Supplementary material

```
TaTOE1-B1-1  ATGGAGCTGGATCTGAACGTGGAGGAGAAGCCGGCGGCCGGTGGCGCGGAGCGACTCCGGGACGTCGGAGTCGTCGGTGCTGAACGCGGAGGCGTCCTGCG  100
TaTOE1-B1-2  ATGGAGCTGGATCTGAACGTGGAGGAGAAGCCGGCGGCCGGTGGCGCGGAGCGACTCCGGGACGTCGGAGTCGTCGGTGCTGAACGCGGAGGCGTCCTGCG  100
TaTOE1-B1-3  ATGGAGCTGGATCTGAACGTGGAGGAGAAGCCGGCGGCCGGTGGCGCGGAGCGACTCCGGGACGTCGGAGTCGTCGGTGCTGAACGCGGAGGCGTCCTGCG  100
Consensus    atggagctggatctgaacgtggaggagaagccggcggccggtggcgcggagcgactccgggacgtcggagtcgtcggtgctgaacgcggaggcgtcctgcg

TaTOE1-B1-1  GCGGGGGCGCCGCGCCGGCCGAGGAGGCCTCCAGCTCGACGCGCCAGCCGGCGCCGGCGCCGCGGGCGGTGCTCGAGTTCAGCATCCTGAGGAGCTCGGC  200
TaTOE1-B1-2  GCGGGGGCGCCGCGCCGGCCGAGGAGGCCTCCAGCTCGACGCGCCAGCCGGCGCCGGCGCCGCGGGCGGTGCTCGAGTTCAGCATCCTGAGGAGCTCGGC  200
TaTOE1-B1-3  GCGGGGGCGCCGCGCCGGCCGAGGAGGCCTCCAGCTCGACGCGCCAGCCGGCGCCGGCGCCGCGGGCGGTGCTCGAGTTCAGCATCCTGAGGAGCTCGGC  200
Consensus    gcggggcgccgcgccggccgaggaggcctccagctcgacgcgccagccggcgccggcgccgcgggcggtgctcgagttcagcatcctgaggagctcggc

TaTOE1-B1-1  GTCCGCCGAGGGCGAGAACGACGTCGGCGCCGACGACGACGAGGAGGAGGCCACTCCCTCGCCTCCACCTCCGCCGACGCGGCACTACCACCAGCACCTG  300
TaTOE1-B1-2  GTCCGCCGAGGGCGAGAACGACGTCGGCGCCGACGACGACGAGGAGGAGGCCACTCCCTCGCCTCCACCTCCGCCGACGCGGCACTACCACCAGCACCTG  300
TaTOE1-B1-3  GTCCGCCGAGGGCGAGAACGACGTCGGCGCCGACGACGACGAGGAGGAGGCCACTCCCTCGCCTCCACCTCCGCCGACGCGGCACTACCACCAGCACCTG  300
Consensus    gtccgccgagggcgagaacgacgtcggcgccgacgacgacgaggaggaggccactccctcgcctccacctccgccgacgcggcactaccaccagcacctg

TaTOE1-B1-1  CTGCAGCCGCAACAACTCGTCACCCAAGAGCTGTTCCCCGCCGCGGCCACCGCCGGCGGTCCGCCGCCGATGTCCGTGCCGCAGCATTGGGCCGAGCTCG  400
TaTOE1-B1-2  CTGCAGCCGCAACAACTCGTCACCCAAGAGCTGTTCCCCGCCGCGGCCACCGCCGGCGGTCCGCCGCCGATGTCCGTGCCGCAGCATTGGGCCGAGCTCG  400
TaTOE1-B1-3  CTGCAGCCGCAACAACTCGTCACCCAAGAGCTGTTCCCCGCCGCGGCCACCGCCGGCGGTCCGCCGCCGATGTCCGTGCCGCAGCATTGGGCCGAGCTCG  400
Consensus    ctgcagccgcaacaactcgtcacccaagagctgttccccgccgcggccaccgccggcggtccgccgccgatgtccgtgccgcagcattgggccgagctcg

TaTOE1-B1-1  GCTTCTTCCGCCCCGCGGCGCCGCCTCCGGACATGAGGATCCTGCAGATGCAGCAGCAGCAGCTGCAGGTGCACGCGCAGCCCCGCCGCCGCCGGCGGC  500
TaTOE1-B1-2  GCTTCTTCCGCCCCGCGGCGCCGCCTCCGGACATGAGGATCCTGCAGATGCAGCAGCAGCAGCTGCAGGTGCACGCGCAGCCCCGCCGCCGCCGGCGGC  500
TaTOE1-B1-3  GCTTCTTCCGCCCCGCGGCGCCGCCTCCGGACATGAGGATCCTGCAGATGCAGCAGCAGCAGCTGCAGGTGCACGCGCAGCCCCGCCGCCGCCGGCGGC  500
Consensus    gcttcttccgccccgcggcgccgcctccggacatgaggatcctgcagatgcagcagcagcagctgcaggtgcacgcgcagccccgccgccgccggcggc

TaTOE1-B1-1  CCAGCCGCCGGTGGCCAAGAAGAGCCGCCGCGGCCCGCGCTCCCGCAGCTCGCAGTACCGCGGCGTGACCTTCTACCGCCGCACCGGCCGCTGGGAATCC  600
TaTOE1-B1-2  CCAGCCGCCGGTGGCCAAGAAGAGCCGCCGCGGCCCGCGCTCCCGCAGCTCGCAGTACCGCGGCGTGACCTTCTACCGCCGCACCGGCCGCTGGGAATCC  600
TaTOE1-B1-3  CCAGCCGCCGGTGGCCAAGAAGAGCCGCCGCGGCCCGCGCTCCCGCAGCTCGCAGTACCGCGGCGTGACCTTCTACCGCCGCACCGGCCGCTGGGAATCC  600
Consensus    ccagccgccggtggccaagaagagccgccgcggcccgcgctcccgcagctcgcagtaccgcggcgtgaccttctaccgccgcaccggccgctgggaatcc

TaTOE1-B1-1  CATATCTGGGATTGCGGCAAGCAGGTGTACTTGGGTGGATTTGACACTGCACATGCTGCTGCAAGGGCGTACGATCGAGCGGCGATCAAGTTCCGTGGCG  700
TaTOE1-B1-2  CATATCTGGGATTGCGGCAAGCAGGTGTACTTGGGTGGATTTGACACTGCACATGCTGCTGCAAGGGCGTACGATCGAGCGGCGATCAAGTTCCGTGGCG  700
TaTOE1-B1-3  CATATCTGGGATTGCGGCAAGCAGGTGTACTTGGGTGGATTTGACACTGCACATGCTGCTGCAAGGGCGTACGATCGAGCGGCGATCAAGTTCCGTGGCG  700
Consensus    catatctgggattgcggcaagcaggtgtacttgggtggatttgacactgcacatgctgctgcaagggcgtacgatcgagcggcgatcaagttccgtggcg

TaTOE1-B1-1  TCGACGCCGACATAAACTTCAACCTCAGCGACTACGAGGACGACATGAAGCAGATGAAGGGCCTGTCCAAGGAGGAGTTCGTGCACGTGCTGCGGCGGCA  800
TaTOE1-B1-2  TCGACGCCGACATAAACTTCAACCTCAGCGACTACGAGGACGACATGAAGCAGATGAAGGGCCTGTCCAAGGAGGAGTTCGTGCACGTGCTGCGGCGGCA  800
TaTOE1-B1-3  TCGACGCCGACATAAACTTCAACCTCAGCGACTACGAGGACGACATGAAGCAGATGAAGGGCCTGTCCAAGGAGGAGTTCGTGCACGTGCTGCGGCGGCA  800
Consensus    tcgacgccgacataaacttcaacctcagcgactacgaggacgacatgaagcagatgaagggcctgtccaaggaggagttcgtgcacgtgctgcggcggca

TaTOE1-B1-1  GAGCACCGGCTTCTCGCGGGGCAGCTCCAAGTACAGAGGCGTCACCCTGCACAAGTGCGGCCGGTGGGAGGCGCGCATGGGCCAGTTCCTCGGCAAGAAG  900
TaTOE1-B1-2  GAGCACCGGCTTCTCGCGGGGCAGCTCCAAGTACAGAGGCGTCACCCTGCACAAGTGCGGCCGGTGGGAGGCGCGCATGGGCCAGTTCCTCGGCAAGAAG  900
TaTOE1-B1-3  GAGCACCGGCTTCTCGCGGGGCAGCTCCAAGTACAGAGGCGTCACCCTGCACAAGTGCGGCCGGTGGGAGGCGCGCATGGGCCAGTTCCTCGGCAAGAAG  900
Consensus    gagcaccggcttctcgcggggcagctccaagtacagaggcgtcaccctgcacaagtgcggccggtgggaggcgcgcatgggccagttcctcggcaagaag

                          45 bp
TaTOE1-B1-1  TACATATATCTTGGGCTATTCGACAATGAAGTAGAGGCTGCAAGG GCTTACGACAAGGCGGCGATCAAATGCAACGGTAGGGAGGCCGTGACGAACTTCG  1000
TaTOE1-B1-2  ............................................. GCTTACGACAAGGCGGCGATCAAATGCAACGGTAGGGAGGCCGTGACGAACTTCG   955
TaTOE1-B1-3  ............................................. GCTTACGACAAGGCGGCGATCAAATGCAACGGTAGGGAGGCCGTGACGAACTTCG   955
Consensus                                                  gcttacgacaaggcggcgatcaaatgcaacggtagggaggccgtgacgaacttcg

TaTOE1-B1-1  AGCCGAGCACCTATGATGCGGAGCTGCTCAGTGAGGTTGCTGCTGAAGGCGCAGATGTCGACCTCAACTTGAGCATATCTCAACCAACTTCACAAAGTCC  1100
TaTOE1-B1-2  AGCCGAGCACCTATGATGCGGAGCTGCTCAGTGAGGTTGCTGCTGAAGGCGCAGATGTCGACCTCAACTTGAGCATATCTCAACCAACTTCACAAAGTCC  1055
TaTOE1-B1-3  AGCCGAGCACCTATGATGCGGAGCTGCTCAGTGAGGTTGCTGCTGAAGGCGCAGATGTCGACCTCAACTTGAGCATATCTCAACCAACTTCACAAAGTCC  1055
Consensus    agccgagcacctatgatgcggagctgctcagtgaggttgctgctgaaggcgcagatgtcgacctcaacttgagcatatctcaaccaacttcacaaagtcc

TaTOE1-B1-1  CAAAAGGGATAAGAGCAGCCTTGGCCTGCAACTCCACCATGGATCATATGAAGGCTCTGAACTAAAGAGACCAAAGGTCGATGCGCCCCCTGAGATGGTC  1200
TaTOE1-B1-2  CAAAAGGGATAAGAGCAGCCTTGGCCTGCAACTCCACCATGGATCATATGAAGGCTCTGAACTAAAGAGACCAAAGGTCGATGCGCCCCCTGAGATGGTC  1155
TaTOE1-B1-3  CAAAAGGGATAAGAGCAGCCTTGGCCTGCAACTCCACCATGGATCATATGAAGGCTCTGAACTAAAGAGACCAAAGGTCGATGCGCCCCCTGAGATGGTC  1155
Consensus    caaaagggataagagcagccttggcctgcaactccaccatggatcatatgaaggctctgaactaaagagaccaaaggtcgatgcgccccctgagatggtc

                                                                                    7 bp
TaTOE1-B1-1  GCAATCCCTCATCGATACCCCCTTCTGACCGAGCATCCACCAATCTGGCATGGCCAATCATATCCCATCTTTTTAAATAATGAGGATGCAGCCAGAGATC  1300
TaTOE1-B1-2  GCAATCCCTCATCGATACCCCCTTCTGACCGAGCATCCACCAATCTGGCATGGCCAATCATATCCCATCTTTTTAAATAATGAG......CCAGAGATC  1248
TaTOE1-B1-3  GCAATCCCTCATCGATACCCCCTTCTGACCGAGCATCCACCAATCTGGCATGGCCAATCATATCCCATCTTTTTAAATAATGAGCATGCAGCCAGAGATC  1255
Consensus    gcaatccctcatcgataccccct tctgaccgagcatccaccaatctggcatggccaatcatatcccatctttttaaataatgag      ccagagatc

TaTOE1-B1-1  ATAGCAGGAGGCCAGAGGTGGCCACAGGGGGTGTTCCAACCTGGGCATGGAGTGTGAGCCACCCTCCTCCAACACAACCCATGCCACTCTTCTCGTCGTC  1400
TaTOE1-B1-2  ATAGCAGGAGGCCAGAGGTGGCCACAGGGGGTGTTCCAACCTGGGCATGGAGTGTGA..........................................  1305
TaTOE1-B1-3  ATAGCAGGAGGCCAGAGGTGGCCACAGGGGGTGTTCCAACCTGGGCATGGAGTGTGAGCCACCCTCCTCCAACACAACCCATGCCACTCTTCTCGTCGTC  1355
Consensus    atagcaggaggccagaggtggccacaggggtgttccaacctgggcatggagtgtga

TaTOE1-B1-1  ATCGTCCGCTGCAGCATCATCAGGATTCTCCAAAACCGCCGCGGCAGCTGCCCCCGGCGCCCCATCGGCCTCATTCCGGTTCGACCCGATGGCGCCATCA  1500
TaTOE1-B1-2  ..................................................................................................  1305
TaTOE1-B1-3  ATCGTCCGCTGCAGCATCATCAGGATTCTCCAAAACCGCCGCGGCAGCTGCCCCCGGCGCCCCATCGGCCTCATTCCGGTTCGACCCGATGGCGCCATCA  1455
Consensus

TaTOE1-B1-1  TCATCGTCAAGCAACCAACACCACCACCACCCCCGCTG  1538
TaTOE1-B1-2  ......................................  1305
TaTOE1-B1-3  TCATCGTCAAGCAACCAACACCACCACCACCCCCGCTG  1493
Consensus
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Figure S1. Coding Sequence alignment of the three transcripts produced by *TaTOE1-B1* in this syudy. *TaTOE1-B1-1* (ID: TraesCS1B02G076300.1), *TaTOE-B1-2* (ID: TraesCS1B02G076300.2) and *TaTOE1-B1-3* (ID: TraesCS1B02G076300.3); The red boxes show the locations of the 45bp (1219-1264) and 7bp (1603-1611) differential loci, respectively.

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TaTOE1-B1-1    MELDLNVEEKPAAVARSDSGTSESSVLNAEASCGGGAAPAEEASSSTRQPAPAPRAVLEFSILRSSASAEGENDVGADDDEEEATPSPPPPPTRHYHQHL    100
TaTOE1-B1-2    MELDLNVEEKPAAVARSDSGTSESSVLNAEASCGGGAAPAEEASSSTRQPAPAPRAVLEFSILRSSASAEGENDVGADDDEEEATPSPPPPPTRHYHQHL    100
TaTOE1-B1-3    MELDLNVEEKPAAVARSDSGTSESSVLNAEASCGGGAAPAEEASSSTRQPAPAPRAVLEFSILRSSASAEGENDVGADDDEEEATPSPPPPPTRHYHQHL    100
Consensus      meldlnveekpaavarsdsgtsessvlnaeascgggaapaeeassstrqpapapravlefsilrssasaegendvgadddeeeatpsppppptrhyhqhl

TaTOE1-B1-1    LQPQQLVTQELFPAAATAGGPPPMSVPQHWAELGFFRPAAPPPDMRILQMQQQQLQVHAQPPPPPAAQPPVAKKSRRGPRSRSSQYRGVTFYRRTGRWES    200
TaTOE1-B1-2    LQPQQLVTQELFPAAATAGGPPPMSVPQHWAELGFFRPAAPPPDMRILQMQQQQLQVHAQPPPPPAAQPPVAKKSRRGPRSRSSQYRGVTFYRRTGRWES    200
TaTOE1-B1-3    LQPQQLVTQELFPAAATAGGPPPMSVPQHWAELGFFRPAAPPPDMRILQMQQQQLQVHAQPPPPPAAQPPVAKKSRRGPRSRSSQYRGVTFYRRTGRWES    200
Consensus      lqpqqlvtqelfpaaataggpppmsvpqhwaelgffrpaapppdmrilqmqqqqlqvhaqpppppaaqppvakksrrgprsrssqyrgvtfyrrtgrwes

                         AP2-Domain1
TaTOE1-B1-1    HIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGVDADINFNLSDYCDDMKQMKGLSKEEFVHVLRRQSTGFSRGSSXYRGVTLHKCGRWEARMGQFLGKK    300
TaTOE1-B1-2    HIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGVDADINFNLSDYCDDMKQMKGLSKEEFVHVLRRQSTGFSRGSSXYRGVTLHKCGRWEARMGQFLGKK    300
TaTOE1-B1-3    HIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGVDADINFNLSDYCDDMKQMKGLSKEEFVHVLRRQSTGFSRGSSXYRGVTLHKCGRWEARMGQFLGKK    300
Consensus      hiwdcgkqvylggfdtahaaaraydraaikfrgvdadinfnlsdyeddmkqmkglskeefvhvlrrqstgfsrgsskyrgvtlhkcgrwearmgqflgkk

                         AP2-Domain2
TaTOE1-B1-1    YIYLGLFDNEVEAARAYDKAAIKCNGREAVTNFEPSTYDAELLSEVAAEGADVDLNLSISQPTSQSPKRDKSSLGLQLHHGSYEGSELKRPKVDAPPEMV    400
TaTOE1-B1-2    ...............AYDKAAIKCNGREAVTNFEPSTYDAELLSEVAAEGADVDLNLSISQPTSQSPKRDKSSLGLQLHHGSYEGSELKRPKVDAPPEMV    385
TaTOE1-B1-3    ...............AYDKAAIKCNGREAVTNFEPSTYDAELLSEVAAEGADVDLNLSISQPTSQSPKRDKSSLGLQLHHGSYEGSELKRPKVDAPPEMV    385
Consensus                     aydkaaikcngreavtnfepstydaellsevaaegadvdlnlsisqptsqspkrdksslglqlhhgsyegselkrpkvdappemv
               15 amino acids
TaTOE1-B1-1    AIPHRYPLLTEHPPIWHGQSYPIFLNNEDAARDHSRRPPVATGGVPTWAWSVSHPPTQPMPLFSSSSSAAASSGFSKTAAAAAPGAPSASFRFDPMAPS    500
TaTOE1-B1-2    AIPHRYPLLTEHPPIWHGQSYPIFLNNE.........PPIIAGGQ.RWPQGVFQFGHGV......................................    434
TaTOE1-B1-3    AIPHRYPLLTEHPPIWHGQSYPIFLNNEDAARDHSRRPPVATGGVPTWAWSVSHPPTQPMPLFSSSSSAAASSGFSKTAAAAAPGAPSASFRFDPMAPS    485
Consensus      aiphrypplltehppiwhgqsypiflnne             pe   gg    w   v   p

TaTOE1-B1-1    SSSSNQHHHHP    511
TaTOE1-B1-2    ...........    434
TaTOE1-B1-3    SSSSNQHHHHP    496
Consensus
```

Figure S2. Protein sequence alignment of TaTOE1-B1-1, TaTOE-B1-2 and TaTOE1-B1-3. The red box represents the first AP2 domain (185-246), and the yellow box represents the second (277-338); The blue line shows 15 different amino acid locations.

Table S1. Primers used in this study

Primer name	Sequences (5'-3')
Clone-F	ATGGAGCTGGATCTGAACGTGGAGGAG
Clone-R	TTTTCAGCGGGGGTGGTGGTGGTG
pBI-CDs-F	acgggggactctaga<u>ggatcc</u>ATGGAGCTGGATCTGAACGTGG
pBI-CDs-R	cgatcggggaaattc<u>gagctc</u>TCAGCGGGGGTGGTGGTG
FT-F	CTGGAACAACCTTTGGCAAT
FT-R	AGCCACTCTCCCTCTGACAA
CO-F	ATTCTGCAAACCCACTTGCT
CO-R	CCTCCTTGGCATCCTTATCA
FLC-F	AGCCAAGAAGACCGAACTCA
FLC-R	GGAGATTTGTCCAGCAGGTG
SOC1-F	AATTCGCCAGCTCCAATATG
SOC1-R	CCTCGATTGAGCATGTTCCTA
PP2A-F	TAACGTGGCCAAAATGATGC
PP2A-R	GTTCTCCACAACCGCTTGGT
Sub-F	atctcgagctcaagc<u>ttcgaa</u>ATGGAGCTGGATCTGAACGTGG
Sub-R	ccgtcgactgcagaa<u>ttcgaa</u>GCGGGGGTGGTGGTGGTG
PGBKT7-F	atggccatggaggcc<u>gaattc</u>ATGGAGCTGGATCTGAACGTGG
PGBKT7-R	atgcggccgctgcag<u>gtcgac</u>TCAGCGGGGGTGGTGGTG
N-R	atgcggccgctgcag<u>gtcgac</u>CGAGCTGCGGGAGCG
N+Domain-R	atgcggccgctgcag<u>gtcgac</u>ATCATAGGTGCTCGGCTC
C-F	atggccatggaggcc<u>gaattc</u>ATGGCGGAGCTGCTCAATG
AD-TaTCP5-A1-F	gccatggaggccagt<u>gaattc</u>ATGATAAGCGCCGGCGAC
AD-TaTCP5-A1-R	cagctcgagctcgatg<u>gatcc</u>TCATCGATCAACCCTGGCTT
AD-TaARF16-B1-F	gccatggaggccagt<u>gaattc</u>ATGAAGGAGGTGGGCGAGG
AD-TaARF16-B1-R	cagctcgagctcgatg<u>gatcc</u>TCACACCCGCTGAACCATG
AD-TaSBP1-D6-F	gccatggaggccagt<u>gaattc</u>ATGGCTGTGCAGGCCCAG
AD-TaSBP1-D6-R	cagctcgagctcgatg<u>gatcc</u>TCAACACAGGATGGCCTCCA
AD-TaMYB85-D5-F	gccatggaggccagt<u>gaattc</u>ATGGGGCGGCAGCCGTGC
AD-TaMYB85-D5-R	cagctcgagctcgatg<u>gatcc</u>CTAGAGATTTGATCCACTTGAGCTGT
TaTOE1-B1-3-NYFP-F	atctcgagctcaagc<u>ttcgaa</u>ATGGAGCTGGATCTGAACGTGG
TaTOE1-B1-3-NYFP-R	ccgtcgactgcagaa<u>ttcgaa</u>GCGGGGGTGGTGGTGGTG
TaARF16-B1-CYFP-F	atctcgagctcaagc<u>ttcgaa</u>ATGAAGGAGGTGGGCGAGG
TaARF16-B1-CYFP-R	ccgtcgactgcagaa<u>ttcgaa</u>TCACACCCGCTGAACCATG
TaPIFI-CYFP-F	atctcgagctcaagc<u>ttcgaa</u>ATGGCCACCATCTCTTCTTGC
TaPIFI-CYFP-R	ccgtcgactgcagaa<u>ttcgaa</u>CTCCTCCGTATCAGAGTCCAGC

The lowercase letters indicate homologous arm sequences, and the underscores indicate the restriction site sequence.