

Supplementary material.

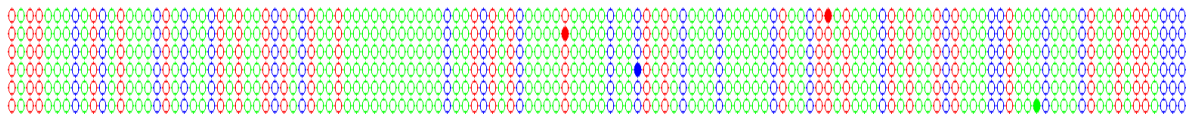


Figure S1. Atp1 gene dotplots obtained from Kismeth software. Filled circles represent methylated cytosines, while empty circles represent unmethylated cytosines. Green, blue and red circles, represent cytosines in CHH, CHG and CG contexts respectively.

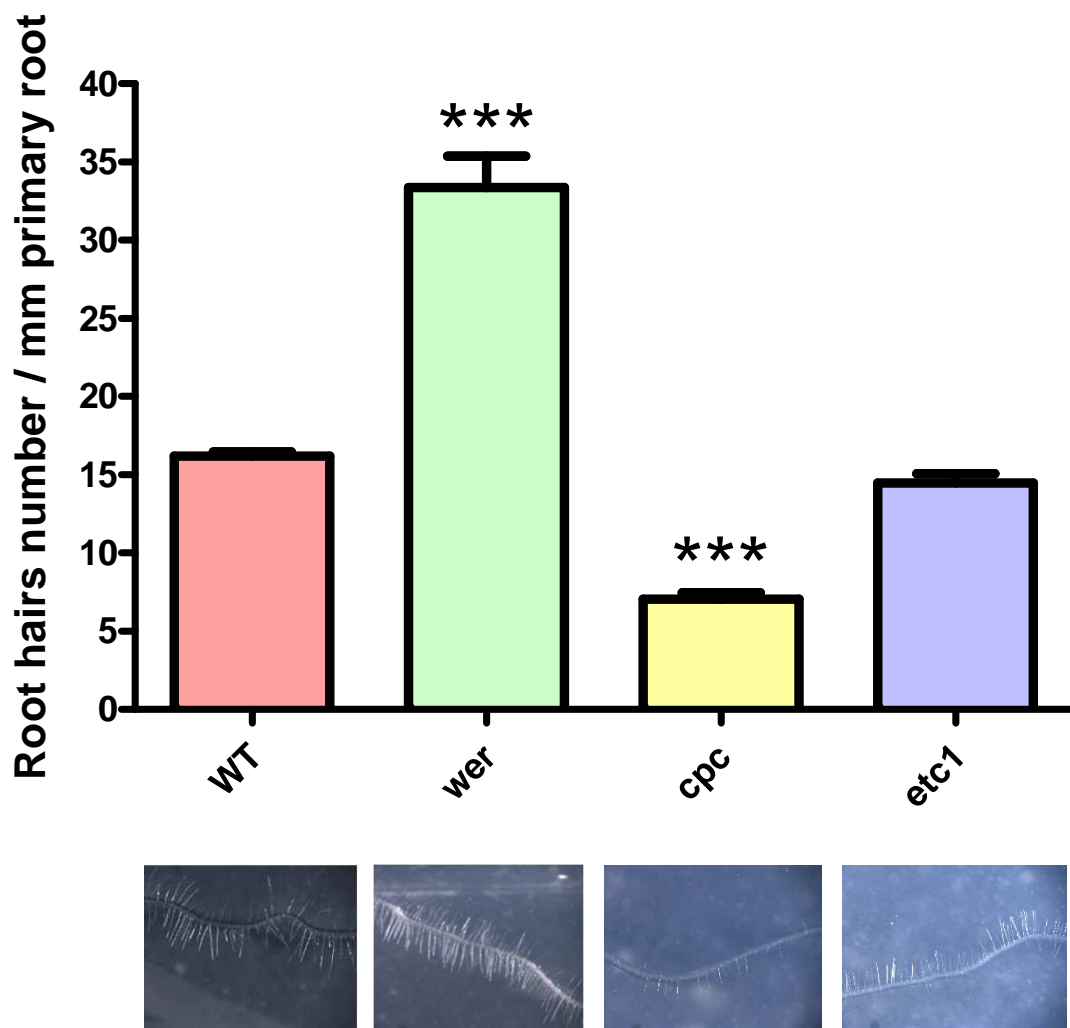
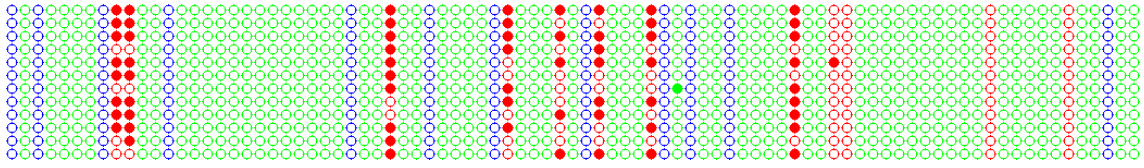


Figure S2. Root hairs density in WT, *wer*, *cpc* and *etc1* plants. Photographs below represent one plant root of each line. A total of 22 roots were measured in each case. *** $p < 0.001$ (One-way ANOVA, Bonferroni post-tests) against WT plants in both cases.

Non-Specific primers



Epidermal specific primers

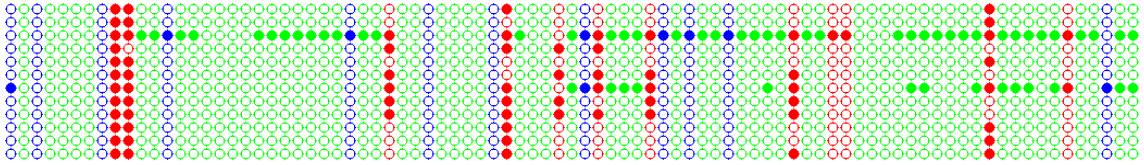
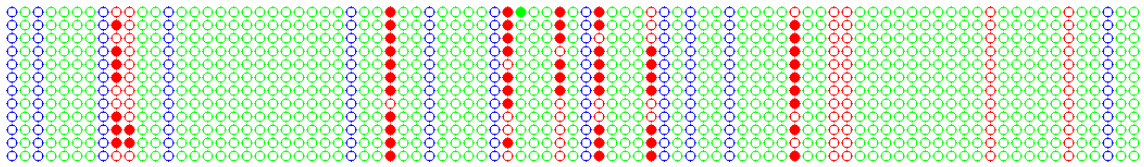


Figure S3. Gl2 gene dotplots from roots of *cpc* plants obtained from Kismeth software (only the region in which both amplicons overlap is shown). Filled circles represent methylated cytosines, while empty circles represent unmethylated cytosines. Green, blue and red circles, represent cytosines in CHH, CHG and CG contexts respectively.

Non-specific primers



Epidermal specific primers

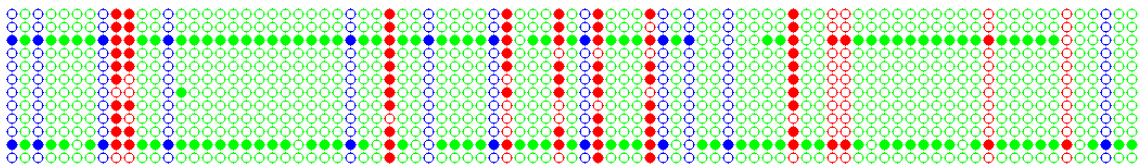
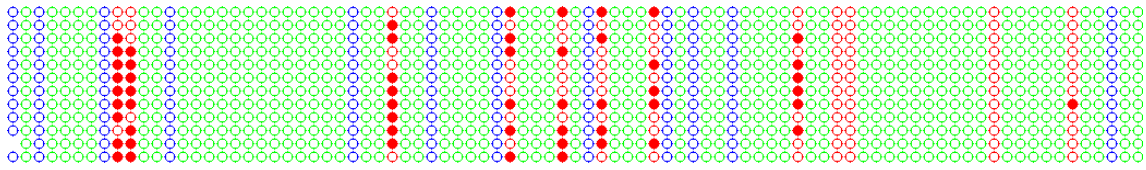


Figure S4. Gl2 gene dotplots from roots of *etc1* plants obtained from Kismeth software (only the region in which both amplicons overlap is shown). Filled circles represent methylated cytosines, while empty circles represent unmethylated cytosines. Green, blue and red circles, represent cytosines in CHH, CHG and CG contexts respectively.

Non-specific primers



Epidermal specific primers

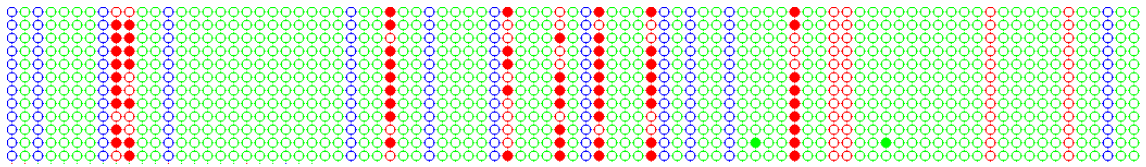


Figure S5. Gl2 gene dotplots from roots of WT plants obtained from Kismeth software (only the region in which both amplicons overlap is shown). Filled circles represent methylated cytosines, while empty circles represent unmethylated cytosines. Green, blue and red circles, represent cytosines in CHH, CHG and CG contexts respectively.