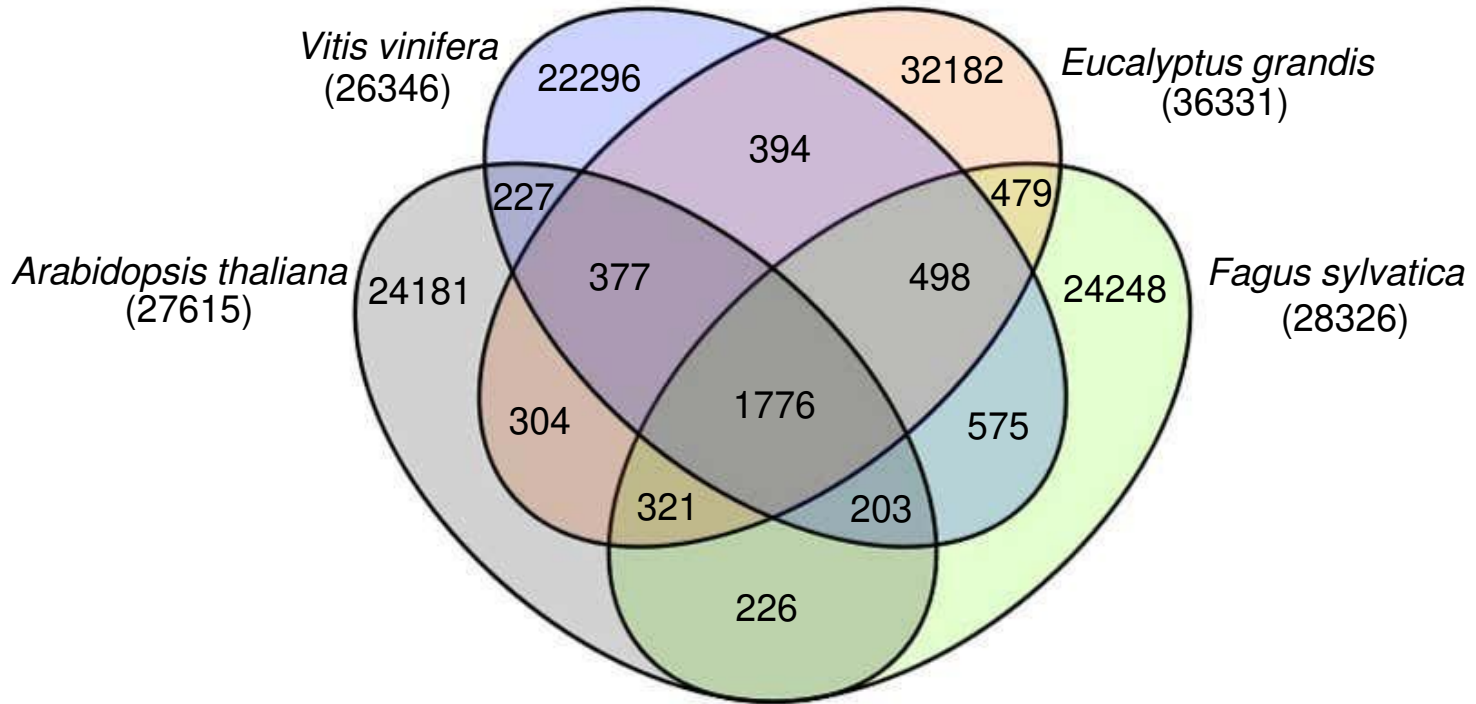


Supplementary File 1. Details of annotated repeat elements in *Fagus sylvatica*.

Repeat elements	# of elements	size	percentage of genome
Retroelements	87628	81859802 bp	15.15 %
LINES:	36016	19755558 bp	3.66 %
RTE/Bov-B	5707	963701 bp	0.18 %
L1/CIN4	30309	18791857 bp	3.48 %
LTR elements:	51612	62104244 bp	11.49 %
Ty1/Copia	26740	25500497 bp	4.72 %
Gypsy/DIRS1	22010	34391985 bp	6.36 %
DNA transposons	27884	14339425 bp	2.65 %
hobo-Activator	14367	4870881 bp	0.90 %
Tourist/Harbinger	4205	1873197 bp	0.35 %
Rolling-circles	7484	3397980 bp	0.63 %

Supplementary File 2. Number of PLAZA genes shared between selected highly resolved plant genomes.



Supplementary File 3. Annotation of centromere-associated features along the 12 chromosomes.

10Mb

20Mb

30Mb

40Mb

50Mb

60Mb

70Mb

Chr 1

Chr 2

Chr 3

Chr 4

Chr 5

Chr 6

Chr 7

Chr 8

Chr 9

Chr 10

Chr 11

Chr 12

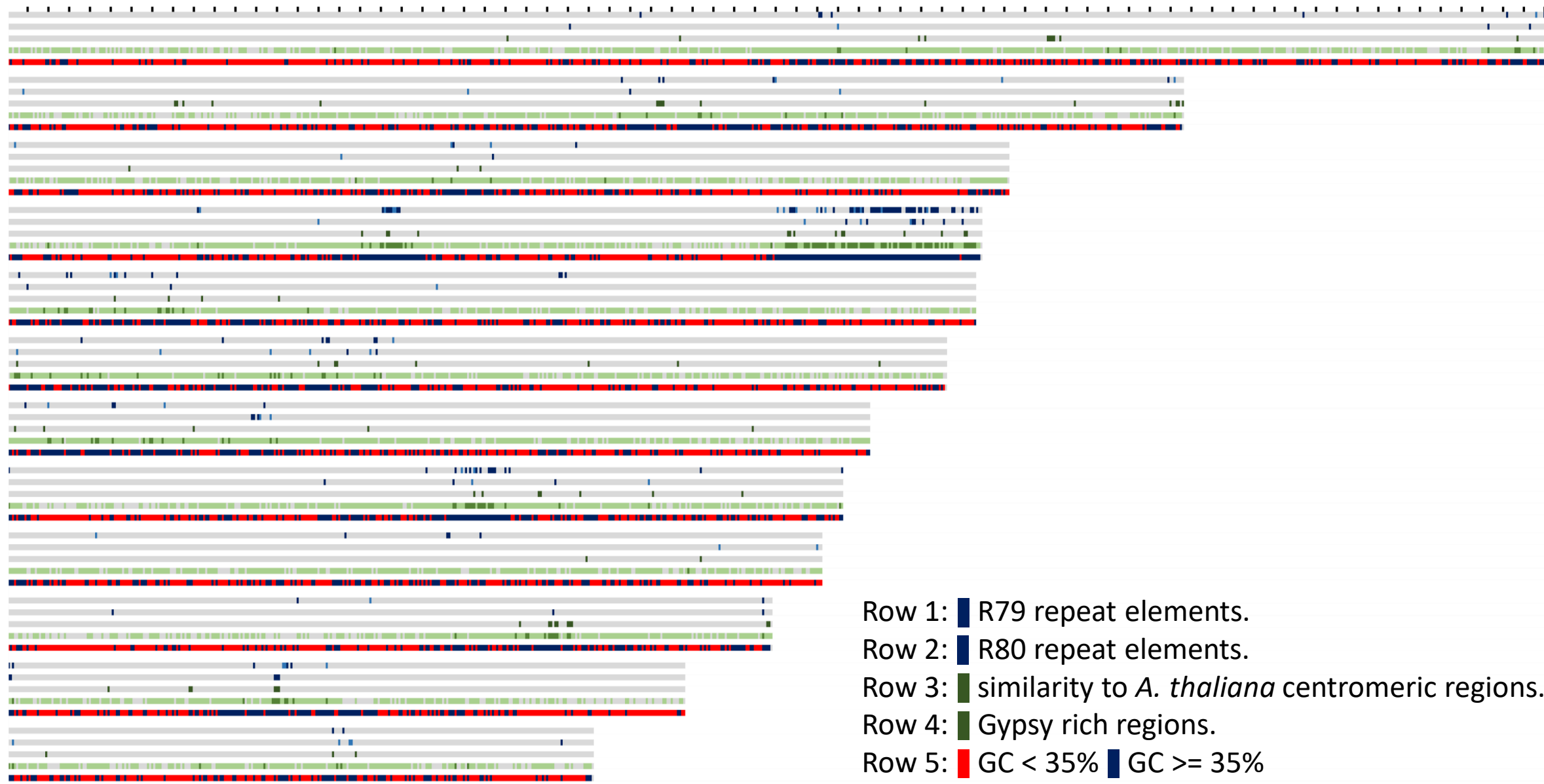
Row 1: R79 repeat elements.

Row 2: R80 repeat elements.

Row 3: similarity to *A. thaliana* centromeric regions.

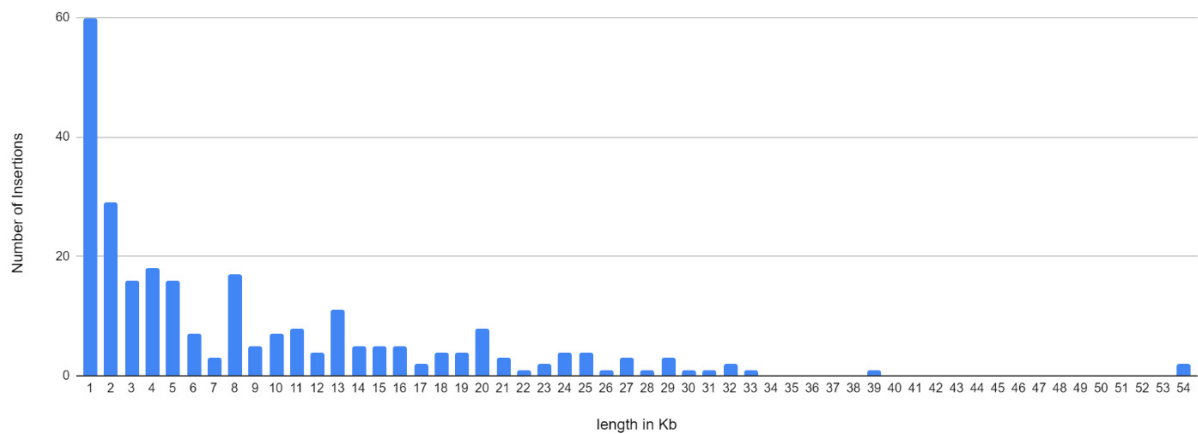
Row 4: Gypsy rich regions.

Row 5: GC < 35% GC >= 35%

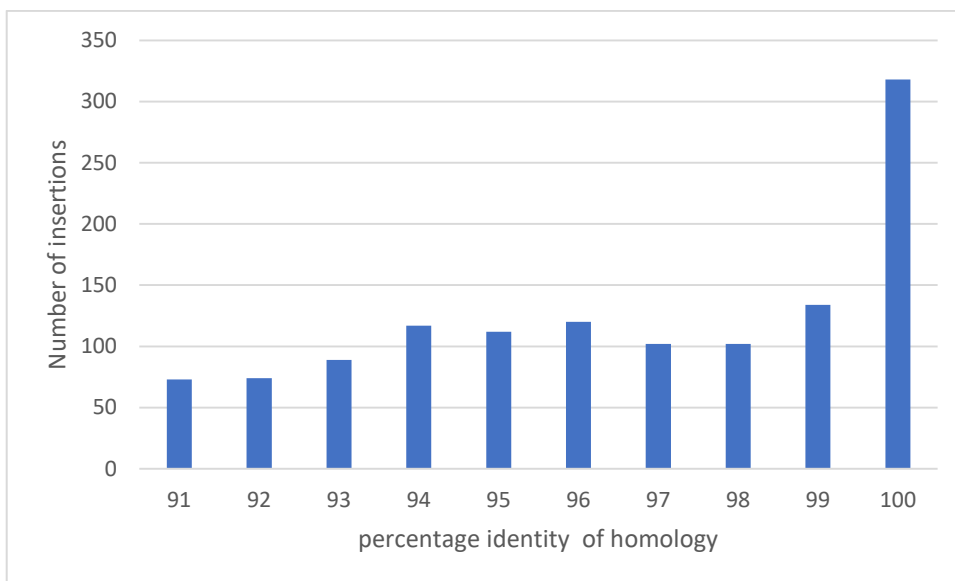


Supplementary File 4. Details of the insertion of organelle genome fragments into the nuclear genome.

Chloroplast Insertions

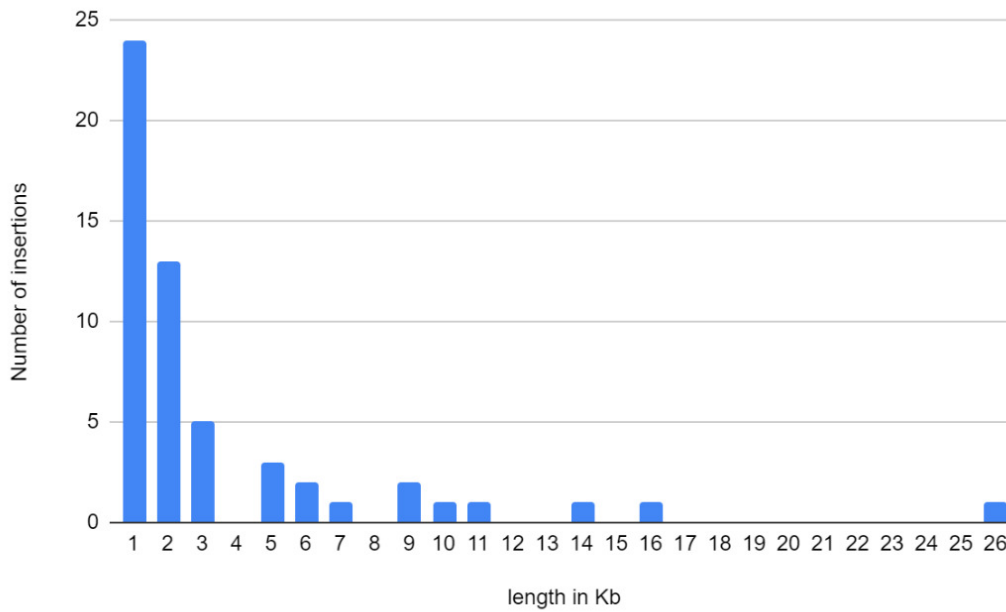


Column chart showing number of insertions for different fragment sizes of chloroplast DNA. The horizontal axis shows the sizes of the fragments (in kb). The vertical axis shows the numbers of insertions for the specified fragment sizes. Inserted fragments less than 1 kb in length are not included in this plot.

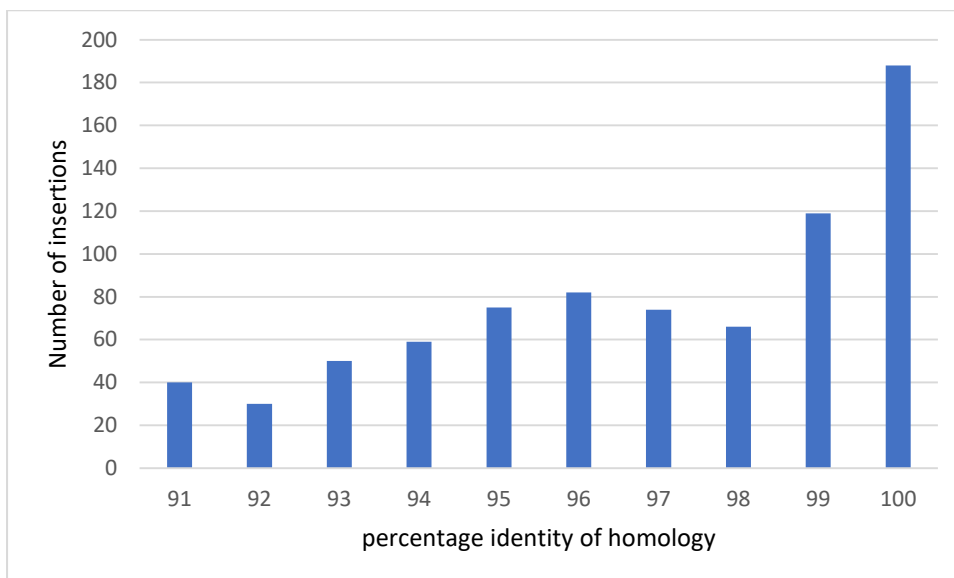


Column chart showing number of insertions at different percentage identity level of the chloroplast genome fragments from 90% to 100% identity. Inserted fragments less than 100 bp in length are excluded for this analysis.

Mitochondrial insertions



Column chart showing number of insertions for different fragment sizes of mitochondrion DNA. The horizontal axis shows the sizes of the fragments (in kb). The vertical axis shows the numbers of insertions for the specified fragment sizes. Inserted fragments less than 1 kb in length are not included in this plot.



Column chart showing number of insertions at different percentage identity level of the mitochondrion genome fragments from 90% to 100% identity. Inserted fragments less than 100 bp in length are excluded for this analysis.

