

Supplemental Table S1. Oligonucleotides used in this study.

T-DNA identification for SALK_021164	
F1	5'-GAGTTAAAGATGCTTATCCCATTG-3'
R1	5'-CTCCAGGACAGCTTGAATCTG-3'
T-DNA identification for GABI_826F11	
F2	5'-TGAGAAATGTACAAATGCAAGAGG-3'
R2	5'-CACACAATCGCAGAGAATCTC-3'
T-DNA-specific primers	
LB-SALK-b1.3	5'-ATTTTGCCGATTTCGGAAC-3'
LB-GABI	5'-CCCATTGACGTGAATGTAGACAC-3'
Pkan	5'-ATCGCCATGGGTCACGACGAGAT-3'
Vector construction for subcellular localization analysis of the TAD1 protein	
F3	5'-CACCATGGAGGAGGATTGGGGAAAGAC-3'
R3	5'-ATTTATCAGAAAATCCTCGCAATTC-3'
RT-PCR for detection of <i>TAD1</i> transcripts	
F4	5'-ATGGAGGAGGATTGGGGAAAGAC-3'
R4	5'-TGGAGGACTTGGTAAAGCAATGC-3'
RT-PCR for <i>TAD1</i> expression analysis	
F5	5'-ATGGAGGAGGATTGGGGAAAGAC-3'
R5	5'-ATTTATCAGAAAATCCTCGCAATTC-3'
RT-PCR for <i>ACTIN2</i> as internal control	
Actin2-F	5'-TCTTCTTCCGCTCTTTCTTTCC-3'
Actin2-R	5'-TCTTACAATTTCCCGCTCTGC-3'
qRT-PCR for determination of <i>TAD1</i> expression levels	
F6	5'-ATGGAGGAGGATTGGGGAAAGAC-3'
R6	5'-TTGGTCCCCGTCCTAACGCTATC-3'
qRT-PCR for <i>EF1alpha</i> as internal control	
<i>EF1-alpha-F</i>	5'-TGAGCACGCTCTTCTTGCTTTCA-3'
<i>EF1-alpha-R</i>	5'-GGTGGTGGCATCCATCTTGTTACA-3'
Primers for tRNA^{Ala} (AGC)	
F7	5'-GGGGATGTAGCTCAGATGGTAG-3'
R7	5'-TGGTGGAGATGCGGGGTATC-3'
Primers for tRNA^{Thr} (AGT)	
F8	5'-GCTTTCATAGCTCAGTTGG-3'
R8	5'-TGGTGCTTTCGTTGAGAGTTG-3'
Primers for tRNA^{Val} (AAC)	
F9	5'-GGTTTCGTGGTGTAGTTGG-3'
R9	5'-TGGTGGCTTCGCCCCGGTTC-3'
Primers for tRNA^{Ser} (AGA)	

F10	5'-GTGGACGTGCCGGAGTGGTTATC-3'
R10	5'-CGTGAACGGCAGGATTCGAAC-3'
Oligonucleotide probe for detection of tRNA^{Ala} (AGC)	
antiAlaAGC	5'-AAGCGAGCGCTCTACCATCTGAGCTACATCCCC-3'
Primers for mitochondrial tRNA^{Cys} (GCA)	
F11	5'-GGCTAGGTAACATAATGGAAATGTATC-3'
R11	5'-GCTTTCCTTTGTTCCAGTTATTTC-3'
Primers for mitochondrial 5S rRNA	
F5S	5'-AAACCGGGCACTACGGTGAG-3'
R5S	5'-TCACCGGGCTTGGACCATG-3'

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AtTAD1 1  -----MEEDWGKTVSEKVISAYMS-LPKKG---KPOGREVTVLSAFLVSSPS-----
Tad1p 1  MVSCQGTRPCIVNLLTMPSEDKLGEETSTRVINEYSKLSACRP IIRP SGIREWTILAGVRAINRDGGAN
dADAT1 1  -----MCDNKKPTVKEIAELCLKKFS-LPKTIG---KPTAN-QWTILAGIVFNR-NTEA
hADAT1 1  -----MWTADEIAQLCYEHYGR LPKKG---KPEFNHEWTL LA VVKIQSPADKA

AtTAD1 43  -----QDPKVI ALGTGTCVSGSLLS-PRGDI VND SHA EVVARRALIRFFYSEIQRMQLTSGKSNE
Tad1p 70  -----KI E I L S T A T G V K A L P D S E L Q R S E G K I L H Q C H A E I L A L R G A N T V L L N R I Q N Y N P S -----
dADAT1 50  C-----QLVSLGCGTKCIGESKLC-PNGLILND SHA EVLARRGFLRFLYQEL-----
hADAT1 48  CDTPDKPVQVTK EVVSMGTGTCIGQSKMR-KNGDILND SHA EVIARRSFRORYLLHQLQLAATL-----

AtTAD1 104 AKRQRIDSE T S S I L E S A D S S C P G E V K Y K L S G C L L H L Y I S Q L P C G Y A S T S S P L Y A L K K I P -----
Tad1p 124  -----S G D K F I Q H N D E I P ---A R F N L K E N W E L A L Y I S R L P C G D A S M S F L N -----
dADAT1 95  -----K Q D R I F H W N S T L S ---T Y D M D E H V E F H F L S T Q T P C G D A C T I L E ---E E Q P -----
hADAT1 110  -----K E D S I F V P G T Q K G ---V W K L R R D L I F V F S S H T P C G D A S I I P M L E F E D Q P C C P V F R N W A H N

AtTAD1 163  -----S T Q V D D S L V Q A S -----
Tad1p 100  -----D M C K N D D F I K I E D S -----
dADAT1 138  -----A A R A K R O R L D -----E D S -----
hADAT1 169  S S V E A S S N L E A P G N E R K C E D P D S P V T K K M R L E P G T A A R E V T N G A A H H Q S F G K Q K S G P I S P G I H S C D L T V E

AtTAD1 178  -----D I C S S R H S D V P E I G S N S N K - G N G S Q V A D M V Q R K P G R G E T --T L S V S C S D K I A R W
Tad1p 180  -----D E F Q Y V D R S V K T I L R G R L N ---F N R R N V V R T K P G R Y D S N I T L S K S C S D K L L M K
dADAT1 151  -----E M V Y T G A K L I S D L S D D P ---M L Q T P G A L R T K P G R G E R --T L S M S C S D K I A R W
hADAT1 239  G L A T V T R I A P G S A K V I D Y Y R T G A K C V P G E A G D S G K P G A A F H Q V G L L R V K P G R G D R --T R S M S C S D K M A R W

AtTAD1 228  N V L G V Q G A L L Y Q V L Q P - V Y I S T I T V G - Q S L H S P D N F S L A D H L R R S L Y E R I L P L S D E L L T S F R L N K P L F E V
Tad1p 231  Q R S S V L N C L N Y E L F E K P V L K Y I V I P N L E D E T K H H L E Q S F H T R L P N L O N E I K F L N C L K P F Y D D K L D E E D V
dADAT1 199  N V I G V Q G A L L D V L I S K P I Y F S S L N F C - C D D A Q L E S L E R A I F K R F D C R T F K H T R F Q P Q R P O I N I D P G I R F E
hADAT1 307  N V L G C Q G A L L M H L L E E P I Y L S A V V I G - K C P Y S Q E A M Q R A L I G R C Q N V S A L P K G F G V Q E L K I - L Q S D L L F E

AtTAD1 296  A P V P P S E F Q H S E T A Q A T L T C G Y S L C W N Y S G L H - - E V I L G T T G R K Q G T S A R G A L Y P S T O S S I C K O R L L E L F
Tad1p 301  P G -----L M C S V K L F M D D F S T E A I L N G V R N G F Y T K S S K P - - L R K H C Q S Q V S R F A Q W E L F
dADAT1 268  F S -----Q R S D ---W O P S P N G L I W S O V P E E L R P Y E I S V N G K R Q G V T K K M K T S Q A A L A I S K Y K L F L T F
hADAT1 375  Q S R S A V Q A K R A D S P G R L V P C G A A I S W S A V P E Q - - P L D V T A N G F P Q G T T K K T I G S L Q A R S Q I S K V E L F R S F

AtTAD1 364  L K E T H G - - - - - H K R E S S K S K K S Y R E L K N K A T E Y Y L M S K I F K G K Y P E N N W L R K P L N C E D F L I N - - -
Tad1p 354  K K I R P E Y - - - - - E G I S Y L E F K S R Q K K R S Q L I I A I K N I L S P D G W I P T R T D V K - - - - -
dADAT1 328  L E L V K F N P K L S E M F D Q Q L S D P E R I A Y A S C K D L A R D Y Q F A W R E I K E K Y - F L Q W T K K P H E L L D F N P M S N K
hADAT1 443  Q K L L S R - - I A R D K W P H S L R V Q K L D T Y Q E Y K E A A S S Y Q E A W S T L R K Q V - F G S W I R N P P D Y H Q F K - - - - -

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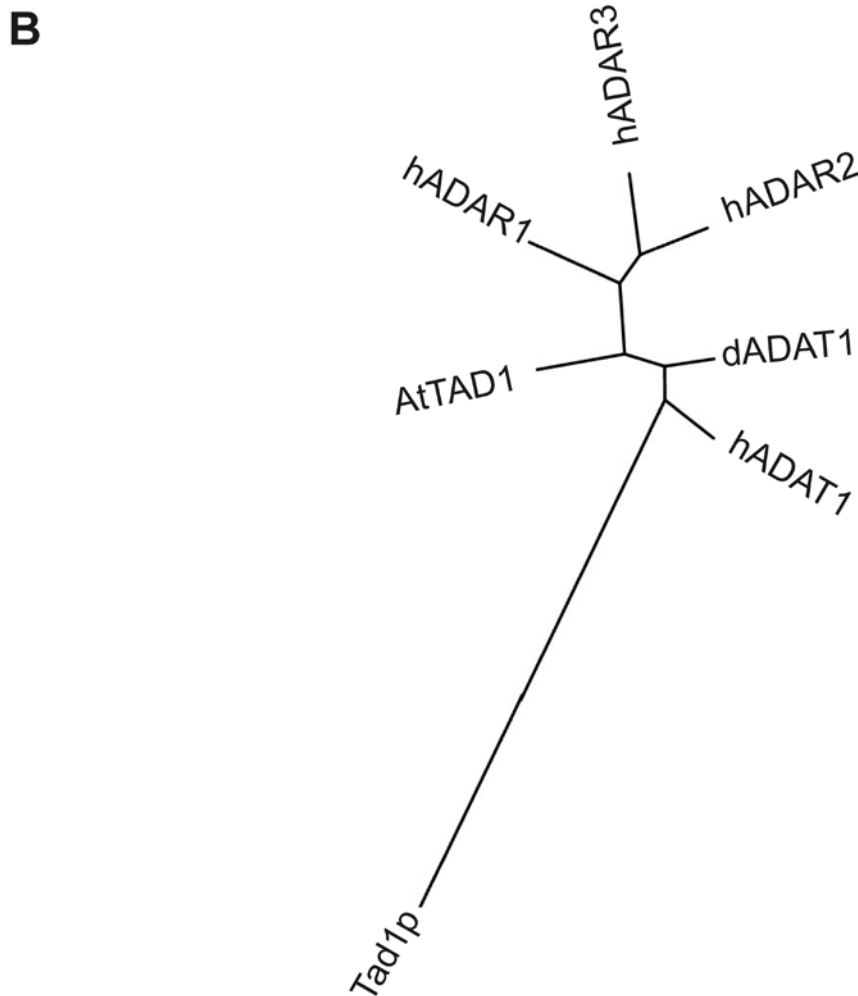


FIGURE S1. Identification of a putative *TAD1* gene in the genome of the model plant *Arabidopsis thaliana*. **(A)** Amino acid sequence alignment of the candidate TAD1 protein from *Arabidopsis* with the Tad1p protein from the yeast *Saccharomyces cerevisiae* and its homologues dADAT1 from *Drosophila melanogaster* and hADAT1 from humans. Black and gray boxes indicate identical and similar amino acids, respectively. Dashed lines represent gaps in the sequence. The histidine and two cysteine residues involved in coordination of a zinc ion are marked with asterisks, the essential glutamate residue in the active site of the enzyme is marked with a filled triangle. **(B)** Unrooted phylogenetic tree of adenosine deaminases acting on tRNAs and adenosine deaminases acting on mRNAs. The GenBank accession numbers are as follows: Tad1p, *Saccharomyces cerevisiae* (CAA07438.1); AtTAD1, *Arabidopsis thaliana* (At1g01760); dADAT1, *Drosophila melanogaster* (AAF53333.1); hADAT1, *Homo sapiens* (AAD48376.1); hADAR1, *Homo sapiens* (NP_001180424.1); hADAR2, *Homo sapiens* (NP_001103.1); hADAR3, *Homo sapiens* (AAI40853.1). The phylogenetic tree was prepared by construction of an amino acid sequence alignment with MUSCLE, subsequent curation with Gblocks (<http://molevol.cmima.csic.es/castresana/Gblocks.html>), phylogenetic analysis by PhyML (<http://www.atgc-montpellier.fr/phyml/>), and visualization with DrawTree (<http://evolution.genetics.washington.edu/phylip/doc/drawtree.html>).

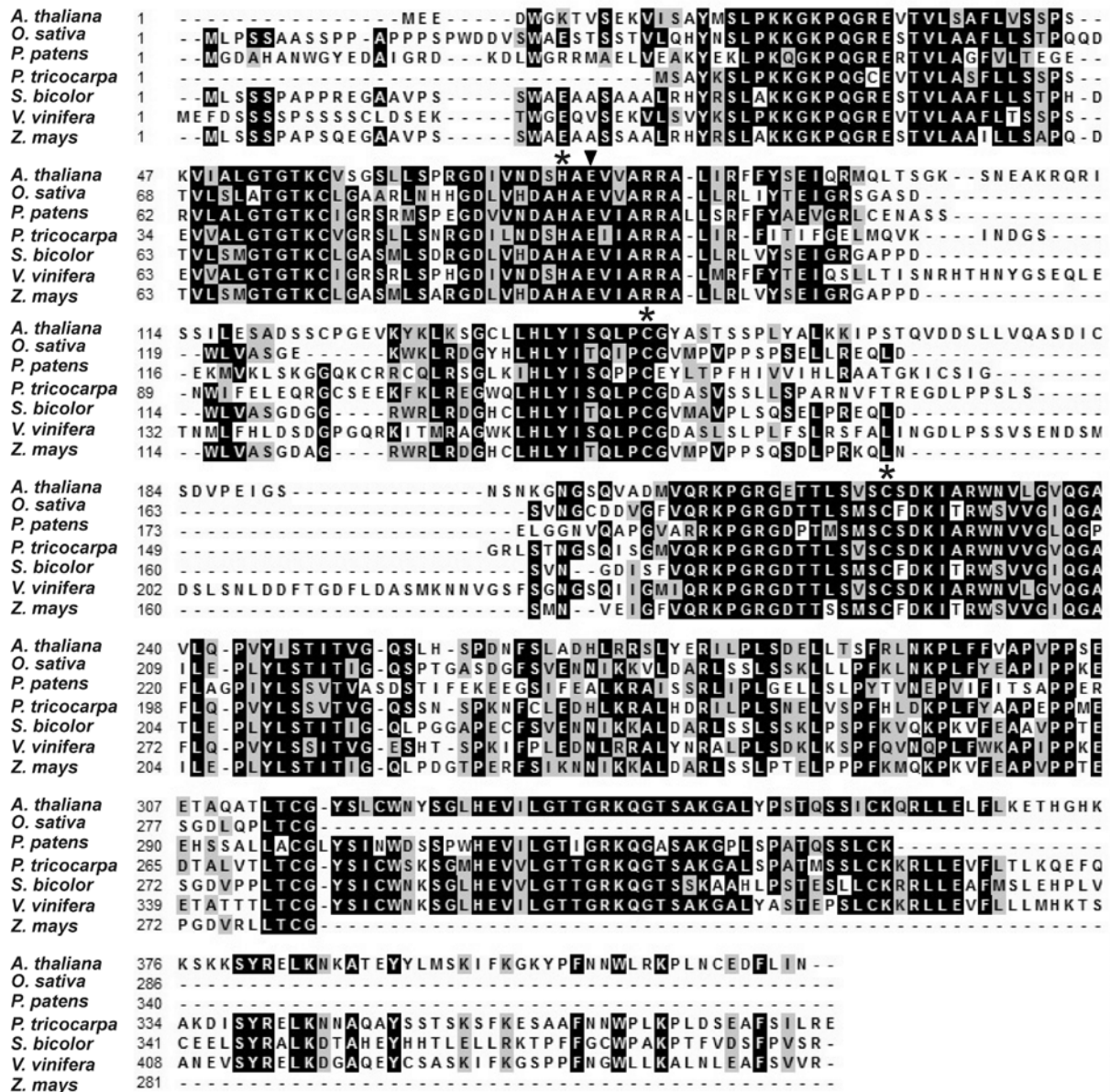


FIGURE S2. Amino acid sequence alignment of the TAD1 protein from *Arabidopsis thaliana* and homologous proteins from other plant species. The amino acid sequence of TAD1 was aligned with its putative homologues in the dicotyledonous plants *Populus trichocarpa* (XP_002320118) and *Vitis vinifera* (XP_002273023.1), the monocotyledonous plants *Oryza sativa* (Os04g0683500), *Sorghum bicolor* (XP_002447262.1) and *Zea mays* (ACF86175.1) and the moss *Physcomitrella patens* (XP_001777317.1). The black and gray boxes indicate identical and similar amino acids, respectively. Dashes represent gaps in the sequence. The sequences were aligned with ClustalW. The histidine and two cysteine residues

involved in coordination of a zinc ion are marked with asterisks, the essential glutamate residue in the active site of the enzyme is marked with a filled triangle. Abbreviations for species names are *O. sativa*: *Oryza sativa*; *P. patens*: *Physcomitrella patens*; *P. trichocarpa*: *Populus trichocarpa*; *S. bicolor*: *Sorghum bicolor*; *V. vinifera*: *Vitis vinifera*; *Z. mays*: *Zea mays*.