Legends for supplementary data:

Supplemental Table S1 Primers used in this study

Supplemental Table S2 List of the 111 genes up- or down-regulated at the 3 timepoints (2, 6 and 30 h) of analysis. For each of the 111 genes the first sheet, "data", indicates: CATMA id, TAIR ID, gene model description, name, the mean gene expression value (log2 ratio) at the 3 time-points in the transcriptome experiment (significantly differentially expressed at each time point: 2, 6 and 30 h after a Benjamini-Hochberg correction procedure using a P-value threshold of 0.001) and the gene expression value at the 3 timepoints in the two different experiments (1 and 2). The second sheet, "FunCat.output", is the complete functional analysis of the 111 genes performed using the "FunCat" catalogue, as described in the "Results" section. The third sheet, "integration", summarizes the information from the first two sheets. Genes highlighted in yellow are those used in qRT-PCR experiments.

Supplemental Table S3 Selection of differentially expressed genes under 50 µM uranyle nitrate treatment at the 3 timepoints of analysis. Values at 2, 6 or 30 h of U exposition are log2 Ratio U-treated/control. Bold ratios were found to be statistically significant with a P-value < 0.05) and bold and underlined ratios were found to be statistically significant after Benjamini-Hochberg correction (P-value < 0.001).

Supplemental Table S4 Microarray experiments used to build the transcriptional module with *FIT1*, *FRO2* and *IRT1* as bait genes; the experiment name refers to the corresponding CATdb project name; # Edges: number of edges that each experiment supports in the final co-expression graph; #arrays: number of hybridization experiments; Description of the experiment: full description of the experiment as provided by CATdb. The experiment name in CATdb refers to the corresponding project name as listed in the CATdb repository (http://urgv.evry.inra.fr/cgi-bin/projects/CATdb/catdb_projects.pl).

Supplemental Table S5 Co-expression analysis with *FRO2*, *FIT1* and *IRT1*. Gene names, symbols, description and GO term annotations (BP: biological process, MF: molecular function, CC: cellular component) were retrieved from the Arabidopsis Information Resource (TAIR, release 10). Only GO term annotations with experimental, author statement and curator statement evidence codes were kept. *: guide genes used to build co-expression graphs.

Supplemental Figure S1. Venn diagram showing the number of genes whose expression was modulated in the roots of 7-week-old Arabidopsis thaliana plants treated with 50 μM uranyl nitrate for 2, 6 and 30 h. Differentially expressed genes were selected after statistical analysis based on the Benjamini-Hochberg method using a P-value threshold of 0.001.

Supplemental Figure S2. Histograms showing expression values (log2 ratio) for the 111 genes (significantly differentially expressed after Benjamini-Hochberg correction (P-value < 0.001) at each time point: 2, 6 and 30 h) in the uranyl treatment microarray experiment (1 and 2).