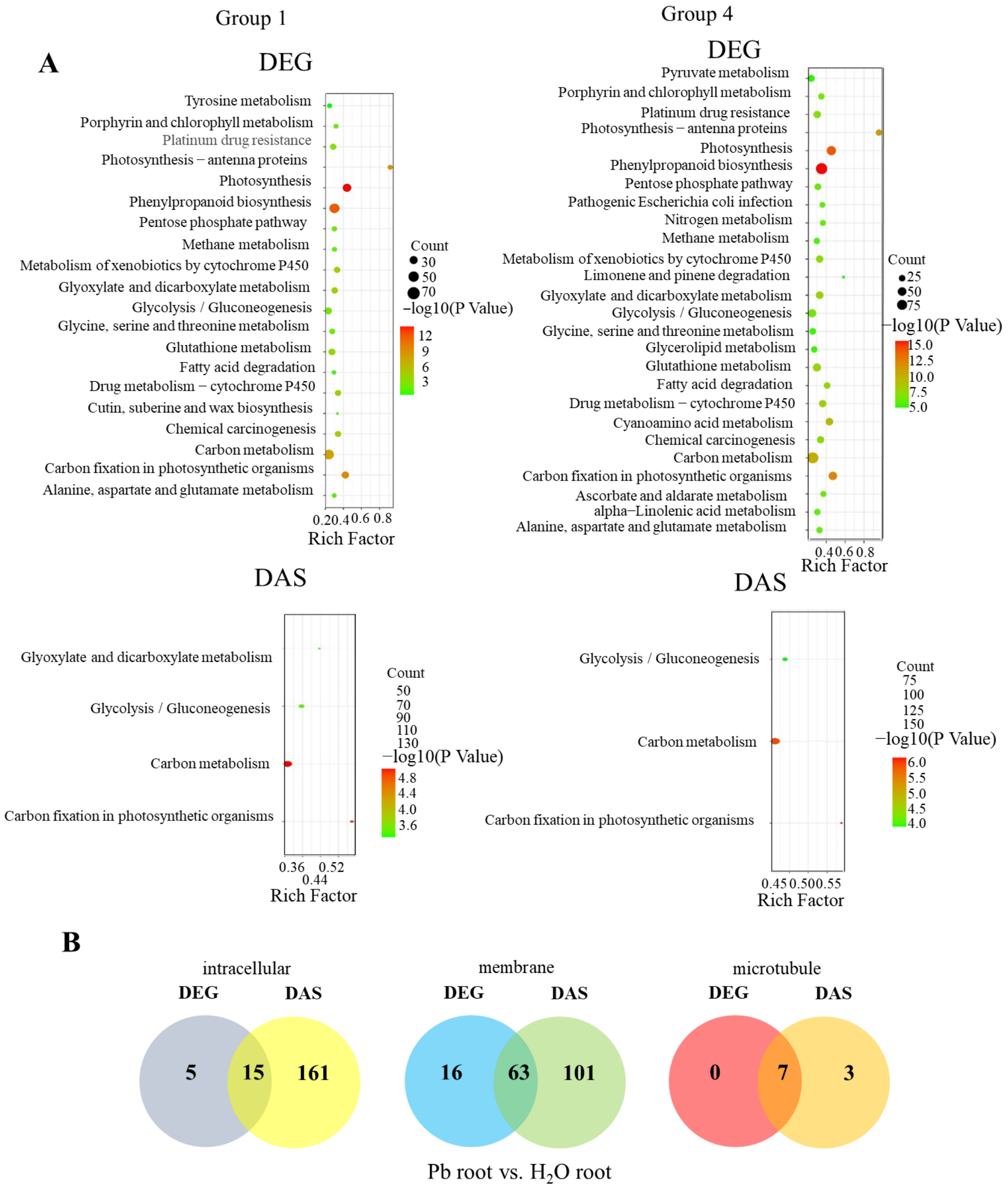


Figure S1. (A) KEGG pathway enrichment analysis of DEGs and genes subjected to DAS events in Group 1 and Group 4. (B) Overlapping GO pathways between DEGs and genes subjected to DAS events in the cellular component category. Group 1 represents H2O shoots vs. H2O roots; Group 2 represents Pb roots vs. H2O roots; Group 3 represents Pb shoots vs. H2O shoots; and Group 4 represents Pb shoots vs. Pb roots.

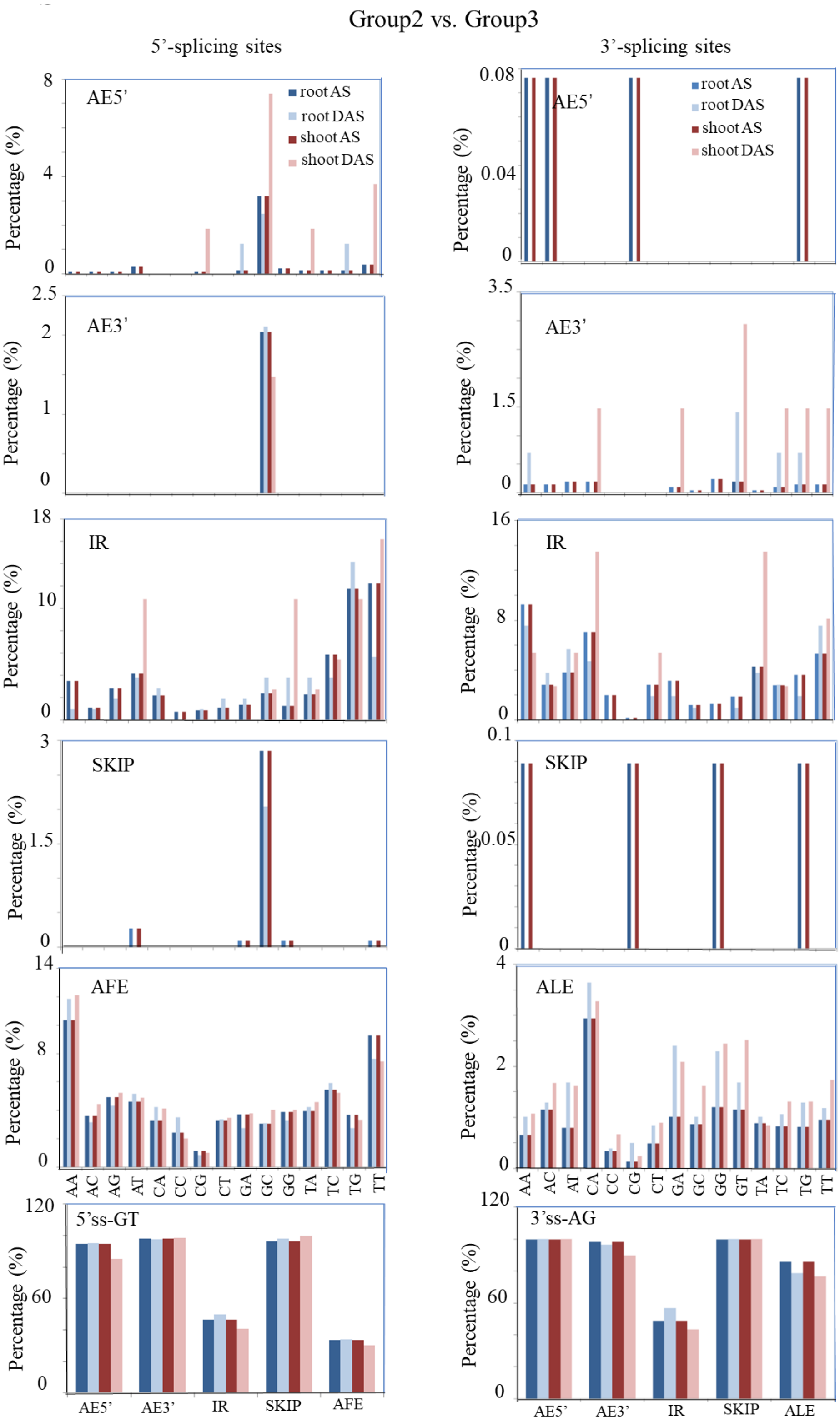


Figure S2. Frequency of traditional and nonconventional splice site selection in specific splicing events in Group 2 and Group 3 members between the shoots and roots. Group 1 represents H_2O shoots vs. H_2O roots; Group 2 represents Pb roots vs. H_2O roots; Group 3 represents Pb shoots vs. H_2O shoots; and Group 4 represents Pb shoots vs. Pb roots.

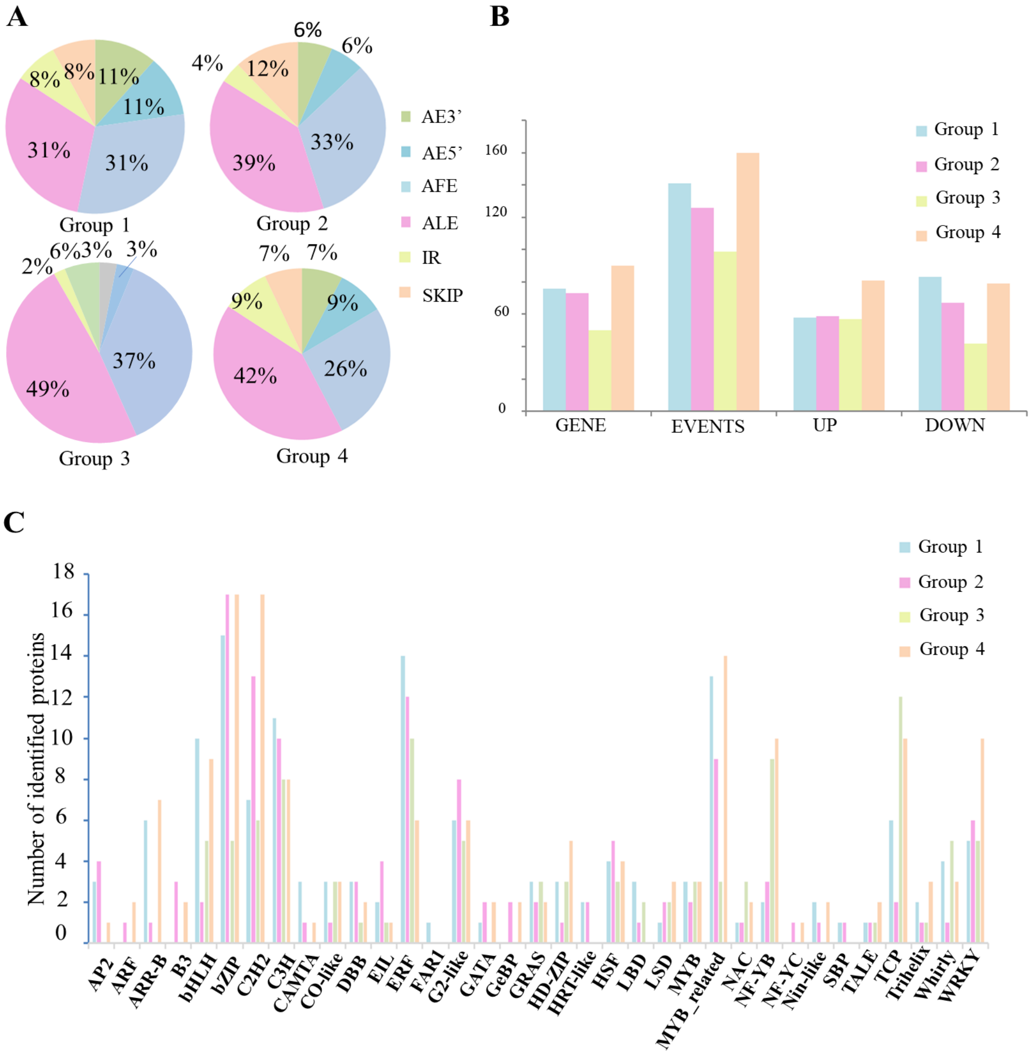
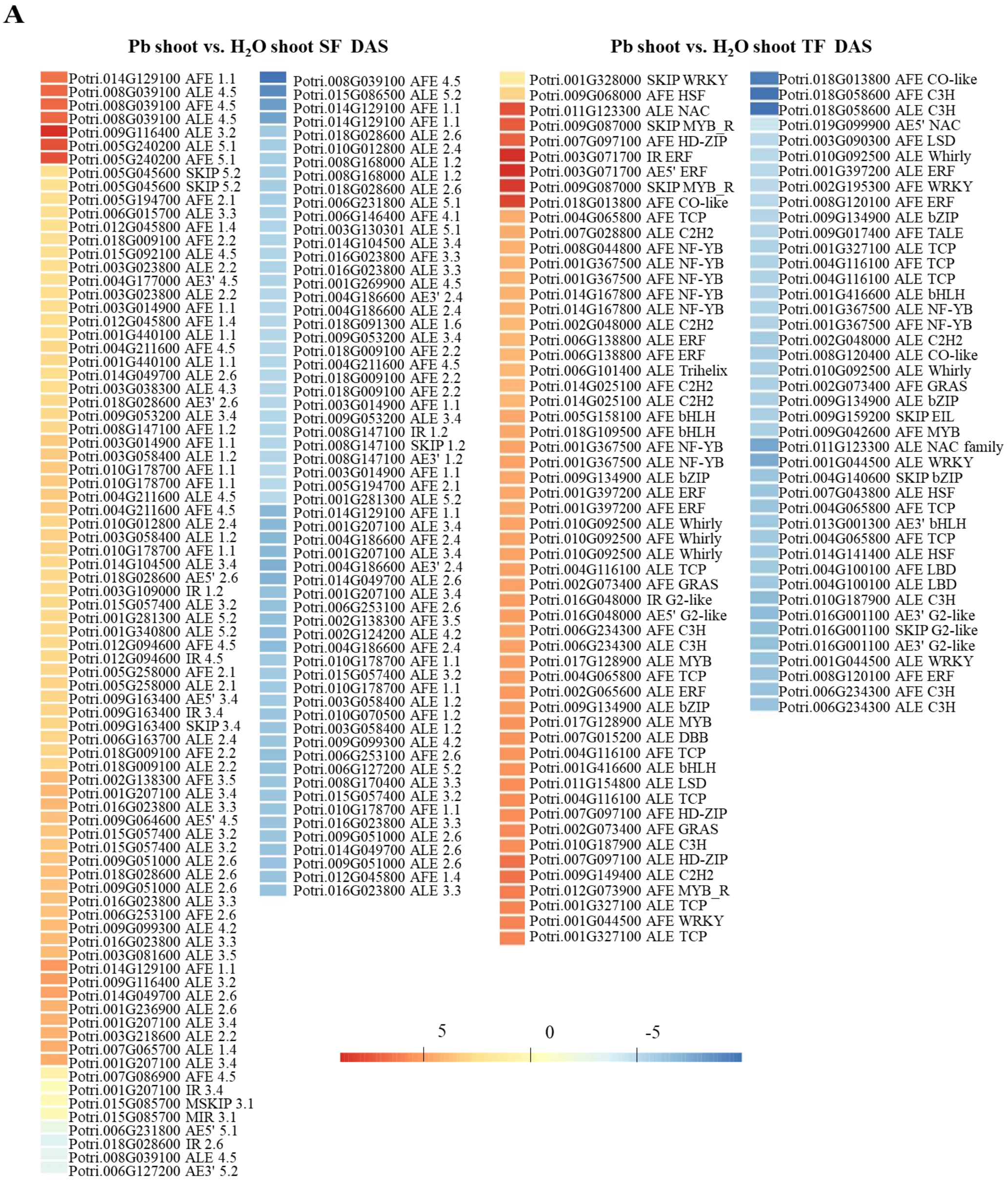


Figure S3. Splicing event statistics and groups of TFs. (A) Proportion of splicing events in each compared group. (B) Number of identified proteins in each TF family. (C) Numbers of genes, events, increased events and decreased events. Group 1 represents H_2O shoots vs. H_2O roots; Group 2 represents Pb roots vs. H_2O roots; Group 3 represents Pb shoots vs. H_2O shoots; and Group 4 represents Pb shoots vs. Pb roots.


A
Pb shoot vs. H2O shoot SF DAS
Potri.014G129100 AFE 1.1
Potri.008G039100 ALE 4.5
Potri.008G039100 AFE 4.5
Potri.008G039100 ALE 4.5
Potri.009G116400 ALE 3.2
Potri.005G240200 ALE 5.1
Potri.005G240200 AFE 5.1
Potri.005G045600 SKIP 5.2
Potri.005G045600 SKIP 5.2
Potri.005G194700 AFE 2.1
Potri.006G015700 ALE 3.3
Potri.012G045800 AFE 1.4
Potri.018G009100 AFE 2.2
Potri.015G092100 ALE 4.5
Potri.003G023800 ALE 2.2
Potri.004G177000 AE3' 4.5
Potri.003G023800 ALE 2.2
Potri.003G014900 AFE 1.1
Potri.012G045800 AFE 1.4
Potri.001G440100 ALE 1.1
Potri.004G211600 AFE 4.5
Potri.001G440100 ALE 1.1
Potri.014G049700 ALE 2.6
Potri.003G038300 ALE 4.3
Potri.018G028600 AE3' 2.6
Potri.009G053200 ALE 3.4
Potri.008G147100 AFE 1.2
Potri.003G014900 AFE 1.1
Potri.003G058400 ALE 1.2
Potri.010G178700 AFE 1.1
Potri.010G178700 AFE 1.1
Potri.004G211600 ALE 4.5
Potri.004G211600 AFE 4.5
Potri.010G012800 ALE 2.4
Potri.003G058400 ALE 1.2
Potri.010G178700 AFE 1.1
Potri.014G104500 ALE 3.4
Potri.018G028600 AE5' 2.6
Potri.003G109000 IR 1.2
Potri.015G057400 ALE 3.2
Potri.001G281300 ALE 5.2
Potri.001G340800 ALE 5.2
Potri.012G094600 AFE 4.5
Potri.012G094600 IR 4.5
Potri.005G258000 AFE 2.1
Potri.005G258000 ALE 2.1
Potri.009G163400 AE5' 3.4
Potri.009G163400 IR 3.4
Potri.009G163400 SKIP 3.4
Potri.006G163700 ALE 2.4
Potri.018G009100 AFE 2.2
Potri.018G009100 ALE 2.2
Potri.002G138300 AFE 3.5
Potri.001G207100 ALE 3.4
Potri.016G023800 ALE 3.3
Potri.009G064600 AE5' 4.5
Potri.015G057400 ALE 3.2
Potri.015G057400 ALE 3.2
Potri.009G051000 ALE 2.6
Potri.018G028600 ALE 2.6
Potri.009G051000 ALE 2.6
Potri.016G023800 ALE 3.3
Potri.006G253100 AFE 2.6
Potri.009G099300 ALE 4.2
Potri.016G023800 ALE 3.3
Potri.003G081600 ALE 3.5
Potri.014G129100 AFE 1.1
Potri.009G116400 ALE 3.2
Potri.014G049700 ALE 2.6
Potri.001G236900 ALE 2.6
Potri.001G207100 ALE 3.4
Potri.003G218600 ALE 2.2
Potri.007G065700 ALE 1.4
Potri.001G207100 ALE 3.4
Potri.007G086900 AFE 4.5
Potri.001G207100 IR 3.4
Potri.015G085700 MSKIP 3.1
Potri.015G085700 MIR 3.1
Potri.006G231800 AE5' 5.1
Potri.018G028600 IR 2.6
Potri.008G039100 ALE 4.5
Potri.006G127200 AE3' 5.2
Potri.008G039100 AFE 4.5
Potri.015G086500 ALE 5.2
Potri.014G129100 AFE 1.1
Potri.014G129100 AFE 1.1
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Potri.010G012800 ALE 2.4
Potri.008G168000 ALE 1.2
Potri.008G168000 ALE 1.2
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Potri.006G146400 AFE 4.1
Potri.003G130301 ALE 5.1
Potri.014G104500 ALE 3.4
Potri.016G023800 AFE 3.3
Potri.016G023800 ALE 3.3
Potri.001G269900 ALE 4.5
Potri.004G186600 AE3' 2.4
Potri.004G186600 ALE 2.4
Potri.018G091300 ALE 1.6
Potri.009G053200 ALE 3.4
Potri.018G009100 AFE 2.2
Potri.004G211600 AFE 4.5
Potri.018G009100 AFE 2.2
Potri.018G009100 AFE 2.2
Potri.003G014900 AFE 1.1
Potri.009G053200 ALE 3.4
Potri.008G147100 IR 1.2
Potri.008G147100 SKIP 1.2
Potri.008G147100 AE3' 1.2
Potri.003G014900 AFE 1.1
Potri.005G194700 AFE 2.1
Potri.001G281300 ALE 5.2
Potri.014G129100 AFE 1.1
Potri.001G207100 ALE 3.4
Potri.004G186600 AFE 2.4
Potri.001G207100 ALE 3.4
Potri.004G186600 AE3' 2.4
Potri.014G049700 ALE 2.6
Potri.001G207100 ALE 3.4
Potri.006G253100 AFE 2.6
Potri.002G138300 AFE 3.5
Potri.002G124200 ALE 4.2
Potri.004G186600 AFE 2.4
Potri.010G178700 AFE 1.1
Potri.015G057400 ALE 3.2
Potri.010G178700 AFE 1.1
Potri.003G058400 ALE 1.2
Potri.010G070500 AFE 1.2
Potri.003G058400 ALE 1.2
Potri.009G099300 ALE 4.2
Potri.006G253100 AFE 2.6
Potri.006G127200 ALE 5.2
Potri.008G170400 ALE 3.3
Potri.015G057400 ALE 3.2
Potri.010G178700 AFE 1.1
Potri.016G023800 ALE 3.3
Potri.009G051000 ALE 2.6
Potri.014G049700 ALE 2.6
Potri.009G051000 ALE 2.6
Potri.012G045800 AFE 1.4
Potri.016G023800 ALE 3.3
Pb shoot vs. H2O shoot TF DAS
Potri.001G328000 SKIP WRKY
Potri.009G068000 AFE HSF
Potri.011G123300 ALE NAC
Potri.009G087000 SKIP MYB_R
Potri.007G097100 AFE HD-ZIP
Potri.003G071700 IR ERF
Potri.003G071700 AE5' ERF
Potri.009G087000 SKIP MYB_R
Potri.018G013800 AFE CO-like
Potri.004G065800 AFE TCP
Potri.007G028800 ALE C2H2
Potri.008G044800 AFE NF-YB
Potri.001G367500 ALE NF-YB
Potri.001G367500 AFE NF-YB
Potri.014G167800 AFE NF-YB
Potri.014G167800 ALE NF-YB
Potri.002G048000 ALE C2H2
Potri.006G138800 ALE ERF
Potri.006G138800 AFE ERF
Potri.006G101400 ALE Trihelix
Potri.014G025100 AFE C2H2
Potri.014G025100 ALE C2H2
Potri.005G158100 AFE bHLH
Potri.018G109500 AFE bHLH
Potri.001G367500 AFE NF-YB
Potri.001G367500 ALE NF-YB
Potri.009G134900 ALE bZIP
Potri.001G397200 ALE ERF
Potri.001G397200 AFE ERF
Potri.010G092500 ALE Whirly
Potri.010G092500 AFE Whirly
Potri.010G092500 ALE Whirly
Potri.004G116100 ALE TCP
Potri.002G073400 AFE GRAS
Potri.016G048000 IR G2-like
Potri.016G048000 AE5' G2-like
Potri.006G234300 AFE C3H
Potri.006G234300 ALE C3H
Potri.017G128900 ALE MYB
Potri.004G065800 AFE TCP
Potri.002G065600 ALE ERF
Potri.009G134900 ALE bZIP
Potri.017G128900 ALE MYB
Potri.007G015200 ALE DBB
Potri.004G116100 AFE TCP
Potri.001G416600 ALE bHLH
Potri.011G154800 ALE LSD
Potri.004G116100 ALE TCP
Potri.007G097100 AFE HD-ZIP
Potri.002G073400 AFE GRAS
Potri.010G187900 ALE C3H
Potri.007G097100 ALE HD-ZIP
Potri.009G149400 ALE C2H2
Potri.012G073900 AFE MYB_R
Potri.001G327100 ALE TCP
Potri.001G044500 AFE WRKY
Potri.001G327100 ALE TCP
Potri.018G013800 AFE CO-like
Potri.018G058600 AFE C3H
Potri.018G058600 ALE C3H
Potri.019G099900 AE5' NAC
Potri.003G090300 AFE LSD
Potri.010G092500 ALE Whirly
Potri.001G397200 ALE ERF
Potri.002G195300 AFE WRKY
Potri.008G120100 AFE ERF
Potri.009G134900 ALE bZIP
Potri.009G017400 AFE TALE
Potri.001G327100 ALE TCP
Potri.004G116100 AFE TCP
Potri.004G116100 ALE TCP
Potri.001G416600 ALE bHLH
Potri.001G367500 ALE NF-YB
Potri.001G367500 AFE NF-YB
Potri.002G048000 ALE C2H2
Potri.008G120400 ALE CO-like
Potri.010G092500 ALE Whirly
Potri.002G073400 AFE GRAS
Potri.009G134900 ALE bZIP
Potri.009G159200 SKIP EIL
Potri.009G042600 AFE MYB
Potri.011G123300 ALE NAC family
Potri.001G044500 ALE WRKY
Potri.004G140600 SKIP bZIP
Potri.007G043800 ALE HSF
Potri.004G065800 AFE TCP
Potri.013G001300 AE3' bHLH
Potri.004G065800 AFE TCP
Potri.014G141400 ALE HSF
Potri.004G100100 AFE LBD
Potri.004G100100 ALE LBD
Potri.010G187900 ALE C3H
Potri.016G001100 AE3' G2-like
Potri.016G001100 SKIP G2-like
Potri.016G001100 AE3' G2-like
Potri.001G044500 ALE WRKY
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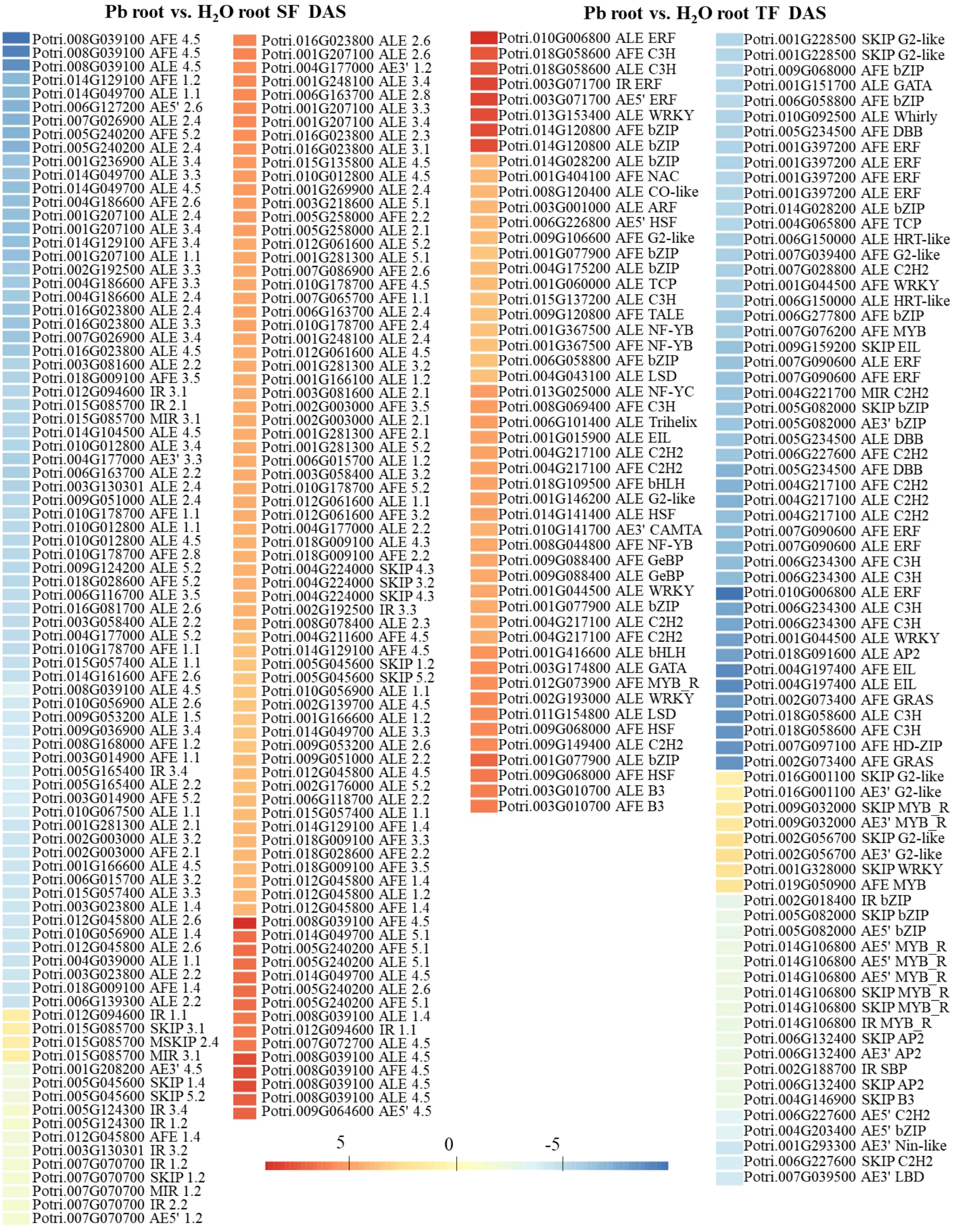
5
0
-5



Pb root vs. H_2O root SF DAS

Pb root vs. H_2O root TF DAS

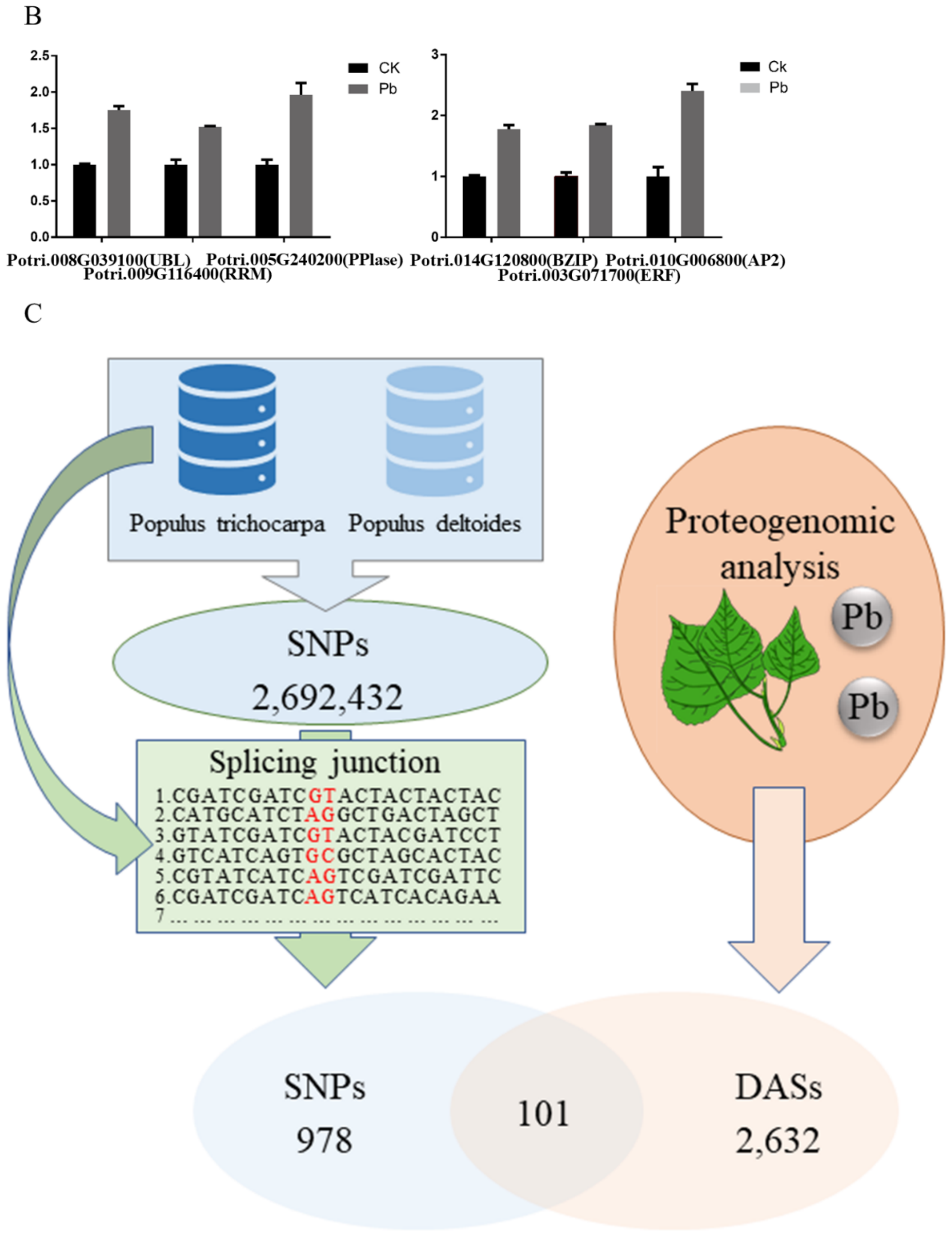
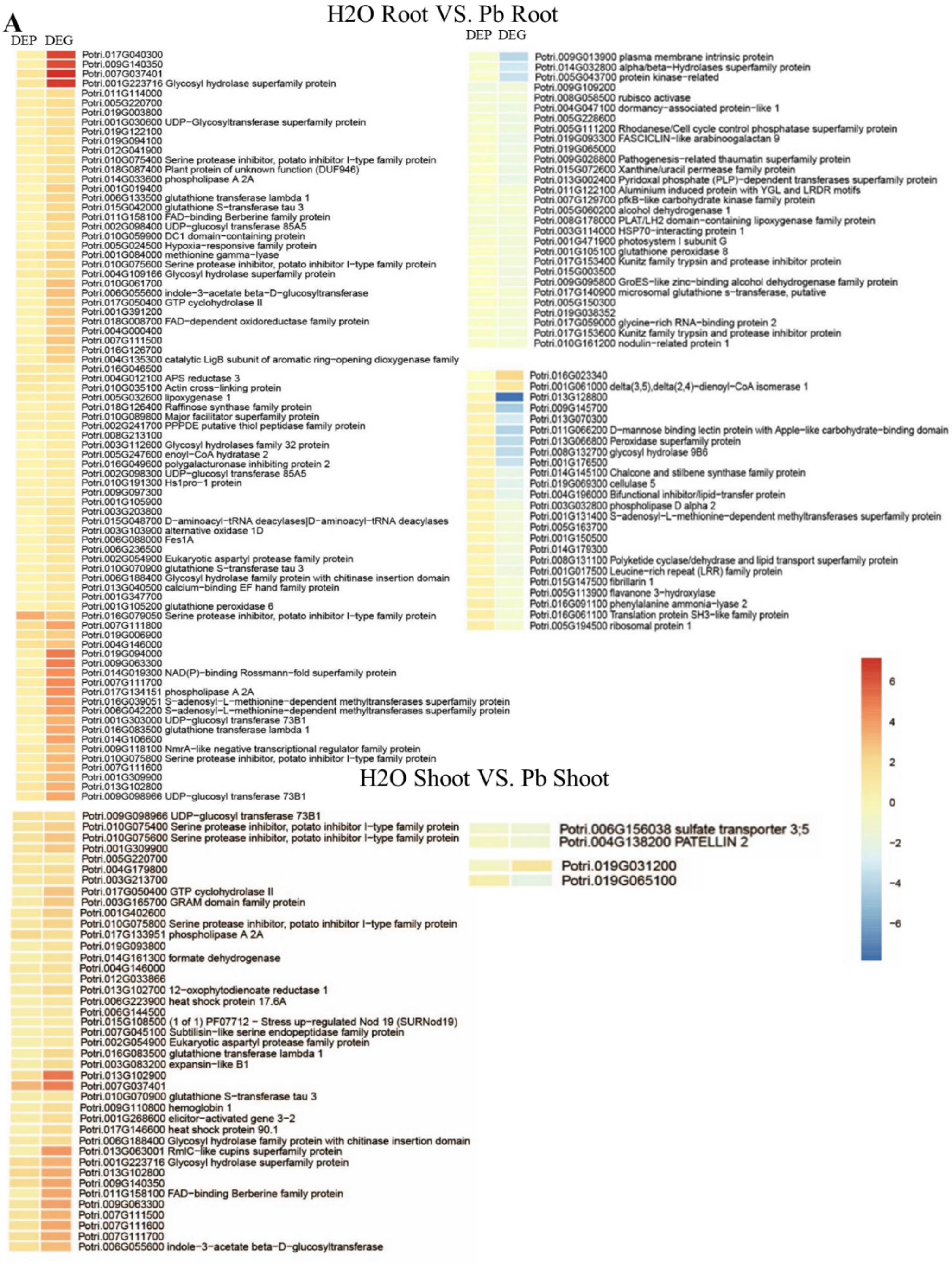


Figure S4. (A) Heatmap showing the expression levels of SF- and TF-encoding genes subjected to DAS events in Group 2 and Group 3. (B) RT–qPCR validation of the WRKY gene. (C) The process of SNP identification.


A
H2O Root VS. Pb Root
DEP
DEG
Potri.017G040300
Potri.009G140350
Potri.007G037401
Potri.001G223716 Glycosyl hydrolase superfamily protein
Potri.011G114000
Potri.005G220700
Potri.019G003800
Potri.001G030600 UDP−Glycosyltransferase superfamily protein
Potri.019G122100
Potri.019G094100
Potri.012G041900
Potri.010G075400 Serine protease inhibitor, potato inhibitor I−type family protein
Potri.018G087400 Plant protein of unknown function (DUF946)
Potri.014G033600 phospholipase A 2A
Potri.001G019400
Potri.006G133500 glutathione transferase lambda 1
Potri.015G042000 glutathione S−transferase tau 3
Potri.011G158100 FAD−binding Berberine family protein
Potri.002G098400 UDP−glucosyl transferase 85A5
Potri.010G059900 DC1 domain−containing protein
Potri.005G024500 Hypoxia−responsive family protein
Potri.001G084000 methionine gamma−lyase
Potri.010G075600 Serine protease inhibitor, potato inhibitor I−type family protein
Potri.004G109166 Glycosyl hydrolase superfamily protein
Potri.010G061700
Potri.006G055600 indole−3−acetate beta−D−glucosyltransferase
Potri.017G050400 GTP cyclohydrolase II
Potri.001G391200
Potri.018G008700 FAD−dependent oxidoreductase family protein
Potri.004G000400
Potri.007G111500
Potri.016G126700
Potri.004G135300 catalytic LigB subunit of aromatic ring−opening dioxygenase family
Potri.016G046500
Potri.004G012100 APS reductase 3
Potri.010G035100 Actin cross−linking protein
Potri.005G032600 lipoxygenase 1
Potri.018G126400 Raffinose synthase family protein
Potri.010G089800 Major facilitator superfamily protein
Potri.002G241700 PPPDE putative thiol peptidase family protein
Potri.008G213100
Potri.003G112600 Glycosyl hydrolases family 32 protein
Potri.005G247600 enoyl−CoA hydratase 2
Potri.016G049600 polygalacturonase inhibiting protein 2
Potri.002G098300 UDP−glucosyl transferase 85A5
Potri.010G191300 Hs1pro−1 protein
Potri.009G097300
Potri.001G105900
Potri.003G203800
Potri.015G048700 D−aminoacyl−tRNA deacylases|D−aminoacyl−tRNA deacylases
Potri.003G103900 alternative oxidase 1D
Potri.006G088000 Fes1A
Potri.006G236500
Potri.002G054900 Eukaryotic aspartyl protease family protein
Potri.010G070900 glutathione S−transferase tau 3
Potri.006G188400 Glycosyl hydrolase family protein with chitinase insertion domain
Potri.013G040500 calcium−binding EF hand family protein
Potri.001G347700
Potri.001G105200 glutathione peroxidase 6
Potri.016G079050 Serine protease inhibitor, potato inhibitor I−type family protein
Potri.007G111800
Potri.019G006900
Potri.004G146000
Potri.019G094000
Potri.009G063300
Potri.014G019300 NAD(P)−binding Rossmann−fold superfamily protein
Potri.007G111700
Potri.017G134151 phospholipase A 2A
Potri.016G039051 S−adenosyl−L−methionine−dependent methyltransferases superfamily protein
Potri.006G042200 S−adenosyl−L−methionine−dependent methyltransferases superfamily protein
Potri.001G303000 UDP−glucosyl transferase 73B1
Potri.016G083500 glutathione transferase lambda 1
Potri.014G106600
Potri.009G118100 NmrA−like negative transcriptional regulator family protein
Potri.010G075800 Serine protease inhibitor, potato inhibitor I−type family protein
Potri.007G111600
Potri.001G309900
Potri.013G102800
Potri.009G098966 UDP−glucosyl transferase 73B1
DEP
DEG
Potri.009G013900 plasma membrane intrinsic protein
Potri.014G032800 alpha/beta−Hydrolases superfamily protein
Potri.005G043700 protein kinase−related
Potri.009G109200
Potri.008G058500 rubisco activase
Potri.004G047100 dormancy−associated protein−like 1
Potri.005G228600
Potri.005G111200 Rhodanese/Cell cycle control phosphatase superfamily protein
Potri.019G093300 FASCICLIN−like arabinoogalactan 9
Potri.019G065000
Potri.009G028800 Pathogenesis−related thaumatin superfamily protein
Potri.015G072600 Xanthine/uracil permease family protein
Potri.013G002400 Pyridoxal phosphate (PLP)−dependent transferases superfamily protein
Potri.011G122100 Aluminium induced protein with YGL and LRDR motifs
Potri.007G129700 pfkB−like carbohydrate kinase family protein
Potri.005G060200 alcohol dehydrogenase 1
Potri.008G178000 PLAT/LH2 domain−containing lipoxygenase family protein
Potri.003G114000 HSP70−interacting protein 1
Potri.001G471900 photosystem I subunit G
Potri.001G105100 glutathione peroxidase 8
Potri.017G153400 Kunitz family trypsin and protease inhibitor protein
Potri.015G003500
Potri.009G095800 GroES−like zinc−binding alcohol dehydrogenase family protein
Potri.017G140900 microsomal glutathione s−transferase, putative
Potri.005G150300
Potri.019G038352
Potri.017G059000 glycine−rich RNA−binding protein 2
Potri.017G153600 Kunitz family trypsin and protease inhibitor protein
Potri.010G161200 nodulin−related protein 1
Potri.016G023340
Potri.001G061000 delta(3,5),delta(2,4)−dienoyl−CoA isomerase 1
Potri.013G128800
Potri.009G145700
Potri.013G070300
Potri.011G066200 D−mannose binding lectin protein with Apple−like carbohydrate−binding domain
Potri.013G066800 Peroxidase superfamily protein
Potri.008G132700 glycosyl hydrolase 9B6
Potri.001G176500
Potri.014G145100 Chalcone and stilbene synthase family protein
Potri.019G069300 cellulase 5
Potri.004G196000 Bifunctional inhibitor/lipid−transfer protein
Potri.003G032800 phospholipase D alpha 2
Potri.001G131400 S−adenosyl−L−methionine−dependent methyltransferases superfamily protein
Potri.005G163700
Potri.001G150500
Potri.014G179300
Potri.008G131100 Polyketide cyclase/dehydrase and lipid transport superfamily protein
Potri.001G017500 Leucine−rich repeat (LRR) family protein
Potri.015G147500 fibrillarin 1
Potri.005G113900 flavanone 3−hydroxylase
Potri.016G091100 phenylalanine ammonia−lyase 2
Potri.016G061100 Translation protein SH3−like family protein
Potri.005G194500 ribosomal protein 1
6
4
2
0
-2
-4
-6
H2O Shoot VS. Pb Shoot
Potri.009G098966 UDP−glucosyl transferase 73B1
Potri.010G075400 Serine protease inhibitor, potato inhibitor I−type family protein
Potri.010G075600 Serine protease inhibitor, potato inhibitor I−type family protein
Potri.001G309900
Potri.005G220700
Potri.004G179800
Potri.003G213700
Potri.017G050400 GTP cyclohydrolase II
Potri.003G165700 GRAM domain family protein
Potri.001G402600
Potri.010G075800 Serine protease inhibitor, potato inhibitor I−type family protein
Potri.017G133951 phospholipase A 2A
Potri.019G093800
Potri.014G161300 formate dehydrogenase
Potri.004G146000
Potri.012G033866
Potri.013G102700 12−oxophytodienoate reductase 1
Potri.006G223900 heat shock protein 17.6A
Potri.006G144500
Potri.015G108500 (1 of 1) PF07712 − Stress up−regulated Nod 19 (SURNod19)
Potri.007G045100 Subtilisin−like serine endopeptidase family protein
Potri.002G054900 Eukaryotic aspartyl protease family protein
Potri.016G083500 glutathione transferase lambda 1
Potri.003G083200 expansin−like B1
Potri.013G102900
Potri.007G037401
Potri.010G070900 glutathione S−transferase tau 3
Potri.009G110800 hemoglobin 1
Potri.001G268600 elicitor−activated gene 3−2
Potri.017G146600 heat shock protein 90.1
Potri.006G188400 Glycosyl hydrolase family protein with chitinase insertion domain
Potri.013G063001 RmlC−like cupins superfamily protein
Potri.001G223716 Glycosyl hydrolase superfamily protein
Potri.013G102800
Potri.009G140350
Potri.011G158100 FAD−binding Berberine family protein
Potri.009G063300
Potri.007G111500
Potri.007G111600
Potri.007G111700
Potri.006G055600 indole−3−acetate beta−D−glucosyltransferase
Potri.006G156038 sulfate transporter 3;5
Potri.004G138200 PATELLIN 2
Potri.019G031200
Potri.019G065100

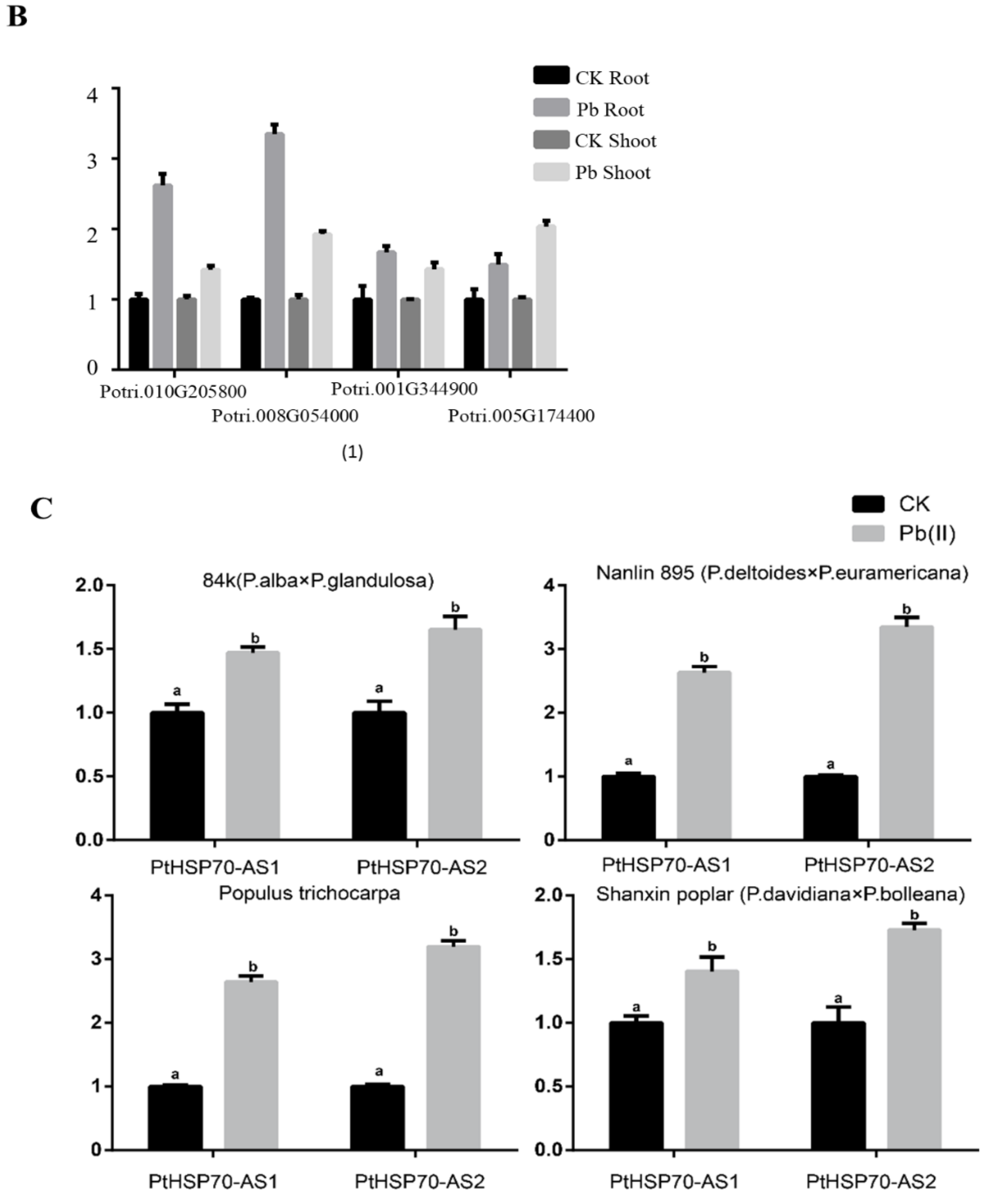


Figure S5. Correlation analysis of DEGs and DEPs. (A) Heatmaps of DEP and DEG correlations. (B) RT–qPCR validation of DEGs. (C) The expression of PtHSP70 under Pb resistance among 4 poplar species.

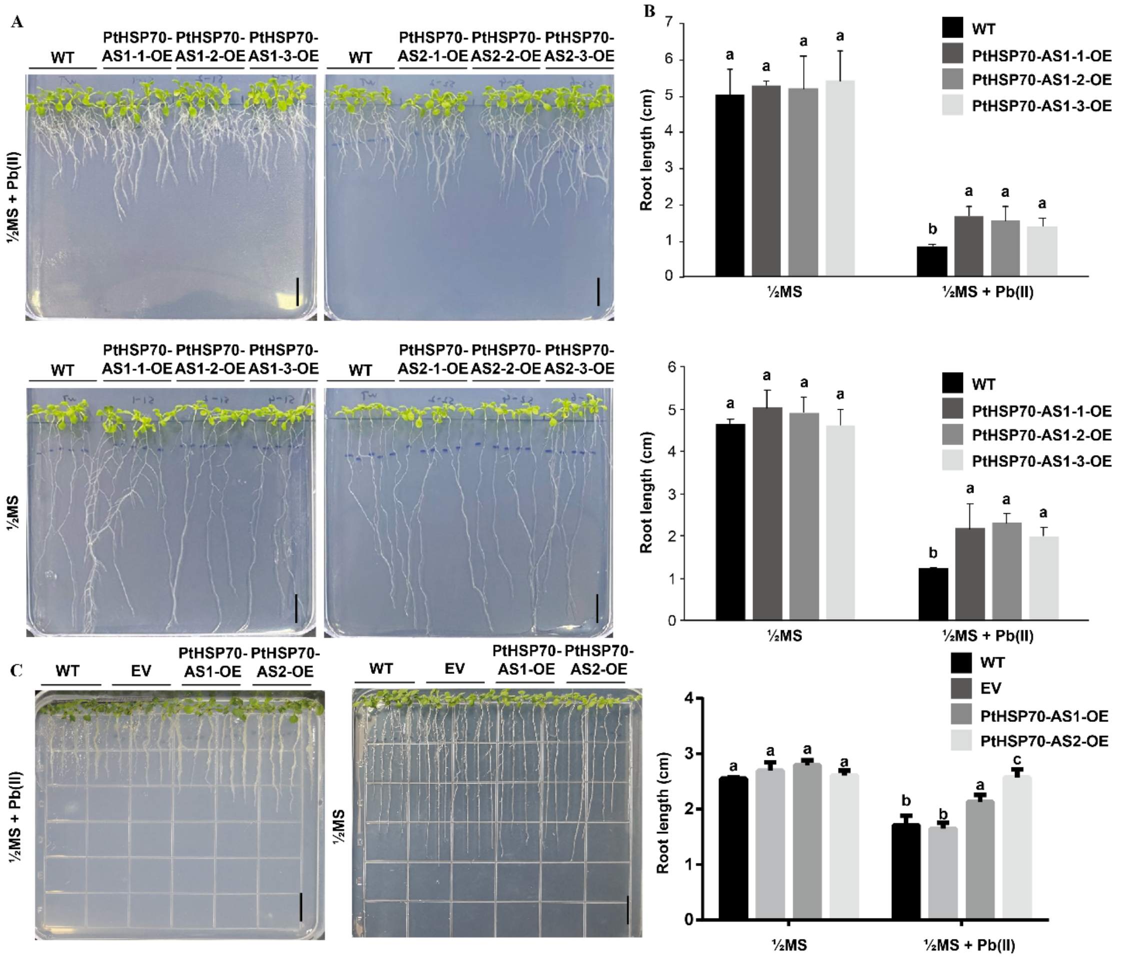


Figure S6. Phenotypic analysis of transgenic Arabidopsis overexpressing PtHSP70-AS1 and PtHSP70-AS2. (A, B and C) Phenotypic analysis of transgenic Arabidopsis overexpressing PtHSP70-AS1 and PtHSP70-AS2 and EV with and without Pb treatment. (A) Phenotype of transgenic Arabidopsis overexpressing PtHSP70-AS1 and PtHSP70-AS2. Scale bars denote 1 cm (B) Root length of transgenic Arabidopsis overexpressing PtHSP70-AS1 and PtHSP70-AS2. Values represent mean ± SD (n = 10). Asterisks represent significant differences WT and transgenic lines (ANOVA, $P < 0.05$). (C) Phenotype of transgenic Arabidopsis of EV and the root length of them.

CK, control sample grown the absence of Pb; Pb, sample grown in the presence of Pb; WT, wild type; PtHSP70-AS1-1–3, transgenic Arabidopsis overexpressing PtHSP70-AS1 line 1–3; PtHSP70-AS2-1–3, transgenic Arabidopsis overexpressing PtHSP70-AS2 line 1–3.

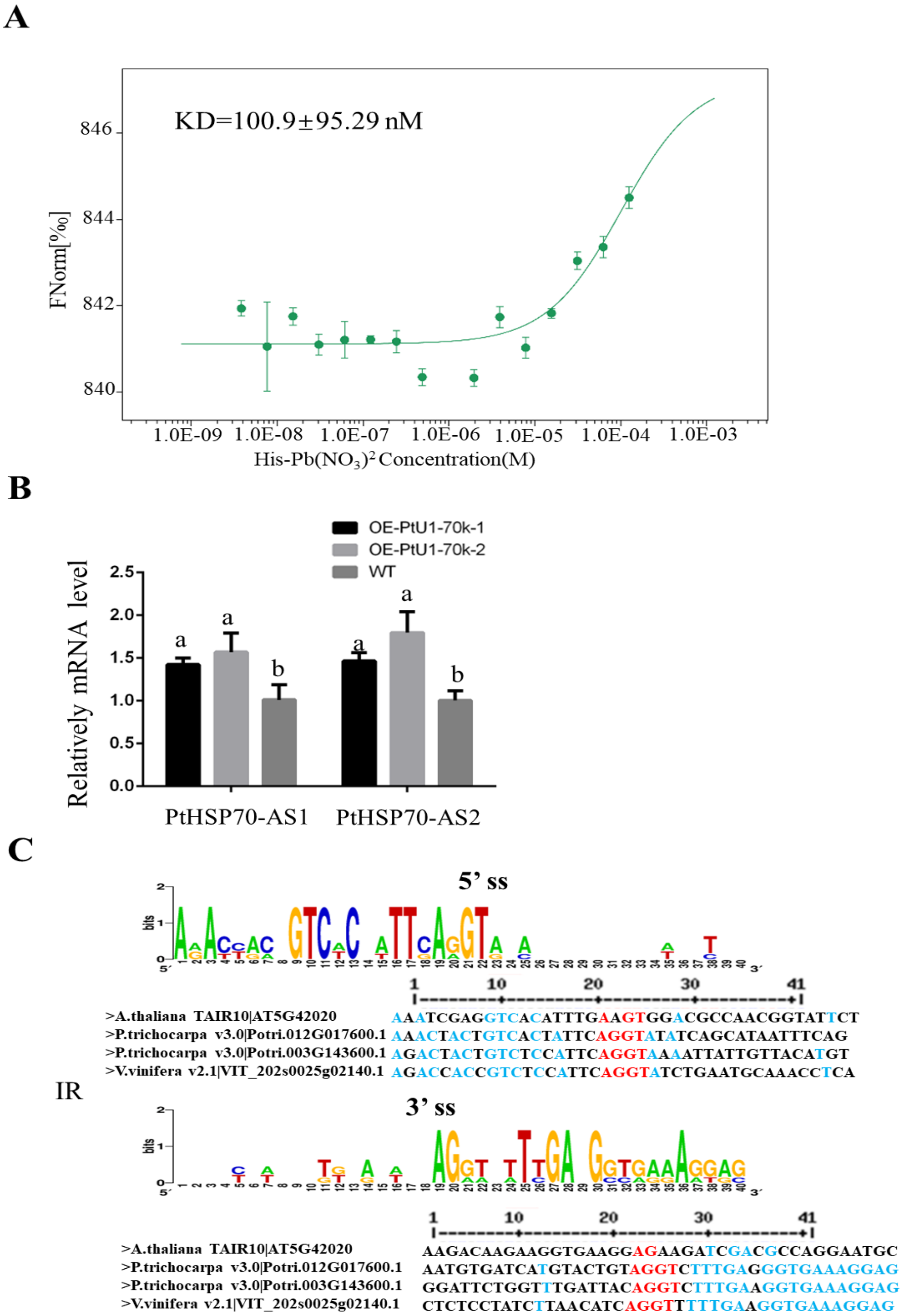


Figure S7. (A) Results of the MST binding assay used to determine the Kd value for the binding of His proteins to Pb(II). (B) Results of the RT–qPCR validation of the expression of PtHSP70.1/PtHSP70.2 in transgenic poplar lines overexpressing PtU1-70k. (C) Analysis of conserved AS site sequences (IR events) in plant HSP70 genes. The flanking sequences (20 bp on each side, as indicated by coloured arrows in Figure 7(A)) of plant HSP70 genes were analysed to determine their consensus sequences using WebLogo and multiple alignment.

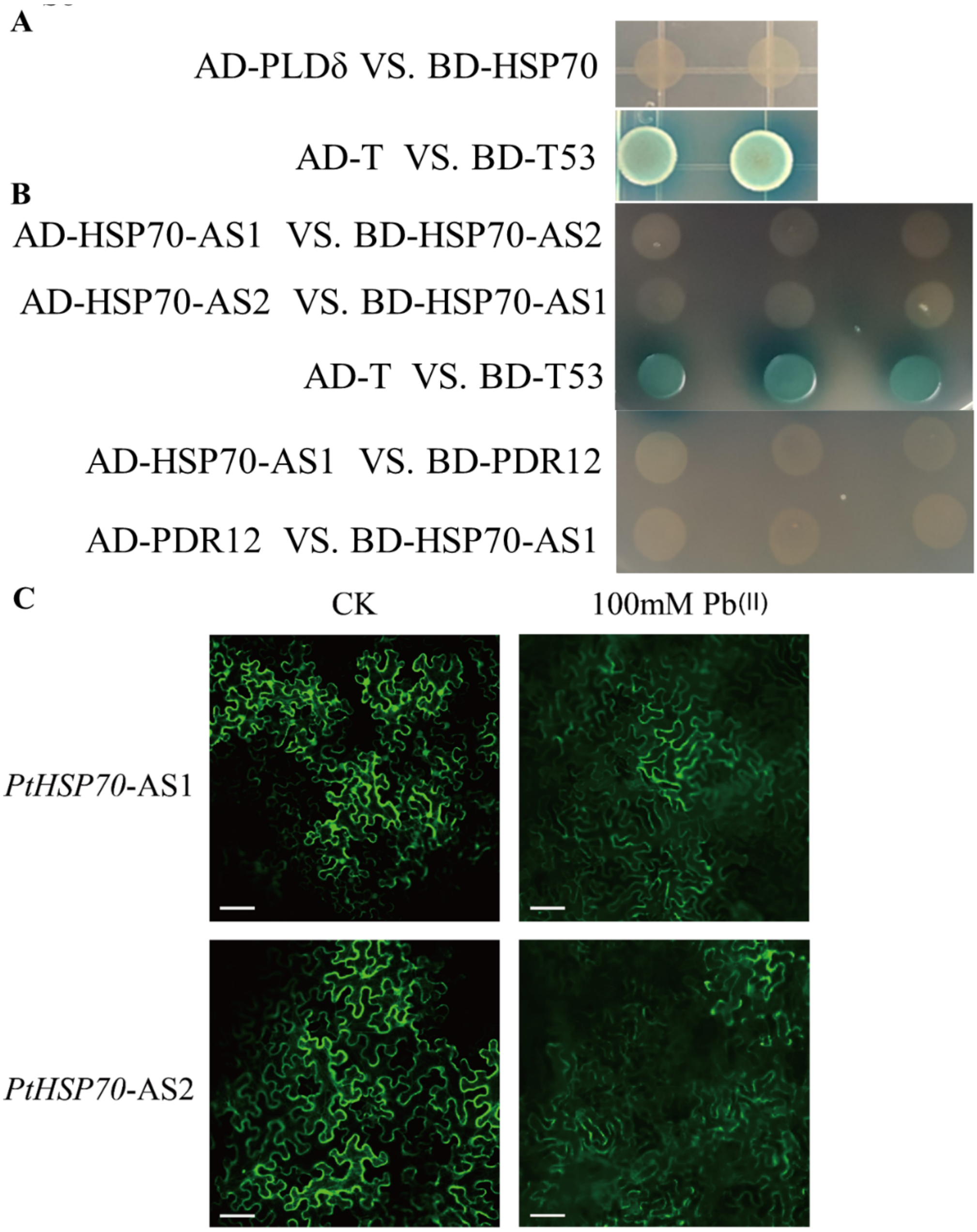


Figure S8. Analysis of the interactions via a Y2H assay and subcellular localization of PtHSP70. (A) The interaction between PtHSP70 and PtPLDδ (B) The interaction between HSP70-AS1 and HSP70-AS2 and HSP70 with PDR12. Plasmids were cotransfected into yeast cells and selected on SD-Leu/-Trp and SD-Leu/-Trp/-His/-Ade media. T and T53 were used as positive controls. (C) The subcellular localization of PtHSP70 with and without Pb(II).

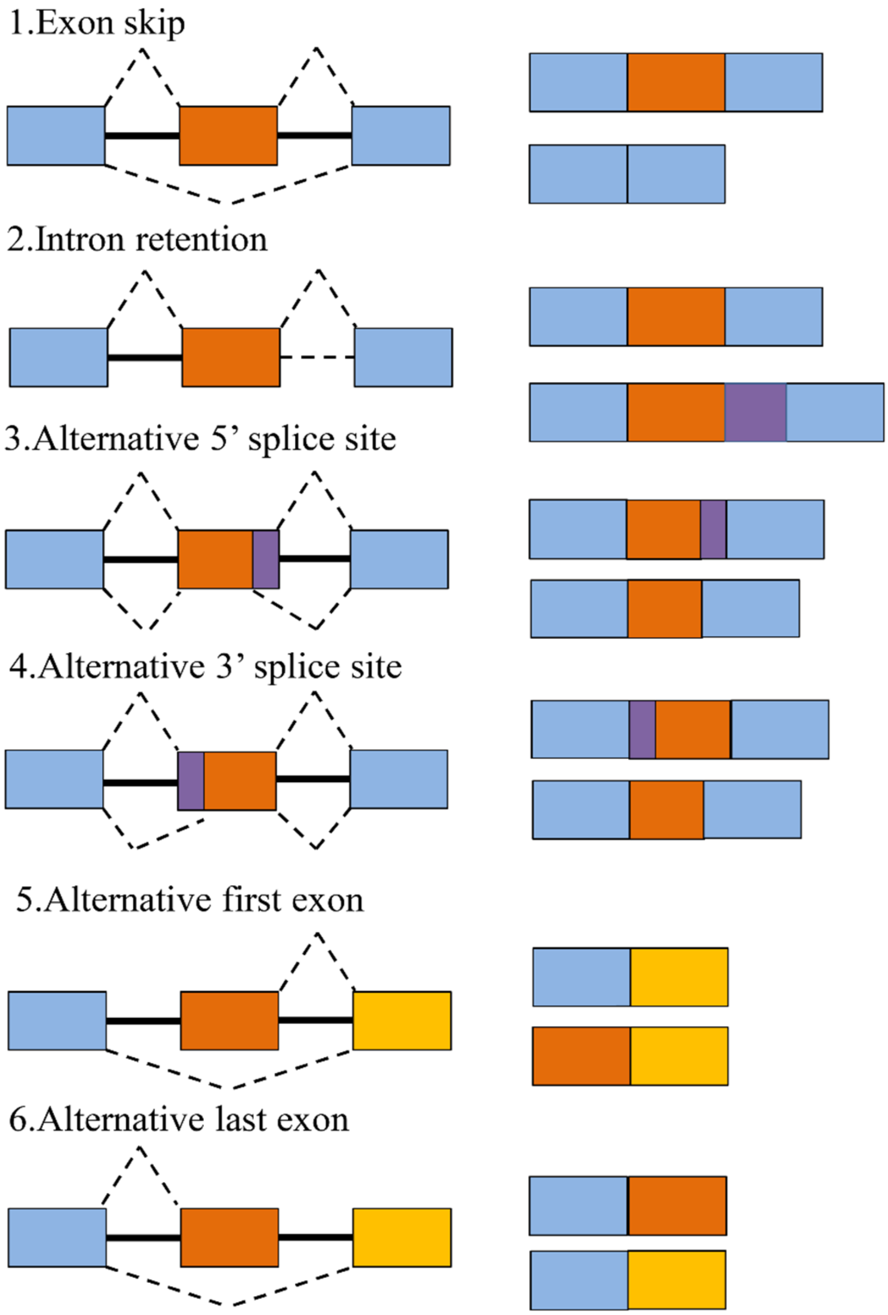


Figure S9. Pattern diagram for identifying AS events.

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Potri.010G205800.2|P.trichocarpa       ------------------------------------------------------- 0
transcript/13815.p1                    MAGKGEGPAIGIDLGTTYSCVGVWQHDRVEIIANDQGNRTTPSYVAFTDSERLIG 55
transcript/15043.p1                    MAGKGEGPAIGIDLGTTYSCVGVWQHDRVEIIANDQGNRTTPSYVAFTDSERLIG 55
transcript/15210.p1                    MAGKGEGPAIGIDLGTTYSCVGVWQHDRVEIIANDQGNRTTPSYVAFTDSERLIG 55
transcript/15677.p1                    MAGKGEGPAIGIDLGTTYSCVGVWQHDRVEIIANDQGNRTTPSYVAFTDSERLIG 55

m64114_210318_184623/113051804/ccs.p1  DAAKNQVAMNPINTVFDAKRLIGRRFTDASVQSDIKLWPFKVISGPGDKPMIGVT 110
Potri.010G205800.1|P.trichocarpa       DAAKNQVAMNPINTVFDAKRLIGRRFTDASVQSDIKLWPFKVISGPGDKPMIGVT 110
Potri.010G205800.2|P.trichocarpa       --------------------------------------------------MIGVT 5
transcript/13815.p1                    DAAKNQVAMNPINTVFDAKRLIGRRFTDASVQSDIKLWPFKVISGPGDKPMIGVT 110
transcript/15043.p1                    DAAKNQVAMNPINTVFDAKRLIGRRFTDASVQSDIKLWPFKVISGPGDKPMIGVT 110
transcript/15210.p1                    DAAKNQVAMNPINTVFDAKRLIGRRFTDASVQSDIKLWPFKVISGPGDKPMIGVT 110
transcript/15677.p1                    DAAKNQVAMNPINTVFDAKRLIGRRFTDASVQSDIKLWPFKVISGPGDKPMIGVT 110

m64114_210318_184623/113051804/ccs.p1  YKGEEKQFSAEEISSMVLIKMREIAEAYLGTAIKNAVVTVPAYFNDSQRQATKDA 165
Potri.010G205800.1|P.trichocarpa       YKGEEKQFSAEEISSMVLIKMREIAEAYLGTAIKNAVVTVPAYFNDSQRQATKDA 165
Potri.010G205800.2|P.trichocarpa       YKGEEKQFSAEEISSMVLIKMREIAEAYLGTAIKNAVVTVPAYFNDSQRQATKDA 60
transcript/13815.p1                    YKGEEKQFSAEEISSMVLIKMREIAEAYLGTAIKNAVVTVPAYFNDSQRQATKDA 165
transcript/15043.p1                    YKGEEKQFSAEEISSMVLIKMREIAEAYLGTAIKNAVVTVPAYFNDSQRQATKDA 165
transcript/15210.p1                    YKGEEKQFSAEEISSMVLIKMREIAEAYLGTAIKNAVVTVPAYFNDSQRQATKDA 165
transcript/15677.p1                    YKGEEKQFSAEEISSMVLIKMREIAEAYLGTAIKNAVVTVPAYFNDSQRQATKDA 165

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Potri.010G205800.2|P.trichocarpa       GVIAGLNVMRIINEPTAAAIAYGLDKKATSVGEKNVLIFDLGGGTFDVSLLTIEE 115
transcript/13815.p1                    GVIAGLNVMRIINEPTAAAIAYGLDKKATSVGEKNVLIFDLGGGTFDVSLLTIEE 220
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transcript/15210.p1                    GVIAGLNVMRIINEPTAAAIAYGLDKKATSVGEKNVLIFDLGGGTFDVSLLTIEE 220
transcript/15677.p1                    GVIAGLNVMRIINEPTAAAIAYGLDKKATSVGEKNVLIFDLGGGTFDVSLLTIEE 220
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Peptide	Protein information
FTDASVQSDIK	PtHSP70. 1
RFTDASVQSDIK	PtHSP70. 1
VISGPGDKPMIGVTYK	PtHSP70. 1
EIAEAYLGTALK	PtHSP70. 2
KIEDAIDQAIQWLDSNQLAEADEFEDK	PtHSP70. 2
NALENYAYNMR	PtHSP70. 2

Figure S10. The spectrum information of SWATH-MS.

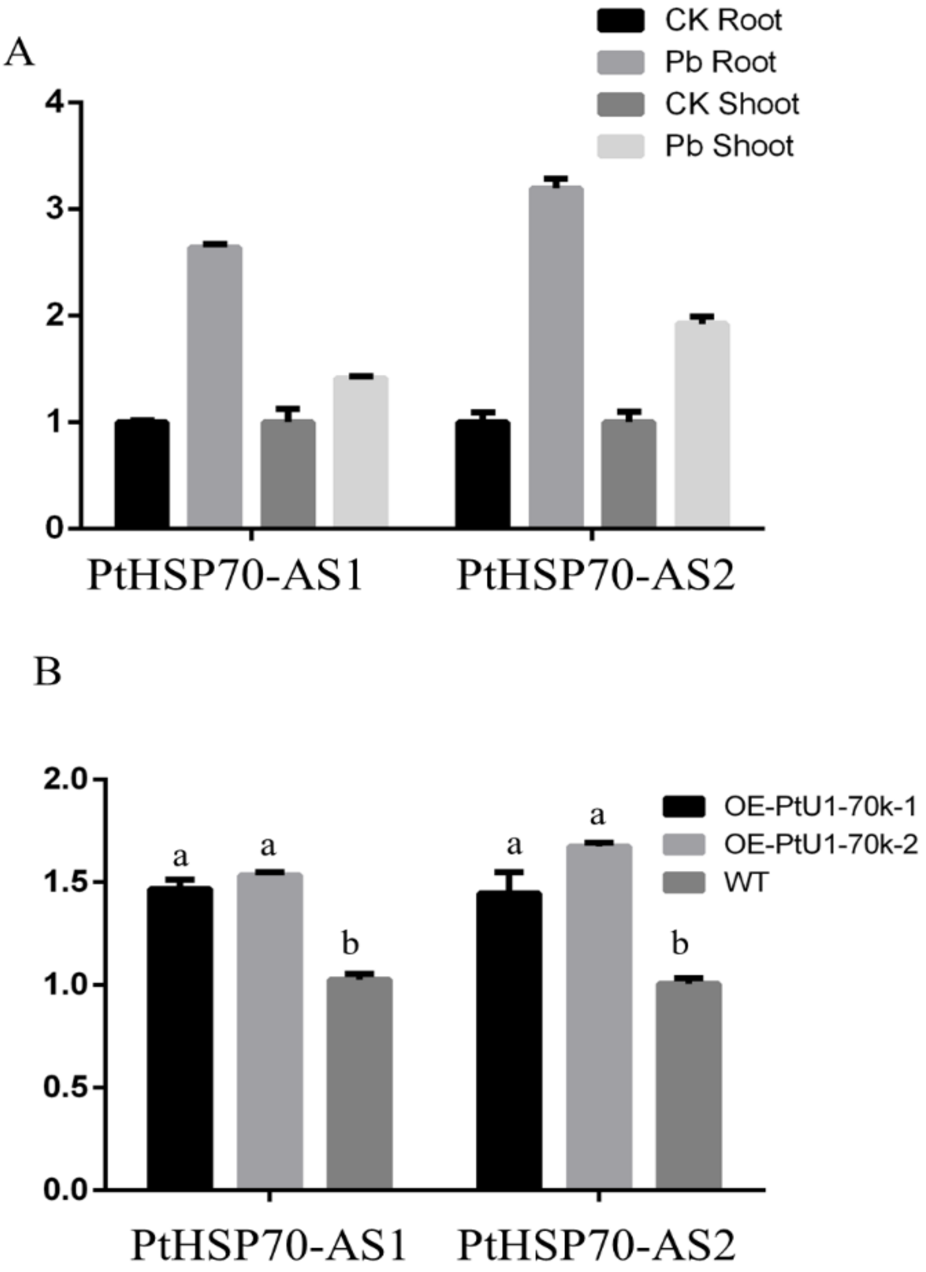

Figure S11. The expression of RT-qPCR in the reference of *PtACT6*.