

Figure S2. Distribution of the *MsCLBDs* in *M. sativa* spp. *Caerulea* chromosome. *MsCLBDs*, *M. sativa* spp. *Caerulea* lateral organ boundaries domain genes.



Figure S3. Conserved motifs of MsLBDs proteins

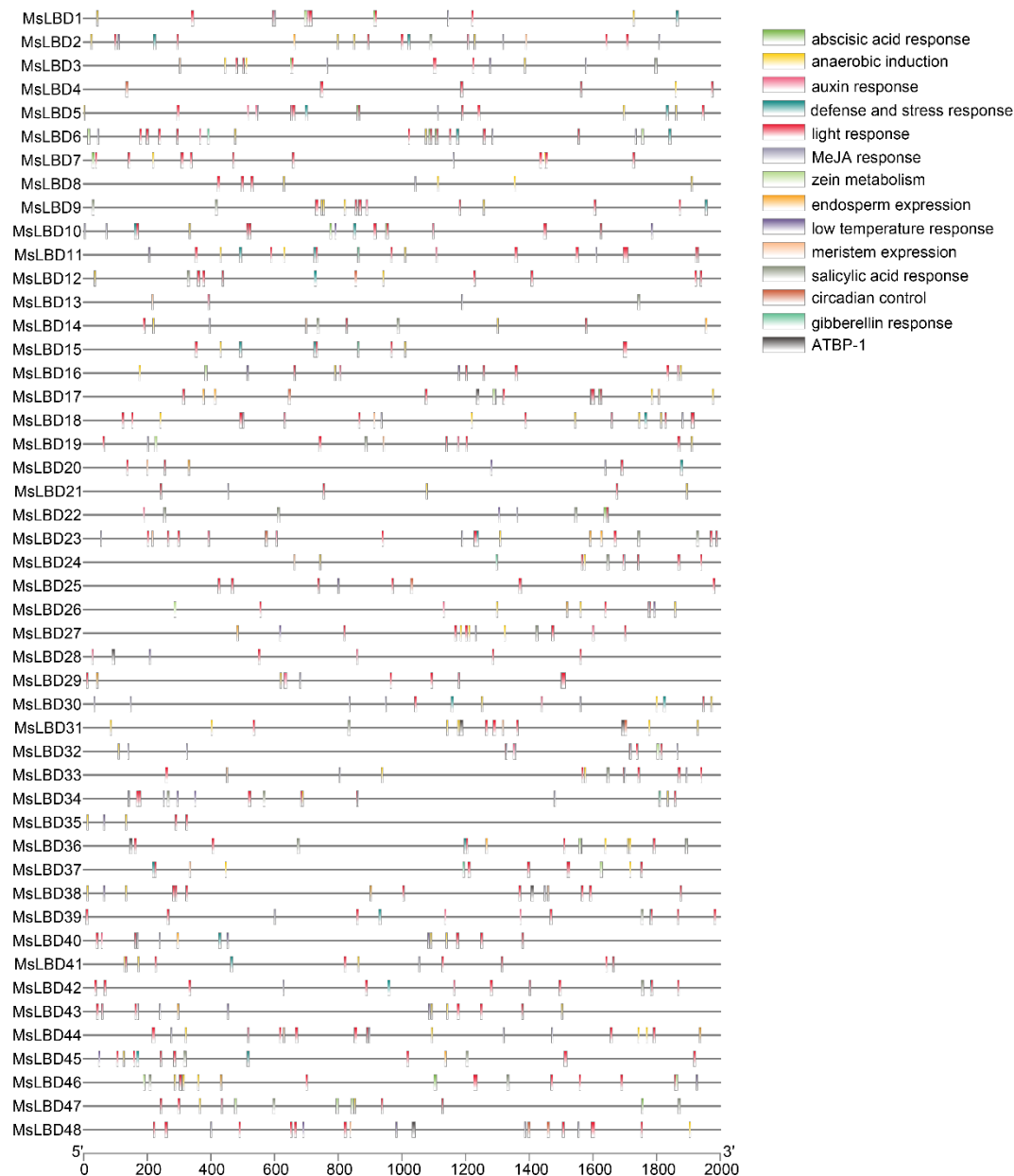


Figure S4. Promoter element of *MsLBDs* genes

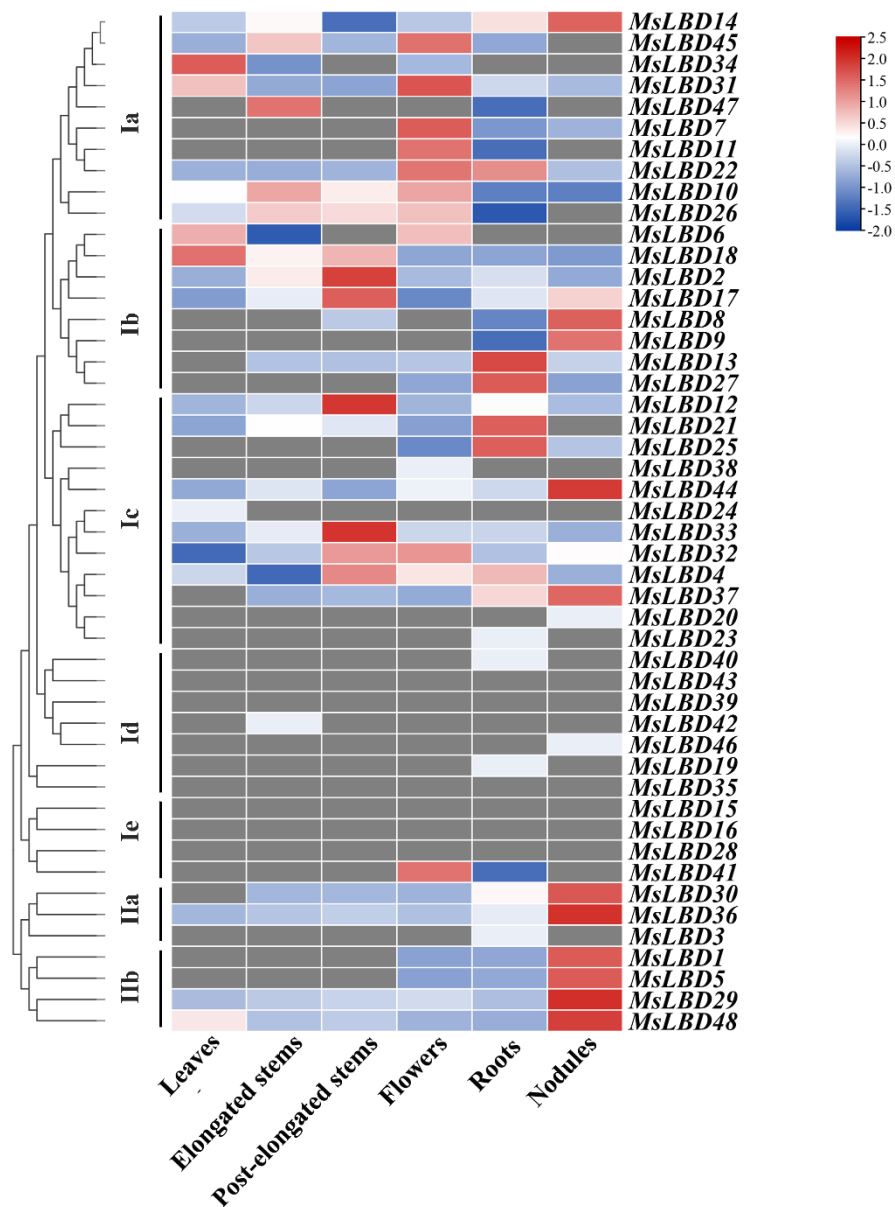


Figure S5. Heatmap of the expression profile of *MsLBD* genes. The relative expression of each *MsLBD* gene was normalized by TBtools software in different tissue. Blue indicated down-regulation, red for up-regulation, the grey for genes undetected in the RNA sequencing data.

Table S1 Basic information of the putative MsLBDs in alfalfa

Gene_name	Gene_id	Location	Size	MW(kDa)	pI	Location prediction
MsLBD14	MS.gene022331	chr3.4:74172606:74173187	193 a.a.	20.94	7.63	nucleus
MsLBD45	MS.gene011318	chr8.4:21137334:21137906	190 a.a.	20.71	7.63	nucleus
MsLBD34	MS.gene30077	chr7.1:63714330:63714848	172 a.a.	18.77	5.52	nucleus
MsLBD31	MS.gene032616	chr6.3:1161920:1162375	151 a.a.	16.62	6.57	nucleus
MsLBD47	MS.gene87198	chr8.4:58297179:58297874	231 a.a.	25.39	8.26	nucleus
MsLBD7	MS.gene068854	chr3.2:41474825:41475718	297 a.a.	31.9	5.91	nucleus
MsLBD11	MS.gene35626	chr3.3:63690097:63690793	204 a.a.	22.72	8.71	nucleus
MsLBD22	MS.gene010395	chr5.4:10916826:10917782	318 a.a.	34.77	6.56	nucleus
MsLBD10	MS.gene008030	chr3.3:62078169:62078726	185 a.a.	20.59	8.1	nucleus
MsLBD26	MS.gene94227	chr5.4:65755991:65756530	179 a.a.	19.98	6.81	nucleus
MsLBD6	MS.gene31331	chr2.4:8424586:8427204:-	174 a.a.	19.46	5.16	nucleus
MsLBD18	MS.gene049862	chr4.4:44081649:44083790	185 a.a.	20.26	5.49	nucleus
MsLBD2	MS.gene54754	chr1.2:72649812:72651370	230 a.a.	25.22	6.43	nucleus
MsLBD17	MS.gene56569	chr4.4:29258656:29262353	174 a.a.	18.92	7.7	nucleus
MsLBD8	MS.gene92645	chr3.3:33819966:33823100	147 a.a.	16.56	8.54	nucleus
MsLBD9	MS.gene048563	chr3.3:53189343:53190643	176 a.a.	19.7	5.88	nucleus
MsLBD13	MS.gene031929	chr3.4:70837285:70838290	160 a.a.	18.06	7.64	nucleus
MsLBD27	MS.gene29689	chr5.1:65545351:65546630	166 a.a.	18.69	6.5	nucleus
MsLBD12	MS.gene31052	chr3.3:78615404:78616107	205 a.a.	22.45	8.63	nucleus
MsLBD21	MS.gene98872	chr5.2:71826185:71827588	196 a.a.	21.83	7.64	nucleus
MsLBD25	MS.gene26285	chr5.4:59341388:59342282	142 a.a.	15.56	6.41	nucleus
MsLBD38	MS.gene96098	chr7.4:30185115:30188016	197 a.a.	21.91	6.58	nucleus
MsLBD44	MS.gene019357	chr8.3:59598280:59606588	259 a.a.	28.31	6.49	nucleus
MsLBD24	MS.gene032845	chr5.4:29480141:29480862	202 a.a.	21.58	9.35	nucleus
MsLBD33	MS.gene47300	chr6.4:2862808:2863768	227 a.a.	24.44	9.2	nucleus
MsLBD32	MS.gene49826	chr6.3:19474848:19475838	209 a.a.	23.06	8.78	nucleus
MsLBD4	MS.gene39880	chr1.3:50204038:50205951	204 a.a.	22.38	6.79	nucleus
MsLBD37	MS.gene23507	chr7.3:14703507:14704706	218 a.a.	24.15	7.05	nucleus
MsLBD20	MS.gene57863	chr5.2:68313632:68314864	194 a.a.	21.3	5.67	nucleus
MsLBD23	MS.gene027499	chr5.4:26000842:26002006	224 a.a.	25.16	5.94	nucleus
MsLBD40	MS.gene011859	chr8.2:26259985:26260641	218 a.a.	24.31	5.76	nucleus
MsLBD43	MS.gene87329	chr8.3:24663882:24664565	227 a.a.	25.15	5.57	nucleus
MsLBD39	MS.gene44932	chr8.1:28095019:28095934	231 a.a.	24.87	5.05	nucleus
MsLBD42	MS.gene87327	chr8.3:24626480:24627396	271 a.a.	29.32	5.5	nucleus
MsLBD46	MS.gene28573	chr8.4:27097987:27098778	263 a.a.	28.09	6.24	nucleus
MsLBD19	MS.gene062277	chr5.1:74140421:74141954	157 a.a.	18.1	8.98	nucleus
MsLBD35	MS.gene98098	chr7.2:71052146:71052981	157 a.a.	18.01	8.23	nucleus
MsLBD15	MS.gene39546	chr4.2:23249084:23249914	276 a.a.	31.48	8.74	nucleus
MsLBD16	MS.gene045528	chr4.3:29689620:29690594	196 a.a.	22.78	8.75	nucleus
MsLBD28	MS.gene057889	chr5.3:69179502:69180203	233 a.a.	26.31	5.1	nucleus
MsLBD41	MS.gene72374	chr8.3:21407143:21407616	157 a.a.	17.37	7.65	nucleus
MsLBD30	MS.gene074251	chr6.2:14344708:14346344	278 a.a.	30.54	8.03	nucleus
MsLBD36	MS.gene76902	chr7.2:91305148:91306331	301 a.a.	32.99	8.07	nucleus
MsLBD3	MS.gene71832	chr1.3:75557737:75558748	231 a.a.	25.24	8.99	nucleus
MsLBD1	MS.gene76816	chr1.1:76542635:76543444	212 a.a.	23.8	5.74	nucleus
MsLBD5	MS.gene71626	chr1.4:82355009:82355729	179 a.a.	19.96	5.93	nucleus
MsLBD29	MS.gene57207	chr5.3:8766360:8767197	231 a.a.	25.2	8.62	nucleus
MsLBD48	MS.gene041894	32644:18066:18887	233 a.a.	25.29	8.1	nucleus

Note: *M. sativa* LATERAL ORGAN BOUNDARIES DOMAIN transcription factors(MsLBDs).

Table S2 Preliminary information of the putative MsCLBDs in *M. sativa* spp. *Caerulea*

Gene name	Gene_id	Location	Size	MW (kDa)	pI	Location prediction
MsCLBD12	MsaT015364	Chr3: 85959009: 85959590	193 a.a.	20.93	7.8	nucleus
MsCLBD26	MsaT030281	Chr6: 5819528: 5819983	151 a.a.	16.62	6.57	nucleus
MsCLBD27	MsaT030282	Chr6: 5831713: 5832141	142 a.a.	15.84	6.18	nucleus
MsCLBD31	MsaT036548	Chr7: 37357894: 37358412	172 a.a.	18.83	5.52	nucleus
MsCLBD40	MsaT042594	Chr8: 24599747: 24600418	223 a.a.	24.47	8.26	nucleus
MsCLBD7	MsaT013595	Chr3: 57010098: 57010985	295 a.a.	31.78	5.83	nucleus
MsCLBD11	MsaT015211	Chr3: 83940752: 83941358	204 a.a.	22.75	8.71	nucleus
MsCLBD23	MsaT025540	Chr5: 9684729: 9685685	318 a.a.	34.77	6.56	nucleus
MsCLBD18	MsaT028821	Chr5: 69255786: 69256319	177 a.a.	19.79	6.81	nucleus
MsCLBD9	MsaT015066	Chr3: 82291736: 82292293	185 a.a.	20.59	8.1	nucleus
MsCLBD8	MsaT014481	Chr3: 73792224: 73792595	176 a.a.	19.69	5.88	nucleus
MsCLBD10	MsaT015081	Chr3: 82450564: 82450881	159 a.a.	17.92	7.64	nucleus
MsCLBD19	MsaT028836	Chr5: 69470495: 69470839	166 a.a.	18.69	6.5	nucleus
MsCLBD6	MsaT013281	Chr3: 47321941: 47322096	145 a.a.	16.3	7.61	nucleus
MsCLBD4	MsaT009292	Chr2: 56843376: 56843534	164 a.a.	18.36	8.28	nucleus
MsCLBD1	MsaT004729	Chr1: 73159722: 73160078	230 a.a.	25.22	6.43	nucleus
MsCLBD5	MsaT010576	Chr2: 75127349: 75127708	198 a.a.	22.1	5.2	nucleus
MsCLBD14	MsaT020688	Chr4: 57175175: 57175369	185 a.a.	20.26	5.49	nucleus
MsCLBD13	MsaT016470	Chr3: 98270810: 98271001	122 a.a.	13.51	8.61	nucleus
MsCLBD20	MsaT028887	Chr5: 70118385: 70118398	196 a.a.	21.8	7.64	nucleus
MsCLBD17	MsaT028528	Chr5: 63567376: 63567401	180 a.a.	19.73	8.11	nucleus
MsCLBD38	MsaT042385	Chr8: 21091421: 21091448	273 a.a.	29.36	8.76	nucleus
MsCLBD34	MsaT038370	Chr7: 75720732: 75721124	236 a.a.	24.74	8.72	nucleus
MsCLBD39	MsaT042387	Chr8: 21145858: 21146196	216 a.a.	23.6	7.1	nucleus
MsCLBD33	MsaT038369	Chr7: 75694211: 75694510	195 a.a.	21.61	6.58	nucleus
MsCLBD37	MsaT039690	Chr7: 91946121: 91946402	223 a.a.	24.93	5.93	nucleus
MsCLBD36	MsaT039686	Chr7: 91909434: 91909790	218 a.a.	24.14	7.05	nucleus
MsCLBD16	MsaT028214	Chr5: 59062539: 59062817	193 a.a.	21.26	5.84	nucleus
MsCLBD29	MsaT030527	Chr6: 9459093: 9459443	209 a.a.	23.06	8.78	nucleus
MsCLBD28	MsaT030526	Chr6: 9454875: 9455180	227 a.a.	24.44	9.2	nucleus
MsCLBD15	MsaT026939	Chr5: 31658872: 31659246	202 a.a.	21.6	9.35	nucleus
MsCLBD30	MsaT036316	Chr7: 31931914: 31932234	156 a.a.	17.82	8.23	nucleus
MsCLBD25	MsaT029978	Chr6: 570228: 570248	241 a.a.	27.22	7.55	nucleus
MsCLBD21	MsaT028964	Chr5: 71237317: 71238012	231 a.a.	26.25	5.68	nucleus
MsCLBD46	MsaT044729	Chr8: 64091129: 64091599	156 a.a.	17.26	8.21	nucleus
MsCLBD42	MsaT044430	Chr8: 60119992: 60120492	166 a.a.	18.88	6.9	nucleus
MsCLBD45	MsaT044701	Chr8: 63676605: 63676646	86 a.a.	9.65	7.73	nucleus
MsCLBD41	MsaT044429	Chr8: 60093732: 60094049	220 a.a.	23.61	6.58	nucleus
MsCLBD43	MsaT044434	Chr8: 60184159: 60184953	264 a.a.	28.91	5.6	nucleus
MsCLBD44	MsaT044566	Chr8: 62087191: 62087374	233 a.a.	25.32	7.53	nucleus
MsCLBD22	MsaT025414	Chr5: 8043179: 8043690	231 a.a.	25.07	8.4	nucleus
MsCLBD2	MsaT005365	Chr6: 80640560: 80641011	211 a.a.	23.66	5.96	nucleus
MsCLBD3	MsaT005565	Chr1: 82906029: 82906528	231 a.a.	25.24	8.99	nucleus
MsCLBD24	MsaT030850	Chr6: 15116464: 15117110	278 a.a.	30.43	8.03	nucleus
MsCLBD35	MsaT035149	Chr7: 8072569: 8072758	301 a.a.	32.99	8.56	nucleus
MsCLBD32	MsaT034983	Chr7: 5538972: 5539161	301 a.a.	32.96	8.07	nucleus

Note: *M. sativa* spp. *Caerulea* LATERAL ORGAN BOUNDARIES DOMAIN transcription factors(MsCLBDs).

Table S3 Classification of the LBD members in select species.

	<i>M. sativa</i> L. Xinjiandaye (4x = 32)	<i>M. sativa</i> spp. <i>Caerulea</i> (2x = 16)	<i>M. truncatula</i> (2x = 16)	<i>A.thaliana</i> (2x = 10)	Average
Genome (Mb)	3,150	793.2	420	125	
No. LBDs	48	46	57	42	48.25
Class I					
I a	10 (20.83%)	10 (21.74%)	11 (19.30%)	6 (14.29%)	19.04%
I b	11 (22.92%)	11 (23.91%)	11 (19.30%)	7 (16.67%)	20.70%
I c	9 (18.75%)	10 (21.74%)	11 (19.30%)	10 (23.81%)	20.90%
I d	7 (14.58%)	5 (10.87%)	5 (8.77%)	5 (11.90%)	11.53%
I e	4 (8.33%)	3 (6.52%)	10 (17.54%)	8 (19.05%)	12.86%
sum	41 (85.42%)	39 (84.78%)	48 (84.21%)	36 (85.71%)	85.03%
Class II					
II a	3 (6.25%)	4 (8.70%)	6 (10.53%)	3 (7.14%)	8.15%
II b	4 (8.33%)	3 (6.52%)	3 (5.26%)	3 (7.14%)	6.82%
sum	7 (14.58%)	7 (15.22%)	9 (15.79%)	6 (14.29%)	14.97%

Table S4 Homology analysis of MsLBDs from the different subclasses.

		I a	I b	I c	I d	I e	II a	II b	
	<div>maximum minimum</div>	98.80%	79%	74.10%	64.20%	50.60%	30.90%	32.10%	I a
I a	60.50%		91.40%	79%	61.70%	48.10%	28.40%	30.90%	I b
I b	58%	65.40%		95.10%	59.30%	45.70%	29.60%	30.90%	I c
I c	48.10%	43.20%	48.10%		98.80%	44.40%	27.20%	27.20%	I d
I d	46.90%	45.70%	39.50%	42%		70.40%	29.60%	33.30%	I e
I e	33.30%	35.80%	28.40%	30.90%	30.90%		91.40%	72.80%	II a
II a	25.60%	22.20%	23.50%	21%	18.50%	66.70%		98.80%	II b
II b	27.20%	25.90%	21%	21%	21%	54.30%	76.50%		
	I a	I b	I c	I d	I e	II a	II b		

Table S5 Homology analysis of MsCLBDs from the different subclasses.

		I a	I b	I c	I d	I e	II a	II b	
	<div>maximum minimum</div>	98.00%	73.50%	74.10%	59.20%	61.20%	32.70%	26.50%	I a
I a	55.10%		89.80%	77.60%	57.10%	57.10%	30.60%	26.50%	Ib
I b	53.10%	65.30%		93.90%	57.10%	53.10%	38.80%	28.60%	Ic
Ic	46.90%	42.90%	46.90%		77.6%	55.10%	24.50%	20.40%	Id
Id	40.80%	40.80%	32.70%	42.90%		79.60%	26.50%	20.40%	Ie
Ie	36.70%	38.80%	34.70%	36.70%	53.10%		95.90%	73.50%	II a
IIa	20.40%	22.40%	22.40%	18.40%	18.40%	75.50%		98.67%	II b
IIb	16.30%	16.30%	18.40%	16.30%	14.30%	51.00%	67.30%		
	I a	I b	I c	I d	I e	II a	II b		

Table S6 sequence homology of MsLBD48 with three Arabidopsis LBD homologues

protein		identity			
MsLBD48	100%				
AtLBD37	61.60%	100%			
AtLBD38	63.00%	83.10%	100%		
AtLBD39	63.50%	63.00%	64.80%	100%	

Table S7 sequence of primers used in this study

Gene	Purpose/details	Primer sequence (5' to 3')
<i>MsLBD1</i>	qRT-PCR	F: 5'-GCAGTTGGGCTGTTATGGA-3' R: 5'-ATCAGGGAGTGCGGTCAAT-3'
<i>MsLBD3</i>	qRT-PCR	F: 5'-TGAAGCCCAAGCCACGAGTT-3' R: 5'-AAGCCAAGAGTGAGTTCCAAAT-3'
<i>MsLBD5</i>	qRT-PCR	F: 5'-TAACGCCACTGTCTTTGTC-3' R: 5'-CCCAACTGCTCCATTTACT-3'
<i>MsLBD18</i>	qRT-PCR	F: 5'-CTTCCCATAGCAATGGACAT-3' R: 5'-TGAGCATAGGCTAGTGTTGT-3'
<i>MsLBD29</i>	qRT-PCR	F: 5'-GCGGCGACGACTGATCTTA-3' R: 5'-TCCTCCCATCCCACTTTCC-3'
<i>MsLBD30</i>	qRT-PCR	F: 5'-AAGGGTGTAGTGAAGATTGTAAC-3' R: 5'-GATGAGACCAGCACGACCA-3'
<i>MsLBD36</i>	qRT-PCR	F: 5'-AAAGCCCTGAATCACAAGC-3' R: 5'-ACCAGCACGACCGTAGAAT-3'
<i>MsLBD48</i>	qRT-PCR	F: 5'-TGGCGCTGCTGCTATTTGG-3' R: 5'-CGTTCCTCCACTGCCTTCTGT-3'
<i>AtNRT1.1</i>	qRT-PCR	F: 5'-CTGCCACACACTGAACAATTCC-3' R: 5'-CCCGCTTCCTGATCCCTTAT-3'
<i>AtNRT2.1</i>	qRT-PCR	F: 5'-TTGCTTTCTCGGTGCAATCAC-3' R: 5'-TGCTCTGTGTCCACCGGAA-3'
<i>AtNIA1</i>	qRT-PCR	F: 5'-GGCTACGCTTATTCTGGAGGAGGT-3' R: 5'-TGGTGGTCAAGCTCACAAACACTC-3'
<i>AtNIA2</i>	qRT-PCR	F: 5'-GCCGACGAAGAAGGTTGGTGGTAT-3' R: 5'-GAAGAATCTCCTCGTGACATGGCG-3'
<i>MsLBD48</i>	Isolation of CDS	F: 5'-AACAATGATGTCGTCGTGTAAT-3' R: 5'-TCATCATATAAGATTACCCTCTCCA-3'
<i>MsLBD48</i>	over expression	F: 5'-gaacacgggggactcttgacATGGACAAAGCATGGGGT-3' R: 5'-atttaccctcagatctaccatGTTTCCTGAAAAGTTGCT-3'
<i>MsLBD48</i>	GFP	F: 5'-agaacacgggggactcttgaATGGACAAAGCATGGGGT-3' R: 5'-cctttactagttagatctaccatGTTTCCTGAAAAGTTGCT-3'