Erratum

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A gene-based RFLP map of petunia Theor Appl Genet (2000) 100:899–905

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Due to a technical error, the Figure 2 was unfortunately not completely included in the above-mentioned article. We apologize for this error and print the missing figure.

Abstract Due in large part to the data accumulated from years of classic genetic analysis, petunia (*Petunia hybrida* Vilm) has remained a useful model system, particularly for studies of gene regulation and genome structure. We have used three segregating populations of petunia, including those serving as the source of an earlier actin gene RFLP map, for RFLP mapping of several additional genes. Twenty-seven loci have been merged with 11 previously mapped morphological and biochemical markers. Our results contribute additional evidence to reports of a high degree of genome plasticity and segregation distortion in this species and suggest that petunia may be a useful plant system for detailed analysis of plant genome organization, activity and evolution.

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