

Supplementary Figures- The first complete chloroplast genome sequence of mortiño (*Vaccinium floribundum*) and comparative analyses with other *Vaccinium* species

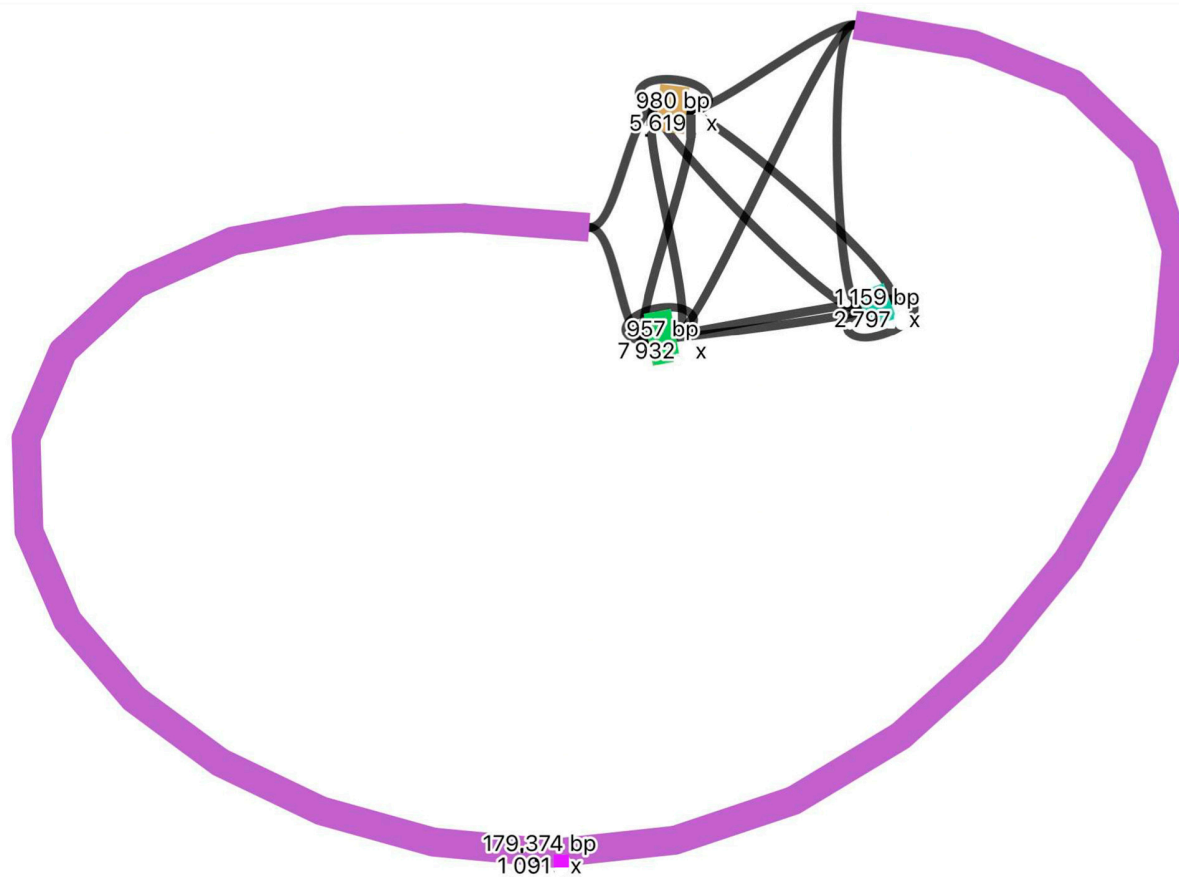


Figure S1. Bandage graph result from Flye genome assembly of *V. floribundum* cp genome. A quadripartite structure characteristic of cp genomes is not evident. There are a total of 4 fragments (1 that is composed of the majority of the genome size: 179,374 bp and three others with sizes: 957 bp, 980 bp and 1,159 bp). Numbers with x represent the coverage for each fragment.

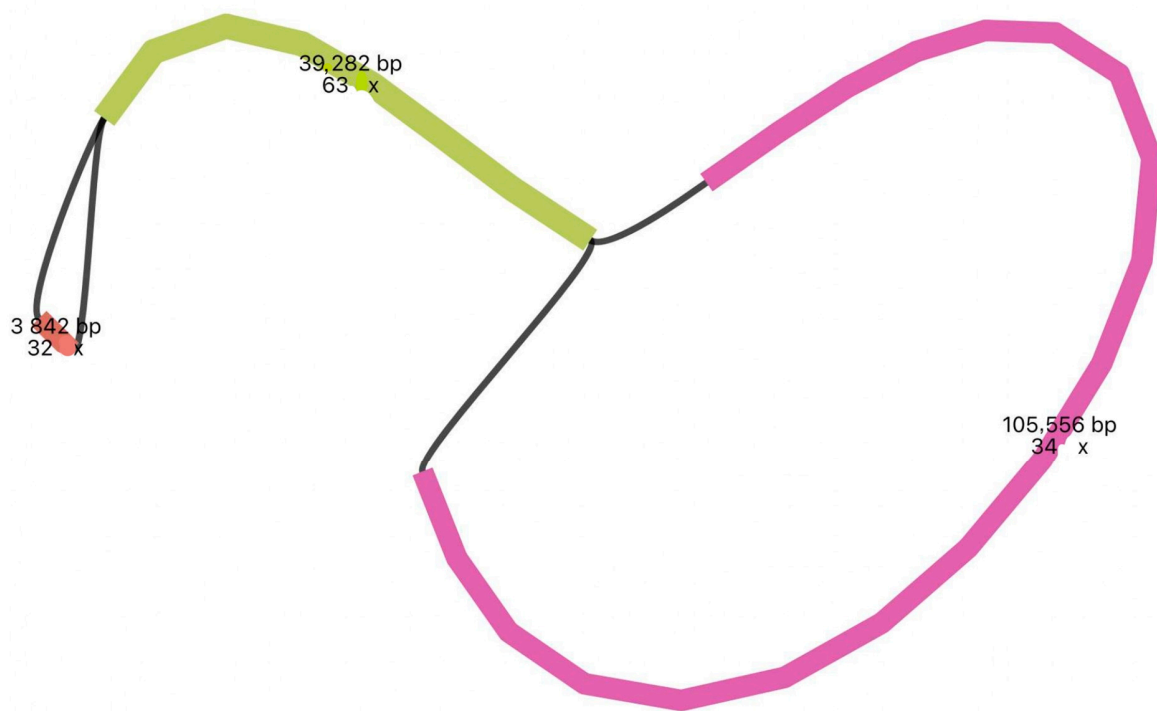


Figure S2. Bandage graph result from ptGAUL genome assembly of *V. floribundum* cp genome. A quadripartite structure characteristic of cp genomes is evident. There are a total of 3 fragments (1 similar to the size expected for the LSC region: 105,556 bp, 1 for the SSC region: 39,282 bp and 1 for the IR regions: 3,842 bp). Numbers with x represent the coverage for each fragment.

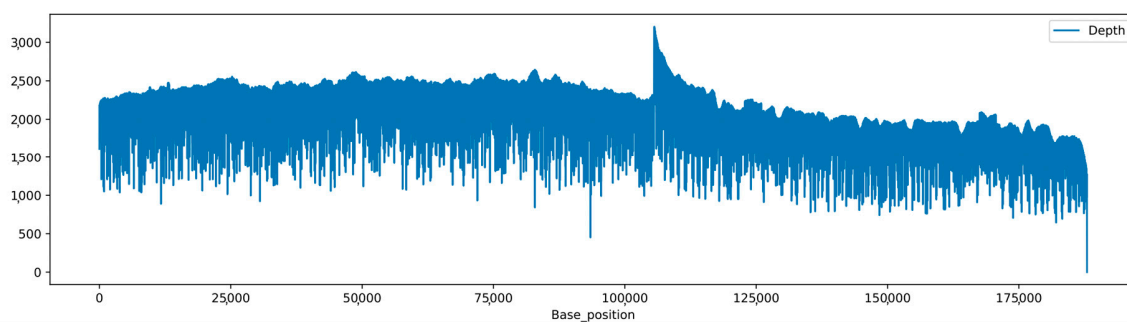


Figure S3. Depth coverage of *V. floribundum* cp genome by base position. The y-axis represents the depth of coverage, and the x-axis represents the base position in bp.

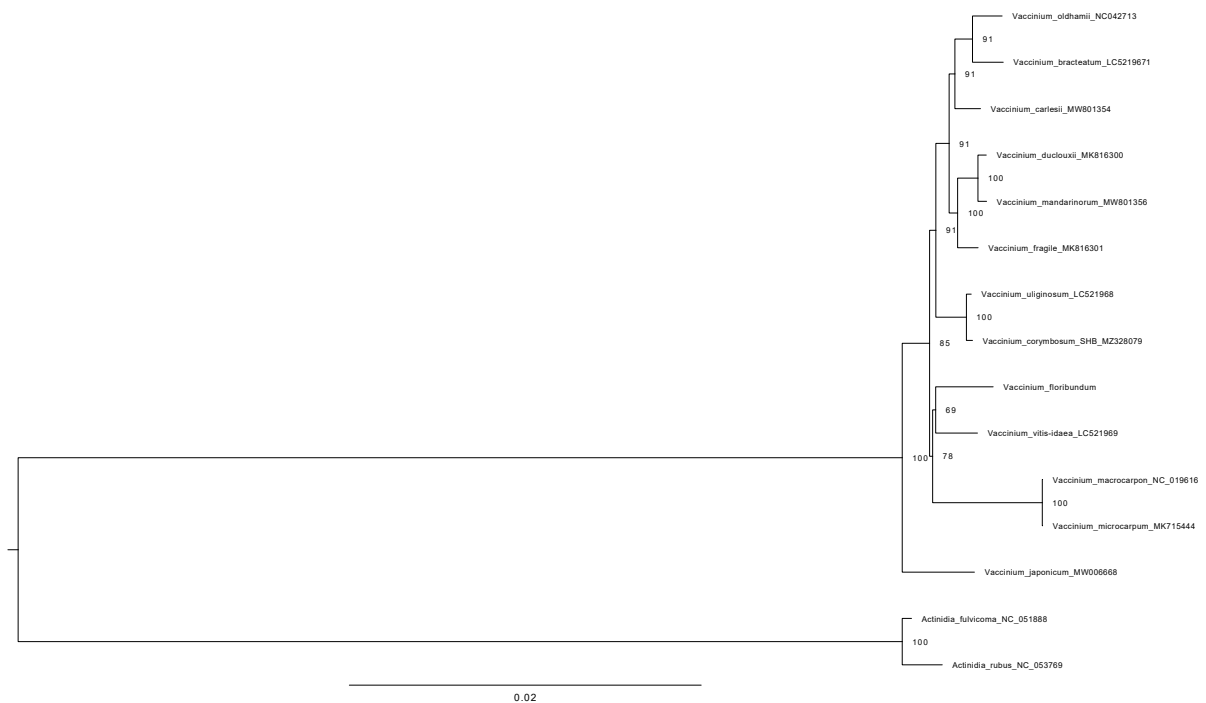


Figure S4. Preliminary phylogenetic tree constructed with 87 genes of 13 *Vaccinium* species cp genomes including *V. floribundum* cp genome using RAxML. Branch labels indicate the bootstrap support (BS) values (%). The scale bar represents nucleotide substitutions per site. Two sequences of *Actinidia* genus (*A. rubus* and *A. fulvicoma*) were used as an outgroup to root the tree.

Supplementary Material

Material S1- In-house script to create the *V. floribundum* cp genome coverage graph.

```
import matplotlib.pyplot as plt
import pandas as pd
```

```
df = pd.read_csv('samtools_depth', sep='\t', names=["Sequence", "Base_position", "Depth"], index_col=0)
fig=df.plot(x='Base_position', y='Depth', kind='line', figsize=(16, 4)).get_figure()
fig.savefig("Coverage_plot.pdf")
plt.show()
```

Material S2- List of genes used to create the phylogenetic tree of *Vaccinium*.

accD
atpA
atpB
atpE
atpF
atpH
atpI
ccsA
cemA
clpP
matK
ndhA
ndhB
ndhC
ndhD
ndhE
ndhF
ndhG
ndhH
ndhI
ndhJ
ndhK
petA
petB
petD
petG
petL
petN
psaA
psaB
psaC
psaI
psaJ
psbA

psbB
psbC
psbD
psbE
psbF
psbG
psbH
psbI
psbJ
psbK
psbL
psbM
psbN
psbT
psbZ
rbcL
rpl14
rpl16
rpl2
rpl20
rpl22
rpl23
rpl32
rpl33
rpl36
rpoA
rpoB
rpoC1
rpoC2
rps11
rps12
rps14
rps15
rps16
rps18
rps19
rps2
rps3
rps4
rps7

rps8
rrn16
rrn23
rrn4.5
rrn5
ycf1
ycf10
ycf15
ycf2
ycf3
ycf4
ycf68
ycf9
