**De novo transcriptome 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**

1. Andrews, S. (2010). FastQC:  A Quality Control Tool for High Throughput Sequence Data [Online]. Available online at: <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>
2. Bolger, Anthony M., Marc Lohse, and Bjoern Usadel. “Trimmomatic: A Flexible Trimmer for Illumina Sequence Data.” *Bioinformatics* 30, no. 15 (August 1, 2014): 2114–20. <https://doi.org/10.1093/bioinformatics/btu170>.
3. Grabherr, Manfred G, Brian J Haas, Moran Yassour, Joshua Z Levin, Dawn A Thompson, Ido Amit, Xian Adiconis, et al. “Full-Length Transcriptome Assembly from RNA-Seq Data without a Reference Genome.” *Nature Biotechnology* 29, no. 7 (July 2011): 644–52. <https://doi.org/10.1038/nbt.1883>.
4. Langmead, Ben, and Steven L Salzberg. “Fast Gapped-Read Alignment with Bowtie 2.” *Nature Methods* 9, no. 4 (April 2012): 357–59. <https://doi.org/10.1038/nmeth.1923>.
5. Li, Bo, and Colin N Dewey. “RSEM: Accurate Transcript Quantification from RNA-Seq Data with or without a Reference Genome.” *BMC Bioinformatics* 12, no. 1 (December 2011): 323. <https://doi.org/10.1186/1471-2105-12-323>.
6. Love, Michael I, Wolfgang Huber, and Simon Anders. “Moderated Estimation of Fold Change and Dispersion for RNA-Seq Data with DESeq2.” *Genome Biology* 15, no. 12 (December 2014): 550. <https://doi.org/10.1186/s13059-014-0550-8>.