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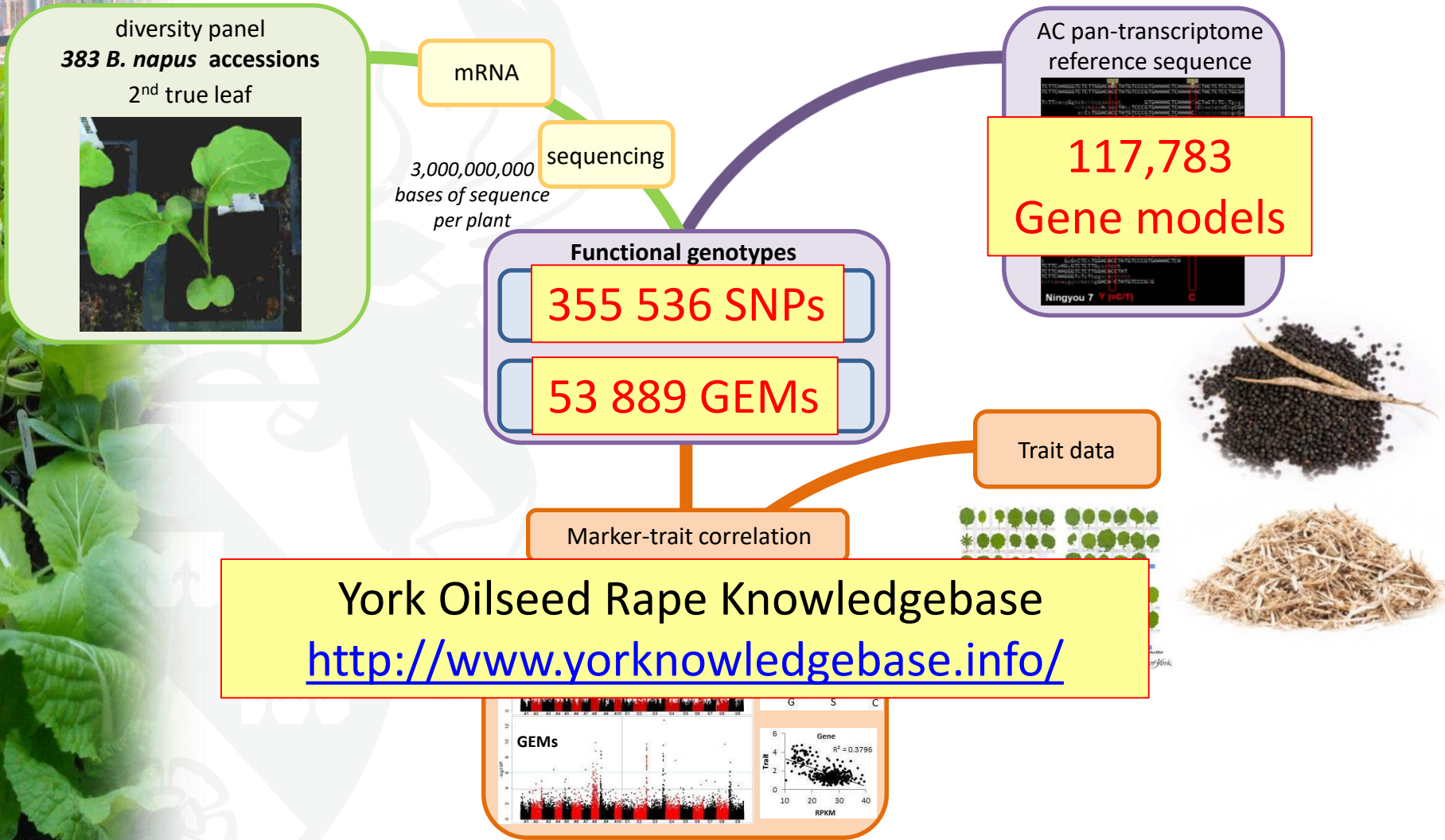
An updated Associative Transcriptomics platform for *Brassica napus*

Lenka Havlickova

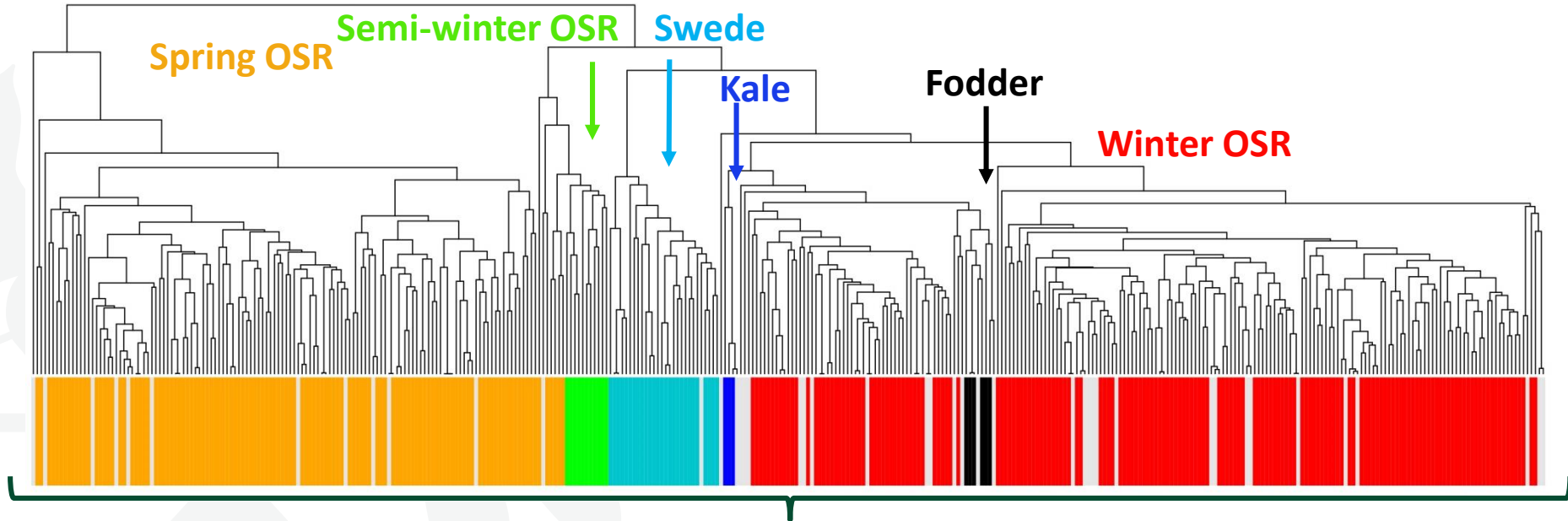
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Associative Transcriptomics platform

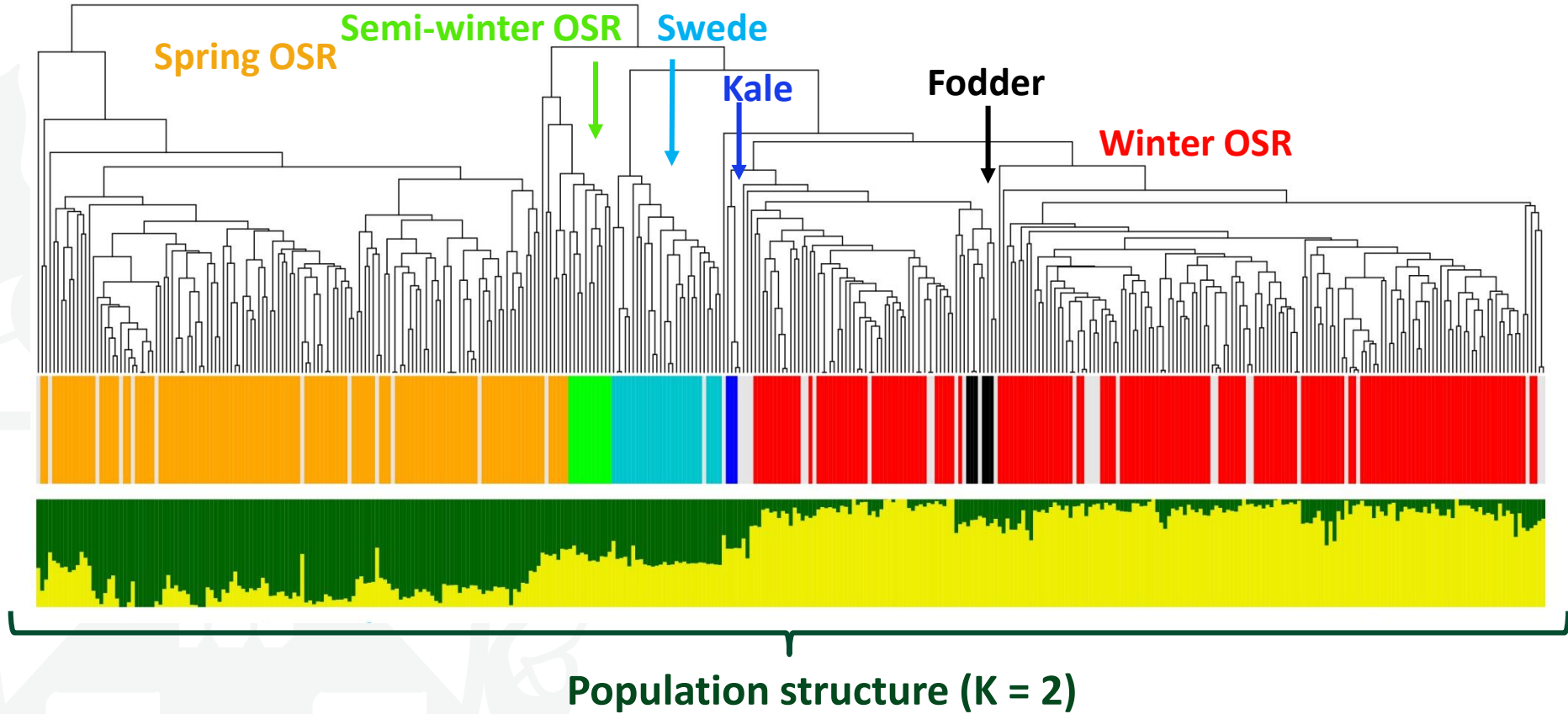


Population structure across 383 accessions of *B. napus*

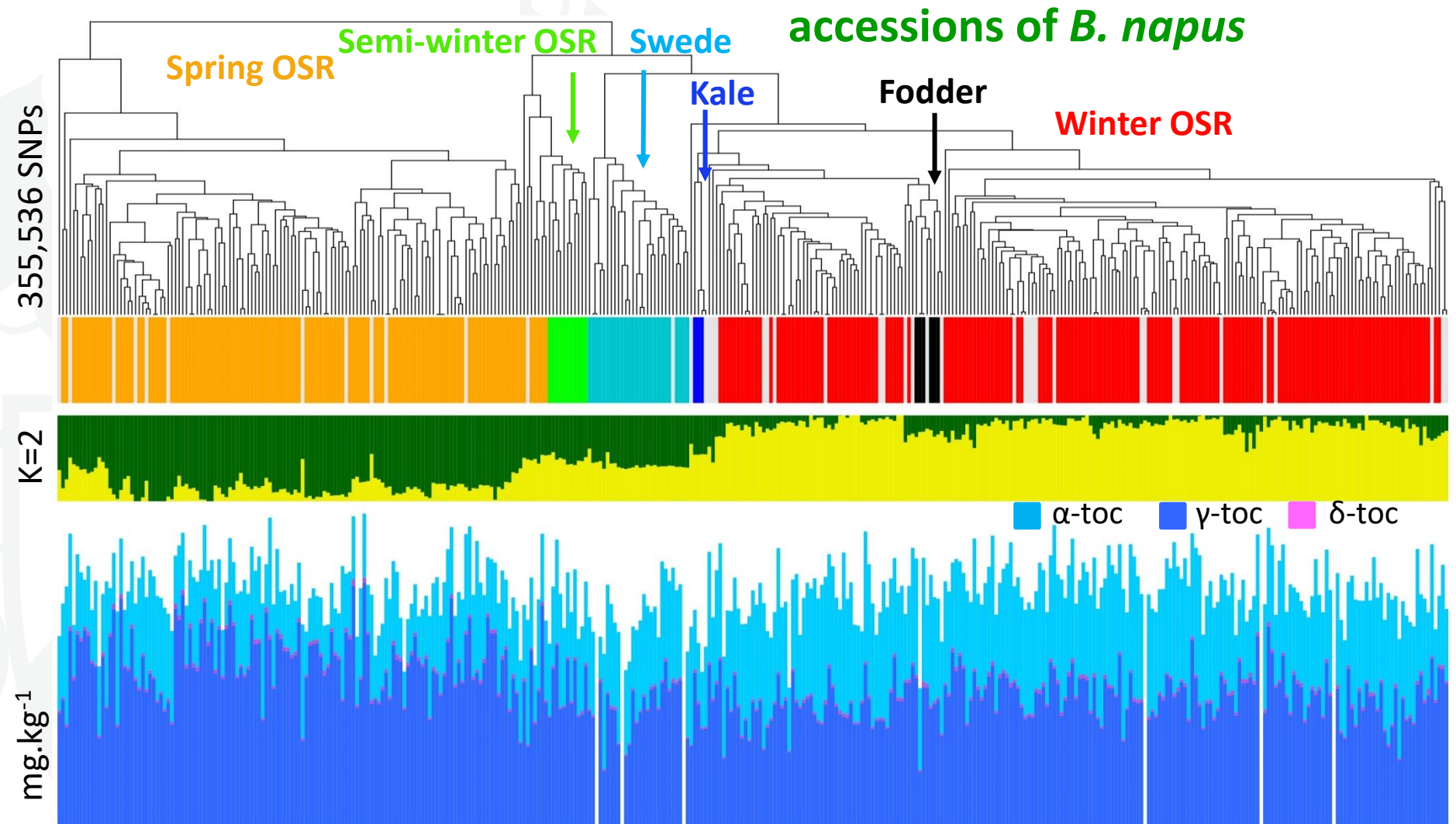


Dendrogram based on 355,536 transcriptome SNPs scored across 383 accessions

Population structure across 383 accessions of *B. napus*



Population structure and tocopherol variation across 377 accessions of *B. napus*



the plant journal Havlickova et al. (2017) Validation of an updated Associative Transcriptomics platform for the polyploid crop species *Brassica napus* by dissection of the genetic architecture of erucic acid and tocopherol isoform variation in seeds. *The Plant Journal*; doi:10.1111/tpj.13767

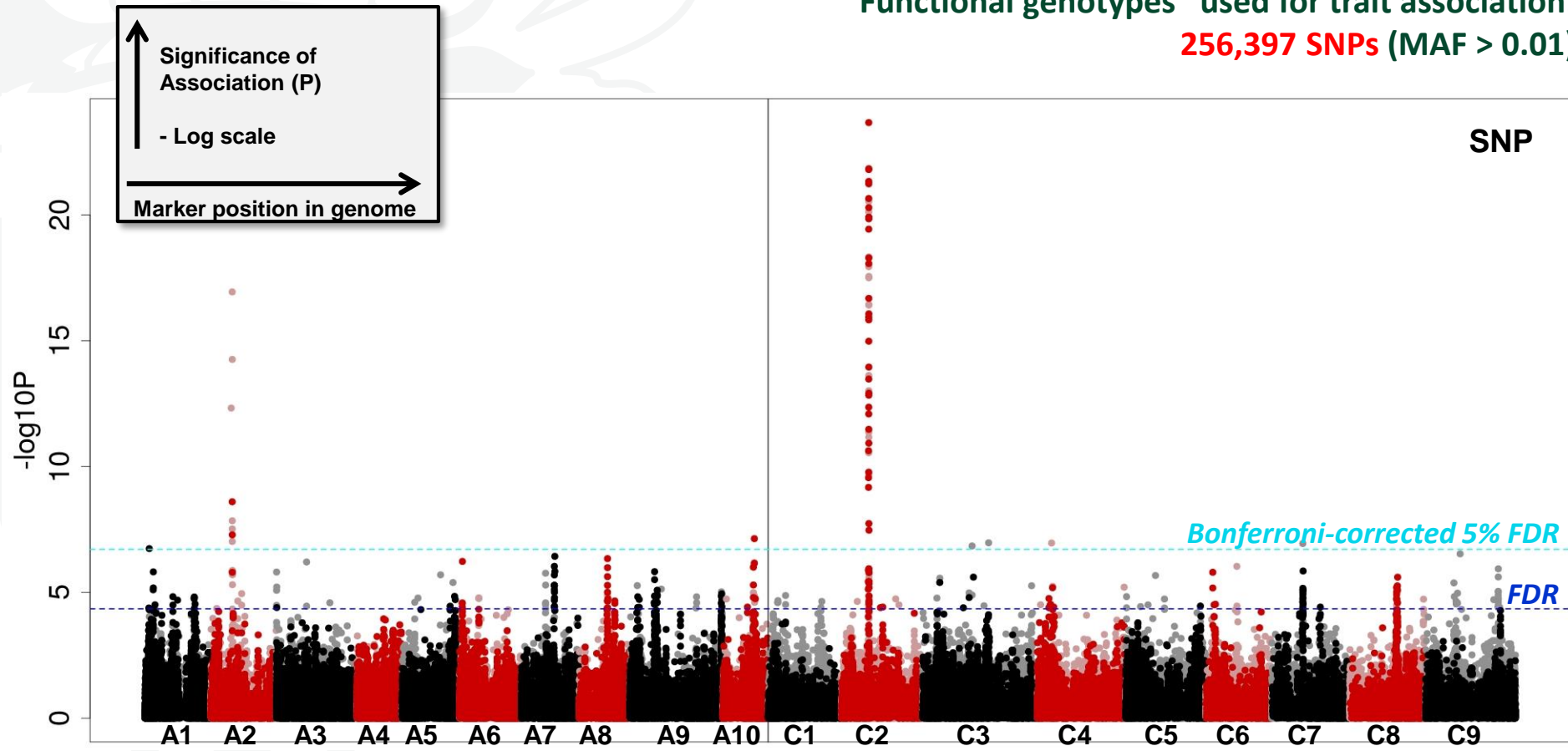
Associative Transcriptomics platform: Case of tocopherols

- Proportion of gamma/alpha tocopherol in seeds of *B. napus*

~1,000,000,000,000 bp of sequence data from a diversity panel of 383 varieties

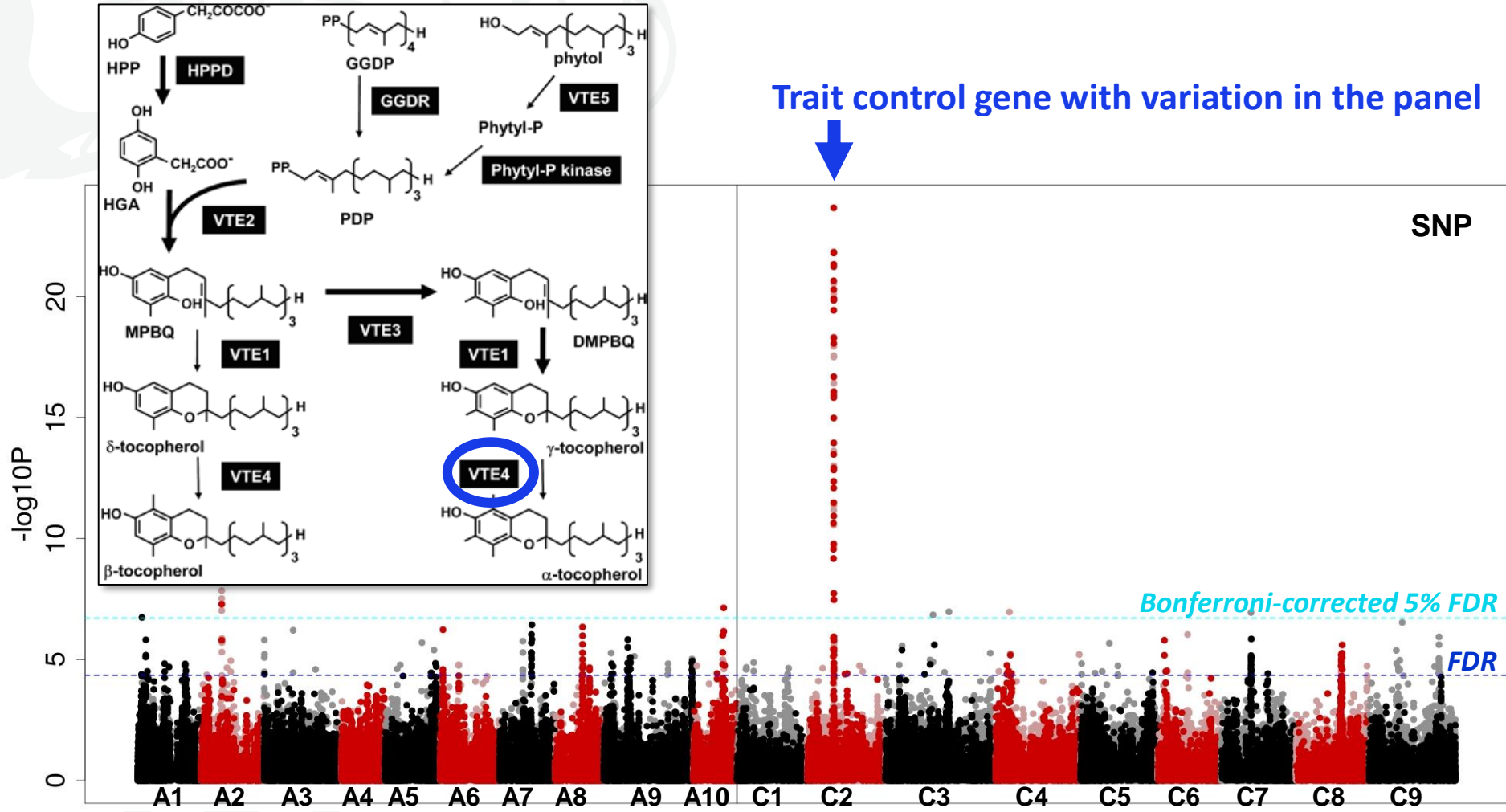
“Functional genotypes” used for trait association:

256,397 SNPs (MAF > 0.01)



Associative Transcriptomics platform: Case of tocopherols

- Proportion of gamma/alpha tocopherol in seeds of *B. napus*

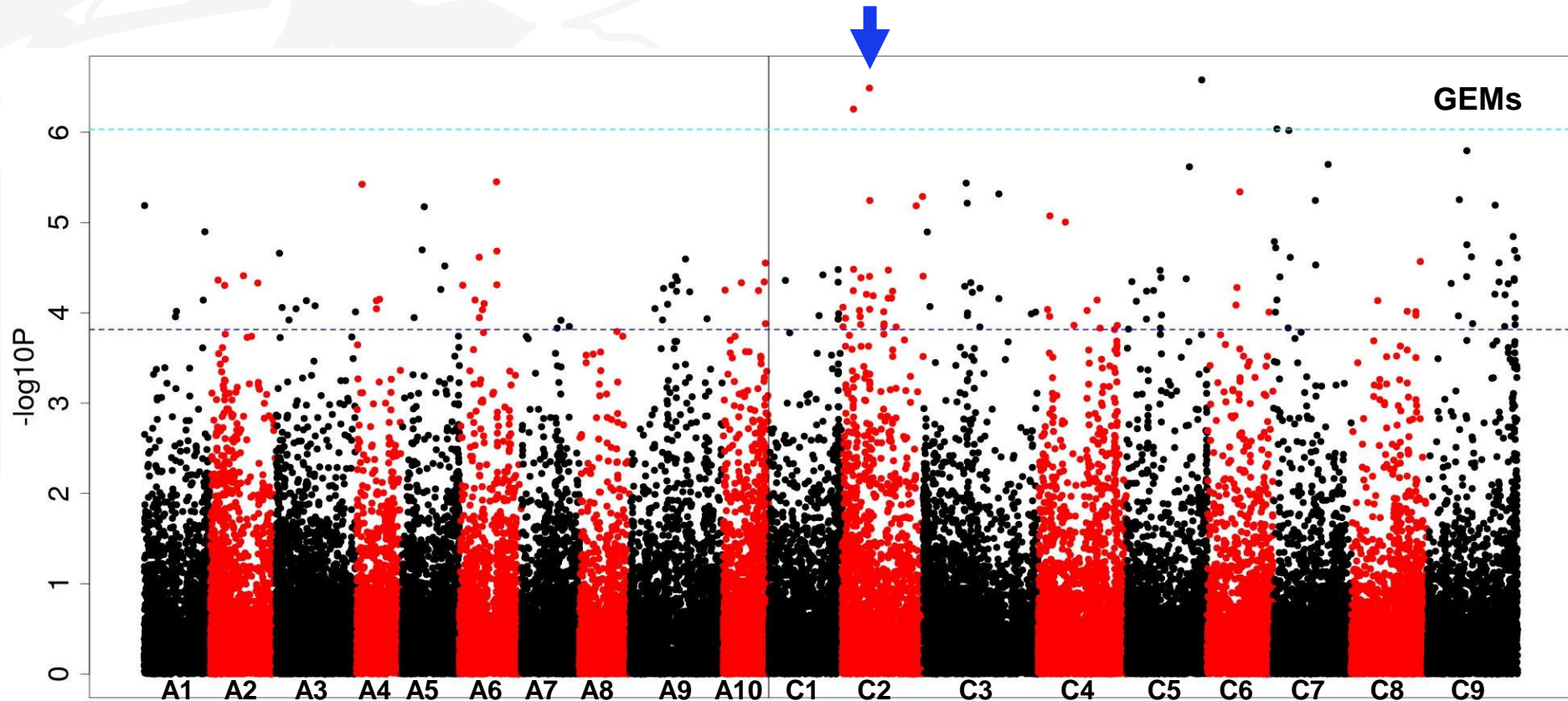


Associative Transcriptomics platform: Case of tocopherols

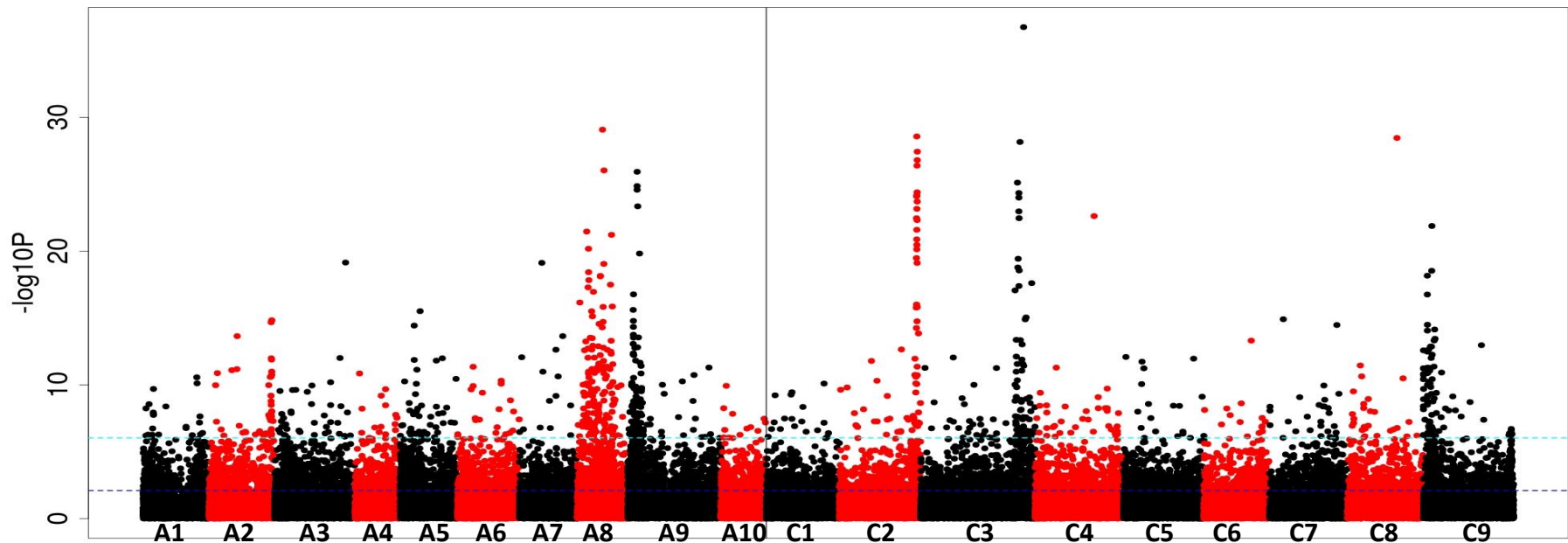
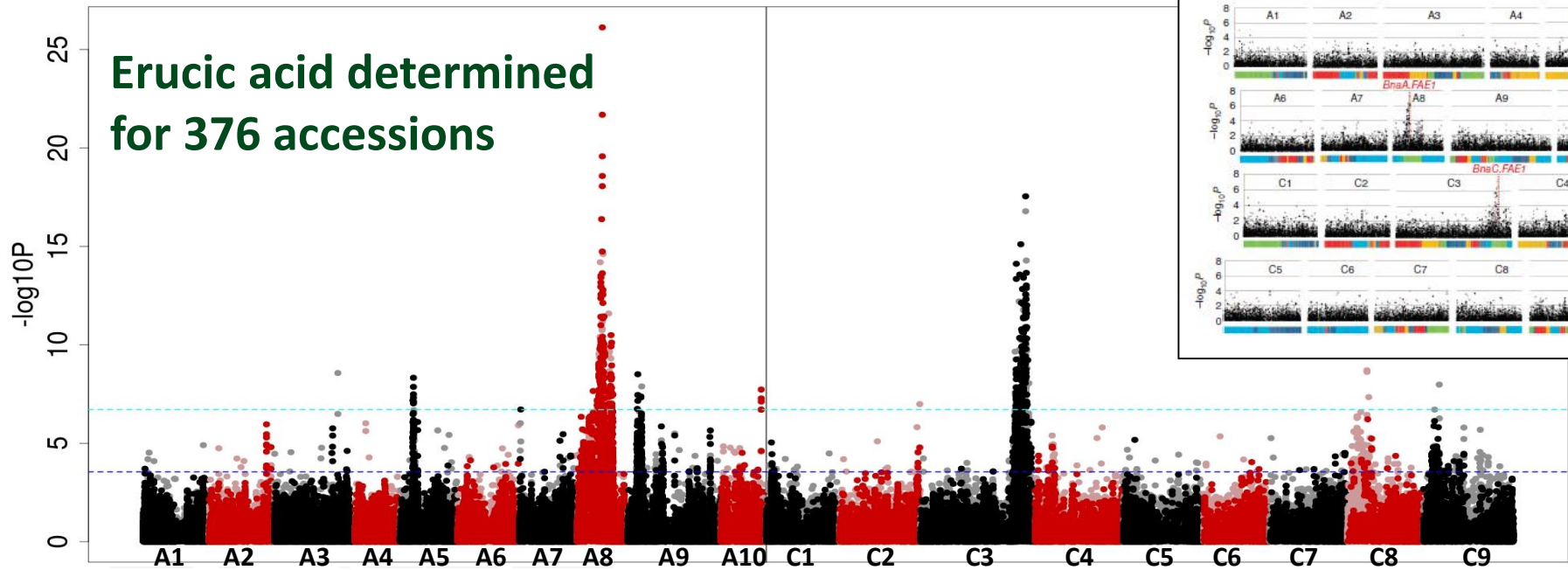
- Proportion of gamma/alpha tocopherol in seeds of *B. napus*

Expression data for 53,180 genes (>0.4 RPKM)

Trait control gene with variation in the panel



Erucic acid determined
for 376 accessions



The Bancroft group



Thank you for your attention!

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