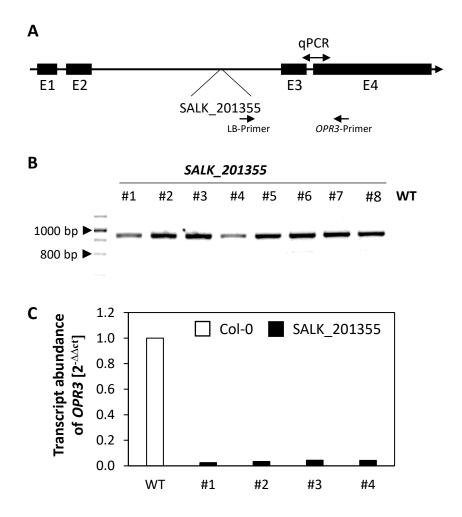
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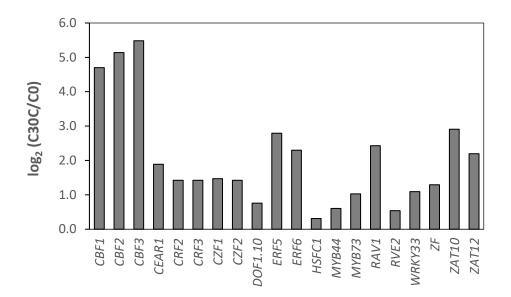
Suppl. Fig. S1



**Suppl. Fig. S1: Genotyping and characterization of the** *OPR3-T-DNA* insertion line **SALK\_201355: A)** The T-DNA is inserted in the intron between exon 2 and exon 3. The black arrows show the primer position for qPCR-based *OPR3* transcript analysis and for PCR-based genotyping with an *OPR3*-specific and the T-DNA-specific left border primer (LB). **B)** For identity checking, PCR reaction were performed with the T-DNA-specific left-border primer (LB) and the gene-specific *OPR3*-primer and DNA of 8 independent SALK\_201355 plants and one wild type Col-0 plant. The mutant allele gave the expected product of 900 base pairs (bp). **C)** The transcript abundance of *OPR3* was analysed in Col-0 (grey) and four homozygote SALK\_201355 plants (green) by quantitative qPCR analysis. The transcript levels were normalized against the transcript abundance of the reference gene *YLS8*.

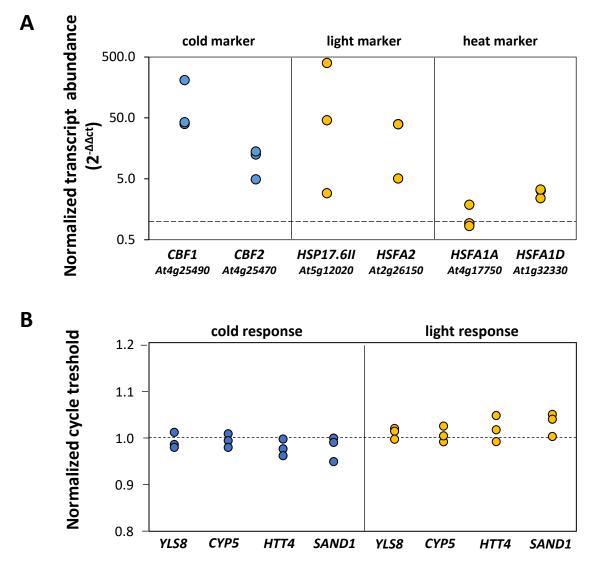
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### Suppl. Fig. S2



Suppl. Fig. S2: Relative transcript accumulation for 20 of the genes identified by Park *et al.* (2015) as 'first-wave' cold-induced genes and represented with an FPKM higher than 0.5 in our data set as observed after 30 min of cold-triggering.

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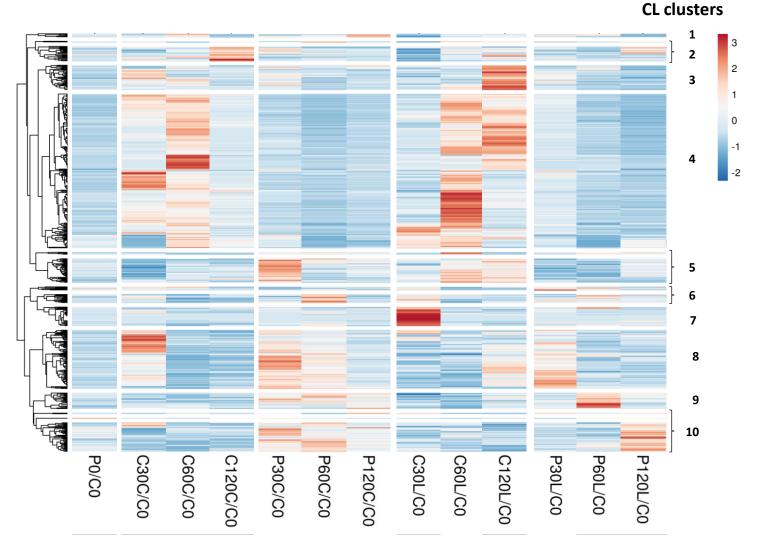


Suppl. Fig. S3

Suppl. Fig. S3: Transcript abundances of stress-responsive and reference genes as determined by qPCR to confirm the reliability of the RNA-seq data: A) Transcript abundances of the cold responsive genes *CBF1* and *CBF2*, the excess light responsive genes *HSP17.6II* and *HSFA2* and of the non-heat filtered light responsive genes were analysed in four-weak-old plants, which were either exposed for 60 min to 4°C (blue) or to heat-filtered excess light (800 µmol m<sup>-2</sup> s<sup>-1</sup>, yellow circle). The transcript values were normalized on the transcript abundances of *YLS8* and standardized to the transcript abundances in control plants (n=3) **B)** Transcript abundances of four reference genes, namely *YLS8*, CYP5, *HTT4* and *SAND1*, were analysed in untreated control plants and after 60 min in the cold or in high-light. The transcript abundances are shown as cycle-thresholds relative to the control cycle threshold (n=3).

Andras Bittner<sup>1</sup>, Bettina Hause<sup>2</sup> and Margarete Baier<sup>1\*</sup>





Suppl. Fig. 4A: Cluster analysis of genes with at least 1.5-fold priming effects in the cold and in the light. Mean-centered heatmap and cluster-definition as obtained by ClustVis with the C0-normalized FPKM data listed in Suppl. Tab. S9.

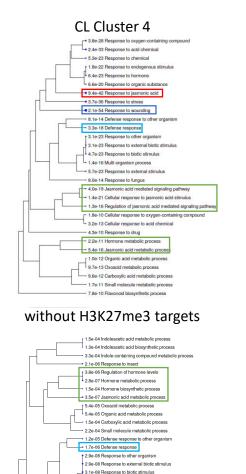
overlap [+-]-genes dehydration stress

- 3.6e-22 Response to oxygen-containing compound

1.9e-28 Response to stress
7.7e-52 Response to wounding

Andras Bittner<sup>1</sup>, Bettina Hause<sup>2</sup> and Margarete Baier<sup>1\*</sup>

#### Suppl. Fig. S4B



8.4e-06 Multi-organism process

4.8e-10 Response to acid chemical
8.7e-07 Response to chemical

7.4e-07 Response to hormone

9.1e-07 Response to endogenous stimulus

3.0e-06 Response to organic substance

1.2e-13 Response to lasmonic acid

1 2.9e-04 Flavonoid metabolic process

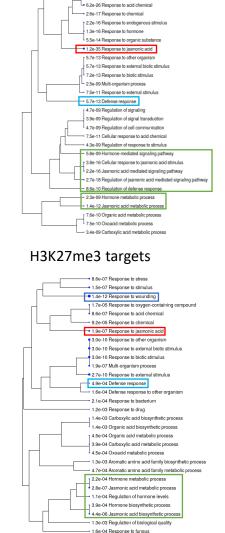
1.2e-04 Flavonoid biosynthetic process

• 1.2e-13 Response to wounding

3.6e-10 Response to stress

1.9e-07 Response to external stimulus

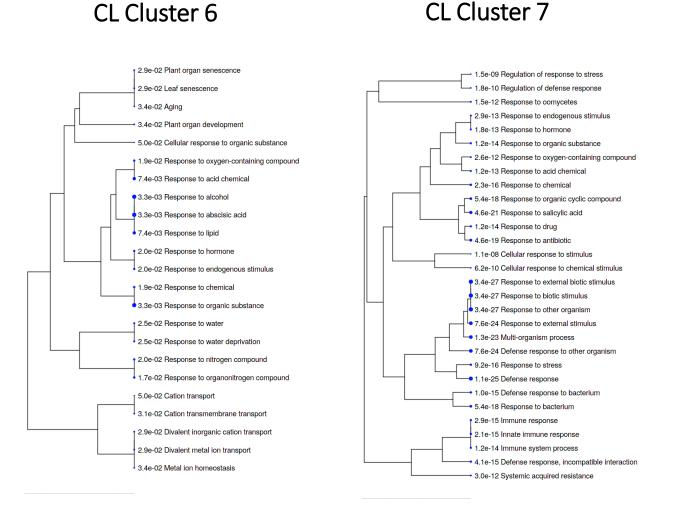
- 5.7e-09 Response to oxygen-containing compound



**Suppl. Fig. 4B:** Results on GO-term analysis for functional categories on the CL cluster 4: all genes (top left), genes overlapping with the [+ -] cluster of dehydration primingresponsive genes (top right), CL cluster 4 genes with are no H3K27me3 targets (bottom left) and the H3K27me3 target genes of CL cluster 4.

Andras Bittner<sup>1</sup>, Bettina Hause<sup>2</sup> and Margarete Baier<sup>1\*</sup>

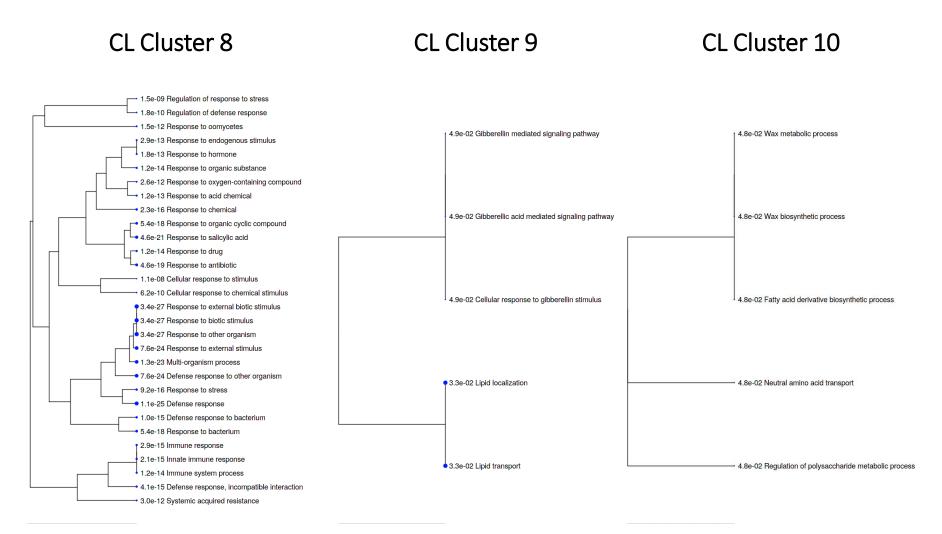
#### Suppl. Fig. S4C



Suppl. Fig. S4C: Results on GO-term analysis for functional categories on the CL cluster 6 and 7.

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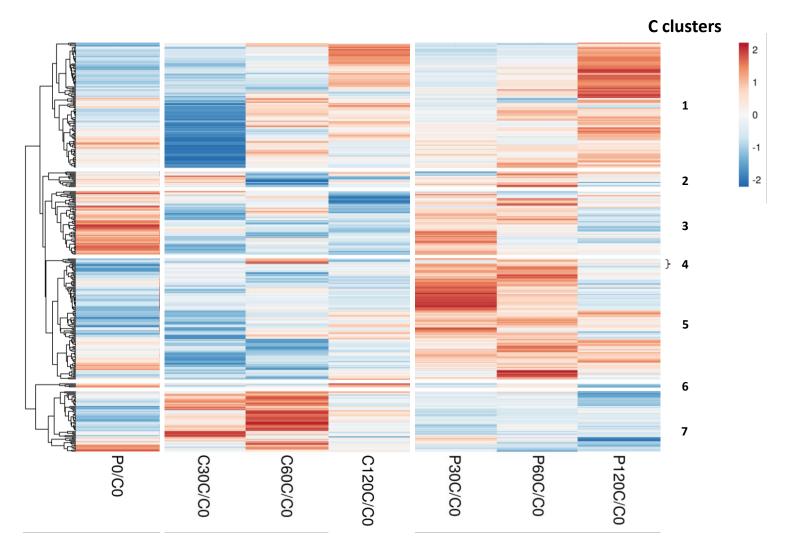
Suppl. Fig. S4D



Suppl. Fig. S4D: Results on GO-term analysis for functional categories on the CL clusters 8, 9 and 10.

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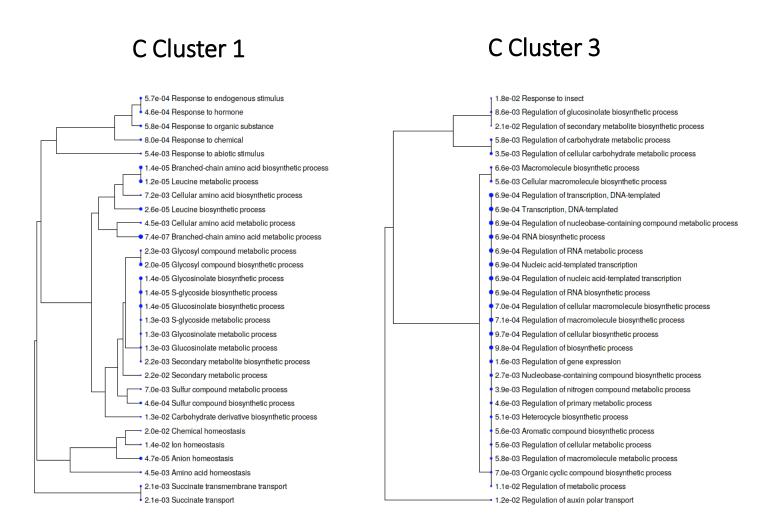
Suppl. Fig. S5A



Suppl. Fig. S5A: Cluster analysis of genes with at least 1.5-fold priming effects in the cold and weaker priming effects in the light. Mean-centered heatmap and cluster-definition as obtained by ClustVis with the C0-normalized FPKM data listed in Suppl. Tab. S7.

Andras Bittner<sup>1</sup>, Bettina Hause<sup>2</sup> and Margarete Baier<sup>1\*</sup>

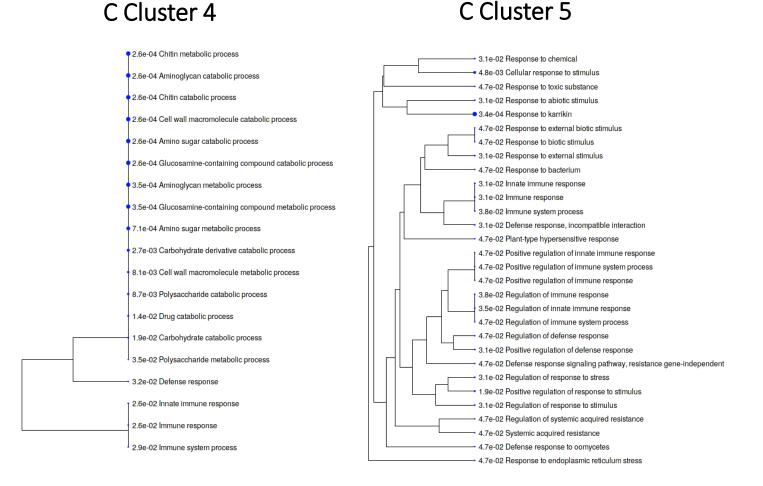
#### Suppl. Fig. S5B



Suppl. Fig. S6B: Results on GO-term analysis for functional categories on the C cluster 1 and 3.

Andras Bittner<sup>1</sup>, Bettina Hause<sup>2</sup> and Margarete Baier<sup>1\*</sup>

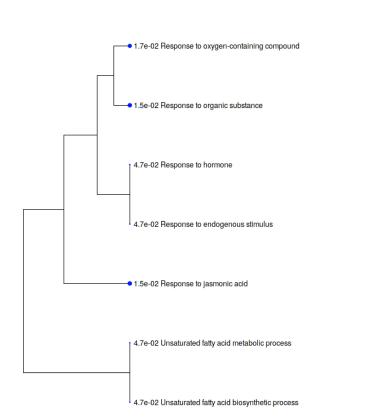
### Suppl. Fig. S5C



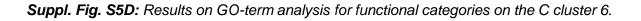
Suppl. Fig. S5C: Results on GO-term analysis for functional categories on the C cluster 4 and 5.

Andras Bittner<sup>1</sup>, Bettina Hause<sup>2</sup> and Margarete Baier<sup>1\*</sup>

Suppl. Fig. S5D

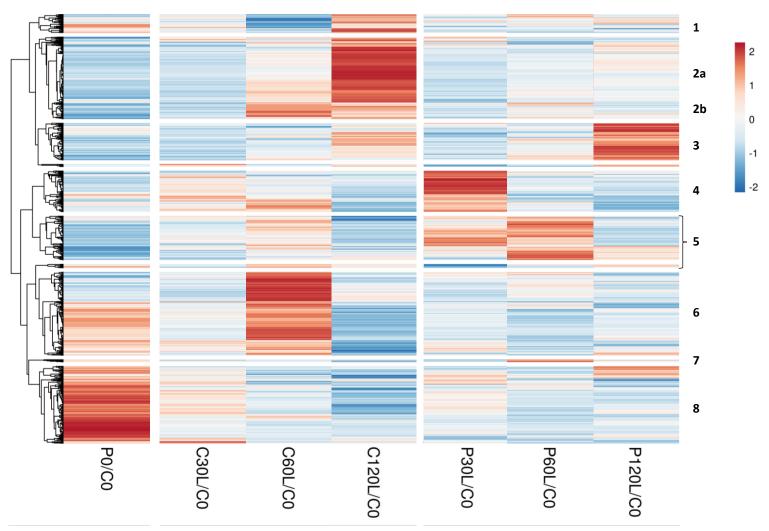


C Cluster 6



Andras Bittner<sup>1</sup>, Bettina Hause<sup>2</sup> and Margarete Baier<sup>1\*</sup>



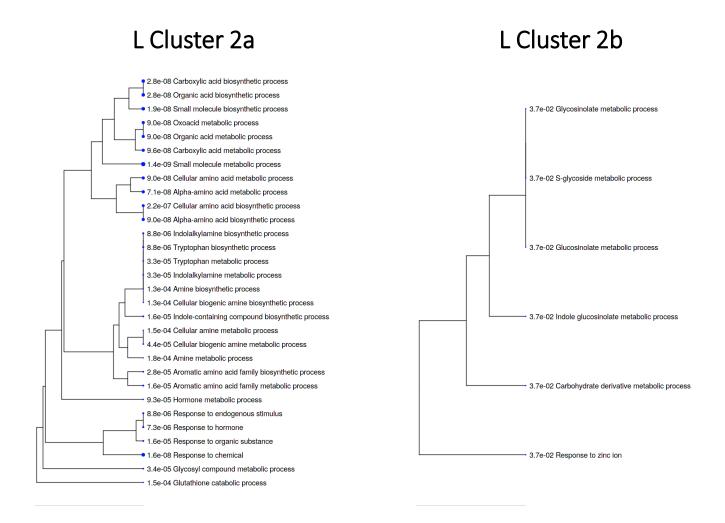


L clusters

Suppl. Fig. S6A: Cluster analysis of genes with at least 1.5-fold priming effects in the light and weaker priming effects in the cold. Mean-centered heatmap and cluster-definition as obtained by ClustVis with the C0-normalized FPKM data listed in Suppl. Tab. S8.

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#### Suppl. Fig. S6B



Suppl. Fig. S6B: Results on GO-term analysis for functional categories on the L cluster 2a and 2b.

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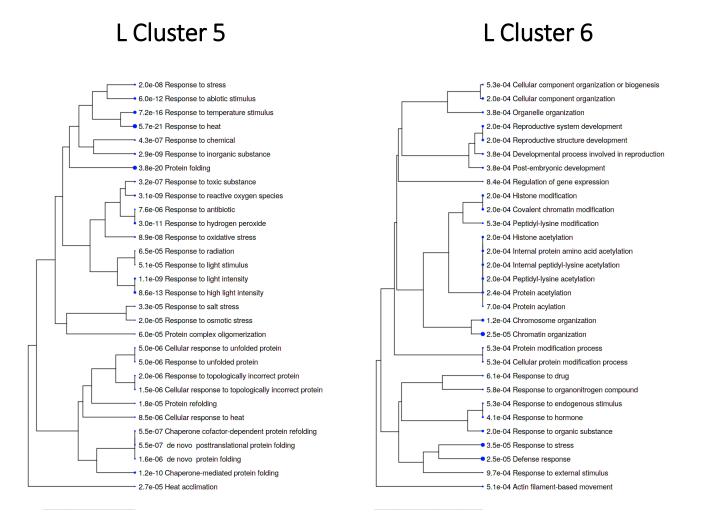
#### Suppl. Fig. S6C

L Cluster 3 L Cluster 4 2.1e-02 Response to water deprivation 3.6e-04 Defense response to bacterium 9.5e-03 Response to water 3.4e-05 Response to bacterium 2.1e-02 Response to inorganic substance 2.0e-04 Immune response 4e-03 Cold acclimation 1.8e-04 Innate immune response 1.9e-04 Response to cold 3.6e-04 Immune system process 1.9e-04 Response to temperature stimulus 4.6e-04 Response to other organism 2.6e-05 Response to abiotic stimulus 4.6e-04 Response to external biotic stimulus 1.0e-02 Response to endogenous stimulus 4.9e-04 Response to biotic stimulus 9.6e-03 Response to hormone 8.5e-05 Defense response 2.3e-02 Response to organic substance 6.3e-04 Indole-containing compound biosynthetic process 7.3e-03 Response to chemical 4.6e-04 Indole-containing compound metabolic process 1.2e-02 Response to lipid 7.7e-07 Signaling 5.8e-07 Signal transduction 2.0e-02 Fruit development 1.2e-02 Cotyledon development 1.5e-06 Cell communication 2.1e-02 System development 1.2e-07 Cellular response to stimulus 2.1e-02 Multicellular organism development 2.0e-05 Response to abiotic stimulus 1.2e-02 Post-embryonic development 8.6e-06 Response to temperature stimulus 2.0e-02 Shoot system development 3.5e-04 Response to heat 7.6e-04 Phyllome development 5.7e-08 Response to oxygen-containing compound 1.2e-02 Plant organ development 2.8e-16 Response to drug 1.4e-03 Leaf development 1.5e-05 Response to chemical 1.4e-03 Exit from dormancy 5.8e-07 Response to organic substance 1.4e-03 Release of seed from dormancy • 5.5e-16 Response to nitrogen compound 7.1e-18 Response to organonitrogen compound 2.2e-03 Positive regulation of seed germination 2.1e-02 Response to red light - 3.1e-21 Response to chitin 2.1e-02 Monocarboxylic acid catabolic process 4.9e-04 Aromatic compound biosynthetic process 2.1e-02 Lipid metabolic process 4.2e-09 Response to stress 1.0e-02 Fatty acid derivative metabolic process 8.1e-04 Response to water 2.3e-02 Very long-chain fatty acid metabolic process 7.5e-04 Response to water deprivation 2.1e-02 Very long-chain fatty acid biosynthetic process 6.9e-04 Response to UV

Suppl. Fig. S6C: Results on GO-term analysis for functional categories on the L cluster 3 and 4.

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#### Suppl. Fig. S6D



Suppl. Fig. S6D: Results on GO-term analysis for functional categories on the L clusters 5 and 6.