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Author Correction: An integrated multi-omics analysis of the NK603 Roundup-tolerant GM maize reveals metabolism disturbances caused by the transformation process

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This Article contains errors.

In the Methods section under the heading ‘Proteome analysis’, subheading ‘Data Processing’:

“Precursor mass tolerance for the searches was set at 20ppm and fragment mass tolerance at 0.8ppm.”

should read:

“Precursor mass tolerance for the searches was set at 20ppm and fragment mass tolerance at 0.8 Daltons.”

The Data Availability section was omitted from the Article and is included below.

Data Availability

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the MassIVE partner repository [<https://massive.ucsd.edu/ProteoSAFe/static/massive.jsp>] with the dataset identifier PXD011363.

Additional Information

These changes do not affect the conclusions of the Article. The Authors apologise for the errors.

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