Supplementary File 1 - Including the description of experiments which have been used in the paper

Nooshin Omranian[*a,b], **Bernd Mueller-Roeber**[a] **and Zoran Nikoloski**[a,b]

Received Xth XXXXXXXXXX 20XX, Accepted Xth XXXXXXXXX 20XX
First published on the web Xth XXXXXXXXXX 200X
DOI: 10.1039/b000000x

The lists of all experiments for the four signals (nitrate, iron, sulfur and hormones) are given in the following tables. Microarrays seletected for the analysis of fewer signals (see Supplementary file 2) are marked with # in Tables 1 to 4.

Table 1 Nitrate experiments. The names of the microarray experiments, the number of chips and conditions, the average number of replicates in addition to the accession ids are shown in the respective columns. Experiments were imported from different sources

Microarray Experiment Name	# of Chips	# of Cond.	Avg. # of Rep.	Accession-ID
# Treatment of *Arabidopsis* with low concentration of nitrate	8	4	2	NASCARRAYS-479
WT vs NR null mutant high nitrate concentration treatment	16	8	2	NASCARRAYS-480
# Genome-wide reprogramming of primary and secondary metabolism, protein synthesis, cellular growth processes, and the regulatory infrastructure of *Arabidopsis* in response to nitrogen	14	6	2.3	Scheible*
# Transcription profiling of *Arabidopsis* roots from plants grown in nutrient solutions with various concentrations of nitrate and sucrose	34	16	2.12	E-MEXP-828
# High resolution NO_3 response of *Arabidopsis* roots	26	13	2	GSE20044

*Data kindly provided by Dr. Wolf-Ruediger Scheible, Max-Plank Institute of Molecular Plant Phisiology, Potsdam, Germany. Experimental setup reported in [11].

---

[a] *Address, Institute of Biochemistry and Biology, University of Potsdam, Karl-Liebknecht-Str. 24-25, 14476 Potsdam,Germany. Tel: 33 1977 2810; E-mail: omranian@uni-potsdam.de and bmr@uni-potsdam.de*
[b] *Address, Systems Biology and Mathematical Modeling, Max-Planck-Institute for Molecular Plant Physiology, Am Mühlenberg 1, 14476 Potsdam, Germany. Tel: 33 1567 8548; E-mail: Nikoloski@mpimp-golm.mpg.de*

Table 2 Iron deficiency experiments. The names of the microarray experiments, the number of chips and conditions, the average number of replicates in addition to the accession ids are included in the respective columns. All experiments were obtained from the GEO database

Microarray Experiment Name	# of Chips	# of Cond.	Avg. # of Rep.	Accession-ID
# Expression analysis of the effect of protoplasting and FACS sorting in roots exposed to iron deficiency (-Fe)	6	2	3	GSE10496
Expression analysis of root developmental zones after iron deficiency (-Fe) treatment	16	8	2	GSE10497
# Expression analysis of root cell-types after iron deficiency (-Fe) treatment	16	5	3.2	GSE10501
# Time course expression analysis of the iron deficiency (-Fe) response in *Arabidopsis* roots Experiment Overall Design	14	7	2	GSE10502
Expression analysis of the response to wild-type and pye-1 mutants to iron sufficient or iron deficient conditions	8	4	2	GSE21443
# Early iron deficiency induced changes in *Arabidopsis* roots	22	8	2.75	GSE15189

Table 3 Sulfur limitation experiments. The names of the microarray experiments, the number of chips and conditions, the average number of replicates in addition to the accession ids are included in the respective columns. Experiments were obtained from the ArrayExpress database

Microarray Experiment Name	# of Chips	# of Cond.	Avg. # of Rep.	Accession-ID
# Transcription profiling of *Arabidopsis* response to sulfate limitation	22	11	2	E-GEOD-5688
# Transcription profiling of *Arabidopsis* wild type seeds grown under sulfur-deficient condition	4	2	2	E-ATMX-1

Table 4 Hormone experiments. The names of the microarray experiments, the number of chips and conditions, the average number of replicates in addition to the accession ids appear in the respective columns. Most of the experiments were obtained from the TAIR database

Microarray Experiment Name	# of Chips	# of Cond.	Avg. # of Rep.	Accession-ID
# AtGenExpress: ACC time course in wildtype seedlings	12	6	2	TAIR-ME00334
AtGenExpress: Zeatin time course in wildtype seedlings	12	6	2	TAIR-ME00344
# AtGenExpress: Methyl Jasmonate time course in wildtype seedlings	12	6	2	TAIR-ME00337
AtGenExpress: IAA time course in wildtype seedlings	12	6	2	TAIR-ME00336
# AtGenExpress: ABA time course in wildtype seedlings	12	6	2	TAIR-ME00333
AtGenExpress: GA3 time course in wildtype and ga1-5 mutant seedlings	24	12	2	TAIR-ME00343
AtGenExpress: Brassinolide time course in wildtype and det2-1 mutant seedlings	24	12	2	TAIR-ME00335
AtGenExpress: Effect of Brassinosteroids on seedlings	26	13	2	TAIR-ME00352
AtGenExpress: Cytokinin treatment of seedlings	12	4	3	TAIR-ME00356
# AtGenExpress: Effect of ABA during seed imbibition	8	4	2	TAIR-ME00351
AtGenExpress: Basic hormone treatment of seeds	12	6	2	TAIR-ME00350
AtGenExpress: Effect of gibberellic acid inhibitors on seedlings	20	10	2	TAIR-ME00357
AtGenExpress: Effect of auxin inhibitors on seedlings	10	5	2	TAIR-ME00358
AtGenExpress: Effect of brassinosteroid inhibitors on seedlings	16	8	2	TAIR-ME00359
AtGenExpress: Effect of ethylene inhibitors on seedlings	6	3	2	TAIR-ME00360
AtGenExpress: Effect of ibuprofen, salicylic acid and daminozide on seedlings	8	4	2	TAIR-ME00364
Cytokinin treatment on roots of seedlings	12	4	3	GSE20232
Cytokinin treatment on aerial parts of seedlings	12	4	3	GSE6832
Gibberellin and ethylene cross-talk at the level of transcriptional regulation in *Arabidopsis*	18	9	2	GSE6150
Transcript profiling of auxin/cytokinin crosstalk in the *Arabidopsis* primary root apex	14	6	2.3	GSE20231