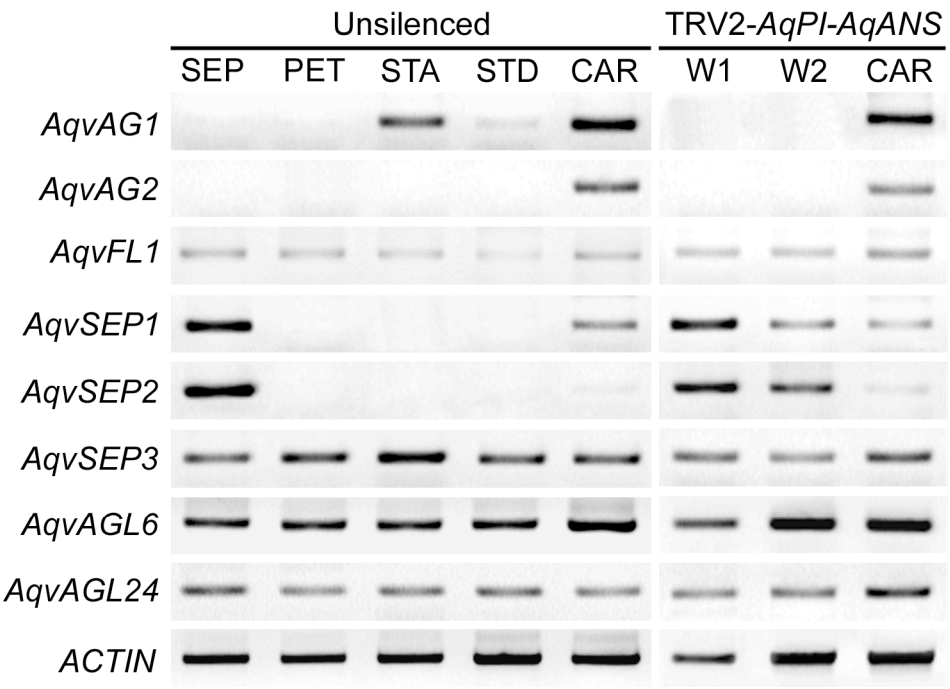

Supplemental Figure 6. Locus specific RT-PCR reactions on RNA prepared from organs of VIGS-treated flowers. RNA samples from eight tissue types were tested: five organ types from flowers that were treated with TRV2-*AqvPI-AqvANS* but did not show silencing (SEP=sepal, PET=petal, STA=stamen, STD=staminodium, CAR=carpel) and three organ types from strongly silenced flowers treated with TRV2-*AqvPI-AqvANS* (W1=first whorl sepals, W2=second whorl sepals, CAR=carpeloid organs). The homology of the loci examined are as follows (Kramer et al., 2004 and unpub. data): *AqvAG1* [AY464111] and *AqvAG2* [AY464110] are representatives of the *AGAMOUS* lineage; *AqvFL1* [DT758909], of the *APETALA1* lineage (Litt and Irish, 2003), *AqvSEP1* [DT728412] and *AqvSEP2* [DR933608], of the *SEP1*/*2*/*4* lineage (Zahn et al., 2005); *AqvSEP3* [DR945848], of the *SEP3* lineage (Zahn et al., 2005); *AqvAGL6* [DR925490], of the *AGL6* lineage (Litt and Irish, 2003; Zahn et al., 2005); and *AqvAGL24* [DT755130], of the *AGL24* lineage (Becker and Theissen, 2003). All PCR primers are shown in Suppl. Table 1. Note that none of the loci show down-regulation in the TRV2-*AqPI-AqANS* silenced floral organs. The *AqvSEP1* and *AqvSEP2* loci are of interest since their wildtype expression is primarily detected

in the first whorl sepals. In strongly silenced flowers, the expression of these genes is detected in the second whorl organs, consistent with their transformation to sepal identity.

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