

AUTHOR CORRECTION

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Author Correction: Single-cell resolution analysis reveals the preparation for reprogramming the fate of stem cell niche in cotton lateral meristem

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The original article can be found online at <https://doi.org/10.1186/s13059-023-03032-6>.

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Following publication of the original article [1], the authors reported an error in Fig. 9, namely a missing significant difference symbol for JCR1 and a redundant significant difference symbol for JOE1. The updated Fig. 9 is available in this Correction.

Additionally, the following text describing the experimental results shown in Fig. 9 has been amended as follows:

Previous text: Although all explants (CRISPR and overexpression) produced callus after 20 days of induction (Fig. 9c and Additional file 1: Figure. S11a), the callus proliferation rate (CPR) after 20 days of induction showed that the CPR of JCR1 was 58% and for JOE1, 130%, both significantly different to control (88%) in Jin668 (t-test, $P < 0.05$), suggesting that these *LAX* genes may play import roles in callus proliferation in Jin668. Notably, there was no significant difference between TCR1 and TP7N (71% Vs 77%; Fig. 9c).

Updated text: Although all explants (CRISPR and overexpression) produced callus after 20 days of induction (Fig. 9c and Additional file 1: Fig. S11a), the callus proliferation rate (CPR) after 20 days of induction showed that the CPR of JCR1 was 58% and for JOE1, 130%. JCR1 showed significantly different to control (88%) in Jin668 (t-test, $P < 0.05$), suggesting that these *LAX* genes may play import roles in callus proliferation in Jin668. Notably, there was no significant difference between TCR1 and TP7N (71% Vs 77%; Fig. 9c).

The original article has been updated.



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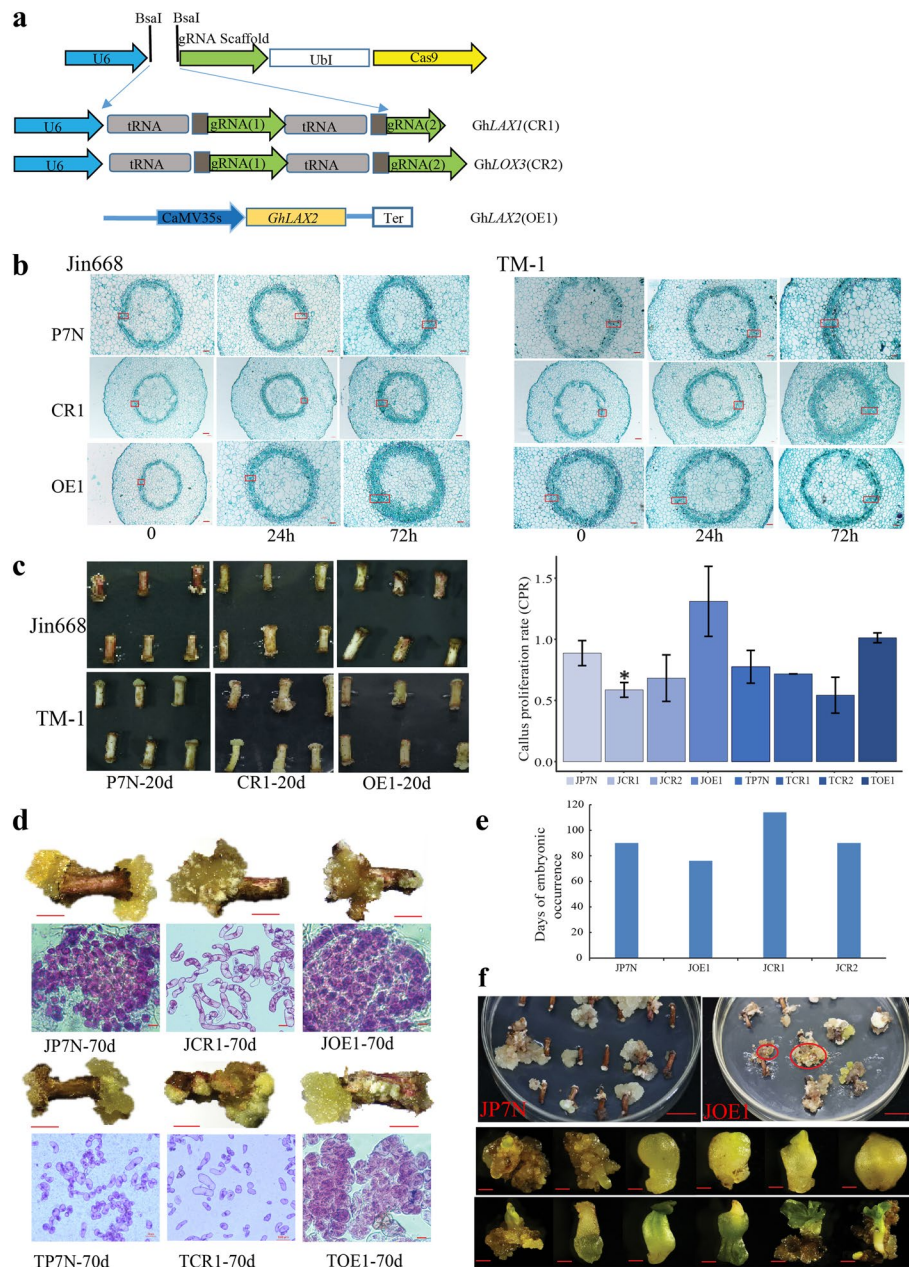


Fig. 9 Phenotype of *GhLAX1*, *GhLAX2*, *GhLOX3* knock out and overexpression callus with hypocotyls as explants. **a** Schematic view of gRNA1, gRNA2 target sites in the *GhLAX1*, and *GhLOX3* and overexpression cassette of *GhLAX2*. **b** Paraffin sections of hypocotyls infected with *Agrobacterium* after induction on callus induction medium for 0, 24, and 72 h. The red box represents the proliferation site. **c** The phenotypes of different transgenic explants and control (P7N) at 20 days post-induction and the callus proliferation rate (CPR) of explants and control at 20 days post-induction. **d** The phenotype of callus on the *GhLAX1* knock out and *GhLAX2* overexpression explants at about 70 days post-induction. Scale bar, 100 μ m. **e** Days of embryonic callus occurrence of different transgenic explants. **f** Morphology of somatic cell embryos of JOE1. Scale bar, 100 μ m

Reference

1. Zhu X, Xu Z, Wang G, et al. Single-cell resolution analysis reveals the preparation for reprogramming the fate of stem cell niche in cotton lateral meristem. *Genome Biol.* 2023;24:194. <https://doi.org/10.1186/s13059-023-03032-6>.