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ERRATUM

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Multiplex-endonuclease genotyping approach (MEGA): a tool for the fine-scale detection of unlinked polymorphic DNA markers

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The authors have noted that Table 2 of the above paper contained two errors:

i. The 5′-3′ *Mun*I adapter oligonucleotide sequence and FAM-labelled *Mun*I primer were shuffled in the print version, which seems to be a type-setting error.
ii. There was inadvertent addition of extra nucleotides (T and G) to the *Bgl*II and *Mun*I primer and adapter sequences in the table by us. The sequences should read $^{5'}$-GAG TAC ACT GTC GAT C and $^{5'}$-6 FAM-GAG AGC TCT TGG AAT T, respectively (without the 3′ T and G).
Since our data were generated with these primers, this correction does not alter the results and conclusions of the paper in any way.

The corrected Table 2 is shown below:

Acknowledgement We thank Drs E. Vansnick and Dirk Geysen (Institute of Tropical Medicine, Antwerp, Belgium) for drawing attention to these points.

Table 2 The complementary sets of *Bgl*II and *Mun*I adapters and polymerase chain reaction primers. (6-FAM is 6-carboxyfluorescein)

Endonuclease	Adapter	Primer core sequence
*Bgl*II (A/GATCT)	5′-CGG ACT AGA GTA CAC TGT C 3′-C TGA TCT CAT GTG ACA GCT AG	5′-GAG TAC ACT GTC GAT C
*Mun*I (C/AATTG)	5′-AAT TC CAA GAG CTC TCC AGT AC 3′-G GTT CTC GAG AGG TCA TGA T	5′-6-FAM-GAG AGC TCT TGG AAT T

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