

Supplementary Information

Additional file 1:

Fig. S1. Total length of the LSC, IRs, and SSC sequences in the Ranunculeae plastomes examined in this study. IR, inverted repeats; SSC, small single-copy; LSC, large single-copy.

Fig. S2. Plastomes of seven species from four genera of Ranunculeae. (a) *Ficaria verna*, (b) *Halerpestes sarmentosa*, (c) *Oxygraphis glacialis*, (d) four species of *Ranunculus*. The genes inside and outside of the circle are transcribed in clockwise and counterclockwise directions, respectively. Genes belonging to different functional groups are shown in different colors. The thick lines indicate the extent of IR_A and IR_B that separate the genomes into SSC and LSC regions. IR, inverted repeats; SSC, small single-copy; LSC, large single-copy.

Fig. S3. Scatter plot of GC3s contents of protein-coding genes of Ranunculeae plastomes. GC3s, G or C in the third codon positions.

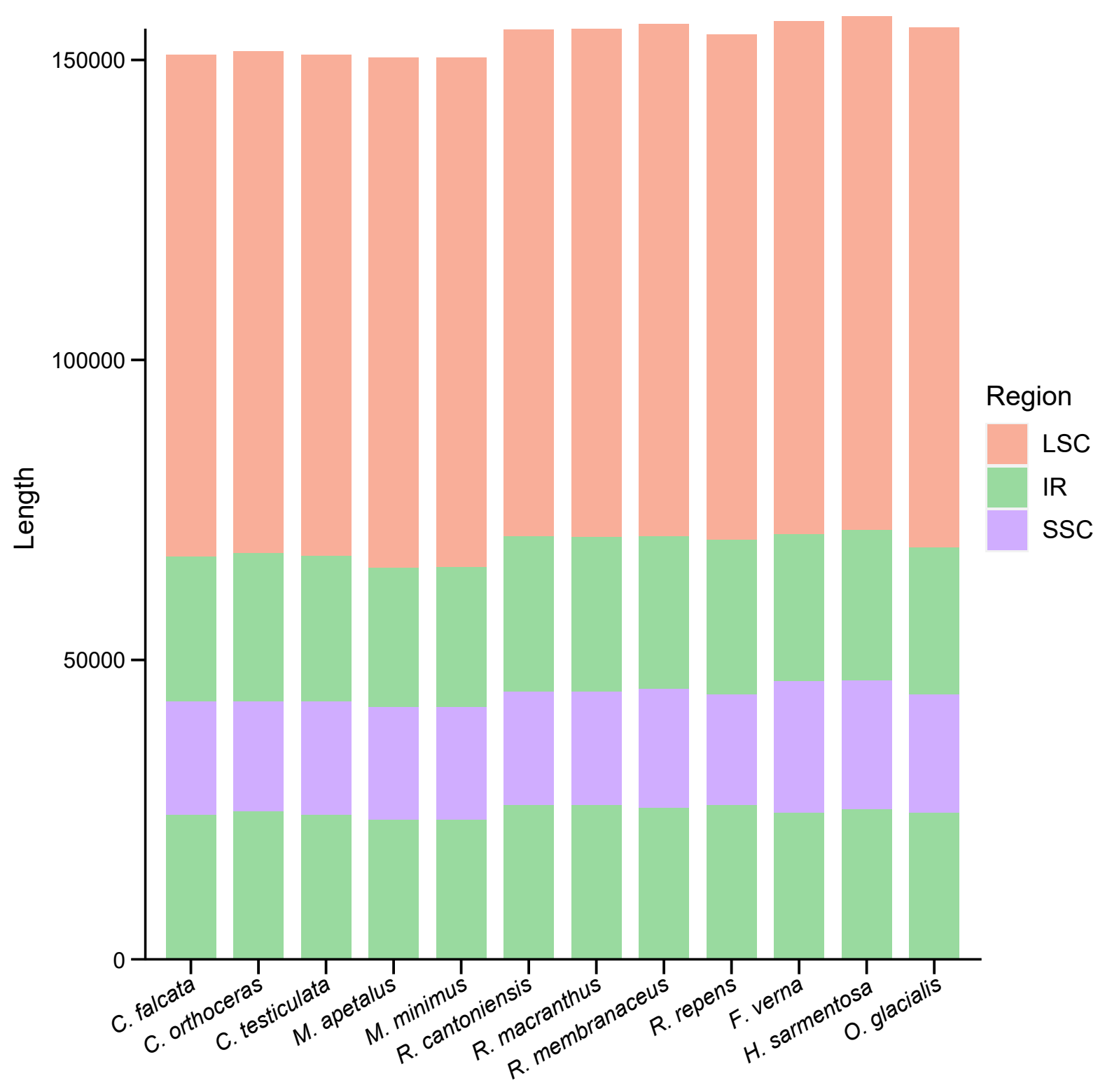
Fig. S4. The plastid phylogenomic tree of Ranunculeae. Maximum likelihood bootstrap support values are shown above the branches.

Fig. S5. Comparison of the LSC, IRs, and SSC region boundaries of plastomes within Ranunculeae. IR, inverted repeats; SSC, small single-copy; LSC, large single-copy.

Fig. S6. Character reconstructions for amino acid sites of the eleven genes under positive selection. Amino acid sites are listed in Table S7 in details. Character states

of amino acid sequences were coded A, B, C, and D, as referred to Table S7. Genes positively selected in *Ceratocephala* and *Myosurus* are in red; genes positively selected in *Ceratocephala* are in blue; genes positively selected in *Myosurus* are in green.

Fig. S7. Changes through time plots generated from sampled stochastic character maps for the eleven genes under positive selection. For each gene the mean rate of changes per unit time is shown. Gene names are given above the plots and their colors are the same with those in Fig. S6. The five dashed lines in each graph represented 34, 23.03, 17, 13.9 and 3.3 Ma, respectively; the colored line indicates the significant rate change point. Asterisk indicates a significant difference ($p < 0.05$; see Table S8 for details).



Ficaria verna
chloroplast genome
156,439 bp

The circular map displays the following genes and features:

- LSC (Large Single Copy) Region:** Contains most of the large genes, including *rbcL*, *psaA-psaJ*, *ycf1*, *ndhA-ndhG*, *atpA-atpH*, *accD*, *psaI-psaN*, *psaB-psaF*, *psaC-psaE*, *psaJ-psaK*, *psaM-psaX*, *psaY-psaZ*, *psaW-psaV*, *psaU-psaT*, *psaS-psaR*, *psaQ-psaP*, *psaO-psaN*, *psaM-psaL*, *psaK-psaJ*, *psaI-psaH*, *psaG-psaF*, *psaE-psaD*, *psaC-psaB*, *psaA-psaZ*, *psaY-psaX*, *psaW-psaV*, *psaU-psaT*, *psaS-psaR*, *psaQ-psaP*, *psaO-psaN*, *psaM-psaL*, *psaK-psaJ*, *psaI-psaH*, *psaG-psaF*, *psaE-psaD*, *psaC-psaB*, *psaA-psaZ*.
- SSC (Small Single Copy) Region:** Contains smaller genes like *ycf2*, *ycf1*, *ycf2*, *ycf3*, *ycf4*, *ycf5*, *ycf6*, *ycf7*, *ycf8*, *ycf9*, *ycf10*, *ycf11*, *ycf12*, *ycf13*, *ycf14*, *ycf15*, *ycf16*, *ycf17*, *ycf18*, *ycf19*, *ycf20*, *ycf21*, *ycf22*, *ycf23*, *ycf24*, *ycf25*, *ycf26*, *ycf27*, *ycf28*, *ycf29*, *ycf30*, *ycf31*, *ycf32*, *ycf33*, *ycf34*, *ycf35*, *ycf36*, *ycf37*, *ycf38*, *ycf39*, *ycf40*, *ycf41*, *ycf42*, *ycf43*, *ycf44*, *ycf45*, *ycf46*, *ycf47*, *ycf48*, *ycf49*, *ycf50*, *ycf51*, *ycf52*, *ycf53*, *ycf54*, *ycf55*, *ycf56*, *ycf57*, *ycf58*, *ycf59*, *ycf60*, *ycf61*, *ycf62*, *ycf63*, *ycf64*, *ycf65*, *ycf66*, *ycf67*, *ycf68*, *ycf69*, *ycf70*, *ycf71*, *ycf72*, *ycf73*, *ycf74*, *ycf75*, *ycf76*, *ycf77*, *ycf78*, *ycf79*, *ycf80*, *ycf81*, *ycf82*, *ycf83*, *ycf84*, *ycf85*, *ycf86*, *ycf87*, *ycf88*, *ycf89*, *ycf90*, *ycf91*, *ycf92*, *ycf93*, *ycf94*, *ycf95*, *ycf96*, *ycf97*, *ycf98*, *ycf99*, *ycf100*.
- IR (Inverted Repeat) Regions:** Located between LSC and SSC, containing inverted copies of some genes.

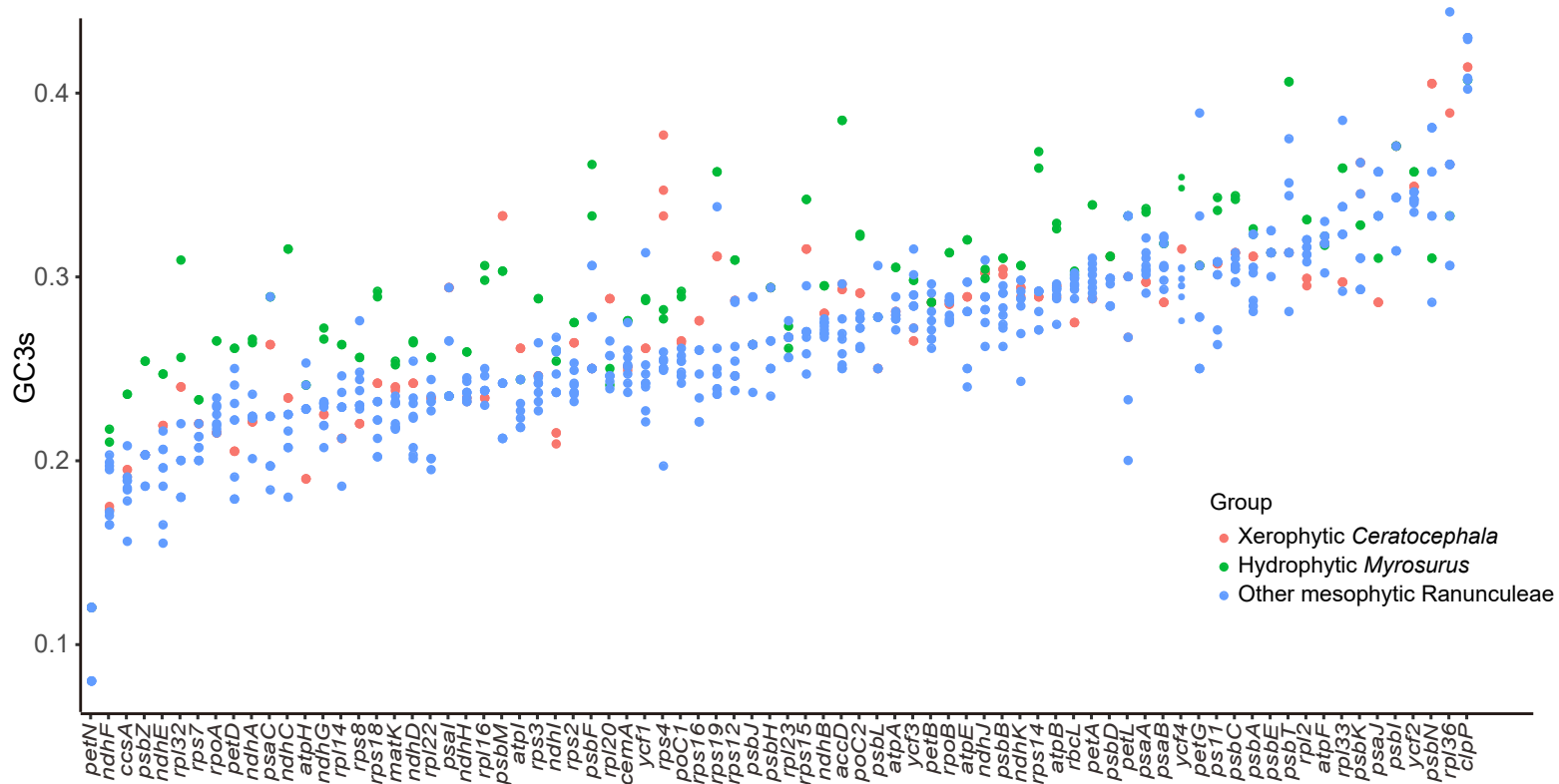
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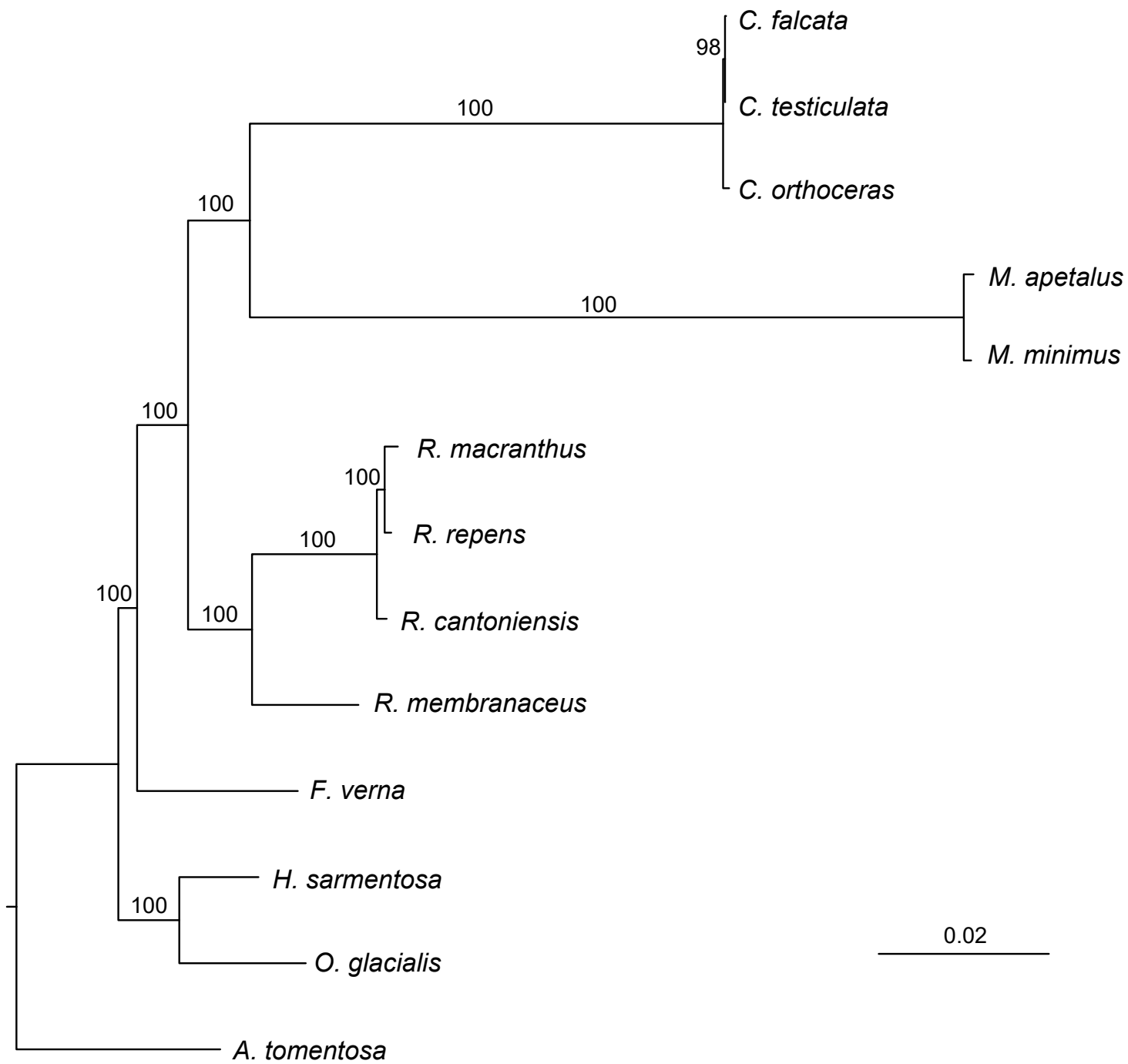
Oxygraphis glacialis
chloroplast genome
155,434 bp

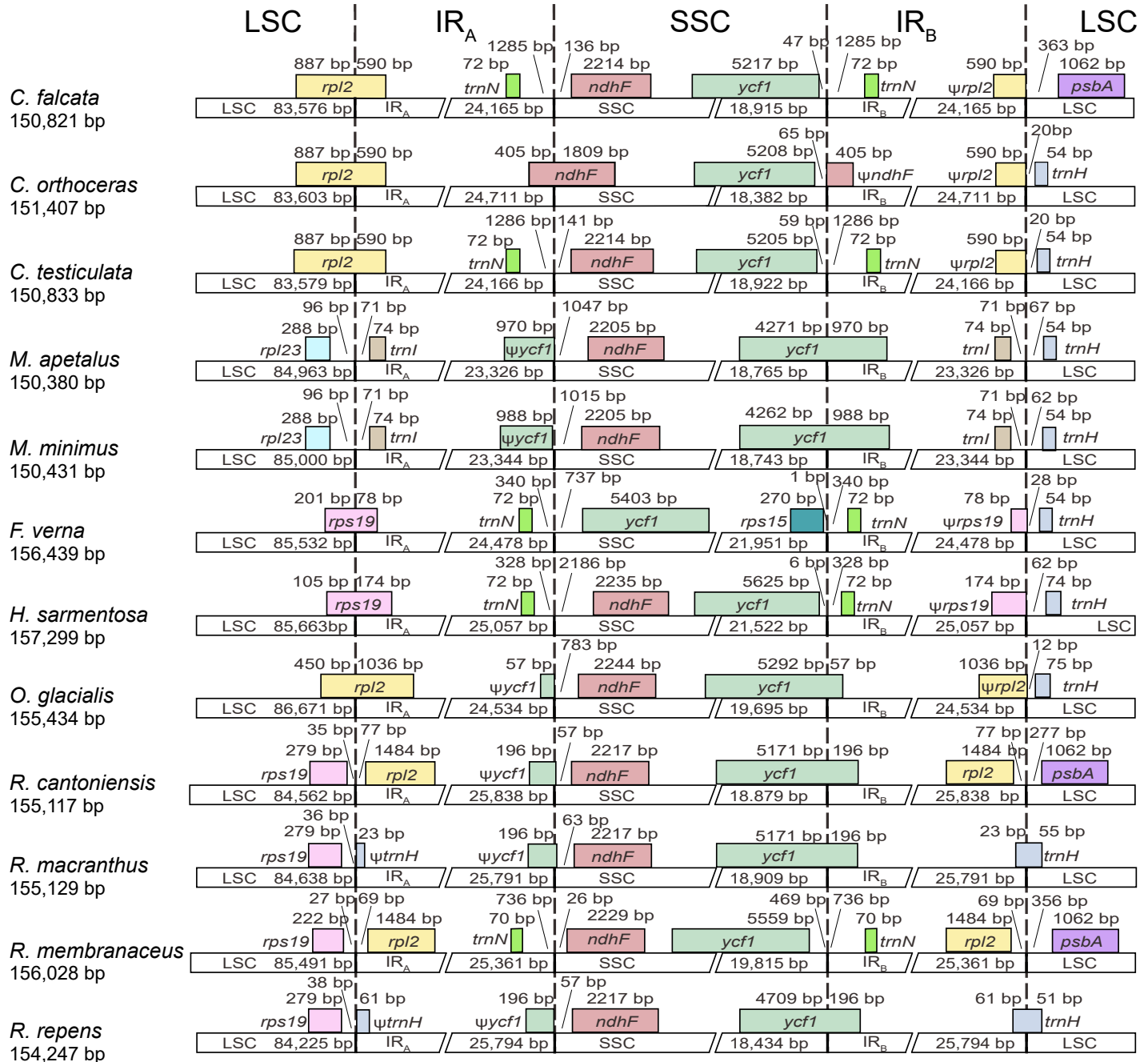
Legend:

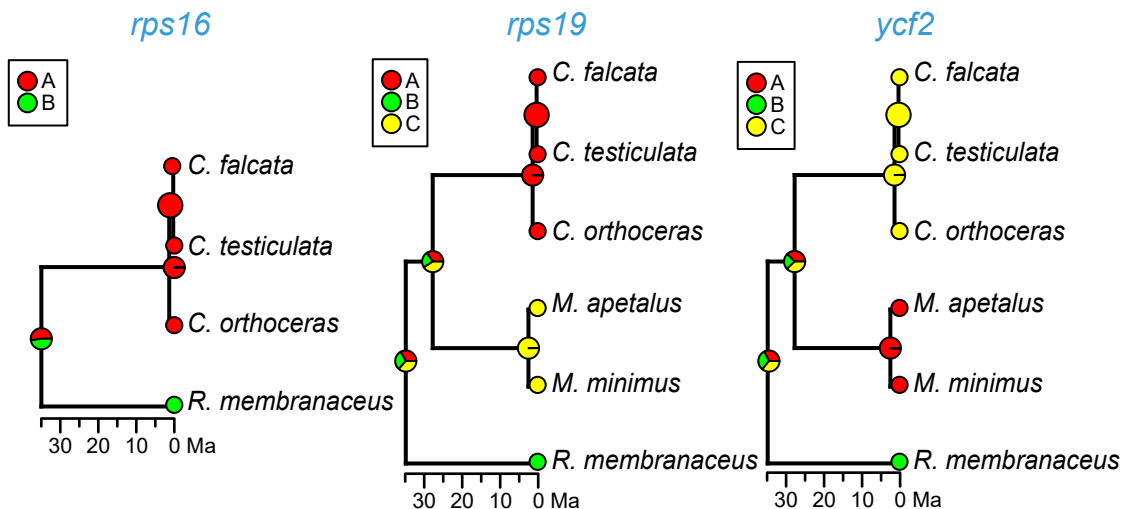
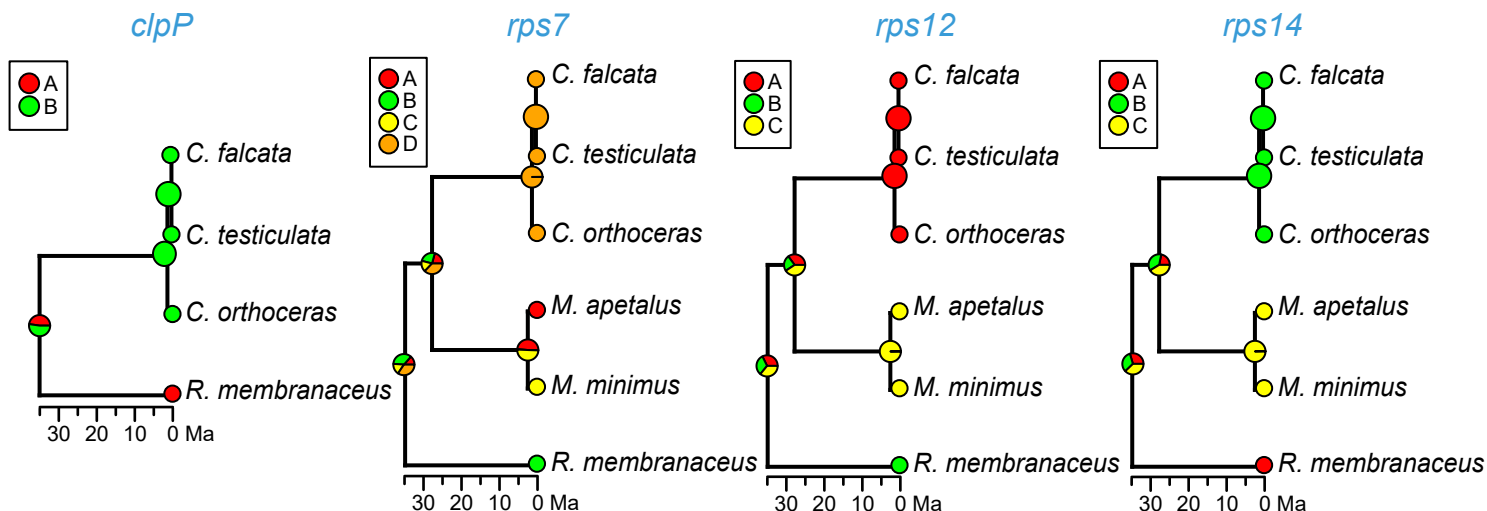
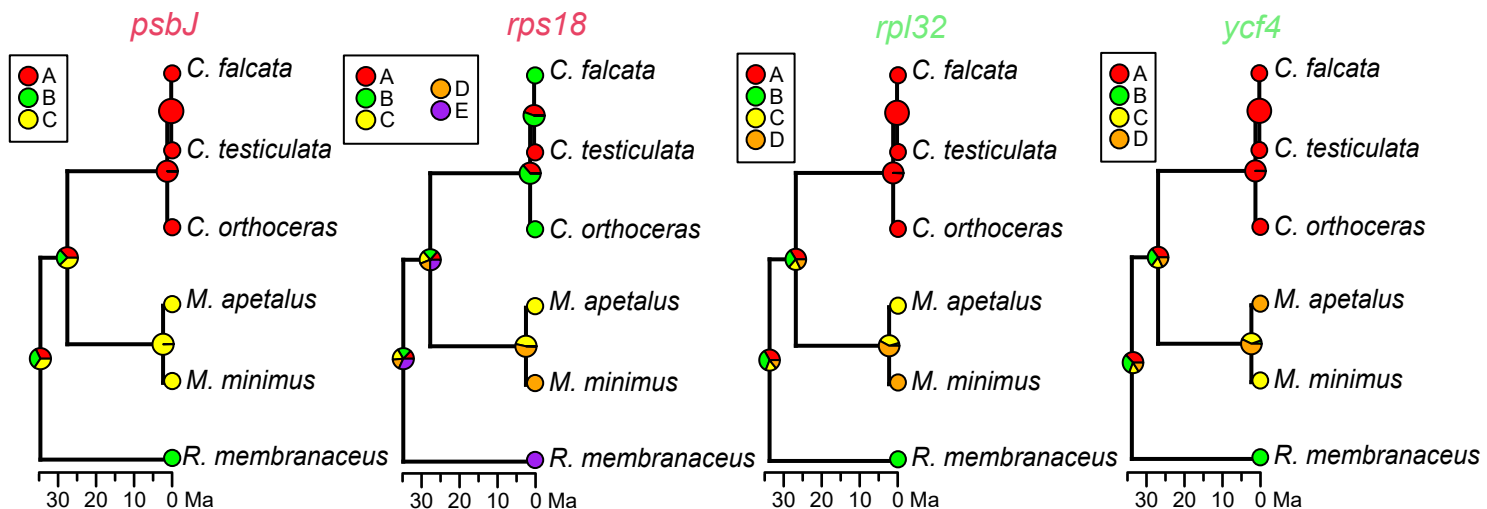
- Photosynthesis (green)
- Photosynthesis-related (light green)
- Cytochrome (yellow)
- ATP (orange)
- NADH dehydrogenase (red)
- Rubisco (dark green)

- Photosystem I
- Photosystem II
- Cytochrome b/f complex
- ATP synthase
- NADH dehydrogenase
- RubisCO large subunit
- RNA polymerase
- Ribosomal proteins (SSU)
- Ribosomal proteins (LSU)
- Transfer RNAs
- Ribosomal RNAs
- clpP, matK
- Other genes
- Hypothetical chloroplast reading frames (ycf)



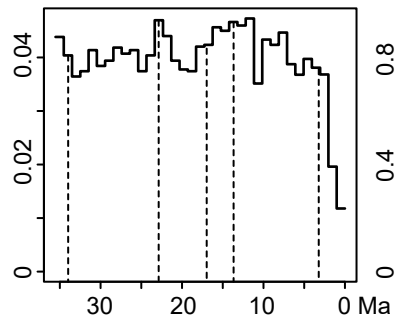




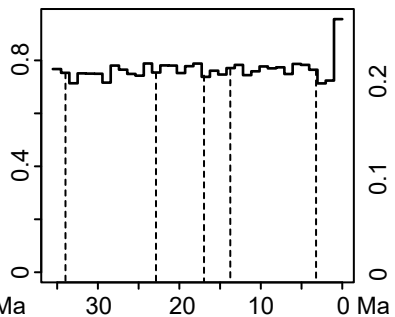


Mean number of changes / Total edge length

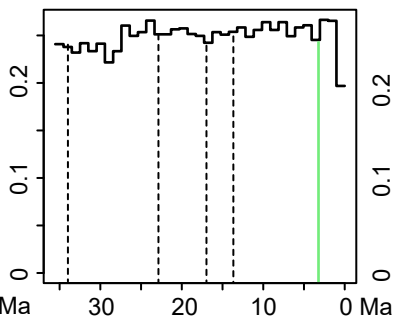
psbJ



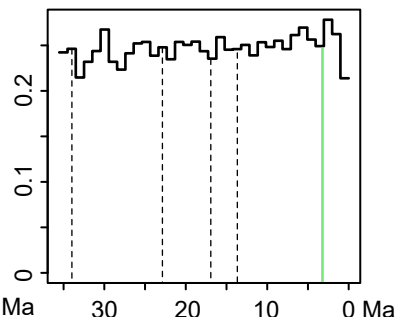
*rps18**



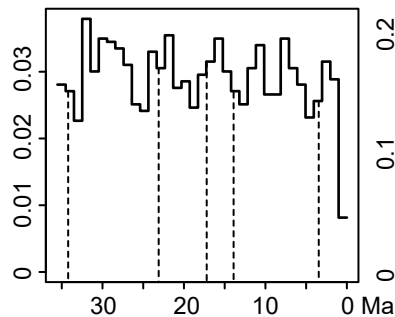
*rpl32**



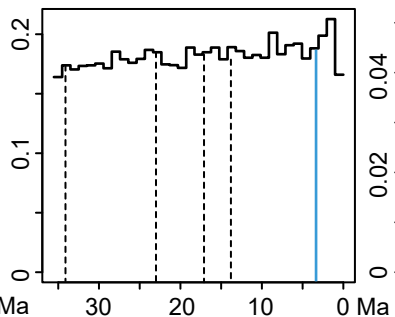
*ycf4**



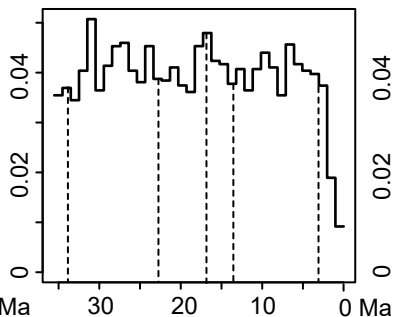
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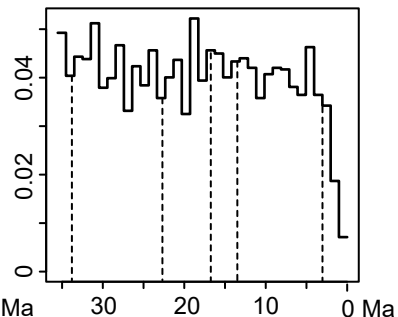
*rps7**



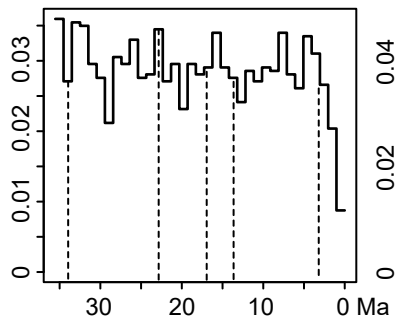
rps12



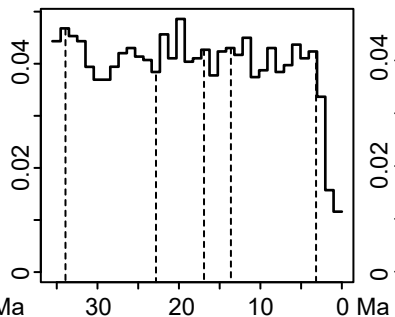
rps14



rps16



rps19



ycf2

