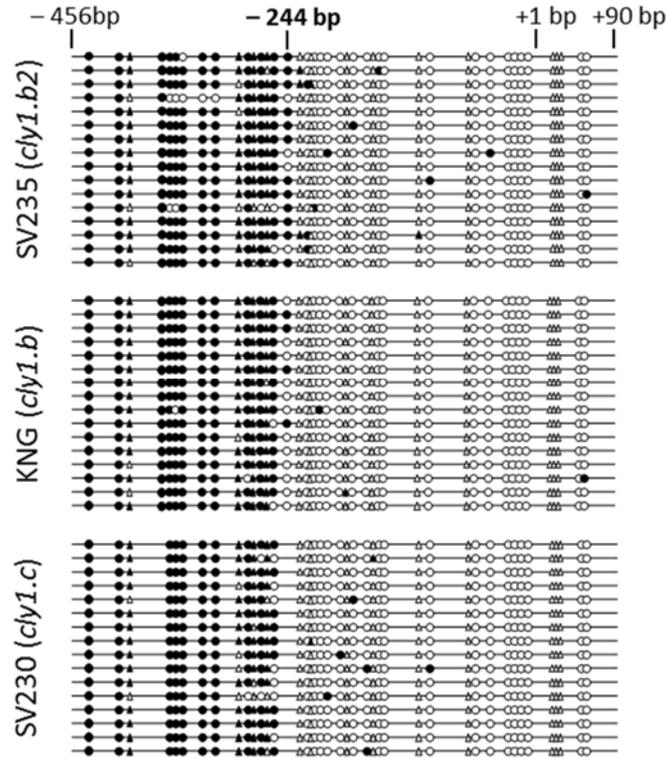


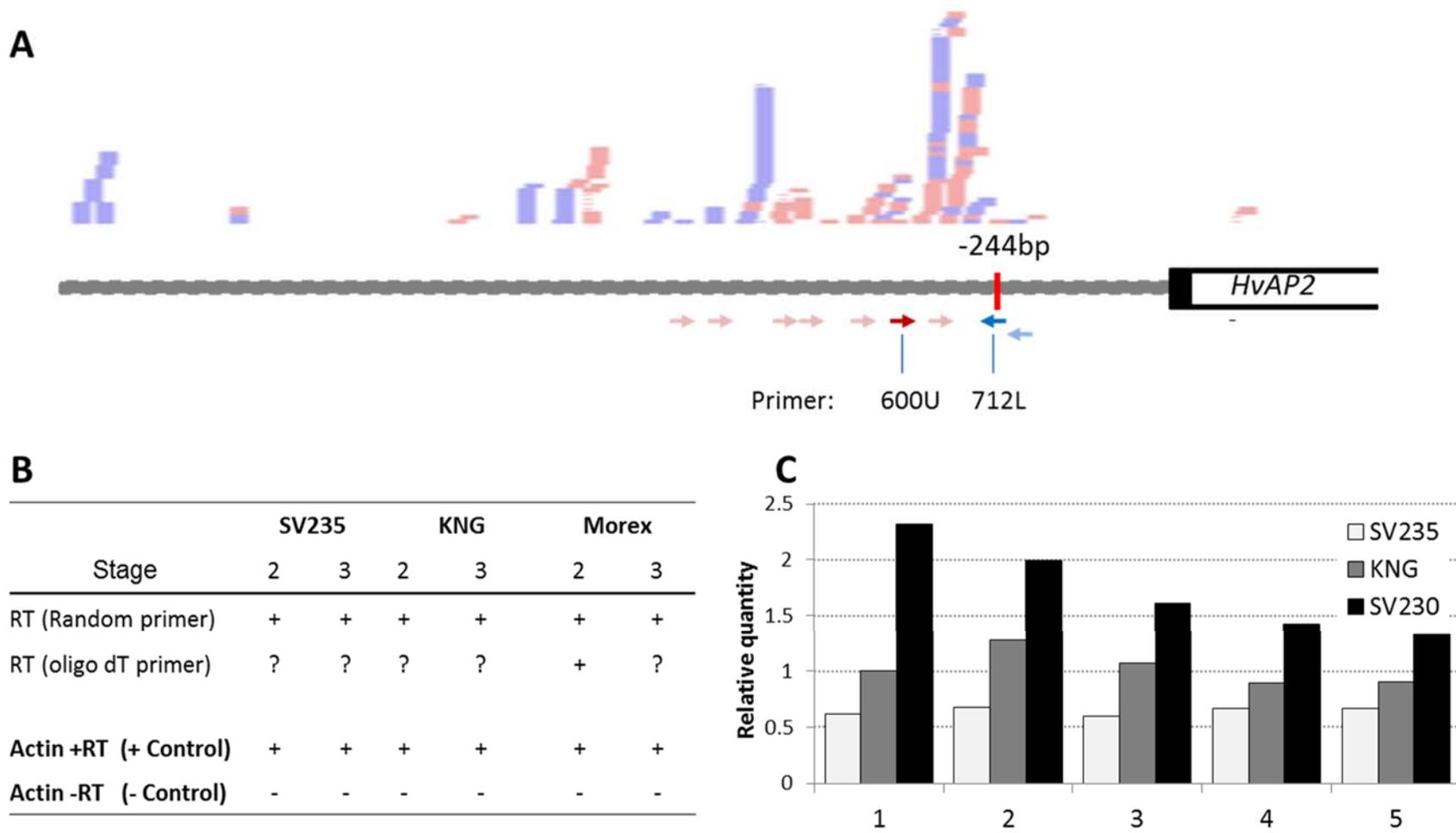
**Figure S1** Measuring lodicule vascularization from (A) stereomicroscope images and (B) transverse sections from the same floret. The width of transparent tissue (red line) correlates with the volume of vascularized tissue.



**Figure S2** Anther extrusion in SV235 at anthesis. (A) Untreated spikes, (B) spikes exposed to 100 ppm 2,4-D for three days.



**Figure S3** DNA methylation at CpG sites in the upstream region of *cly1*. Methylation level within a specific upstream region revealed the key -245/-244 CpG site. Filled circles indicate methylated CpG sites and empty ones non-methylated CpG sites; filled triangles indicate methylated CpNpG sites and empty ones non-methylated CpNpG sites.



**Figure S4** Transcription of putative lncRNA from the upstream sequence of *cly1*. Stages assayed as given in the legend to Fig. 4. Barley *actin* was used as the reference gene. (A) All the primer combinations generated a clear amplicon from genomic DNA template, but the pair SV235-244RT\_600U / SV235-244RT\_712L was the only one to successfully amplify from cDNA template. (B) A comparison between cDNA template produced using an oligo dT primer and a random primer for lncRNA detection. Stage 2, stamen primordium stage; stage 3, awn primordium stage. ?: no clear amplification, +: clear amplicon, -: no amplicon. Actin: *actin* fragment amplicon from cDNA template produced using an oligo dT primer. (C) Relative abundance of SV235 (light gray bar), KNG (dark gray bar) and SV230 (black bar) message. KNG stage 1 (lemma primordium) was used as the reference sample for quantification. Data shown derived from the mean of at least three biological replicates.

**Tables S1-S3**

Available for download as Excel files at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.171652/-/DC1>.

**Table S1** Sequences of PCR primers targeted at *cly1*.

**Table S2** Dominance relationships for alleles determining the volume of transparent tissue in the lodicule.

**Table S3** Location of inter-cultivar sequence polymorphisms within an 11.2 kb region encompassing *cly1*.