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Title	Identification of Arabidopsis thaliana upstream open reading frames encoding peptide sequences that cause ribosomal arrest
Author(s)	Hayashi, Noriya; Sasaki, Shun; Takahashi, Hiro et al.
Citation	Nucleic acids research, 45(15), 8844-8858 https://doi.org/10.1093/nar/gkx528
Issue Date	2017-09-06
Doc URL	https://hdl.handle.net/2115/67324
Rights(URL)	https://creativecommons.org/licenses/by-nc/4.0/
Type	journal article
File Information	gkx528_Su.pdf, Supplementary data



Supplementary Figure S1

A AT2G27230 (HG2)

1 CCAAGAAGCAGAGAAAAGAAACATTAAAGCAGAGAAAAACAAAGACAAATAATCTCCAT

61 TTGCTTTCTTCTCCATCTTCTTCTAATTTTCTTCAAGTTTTATCAATGGCTGGTGTACT

121 GGAATCTTAAAGCTTGAAGCTTGGAGCATCTTGTGAAGAAGATTAAGTAGTTTCTTGTAT

181 TTTTCTTTTCTGGGGTTTTGAGTTTTTTTTTCTCTTCCTTATTACCGGAAGTAATGGCAT
M A C
M A C

241 GTCGGAGTATGATCGCTTTTAGTTTAGATCCTGAAAGAAAACAAAGTGGAGGACTTAGGA
R S M I A F S L D P E R K Q S G G L R T
R S M I A F S L D P E E N K V E D L G

301 CAAAACAAGCTGGAAGAGGATCTTGCCGTGGAAGTTAGTCTTTGTTCAAATCCATTTTCC
K Q A G R G S C R G S *
Q N K L E E D L A V G S *

361 TCTTAAAGAATTTTGAAATTGCACTGTTGCAAGTGAAAAAGTTTGTCTTGTTGGAGCTT

421 AAAGAAGAGAGAAGAGAAAGAGAAAAGCTATG

B AT5G52550 (HG4)

1 AAAATCTTCTTTCTCAAAATCTTCTTCTCTCGTCTCTGCGTTTATTCTCTCTGGATCGA

61 AGTAGTAACTTTACGTCCGCGATTTGGTCTCTCTCTCTCTCTCTTTCTATCCGATAAA

121 TCTCAGGAGAAGTTAGTCGAGGTAGTCTGCTTCTATGCCATTTTGCCGAGAAAATGGGAG
M G E
M G E

181 AAGTTAAGGGATGTTGGAATTAGGACGAATGCTTTCAAAGGATAACTCTGCAAACCTCT
V K G C W K L G R M L S K D N S A N S Y
V K G C W K L G R M L S K D N S A N S Y

241 ACAACGTCTCCCTTCTCTTATCTCCTGTTGTTTCTGTTTGGGATTGTATTGTCCGTAAAA
N V S L L L S P V V S V W D C I V R K M
N V S L L L S P V V S V W D C I V R K M

301 TGAGGTATACCTACATACCTGAGTGGGTGTAGTAGTCATTGAGATCATCGCGCCTTGGTG
R Y T Y I P E W V *
R Y T Y I P E W V *

361 TAGTGAGTTTGGTAGAATCAAAGTAAAAGGAAACAACCAACTAAAAGAAGAAGCCAGTTA

421 ACAAAGCAAGGCAAAACAAAGACTTGTAGCAATCATG

C AT5G07840 (HG5)

1 CTAAGCTACGACGCCTACAGATCTGGCTGGTAAAAATCACGCAGATAGAGACTCTGGCCC
61 GATGCTCTCTTTACCCATTGATCCAGGCTTTTCTGATTTCTCTTTGTTCTAGAAACCA
121 TTAAGCTCCTACCTCTTTCTAGTTGATGCTCGTGTTCTCTTCACTGTCTATGACTCCAGT
M L V F S S L S M T P V
181 **TGTGATCCCTCAAAATCTCCGTGTCTTTGGCCCTGGTTTGAATCCCTCTTTCCCTTACTG**
V I P Q N L R V F G P G L N P S F P Y C
241 **CATTGCTAATCACTTCCCTTGAT**TGAGTTGCTCCATTCCAACGAATCATCTCAATCTGC
I A N H F P *
301 CTCTCCATAAGTTCTTATTCTGAGTGATATTGGTTGATGATTCTACCCACAAGTAGTG
361 TTCCTGCTTTAGACATTCTTGTATAAGATTGTAACCAAATTATGTAAATCTGAGTCACT
421 CCTAGAATCTCCTTGTCTAGTAAGTTTCCCTTAGGAAATATCCTTTGAGTCTTTCATCTG
481 TGAATTCTAGTCAGTTCTGGTTTATCTGCAAGATG

D AT2G43020 (HG6)

1 CCAAAGCCTAAAAAATCCGACCTTTTTTTGTTTTCTCTCTCTAGAAGTCTCTCTGTTTTTC
61 ATCTTTCTCTCTCTCTCTCTAGCTCTTCTTCCTCGTTTCTGGCTTTTCTGGGAATTTTGA
121 TCCTTTGGCCCCCATTGCTCGCTTGAATTACGAATCAGATATCGCCGATCGTCGTAGATC
181 TGC GTTGATACTGTCCGGCTGAGTAAACAGGGTGAACAAAAACAAAAACAGAGAGGGGG
241 TTTAAAAATCCTGAAGAAAATCGC**ATGAATTGTTTGGAAGCCTG**ATTTTTTTCATCTTCG
M N L F G S L I F S S S
301 **ATTTGAGCCACTTCACGACTTGTCTTCTCATCTTTATTCTTCATTTCTCTCCCCAGCTT**
I S S H F T T C L L I F I L H F S P Q L
361 **AATAGTAATAATAATAATAATAATAGTAATCGTAATTCCAATAATCTCGAGAGTAATCGT**
N S N N N N N N S N R N S N N L E S N R
421 **TTGATCAATTGA**AAAAAAATCATGGAGTCCAGGAAAACTCTGATCGTCAAATGCGTAG
L I N *
481 AGCTAATTGCTTTTCAGCTGGTGAGAGGATGAAGACAAGGTCGCCCTCCGTGATTGTGAT
541 CGGA

E AT1G36730 (HG7)

1 ACAATCACGCGTCTTCTCATTTCTAGTTTCTCAGCCTCCTCCTTCTCTTCCTTCTTA
61 TATATAAATATATCCACAAAATCATCTCTTTTGCTTCGCTGTTTCTCTCATTATTCCATC
121 TCTCTTATCGCCGCTACAAACGTTTCTTCTTCAACCTCGTTCAGAGATTATCCTCCCTTC
181 TTTTCTCATCTTACAAGGAAGTTGGGCAGTTAAAGCTGCTGGGATCACCAGTTTTGTCAA
241 AAGTGGAGTGTGAAGAATCTTTT**ATGTCTGAACAGGCTTCTCTCTTT****CAATCATCTATCC**
M S E Q A S L F Q S S I R
301 **GGCTTTTAGGAGAGTACTGTCCTATATCTAGGAAAAAGTCCACTCATAAAGTTGGTGGTT**
L L G E Y C P I S R K K S T H K V G G L
361 **TGCGTTTTGAGGAGGACATCACGAGCTGTATTGGATTTCAGTTTATGCAACTGAGTGATT**
R F E E D I T S C I G F Q F M Q L S D Y
421 **ATCACTGCCTCTTCTGA**CATCCCTTGTTTGTTTACGTTTGTTGAATCAAG**AT**GGCTTTGC
H C L F *
481 AAAACATTGGTGCCTCCAACCGCGATGATGCCTTTTATAGGTATAAGATGCCGAGGATGA
541 TGAC

F AT3G12010 (HG8)

1 GGTGATCGTTTGTTCGTTGAAGAAGAACAACAACCATCAATTTCCGGACGAGCAAGCCGA
61 GGAGGTCTGTTTGTACAAAACTCGAACTACTACTCTTCTGTCTGATTGTAGCAACTCC
121 ATCACTGTATTTATATTCATCTCCATCTGGGTTTTCGAAGCTTTAGCAATGCAGGC**ATGA**
M K
M K
181 **AAGAAAAGAATTCCACTACCGCTCTACACTTGGACGGATTTTAGCTACTTGTTCTAAAC**
E K N S T T A S T L G R I L A T C S K Q
E K N S T T A S T L G R I L A T C S K Q
241 **AGGCCAAAGACTACGGGAGCTGTGTTGCATCTAAAGTTCATGAGGTTGAAAGAGATATAT**
A K D Y G S C V A S K V H E V E R D I C
A K D Y G S C V A S K V H E V E K R Y M
301 **GTTTGAAAGAGTTTCTTGCGCTGAAGAGTTGTATGCA**GCATACGATCCGAGGAAAGGCTT
L K E F L A L K S C M Q H T I R G K A *
F E R V S C A E E L Y A H T I R G K A *
361 GAATCACAATTATATTCTCCTTTTCGTTAGAGGCATTTATCAGCACTGCTTGAAGTTTTA
421 ACATGAATTCAAGTGCACAGGCAGGTGTTGGTTCTGGTGCTTTATCAC

G AT5G09670 (HG9)

1 GCCAATAATCTTTTTGTCTTCTATCTTCGACACCTGTTTCTGAAATCTTCTTCTGTCTT

61 CTCCTTGGAATTCTATCTGTGAGCCCGAGTTTCAGATCCACCAGGTCATGTGGACAGTTC

121 TCAACAGTAGCATACTTCAACAAAGATCATTGCTTTTCAGCGGAACCTGATAATCTCCAA

181 CAAACATTCTTCGGTTTACAGTATTAACACCAGCAGGATAGTGCTGTTTTCCATTCTTG

241 AAG**ATGGACAGGGCAGATACGTCGGGCTTTGTAAGTGGCGGAAGTTGTTCATCTCTCAAC**
M D R A D T S G F V S G G S C S S L N
M D R A D H V G L C K W G S C S S L N

281 **TTGCTCCAATATATGCTTATAGCTACAAGTATGATGTGCTAAG**TGGTACTATTTTCGGAGC
L L Q Y M L I A T S M M C *
L L Q Y M L I A T S M M C *

321 TCTCTTTCATCTATATCCTTTTCATCTTCATGTGAATTTGGACAAAGGTGTAGTTCCATT

361 CTCTAGTGCCATTAATATGGGTGACACC

H AT5G45430 (HG10)

1 ATCACGAGAACCACACAAATACGCGGCAAAGAGAGAGAAAGATAGAGAGAGAGAGAGAGA
61 GAGAGAGAGAAAGCGGTGGAGTCGTGATAAGGGAGAAGCTCTGGATACAGTCTCTTCCCG
121 TCGTCGGAGACGGAGTTTATGCCTATTGGCTCCTGAGGTTAGATTAAGCTTCGTATTTAG
181 TGGATTTTCTTCTTTTGAGATATGGAACAAGATTACATCTGCTCAGGGTGCTACCAGTAT
M E Q D Y I C S G C Y Q Y
M E Q D Y I C S G C Y Q Y
241 CGAGTTTTTTCATTGCAAGAAGCACTCGATTGGCGGTTTCTTGTGCACTCAGATTCCTT
R V F S L Q E A L D W R F L V H S D F L
R V F S L Q R S T R L A V S C A L R F P
301 ATCGGCTCTTTCGTGAACCTGCACCTAGTGGTCAGACCTTCTGCGATCTTTACGGAAGGTG
I G S F V N C T *
Y R L F R E C T *
361 TGATGCAAATTTCTGATTCAGGGCTGATGTTTGCAAGTTATCCTACCTTCACACAGTCCT
421 AGAGTGTCATCTAAATCTGTTCCCTGCACTCAAAACTAGTTGGTCCTTCTTCCATATCC
481 TGTTCCTTATGAGAGCTTGTTGAAGAAGGATGAATCAGTTTTTTTTCAAGTTATGACTTTT
541 CTTAGCTGTGTCTTTTCCTCGAGTCTCTGAACCCCTTGAGTGAAATGTTGTGAGCATAAG
601 TTTCGTCCAGCTACCCAGAACATTACTTTTTGTTAGTGCGTCTTCCAATTCTCAGTATGT
661 TTTGTCTTTTTCTCTTAGCGTCTTTCTTTTGCCTTGTTGGTCAACCCATTGATGTTCAAA
721 CTTCAAAGTAAATAAGGGTCAGTCTACCCAGCGGGAGAATCATTGATCTTGCTGCCATAC
781 GAACAACTGGAAGATTAAAGTGATAGACATATTTCAGAAGTCTTTACAGAGAAATACTT
841 AAGGGGATACTTTGCTTCACCTAGAGGCGATC

I

AT4G22590 (HG11)

1 CTCCTCTTTCCAAATTCGGATTTTTAGTGAGCTCTTTGCAATTTTtagggTTTTCTTCG

61 AATAAAGAAAAAAATCCCTGATCTTCCTCTTAGTGATTTCTCCTTTCGAGATCCCTG

121 AGATTCCGAGAAAATCTGCATTTTTTCTCGTGATTCTCTAGCTCTGTTTTGTGTTTTAC

181 ACAGCTCTTTTGAATCAGGTTTGTGTGTGATAGCGTTGTTGTGGTAAAAGCTTTGTACAT

241 TTGAAGATTTAGAGATGATAAGTTTTCAGGTAACCTACTTTTAATGGACAGTTCAACAAC

M D S S T T
M D S S T T

301 AAGCAGTGATAAGAAAACACTAAAGAGGTGGTTTTTCATTGACAAAAGAGTTGGATAAAG

S S D K K T L K R W F F I D K R V G *
S S D K K T L K G G F S L T K E L R *

361 TGTGTTTAGAAGAAGCCGTCGAATTTCTTAGTTTGAAGCATTTTATTGTTTGGAGAGTTC

421 GATGATTTGAATATAACAAGACGACCCCTGTTCTTAGTGACCCTACTACACCAGTAAG

481 T

J

AT1G70780 (HG12)

1
ACCAACAATCACATTCTTCTCCATAAGAAAAAAAAAATAATCAAATCCTCCTCCTCTGC

61 TTCACCACCAAAAAGCATATTCTTCTCTCGTCTTCTCCGGTTAATCAAAATCTCTCCGTG

121 TGAATCGTTTGTGAATGGTGAAACTAATCCGATCGGTGGTAAGTTTACGCTCTCCCTTT

M V E T N P I G G K F T L S L S
M V E T N P I G G K F T L S L S

181 CCATCAAAAGGGCGAGCTTTTCTCTTCCTCTCTCGACATCCTCTGTTTTCGCTTTCGGAT

I K R A S F S L P L S T S S V F A F G S
I K R A S F S L P L S H P L F S L S D

241 CTTGCAAAGAAGGCTGGTACTTTTCGCTGCCTTGGCCTCGACCCGTGAACGATTCGCCCCCT

C K E G W Y F R C L G L D P *
L A K K A G T F A A L A S T A *

301 AAAATTCACAACCCGGAACCCTAATTCCTAAAAAGTGGTTCTTTTTTTATTGATTCTGT

361 TACTTGTGAGATTGCTCTGTTTTTTGTTCTCTCGATTTCGAAGATGTT

←-----
AT1G70780 TP2

K AT3G18000 (HG13)

1 ACACTCTTTTCGCTCTCAGATCTGAAACCTTATCTGAATTACATTTCCCCGATTGACGT
61 TGTGCGAATTG**ATGCAGCAGAGAGGACGATCCGTCAACCGCAGATCACGAAGCTTCTCTA**
M Q Q R G R S V N R R S R S F S R
121 **GATCCAGACTCGCCGTCGAAGGCCACTGA**ATTACTCTCTCCCCTCTCTTGGCAGATCTTC
S R L A V E G H *
181 TTCTTCGTTTTTTCCCGACAAACGACATTTCCGAAATGGCTGCATCGTACGAAGAAGAGC
241 GTGATATTCAGAAGAATTAC

L AT3G01470 (HG14)

1 GAGACGCTCACATTGCAAAAACAAAACCAACAAGGAACTTGTCTCTCTCTCTGGCTCTCT
61 TTCTCTTAACGTGATCATAACGTGATTCGAAAATTGGATATAGATAGGTTTCTTGTTGGA
121 TCTTGATCCCTCTGGAAAAGGAGGGGAGAATAGCAGTTC**ATGATGGGATTTTGTATCTGC**
M M G F C I C
M M G F V S A
181 CCGTTGGAGTCACCTGCGAGATTACTATGGAGTACAAGCTTCTTCCGCCATAAGATCATG
P L E S P A R L L W S T S F F R H K I M
R W S H L R D Y Y G V Q A S S A I R I M
241 **ATCTTCTAA**TCCTTCCTACTTCTTCCCATCTTTTAAATCATCTTCTCGCTATCTCTGCTT
I F *
I F *
301 CCTCTTCTCTCTGTTTCCTCTTCTCAGAACTCAGAAGTAGTTGTTGTTTTATTTCTGT
361 TGATCAAAAATG

M AT3G51630 (HG16)

1 CAAGAACAAAGAAGAAGGAAAAAGTAGAGCTTTTTTGGGAATCAGAATCATCATCGATGG
61 TGAATCCAAAGCGTGGCAATAGGTTTTTCAAATACAGAATTGTGTAAATTGCTCTCTATC
121 TTCTTCTCTTTCAAATTCTCTTCCTTTTGTGTATTCAATAACTTTTTCCCCACTTTGAT
181 GGGCTGCAACCACATATTCTTCTTCTATCTTTAACTTTTCCCACCAAACCTTCTCCTTTTT
241 TTTCTTTTTTTTTTGGGTTCTGGGTCTGCTTTTTTGTGTGTTGTTGTTGTTGAATGAAGGTC
M K V
M K V
301 CGTAAGGGAAGAAGACAGATGATTGCGAAAGAGCAAGACGAATACAAATTACGCCAACAA
R K G R R Q M I A K E Q D E Y K L R Q Q
R K G R R Q M I A K E Q D E Y K L R Q Q
361 GGTCTTGTTTTTCAAATGGCTTCTCTTTTCCTCTCTTTCGATTACTCCTTACTCTTCTTT
G L V F Q M A S L F L S F D Y S L L F F
G L V F Q M A S L F L S F D Y S Y S S F
421 TGGTTGCTCTTCCGCGTTTTCTTATACGAGAATCACGAACGAAAACCTCCAGATTTTCTAG
W L L F R V F L Y E N H E R K L Q I F *
G C S S A F S Y T E N H E R K L Q I F *
481 CACACCTCTTCTCTCTGCATCGCCATCTTGTTTTTTCCCCCAAATTTTCGATTTTTTTTT
541 TGTATAACTTTTGAGATTCTGATAGATCCGGTACGGAGTCATGTATATGGAGAT

N AT1G58120 (HG17)

1 ATTGCGAGAAACAAAGAAACTTAAGCCTCAAGAAATCAAACCCACAAAAAATCAATTCA
61 ACAAACCTCTTTCTGCTCTCTCTCTCTTTTTTCATTCCCATATGTTGCTTCCTTGAGTTT
121 ATCTCTTCCCAAAGAATGGGAAGCAACATCTGAGGATCCATTTGATTACCATACATATAT
181 TAAAAACAAAACATATATCTTTGTGTGTGCGCGTTAATGATGAAATAGCAGATTGAGAG
241 CAAGAAAGAGGTCATAGCTGATAACCACAATGGAGATTCAGAGGATGAGGCAGTTGATGT
M E I Q R M R Q L M S
301 CTCTTTGGTCTAATTTGAAGAGTAGCCGCGTTTCTCTCACC GGTGGGAATCATA CAGCCG
L W S N L K S S R V S L T G G N H T A A
361 CAAGGTTCTGCACTCGCTAGGCTCGCCTCTTCTCTCGCTAGCTTTTTCTTTCTTCTTTCT
R F C T R *
421 CTTCTTCTTACTTCCTTTTGATTCTCTTTAGCTCTCTATTCTCTTCTCTTCTTCTCTCT
481 TTTTCCTATTTCTTTAACTTTCAACTGTACATTTTCGCGCGCGCTCTTTGTCTCAGCTTT
541 TAAGACATAACAAAACAAGATATG

O AT4G36990 (HG18)

1 GACATAACACTTAACTCGTTTATATATTTGTTTACTTGTTTTGCACATACACACAAAAA

61 TAAAAAAGACTTTATATTTATTTACTTTTTAATCACACGGATTAGCTCCGGCGAAGTATG

121 GTCGTCGTCTTCATCTTCTTCCTCCATCATCAGATTTTTCCTTAAATGGAAGAAACCAAA

M E E T K
M E E P N

181 CGAAACTCCGATCTTCTCCGTTCTCGTGTTTTCTCTGGCTTTTATTGCTGGGATTGG

R N S D L L R S R V F L S G F Y C W D W
E T P I F S V L V F S S L A F I A G I G

241 GAATTTCTACCGCTCTCTTGCTTTTATGTTGCTGATTCTTTTTCCTTCGACTTTCTATT

E F L T A L L L F S C *
N F S P L S C F L R C *

301 TCCAATCTTTCTTCTCTTTGTGTATTAGATTATTTTATGTTTATTTTTCTGTGGTA

HsfB1 TP1

361 AAATAAAAAAAGTTGCGCCGGAGATGAC

P AT5G53590 (HG19)

1 ACCTCCTCTAAAAAACCAAATAAAAACCTTTTTTCTCTCTTCATGCTTAGCCTATCATG
M
M

61 AGCAACATCCCTAGATCTCTCACCGACTCAGATCTTTCTCTATTTACTCTCATAATCTCT
S N I P R S L T D S D L S L F T L I I S
S N I P R S L T D S D L S L F T L I I S

121 TCTGCTGTTGATCCTTGGCCTTTTTCTATCACCGTTTTTTAGCATCAACAAAACTCACCG
S A V D P W P F S I T V F *
S A V D S L A F F Y T V F *

181 GAAAATCTCTAACAACCACCACCGTTTAACACTTCTCTTCCTCCTCGTCGATCGTTTTTA
SAUR30 TP1

241 AACCAATCTTTGTGTTTCTTGTTTGGTTTTTCGGTGAAAAAGATTCCCTTCTTCTTAATG

301 G

Q AT2G37480 (HG20)

1 ATTATTCATTTCTTCTTCGTCTTCTTCTTCTTCTCAAATTAGCTTTTCTTTATCGTCTT

61 CCTCAAGCGTGAGATTCGTTGTGGATATAGTTTTTCTCCTTGATTCTCTGGTTCTTTCCA

121 TGATCCAATTTTAAGGGTTTCACGGCTTCGTTTTTTTTGGGTATATCTAGCTCTATCGTTC

181 GTGGTGGTTTTCTTTCTGGATCAAAGTTTTCTGAGATCTCTGCGATTTCTGGGATTTCGAA

241 AATTGGAGAATTAGGGCTTTTTTACGGTAACAGGGTTTCGAAGAGCATAAGATAAGAATG
M
M

301 CCTTCGGTGCCCTCTAAGCTTCTTCCTCTCCTGTCTTTGATTCCTTCGTTGACTCCTTAT
P S V P S K L L P L L S L I P S L T P Y
P S V P S K L L P L L S L I P S L T P Y

361 CATTCTGGTTTGAGTTCTAATCGTTTGAAACCTCTTGAAAAGTGTGATTGGCGTGGAAT
H S G L S S N R L K P L E K C D W R G N
H S G L S S N R L N L L K S V I G V V I

421 CTTAGTTAACATTTTCCTTTCCTTCTTCTCTCCTTTTTTACCCTTCTTCTCTCGCCCTCGT
L S *
L S *

481 TTA

541 TTTGATTTGCAGCACAAAAAGTTACTACTACTACTGTGATTACCTTGTACTGTTAGTTGGA

601 TATG

R AT1G68550 (HG21)

1 ATTCACAAGAAGAAAAAAAAAAGTGTGAAAGGAAAAGAGAGAGAGAAAAAAAAATCAGAAGA
61 AACAAACAGCAACAAGGAACAGTGAAAGGTTTCGGTTTTTTGGGTTTCGATCTGATAATCAA
121 CAAGAAAAAAGGGTTTGATTTATGTCGGCTGGGTTTGAATCGACTGTGATTTTGTCTTTG
M S A G F E S T V I L S L
M S A G F E S T V I L S L
181 ATTCATATCTCTTCTCCGATTTTCATCATCATCTTCCCCATCATCGTCGTCTTTGAAATCT
I H I S S P I S S S S S P S S S S L K S
I H I S S P I S S S S S P S S S S L K S
241 TGTCTTCTCAACGCTCTTCACTTCTGCTGTAATAAGCAGAGGCTTGTTCTGGAGACTCCT
C L L N A L H F C C N K Q R L V L E T P
C L L N A L H F C C N K Q R L V L E T P
301 TCTCTTTCCATGCGCTTAAGACCCAAAAGGACTTGTTCTAGTGTTGAAGTCTTTGGGGGT
S L S M R L R P K R T C S S V E V F G G
S L S M R L D P K G L V L V L K S L G V
A
361 TTTACATAAAGCAGCAAAAGTTTTCTTTTTTTCATAGTTCGCTGAGAGTTTTGAGTTTTG
F H I K Q Q K F S F F I V R *
F T I K Q Q K F S F F I V R *
421 ATACCAAAAAGTTTTGACCTTTTAGAGTGATTTTTTGTTCCTTCTGTTTTCTGGGTATT
481 TTTGAGGAGTGGGTTTAACAATGCGTTGCGATTAGAAAG

S AT1G64630 (HG23)

1 CAAATCCTCAATCTGTTTTTAGGGTTTCGAGAGAGAGAGAGAAATTGATTTTTGTGATA
61 TTTGTGAAATTTGGTGGCGAAATTGAAGCTTCTTCATCGGTCGTTGTCTAAAAGCAATGG
121 TGGATGGTTGATGAATGGAGGAGATGCTCTTCTTCTTCTATCCAATAACAATAAAGAG
M E E M L F F F Y P I T I I R D
181 ACACGACGCTGACACAAACGCAGAACCATCTCACCACCGTCATCATCTCGGAGATGGCCG
T T L T Q T Q N H L T T V I I S E M A A
241 CCACACTCCTCTGTTCCCGATCTCGATTCCGATCGGCGATCGACTCCTATTGCTTCGCCC
T L L C S R S R F R S A I D S Y C F A R
301 GTGAGGCCTTCTCCGATCCAATCTCCTTCCATCTCCTCACCCTTCTGTAAACCACCAATCA
E A F S D P I S F H L L T L L *
361 TCATCCCTCCTTTCTTCTTCTTCTTCTTCTGCTTCCGGATTATTAGTATCATTAGGTTAG
421 AATATCTGCCATGGAAGAGGCTGACTTCGTCCAGAAAG

T AT3G22970 (HG24)

1 ACAATCCACACACACACACATAAGAAAAGAAATTAACAAATTATCACAAAAATACGTTTT

61 CTTGTATAATAATTTTTCTCTAGATTTGTCGCTTACCTTTTGAAATTCTCCGGCG**ATGAA**
M N
M N

121 TCTCGCCGGGAAAAGGAATATTCCGGTTATTATTTCTGTTTCCGTT**ACTAGT**GA**CTCTTA**
L A G K R N I P V I I S V S V T S D S Y
L A G K R N I P V I I S V S V L V T L T

181 CCATCGCCGTCATGTCTTCCGTGAACATCGTCGGACCTGAAAAATCCTTCTCCTAGACTT
H R R H V F R E H R R T *
I A V N V F R E H R R T *

241 TTTTTTTTTCTTTCTTCTTTGTATTATTATTCTTTGCTTCGTTTTTGTGAAGAAGATG

301 ATCCGCTGATTTCAGAAGTTTTCTTCTTCTGGATTTTAGCTGAGAGGTTTTTGGTAGATT

361 CTGTTTCTTCTTCTCCTCTGTGGTTTTCGAATCCAGTTTTGGAATTTTGAAGATTTTG

421 TTTAGTTTCTGTTGAAGAGATCTGAGATATTTGAACGAAGCAGAGTGTATATGAAATCAA

481 ATCTGTGAAAATTTCTTTGAATTTGAATTGACTTTGGACTTGTGAGAGAAGTTAGATCTT

541 CTTCTTCGTGAGCT**ATG**

U AT5G60550 (HG25)

1 GGGGAGAGAATCTCGATCAAAGGCTTCGAAGCTCTCTCTTTTTTTTTTTGGTGTGTCTAAA

61 TCTCTCACGCACGACGTTGAGAGAGCTCTTTCCTTTGCGATCTTGTTGTCTTCCTCTGCT

121 CCGATCGAATTCACAACCAGCTTTAATAAGCATTGTAGTTCAACTTGAATTTATTGGCGG

181 TTGTTGAAGCTGTGTAGCTATTAACAATTGGGGCTATGCATTCAACGATTTTCTGCTCGT

241 GAAGAAGGAATATAACTTATTTATAAGGTTTCAGTCTTAGAC**ATGTCGTTTCGATTGC**
M S C F D C

301 AGTGGTTATGATGTCTCAAGTTGTCTTATTCATCTCGCTGAATGGCATCCTTTGGAATAG
S G Y D V S S C L I H L A E W H P L E *

361 TCAAGTTCTCCGGGCTTGAAGCCCTCGAAACCCCTTTATCGCGGGGTTCTCAGTTAAC

421 TTGAGGATTTTATATTTTCATCATACATTTGAGGAGCAATTTGTTTTTTATTTTATTTT

481 GAGAAGGAGATC**ATG**TTTCGTG

V AT5G05280 (HG26)

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1 CTATTACTAGCCTATTTCTACTCTTATAGTACAACCTATTTTCCTTATGTGTAAAACCCA
61 AAGAAGAACTTGTATAAAGAAACAGATCATAAAGGATTTGAGCTTTGATTTTTCTCCATG
121 GATTTATCAAGTCTTTGAGTTTCAGACTGGAACTAAGCCTCGGAGTAAAAGAGAGAACA
181 AAAGCACTCTTGTGCTTATCATAGCATGAAGAACTTGACTCTTTCATCTCAGTCTCTTT
                                M K K L D S F I S V S F
241 CGTAGTCCGATTCGAACAGAACTGGAGCAATAAGAAAAAGAAGAAGAAGAACCTTGAAG
    V V R F E Q K L E Q *
301 GTGAGTTAAAAAAGAAAGATTTGTGCATCTGTTTCTGAAACGTTTACAGATGGCTAG
361 ATTTTACTTGCGACGCAAGCTACC

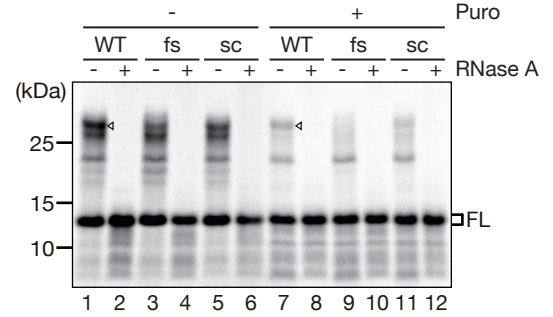
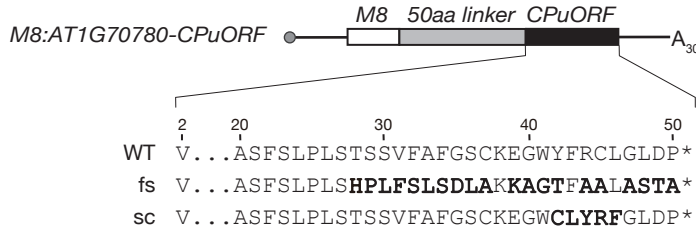
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Supplementary Figure S1. Nucleotide sequences of the 5'-UTRs and deduced amino acid sequences of the CPuORFs analyzed in this study

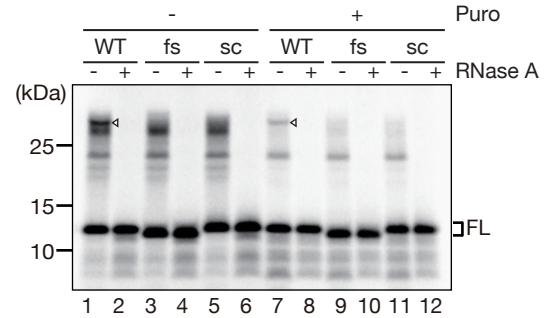
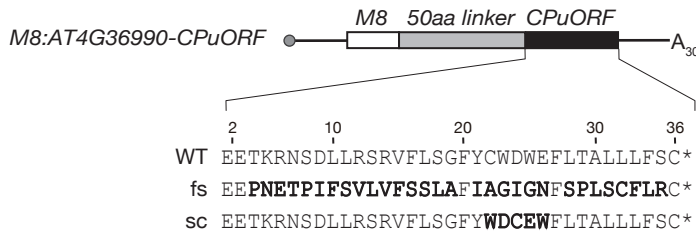
The nucleotide sequences of the 5'-UTRs are based on the full-length cDNA sequences of the TAIR gene models AT2G27230.2 (A), AT5G52550.1 (B), AT5G07840.1 (C), AT2G43020.1 (D), AT1G36730.1 (E), AT3G12010.1 (F), AT5G09670.1 (G), AT5G45430.1 (H), AT4G22590.1 (I), AT1G70780.1 (J), AT3G18000.1 (K), AT3G01470.1 (L), AT3G51630.1 (M), AT1G58120.1 (N), AT4G36990.1 (O), AT5G53590.1 (P), AT2G37480.1 (Q), AT1G68550.1 (R), AT1G64630.1 (S), AT3G22970.1 (T), AT5G60550.1 (U) and AT5G05280.1 (V) (<http://arabidopsis.org/>). The nucleotide sequences and the deduced amino sequences of the CPuORFs are shown in bold. The initiation codon of the main ORF in each sequence is boxed. Thin arrows indicate the positions of the primers used for the cloning of the CPuORFs for the in vitro translation experiments. In (A), (B), (C), (F), (G), (H), (I), (L), (M), (N), (O), (P), (Q), (S), (T), (U) and (V), the nucleotide sequences of uORFs other than the CPuORFs are underlined. In (A), (B), (F), (G), (H), (I), (J), (L), (M), (N), (O), (P), (Q), (R) and (T), the nucleotides that were deleted and inserted in the fs mutants are shaded, and the deduced amino sequences of the fs mutant CPuORFs are indicated. In (J), (O) and (P), thick and dashed arrows mark the positions of primers used for the toeprint analysis and the cloning of the 5'-UTRs for the transient expression assay. It should be noted that the toeprint primer for AT4G36990, HsfB1TP1, anneals to a region in the pNH002 plasmid vector at its 5' end in addition to the position indicated in (O).

Supplementary Figure S2

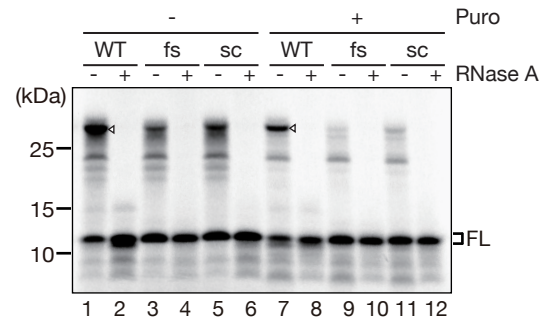
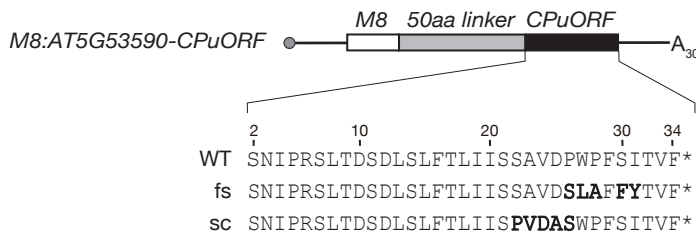
A AT1G70780 (HG12)



B AT4G36990 (HG18)



C AT5G53590 (HG19)



Supplementary Figure S2. RNase A treatment of the *in vitro* translation products of *M8:CPuORF* RNAs

(A-C) SDS-PAGE analysis of [³⁵S]methionine-labeled *in vitro* translation products. Schematic representation of *M8:CPuORF* RNAs and the amino acid sequences of the WT and fs and sc mutant versions of the AT1G70780 (A), AT4G36990 (B) and AT5G53590 (C) CPuORFs are indicated. Asterisks represent stop codons. Altered amino acids in the mutants are shown in bold. *M8:CPuORF* RNAs containing the WT and mutated versions of each CPuORF were separately translated in WGE supplemented with [³⁵S]methionine for 15 min. Translation products were treated with (+ Puro) or without (- Puro) 2 mM puromycin for 30 seconds, and then treated with (+) or without (-) 0.5 mg ml⁻¹ RNase A for 15 min. The translation products were separated by SDS-PAGE and visualized by autoradiography. The positions of molecular mass standards and full-length translation products (FL) are indicated. The open arrowheads mark the WT CPuORF sequence-dependent peptidyl-tRNAs.

Supplementary Table S1

Supplementary Table S1. Plasmids used in this study and primers used for plasmid construction

Plasmid	Construct	Primer	
		Forward	Reverse
pNH001	<i>HA::poly(A)</i>	SP6HAfor	HABKXSrev
pNH002	<i>GST::poly(A)</i>	GSTfor	GSTrev
pNH003	<i>HA-75aa linker::poly(A)</i>	SP6for	HArev
		DAP2-75aaF	DAP2-75aaR
pNH004	<i>M8::poly(A)</i>	M8for	M8rev
pNH005	<i>M8-50aa linker::poly(A)</i>	SP6for	M8rev2
		DAP2-50aaF	DAP2-50aaR
pKM56	<i>35S::ELuc-PEST</i>	ELucfor	ELucrev
		HSPterF	HSPterR
pKM5	<i>35S::RLuc</i>	RLucATGfor	NOSterR
pNH01	<i>GST:AT2G27230-CPuORF(WT)</i>	AT2G27230 for	AT2G27230 rev
pNH02	<i>GST:AT5G52550-CPuORF(WT)</i>	AT5G52550 for	AT5G52550 rev
pNH03	<i>GST:AT5G07840-CPuORF(WT)</i>	AT5G07840 for	AT5G07840 rev
pNH04	<i>GST:AT2G43020-CPuORF(WT)</i>	AT2G43020 for	AT2G43020 rev
pNH05	<i>GST:AT1G36730-CPuORF(WT)</i>	AT1G36730 for	AT1G36730 rev
pNH06	<i>GST:AT3G12010-CPuORF(WT)</i>	AT3G12010 for	AT3G12010 rev
pNH07	<i>GST:AT5G09670-CPuORF(WT)</i>	AT5G09670 for	AT5G09670 rev
pNH08	<i>GST:AT5G45430-CPuORF(WT)</i>	AT5G45430 for	AT5G45430 rev
pNH09	<i>GST:AT4G22590-CPuORF(WT)</i>	AT4G22590 for	AT4G22590 rev
pNH10	<i>GST:AT1G70780-CPuORF(WT)</i>	AT1G70780 for	AT1G70780 rev
pNH11	<i>GST:AT3G18000-CPuORF(WT)</i>	AT3G18000 for	AT3G18000 rev
pNH12	<i>GST:AT3G01470-CPuORF(WT)</i>	AT3G01470 for	AT3G01470 rev
pNH13	<i>GST:AT3G51630-CPuORF(WT)</i>	AT3G51630 for	AT3G51630 rev
pNH14	<i>GST:AT1G58120-CPuORF(WT)</i>	AT1G58120 for	AT1G58120 rev
pNH15	<i>GST:AT4G36990-CPuORF(WT)</i>	AT4G36990 for	AT4G36990 rev
pNH16	<i>GST:AT5G53590-CPuORF(WT)</i>	AT5G53590 for	AT5G53590 rev
pNH17	<i>GST:AT2G37480-CPuORF(WT)</i>	AT2G37480 for	AT2G37480 rev
pNH18	<i>GST:AT1G68550-CPuORF(WT)</i>	AT1G68550 for	AT1G68550 rev
pNH19	<i>GST:AT1G64630-CPuORF(WT)</i>	AT1G64630 for	AT1G64630 rev
pNH20	<i>GST:AT3G22970-CPuORF(WT)</i>	AT3G22970 for	AT3G22970 rev
pNH21	<i>GST:AT5G60550-CPuORF(WT)</i>	AT5G60550 for	AT5G60550 rev
pNH22	<i>GST:AT5G05280-CPuORF(WT)</i>	AT5G05280 for	AT5G05280 rev
pNH23	<i>GST:AT2G27230-CPuORF(fs)</i>	AT2G27230 fs for1	AT2G27230 fs rev1
		AT2G27230 fs for2	AT2G27230 fs rev2
pNH24	<i>GST:AT5G52550-CPuORF(fs)</i>	AT5G52550 fs for1	AT5G52550 fs rev1
		AT5G52550 fs for2	AT5G52550 fs rev2
		AT5G52550 fs for3	AT5G52550 fs rev3
		AT5G52550 fs for4	AT5G52550 fs rev4
pNH25	<i>GST:AT3G12010-CPuORF(fs)</i>	AT3G12010 fs for1	AT3G12010 fs rev1
		AT3G12010 fs for2	AT3G12010 fs rev2
pNH26	<i>GST:AT5G09670-CPuORF(fs)</i>	AT5G09670 fs for1	AT5G09670 fs rev2
		AT5G09670 fs for2	AT5G09670 fs rev2
pNH27	<i>GST:AT5G45430-CPuORF(fs)</i>	AT5G45430 fs for1	AT5G45430 fs rev1
		AT5G45430 fs for2	AT5G45430 fs rev2
pNH28	<i>GST:AT4G22590-CPuORF(fs)</i>	AT4G22590 fs for1	AT4G22590 fs rev1
pNH29	<i>GST:AT1G70780-CPuORF(fs)</i>	AT1G70780 fs for1	AT1G70780 fs rev1
		AT1G70780 fs for2	AT1G70780 fs rev2
pNH30	<i>GST:AT3G01470-CPuORF(fs)</i>	AT3G01470 fs for1	AT3G01470 fs rev1
		AT3G01470 fs for2	AT3G01470 fs rev2
pNH31	<i>GST:AT3G51630-CPuORF(fs)</i>	AT3G51630 fs for1	AT3G51630 fs rev1
		AT3G51630 fs for2	AT3G51630 fs rev2
pNH32	<i>GST:AT1G58120-CPuORF(fs)</i>	AT1G58120 fs for1	AT1G58120 fs rev1
pNH33	<i>GST:AT4G36990-CPuORF(fs)</i>	AT4G36990 fs for1	AT4G36990 fs rev2
		AT4G36990 fs for2	AT4G36990 fs rev2

Plasmid	Construct	Primer	
		Forward	Reverse
pNH34	<i>GST:AT5G53590-CPuORF(fs)</i>	AT5G53590 fs for1	AT5G53590 fs rev1
pNH35	<i>GST:AT2G37480-CPuORF(fs)</i>	AT2G37480 fs for1	AT2G37480 fs rev1
		AT2G37480 fs for2	AT2G37480 fs rev2
pNH36	<i>GST:AT1G68550-CPuORF(fs)</i>	AT1G68550 fs for1	AT1G68550 fs rev1
		AT1G68550 fs for2	AT1G68550 fs rev2
pNH37	<i>GST:AT3G22970-CPuORF(fs)</i>	AT3G22970 fs for1	AT3G22970 fs rev1
pNH38	<i>HA:AT1G70780-CPuORF(WT)</i>	AT1G70780 for	AT1G70780 rev
pNH39	<i>HA:AT1G70780-CPuORF(sc)</i>	AT1G70780 sc for	AT1G70780 sc rev
pNH40	<i>HA:AT4G36990-CPuORF(WT)</i>	AT4G36990 for	AT4G36990 rev
pNH41	<i>HA:AT4G36990-CPuORF(sc)</i>	AT4G36990 sc for	AT4G36990 sc rev
pNH42	<i>HA:AT5G53590-CPuORF(WT)</i>	AT5G53590 for	AT5G53590 rev
pNH43	<i>HA:AT5G53590-CPuORF(sc)</i>	AT5G53590 sc for	AT5G53590 sc rev
pNH44	<i>M8:AT1G70780-CPuORF(WT)</i>	AT1G70780 for	AT1G70780 rev
pNH45	<i>M8:AT1G70780-CPuORF(fs)</i>	AT1G70780 fs for1	AT1G70780 fs rev1
		AT1G70780 fs for2	AT1G70780 fs rev2
pNH46	<i>M8:AT1G70780-CPuORF(sc)</i>	AT1G70780 sc for	AT1G70780 sc rev
pNH47	<i>M8:AT1G70780-CPuORF(Δ2-29)</i>	AT1G70780 Δ 2-29 for	AT1G70780 rev
pNH48	<i>M8:AT1G70780-CPuORF(Δ2-33)</i>	AT1G70780 Δ 2-33 for	AT1G70780 rev
pNH49	<i>M8:AT1G70780-CPuORF(Δ2-38)</i>	AT1G70780 Δ 2-38 for	AT1G70780 rev
pNH50	<i>M8:AT1G70780-CPuORF(G47*)</i>	AT1G70780 G47* for	AT1G70780 G47* rev
pNH51	<i>M8:AT1G70780-CPuORF(L48*)</i>	AT1G70780 L48* for	AT1G70780 L48* rev
pNH52	<i>M8:AT1G70780-CPuORF(D49*)</i>	AT1G70780 D49* for	AT1G70780 D49* rev
pNH53	<i>M8:AT1G70780-CPuORF(P50*)</i>	AT1G70780 P50* for	AT1G70780 P50* rev
pNH54	<i>M8:AT1G70780-CPuORF(*51A/52*)</i>	AT1G70780 *51A/52* for	AT1G70780 *51A/52* rev
pNH55	<i>M8:AT4G36990-CPuORF(WT)</i>	AT4G36990 for	AT4G36990 rev
pNH56	<i>M8:AT4G36990-CPuORF(fs)</i>	AT4G36990 fs for1	AT4G36990 fs rev2
		AT4G36990 fs for2	AT4G36990 fs rev2
pNH57	<i>M8:AT4G36990-CPuORF(sc)</i>	AT4G36990 sc for	AT4G36990 sc rev
pNH58	<i>M8:AT4G36990-CPuORF(Δ2-18)</i>	AT4G736990 Δ 2-18 for	AT4G36990 rev
pNH59	<i>M8:AT4G36990-CPuORF(Δ2-24)</i>	AT4G736990 Δ 2-24 for	AT4G36990 rev
pNH60	<i>M8:AT4G36990-CPuORF(Δ2-28)</i>	AT4G736990 Δ 2-28 for	AT4G36990 rev
pNH61	<i>M8:AT4G36990-CPuORF(F34*)</i>	AT4G36990 F34* for	AT4G36990 F34* rev
pNH62	<i>M8:AT4G36990-CPuORF(S35*)</i>	AT4G36990 S35* for	AT4G36990 S35* rev
pNH63	<i>M8:AT4G36990-CPuORF(C36*)</i>	AT4G36990 C36* for	AT4G36990 C36* rev
pNH64	<i>M8:AT4G36990-CPuORF(*37A/38*)</i>	AT4G36990 *37A/38* for	AT4G36990 *37A/38* rev
pNH65	<i>M8:AT5G53590-CPuORF(WT)</i>	AT5G53590 for	AT5G53590 rev
pNH66	<i>M8:AT5G53590-CPuORF(fs)</i>	AT5G53590 fs for1	AT5G53590 fs rev1
pNH67	<i>M8:AT5G53590-CPuORF(sc)</i>	AT5G53590 sc for	AT5G53590 sc rev
pNH68	<i>M8:AT5G53590-CPuORF(Δ2-12)</i>	AT5G53590 Δ 2-12 for	AT5G53590 rev
pNH69	<i>M8:AT5G53590-CPuORF(Δ2-17)</i>	AT5G53590 Δ 2-17 for	AT5G53590 rev
pNH70	<i>M8:AT5G53590-CPuORF(Δ2-24)</i>	AT5G53590 Δ 2-24 for	AT5G53590 rev
pNH71	<i>M8:AT5G53590-CPuORF(Δ2-27)</i>	AT5G53590 Δ 2-27 for	AT5G53590 rev
pNH72	<i>M8:AT5G53590-CPuORF(P28*)</i>	AT5G53590 P28* for	AT5G53590 P28* rev
pNH73	<i>M8:AT5G53590-CPuORF(F29*)</i>	AT5G53590 F29* for	AT5G53590 F29* rev
pNH74	<i>M8:AT5G53590-CPuORF(S30*)</i>	AT5G53590 S30* for	AT5G53590 S30* rev
pNH75	<i>M8:AT5G53590-CPuORF(I31*)</i>	AT5G53590 I31* for	AT5G53590 I31* rev
pNH76	<i>M8:AT5G53590-CPuORF(T32*)</i>	AT5G53590 T32* for	AT5G53590 T32* rev
pNH77	<i>GST:AT1G70780-CPuORF(sc)</i>	AT1G70780 sc for	AT1G70780 sc rev
pNH78	<i>GST:AT4G36990-CPuORF(sc)</i>	AT4G36990 sc for	AT4G36990 sc rev
pNH79	<i>GST:AT5G53590-CPuORF(sc)</i>	AT5G53590 sc for	AT5G53590 sc rev

Plasmid	Construct	Primer	
		Forward	Reverse
pNH80	35S::AT1G70780 5'UTR(WT):ELuc-PEST	pUC19 rev3	AT1G70780 35S rev
pNH81	35S::AT1G70780 5'UTR(fs):ELuc-PEST	AT1G70780 5' UTR for	AT1G70780 5' UTR rev
		AT1G70780 fs for1	AT1G70780 fs rev1
		AT1G70780 fs for2	AT1G70780 fs rev2
pNH82	35S::AT1G70780 5'UTR(Δ AUG):ELuc-PEST	AT1G70780 Δ AUG for	AT1G70780 Δ AUG rev
pNH83	35S::AT1G70780 5'UTR(fs Δ AUG):ELuc-PEST	AT1G70780 Δ AUG for	AT1G70780 Δ AUG rev
pNH84	35S::AT4G36990 5'UTR(WT):ELuc-PEST	pUC19 rev3	AT4G36990 35S rev
pNH85	35S::AT4G36990 5'UTR(fs):ELuc-PEST	AT4G36990 5' UTR for	AT4G36990 5' UTR rev
		AT4G36990 fs for1-2	AT4G36990 fs rev1
		AT4G36990 fs for2	AT4G36990 fs rev2
pNH86	35S::AT4G36990 5'UTR(Δ AUG):ELuc-PEST	AT4G36990 Δ AUG for	AT4G36990 Δ AUG rev
pNH87	35S::AT4G36990 5'UTR(fs Δ AUG):ELuc-PEST	AT4G36990 fs Δ AUG for	AT4G36990 fs Δ AUG rev
pNH88	35S::AT5G53590 5'UTR(WT):ELuc-PEST	pUC19 rev3	AT5G53590 35S rev
pNH89	35S::AT5G53590 5'UTR(fs):ELuc-PEST	AT5G53590 5' UTR for	AT5G53590 5' UTR rev
		AT5G53590 fs for1	AT5G53590 fs rev1
		AT5G53590 Δ AUG for	AT5G53590 Δ AUG rev
pNH90	35S::AT5G53590 5'UTR(Δ AUG):ELuc-PEST	AT5G53590 Δ AUG for	AT5G53590 Δ AUG rev
pNH91	35S::AT5G53590 5'UTR(fs Δ AUG):ELuc-PEST	AT5G53590 Δ AUG for	AT5G53590 Δ AUG rev

Supplementary Table S2

Supplementary Table S2. Oligonucleotides used in this study

Name	Oligonucleotide sequence
Preparation of a template for <i>in vitro</i> transcription	
SP6for	5'-CTGCTTCAGTAAGCCAGATGCTA-3'
SP63'rev	5'-TTTATGCTTCCGGCTCGTAT-3'
Toeprint analyses	
AT1G70780TP2	5'-CAAAAAACAGAGCAAATCTCACAA-3
HsfB1TP1	5'-CTCAGTCTAGATTATTTTACCACAGAA-3'
SAUR30TP1	5'-AGATTGGTTTAAAAACGATCGAC-3'
Plasmid construction	
SP6HAfor	5'-TCTGTGCGACACTAGAAATGGAGTATCCTTACGACGTTCTGATTACGCTGGTGGA-3'
HABKXSrev	5'-GAAGAGCTCAGTCTAGAAGAGGTACCAGCGGATCCACCAGCGTAATCAGGAACGTC-3'
GSTfor	5'-TGGGCTGCAGGTCGACACTAGAAATGTCCCCTATACT-3'
GSTrev	5'-GGTGGCCTCCGGATCCATCCGATTTTGGAGGATGG-3'
SP6for	5'-CTGCTTCAGTAAGCCAGATGCTA-3'
HArev	5'-ACCAGCGTAATCAGGAACGTC-3'
DAP2-75aaF	5'-GACGTTCTGATTACGCTGGTGAAGGTGGCGAAGAAGAAGTTGA-3'
DAP2-75aaR	5'-ACAGGATCCAACAGAAAACGACACCTTTAATTTCC-3'
M8for	5'-TCGACACTAGAAATGATGATGATGATGATGATGATGATGGAGG-3'
M8rev	5'-GATCCCTCCATCATCATCATCATCATCATCATCTTAGTG-3'
M8rev2	5'-CTCCATCATCATCATCATCATC-3'
DAP2-50aaF	5'-GATGATGATGATGATGATGATGGAGCCTCACCATTCAAACACACC-3'
DAP2-50aaR	5'-TCTGGATCCTTCAATTTTATTGTCACTAATCCATTG-3'
ELucfor	5'-TCCTCTAGAAAAGATGGCGTCGACGGAGAGAGAGAAGAACGTG-3'
ELucrev	5'-GTGGAGCTCGAATGGCATCTACACATTGATCCT-3'
HSPterF	5'-CCTGAGCTCGAAGATGAAGATGAAATATTTGGTGTGTCA-3'
HSPterR	5'-CCAGAATTCCATAGTCCATACCATAGCACA-3'
RLucATGfor	5'-TCCTCTAGAAAAGATGGCGTCGACTCTAGCC-3'
NOSterR	5'-CAAGACCGGCAACAGGATT-3'
AT2G27230 for	5'-TCTGGATCCGCATGTCGGAGTATGATCGCTTTTAG-3'
AT2G27230 rev	5'-GTGTCTAGACTTTCTCTTCTCTTCTTTAAGCTCCAAC-3'
AT5G52550 for	5'-TCTGGATCCGAGAGAAGTTAAGGGATGTTG-3'
AT5G52550 rev	5'-GTGTCTAGATGCTACAAGTCTTTGTTTGCC-3'
AT5G07840 for	5'-TCTGGATCCCTCGTGTCTCTTCACTGTCTATGA-3'
AT5G07840 rev	5'-GTGTCTAGATGGGTAGAAATCATCAACCAATATC-3'
AT2G43020 for	5'-TCTGGATCCAAATTTGTTTGGAAGCCTGA-3'
AT2G43020 rev	5'-GTGTCTAGATCCGATCACAATCACGGA-3'
AT1G36730 for	5'-TCTGGATCCTCTGAACAGGCTTCTCTCTTTC-3'
AT1G36730 rev	5'-GTGTCTAGAGTCATCATCCTCGGCATC-3'
AT3G12010 for	5'-TCTGGATCCAAAGAAAAGAATCCACTACCGC-3'
AT3G12010 rev	5'-GTGTCTAGAGTGATAAAGCACCAGAACCAACAC-3'
AT5G09670 for	5'-TCTGGATCCGACAGGGCAGATACGTCGG-3'
AT5G09670 rev	5'-GTGTCTAGAGGTGTCACCCATATTAATGGCAC-3'
AT5G45430 for	5'-TCTGGATCCGAACAAGATTACATCTGCTCAG-3'
AT5G45430 rev	5'-GTGTCTAGAAAGATGACACTCTAGGACTGTGTGA-3'
AT4G22590 for	5'-TCTGGATCCGACAGTTCAACAACAAGCAGTGA-3'
AT4G22590 rev	5'-GTGTCTAGAACTTACTGGTGTAGTAGGGTCACTAAG-3'
AT1G70780 for	5'-TCTGGATCCGTGGAACTAATCCGATCG-3'
AT1G70780 rev	5'-GAGTCTAGATCGAGAGAACAAAAACAGAG-3'
AT3G18000 for	5'-TCTGGATCCCAGCAGAGAGGACGATCCGT-3'
AT3G18000 rev	5'-GTGTCTAGAGTAATCTTCTGAATATCACGCTCTTC-3'
AT3G01470 for	5'-TCTGGATCCGGATTTTGTATCTGCCCCGTTG-3'
AT3G01470 rev	5'-GTGTCTAGAGATCAACAGAAATAAAACAACAACACTTTC-3'
AT3G51630 for	5'-TCTGGATCCAAAGGTCCGTAAGGGAAGAAGAC-3'
AT3G51630 rev	5'-GTGTCTAGAAATCTCCATATACATGACTCCGTACC-3'
AT1G58120 for	5'-TCTGGATCCGAGATTGAGAGGATGAGGCA-3'
AT1G58120 rev	5'-GTGTCTAGAGTTGAAAGTTAAAGAAATAGGAAAAAGAG-3'

Name	Oligonucleotide sequence
AT4G36990 for	5'-TCTGGATCCGAAGAAACCAAACGAAAC-3'
AT4G36990 rev	5'-GTGTCTAGATTATTTTACCACAGAAAAATAAAC-3'
AT5G53590 for	5'-TCTGGATCCAGCAACATCCCTAGATCTCTCA-3'
AT5G53590 rev	5'-GTGTCTAGATTAAAGAAGAAGGAATCTTTTACC-3'
AT2G37480 for	5'-TCTGGATCCCCTTCGGTGCCCTCTAAGC-3'
AT2G37480 rev	5'-GTGTCTAGATCAAACACCGCCAGAAGTTAAAGC-3'
AT1G68550 for	5'-TCTGGATCCTCGGCTGGGTTTGAATCGA-3'
AT1G68550 rev	5'-GTGTCTAGACTTTCTAATCGCAACCATTGTAAAC-3'
AT1G64630 for	5'-TCTGGATCCGAGGAGATGCTCTTCTTCTATCC-3'
AT1G64630 rev	5'-GTGTCTAGACTTTCTGGACGAAGTCAGCC-3'
AT3G22970 for	5'-TCTGGATCCAATCTCGCCGGGAAAAGGA-3'
AT3G22970 rev	5'-GTGTCTAGAAACTTCTGAAATCAGCGGATCATC-3'
AT5G60550 for	5'-TCTGGATCCTCGTGTTTCGATTGCAGTG-3'
AT5G60550 rev	5'-GTGTCTAGACACGAAACATGATCTCCTTCTCA-3'
AT5G05280 for	5'-TCTGGATCCAAGAAACTGACTCTTTCATCTCAGTCTC-3'
AT5G05280 rev	5'-GTGTCTAGAGGTAGCTTGCGTCGCAAGTA-3'
AT2G27230 fs for1	5'-CGCTTTAGTTAGATCCTGAAGAAAACAAAGTG-3'
AT2G27230 fs rev1	5'-CTTTGTTTTCTTCAGGATCTAACTAAAAGCGATC-3'
AT2G27230 fs for2	5'-GATCTTGCCGTTGGAAGTTAGTCTTTGTTTC-3'
AT2G27230 fs rev2	5'-GACTAACTTCCAACGGCAAGATCCTC-3'
AT5G52550 fs for1	5'-CTCTTATCTCCTTTGTTTCTGTTTGG-3'
AT5G52550 fs rev1	5'-CAAACAGAAACAAAGGAGATAAGAGAAG-3'
AT5G52550 fs for2	5'-TGTATTGTCGCGTAAAATGAGGTAT-3'
AT5G52550 fs rev2	5'-ATACCTCATTTTACGCGACAATACA-3'
AT5G52550 fs for3	5'-TAAATGAGGTATACCACATACCTGAGTG-3'
AT5G52550 fs rev3	5'-CACTCAGGTATGTGGTATACCTCATTTTA-3'
AT5G52550 fs for4	5'-CATACCTGAGTGGTGTGTAGTAGTCATTGA-3'
AT5G52550 fs rev4	5'-TCAATGACTACTACACCACTCAGGTATG-3'
AT3G12010 fs for1	5'-GTTTCATGAGGTTGAAAAGAGATATATGTTTGAA-3'
AT3G12010 fs rev1	5'-ACATATATCTCTTTTCAACCTCATGAACTTTGA-3'
AT3G12010 fs for2	5'-GAAGAGTTGTATGCGCATACGATCCGAGGAA-3'
AT3G12010 fs rev2	5'-TCGGATCGTATGCGCATACAACCTTTCAGCGCA-3'
AT5G09670 fs for1	5'-TCTGGATCCGACCAGGGCAGATACGTCGG-3'
AT5G09670 fs for2	5'-CTTTGTAAGTGGGGAAGTTGTTTCATC-3'
AT5G09670 fs rev2	5'-GAACAACTTCCCCACTTACAAAGCC-3'
AT5G45430 fs for1	5'-TTTCATTGCAACGAAGCACTCGATT-3'
AT5G45430 fs rev1	5'-AGTGCTTCGTTGCAATGAAAAAAC-3'
AT5G45430 fs for2	5'-TCTTTCGTGAATGCACCTAGTGGTCA-3'
AT5G45430 fs rev2	5'-CACTAGGTGCATTACGAAAGAGC-3'
AT4G22590 fs for1	5'-GTGGTTTTTCATTGACAAAAGAGTTGAGATAAAGTGTTTGA-3'
AT4G22590 fs rev1	5'-CAACTCTTTTGTCAATGAAAAACCACCCTTTAGTGTTTTTC-3'
AT1G70780 fs for1	5'-TCTTCTCTCTCACATCCTCTGTTTTTC-3'
AT1G70780 fs rev1	5'-GAAAACAGAGGATGTGAGAGAGGAAGA-3'
AT1G70780 fs for2	5'-GCCTCGACCGCGTGAACGATTCGCCC-3'
AT1G70780 fs rev2	5'-GAATCGTTCACGCGGTGAGGCCAAGG-3'
AT3G01470 fs for1	5'-CATGATGGGATTTGTATCTGCCC-3'
AT3G01470 fs rev1	5'-CCATAAAGAATCATGATCTTCTAATCCTTC-3'
AT3G01470 fs for2	5'-GGCAGATACAAATCCCATCATGAAC-3'
AT3G01470 fs rev2	5'-GGATTAGAAGATCATGATTCTTATGGC-3'
AT3G51630 fs for1	5'-TCGATTACTCCTACTCTCTTTTGG-3'
AT3G51630 fs rev1	5'-AAAAGAAGAGTAGGAGTAATCGAAAGA-3'
AT3G51630 fs for2	5'-TTTCTTATACTGAGAATCACGAACGA-3'
AT3G51630 fs rev2	5'-TTCGTGATTCTCAGTATAAGAAAACGC-3'
AT1G58120 fs for1	5'-GAATCATACAGCCGAAGGTTCTGCACATCGCTAGGCTCGCCTC-3'
AT1G58120 fs rev1	5'-GAACCTTGCGGCTGTATGATTCCCACCGGGAGAGAAACGCGGCTA-3'
AT4G36990 fs for1	5'-TCTGGATCCGAAGAACCAAACGAAACTC-3'
AT4G36990 fs for2	5'-CTTGCTTTTTACGTTGCTGTTGTTTTTC-3'
AT4G36990 fs rev2	5'-AAAAAGAATCAGCAACGTAAAAAGCAAGAG-3'

Name	Oligonucleotide sequence
AT5G53590 fs for1	5'-GATTCCTTGGCCTTTTCTACACCGTTTTTAGCATCAACAA-3'
AT5G53590 fs rev1	5'-GTGTAGAAAAAGGCCAAGGAATCAACAGCAGAAGAGATTATGA-3'
AT2G37480 fs for1	5'-TCTAATCGTTTGAACCTCTTGAAAAGTGTGA-3'
AT2G37480 fs rev1	5'-ACTTTTCAAGAGGTTCAAACGATTAGAACTCA-3'
AT2G37480 fs for2	5'-TTGGCGTGGTAATACTTAGTTAACATTTC-3'
AT2G37480 fs rev2	5'-TGTTAACTAAGTATTACCACGCCAATCACAC-3'
AT1G68550 fs for1	5'-CCATGCGCTTAGACCCAAAAGGACTTGTTTC-3'
AT1G68550 fs rev1	5'-CCTTTTGGGTCTAAGCGCATGGAAAGA-3'
AT1G68550 fs for2	5'-GGTTTTCACATAAAGCAGCAAAAGTTTTTC-3'
AT1G68550 fs rev2	5'-ACTTTTGCTGCTTTATTGTGAAAACCCCCAAAG-3'
AT3G22970 fs for1	5'-TAGTGACTCTTACCATCGCCGTCAATGTCTTCCGTGAACA-3'
AT3G22970 fs rev1	5'-GGCGATGGTAAGAGTCACTAGAACGGAACAGAAATAATAAC-3'
AT1G70780 sc for	5'-GCTGGTGCCTTTACCGCTTTGGCCTCGACCCGTGAACGA-3'
AT1G70780 sc rev	5'-AAAGCGGTAAAGGCACCAGCCTTCTTTGCAAGATC-3'
AT4G36990 sc for	5'-TATTGGGATTGCGAATGGTTTCTACCGCTCTCTTGC-3'
AT4G36990 sc rev	5'-CCATTGCGAATCCCAATAAAAGCCAGAGAGGAAAACAC-3'
AT5G53590 sc for	5'-TCTCTCCTGTTGATGCTTCTTGGCCTTTTTCTATCACCGTT-3'
AT5G53590 sc rev	5'-AGAAGCATCAACAGGAGAGATTATGAGAGTAAATAGAGAAAGATC-3'
AT1G70780 Δ2-29 for	5'-TCTGGATCCCTCTGTTTTCGCTTTTCGGATC-3'
AT1G70780 Δ2-33 for	5'-TCTGGATCCCTTCGGATCTTGCAAAGAAGGC-3'
AT1G70780 Δ2-38 for	5'-TCTGGATCCGAAGGCTGGTACTTTTCGCTG-3'
AT1G70780 G47* for	5'-TCGCTGCCTTTGACTCGACCCGTG-3'
AT1G70780 G47* rev	5'-CACGGGTCGAGTCAAAGGCAGCGA-3'
AT1G70780 L48* for	5'-CCTTGGCTGAGACCCGTGAACGATTC-3'
AT1G70780 L48* rev	5'-TCACGGGTCTCAGCCAAGGCAGC-3'
AT1G70780 D49* for	5'-CTTGGCCTCTGACCGTGAACGATTC-3'
AT1G70780 D49* rev	5'-CGTTCACGGTCAGAGGCCAAGGCA-3'
AT1G70780 P50* for	5'-GGCCTCGACTGATGAACGATTCGC-3'
AT1G70780 P50* rev	5'-GAATCGTTCATCAGTCGAGGCCAAGGCA-3'
AT1G70780 *51A/52* for	5'-GCCTCGACCCGGCATAAATTCGCC-3'
AT1G70780 *51A/52* rev	5'-GGCGAATTTATGCCGGGTGAGGC-3'
AT4G736990 Δ2-18 for	5'-TCTGGATCCGGCTTTTATTGCTGGGATTGGGA-3'
AT4G736990 Δ2-24 for	5'-TCTGGATCCCTGGGAATTTCTACCGCTCTC-3'
AT4G736990 Δ2-28 for	5'-TCTGGATCCACCGCTCTCTTGCTTTTTAGTTGC-3'
AT4G36990 F34* for	5'-GCTCTCTTGCTTTGAAGTTGCTGATTC-3'
AT4G36990 F34* rev	5'-GAATCAGCAACTTCAAAGCAAGAGAGC-3'
AT4G36990 S35* for	5'-CTTGCTTTTTTGATGCTGATTCTTTTCC-3'
AT4G36990 S35* rev	5'-GAATCAGCATCAAAAAAGCAAGAGAGCGG-3'
AT4G36990 C36* for	5'-CTTGCTTTTTAGTTGATGATTCTTTTCCCTTC-3'
AT4G36990 C36* rev	5'-GAAGGAAAAAGAATCATCAACTAAAAAGCAAG-3'
AT4G36990 *37A/38* for	5'-CTTTTTAGTTGCGCATGATTTTTCCCTT-3'
AT4G36990 *37A/38* rev	5'-AAGGAAAAATCATGCGCAACTAAAAAG-3'
AT5G53590 Δ2-12 for	5'-TCTGGATCCCTTTCTCTATTTACTCTCATAATCTCTTCTGC-3'
AT5G53590 Δ2-17 for	5'-TCTGGATCCCTCATAATCTCTTCTGCTGTTGATCC-3'
AT5G53590 Δ2-24 for	5'-TCTGGATCCGATCCTTGGCCTTTTTCTATCAC-3'
AT5G53590 Δ2-27 for	5'-TCTGGATCCCTTTTTCTATCACCGTTTTTTAGCA-3'
AT5G53590 P28* for	5'-CTGTTGATCCTTGGTAGTTTTCTATCACC-3'
AT5G53590 P28* rev	5'-GGTGATAGAAAACACCAAGGATCAACAG-3'
AT5G53590 F29* for	5'-TTGATCCTTGGCCTTAGTCTATCACCGTTTTTAG-3'
AT5G53590 F29* rev	5'-CGGTGATAGACTAAGGCCAAGGATCAACA-3'
AT5G53590 S30* for	5'-CCTTGGCCTTTTTAGATCACCGTTTTTTAGC-3'
AT5G53590 S30* rev	5'-AAACGGTGATCTAAAAAGGCCAAGGATC-3'
AT5G53590 I31* for	5'-GGCCTTTTTCTTAGACCGTTTTTTAGC-3'
AT5G53590 I31* rev	5'-GCTAAAAACGGTCTAAGAAAAAGGCC-3'
AT5G53590 T32* for	5'-GCCTTTTTCTATCTAGTTTTTTAGCATCAACA-3'
AT5G53590 T32* rev	5'-TGTTGATGCTAAAAACCTAGATAGAAAAAGGC-3'

Name	Oligonucleotide sequence
pUC19 rev3	5'-GACCATGATTACGCCAAGCT-3'
AT1G70780 35S rev	5'-TGTGATTGTTGGTTCTCTCCAAATGAAATGAACT-3'
AT1G70780 5' UTR for	5'-ATTTGGAGAGAACCAACAATCACATTCTTCTC-3'
AT1G70780 5' UTR rev	5'-AGAGTCGACAACATCTTCGAAATCGAGAGA-3'
AT1G70780 ΔAUG for	5'-CGTTTGTGAAAGGTGGAAACTA-3'
AT1G70780 ΔAUG rev	5'-TAGTTTCCACCTTTCACAAACG-3'
AT4G36990 35S rev	5'-GTTAAGTGTTATGTCTCTCTCCAAATGAAATGAACTTCCT-3'
AT4G36990 5' UTR for	5'-CATTTGGAGAGAGACATAACACTTAACTCGTTTA-3'
AT4G36990 5' UTR rev	5'-AGAGTCGACGTCATCTCCGGCGAACTT-3'
AT4G36990 fs for1-2	5'-CTTAAATGGAAGAACCAACGAAACTC-3'
AT4G36990 ΔAUG for	5'-TTTTTCCTTAAAAGGAAGAAACCA-3'
AT4G36990 ΔAUG rev	5'-TGGTTTCTTCCTTTTAAGGAAAA-3'
AT4G36990 fs ΔAUG for	5'-GATTTTTCCTTAAAAGGAAGAACCAAC-3'
AT4G36990 fs ΔAUG rev	5'-GTTTGGTTCTTCCTTTTAAGGAAAAATC-3'
AT5G53590 35S rev	5'-GTTTTTTAGAGGAGGTTCTCTCCAAATGAAATGAACT-3'
AT5G53590 5' UTR for	5'-ATTTGGAGAGAACCTCCTCTAAAAAACCAAAATAAAAAC-3'
AT5G53590 5' UTR rev	5'-AGAGTCGACCCCATTAAGAAGAAGGAATCTTTTC-3'
AT5G53590 ΔAUG for	5'-GCCTATCATAAGCAACATCCCTAGATC-3'
AT5G53590 ΔAUG rev	5'-TGTTGCTCACGATAGGCTAAGCATGAAG-3'

The recognition sites of restriction enzymes are underlined.

Supplementary Table S3

Supplementary Table S3. Genbank accession numbers of Refseqs used for the alignments in Figure 4

Homology Group (HG)	Species	Genbank accession number of Refseq
12	<i>Oryza sativa</i>	XM_015771912.1
	<i>Zea mays</i>	NM_001157013.2
	<i>Populus trichocarpa</i>	XM_002311473.2
	<i>Glycine max</i>	NM_001249805.1
	<i>Medicago truncatula</i>	XM_003589610.2
	<i>Arabidopsis thaliana</i> (AT1G70780)	NM_105746.3
	<i>Arabidopsis thaliana</i> (AT1G23150)	NM_102163.4
	<i>Gossypium raimondii</i>	XM_012611812.1
	<i>Solanum lycopersicum</i>	XM_004237858.3
	<i>Nicotiana tabacum</i>	XM_016630751.1
18	<i>Oryza sativa</i>	XM_015756373.1
	<i>Zea mays</i>	NM_001156846.1
	<i>Ricinus communis</i>	XM_015722026.1
	<i>Glycine max</i>	NM_001254668.1
	<i>Medicago truncatula</i>	XM_003611703.2
	<i>Arabidopsis thaliana</i> (AT4G36990)	NM_119862.3
	<i>Gossypium raimondii</i>	XM_012601569.1
	<i>Vitis vinifera</i>	XM_002277729.4
	<i>Solanum lycopersicum</i>	NM_001321450.1
	<i>Nicotiana tabacum</i>	NM_001325866.1
19	<i>Oryza sativa</i>	XM_015757422.1
	<i>Zea mays</i>	NM_001156710.1
	<i>Ricinus communis</i>	XM_002511629.2
	<i>Glycine max</i>	XM_003523285.2
	<i>Medicago truncatula</i>	XM_003602279.2
	<i>Malus x domestica</i>	XM_008383208.2
	<i>Arabidopsis thaliana</i> (AT5G53590)	NM_124739.4
	<i>Gossypium raimondii</i>	XM_012584501.1
	<i>Vitis vinifera</i>	XM_002273056.3
	<i>Solanum lycopersicum</i>	XM_004240931.3