Supplemental Table 1.
Summarized data of Real Time PCR experiments analyzing AtMUS81, AtEME1A and 1B expression in different tissues.

tissue / gene	flower		stem		leaf		root	
	cycles[a]	(relative %)[b]	cycles[a]	(relative %)[b]	cycles[a]	(relative %)[b]	cycles[a]	(relative %)[b]
At*MUS81*	24.5 [c]		24.4		24		24.5	
At*EME1A*	25.5 [c]	(50%)	27.4	(13%)	27.5	(9%)	26.9	(19%)
At*EME1B*	27.5 [c]	(13%)	27.3	(13%)	26.4	(19%)	28	(9%)
At*L27A*	16.1		17.1		17.3		17	

[a] The given cycles correspond to the respective calculated threshold value results from a triplicate experiment. One cycle difference between the respective gene expression data equals a 2-fold, 2 cycles a 4-fold, 3 cycles a 8-fold higher or lower expression level, respectively.
[b] The respective expression level of AtEME1A and 1B is shown in brackets as percentage in comparison to the AtMUS81 expression.
[c] As the cDNA amount used of flower tissue was approximately double of the cDNA used from other tissues the calculated threshold values have been normalized in comparison to the expression of the 60S ribosomal protein L27A (At1g70600), which we use as standard loading control.