



Correction to: Inducible epigenome editing probes for the role of histone H3K4 methylation in Arabidopsis heat stress memory

Correction

This is a correction to: Vicky Oberkofler, Isabel Bäurle, Inducible epigenome editing probes for the role of histone H3K4 methylation in Arabidopsis heat stress memory, *Plant Physiology*, Volume 189, Issue 2, June 2022, Pages 703–714, <https://doi.org/10.1093/plphys/kiac113>

The authors state that due to a software error converting Figure 4 from one file type to another, several of the

letters in panel B shifted out of place in the version of the file sent to production. Upon noticing the error, the authors submitted a revised figure containing realigned letters as part of their proof corrections that was mistakenly not included in the final, published version of the article. The revised figure 4 appears below and has been replaced in the article.

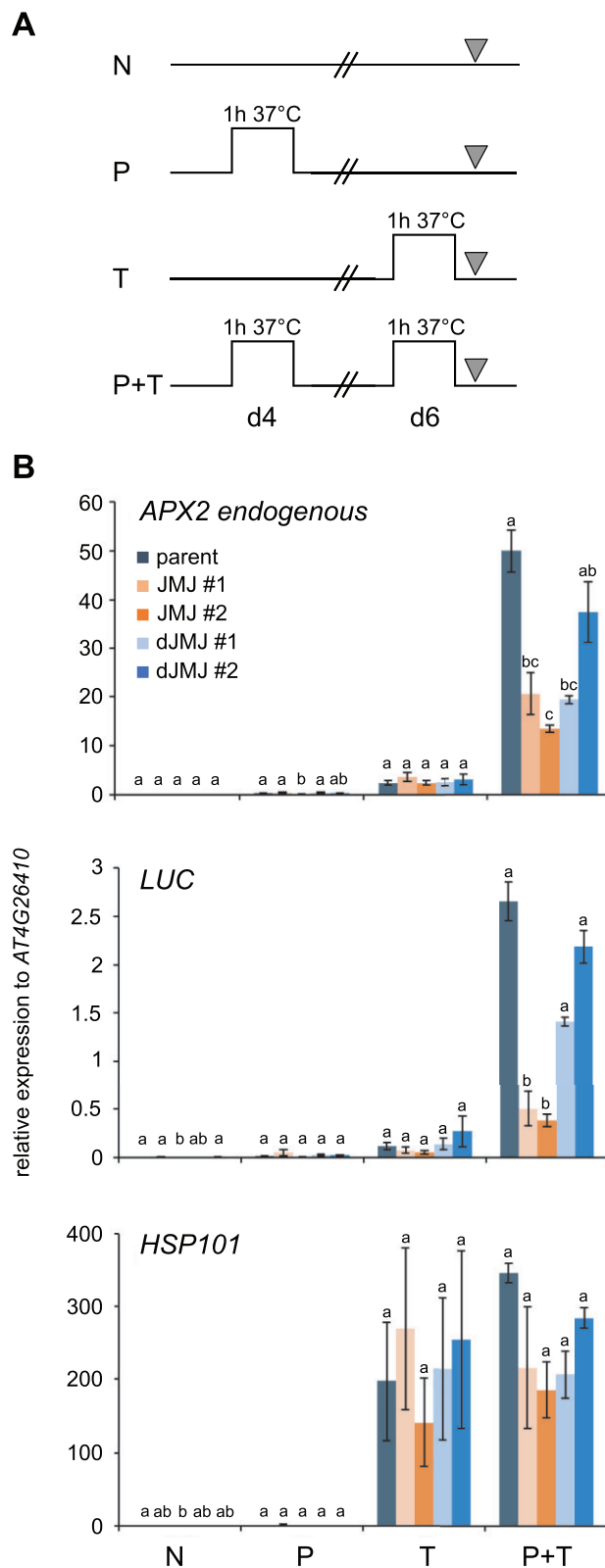


Figure 4 Type II transcriptional memory of endogenous *APX2* and *pAPX2::LUC* after recurrent HS is reduced in *dCas9-JMJ* lines. A, Treatment scheme for RT-qPCR-based type II transcriptional memory assay. Four-day-old seedlings were either exposed to priming HS (P) on Day 4, exposed to a triggering HS (T) on Day 6, exposed to a priming and a triggering HS (P + T), or not exposed to any HS (N). All samples were taken on d6 corresponding to the end of the HS treatment. B, Transcript levels of endogenous *APX2* (*At3g09640*), *LUC* (*pAPX2₆₀₀bp::LUC*), and *HSP101* (*At1g74310*) in parent, two *dCas9-JMJ* lines (JMJ #1 and JMJ #2), and two *dCas9-dJMJ* lines (dJMJ #1 and dJMJ #2) as measured by RT-qPCR. Expression values are relative to *At4g26410*. Data are mean \pm SEM of three independent experiments. Transcript levels were statistically evaluated for all genotypes within each time point by Tukey's HSD ($P < 0.05$). Genotypes are assigned one or more letters based on their statistical group. Genotypes sharing one letter are not significantly different.