Table 1 Suppl. Plant material used in this study. S - inbred maize lines sensitive to low nitrogen, R - tolerant lines to low nitrogen.

Inbred Line	Sensitivity to low nitrogen	Inbred Line	Sensitivity to low nitrogen
B09	S	LH194	S
B73	S	LH214	S
PHG50	S	MBSJ	S
N-PH-P	R	MBST	R
PHG86	S	PHH93	S
F118	S	PHP02	S
G80	S	PHT69	S
GP156	S	PHV78	S
IBC2	S	PHW20	S
K64	S	Q381	S
LH23Ht	S	S-8326	S
LH181	S	2FACC	S
LH93	S	33-56	S
LH190	S	Dec-45	S
LH192	S	6M502	R

Table 2*A* Suppl. Primers used in this study.

Gene family	Gene locus	Gene name	Primer sequence (5'-3')	Usage	Reference
NRTs	*GRMZM2G086496*	*NRT1.1A/NPF6.4*	F: ATGTCCGTGTTCTGGCTCAT	qPCR	this study
			R: TGACGAAGAATCCCAGCGAC	qPCR	this study
	GRMZM2G161459	*NRT1.1B/NPF6.6*	F: TCCGTCCTGCCGGATAC	qPCR	this study
			R: AGCTCCGCGCCTAGTATCAT	qPCR	this study
	GRMZM2G161483	*NRT1.1D/ NPF6.5*	F: CAGCACCGCCATCGTCAG	qPCR	Garnett *et al.* 2013
			R: GCCAGCAGCCAATAGAACTTG	qPCR	Garnett *et al.* 2013
	GRMZM2G137421	*NRT1.2/ NPF4.10*	F: GGTGCTGCCCATCTTCTTGT	qPCR	Garnett *et al.* 2013
			R: ATGATGTGGTCGTAGACGGG	qPCR	Garnett *et al.* 2013
	GRMZM2G176253	*NRT1.3/NPF6.8*	F: CCAAGGTCGCACACACTGA	qPCR	this study
			R: GACCGTCCAGAAGAGGATGC	qPCR	this study
	GRMZM2G064091	*NRT1.4A/NPF6.2*	F: CCACAAGTGGCGTAGCAGG	qPCR	this study
			R: GGCGACCTCGTGATGAAGAA	qPCR	this study
	GRMZM2G044851	*NRT1.5A/NPF7.0/*NPF7.10	F: GGTTCAGTTTCTTGGACCGC	qPCR	this study
			R: GTAGAGGATGGTGCAGAGCC	qPCR	this study
	GRMZM2G061303	*NRT1.5B/ NPF7.12*	F: GCCAACAGCATCAGCAAGTG	qPCR	Garnett *et al.* 2013
			R: CGAGCGACAGGACCACCAG	qPCR	Garnett *et al.* 2013
	GRMZM2G010280	*NRT2.1*	F: AGTGGGGGTCCATGTTCTTC	qPCR	this study
			R: GAGGCTAGCGCTATGGAGTC	qPCR	this study
	GRMZM2G010251	*NRT2.2*	F: CGACGAGAAGAGCAAGGGACT	qPCR	Garnett *et al.* 2013
			R: AGGTGAACATGGATGATGGAT	qPCR	Garnett *et al.* 2013
	GRMZM2G163866	*NRT2.3*	F: AGGAAGGGCATCGAGAACAT	qPCR	Garnett *et al.* 2013
			R: CTTGCGCTGTGACGGCCTAC	qPCR	Garnett *et al.* 2013
	GRMZM2G455124	*NRT2.5*	F: GCATCGTCCCGTTCGTCTC	qPCR	Garnett *et al.* 2013
			R: CCGTCTCCGTCTTGTACTTGG	qPCR	Garnett *et al.* 2013
	GRMZM2G179294	*NRT3.1A*	F: GCATCCACGCCTCTCTCAAG	qPCR	Garnett *et al.* 2013
			R: TCAGCAACGACAGCCACTCAT	qPCR	Garnett *et al.* 2013
	GRMZM2G163494	*NRT3.1B*	F: CACCTCGTCACACACCACAG	qPCR	Garnett *et al.* 2013
			R: CCAGCAGCAGCGGCAAAG	qPCR	Garnett *et al.* 2013
			pF1: ACACCCTGCAATGGTCACAT	Promoter cloning	this study
			pR1:AGTTCACTGTCGGTCGGTTG	Promoter cloning	this study
			pF2: CGACATATATGATGCACACGTAACGTACG	Promoter cloning	this study
			pR2: TGGTGTGTGACGAGGTGAAC	Promoter cloning	this study

Table 2*B* Suppl. Primers used in this study. qPCR - quantitative PCR.

Gene family	Gene locus	Gene name	Primer sequence (5'-3')	Usage	References
NLPs	*GRMZM2G109509*	*ZmNLP1.1*	F: ACGCCAATCCCCGAAGTAAT	qPCR	this study
			R: ATGCAGGGTATCCACGTCTG	qPCR	this study
	GRMZM2G053298	*ZmNLP1.2*	F: TCGCTACCACTGATGACTGA	qPCR	this study
			R: CGGACAGTAGCTGCTCAAGG	qPCR	this study
	GRMZM2G048582	*ZmNLP1.3*	F: TGGAACGTTCTCACCTGTGG	qPCR	this study
			R: ACACACTCCAAGGCTTCTCG	qPCR	this study
	GRMZM2G105004	*ZmNLP2.1*	F: GCGCCCAGTCTCCTAGATG	qPCR	this study
			R: TCGAAGTCCATCCCGTAAGA	qPCR	this study
	GMRZM2G031398	*ZmNLP2.2*	F: AGGTACCGACGTGCTCCCCT	qPCR	Wang *et al.* 2018
			R: CAGTGCGGCGGTCTCCCATC	qPCR	Wang *et al.* 2018
	GRMZM2G375675	*ZmNLP3.1*	F: TGTGCAGAACGCACTTGTAG	qPCR	this study
			R: CCCAACACTGTTCTGTGCAAAT	qPCR	this study
	GRMZM2G475305	*ZmNLP3.2*	F: AGCTCCGGTTGATATGCCTG	qPCR	this study
			R: AAGCAACTAATGCTCCCGCT	qPCR	this study
	GRMZM2G176655	*ZmNLP3.3*	F: AAAGAGGACCTGCGGTTTCATG	qPCR	Wang *et al.*2018
			R: GATGAGACTGCCTGGACATGTT	qPCR	Wang *et al.*2018
	GRMZM2G042278	*ZmNLP3.4*	F: ACTGGCATGTGTCTGTCTCT	qPCR	this study
			R: GCGAATACCAGTGCTAGATCA	qPCR	this study
NPFs	*GRMZM2G085411*	*NPF2.1*	F :TCATAGGGAACGAGACGTGC	qPCR	this study
			R: CCATGTAGGTGTCGCTGAGG	qPCR	this study
	GRMZM2G361652	*NPF3.1*	F: GGAGCTCAAGTCGGTGATCC	qPCR	this study
			R: GATCTCGAACGTGGAGAGGC	qPCR	this study
	GRMZM2G127134	*NPF4.1*	F: CCGTCCATGAGATGTCCGTT	qPCR	this study
			R: CTGCTGGCGTGCACATAATC	qPCR	this study
	GRMZM2G138731	*NPF4.7*	F: AGGAGCTTTCCTCTCGGACT	qPCR	this study
			R: TGCAGTTACTTGGTTCGGCT	qPCR	this study
	GRMZM2G001764	*NPF5.2*	F: GAGAGCATGAAGAGCCTCGG	qPCR	this study
			R: TAGTACCAGTCGAGGTGCGA	qPCR	this study
	GRMZM2G001676	*NPF5.4*	F: ACTACGCCTTCTTCGCCATT	qPCR	this study
			R: ACTTCCCGCTTCTGCTTACTG	qPCR	this study
	GRMZM2G400602	*NPF5.9*	F: CTTCGCGCTCCTCATGTTCT	qPCR	this study
			R: CAAGAGTGCCGTCATGTTGTC	qPCR	this study
	GRMZM2G316889	*NPF5.13*	F: CGAAAGGCTCTTCAGCATGG	qPCR	this study
			R: ACGGAGGATGTCCTTGGTCT	qPCR	this study
	GRMZM2G375113	*NPF7.2*	F: TACGCTATCGTGGCAGCATT	qPCR	this study
			R: AAGTTGAGCGCTGAAATGGC	qPCR	this study
	GRMZM2G012242	*NPF7.3*	F: GCATTTGGGCTAACGGACTC	qPCR	this study
			R: GAGGAAGGCGACGGTCTTG	qPCR	this study
	GRMZM2G076313	*NPF7.4*	F: GACATGCTCTACGAGGTCGG	qPCR	this study
			R: GCATCTCCTCCATGTCCGAT	qPCR	this study
	GRMZM5G867390	*NPF8.8*	F: ATTCACTGGCAACGAGAGGG	qPCR	this study
			R: TTCTGATCCACCAGGTGTGC	qPCR	this study
	GRMZM2G079889	*NPF8.9*	F: CCCACTCTATGACCGCATCC	qPCR	this study
			R: AGAGCTGCAGATACCATCGC	qPCR	this study
	GRMZM2G158807	*NPF1.1*	F: AGCTTCTTGCTGGGATCGAG	qPCR	this study
			R: TTGAGGTGATGGTACACGCC	qPCR	this study
	GRMZM2G035790	*NPF1.4*	F: ACCTAGGACTCCCACGAACA	qPCR	this study
			R: TCGACCATATCGGAAGCACG	qPCR	this study
	GRMZM2G104542	*NPF2.2*	F: GTCAAGTACCACGGCTGGAA	qPCR	this study
			R: AACACCTGCGTCAGGTACAC	qPCR	this study
	GRMZM2G122251	*NPF2.3*	F: CGTGGACAAGATGGAGAACG	qPCR	this study
			R: TCGTTCCCGATGATGAAGGG	qPCR	this study
	GRMZM5G827496	*NPF3.2*	F: AGCTCGCACAACTACACCTT	qPCR	this study
			R: CGCGTTCGAGAAGATGGACA	qPCR	this study
	GRMZM2G322220	*NPF3.5*	F: CAGACGTTGGTTTCATGTGC	qPCR	this study
			R: GCATGCGGACGATGGATTTG	qPCR	this study

Table 2*C* Suppl. Primers used in this study. qPCR - quantitative PCR.

Gene family	Gene locus	Gene name	Primer sequence (5'-3')	Usage	References
NPFs	*GRMZM2G026523*	*NPF3.6*	F: CCCTTCATCCTAGCGAATGACT	qPCR	this study
			R: AGCGGAGTGAGGTTAGCAGT	qPCR	this study
	GRMZM2G026459	*NPF4.3*	F: CTGTCGGAGCTGTTCACCAA	qPCR	this study
			R: AGCACCGAGCTGAGGTAGAA	qPCR	this study
	GRMZM2G055545	*NPF4.5*	F: GTAGACTGGAAGGGACAGCC	qPCR	this study
			R: CATCACAACCAGGAAGTAGATGA	qPCR	this study
	GRMZM2G137421	*NPF4.10*	F: GCTACGTGGACTGGAGGAAC	qPCR	this study
			R: CATGGACCCCATCAGGTACG	qPCR	this study
	GRMZM2G043926	*NPF4.12*	F: GACGCTTCAAACCTGCTGAC	qPCR	this study
			R: TCATGTATCGGCCGACGAAG	qPCR	this study
	GRMZM2G472167	*NPF5.1*	F: TTTACCTGCTGGGGATGGTG	qPCR	this study
			R: CCCAGGGCCACGATGTAGAG	qPCR	this study
	GRMZM2G055834	*NPF5.5*	F: CTTCAACTGGTGGAACTGCG	qPCR	this study
			R: GAAGACGGCGAGCGAGG	qPCR	this study
	GRMZM2G143998	*NPF5.6*	F: CTTGGAGGTTGCTAGGGGC	qPCR	this study
			R: GGCTATGCCGAAGTAGCTCA	qPCR	this study
	GRMZM2G148800	*NPF5.10*	F: TGTCATCGGACTAGCAAGGG	qPCR	this study
			R: CCATCGCCATGACGAAAACC	qPCR	this study
	GRMZM2G085210	*NPF5.12*	F: GCCAGAGCTGGTTCTCAGATA	qPCR	this study
			R: TCTCGGCTCCAACGTTCTGT	qPCR	this study
	GRMZM2G378604	*NPF5.14*	F: GGACGGTGACGAGCAGG	qPCR	this study
			R: GCGATCTCCACCGCTATGAT	qPCR	this study
	GRMZM2G083176	*NPF6.1*	F: CTTCTCCATCCTGTCCGTGG	qPCR	this study
			R: CTGGATGAGCAGCCAGTAGG	qPCR	this study
	GRMZM2G476069	*NPF6.3*	F: CGTCTTCCTATCAGGCACCAG	qPCR	this study
			R: GTTTTCGGGTGGCAGCAACTA	qPCR	this study
	GRMZM2G112154	*NPF6.7*	F: CGAGCTCGGAGTCACCATTA	qPCR	this study
			R: GCTCATGGTCTTCATGCCCT	qPCR	this study
	AC208110.2_FGT011	*NPF7.5*	F: GCGTTATTCCTCGGCCTCTA	qPCR	this study
			R: AAGAAGGACATCCTGCGCTC	qPCR	this study
	GRMZM2G012434	*NPF7.7*	F: CCTCGCTACAGTTCTCGTGT	qPCR	this study
			R: GATTCGCTGAGGAAACCTGC	qPCR	this study
	GRMZM2G012306	*NPF7.8*	F: CATCGTCATGGACGGAGACA	qPCR	this study
			R: CCATCCCCTGCTGGATGAAG	qPCR	this study
	GRMZM2G156794	*NPF7.9*	F: GGCTGAGGGTAGCTGGACC	qPCR	this study
			R: ATGCTGCTTCTCCTGGACCAC	qPCR	this study
	GRMZM2G061303	*NPF7.12*	F: GTCATGGCTCTTGCTGGTGA	qPCR	this study
			R: CCGAACGCGATCATGTAGGT	qPCR	this study
	GRMZM2G020484	*NPF8.1*	F: GTGTACTCGCAGATGAGCA	qPCR	this study
			R: AGACGATGACGCTGATGGTG	qPCR	this study
	GRMZM2G101576	*NPF8.12*	F: GAGTGGGAACTCCAACGAGG	qPCR	this study
			R: GGACTTTCTTCCCTGTGCGA	qPCR	this study
	GRMZM2G041631	*NPF8.13*	F: CTGGCACCGTGATTGTTTGG	qPCR	this study
			R: CACCCTGGAGCCAGCTAAAA	qPCR	this study
	GRMZM2G015767	*NPF8.15*	F: GATTGGCAGCTGCTACCTCA	qPCR	this study
			R: GCTGTTGTCAGGTGAGTCGT	qPCR	this study

Table 2*D* Suppl. Primers used in this study. qPCR - quantitative PCR.

Gene family	Gene locus	Gene name	Primer sequence (5'-3')	Usage	References
AMT	*GRMZM2G118950*	*AMT1A*	F: AGATCGTCCAGATCGTGGTG	qPCR	this study
			R: TCGCCAGGGTCCTCGTAA	qPCR	this study
	GRMZM2G028736	*AMT1B*	F: AGGGAGTACGTGGAGCAGAT	qPCR	this study
			R: GAGCAGCCCCATCTTGTTGA	qPCR	this study
	GRMZM2G175140	*AMT1C*	F: GCTTCATCGGCAAGCAGTTC	qPCR	this study
			R: AAGGCCCACTGGTAGAGGAA	qPCR	this study
	GRMZM2G473697	*AMT2B*	F: GACGCTCCTCTTCTTCCAGTT	qPCR	this study
			R: GGCCTTGAAAAGGAACCCGT	qPCR	this study
	GRMZM2G043193	*AMT2C*	F: ATGCAGAGGATCGACGACAC	qPCR	this study
			R: CAGAGGACAGGCTCAGCAAA	qPCR	this study
	GRMZM2G080045	*AMT2D*	F: AGAAGAAGTGGGCGGTGAAC	qPCR	this study
			R: GACCAGGTAGCCCTGGGAG	qPCR	this study
	GMRZM2G335218	*AMT2E*	F: CATACCGGACTGGCTGAACA	qPCR	this study
			R: GGCCCACTTCTTCTTCACGA	qPCR	this study
	GMRZM2G338809	*AMT2A*	F: TGAAGAAGAAGTGGGCCGTG	qPCR	this study
			R: ATGTTGTAGGCCCAGGTCAC	qPCR	this study
Nitrogen metabolism	*GRMZM2G568636*	*Nitrate reductase*	F: GGCTACAGCTCCGACAACTC	qPCR	this study
			R: GAGGCGGCAGTGGATCTTTT	qPCR	this study
	GRMZM2G079381	*Ferredoxin-nitrite reductase 2*	F: GTGAAGCTGGAGAAGGAGCC	qPCR	this study
			R: CGATCTGCTCCATGGGGACC	qPCR	this study
	GRMZM2G098290	*Glutamine synthetase*	F: AACAAGTGCCATGGTTTGGC	qPCR	this study
			R: CGGCACAGTAGTATGGACCC	qPCR	this study
	GRMZM2G046601	*Glutamine synthetase 3*	F: TCGACCTGAGTGACTGCAC	qPCR	this study
			R: CAGTCACACATCACCCTTGCT	qPCR	this study
	GRMZM2G036609	*Ferredoxin-dependent glutamate synthase*	F: GACGGTGGATTCAGGAGTGG	qPCR	this study
			R: ACCAGGAAACCTTGCACGAA	qPCR	this study
	GRMZM2G105604	*Siroheme uroporphyrinogen methyltransferase 1*	F: GTCACCCTTCTGGGTTGAGT	qPCR	this study
			R: CGAACCTGTGCTCCCATATCT	qPCR	this study
	GRMZM2G000739	*Urophorphyrin methylase 1*	F: AAATGCAGCCGATCCTGACA	qPCR	this study
			R: ACGCAAACACCATTCGTTGT	qPCR	this study
	GRMZM2G004590	*Shikimate kinase 1*	F: ATGCATCGGTTGGTTGTTGC	qPCR	this study
			R: ATGCAAGAGTGGTCGAGACG	qPCR	this study
	GRMZM2G365961	*Arogenate dehydrogenase isoform 2*	F: AGCTTCGACCTGTACAACGG	qPCR	this study
			R: TACTTGCGCACGTTGGAGG	qPCR	this study
	GRMZM5G811593	*Peptide transporter PTR2*	F: CTCGGAAGCAGAGAACTGGG	qPCR	this study
			R: GATCCAGGTGGACACAGTCG	qPCR	this study

Table 2*E* Suppl. Primers used in this study. qPCR - quantitative PCR

Gene family	Gene locus	Gene name	Primer sequence (5'-3')	Usage	References
Carbon metabolism	*GRMZM2G177077*	*Glucose-6-phosphate-1-dehydrogenase* (*ZmGPDH*)	F: GCGGTCTGAAGCAGTACCTT	qPCR	this study
			R: AGAAGCGCAGGACAGACAAA	qPCR	this study
	GRMZM2G076075	*Glucose-6-phosphate isomerase 1* (*ZmGPI*)	F: TCATCAGCCTGGTGTTGAGG	qPCR	this study
			R: AAGAACACAGGTCAGAAGTTCCA	qPCR	this study
	GRMZM2G180720	*Glucose-6-phosphate/phosphate-translocator 1* (*ZmGPT*)	F: TGGTGGGCGCTTAATGTGAT	qPCR	this study
			R: ATCATAGCAGAGCCACAGGC	qPCR	this study
	GRMZM2G009223	*Glucose-6-phosphate/phosphate translocator 2*(*ZmGPT*)	F: TGGGCGCTGAACGTTATCTT	qPCR	this study
			R: CGCCTTCCAGAAATCGAGGT	qPCR	this study
Others	*GRMZM2G049852*	*Protein DETOXIFICATION 49*	F: CAAGGACGTTACTGGGTGGA	qPCR	this study
			R: GACGTGGTCTGGATGAGGAC	qPCR	this study
	GRMZM2G058760	*Ferredoxin--NADP reductase root isozyme 1* (*ZmFENR*)	F: AGGATCCAAACGCAACCCAT	qPCR	this study
			R: CTGTCTGAATTGGCAACGCC	qPCR	this study
	GRMZM2G181081	*CBL-interacting kinase*	F: TGCAATGGCTGATCTGTGGT	qPCR	this study
			R: CAACAACCTCTTGGCAGGGA	qPCR	this study
	GRMZM2G001205	*C2H2-type zinc finger family protein*	F: TTTGCAGTTCAGGAGAGCGA	qPCR	this study
			R: GGCAGGCCGACAGTGG	qPCR	this study
	GRMZM2G168898	*Hemoglobin 2*	F: GTCACCGTCTTCGTTATGGC	qPCR	this study
			R: GTCTTGACGACCTCGAAATGC	qPCR	this study
	GRMZM2G126190	*Actin*	F: GCATCCATGAGACCACCTACAAC	internal control	Chen *et al.* 2018
			R: GATGGACCCTCCTATCCAGACAC		Chen *et al.* 2018

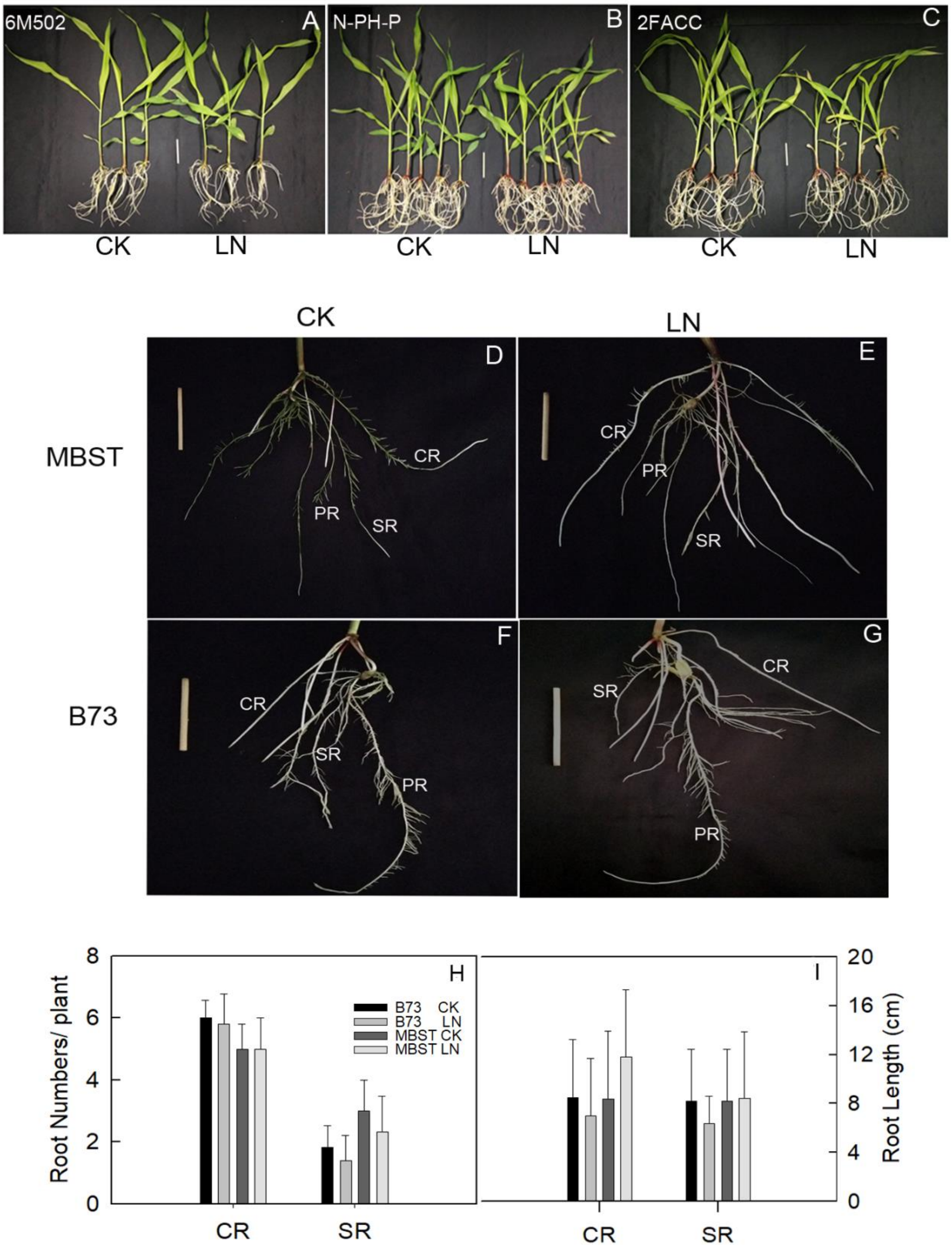

Fig. 1 Suppl. The phenotype of maize inbred lines under normal (CK) and low nitrogen conditions (LN). 6M502 (*A*) and N-PH-P (*B*) are LN-tolerant lines, 2FACC(C) is an LN-sensitive line. *D* to *G* - The root phenotype of B73 and MBST; PR - primary root, SR - seminal root, CR - crown root; the *bar* is 5 cm). *H* - The number of CR and SR in B73 and MBST. *I* - Root lengths of B73 and MBST. For CK: 6 mM nitrate + 1 mM ammonium for LN: 0.5 mM nitrate + 1 mM ammonium. Plants were harvested after 10 d LN treatment of 9-d-old seedlings.

```
-3338 B73     ACACCCTGCAATGGTCACATAGAACATATCCAAACACAGGAATAACCCAAACTAAAGTCA
      MBST    ------------------------------------------------------------

-3278 B73     GAGTGAACTTAGCTCTTTTGGGTGGCTTCTAGGTTCTAGCTTTGACACTTCTACTTCTAG
      MBST    ------------------------------------------------------------

-3218 B73    TGACCTTGTCCTACCACTTGAGCTTGATCTTGAGCCTTATGACTTGAACCATAAATCATA
      MBST   -------------------------------------------------------C----

-3158 B73     AGAATTACCTCAGTGGTACCAAGTCACGTCCTTAGGTAGTGATCTTCCATGCACCATAAC
      MBST    ----------------------------------------------------------G-

-3098 B73     TTTTCTCAACTCGATCAACCTTGACTTTATAAGTCTTCTTCTTCACCCTTGGCCTTGACC
      MBST    ------------------------------------------------------------

-3038 B73     TTCTCCCTTGCACTCGGTACCTCGAAGTTATTCTTGCCTCCATCCTCGCCTTGACCACTT
      MBST    ------------------------------------------------------------

-2978 B73-    GTCTCCAAGTTATGCACATCGATTCTCACATAAGCAATGTCCATCCTTCACTTAGCTTGT
      MBST    ------------------------------------------------------------

-2918 B73     GATGTTCATTATCCATAGGTATCTCAACCTTTGGACCATTAGACTTGATCACTTGTGTTG
      MBST    ------------------------------------------------------------

-2858 B73     GGCCTTATGAGCTTTGCACTAAGCACATGTTCGACACTTACCACACACATCGGTCCTTTA
      MBST    --------------------------------C---------------------------

-2798 B73    ATTGGGTTGTCATCCAAATCAACAAAACCCACAAGGGAGCTTTCAAAGACCCTGACAGGT
      MBST   --------------------------------  --------------------------

-2738 B73     GAGTCTAAGGGCTCGACCACGGTGCCCAAGGGCTTGAACCACATGTCAACAAGTTGCTTG
      MBST    -----C------------------------------------------------------

-2678 B73     ACTCGTCTAGAGGAGATAAGGACACGATGTCTTATCAAGGTCGATAGATTAGATTGGTAT
      MBST    ------------------------------------------------------------

-2618 B73     CGATGTAAATATGGTAAAGCCAGATGATAAGGGTAATCTACATGTAAATATAGATATAAG
      MBST    ------------------------------------------------------------

-2558 B73     AGTCCTTATAACTAGGGACTGACTTGGCTAGGATAATCTG----TATCCTTATCTGGCGA
      MBST    ----------------------------------------TATA----------------

-2502 B73     GAGACTAGGTAACTTTTGTGTAAGTATTCCCTTCTTTGGATTATTAAAGAATGAATGAAA
      MBST    GAGACTAGGTAACTTTTGTGTAAGTATTCCCTTCTTTGGATTATTAAAGAATGAATGAGA

-2442 B73     CGCTCTAAAAGGGCATATCATCTTATTATATTGAATAGACAATAGACATTATGACACAGA
      MBST    ------------------------------------------------------------

-2382 B73     AAATGTAGGGTATTATCTCCCAACATTGTTGAGAGTATCAACAAATCTAAACCTTCCAAG
      MBST    ------------------------------------------------------------

-2322 B73     ACTATTGTATATTTATCTTCATTTCTGGATCTCACGATCACTCGGTAGTCGGTAGTCTTC
      MBST    ACTATTGTATATTTATCTTCATTTCTGGATCTCACGATCACTCGGTAGTCGGTAGTCTTC

-2262 B73     AGTGTGGAGCCAACCGACCGACAGTGAACT   -2232
      MBST    ------------------------------
```

Fig. 2 Suppl. The promoter sequence alignment of *ZmNRT3.1B* from two maize inbred lines. Single nucleotide polymorphisms or small insertion/deletions are shown in *red*. Other regions without sequence differences are not shown.

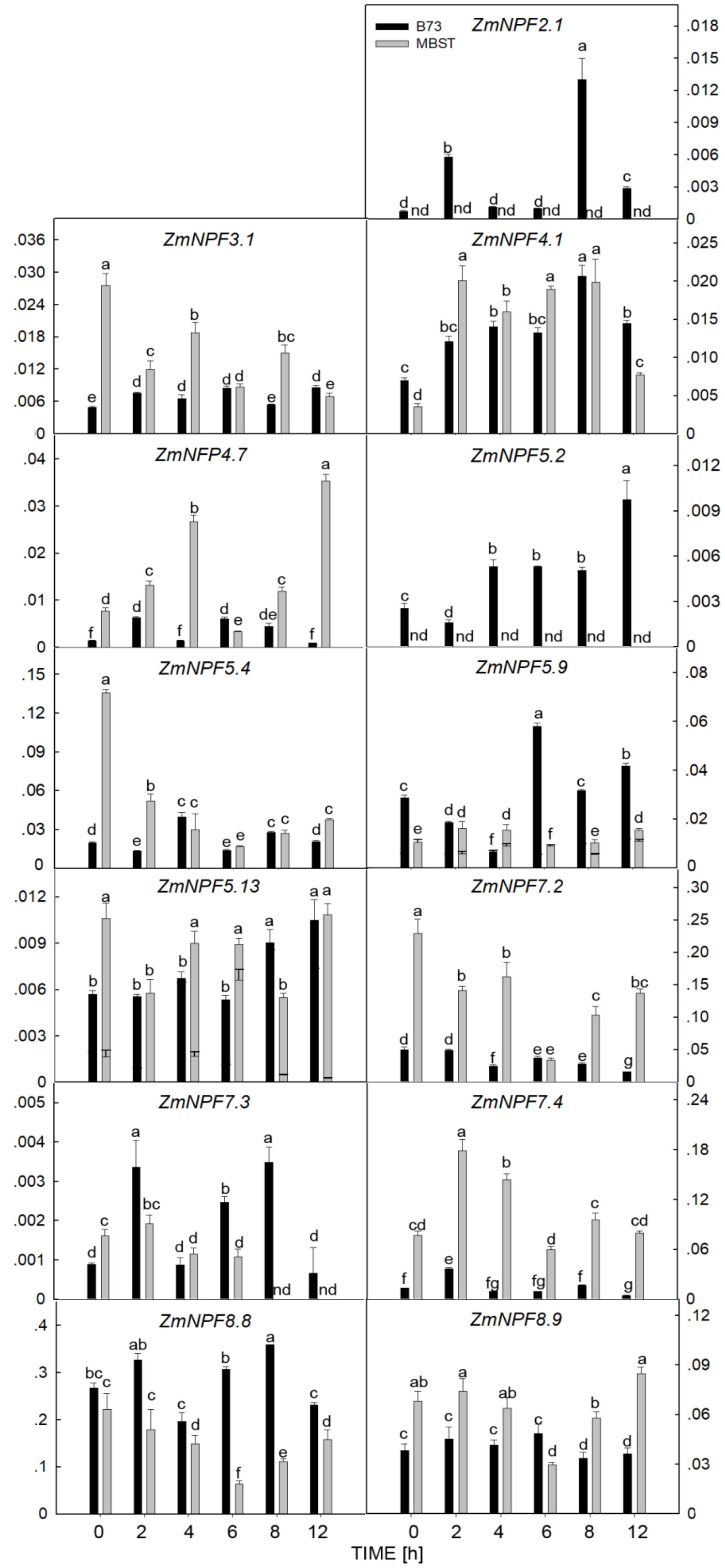

Fig. 3 Suppl. Nitrate-depended expression patterns of *ZmNPFs.* Genes were detected after low-nitrogen (LN) treatment for 0, 2, 4, 6, 8, or 12 h. All gene expressions were normalized to *actin* (*GRMZM2G126190*) expression. Maize plants were pre-cultured hydroponically in 6 mM NO_3^- + 1 mM NH_4^+ for 9 d before transfer to a 0.5 mM NO_3^- + 1 mM NH_4^+ solution for LN treatment. Means ± SDs of at least two biological and three technical replicates. Gene expressions are shown in *black* for B73 and in *gray* for MBS. Different letters indicate significant differences at $P < 0.05$ (Student's *t*-test).

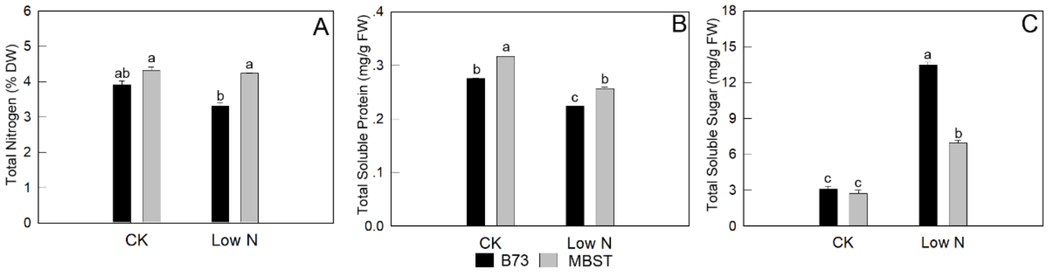

Fig. 4 Suppl. The content of total nitrogen (*A*), soluble proteins (*B*), and soluble sugars (*C*) in B73 and MBST maize plants. The plants were pre-cultured hydroponically in 6 mM NO_3^- + 1 mM NH_4^+ for 9 d before transfer to a 0.5 mM NO_3^- + 1 mM NH_4^+ solution for low N treatment. Means ± SDs, $n \geq 3$, different letters indicate significant differences at $P < 0.05$ (Student's *t*-test).