**De novo assembly**

First the quality visualization was performed with FastQC (version 0.11.5) (1). After we used Trimmomatic (version 0.36) (2) to remove the sequencing adapters, ambiguous nucleotides and filter the quality of the reads with a sliding window of 4 bases and a minimum Phred score > 20. Those quality filtered reads were the input for the ‘de novo’ transcriptome assembly with Trinity transcriptome assembler (version 2.5.1) (3) with the default parameters and the metadata file containing all the samples separated by their treatment (day\_0, day\_3\_amb-temp, day\_3\_15C\_temp, day\_6\_amb-temp, day\_6\_15C\_temp and day\_9\_15C\_temp). To validate the assembly, the reads of each sample were realigned to the transcriptome using Bowtie2 (version 2.3.0) (4).

**Differential expression analysis**

The expression was calculated with RSEM (RNA-Seq by Expectation Maximization) (version 1.2.31) (5), filtering the features with an FPKM < 1. After, we use DESeq2 (version 1.26.0) (6) R package to obtain the differentially expressed genes and isoforms. Only the genes and isoforms with a log2 fold change > 2 and False Discovery Rate (FDR) < 0.005 were considered as differentially expressed between treatments.

**Code availability**

All the scrips and their description were temporarily deposited in this GitHub repository: https://github.com/LuiguiGallardo/transcriptome\_soursop-guanabana.git

**References**

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