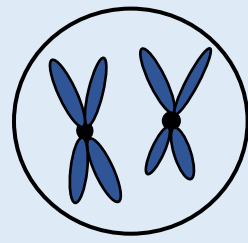
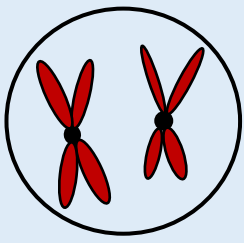
The background of the slide features a light blue gradient with several semi-transparent, golden-brown molecular models scattered across it. These models consist of spheres of varying sizes connected by thin lines, representing chemical structures. The models are out of focus, creating a sense of depth and a scientific atmosphere.

# Effect of gene copy number variation on fatty acid biosynthesis in *Brassica* species and hybrids

Shima Mahmoudi  
Supervisor: Prof. Dr. Annaliese Mason

IRC-2023 Sydney

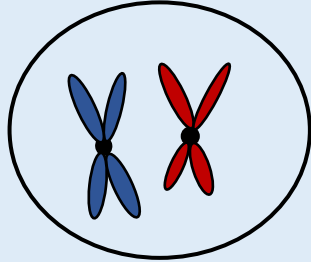
*B. rapa*  
AA, 2n=20



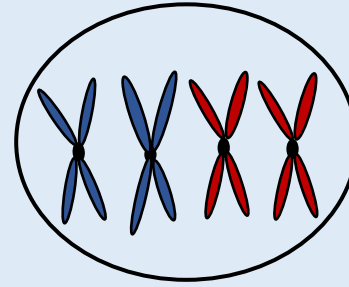
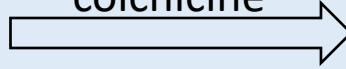
*B. oleracea*  
CC, 2n=18

Resynthesised *Brassica napus*

Allohaploid  
hybrid (AC)



Chromosome  
doubling via  
colchicine

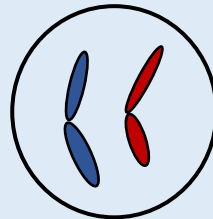


Resynthesized *B.napus*  
AACC, 2n=38

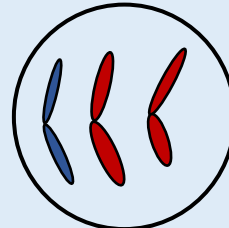


Homoeologous chromosome pairing

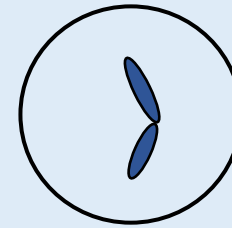
Possible gametes



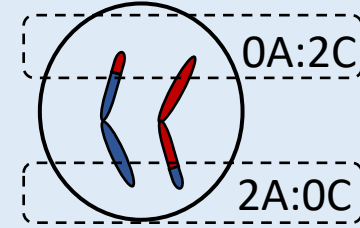
Expected  
copies



Extra copy



Missing  
copy



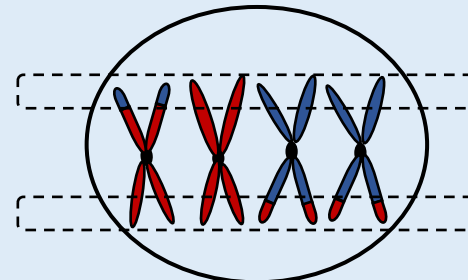
Duplication/  
deletion



Self-pollination

A:extra copy  
C:reduced copy


3A:1C




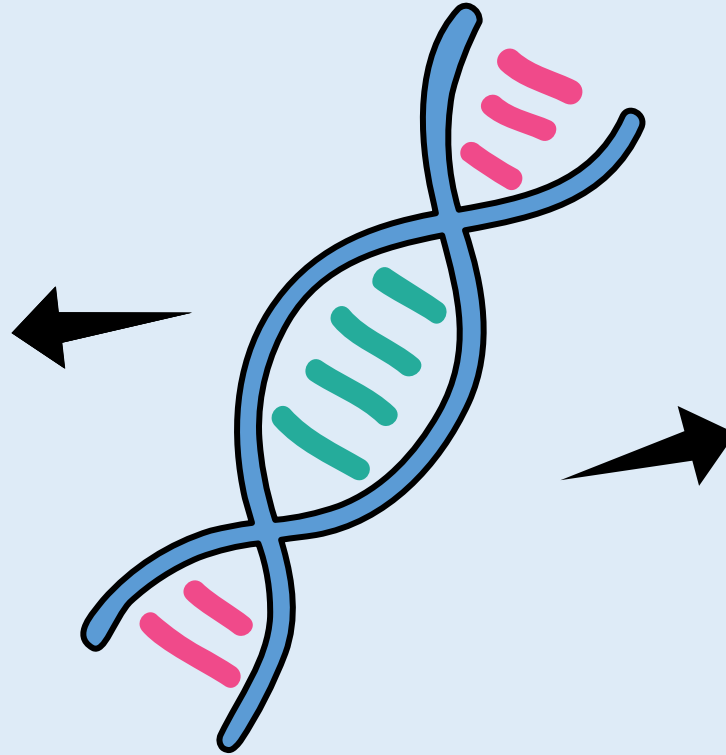
0A:4C

A:deletion  
C:extra copy

# Hypotheses

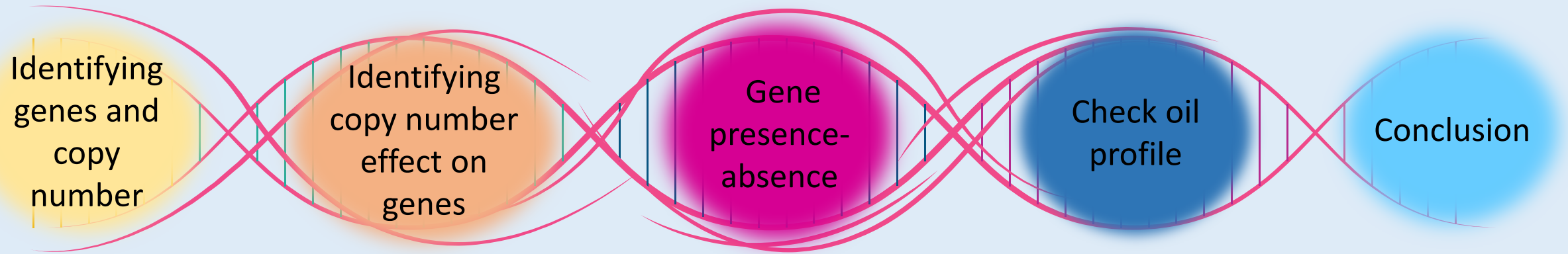


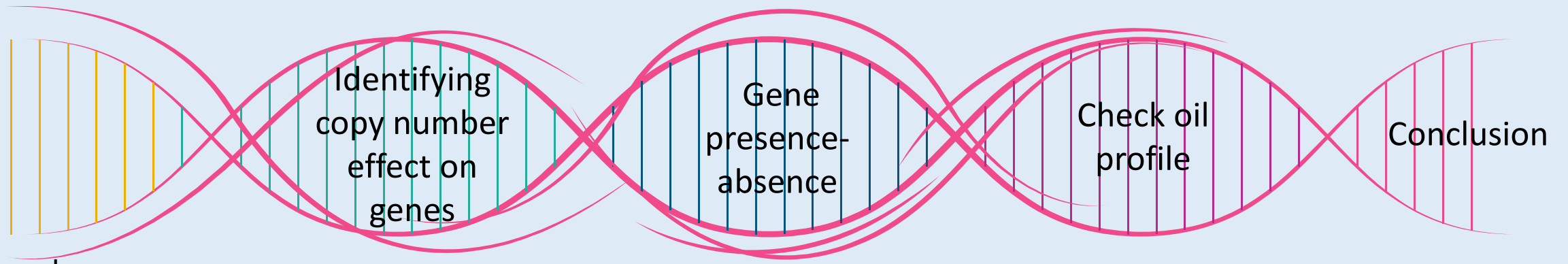
Different oil composition between lines from homozygous genotypes



Different copy numbers and whole or partial deletions of interesting genes or gene regulators will alter oil quality

# Workflow

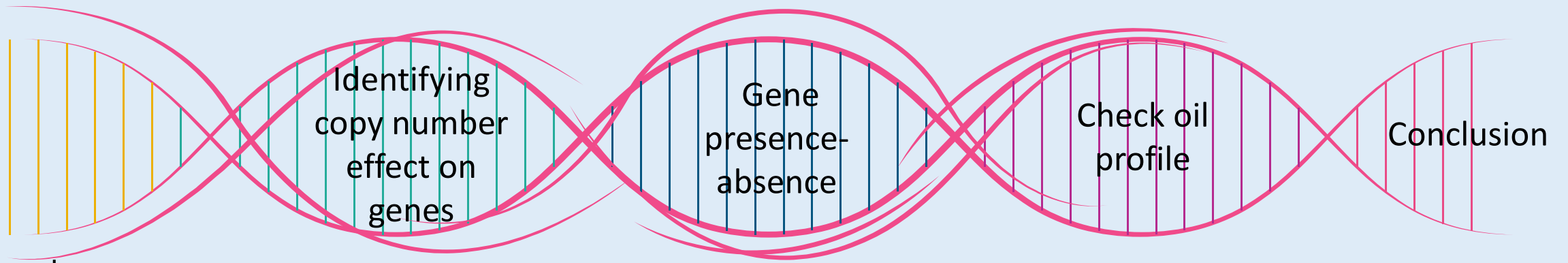




Identifying genes and copy number



- Identifying key oil related genes → 48 genes in *Arabidopsis*
- Identification of homologs of these genes in *Brassica* species
- Determine the number of copies of these genes



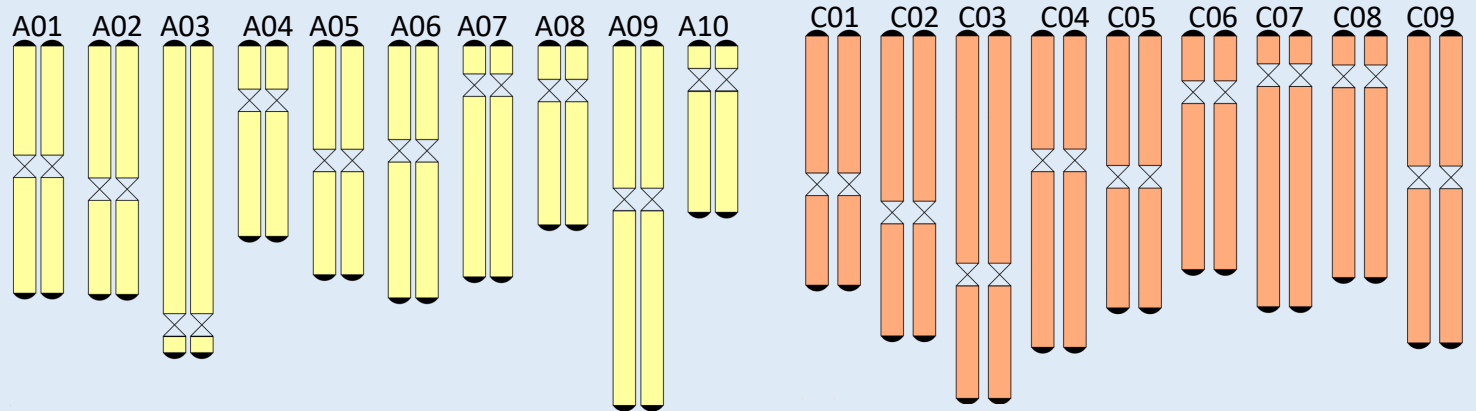
Identifying genes and copy number

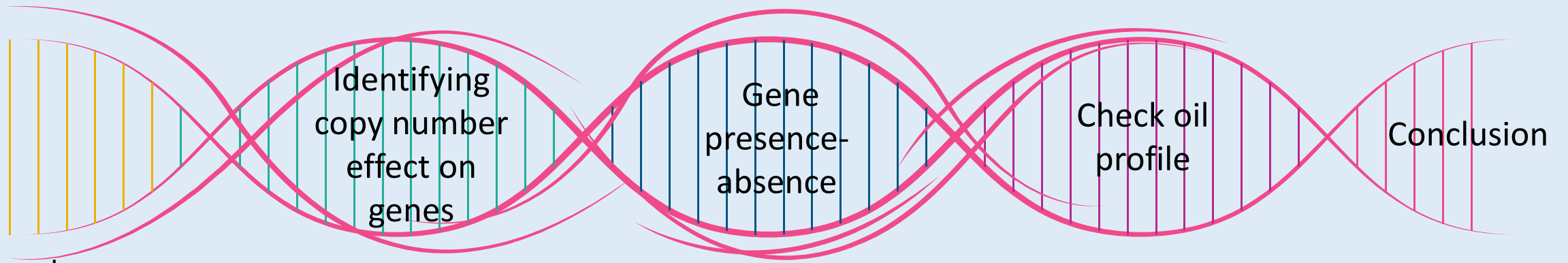


➤ Determine the number of copies of these genes

✓ (1-13)

*B.napus* reference genome (Darmor-bzh v8.1)





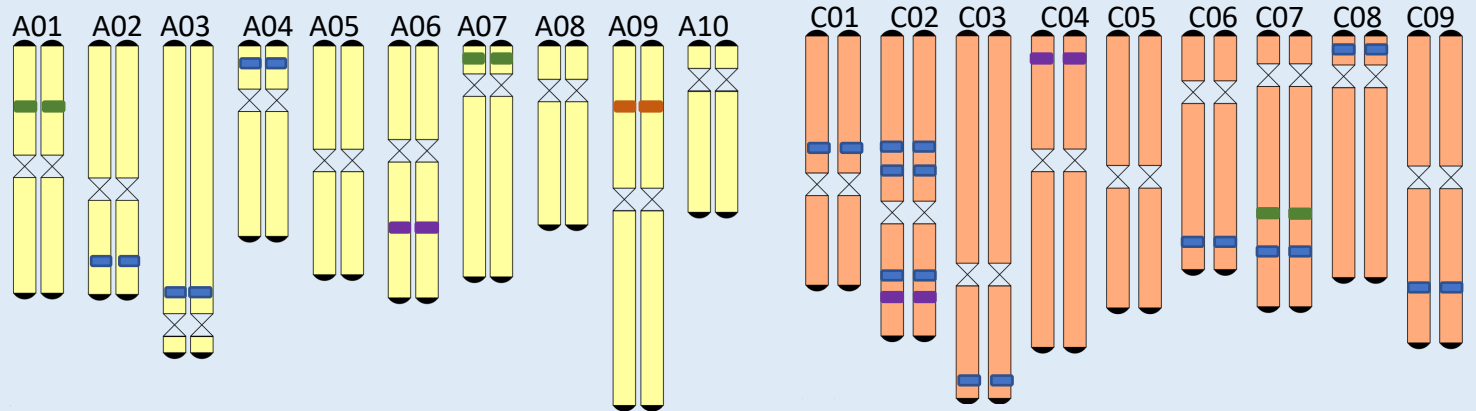
Identifying genes and copy number



- Determine the number of copies of these genes
- Location of copies on the reference genome

✓ (1-13)

*B.napus* reference genome (Darmor-bzh v8.1)



Identifying genes and copy number

Gene presence-absence

Check oil profile

Conclusion

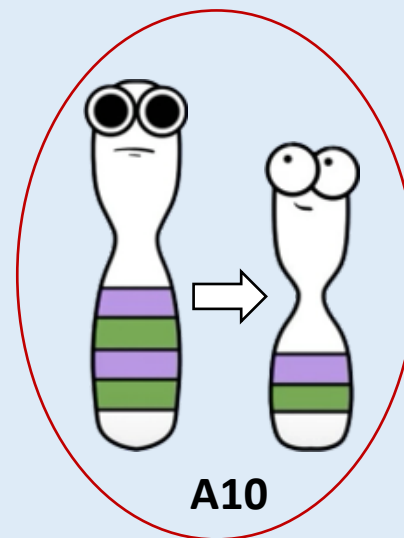
Identifying copy number effect on genes



Resynthesised *B.napus* genotypes

Look for copies located in CNV region from SNP data

**GPAT7**



A9C47  
A4C47

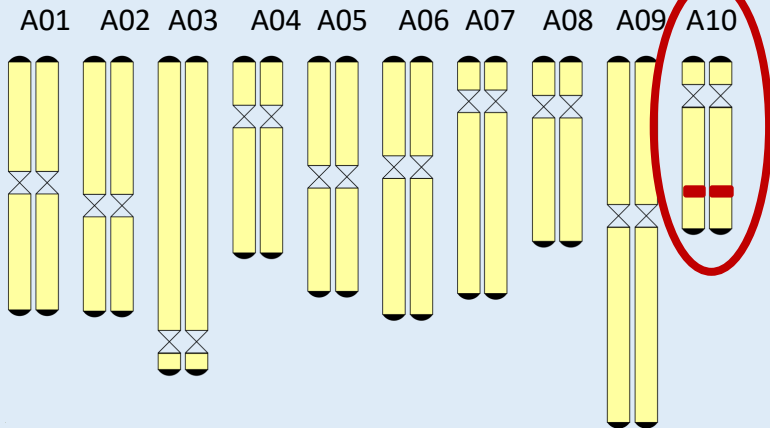
Identifying genes and copy number

Identifying copy number effect on genes

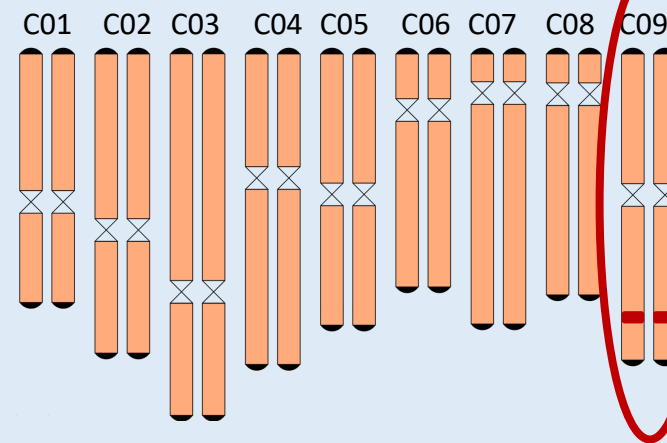
Check oil profile

Conclusion

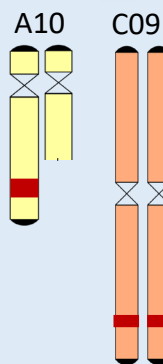
Expected copy number for *GPAT7*:



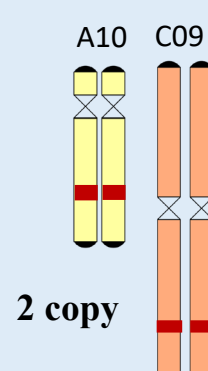
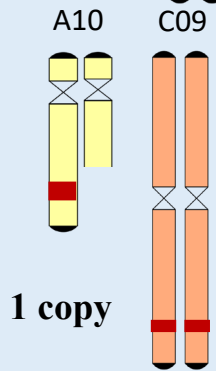
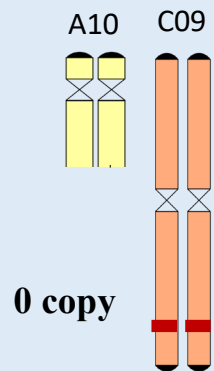
Gene presence-absence



Selected lines: A9C47, A4C47



expected segregation of progeny:



Identifying genes and copy number

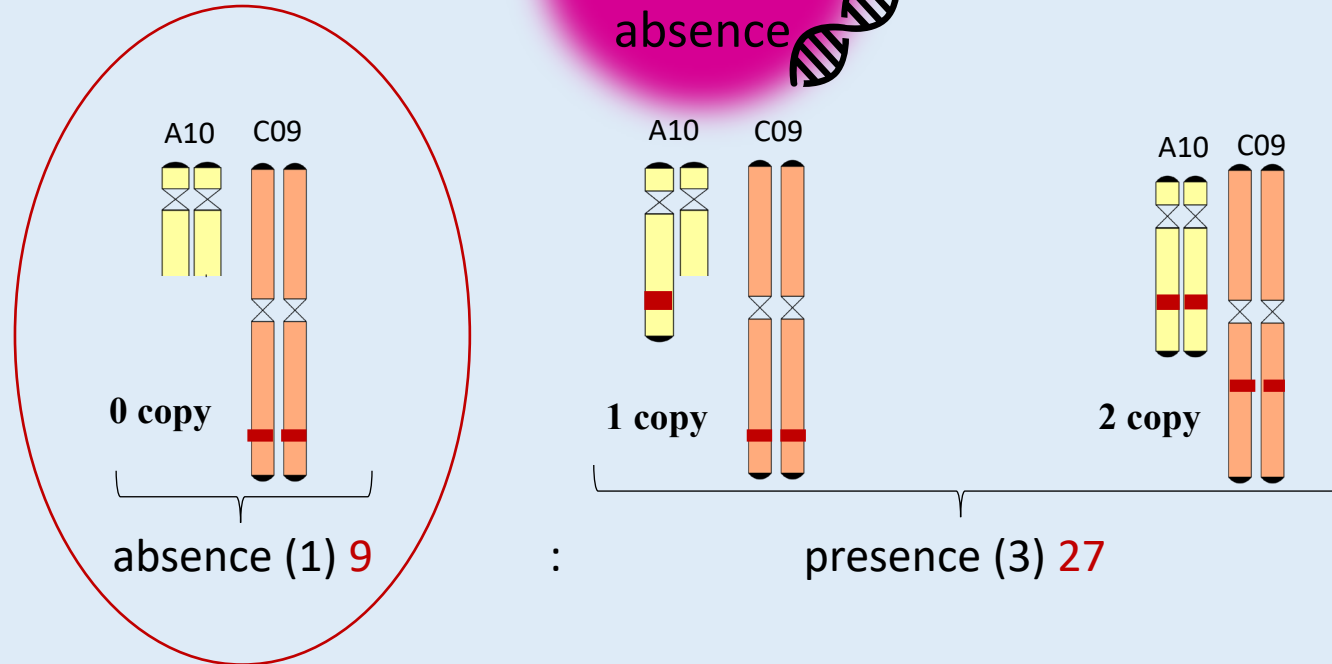
Identifying copy number effect on genes

Check oil profile

Conclusion

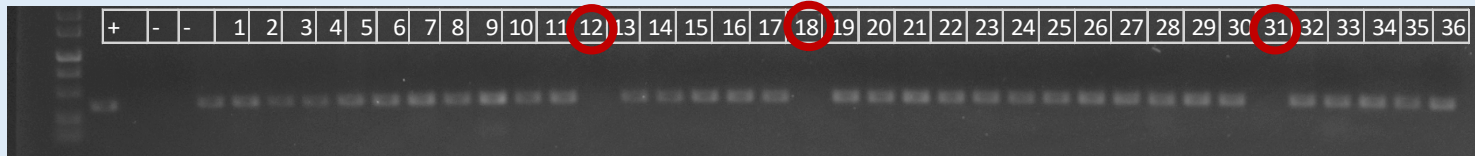
Gene presence-absence

expected segregation of progeny:



A9C47 plant lines from 1-36

Primer:  
(*Bna.GPAT7.A10*)



observed ratio → 3:33  
p-value = 0.020

Identifying genes and copy number

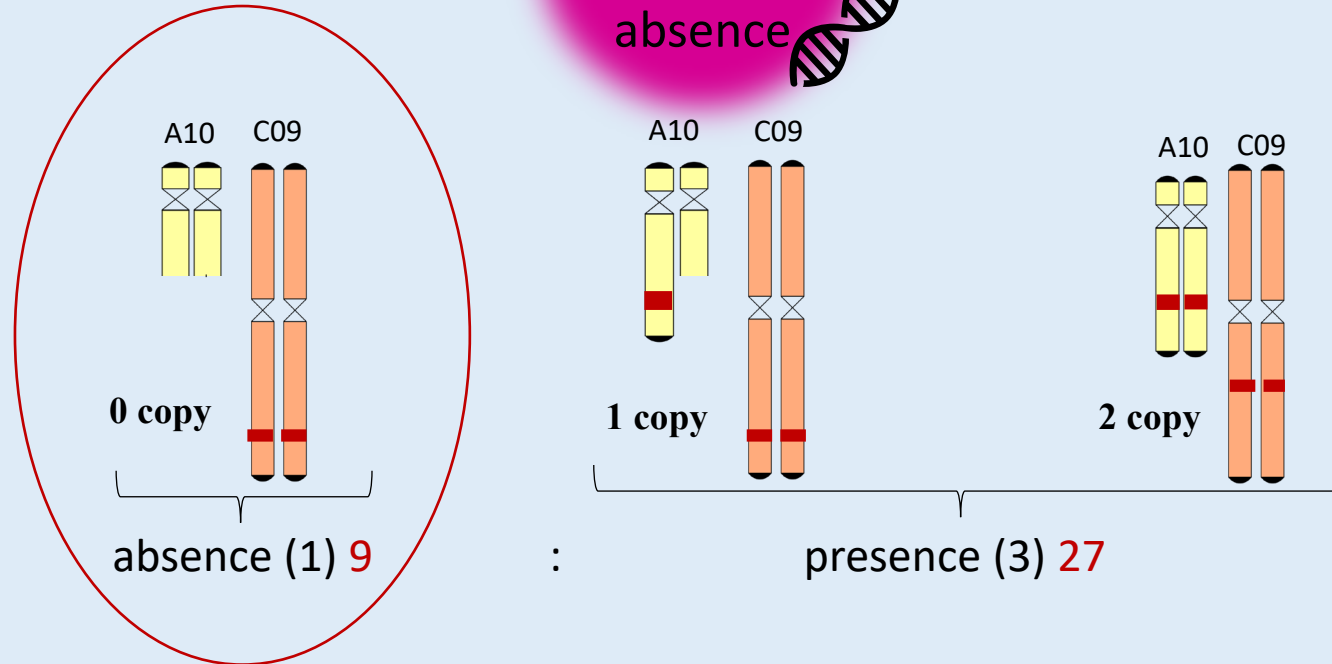
Identifying copy number effect on genes

Check oil profile

Conclusion

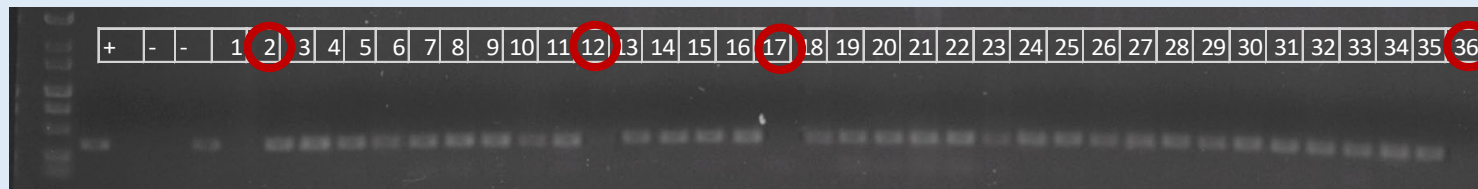
Gene presence-absence

expected segregation of progeny:



A4C47 plant lines from 1-36

Primer: (Bna.GPAT7.A10)



observed ratio → 4:32  
p-value = 0.054

Identifying genes and copy number

Identifying copy number effect on genes

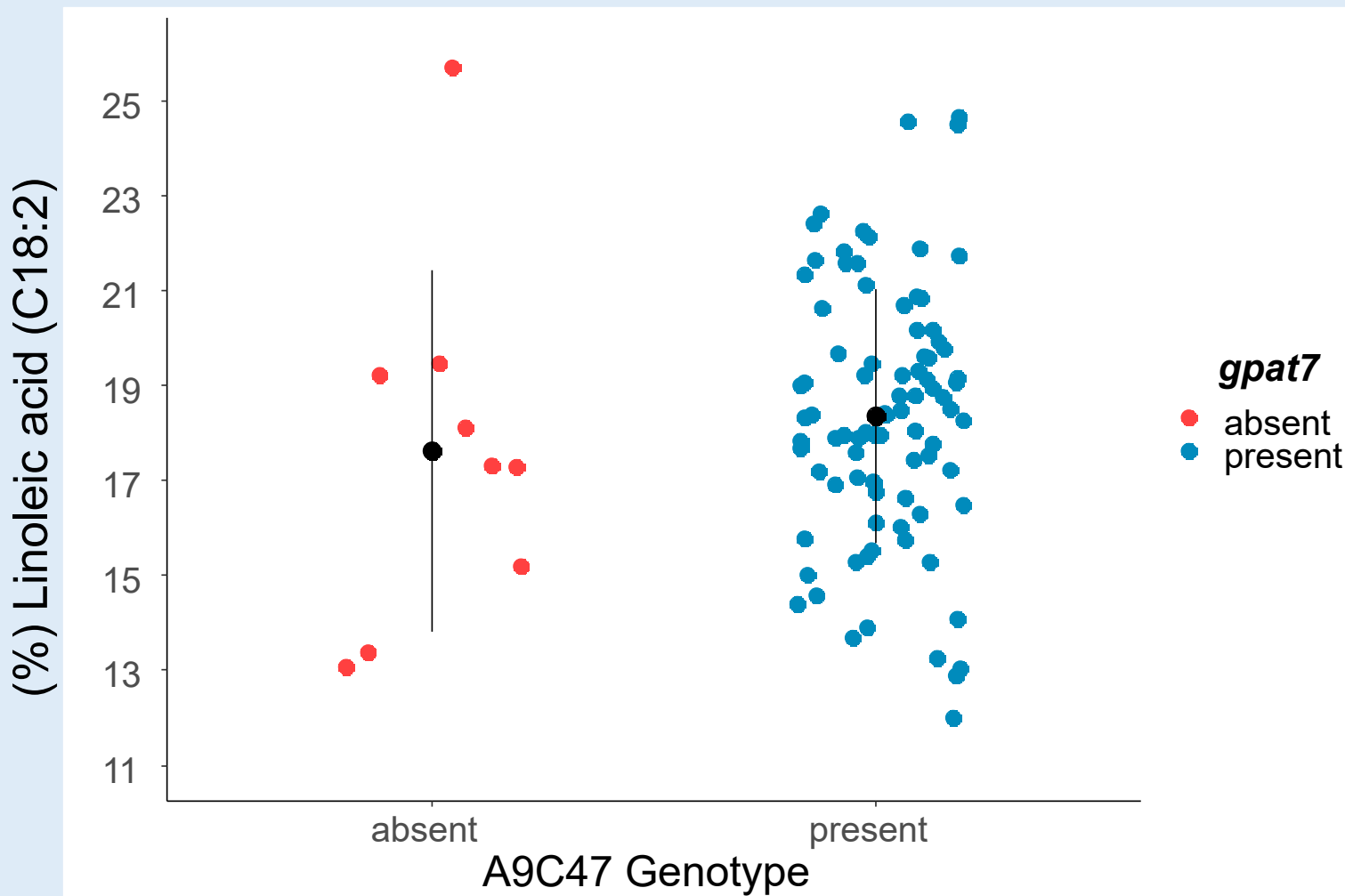
Gene presence-absence

Conclusion

Check oil profile



**p-value = 0.52**



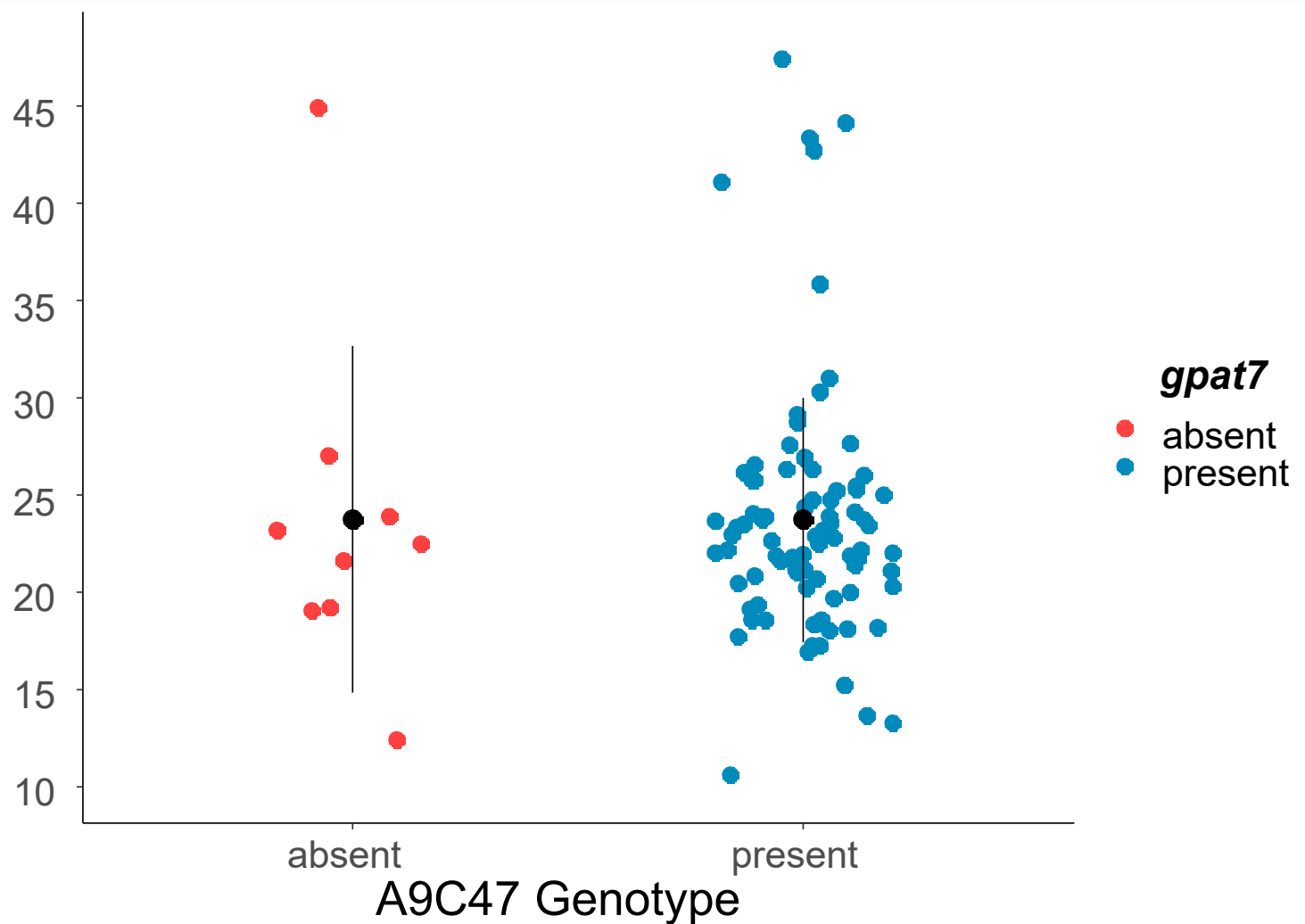
Identifying genes and copy number

Identifying copy number effect on genes

Gene presence-absence

Conclusion

(%) Erucic acid (C22:1)



Check oil profile



**p-value = 0.97**

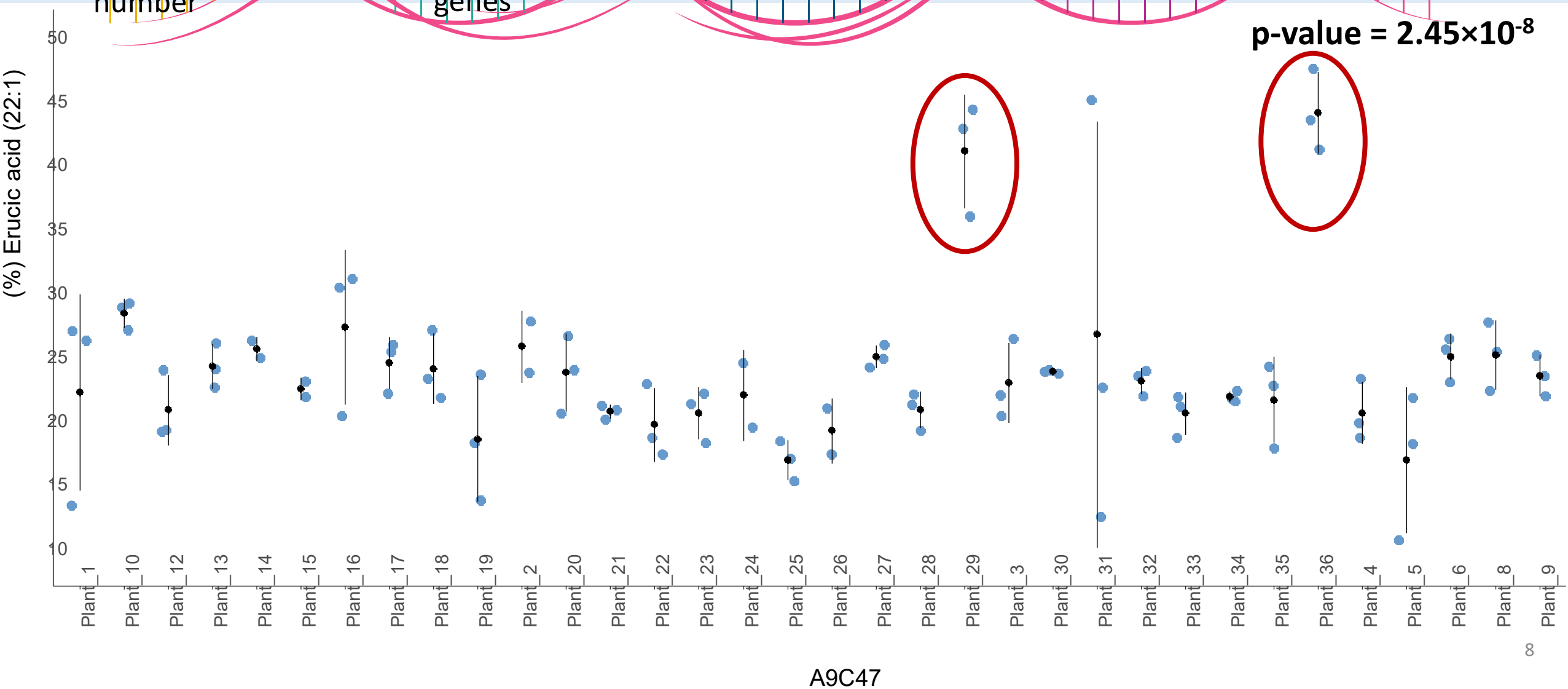
Identifying genes and copy number

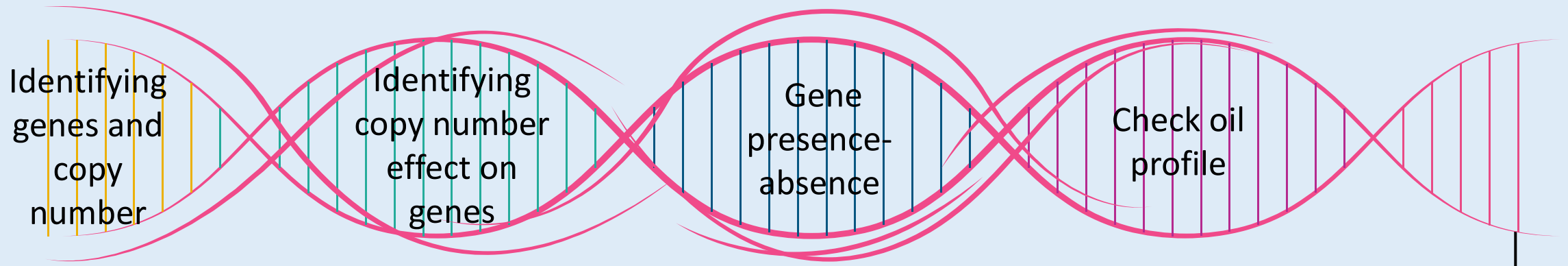
Identifying copy number effect on genes

Gene presence-absence

Check oil profile

Conclusion





## Conclusions and future work

- No significant differences in fatty acid profiles were observed based on segregation of *GPAT7* copy numbers
- However, some individuals within the allelically homozygous progeny sets demonstrated radical changes in fatty acid profiles, putatively due to non-homologous chromosome rearrangements
- Further validation will be carried out using a combination of sequencing, gene expression analysis and molecular cytogenetics as appropriate
- Our results so far suggest that copy number variation can potentially majorly contribute to fatty acid profiles in rapeseed

# Acknowledgements



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**DAAD**  
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German Academic Exchange Service

