

## ERRATUM

# Further mapping of quantitative trait loci for postnatal growth in an intersubspecific backcross of wild *Mus musculus castaneus* and C57BL/6J mice

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We regret that in the article by Akira Ishikawa *et al.* in *Genetical Research* (2005) Vol. 85, No. 2, pp. 127–137, Fig. 1 on page 131 should have been reproduced in colour, not in black and white. Please find the correct version below.

We apologise to the authors and readers for this error.

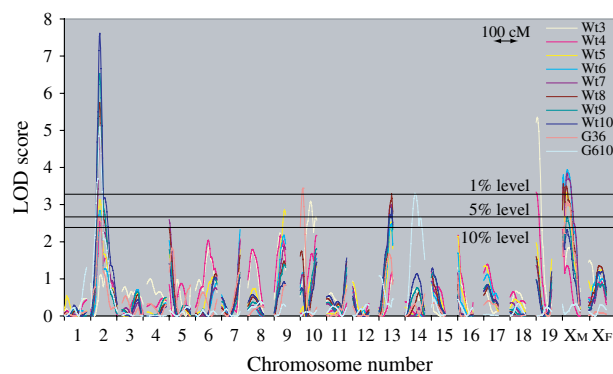


Fig. 1. LOD score plots of QTLs with main effects on postnatal growth. Simple interval mapping (SIM) of eight once-weekly measurements of body weight (Wt3–Wt10) and two weight gains (G36 and G610) (Table 1) was performed with the computer package QTL Cartographer (Basten *et al.*, 2000). The horizontal lines show the genome-wide 10%, 5% and 1% significance levels computed by 1,000 permutations. Map positions in cM were estimated from sex-combined data using Kosambi map function. X<sub>M</sub> and X<sub>F</sub> specify the X chromosome for males and females, respectively.