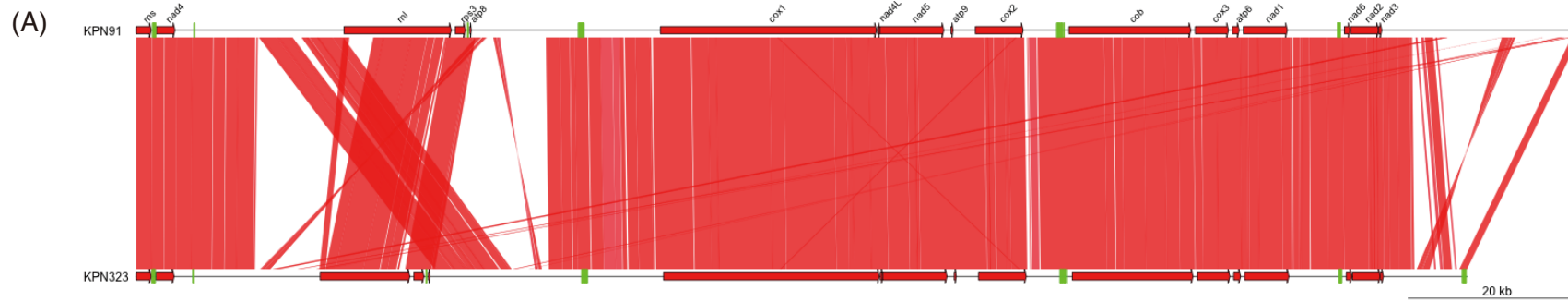
(A)

KPN91

KPN323

20 kb

(B)

KPN91

KPN130

20 kb

(C)

KPN91

Pn081

20 kb

(D)

KPN91

Pn035

20 kb

Figure S9: Pairwise identity of concatenated intronic sequences. The dendrogram is clustered using gap-compressed identities in (A) with 'hclust' function in R. The axis labels of both plots are in same order.

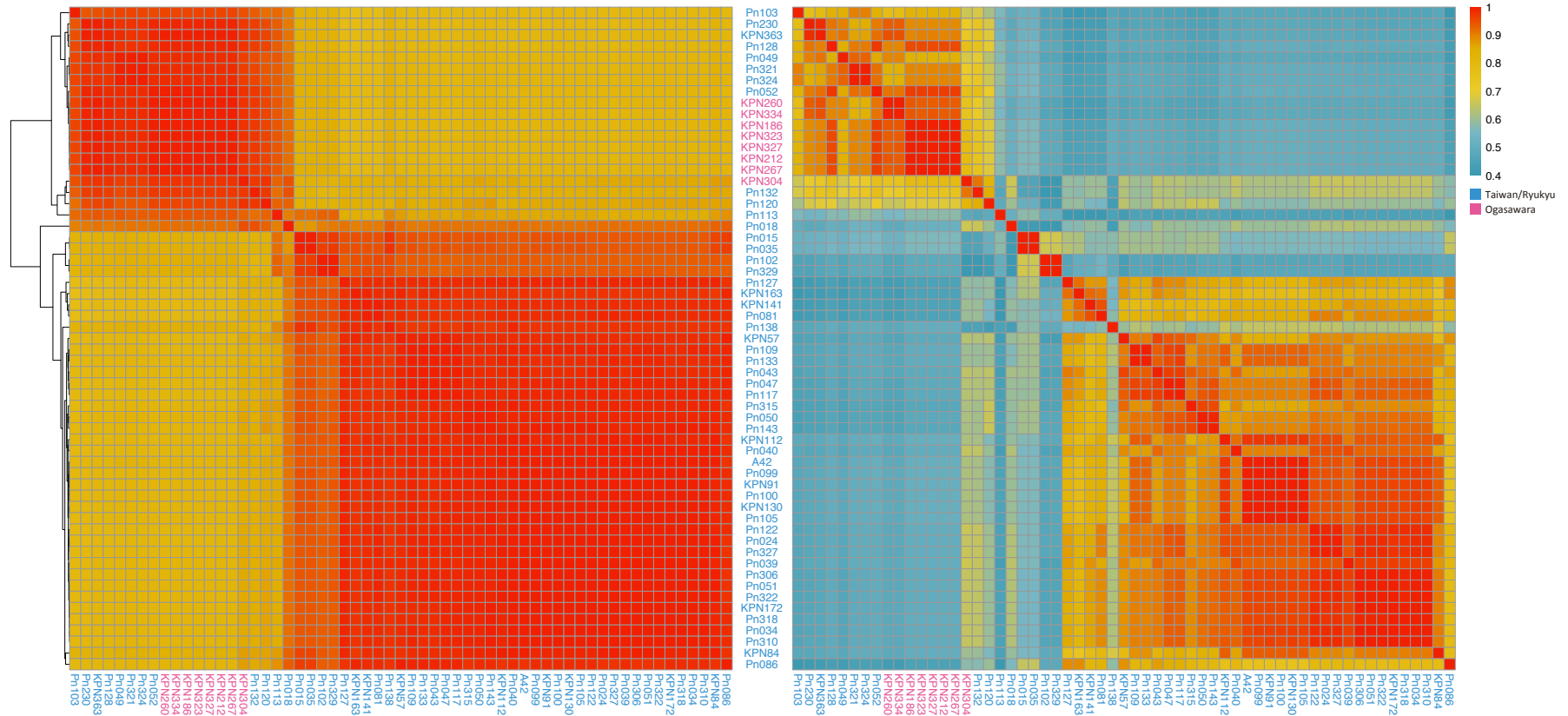(A) Gap-compressed identity

(B) Direct identity

Figure S10: Classification of intergene rearrangement events against KPN91 (Taiwan/Ryukyu lineage) and KPN323 (Ogasawara lineage). A rearrangement event is defined according to examples in figure S8. Prefixes of x labels represent intra- and inter-rearrangement, respectively; suffixes represent intergenic regions defined in fig. 1. No: no rearrangement against reference.