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Corrigendum: Genomic regions associated with tuber traits in tetraploid potatoes and identification of superior clones for breeding purposes

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KEYWORDS

tuber morphology, genome-wide association studies, single-nucleotide polymorphism, *Solanum tuberosum* ssp. *tuberosum* L., genomic prediction

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A Corrigendum on

Genomic regions associated with tuber traits in tetraploid potatoes and identification of superior clones for breeding purposes

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Text Correction

In the published article, there was an error. Due to a misreading of the QTL position for eye depth, we mentioned that a QTL for eye depth was identified near the *CDF1* gene.

A correction has been made to the Abstract, Discussion, and Reference sections.

The following sentences have been removed from the abstract and discussion:

Abstract: “Another QTL peak for eye depth on chromosome 5 was located near the *CDF1* gene, an important regulator of maturity in potato”.

Discussion (Paragraph number 5): “The SNP at the peak of the QTL for eye depth on chromosome 5 is located near the *CDF1* gene, an important regulator of maturity in potato (Kloosterman et al., 2013)”.

The following reference has been removed:

Kloosterman, B., Abelenda, J. A., Gomez, M. D. M. C., Oortwijn, M., de Boer, J. M., and Kowitwanich, K. (2013). Naturally occurring allele diversity allows potato cultivation in northern latitudes. *Nature* 495, 246–250. doi: 10.1038/nature11912

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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