

Supplementary Information:

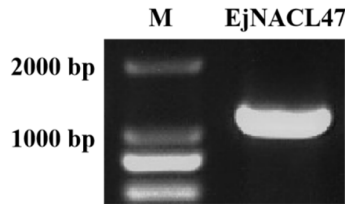
Supplementary Table S1. Gene-specific primers used in isolation of *EjNACL47* genes and vector construction.

Primer name	Primer sequence (5'-3')
DN242232-F	GACCAAGGCTTTGCAGGTTC
DN242232-R	GAGGATGCAAAACCCAGAATC
P2300-EjNACL47-eGFP-F	cggggtaccATGGAAGATGTGGAGATGGAG
P2300-EjNACL47-eGFP-R	cgcggatccCCAATCACTATAAAGCAATGAATCACC
pGBKT7-EjNACL47-F	catggaggccgaattcccGAGGATGCAAAACCCAGAATC
pGBKT7-EjNACL47-R	aggtcgacggatccccGACCAAGGCGACCAAGGCTTT
pGBKT7-EjNACL47-N-R	ggtcgacggatccccTAAATCTTTGAGCTTCATGGC
pGBKT7-EjNACL47-C-F	tggccatggaggccgaattcTCCATGAGGTGGGATGATT
pGBKT7-EjNACL47-C-R	cgtctcaggtcgacggatccGACCAAGGCGACCAAGGCTTT
PLGN-EjNACL47-F	ggtaccatgtcgacgggcccGACCAAGGCTTTGCAGGTTC
PLGN-EjNACL47-R	gtacggatccgtactagtcccGAGGATGCAAAACCCAGAATC

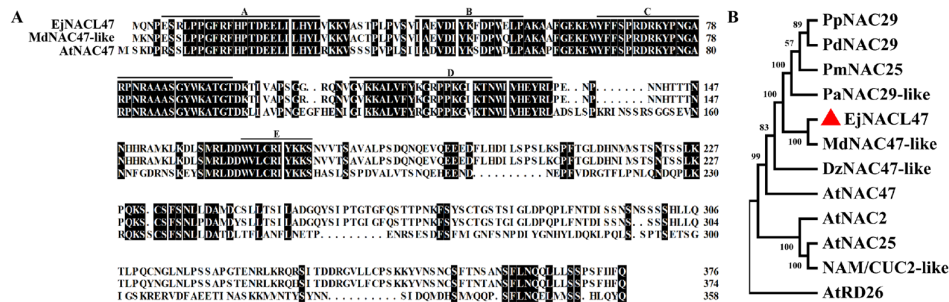
Supplementary Table S2. Gene-specific primers used in RT-PCR analysis.

Primer name	Primer sequence (5'-3')
q-EjNACL47-F	TATTGGAAGGCAACCGGAAC
q-EjNACL47-R	AGATTGACAAAGAACCCAA
q-EjActin-F	AATGGAAGTGAATGGTCAAGGC
q-EjActin-R	TGCCAGATCTTCTCCATGTCATCCCA
q-EjActin-F	TATCGCTGACCGTATGAG
q-AtActin-R	CTGAGGGAAGCAAGAATG
q-AtEXPA3-F	TCCTTTCTCTTAACCGCAACAAAC
q-AtEXPA3-R	CCAATCTGTCTTTGATCCCTTTAC
q-AtEXPB3-F	TTCCAGTCATGTTAGCCACACTC
q-AtEXPB3-R	CGATCACACGAGTAGTAGTAATAGAAC
q-AtEXPA8-F	CAAGGAACTCATGGAGACGACGGAGGT
q-AtEXPA8-R	TGCTCTGCCAGTTTTGTCCCCAGTT
q-AtEXPA10-F	TAACCGCTACAACTTCTGCCCCGCAAA
q-AtEXPA10-R	ATATGGAAGAGAGATTAACCAACTTGCCCT
q-AtEXPA11-F	TTATTGCGTTGATGCGTTTAG
q-AtEXPA11-R	GACCACTGCCAATGATATTTTCATAC
q-AtEXPA15-F	GGTCTTTTGGGAATTGCTCTGTT
q-AtEXPA15-R	CCTAAACTATATAAAACCGAACTTGACTCA
q-AtXTH8-F	TTTGTTTTGAGTGTATTAAAGTGGAATG
q-AtXTH8-R	ATAAATAAACAGAGGATATAGTCCATAACAAAAT
q-AtXTH9-F	ACCAACTGTCTCTGAGCTTAGCCT
q-AtXTH9-R	ATGATGTTGGCACTCAAGAGGA
q-AtXTH16-F	CCGGTAACTCCGCTGGAA

q-AtXTH16-R	TCTCGTCGTGTGTTGGTCCTT
q-AtXTH17-F	ATGGGCTAATGGAAAATCATCTTGTT
q-AtXTH17-R	TACTTTGCACACCTTTCATTCTTGTC
q-AtXTH32-F	CATACCGTTCTGGCGGATTAA
q-AtXTH32-R	CTTTGCAATAATTGTATACCATACTATGTG



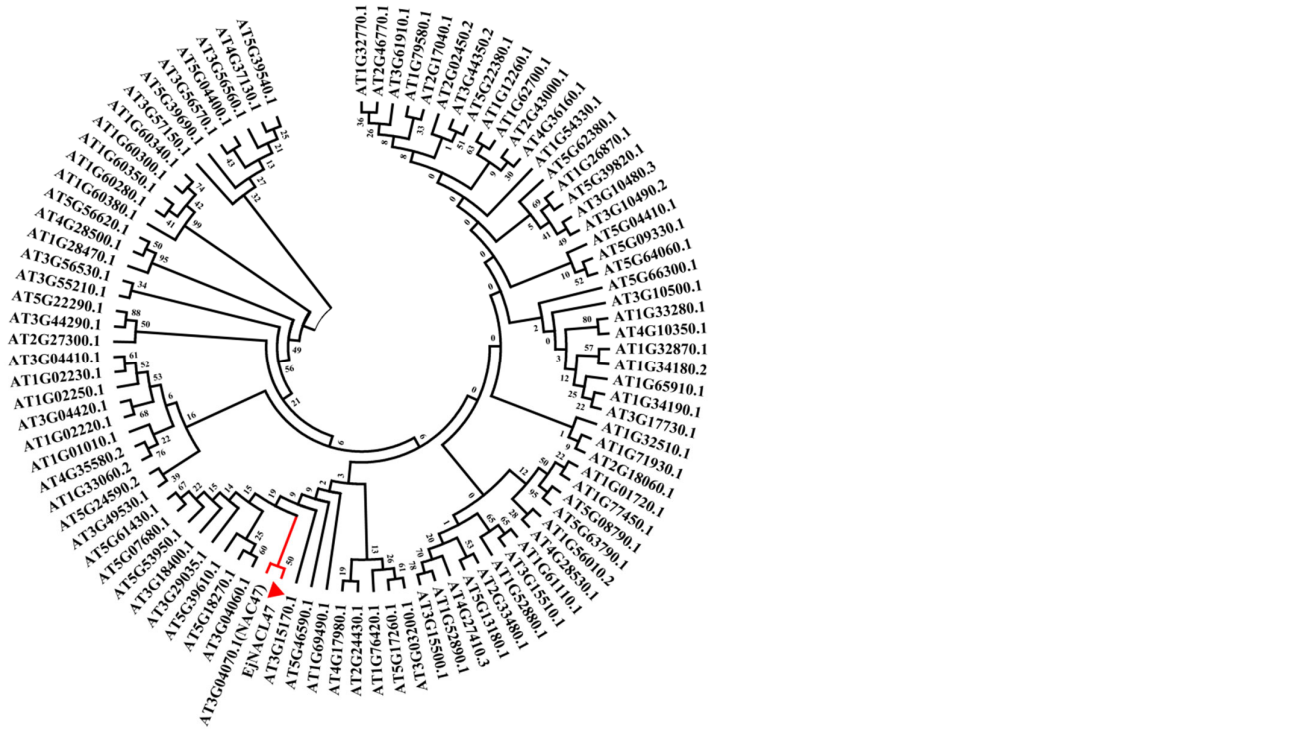
Supplementary Figure S1. Cloning of EjNACL47. M: Marker 2000.



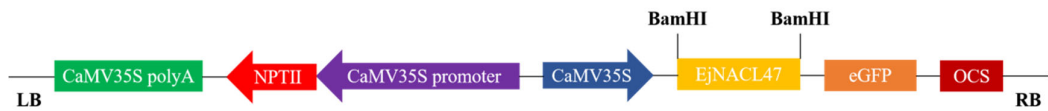
Supplementary Figure S2. Sequence analysis of EjNACL47. (A) Multiple sequence alignment of EjNACL47 with other NAC proteins. Gene codes are as follows: MdNAC47-like, XP028946255.1; AtNAC47, NP187057.2. Horizontal lines represent conserved NAC binding domains (five subdomains, A–E). Black shading represents conserved amino acid residues. (B) Phylogenetic analysis of EjNACL47. Phylogenetic analysis was performed using MEGA7.0 software with the neighbor-joining (NJ) method under 1000 bootstrap replicates. The analysis involved 12 amino acid sequences. ▲ represents EjNACL47.

Sequences producing significant alignments:	Score (bits)	E Value
GWHAAZU00000017#Chromosome 17#Complete=T#Circular=F#OriSeqID=LGI...	1292	0.0
GWHAAZU00000003#Chromosome 3#Complete=T#Circular=F#OriSeqID=L903...	563	e-158
GWHAAZU00000001#Chromosome 1#Complete=T#Circular=F#OriSeqID=L901...	88	3e-015
GWHAAZU00000007#Chromosome 7#Complete=T#Circular=F#OriSeqID=L907...	64	5e-008
GWHAAZU00000002#Chromosome 2#Complete=T#Circular=F#OriSeqID=L902...	64	5e-008
GWHAAZU000000172#OriSeqID=Contig00301#Len=265256	52	2e-004
GWHAAZU000000132#OriSeqID=Contig00299_ERRORPOS333418#Len=333418	52	2e-004
GWHAAZU00000013#Chromosome 13#Complete=T#Circular=F#OriSeqID=L91...	50	7e-004
GWHAAZU00000011#Chromosome 11#Complete=T#Circular=F#OriSeqID=L91...	50	7e-004
GWHAAZU00000004#Chromosome 4#Complete=T#Circular=F#OriSeqID=L904...	50	7e-004

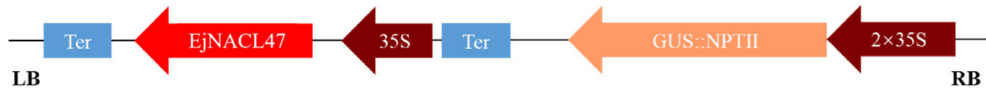
Supplementary Figure S3. The chromosome locations of EjNACL47.



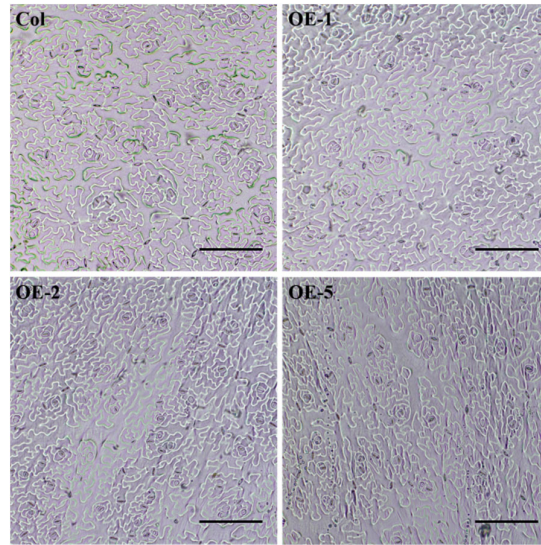
Supplementary Figure S4. Phylogenetic analysis of NAC members from loquat and Arabidopsis. Full length NAC protein sequences from Arabidopsis were downloaded from The Arabidopsis Information Resource (TAIR). ▲ represents EjNACL47.



Supplementary Figure S5 CaMV35S::EjNACL47-eGFP vector construction. LB: The left border of T-DNA; CaMV35S: promoter; RB: The right border of T-DNA; OCS: terminator; BamHI indicate multiple cloning sites for EjNACL47 insertion.



Supplementary Figure S6. PLGN-35S-EjNACL47-NOS-BE vector construction. LB: The left border of the T-DNA; Ter: Terminator; 35S: The CaMV 35S promoter; GUS::NPTII: The integration of GUS and NPTII gene; RB: The right border of the T-DNA



Supplementary Figure S7. *Lower epidermal cell changes of transgenic Arabidopsis. Scale bar: 200 μ m*