

## Table Supplementary

**Table S1.** Nucleotides sequence of *Atorel* gene.

ATGGATTACGAGGCATCAAGAATCGTCGAAATGGTAGAAGATGAAGAACATATAGATCTACCACCAG	
GATTCAGATTTTACCCTACTGATGAAGAACTCATAACTCACTACCTCAAACCAAAGGTTTTCAACAC	
TTTCTTCTCTGCTACTGCCATTGGTGAAGTTGATCTCAACAAGATTGAGCCTTGGGACTTACCATGT	intron 1
AAGTTTTCACACCTTATCTTTCTATTTCTCAAGTCTTTTGTGTTGTCTTTCTTACCATTAAACTCA	
TGGTTCTGAATTCTGATACATGGCTGGTTTTGTTGGAACAGGGAAGGCTAAGATGGGAGAAAAAGAA	
TGGTATTTCTTCTGTGTGAGAGACCGGAAATACCCGACCGGTTTAAGGACAAACCGGGCGACAGAAG	
CCGGTTATTGGAAAGCCACAGGAAAAGACAAAGAGATATTCAAGGGAAAATCACTTGTGGGTATGAA	
GAAAACTTTGGTTTTTCTATAAAGGAAGAGCTCCTAAAGGAGTTAAAACCAATTGGGTTATGCATGAA	
TATCGTTTTAGAAGGCAAATATTGTATTGAAAATCTTCCCCAAACAGCTAAGGTAATAACATTAAAGAG	intron 2
ATTTTGTGTGTTTCTGTCTTTTGTGTTTTTTTGGGGACTTGAAATTAATTCTTTTGTGTTGGTTGTTTG	
TGAATGTAGAACGAATGGGTTATATGTCGTGTTTCCAAAAACGTGCCGATGGTACAAAGGTTCCAA	
TGTCAATGCTTGATCCACACATTAACCGAATGGAACCAGCCGGTTTACCTTCGTTAATGGATTGTTC	
TCAACGAGACTCCTTCACCGGTTTCGTCGTCTCACGTGACCTGCTTCTCCGACCAAGAAACCGAAGAC	
AAAAGACTTGTCCACGAGTCCAAAGACGGTTTTTGGTTCTCTGTTTTTACTCGGATCCTCTGTTTTTAC	
AAGACAATTGTCTTGGAACCTACAGAGGATGCGCGTAAAACAGAGAAGCTAAATCGGGTTTGGACTCG	T-DNA insert region
AGGACAAGTCTTTTGTCTTCAGTGTCTTGGCCGGATAAGCGGGTCTCGTGAAACGACGATCCGGTGA	
GAGAGTCTCTTTGAGAACAGTCCATTATCGAGCGTACTCCGGCTGGTGTCTTCAGATAGTGTGTGG	
ATCGAGCATTGTTCTTCGGAGCCTTTGTACCATAGAGCCCGGTTTTTGGATCACGCGACATATAACCC	
ATTTTATTCGCTAATGAAGCTGTTGCTTGACGGTCAAGAACTCAATTCTCCGGCAAACCTTTTCGAC	
GGTCGTGATTCGTCCGGTACAGAAGAATTGGATTGCGTTTGGAAATTC	

Note: *Atorel* gene made by T-DNA insertion in the third exon of the *Atorel* genomic sequence between position 743 and 744 of the coding region, from start codon ATG, which is indicated by nucleotides sequence under grey color. In the CDS sequence of *Atorel* (855 bp) include two intron position, which is indicate by light grey color.

**Table S2.** Sequences of oligonucleotide of *Atore1* included *cis*-regulatory element motifs identified.

AAGAACTTGATACGAAAAAATTGACCAATTATTGGTCAATATATTAAAAAGAATAAATTATTTTAGTGTTCTTATTTCTCAAATGAAAA  
CTAGTATATAGAGAGGAGCTTCGTTGCTCAAACACTTTCCTCTCTCTTAAAAACCTCAACTTTCTTCTCTCTCTCAAAAACCCTTCCC  
TCTTCGTCTCCAAACAACAACAACACAACAACAAAAATCTTACAAGAAGATCATTTTTAGAAACCCTATTAGGATAAAATGGATT  
ACGAGGCATCAAGAATCGTCGAAATGGTAGAAGATGAAGAACATATAGATCTACCACCAGGATTGAGATTTACCCCTACTGATGAAGAA  
CTCATAACTCACTACCTCAAACCAAGGTTTTCAACACTTTCCTCTCTGCTACTGCCATTGGTGAAGTTGATCTCAACAAGATTGAGCC  
TTGGGACTTACCATGTAAAGTTTCACACCTTATCTTTCTATTTCTCAAGTCTTTTGTTTGTCTTCTTTCTACCATTAACTCATGGTTC  
TGAATTCTGATACATGGCTGGTTTTGTTGGAACAGGGAAGGCTAAGATGGGAGAAAAAGAATGGTATTTCTTCTGTGTGAGAGACCGGA  
AATACCCGACCGGTTTAAGGACAAACCGGGCGACAGAAGCCGGTTATTGGAAAGCCACAGGAAAAGACAAAGAGATATTCAAGGGAAAA  
TCACTTGTGGGTATGAAGAAAACCTTTGGTTTTCTATAAAGGAAGAGCTCCTAAAGGAGTTAAACCAATTGGGTTATGCATGAATATCG  
TTTAGAAGGCAAATATTGTATTGAAAATCTTCCCCAAACAGCTAAGGTAATAACATTAAAGAGATTTTGTGTGTTTCTGTCTTTTGT  
TTTTGGGGACTTGAAATTAATTCTTTTGTGTTGGTTGTTTGTGAATGTAGAACGAATGGGTTATATGTCGTGTTTTCCAAAAACGTGCCG  
ATGGTACAAAGGTTCCAATGTCAATGCTTGATCCACACATTAACCGAATGGAACCAGCCGGTTTACCTTCGTAATGGATTGTTCTCAAC  
GAGACTCCTTCACCGGTTTCGTCGTCTCACGTGCTTCTCCGACCAAGAAACCGAAGACAAAAGACTTGTCCACGAGTCCAAAGAC  
GGTTTTGGTTCTCTGTTTTACTCGGATCCTCTGTTTTTACAAGACAATTGTCTTGGAACACTACAGAGGATGCGCGTAAACAGAGAAGCT  
AAATCGGGTTTGGACTCGAGGACAAGTCTTTTGTCTTCAGTGTCTTGGCCGGATAAGCGGGTCTCGTGAACCGACGATCCGGTGAGAGA  
GTCTCTTTGAGAACAGTCCATTATCGAGCGTACTCCGGCTGGTGTCTTCAAGATGTGTGGATCGAGCATTGTTCTTCGGAGCCTTT  
GTACCATAGAGCCCGGTTTTGGATCACGCGACATATAACCCATTTTATTCGCTAATGAAGCTGTTGCTTGACGTTCAAGAACTCAATT  
CTCCGGCAAACCTTTTCGACGGTCGTGATTCGTCCGGTACAGAAGAATTGGATTGCGTTTGGAAATTTCTGAGTTGTATAAGTTATGTTGT  
AGACTTGTAGTAGTCATGTGTTTCGTGTGTGTGAATGAATATTCTTGTTACATTTTTTTGTAAAAAAGGAGAAAAAATATGCTAGAAAG  
TCAATTGCTTTTGTATGTAGCATTAGTGTTTTTTATGTACTCAATAGACTTCCTAATTAAATAAAAATCTTAATTTATTTGCC

Note: *cis*-regulatory element motifs were scanned by the PlantCARE (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>). The motifs related in abscisic acid, auxin, chlorophyll and MeJA-responsiveness were highlighted. Sequences in the dark red are ABRE motif (5'-ACGTG-3'), blue sequence indicates TGA element (5'-AACGAC-3'), bright green sequence is GATA box (5'-GATA-3') and yellow is TGACG-motif (5'-TGACG-3').

**Table S3.** Sequences of oligonucleotide primers used for the qPCR.

No	Name	Gene ID	Forward sequence of primers (5'-3')	Reverse sequence of primers (5'-3')	Tm (°C)
1	GmActin	NM_001252731.3	F: 5'-TTCTCTCGCTCTCTGCCTTC- 3'	R: 5'-TTGTGCCTCATCACCAACAT- 3'	58
2	GmCHLG	XM_014768972.3	F: 5'-AGGGCTCTAGGGCTTCAGTC- 3'	R: 5'-AGGGTCCTTGCGGAAATACT- 3'	60
3	GmSGR1	AY850141.1	F: 5'-GGTTCCTGTTGCAAGGTTGT- 3'	R: 5'-GAGAGATTGCCAAGGTGAGC- 3'	60
4	GmNYC1	NM_001358945.1	F: 5'-TATAGACGGGGCAGGTTTCAG- 3'	R: 5'-CCATTCCTGGCGAAAGATTA- 3'	60
5	GmSAG39	XM_026124662.1	F: 5'-AGGGAAAAGCGTTTCAGGAT- 3'	R: 5'-ATGGATGGTACTGCCCTCAC- 3'	60
6	GmRBOH-E	XM_014767463.2	F: 5'-TCCACAACAAAAGACCCACA- 3'	R: 5'-ACCAGACCAAAGAGGTGGTG - 3'	58
8	GmVPE	NM_001249749.2	F: 5'-GTGAAAGTGGGAGCGTGTTT- 3'	R: 5'-CCGTTGCTTTACCGATTTGT- 3'	60
8	GmABI5	XM_014765566.1	F: 5'-GGAGAGTGGCAAGAACTTCG- 3'	R: 5'-CCAAACCTCGTCCACTGTTT- 3'	59
9	GmNAC081	DQ028774.1	F: 5'-CTTTAGCAGCCCACAGGAAG- 3'	R: 5'- TTCCCAAAGGGCATTTGTAG - 3'	58
10	GmNAC065	NM_001251701.2	F: 5'-ATTTGCCAGGTGATTTGGAG- 3'	R: 5'-TGGATCCATTAGGAGGCTTG- 3'	59
12	GmNECD3	Glyma.15g250100	F: 5'- CGAATCCCAACAGGTCAACT- 3'	R: 5'-CTTTCGTCCGAGCTTGTTTC- 3'	58
13	GmICS1	XM_003522145.4	F: 5'-GGCATTGTAAGGTTGCAGGT- 3'	R: 5'-GATGTGGCTGGGAAAAGAAA- 3'	60
14	GmYUUCA6	XM_003550066.5	F: 5'-GGGCCATAAAGCACACAAGT- 3'	R: 5'-ACCAATCCACAAACCGGATA- 3'	58
15	GmNPR1	FJ418595.1	F: 5'-CGCATGCTGAGACAACATCT- 3'	R: 5'-CCCATCTCCACTGTTTTTCGT- 3'	60
16	GmARF2	Glyma01g25270	F: 5'-CACCCCTCAAAATTCAACAG- 3'	R: 5'-AGAGTAAGTAGGTCTTCTCCCAGTG- 3'	57