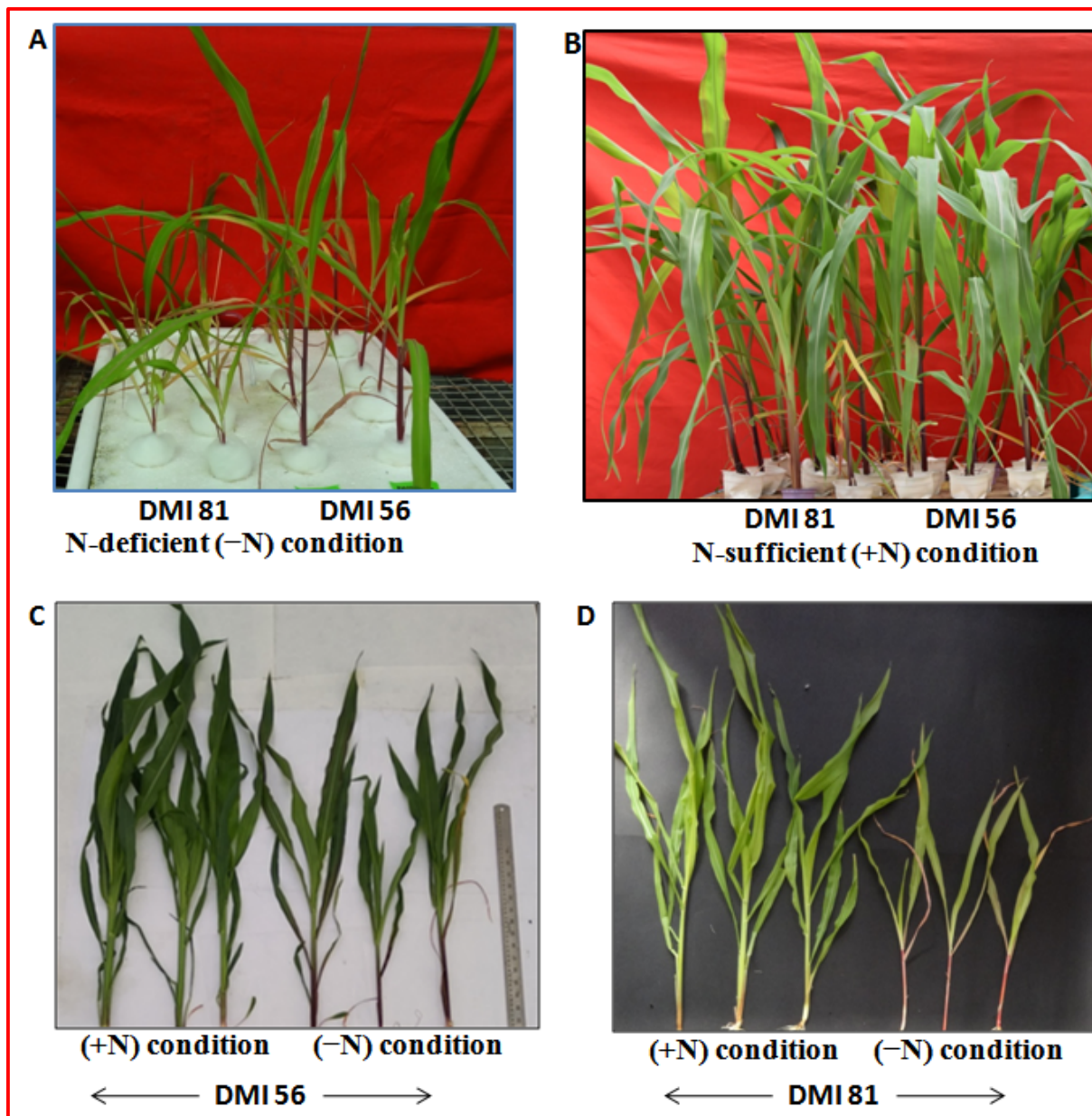


**Global gene expression profiling under nitrogen stress identifies key genes involved in
nitrogen stress adaptation in maize (*Zea mays* L.)**

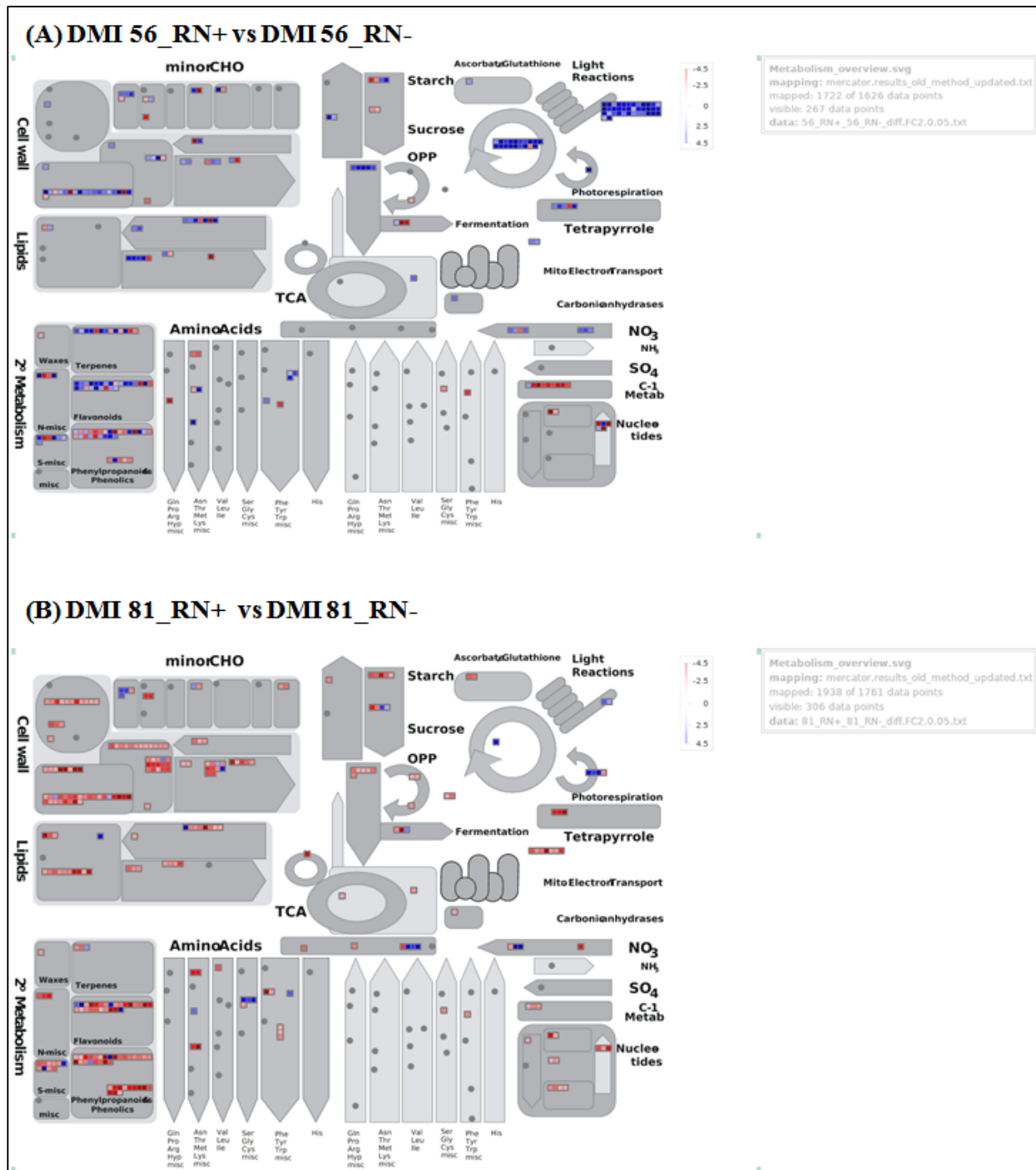
Prabha Singh^{1,2,3*}, Krishan Kumar^{1*}, Abhishek Kumar Jha¹, Pranjal Yadava², Madan Pal², Sujay Rakshit¹ and Ishwar Singh^{1#}

*Krishan Kumar contributed equally and considered as co-first author.

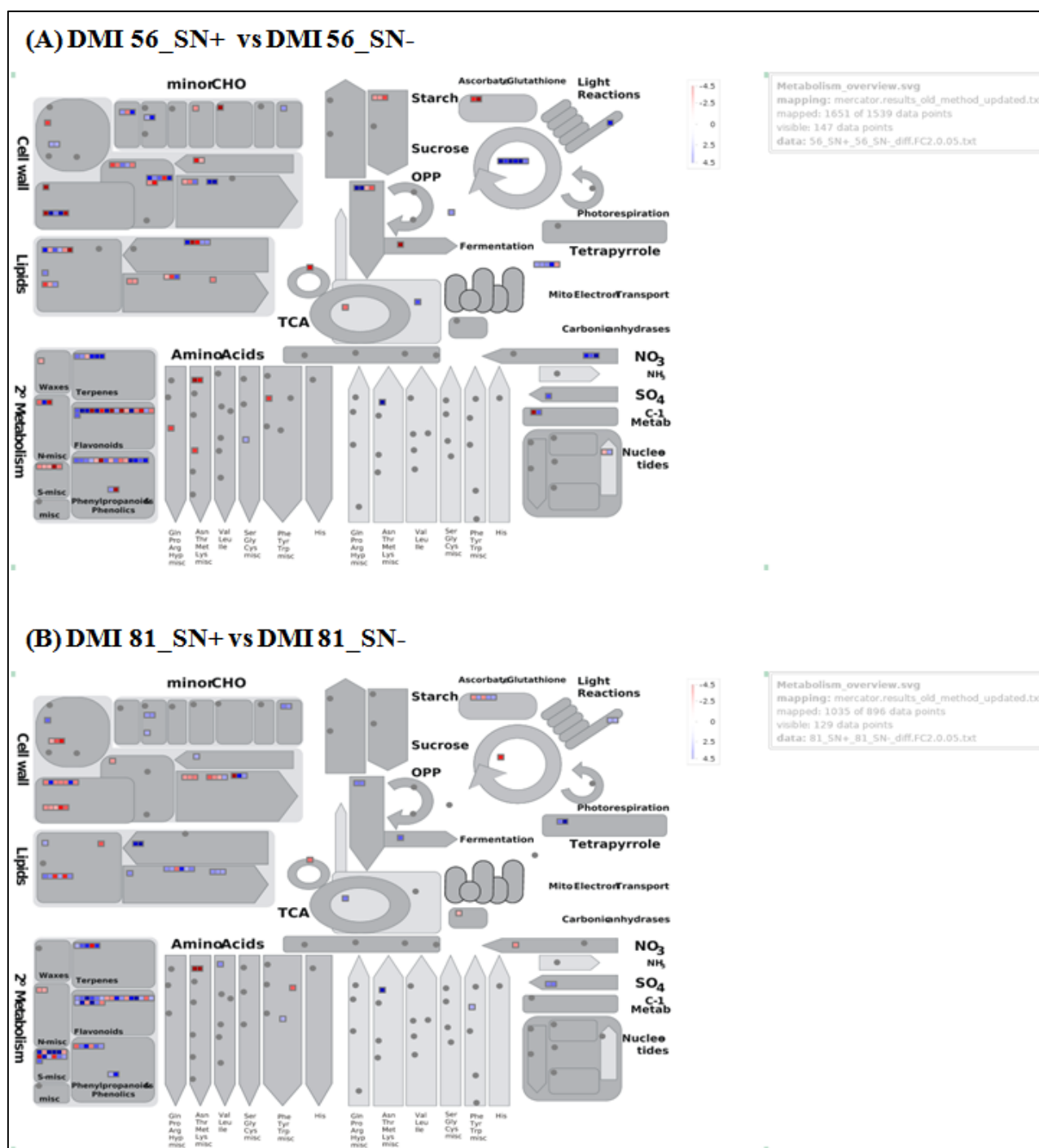
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Supplementary Fig S1. Effect of N-stress on two contrasting maize inbred lines DMI 56 (tolerance to nitrogen stress) and DMI 81 (susceptible to nitrogen stress). Plants were grown hydroponically under N-deficient (**A**) and sufficient/control (**B**) conditions for 21 days. DMI 56 (**C**) and DMI 81 (**D**) lines under N-sufficient and -deficient conditions.

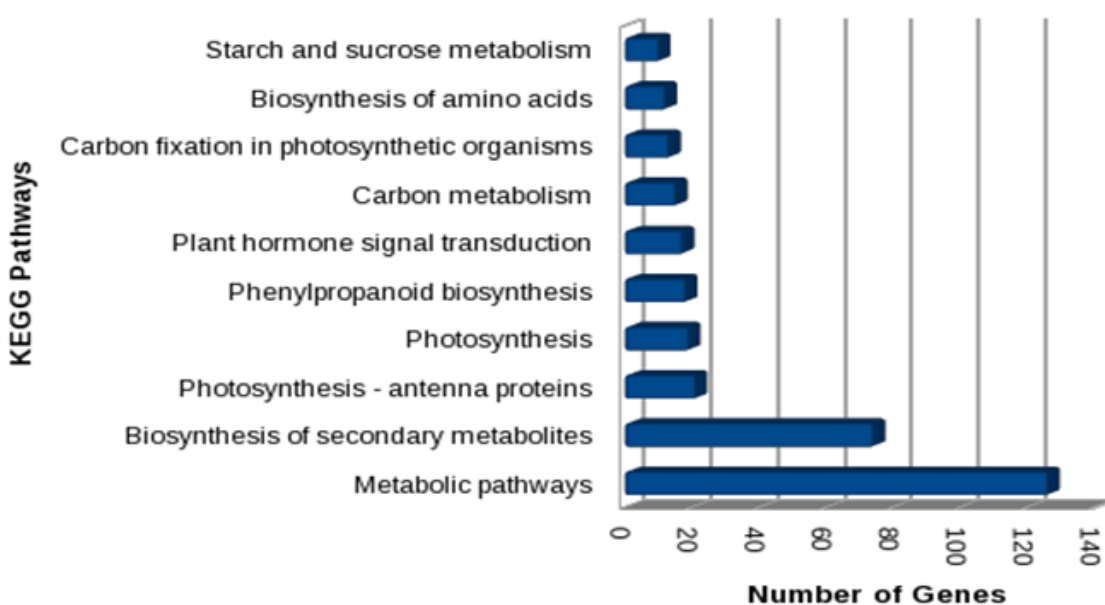


Supplemental Fig S2: MapMan-based visualization of the DEGs in root tissues of **(A)** DMI 56 (tolerant to low-N stress) and **(B)** DMI 81 (susceptible to low-N stress) under low-nitrogen stress compared to their respective control (sufficient-N sample). Small blue and red colour squares represent up- and down-regulated genes, respectively at the amplitude of 4.5 to -4.5 (log₂-value). Letters R, N+, and N- represent root, sufficient nitrogen, and nitrogen deficiency conditions, respectively.

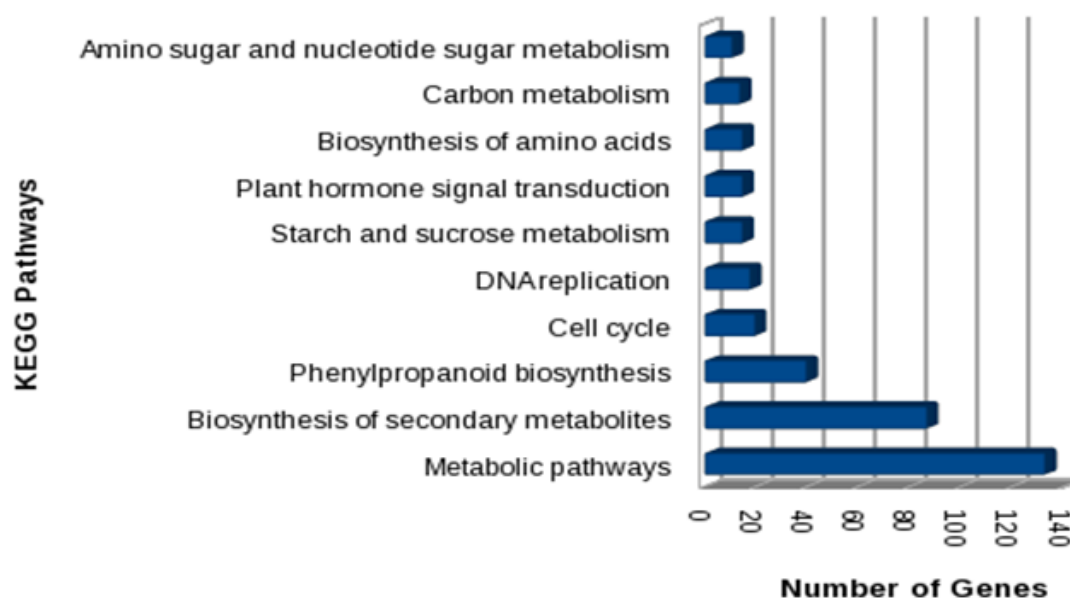


Supplemental Fig S3: MapMan-based visualization of the DEGs in leaf tissues of **(A)** DMI 56 (tolerant to low-N stress) and **(B)** DMI 81 (susceptible to low-N stress) under low-nitrogen stress as compared to their respective control (sufficient-N sample). Small blue and red colour squares represents up- and down-regulated genes, respectively at the amplitude of 4.5 to -4.5 (log2-value). Letters S, N+, and N- represent leaf, sufficient nitrogen, and nitrogen deficiency conditions, respectively.

(A) DMI 56_RN+ vs DMI 56_RN-

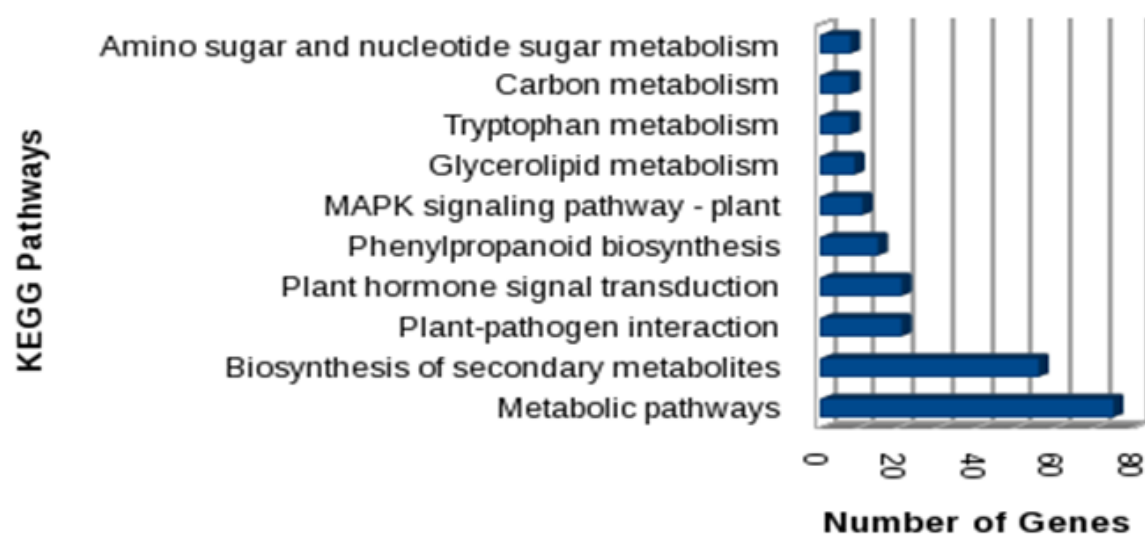


(B) DMI 81_RN+ vs DMI 81_RN-

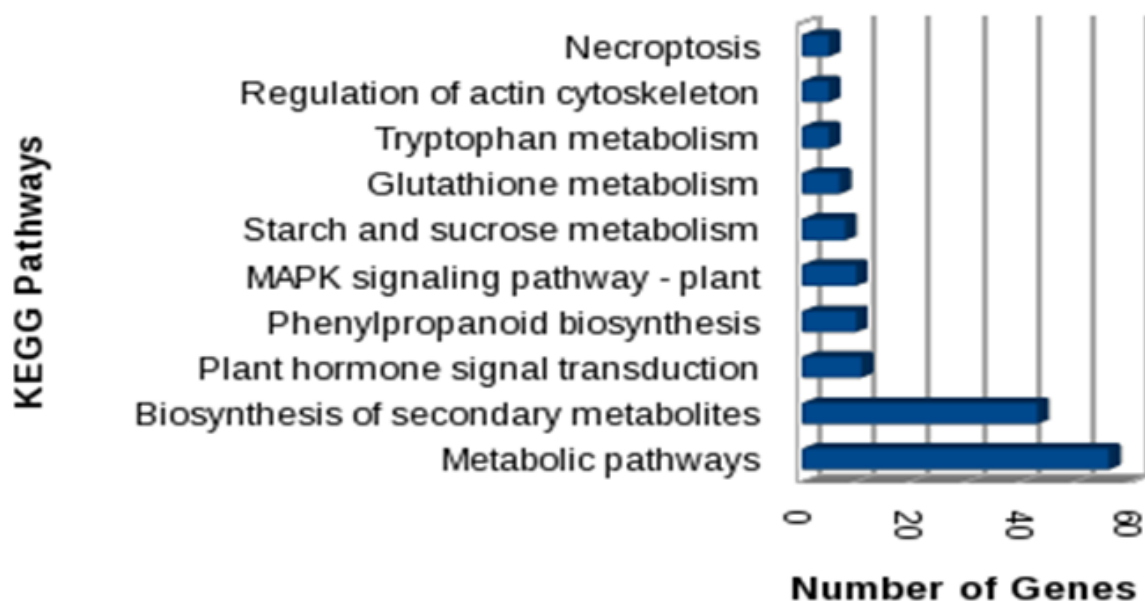


Supplemental Fig S4: KEGG pathway enrichment analysis of DEGs in comparison **(A)** (DMI 56_RN+ vs DMI 56_RN-) **(B)** (DMI 81_RN+ vs DMI 81_RN-). The top 10 pathways from the KEGG enrichment analysis are shown as a bar chart. The terms of the KEGG pathways are depicted on the y-axis. The no of DEGs is shown as the length of the histogram. Letters R, N+, and N- represent root, nitrogen-sufficient, and nitrogen- deficiency conditions, respectively.

(A) DMI 56_SN+ vs DMI 56_SN-

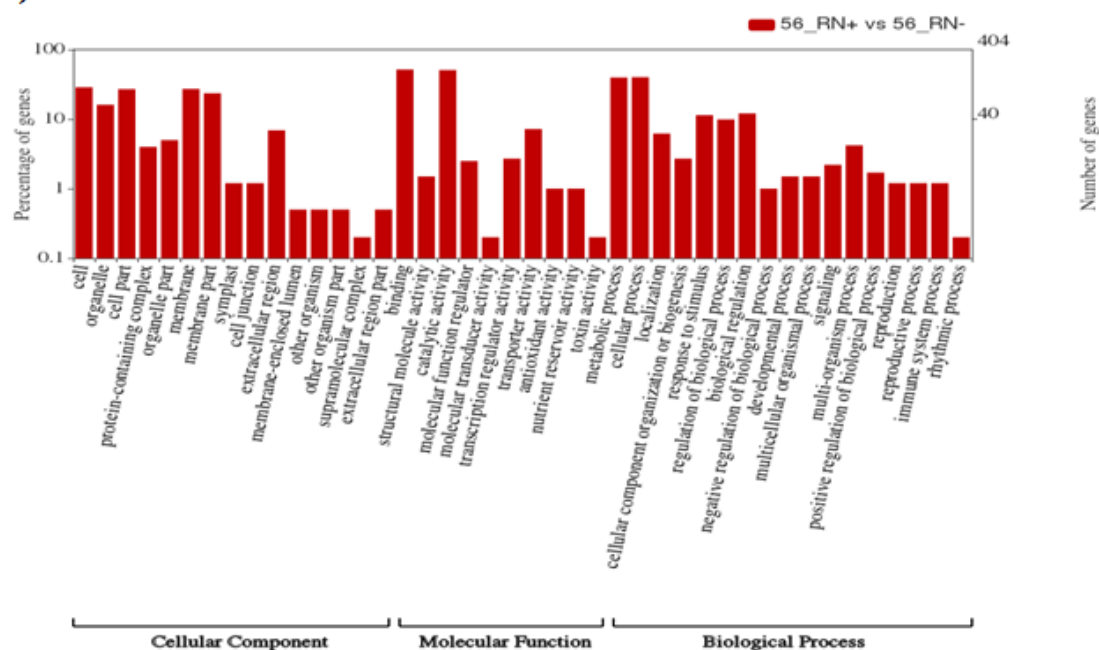


(B) DMI 81_SN+ vs DMI 81_SN-

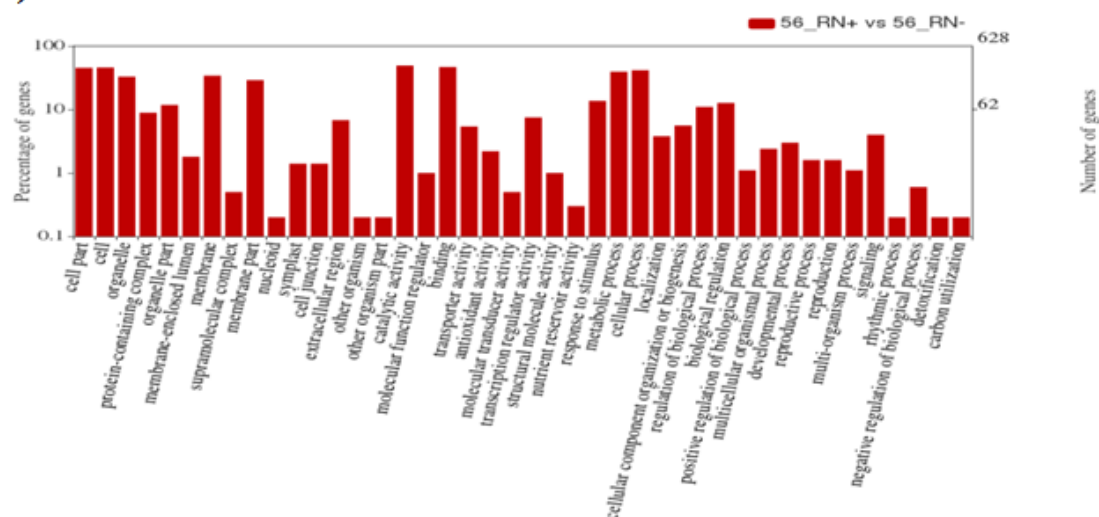


Supplemental Fig S5: KEGG pathway enrichment analysis of DEGs in comparison **(A)** (DMI 56_SN+ vs DMI 56_SN-) **(B)** (DMI 81_SN+ vs DMI 81_SN-). The top 10 pathways from the KEGG enrichment analysis are shown as a bar chart. The terms of the KEGG pathways are depicted on the y-axis. The no of DEGs is shown as the length of the histogram. Letter S, N+, and N- represents leaf, nitrogen-sufficient, and nitrogen- deficiency conditions, respectively.

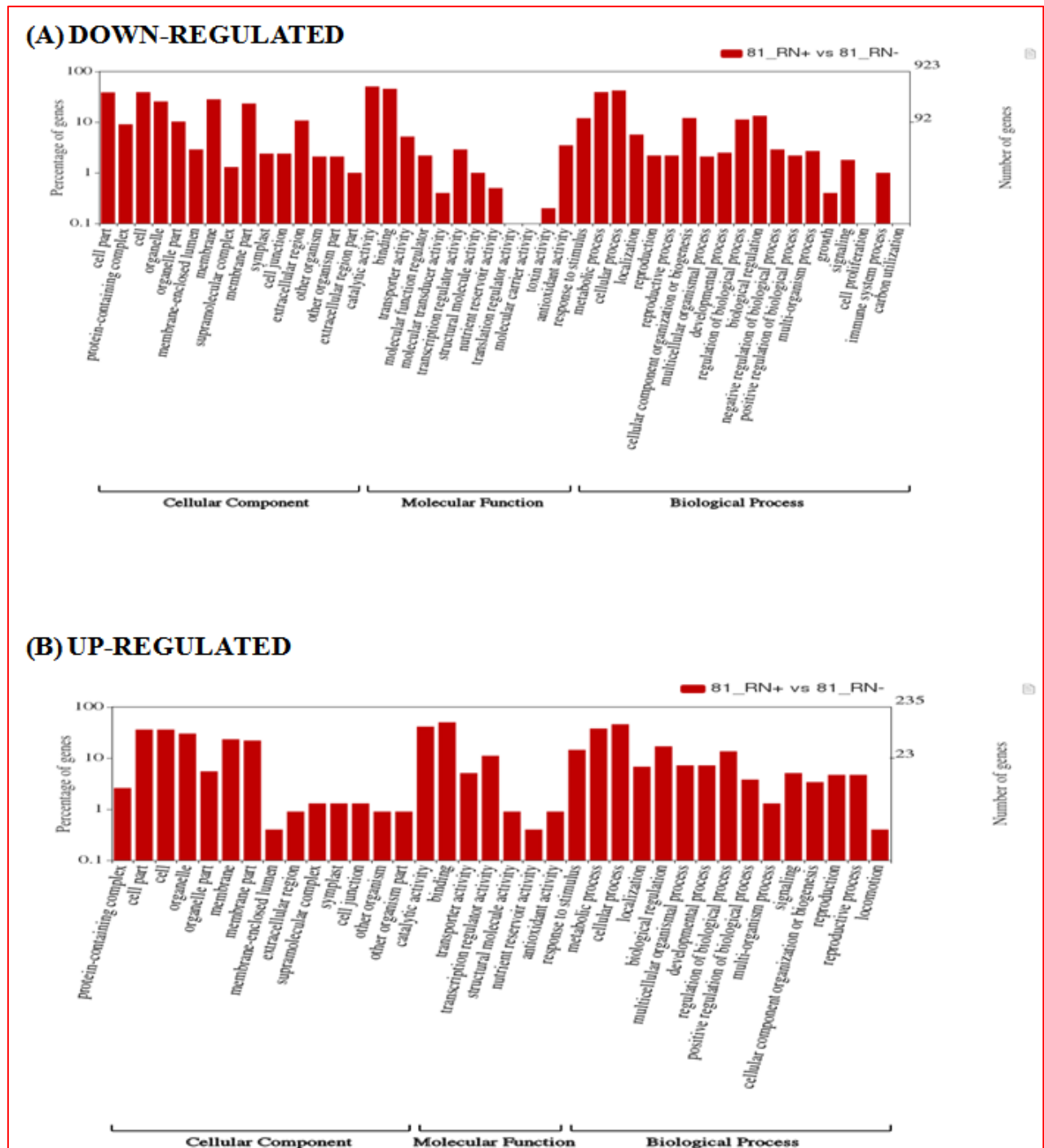
(A) DOWN-REGULATED



(B) UP-REGULATED

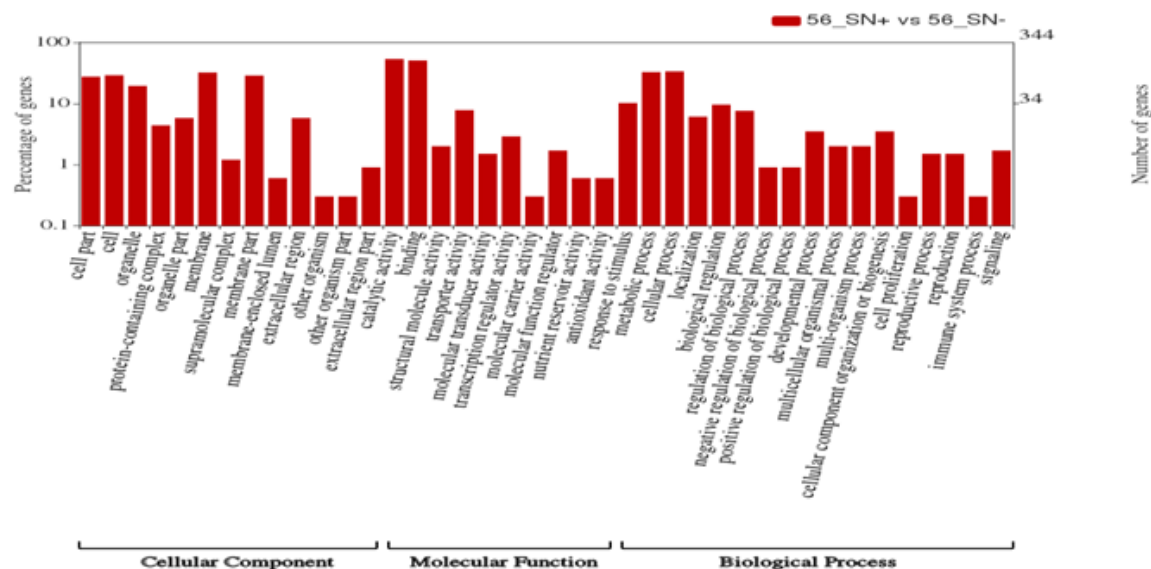


Supplemental Fig S6: Wego plot for (A) down-regulated and (B) up-regulated GO classification in accordance to GO groups: molecular function, biological process and cellular component in DMI 56 root under low-N stress compared to its control (sufficient N) (named as DMI 56_RN+ vs DMI 56_RN-).

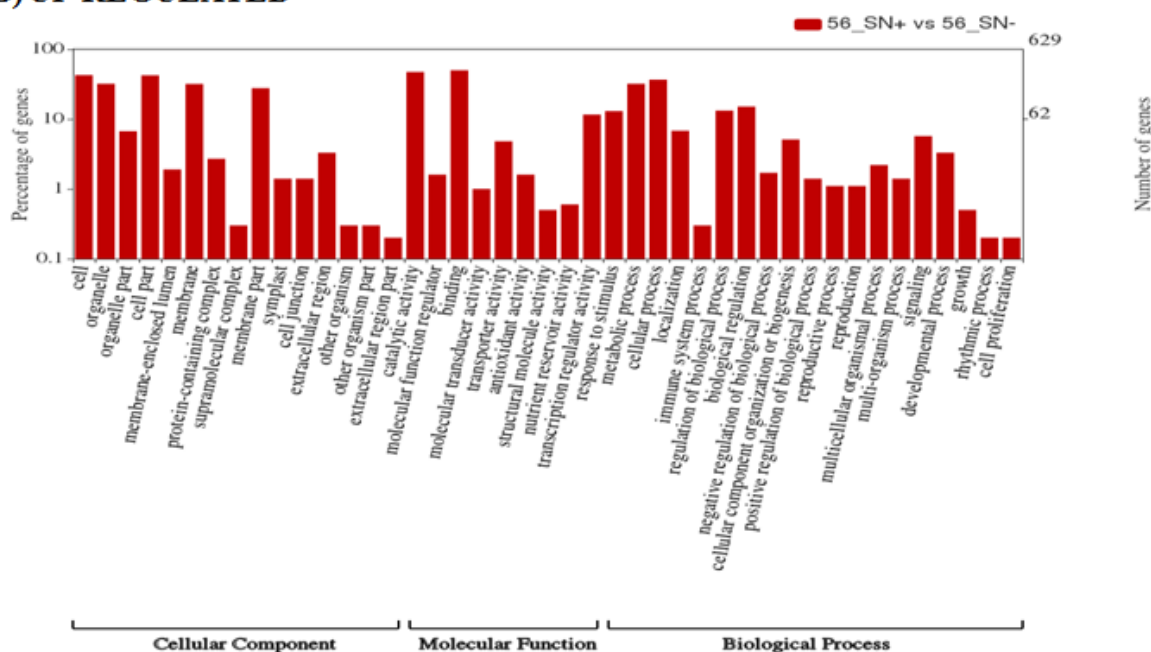


Supplemental Fig S7: Wego plot for **(A)** down-regulated and **(B)** up-regulated GO classification in accordance to GO groups: molecular function, biological process and cellular component in DMI 81 root under low-N stress compared to its control (sufficient N) (named as DMI 81_RN+ vs DMI81_RN-).

(A) DOWN-REGULATED

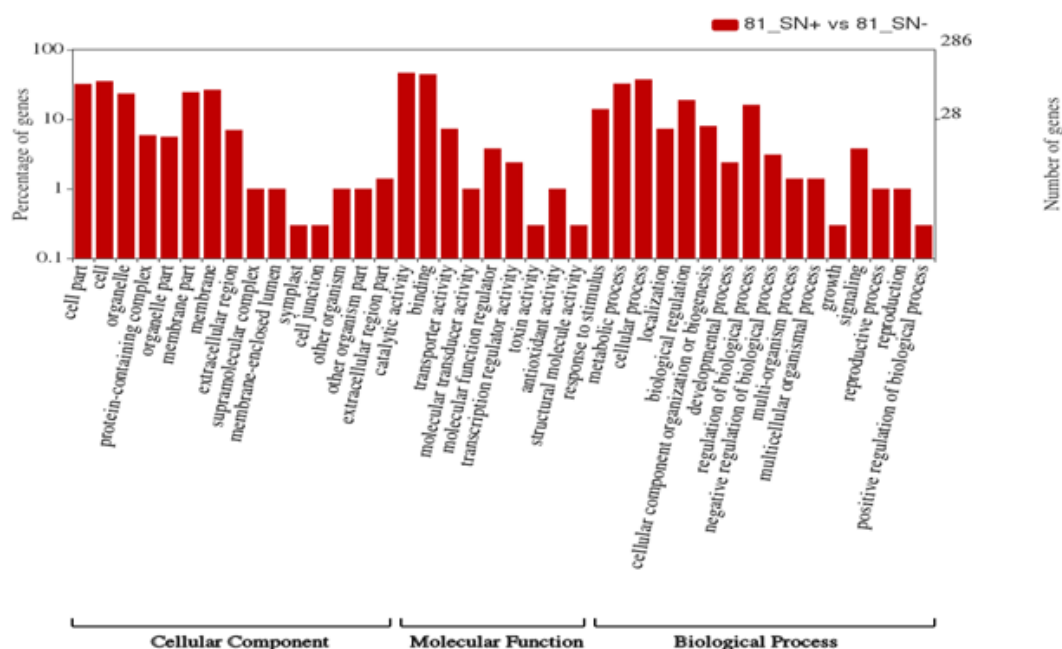


(B) UP-REGULATED

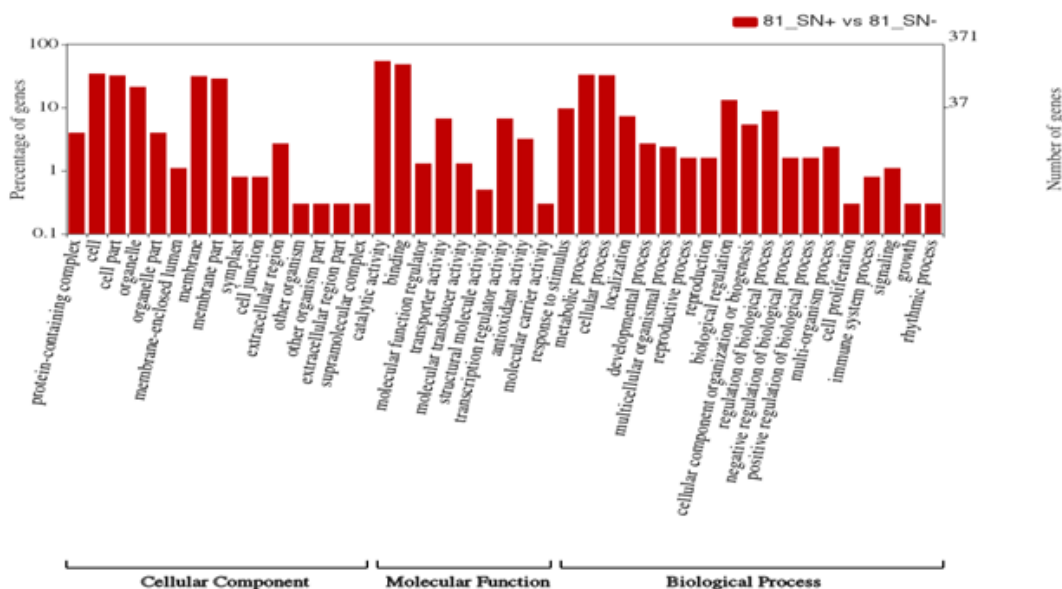


Supplemental Fig S8: Wego plot for (A) down-regulated and (B) up-regulated GO classification in accordance to GO groups: molecular function, biological process and cellular component in DMI 56 leaf under low-N stress compared to its control (sufficient N) (named as DMI 56_SN+ vs DMI56_SN).

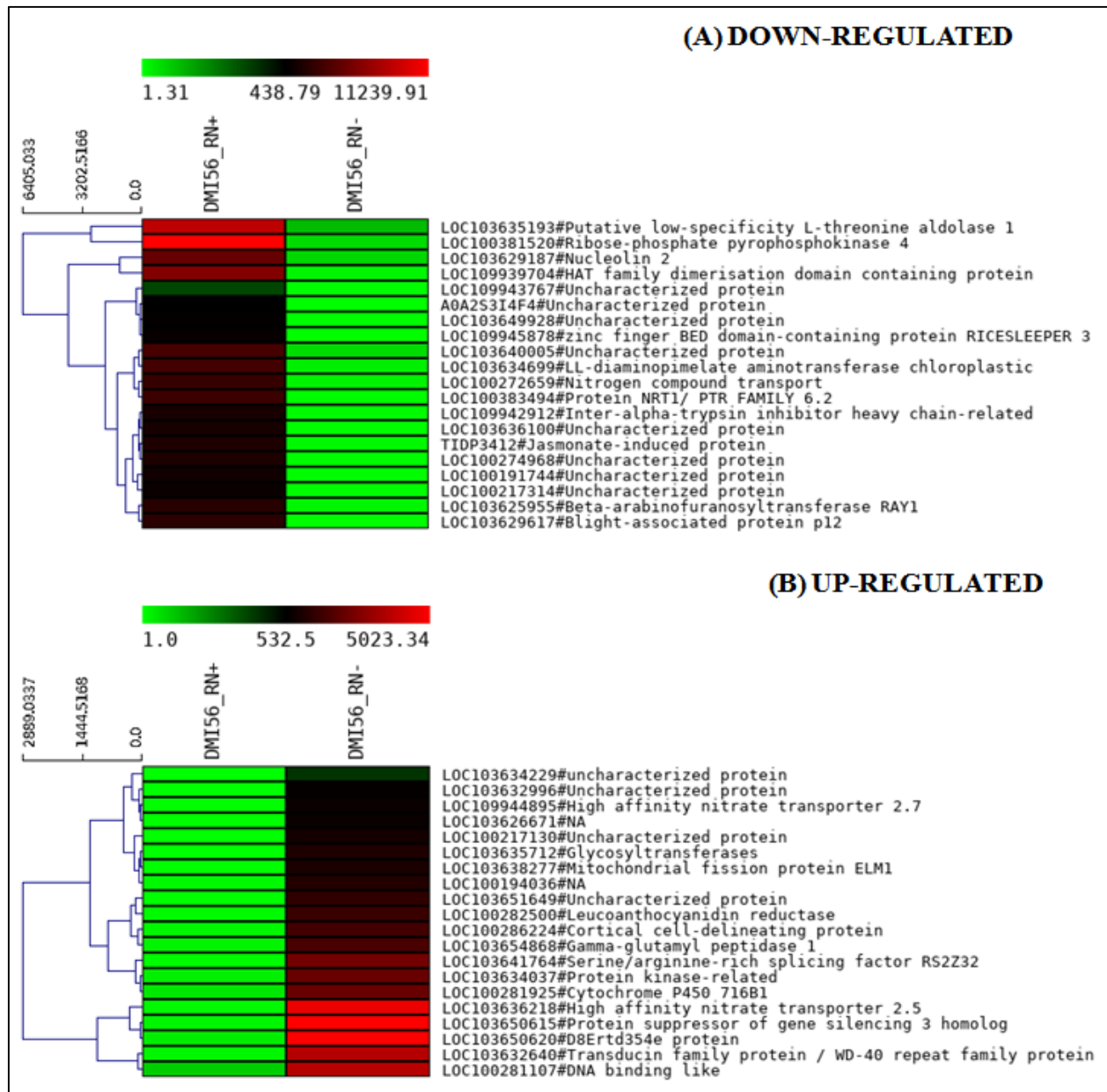
(A) DOWN-REGULATED



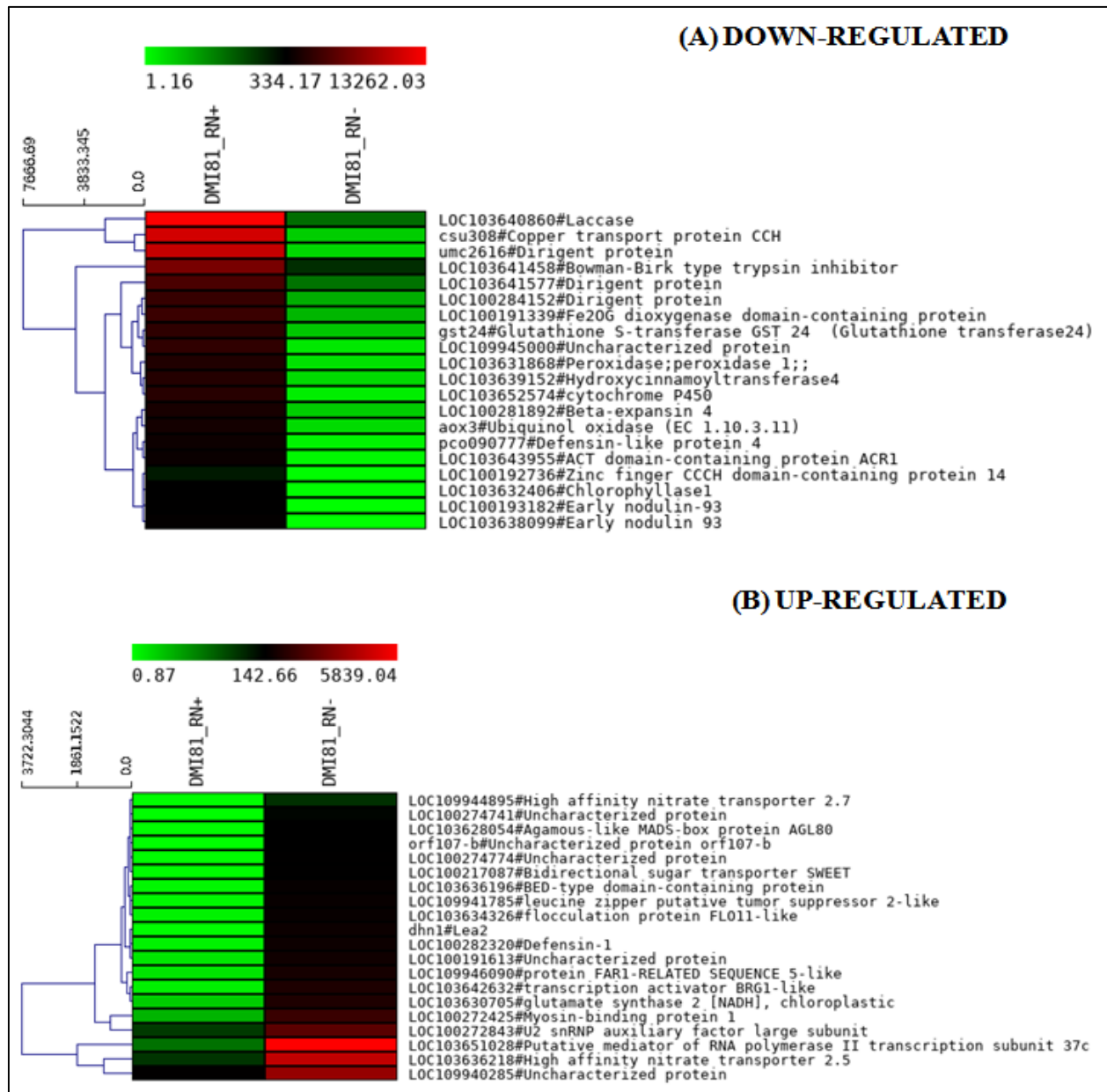
(B) UP-REGULATED



Supplemental Fig S9: Wego plot for (A) down-regulated and (B) up-regulated GO classification in accordance to GO groups: molecular function, biological process and cellular component in DMI 81 leaf under low-N stress compared to its control (sufficient N) (named as DMI 81_SN+ vs DMI81_SN-).



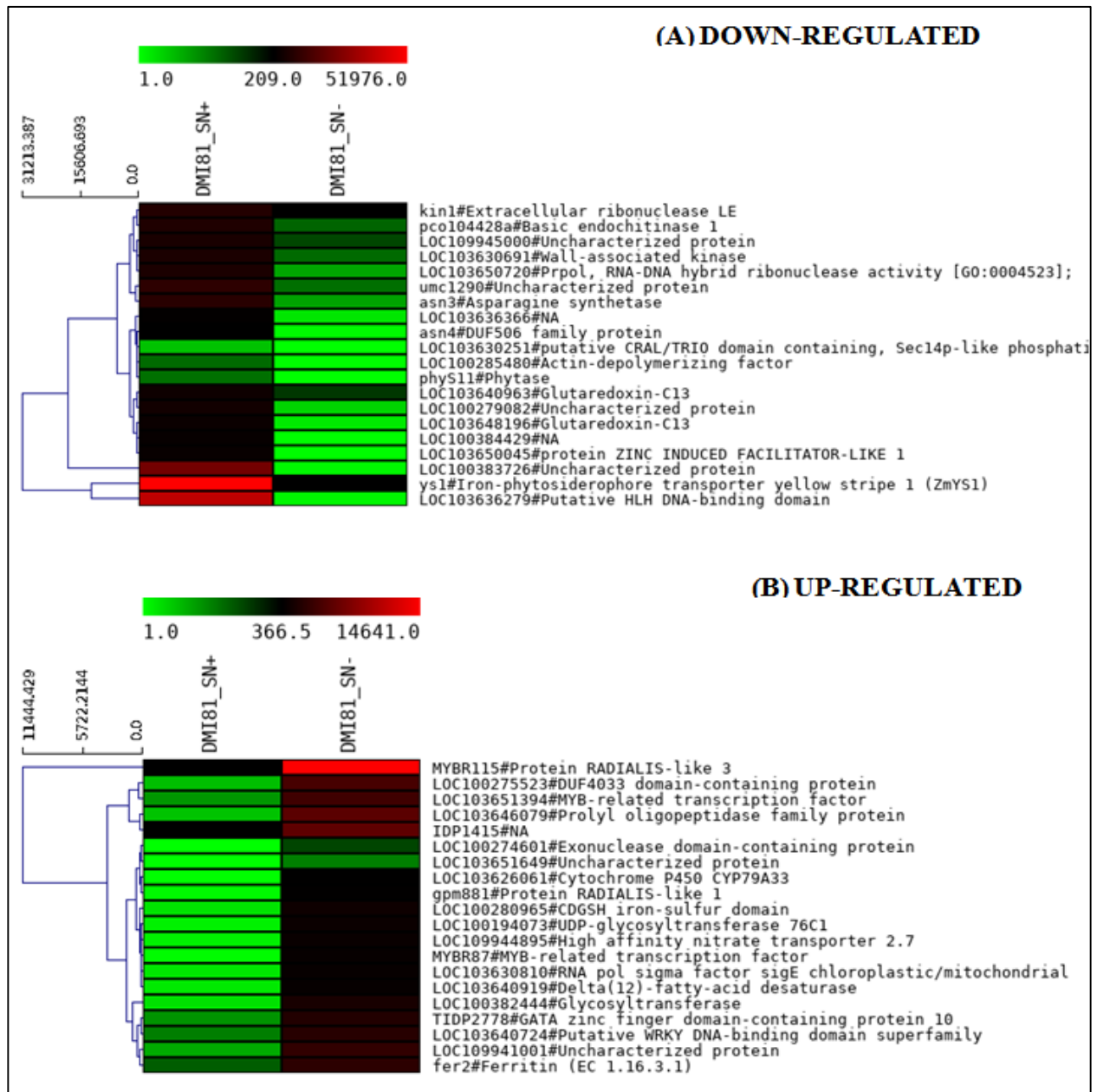
Supplemental Fig S10: Heat map depicting top 20 down-regulated **(A)** and up-regulated **(B)** genes with p -value < 0.05 in DMI 56 root under low-N stress compared to its control (sufficient N) (named as DMI 56_RN+ vs DMI 56_RN-). The plants were grown in hydroponic culture with low N and sufficient N supply. In the heat maps, each horizontal line refers to a gene. Relatively up-regulated genes are shown in red colour, whereas down-regulated genes are shown in green colour.



Supplemental Fig S11: Heat map depicting top 20 down-regulated **(A)** and up-regulated **(B)** genes with p -value < 0.05 in DMI 81 root under low-N stress compared to its control (sufficient N) (named as DMI 81_RN+ vs DMI 81_RN-). The plants were grown in hydroponic culture with low N and sufficient N supply. In the heat maps, each horizontal line refers to a gene. Relatively up-regulated genes are shown in red colour, whereas down-regulated genes are shown in green colour.



Supplemental Fig S12: Heat map depicting top 20 down-regulated **(A)** and up-regulated **(B)** genes with p -value < 0.05 in DMI 56 leaf under low-N stress compared to its control (sufficient N) (named as DMI 56_SN+ vs DMI 56_SN-). The plants were grown in hydroponic culture with low N and sufficient N supply. In the heat maps, each horizontal line refers to a gene. Relatively up-regulated genes are shown in red colour, whereas down-regulated genes are shown in green colour.



Supplemental Fig S13: Heat map depicting top 20 down-regulated **(A)** and up-regulated **(B)** genes with p -value < 0.05 in DMI 81 leaf under low-N stress compared to its control (sufficient N) (named as DMI 81_SN+ vs DMI 81_SN-). The plants were grown in hydroponic culture with low N and sufficient N supply. In the heat maps, each horizontal line refers to a gene. Relatively up-regulated genes are shown in red colour, whereas down-regulated genes are shown in green colour.

Supplementary Table S2: Selected top 20 up-regulated genes in DMI 56 root under low-N stress compared to its control (sufficient N) (named as DMI 56_RN+ vs DMI 56_RN-). Letters R, N+ and N- represent root, sufficient nitrogen, and nitrogen-deficiency conditions, respectively.

DMI 56_RN+ vs DMI 56_RN-					
ID	Gene ID	Log ₂ fold change	P value	FDR	Gene Description
NC_024466.2:158415465-158417502(+)	LOC103636218	8.41963	7.90E-19	2.43E-14	High-affinity nitrate transporter 2.5
NC_024461.2:138093686-138100193(-)	LOC103650615	7.930844	9.84E-18	8.24E-14	Protein suppressor of gene silencing 3 homolog
NC_024468.2:126118262-126120658(+)	LOC103641764	8.547843	1.47E-17	1.02E-13	Serine/arginine-rich splicing factor RS2Z32
NC_024461.2:232951331-232954396(-)	LOC103651649	Inf	2.72E-17	1.62E-13	Uncharacterized protein
NC_024465.2:101004710-101009817(-)	LOC103632640	7.863483	3.19E-17	1.67E-13	Transducin family protein / WD-40 repeat family protein
NC_024461.2:138805064-138814004(+)	LOC103650620	7.041498	1.72E-15	5.53E-12	D8Ert354e protein
NC_024466.2:113319211-113321231(-)	LOC103635712	Inf	2.85E-15	8.53E-12	Glycosyltransferases
NC_024460.2:195290931-195293498(+)	LOC100217130	Inf	5.44E-14	1.27E-10	Uncharacterized protein
NC_024467.2:37432851-37435462(+)	LOC103638277	9.411959	2.16E-13	4.53E-10	Mitochondrial fission protein ELM1
NC_024468.2:144452238-144454289(-)	LOC100282500	7.314584	4.79E-13	9.12E-10	Leucoanthocyanidin reductase
NC_024465.2:98116798-98117776(-)	LOC103634037	6.252393	2.06E-12	3.31E-09	Protein kinase-related
NC_024462.2:156545940-156546701(+)	LOC100286224	6.61879	4.18E-12	6.04E-09	Cortical cell-delineating protein

NC_024465.2:140065077-140066304(-)	LOC103632996	Inf	1.05E-11	1.29E-08	Uncharacterized protein
NC_024462.2:240079626-240080879(-)	LOC103654868	6.284761	1.16E-11	1.38E-08	Gamma-glutamyl peptidase 1
NC_024462.2:5969504-5971912(+)	LOC100281925	5.574259	8.09E-11	8.91E-08	Cytochrome P450 716B1
NC_024461.2:230035429-230038824(-)	LOC109944895	8.347387	1.02E-10	1.10E-07	High-affinity nitrate transporter 2.7
NC_024468.2:106318814-106321232(-)	LOC100281107	5.201142	1.69E-10	1.68E-07	DNA binding like
NC_024465.2:101003482-101007474(+)	LOC100194036	6.476499	3.12E-10	2.97E-07	NA
NC_024463.2:88008903-88012287(-)	LOC103626671	7.563962	8.17E-10	7.28E-07	NA
NC_024465.2:140066671-140067924(-)	LOC103634229	Inf	1.13E-09	9.69E-07	uncharacterized protein

Supplementary Table S3: Selected top 20 down-regulated genes in DMI 56 root under low-N stress compared to its control (sufficient N) (named as DMI 56_RN+ vs DMI 56_RN-).

DMI 56_RN+ vs DMI 56_RN-					
ID	Gene I'D	Log ₂ fold change	P value	FDR	Gene Description
NC_024463.2:72705848-72708598(-)	LOC109939704	-8.47587	1.16E-18	2.43E-14	HAT family dimerisation domain-containing protein
NC_024466.2:62579423-62581864(-)	LOC100383494	-9.15771	2.46E-18	3.43E-14	Protein NRT1/ PTR FAMILY Y 6.2
NC_024464.2:91462875-91463803(+)	LOC103629617	-9.81172	7.20E-18	7.54E-14	Blight-associated protein p12
NC_024462.2:181681444-181682786(-)	LOC109945878	-8.17014	6.05E-10	5.63E-07	zinc finger BED domain-containing protein RICESLEEPER 3

NC_024461.2:323934 07-32394800(-)	LOC103649928	-8.01991	2.17E-09	1.69E-06	Uncharacterized protein
NC_024462.2:165271 169-165273576(+)	LOC100381520	-7.51045	1.29E-15	4.91E-12	Ribose-phosphate pyrophosphokinase 4
NC_024461.2:541392 02-54139903(+)	LOC100274968	-9.36206	1.52E-15	5.31E-12	Uncharacterized protein
NC_024466.2:149851 012-149852859(-)	LOC103636100	-9.14369	2.10E-14	5.87E-11	Uncharacterized protein
NC_024466.2:587511 8-5881172(+)	LOC103634699	-6.83244	2.66E-14	6.97E-11	LL-diaminopimelate aminotransferase chloroplastic
NC_024464.2:100698 49-10071772(+)	LOC100272659	-6.89883	4.21E-14	1.04E-10	Nitrogen compound transport
NC_024462.2:198407 157-198409508(-)	A0A2S3I4F4	-7.73507	1.91E-08	1.08E-05	Uncharacterized protein
NC_024463.2:118556 24-11859798(-)	LOC103625955	-7.09084	1.44E-13	3.16E-10	Beta- arabinofuranosyltransferase RAY1
NC_024468.2:122393 248-122395555(-)	LOC109942912	-7.64506	4.63E-13	9.12E-10	Inter-alpha-trypsin inhibitor heavy chain- related
NC_024464.2:289284 93-28931803(+)	LOC103629187	-6.11678	5.63E-13	1.02E-09	Nucleolin 2
NC_024459.2:633178 28-63324872(+)	LOC103635193	-6.18538	7.45E-13	1.30E-09	Putative low-specificity L- threonine aldolase 1
NC_024461.2:132539 492-132540473(-)	TIDP3412	-7.0791	9.67E-13	1.62E-09	Jasmonate-induced protein
NC_024462.2:196029 366-196032725(-)	LOC100217314	-9.55279	3.70E-12	5.59E-09	Uncharacterized protein
NC_024459.2:249828 810-249830061(+)	LOC109943767	-7.92476	8.50E-07	0.000254	Uncharacterized protein
NC_024461.2:231817 612-231818726(+)	LOC100191744	-7.87561	4.40E-12	6.15E-09	Uncharacterized protein

NC_024467.2:66116173-66116535(-)	LOC103640005	-5.8496	4.91E-12	6.63E-09	Uncharacterized protein
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Supplementary Table S4: Selected top 20 up-regulated genes in DMI 81 root under low-N stress compared to its control (sufficient N) (named as DMI 81_RN+ vs DMI 81_RN-).

DMI 81_RN+ vs DMI 81_RN-					
ID	Gene ID	Log ₂ fold change	P value	FDR	Gene Description
NC_024461.2:184004253-184007904(-)	LOC103651028	6.195975	1.52E-10	1.26E-06	Putative mediator of RNA polymerase II transcription subunit 37c
NC_024464.2:141324558-141325543(-)	dhn1	Inf	3.38E-09	1.99E-05	Lea2
NC_024466.2:158415465-158417502(+)	LOC103636218	5.295507	7.57E-09	3.13E-05	High affinity nitrate transporter 2.5
NC_024468.2:92359187-92360695(-)	LOC103642632	6.579942	4.13E-08	9.49E-05	transcription activator BRG1-like
NC_024459.2:244884706-244894283(-)	LOC100272425	5.095952	2.47E-07	0.000463	Myosin-binding protein 1
NC_024460.2:231129791-231130667(+)	LOC100274774	Inf	2.93E-07	0.000527	Uncharacterized protein
NC_024460.2:236537682-236544091(-)	LOC100272843	4.309235	1.38E-06	0.00178	U2 snRNP auxiliary factor large subunit
NC_024463.2:20265968-20266894(-)	LOC103628054	Inf	1.56E-06	0.00189	Agamous-like MADS-box protein AGL80
NC_024468.2:110200453-110201623(+)	LOC100274741	Inf	1.91E-06	0.002085	Uncharacterized protein
NC_024463.2:192005501-192006241(+)	LOC100282320	5.932617	2.54E-06	0.002585	Defensin-1
NC_024466.2:68841087-68842987(+)	LOC109941785	6.327733	2.58E-06	0.002585	leucine zipper putative tumor suppressor 2-like

NC_024462.2:208046149-208049422(-)	LOC109946090	5.428511	2.92E-06	0.002682	protein FAR1-RELATED SEQUENCE 5-like
NC_024464.2:14454177-14465023(-)	LOC109940285	3.922351	4.61E-06	0.003963	Uncharacterized protein
NC_024461.2:230035429-230038824(-)	LOC109944895	Inf	5.00E-06	0.004133	High affinity nitrate transporter 2.7
NC_024464.2:167441703-167453268(+)	LOC103630705	4.906922	5.26E-06	0.004211	glutamate synthase 2 [NADH], chloroplastic
NC_024459.2:59948045-59951123(-)	LOC100217087	6.791081	5.95E-06	0.004391	Bidirectional sugar transporter SWEET
NC_007982.1:372870-373193(-)	orf107-b	7.404726	7.31E-06	0.004953	Uncharacterized protein orf107-b
NC_024466.2:156961406-156962581(+)	LOC103636196	5.847887	9.71E-06	0.006469	BED-type domain-containing protein
NC_024459.2:227680106-227684609(+)	LOC100191613	5.161468	1.32E-05	0.008281	Uncharacterized protein
NC_024465.2:161004438-161005368(+)	LOC103634326	5.522241	1.34E-05	0.008281	flocculation protein FLO11-like

Supplementary Table S5: Selected top 20 down-regulated genes in DMI 81 root under low-N stress compared to its control (sufficient N) (named as DMI 81_RN+ vs DMI 81_RN-).

DMI 81_RN+ vs DMI 81_RN-					
ID	Gene ID	Log ₂ fold change	P Value	FDR	Gene Description
NC_024463.2:149398951-149400833(+)	umc2616	- 7.6386 4	3.05E-12	1.26E-07	Dirigent protein
NC_024463.2:172644130-172645527(+)	csu308	- 7.3892	1.31E-11	2.71E-07	Copper transport protein CCH

		8			
NC_024461.2:58127334-58128164(-)	LOC109945000	- 6.5735 2	2.78E -11	3.23E- 07	Uncharacterized protein
NC_024461.2:220486444-220488718	-	- 6.7034 2	3.13E -11	3.23E- 07	cytochrome P450
NC_024465.2:1175473-1177144(+)	LOC103631868	- 5.7355 5	4.09E -09	2.11E- 05	Peroxidase;peroxidase 1;;
NC_024459.2:142569164-142571276(-)	LOC103639152	- 5.5387 1	6.02E -09	2.76E- 05	Hydroxycinnamoyltransferase4
NC_024468.2:12275223-12278091(-)	LOC103640860	- 6.1119 5	8.35E -09	3.14E- 05	Laccase
NC_024467.2:20480643-20481654(+)	LOC103638099	- 8.9546 5	1.06E -08	3.65E- 05	Early nodulin 93
NC_024463.2:216862611-216863602(-)	gst24	- 5.2214 9	1.38E -08	4.38E- 05	Glutathione S-transferase GST 24 (Glutathione transferase24)
NC_024461.2:135359547-135361124(-)	LOC100191339	- 5.1303 9	1.69E -08	4.98E- 05	Fe ₂ OG dioxygenase domain-containing protein
NC_024459.2:277214406-277217329(+)	LOC103643955	- 6.6594 4	2.22E -08	6.10E- 05	ACT domain-containing protein ACR1
NC_024468.2:132238491-132239276(+)	pco090777	- 6.1758 4	3.37E -08	8.20E- 05	Defensin-like protein 4
NC_024459.2:187013824-187015222(+)	LOC100284152	- 4.8769 8	5.80E -08	0.00012 3	Dirigent protein
NC_024466.2:151370	LOC100192736	- 6.4419	4.83E -06	0.00407 1	Zinc finger CCCH domain-

661-151372724(-)		4			containing protein 14
NC_024467.2:204028 28-20403920(-)	LOC100193182	- 8.5951 9	6.52E -08	0.00012 8	Early nodulin-93
NC_024459.2:186945 224-186946587(+)	LOC103641577	- 4.4947 8	3.40E -07	0.00058 6	Dirigent protein
NC_024468.2:969377 63-96938529(+)	LOC103641458	- 4.5647	4.36E -07	0.00072 1	Bowman-Birk type trypsin inhibitor
NC_024460.2:125656 21-12567188(+)	aox3	- 4.9259 8	5.45E -07	0.00086 5	Ubiquinol oxidase (EC 1.10.3.11)
NC_024465.2:568658 86-56867259(-)	LOC103632406	- 7.3118 8	6.91E -07	0.00105 8	Chlorophyllase1
NC_024463.2:197531 995-197533772(+)	LOC100281892	- 4.6314 2	9.96E -07	0.00146 9	Beta-expansin 4

Supplementary Table S6: Selected top 20 up-regulated genes in DMI 56 leaf under low-N stress compared to its control (sufficient N) (named DMI 56_SN+ vs DMI 56_SN-).

DMI 56_SN+vs DMI_56SN-					
ID	Gene ID	Log ₂ fold change	P value	FDR	Gene Description
NC_024466.2:113319211- 113321231(-)	LOC103635712	8.807695	7.31E- 10	5.19E- 07	carbohydrate metabolic process [GO:0005975]
NC_024461.2:138093686- 138100193(-)	LOC103650615	8.125569	6.39E- 19	8.63E- 15	protein suppressor of gene silencing 3 homolog
NC_024467.2:37432851- 37435462(+)	LOC103638277	7.708985	6.41E- 09	3.37E- 06	microtubule-based movement [GO:0007018]
NC_024459.2:174658843-	LOC103645065	Inf	1.48E-	1.46E-	ubiquitin protein ligase

174660244(+)			10	07	activity [GO:0061630]
NC_024463.2:203485460-203489985(-)	LOC103627571	Inf	1.85E-08	8.82E-06	Plant elicitor peptide 4, Protein NRT1/ PTR FAMILY 7.2 (Protein NRT1/ PTR FAMILY 7.3)
NC_024461.2:146542784-146543596(-)	LOC103650692	8.011858	4.01E-16	1.81E-12	AP2-EREBP transcription factor
NC_024461.2:138805064-138814004(+)	LOC103650620	6.974394	4.94E-16	2.00E-12	D8Ertd354e protein
NC_024463.2:201022527-201023593(+)	LOC100284491	6.307505	9.09E-14	2.05E-10	Dehydration-responsive element-binding protein 1A
NC_024467.2:60442035-60447747(+)	LOC103638554	6.096847	1.97E-13	4.20E-10	Interferon-related developmental regulator family
NC_024462.2:150629045-150631230(+)	LOC100191789	6.606741	3.70E-13	6.82E-10	oxidation-reduction process [GO:0055114]
NC_024465.2:101004710-101009817(-)	LOC103632640	6.563266	4.55E-12	6.82E-09	Transducin family protein
NC_024463.2:216589025-216592463(-)	LOC100383210	5.773044	7.06E-12	9.34E-09	oxidoreductase activity [GO:0016491]
NC_024461.2:232951331-232954396(-)	LOC103651649	8.427881	7.42E-12	9.40E-09	Uncharacterized protein#integral component of membrane [GO:0016021]
NC_024468.2:71754071-71755095(-)	LOC103642522	5.628917	2.57E-11	3.06E-08	Uncharacterized protein
NC_024466.2:104190500-104193277(+)	LOC100284502	5.769391	4.90E-11	5.52E-08	Universal stress protein family protein
NC_024460.2:39565956-39567856(+)	LOC103646320	6.676106	1.04E-10	1.14E-07	Zinc knuckle (CCHC-type) family protein
NC_024464.2:65322405-	DBP4	5.216594	1.29E-	1.35E-	Dehydration-responsive element-

65323578(+)			10	07	binding protein 1C
NC_024465.2:10857307-10858459(-)	LOC100280478	6.769611	6.38E-10	5.03E-07	xylan catabolic process [GO:0045493]
NC_024463.2:7406160-7408459(-)	LOC100194167	Inf	2.04E-10	1.97E-07	Transcriptional adapter ADA2b
NC_024461.2:172146140-172147330(+)	LOC100279664	Inf	2.22E-10	2.09E-07	Uncharacterized protein

Supplementary Table S7: Selected top 20 down-regulated genes in DMI 56 leaf under low-N stress compared to its control (sufficient N) (named DMI 56_SN+ vs DMI 56_SN-).

DMI 56_SN+ vs DMI 56_SN-					
ID	Gene ID	Log ₂ fold change	P value	FDR	Gene Description
NC_024464.2:28923624-28924298(-)	LOC103630947	-8.10065	4.35E-10	3.69E-07	uncharacterized protein LOC103630947
NC_024459.2:282687219-282688648(+)	LOC103644023	-8.05002	3.91E-07	0.000117	Regulator of Vps4 activity in the MVB pathway protein transport
NC_024466.2:171431000-171436167(+)	LOC100382585	-9.30495	1.30E-15	4.80E-12	Uncharacterized protein
NC_024463.2:72705848-72708598(-)	LOC109939704	-7.70979	1.75E-15	5.90E-12	HAT family dimerisation domain containing protein
NC_024468.2:142619140-142622387(-)	LOC100279863	-7.74016	1.00E-08	5.00E-06	Uncharacterized protein
NC_024466.2:162651852-162658240(+)	LOC103636279	-6.91398	3.51E-15	1.02E-11	Putative HLH DNA-binding domain superfamily protein
NC_024461.2:140251533-140253626(+)	LOC103650635	-6.65397	5.18E-15	1.40E-11	Amino acid permease 2

NC_024463.2:65058208-65059377(+)	pco104428a	-7.01388	5.40E-14	1.37E-10	Basic endochitinase 1
NC_024465.2:3653592-3654276(+)	prp4	-6.17621	6.37E-14	1.52E-10	Pathogenesis related protein4
NC_024461.2:18481283-18484038(+)	LOC103649793	-7.78747	3.05E-13	6.18E-10	Uncharacterized protein
NC_024466.2:167594748-167596284(+)	LOC103636366	-8.80625	3.26E-13	6.28E-10	DUF506 family protein
NC_024466.2:171234104-171236206(-)	LOC100383726	-7.30156	7.15E-12	9.34E-09	C0PIK5
NC_024464.2:28928493-28931803(+)	LOC103629187	-6.02827	7.54E-13	1.33E-09	Nucleolin 2
NC_024461.2:178451617-178453328(-)	LOC100272433	-7.92669	8.56E-13	1.44E-09	DBD_Tnp_Mut domain-containing protein
NC_024459.2:45286561-45290000(-)	asn3	-6.79721	1.68E-12	2.72E-09	Asparagine synthetase
NC_024468.2:122393248-122395555(-)	LOC109942912	-7.31507	4.37E-10	3.69E-07	Inter-alpha-trypsin inhibitor heavy chain-related
NC_024461.2:231817612-231818726(+)	LOC100191744	-6.54629	5.75E-12	8.32E-09	Uncharacterized protein
NC_024462.2:181681444-181682786(-)	LOC109945878	-7.1094	8.59E-07	0.000238	zinc finger BED domain-containing protein RICESLEEPER 3
NC_024464.2:28920057-28921765(+)	LOC109940384	-6.62009	5.35E-09	2.96E-06	cytochrome P450 714C3
NC_024460.2:219038973-219039945(+)	LOC109944405	-7.085938687	3.68E-09	5.05E-03	wiskott-Aldrich syndrome protein homolog 1-like

Supplementary Table S8: Selected top 20 up-regulated genes in DMI 81 leaf under low-N stress compared to its control (sufficient N) (named DMI 81_SN+ vs DMI 81_SN-).

DMI 81_SN+ vs DMI 81_SN-					
ID	Gene I'D	Log ₂ fold change	P value	FDR	Gene Description
NC_024460.2:19078363-19082101(-)	LOC103646079	5.975173	9.98E-19	3.13E-15	Prolyl oligopeptidase family protein
NC_024466.2:72403032-72404407(+)	MYBR87	7.733015	7.16E-18	1.94E-14	MYB-related transcription factor
NC_024464.2:4037971-4039290(-)	LOC100275523	5.574258	1.69E-17	4.31E-14	DUF4033 domain-containing protein
NC_024459.2:224454964-224456636(-)	LOC100382444	5.376252	1.63E-15	3.32E-12	Glycosyltransferase
NC_024463.2:19357180-19359209(+)	LOC103626061	8.02514	3.58E-15	6.94E-12	Cytochrome P450 CYP79A33
NC_024460.2:174867030-174869050(-)	LOC100194073	5.653442	1.84E-14	3.25E-11	UDP-glycosyltransferase 76C1
NC_024465.2:181006315-181007733(-)	LOC109941001	4.741017	3.34E-14	5.44E-11	Uncharacterized protein
NC_024461.2:215275386-215276968(+)	LOC103651394	4.712516	4.27E-14	6.68E-11	MYB-related transcription factor
NC_024461.2:230035429-230038824(-)	LOC109944895	5.439925	1.81E-13	2.63E-10	High affinity nitrate transporter 2.7
NC_024466.2:153108122-153110782(-)	MYBR115	5.310249	5.43E-13	7.63E-10	Protein RADIALIS-like 3
NC_024465.2:149842408-149844850(-)	LOC100280965	4.929006	6.75E-13	9.16E-10	CDGSH iron-sulfur domain
NC_024464.2:169245888-169247273(+)	gpm881	6.01495	8.35E-13	1.10E-09	Protein RADIALIS-like 1
NC_024461.2:29625385-29627271(-)	LOC100274601	Inf	1.87E-12	2.30E-09	Exonuclease domain-containing protein

NC_024459.2:8372130-8373575(+)	TIDP2778	3.93637 2	8.19E -11	9.02E -08	GATA zinc finger domain-containing protein 10
NC_024460.2:50474639-50478074(-)	IDP1415	3.97046 9	1.04E -10	1.11E -07	NA
NC_024468.2:823896-825905(-)	fer2	3.64584 5	7.12E -10	6.31E -07	Ferritin (EC 1.16.3.1)
NC_024464.2:172322009-172324235(-)	LOC103630810	4.60253 5	1.16E -10	1.21E -07	RNA pol sigma factor sigE chloroplastic/mitochondrial
NC_024468.2:3630797-3632942(+)	LOC103640724	3.82781 9	1.68E -10	1.71E -07	Putative WRKY DNA-binding domain superfamily
NC_024468.2:19502940-19504931(-)	LOC103640919	4.57742 9	2.28E -10	2.21E -07	Delta(12)-fatty-acid desaturase
NC_024461.2:232951331-232954396(-)	LOC103651649	Inf	2.43E -10	2.30E -07	Uncharacterized protein

Supplementary Table S9: Selected top 20 down-regulated genes in DMI 81 leaf under low-N stress compared to its control (sufficient N) (named DMI 81_SN+ vs DMI 81_SN-).

DMI 81_SN+ vs DMI81_SN-					
ID	Gene ID	Log ₂ fold change	P value	FDR	Gene Description
NC_024463.2:195832851-195835981(-)	ys1	- 7.21435	4.35E-11	4.93E-08	Iron-phytosiderophore transporter yellow stripe 1 (ZmYS1)
NC_024461.2:132281202-132282700(-)	phyS11	- 6.87036	1.94E-07	9.06E-05	Phytase
NC_024461.2:47342404-47360743(-)	LOC103650045	- 10.0821	5.06E-28	6.86E-24	protein ZINC INDUCED FACILITATOR-LIKE 1

NC_024466.2:171234104-171236206(-)	LOC100383726	- 11.9543	2.65E-27	2.70E-23	Uncharacterized protein
NC_024460.2:174319805-174320236(-)	LOC100384429	- 9.87882	1.08E-26	8.79E-23	NA
NC_024468.2:25871996-25872962(-)	LOC103648196	- 7.22347	4.22E-23	2.86E-19	Glutaredoxin-C13
NC_024466.2:162651852-162658240(+)	LOC103636279	- 12.4476	5.90E-23	3.18E-19	Putative HLH DNA-binding domain
NC_024459.2:81672408-81675503(-)	LOC100285480	- 5.93074	5.32E-07	0.000209	Actin-depolymerizing factor
NC_024461.2:191129385-191130502(-)	LOC100279082	- 6.89655	1.12E-22	4.57E-19	Uncharacterized protein
NC_024459.2:45286561-45290000(-)	asn3	- 6.82001	1.60E-20	5.91E-17	Asparagine synthetase
NC_024461.2:149339751-149371343(+)	LOC103650720	- 6.37456	4.99E-20	1.69E-16	Prpol, RNA-DNA hybrid ribonuclease activity [GO:0004523];
NC_024459.2:275610625-275611161(+)	umc1290	- 6.34933	2.41E-18	7.02E-15	Uncharacterized protein
NC_024463.2:65058208-65059377(+)	pco104428a	- 5.76077	2.76E-17	6.62E-14	Basic endochitinase 1
NC_024464.2:166878688-166882923(+)	LOC103630691	- 5.63793	3.85E-17	8.71E-14	Wall-associated kinase
NC_024461.2:58127334-58128164(-)	LOC109945000	- 5.19518	1.35E-15	2.89E-12	Uncharacterized protein
NC_024466.2:167594748-167596284(+)	LOC103636366	- 5.68049	1.29E-14	2.39E-11	NA
NC_024467.2:140318846-140322386(+)	asn4	- 6.69697	2.07E-12	2.47E-09	DUF506 family protein

NC_024464.2:144377375-144377968(-)	LOC103630251	- 5.64386	0.000153	0.021183	putative CRAL/TRIO domain containing, Sec14p-like phosphatidylinositol transfer family protein isoform X1
NC_024465.2:181798111-181799403(+)	kin1	- 4.91294	1.01E-13	1.52E-10	Extracellular ribonuclease LE
NC_024468.2:25661576-25662576(-)	LOC103640963	- 4.37758	8.98E-13	1.14E-09	Glutaredoxin-C13

Supplementary Table S10: Mapping percentage with reference B73 (version 4) genome

Genotype	Tissue	Stress treatment	Sample code	Mapping %
DMI 56	Root	N-	56_RN-	93.25%
DMI 56	Root	N+	56_RN+	88.10%
DMI 56	leaf	N-	56_SN-	97.03%
DMI 56	leaf	N+	56_SN+	96.83%
DMI 81	Root	N-	81_RN-	94.63%
DMI 81	Root	N+	81_RN+	95.91%
DMI 81	leaf	N-	81_SN-	95.55%
DMI 81	leaf	N+	81_SN+	97.55%

Letter N+, and N- represent sufficient nitrogen, and nitrogen-deficiency conditions, respectively.

Supplementary Table S11: List of shortlisted genes with their primer sequences for validation through qRT-PCR.

S.No.	Gene Name	Primer name	Primer sequence
1	Asparagine synthetase	XM_008659820.2_F	ACGTGTCTGTGTAGTGCCTC
		XM_008659820.2_R	GCTCGGACAGAAAATGCCTG

2	High affinity transporter 2.3	_XM_008658573.2_F	TACAAGACGGAGACGGGGAT
		XM_008658573.2_R	GCGGTGTTGAAACCCTTGTC
3	Nodulin-related protein 1_	NM_001165453.1_F	CAAGTCGTCGGAGGGGTTTC
		NM_001165453.1_R	CATCTTAAACAGCCCACCGC
4	Basic endochitinase	NM_001137022.1_F	ATACGGCCTGACCACGAAC
		NM_001137022.1_R	TCCGTAAGGCTTCTGGCTC
5	Amino acid permease 3	XM_008676200.2_F	CGTTCGCCCTCAGCCCTTT
		XM_008676200.2_R	TGTACATCTCGACGGGGAAGT
6	Glutathione transferase 31	NM_001279823.2_F	GTGGGCTGATCGTCTGTGTG
		NM_001279823.2_R	AGGCTTGGAGAAGGAGCCAT
7	Transcription factor MYB 36	XM_008671987.3_F	CTACGCAGGAGGTAGAGTGC
		XM_008671987.3_R	CTACTCTCAAACGTCGCGGA
8	Transcription factor AP2-EREBP	XM_008676258.2_F	TCTTTGACATGCCAGGGCTC
		XM_008676258.2_R	GTGCAGTCGACGTGGCTAT
9	Nitrate transport1:	NM_001279422.1_F	ATCTTCGGGGTTCATCCCCTT
		NM_001279422.1_R	GTGCACGAACACCACAGGTA