A study of crop-to-crop gene flow using farm scale sites of fodder maize (*Zea mays* L.) in the UK

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Due to an unfortunate mistake, an incorrect version of Fig. 2 has been used in the above mentioned publication. The y-axis scale is incorrect as the values in this scale should have been multiplied by 0.58 as described

in the text. Correspondingly, the bottom line in the left hand column on p. 207 should have read:

‘...recorded was 38%; the mean value was 4.8%.’

The correct representation of Fig. 2 is published on the following page and should be treated as definitive by the reader.

The online version of the original article can be found under doi:[10.1007/s11248-006-9036-0](https://doi.org/10.1007/s11248-006-9036-0).

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Fig. 2 Plot of %GM DNA as measured in all maize FSE samples versus distance. The dashed line shows the upper 98th percentile and the solid line the mean for the fitted two-step model