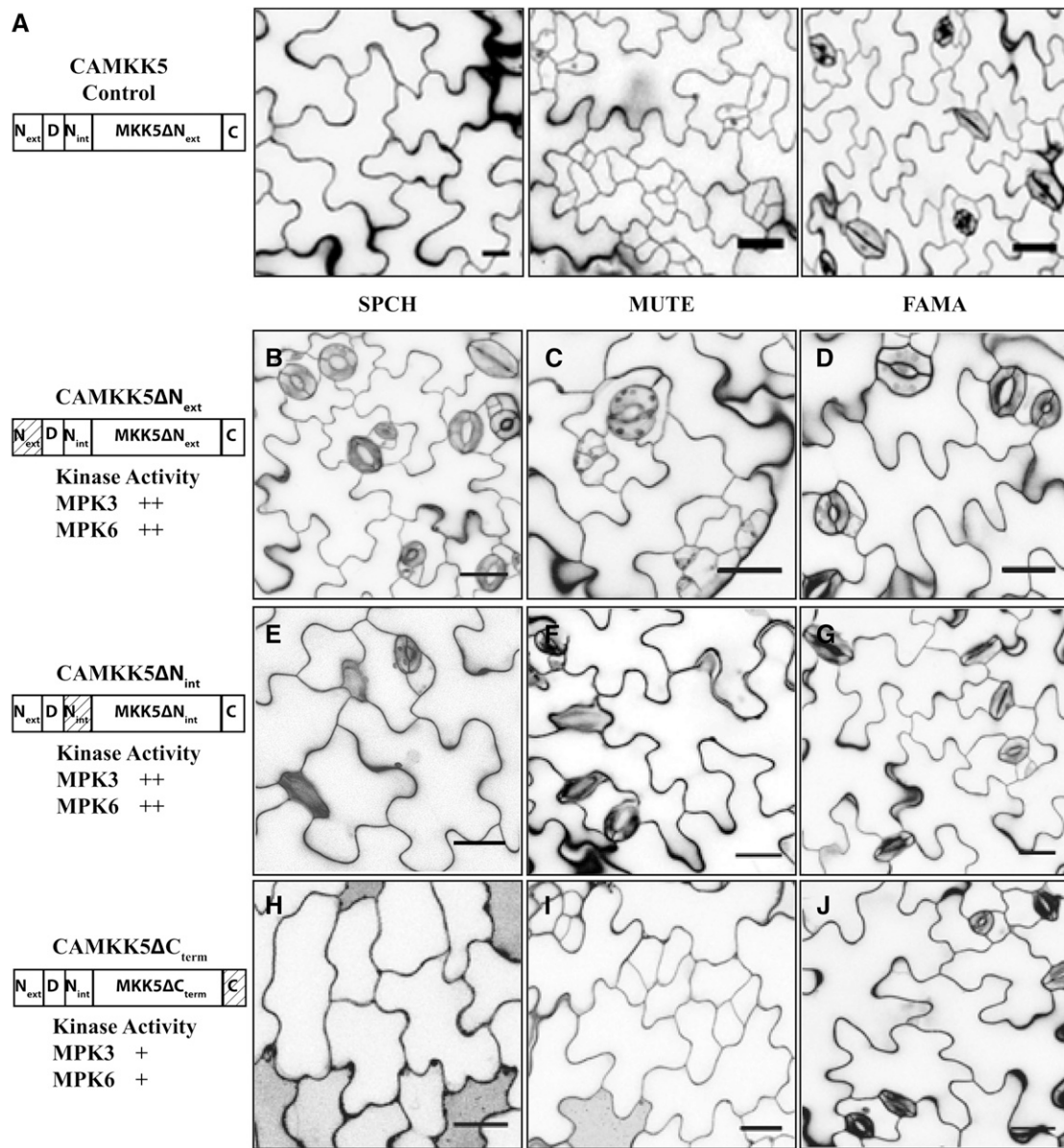


## Correction

**Lampard, G.R., Wengier, D.L., and Bergmann, D.C.** (2014). Manipulation of mitogen-activated protein kinase kinase signaling in the *Arabidopsis* stomatal lineage reveals motifs that contribute to protein localization and signaling specificity. *Plant Cell* **26**: 3358–3371.

The image in Figure 6E was inadvertently duplicated from Figure 6D. The corrected version of Figure 6 is shown below, wherein panel 6E has been replaced with the correct image representing SPCHp:CAMKK5 $\Delta$ N<sub>INT</sub>. The figure legend and remaining figure panels are unaltered from the original.



**Figure 6.** N-Terminal Extensions in CAMKK4/5 Promote Stomatal Inhibition in the SPCH and MUTE Stages.

**(A)** Protein schematic (left) and images of phenotypes associated with expressing CAMKK5 in the SPCH, MUTE, and FAMA stages of stomatal development as indicated.

**(B) to (D)** The 10-DPG seedlings expressing CAMKK5ΔN<sub>ext</sub> in the SPCH **(B)**, MUTE **(C)**, and FAMA **(D)** stages show wild-type stomatal development patterns.

**(E) to (G)** The 10-DPG seedlings expressing CAMKK5ΔN<sub>int</sub> in the SPCH **(E)**, MUTE **(F)**, and FAMA **(G)** stages show wild-type stomatal development patterns. Thus, both N<sub>ext</sub> and N<sub>int</sub> have a positive function in inhibiting stomatal development but do not prevent CAMKK4/5 from inducing stomatal clustering in the FAMA stage.

**(H) to (J)** The 10-DPG seedlings expressing CAMKK5ΔC<sub>term</sub> in the SPCH **(H)**, MUTE **(I)**, and FAMA **(J)** stages show the same stomatal development patterns as controls **(A)**.

The relative activity of each kinase variant in *in vitro* kinase assays is depicted as follows (+, less active than full length; ++, comparable activity to the full-length CAMKK). Hashed boxes in schematic representations of kinase variants indicate the region(s) that were removed. All images are of 10-DPG abaxial cotyledons, and bars = 25 μm.