Corrigendum: LocoGSE, a sequence-based genome size estimator for plants

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A corrigendum on

LocoGSE, a sequence-based genome size estimator for plants

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In the published article, there was an error in Figure 2 as published. The same formula
"y=1.59x R2 = 0.99" was displayed on all panels, whereas it was supposed to vary across
lineages. The corrected Figure 2 and its caption appear below.

The authors apologize for this error and state that this does not change the scientific
conclusions of the article in any way. The original article has been updated.

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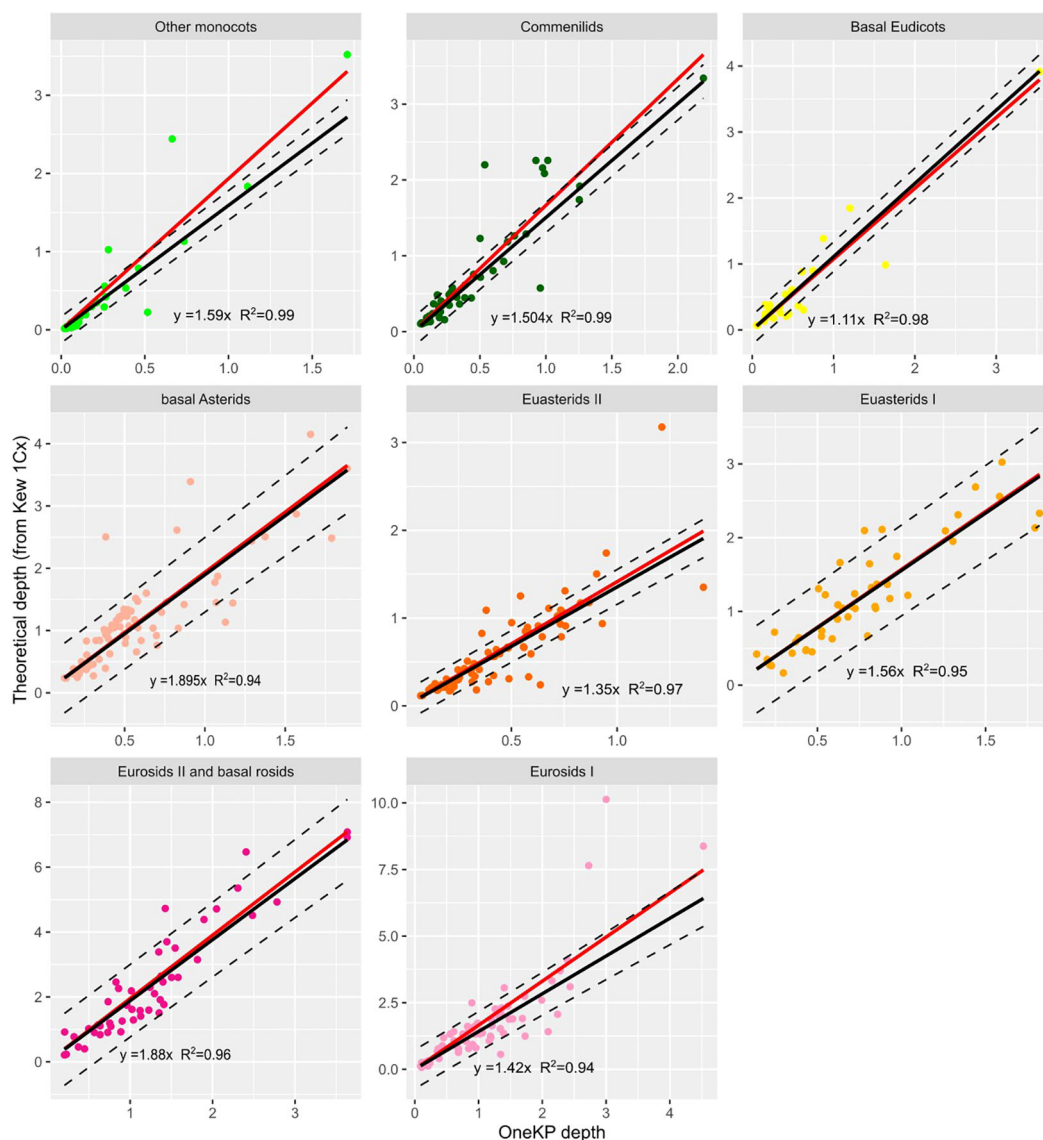its manufacturer, is not guaranteed or endorsed by the publisher.

FIGURE 2
Relationship between depth on OneKP single copy genes and theoretical depth (calculated from Kew 1Cx) in the training set, for 8 plant lineages. Black line is the regression line obtained after robust regression, red line is the regression line obtained with standard regression. Regression line equations and R coefficients are displayed for each lineage.