

# Hybrid *de novo* transcriptome assembly of Poinsettia (*Euphorbia pulcherrima* Willd. Ex Klotsch).

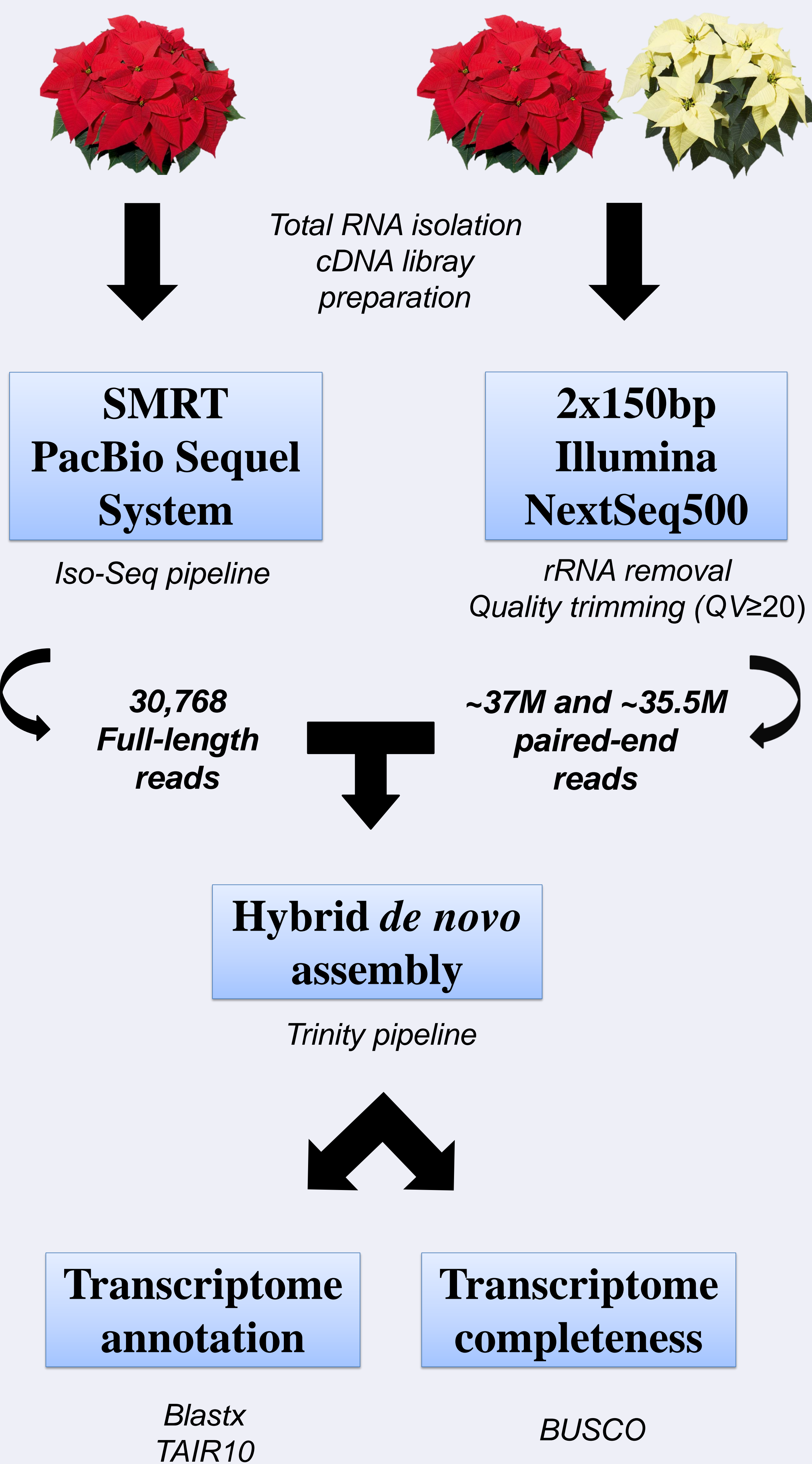
## Introduction

Poinsettia is a popular and important ornamental crop, mostly during the Christmas season, due to its bract colouration, which ranges from pink/red to creamy/white shades (Fig. 1). Despite its ornamental value, there is a lack of knowledge about the genetics and molecular biology of poinsettia. Therefore, we performed an **RNA-Seq** analysis in order to shed light on the transcriptome of poinsettia bracts.



Fig. 1. Red and white Poinsettia plants  
(Source: www.selecta-one.com).

## Methods



## Results and discussion

The final transcriptome contains **288,524** contigs, with **33%** showing confident protein annotation against TAIR10 database. **14,623** distinct protein alignments were identified in the transcriptome, with 54% of them showing a coverage between 80-100%.

The BUSCO pipeline, which is based on near-universal ortholog gene groups, was applied in order to assess the transcriptome completeness. From a total of 1,440 BUSCO (embryophyta\_odb9 database) groups searched, **77% were categorized as complete** (41% as single-copy and 36% as duplicated), 10% as fragmented and 13% as missing BUSCOs (Fig. 2)

### BUSCOs in the Poinsettia transcriptome

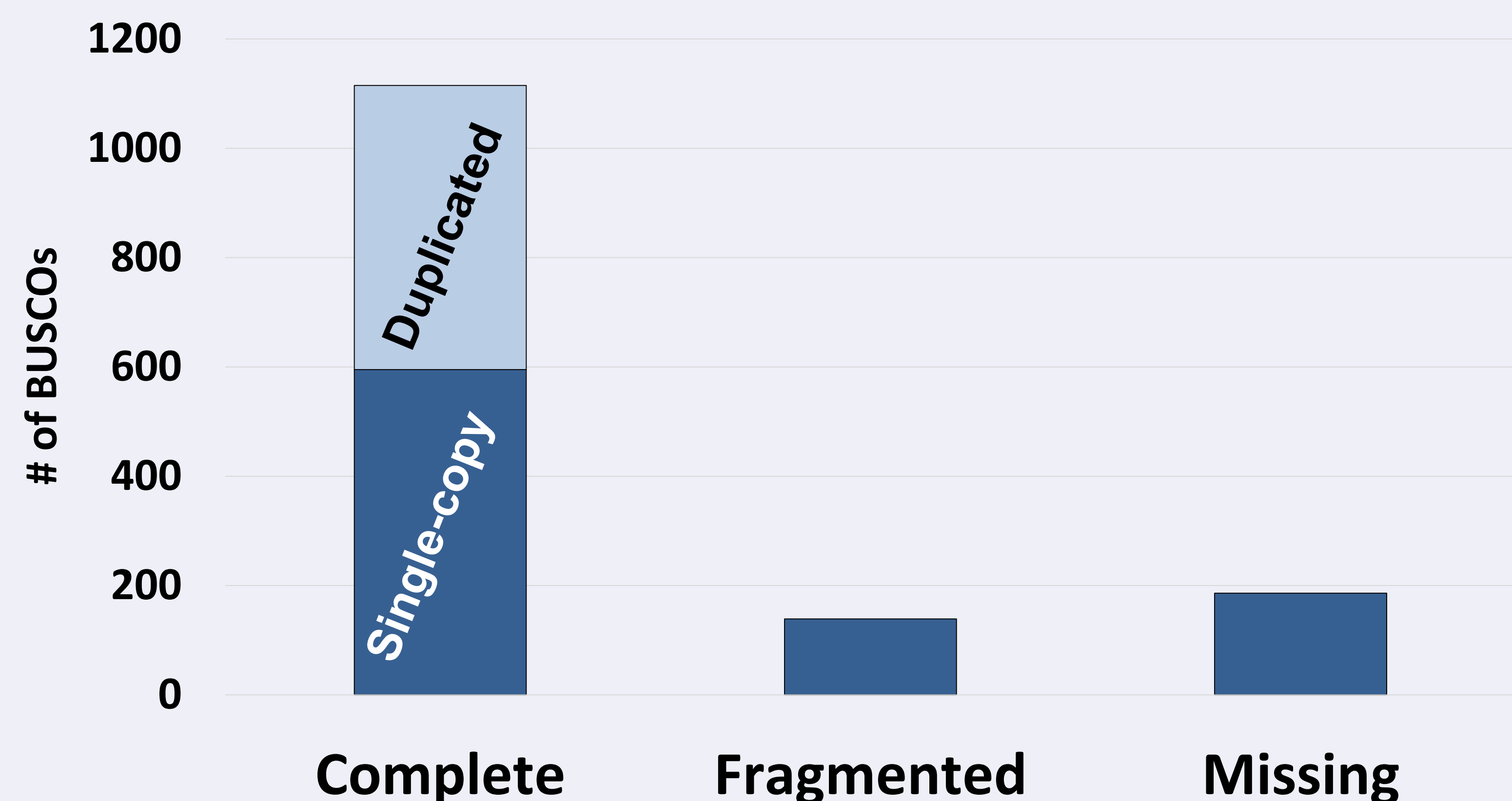


Fig. 2. Number of BUSCOs present in the Poinsettia transcriptome for each of the categories.

When comparing with other transcriptome plant species, some have showed a higher number of complete BUSCOs (e.g. *C. longepaniculatum* - 91%, and *N. caerulescens* - 90%), but also similar values as the ones in our transcriptome (*C. nitidissima* - 76%).

## Conclusions

This transcriptome analysis provides a valuable foundation for further studies on *E. pulcherrima* and related species, such as plant molecular breeding and genetics.

## References

Zhou et al. De novo Assembly of the *C. nitidissima* transcriptome reveals key genes of flower pigment biosynthesis. *Front. Plant Sci.* 8:1545, 2017.

Yan et al. Transcriptome analysis of *C. longepaniculatum* by high-throughput sequencing. *Electronic J. of Biotechnology.* 28:58–66, 2017.

Blande et al. De novo transcriptome assemblies of four accessions of the metal hyperaccumulator plant *N. caerulescens*. *Scientific Data.* 4:160131, 2017.