



Is a member of UDP-glycosyltransferase regulating ellagitannins metabolism in strawberry?



José Mora¹, Delphine M. Pott¹, Iraida Amaya², José G. Vallarino¹ and Sonia Osorio¹

¹Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora". Departamento de Biología Molecular y Bioquímica, Consejo Superior de Investigaciones Científicas –Universidad de Málaga- (IHSM-CSIC-UMA)

²IFAPA Centro Málaga, Instituto Andaluz de Investigación y Formación Agraria y Pesquera (IFAPA), Cortijo de la Cruz s/n, 29140, Churriana, Málaga, Spain

José Mora: mora@uma.es

Corresponding autor:
Sonia Osorio: sosorio@uma.es



Domestic strawberries (*Fragaria × ananassa*) are widely consumed worldwide. Their high nutritive value and their organoleptic characteristics are related to the secondary metabolism in fruits. Specifically the phenylpropanoids' pathway produces many chemicals that contribute to flavour and offer antioxidant protection. Among them, the hydrolysable tannins, like ellagitannins and ellagic acid, have an effect on health in some human diseases such as breast and prostate cancers or neurodegenerative diseases.

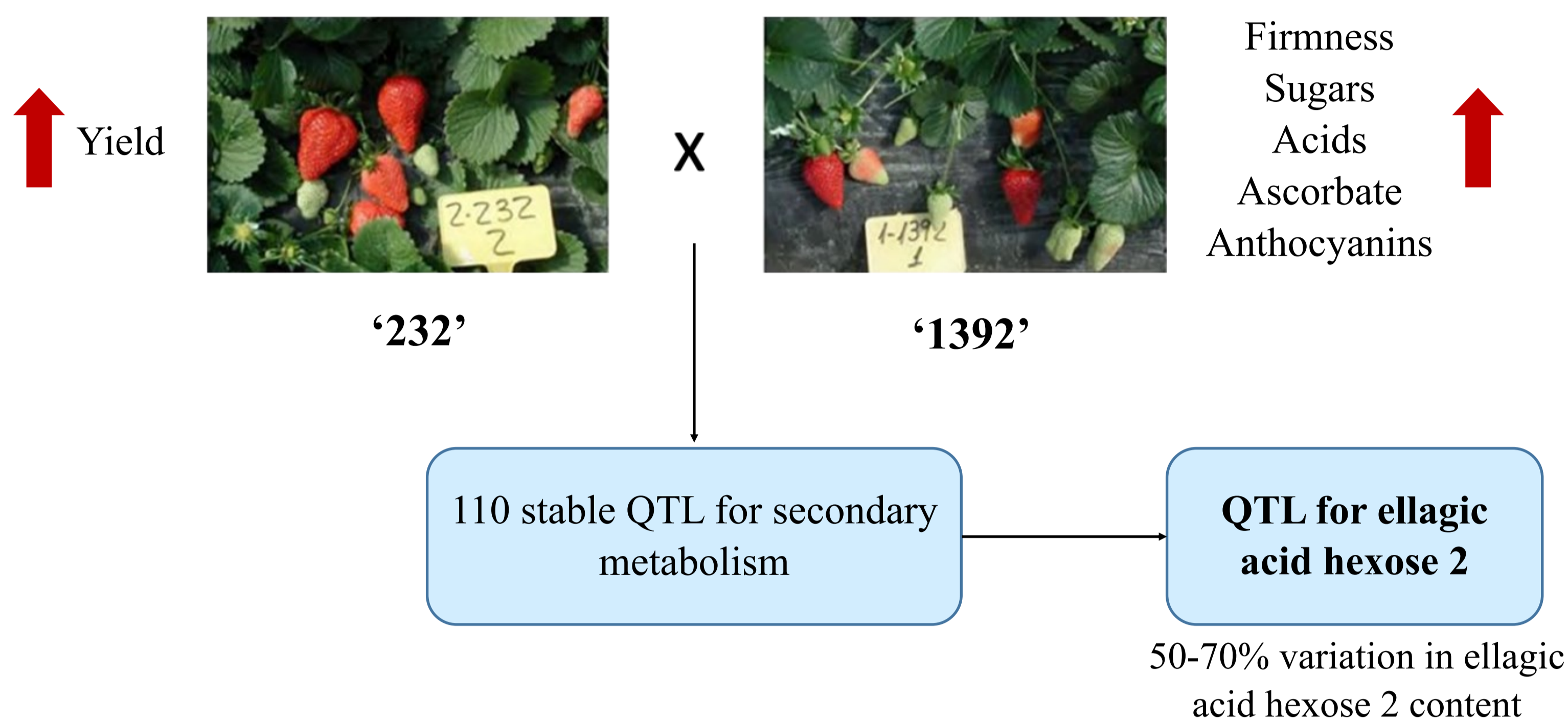


Figure 1. Scheme of the detection of the candidate gene for the mQTL responsible of ellagic acid hexose 2 content. The mQTL were performed with F₁ individuals derived from the crossing of '232' and '1392'.

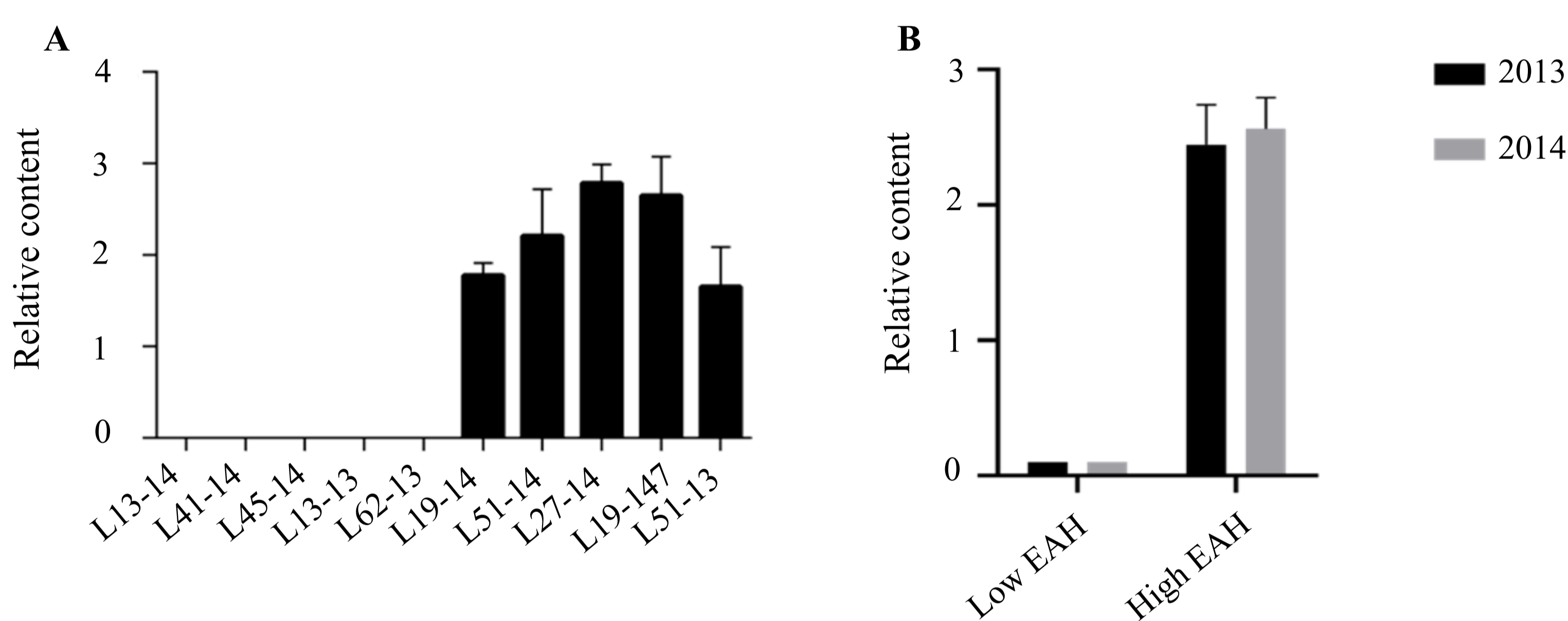


Figure 2. Constrasting lines in ellagic acid hexose 2 (EAH) content used in RNAseq. In A we show the F₁ individuals derived from the crossing of '232' and '1392' that were selected for the RNAseq. In B we show the difference in ellagic acid hexose 2 content in two years within two groups: high and low ellagic acid hexose 2 content lines.

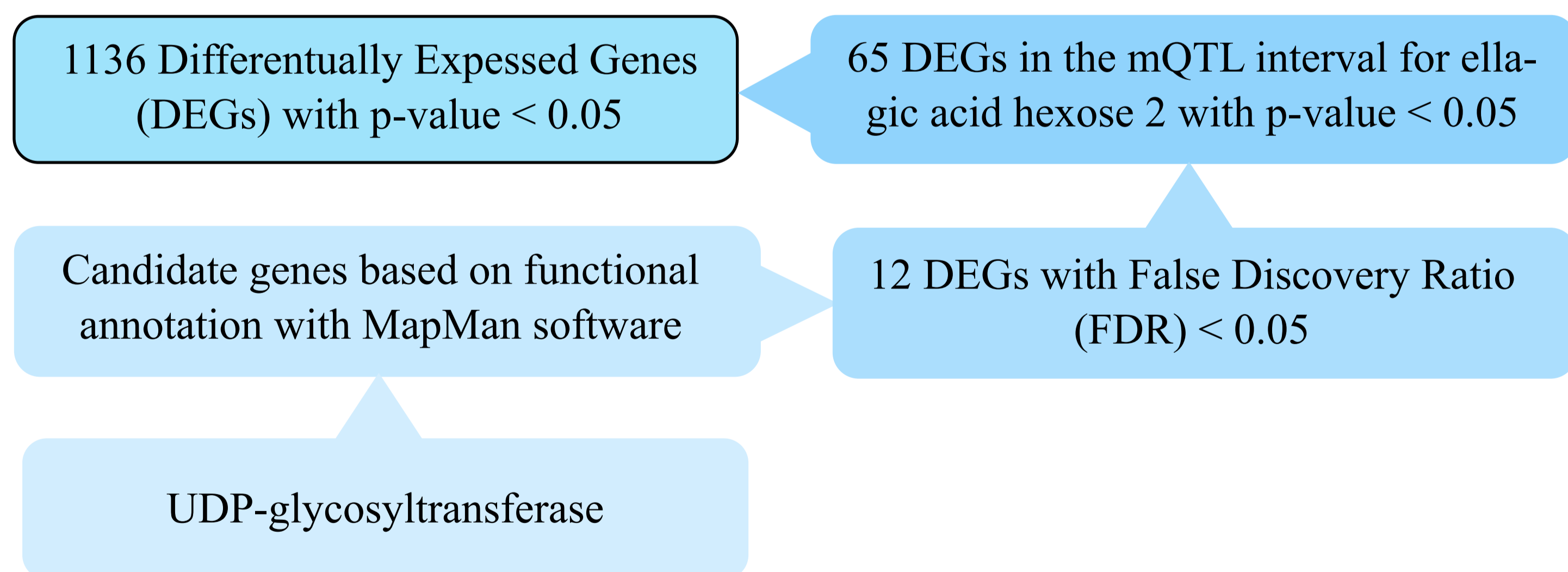


Figure 3. Summary of RNAseq analysis of F₁ individual with contrasting ellagic acid hexose 2 content. The RNAseq analysis from high and low content lines revealed several Differentially Expressed Genes (DEGs). Those genes were filtered with p-value, False Discovery Ratio (FDR) and functional annotation criteria. Finally, we selected a UDP-glycosyltransferase as a candidate gene for the mQTL due to its possible implication in ellagitannins metabolism.

To further confirm the hypothesis that this UDP-glycosyltransferase, detected in the mQTL from the population showed in **Figure 1**, is involved in ellagic acid hexose 2 metabolism we moved forward to study the expression and the metabolites content in another population.

For this purpose, we used the Goodberry population (F₁ population derived from the crossing of 'Candongga' and 'Senga Sengana' varieties).

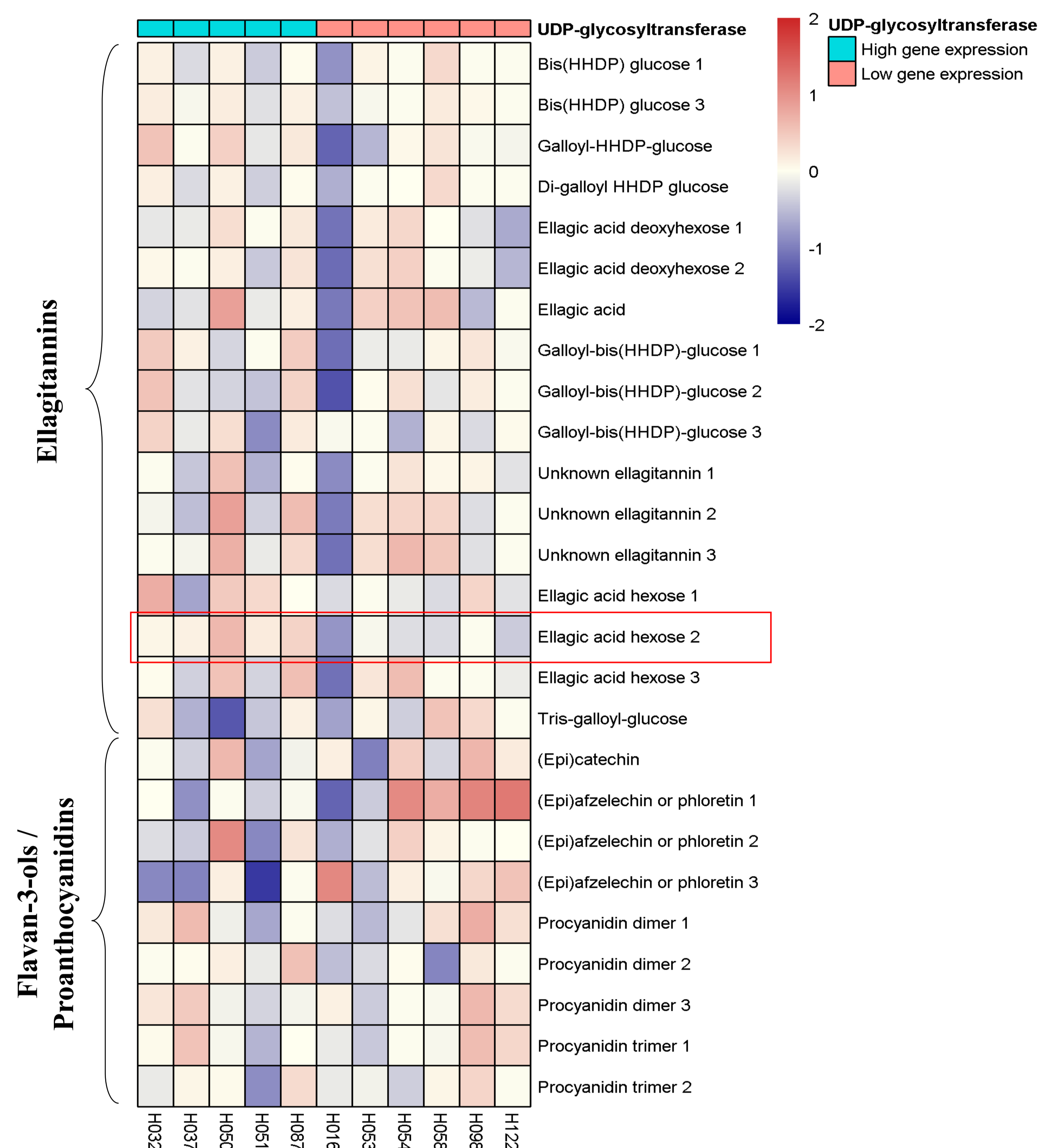


Figure 4. Metabolic profiling of ellagitannins and flavan-3-ols/proanthocyanidins in Goodberry individuals. The Goodberry individuals are separated depending on the UDP-glycosyltransferase gene expression in two categories: high and low expression. Highlighted in red we show the compound responsible of the detection of the mQTL for ellagic acid hexose variation.

Conclusions

- An UDP-glycosyltransferase were selected as a candidate gene for a mQTL responsible of the 50-70% of the variation of ellagic acid hexose 2
- The expression of the gene were studied in a different population to further confirm the relationship between this gene expression and the ellagic acid hexose 2 content
- Metabolic profiling of ellagitannins, flavan-3-ols and proanthocyanidins were performed to confirm a positive correlation between UDP-glycosyltransferase expression and ellagic acid hexose 2 content.
- The expression of the UDP-glycosyltransferase seems to have a negative correlation with the flavan-3-ols and proanthocyanidins content, maybe indicating a possible metabolic flux redirection through the synthesis of ellagitannins.

References

- Basu, A., Nguyen, A., Betts, N. M., and Lyons, T. J. (2014). Strawberry as a functional food: An evidence-based review. *Crit. Rev. Food Sci. Nutr.* 54, 790–806. doi:10.1080/10408398.2011.608174
- Pott, D. M., Vallarino, J. G., Cruz-Rus, E., Willmitzer, L., Sánchez-Sevilla, J. F., Amaya, I., et al. (2020). Genetic analysis of phenylpropanoids and antioxidant capacity in strawberry fruit reveals mQTL hotspots and candidate genes. *Sci. Reports* 2020 101 10, 1–15. doi:10.1038/s41598-020-76946-x.
- Zorrilla-Fontanesi et al., (2011). *Theoretical and Applied Genetics* 123(5), 755-778. doi: 10.1007/s00122-011-1624-6.

Acknowledgements & Funding

This work was supported by grants RTI 2018-099797-B-I00 (Ministerio de Ciencia, Innovación y Universidades, Spain) and UMA18-FEDERJA-179 (FEDER-Junta Andalucía). In addition, we acknowledge partial funding by PY20_00408 (PAIDI 2020-Junta Andalucía). JGV acknowledges the EMERGIA Programme (EMERGIA20_00309-Junta de Andalucía). J.M. thanks to Ministerio de Ciencia, Innovación y Universidades (PRE2019-091188). The authors also acknowledge the support by the Plan Propio from University of Málaga, Campus de Excelencia Internacional de Andalucía.