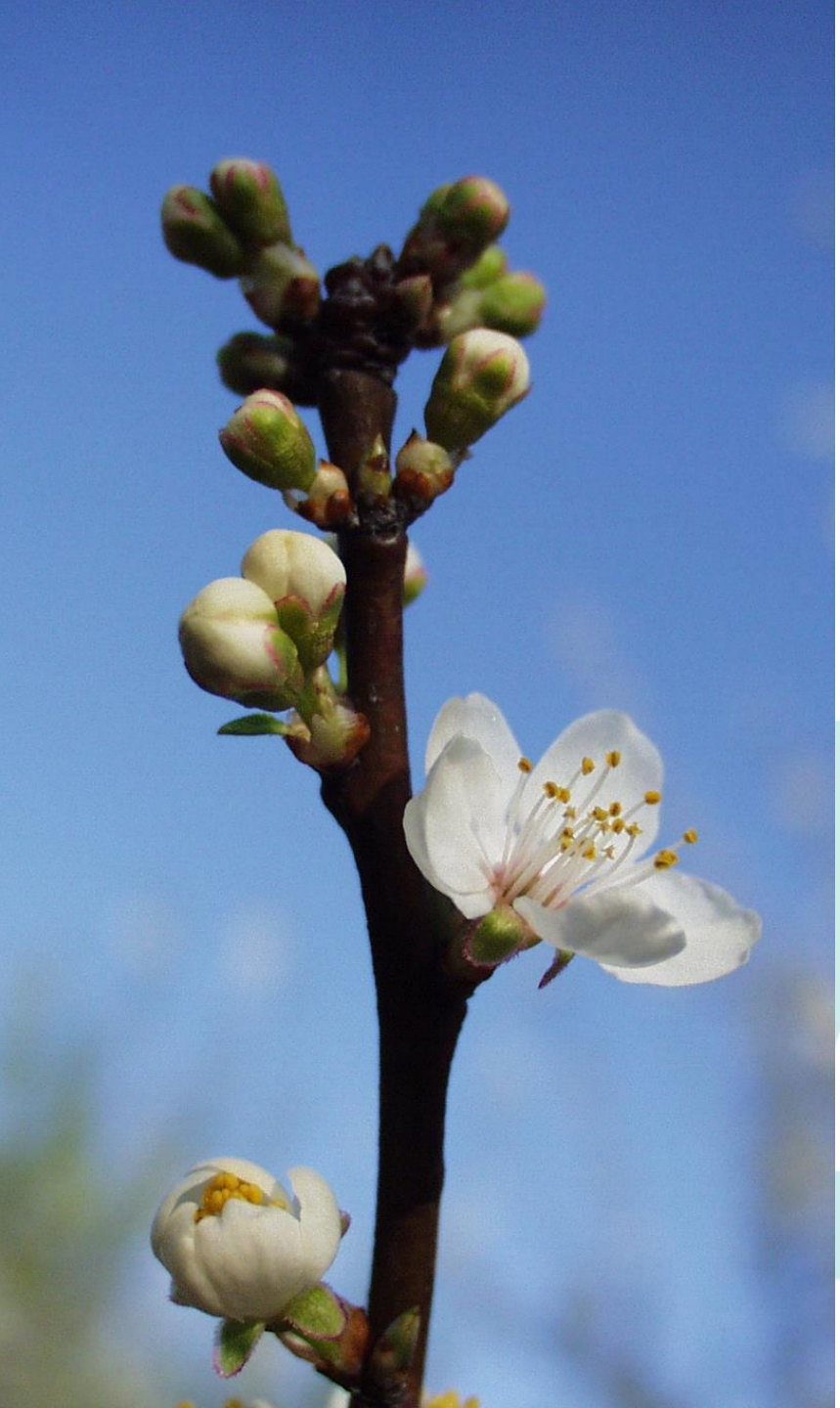
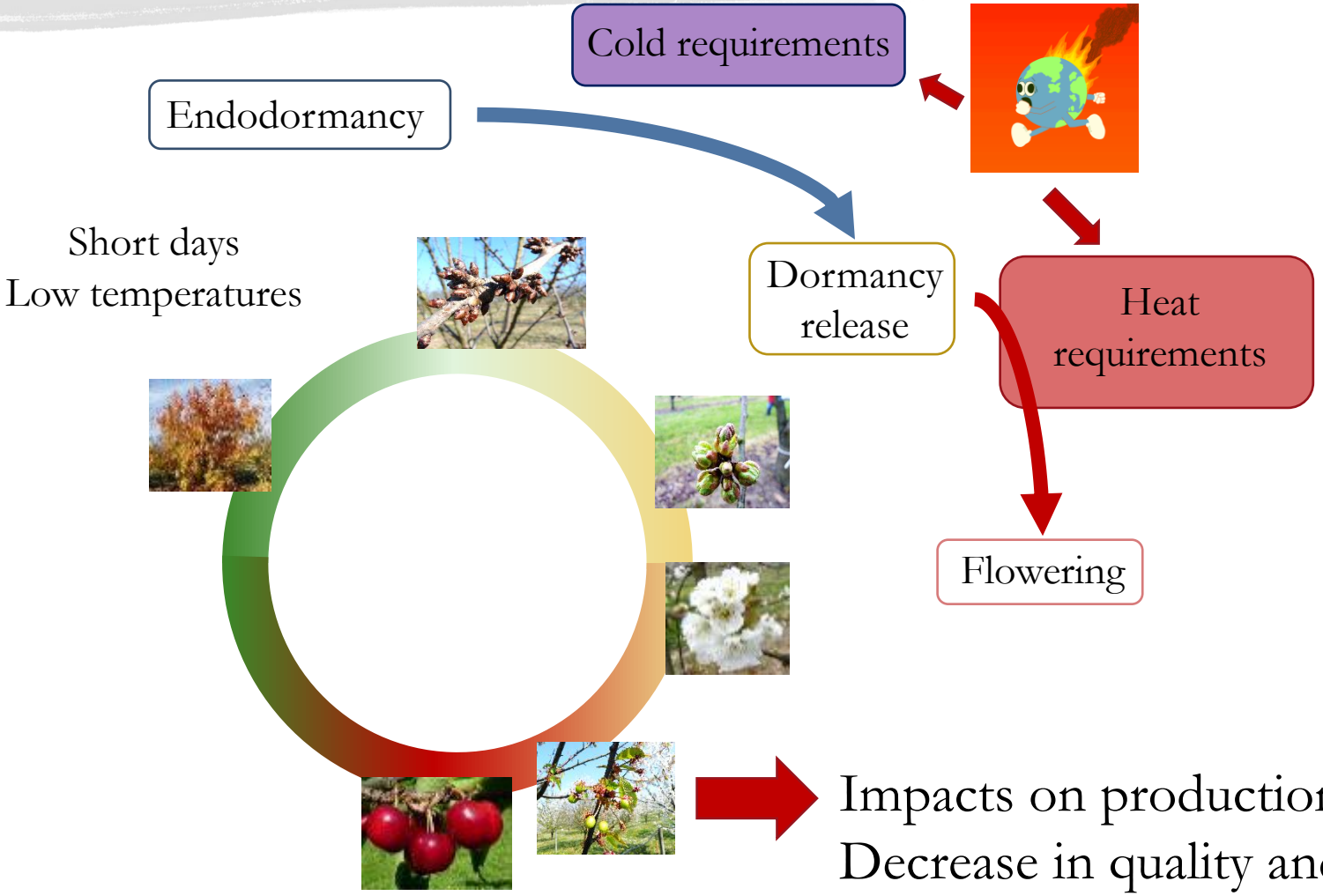


Transcriptomic analyses of molecular pathways involved in the regulation of bud dormancy in sweet cherry

Bénédicte Wenden, Mathieu Fouché, Noémie Vimont
Aline Faure, Sandra Cortijo
INRAE, Univ. Bordeaux
UMR 1332 Biologie du Fruit et Pathologie
Villenave d'Ornon, France

Phenology and climate change



Impacts on production
Decrease in quality and yields

Earlier flowering dates

- Late frost damages
- Desynchronization with pollinators

Insufficient chill accumulation

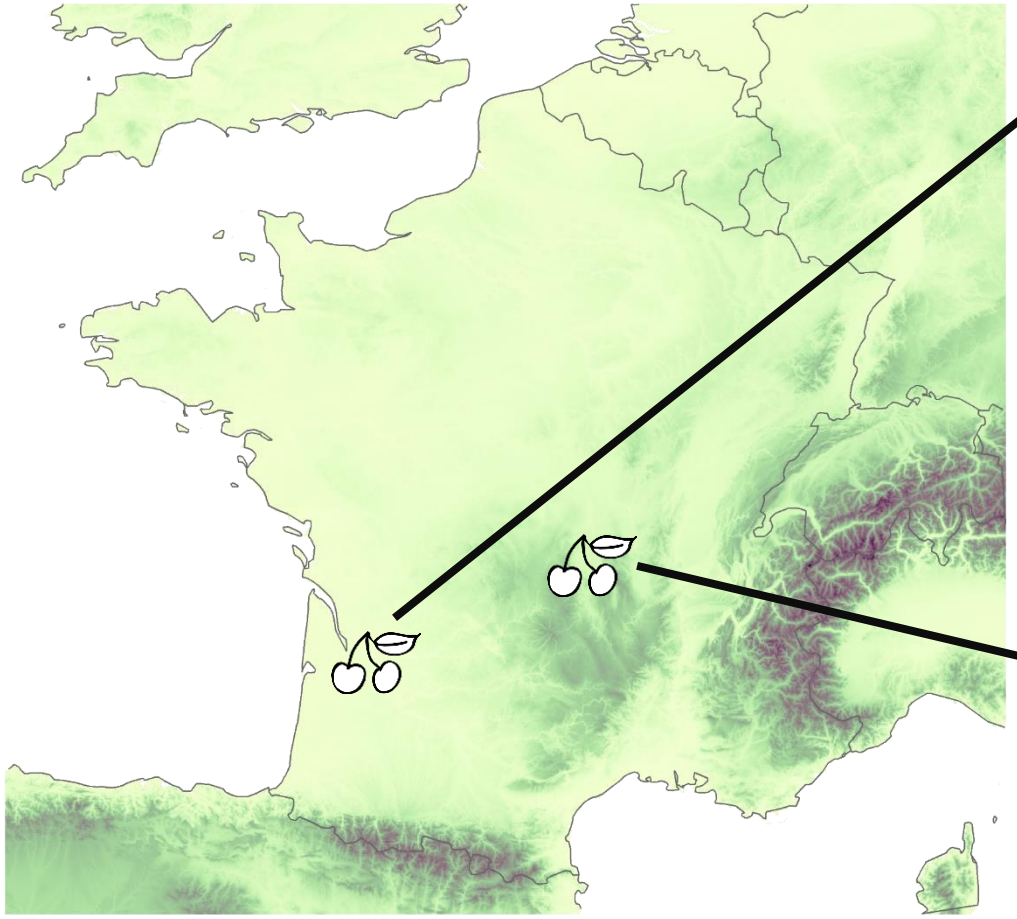
- Inability to complete dormancy
- Budburst delays
- Budburst defaults
- Necrosis
- Extended flowering period

Challenges under shifting climatic conditions

- Better understanding of response to temperatures
- Explore candidate genes and signalling pathways
- Different genotypes and temperature conditions

→ Regulatory networks involved in bud dormancy and temperature regulation

Transcriptomic analysis of flower bud dormancy



Noémie Vimont

Rémi Beauvieux

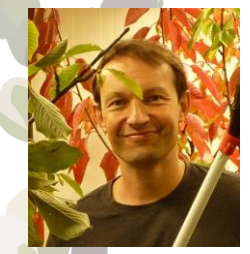
Bordeaux

July 2015 – March 2016

- 3 cultivars: ‘Cristobalina’, ‘Burlat’, ‘Regina’

September 2020 – April 2021

- 3 cultivars: ‘Cristobalina’, ‘Burlat’, ‘Regina’



Mathieu Fouché

Clermont-Ferrand

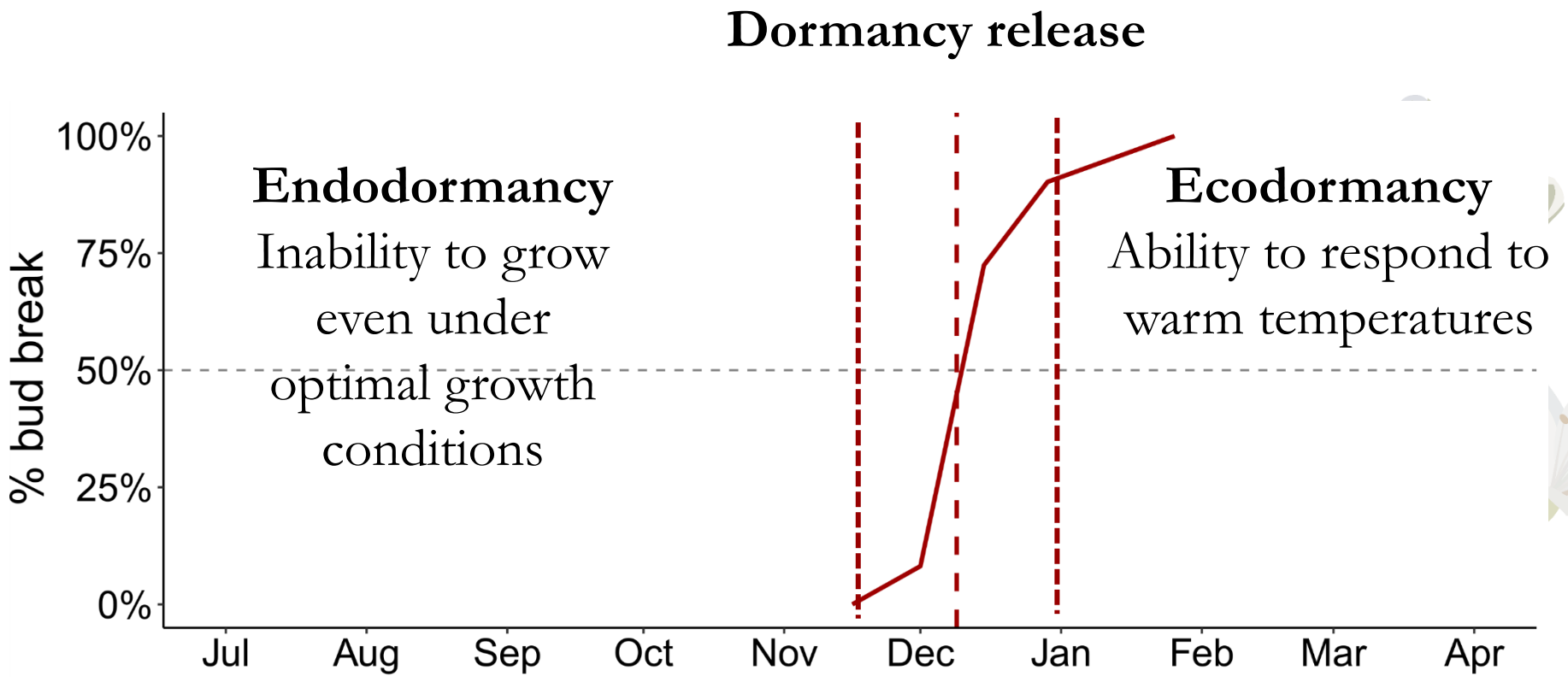
September 2020 – April 2021

- 2 cultivars: ‘Cristobalina’, ‘Regina’

Aline Faure

Transcriptomic analysis of flower bud dormancy

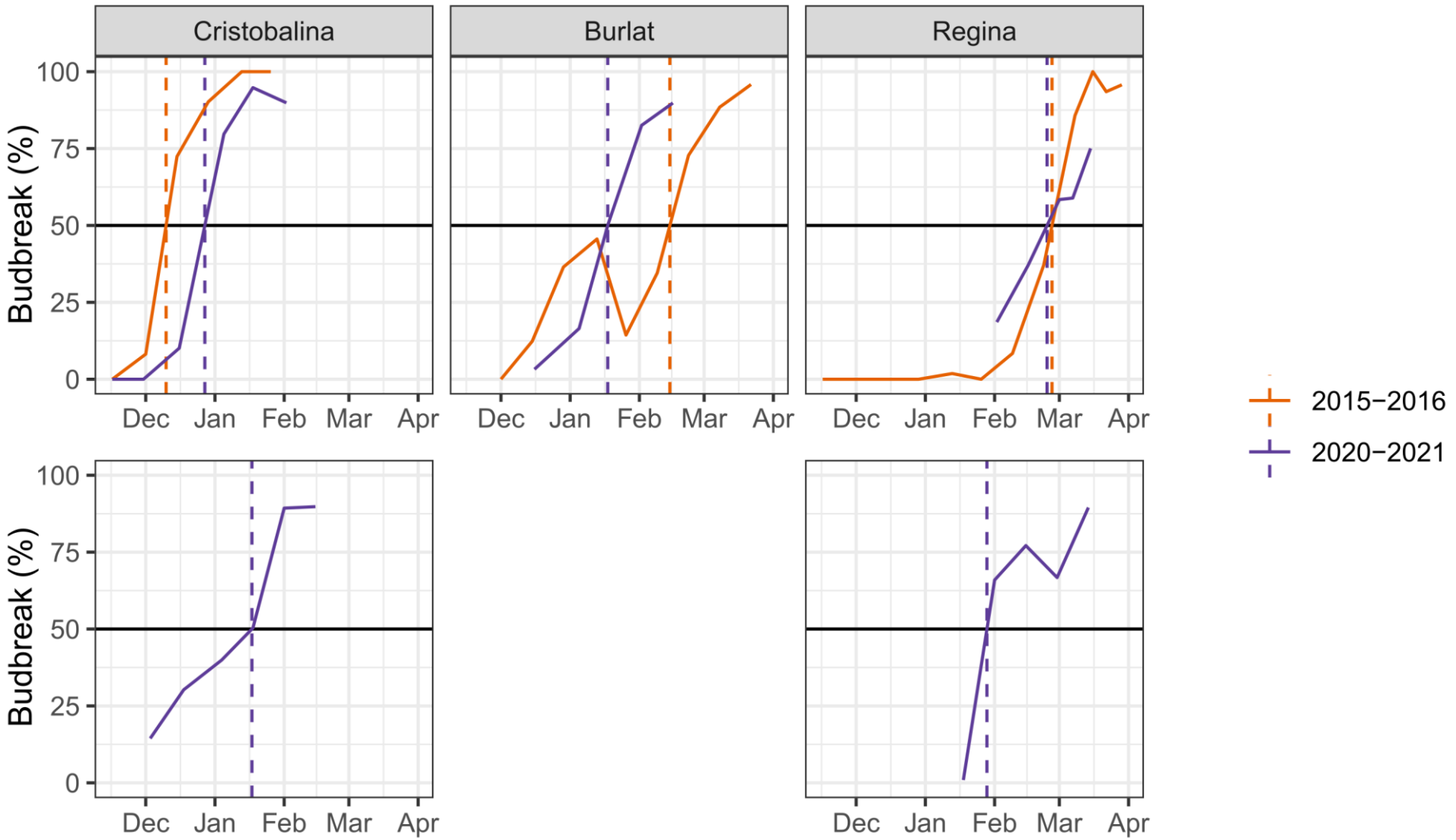
Defining flower bud dormancy stages



Transcriptomic analysis of flower bud dormancy

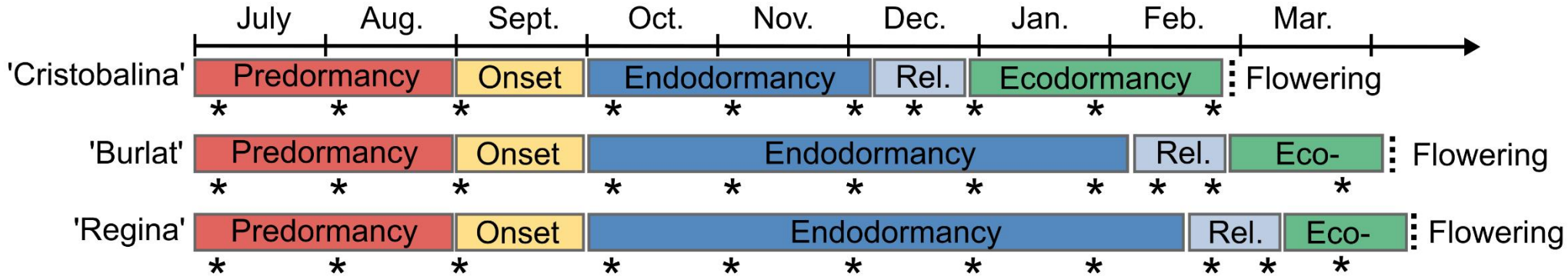
Bordeaux

Clermont-Ferrand

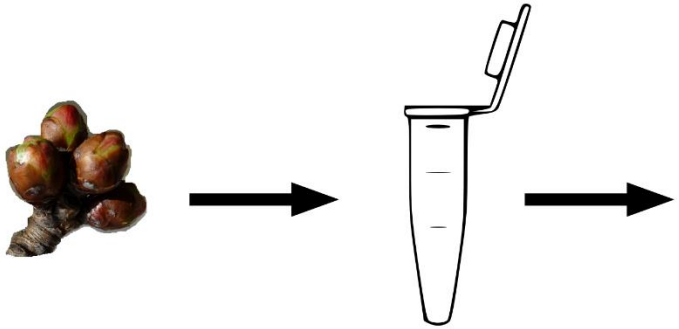


Transcriptomic analysis of flower bud dormancy

Flower bud sampling (*) throughout dormancy



Analyses



RNA-seq

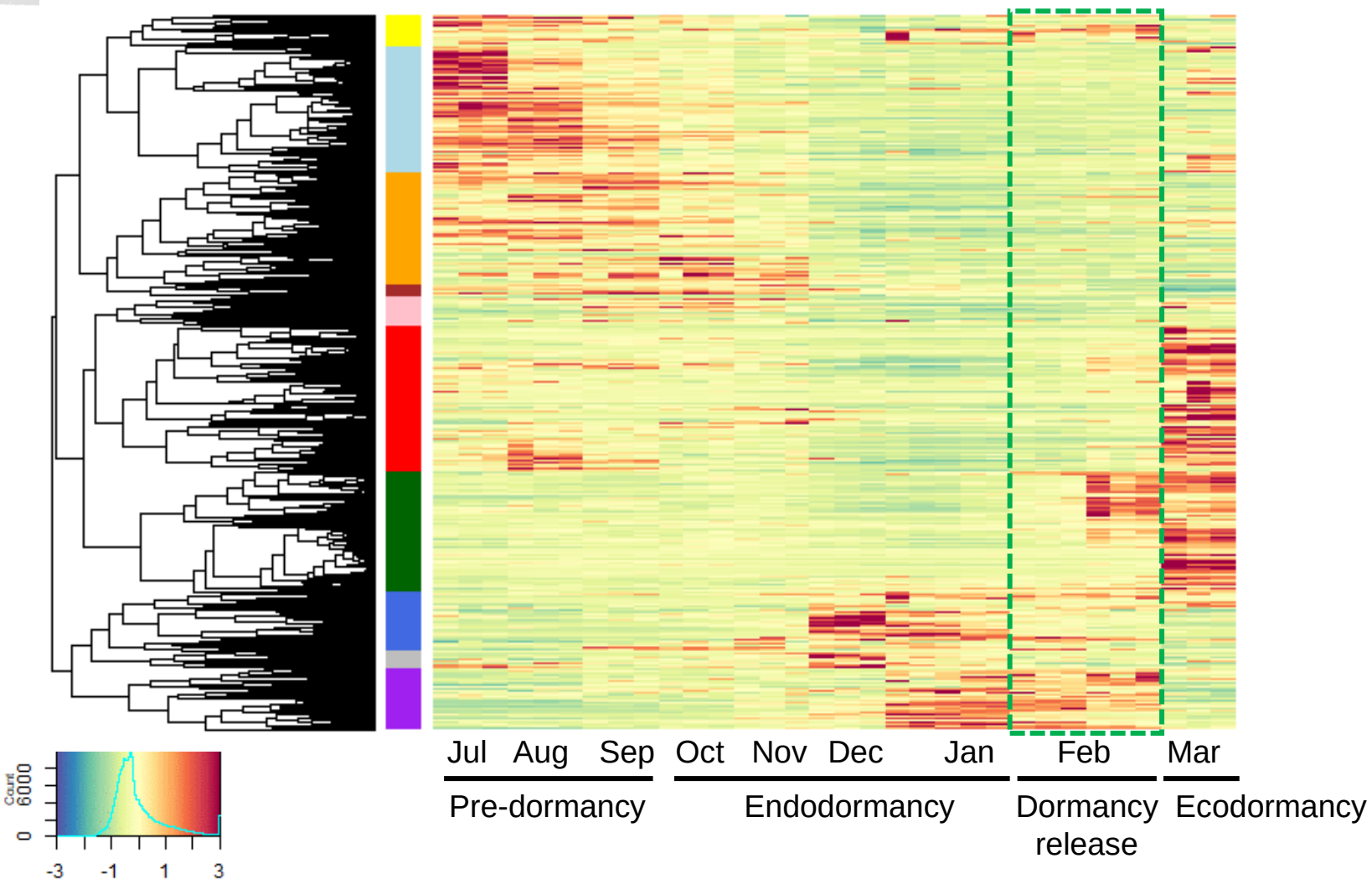
Extraction → Library preparation → Sequencing NextSeq500 (Illumina) → Reads mapped to sweet cherry 'regina' genome

Transcriptomic analysis of flower bud dormancy

- Differential expression analysis on 'Burlat'
  - Genes with statistically significant differences in the expression levels between at least 2 dates
  - Differentially expressed genes (DEG)

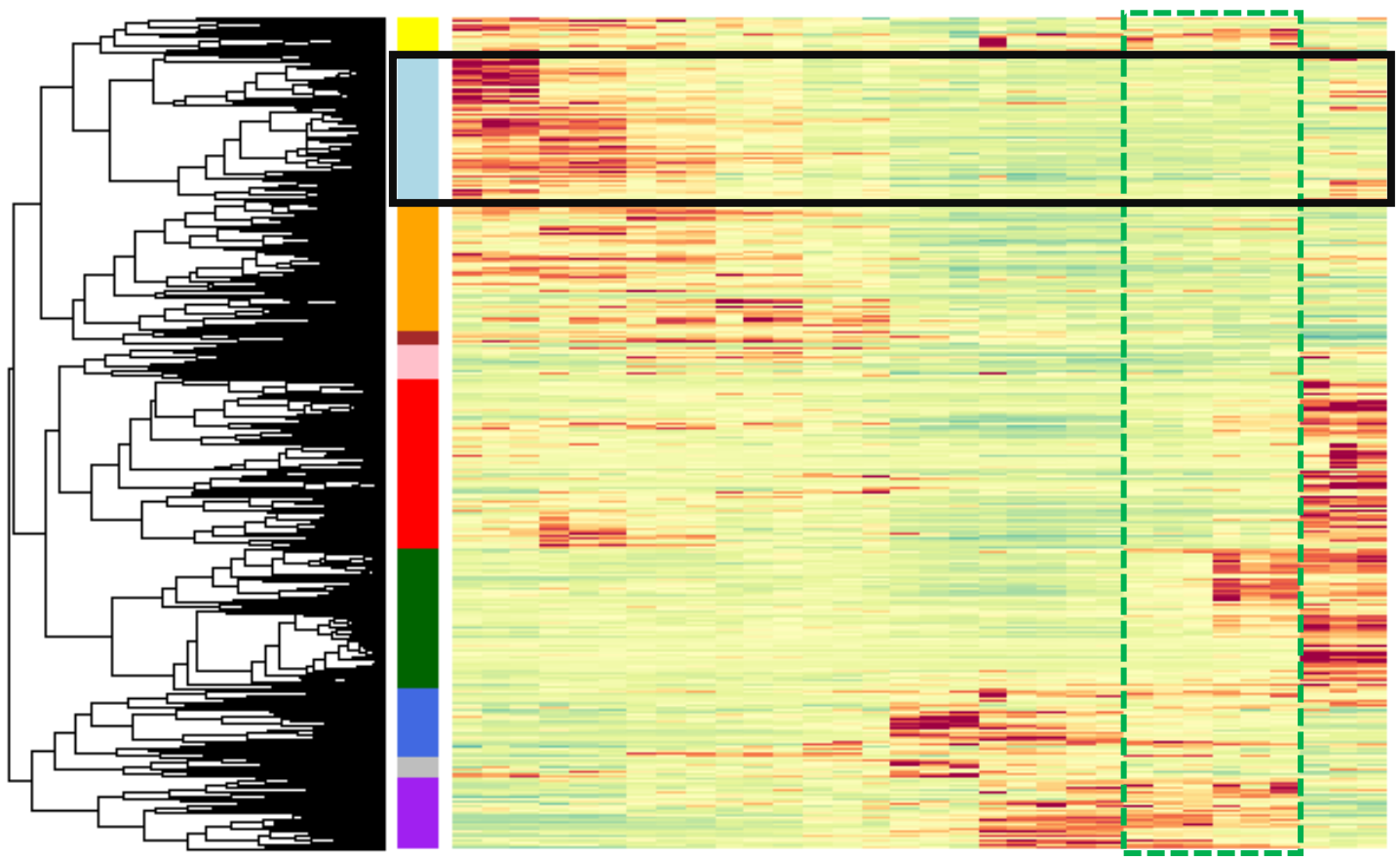
Transcriptomic analysis of flower bud dormancy

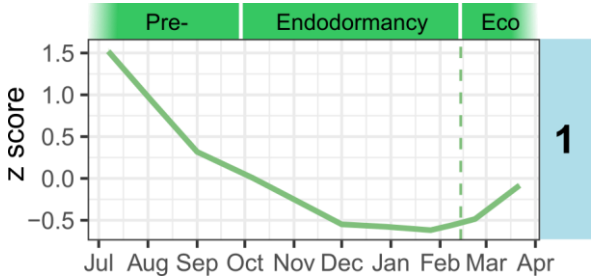
- Clustering on DEG expression patterns



Transcriptomic analysis of flower bud dormancy

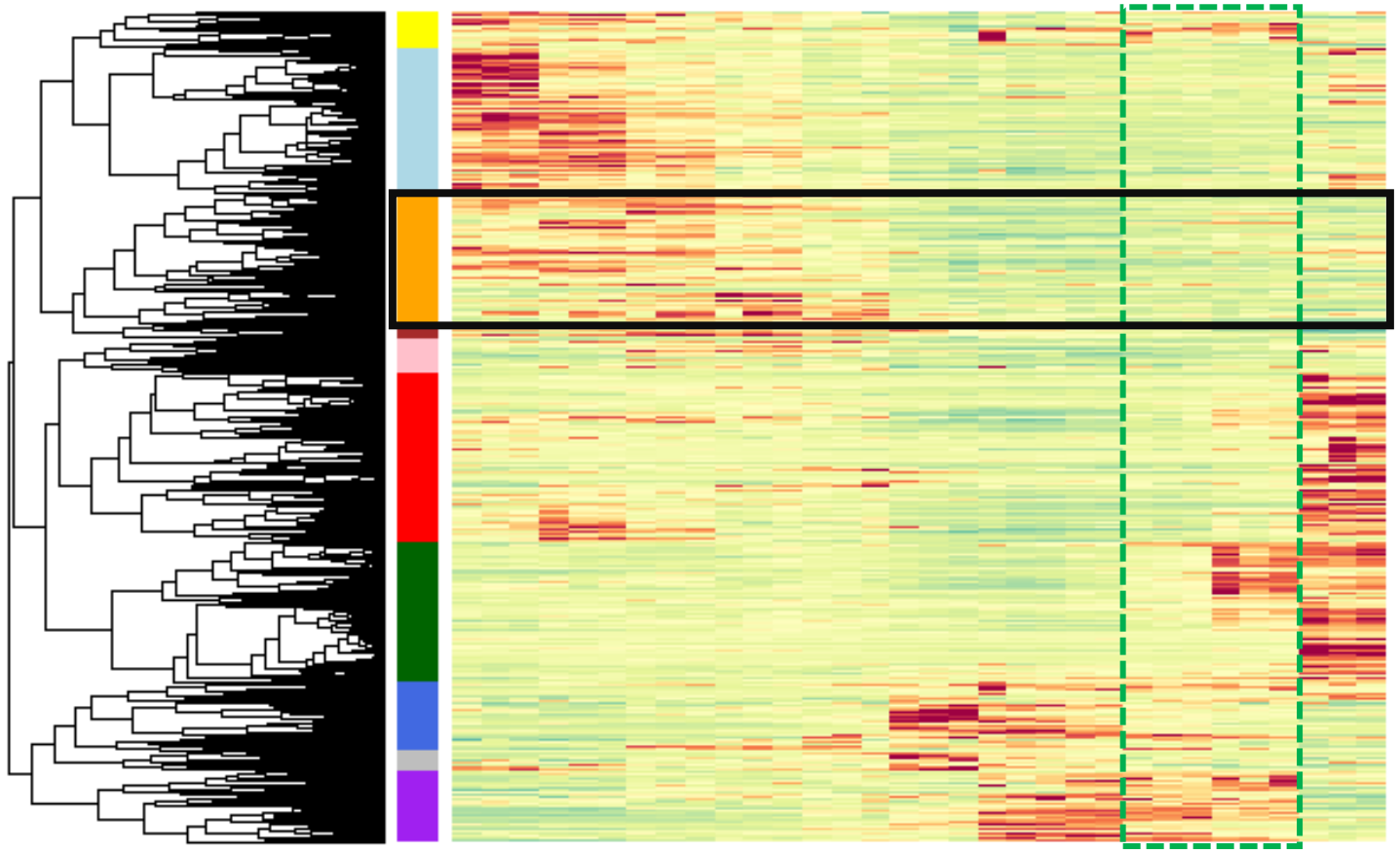
- Clustering on DEG expression patterns

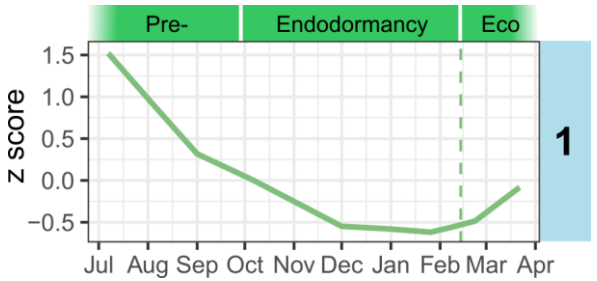


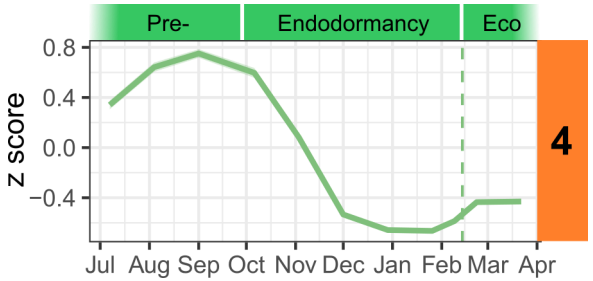


Transcriptomic analysis of flower bud dormancy

- Clustering on DEG expression patterns

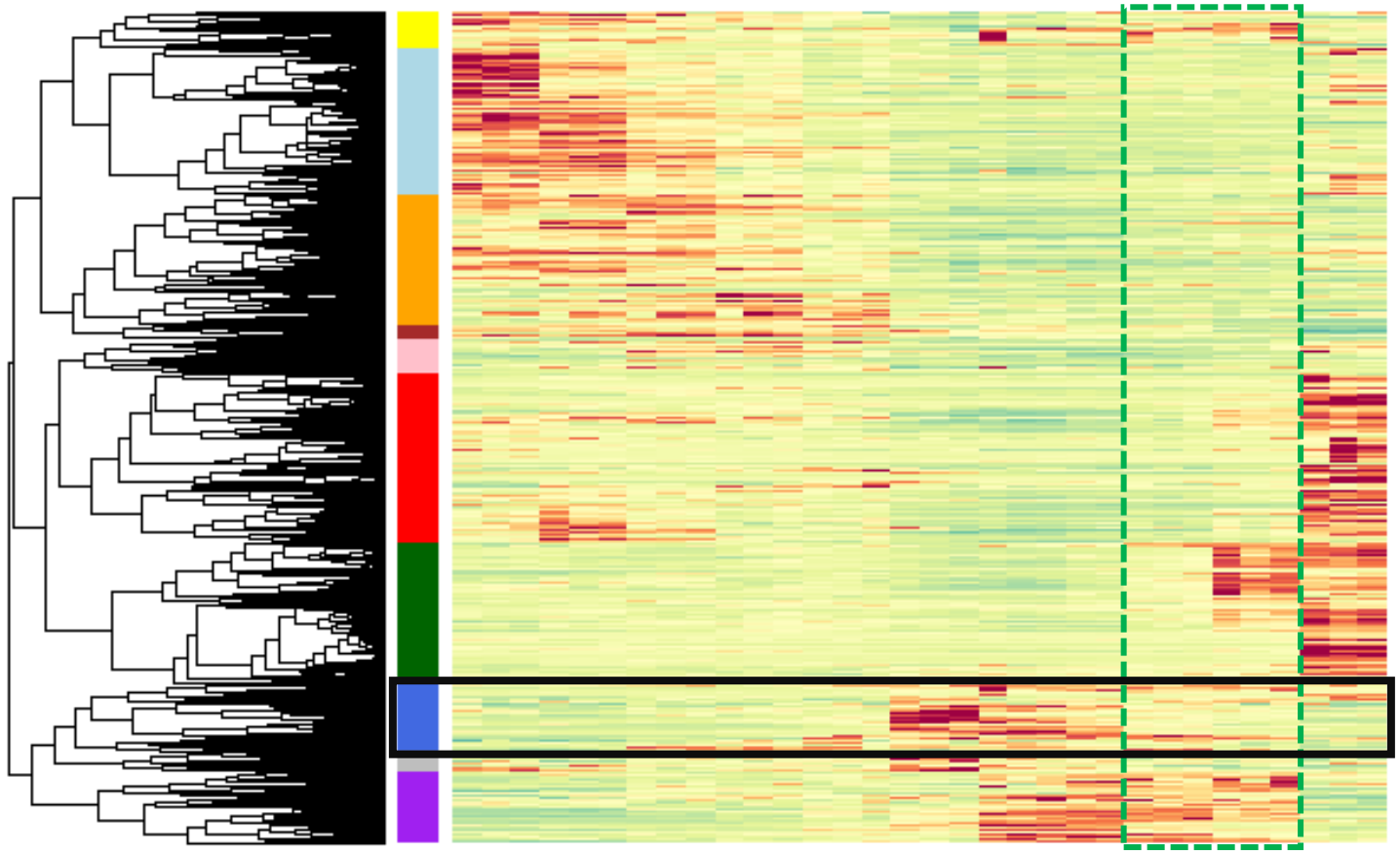


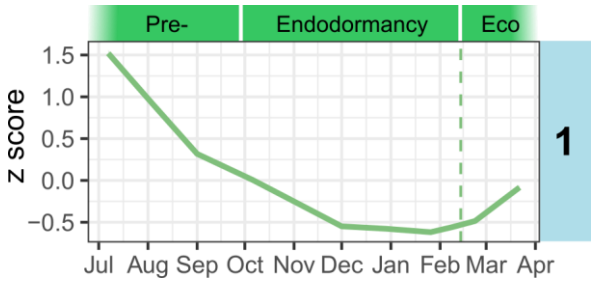


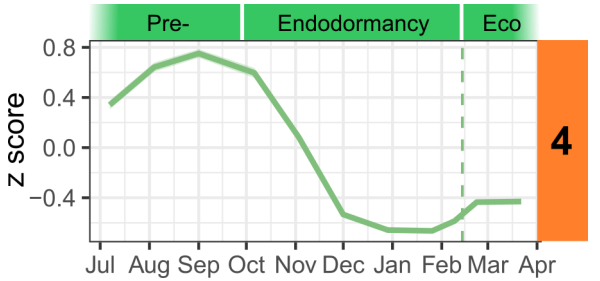


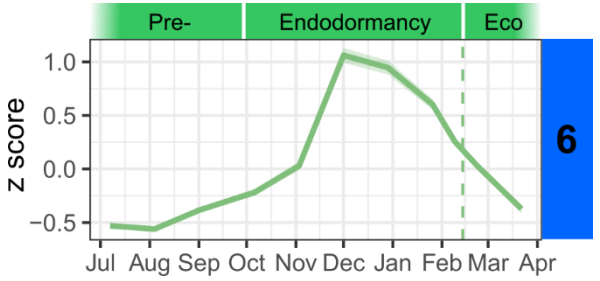
Transcriptomic analysis of flower bud dormancy

- Clustering on DEG expression patterns



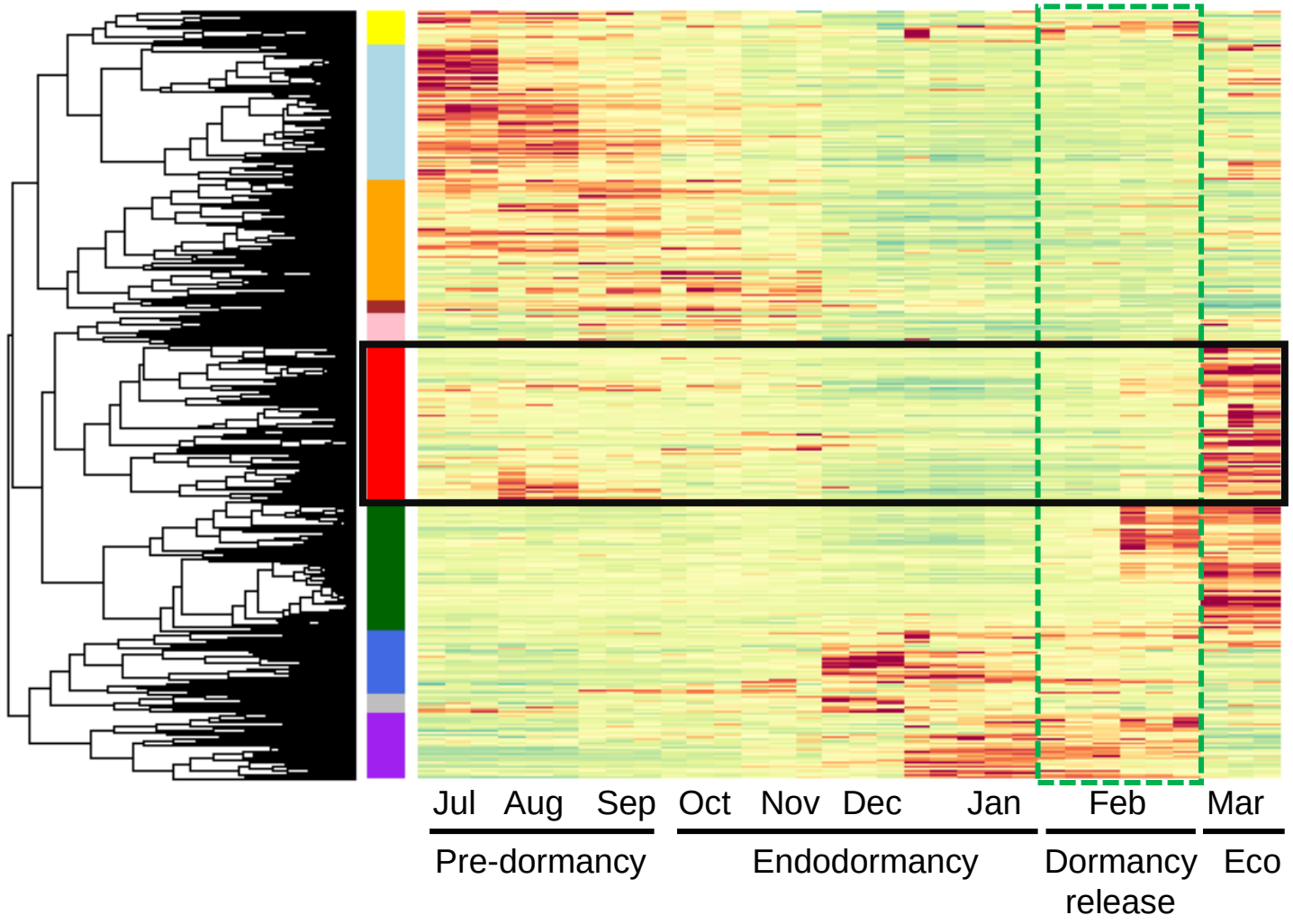


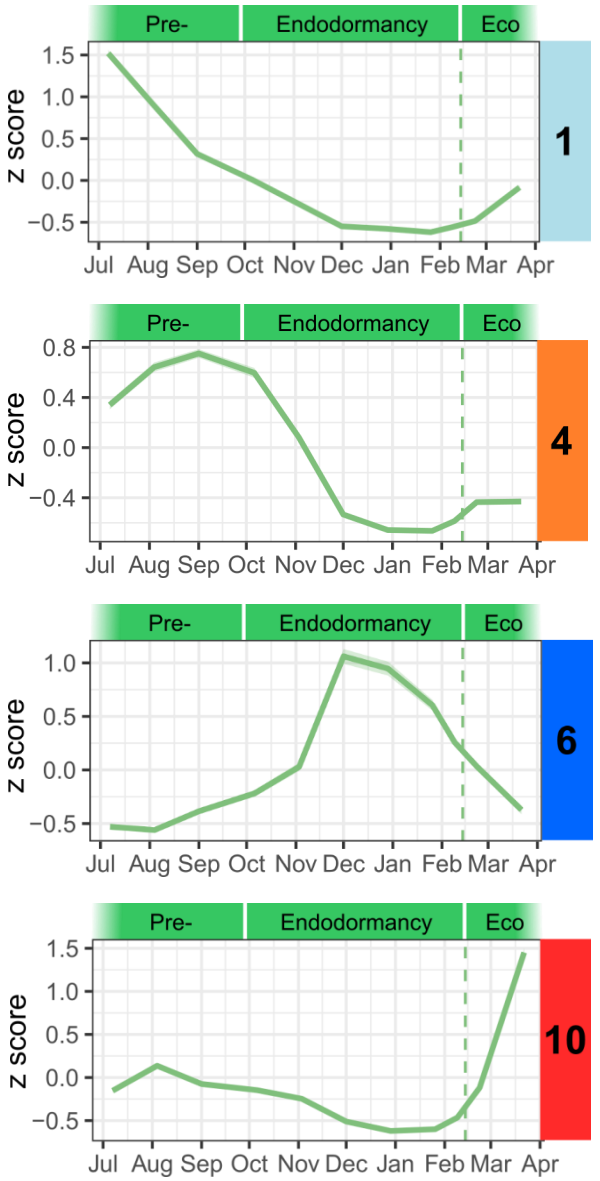




Transcriptomic analysis of flower bud dormancy

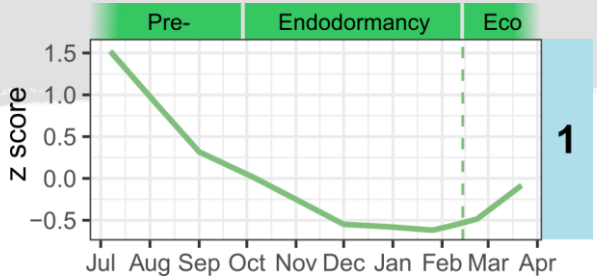
- Clustering on DEG expression patterns



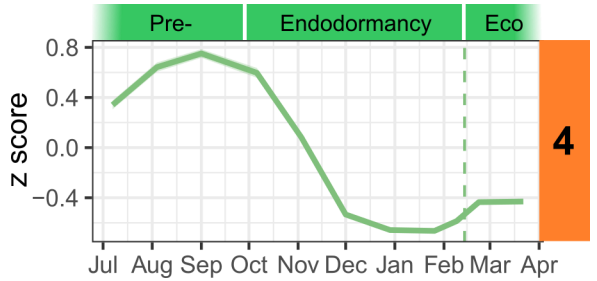


Transcriptomic analysis of flower bud dormancy

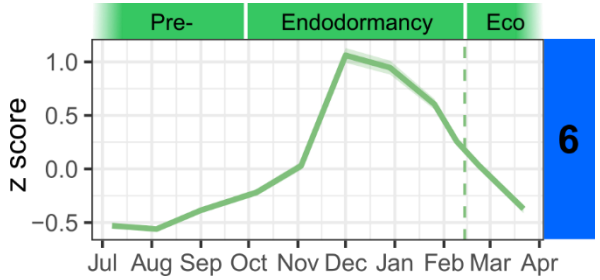
Genes expressed **before** dormancy



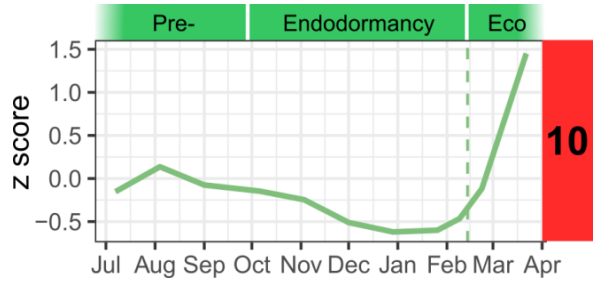
Genes expressed during **dormancy onset**



Genes expressed during **endodormancy**



Genes expressed during **ecodormancy**



→ **Clusters of genes expressed during specific dormancy phases**

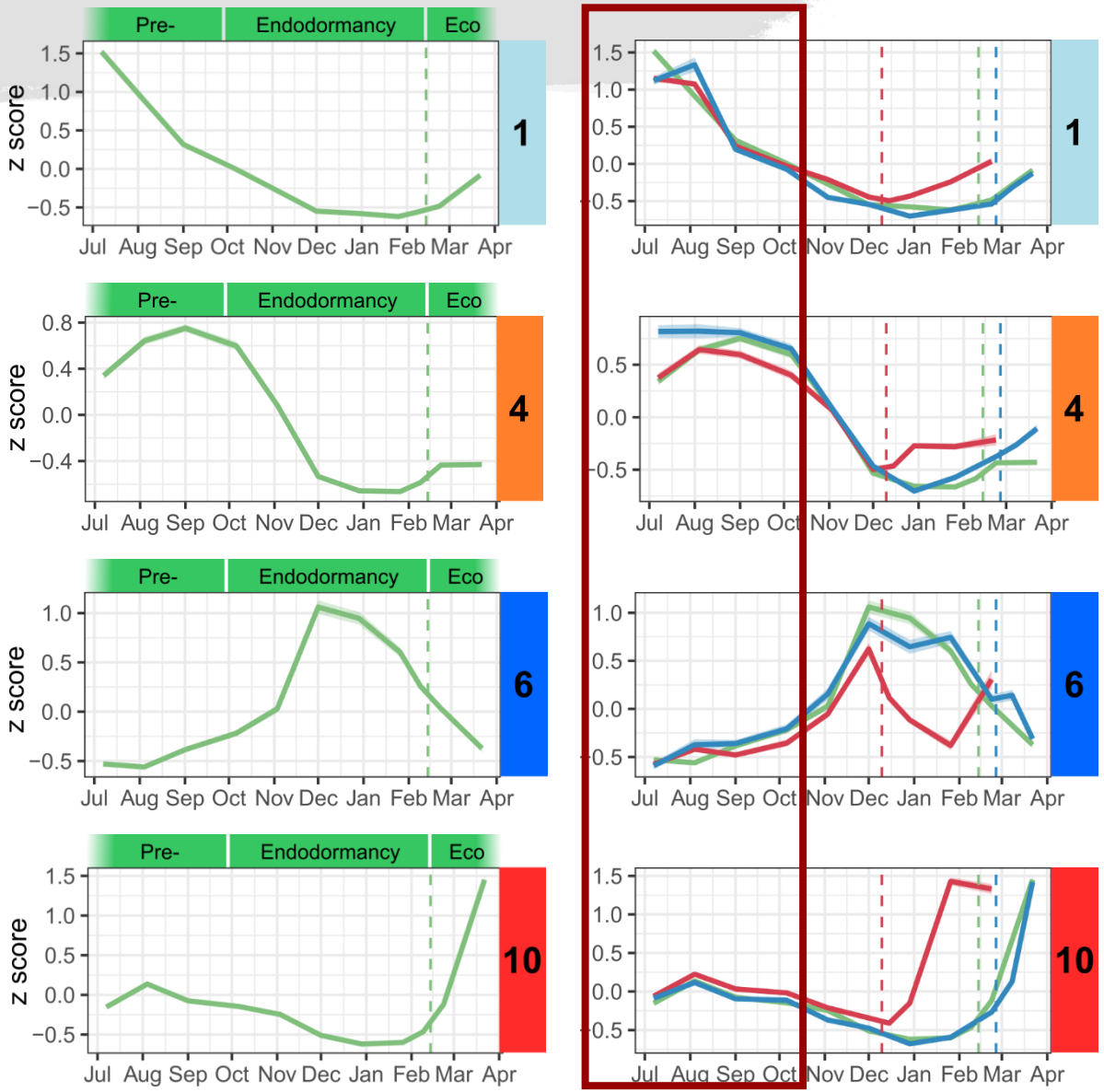
Transcriptomic analysis of flower bud dormancy

Genes expressed **before** dormancy

Genes expressed during **dormancy onset**

Genes expressed during **endodormancy**

Genes expressed during **ecodormancy**



➡ **No differences in gene expression patterns before dormancy between cultivars**

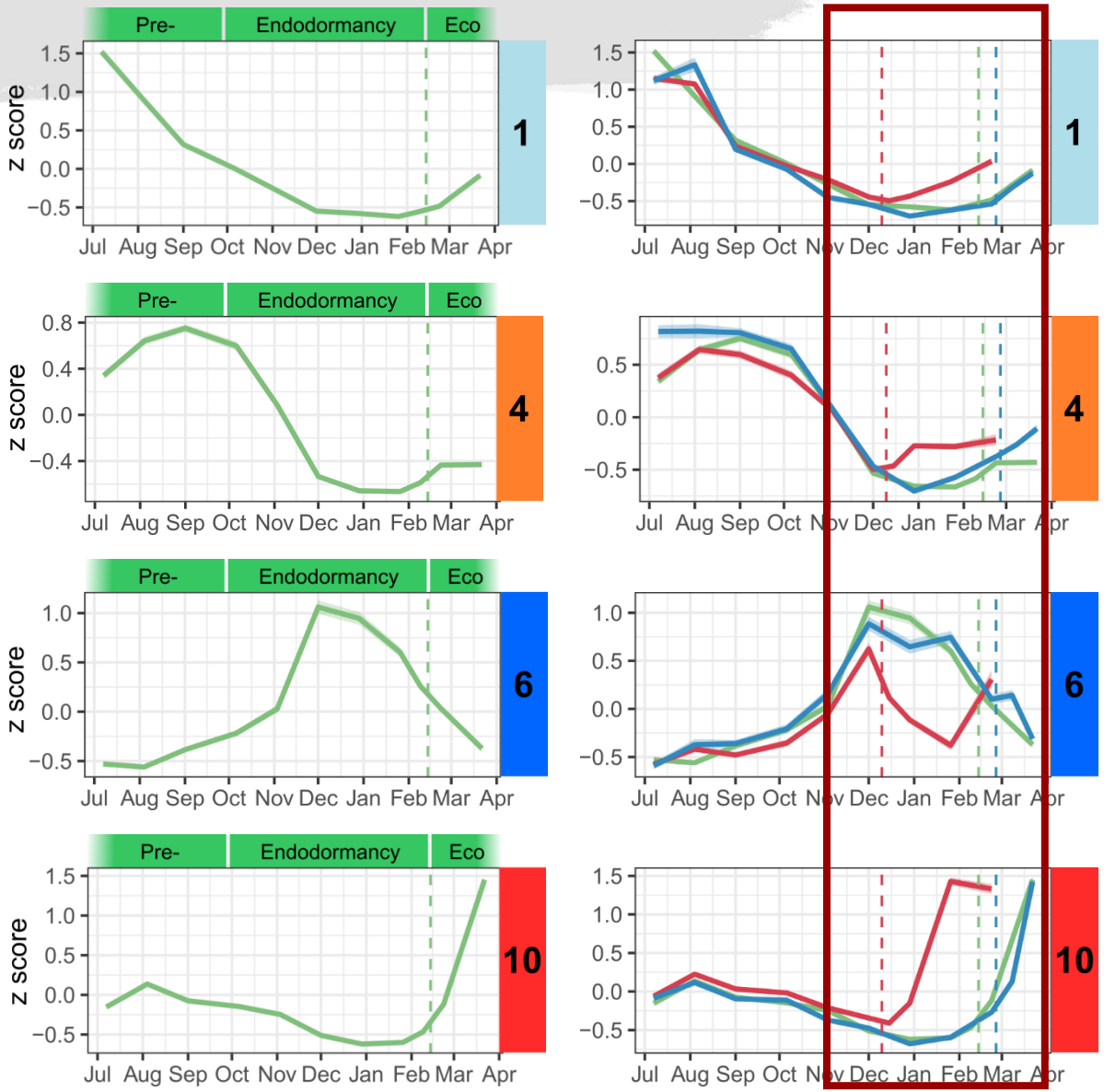
Transcriptomic analysis of flower bud dormancy

Genes expressed **before** dormancy

Genes expressed during **dormancy onset**

Genes expressed during **endodormancy**

Genes expressed during **ecodormancy**

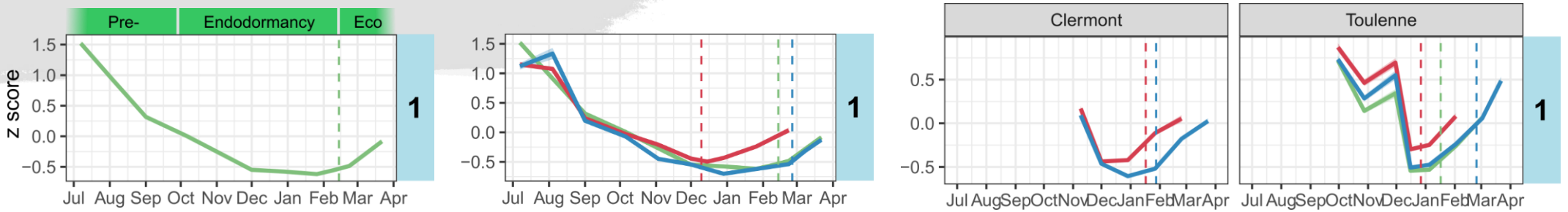


➡ **No differences in gene expression patterns before dormancy between cultivars**

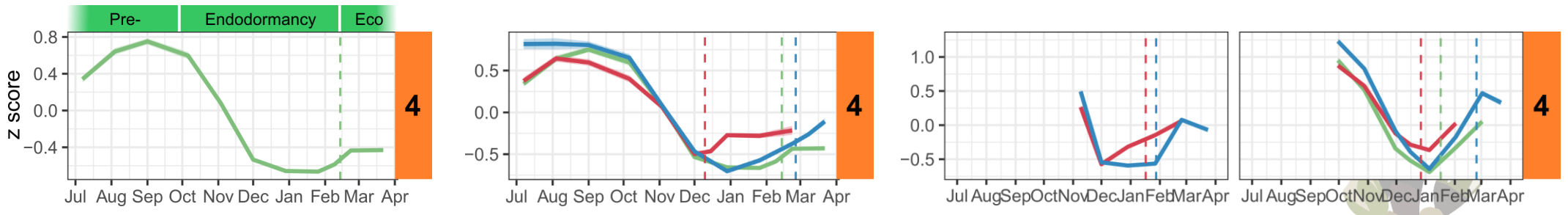
➡ **Gene expression patterns are correlated with the dormancy release date**

Transcriptomic analysis of flower bud dormancy

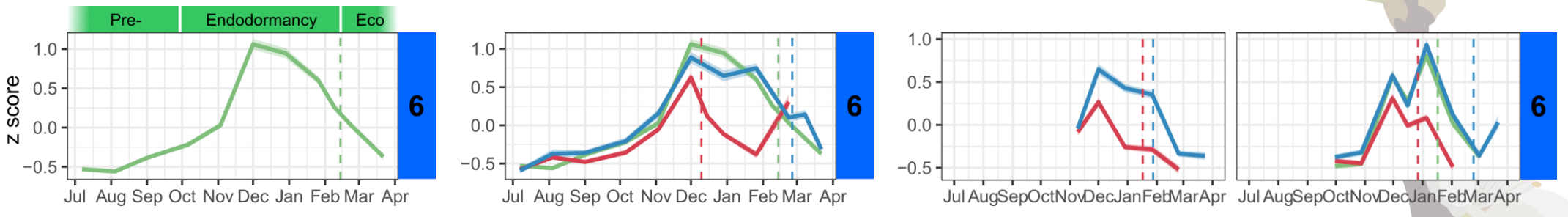
Genes expressed **before** dormancy



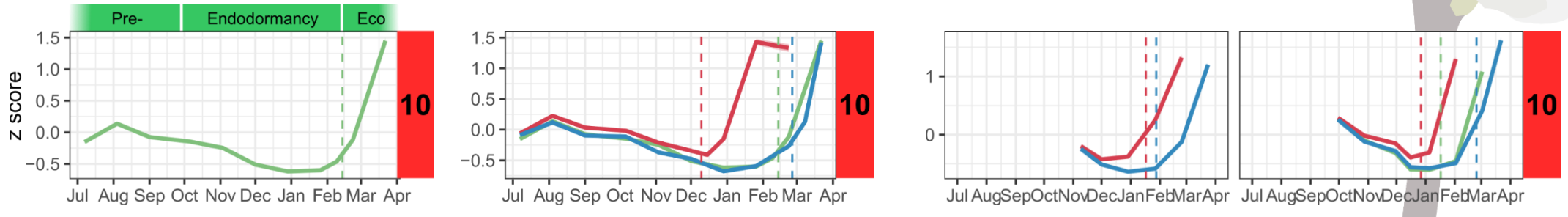
Genes expressed during **dormancy onset**



Genes expressed during **endodormancy**

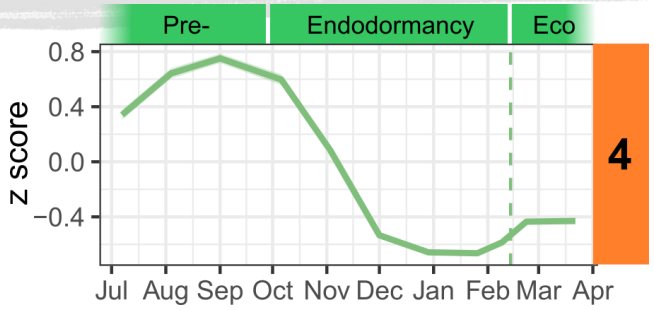


Genes expressed during **ecodormancy**



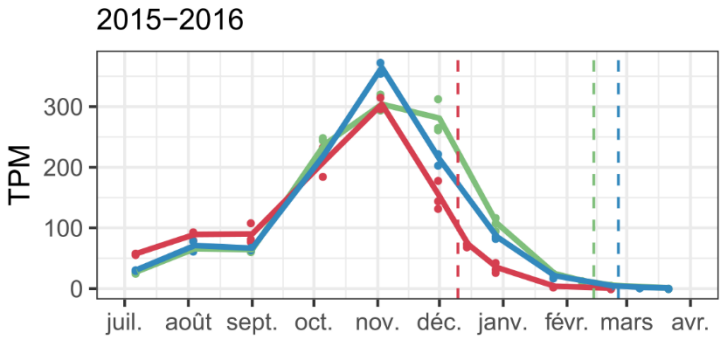
Transcriptomic analysis of flower bud dormancy

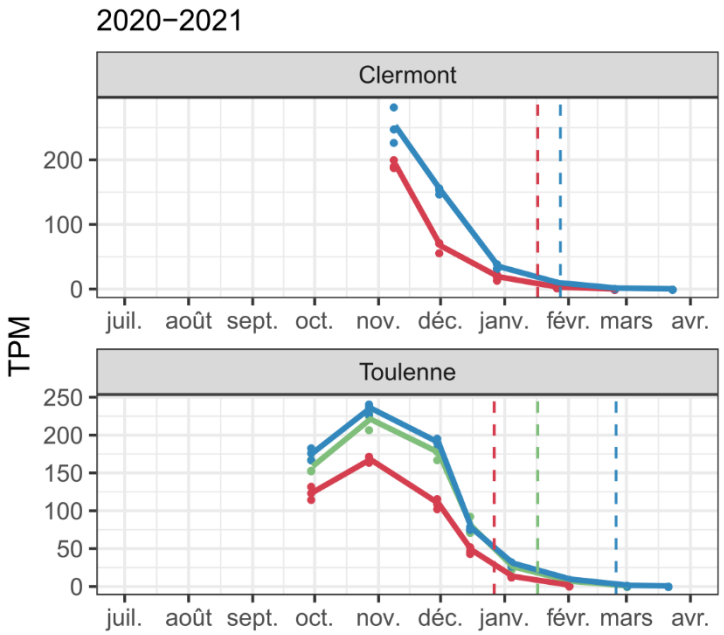
Genes expressed during dormancy onset



- Dormancy Associated MADS-box genes

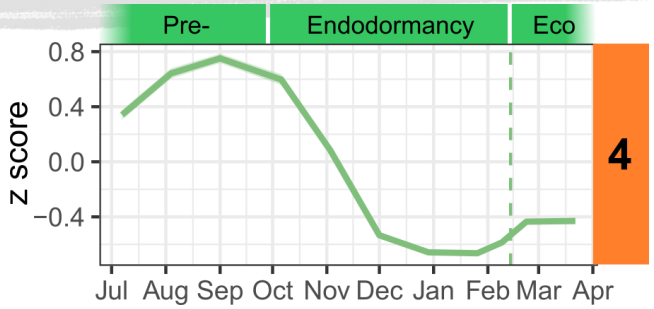
DAM5





Transcriptomic analysis of flower bud dormancy

Genes expressed during dormancy onset



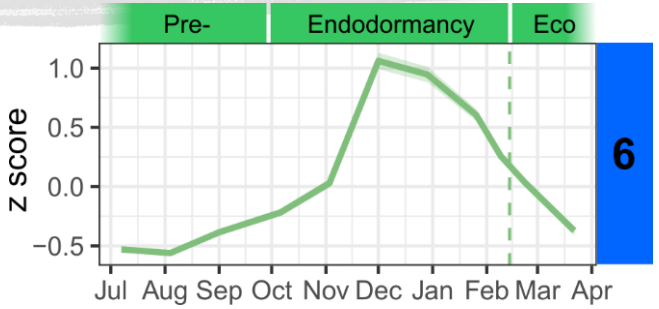
- Dormancy Associated MADS-box genes
- Cell wall biogenesis
- Cell wall organization
- Secondary metabolic processes

➡ **Dormancy onset and maintenance**

➡ **Cellular preparation for winter**

Transcriptomic analysis of flower bud dormancy

Genes expressed during endodormancy



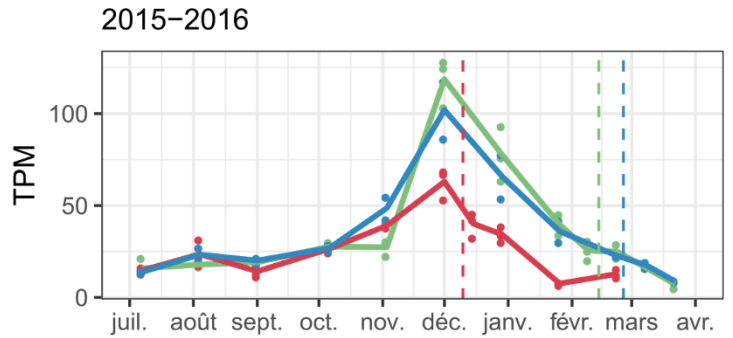
- Response to stimulus
- Response to abscisic acid (ABA)

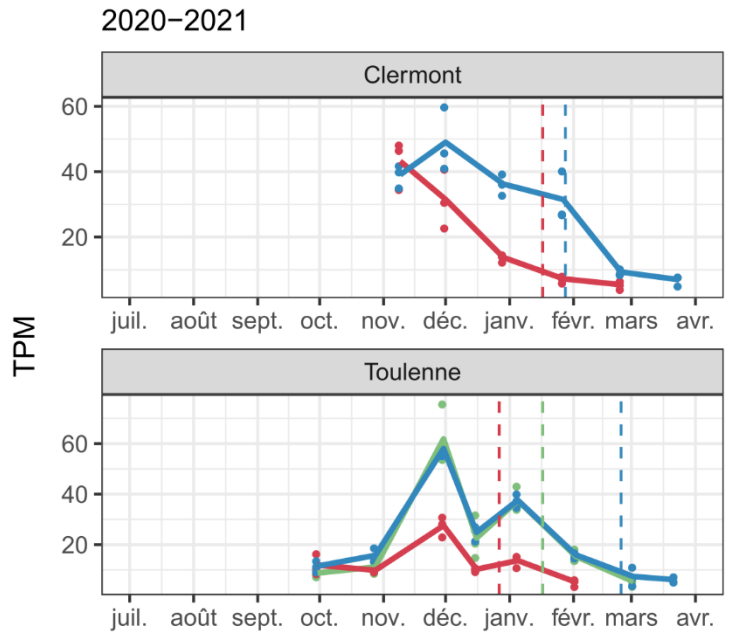
➡ **Dormancy maintenance**

➡ **Response to stress**

➡ **Response to drought**

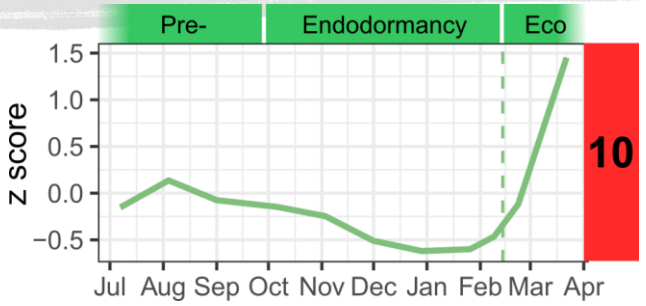
RHA2A





Transcriptomic analysis of flower bud dormancy

Genes expressed during ecodormancy

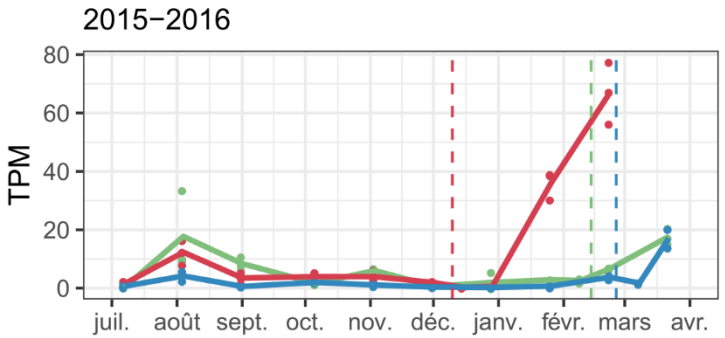


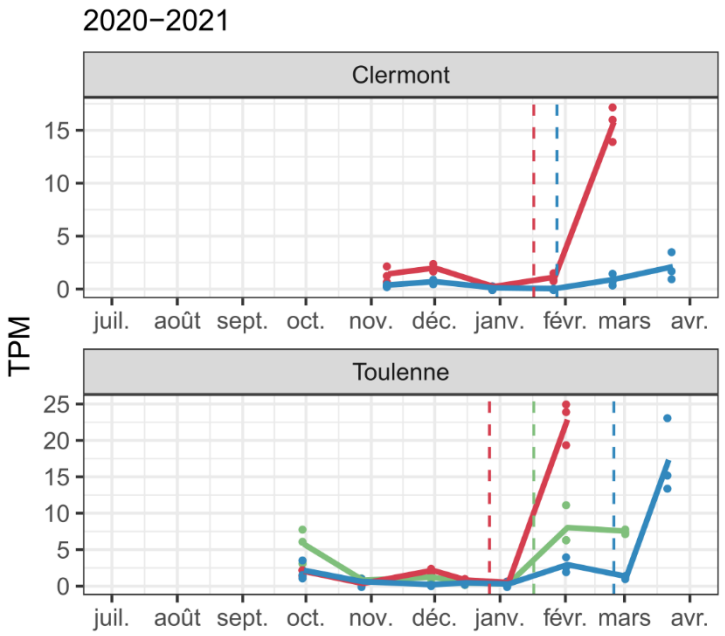
- Gametophyte development
- Pollen development
- Cell reorganization
- Response to gibberellins

➡ **Maturation of flower organs**

➡ **Growth resumption**

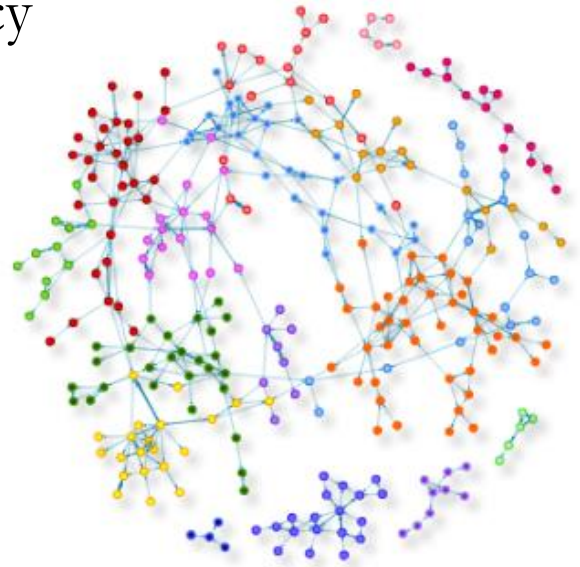
GASA





Take home messages and perspectives

- Transcriptomic analyses of multiple cultivars and environments allow to define groups of genes specifically expressed during the different stages of dormancy
- Gene regulatory network construction to study functional modules
- Multiple cultivars:
  - Genes involved in the genotype-specific regulation of dormancy
- Multiple environments :
  - Genes involved in the response to environment



- Further explore the G x E interaction in the molecular regulation of dormancy
- Identify key candidate genes
- Integrate the gene networks into predictive models

PHENO 2022

INRAE Experimental Station (UEA)

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