

Accessory Publication

Table S1. List of differentially expressed genes identified by the Significance Analysis of Microarrays (SAM) two-class unpaired analysis

Fold change threshold was set at 2.0 and a false discovery rate was 9.42% for the root-forming culture and leaf comparison (RFC/L), and 9.48% for the root-forming culture and non root-forming culture (RFC/NRFC) comparison. The expected proportion of significantly different features (p_0) was set to 0.95.

[\[See FP10159 TableS1.xls\]](#)

Table S2. Gene family classification for transcripts with more than two-fold differential expression

[\[See FP10159 TableS2.xls\]](#)

Table S3. Gene family classification for transcripts with more than two-fold differential expression

Transcription factors that were more than two-fold differentially expressed were predicted by the homology relationship based on members of Database of Arabidopsis Transcription Factors.

[\[See FP10159 TableS3.xls\]](#)

Table S4. Probes representing transcripts encoding peroxidases that are up-regulated in RFC compared leaf

[\[See FP10159 TableS4.xls\]](#)

Fig. S1. Root specific expression of putative Arabidopsis orthologs of selected transcription factors shown in Fig. 3, obtaining from the electronic fluorescent pictograph browser (Winter *et al.* 2007).

[\[See FP10159 Fig S1.tif\]](#)

Fig. S2. Relative transcript expression of *Mt BBM* (Mtr.21627.1.S1_at) and *MtPLT2* (Mtr.23155.1.S1_at) and *MtWOX5* (Mtr.33304.1.S1_at) determined by quantitative real-time RT-PCR. Equal amounts of total RNAs were used for each real-time RT-PCR analysis. Leaf, RFC – 1-week-old root-forming explants cultures (RFC) treated with 10 μ M NAA, NRFC – 1-week-old explants cultures treated with and 10 μ M NAA and 4 μ M BAP. Relative gene expression levels (y-axis) were obtained by normalizing the amplification signals against those of the constitutively expressed *MtUBQ10* gene used as an internal control and plotted against the lowest expressed sample. Data are expressed as fold-difference of gene expression; letters represent where gene expression is significantly different between samples at $P \leq 0.05$; error bars represent standard deviations.

[\[See FP10159 Fig S2.ppt\]](#)