

Legends to supplementary figures

Supplementary Fig. S1 The outputs derived from gene ontology (GOs) term enrichment analysis (https://www.arabidopsis.org/tools/go_term_enrichment.jsp) of the transcripts upregulated (A) or downregulated (B) in the shoots of the NR-null mutant compared with those of the Col exclusively in the absence of ammonium. The transcripts whose expression was at least 1.5-fold higher or at most 2/3-fold lower in the mutant relative to that in the Col were used for the analyses.

Supplementary Fig. S2 The outputs derived from gene ontology (GOs) term enrichment analysis (https://www.arabidopsis.org/tools/go_term_enrichment.jsp) of the transcripts upregulated (A) or downregulated (B) in the roots of the NR-null mutant compared with those of the Col exclusively in the absence of ammonium. The transcripts whose expression was at least 1.5-fold higher or at most 2/3-fold lower in the mutant relative to that in the Col were used for the analyses.

Supplementary Fig. S3 The outputs derived from gene ontology (GOs) term enrichment analysis (https://www.arabidopsis.org/tools/go_term_enrichment.jsp) of the transcripts commonly upregulated (A) or downregulated (B) in the shoots of the NR-null mutant compared with those of the Col. The transcripts whose expression was at least 1.5-fold higher or at most 2/3-fold lower in the mutant relative to that in the Col were used for the analyses.

Supplementary Fig. S4 The outputs derived from gene ontology (GOs) term enrichment analysis (https://www.arabidopsis.org/tools/go_term_enrichment.jsp) of the transcripts commonly upregulated (A) or downregulated (B) in the roots of the NR-null mutant compared with those of the Col. The transcripts whose expression was at least 1.5-fold higher or at most 2/3-fold lower in the mutant relative to that in the Col were used for the analyses.

Supplementary Fig. S5 Cytokinin concentrations in the shoots of the Col and the NR-null mutant under 0.2 mM ammonium (NH_4^+) or N-starvation (-N) conditions. *tZR*, *trans*-zeatin riboside; *tZRP*s, *trans*-zeatin ribotides; *cZ*, *cis*-zeatin; *cZR*, *cis*-zeatin riboside; *cZRP*s, *cis*-zeatin ribotides; *iPRP*s, N^6 -(Δ^2 -isopentenyl)adenine ribotides; *tZ7G*, *tZ*-7-N-glucoside; *tZ9G*,

*t*Z-9-N-glucoside; *t*ZOG, *t*Z-O-glucoside; *c*ZOG, *c*Z-O-glucoside; *t*ZROG, *t*ZR-O-glucoside; *c*ZROG, *c*ZR-O-glucoside; iP7G, iP-7-N-glucoside; iP9G, iP-9-N-glucoside.

Supplementary Fig. S6 The outputs derived from gene ontology (GOs) term enrichment analysis (https://www.arabidopsis.org/tools/go_term_enrichment.jsp) of the transcripts commonly upregulated in the shoots of the NR-null mutant compared with those of the Col. The transcripts whose expression was at least 2-fold (A) or 3-fold (B) higher in the mutant relative to that in the Col were used for the analyses.

Figure S1**(A)**

GO enrichment
(1858 up-transcripts in the shoot)

GO biological process complete	upload_1 (fold Enrichment)	upload_1 (P-value)
ribosomal small subunit assembly (GO:0000028)	7.32	3.07E-04
S-glycoside biosynthetic process (GO:0016144)	7.24	1.22E-04
glucosinolate biosynthetic process (GO:0019761)	7.24	1.22E-04
glycosinolate biosynthetic process (GO:0019758)	7.24	1.22E-04
ribosome assembly (GO:0042255)	6.56	2.00E-10
ribosomal large subunit assembly (GO:0000027)	6.13	1.81E-03
cytoplasmic translation (GO:0002181)	5.91	2.14E-06
glycosyl compound biosynthetic process (GO:1901659)	5.29	3.03E-04
ribosomal small subunit biogenesis (GO:0042274)	5.21	6.86E-06
plant-type secondary cell wall biogenesis (GO:0009834)	5.19	1.90E-03
GO molecular function complete	upload_1 (fold Enrichment)	upload_1 (P-value)
structural constituent of ribosome (GO:0003735)	5.13	4.56E-26
rRNA binding (GO:0019843)	4.92	1.20E-07
structural molecule activity (GO:0005198)	3.78	2.27E-19
translation factor activity, RNA binding (GO:0008135)	2.99	1.44E-02
mRNA binding (GO:0003729)	2.89	2.65E-09
translation regulator activity, nucleic acid binding (GO:0090079)	2.89	1.63E-02
translation regulator activity (GO:0045182)	2.85	1.97E-02
RNA binding (GO:0003723)	2.12	6.29E-12
transition metal ion binding (GO:0046914)	1.74	5.64E-04
nucleic acid binding (GO:0003676)	1.61	2.61E-13
GO cellular component complete	upload_1 (fold Enrichment)	upload_1 (P-value)
cytosolic small ribosomal subunit (GO:0022627)	8.12	9.44E-20
small ribosomal subunit (GO:0015935)	6.81	3.22E-18
cytosolic large ribosomal subunit (GO:0022625)	6.75	1.66E-18
ribosomal subunit (GO:0044391)	6.08	3.39E-37
cytosolic ribosome (GO:0022626)	5.94	2.83E-35
large ribosomal subunit (GO:0015934)	5.56	1.65E-17
ribosome (GO:0005840)	4.47	6.41E-32
nucleolus (GO:0005730)	3.42	8.10E-18
ribonucleoprotein complex (GO:1990904)	3.27	2.29E-24
cell wall (GO:0005618)	2.54	1.00E-11

(B)

GO enrichment
(730 down-transcripts in the shoot)

GO biological process complete	upload_1 (fold Enrichment)	upload_1 (P-value)
photosynthesis, light harvesting in photosystem I (GO:0009768)	13.15	4.73E-02
photosynthesis, light reaction (GO:0019684)	5.12	1.12E-02
response to starvation (GO:0042594)	4.51	4.22E-03
cellular response to starvation (GO:0009267)	4.46	4.45E-02
photosynthesis (GO:0015979)	4.29	4.43E-04
response to drug (GO:0042493)	3.2	7.17E-05
response to endogenous stimulus (GO:0009719)	2	1.12E-03
response to organic substance (GO:0010033)	1.93	6.65E-04
response to hormone (GO:0009725)	1.93	7.04E-03
response to external stimulus (GO:0009605)	1.84	1.38E-02
GO molecular function complete	upload_1 (fold Enrichment)	upload_1 (P-value)
monovalent inorganic cation transmembrane transporter activity (GO:0015077)	3.23	2.74E-02
inorganic cation transmembrane transporter activity (GO:0022890)	3.22	2.89E-04
cation transmembrane transporter activity (GO:0008324)	3.16	1.53E-04
inorganic molecular entity transmembrane transporter activity (GO:0015318)	2.71	9.18E-05
ion transmembrane transporter activity (GO:0015075)	2.64	1.27E-04
transmembrane transporter activity (GO:0022857)	2.26	1.52E-04
transporter activity (GO:0005215)	2.21	1.57E-04
DNA-binding transcription factor activity (GO:0003700)	1.81	4.89E-02
-	-	-
-	-	-
GO cellular component complete	upload_1 (fold Enrichment)	upload_1 (P-value)
photosystem I (GO:0009522)	11.07	3.07E-04
photosystem (GO:0009521)	8.22	1.73E-06
photosystem II (GO:0009523)	7.53	1.62E-03
chloroplast thylakoid membrane (GO:0009535)	3.87	2.38E-07
plastid thylakoid membrane (GO:0055035)	3.87	2.38E-07
thylakoid membrane (GO:0042651)	3.83	1.65E-07
photosynthetic membrane (GO:0034357)	3.82	1.75E-07
chloroplast thylakoid (GO:0009534)	3.46	5.73E-07
plastid thylakoid (GO:0031976)	3.46	5.73E-07
thylakoid (GO:0009579)	3.3	3.64E-07

Figure S2

GO enrichment (530 up-transcripts in the root)

GO biological process complete	upload_1 (fold Enrichment)	upload_1 (P-value)
photosynthetic electron transport in photosystem II (GO:0009772)	33.47	4.97E-03
photosynthetic electron transport in photosystem I (GO:0009773)	23.63	2.22E-03
photosynthetic electron transport chain (GO:0009767)	17.46	1.18E-07
photosystem II assembly (GO:0010207)	16.07	1.46E-02
photosynthesis, light reaction (GO:0019684)	12.55	1.48E-14
protein-chromophore linkage (GO:0018298)	12.17	2.44E-03
photosynthesis, light harvesting (GO:0009765)	10.65	2.61E-02
photosynthesis (GO:0015979)	9.4	2.29E-17
electron transport chain (GO:0022900)	8.13	7.36E-05
response to light intensity (GO:0009642)	6	1.88E-03
GO molecular function complete	upload_1 (fold Enrichment)	upload_1 (P-value)
chlorophyll binding (GO:0016168)	13.78	3.53E-03
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
GO cellular component complete	upload_1 (fold Enrichment)	upload_1 (P-value)
chloroplast thylakoid membrane protein complex (GO:0098807)	17.62	1.52E-02
chloroplast thylakoid lumen (GO:0009543)	14.75	2.72E-08
plastid thylakoid lumen (GO:0031978)	14.75	2.72E-08
thylakoid lumen (GO:0031977)	12.67	2.87E-08
photosystem II (GO:0009523)	10.99	1.32E-05
photosystem (GO:0009521)	10.19	3.71E-07
photosystem I (GO:0009522)	9.8	4.22E-02
plastoglobule (GO:0010287)	9.44	5.36E-05
chloroplast thylakoid membrane (GO:0009535)	6.9	3.48E-19
plastid thylakoid membrane (GO:0055035)	6.9	3.48E-19

(B)

GO enrichment (581 down-transcripts in this root)

Figure S3**(A)**

GO enrichment
(1417 up-transcripts in the shoot)

GO biological process complete	upload_1 (fold Enrichment)	upload_1 (P-value)
maturity of LSU-rRNA (GO:0000470)	13.68	2.74E-09
maturity of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000463)	12.88	4.35E-03
ribosomal large subunit biogenesis (GO:0042273)	12.32	7.42E-26
maturity of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000462)	10.3	3.60E-07
ribosomal large subunit assembly (GO:0000027)	9.81	6.45E-07
rRNA processing (GO:0006364)	9.15	5.30E-39
maturity of SSU-rRNA (GO:0030490)	9.09	1.36E-07
rRNA metabolic process (GO:0016072)	8.9	2.59E-38
ribosome biogenesis (GO:0042254)	8.65	1.38E-65
ribosomal small subunit biogenesis (GO:0042274)	7.66	5.98E-10
GO molecular function complete	upload_1 (fold Enrichment)	upload_1 (P-value)
snoRNA binding (GO:0030515)	18.03	1.10E-08
structural constituent of ribosome (GO:0003735)	7.19	1.49E-44
structural molecule activity (GO:0005198)	5.54	3.72E-39
tRNA binding (GO:0019843)	4.04	1.41E-02
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616)	3.13	2.23E-02
RNA binding (GO:0003723)	2.74	2.47E-18
mRNA binding (GO:0003729)	2.7	3.15E-05
nucleic acid binding (GO:0003676)	1.67	4.76E-10
heterocyclic compound binding (GO:1901363)	1.48	1.34E-10
organic cyclic compound binding (GO:0097159)	1.48	1.44E-10
GO cellular component complete	upload_1 (fold Enrichment)	upload_1 (P-value)
box C/D snoRNP complex (GO:0031428)	18.73	1.27E-04
90S preribosome (GO:0030686)	18.12	6.75E-13
preribosome, large subunit precursor (GO:0030687)	16.74	4.82E-08
preribosome (GO:0030684)	16.36	1.06E-37
small-subunit processome (GO:0032040)	16.29	5.97E-21
preribosome, small subunit precursor (GO:0030688)	14.05	1.52E-02
cytosolic large ribosomal subunit (GO:0022625)	12.59	1.15E-41
nucleolar part (GO:0044452)	11.63	8.41E-16
cytosolic ribosome (GO:0022626)	9.17	1.60E-58
small nucleolar ribonucleoprotein complex (GO:0005732)	9.16	3.53E-07

(B)

GO enrichment
(545 down-transcripts in the shoot)

GO biological process complete	upload_1 (fold Enrichment)	upload_1 (P-value)
photosynthesis, light harvesting in photosystem I (GO:0009768)	16.86	1.12E-02
protein-chromophore linkage (GO:0018298)	14.45	2.42E-02
response to light stimulus (GO:0009416)	2.83	1.21E-03
response to radiation (GO:0009314)	2.75	2.13E-03
response to external stimulus (GO:0009605)	2.09	2.05E-02
response to chemical (GO:0042221)	1.7	4.11E-02
response to stimulus (GO:0050896)	1.6	1.72E-05
-	-	-
-	-	-
-	-	-
GO molecular function complete	upload_1 (fold Enrichment)	upload_1 (P-value)
oxidoreductase activity, oxidizing metal ions, NAD or NADP as acceptor (GO:0016723)	33.72	3.38E-02
ferric-chelate reductase activity (GO:0000293)	33.72	3.38E-02
chlorophyll binding (GO:0016168)	13.88	3.30E-03
tetrapyrrole binding (GO:0046906)	4.67	6.04E-05
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
GO cellular component complete	upload_1 (fold Enrichment)	upload_1 (P-value)
light-harvesting complex (GO:0030076)	16.18	3.31E-03
photosystem I (GO:0009522)	13.16	3.38E-04
chloroplast thylakoid membrane protein complex (GO:0098807)	11.9	1.54E-02
photosystem II (GO:0009523)	8.3	7.42E-03
photosystem (GO:0009521)	7.49	1.39E-03
plastoglobule (GO:0010287)	6.83	2.70E-02
chloroplast thylakoid (GO:0009534)	2.73	3.52E-02
plastid thylakoid (GO:0031976)	2.72	3.61E-02
-	-	-
-	-	-

Figure S4

GO enrichment (294 up-transcripts in the root)

GO biological process complete	upload_1 (fold Enrichment)	upload_1 (P-value)
photosynthesis, light harvesting in photosystem I (GO:0009768)	80.04	1.53E-17
carbon fixation (GO:0015977)	54.89	4.87E-08
protein-chromophore linkage (GO:0018298)	53.91	8.23E-12
reductive pentose-phosphate cycle (GO:0019253)	52.78	4.07E-04
photosynthesis, dark reaction (GO:0019685)	49.01	5.48E-04
photosynthesis, light harvesting (GO:0009765)	41.76	2.40E-14
response to low light intensity stimulus (GO:0009645)	36.11	1.95E-03
photosynthetic electron transport chain (GO:0009767)	31.67	1.62E-07
photosynthesis, light reaction (GO:0019684)	27.01	2.28E-23
photosynthesis (GO:0015979)	26.86	6.94E-36
GO molecular function complete	upload_1 (fold Enrichment)	upload_1 (P-value)
glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) activity (GO:0047100)	> 100	1.22E-02
ribulose-bisphosphate carboxylase activity (GO:0016984)	> 100	2.13E-02
chlorophyll binding (GO:0016168)	56.5	4.41E-16
poly(U) RNA binding (GO:0008266)	26.39	4.59E-03
poly-pyrimidine tract binding (GO:0008187)	22.87	8.56E-03
single-stranded RNA binding (GO:0003727)	13.92	2.23E-03
tetrapyrrole binding (GO:0046906)	7.6	1.49E-06
cofactor binding (GO:0048037)	4.54	9.27E-07
-	-	-
-	-	-
GO cellular component complete	upload_1 (fold Enrichment)	upload_1 (P-value)
chloroplast ribulose bisphosphate carboxylase complex (GO:0009573)	> 100	4.79E-03
ribulose bisphosphate carboxylase complex (GO:0048492)	> 100	4.79E-03
photosystem I reaction center (GO:0009538)	99.8	3.00E-10
photosystem I (GO:0009522)	73.63	6.60E-29
light-harvesting complex (GO:0030076)	65.87	1.52E-14
chloroplast photosystem II (GO:0030095)	50.55	3.57E-07
photosystem (GO:0009521)	48.79	2.30E-38
chloroplast thylakoid membrane protein complex (GO:0098807)	48.43	3.02E-13
plastoglobule (GO:0010287)	36.48	3.11E-22
photosystem II (GO:0009523)	35.89	1.43E-17

GO enrichment (243 down-transcripts in ths root)

Figure S5**Cytokinin concentrations in the shoot**

pmol g ⁻¹	1st experiment				2nd experiment			
	Col NH ₄ ⁺	NR-null NH ₄ ⁺	Col -N	NR-null -N	Col NH ₄ ⁺	NR-null NH ₄ ⁺	Col -N	NR-null -N
tZR	0.483	0.464	0.189	0.312	0.512	0.588	0.143	0.239
tZRP_s	6.574	7.440	2.560	4.063	8.086	9.315	2.289	3.625
tZ7G	25.685	23.821	21.573	19.404	25.845	22.744	24.346	22.003
tZ9G	8.400	7.763	6.248	6.082	8.435	7.570	7.050	6.917
tZOG	9.102	8.494	7.451	6.222	10.208	7.640	9.507	7.007
tZROG	1.653	2.522	1.411	2.002	1.863	2.335	1.752	2.234
iPRP_s	7.416	15.251	4.451	9.472	7.880	13.259	4.086	8.224
iP7G	117.366	162.300	118.657	157.471	114.305	149.376	123.557	155.927
iP9G	2.225	3.624	1.929	3.295	2.271	3.013	2.194	3.277
cZ	0.237	0.326	0.283	0.293	0.207	0.286	0.288	0.322
cZR	0.376	0.300	0.397	0.292	0.301	0.233	0.231	0.222
cZRP_s	2.511	2.917	2.306	2.380	2.509	2.828	2.060	2.300
cZOG	2.019	1.873	3.167	2.648	2.030	1.557	3.522	2.635
cZROG	2.963	2.636	4.672	3.405	2.712	2.324	4.395	2.980

Figure S6

GO enrichment (371 up-transcripts in the shoot)

GO enrichment (154 up-transcripts in ths shoot)