

S1 Method. Expression analysis by quantitative real-time PCR.

RNA extraction and cDNA analysis was performed as described before. The resulting cDNA was used as template, combined with 5 µl 2x qPCR Master Mix KAPA SYBR FAST containing SYBR Green dye (Kapa Biosystems), 0.5 µl of each primer (10 mM) and distilled water in an overall volume of 10 µl. The Light Cycler 480 instrument (Roche Diagnostics) was used with a 384-well block system. Three locations in the genome were analysed by corresponding primer pairs, targeting 5' and 3' of the T-DNA insertion as well as the T-DNA insertion site itself (S1 Table). The results of two different constitutively expressed genes (At3g18780 and At4g34270) were applied for normalisation (S1 Table).