CORRIGENDUM

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Genome sequence of the palaeopolyploid soybean

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During resubmission of this work, a paper was published¹ that used a comparative genomics approach between soybean and maize to show that a single-base mutation in chromosome 19 accounts for the duplicate recessive epistasis needed to greatly reduce phytate production in soybean seed.

In this Article, the statement that: “31,264 high-confidence soybean genes have recent paralogues with $K_s \approx 0.13$ synonymous substitutions per site and $4dTv \approx 0.0566$ synonymous transversions per site” is inadvertently incorrect, and instead the correct statement is that “26,501 high-confidence soybean genes have recent paralogues with $K_s \approx 0.13$ synonymous substitutions per site and $4dTv \approx 0.0566$ synonymous transversions per site”. This change does not affect the overall conclusions.

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1. Gillman, J. D., Pantalone, V. R. & Bilyeu, K. The low phytic acid phenotype in soybean line CX1834 is due to mutations in two homologs of the maize *low phytic acid* gene. *Plant Genome* 2, 179–190 (2009).