Supplemental Figure 1. Separation and size distribution of EXP7 protoplasts. (a) Number of GFP (R5) and non-GFP protoplasts (R7). (b) Size distribution of GFP-expressing protoplast.
**Supplemental Figure 2.** Validation of the expression level of selected genes by qRT-PCR.
Supplemental Figure 3. Co-expression relationships of genes preferentially expressed in root hairs. The network was generated by clustering genes that are preferentially expressed in root hairs against a selected database. Differences in color indicate differences in transcript level between EXP7 and non-GFP cells expressed as log fold-change. Diamond-shaped nodes indicate the detection of proteins preferentially expressed in EXP7 cells. Graph was generated with the Cytoscape software (Cline et al., 2007).
Supplemental Figure 4. Root hair phenotypes of mutants harboring defects in the expression of genes from the co-expression network (a). (b) root hair length, (c) root hair number. For root hair length, 100 root hairs from 10 plants were measured. Root hair number was determined from 10 primary roots. P values derived from t-test. Red line in boxes indicate mean, black lines denote median.
**Supplemental Figure 5.** Validation of alternative splice feature. Numbers in parentheses gives the number of the validated features.
Supplemental Figure 6. Scheme for the identification and quantification of proteins in EXP7 and non-GFP cells. All identified proteins in root protoplasts (12,492) were first filtered for reliable identification (detected in two independent experiments or by at least two peptides in one of the two runs). Proteins that could be quantified by the normalized spectral abundance factor (NSAF) method were further classified into those that showed enriched or decreased abundance in EXP7 cells with 95% confidence. Threshold values were validated by power analysis.
Supplemental Figure 7. Distributions of molecular weight (MW) and isoelectric point (PI) of root protoplast proteins (a, b) and the Arabidopsis proteome annotated in TAIR10 (c,d).
Supplementary Figure 8. The interactome of root hairs. Protein-protein interactions in EXP7 cells based on confirmed interactions provided by the Arabidopsis Interactome Mapping Consortium (2011). Color codes refer to the regulation at the mRNA level; red nodes denote higher, green nodes lower mRNA abundance in EXP7 cells compared with non-GFP cells. Grey nodes indicate proteins for which no cognate mRNA was detected in EXP7 cells. Graph was generated with the Cytoscape software (Cline et al., 2007).