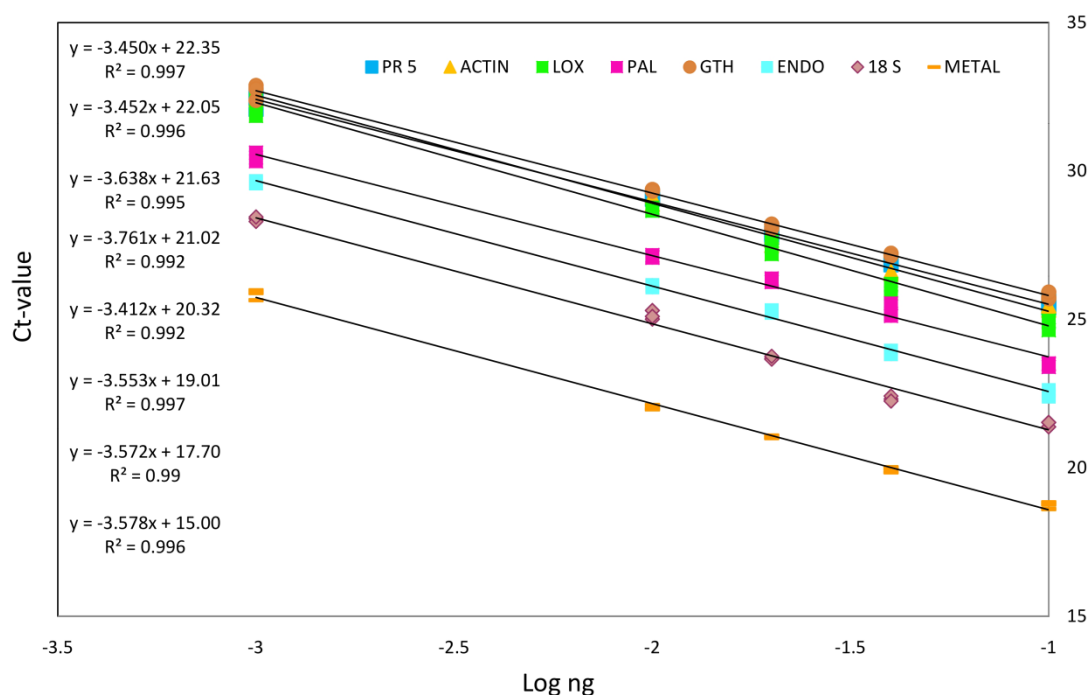


Lanes: M, 100-bp molecular weight standard; 1, negative control; 2, 1221-bp genomic DNA control; 3 to 11, 241-bp PCR products from avocado root cDNA.

**Supplementary figure 1:** PCR products with F3H-based control primers for monitoring genomic DNA contamination of avocado cDNA.



**Supplementary figure 2:** Standard regression curve plots. A dilution series of a mixture of cDNA spanning five orders of magnitude (1:10, 1:25, 1:50, 1:100 and 1:1000) was used to generate standard curves for each separate primer pair: *r18S*, *actin*, *lipoxxygenase*, *phenylalanine ammonia lyase*, *PR5*, *gluthathionine S-transferase*, *metallothionein-like protein* and *endochitinase*. The resulting crossing point values for each input amount of template were plotted as a function of the log<sub>10</sub> concentration of input amounts and a linear trend line was imposed on the data. R<sup>2</sup> is the proportion of variability that the data set is accounted for by a statistical model; thus, R<sup>2</sup>=1 indicates that the fitted model explains all variability in y, while R<sup>2</sup>=0 indicates no linear relationship between the response variable and regressors.