S12 Figure: Expression analysis of *MeGI/SiMeGI* in laser capture microdissection (LCM)

Longitudinal (**a**) and cross (**b**) sections of buds from *D. lotus*, Kunsenshi-male, and the target of the LCM. We targeted flower buds (red), young leaf or leaf buds (blue), and pith or cambium (green). **c**, the section after laser captions. **d**, qRT-PCR analysis to detect relative expression of the *MeGI* and *SiMeGI* among the organs, at early developmental stages (Jun-Jul) when the flower primordia form. Consistent with the results of the in situ hybridization (S11 Figure), *MeGI* expression was much stronger in flower buds than in pith or young leaves, while the difference in expression levels between the three organs was less drastic for *SiMeGI*. For both graphs, the expression level in flower buds was defined as "1". **e**, comparison of the expression level of *MeGI* and *SiMeGI* in the developing flower buds. Illumina mRNA-Seq analysis was conducted on the LCM samples to detect RPKM values of *MeGI* and *SiMeGI*. *SiMeGI* was expressed higher than or comparative to the *MeGI,* in the developing flower buds. Notwithstanding, the reduction in *MeGI* expression in this stage affect the flower sexuality and the inflorescent structure (Akagi et al., 2014). **f**, relative expression of the *MeGI* and *SiMeGI* in different organs, during dormancy stage (Dec) when the development of flower primordia halt. Flower buds showed no significant expression of either *MeGI* or *SiMeGI*.