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FaRIF* TRANSCRIPTION FACTOR PLAYS A KEY ROLE IN THE REGULATION OF FRUIT RIPENING IN THE CULTIVATED STRAWBERRY *Fragaria* × *ananassa

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Strawberry is becoming a model for studying the molecular mechanism of ripening in non-climacteric fruits. However, a limited number of transcriptional regulators of this process have been identified so far. In this study, we have identified and characterized a gene encoding for a NAC transcription factor (TF), named as *FaRIF* (*Ripening Inducing Factor*). *FaRIF* expression presents a fruit-specific pattern being upregulated during ripening. In order to functionally characterize this TF, we have generated silencing (*35S::RIF-RNAi*) and overexpressing (*35S::RIF-GFP*) stable transgenic lines. While the RNAi lines showed an apparent delay of fruit ripening, the overexpressing lines displayed an acceleration of this process. Transcriptomic analysis by RNA-seq of the silenced lines showed a significantly altered expression of genes involved in the flavonoids pathway, as well as genes of the metabolism of the main sugars of the fruit. Metabolomics analysis confirmed these changes in the transgenic fruits. Both, transcriptomic and metabolomics data, were in agreement with the general phenotype observed in the fruits of the *FaRIF*-silenced lines. All

together, our results support a main role of *FaRIF* in the control of relevant ripening-associated processes in strawberry fruit.

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