

# SCIENTIFIC REPORTS

**OPEN**

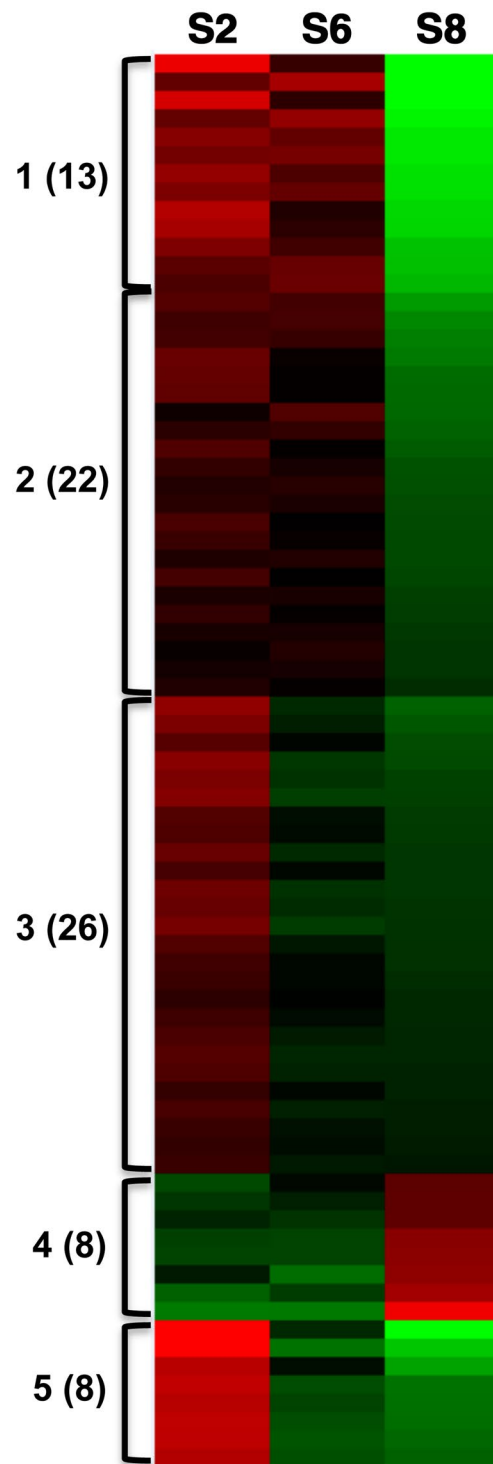
## **Author Correction:** Dynamic Changes of Genome-Wide DNA Methylation during Soybean Seed Development

Yong-qiang Charles An<sup>1</sup>, Wolfgang Goettel<sup>1</sup>, Qiang Han<sup>2</sup>, Arthur Bartels<sup>2</sup>, Zongrang Liu<sup>3</sup> & Wenyan Xiao<sup>2</sup>

Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-017-12510-4>, published online 25 September 2017

In Figure 4, the labels 'S2, S6, S8' are incorrectly given as 'S2, S4, S6'. The correct Figure 4 appears below as Figure 1.

<sup>1</sup>US Department of Agriculture, Agricultural Research Service, Midwest Area, Plant Genetics Research Unit, Donald Danforth Plant Science Center, St. Louis, MO, 63132, USA. <sup>2</sup>Department of Biology, Saint Louis University, St. Louis, MO, 63103, USA. <sup>3</sup>US Department of Agriculture, Agricultural Research Service, Appalachian Fruit Research Station, Kearneysville, WV, 25430, USA. Correspondence and requests for materials should be addressed to Y.-q.C.A. (email: [yong-qiang.an@ars.usda.gov](mailto:yong-qiang.an@ars.usda.gov)) or W.X. (email: [wxiao@slu.edu](mailto:wxiao@slu.edu))



**Figure 1.** Cluster analysis of 77 genes with seed-specific CHH DMRs based on gene expression at stages S2, S6, and S8. Gene clusters based on gene transcription patterns in cotyledon at three stages and DNA methylation in DMRs in <sup>m</sup>CHH, <sup>m</sup>CHG and <sup>m</sup>CG contexts. The green to red color gradient represents low to high gene expression, respectively. Genes with 1) more than 30% DNA methylation changes among three different seed stages S2, S6, and S8, 2). statistically significant changes in gene expression and 3). a negative correlation ( $PCC < -0.85$ ) between gene expression and methylation level were used for cluster analysis.



**Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit <http://creativecommons.org/licenses/by/4.0/>.

© The Author(s) 2018