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Correction to: Functional characterization of genes mediating cell wall metabolism and responses to plant cell wall integrity impairment



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Following publication of the original article [1], the author reported that the two curves in the sub-diagram WSR4 in Fig. 2a should be the other way round.

Correct Fig. 2 is as follows:

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Engelsdorf et al. BMC Plant Biology

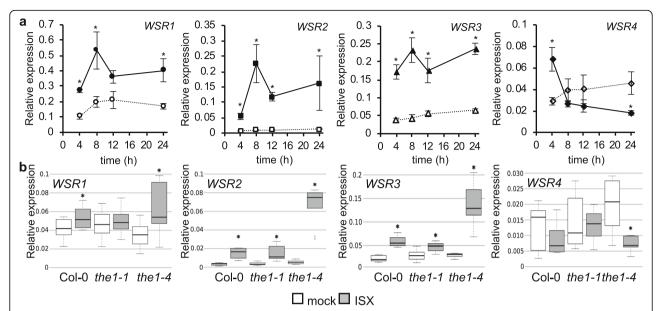


Fig. 2 Candidate gene expression profiling in seedlings exposed to cellulose biosynthesis inhibition. **a** Gene expression of *WSR1*, *2*, *3* and *4* in Col-0 seedlings at the indicated time points after mock (DMSO; empty symbols, dotted lines) or ISX (filled symbols, solid lines) treatment according to qRT-PCR analysis. Values were normalized to *ACT2* and represent means from 3 independent experiments (one replicate per experiment with multiple seedlings pooled for each replicate). Error bars indicate SD. Asterisks indicate statistically significant differences (*p < 0.05) to mock controls according to Student's t test. **b** Transcript levels of *WSR1*, *2*, *3* and *4* in Col-0, *the1*–1 and the1–4 seedlings mock (DMSO) or ISX-treated for 8 h. Values were normalized to *ACT2* and represent means from 3 independent experiments (*n* = 8–9). Asterisks indicate statistically significant differences to mock controls according to Student's t test (*p < 0.05). The boxes in the boxplot indicate interquartile range (IQR, between 25th and 75th percentile) and the black line in the middle of the box marks the median. The whiskers indicate data points furthest from the median, if they are still within 1.5xIQR from the closest quartile. The data points outside this range are plotted individually