Supplemental Figure 2. Expression analysis of cytokinin signaling genes in wild-type versus *A. rhizogenes*-transformed *GUS* RNAi roots

Real-time RT-PCR analysis was used to analyze expression levels of the indicated cytokinin signaling genes in both roots types. Histogram represents the quantification of specific RT-PCR amplification product normalized to the constitutive control Mt *ACTIN11*. The value of gene expression in wild-type roots is set up at 100%. Error bars represent standard deviation for 3 technical replicates.