

## ERRATUM

## Open Access



# Erratum to: Chromosome doubling to overcome the chrysanthemum cross barrier based on insight from transcriptomic and proteomic analyses

Fengjiao Zhang<sup>1,2</sup>, Lichun Hua<sup>1</sup>, Jiangsong Fei<sup>1</sup>, Fan Wang<sup>1</sup>, Yuan Liao<sup>1</sup>, Weimin Fang<sup>1</sup>, Fadi Chen<sup>1</sup> and Nianjun Teng<sup>1,2\*</sup>

## Erratum

Unfortunately, the original version of this article [1] contained an error. The Figure legends for Figs. 3, 4, 5 and 6 are incorrect. The correct version of Figs. 3, 4, 5 and 6 can be found below.

The correct match is as follows:

Received: 16 August 2016 Accepted: 2 September 2016

Published online: 07 September 2016

## Reference

1. Zhang F, et al. Chromosome doubling to overcome the chrysanthemum cross barrier based on insight from transcriptomic and proteomic analyses. *BMC Genomics*. 2016;17:585. doi:10.1186/s12864-016-2939-0.

\* Correspondence: nianjunteng@163.com; njteng@njau.edu.cn

<sup>1</sup>College of Horticulture, Nanjing Agricultural University, Nanjing 210095, China

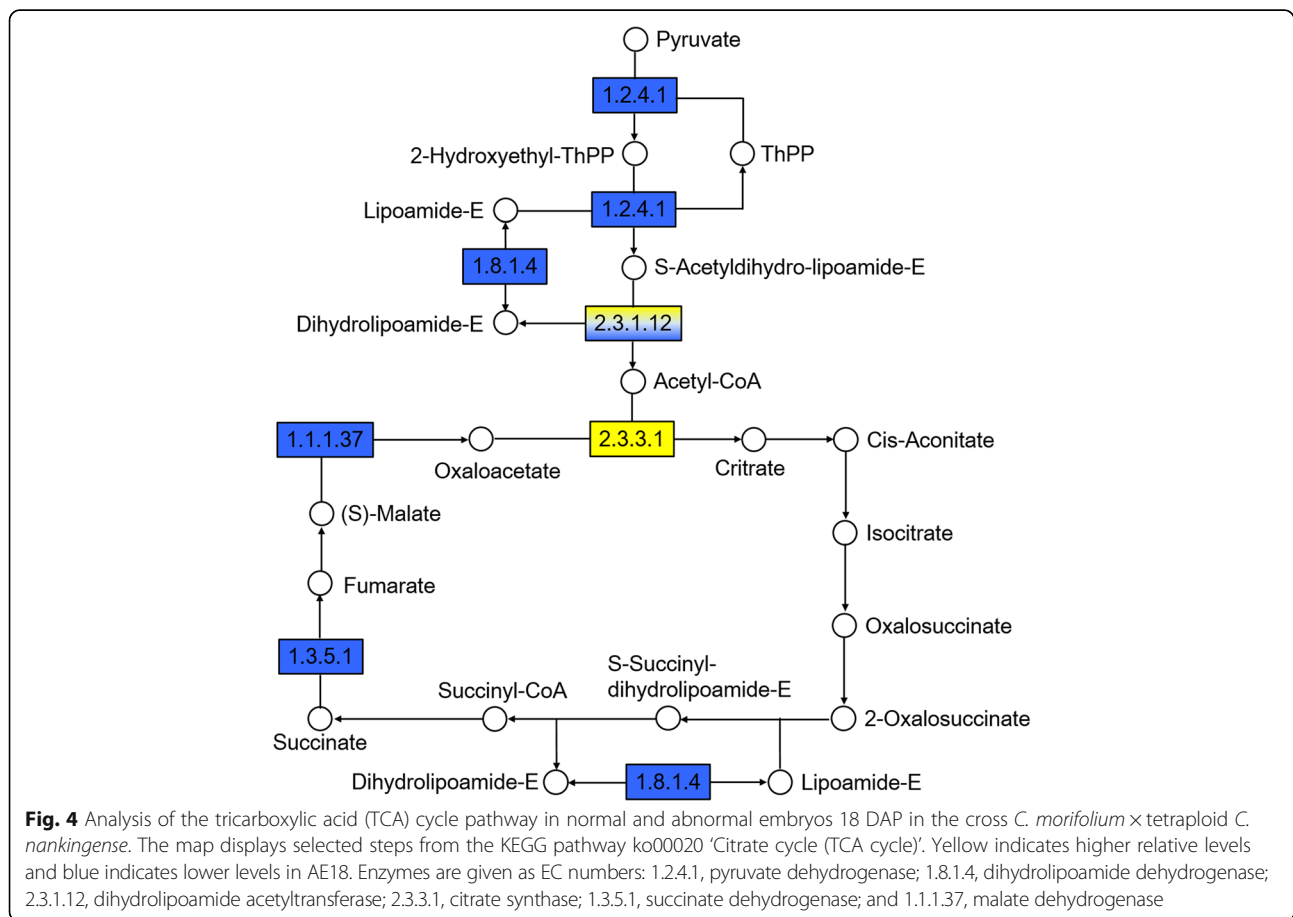
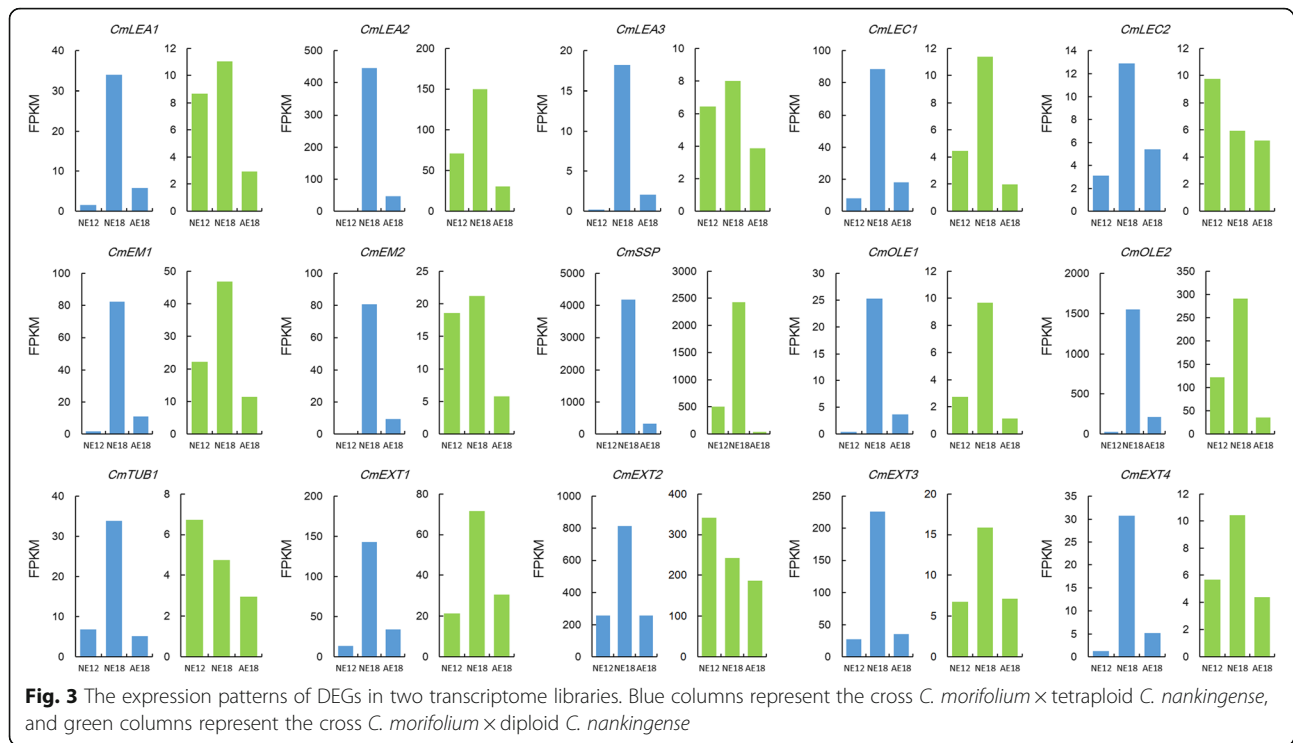
<sup>2</sup>Jiangsu Province Engineering Lab for Modern Facility Agriculture Technology and Equipment, Nanjing 210095, China

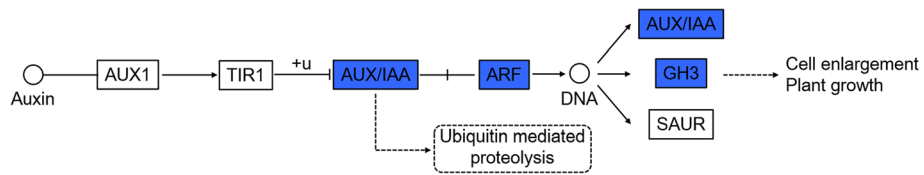
Submit your next manuscript to BioMed Central and we will help you at every step:

- We accept pre-submission inquiries
- Our selector tool helps you to find the most relevant journal
- We provide round the clock customer support
- Convenient online submission
- Thorough peer review
- Inclusion in PubMed and all major indexing services
- Maximum visibility for your research

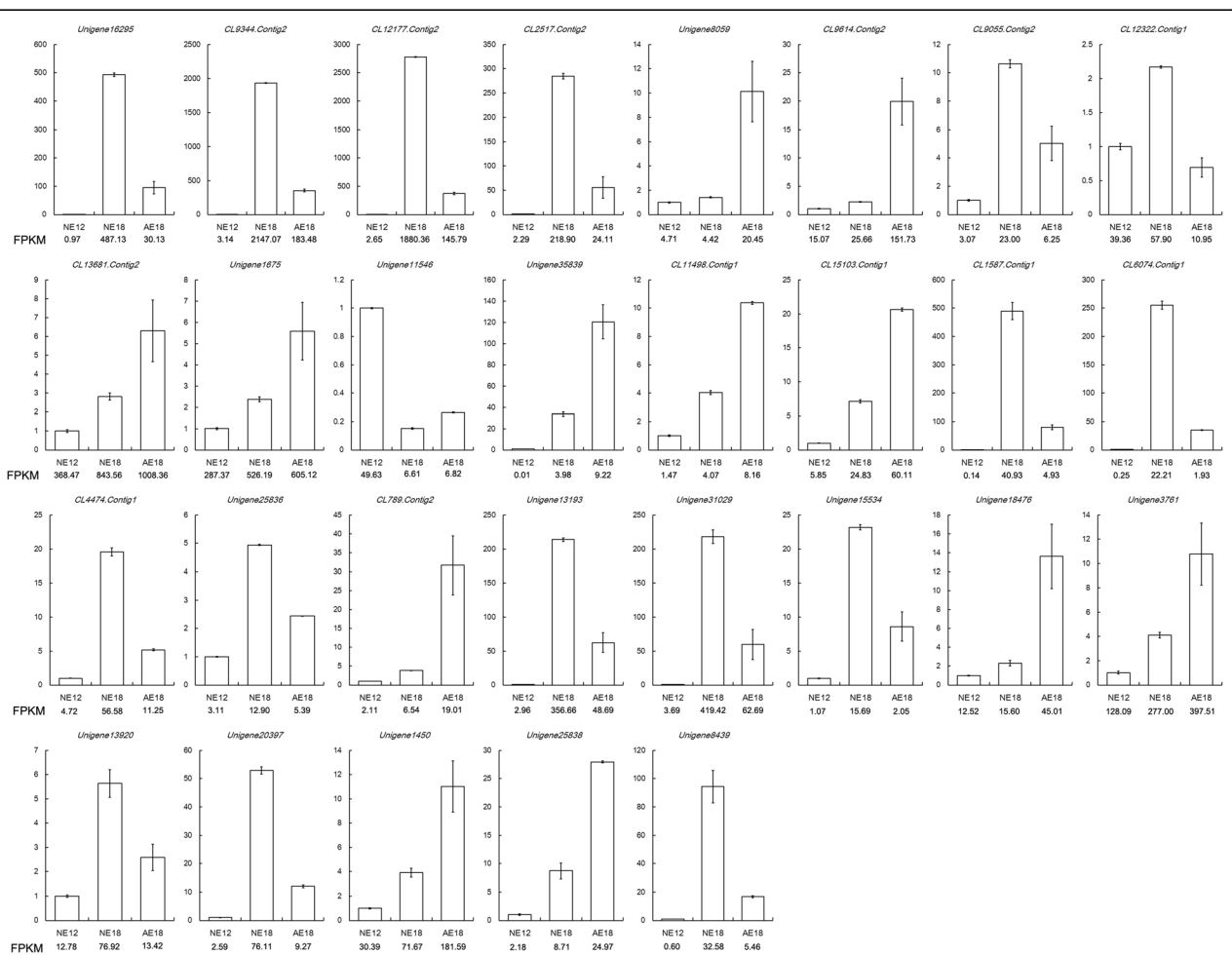
Submit your manuscript at  
[www.biomedcentral.com/submit](http://www.biomedcentral.com/submit)







**Fig. 5** Analysis of the pathway related to auxin signal transduction in normal and abnormal embryos 18 DAP in the cross *C. morifolium* × tetraploid *C. nankingense*. The map displays selected steps from the KEGG pathway ko04075 'Plant hormone signal transduction'. Blue indicates the lower expression level of genes in AE18



**Fig. 6** Validation of the RNA-Seq results by qRT-PCR. FPKM represents the gene abundance in the sequencing data of the transcriptome libraries