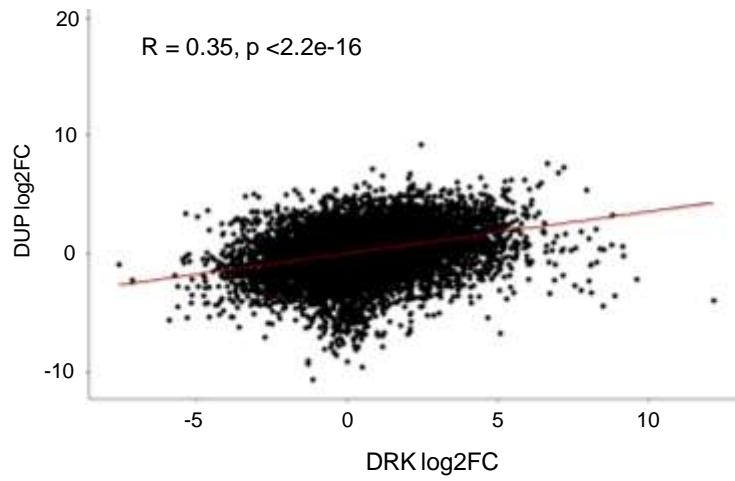
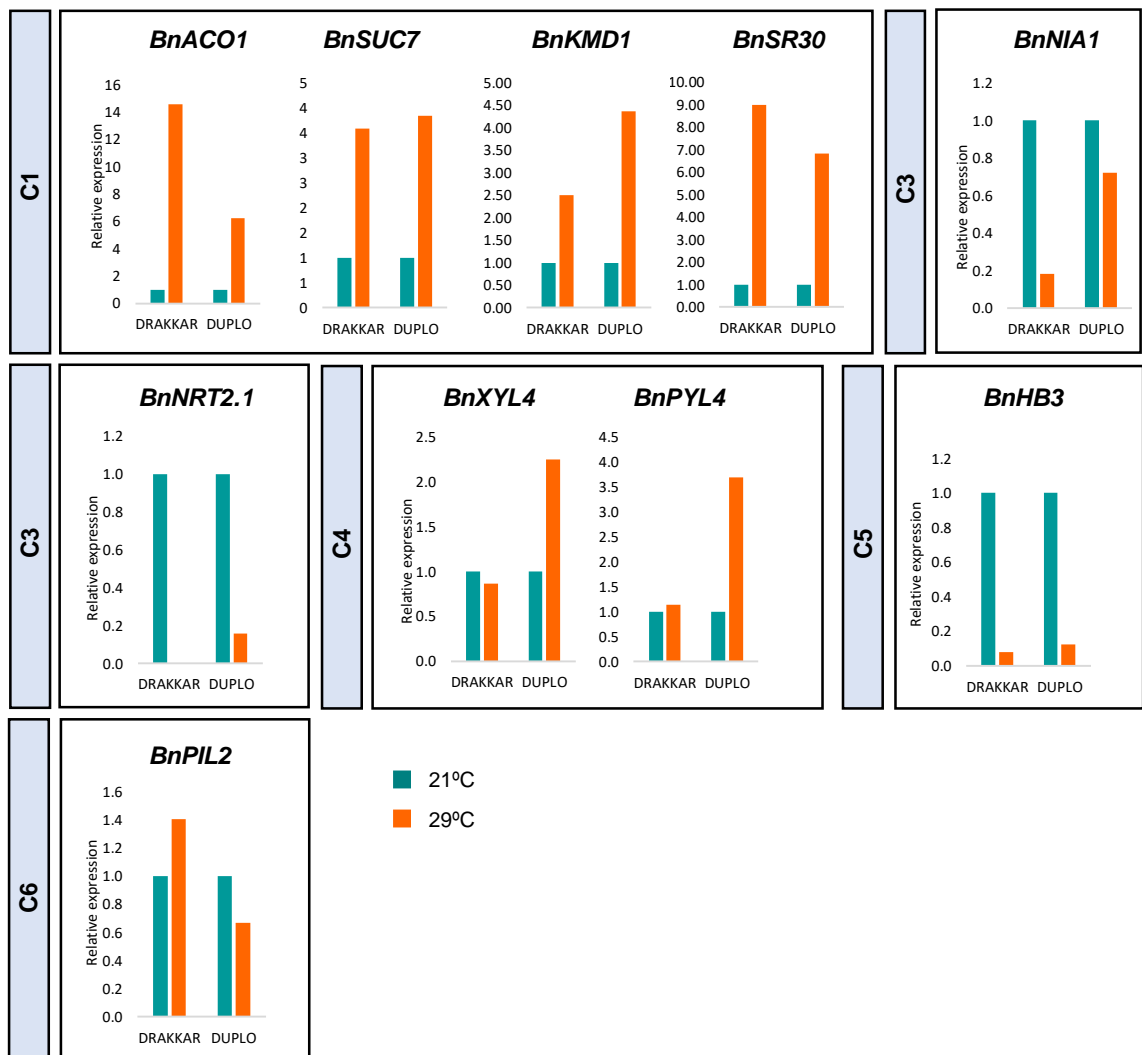


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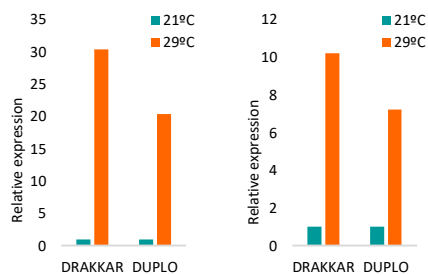


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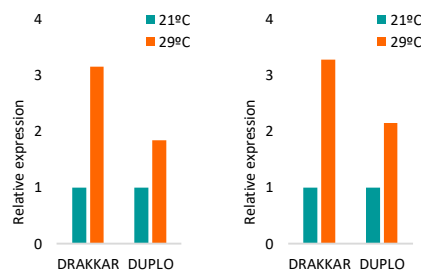


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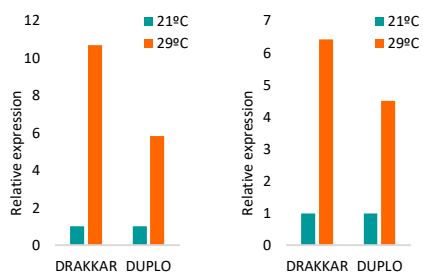
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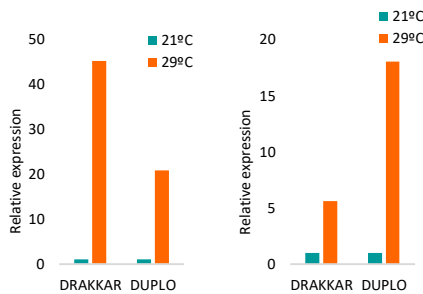
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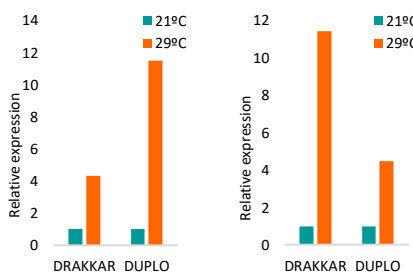
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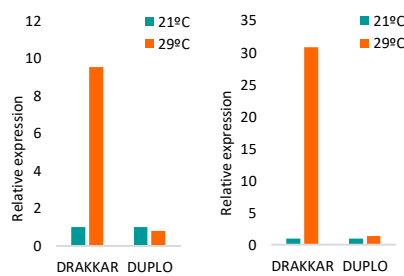
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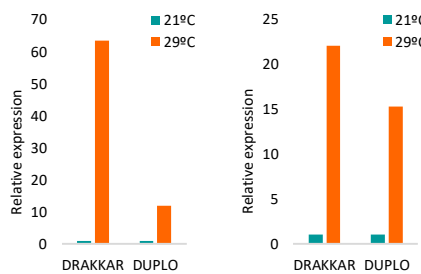
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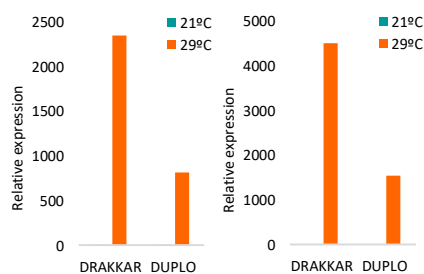
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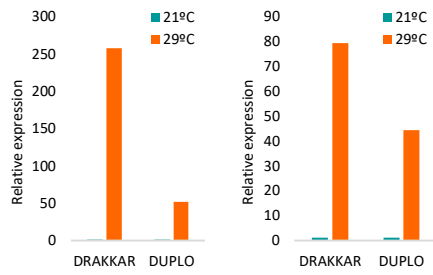
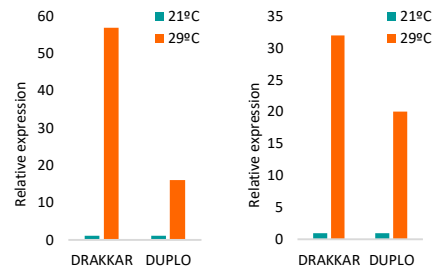
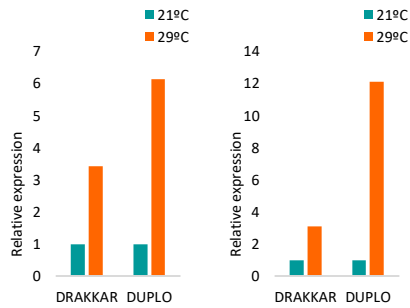
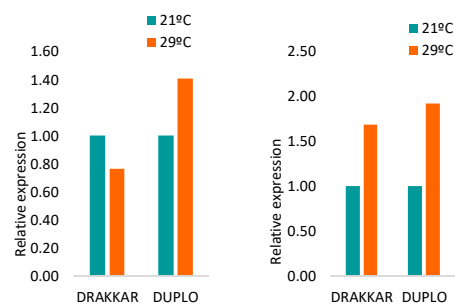
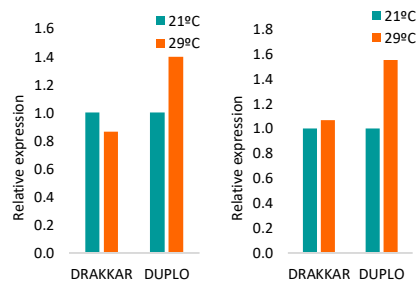
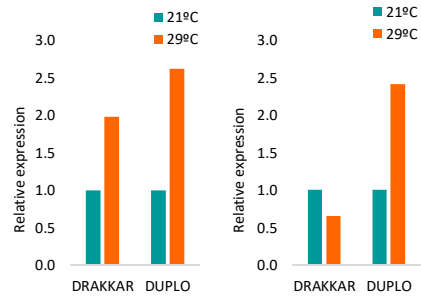
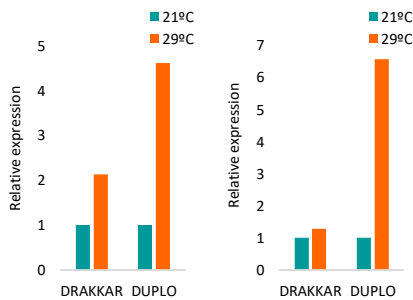
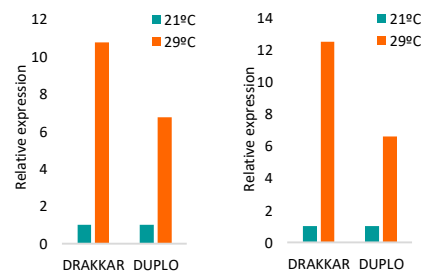


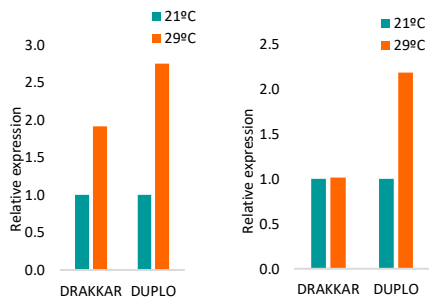
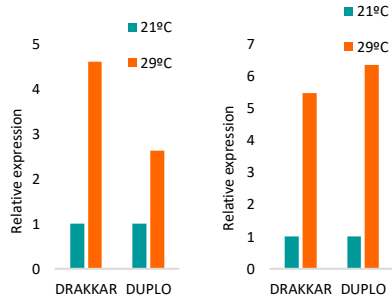
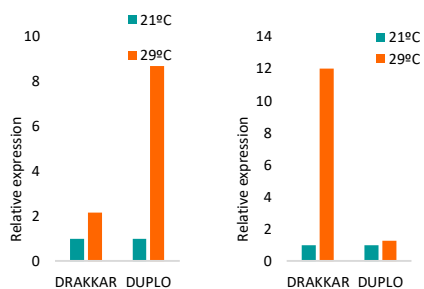
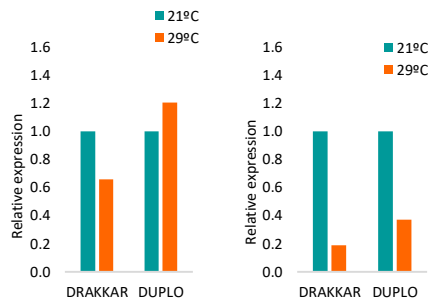
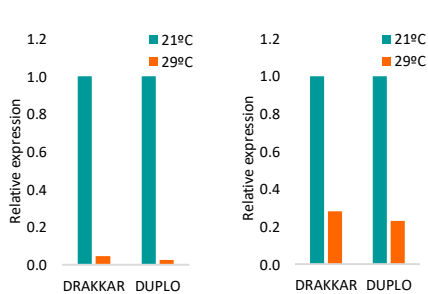
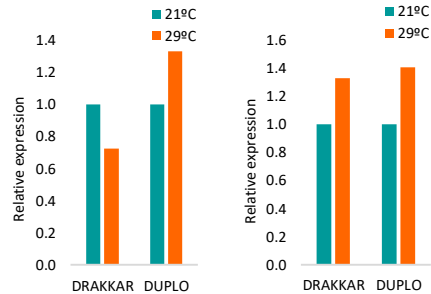
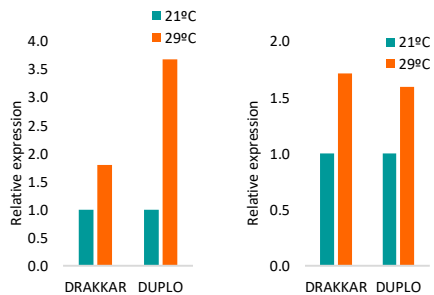
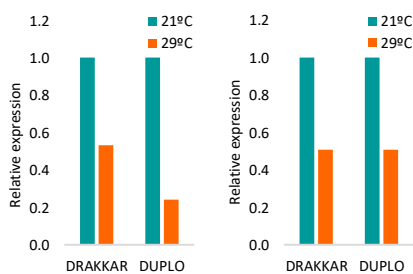
BnGolS1



Bnp23



BnHSA32**BnHSP15.7****BnXTR6****BnEXPA8****BnPYL5****BnSTE1****BnGA2OX2****BnSR30**

BnACO1**BnSUC7****BnKMD1****BnNIA1****BnNRT2.1****BnXYL4****BnPYL4****BnHB3**

BnPIL2

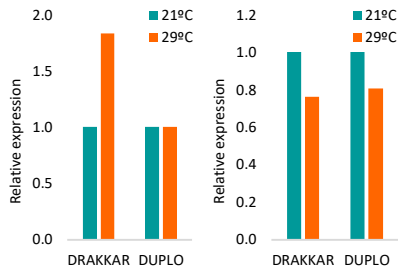


Figure S3. Differential gene expression patterns determine the variability of root response to warm temperature in *B. napus*. **(A)** Correlation analysis of gene expression between Drakkar and Duplo root tips grown at 21°C and 29°C. **(B)** Relative gene expression values of genes, as measured using quantitative RT-PCR (qPCR), from Cluster 1: related with ethylene (ET) biosynthesis genes, *BnACO1*; mechanisms of temperature sensing and signalling like sugar transport, *BnSUC7*, and splicing machinery, *BnSR30* and degradation of CKs, *BnKMD1*; from Cluster 3: related with nitrate assimilation and transport, *BnNIA1* and *BnNRT2.1*; from Cluster 4: related with cell wall biogenesis and organization, *BnXYL4* and ABA sensing, *BnPYL4*; from Cluster 5: related to CK signalling, *BnHB3*; and from Cluster 6: related to negative regulation of photomorphogenesis, *BnPIL2*, identified by hierarchical clustering analysis of Drakkar and Duplo root tips grown at 21°C compared to 29°C. The second and third biological replicates can be found in Figure. S2C. **(C)** Second and third biological replicates of qPCRs of DEGs between Drakkar and Duplo root tips grown at 21°C and to 29°C from all the clusters analysed. The first biological replicates are shown in Figure. 6 and Figure. S3B.