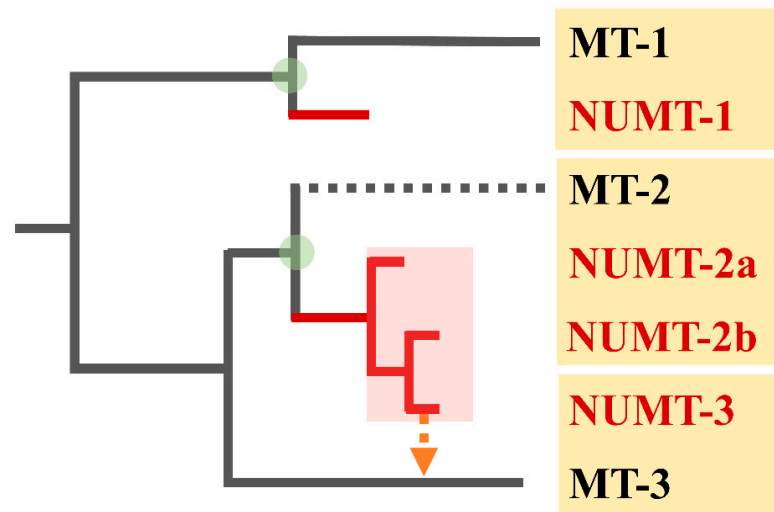


Evolutionary Histories

- transfer of mt DNA to the nucleus
- duplication of NUMT in the nucleus
- derived from the same individual
- ⇩ transfer of NUMT by interbreeding



Phylogenetic Reconstructions

- branch with a mixed evolutionary history
- extinction or unsampled of mt lineage 2
- evolutionary history of mt protein-coding gene
- evolutionary history of NUMT

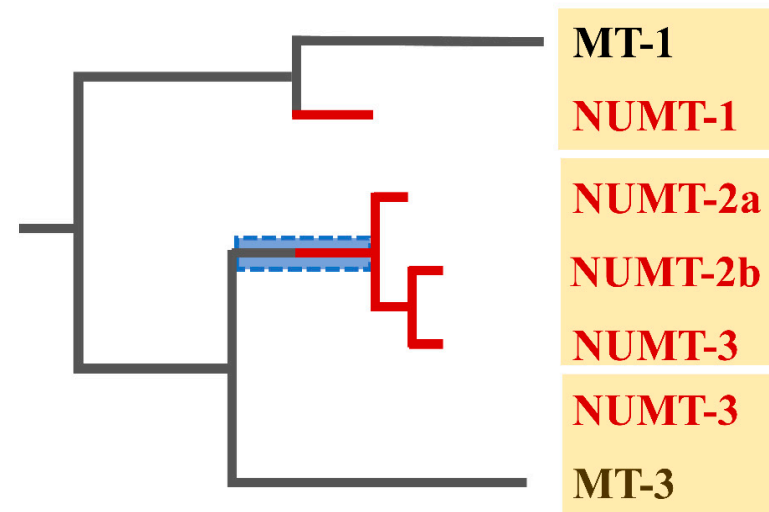
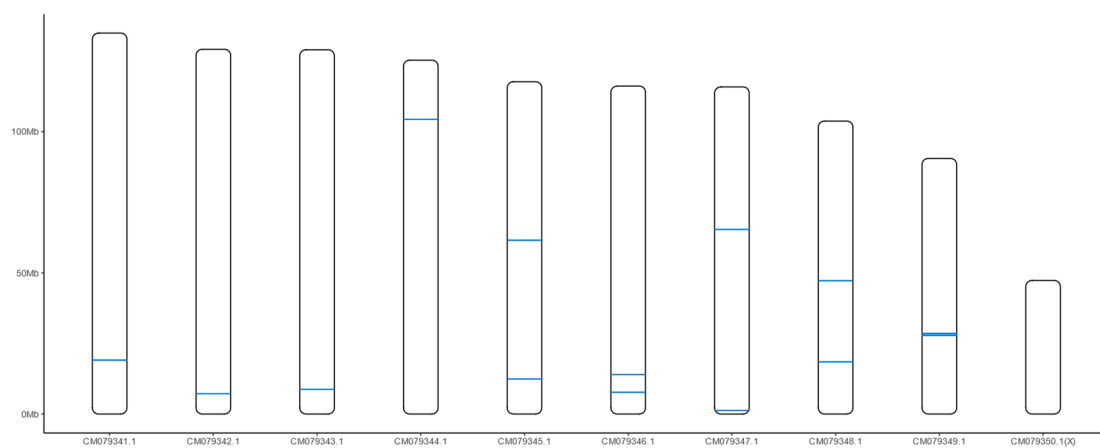
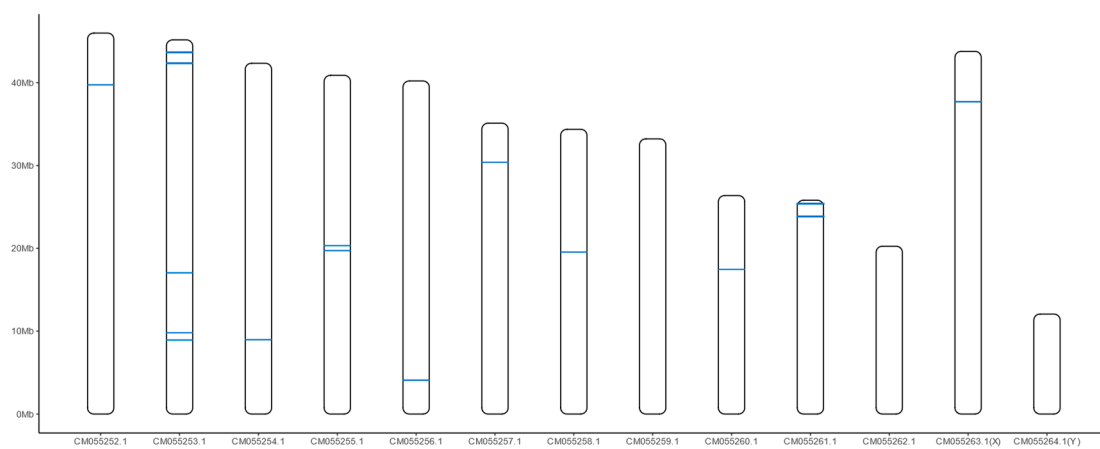


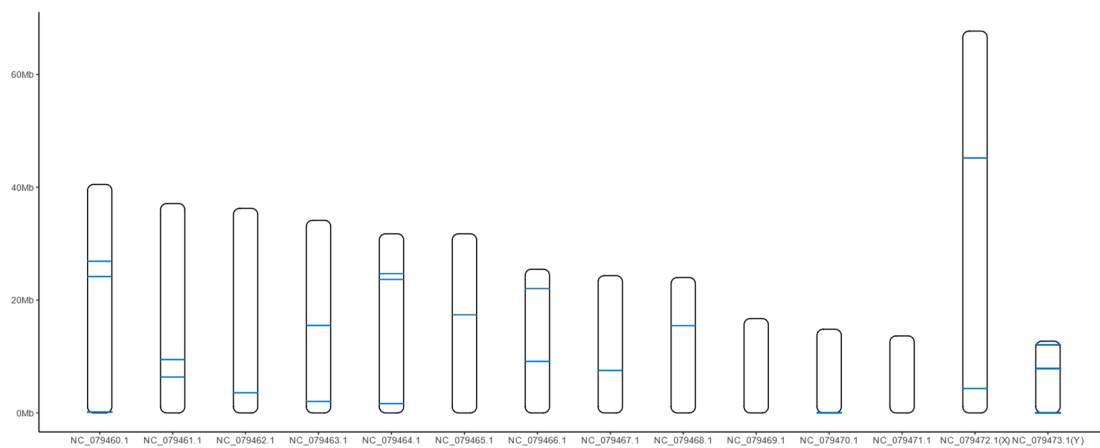
Figure S1: Dynamics of NUMTs generation and evolution along mitochondrial (mt) lineages (left) and the resulting phylogenetic reconstructions (right). Based on Baldo et al., with significant modifications by the authors. The third-codon-position bias should not be observed between the paired sequences of NUMT-2a, NUMT-2b, and NUMT-3, as well as between MT-1 and NUMT-1. However, the mutation pattern of the paired sequences from the same individual, MT-3 and NUMT-3, should exhibit the third-codon-position bias.



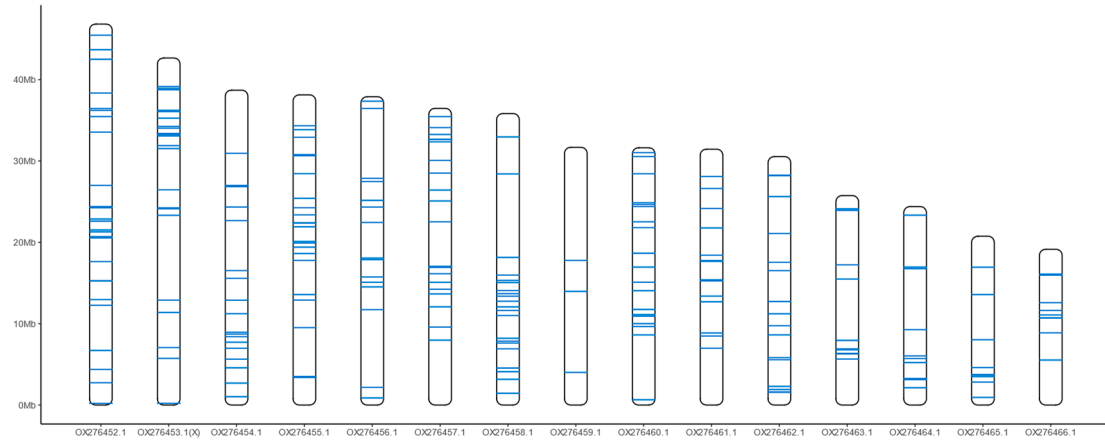
(a) *Callosobruchus maculatus*



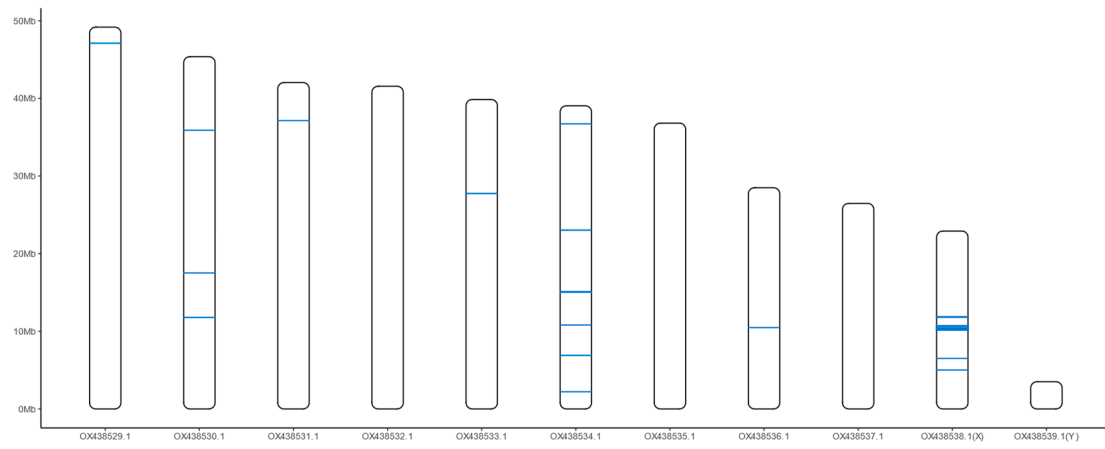
(b) *Diorhabda carinata*



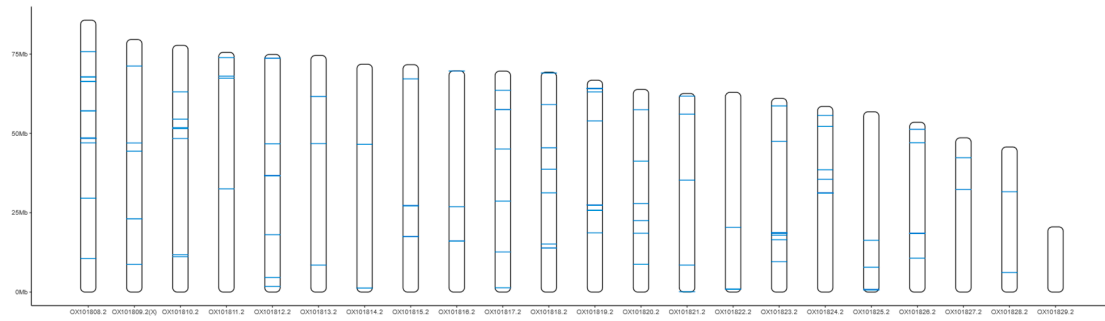
(c) *Diorhabda carinulata*



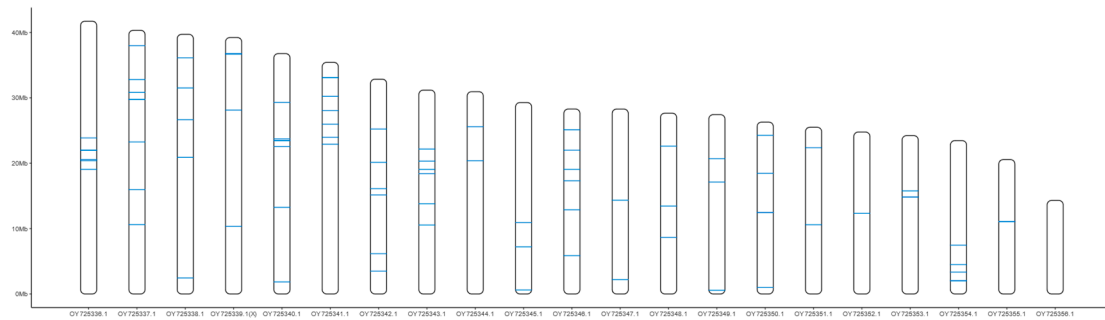
(d) *Cryptocephalus moraei*



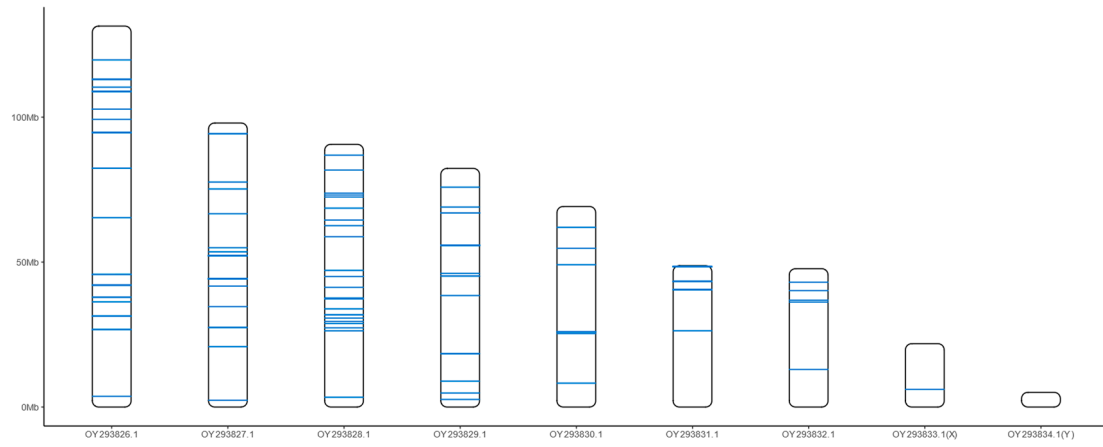
(e) *Bruchidius siliquastri*



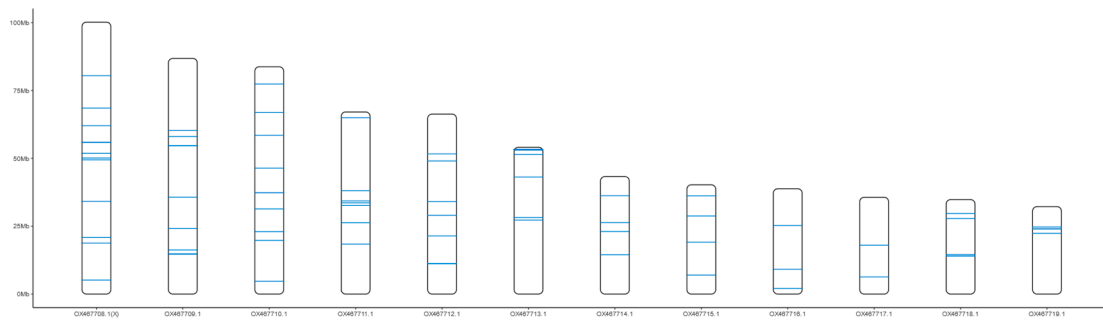
(f) *Chrysolina oricalcia*



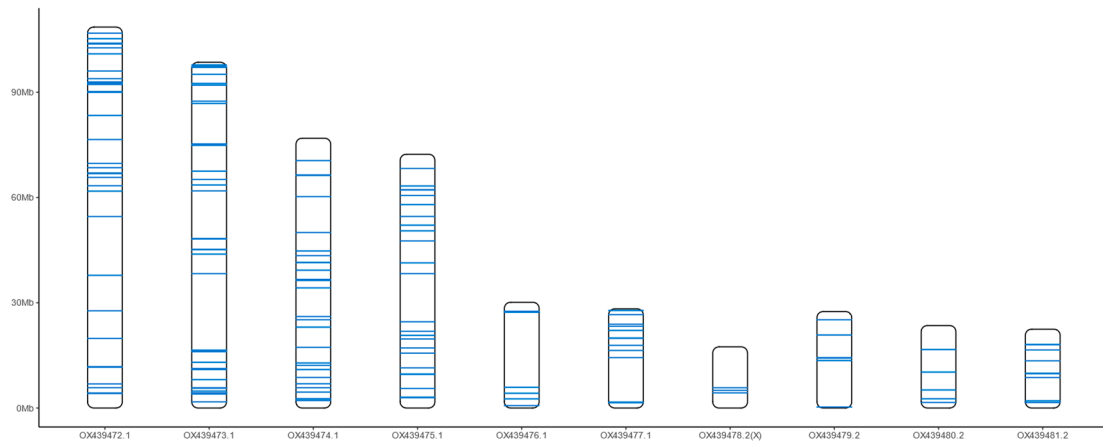
(g) *Neocrepidodera transversa*



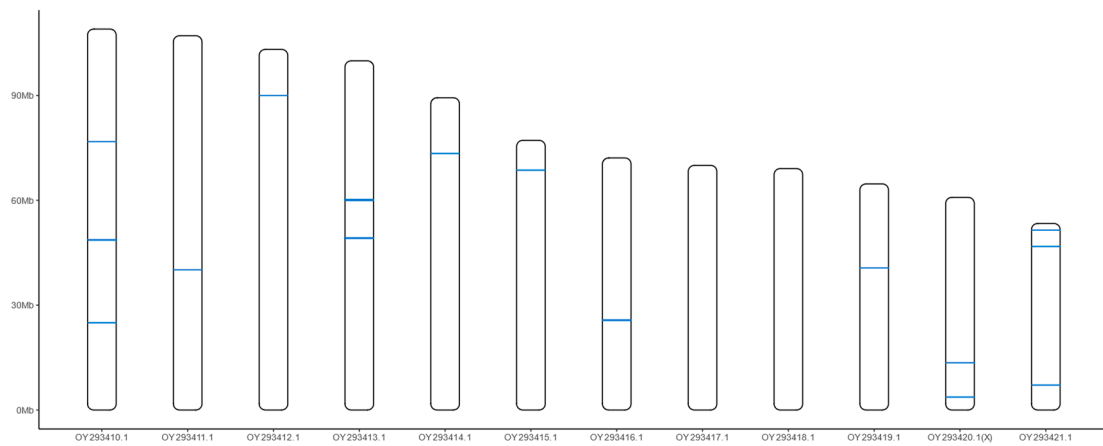
(h) *Crioceris asparagi*



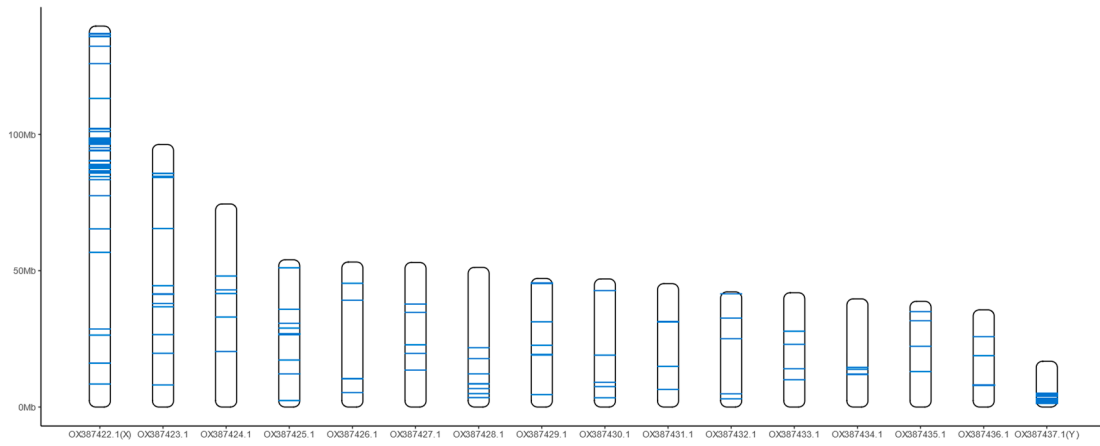
(i) *Agelastica alni*



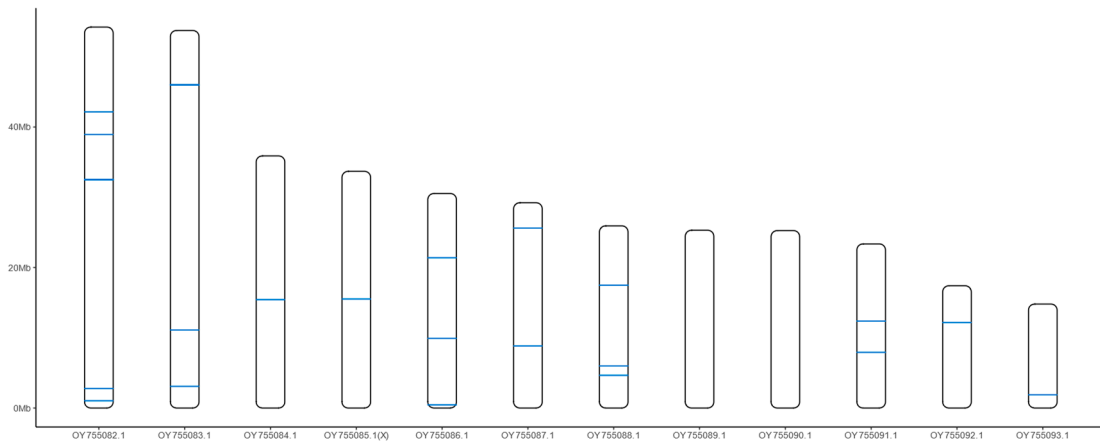
(j) *Crepidodera aurea*



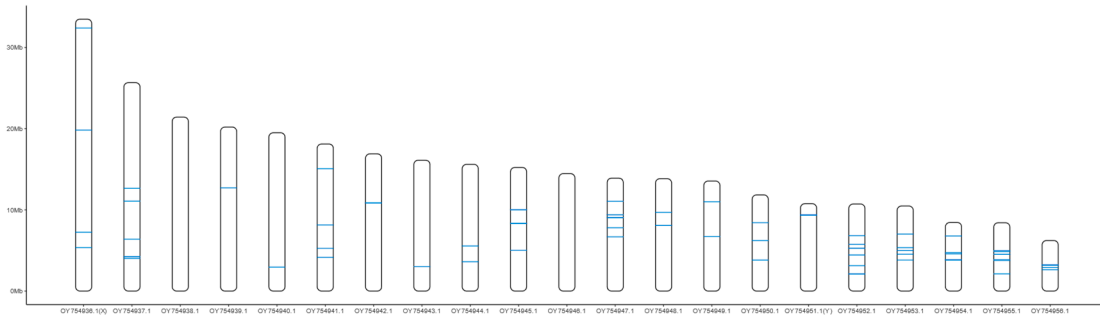
(k) *Chrysolina americana*



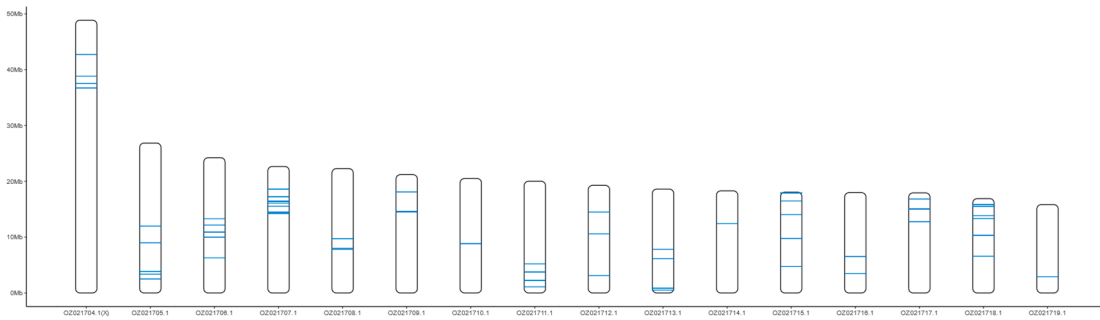
(l) *Lochmaea crataegi*



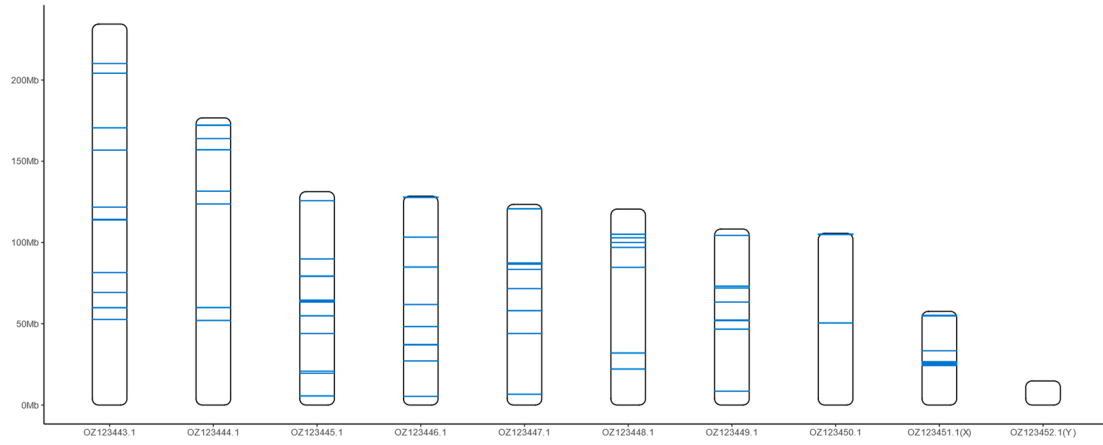
(m) *Gastrophysa polygoni*



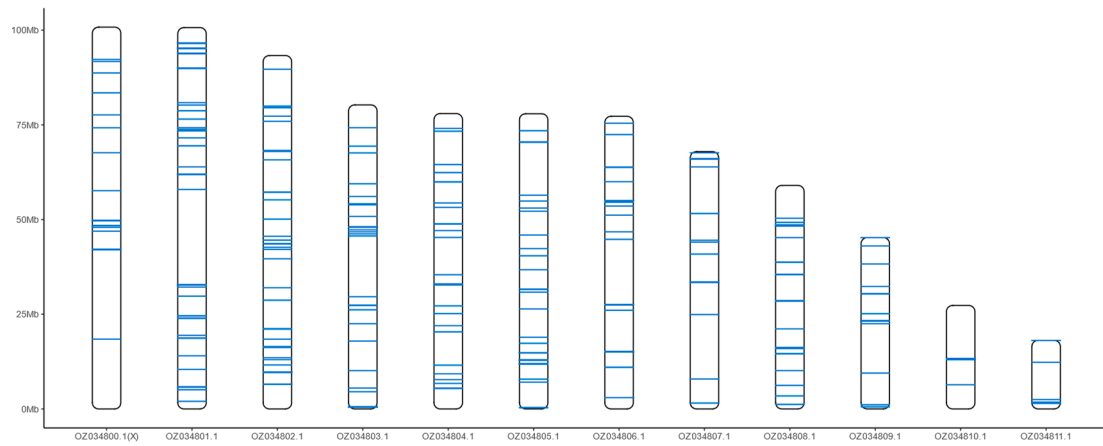
(n) *Cryptocephalus primarius*



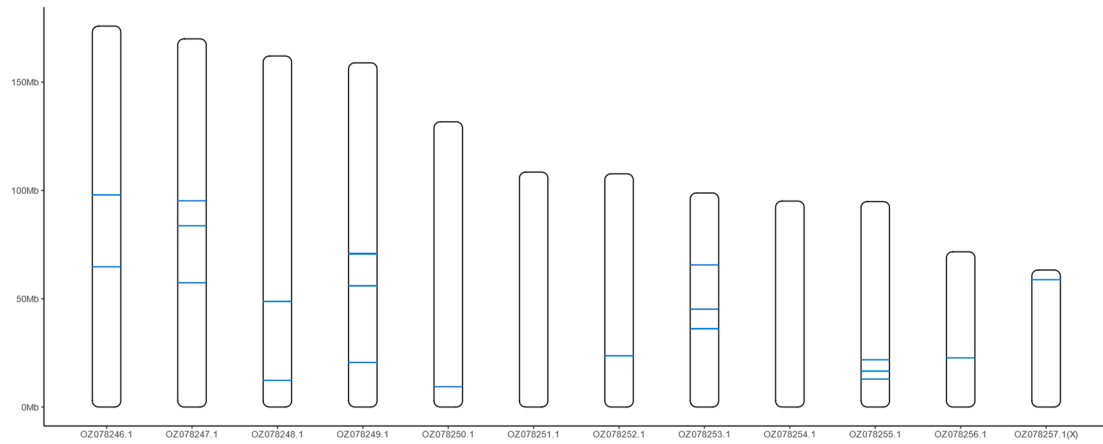
(o) *Galerucella nymphaeae*



(p) *Bruchidius varius*



(q) *Altica lythri*



(r) *Chrysolina graminis*

Figure S2: Chromosomal localization of NUMTs derived from 13 mitochondrial PCGs in Chrysomelidae species with annotated sex chromosomes. (a) *Callosobruchus maculatus*; (b) *Diorhabda carinata*; (c) *Diorhabda carinulata*; (d) *Cryptocephalus moraei*; (e) *Bruchidius siliquastri*; (f) *Chrysolina oricalcia*; (g) *Neocrepidodera transversa*; (h) *Crioceris asparagi*; (i) *Agelastica alni*; (j) *Crepidodera aurea*; (k) *Chrysolina americana*; (l) *Lochmaea crataegi*; (m) *Gastrophysa polygoni*; (n) *Cryptocephalus primaries*; (o) *Galerucella nymphalaeae*; (p) *Bruchidius varius*; (q) *Altica lythri*; (r) *Chrysolina graminis*.

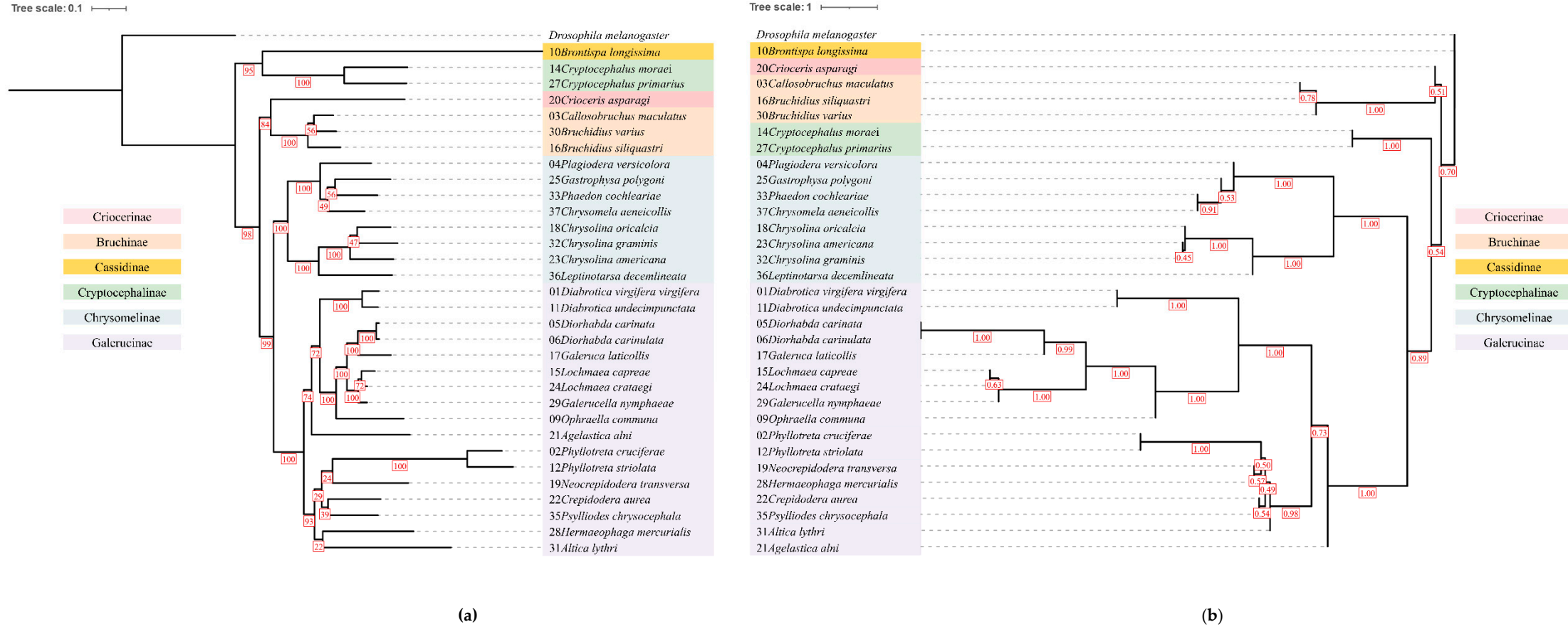
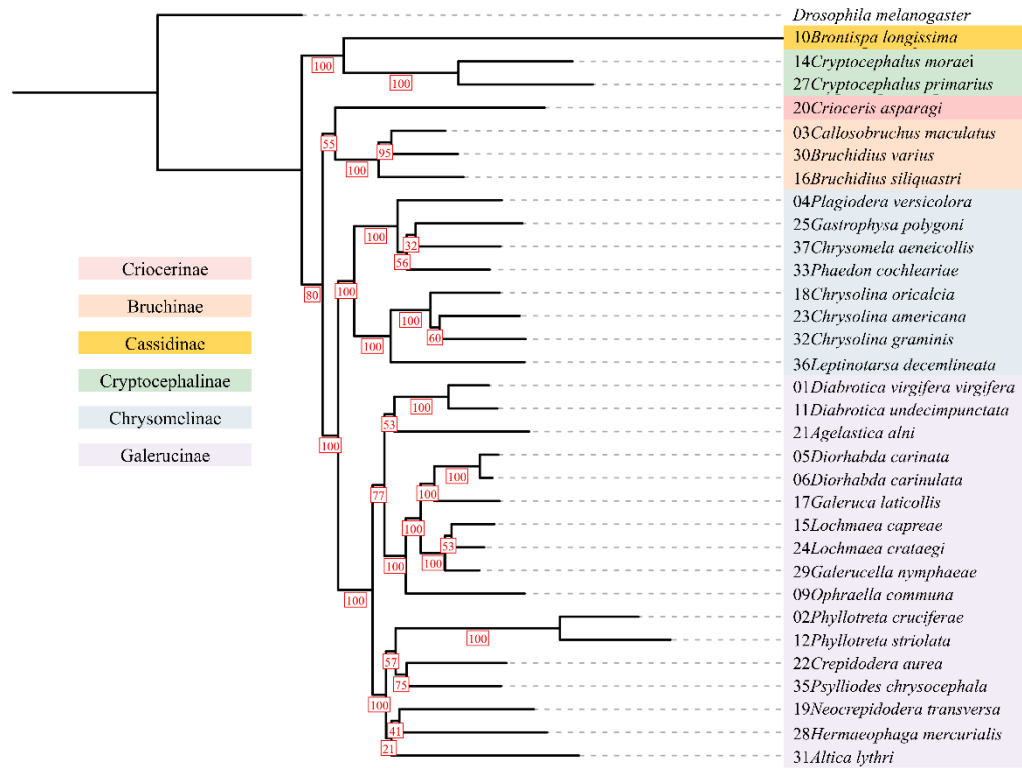


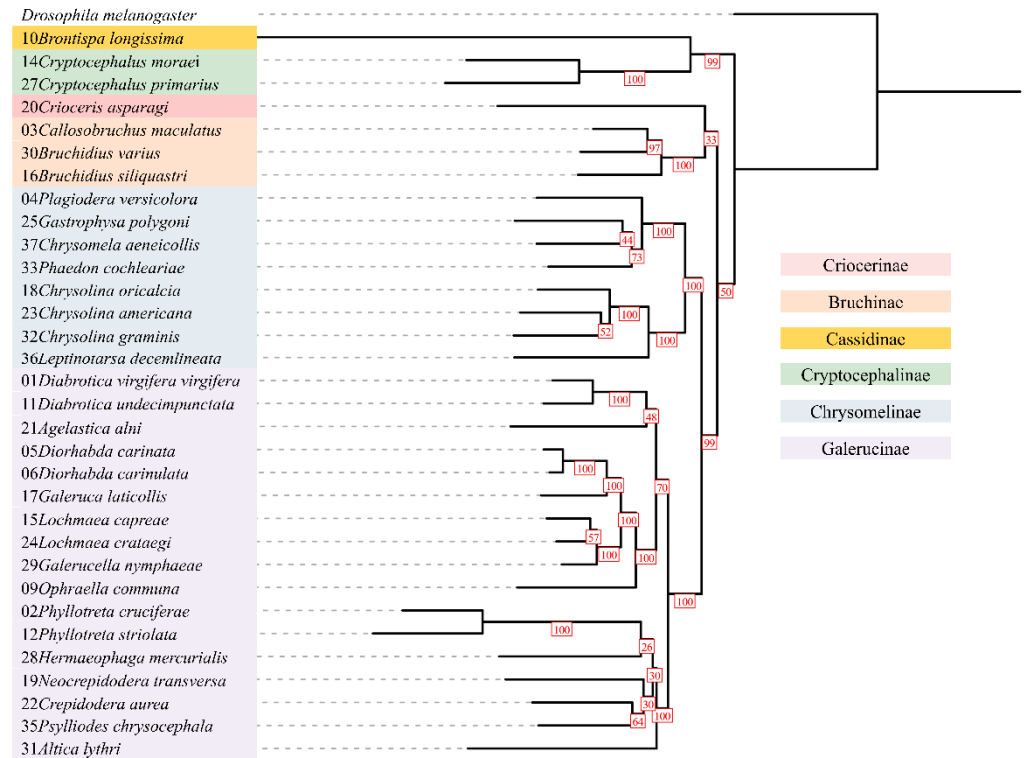
Figure S3: ML tree based on the 13 PCGs amino acid sequence (13PCGs-AA) dataset. **(a)** Supermatrix concatenation method, with red-boxed numbers indicating node support as bootstrap values; **(b)** Multispecies coalescent method, with red-boxed numbers indicating node support as local posterior probabilities.

Tree scale: 0.1



(a)

Tree scale: 0.1



(b)

Figure S5: ML tree based on two nucleotide sequence datasets. **(a)** the 13PCGs-CDS dataset; **(b)** the 11PCGs-CDS dataset. The numbers in red boxes indicate node support as bootstrap values.

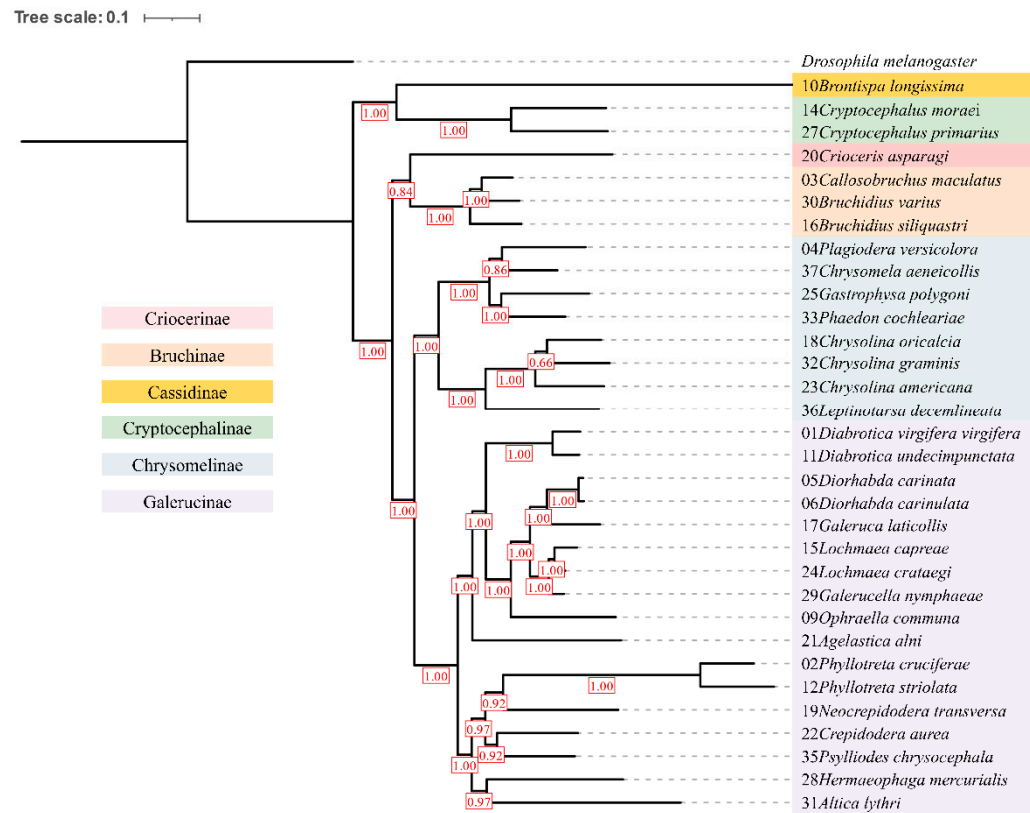
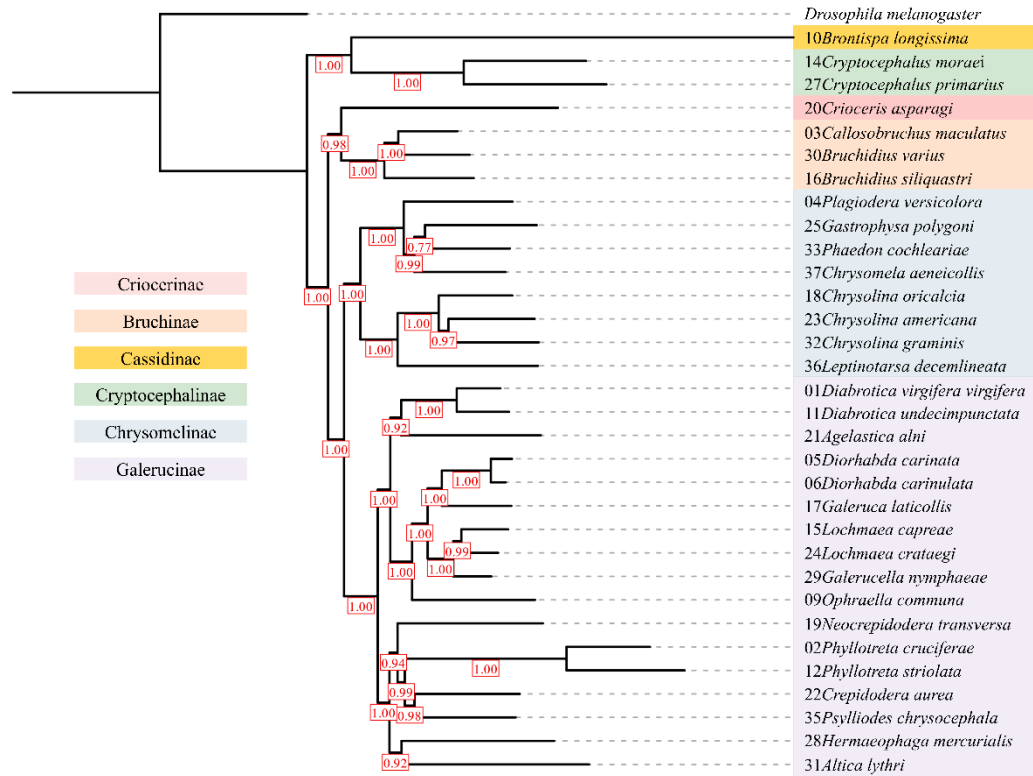


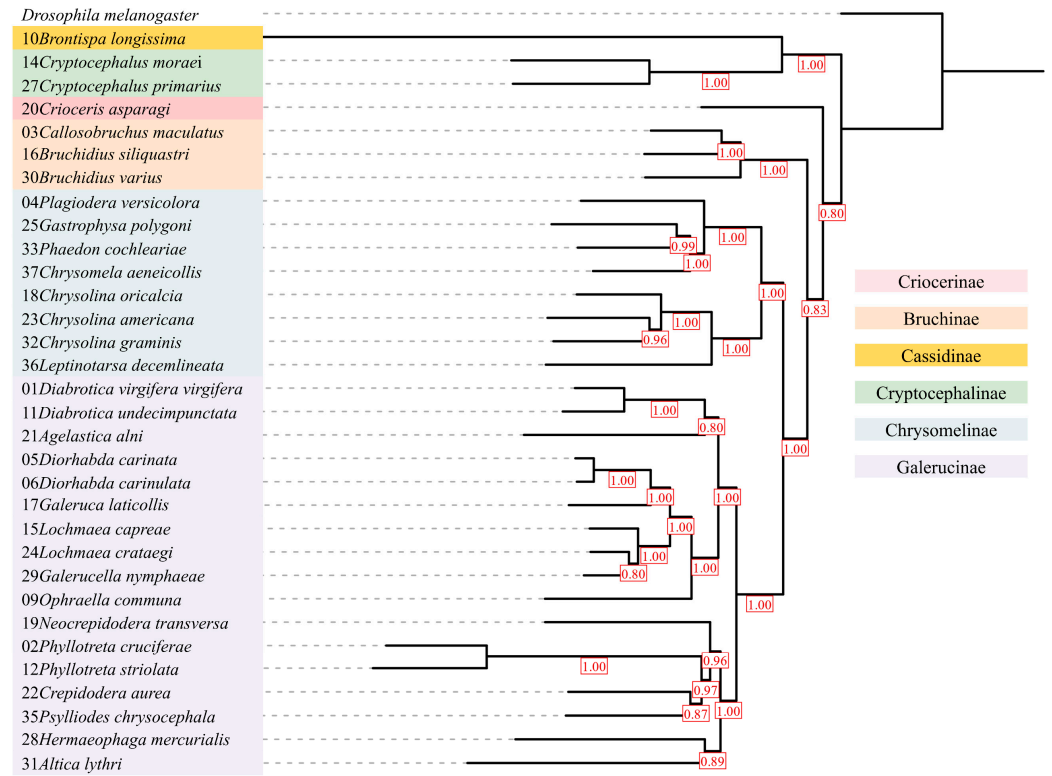
Figure S6: BI tree based on the 13PCGs-AA dataset. The numbers in red boxes indicate node support as posterior probabilities.

Tree scale: 0.1



(a)

Tree scale: 0.1



(b)

Figure S7: BI tree based on two nucleotide sequence datasets. (a) the 13PCGs-CDS dataset; (b) the 11PCGs-CDS dataset. The numbers in red boxes indicate node support as posterior probabilities.

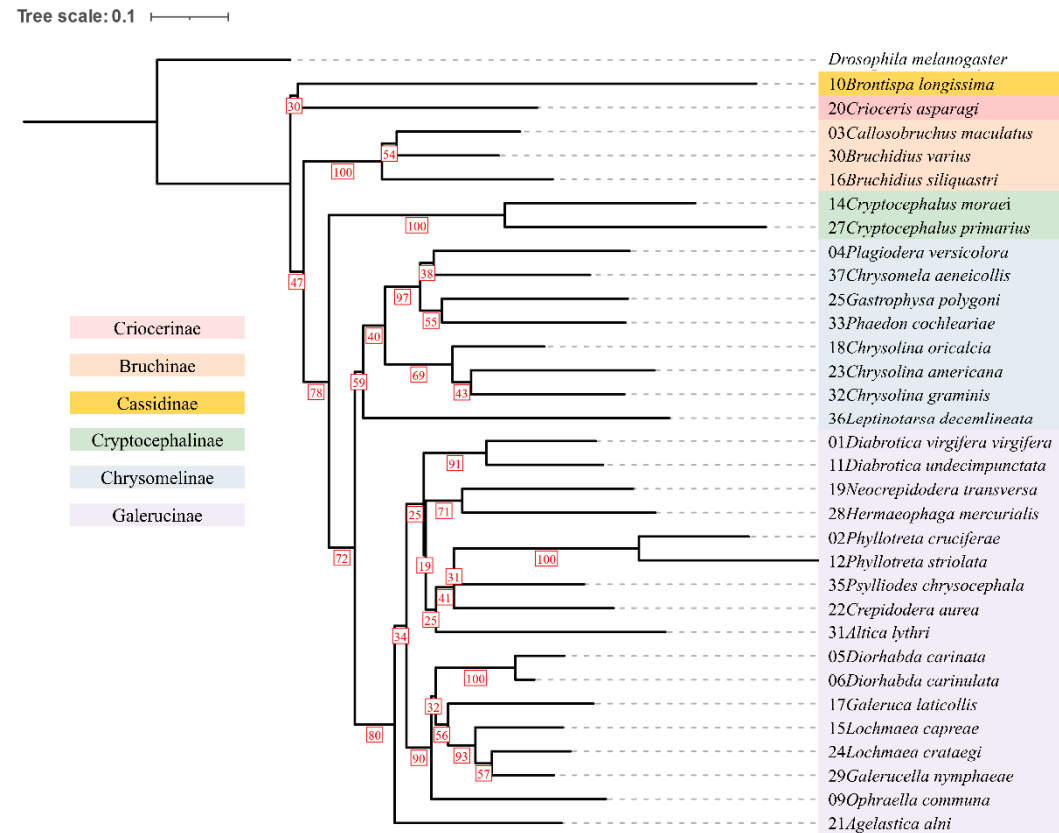


Figure S8: ML tree based on the COX1 dataset. The numbers in red boxes indicate node support as bootstrap values.

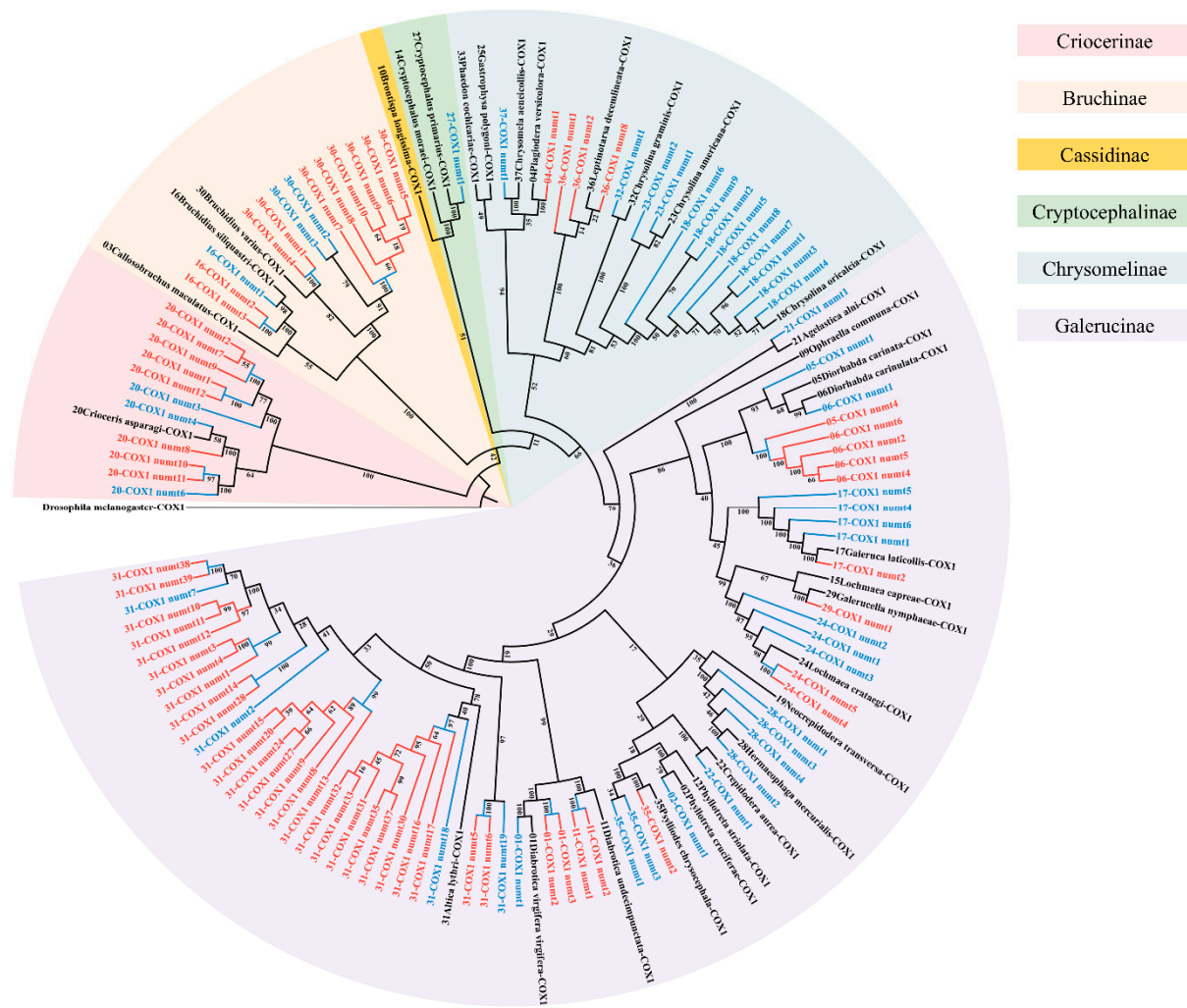


Figure S9: ML tree of the COX1 and NUMT dataset without branch lengths.