SUPPLEMENTARY DATA

Fig. S1. Genome-wide multi-trait QTL mapping scan for mean average petal number and Levene's statistic on flowers 1–24. The upper panel shows the log transformed test statistic [$-\log_{10}$(P)] plotted against genetic position. Chromosomes 1–8 are labelled on the *x*-axis and the significance threshold (α=0.05) is indicated by the horizontal red line. The lower panel represents significant allelic effects of the QTL, as a heat-map scale, on multiple traits indicated on the *y*-axis: muPN - mean average petal number, LS - Levene's statistic. QTL effects where the Wa allele reduces the trait are shown in blue and those where the Wa allele increases the trait in yellow-red. Darker shades represent stronger effects.