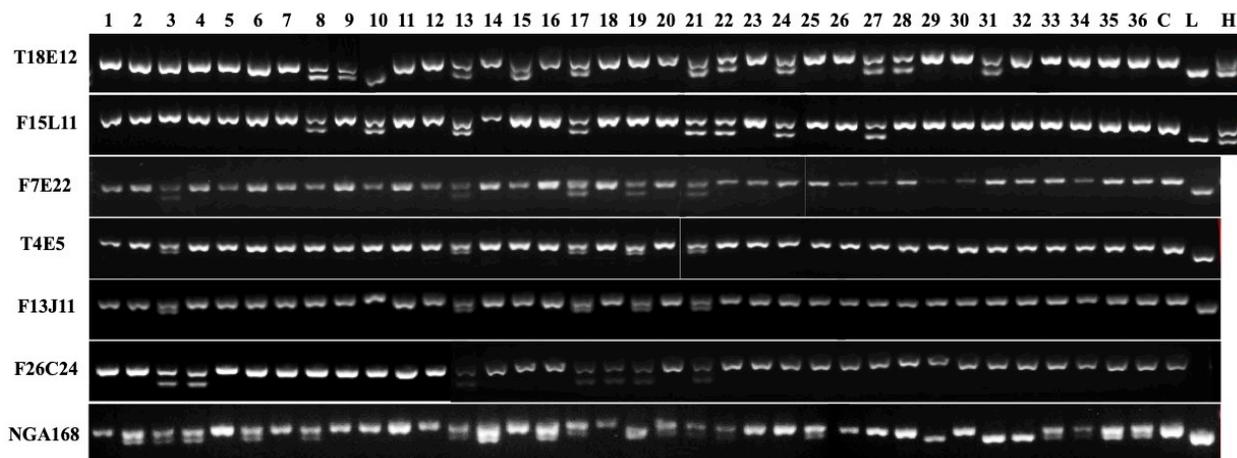


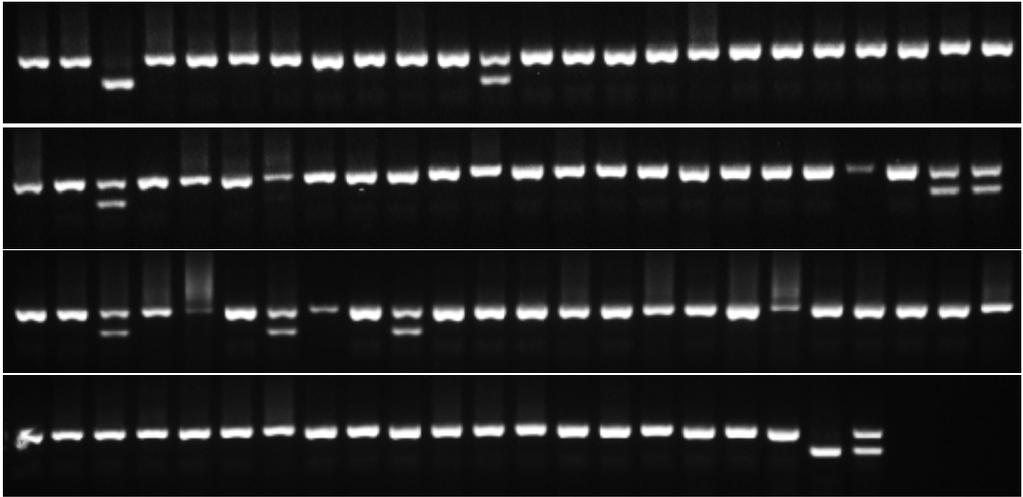
**Fig S1.** Initial mapping of the causal mutation in *ewe1*.  
C, Columbia; L, *Ler*; H, mix of Columbia and *Ler* DNA.

## Chr2

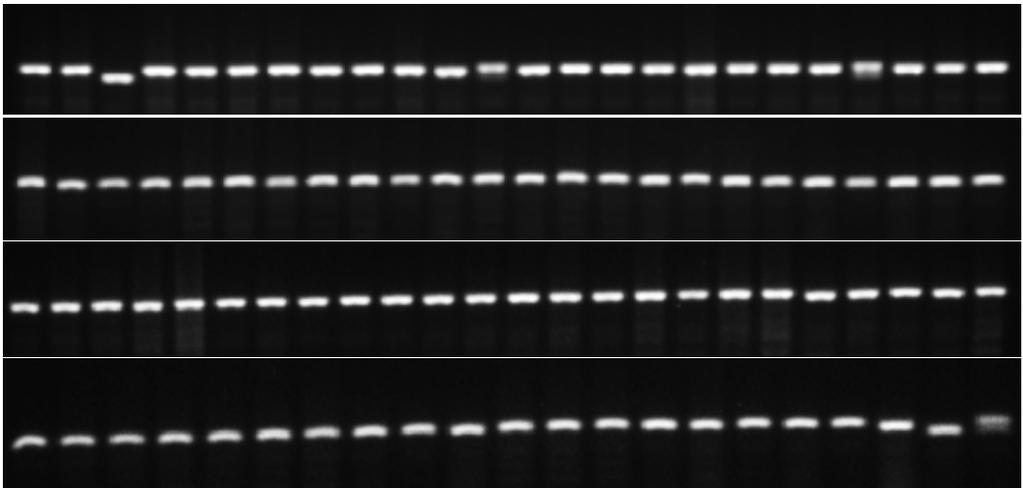


**Fig S2.** Refined mapping of the causal mutation in *ewe1*.  
C. Columbia; L, *Ler*; H, mix of Columbia and *Ler* DNA.

F15L11

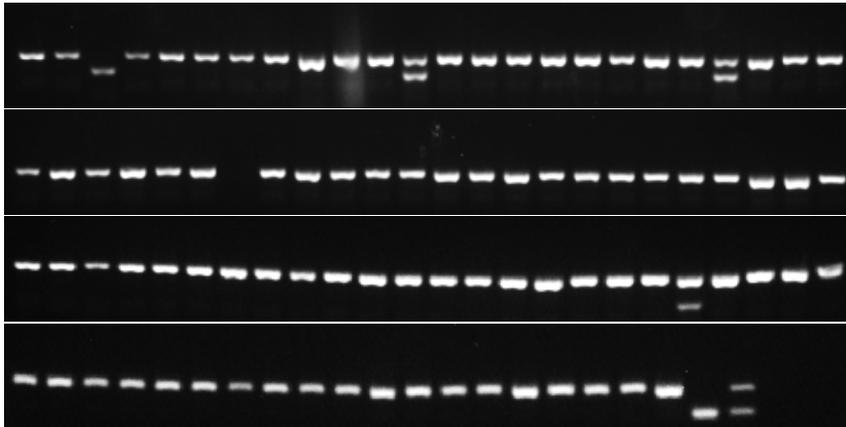


T16I21

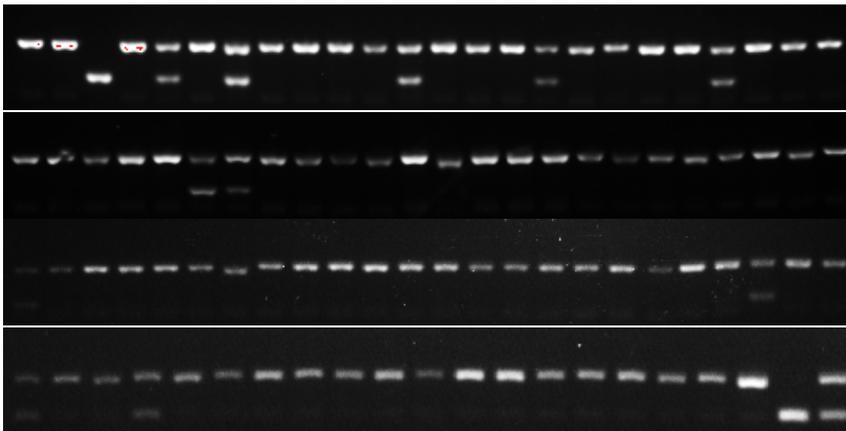


**Fig S3.** Initial mapping of the causal mutation in *ewe2*.  
C, Columbia; L, *Ler*; H, mix of Columbia and *Ler* DNA.

F7E22

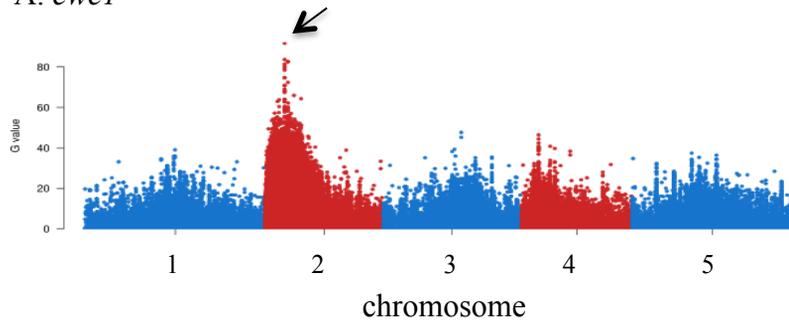


F26C24

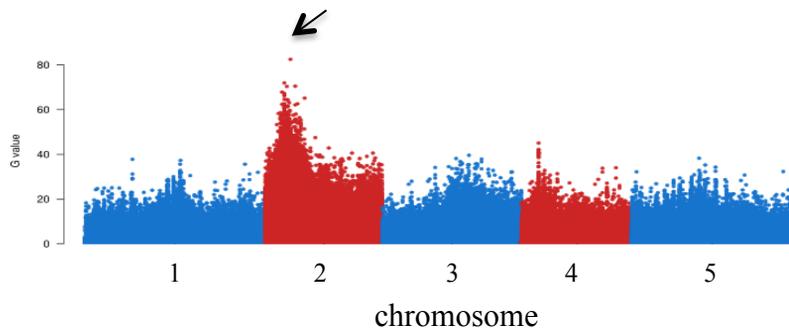


**Fig S4.** Refined mapping of the causal mutation in *ewe2*.  
C. Columbia; L, *Ler*; H, mix of Columbia and *Ler* DNA.

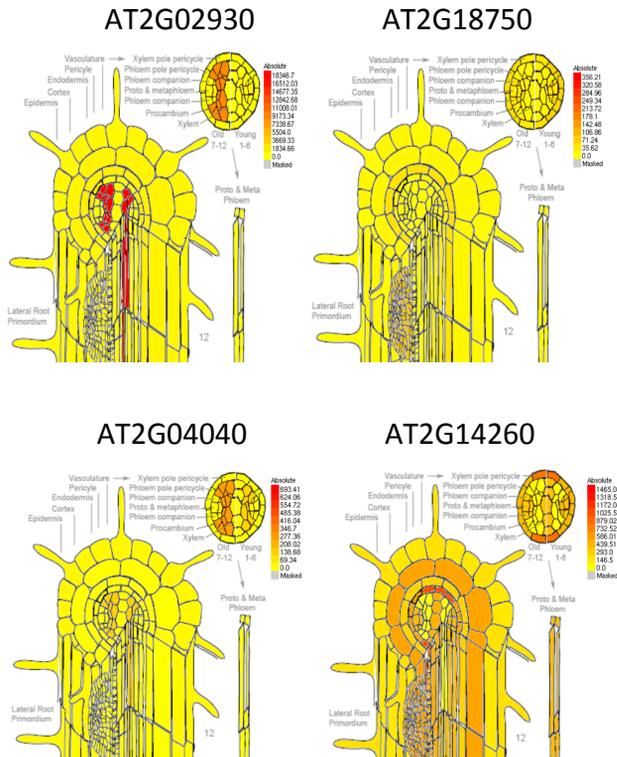
A. *ewe1*



B. *ewe2*



**Fig S5.** Manhattan plots showing the approximate locations (arrows) of the causal SNPs in *ewe1* and *ewe2* mutants. The comparison was between F2 normal plants and F2 mutants.



**Fig S6.** Digital spatial expression pattern of candidate genes in root, according to the eFP tool (Bar.utoronto.ca). Shown in the right of each image is the color code for gene expression level.