```
                    10        20        30        40        50        60        70        80        90        100       110
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AtZAT4      ------------------------------------MERYK-----CRFCFKSFINGRALGGHMRSHMLTLSAERC------------------------------------
PEThyZPT3-3 ------------------------------------MEKHKS----CKLCFRKFANGRALGGHMRSHMMNLYVQKQ-------------------------------------
SlZPT3-1    ------------------------------------MEKQR-----CKLCYRRFSNGRALGGHMRSHMMNMPVTRK-------------------------------------
BcMF20      -----------------------------------MEQFKERKFVCKFCSKRFACGKSLGGHIRTHMNKENSADSDEDEHNKFRID---------------------------
AtDAZ1      -----------------------------------------MSN-TSNSDPNSDIPFASSNVTLP---------------------------------------------
AtDAZ2      --------------------------------------MNNNHSYDDRSFHIPLHPSNTSNPNPNL------------------------------------------
AtMAZ1      -------------------------------MEDEHQDLHKPINGALRDLKITRSQKETEKSTNQ---------------------------------------
PEThyMEZ1   --------------------------------------------------------------------------------------------------------
PEThyTAZ1   MVDYQDLQVGMSGTLWIQLKIEDKQVQELDHSQDIMDYEVPKNNDHTRICEVCNKGFSSGKALGGHMRIHVQAAKKLLSVG--------------------------------
PEThyZPT4-1 ----------------------------MDCIDQEQQQQQPVFKHYCRVCKKGFVCGRALGGHMRAHGIGDEVVTMDDDDQASDWEDKFG--------------------
BrZFP38     ------------------------------------------MSDPEKTKVN----------------------------------------
PEThyZPT4-2 ------------------------------------MEEGQDLKYFCKLCNKRYPCGKSFGGHMRSHVLANSAKLEBKVEFKQKKVPSWTNGGKIHKR------------
PEThyZPT4-3 ------------------------------------MEEDQDLKFVCKVCNKKYPCGKSLGGHMRSHVLDNSTEFEEKVEDKLEKLEYWSSDEKNSNREKASLVDAGFEE

                    170       180       190       200       210       220       230       240       250       260       270
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|...
AtZAT4      ----------SDASSSGEFDNQKMNRLDDELEFDFAE-------DDDVESETESSRINPTRRRSKRTRKLGSFDFDFEKLT-------TSQPSELVAEPEHHSSASDTTTEE
PEThyZPT3-3 ----------GDADDSGIVLP-------------------------DKESETESSRNQAPFRKSKRSRK--SRIVK-----------VKEYSSLVDTEP-VSSISENSPEE
SlZPT3-1    ----------GNS--SSVTLQ------------------------DRGSDTESTKNVTRMRRSKRARKPVSSILLRNSHDYKLSWDSFDNYYNDVEQQTGSSSISEVTSEE
BcMF20      QQQLLYCRECGKGFTSSKALCGHMACHSBREK-------------IVMDSQFDTEASSSPIRRRSKRAVKHHHHHKDDAFVD------GGSIMDQSDSSASSDDDEIEPEQE
AtDAZ1      ----------SSS-SSPRPKP-------------------------VTQPDPDASQIARPCTECGKQFGSLKALFGHMR--------CHPERQWRGINPPSNFKRRINSN
AtDAZ2      ----------SSPKSASKPKY-------------------------TKKPDPNAPKITRPCTECGRKFWSWKALPGHMR--------CHPERQWRGINPPPNYRVPTAAS
AtMAZ1      ------CEECGKGFRYEKYFKNHR------------------SMMHLSPNEKVCEESLMTLSRSLGFVKKKKRSRLG------RSGKTLFTTFLEPSSIFDATDEEL
PEThyMEZ1   -----------------------------------------------------------MVALSTKREREEDNPYSIT
PEThyTAZ1   NQLAPICSVCGKNFPSMKSLFGHMRSHPERAWRGIQPPAP-----NKNSCLSSASNEIAATTKSGDLSVPGWSVKAKRGRKGTIAEASSNSSLGSRSFSFDQEKDDEEHELHD
PEThyZPT4-1 ---------CGKEFSSWKSFLEHGKCSSEDAEESLVSS---------PGSEGEDYIYDGRKEKGYGWSKRKRSLRTKVGGLST-------STYQSSEEEDLLLAKCLIDLANA
BrZFP38     ----------GEMREIVLALP------------------------ALSLSDPPDEITRQKAVAAADLLVAAAQEAAVTKGN-------MDQQQFGGSGETAKKEKSRRPRT
PEThyZPT4-2 -----VCQQCGKVFQSLKALCGHMACHSGKDRGMKDDNSWTSETKNLVMDSNSDTEAEEPRLRSKSNSKRYNRLIAKSSSFCF------VNNKSVS---SSVSEID--DQEQE
PEThyZPT4-3 -----MCQQCGKVFQSLKALCGHMACHSEKDKGALIDS-----------NSDSEAEEEELRLRTRSKTKRYKTIVVKPSSFCL------VNSSTVNNSSSSVSEID--EQEQE

                    330       340       350       360       370       380       390       400       410       420       430
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|...
AtZAT4      ------------------------------------------------------------------------------------------------------------
PEThyZPT3-3 ------------------------------------------------------------------------------------------------------------
SlZPT3-1    ------------------------------------------------------------------------------------------------------------
BcMF20      ------LKILNVKNVEEFCKK--DKLGGVDNGDVLYDSDNSDSGYFRNGPKKLDSDVSVDGFLKN-NAFSNKSAMG----FNSYTPKQEKSLNRFRNEWSGSG----------
AtDAZ1      ------------------------------------------------------------------------------------------------------------
AtDAZ2      ------------------------------------------------------------------------------------------------------------
AtMAZ1      ------------------------------------------------------------------------------------------------------------
PEThyMEZ1   ------------------------------------------------------------------------------------------------------------
PEThyTAZ1   ------------------------------------------------------------------------------------------------------------
PEThyZPT4-1 ------------------------------------------------------------------------------------------------------------
BrZFP38     ------------------------------------------------------------------------------------------------------------
PEThyZPT4-2 IERKDSPKCVNNLDETPRSKKKADRNLKLDLLNAEAQSENSDSEYFLGEYKKVESDASVDEFHRNGNYQWNTSNTSLGCWFDESGPABKKELTRMKNYVTDSRKDLSKDYKYD
PEThyZPT4-3 FGRKDSLKRVYNQDETPPTKNKEDRNLKLSVSDAEAQSESSDSAYFLEENAIVESDVSVDGFGINGNSKWITSKMSNAAWCDESRTHKEKGLNRNKRNTIDSSKDITEECEDD

                    490       500       510       520       530       540       550       560       570       580       590
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|...
AtZAT4      -SRGRPKCETCGKVFKSYQALGGHRASHKKNK---------------------------------ACMTKTEQVETEYVLG---VKEKKVHECPICFRVFTSGQALGGHKRSH
PEThyZPT3-3 GSRGKYRCETCNKVFRSYQALGGHRASHKKIK-------------------------------VSSSSTNQVEN--------VVEEKIHECPVCFRVFSSGQALGGHKRTH
SlZPT3-1    -YKKKYKCDTCNKVFRSYQALGGHRASHKKTR--------------------------------VTAPDDDHREKNRNVVATKEGEKKIHKCPICFRVFASGQALGGHKRSH
BcMF20      GDQLSLETDSCADTNRSIKKIHNSKPPMVK-----------------------------------KPSGGVK------------KKSKGHECPICFRVFKSGQALGGHKRSH
AtDAZ1      EVEERFECDGCKKVFGSHQALGGHRATHKDVKGCFANKNITED--------------------PPPPPPQEIVDQDKGKSVKLVSGMNHRCNICSRVFSSGQALGGHMRCH
AtDAZ2      SSIERFECGGCKKVFGSHQALGGHRASHKNVKGCFAITNVTDD------------------PMTVSTSSGHDH-QGKILTFSG--HHKCNICFRVFSSGQALGGHMRCH
AtMAZ1      LMEEGFSSYGTSKEPASFLRDENRLDQQKRRKDGEFESGLLS-----------------NEQRLLEEEITTPVTFKGPASSLRHKCALDRNGGEFGPEFLSNEQTL
PEThyMEZ1   STSRVFECKTCNRQFSSFQALGGHRASHKKPR----------------------------LMGELHNLQLFHELPKRKTHECSICGLEFAIGQALGGHMRRH
PEThyTAZ1   DTPBKYKCNTCEKSFATHQALGGHRSSHNKFRMVIQNSVEDD-----------------VVTNVATSSIIGPVEEREEAAASTSKLLVDHNKNASASQVLGVQNRCQ
PEThyZPT4-1 SSKGLFECKACKHKVFNSHQALGGHRASHKKVKGCYAAKQDQLDDILID--------------DQDVNITHDQEFLQSSKSMRKSKIHECSICHRVFSTGQALGGHKRSH
BrZFP38     PPEGPPKCNVCGRSFLSWKAVFGHLRSHRDRG--------------------------YSGFLPPPTFNAAVKASGGDVAASCGDGGLGLGTGGLNIDL
PEThyZPT4-2 QKKKKYECLNCKKTFSSYQALGGHRPCNKNTNAYFESTYETGENSRDADNGPNYINKGKHRETLSNKPAAHSHDYSSNPEKKMKPKKFKGHACPFCPRMFKSGQALGGHKRSH
PEThyZPT4-3 HNKKKYECLNCKKIFGSYQALGGHRPCHKKANSYVESINGTGENSLDADHD--------------GKPFSAVKEPSYNPEKKIKPKKVKGHECPYCDRVFKSGQALGGHKRSH

                    650       660       670       680       690       700       710       720       730       740       750
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|...
AtZAT4      IDLNLPAPNEEDETSLVFDEW--------------------------------------------------
PEThyZPT3-3 IDLNLPPPMEDDDE--IISHVEVSTVSEAELVNPIKY-------------------------------
SlZPT3-1    IDLNLPAPIDDDEEEEIVSQIATSSVSHVHL--------------------------------------
BcMF20      IDLNLPAPIDE---------------------------------------------------------
AtDAZ1      IDLNVP---AATSSDTTLGCSLDLRLGL-----------------------------------------
AtDAZ2      LDLNVPPTIQDLSTSDTSGCCLDLRLGL-----------------------------------------
AtMAZ1      SDTDMLTQSDKKNVEHRCRLCNKIFSSYQALGGHQTFHRMSKCKNKKNGIEESVEPRMTL---------
PEThyMEZ1   LDLNLTPLENDLEFDLRKSNTAPMVDCFL---------------------------------------
PEThyTAZ1   FDLNELPPQEDEIAGGRDHQYFTFFPI-----------------------------------------
PEThyZPT4-1 LDLNNLPTHEDMSRIRRDPFNPLSFEVSTDIHLQYPWSCAPKNDDNDNYYLEEIKIDSNANNGKYNINNGATQNVEDDEADSKLKLAKLSDLKDMNTNSDNPAHWLQVGIGST
BrZFP38     FDLNRSPPQDEEDAKEDKAE------------------------------------------------
PEThyZPT4-2 LDLNLPAPVEDVNGEPA-FVSW----------------------------------------------
PEThyZPT4-3 LDLNLPAPIDDEDNEHAHFVSW----------------------------------------------
```

Figure S1. Multiple sequence alignment of deduced amino acid sequences of AtZAT4 and others C_2H_2 zinc-finger proteins (C_2H_2-ZFPs). The multiple alignment was done by using the MEGA X software (version 11.0) with ClustalW, and default parameters. Alignment editing was performed in BioEdit (version 7.2). Identification of conserved domains was performed in InterProScan, NLStradamus, and by previous literature. AtZAT4 C_2H_2-zinc finger domains, the Nuclear Localization Sequence, and the EAR motif are underlined in red, green, and yellow, respectively. For details, see the Materials and Methods section.
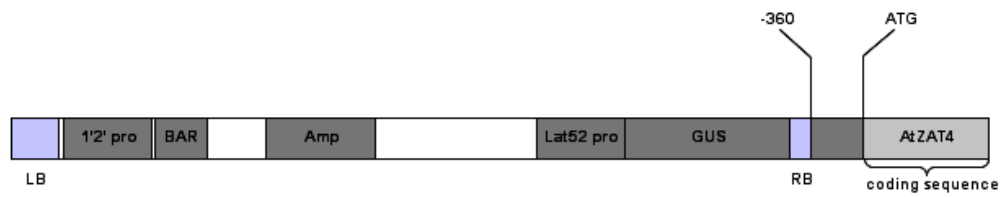
Figure S2. Proportional schematic representation of T-DNA insertion into the *Arabidopsis thaliana* genome and inside the *AtZAT4* promoter region. The T-DNA is the vector pCSA110, which carries the resistance to phosphinothricin gene (BAR; controlled by the 1'2' promoter), the ampicillin resistance gene (Amp), and the GUS marker gene (controlled by Lat52 promoter). RB and LB, right and left border of the T-DNA, respectively.

(A)
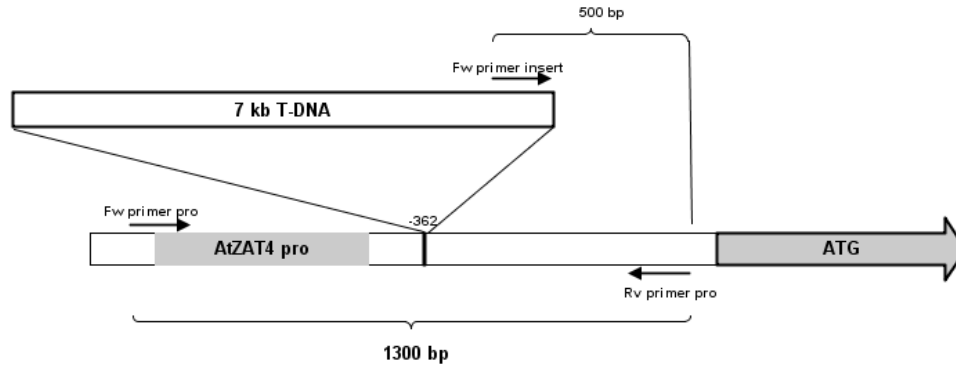
(B)
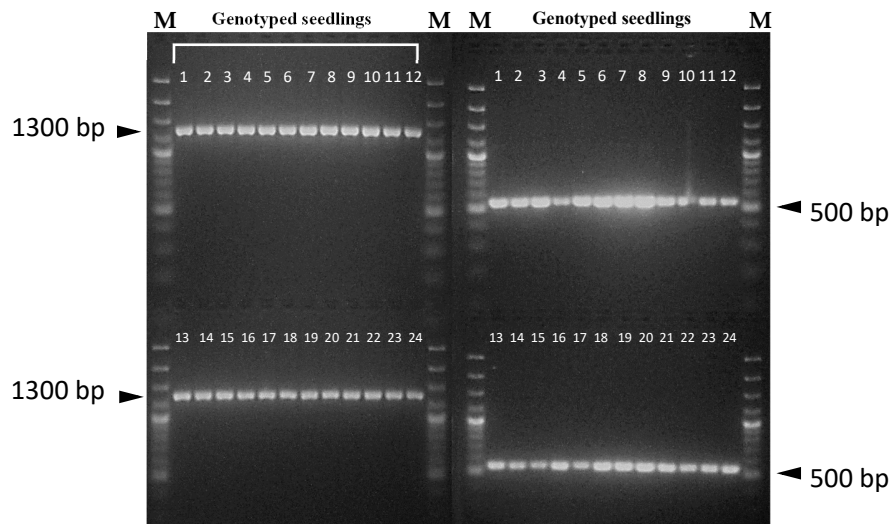
Figure S3. *Atzat4* (+/-) mutant genotyping from *Arabidopsis thaliana*. (**A**) Graphical representation of T-DNA insertion site and primers binding sites. Primer pro: primer promoter *AtZAT4* (pro*AtZAT4*), primer insert: primer T-DNA (pCSA110), see Table S1. (**B**) PCR products from 24 genotyped *A. thaliana* seedlings. The 1300 bp band represents the non-disrupted promoter and the 500 bp band indicated the T-DNA presence. M: 100 bp plus (Thermo Scientific, Waltham, MA, USA).

Table S1. Nucleotide sequence of primers used in RT-qPCR and in genotyping analyses.

Gene	Primer sequence (5′→3′)	Annealing temperature (°C)
AtZAT4	F: ACGGAAGTAACATCGGAGCAGGAA	60
	R: CCCGAATCACGCAAAGTCTGTTGT	60
AtF-box	F: TTTCGGCTGAGAGGTTCGAGT	60
	R: GATTCCAAGACGTAAAGCAGATCAA	60
pCSA110	F: ATTGATGAAACTGCTGCTGT	58
	R: GGTGATACATATCCAGCCAT	58
pro*AtZAT4*	F: GAGATCTAGAGGTTTGGCACCACCAT	57
	R: CGACGAGCTCGTACAGAACAGAGATA	57