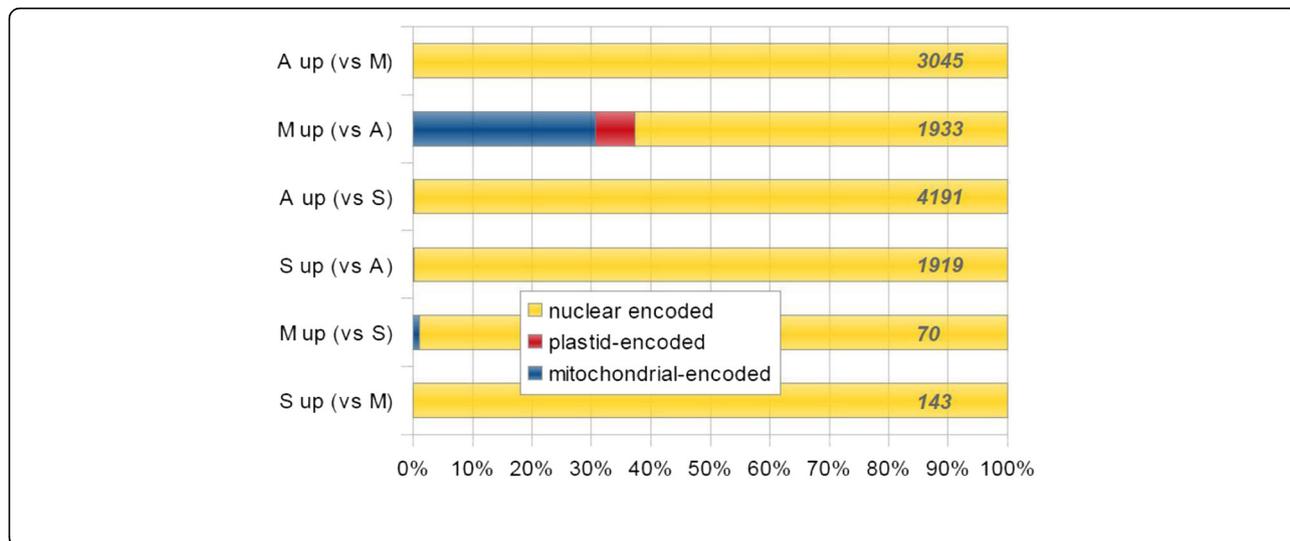**BMC Plant Biology**

CORRECTION

Open Access

Correction to: The transcriptome landscape of early maize meiosis

Stefanie Dukowic-Schulze[1], Anitha Sundararajan[2], Joann Mudge[2], Thiruvarangan Ramaraj[2], Andrew D. Farmer[2], Minghui Wang[3,4], Qi Sun[4], Jaroslaw Pillardy[4], Shahryar Kianian[5], Ernest F. Retzel[2], Wojciech P. Pawlowski[3] and Changbin Chen[1*]

Correction

Following publication of the original article [1], the authors reported that the number of genes overlaying the bar graph in Fig. 3A were incorrectly counted and inserted (i.e. including a title tile, and in inverse order). The corrected numbers are below and match with the listed genes supplied in Additional File: Table S2.
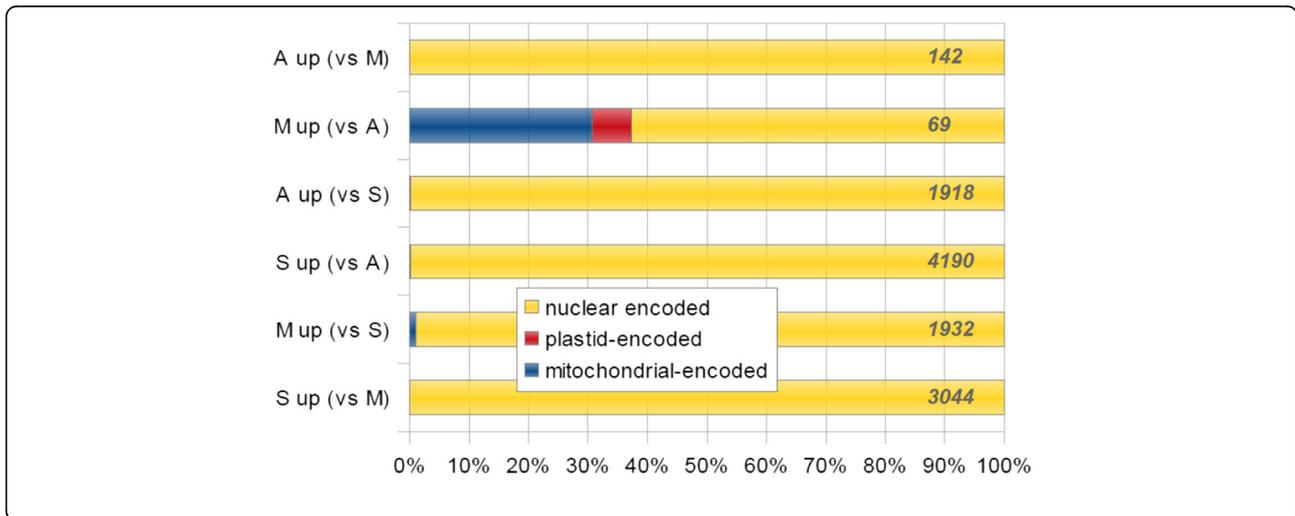
Previous, published version of Fig. 3A:

* Correspondence: chenx481@umn.edu
[1]Department of Horticultural Science, University of Minnesota, St. Paul, MN 55108, USA

Dukowic-Schulze *et al. BMC Plant Biology* (2018) 18:12

Page 2 of 2

New, corrected version of Fig. 3A:

Author details

[1]Department of Horticultural Science, University of Minnesota, St. Paul, MN 55108, USA. [2]National Center for Genome Resources, Santa Fe, NM 87505, USA. [3]Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY 14850, USA. [4]Computational Biology Service Unit, Cornell University, Ithaca, NY 14850, USA. [5]USDA-ARS Cereal Disease Laboratory, University of Minnesota, St. Paul, MN 55108, USA.

Reference

1.   Dukowic-Schulze S, Sundararajan A, Mudge J, Ramaraj T, Farmer AD, Wang M, Sun Q, Pillardy J, Kianian S, Retzel EF, Pawlowski WP, Chen C. The transcriptome landscape of early maize meiosis. BMC Plant Biol. 2014;14:118. https://doi.org/10.1186/1471-2229-14-118.