



Supplemental Figure 1. Expression patterns of cyclamen MADS-box genes during flower development.

For expression analysis of different stages of flower development, total RNA was isolated from whole floral buds (removed from flower stalks) grouped into nine developmental stages according to bud size. RT-sqPCR analysis was performed according to the same protocols used in expression analysis of various tissues. (A) Stages of flower development in cyclamen (1–9). Bud size is approximately $0.5 \, \text{mm}$ in Stage 1 and 2 cm in Stage 8. Bar = 1 cm. (B) Results of RT-sqPCR analysis. The names of corresponding genes and ABCDE classes are indicated at the left. The actin gene (CpACT) was amplified from the same cDNA as a standard control to normalize the cDNA amount used in RT-sqPCR.