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ERRATUM

Erratum to: Genome-wide association study (GWAS) of carbon isotope ratio ($\delta^{13}C$) in diverse soybean [*Glycine max* (L.) Merr.] genotypes

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The Manhattan plot in Fig. 7 was erroneously published. The correct figure is given below:

The online version of the original article can be found under doi:10.1007/s00122-014-2413-9.

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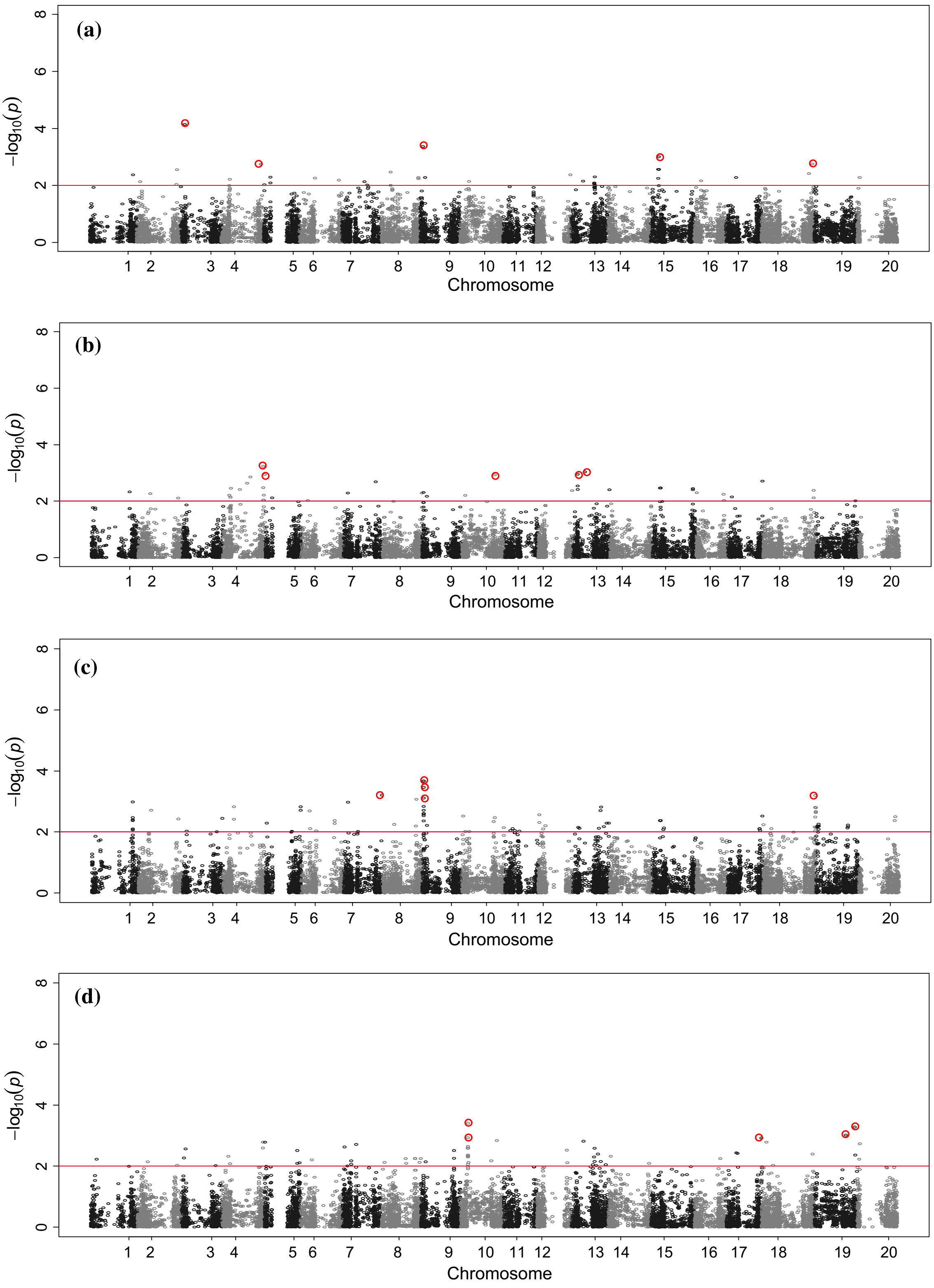

Fig. 7 Manhattan plot of −Log10 (*P*) vs. chromosomal position of SNP markers from MLM (Q + K) model for two locations in two consecutive years 2009 and 2010. The plot shows −Log10 *P* values for each SNP against chromosomal location. (**a**) Columbia 2009; (**b**) Columbia 2010; (**c**) Stuttgart 2009; (**d**) Stuttgart 2010. *Red line* represent the association threshold (−Log 10 $P \geq 2.00$, $P \leq 0.01$). Top five SNPs that showed highest significant association are circled in *red*