Table S1. GmNTLs identified and characterized in this study.

Name	Previous names[a]	Previous names[b]	Glyma1.1 ID	Glycine max Wm82.a2.v1	Domain start	Domain end	Length (a.a)	PFAM domain	Domain name	Predicted by TMHMM Number of predicted TMHs	Predicted by Tmpred Number of predicted TMHs	Number of Alternative Transcripts	Transcript Lack TMH
GmNTL1	GmNAC012	GmNAC027	Glyma02g38710.1	Glyma.02G222300.1	21	147	589	PF02365	NAM	1	1	-	-
GmNTL2	GmNAC013		Glyma02g40750.1	Glyma.02G240500.1	5	132	643	PF02365	NAM	2	2	-	-
GmNTL3	GmNAC021	GmNAC025	Glyma04g40450.1	Glyma.04G226700.1	22	148	603	PF02365	NAM	1	1	-	-
GmNTL4	GmNAC036	GmNAC26	Glyma06g14290.1	Glyma.06G138100.1	22	148	598	PF02365	NAM	1	1	-	-
GmNTL5			Glyma07g05351.1	Glyma.07G047900.1	12	141	497	PF02365	NAM	1	1	-	-
GmNTL6			Glyma10g197600.1	Glyma.10G197600.1	4	111	448	PF02365	NAM	1	1	3	Glyma.10G197600.2; Glyma.10G197600.3
GmNTL7	GmNAC074		Glyma10g36360.1	Glyma.10G219600.1	20	146	560	PF02365	NAM	1	1	-	-
GmNTL8			Glyma11g33210.1	Glyma.11G212400.1	8	135	672	PF02365	NAM	0	2	-	-
GmNTL9			Glyma12g186900.1	Glyma.12G186900.1	17	144	493	PF02365	NAM	1	1	-	-
GmNTL10	GmNAC103		Glyma13g39090.2	Glyma.13G314600.1	18	144	371	PF02365	NAM	1	1	-	-
GmNTL11	GmNAC110		Glyma14g36840.1	Glyma.14G189300.1	21	147	590	PF02365	NAM	1	1	2	-
GmNTL12	GmNAC111		Glyma14g39080.1	Glyma.14G210000.1	5	132	644	PF02365	NAM	1	1	-	-
GmNTL13	GmNAC136		Glyma18g05020.1	Glyma.18G043900.1	6	133	678	PF02365	NAM	2	2	-	-
GmNTL14	GmNAC149		Glyma20g31210.4/ Glyma20g31210.1	Glyma.20G172100.1/ Glyma.20G172100.2	20	146	549	PF02365	NAM	1	1	4	Glyma.20G172100.4
GmNTL15	GmNAC151		Glyma20g33390.1	Glyma.20G192300.1	6	131	604	PF02365	NAM	1	1	-	-

[a] According to Le et al. 2011 (Ref. 30)

[b] According to Tran et al. 2004 (Ref. 53)

Table S2. Conserved motifs in NTLs.

	Logo	E-value	Sites	Width
1.		6.0e-1481	50	41
2.		6.6e-1743	50	50
3.		7.6e-1319	50	41
4.		3.4e-338	50	14
5.		6.0e-279	22	21
6.		2.5e-170	13	27
7.		3.6e-168	11	32
8.		1.1e-141	11	21
9.		2.4e-138	23	21
10.		8.2e-126	25	15
11.		2.0e-111	13	15
12.		1.9e-137	8	41
13.		2.2e-136	10	28
14.		3.5e-110	21	20
15.		5.9e-098	13	21
16.		1.8e-097	9	23
17.		7.9e-153	8	50
18.		8.8e-099	7	50
19.		4.3e-092	7	29
20.		3.5e-086	8	22

Table S3 Flanking sequences of GmNTL within 140 Kb

Gene	Locus	Chr	Start	Stop	Function
	Glyma.02G221300	Chr02	40900121	40918108	DNA mismatch repair protein MutS, type 2
	Glyma.02G221700	Chr02	40927646	40928737	serine protease inhibitor, Kazal-type family protein
	Glyma.02G221900	Chr02	40932876	40935807	Concanavalin A-like lectin protein kinase family protein
	Glyma.02G222000	Chr02	40953440	40959908	nodulin MtN21 /EamA-like transporter family protein
	Glyma.02G222100	Chr02	40962524	40968028	nodulin MtN21 /EamA-like transporter family protein
	Glyma.02G222200	Chr02	40976865	40982917	Calcium-binding endonuclease/exonuclease/phosphatase
	Glyma.02G222200	Chr02	40976865	40982917	Calcium-binding endonuclease/exonuclease/phosphatase
GmNTL1	Glyma.02G222300	Chr02	40991314	40995436	NAC transcription factor-like 9
	Glyma.02G222400	Chr02	40998557	41001678	Aldolase superfamily protein
	Glyma.02G222600	Chr02	41020144	41023345	Heavy metal transport/detoxification superfamily protein
	Glyma.02G222700	Chr02	41029187	41031367	Heavy metal transport/detoxification superfamily protein
	Glyma.02G222800	Chr02	41032232	41033043	Unknown
	Glyma.02G240000	Chr02	42859034	42866507	polyamine oxidase 4
	Glyma.02G240100	Chr02	42866887	42869864	AMP-dependent synthetase and ligase family protein
	Glyma.02G240200	Chr02	42872399	42878160	PHYTOENE SYNTHASE
	Glyma.02G240300	Chr02	42883817	42887882	SET domain group 40
	Glyma.02G240400	Chr02	42892680	42898279	sucrose synthase 6
GmNTL2	Glyma.02G240500	Chr02	42900252	42904927	NAC domain containing protein 28
	Glyma.02G240600	Chr02	42908973	42910047	glutathione S-transferase TAU 19
	Glyma.02G240700	Chr02	42910921	42918001	autophagy protein Apg5 family
	Glyma.02G240800	Chr02	42920379	42922319	Unknown
	Glyma.02G240900	Chr02	42923065	42925453	expansin A13
	Glyma.02G241000	Chr02	42928962	42932788	Homeodomain-like superfamily protein
	Glyma.04G226400	Chr04	49605506	49609864	SPFH/Band 7/PHB domain-containing membrane-associated protein family
	Glyma.04G226500	Chr04	49611490	49612657	Ribosomal protein L6 family
	Glyma.04G226600	Chr04	49617121	49622404	IAA-leucine-resistant (ILR1)-like 3
GmNTL3	Glyma.04G226700	Chr04	49623094	49626512	NAC 014
	Glyma.04G226800	Chr04	49639118	49643847	Calcium-binding endonuclease/exonuclease/phosphatase
	Glyma.04G226900	Chr04	49655093	49656271	Ribosomal protein L6 family
	Glyma.04G227000	Chr04	49667985	49672223	Heavy metal transport/detoxification superfamily protein
	Glyma.04G227100	Chr04	49679446	49684761	Unknown
	Glyma.04G227200	Chr04	49687315	49689108	Peroxidase superfamily protein
	Glyma.04G227300	Chr04	49689541	49691300	nascent polypeptide-associated complex subunit alpha-like protein 2
	Glyma.04G227400	Chr04	49692001	49694593	nascent polypeptide-associated complex subunit alpha-like protein 2
	Glyma.04G227500	Chr04	49695529	49696967	Unknown
	Glyma.06G137600	Chr06	11250524	11251867	Unknown
	Glyma.06G137700	Chr06	11252976	11255680	nascent polypeptide-associated complex subunit alpha-like protein 2
	Glyma.06G137800	Chr06	11256521	11258533	nascent polypeptide-associated complex subunit alpha-like protein 2
	Glyma.06G137900	Chr06	11258699	11260675	Peroxidase superfamily protein
	Glyma.06G138000	Chr06	11261314	11266797	Unknown
GmNTL4	Glyma.06G138100	Chr06	11272268	11275624	NAC transcription factor-like 9
	Glyma.06G138200	Chr06	11287872	11292405	Calcium-binding endonuclease/exonuclease/phosphatase
	Glyma.06G138300	Chr06	11295254	11301172	nodulin MtN21 /EamA-like transporter family protein
	Glyma.06G138400	Chr06	11302499	11303644	Ribosomal protein L6 family
	Glyma.06G138500	Chr06	11306829	11310909	SPFH/Band 7/PHB domain-containing membrane-associated protein family
	Glyma.06G138600	Chr06	11318029	11319071	Ribosomal protein L6 family
	Glyma.07G047400	Chr07	3977971	3979901	Protein of unknown function (DUF1295)
	Glyma.07G047500	Chr07	3985133	3990296	purple acid phosphatase 29
	Glyma.07G047600	Chr07	3991009	3993352	photosystem I light harvesting complex gene 2
	Glyma.07G047700	Chr07	3995501	3999612	Ribosomal RNA processing Brix domain protein
	Glyma.07G047800	Chr07	4004367	4008503	Calcium-binding endonuclease/exonuclease/phosphatase
GmNTL5	Glyma.07G047900	Chr07	4016419	4019905	NAC domain containing protein 62

	Glyma.07G048000	Chr07	4026951	4029750	NAC transcription factor-like 9
	Glyma.07G048100	Chr07	4042093	4044551	NAC transcription factor-like 9
	Glyma.07G048200	Chr07	4061864	4064513	AP2/B3-like transcriptional factor family protein
	Glyma.07G048300	Chr07	4086892	4090342	pyrophosphorylase 1
	Glyma.07G048400	Chr07	4096301	4102195	Protein kinase superfamily protein
	Glyma.10G067900	Chr10	6697335	6700998	IQ calmodulin-binding motif family protein
	Glyma.10G068900	Chr10	6788893	6792760	vascular plant one zinc finger protein
	Glyma.10G197300	Chr10	42857995	42860990	SKU5 similar 3
	Glyma.10G197400	Chr10	42863093	42868252	RAB GTPase homolog C2A
	Glyma.10G197500	Chr10	42882331	42888608	NAC domain containing protein 52
GmNTL6	Glyma.10G197600	Chr10	42899234	42904478	NAC domain containing protein 52
	Glyma.10G197700	Chr10	42905294	42911464	lactate/malate dehydrogenase family protein
	Glyma.10G197800	Chr10	42914376	42918603	OPC-8:0 CoA ligase1
	Glyma.10G198000	Chr10	42923799	42930121	Galactose oxidase/kelch repeat superfamily protein
	Glyma.10G198100	Chr10	42932760	42934470	Peroxidase superfamily protein
	Glyma.10G219100	Chr10	45096674	45100122	Laccase/Diphenol oxidase family protein
	Glyma.10G219200	Chr10	45102350	45106419	laccase 14
	Glyma.10G219300	Chr10	45108514	45111450	Oxidoreductase family protein
	Glyma.10G219400	Chr10	45112587	45115127	cofactor assembly, complex C (B6F)
	Glyma.10G219500	Chr10	45115436	45122237	cleavage stimulating factor 64
GmNTL7	Glyma.10G219600	Chr10	45126440	45130601	NAC domain containing protein 17
	Glyma.10G219700	Chr10	45134028	45138735	sphingoid base hydroxylase 2
	Glyma.10G219800	Chr10	45139887	45141455	Peroxidase superfamily protein
	Glyma.10G219900	Chr10	45144422	45147283	Subunits of heterodimeric actin filament capping protein Capz superfamily
	Glyma.10G220000	Chr10	45149408	45157038	Pseudouridine synthase family protein
	Glyma.10G220100	Chr10	45160713	45166890	RAB GTPase homolog G3A
	Glyma.11G211900	Chr11	30435707	30438967	vascular plant one zinc finger protein
	Glyma.11G212000	Chr11	30452236	30454838	cytochrome P450, family 94, subfamily C, polypeptide 1
	Glyma.11G212100	Chr11	30470250	30473891	IQ calmodulin-binding motif family protein
	Glyma.11G212200	Chr11	30478174	30480634	Unknown
	Glyma.11G212300	Chr11	30507015	30517598	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain
GmNTL8	Glyma.11G212400	Chr11	30521509	30526668	NAC domain containing protein 28
	Glyma.11G212500	Chr11	30536793	30543127	Unknown
	Glyma.11G212600	Chr11	30544163	30545905	Unknown
	Glyma.11G212700	Chr11	30547238	30552421	sucrose synthase 6
	Glyma.11G212800	Chr11	30571422	30573995	LRR and NB-ARC domains-containing disease resistance protein
	Glyma.11G212900	Chr11	30575283	30577501	glutathione S-transferase F11
	Glyma.11G213000	Chr11	30593602	30596478	glutamate decarboxylase
	Glyma.11G213100	Chr11	30598525	30601364	Concanavalin A-like lectin protein kinase family protein
	Glyma.12G186500	Chr12	34725542	34726776	Uncharacterised protein family (UPF0497)
	Glyma.12G186600	Chr12	34727876	34733210	decapping 1
	Glyma.12G186700	Chr12	34736246	34740450	Leucine-rich repeat (LRR) family protein
	Glyma.12G186800	Chr12	34749304	34751194	F-box family protein
GmNTL9	Glyma.12G186900	Chr12	34753427	34763019	NTM1-like 8
	Glyma.12G187000	Chr12	34770351	34771629	Unknown
	Glyma.12G187100	Chr12	34784828	34786462	Unknown
	Glyma.12G187200	Chr12	34824285	34825948	Unknown
	Glyma.12G187400	Chr12	34850968	34852441	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
	Glyma.13G152400	Chr13	26701683	26706699	Ankyrin repeat family protein
	Glyma.13G152500	Chr13	26712715	26718689	UDP-glucose pyrophosphorylase 2
	Glyma.13G314100	Chr13	40937254	40938477	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
	Glyma.13G314200	Chr13	40949752	40951896	Unknown
	Glyma.13G314300	Chr13	40964940	40965184	Unknown
	Glyma.13G314400	Chr13	40977943	40978908	Unknown

	Glyma.13G314500	Chr13	40987411	40991169	Unknown
GmNTL10	Glyma.13G314600	Chr13	40993081	40996703	NTM1-like 8
	Glyma.13G314700	Chr13	40998351	40999331	F-box family protein
	Glyma.13G314800	Chr13	41004969	41008993	Leucine-rich repeat (LRR) family protein
	Glyma.13G314900	Chr13	41018298	41024037	decapping 1
	Glyma.13G315000	Chr13	41028031	41029272	Uncharacterised protein family (UPF0497)
	Glyma.14G188800	Chr14	45344566	45346078	DNA mismatch repair protein MutS, type 2
	Glyma.14G188900	Chr14	45348073	45353965	DNA mismatch repair protein MutS, type 2
	Glyma.14G189000	Chr14	45364719	45365712	serine protease inhibitor, Kazal-type family protein
	Glyma.14G189100	Chr14	45369316	45371858	Concanavalin A-like lectin protein kinase family protein
	Glyma.14G189200	Chr14	45393981	45398605	nodulin MtN21 /EamA-like transporter family protein
GmNTL11	Glyma.14G189300	Chr14	45407343	45411346	NAC transcription factor-like 9
	Glyma.14G189400	Chr14	45416092	45419126	Aldolase superfamily protein
	Glyma.14G189500	Chr14	45437919	45441053	Heavy metal transport/detoxification superfamily protein
	Glyma.14G189600	Chr14	45450173	45452630	Heavy metal transport/detoxification superfamily protein
	Glyma.14G189700	Chr14	45453681	45453860	Unknown
	Glyma.14G209400	Chr14	47475271	47483030	polyamine oxidase 4
	Glyma.14G209500	Chr14	47475331	47475528	Unknown
	Glyma.14G209600	Chr14	47485565	47488948	AMP-dependent synthetase and ligase family protein
	Glyma.14G209700	Chr14	47496019	47500526	PHYTOENE SYNTHASE
	Glyma.14G209800	Chr14	47508042	47511868	SET domain group 40
	Glyma.14G209900	Chr14	47515899	47521687	sucrose synthase 6
GmNTL12	Glyma.14G210000	Chr14	47524327	47529700	NAC domain containing protein 28
	Glyma.14G210100	Chr14	47533732	47535083	glutathione S-transferase TAU 19
	Glyma.14G210200	Chr14	47535839	47545840	autophagy protein Apg5 family
	Glyma.14G210300	Chr14	47537416	47537595	Unknown
	Glyma.14G210400	Chr14	47547994	47549987	Unknown
	Glyma.14G210500	Chr14	47550799	47553102	expansin A13
	Glyma.14G210600	Chr14	47557927	47561596	Homeodomain-like superfamily protein
	Glyma.18G043400	Chr18	3705531	3706973	Pentatricopeptide repeat (PPR) superfamily protein
	Glyma.18G043500	Chr18	3711823	3713856	Concanavalin A-like lectin protein kinase family protein
	Glyma.18G043600	Chr18	3716146	3727012	glutamate decarboxylase 4
	Glyma.18G043700	Chr18	3734876	3739321	glutathione S-transferase F11
	Glyma.18G043800	Chr18	3752591	3759239	Unknown
GmNTL13	Glyma.18G043900	Chr18	3767587	3772179	NAC domain containing protein 28
	Glyma.18G044000	Chr18	3777421	3789101	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain
	Glyma.18G044100	Chr18	3809348	3812858	expansin A13
	Glyma.18G044200	Chr18	3813589	3817289	Homeodomain-like superfamily protein
	Glyma.18G044300	Chr18	3820564	3825063	Ankyrin repeat family protein
	Glyma.18G044400	Chr18	3836270	3837813	UDP-GLUCOSE PYROPHOSPHORYLASE 1
	Glyma.20G171600	Chr20	40934103	40939326	RAB GTPase homolog G3A
	Glyma.20G171700	Chr20	40941339	40957772	Pseudouridine synthase family protein
	Glyma.20G171800	Chr20	40959554	40962492	Subunits of heterodimeric actin filament capping protein Capz superfamily
	Glyma.20G171900	Chr20	40967953	40969568	Peroxidase superfamily protein
	Glyma.20G172000	Chr20	40972828	40977774	sphingoid base hydroxylase 1
GmNTL14	Glyma.20G172100	Chr20	40983077	40987397	NAC domain containing protein 17
	Glyma.20G172200	Chr20	40991514	40998998	cleavage stimulating factor 64
	Glyma.20G172300	Chr20	41000197	41002424	cofactor assembly, complex C (B6F)
	Glyma.20G172400	Chr20	41008497	41011265	Oxidoreductase family protein
	Glyma.20G172500	Chr20	41013531	41015300	cytochrome P450, family 78, subfamily A, polypeptide 7
	Glyma.20G172600	Chr20	41019363	41023633	Laccase/Diphenol oxidase family protein
	Glyma.20G172700	Chr20	41025526	41028921	Laccase/Diphenol oxidase family protein
	Glyma.20G191800	Chr20	43061155	43062135	Peroxidase superfamily protein
	Glyma.20G191900	Chr20	43064269	43071245	Galactose oxidase/kelch repeat superfamily protein
	Glyma.20G192100	Chr20	43072402	43078719	OPC-8:0 CoA ligase1
	Glyma.20G192200	Chr20	43084747	43090392	lactate/malate dehydrogenase family protein
GmNTL15	Glyma.20G192300	Chr20	43096801	43100393	NAC domain containing protein 50

	Glyma.20G192500	Chr20	43138131	43145708	NAC domain containing protein 50
	Glyma.20G192600	Chr20	43158672	43164035	RAB GTPase homolog C2A
	Glyma.20G192700	Chr20	43171939	43184282	cycloartenol synthase 1
	Glyma.20G192800	Chr20	43186683	43190491	Cupredoxin superfamily protein
	Glyma.16G015900	Chr16	1391279	1393670	Protein of unknown function (DUF1295)
	Glyma.16G016000	Chr16	1400064	1404488	SF0 - PHOSPHATASE DCR2-RELATED
	Glyma.16G016100	Chr16	1404906	1407307	photosystem I light harvesting complex gene 2
	Glyma.16G016200	Chr16	1409241	1413726	Ribosomal RNA processing Brix domain protein
	Glyma.16G016300	Chr16	1422524	1426370	Calcium-binding endonuclease/exonuclease/phosphatase
Glyma.16G016400	Glyma.16G016400	Chr16	1431637	1433520	NAC domain containing protein 62
	Glyma.16G016500	Chr16	1440846	1441640	DENTIN SIALOPHOSPHOPROTEIN-LIKE PROTEIN
	Glyma.16G016600	Chr16	1450709	1455979	NAC transcription factor-like 9
	Glyma.16G016700	Chr16	1460102	1463552	NAC transcription factor-like 9
	Glyma.16G016800	Chr16	1467805	1469620	unknown protein
	Glyma.16G016900	Chr16	1481288	1483272	unknown protein
	Glyma.16G017100	Chr16	1483694	1486538	AP2/B3-like transcriptional factor family protein
	Glyma.16G017200	Chr16	1512023	1514299	pyrophosphorylase 1
	Glyma.16G017300	Chr16	1519674	1525290	Protein kinase superfamily protein

Table S4 Stress related cis-acting regulatory elements in GmNTL promoters.

Pair No.	Name	Site Name	Organism	Position	Strand	Matrix score.	sequence	function	Name	Site Name	Organism	Position	Strand	Matrix score.	sequence	function
I	**GmNTL1**	ARE	Zea mays	195	-	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction	**GmNTL11**	ARE	Zea mays	214	-	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
		ERE	Dianthus caryophyllus	263	+	8	ATTTCAAA	ethylene-responsive element		ABRE	Arabidopsis thaliana	348	-	6	TACGTG	cis-acting element involved in the abscisic acid responsiveness
		TC-rich repeats	Nicotiana tabacum	347	-	9	ATTTTCTTCA	cis-acting element involved in defense and stress responsiveness		HSE	Brassica oleracea	543	-	9	AGAAAATTCG	cis-acting element involved in heat stress responsiveness
		TCA-element	Brassica oleracea	836	+	9	GAGAAGAATA	cis-acting element involved in salicylic acid responsiveness		TC-rich repeats	Nicotiana tabacum	546	+	9	ATTTTCTTCA	cis-acting element involved in defense and stress responsiveness
		ABRE	Arabidopsis thaliana	1050	-	7	ACGTGGC	cis-acting element involved in the abscisic acid responsiveness		ERE	Dianthus caryophyllus	608	+	8	ATTTCAAA	ethylene-responsive element
		ABRE	Arabidopsis thaliana	1052	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness		TCA-element	Nicotiana tabacum	817	-	9	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
		CGTCA-motif	Hordeum vulgARE	1340	-	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness		ABRE	Arabidopsis thaliana	1077	-	7	ACGTGGC	cis-acting element involved in the abscisic acid responsiveness
		TGACG-motif	Hordeum vulgARE	1340	+	5	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness		ABRE	Arabidopsis thaliana	1079	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness
		TCA-element	Brassica oleracea	1417	-	9	GAGAAGAATA	cis-acting element involved in salicylic acid responsiveness		CGTCA-motif	Hordeum vulgARE	1343	-	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
										TGACG-motif	Hordeum vulgARE	1343	+	5	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness
II	**GmNTL3**	HSE	Brassica oleracea	27	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness	**GmNTL4**	ABRE	Arabidopsis thaliana	248	-	6	TACGTG	cis-acting element involved in the abscisic acid responsiveness
		MBS	Arabidopsis thaliana	78	-	6	TAACTG	MYB binding site involved in drought-inducibility		TCA-element	Brassica oleracea	296	+	9	CAGAAAAGGA	cis-acting element involved in salicylic acid responsiveness
		TCA-element	Brassica oleracea	145	+	9	CAGAAAAGGA	cis-acting element involved in salicylic acid responsiveness		HSE	Brassica oleracea	548	+	9	AGAAAATTCG	cis-acting element involved in heat stress responsiveness
		ABRE	Arabidopsis thaliana	727	+	6	TACGTG	cis-acting element involved in the abscisic acid responsiveness		TC-rich repeats	Nicotiana tabacum	911	-	9	GTTTTCTTAC	cis-acting element involved in defense and stress responsiveness
		HSE	Brassica oleracea	869	-	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness		TC-rich repeats	Nicotiana tabacum	945	+	9	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
		TC-rich repeats	Nicotiana tabacum	943	+	9	ATTTTCTTCA	cis-acting element involved in defense and stress responsiveness		ARE	Zea mays	1003	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
		TCA-element	Brassica oleracea	944	-	9	GAGAAGAATA	cis-acting element involved in salicylic acid responsiveness		TC-rich repeats	Nicotiana tabacum	1005	+	10	GTTTTCTTAC	cis-acting element involved in defense and stress responsiveness
		TC-rich repeats	Nicotiana tabacum	984	+	10	GTTTTCTTAC	cis-acting element involved in defense and stress responsiveness		CGTCA-motif	Hordeum vulgARE	1021	+	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
		ABRE	Arabidopsis thaliana	998	-	6	TACGTG	cis-acting element involved in the abscisic acid responsiveness		TGACG-motif	Hordeum vulgARE	1021	-	5	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness
		CGTCA-motif	Hordeum vulgARE	1029	-	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness		MBS	Arabidopsis thaliana	1044	+	6	CAACTG	MYB binding site involved in drought-inducibility
		TGACG-motif	Hordeum vulgARE	1029	+	5	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness		ABRE	Hordeum vulgARE	1054	+	9	CGCACGTGTC	cis-acting element involved in the abscisic acid responsiveness
		ABRE	Arabidopsis thaliana	1033	-	7	ACGTGGC	cis-acting element involved in the abscisic acid responsiveness		ABRE	Arabidopsis thaliana	1056	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness
		ABRE	Arabidopsis thaliana	1035	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness		ARE	Zea mays	1486	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
		MBS	Zea mays	1162	-	6	CGGTCA	MYB Binding Site								
		ABRE	Arabidopsis thaliana	1163	-	7	TACGGTC	cis-acting element involved in the abscisic acid responsiveness								
		HSE	Brassica oleracea	1335	+	9	AGAAAATTCG	cis-acting element involved in heat stress responsiveness								
III	**GmNTL2**	TCA-element	Nicotiana tabacum	53	-	9	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness	**GmNTL12**	HSE	Brassica oleracea	146	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		ABRE	Arabidopsis thaliana	144	-	7	ACGTGGC	cis-acting element involved in the abscisic acid responsiveness		MBS	Arabidopsis thaliana	239	-	6	TAACTG	MYB binding site involved in drought-inducibility
		ABRE	Arabidopsis thaliana	146	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness		HSE	Brassica oleracea	284	+	10	AAAAAATTTC	cis-acting element involved in heat stress responsiveness

		ABRE	Arabidopsis thaliana	168	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness
		ABRE	Arabidopsis thaliana	169	+	7	ACGTGGC	cis-acting element involved in the abscisic acid responsiveness
		ARE	Zea mays	214	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
		ABRE	Triticum aestivum	231	-	9	GACACGTGGC	cis-acting element involved in the abscisic acid responsiveness
		ABRE	Arabidopsis thaliana	387	+	6	TACGTG	cis-acting element involved in the abscisic acid responsiveness
		HSE	Brassica oleracea	465	-	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		TC-rich repeats	Nicotiana tabacum	672	-	9	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
		MBS	Arabidopsis thaliana	714	-	6	TAACTG	MYB binding site involved in drought-inducibility
		ARE	Zea mays	737	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
		TCA-element	Nicotiana tabacum	1066	+	9	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
		TCA-element	Brassica oleracea	1085	-	9	GAGAAGAATA	cis-acting element involved in salicylic acid responsiveness
		ARE	Zea mays	1324	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
		SARE	Nicotiana tabacum	1461	-	11	TTCGACCTCCTT	cis-acting element involved in salicylic acid responsiveness
IV	**GmNTL8**	TCA-element	Brassica oleracea	65	+	9	CAGAAAAGGA	cis-acting element involved in salicylic acid responsiveness
		TCA-element	Brassica oleracea	691	+	9	CAGAAAAGGA	cis-acting element involved in salicylic acid responsiveness
		MBS	Arabidopsis thaliana	771	-	6	CAACTG	MYB binding site involved in drought-inducibility
		TC-rich repeats	Nicotiana tabacum	959	-	9	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
		ABRE	Arabidopsis thaliana	1434	+	7	TACGGTC	cis-acting element involved in the abscisic acid responsiveness
		MBS	Zea mays	1436	+	6	CGGTCA	MYB Binding Site
		MBS	Arabidopsis thaliana	1475	-	6	TAACTG	MYB binding site involved in drought-inducibility
V	**GmNTL7**	TC-rich repeats	Nicotiana tabacum	115	-	9	ATTTTCTTCA	cis-acting element involved in defense and stress responsiveness
		TCA-element	Brassica oleracea	137	+	10	GAGAAGAATA	cis-acting element involved in salicylic acid responsiveness
		ERE	Dianthus caryophyllus	385	-	8	ATTTCAAA	ethylene-responsive element
		ARE	Zea mays	454	-	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
		ELI-box3	Brassica oleracea	454	+	9	AAACCAATT	elicitor-responsive element
		HSE	Brassica oleracea	597	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		ARE	Zea mays	862	-	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
		ABRE	Arabidopsis thaliana	907	-	6	TACGTG	cis-acting element involved in the abscisic acid responsiveness
		ABRE	Arabidopsis thaliana	1006	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness
		Box-W1	Petroselinum crispum	1100	+	6	TTGACC	fungal elicitor responsive element
		ARE	Zea mays	1131	-	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
		TCA-element	Brassica oleracea	1218	-	9	CAGAAAAGGA	cis-acting element involved in salicylic acid responsiveness

	TC-rich repeats	Nicotiana tabacum	531	-	9	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
	MBS	Arabidopsis thaliana	573	-	6	TAACTG	MYB binding site involved in drought-inducibility
	ARE	Zea mays	596	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
	TCA-element	Brassica oleracea	890	+	9	CAGAAAAGGA	cis-acting element involved in salicylic acid responsiveness
	TCA-element	Nicotiana tabacum	926	+	9	CCATCTTTT	cis-acting element involved in salicylic acid responsiveness
	ABRE	Arabidopsis thaliana	1249	-	6	TACGTG	cis-acting element involved in the abscisic acid responsiveness
GmNTL13	MBS	Arabidopsis thaliana	260	+	6	TAACTG	MYB binding site involved in drought-inducibility
	TCA-element	Nicotiana tabacum	401	+	9	CCATCTTTT	cis-acting element involved in salicylic acid responsiveness
	TC-rich repeats	Nicotiana tabacum	570	+	9	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness
	TCA-element	Brassica oleracea	693	+	9	CAGAAAAGGA	cis-acting element involved in salicylic acid responsiveness
	MBS	Arabidopsis thaliana	770	-	6	CAACTG	MYB binding site involved in drought-inducibility
	ABRE	Arabidopsis thaliana	812	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness
	ABRE	Arabidopsis thaliana	1432	+	7	TACGGTC	cis-acting element involved in the abscisic acid responsiveness
	MBS	Zea mays	1434	+	6	CGGTCA	MYB Binding Site
GmNTL14	ARE	Zea mays	129	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
	TC-rich repeats	Nicotiana tabacum	378	+	9	GTTTTCTTAC	cis-acting element involved in defense and stress responsiveness
	ARE	Zea mays	897	-	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
	ABRE	Arabidopsis thaliana	1018	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness
	Box-W1	Petroselinum crispum	1111	+	6	TTGACC	fungal elicitor responsive element
	LTR	Hordeum vulgARE	1146	+	6	CCGAAA	cis-acting element involved in low-temperature responsiveness
	LTR	Hordeum vulgARE	1286	-	6	CCGAAA	cis-acting element involved in low-temperature responsiveness
	ARE	Zea mays	1320	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
	MBS	Arabidopsis thaliana	1352	-	6	TAACTG	MYB binding site involved in drought-inducibility
	HSE	Brassica oleracea	1436	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness

		HSE	Brassica oleracea	1312	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		MBS	Arabidopsis thaliana	1353	-	6	TAACTG	MYB binding site involved in drought-inducibility
		ARE	Zea mays	1424	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
VI	**GmNTL9**	ERE	Dianthus caryophyllus	17	+	8	ATTTCAAA	ethylene-responsive element
		HSE	Brassica oleracea	46	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		MBS	Arabidopsis thaliana	274	-	6	TAACTG	MYB binding site involved in drought-inducibility
		LTR	Hordeum vulgARE	434	-	6	CCGAAA	cis-acting element involved in low-temperature responsiveness
		MBS	Arabidopsis thaliana	504	-	6	TAACTG	MYB binding site involved in drought-inducibility
		TCA-element	Brassica oleracea	573	-	9	GAGAAGAATA	cis-acting element involved in salicylic acid responsiveness
		LTR	Hordeum vulgARE	660	+	6	CCGAAA	cis-acting element involved in low-temperature responsiveness
		TCA-element	Brassica oleracea	725	+	9	GAGAAGAATA	cis-acting element involved in salicylic acid responsiveness
		TC-rich repeats	Nicotiana tabacum	885	-	9	ATTTTCTTCA	cis-acting element involved in defense and stress responsiveness
		ABRE	Arabidopsis thaliana	1183	-	7	ACGTGGC	cis-acting element involved in the abscisic acid responsiveness
		ABRE	Arabidopsis thaliana	1185	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness
		ARE	Zea mays	1374	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
VII	**GmNTL6**	TC-rich repeats	Nicotiana tabacum	58	-	9	GTTTTCTTAC	cis-acting element involved in defense and stress responsiveness
		HSE	Lycopersicon esculentum	163	+	8	CNNGAANNTTCNNG	cis-acting element involved in heat stress responsiveness
		HSE	Brassica oleracea	165	-	9	AGAAAATTCG	cis-acting element involved in heat stress responsiveness
		TC-rich repeats	Nicotiana tabacum	168	+	9	ATTTTCTTCA	cis-acting element involved in defense and stress responsiveness
		HSE	Brassica oleracea	549	-	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		TC-rich repeats	Nicotiana tabacum	613	-	9	ATTTTCTTCA	cis-acting element involved in defense and stress responsiveness
		HSE	Brassica oleracea	719	-	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		MBS	Arabidopsis thaliana	942	+	6	TAACTG	MYB binding site involved in drought-inducibility
		HSE	Brassica oleracea	1036	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		HSE	Brassica oleracea	1093	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		HSE	Brassica oleracea	1260	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		ABRE	Arabidopsis thaliana	1330	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness
		ERE	Dianthus caryophyllus	1445	+	8	ATTTCAAA	ethylene-responsive element
	GmNTL5	HSE	Brassica oleracea	124	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		HSE	Brassica oleracea	394	-	10	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
		ARE	Zea mays	421	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
		TC-rich repeats	Nicotiana tabacum	471	-	9	ATTTTCTTCA	cis-acting element involved in defense and stress responsiveness

GmNTL10	MBS	Arabidopsis thaliana	284	-	6	TAACTG	MYB binding site involved in drought-inducibility
	CGTCA-motif	Hordeum vulgARE	384	-	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
	TGACG-motif	Hordeum vulgARE	384	+	5	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness
	MBS	Arabidopsis thaliana	446	-	6	TAACTG	MYB binding site involved in drought-inducibility
	ERE	Dianthus caryophyllus	466	+	8	ATTTCAAA	ethylene-responsive element
	TCA-element	Brassica oleracea	511	-	9	GAGAAGAATA	cis-acting element involved in salicylic acid responsiveness
	TCA-element	Brassica oleracea	641	+	9	GAGAAGAATA	cis-acting element involved in salicylic acid responsiveness
	MBS	Arabidopsis thaliana	673	-	6	TAACTG	MYB binding site involved in drought-inducibility
	ARE	Zea mays	722	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
	MBS	Arabidopsis thaliana	857	-	6	CAACTG	MYB binding site involved in drought-inducibility
	ABRE	Arabidopsis thaliana	1163	-	7	ACGTGGC	cis-acting element involved in the abscisic acid responsiveness
	ABRE	Arabidopsis thaliana	1165	+	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness
GmNTL15	LTR	Hordeum vulgARE	301	-	6	CCGAAA	cis-acting element involved in low-temperature responsiveness
	HSE	Brassica oleracea	395	-	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
	HSE	Brassica oleracea	532	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
	HSE	Brassica oleracea	583	+	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
	MBS	Arabidopsis thaliana	657	+	6	TAACTG	MYB binding site involved in drought-inducibility
	Box-W1	Petroselinum crispum	849	-	6	TTGACC	fungal elicitor responsive element
	HSE	Brassica oleracea	1079	-	9	AAAAAATTTC	cis-acting element involved in heat stress responsiveness
	CGTCA-motif	Hordeum vulgARE	1270	+	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
	TGACG-motif	Hordeum vulgARE	1270	-	5	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness
	CGTCA-motif	Hordeum vulgARE	1279	+	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
	TGACG-motif	Hordeum vulgARE	1279	-	5	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness
	ARE	Zea mays	1378	-	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction

TCA-element	Brassica oleracea	928	-	9	GAGAAGAATA	cis-acting element involved in salicylic acid responsiveness
ARE	Zea mays	1042	+	6	TGGTTT	cis-acting regulatory element essential for the anaerobic induction
TC-rich repeats	Nicotiana tabacum	1188	+	9	ATTTTCTCCA	cis-acting element involved in defense and stress responsiveness
MBS	Arabidopsis thaliana	1476	-	6	TAACTG	MYB binding site involved in drought-inducibility
MBS	Arabidopsis thaliana	1480	+	6	TAACTG	MYB binding site involved in drought-inducibility

Table S5. Functions of NTLs in *A.thaliana*

Name	AGI	Function	Refs
NTM1	At4g01540	Cytokinin signaling	(1)
NTM2	At4g01550	Seed germination under high salinity, auxin signaling	(2,3)
NTL1(ANAC013)	At1g32870	UV response, oxidative stress response	(4,5)
NTL4	At3g10500	ROS - mediated PCD	(6)
NTL6	At3g49530	Cold - induced pathogenesis, ABA signaling	(7-9)
NTL7(ANAC017)	At1g34190	H_2O_2-mediated stress signaling	(10)
NTL8	At2g27300	Salt signaling in seed germination and floral transition	(11-14)
NTL9	At4g35580	Osmotic regulation of leaf senescence, plant immunity	(15,16)
ANAC089	At5g22290	Sugar signaling, ROS signaling, floral transition	(17-19)

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Table S6 Sequences of primer pairs used for the isolation of GmNTL genes.

Name	Forward primer	Reverse primer
GmNTL1	5'-AAAAAGCAGGCTCG ATGGGTGCCGTCGTC-3'	5'-AGAAAGCTGGGTT TTAAGATCTGACATATGCCCA-3'
GmNTL2	5'- AAAAAGCAGGCTCG ATGGCACCTGTTTTGCCT-3'	5'- AGAAAGCTGGGTT TCAAGGGTTAACTACCATATTCTG-3'
GmNTL3	5'-AAAAAGCAGGCTCG ATGGGTTCGGTGGACTG-3'	5'-AGAAAGCTGGGTT TTAAAATTTAAGATATCCCCAAA-3'
GmNTL4	5'-AAAAAGCAGGCTCG ATGGGTTCGGTGGACTGT-3'	5'-AGAAAGCTGGGTT TTAAAATTTAAGATATCCCCAGAT-3'
GmNTL5	5'- AAAAAGCAGGCTCA ATGGAGAACAACATAATTTC-3'	5'- AGAAAGCTGGGTT CTAACATGATAATACATCCCAAC-3'
GmNTL6 (Glyma.10g197600.1)	5'- AAAAAGCAGGCTCA ATGGCACGCATGG-3'	5'-AGAAAGCTGGGT CTATCTGTAGGCAATGATGCTT -3`
GmNTL7	5'-AAAAAGCAGGCTCG ATGGGTGAGGCTTCAGG-3'	5'-AGAAAGCTGGGTT TCAAGGAGAGACACATCTCC-3'
GmNTL8	5'-AAAAAGCAGGCTTA ATGAATATGGCTCCTGTTTC-3'	5'-AGAAAGCTGGGTT GGTACAAAGAGCCTATGATATG-3'
GmNTL9	5'-AAAAAGCAGGCTCG ATGGAAGGGGTTTCGAGG-3'	5'-AGAAAGCTGGGTT CTAAAAACTAAAAAAATAACAAGAT-3'
GmNTL10	5'- AAAAAGCAGGCTCG ATGATGGAAGGGGTTTC-3'	5'-AGAAAGCTGG GTTTAATCCTCTAAAATTTGCTGT-3'
GmNTL11 (Glyma.14g36840.1)	5'- AAAAAGCAGGCTCG ATGGGTGCTGTTGTG -3'	5'-AGAAAGCTGGGTC TTAAGATCTGACATATGC-3'
GmNTL12	5'- AAAAAGCAGGCTCG ATGGCACCTGTTTTGCCT-3'	5'- AGAAAGCTGGGTT TCAAGGGTTAACTATCATATTCTG-3'
GmNTL13	5'- AAAAAGCAGGCTCG ATGGCTCCTGTTTCATTG -3'	5'- AGAAAGCTGGGTT CTAAGAGTCAACTATAACATGGTTA-3'
GmNTL14 (Glyma.20g31210.4/Glyma.20g31210.1)	5'-AAAAAGCAGGCTCG ATGGGTGAGGCTTCGG-3'	5'-AGAAAGCTGGGTT TCAAGGAGAAATACTTCTACCTAC-3'
GmNTL15	5'- AAAAAGCAGGCTCG ATGGCACGGATGGGC-3'	5'- AGAAAGCTGGGTT TCATTTACCAGTATACATGATGCT-

		3'
GmNTL1-ΔC	5'-ATGGGTGCCGTCGTCGAGT-3'	5'-GCCATCGTGTCCATGTTTGGC-3'
Glyma.20G172100.4	5'-CAAGACTCTCTCTCTCGCTC-3'	5'- CTTGAAACTGGCTCGGTTCT-3'
Glyma.10g197600.2/Glyma.10g197600.3	5'-CTTCCACACTCTCCCATTT-3'	5'-ACAGGTAGTCATTTACCAGTATAC-3'

Table S7 Sequences of primer pairs used for qRT-PCR analysis.

Name	Forward primer	Reverse primer
GmNTL1	5'-GCCGTTAGGGTTCCGTTTC-3'	5'-AAGGCTCCCATTTGCAGACA-3'
GmNTL2	5'-TTCAGATTCCACCCTACAGACG-3'	5'-GATTTCCCTGGCAAGTCCC-3'
GmNTL3	5'-CTGAGGAAGAAGTTGGAGGGTC-3'	5'-CTGAATGAATGATTTGGCTGGTA-3'
GmNTL4	5'-GCCGTTAGGGTTCCGTTTC-3'	5'-GCTCCTTCAAAGTGGGACGATA-3'
GmNTL5	5'-GTCTCTAATCTGAATGAAC-3'	5'-ATCTGGAATGATACTCTC-3'
GmNTL6 (compatible for all the alternative transcripts)	5'-GATTGCTCTTGGACTTCA-3'	5'-AGTAATGTCTGTTATGCTGAT-3'
GmNTL7	5'-GGAAAGCAACGGGAAAGGAT-3'	5'-CCAATCAGTCCGCTCACCAC-3'
GmNTL8	5'-CAATATGTGCGGAGGAAG-3'	5'-GTGATGATGAGTAGTTGGATT-3'
GmNTL9	5'-CGCCAGAATAACCATTAG-3'	5'-TGTTGGAAGATTGGAGAT-3'
GmNTL10	5'-ACATAAGGAGGCATCGTGAGGT-3'	5'-ATGTGTAGCCATTGACAAACGAA-3'
GmNTL11 (*Glyma.14g36840.1*)	5'-GCCGTTAGGGTTCCGTTTC-3'	5'-AAGGCTCCCATTTGCAGACA-3'
GmNTL12	5'-GATCTCTATAAGTGTGAACCGTGGG-3'	5'-CGAGGGCTAAAGAAATACCACTCC-3'
GmNTL13	5'-CTCAGAAGGAAGAGGTGAAGTTTTAG-3'	5'-TGTGACCATGTCCCAATGTTATTAT-3'
GmNTL14 (compatible for all the alternative transcripts)	5'-TGAGCGGACTGATTGGGTTAT-3'	5'-CATCTGCCCACTCTTCTTCATT-3'
GmNTL15	5'-AGAAGGAGTGGGATGTTGAGG-3'	5'-ATGTCAAGGTCGTTGGTTTCA-3'

GmTUB	5'-GGCAAGATGAGCACCAAGGAA-3'	5'-GTGGAGGACATGGACAAACCC-3'
Gm60S	5'-AAAGTGGACCAAGGCATATCGTCG-3'	5'-TCAGGACATTCTCCGCAAGATTCC-'
GmELF1b	5'-GTTGAAAAGCCAGGGGACA-3'	5'-TCTTACCCCTTGAGCGTGG-3'
Glyma.10g197600.2	5'-TAAGCAGCAGTCAGTGAA-3'	5'-CGTATGGTTATTCTCCTTACAA-3'
Glyma.10g197600.3	5'-TCTTCATCGTAACTTATACAACA-3'	5'-ATGGACAGCCTCTATCAG-3'
Glyma.20G172100.4	5'-AGGTATAGTAATCAGCACAA-3'	5'-GTCATTCAGGAGCAGTAA-3'
Medtr5g069030	5'-TGATGACACTGGTATAAG-3'	5'-ATCCTCCTAATCGTATTC-3'
Medtr3g093050	5'-TTACAGTATCCACATCAC -3'	5'-CATCATATCCATCGCTAT-3'
Medtr5g076850	5'-GCACTAACTACAATCACA -3'	5'- ATCCTCCTAATCGTATTC-3'
Medtr3g064580	5'- GCTATGAAGTTGTTGAGGAA-3'	5'-CAGAATTGGATTGAGTTGAAC -3'
Medtr1g097300	5'-AAGGTTATGATGGTTCTT -3'	5'-AGGAGTAGTAGGTATTGA -3'
Medtr2g086880	5'-ATCATTCATTCAATCAGATAACG -3'	5'-TTCCAATAGCCACAATCG -3'
Medtr1g090723	5'-TCAGCATTACAGACATTAC -3'	5'-TTAACATCAGTTTGGGAAA -3'
Medtr4g055270(60S)	5'-AATCTCACCACGCTATCA -3'	5'-AATCTCACCACGCTATCA-3'
Medtr5g088660(ELF1b)	5'-GATAAGAAGGCAGCAGAG -3'	5'-TCAAGCAGAATGGAAGAC -3'
Medtr7g026230(ACT)	5'-CACATACAACTCCATCAT -3'	5'-TTCCTTGCTCATTCTATC-3'

Table S8 Sequences of primer pairs used for the semi-quantitative RT-PCR of GmNTL genes.

Name	Forward primer	Reverse primer
GmNTL1-ΔC	5'-TCGAGTGTTACCCACAGCCGC-3'	5'-CAAGGCTCCCATTTGCAGACAT-3'
GmNTL1	5'- GTTAATTGGGATGCGTTCTC-3'	5'- CAGCATGGTTTTCTGATTCTG-3'
GmNTL14	5'- ACTGTTGTGGATCAGTTCTC-3'	5'- GCTGATTACTTTCACCATGC-3'
GmNTL7	5'- AGCATGTGAATGGTTATCCT-3'	5'- GAGAAAGAATCAACAAAGCCT-3'