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## Erratum to: A novel role for STOMATAL CARPENTER 1 in stomata patterning

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## **Erratum**

After publication of this article [1] it was noticed that the picture of a plant that was grown without DEX (and thus intended to be a control), was inadvertently inserted in panel 4C which should represent a DEX-treated plant. The correct version of Fig. 4 can be seen in the next page.

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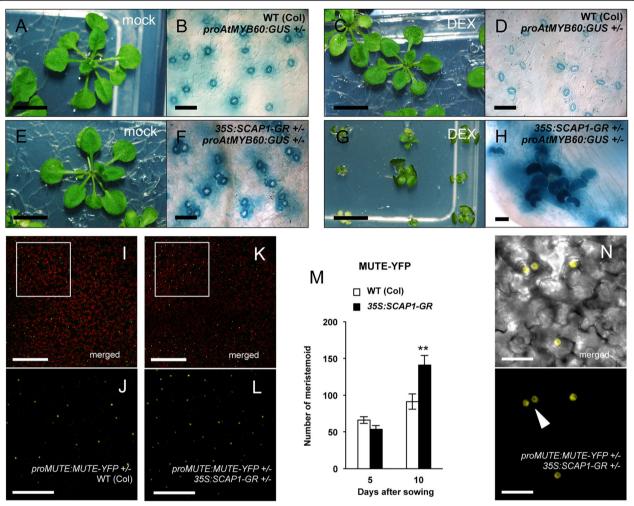
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## Reference

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**Fig. 4** *SCAP1* affect stomata spacing and induce meristemoid production. **a-d** Morphological alterations observed in 4-weeks old wild type (Col) or (**e-h**) *pro35S:SCAP1-GR* (35S:SCAP1-GR) plants grown in presence of DEX (**c-d** and **g-h**) or mock (**a-b** and **e-f**). **f**, **h** GUS staining of double *proAtMYB60:GUS pro35S:SCAP1-GR* or (B, D) single *proAtMYB60:GUS* hemizygous plants. **i-j** Confocal images of MUTE-YFP fusion proteins in hemizygous *proMUTEMUTE-YFP* or (**k-l** and **n**) double hemizygous *proMUTEMUTE-YFP pro35S:SCAP1-GR* transgenic plants. Insets (**j** and **l**) are higher magnification of the areas shown in (**i**) and (**k**), respectively. White arrowhead in (**n**) indicates two adjacent meristemoid. **m** Number of epidermal cells accumulating MUTE-YFP protein in hemizygous *proMUTEMUTE-YFP* or double hemizygous *proMUTEMUTE-YFP pro35S:SCAP1-GR* plants at different developmental stages (5 and 10 das). Shown is the average number of observable nuclei expressing MUTE-YFP in epidermal cells of 10 independent 1st leaf primordia. Note that at stage 5 das, numbers refer to the entire primordium while at 10 das numbers refer to an area of 562 mm<sup>2</sup>. Error bars = Standard Error. \*\*\* = P < 0.01 two tails T Student test. Bars = 1 mm (**a, c, e, g,**); 200 μm (**i, l**); 100 μm (**j, m**); 50 μm (**b, d, f**); 20 μm (**h, o**)