

Table S1. qRT-PCR validation of microarrays.

GENE	Microarray fold change	RTPCR fold change	RTPCR standard deviation
MMP3/10a	1.065	1.126	0.072
TIMP1	0.752	0.406	0.054
Tenascin	0.631	0.853	0.086

A subset of ECM remodeling genes from the microarray analysis were selected for qRT-PCR validation as previously described (Mercer et al., 2012). qRT-PCR was performed with tissue samples at 3 dpa (see Methods). Fold changes are derived from triplicate samples and presented as normalized \log_{10} values. The respective fold changes of the microarray data at 3 dpa are provided for comparison (Figure 1). dpa = days postamputation.