



Author Correction: The genomic landscape of gene-level structural variations in Japanese and global soybean *Glycine max* cultivars

Correction to: *Nature Genetics*
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In the version of the article initially published online, there was a misstatement in the Methods “Phylogenetic tree analysis and PCA” section where in the sentence now reading “The dissimilarity matrix between soybean accessions was calculated with R-poppr⁸⁰ and then used to construct a phylogenetic tree using the unweighted pair group method with arithmetic mean implemented in MEGA (v11)⁸¹,” the text “unweighted pair group method with arithmetic mean” replaced the original phrase “neighbor-joining method.” The error has been corrected in the HTML and PDF versions of the article.

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Author Correction: A likelihood-based framework for demographic inference from genealogical trees

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In the version of the article initially published online, boxed labels in the Fig. 1 “Graph of states” diagram from points $t_2 - t_0$ were missing the final letter “C”, which has now been corrected in the HTML and PDF versions of the article.

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