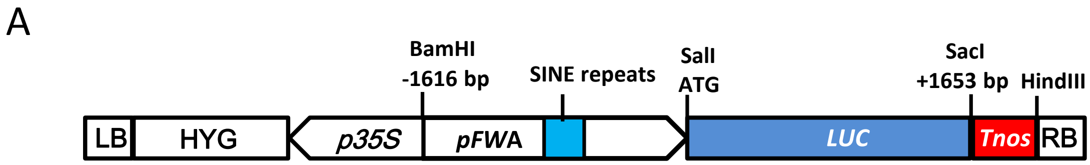
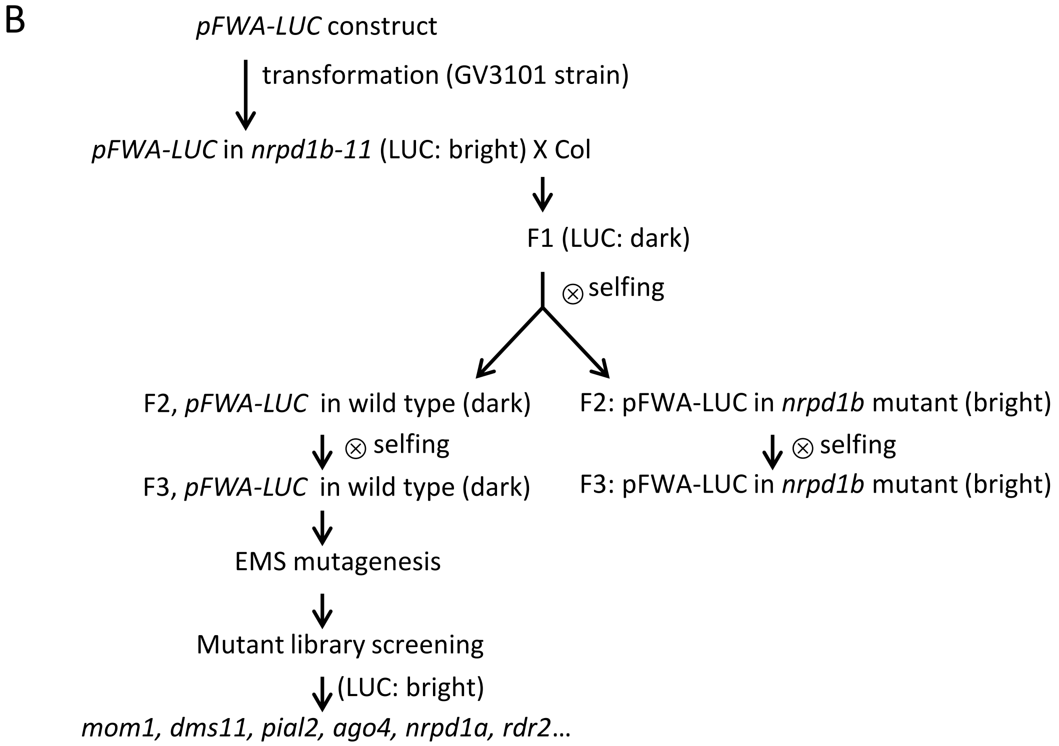
Supplemental Figure 1

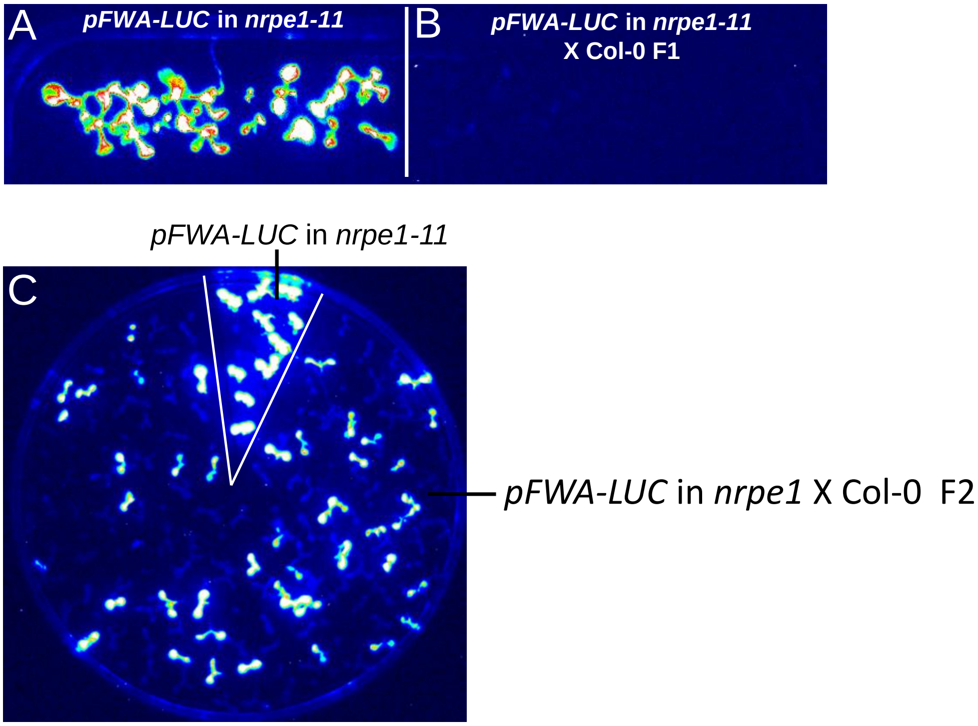


***pFWA*-BamHI-F:** CGGGATCCCGCCTTTCTCTTCCTCATCTGC
***pFWA*-SalI-R:** ACGCGTCGACCATTTTCCCTCAATGCAATAACCTG



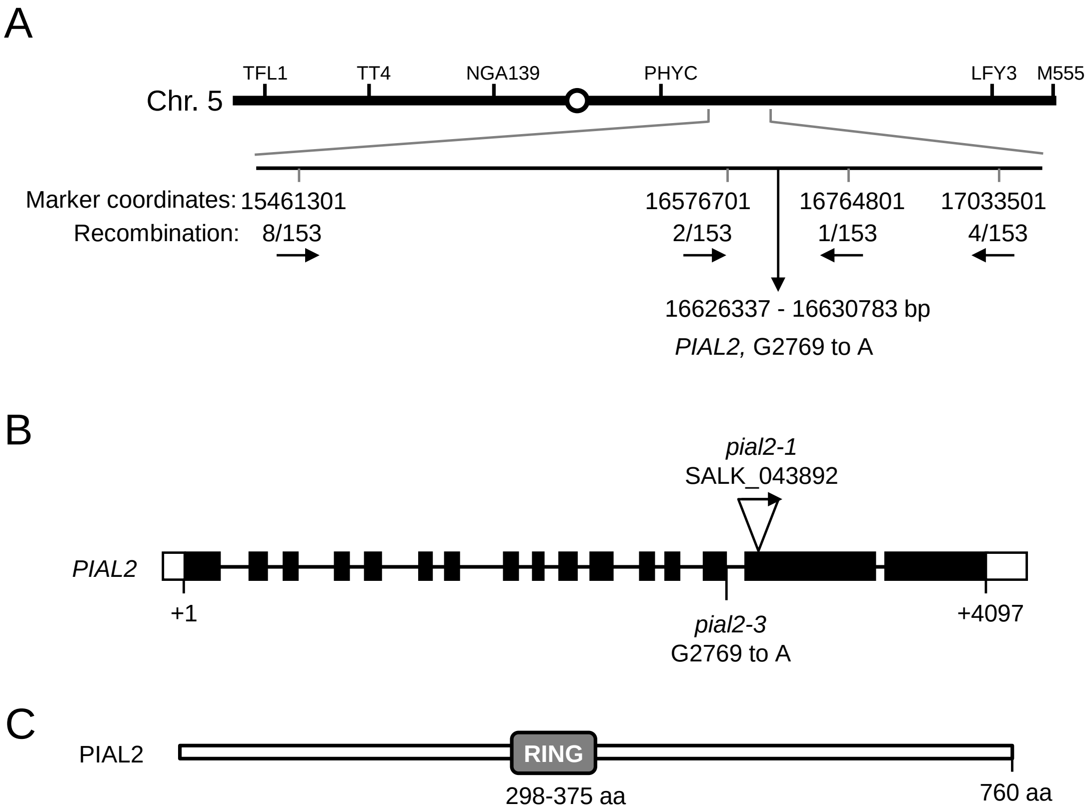
Supplemental Figure 1. The *FWA-LUC* reporter system. **(A)** Schematic representation of the *pFWA-LUC* construct. The primers used to generate the *FWA* promoter sequence are shown. The recognition sites of BamHI and SalI are shown in red in the primer sequences. **(B)** The flow diagram used for mutant library construction and map-based cloning.

Supplemental Figure 2



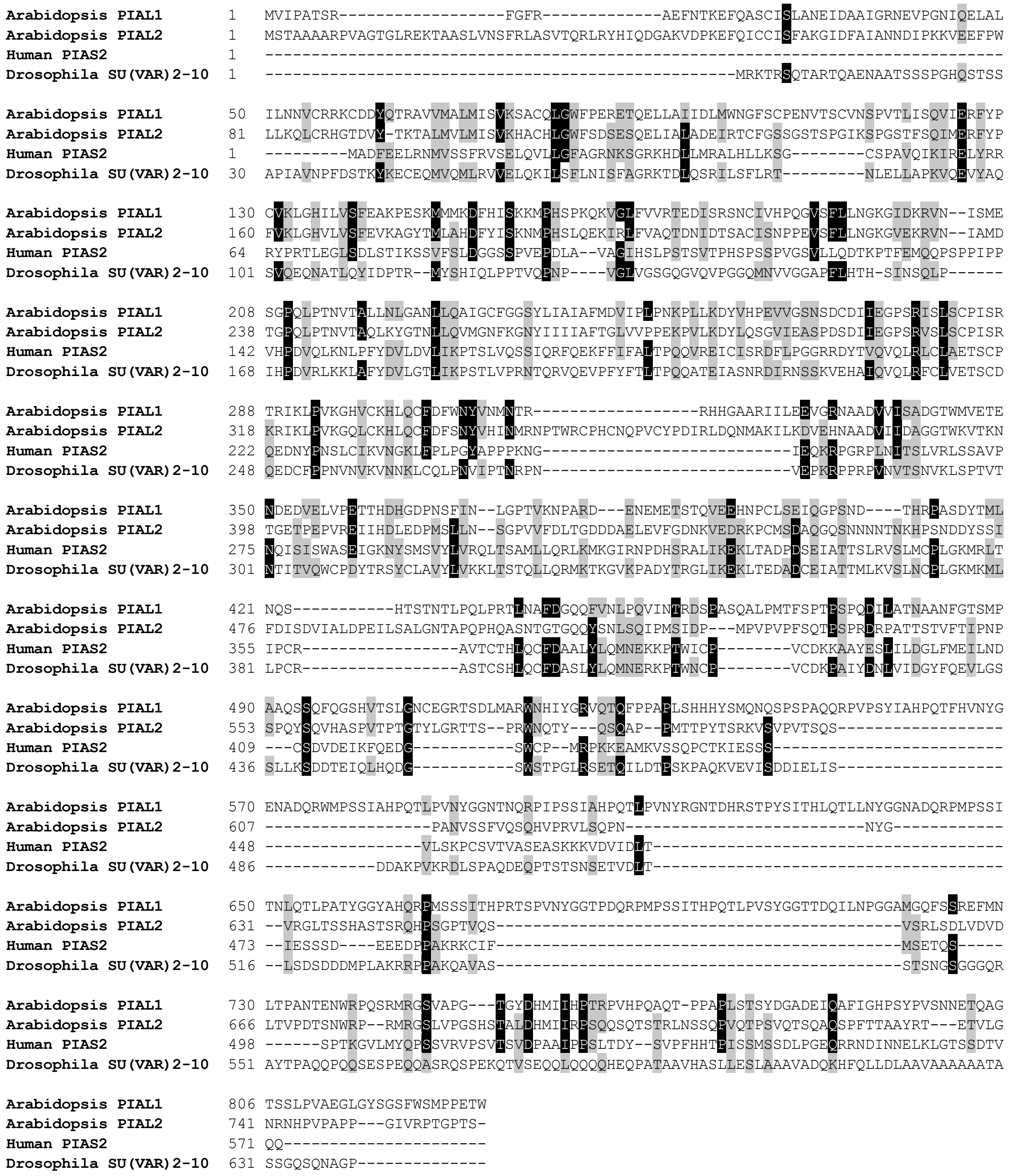
Supplemental Figure 2. Luminescence imaging of *pFWA-LUC* transgenic plants. **(A)** Luminescence imaging of pFWA-LUC transgenic plants in the *nrpe1-11* background. *pFWA-LUC* was transformed into the *nrpe1-11* background and a transgenic line highly expressed the *pFWA* reporter gene. **(B)** The expressed *pFWA-LUC* transgenic line was crossed to the wild-type Col-0 and the *pFWA-LUC* reporter gene was silenced in the F1 plants. **(C)** Luminescence imaging of the F2 plants from the cross of *pFWA-LUC* in *nrpe1* and the wild-type Col-0. The *pFWA-LUC* transgenic plants in the *nrpe1-11* background are shown as a control.

Supplemental Figure 3



Supplemental Figure 3. Map-based cloning and characterization of *PIAL2*. **(A)** Diagram for map-based cloning of *PIAL2*. A ~188-kb region on chromosome 5 was determined by map-based cloning. A mutation was identified by whole-genome DNA deep sequencing at a splice site of *PIAL2* in the ~188-kb region. A black bar with a blank circle represents chromosome 5. The centromere is indicated by the blank circle. Positions of indicated genes and markers are shown on the top of the black bar. **(B)** Schematic representation of the *PIAL1* gene and the mutations in the *pial2-1* and *pial2-3* mutants. Boxes and lines represent exons and introns, respectively. 5’ and 3’ UTRs are indicated by blank boxes, whereas coding regions are indicated by filled boxes. **(C)** The PIAL2 protein contains a RING-type zinc finger motif that is conserved in SUMO E3 ligases. The blank bar represents the full-length PIAL2 proteins. The position and size of the conserved RING-type zinc finger motif are shown.

Supplemental Figure 4



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Arabidopsis PIAL2       1   MSTAAAARPVAGTGLREKTAASLVNSFRLASVTQRLRYHIQDGAKVDPKEFQICCISFAKGIDFAIANNDIPKKVEEFPW
Human PIAS2             1   --------------------------------------------------------------------------------
Drosophila SU(VAR)2-10  1   ---------------------------------------------------MRKTRSQTARTQAENAATSSSPGHQSTSS

Arabidopsis PIAL1       50  ILNNVCRRKCDDYQTRAVVMALMISVKSACQLGWFPERETQELLAIIDLMWNGFSCPENVTSCVNSPVTLISQVIERFYP
Arabidopsis PIAL2       81  LLKQLCRHGTDVY-TKTALMVLMISVKHACHLGWFSDSESQELIALADEIRTCFGSSGSTSPGIKSPGSTFSQIMERFYP
Human PIAS2             1   ---------MADFEELRNMVSSFRVSELQVLLGFAGRNKSGRKHDLLMRALHLLKSG--------CSPAVQIKIRELYRR
Drosophila SU(VAR)2-10  30  APIAVNPFDSTKYKECEQMVQMLRVVELQKILSFLNISFAGRKTDLQSRILSFLRT---------NLELLAPKVQEVYAQ

Arabidopsis PIAL1       130 CVKLGHILVSFEAKPESKMMMKDFHISKKMPHSPKQKVGLFVVRTEDISRSNCIVHPQGVSFLLNGKGIDKRVN--ISME
Arabidopsis PIAL2       160 FVKLGHVLVSFEVKAGYTMLAHDFYISKNMPHSLQEKIRLFVAQTDNIDTSACISNPPEVSFLLNGKGVEKRVN--IAMD
Human PIAS2             64  RYPRTLEGLSDLSTIKSSVFSLDGGSSPVEPDLA--VAGIHSLPSTSVTPHSPSSPVGSVLLQDTKPTFEMQQPSPPIPP
Drosophila SU(VAR)2-10  101 SVQEQNATLQYIDPTR--MYSHIQLPPTVQPNP----VGLVGSGQGVQVPGGQMNVVGGAPFLHTH-SINSQLP------

Arabidopsis PIAL1       208 SGPQLPTNVTALLNLGANLLQAIGCFGGSYLIAIAFMDVIPLPNKPLLKDYVHPEVVGSNSDCDIIEGPSRISLSCPISR
Arabidopsis PIAL2       238 TGPQLPTNVTAQLKYGTNLLQVMGNFKGNYIIIIAFTGLVVPPEKPVLKDYLQSGVIEASPDSDIIEGPSRVSLSCPISR
Human PIAS2             142 VHPDVQLKNLPFYDVLDVLIKPTSLVQSSIQRFQEKFFIFALTPQQVREICISRDFLPGGRRDYTVQVQLRLCLAETSCP
Drosophila SU(VAR)2-10  168 IHPDVRLKKLAFYDVLGTLIKPSTLVPRNTQRVQEVPFYFTLTPQQATEIASNRDIRNSSKVEHAIQVQLRFCLVETSCD

Arabidopsis PIAL1       288 TRIKLPVKGHVCKHLQCFDFWNYVNMNTR------------------RHHGAARIILEEVGRNAADVVISADGTWMVETE
Arabidopsis PIAL2       318 KRIKLPVKGQLCKHLQCFDFSNYVHINMRNPTWRCPHCNQPVCYPDIRLDQNMAKILKDVEHNAADVIIDAGGTWKVTKN
Human PIAS2             222 QEDNYPNSLCIKVNGKLFPLPGYAPPPKNG---------------------------IEQKRPGRPLNITSLVRLSSAVP
Drosophila SU(VAR)2-10  248 QEDCFPPNVNVKVNNKLCQLPNVIPTNRPN---------------------------VEPKRPPRPVNVTSNVKLSPTVT

Arabidopsis PIAL1       350 NDEDVELVPETTHDHGDPNSFIN--LGPTVKNPARD---ENEMETSTQVEEHNPCLSEIQGPSND----THRPASDYTML
Arabidopsis PIAL2       398 TGETPEPVREIIHDLEDPMSLLN--SGPVVFDLTGDDDAELEVFGDNKVEDRKPCMSDAQGQSNNNNTNKHPSNDDYSSI
Human PIAS2             275 NQISISWASEIGKNYSMSVYLVRQLTSAMLLQRLKMKGIRNPDHSRALIKEKLTADPDSEIATTSLRVSLMCPLGKMRLT
Drosophila SU(VAR)2-10  301 NTITVQWCPDYTRSYCLAVYLVKKLTSTQLLQRMKTKGVKPADYTRGLIKEKLTEDADCEIATTMLKVSLNCPLGKMKML

Arabidopsis PIAL1       421 NQS-----------HTSTNTLPQLPRTLNAFDGQQFVNLPQVINTRDSPASQALPMTFSPTPSPQDILATNAANFGTSMP
Arabidopsis PIAL2       476 FDISDVIALDPEILSALGNTAPQPHQASNTGTGQQYSNLSQIPMSIDP---MPVPVPFSQTPSPRDRPATTSTVFTIPNP
Human PIAS2             355 IPCR-----------------AVTCTHLQCFDAALYLQMNEKKPTWICP--------VCDKKAAYESLILDGLFMEILND
Drosophila SU(VAR)2-10  381 LPCR-----------------ASTCSHLQCFDASLYLQMNERKPTWNCP--------VCDKPAIYDNLVIDGYFQEVLGS

Arabidopsis PIAL1       490 AAQSSQFQGSHVTSLGNCEGRTSDLMARWNHIYGRVQTQFPPAPLSHHHYSMQNQSPSPAQQRPVPSYIAHPQTFHVNYG
Arabidopsis PIAL2       553 SPQYSQVHASPVTPTGTYLGRTTS--PRWNQTY---QSQAP--PMTTPYTSRKVSVPVTSQS------------------
Human PIAS2             409 ---CSDVDEIKFQEDG-----------SWCP--MRPKKEAMKVSSQPCTKIESSS-------------------------
Drosophila SU(VAR)2-10  436 SLLKSDDTEIQLHQDG-----------SWSTPGLRSETQILDTPSKPAQKVEVISDDIELIS------------------

Arabidopsis PIAL1       570 ENADQRWMPSSIAHPQTLPVNYGGNTNQRPIPSSIAHPQTLPVNYRGNTDHRSTPYSITHLQTLLNYGGNADQRPMPSSI
Arabidopsis PIAL2       607 ------------------PANVSSFVQSQHVPRVLSQPN--------------------------NYG------------
Human PIAS2             448 -----------------VLSKPCSVTVASEASKKKVDVIDLT--------------------------------------
Drosophila SU(VAR)2-10  486 ------------DDAKPVKRDLSPAQDEQPTSTSNSETVDLT--------------------------------------

Arabidopsis PIAL1       650 TNLQTLPATYGGYAHQRPMSSSITHPRTSPVNYGGTPDQRPMPSSITHPQTLPVSYGGTTDQILNPGGAMGQFSSREFMN
Arabidopsis PIAL2       631 --VRGLTSSHASTSRQHPSGPTVQS--------------------------------------------VSRLSDLVDVD
Human PIAS2             473 --IESSSD----EEEDPPAKRKCIF--------------------------------------------MSETQS-----
Drosophila SU(VAR)2-10  516 --LSDSDDDMPLAKRRPPAKQAVAS--------------------------------------------STSNGSGGGQR

Arabidopsis PIAL1       730 LTPANTENWRPQSRMRGSVAPG---TGYDHMIIHPTRPVHPQAQT-PPAPLSTSYDGADEIQAFIGHPSYPVSNNETQAG
Arabidopsis PIAL2       666 LTVPDTSNWRP--RMRGSLVPGSHSTALDHMIIRPSQQSQTSTRLNSSQPVQTPSVQTSQAQSPFTTAAYRT---ETVLG
Human PIAS2             498 ------SPTKGVLMYQPSSVRVPSVTSVDPAAIPPSLTDY--SVPFHHTPISSMSSDLPGEQRRNDINNELKLGTSSDTV
Drosophila SU(VAR)2-10  551 AYTPAQQPQQSESPEQQASRQSPEKQTVSEQQLQQQQHEQPATAAVHASLLESLAAAVADQKHFQLLDLAAVAAAAAATA

Arabidopsis PIAL1       806 TSSLPVAEGLGYSGSFWSMPPETW
Arabidopsis PIAL2       741 NRNHPVPAPP---GIVRPTGPTS-
Human PIAS2             571 QQ----------------------
Drosophila SU(VAR)2-10  631 SSGQSQNAGP--------------
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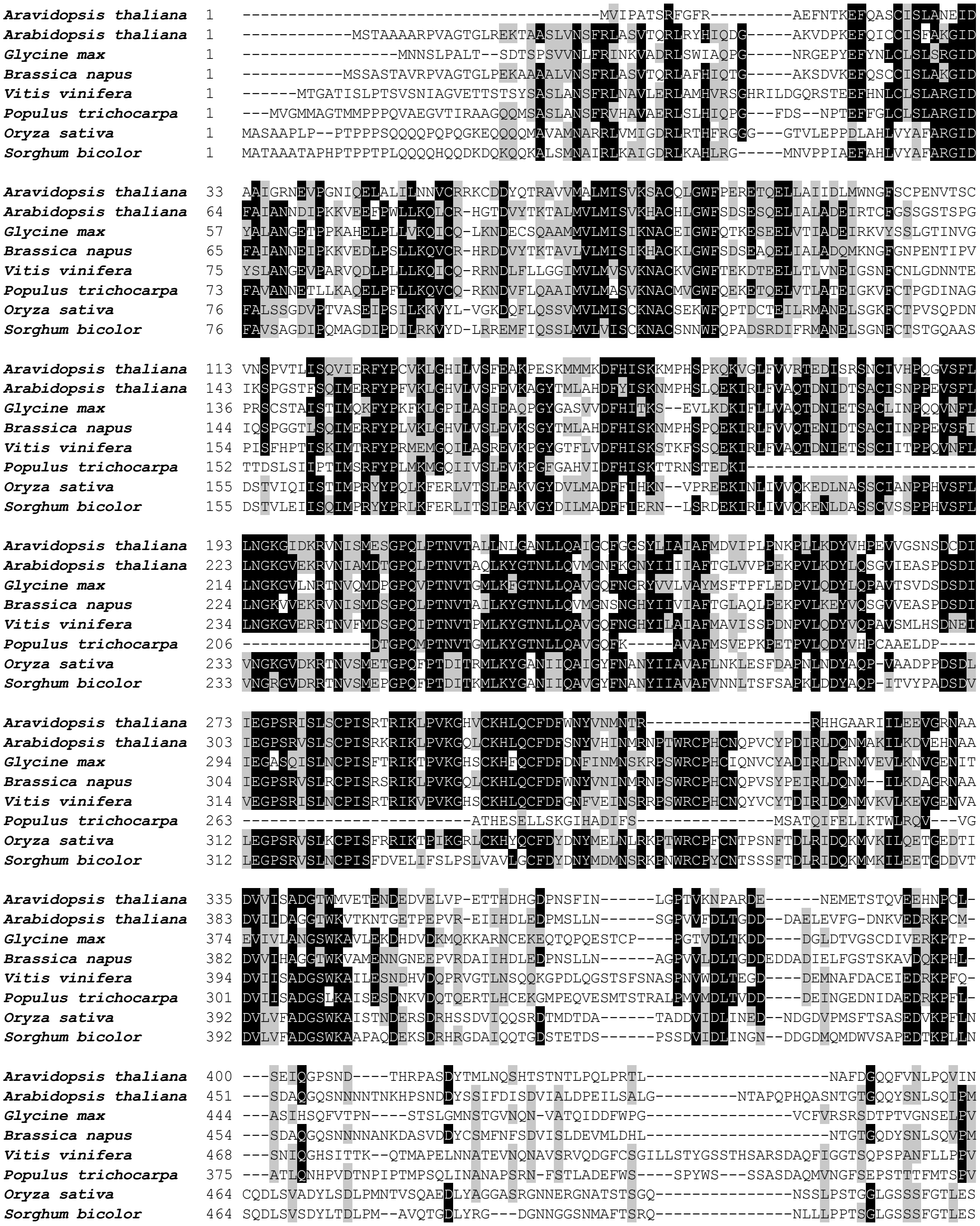
Supplemental Figure 4. Alignment of PIAL1 and PIAL2 in *Arabidopsis*, PIAS2 in human, and SU(VAR)2-10 in *Drosophila*. Black and gray boxes indicate that the residues are highly and weakly conserved, respectively.

Supplemental Figure 5



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Glycine max            1   -----------------MNNSLPALT--SDTSPSVVNLFRINKVADRLSWIAQPG-----NRGEPYEFYNLCLSLSRGID
Brassica napus         1   -----------MSSASTAVRPVAGTGLPEKAAAALVNSFRLASVTQRLAFHIQTG-----AKSDVKEFQSCCISLAKGID
Vitis vinifera         1   ------MTGATISLPTSVSNIAGVETTSTSYSASLANSFRLNAVLERLAMHVRSGHRILDGQRSTEEFHNLCLSLARGID
Populus trichocarpa    1   ---MVGMMAGTMMPPPQVAEGVTIRAAGQQMSASLANSFRVHAVAERLSLHIQPG---FDS--NPTEFFGLCLSLARGID
Oryza sativa           1   MASAAPLP--PTPPPSQQQQPQPQGKEQQQQMAVAMNARRLVMIGDRLRTHFRGGG---GTVLEPPDLAHLVYAFARGID
Sorghum bicolor        1   MATAAATAPHPTPPTPLQQQQHQQDKDQKQQKALSMNAIRLKAIGDRLKAHLRG-----MNVPPIAEFAHLVYAFARGID

Aravidopsis thaliana   33  AAIGRNEVPGNIQELALILNNVCRRKCDDYQTRAVVMALMISVKSACQLGWFPERETQELLAIIDLMWNGFSCPENVTSC
Arabidopsis thaliana   64  FAIANNDIPKKVEEFPWLLKQLCR-HGTDVYTKTALMVLMISVKHACHLGWFSDSESQELIALADEIRTCFGSSGSTSPG
Glycine max            57  YALANGETPPKAHELPLLVKQICQ-LKNDECSQAAMMVLMISIKNACEIGWFQTKESEELVTIADEIRKVYSSLGTINVG
Brassica napus         65  FAIANNEIPKKVEDLPSLLKQVCR-HRDDVYTKTAVLVLMISIKHACKLGWFSDSEAQELIALADQMKNGFGNPENTIPV
Vitis vinifera         75  YSLANGEVPARVQDLPLLLKQICQ-RRNDLFLLGGIMVLMVSVKNACKVGWFTEKDTEELLTLVNEIGSNFCNLGDNNTE
Populus trichocarpa    73  FAVANNETLLKAQELPFLLKQVCQ-RKNDVFLQAAIMVLMASVKNACMVGWFQEKETQELVTLATEIGKVFCTPGDINAG
Oryza sativa           76  FALSSGDVPTVASEIPSILKKVYL-VGKDQFLQSSVMVLMISCKNACSEKWFQPTDCTEILRMANELSGKFCTPVSQPDN
Sorghum bicolor        76  FAVSAGDIPQMAGDIPDILRKVYD-LRREMFIQSSLMVLVISCKNACSNNWFQPADSRDIFRMANELSGNFCTSTGQAAS

Aravidopsis thaliana   113 VNSPVTLISQVIERFYPCVKLGHILVSFEAKPESKMMMKDFHISKKMPHSPKQKVGLFVVRTEDISRSNCIVHPQGVSFL
Arabidopsis thaliana   143 IKSPGSTFSQIMERFYPFVKLGHVLVSFEVKAGYTMLAHDFYISKNMPHSLQEKIRLFVAQTDNIDTSACISNPPEVSFL
Glycine max            136 PRSCSTAISTIMQKFYPKFKLGPILASIEAQPGYGASVVDFHITKS--EVLKDKIFLLVAQTDNIETSACLINPQQVNFL
Brassica napus         144 IQSPGGTLSQIMERFYPLVKLGHVLVSLEVKSGYTMLAHDFHISKNMPHSPQEKIRLFVVQTENIDTSACIINPPEVSFI
Vitis vinifera         154 PISFHPTISKIMTRFYPRMEMGQILASREVKPGYGTFLVDFHISKSTKFSSQEKIRLFVAQTDNIETSSCIITPPQVNFL
Populus trichocarpa    152 TTDSLSIIPTIMSRFYPLMKMGQIIVSLEVKPGFGAHVIDFHISKTTRNSTEDKI-------------------------
Oryza sativa           155 DSTVIQIISTIMPRYYPQLKFERLVTSLEAKVGYDVLMADFFIHKN--VPREEKINLIVVQKEDLNASSCIANPPHVSFL
Sorghum bicolor        155 DSTVLEIISQIMPRYYPRLKFERLITSIEAKVGYDILMADFFIERN--LSRDEKIRLIVVQKENLDASSCVSSPPHVSFL

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Arabidopsis thaliana   223 LNGKGVEKRVNIAMDTGPQLPTNVTAQLKYGTNLLQVMGNFKGNYIIIIAFTGLVVPPEKPVLKDYLQSGVIEASPDSDI
Glycine max            214 LNGKGVLNRTNVQMDPGPQVPTNVTGMLKFGTNLLQAVGQFNGRYVVLVAYMSFTPFLEDPVLQDYLQPAVTSVDSDSDI
Brassica napus         224 LNGKVVEKRVNISMDSGPQLPTNVTAILKYGTNLLQVMGNSNGHYIIVIAFTGLAQLPEKPVLKEYVQSGVVEASPDSDI
Vitis vinifera         234 LNGKGVERRTNVFMDSGPQIPTNVTPMLKYGTNLLQAVGQFNGHYILAIAFMAVISSPDNPVLQDYVQPAVSMLHSDNEI
Populus trichocarpa    206 --------------DTGPQMPTNVTGMLKYGTNLLQAVGQFK-----AVAFMSVEPKPETPVLQDYVHPCAAELDP----
Oryza sativa           233 VNGKGVDKRTNVSMETGPQFPTDITRMLKYGANIIQAIGYFNANYIIAVAFLNKLESFDAPNLNDYAQP-VAADPPDSDL
Sorghum bicolor        233 VNGRGVDRRTNVSMEPGPQFPTDITKMLKYGANIIQAVGYFNANYIIAVAFVNNLTSFSAPKLDDYAQP-ITVYPADSDV

Aravidopsis thaliana   273 IEGPSRISLSCPISRTRIKLPVKGHVCKHLQCFDFWNYVNMNTR------------------RHHGAARIILEEVGRNAA
Arabidopsis thaliana   303 IEGPSRVSLSCPISRKRIKLPVKGQLCKHLQCFDFSNYVHINMRNPTWRCPHCNQPVCYPDIRLDQNMAKILKDVEHNAA
Glycine max            294 IEGASQISLNCPISFTRIKTPVKGHSCKHFQCFDFDNFINMNSKRPSWRCPHCIQNVCYADIRLDRNMVEVLKNVGENIT
Brassica napus         304 IEGPSRVSLRCPISRSRIKLPVKGQLCKHLQCFDFWNYVNINMRNPSWRCPHCNQPVSYPEIRLDQNM--ILKDAGRNAA
Vitis vinifera         314 VEGPSRISLNCPISRTRIKVPVKGHSCKHLQCFDFGNFVEINSRRPSWRCPHCNQYVCYTDIRIDQNMVKVLKEVGENVA
Populus trichocarpa    263 -------------------------ATHESELLSKGIHADIFS---------------MSATQIFELIKTWLRQV---VG
Oryza sativa           312 LEGPSRVSLKCPISFRRIKTPIKGRLCKHYQCFDYDNYMELNLRKPTWRCPFCNTPSNFTDLRIDQKMVKILQETGEDTI
Sorghum bicolor        312 LEGPSRVSLNCPISFDVELIFSLPSLVAVLGCFDYDNYMDMNSRKPNWRCPYCNTSSSFTDLRIDQKMMKILEETGDDVT

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Arabidopsis thaliana   383 DVIIDAGGTWKVTKNTGETPEPVR-EIIHDLEDPMSLLN------SGPVVFDLTGDD--DAELEVFG-DNKVEDRKPCM-
Glycine max            374 EVIVLANGSWKAVLEKDHDVDKMQKKARNCEKEQTQPQESTCP----PGTVDLTKDD----DGLDTVGSCDIVERKPTP-
Brassica napus         382 DVVIHAGGTWKVAMENNGNEEPVRDAIIHDLEDPNSLLN------AGPVVLDLTGDDEDDADIELFGSTSKAVDQKPHL-
Vitis vinifera         394 DVIISADGSWKAILESNDHVDQPRVGTLNSQQKGPDLQGSTSFSNASPNVWDLTEGD----DEMNAFDACEIEDRKPFQ-
Populus trichocarpa    301 DVIISADGSLKAISESDNKVDQTQERTLHCEKGMPEQVESMTSTRALPMVMDLTVDD----DEINGEDNIDAEDRKPFL-
Oryza sativa           392 DVLVFADGSWKAISTNDERSDRHSSDVIQQSRDTMDTDA------TADDVIDLINED--NDGDVPMSFTSASEDVKPFLN
Sorghum bicolor        392 DVLVFADGSWKAAPAQDEKSDRHRGDAIQQTGDSTETDS------PSSDVIDLINGN--DDGDMQMDWVSAPEDTKPLLN

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Arabidopsis thaliana   451 ---SDAQGQSNNNNTNKHPSNDDYSSIFDISDVIALDPEILSALG---------NTAPQPHQASNTGTGQQYSNLSQIPM
Glycine max            444 ---ASIHSQFVTPN----STSLGMNSTGVNQN-VATQIDDFWPG----------------VCFVRSRSDTPTVGNSELPV
Brassica napus         454 ---SDAQGQSNNNNANKDASVDDYCSMFNFSDVISLDEVMLDHL--------------------NTGTGQDYSNLSQVPM
Vitis vinifera         468 ---SNIQGHSITTK--QTMAPELNNATEVNQNAVSRVQDGFCSGILLSTYGSSTHSARSDAQFIGGTSQPSPANFLLPPV
Populus trichocarpa    375 ---ATLQNHPVDTNPIPTMPSQLINANAPSRN-FSTLADEFWS----SPYWS---SSASDAQMVNGFSEPSTTTFMTSPV
Oryza sativa           464 CQDLSVADYLSDLPMNTVSQAEDLYAGGASRGNNERGNATSTSGQ---------------NSSLPSTGGLGSSSFGTLES
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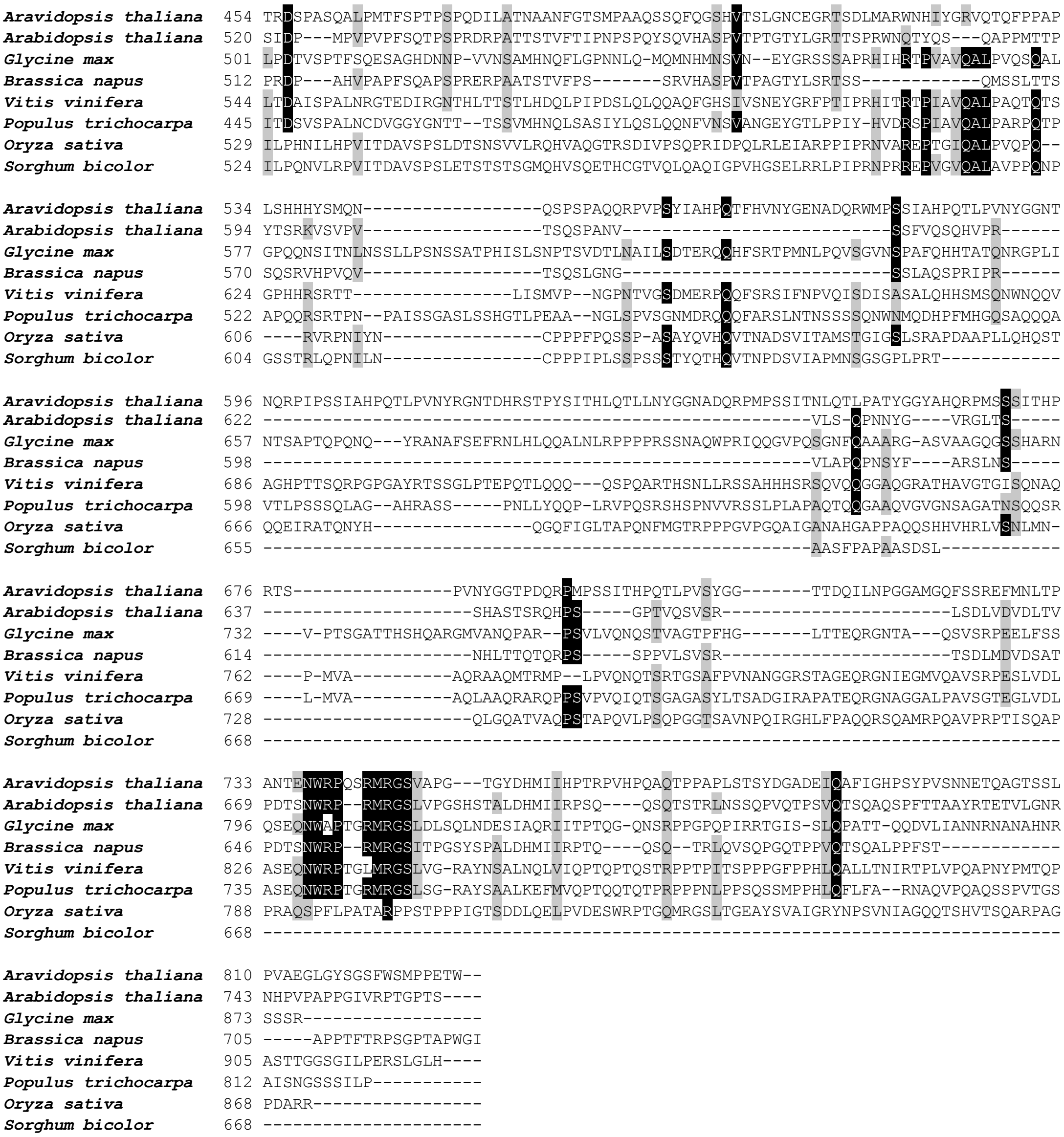

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Arabidopsis thaliana  520 SIDP---MPVPVPFSQTPSPRDRPATTSTVFTIPNPSPQYSQVHASPVTPTGTYLGRTTSPRWNQTYQS---QAPPMTTP
Glycine max           501 LPDTVSPTFSQESAGHDNNP-VVNSAMHNQFLGPNNLQ-MQMNHMNSVN--EYGRSSSAPRHIHRTPVAVQALPVQSQAL
Brassica napus        512 PRDP---AHVPAPFSQAPSPRERPAATSTVFPS-------SRVHASPVTPAGTYLSRTSS------------QMSSLTTS
Vitis vinifera        544 LTDAISPALNRGTEDIRGNTHLTTSTLHDQLPIPDSLQLQQAQFGHSIVSNEYGRFPTIPRHITRTPIAVQALPAQTQTS
Populus trichocarpa   445 ITDSVSPALNCDVGGYGNTT--TSSVMHNQLSASIYLQSLQQNFVNSVANGEYGTLPPIY-HVDRSPIAVQALPARPQTP
Oryza sativa          529 ILPHNILHPVITDAVSPSLDTSNSVVLRQHVAQGTRSDIVPSQPRIDPQLRLEIARPPIPRNVAREPTGIQALPVQPQ--
Sorghum bicolor       524 ILPQNVLRPVITDAVSPSLETSTSTSGMQHVSQETHCGTVQLQAQIGPVHGSELRRLPIPRNPRREPVGVQALAVPPQNP

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Arabidopsis thaliana  594 YTSRKVSVPV------------------TSQSPANV---------------------------SSFVQSQHVPR------
Glycine max           577 GPQQNSITNLNSSLLPSNSSATPHISLSNPTSVDTLNAILSDTERQQHFSRTPMNLPQVSGVNSPAFQHHTATQNRGPLI
Brassica napus        570 SQSRVHPVQV------------------TSQSLGNG---------------------------SSLAQSPRIPR------
Vitis vinifera        624 GPHHRSRTT----------------LISMVP--NGPNTVGSDMERPQQFSRSIFNPVQISDISASALQHHSMSQNWNQQV
Populus trichocarpa   522 APQQRSRTPN--PAISSGASLSSHGTLPEAA--NGLSPVSGNMDRQQQFARSLNTNSSSSQNWNMQDHPFMHGQSAQQQA
Oryza sativa          606 ----RVRPNIYN----------------CPPPFPQSSP-ASAYQVHQVTNADSVITAMSTGIGSLSRAPDAAPLLQHQST
Sorghum bicolor       604 GSSTRLQPNILN----------------CPPPIPLSSPSSSTYQTHQVTNPDSVIAPMNSGSGPLPRT------------

Aravidopsis thaliana  596 NQRPIPSSIAHPQTLPVNYRGNTDHRSTPYSITHLQTLLNYGGNADQRPMPSSITNLQTLPATYGGYAHQRPMSSSITHP
Arabidopsis thaliana  622 -------------------------------------------------------VLS-QPNNYG----VRGLTS-----
Glycine max           657 NTSAPTQPQNQ---YRANAFSEFRNLHLQQALNLRPPPPRSSNAQWPRIQQGVPQSGNFQAAARG-ASVAAGQGSSHARN
Brassica napus        598 -------------------------------------------------------VLAPQPNSYF----ARSLNS-----
Vitis vinifera        686 AGHPTTSQRPGPGAYRTSSGLPTEPQTLQQQ---QSPQARTHSNLLRSSAHHHSRSQVQQGGAQGRATHAVGTGISQNAQ
Populus trichocarpa   598 VTLPSSSQLAG--AHRASS-----PNLLYQQP-LRVPQSRSHSPNVVRSSLPLAPAQTQQGAAQVGVGNSAGATNSQQSR
Oryza sativa          666 QQEIRATQNYH----------------QGQFIGLTAPQNFMGTRPPPGVPGQAIGANAHGAPPAQQSHHVHRLVSNLMN-
Sorghum bicolor       655 -------------------------------------------------------AASFPAPAASDSL------------

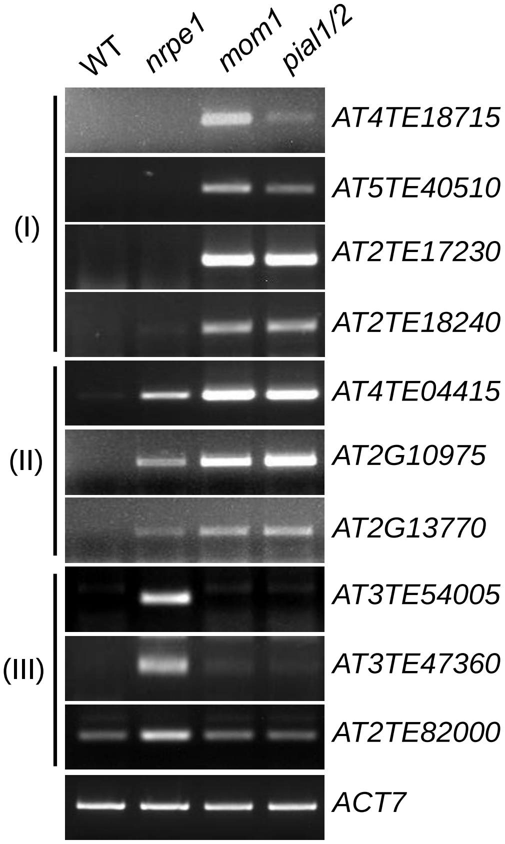
Aravidopsis thaliana  676 RTS----------------PVNYGGTPDQRPMPSSITHPQTLPVSYGG-------TTDQILNPGGAMGQFSSREFMNLTP
Arabidopsis thaliana  637 ---------------------SHASTSRQHPS-----GPTVQSVSR-----------------------LSDLVDVDLTV
Glycine max           732 ----V-PTSGATTHSHQARGMVANQPAR--PSVLVQNQSTVAGTPFHG-------LTTEQRGNTA---QSVSRPEELFSS
Brassica napus        614 ---------------------NHLTTQTQRPS-----SPPVLSVSR-----------------------TSDLMDVDSAT
Vitis vinifera        762 ----P-MVA----------AQRAAQMTRMP--LPVQNQTSRTGSAFPVNANGGRSTAGEQRGNIEGMVQAVSRPESLVDL
Populus trichocarpa   669 ----L-MVA----------AQLAAQRARQPPSVPVQIQTSGAGASYLTSADGIRAPATEQRGNAGGALPAVSGTEGLVDL
Oryza sativa          728 ---------------------QLGQATVAQPSTAPQVLPSQPGGTSAVNPQIRGHLFPAQQRSQAMRPQAVPRPTISQAP
Sorghum bicolor       668 --------------------------------------------------------------------------------

Aravidopsis thaliana  733 ANTENWRPQSRMRGSVAPG---TGYDHMIIHPTRPVHPQAQTPPAPLSTSYDGADEIQAFIGHPSYPVSNNETQAGTSSL
Arabidopsis thaliana  669 PDTSNWRP--RMRGSLVPGSHSTALDHMIIRPSQ----QSQTSTRLNSSQPVQTPSVQTSQAQSPFTTAAYRTETVLGNR
Glycine max           796 QSEQNWAPTGRMRGSLDLSQLNDESIAQRIITPTQG-QNSRPPGPQPIRRTGIS-SLQPATT-QQDVLIANNRNANAHNR
Brassica napus        646 PDTSNWRP--RMRGSITPGSYSPALDHMIIRPTQ----QSQ--TRLQVSQPGQTPPVQTSQALPPFST------------
Vitis vinifera        826 ASEQNWRPTGLMRGSLVG-RAYNSALNQLVIQPTQPTQSTRPPTPITSPPPGFPPHLQALLTNIRTPLVPQAPNYPMTQP
Populus trichocarpa   735 ASEQNWRPTGRMRGSLSG-RAYSAALKEFMVQPTQQTQTPRPPPNLPPSQSSMPPHLQFLFA--RNAQVPQAQSSPVTGS
Oryza sativa          788 PRAQSPFLPATARPPSTPPPIGTSDDLQELPVDESWRPTGQMRGSLTGEAYSVAIGRYNPSVNIAGQQTSHVTSQARPAG
Sorghum bicolor       668 --------------------------------------------------------------------------------

Aravidopsis thaliana  810 PVAEGLGYSGSFWSMPPETW--
Arabidopsis thaliana  743 NHPVPAPPGIVRPTGPTS----
Glycine max           873 SSSR------------------
Brassica napus        705 -----APPTFTRPSGPTAPWGI
Vitis vinifera        905 ASTTGGSGILPERSLGLH----
Populus trichocarpa   812 AISNGSSSILP-----------
Oryza sativa          868 PDARR-----------------
Sorghum bicolor       668 ----------------------
```

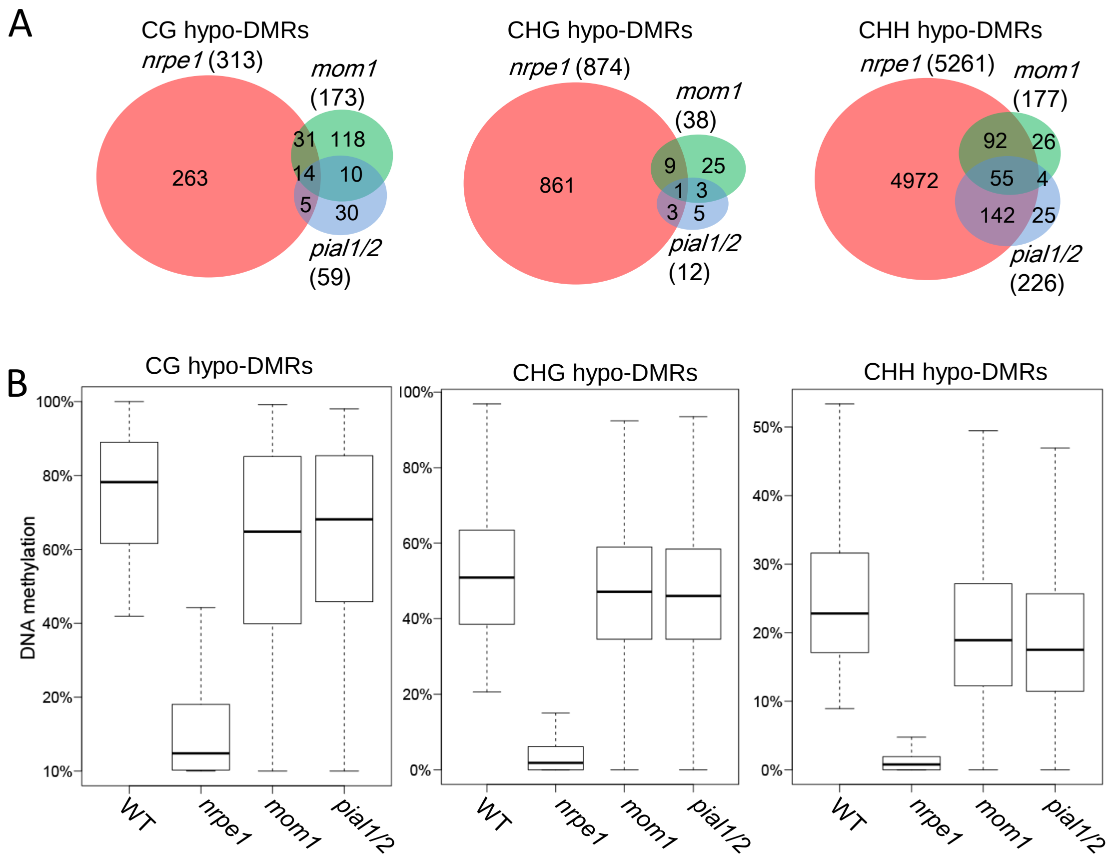
Supplemental Figure 5. Alignment of Arabidopsis PIAL1 and PIAL2 and their homologs in other plants including *Glycine max*, *Brassica napu*s, *Vitis vinifera*, *Populus trichocarpa*, *Oryza sativa*, and *Sorghum bicolor*. Black and gray boxes indicate that the residues are highly and weakly conserved, respectively.

Supplemental Figure 6



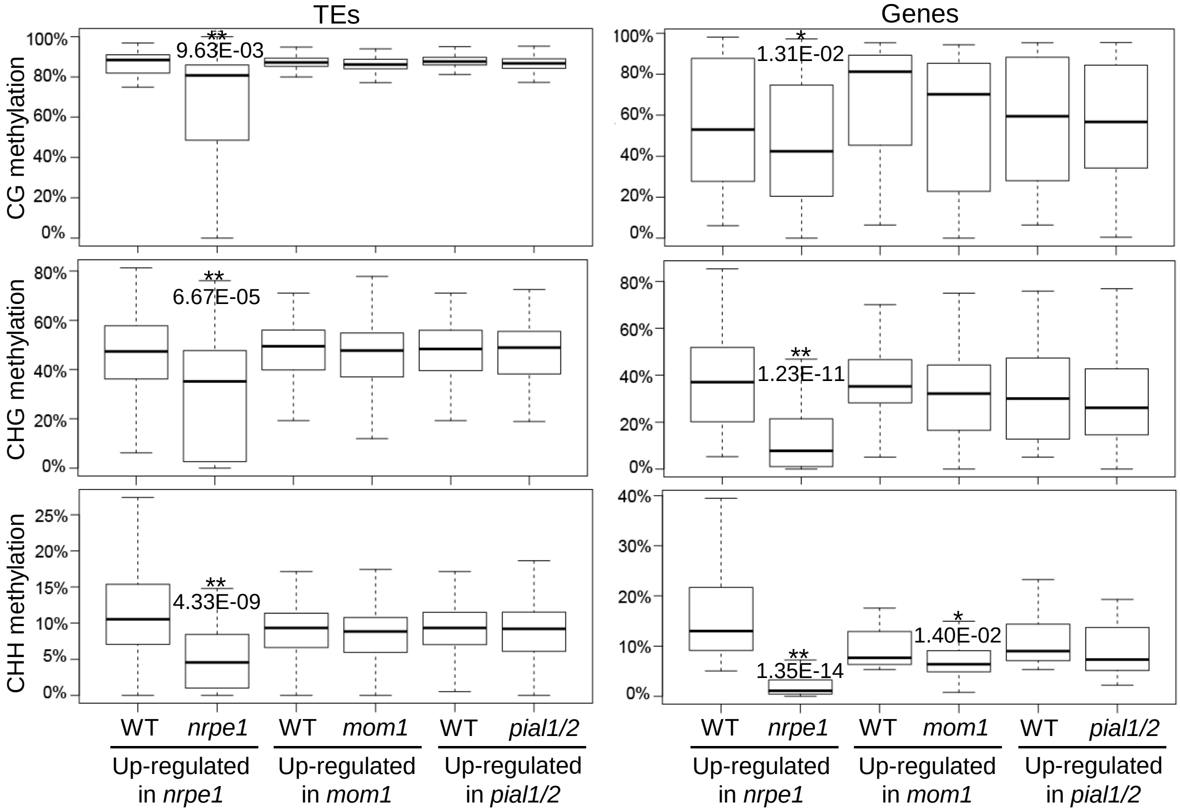
Supplemental Figure 6. Validation of the transcript levels of the MOM1, PIAL1/2, and/or NPRE1 target loci in the wild type, *nrpe1*, *mom1*, and *pial1/2*. Indicated loci were randomly selected from up-regulated loci identified by the RNA deep sequencing analyses. The transcript levels of the indicated loci were determined by RT-PCR. The loci that are transcriptionally up-regulated in *nrpe1*, *mom1*, and/or *pial1/2* were placed into three classes based on the transcript patterns of the loci. I, loci up-regulated in *mom1* and *pial1/2* but not in *nrpe1*; II, loci up-regulated in *nrpe1*, *mom1*, and *pial1/2*; III, loci up-regulated in *nrpe1* but not in *mom1* or *pial/2*. The actin gene *ACT7* was used as an internal control. The RT-PCR experiment was biologically repeated for at least two times and the result of a representative experiment is shown.

Supplemental Figure 7



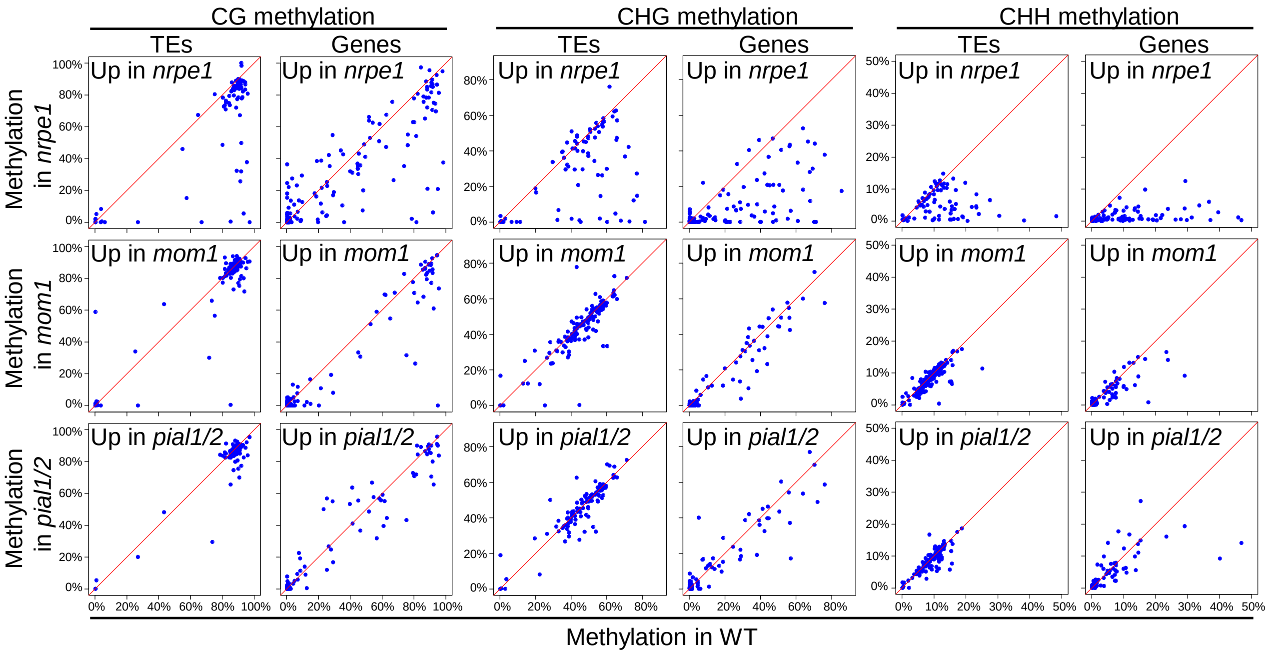
Supplemental Figure 7. Analyses of hypo-DMRs in *nrpe1*, *mom1*, and *pial1/2*. **(A)** Overlaps of hypo-DMRs in *nrpe1*, *mom1*, and *pial1/2* relative to the wild type at CG, CHG, and CHH sites. Hypo-DMRs were separately defined based on the DNA methylation levels of CG. CHG, and CHH sites in the mutants relative to the wild type. Bins were recognized as DMRs when their absolute DNA methylation change is more than 40%, 20%, and 10% for CG, CHG, and CHH, respectively. **(B)** DNA methylation levels of hypo-DMRs in the wild type, *nrpe1*, *mom1*, and *pial1/2*. CG, CHG, and CHH hypo-DMRs in *nrpe1* were separately analyzed.

Supplemental Figure 8



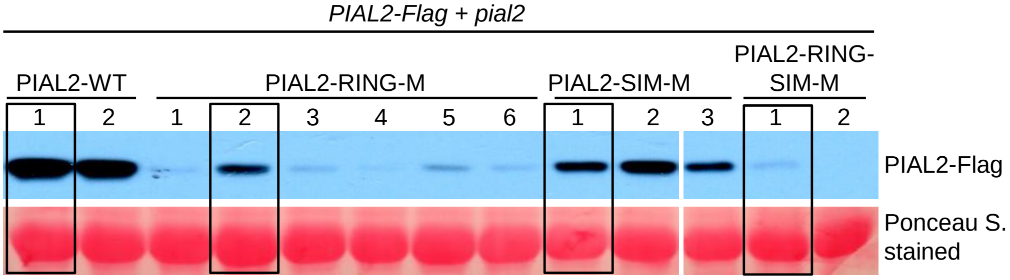
Supplemental Figure 8. Box plots showing CG, CHG, and CHH methylation of transcriptionally up-regulated TEs and genes in *nrpe1*, *mom1*, and *pial1/2* relative to the wild type. *p<0.05 or **p<0.01 was determined by t test. In the box plots, gene promoters were included for DNA methylation analysis only when their DNA methylation levels in the wild type were higher than 5%.

Supplemental Figure 9



Supplemental Figure 9. Scatter plots showing CG, CHG, and CHH methylation of transcriptionally up-regulated TEs or genes in *nrpe1*, *mom1*, and *pial1/2* relative to the wild type. The DNA methylation levels of TEs and genes that are transcriptionally up-regulated in the mutants were analyzed. Diagonal red lines indicate that the DNA methylation levels of mutants are the same as those of the wild-type.

Supplemental Figure 10



Supplemental Figure 10. The expression levels of the wild-type and mutated *PIAL2* transgenes in the *pial2* mutant. The expression levels were determined by immunoblot assays with anti-Flag antibody. Rubisco proteins stained by Ponceau S. are shown as a loading control. Boxed transgenic lines were used for complementation assays by quantitative RT-PCR and the results are shown in Figure 6C. The expression of *PIAL2-Flag* in the boxed transgenic lines is also shown in Figure 6B.

Supplemental Table 1. Full list of mutants identified by map-based cloning in this study.

Mutant No.	Mutant gene	Mutation position related to ATG	Mutation	Code change	Mutation type
84-3	*PIAL2*	2769	C→T		splice site
4-1	*MORC6*	548	G→A	TGG→TGA	premature stop codon
22-1-1	*MORC6*	3049	G→T	GAG→TAG	premature stop codon
59-1	*MORC6*	3031	C→T	CAG→TAG	premature stop codon
138-2	*MORC6*	4123	C→T	CAA→TAA	premature stop codon
215-3	*MORC6*	2904	G→A		splice site
249-1	*MORC6*	3170	G→A	GGA→GAA	G→E
250-1	*MORC6*	3169	G→A	GGA→AGA	G→R
200-1	*MORC6*	315	G→A		splice site
294-1	*MORC6*	1800	C→T	GCT→GTT	A→V
31-2	*MOM1*	4782	G→A		splice site
38-1	*MOM1*	400	C→T	CGA→TGA	premature stop codon
270-2	*MOM1*	1036	C→T	CAA→TAA	premature stop codon
310-9	*MOM1*	2350	G		deletion
13-2	*MOM1*	6181	G→A		splice site
241-1	*MOM1*	3007	G→A	GAA→AAA	E→K
78-2	*AGO4*	2457	C→T		splice site
91-1	*AGO4*	4213	C→T		splice site
139-3	*AGO4*	469	C→T	CAA→TAA	premature stop codon
136-3	*AGO4*	3256	G→A		splice site
62-1	*AGO4*	2555	G→A	GGA→GAA	G→E
227-2	*AGO4*	3893	G→A	TGG→TGA	premature stop codon
310-17	*AGO4*	3370	G→A	TGG→TGA	premature stop codon
190-1	*AGO4*	3785	G→A		splice site
24-1	*AGO4*	199	C→T	CAA→TAA	premature stop codon
144-1	*AGO4*	3148	G→A	GAG→AAG	E→K
178-1	*AGO4*	1789	G→A	TGC→TAC	C→Y
324-2	*AGO4*	3199	G→A	GGG→AGG	G→R
131-1	*NRPD1*	2839	C→T	CAG→TAG	premature stop codon
45-1	*NRPD1*	3412	C→T		splice site
120-3	*NRPD1*	3169	C→T	CAG→TAG	premature stop codon
200-2	*NRPD1*	2752	C→T	CAA→TAA	premature stop codon
268-2	*NRPD1*	225	G→A	GGA→AGA	G→R
95-1	*NRPD1*	1828	C→T	CCT→TCT	P→W
40-1	*DRD1*	2014	C→T	CCA→TCA	P→S
226-1	*DRD1*	3127	G→A	GAA→AAA	E→K
231-1	*DRD1*	3209	G→A	GGG→GAG	G→E
272-5	*RDR2*	2548	C→T	CAG→TAG	premature stop codon
33-1	*RDR2*	3120	C→T	CTT→TTT	L→F
218-2	*NRPD4*	199,200	CC→GG		splice site
139-2	*RDM4*	49	C→T	CCT→TCT	P→S
17-4	*NRPD2*	4022	G→A	GGG→AGG	G→R
25-1	*MET1*	4596	C→T	CCT→CTT	P→L
218-1	*MET1*	3016	G→A	GAG→AAG	E→K
28-6	*MET1*	4557	G→A	CGA→CAA	R→Q
68-2	*FPGS1*	3803	G→A	TGG→TGA	premature stop codon
25-9	*FPGS1*	3403	G→A	TGG→TGA	premature stop codon
104-1	*FAS1*	455	G→A	TGG→TAG	premature stop codon
112-2	*BRU1*	5091	G→A		splice site