irc 2023 SYDNEY
16th INTERNATIONAL RAPESEED CONGRESS
24 - 27 September 2023
GLOBAL CROP - GOLDEN OPPORTUNITIES

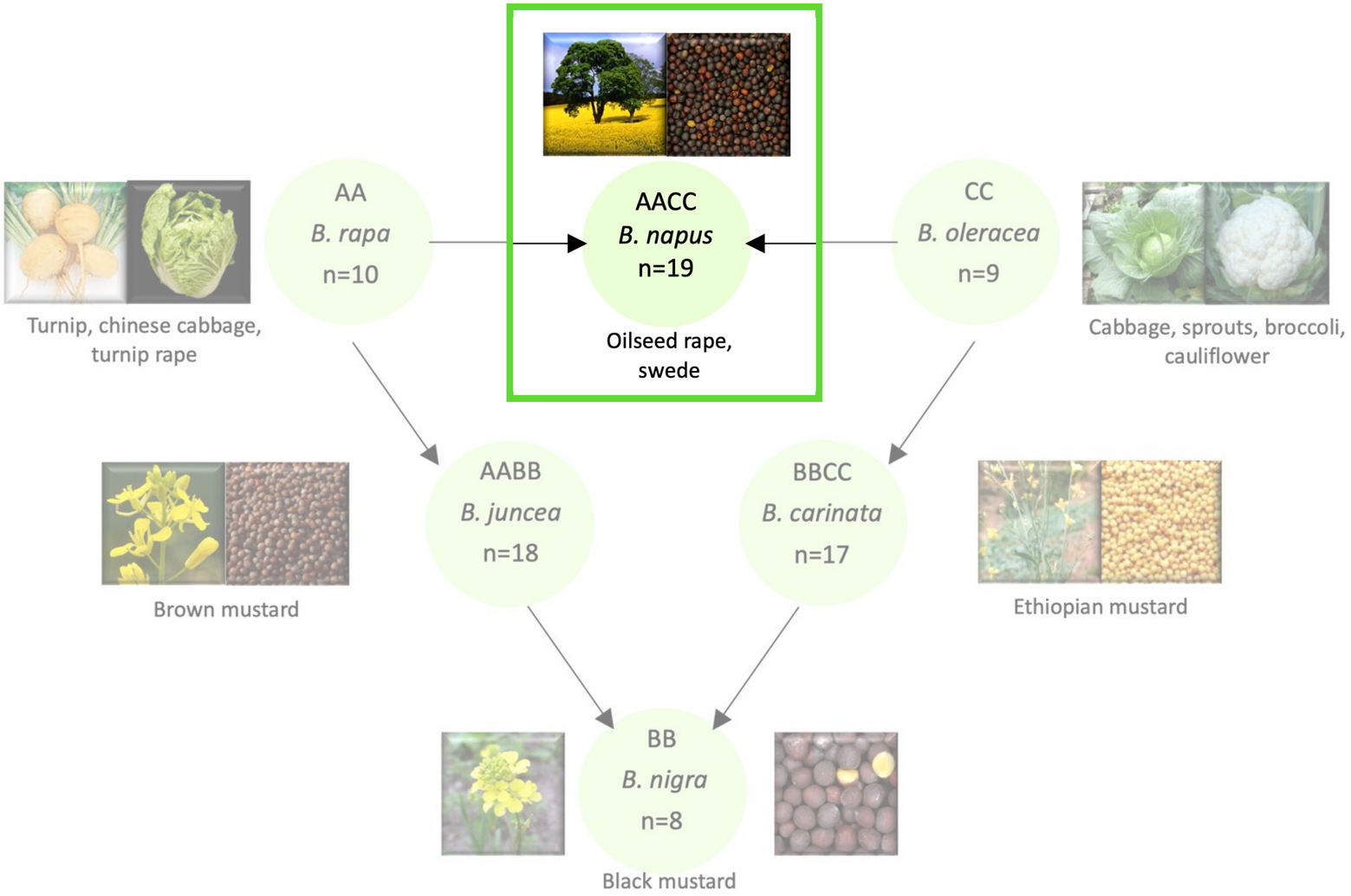
Investigating genome dominance in *Brassica napus*

Hugh Woolfenden

BRAVO
Brassica Rapeseed And Vegetable Optimisation

John Innes Centre

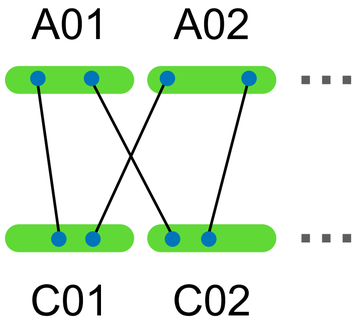
Are the A and C subgenomes in *B. napus* equal partners?



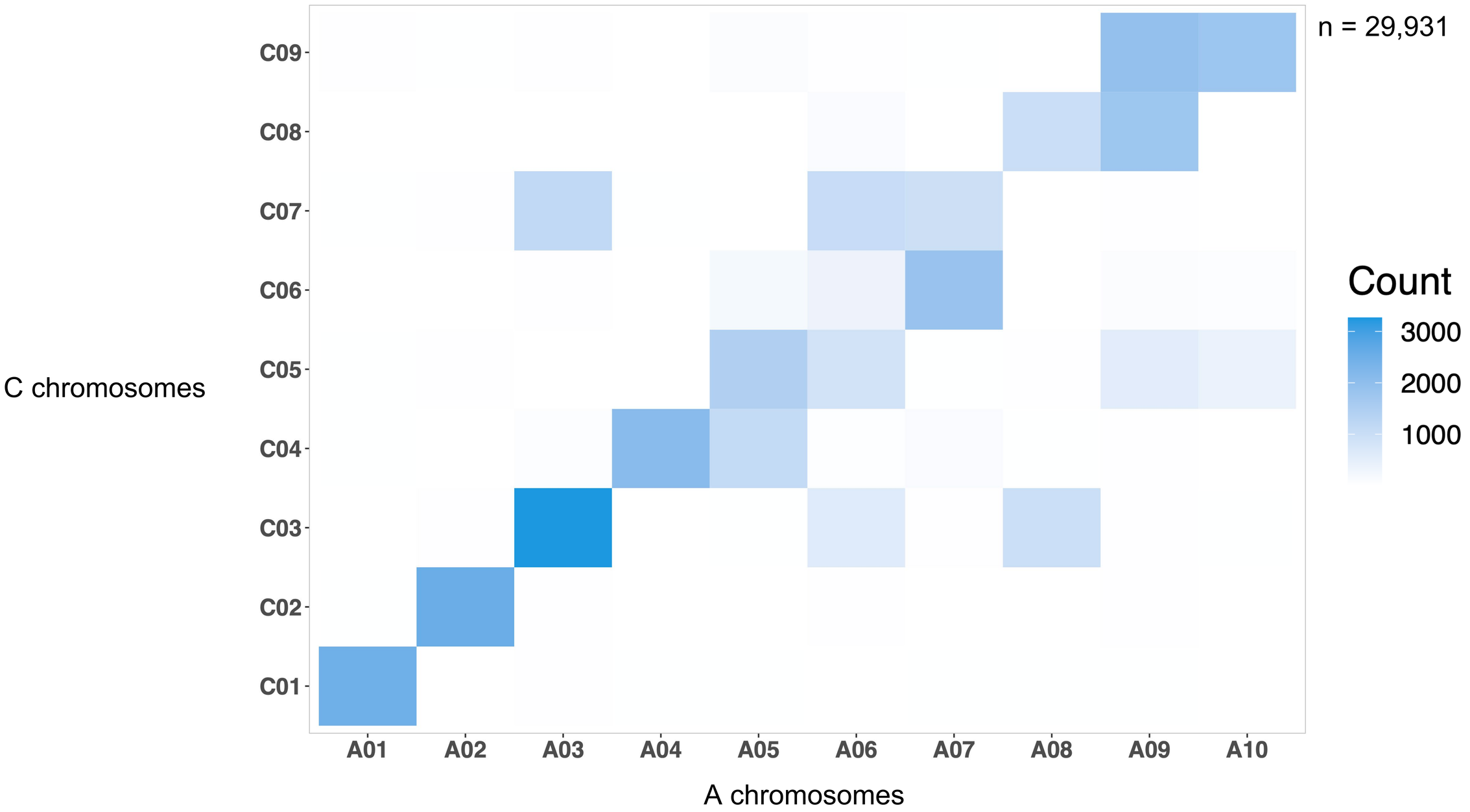
AA_{CC} ?

$_{AA}CC$?

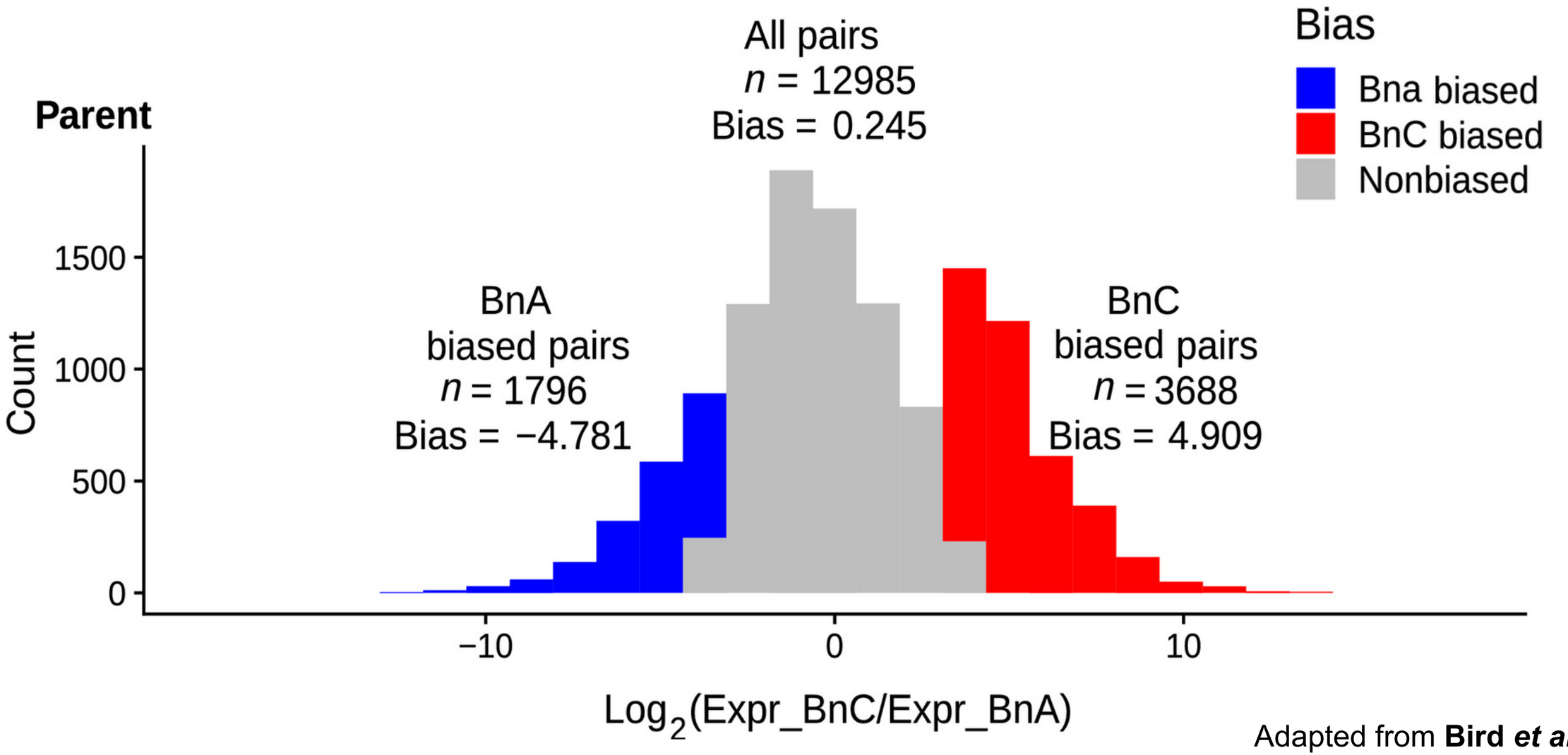
Homoeolog pairs



BLAST analysis identifies 30,000 homoeolog pairs



Bias to C subgenome has been observed in resynthesised *B. napus*



Adapted from **Bird *et al.* (2020)**

~21d leaf

RNA-seq analysis in the semi-winter Zhongshuang11

Thank you

Rachel Wells
Lorelei Bilham

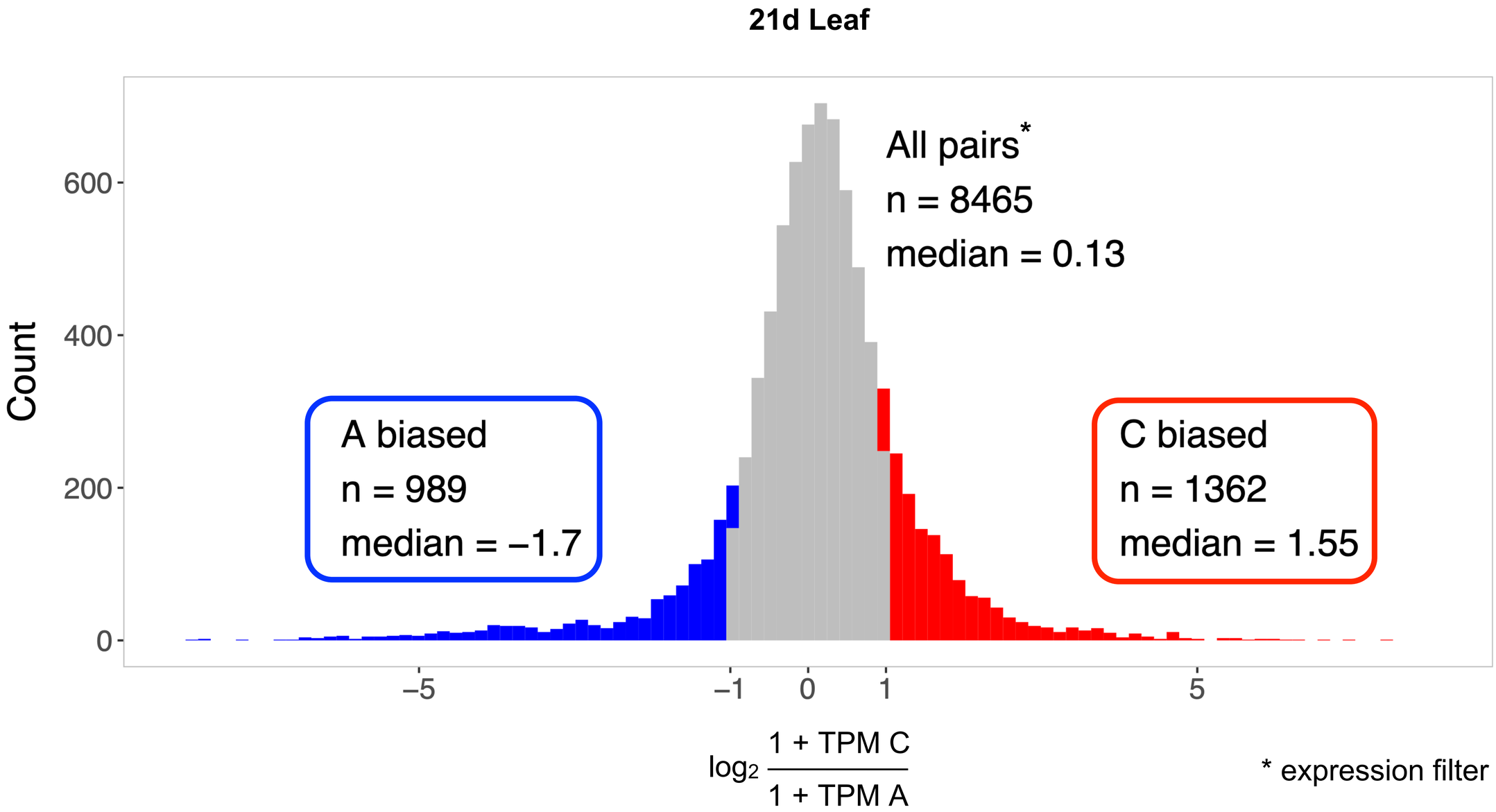
Experiments

3 repetitions in CER

Alignment

Darmor 10 reference
Uniquely mapped reads

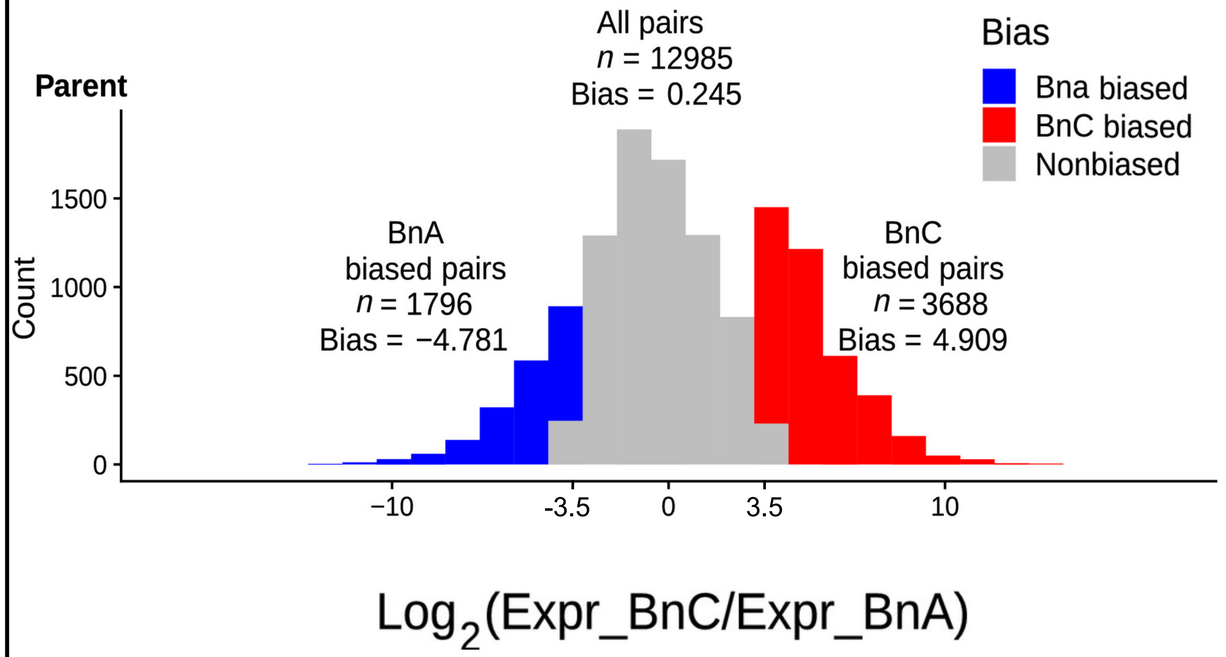
Homoeolog pairs biased to C subgenome



Bimodality is lost in an established cultivar

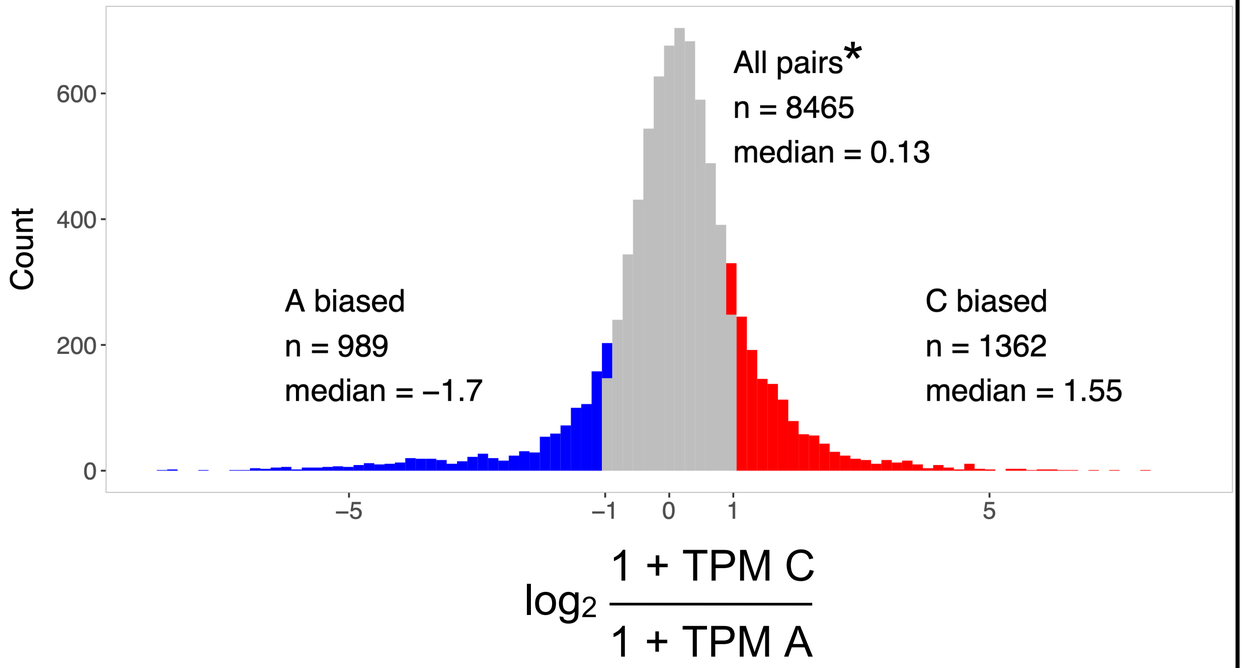
Leaf (21d)

Resynthesised *B. napus*



Bird *et al*. (2020)

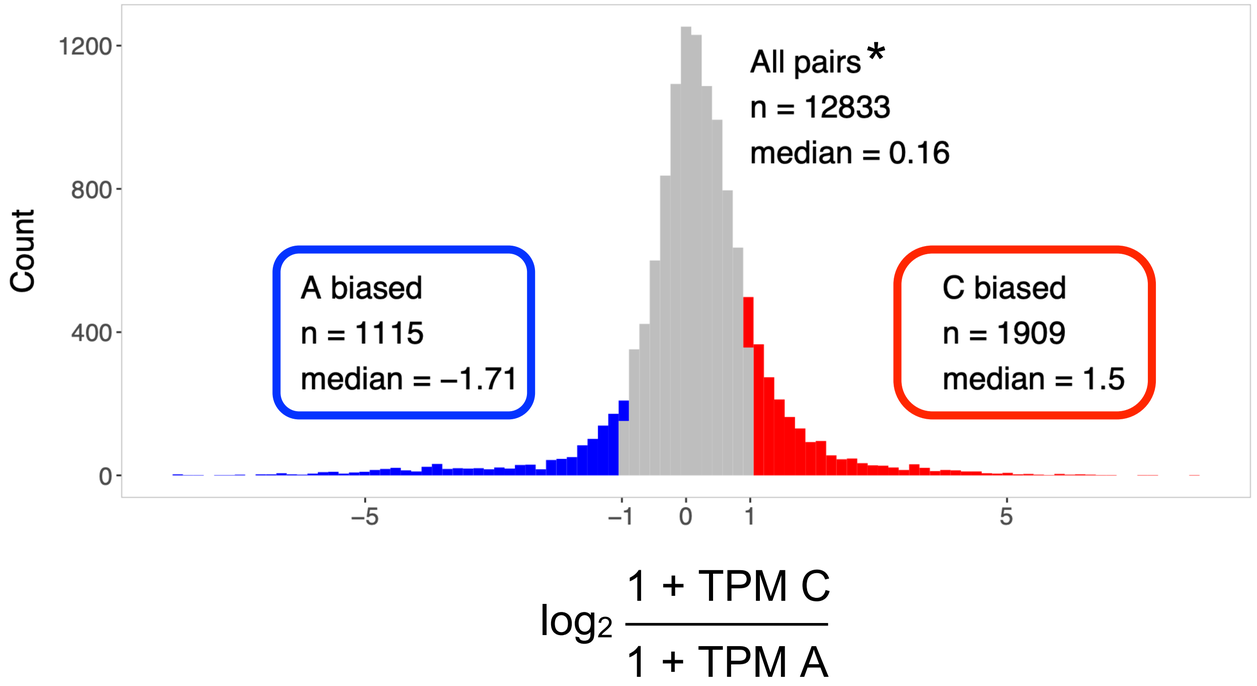
Zhongshuang11

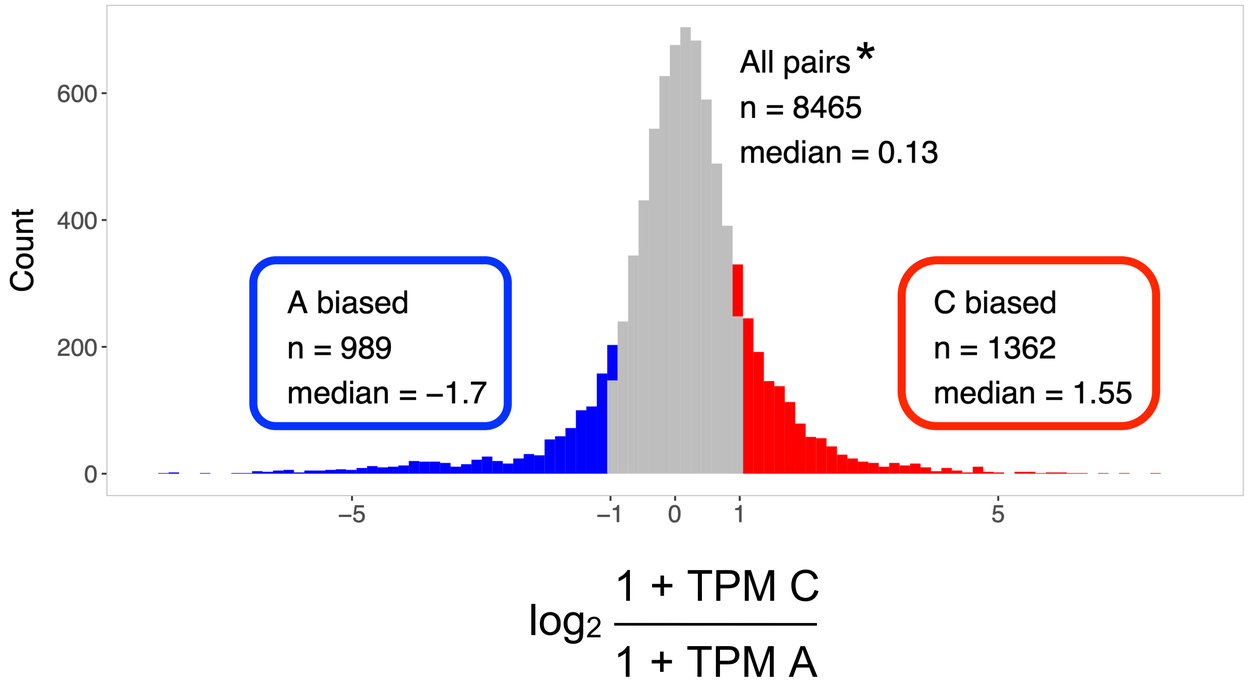


Bias to C subgenome is preserved across tissues

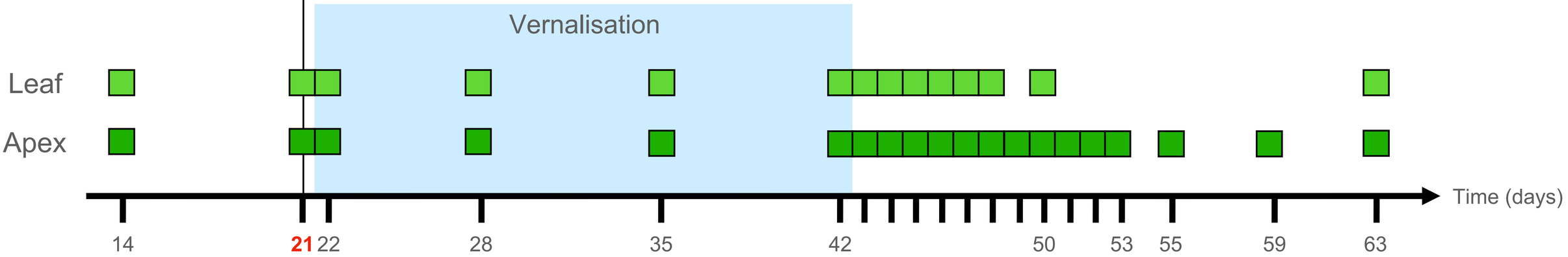
Apex (21d)

Leaf (21d)





What happens during Zhongshuang11 development?



Thank you

Rachel Wells
Lorelei Bilham
Judith Irwin
Steve Penfield
Carmel O'Neill

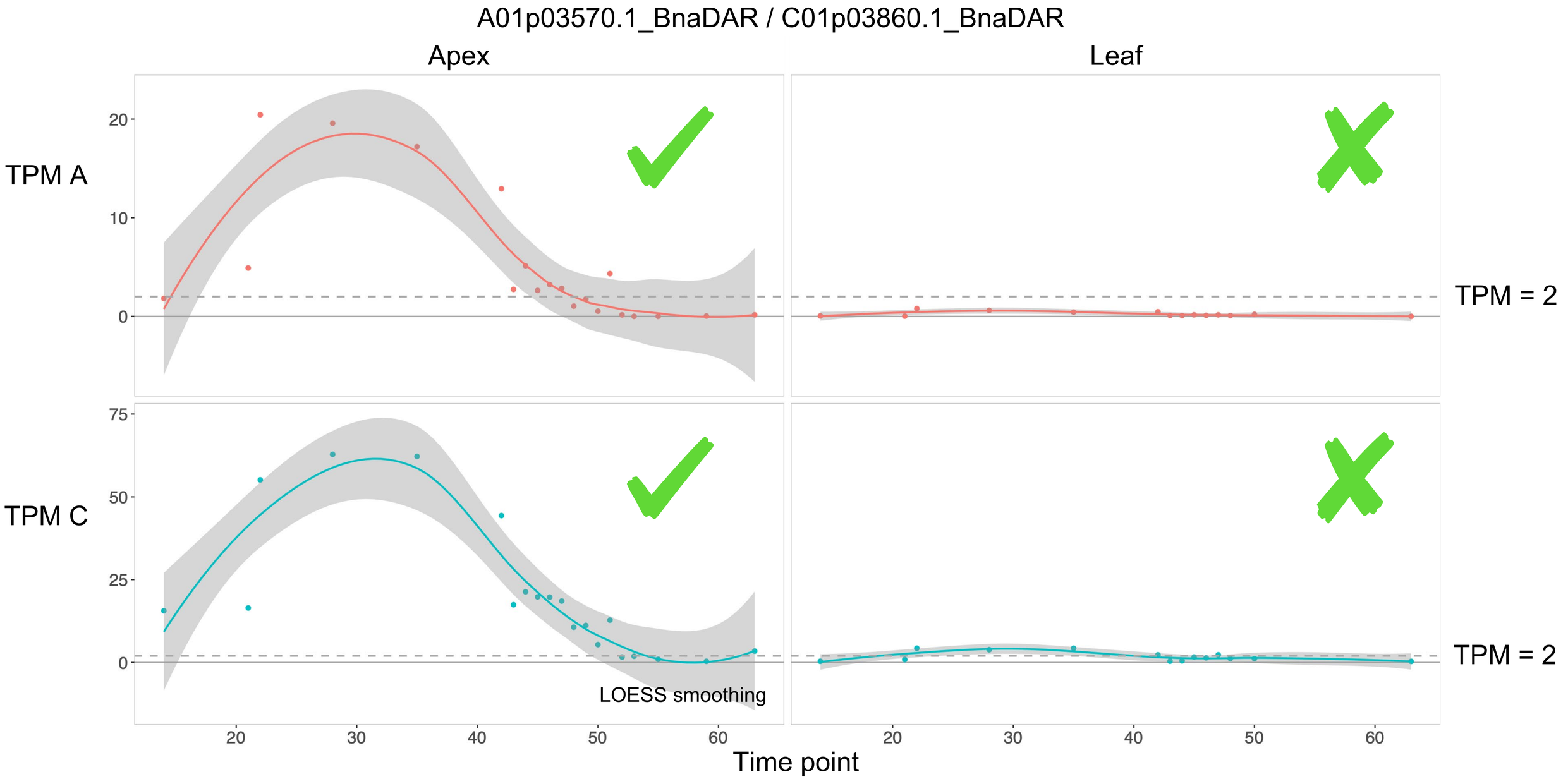
Experiments

3 repetitions in CER

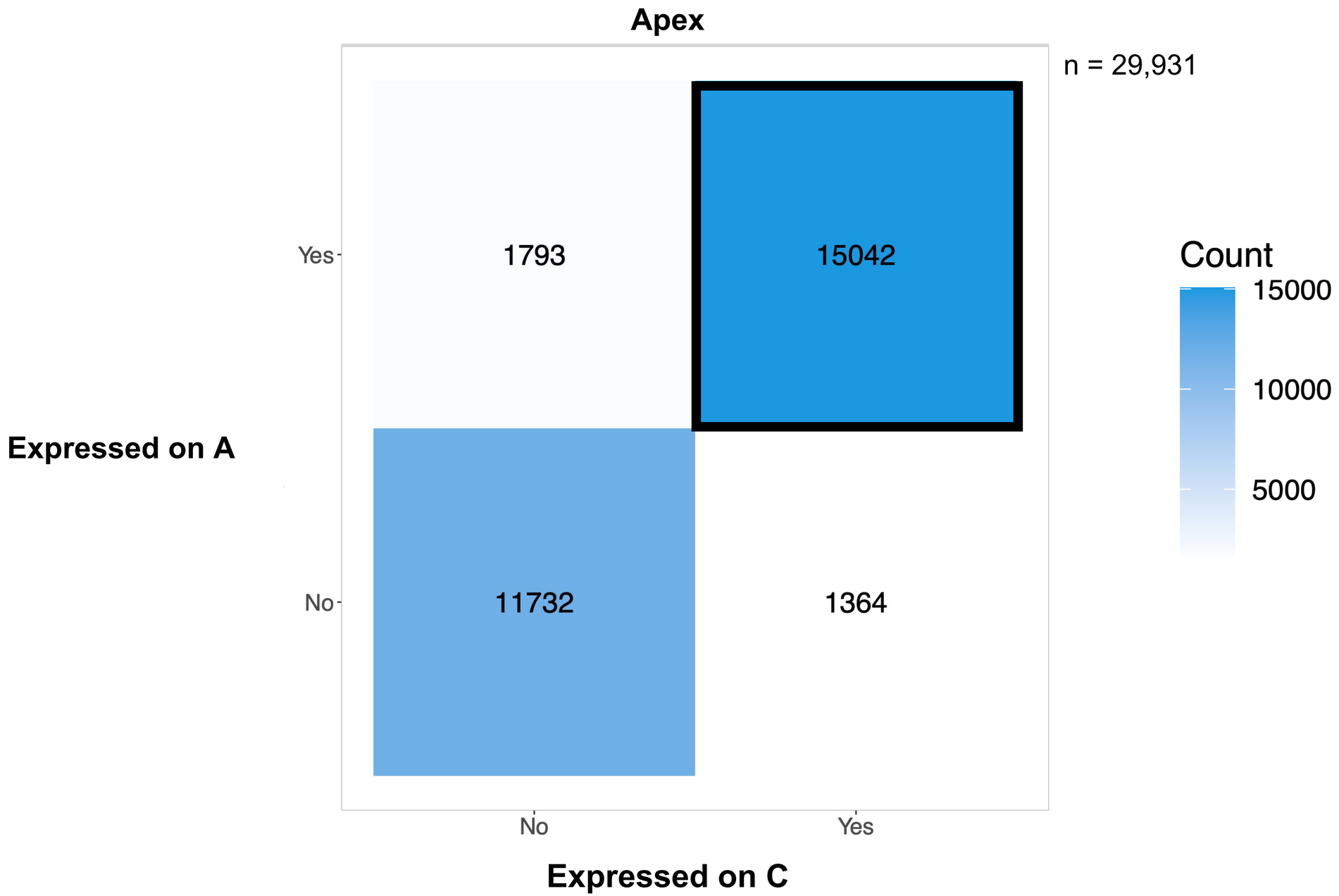
Alignment

Darmor 10 reference
Uniquely mapped reads

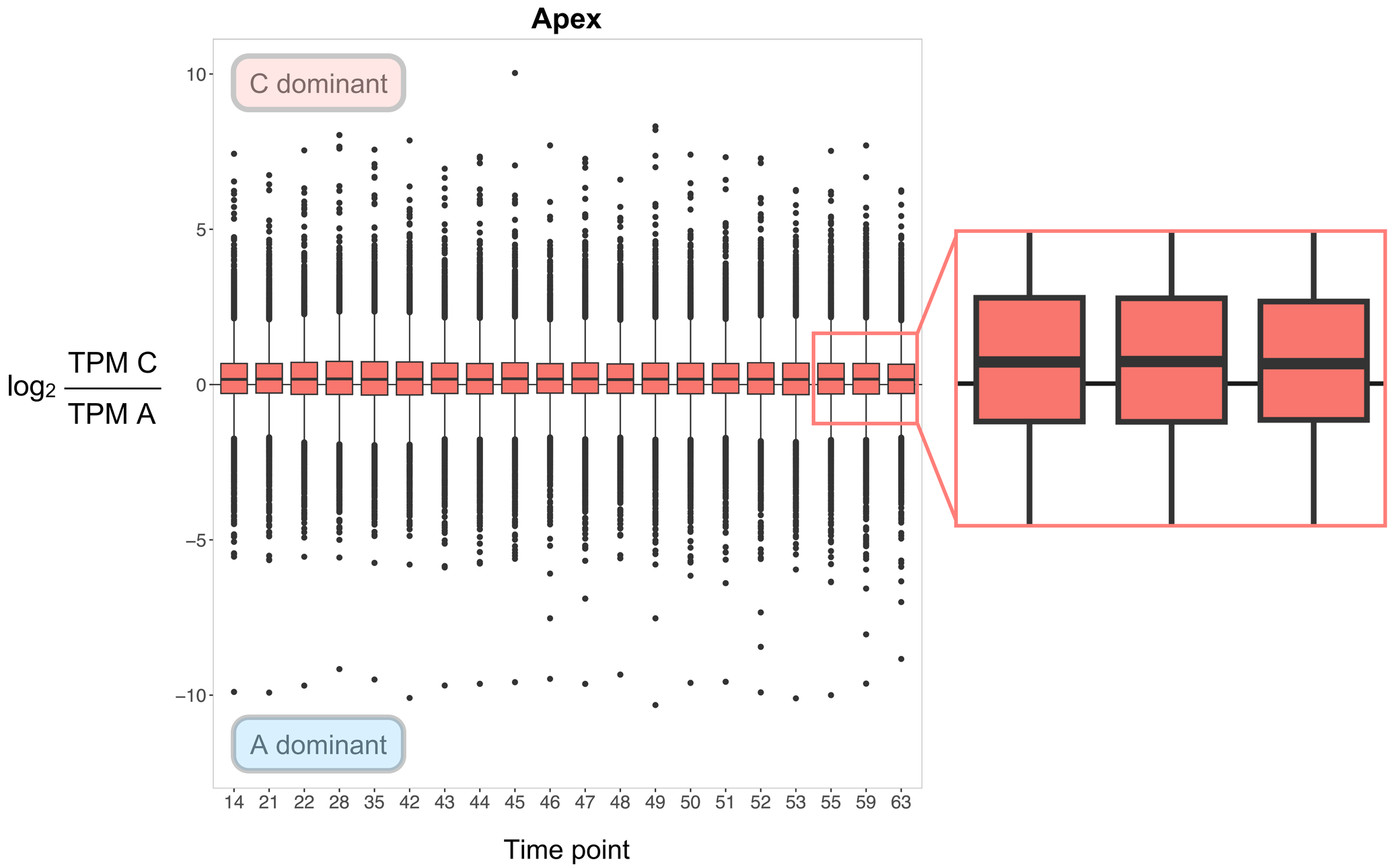
Homoeolog pair expression dynamics are tissue dependent



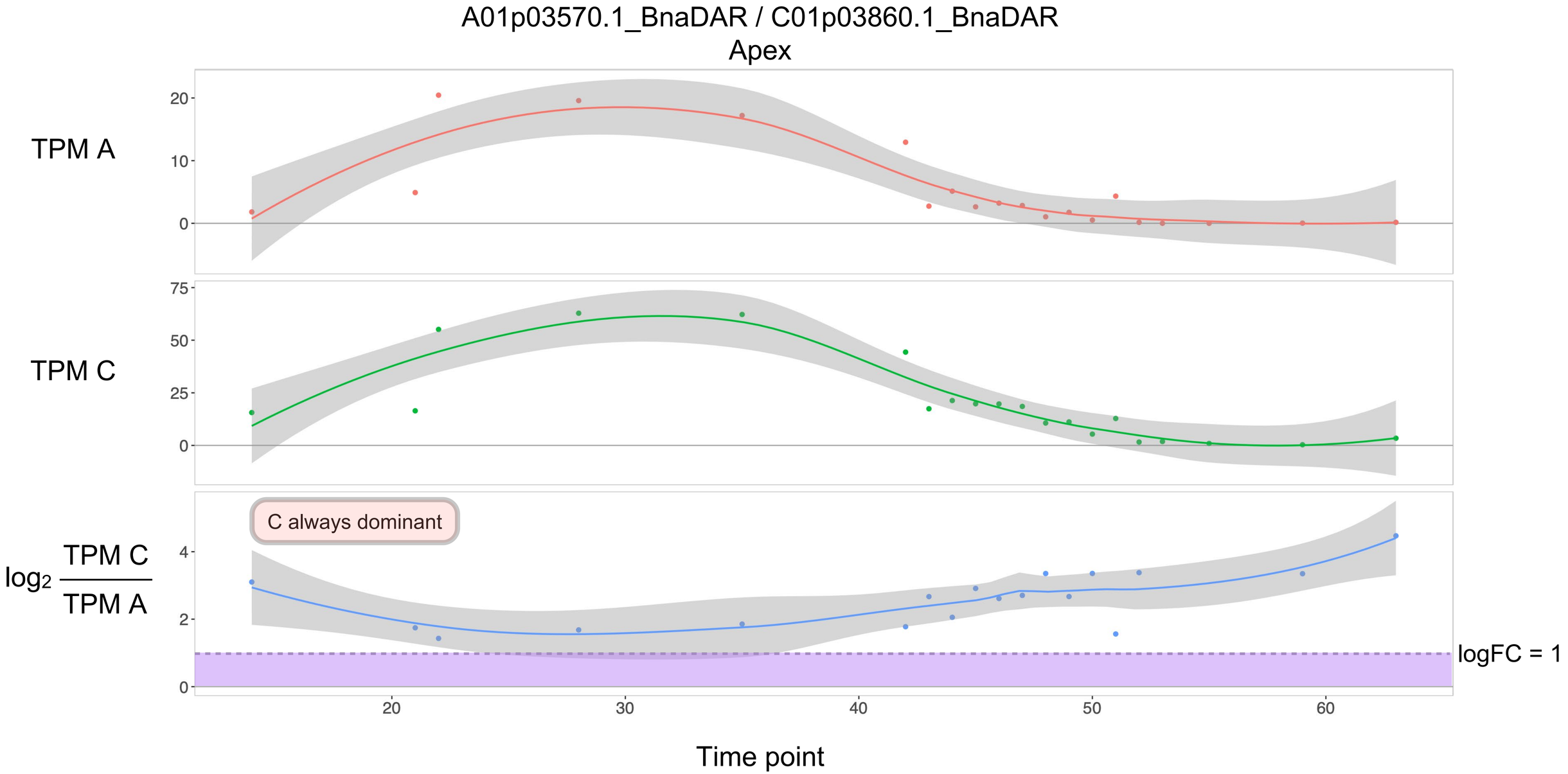
Expression filtering halves number of HPs



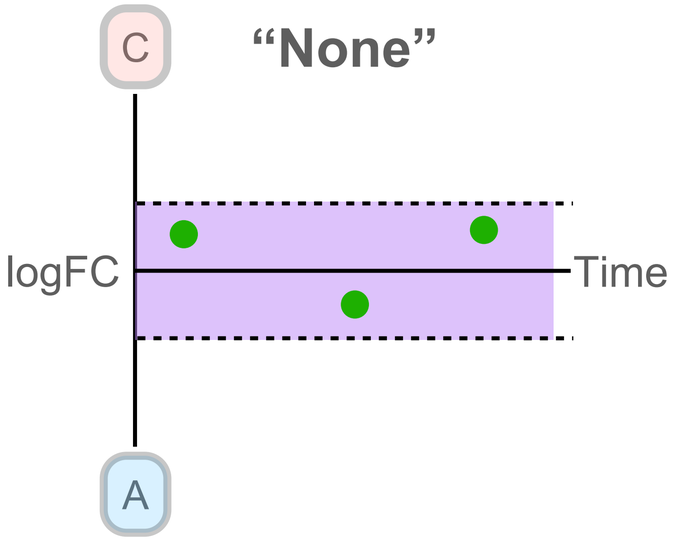
C subgenome bias is preserved across time

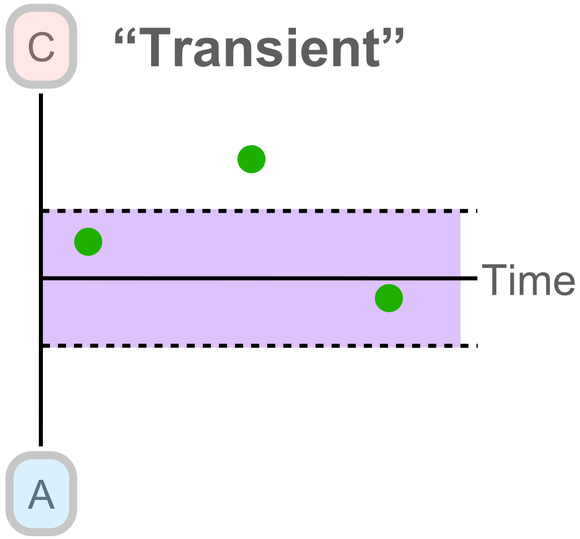


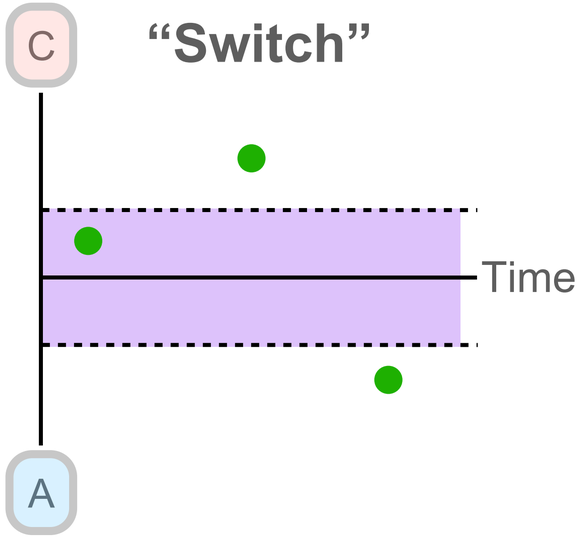
Categorising dominance

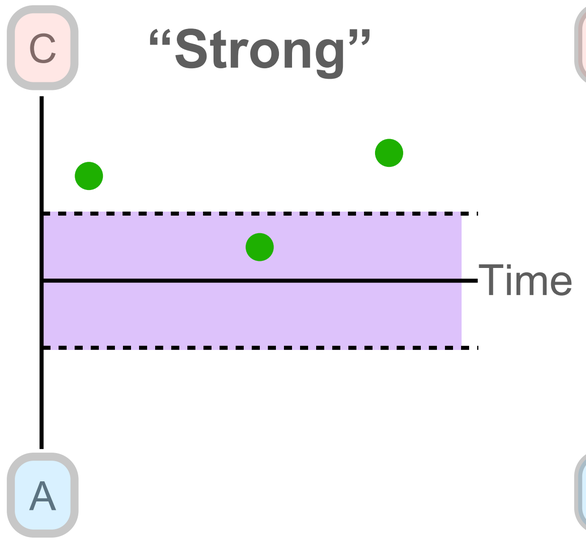


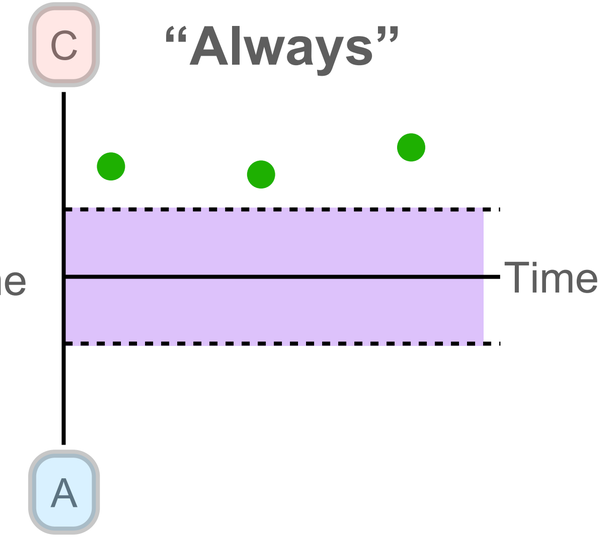
Categorising dominance



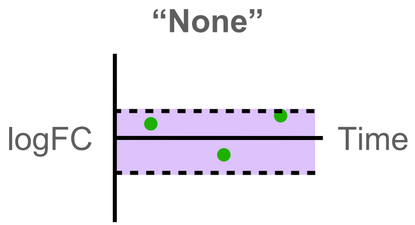


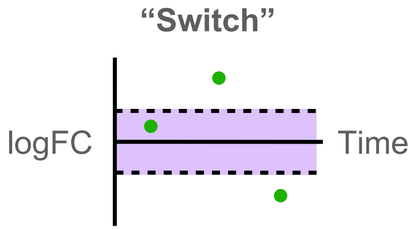


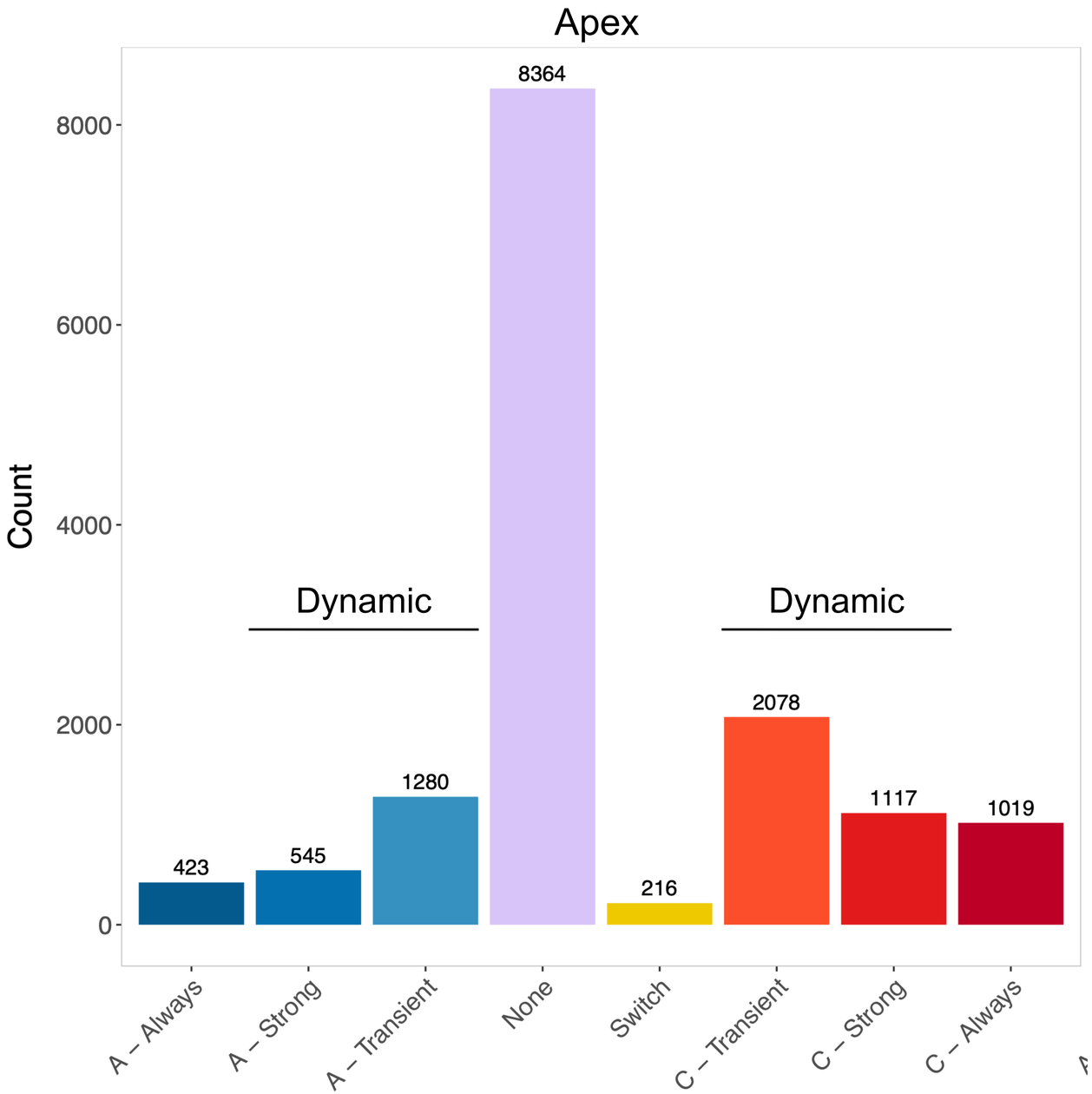


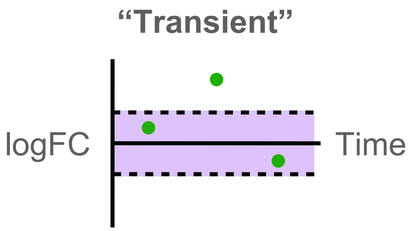


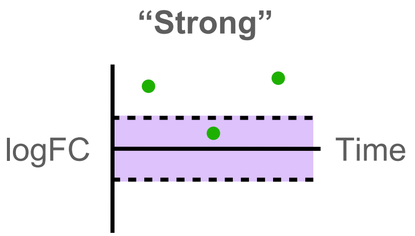
No dominance “wins” - C subgenome dominates

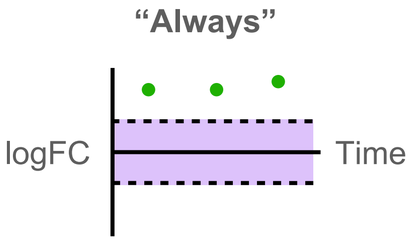










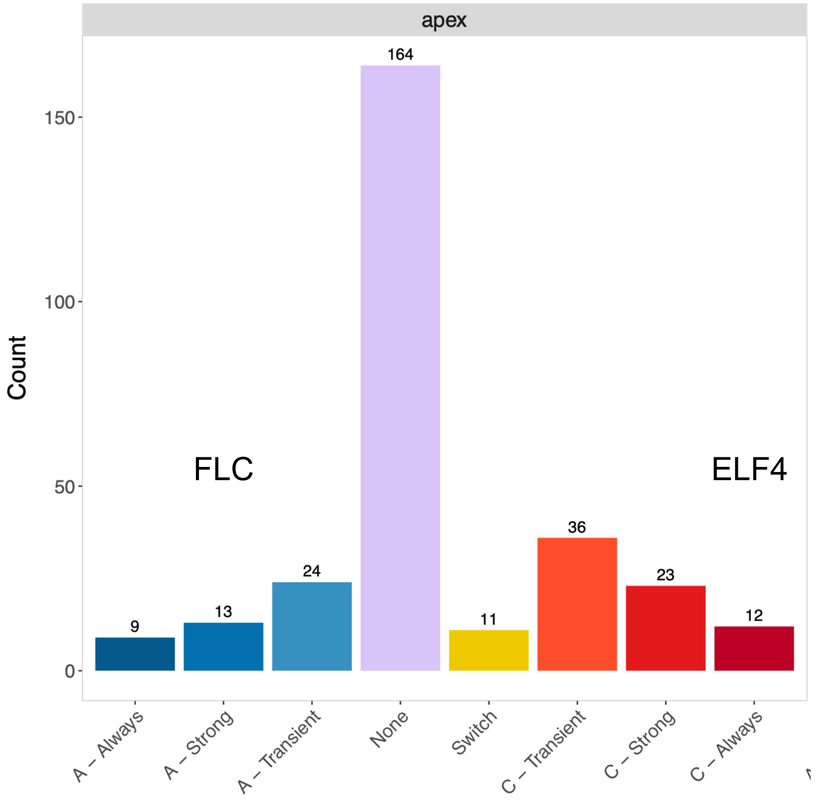


Comparing dominance dynamics to other *B. napus* accessions

Accession	Type	Time (days)
Zhongshuang11	Semi-winter	14 to 63
Express	Winter	21 to 98
Stellar	Spring	14 to 40

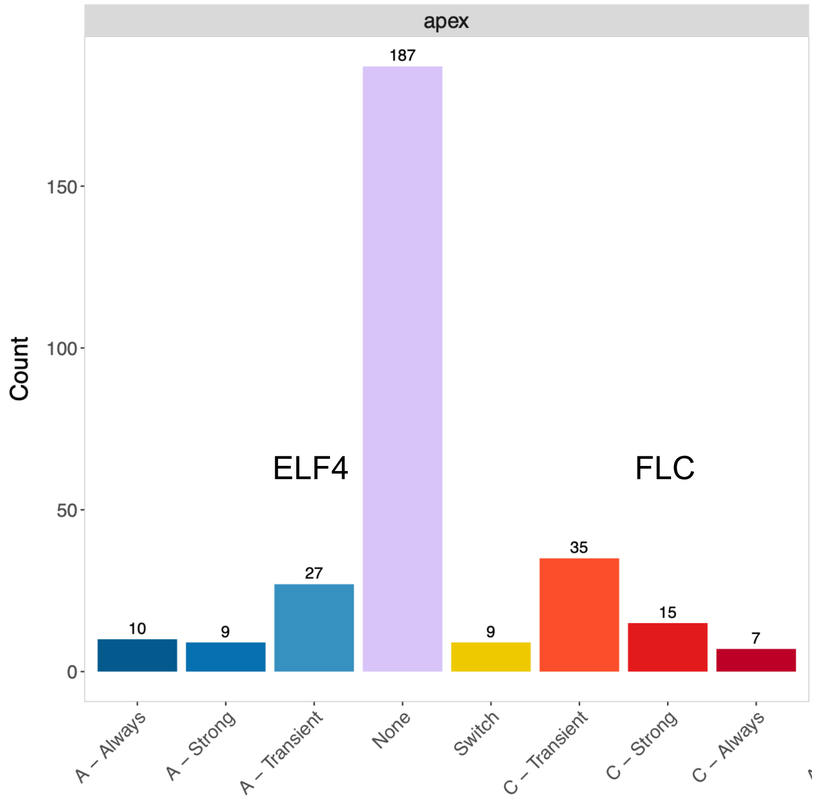
FLOR-ID genes: Type-specific dominance “fingerprinting”

Zhongshuang11



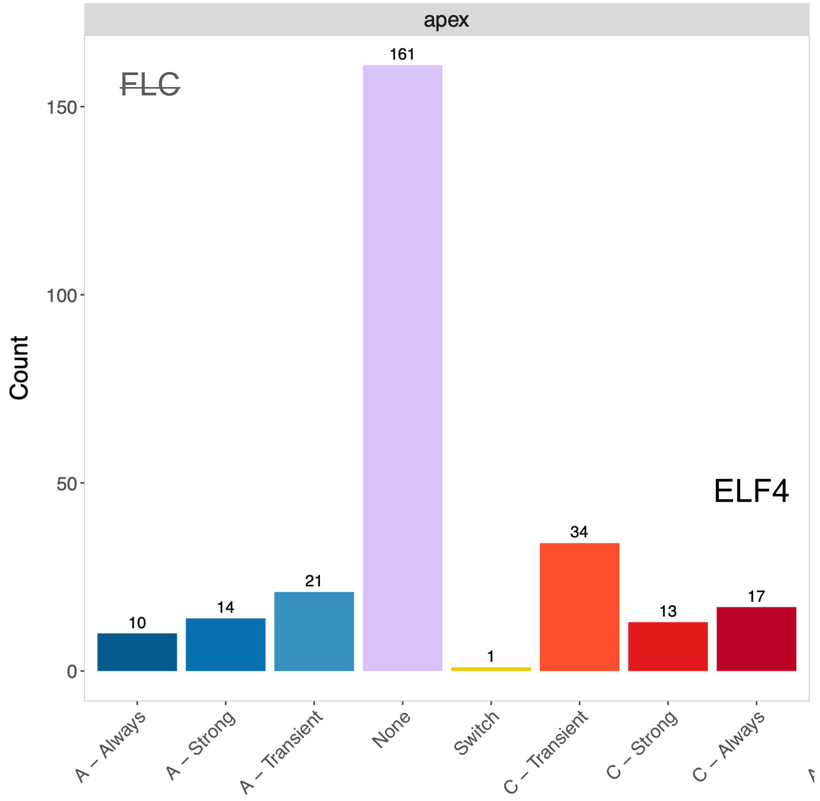
Semi-winter

Express



Winter

Stellar

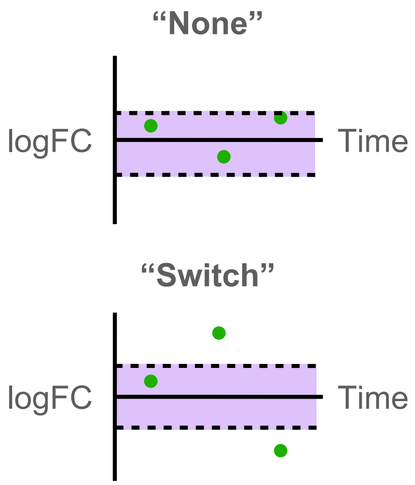


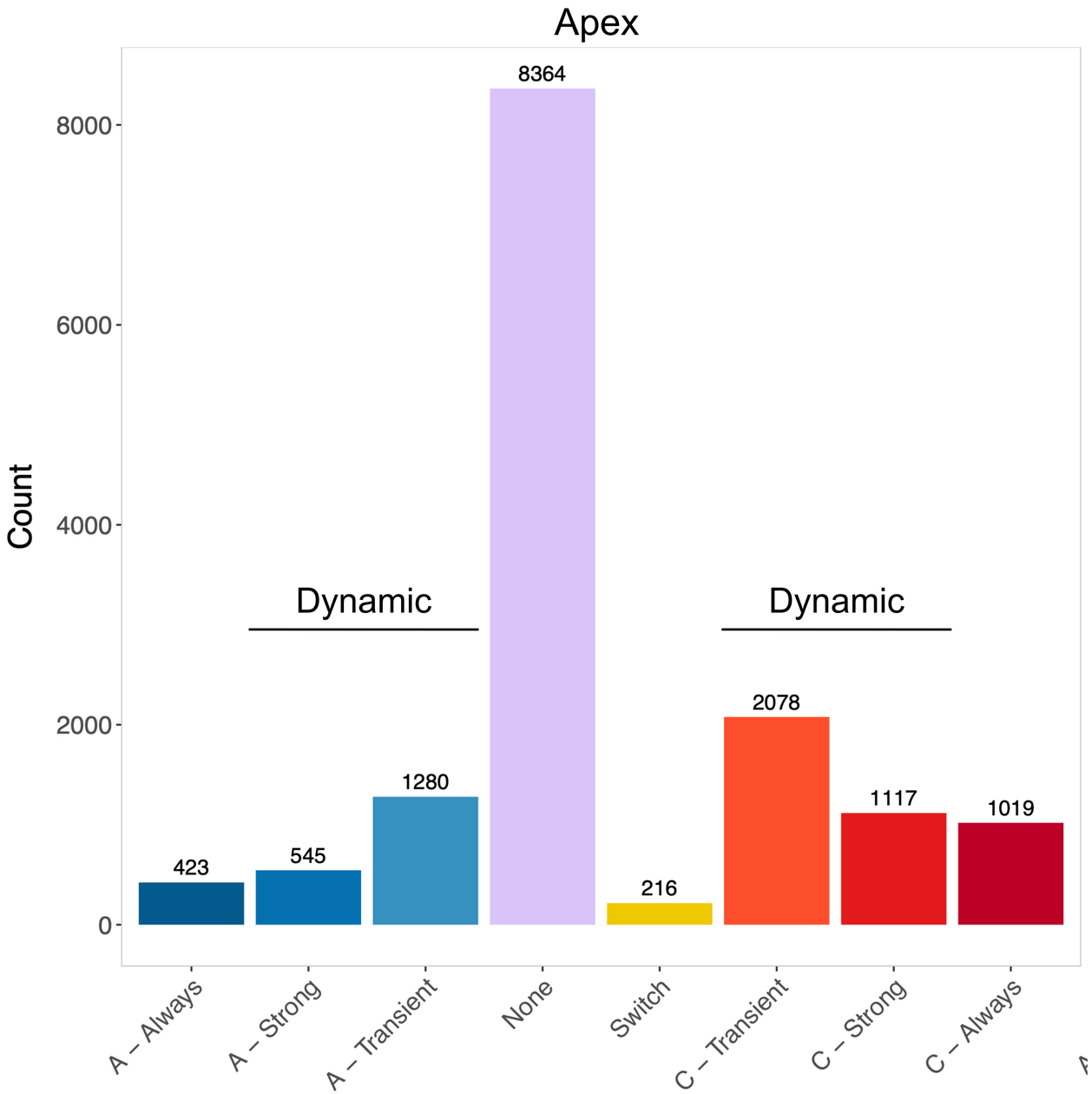
Spring

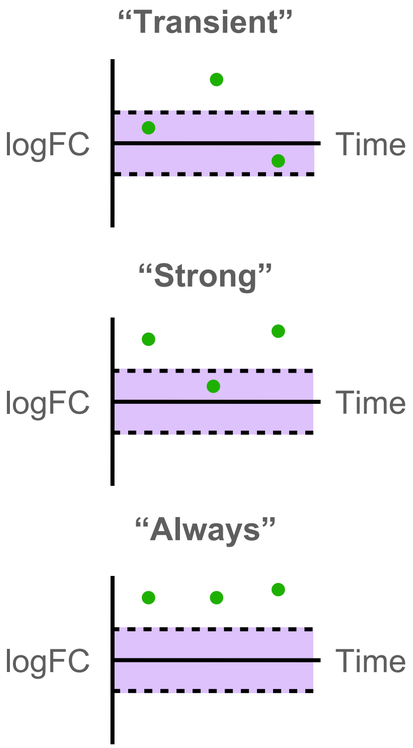
https://www.flor-id.org

Towards linking dominance to function: matching expression dynamics

Zhongshuang11



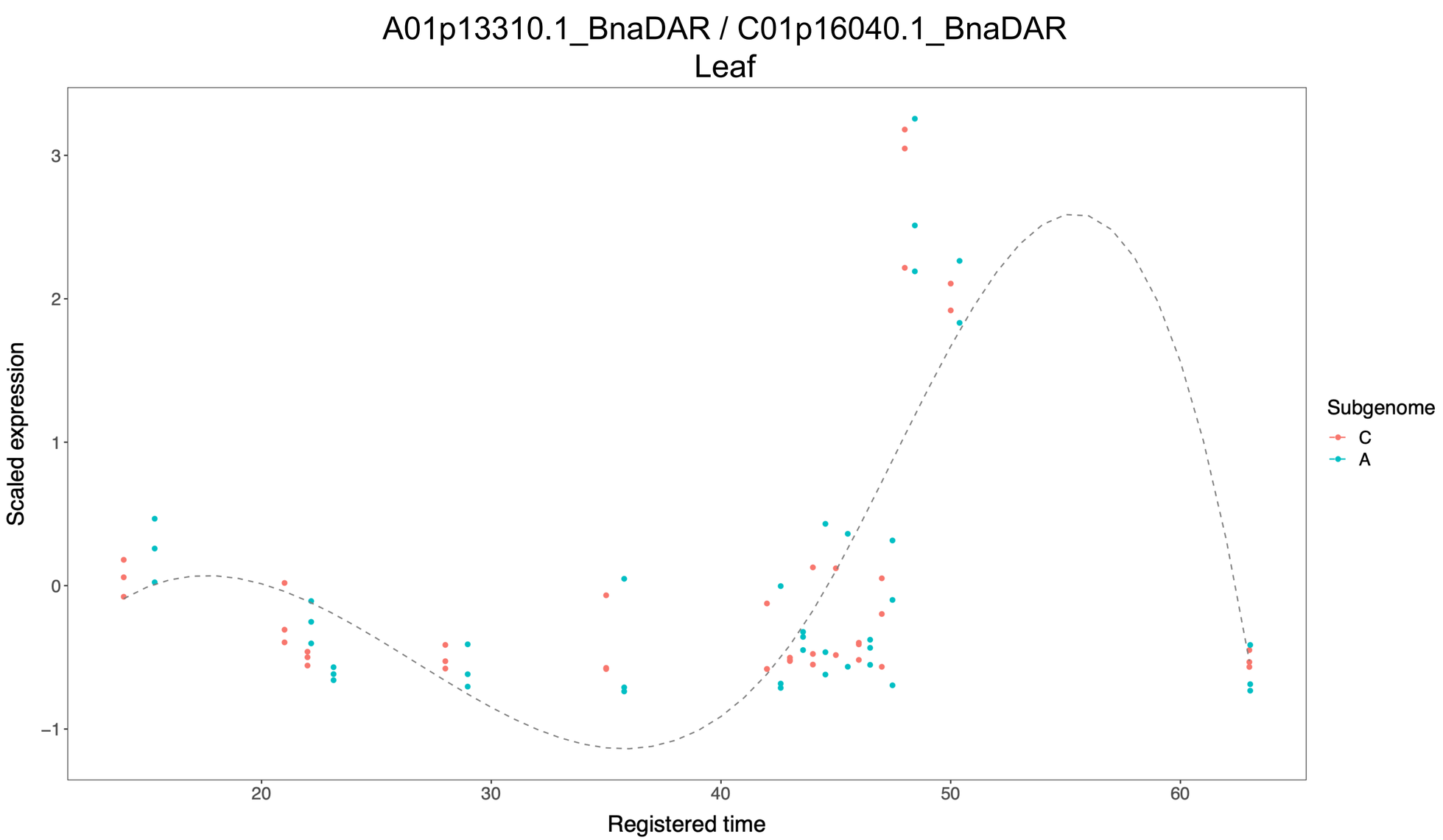




greatR: Gene registration from expression and time courses in R

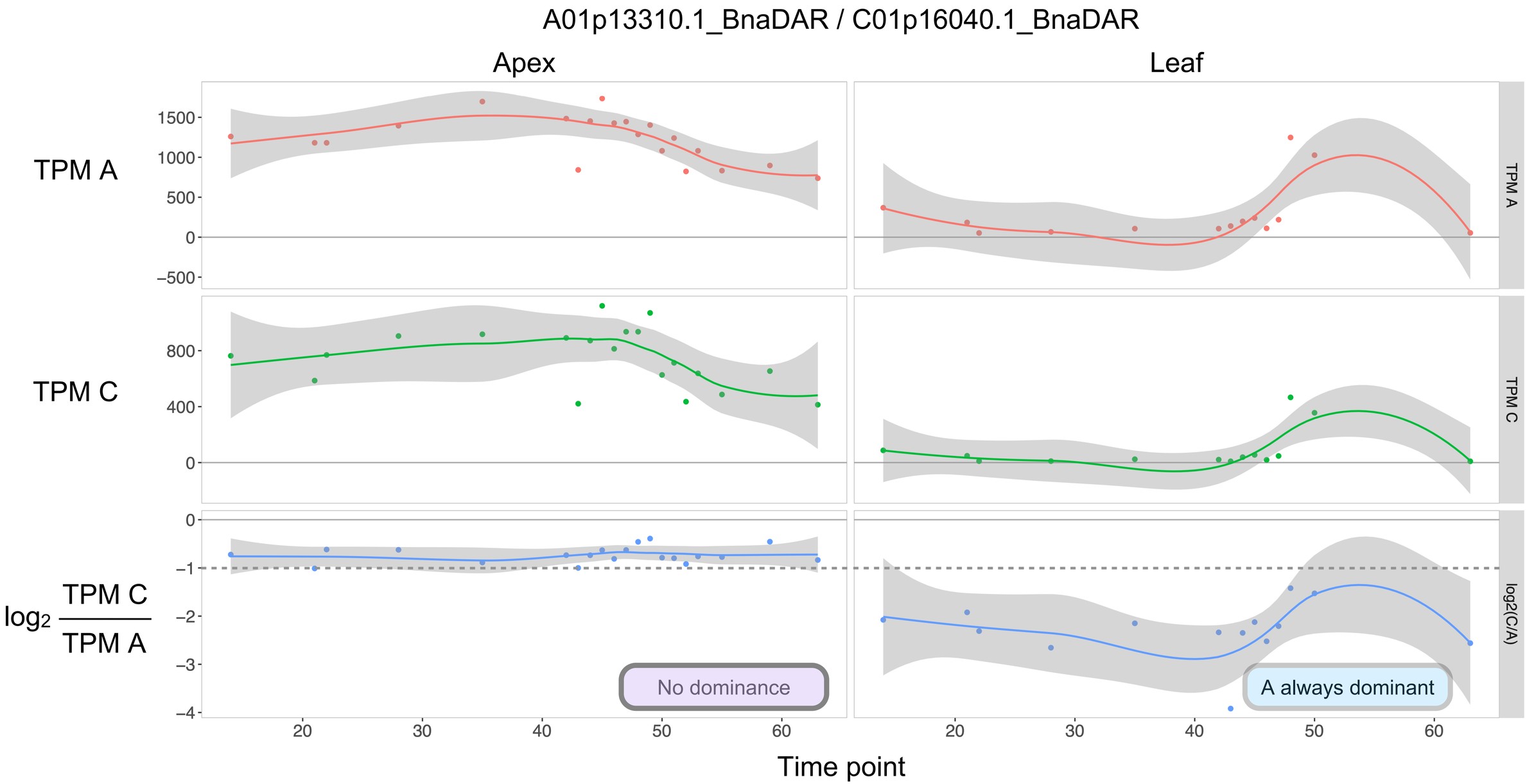
Ruth Kristianingsih

Wed AM

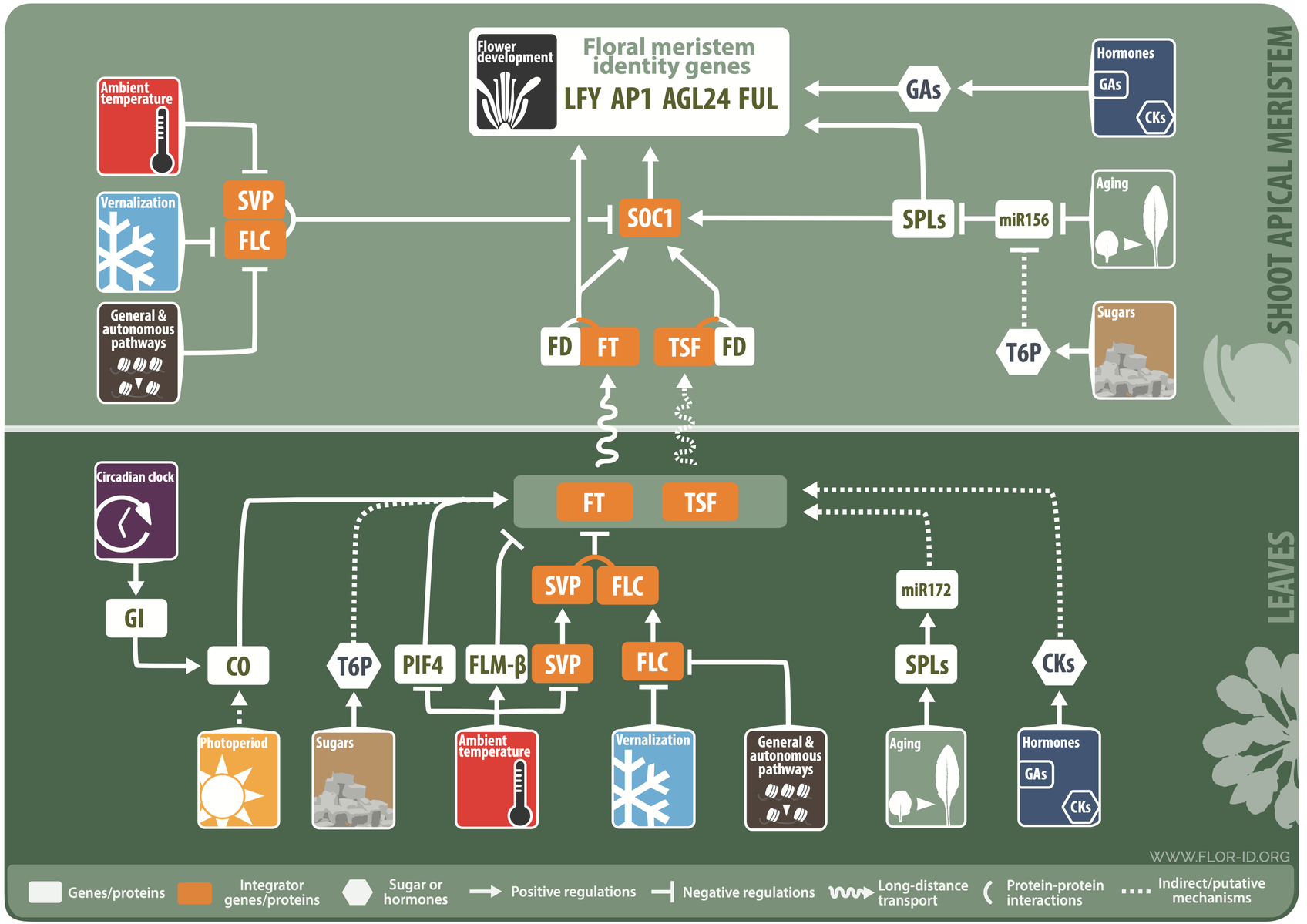


“Registered” time courses: ~10,000 in Apex, ~9,000 in Leaf

Homoeologs with identical protein sequence and same dynamics display dominance



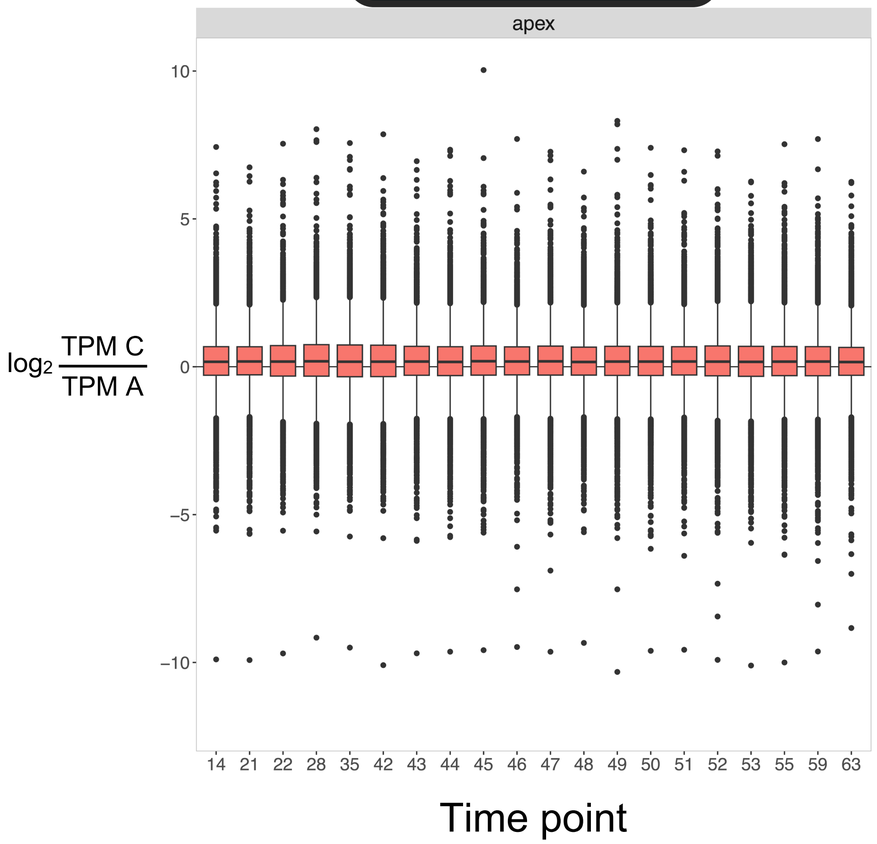
Linking Arabidopsis to *B. napus*



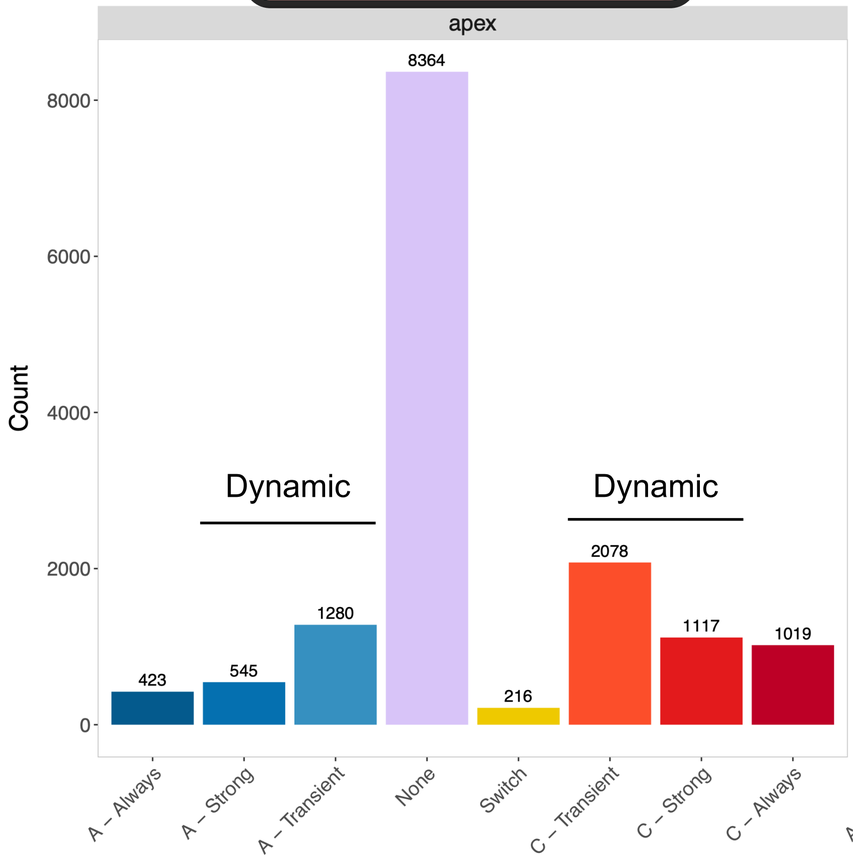
From https://www.flor-id.org

Conclusions: How to understand regulatory mechanisms that lead to subgenome dominance?

C bias preserved



Dominance is dynamic



Hypothesis: Differences in genome dominance between cultivars are the consequences of transcription

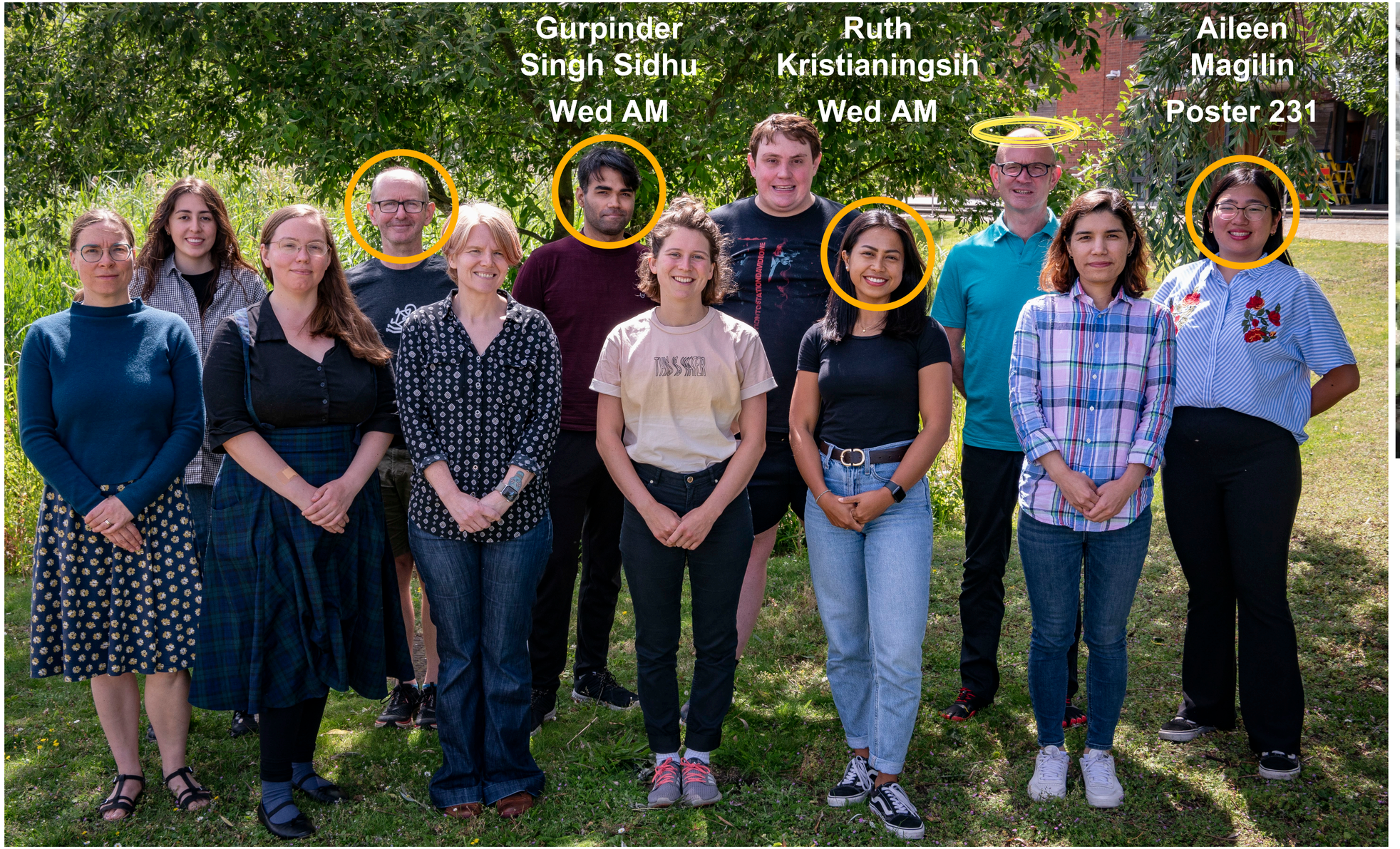
Outlook

Accession	Type	Time (days)
Zhongshuang11	Semi-winter	14 to 63
Stellar	Spring	14 to 40
Express	Winter	21 to 98
Ragged Jack	Biennial	14 to 130

- GO term analysis
- Seed development RNA-seq
- **Ruth**: “Registered” genes 

- **Gurpinder**: Gene Regulatory Networks

Thanks to Richard Morris and Rachel Wells



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