

CORRECTIONS & AMENDMENTS

CORRIGENDUM

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Corrigendum: Carbonic anhydrases, EPF2 and a novel protease mediate CO₂ control of stomatal development

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In this Letter, the RNA-seq insets in Fig. 2a on top of the bar graph showing qPCR data from independent experiments have errors. RNA-seq analyses were originally conducted with BAM files generated by the sequencing service, but we have noticed that these BAM files differ from those generated when using publically available software on the GALAXY platform. The IGV viewer images originally generated from the BAM and BAI files were erroneously formatted, and two of these were inadvertently mis-inserted in the two right insets in Fig. 2a. We apologize for this error. We have now re-analysed the original raw RNA-seq data for the same experiment, and the Fig. 2a insets have been corrected in the online versions of the paper. Analyses were now conducted using the Tuxedo Suite of programs (TopHat and Cuffdiff) with default parameters (aligned to the TAIR10 annotation) on the GALAXY^{1–3} platform, and IGV viewer image files were generated (see Supplementary Information). The large BAM, BAI and TDF files used for this experiment and those generated by using the GALAXY platform are available for public access at the following link at the UCSD library: <http://library.ucsd.edu/dc/collection/bb6929925>.

In addition, in the abstract we have replaced the word ‘transcriptomic’ with ‘transcript’ in the sentence: “Using cell-wall proteomic analyses and CO₂-dependent transcriptomic analyses”, as this more clearly reflects the research following our proteomic identifications, as accurately described in the paper.

Supplementary Information is available in the online version of the paper.

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