

# Appendix I

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**TABLE S1.1.** Abiotic stress-related genes within SUMO-binding proteins.



**Table S1.1.** Abiotic stress-related genes within SUMO-binding proteins. Genes coding SUMO pathway components are highlighted in bold; transcription factors annotated in the AGRIS database (arabidopsis.med.ohio-state.edu/; Yilmaz A et al. 2011) are underlined.

AGI ID	Name	Gene ontology associated with abiotic stress
AT1G48030	<i>mtLPD1</i>	response to radiation
<u>AT3G55730</u>	<u><i>MYB109</i></u>	response to osmotic stress
AT1G77180	<i>SKIP</i>	response to osmotic stress
AT1G04410	<i>C-NAD-MDH1</i>	response to osmotic stress
AT5G17920	<i>ATCIMS, ATMETS, ATMS1</i>	response to osmotic stress
AT1G62380	<i>ACO2</i>	response to osmotic stress
AT3G53870		response to osmotic stress
AT1G49950	<i>TRB1</i>	response to osmotic stress
AT5G59430	<i>TRP1</i>	response to osmotic stress
AT1G65930	<i>cICDH</i>	response to osmotic stress
AT3G09260	<i>BGLU23, LEB, PSR3.1, PYK10</i>	response to osmotic stress; response to temperature stimulus
AT2G21660	<i>GRP7, CCR2, GR-RBP7</i>	response to osmotic stress; response to temperature stimulus
AT5G12250	<i>TUB6</i>	response to osmotic stress; response to temperature stimulus
AT1G07890	<i>APX1, CS1, MEE6</i>	response to osmotic stress; response to temperature stimulus
<u>AT2G38470</u>	<u><i>WRKY33</i></u>	response to osmotic stress; response to temperature; response to water stimulus
AT5G52300	<i>LTI65, RD29B, CAP160</i>	response to osmotic stress; response to temperature stimulus; response to water
AT3G09440	<i>HSP70</i>	response to temperature stimulus
AT4G37930	<i>SHM1, SHMT1</i>	response to temperature stimulus
<b>AT4G26840</b>	<b><i>SUM1</i></b>	response to temperature stimulus
AT1G53540	<i>HSP20</i>	response to temperature stimulus
AT3G01500	<i>BCA1, SABP3, CA1</i>	response to temperature stimulus
AT3G46230	<i>HSP17.4</i>	response to temperature stimulus
<u>AT1G32330</u>	<u><i>HSFA1D</i></u>	response to temperature stimulus
AT1G48050	<i>KU80</i>	response to temperature stimulus
AT3G17390	<i>MAT4, MTO3, SAMS3</i>	response to temperature stimulus
AT5G02500	<i>HSC70-1, HSP70-1</i>	response to temperature stimulus
AT4G03430	<i>STA1</i>	response to temperature stimulus
AT4G31990	<i>AAT3, ASP5, ATAAT1</i>	response to temperature stimulus
<b>AT5G55160</b>	<b><i>SUM2</i></b>	response to temperature stimulus
<b>AT5G60410</b>	<b><i>SIZ1</i></b>	response to temperature stimulus
AT4G16420	<i>ADA2B, PRZ1</i>	response to temperature stimulus
AT3G07740	<i>ADA2A, HAC10, HXA2</i>	response to temperature stimulus
AT1G27650	<i>U2AF35A</i>	response to radiation
AT3G54610	<i>BGT, GCN5, HAC3, HAG01, HAG1, HAT1</i>	response to radiation
AT1G79000	<i>HAC1, PCAT2</i>	response to radiation
AT1G18450	<i>ARP4</i>	response to radiation

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AT3G19210	<i>RAD54, CHR25</i>	response to radiation
<u>AT4G00730</u>	<u><i>AHDP, ANL2</i></u>	response to radiation
<u>AT5G08790</u>	<u><i>ANAC081, ATAF2</i></u>	response to radiation
<u>AT5G25220</u>	<u><i>KNAT3</i></u>	response to radiation
AT3G26650	<i>GAPA-1</i>	response to radiation; response to temperature stimulus
AT3G12580	<i>HSP70</i>	response to radiation; response to temperature stimulus
<u>AT2G26150</u>	<u><i>HSEA2</i></u>	response to radiation; response to temperature stimulus
AT2G41100	<i>CAL4, TCH3</i>	response to radiation; response to mechanical stimulus; response to temperature stimulus
<u>AT2G22430</u>	<u><i>ATHB6</i></u>	response to water
AT1G06770	<i>DRIP1</i>	response to water
<u>AT2G30580</u>	<u><i>DRIP2</i></u>	response to water
AT1G25540	<i>PFT1, MED25</i>	detection of abiotic stimulus; response to radiation
AT2G25930	<i>ELF3, PYK20</i>	detection of abiotic stimulus; response to radiation; response to temperature stimulus
AT1G54990	<i>AXR4, RGR1</i>	response to mechanical stimulus
AT5G19770	<i>TUA3</i>	
AT1G04820	<i>TOR2, TUA4</i>	

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# Appendix II

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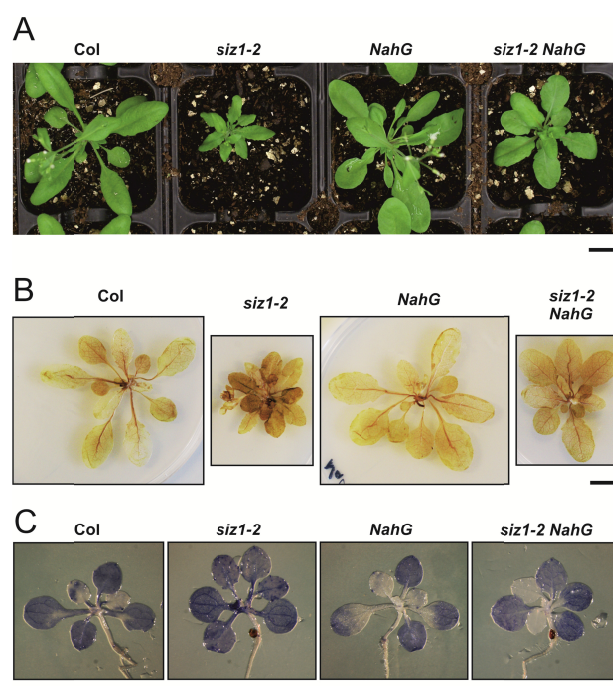
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**Figure S2.1.** Analysis of the influence of salicylic acid (SA) in *siz1* ROS homeostasis and oxidative stress responses, by introgression of *siz1-2* with the transgenic SA hydroxylase *NahG*.

**Table S2.1.** List of primers used for genotyping T-DNA insertion mutants and transgene lines.





**Figure S2.1.** Analysis of the influence of salicylic acid (SA) in *siz1* ROS homeostasis and oxidative stress responses, by introgression of *siz1-2* with the transgenic SA hydroxylase *NahG*. **A**, Morphology of adult Col, *siz1-2*, *NahG* and *siz1-2 NahG* plants. **B**, Histochemical DAB staining of 4-week-old soil-grown plants. **C**, Histochemical NBT staining of 21-day-old in vitro-grown seedlings. Bars indicate 1 cm.

**Table S2.1.** List of primers used for genotyping T-DNA insertion mutants and transgene lines.

Primer name	Primer sequence (5' to 3')	Description
NahG FW	ACTGGAActCTGCCGCTA	Genotyping of the <i>NahG</i> transgene; Previously described by Heck S et al. (2003)
NahG RV	TGAGTFACTAGGGCGTCCG	
SIZ1-2 RP	CACGACAGATGAAGCATTGTG	Genotyping of <i>siz1-2</i> (SALK_065397)
SIZ1-2 LP	GAGCTGAAGCATCTGGTTTTG	
LBb1.3	ATTTTGCCGATTTTCGGAAC	Left border primer for genotyping SALK T-DNA insertion lines

## REFERENCES

**Heck S, Grau T, Buchala A, Metraux JP, Nawrath C** (2003) Genetic evidence that expression of *NahG* modifies defence pathways independent of salicylic acid biosynthesis in the *Arabidopsis-Pseudomonas syringae* pv. *tomato* interaction. *Plant J* **36**: 342-352



# Appendix III

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**Table S3.1.** Common targets/interactors of mitogen activated protein kinases (MPKs) and SUMO.

**Table S3.2.** List of primers used for genotyping T-DNA insertion mutant lines.

**Table S3.3.** List of quantitative RT-PCR (qPCR) primers.

**Table S3.4.** List of primers used for constructs.



**Table S3.1.** Common targets/interactors of mitogen activated protein kinases (MPKs) and SUMO. Number of instances indicates the number of MPKs associated to each protein (less than two are not shown).

AGI code	Name	No. of instances	Annotation
At1g35460	FBH1	8	Basic helix-loop-helix (bHLH) DNA-binding superfamily protein
At1g09770	CDC5	6	Cell division cycle
At4g23650	CDPK6, CPK3	6	Calcium-dependent protein kinase
At2g41630	TFIIB	5	Transcription factor IIB
At5g47660		5	
At5g59430	TRP1	5	Telomeric repeat binding protein
At1g30480	DRT111	4	D111/G-patch domain-containing protein
At5g05610	AL1	4	Alfin-like
At2g02080	IDD4	3	Indeterminate(ID)-domain 4
At3g07740	ADA2A, HAC10, HXA2	3	Homolog of yeast ADA2 2A
At3g13670		3	Protein kinase family protein
At4g34430	SWI3D, CHB3	3	DNA-binding family protein
At3g09030		2	BTB/POZ domain-containing protein
At3g12490	CYS6, CYSB	2	Cystatin B
At3g26744	ICE1, SCRUM	2	Basic helix-loop-helix (bHLH) DNA-binding superfamily protein
At3g58120	BZIP61	2	Basic-leucine zipper (bZIP) transcription factor family protein
At4g16420	ADA2B, PRZ1	2	Homolog of yeast ADA2 2B

**Table S3.2.** List of primers used for genotyping T-DNA insertion mutant lines.

Primer name	Primer sequence (5' to 3')	Description
MKK1-126 RP MKK1-1022 LP	GGAAGCTTATGCCCTAATCCC CACCATTGCGAGATGAAGGAG	Genotyping of <i>mkk1-3</i> (SALK_027645); Previously described by Qiu et al. (2008)
MKK2-1889 LP MKK2-2 RP	GAAGTAGGACGCGAGATTGAT GCGAAGAACGAAGTAGACGAA	Genotyping of <i>mkk2-1</i> (SAIL_551_H_01) Previously described by Qiu et al. (2008)
MPK4 RP MPK4 LP	ACGCACCTTCGGACCTCAACC ATTTGGCGCCGCTGCATGAT	Genotyping of <i>mpk4-2</i> (SALK_056245)
SIZ1-2 RP SIZ1-2 LP	CACGACAGATGAAGCATTGTG GAGCTGAAGCATCTGGTTTTG	Genotyping of <i>siz1-2</i> (SALK_065397)
LBb1.3	ATTTTGCCGATTTTCGGAAC	Left border primer for genotyping SALK T-DNA insertion lines
Garlic-LB	TAGCATCTGAATTCATAACCA ATCTCGATACAC	Left border primer for genotyping SAIL T-DNA insertion lines

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**Table S3.3.** List of quantitative RT-PCR (qPCR) primers.

Gene (AGI code)	Primer name	Primer sequence (5' to 3')	Tm	GC (%)	Product size (bp)
<i>MPK4</i> (AT4G01370)	MPK4 RTf	ACACGAGAGCCCTTGTTCCTCG	59.1	59.1	262
	MPK4 RTr	GGCACAACGCCTCATCAACTGTG	59.0	56.5	
<i>ACT2</i> (At3g18780)	ActinF	CTAAGCTCTCAAGATCAAAGGCTTA	52.7	40.0	211
	ActinR	ACTAAAACGCAAACGAAAGCGGTT	57.2	40.0	

*Tm* - Melting temperature; *bp* - Base pair

**Table S3.4.** List of primers used for constructs.

Primer name	Primer sequence (5' to 3')	Description
MPK4 F1	ATGGCTAGCATGTCGGCGGAGAGTTG	Cloning into pET28b with HexaHis-tag; RS: <i>NheI</i>
MPK4 R1	GTGCTCGAGTCACACTGAGTCTTGAGG	Cloning into pET28b without HexaHis-tag; RS: <i>Ncd</i>
MKK2 F1	ATGGCTAGCATGAAGAAAGGTGG	Cloning into pET28b with HexaHis-tag; RS: <i>NheI</i>
MKK2 R1	GTGCTCGAGTTACACGGAGAACGTAC	Cloning into pET28b without HexaHis-tag; RS: <i>Ncd</i>
MPK4 pENTR Fw1	AAGCGGCCGCCATGTCGGCGGAGAGTTGTTTC	Cloning into pENTR; RS: <i>NotI</i>
MPK4 pENTR Rv1	AAGGCGGCCCCACTGAGTCTTGAGGATTG	Cloning into pENTR; RS: <i>Asd</i>

*RS* - restriction site

## REFERENCES

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# Appendix IV

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**Figure S4.1.** In silico analysis of *ULP1c* and *ULP1d* expression patterns.

**Figure S4.2.** In silico characterization of ULP1c and ULP1d functional redundancy.

**Figure S4.3.** Additional developmental characterization of *ulp1c*, *ulp1d* and *ulp1c ulp1d* mutants.

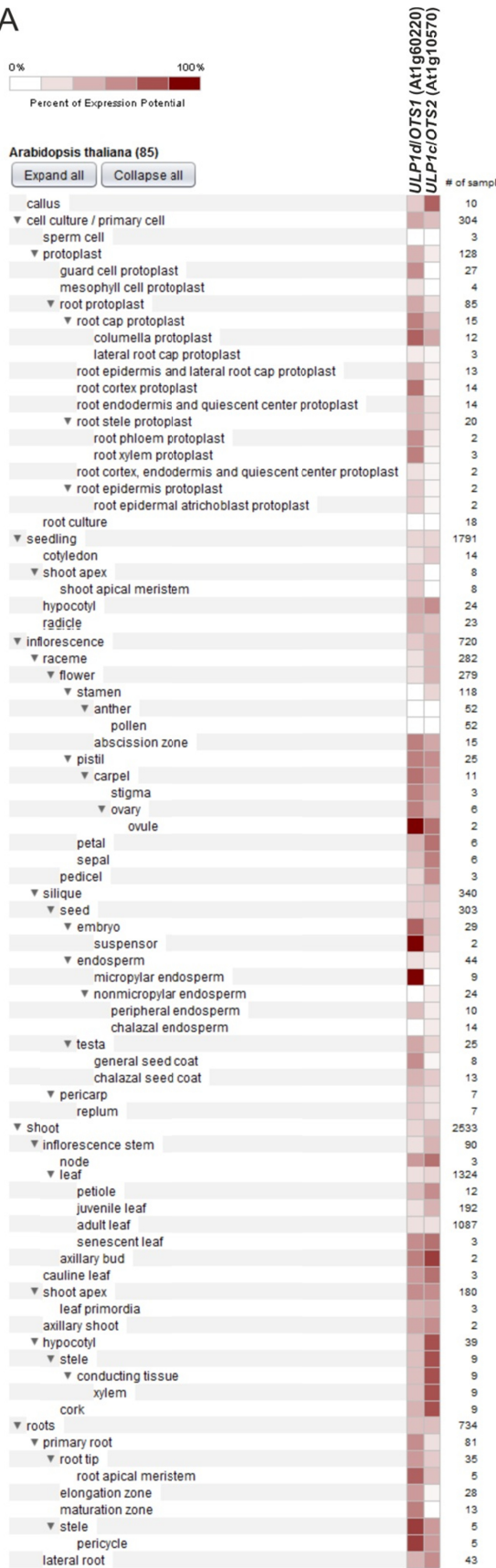
**Figure S4.4.** Complementation of *ulp1c/d* seed germination and mannitol sensitivity phenotypes.

**Table S4.1.** List of primers used for genotyping T-DNA insertion lines.

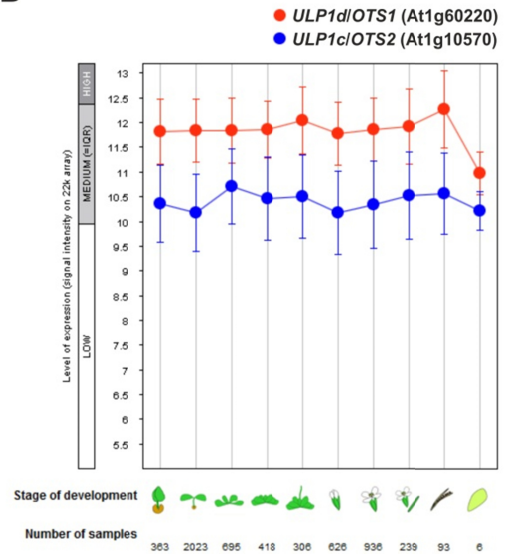
**Table S4.2.** List of quantitative RT-PCR (qPCR) primers.



A

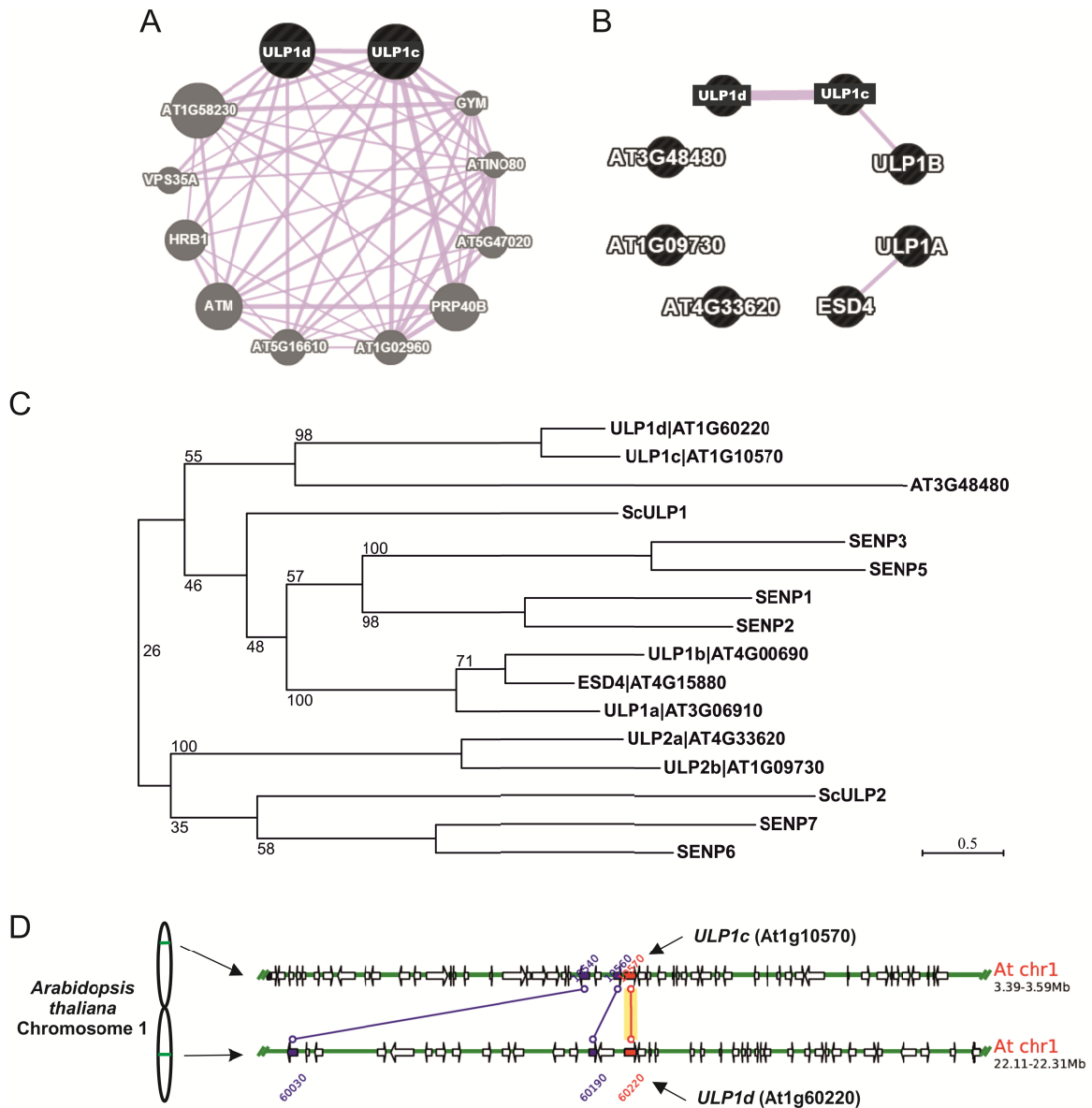


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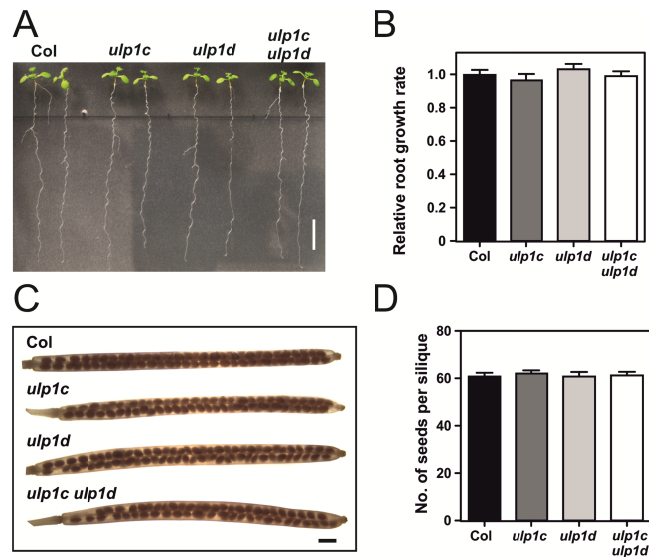


ULP1c and ULP1c displays analysis for v4

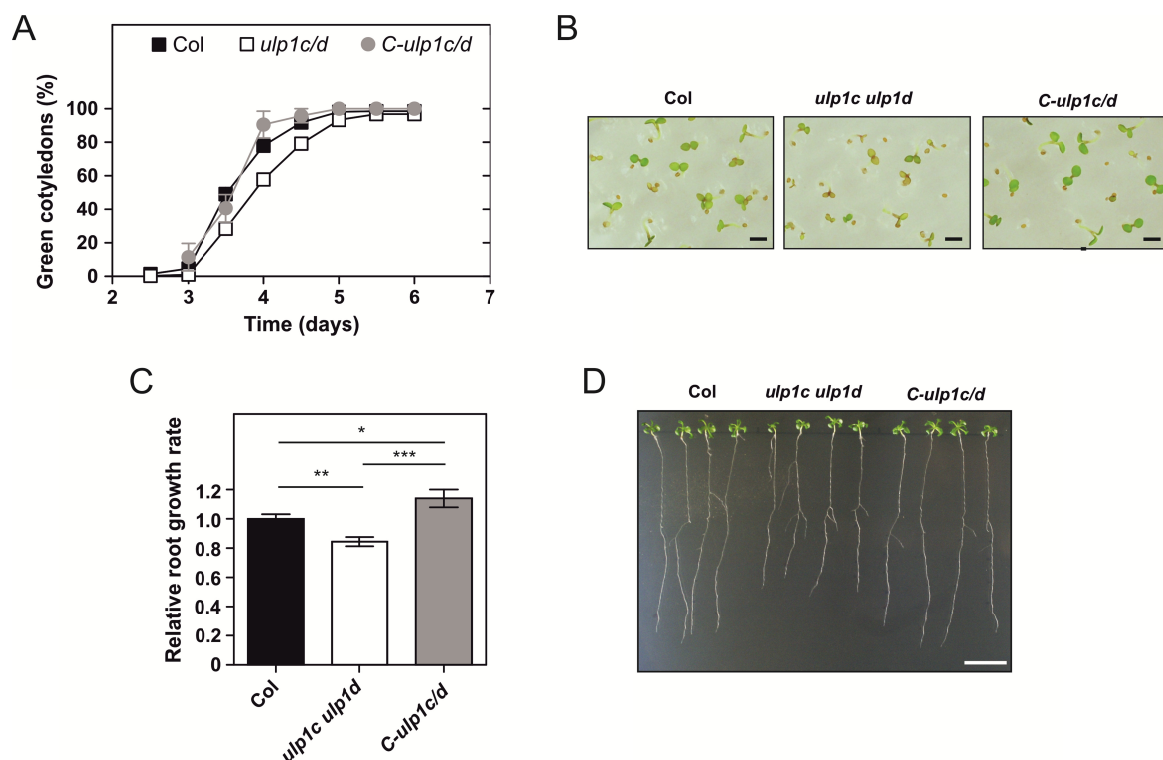
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**Figure S4.2.** In silico characterization of ULP1c and ULP1d functional redundancy. **A**, Co-expression network (10 highest-ranking genes) of *ULP1c* and *ULP1d*. **B**, Co-expression score of annotated ULPs of Arabidopsis. Co-expression analysis was performed using GeneMANIA (genemania.org/; Warde-Farley et al., 2010) with default settings for the co-expression network. Connecting line thickness reflects a weighted sum of co-expression data sources. **C**, Phylogenetic relationship of Arabidopsis ULPs in conjunction with human SENP and yeast (*S. cerevisiae*) ULPs. Arabidopsis ULP homologues were obtained using *Saccharomyces cerevisiae* ULPs and protein DELTA-BLAST analysis at NCBI (www.ncbi.nlm.nih.gov/). SeaView v4 (Gouy et al., 2010) was used to sequentially perform (1) sequence alignment using MUSCLE and (2) tree generation using maximum likelihood (PhyML; Jones-Taylor-Thornton model). Bootstrap values (100 replicates) are indicated. Analysis shows four separate clades, comprising Arabidopsis ULP1a/ULP1b/ESD4, ULP1c/ULP1d, At3g48480 and ULP2a/ULP2b. ULP1c/d display high phylogenetic proximity, which suggests a recent duplication event. **D**, *ULP1c* and *ULP1d* syntenic relationship. Both genes are located within a large genomic block (score 3993.0, E-value 9e-51) with 106 anchors. Analysis was carried out using the Plant Genome Duplication Database (chibba.agtec.uga.edu), which allows the search for intra-genome or cross-genome syntenic relationships.



**Figure S4.3.** Additional developmental characterization of *ulp1c*, *ulp1d* and *ulp1c ulp1d* mutants. **A**, Morphology of in vitro-grown 14-day-old plants; scale bar indicates 1 cm. **B**, Root growth rate of in vitro-grown plants ( $n = 16$ ). **C**, Silique morphology following clearing in ethanol; scale bar indicates 1 mm. **D**, Number of seeds per silique ( $n = 9$ ). Error bars represent standard error of the means (SEM). No statistically significant differences (unpaired t test) of mutants in relation to the wild-type were observed.



**Figure S4.4.** Complementation of *ulp1c/d* seed germination and mannitol sensitivity phenotypes by expression of a *pro35S::ULP1d* construct in the mutant background (*C-ulp1c/d*). **A**, Seed germination rate (formation of green cotyledons;  $n \geq 4$ ). **B**, Seedling morphology four days after germination; scale bar indicates 1 mm. **C**, Relative root growth of 7-day-old seedlings subjected to mannitol-induced osmotic stress; error bars represent SEM ( $n \geq 10$ ). **D**, Root morphology of 7-day-old seedlings transferred to mannitol-supplemented media and grown for 10 days. Scale bars indicate 1 cm. Error bars represent SEM. Asterisks represent statistically significant differences between genotypes (unpaired t test; \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ ).

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**Table S4.1.** List of primers used for genotyping T-DNA insertion lines.

Primer name	Primer sequence (5' to 3')	Description
ULP1c RP ULP1c LP	GACATACCTTCCTGCAGCTTG CTCTGCAATTGCATCATTCTG	Genotyping of <i>ulp1c-1</i> (SALK_050441)
ULP1d RP ULP1d LP	GGCTGAGCTTCTTCTTCATCC TTCAGATGTTTTACCGCAAGG	Genotyping of <i>ulp1d-1</i> (SALK_029340)
SIZ1-2 RP SIZ1-2 LP	CACGACAGATGAAGCATTGTG GAGCTGAAGCATCTGGTTTTG	Genotyping of <i>siz1-2</i> (SALK_065397)
LBb1.3	ATTTTGCCGATTCGGAAC	Left border primer for genotyping SALK T-DNA insertion lines

**Table S4.2.** List of quantitative RT-PCR (qPCR) primers.

Gene (AGI code)	Primer name	Primer sequence (5' to 3')	Tm	GC (%)	Product size (bp)
<i>ULP1c</i> (At1g10570)	ULP1c qRT F1	TGCGAGCGAGTACAGCCTCA	57.9	60.0	232
	ULP1c qRT R1	AATCTTGGCAGCGACCGCCA	59.3	60.0	
<i>ULP1d</i> (At1g60220)	ULP1d qRT F1	GGGAAAGCTGAGCACAGTGCA	57.6	57.1	200
	ULP1d qRT R1	TCCCAAGACCACTCCCTAGGAGT	57.6	56.5	
<i>QQS</i> (At3g30720)	QQS qRT F1	TTCTCCACAGCGACCAGTTG	60.3	55.0	210
	QQS qRT R1	GTAGAAGTGAAGCCCGACCC	60.1	60.0	
<i>RD20</i> (At2g33380)	RD20 qRT Fw1	ACACCGAAGGAAGGTATGTCCAG	57.9	54.2	142
	RD20 qRT Rv1	AGCCATCCAAAAGGATCGATTGCC	57.8	50.0	
<i>GOLS1</i> (At2g47180)	GOLS1 qRT Fw1	GGTTCCTACTGTGCAGCGGGTTC	60.0	58.3	237
	GOLS1 qRT Rv1	GACGGTGCGGTCACGTAGTT	57.1	60.0	
<i>CIPK11</i> (At2g30360)	CIPK11 qRT Fw1	TTGCTTGTTGGTGGAGGCAC	59.8	59.1	127
	CIPK11 qRT Rv1	TAGCCGCGTTTGTGACGACG	58.4	57.1	
<i>RPT2</i> (At2g30520)	RPT2 qRT F1	GTGCTAAGGCTTGCAACGAG	59.8	55.0	207
	RPT2 qRT R1	TGCCTGAATGGTCTCTGACG	59.8	55.0	
<i>CalB</i> (At2g45670)	CalB qRT Fw1	ACGACGGTGGATCCATTCCGGA	59.7	59.1	167
	CalB qRT Rv1	TCTTTCCAGCCAGCAAGTGCCA	59.0	54.6	
<i>ACT2</i> (At3g18780)	ActinF	CTAAGCTCTCAAGATCAAAGGCTTA	52.7	40.0	211
	ActinR	ACTAAAACGCAAACGAAAGCGGTT	57.2	40.0	

*CalB* - Calcineurin B subunit-related; *Tm* - Melting temperature; *bp* - Base pair

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# Appendix V

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- Table S5.1.** Genes deregulated in *ulp1c/d* relatively to the wild-type, specifically in response to *Pst* DC3000.
- Table S5.2.** Gene ontology (GO) terms for *ulp1c/d* differentially expressed genes in response to *Pst* DC3000.
- Table S5.3.** Genes involved in protein modification and metabolism that are differentially expressed in *ulp1c/d* upon *Pst* DC3000 infection.
- Table S5.4.** Genes involved in transcriptional regulation that are deregulated in *ulp1c/d* upon *Pst* DC3000 infection.
- Table S5.5.** *Arabidopsis thaliana* WRKY transcription factors that are modified by SUM1.
- Table S5.6.** List of primers used for genotyping T-DNA insertion lines.
- Table S5.7.** List of quantitative RT-PCR (qPCR) primers.



**Table S5.1.** Genes deregulated in *ulp1c/d* relatively to the wild-type, specifically in response to *Pseudomonas syringae* pv. *tomato* (*Pst*) DC3000. Gene annotation was performed using *\_at* to *AGI Conversion Tool* ([bar.utoronto.ca/ntools/cgi-bin/ntools\\_agi\\_converter.cgi](http://bar.utoronto.ca/ntools/cgi-bin/ntools_agi_converter.cgi)).

Affy ID	AGI ID	Log2 ratio	p-value	Annotation
<b>Down-regulated</b>				
247347_at	At5g63780	-1,67	3,33E-9	SHA1; RING/FYVE/PHD zinc finger superfamily protein
246658_at	At5g35260	-1,52	3,61E-7	
256655_at	At3g18890	-1,52	3,76E-7	Tic62; NAD(P)-binding Rossmann-fold superfamily protein
262866_at	At1g64940	-1,50	6,87E-7	CYP89A6; cytochrome P450, family 87, subfamily A, polypeptide 6
250739_at	At5g05740	-1,43	4,95E-6	EGY2; ethylene-dependent gravitropism-deficient and yellow-green-like 2
257200_at	At3g23720	-1,39	1,66E-5	
249047_at	At5g44410	-1,36	3,30E-5	FAD-binding Berberine family protein
248527_at	At5g50740	-1,36	3,40E-5	Heavy metal transport/detoxification superfamily protein
257331_at	AtMg01330	-1,36	3,86E-5	ORF107H; hypothetical protein
258289_at	At3g23450	-1,35	4,39E-5	Unknown protein
249847_at	At5g23210	-1,35	4,74E-5	SCPL34; serine carboxypeptidase-like 34
259790_s_at	At1g29430	-1,35	4,81E-5	SAUR-like auxin-responsive protein family
252775_s_at	At3g42930	-1,35	5,44E-5	
257207_at	At3g14900	-1,30	1,92E-4	EMB3120; unknown protein
267562_at	At2g39670	-1,30	1,93E-4	Radical SAM superfamily protein
256136_s_at	At1g48720	-1,30	2,08E-4	Unknown protein
252970_at	At4g38850	-1,29	2,28E-4	SAUR15, SAUR-AC1; SAUR-like auxin-responsive protein family
253679_at	At4g29610	-1,28	3,00E-4	Cytidine/deoxycytidylate deaminase family protein
252598_at	At3g45380	-1,26	4,67E-4	
248613_at	At5g49555	-1,26	4,78E-4	FAD/NAD(P)-binding oxidoreductase family protein
252793_at	At3g42250	-1,26	5,19E-4	
258708_at	At3g09580	-1,25	6,15E-4	FAD/NAD(P)-binding oxidoreductase family protein
248667_at	At5g48710	-1,25	6,35E-4	Ubiquitin-like superfamily protein
255897_at	At1g17900	-1,25	6,54E-4	
248617_at	At5g49590	-1,23	1,00E-3	Unknown protein
251956_at	At3g53460	-1,21	1,96E-3	CP29; chloroplast RNA-binding protein 29
266575_at	At2g24060	-1,20	2,18E-3	Translation initiation factor 3 protein
265949_at	At2g18540	-1,20	2,50E-3	RmlC-like cupins superfamily protein
251119_at	At3g63510	-1,18	3,85E-3	FMN-linked oxidoreductases superfamily protein
264963_at	At1g60600	-1,18	3,87E-3	ABC4; UbiA prenyltransferase family protein
247098_at	At5g66470	-1,17	4,80E-3	RNA binding;GTP binding
259784_at	At1g29450	-1,17	5,13E-3	SAUR-like auxin-responsive protein family
264900_at	At1g23080	-1,17	5,32E-3	PIN7; auxin efflux carrier family protein
252660_at	At3g44440	-1,16	6,63E-3	Unknown protein
256228_at	At1g56190	-1,15	6,91E-3	Phosphoglycerate kinase family protein
257961_at	At3g19780	-1,15	7,95E-3	
256676_at	At3g52180	-1,13	1,12E-2	PTPKIS1, SEX4, DSP4; dual specificity protein phosphatase (DsPTP1)
261706_at	At1g32680	-1,13	1,24E-2	
257809_at	At3g27060	-1,13	1,29E-2	TSO2; ferritin/ribonucleotide reductase-like family protein
247639_s_at	At5g60500	-1,12	1,56E-2	Undecaprenyl pyrophosphate synthetase family protein
261507_at	At1g71720	-1,12	1,57E-2	PDE338; nucleic acid-binding proteins superfamily
267639_at	At2g42200	-1,12	1,59E-2	SPL9; squamosa promoter binding protein-like 9
253871_at	At4g27440	-1,12	1,69E-2	PORB; protochlorophyllide oxidoreductase B
267117_at	At2g32560	-1,11	1,82E-2	F-box family protein
259783_at	At1g29510	-1,11	1,88E-2	SAUR68; SAUR-like auxin-responsive protein family
248329_at	At5g52780	-1,10	2,37E-2	Protein of unknown function (DUF3464)
265204_at	At2g36650	-1,10	2,52E-2	
245150_at	At2g47590	-1,10	2,60E-2	PHR2; photolyase/blue-light receptor 2
266478_at	At2g31170	-1,08	3,70E-2	FIONA, SYCO ARATH; cysteinyl-tRNA synthetase, class Ia family protein
258800_at	At3g04550	-1,08	3,72E-2	Unknown protein

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255053_at	At4g09730	-1,08	3,90E-2	RH39
262979_s_at	At1g75610	-1,07	4,74E-2	Histone superfamily protein
<b>Up-regulated</b>				
254806_at	At4g12430	1,07	4,90E-2	TPPF; haloacid dehalogenase-like hydrolase (HAD) superfamily protein
263226_at	At1g30690	1,07	4,76E-2	Sec14p-like phosphatidylinositol transfer family protein
254661_at	At4g18260	1,07	4,75E-2	Cytochrome b561/ferric reductase transmembrane protein family
253407_at	At4g32920	1,07	4,73E-2	Glycine-rich protein
253373_at	At4g33150	1,07	4,68E-2	LKR, SDH; lysine-ketoglutarate reductase/saccharopine dehydrogenase
247925_at	At5g57560	1,07	4,54E-2	TCH4, XTH22; xyloglucan endotransglucosylase/hydrolase family
250449_at	At5g10830	1,07	4,48E-2	S-adenosyl-L-methionine-dependent methyltransferases superfamily
255319_at	At4g04220	1,07	4,26E-2	RLP46; receptor like protein 46
264238_at	At1g54740	1,08	3,79E-2	Protein of unknown function (DUF3049)
266180_at	At2g02470	1,08	3,66E-2	AL6; alfin-like 6
247388_s_at	At5g63470	1,08	3,56E-2	HAP5A, NF-YC1; nuclear factor Y, subunit C1
254200_at	At4g24110	1,09	3,34E-2	Unknown protein
265339_at	At2g18230	1,09	3,34E-2	PPa2; pyrophosphorylase 2
262876_at	At1g64750	1,09	3,33E-2	DSS1(l); deletion of SUV3 suppressor 1(l)
261481_at	At1g14260	1,09	3,11E-2	RING/FYVE/PHD zinc finger superfamily protein
249544_at	At5g38110	1,09	3,03E-2	ASF1B, SGA1; anti-silencing function 1b
258338_at	At3g16150	1,09	2,92E-2	ASPGB1; N-terminal nucleophile aminohydrolases (Ntn hydrolases)
244973_at	AtCg00690	1,09	2,71E-2	PSBT, PSBTC; photosystem II reaction center protein T
250072_at	At5g17210	1,10	2,67E-2	Protein of unknown function (DUF1218)
255549_at	At4g01950	1,10	2,60E-2	GPAT3; glycerol-3-phosphate acyltransferase 3
257315_at	At3g30775	1,10	2,49E-2	POX, PDH1, ERD5, PRO1, PRODH; methylenetetrahydrofolate reductase
253392_at	At4g32650	1,10	2,21E-2	KC1, LKT1, KAT3; potassium channel in Arabidopsis thaliana 3
247707_at	At5g59450	1,11	2,11E-2	GRAS family transcription factor
245136_at	At2g45210	1,11	2,07E-2	SAUR-like auxin-responsive protein family
252624_at	At3g44735	1,11	2,07E-2	PSK3, PSK1; phyto-sulfokine 3 precursor
260915_at	At1g02660	1,11	1,94E-2	alpha/beta-hydrolases superfamily protein
251090_at	At5g01340	1,11	1,86E-2	mSFC1, mitochondrial substrate carrier family protein
265674_at	At2g32190	1,11	1,81E-2	Unknown protein
254158_at	At4g24380	1,12	1,61E-2	
246155_at	At5g20030	1,12	1,55E-2	Plant Tudor-like RNA-binding protein
258851_at	At3g03190	1,12	1,44E-2	GSTF11, GSTF6; glutathione S-transferase F11
260276_at	At1g80450	1,13	1,36E-2	VQ motif-containing protein
244901_at	AtMg00640	1,13	1,36E-2	ORF25; hydrogen ion transporting ATP synthases
254424_at	At4g21510	1,13	1,32E-2	F-box family protein
260522_x_at	At2g41730	1,13	1,27E-2	Unknown protein
266021_at	At2g05910	1,13	1,25E-2	Protein of unknown function (DUF567)
256664_at	At3g12040	1,13	1,21E-2	DNA-3-methyladenine glycosylase (MAG)
261957_at	At1g64660	1,13	1,19E-2	MGL, methionine gamma-lyase
252437_at	At3g47380	1,13	1,14E-2	Plant invertase/pectin methylesterase inhibitor superfamily
259235_at	At3g11600	1,13	1,09E-2	Unknown protein
260553_at	At2g41800	1,14	1,08E-2	Protein of unknown function (DUF642)
249336_at	At5g41070	1,14	1,08E-2	DRB5; dsRNA-binding protein 5
263120_at	At1g78490	1,14	1,06E-2	CYP708A3; cytochrome P450, family 708, subfamily A, polypeptide 3
255985_at	At1g34150	1,14	9,77E-3	Pseudouridine synthase family protein
255605_at	At4g01090	1,14	9,46E-3	Protein of unknown function (DUF3133)
264692_at	At1g70000	1,14	9,41E-3	Myb-like transcription factor family protein
253093_at	At4g37460	1,14	9,36E-3	SRFR1; tetratricopeptide repeat (TPR)-like superfamily protein
264636_at	At1g65490	1,15	8,42E-3	Unknown protein
246999_at	At5g67440	1,15	6,97E-3	MEL2, NPY3; Phototropic-responsive NPH3 family protein
245349_at	At4g16690	1,16	6,25E-3	MES16; methyl esterase 16
255900_at	At1g17830	1,16	6,05E-3	Protein of unknown function (DUF789)
252989_at	At4g38420	1,17	5,22E-3	SKS9; SKU5 similar 9
266910_at	At2g45920	1,17	4,95E-3	U-box domain-containing protein
255080_at	At4g09030	1,17	4,78E-3	AGP10; arabinogalactan protein 10
259753_at	At1g71050	1,17	4,73E-3	HIPP20; heavy metal transport/detoxification superfamily
265573_at	At2g28200	1,17	4,63E-3	C2H2-type zinc finger family protein
259875_s_at	At1g76690	1,17	4,61E-3	OPR2; 12-oxophytodienoate reductase 2
258566_at	At3g04110	1,17	4,48E-3	GLR1.1, GLR1; glutamate receptor 1.1
248607_at	At5g49480	1,18	4,17E-3	CP1; Ca <sup>2+</sup> -binding protein 1

250741_at	At5g05790	1,18	4,11E-3	Duplicated homeodomain-like superfamily protein
261745_at	At1g08500	1,18	3,73E-3	ENODL18; early nodulin-like protein 18
253749_at	At4g29080	1,19	3,33E-3	IAA27, PAP2; phytochrome-associated protein 2
251436_at	At3g59900	1,19	3,31E-3	ARGOS; auxin-regulated gene involved in organ size
264867_at	At1g24150	1,19	2,97E-3	FH4; formin homologue 4
253224_at	At4g34860	1,19	2,95E-3	A/N-InvB; plant neutral invertase family protein
262099_s_at	At1g59500	1,19	2,95E-3	GH3.4; Auxin-responsive GH3 family protein
266100_at	At2g37980	1,20	2,54E-3	O-fucosyltransferase family protein
266635_at	At2g35470	1,20	2,45E-3	Unknown protein
259979_at	At1g76600	1,20	2,33E-3	Unknown protein
265116_at	At1g62480	1,20	2,31E-3	Vacuolar calcium-binding protein-related
265499_at	At2g15480	1,20	2,12E-3	UGT73B5; UDP-glucosyl transferase 73B5
257978_at	At3g20860	1,21	1,70E-3	NEK5; NIMA-related kinase 5
246825_at	At5g26260	1,21	1,62E-3	TRAF-like family protein
258078_at	At3g25870	1,22	1,38E-3	Unknown protein
252852_at	At4g39900	1,22	1,28E-3	Unknown protein
264547_at	At1g55620	1,23	1,15E-3	CLC-F; chloride channel F
267226_at	At2g44010	1,23	1,12E-3	Unknown protein
267591_at	At2g39705	1,23	1,02E-3	DVL11, RTFL8; ROTUNDIFOLIA like 8
259987_at	At1g75030	1,24	9,41E-4	TLP-3; thaumatin-like protein 3
258139_at	At3g24520	1,24	8,33E-4	HSFC1; heat shock transcription factor C1
259478_at	At1g18980	1,24	7,85E-4	RmlC-like cupins superfamily protein
259976_at	At1g76560	1,25	6,97E-4	CP12-3; CP12 domain-containing protein 3
254759_at	At4g13180	1,26	4,96E-4	NAD(P)-binding Rossmann-fold superfamily protein
265184_at	At1g23710	1,26	4,72E-4	Protein of unknown function (DUF1645)
254638_at	At4g18740	1,26	4,66E-4	Rho termination factor
246584_at	At5g14730	1,26	4,66E-4	Unknown protein
254318_at	At4g22530	1,27	4,13E-4	S-adenosyl-L-methionine-dependent methyltransferases
254201_at	At4g24130	1,27	3,56E-4	Protein of unknown function (DUF538)
244921_s_at	AtMg01000	1,28	2,82E-4	ORF114; hypothetical protein
249255_at	At5g41610	1,29	2,48E-4	CHX18; cation/H <sup>+</sup> exchanger 18
264661_at	At1g09950	1,29	2,15E-4	RAS1; RESPONSE TO ABA AND SALT 1
259651_at	At1g55280	1,30	1,89E-4	Lipase/lipoxygenase, PLAT/LH2 family protein
263259_at	At1g10560	1,30	1,85E-4	PUB18; plant U-box 18
244939_at	AtCg00065	1,30	1,83E-4	RPS12A; ribosomal protein S12A
252563_at	At3g45970	1,31	1,55E-4	EXLA1, EXPL1, HEXP BETA 2.1; expansin-like A1
259682_at	At1g63040	1,31	1,53E-4	
266732_at	At2g03240	1,32	1,04E-4	EXS (ERD1/XPR1/SYG1) family protein
249329_at	At5g40960	1,33	7,91E-5	Protein of unknown function (DUF 3339)
256720_at	At2g34140	1,34	6,58E-5	Dof-type zinc finger DNA-binding family protein
244903_at	AtMg00660	1,34	6,25E-5	ORF149; hypothetical protein
260876_at	At1g21460	1,34	6,23E-5	SWEET1; nodulin MtN3 family protein
266545_at	At2g35290	1,35	5,03E-5	Unknown protein
255884_at	At1g20310	1,35	4,60E-5	Unknown protein
248189_at	At5g54090	1,36	3,82E-5	DNA mismatch repair protein MutS, type 2
250732_at	At5g06480	1,37	2,59E-5	Immunoglobulin E-set superfamily protein
252350_at	At3g48190	1,38	1,91E-5	ATM, PIG1; ataxia-telangiectasia mutated
254304_at	At4g22270	1,39	1,51E-5	MRB1; protein of unknown function (DUF3537)
249459_at	At5g39580	1,40	1,23E-5	peroxidase superfamily protein
258075_at	At3g25900	1,41	9,46E-6	HMT-1; homocysteine S-methyltransferase family protein
248564_at	At5g49700	1,42	6,44E-6	Predicted AT-hook DNA-binding family protein
253963_at	At4g26470	1,42	6,22E-6	Calcium-binding EF-hand family protein
253177_s_at	At4g35150	1,43	4,98E-6	O-methyltransferase family protein
253608_at	At4g30290	1,43	4,91E-6	XTH19; xyloglucan endotransglucosylase/hydrolase 19
256340_at	At1g72070	1,44	4,12E-6	Chaperone DnaJ-domain superfamily protein
258953_at	At3g01430	1,44	3,88E-6	
245641_at	At1g25370	1,44	3,61E-6	Protein of unknown function (DUF1639)
257418_at	At1g30850	1,45	2,71E-6	RSH4; root hair specific 4
248895_at	At5g46330	1,45	2,63E-6	FLS2; leucine-rich receptor-like protein kinase family protein
260655_at	At1g19320	1,47	1,84E-6	Pathogenesis-related thaumatin superfamily protein
245363_at	At4g15120	1,47	1,82E-6	VQ motif-containing protein
265122_at	At1g62540	1,47	1,82E-6	FMO GS-OX2; flavin-monooxygenase glucosinolate S-oxygenase 2
260841_at	At1g29195	1,47	1,80E-6	Unknown protein

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260335_at	At1g74000	1,47	1,75E-6	SS3; strictosidine synthase 3
248090_at	At5g55090	1,47	1,41E-6	MAPKKK15; mitogen-activated protein kinase kinase kinase 15
266798_at	At2g22850	1,48	1,17E-6	bZIP6; basic leucine-zipper 6
247693_at	At5g59730	1,49	9,12E-7	EXO70H7; exocyst subunit exo70 family protein H7
264005_at	At2g22470	1,49	8,31E-7	AGP2; arabinogalactan protein 2
247151_at	At5g65640	1,49	8,24E-7	bHLH093; beta HLH protein 93
250211_at	At5g13880	1,50	7,46E-7	Unknown protein
250860_at	At5g04770	1,50	5,66E-7	CAT6; cationic amino acid transporter 6
247215_at	At5g64905	1,52	3,37E-7	PROPEP3; elicitor peptide 3 precursor
265634_at	At2g25530	1,52	3,26E-7	AFG1-like ATPase family protein
258429_at	At3g16620	1,54	2,01E-7	TOC120; translocon outer complex protein 120
253628_at	At4g30280	1,56	1,09E-7	XTH18; xyloglucan endotransglucosylase/hydrolase 18
265482_at	At2g15780	1,57	8,37E-8	Cupredoxin superfamily protein
253649_at	At4g29790	1,61	2,25E-8	Unknown protein
258887_at	At3g05630	1,62	1,64E-8	PDLZ2, PLDP2; phospholipase D P2
255059_at	At4g09420	1,62	1,62E-8	Disease resistance protein (TIR-NBS class)
247243_at	At5g64700	1,62	1,53E-8	Nodulin MtN21 / EamA-like transporter family protein
248424_at	At5g51680	1,63	1,17E-8	Hydroxyproline-rich glycoprotein family protein
256044_at	At1g07160	1,63	1,14E-8	Protein phosphatase 2C family protein
245411_at	At4g17240	1,63	1,01E-8	Unknown protein
254413_at	At4g21440	1,63	9,68E-9	ATM4, MYB102; MYB-like 102
246984_at	At5g67310	1,65	5,84E-9	CYP81G1; cytochrome P450, family 81, subfamily G, polypeptide 1
265796_at	At2g35730	1,65	5,08E-9	Heavy metal transport/detoxification superfamily protein
256937_at	At3g22620	1,66	4,25E-9	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
253271_s_at	At4g34210	1,67	3,09E-9	ASK11, SK11; SKP1-like 11
245840_at	At1g58420	1,69	1,42E-9	Uncharacterised conserved protein UCPO31279
259339_at	At3g03900	1,71	7,42E-10	APK3; adenosine-5'-phosphosulfate (APS) kinase 3
263151_at	At1g54120	1,73	3,86E-10	Unknown protein
253066_at	At4g37770	1,77	9,90E-11	ACS8; 1-amino-cyclopropane-1-carboxylate synthase 8
258840_at	At3g04620	1,80	3,96E-11	DAN1; Alba DNA/RNA-binding protein
264773_at	At1g22900	1,82	1,98E-11	Disease resistance-responsive (dirigent-like protein) family
249032_at	At5g44910	1,83	9,90E-12	Toll-Interleukin-Resistance (TIR) domain family protein
247734_at	At5g59400	1,83	9,90E-12	Unknown protein
250098_at	At5g17350	1,85	4,95E-12	Unknown protein
252136_at	At3g50770	1,88	0,00E+0	CML41; calmodulin-like 41
262133_at	At1g78000	1,94	0,00E+0	SEL1, SULTR1;2; sulfate transporter 1;2
254915_s_at	At4g11310	1,96	0,00E+0	Papain family cysteine protease
252320_at	At3g48580	2,00	0,00E+0	XTH11; xyloglucan endotransglucosylase/hydrolase 11
267178_at	At2g37750	2,05	0,00E+0	Unknown protein
253880_at	At4g27590	2,07	0,00E+0	Heavy metal transport/detoxification superfamily protein
247704_at	At5g59510	2,18	0,00E+0	DVL18, RTFL5; ROTUNDIFOLIA like 5
260560_at	At2g43590	2,24	0,00E+0	Chitinase family protein
262630_at	At1g06520	2,36	0,00E+0	GPAT1; glycerol-3-phosphate acyltransferase 1
251780_s_at	At3g55310	2,38	0,00E+0	NAD(P)-binding Rossmann-fold superfamily protein

**Table S5.2.** Gene ontology (GO) terms for *ulp1c/d* differentially expressed genes (DEGs) in response to *Pst* DC3000. GO term functional categorization was performed using *Classification SuperViewer* (bar.utoronto.ca/nTOOLS/cgi-bin/nTOOLS\_classification\_superviewer.cgi). Only statistically significant terms are shown ( $p$ -value < 0.05).

Gene Ontology term	Normed to frequency	$\pm$ bootstrap standard deviation	$p$ -value
<b>Down-regulated DEGs</b>			
<b>Biological process</b>			
Electron transport or energy pathways	4.65	1.745	3,56E+00
Developmental processes	2.23	0.526	2,42E+00
Other biological processes	1.84	0.504	0.023
Cell organization and biogenesis	1.74	0.591	0.037
Unknown biological processes	0.68	0.175	0.045
Response to abiotic or biotic stimulus	0.34	0.199	0.045
<b>Molecular function</b>			
Other enzyme activity	1.93	0.534	0.013
<b>Cellular component</b>			
Plastid	4.67	1.27	3,27E-02
Chloroplast	3.26	0.485	3,55E-04
Other cytoplasmic components	1.57	0.343	0.021
Unknown cellular components	0.59	0.214	0.039
Nucleus	0.4	0.165	1,93E+00
<b>Up-regulated DEGs</b>			
<b>Biological process</b>			
Other biological processes	1.87	0.259	4,99E-02
Transport	1.7	0.283	4,97E-01
Response to abiotic or biotic stimulus	1.57	0.233	2,10E+00
Response to stress	1.55	0.204	1,75E+00
Other cellular processes	1.12	0.082	0.017
Other metabolic processes	1.06	0.083	0.046
Unknown biological processes	0.86	0.11	0.030
Protein metabolism	0.77	0.157	0.033
Developmental processes	0.64	0.167	0.018
Cell organization and biogenesis	0.57	0.139	0.012
<b>Molecular function</b>			
Nucleotide binding	0.71	0.187	0.040
DNA or RNA binding	0.71	0.184	0.040
Nucleic acid binding	0.32	0.181	0.011
<b>Cellular component</b>			
Cell wall	2.81	0.906	2,24E+00
Other intracellular components	0.76	0.139	0.030
Unknown cellular components	0.63	0.098	1,12E+00

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**Table S5.3.** Genes involved in protein modification and metabolism that are differentially expressed in *ulp1c/d* upon *Pst* DC3000 infection.

AGI ID	Gene name	Log2 ratio	p-value	Description
<b>Down-regulated genes</b>				
<i>Peptide modifier</i>				
At5g48710	<i>SUM4</i>	-1,25	6,35E-4	Small ubiquitin-related modifier
<i>Protease</i>				
At5g05740	<i>EGY2</i>	-1,43	4,95E-6	Metalloendopeptidase
At5g23210	<i>SCPL34</i>	-1,35	4,74E-5	Serine-type carboxypeptidase
<i>Ubiquitin E3 ligase</i>				
At5g63780	<i>SHA1</i>	-1,67	3,33E-9	RING finger protein
At2g32560		-1,11	1,82E-2	F-box family protein
<b>Up-regulated genes</b>				
<i>Phosphorylation /dephosphorylation</i>				
At3g20860	<i>NEK5</i>	1,21	1,70E-3	Serine/threonine kinase, protein tyrosine kinase
At3g48190	<i>ATM, PIG1</i>	1,38	1,91E-5	1-phosphatidylinositol-3-phosphate 5-kinase
At5g55090	<i>MAPKKK15</i>	1,47	1,41E-6	Serine/threonine kinase
At1g07160	<i>AP2C2</i>	1,63	1,14E-8	Putative protein phosphatase 2C
<i>Protease</i>				
At4g11310		1,96	0,00E+0	Putative cysteine proteinase
<i>Ubiquitin E3 ligase</i>				
At1g14260		1,09	3,11E-2	C3HC4-type RING finger family protein
At4g21510	<i>FBS2</i>	1,13	1,32E-2	F-box family protein
At2g45920	<i>PUB37</i>	1,17	4,95E-3	U-box domain-containing protein
At1g10560	<i>PUB18</i>	1,30	1,85E-4	U-box domain-containing protein
At4g34210	<i>ASK11</i>	1,67	3,09E-9	Skp subunit of SCF complex

**Table S5.4.** Genes involved in transcriptional regulation that are up-regulated in *ulp1c/d* upon *Pst* DC3000 infection.

Transcription regulator family	AGI ID	Gene name	Log2 ratio	P-value
Alfin-like	At2g02470	<i>AL6</i>	1,08	3,66E-2
AP2/ERF	At1g63040		1,31	1,53E-4
Aux/IAA	At4g29080	<i>IAA27, PAP2</i>	1,19	3,33E-3
bHLH	At5g65640	<i>bHLH093</i>	1,49	8,24E-7
bZIP	At2g22850	<i>bZIP6</i>	1,48	1,17E-6
C2C2 (Zn) Dof (Zn)	At2g34140	<i>DOF2.3</i>	1,34	6,58E-5
C2H2 (Zn)	At2g28200		1,17	4,63E-3
CCAAT	At5g63470	<i>NF-YC4</i>	1,08	3,56E-2
HSF	At3g24520	<i>HSFC1</i>	1,24	8,33E-4
MYB-related	At1g70000		1,14	9,41E-3
	At5g05790		1,18	4,11E-3
	At4g21440	<i>MYB102</i>	1,63	9,68E-9
GRAS	At5g59450	<i>SCL11</i>	1,11	2,11E-2
Putative transcription regulator	At1g09950	<i>RAS1</i>	1,29	2,15E-4
	At5g49700		1,42	6,44E-6

Zn - zinc finger



**Table S5.5.** *Arabidopsis thaliana* WRKY transcription factors that are modified by SUM1 (Miller et al., 2010). \* represents the lysine that is subject of SUMO modification and the experimental condition involved. *SUMO plot Analysis Program* was used to predict the highest probable SUMO attachment lysine ([www.abgent.com/tools/](http://www.abgent.com/tools/)), the score is presented in parenthesis.

	AGI ID	SUMO site *	SUMO plot	Observations	References
WRKY3	At2g03340	K508 (heat)	K508 (91%)	Pathogen infection and salicylic acid	Lai et al. (2008)
WRKY4	At1g13960	K509 (untreated, heat, H <sub>2</sub> O <sub>2</sub> )	K509 (91%)	Pathogen infection and salicylic acid	Lai et al. (2008)
WRKY6	At1g62300		K111 (93%)	Senescence- and defense-associated	Robatzek & Somssich (2002)
WRKY33	At2g38470		K504 (79%)	Response to pathogen attack	Lippok et al., (2007)
WRKY72	At5g15130		K47 (93%)	SA-independent defense mechanisms	Bhattarai et al., (2010)

**Table S5.6.** List of primers used for genotyping T-DNA insertion lines.

Primer name	Primer sequence (5' to 3')	Description
ULP1c RP ULP1c LP	GACATACCTTCCTGCAGCTTG CTCTGCAATTGCATCATTCTG	Genotyping of <i>ulp1c-1</i> (SALK_050441)
ULP1d RP ULP1d LP	GGCTGAGCTTCTTCTTCATCC TTCAGATGTTTTACCGCAAGG	Genotyping of <i>ulp1d-1</i> (SALK_029340)
SIZ1-2 RP SIZ1-2 LP	CACGACAGATGAAGCATTGTG GAGCTGAAGCATCTGGTTTTG	Genotyping of <i>siz1-2</i> (SALK_065397)
35S:ULP1s F1 35S:ULP1c R1 35S:ULP1d R1	CTCGCCGTGAAGACTGGCGAA CGGCGGGTTCATAGCCGGAAA AACAACCGCCACCCGTTGCT	Genotyping of <i>ULP1c</i> and <i>ULP1d</i> overexpression lines
GUS M116 GUS M117	TTGAAGCCGATGTCACGCCG TTATCGAATCCTTTGCCACG	Genotyping <i>proDR5::GUS</i> lines
LBb1.3	ATTTTGCCGATTTCCGGAAC	Left border primer for genotyping SALK T-DNA insertion lines

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**Table S5.7.** List of quantitative RT-PCR (qPCR) primers.

Gene (AGI code)	Primer name	Primer sequence (5' to 3')	T <sub>m</sub>	GC (%)	Product size (bp)
<i>ULP1c</i> (At1g10570)	ULP1c qRT F1	TGCGAGCGAGTACAGCCTCA	57.9	60.0	232
	ULP1c qRT R1	AATCTTGGCAGCGACCGCCA	59.3	60.0	
<i>ULP1d</i> (At1g60220)	ULP1d qRT F1	GGGAAAGCTGAGCACAGTGCA	57.6	57.1	200
	ULP1d qRT R1	TCCCAAGACCACTCCCTAGGAGT	57.6	56.5	
<i>FLS2</i> (At5g46330)	FLS2 RT Fw1	ACCATTACGGCTCTGCAGCA	59.0	57.1	176
	FLS2 RT Rv1	TCGCTTACGTGAGCAACGCG	58.4	60.0	
<i>TUR1</i> (At5g11250)	TIRm2 Fw1	TCCTTACCACTGTTGCAGCTGC	57.4	54.6	206
	TIRm2 Rv1	ACGGACATCTTCCCGCTGA	57.5	60.0	
<i>XTH22</i> (At5g57560)	TCH4 RT Fw1	AGCTCTTGTGACAACCACGAGCC	59.4	56.5	167
	TCH4 RT Rv1	GGGCAACGAGAGGTGGTTTGGT	59.3	59.1	
<i>CalB</i> (At2g45670)	CalB qRT Fw1	ACGACGGTGGATCCATTCCGGA	59.7	59.1	167
	CalB qRT Rv1	TCTTTCCAGCCAGCAAGTGCCA	59.0	54.6	
<i>PIN7</i> (At1g23080)	PIN7 RT Fw1	GCTGGTCCGATGAACGGGGACTAT	60.1	58.3	177
	PIN7 RT Rv1	AGTCATCACACTCGCTGGTGGC	59.2	59.1	
<i>ACT2</i> (At3g18780)	ActinF	CTAAGCTCTCAAGATCAAAGGCTTA	52.7	40.0	211
	ActinR	ACTAAAACGCAAACGAAAGCGGTT	57.2	40.0	

*CalB* - Calcineurin B subunit-related; *TUR1* - TIR-NBS-LRR *ULP1c/d-regulated 1* gene; *T<sub>m</sub>* - Melting temperature; *bp* - Base pair

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# Appendix VI

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**Figure S6.1.** Protein sequence alignment of the catalytic domain of ULP2 subgroup members.

**Figure S6.2.** In silico analysis of *ULP2a* and *ULP2b* expression patterns.

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**Figure S6.4.** *ULP2a* and *ULP2b* second allele T-DNA mutants.

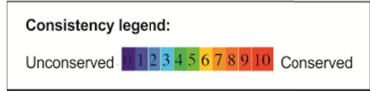
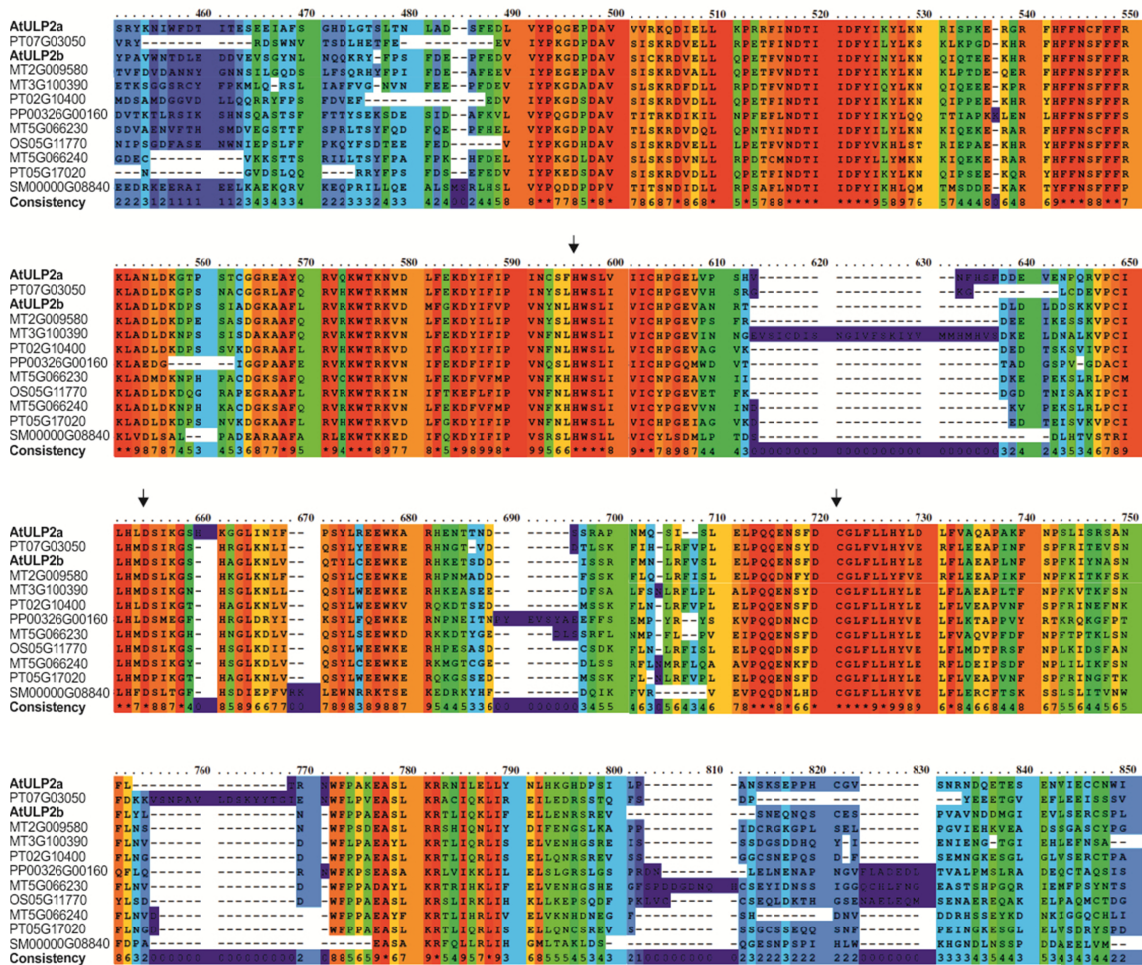
**Figure S6.5.** Subcellular localization prediction for ULP2a and ULP2b.

**Figure S6.6.** Comparison of the most deregulated genes in microarray data of 10-day-old *ulp2a/b* seedlings against available transcriptomic profiles.

**Table S6.1** – List of primers used for genotyping T-DNA insertion lines.

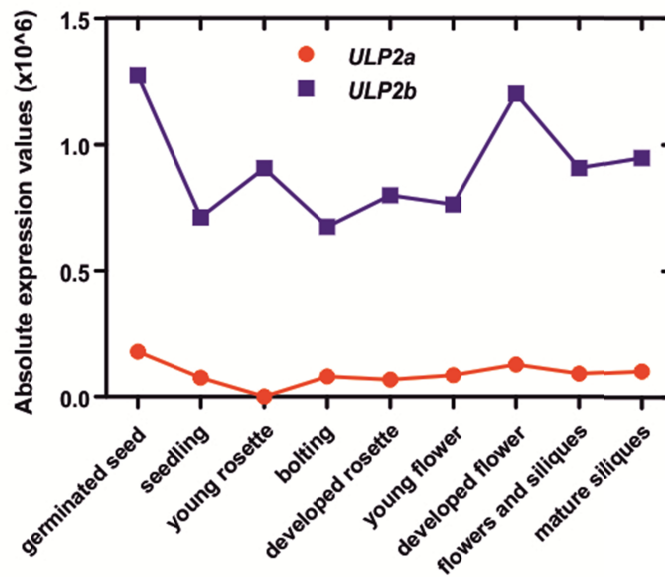
**Table S6.2** – List of quantitative RT-PCR (qPCR) primers.



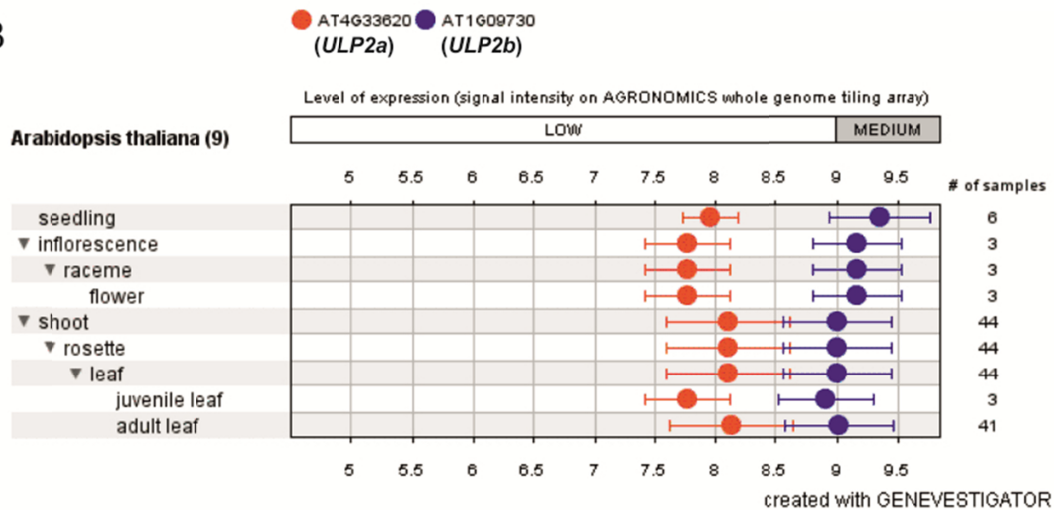


**Figure S6.1.** Protein sequence alignment of the catalytic domain of ULP2 subgroup members identified in *Arabidopsis thaliana*, *Physcomitrella patens*, *Selaginella moellendorffii*, *Oryza sativa* ssp. Japonica, *Medicago truncatula* and *Populus trichocarpa*. Only protein sequences with three conserved catalytic residues (indicated with arrows) were used. Consistency between sequences (color gradient) indicates the level of conservation of each residue. Protein sequence alignment was performed using PRALINE (Simossis and Heringa, 2005).

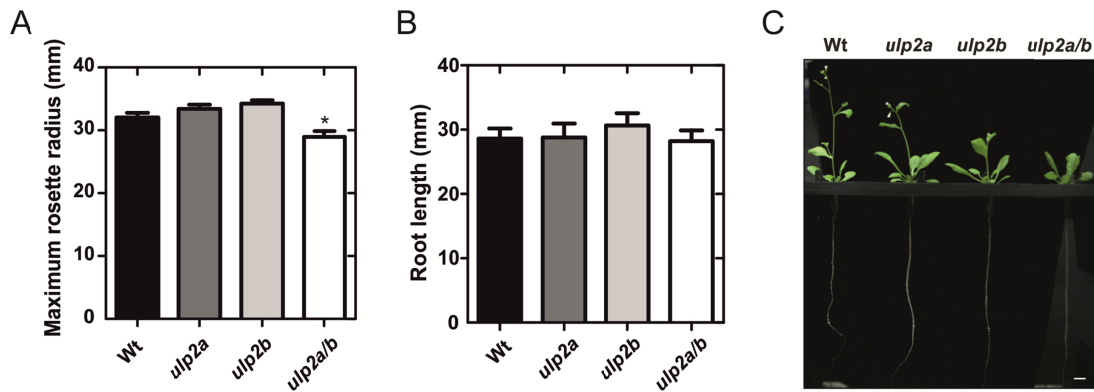
A



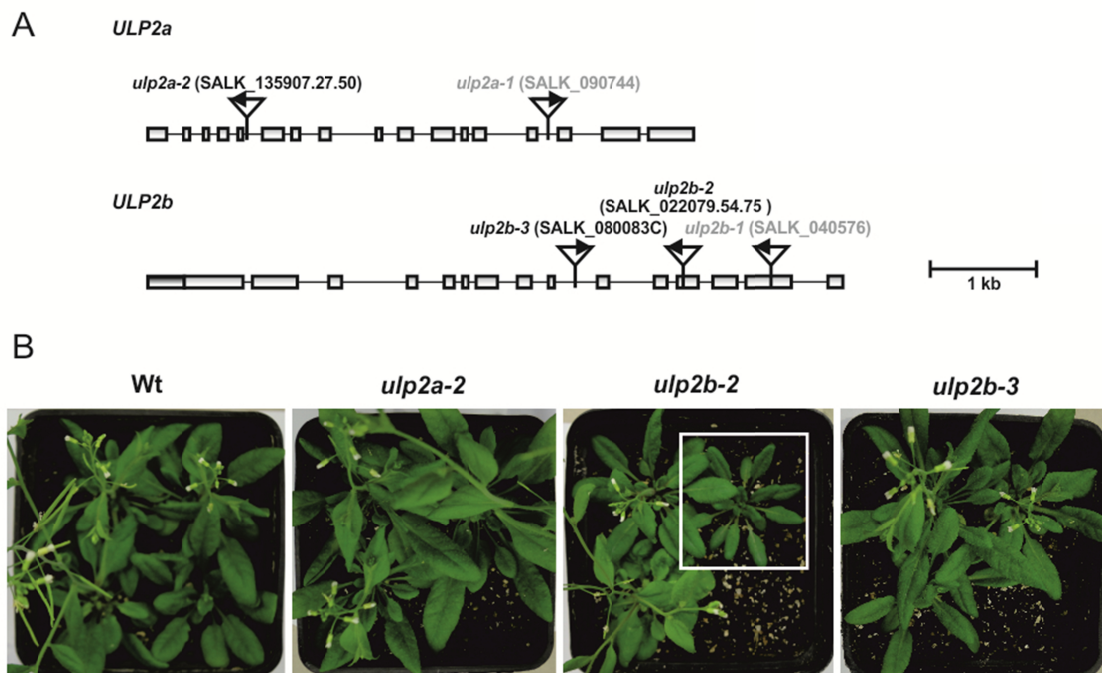
B



**Figure S6.2.** In silico analysis of *ULP2a* and *ULP2b* expression patterns. Expression profile of Arabidopsis *ULP2a* (red) and *ULP2b* (blue) during development (A) and in different plant organs (B). Analysis was conducted in Genevestigator (genevestigator.com; Hruz et al., 2008).



**Figure S6.3.** Developmental characterization of wild-type (Wt), *ulp2a*, *ulp2b* and *ulp2a/b* mutants. **A**, Maximum rosette radius of 1-month-old plants (n=12). **B**, Seedling root length after transfer onto 0.5x MS media and growth for 6 days (n≥14). Error bars represent standard error of the means (SEM). Asterisks indicate statistically significant differences with respect to the wild-type (One-way ANOVA with Dunnett's Multiple Comparison test; \*, P < 0.05). **C**, Plants grown for 1 month in a hydroponic system (*Araponics*). Scale bar indicates 1 cm.



**Figure S6.4.** *ULP2a* and *ULP2b* second allele T-DNA mutants. **A**, Schematic representation of *ULP2a* and *ULP2b*, displaying exons (grey boxes), introns (thin lines), and UTRs (black boxes). The site and orientation of T-DNA insertions (triangles with SALK line code) are represented in grey for the lines described in Chapter 6 and black for SALK\_135907.27.50 (*ulp2a-2*), SALK\_022079.54.75 (*ulp2b-2*) and SALK\_080083C (*ulp2b-3*); scale bar indicates 1 kb. **B**, Morphology of 45-day-old plants. Square shows a homozygous plant for *ulp2b-2*.



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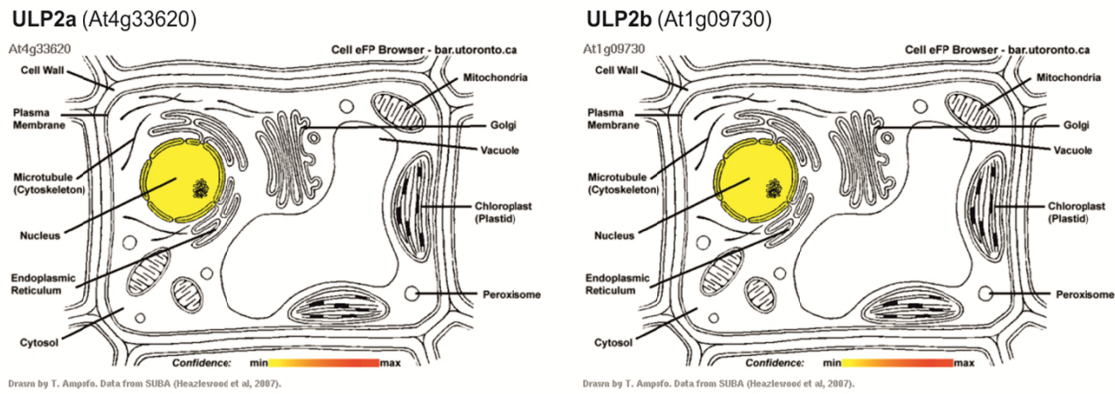


Figure S6.5. Subcellular localization prediction for ULP2a and ULP2b using Cell eFP Browser (bar.utoronto.ca; Winter et al., 2007).

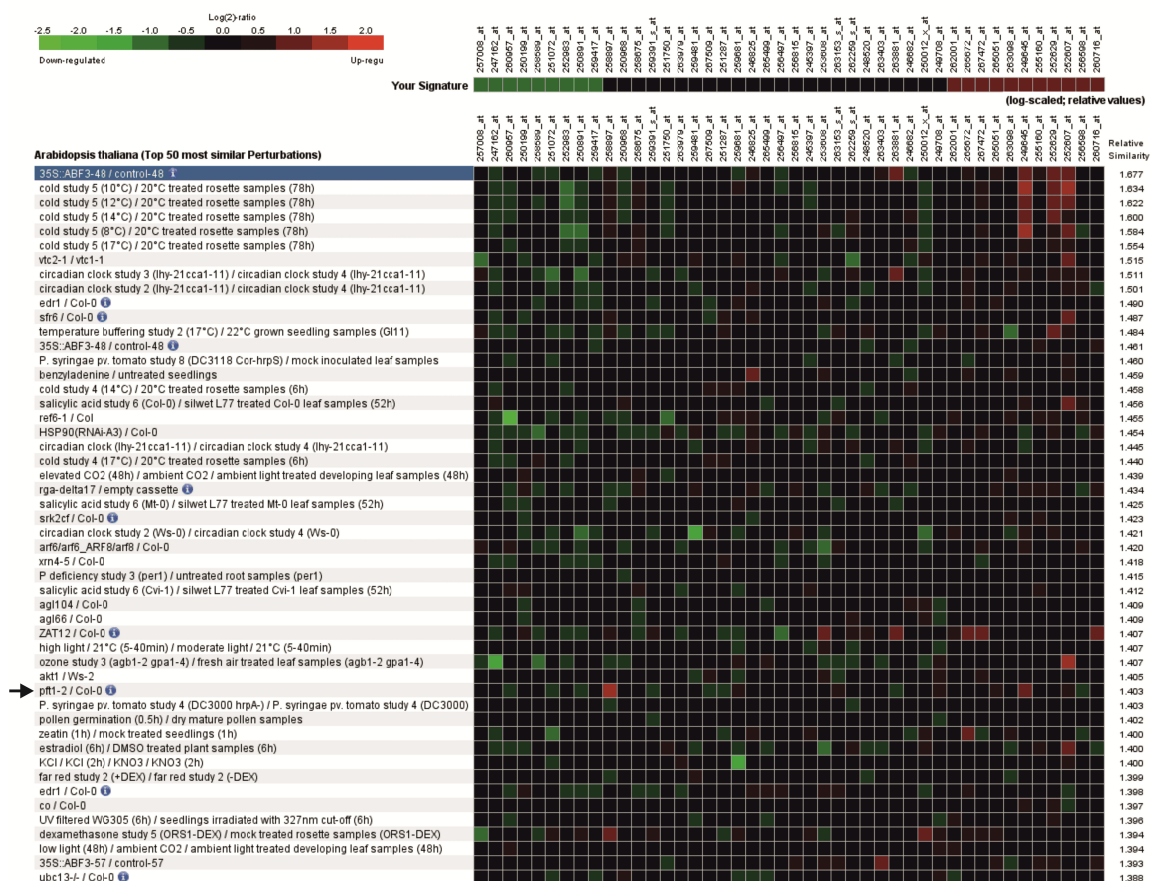


Figure S6.6. Comparison of the most deregulated genes in microarray data of 10-day-old *ulp2a/b* seedlings against available transcriptomic profiles, using the Signature tool in Genevestigator v4 (Hruz et al., 2008); arrows indicate the *pft1-2* transcriptome profile.



**Table S6.1** – List of primers used for genotyping T-DNA insertion lines.

Primer name	Primer sequence (5' to 3')	Description
ULP2a LP ULP2a RP	ACCCACAAAGGGTTCCTGCAT TCTCTTGCTGCGGGAGCTGA	Genotyping of <i>ulp2a-1</i> (SALK_090744)
ULP2b RP ULP2b LP	TCCGCCTAGCTGGCAAGAGA CCGGTTCTGCAACGCCAACG	Genotyping of <i>ulp2b-1</i> (SALK_040576)
SIZ1-2 RP SIZ1-2 LP	CACGACAGATGAAGCATTGTG GAGCTGAAGCATCTGGTTTTG	Genotyping of <i>siz1-2</i> (SALK_065397)
LBb1.3	ATTTTGCCGATTTCCGGAAC	Left border primer for genotyping SALK T-DNA insertion lines

**Table S6.2** – List of quantitative RT-PCR (qPCR) primers.

Gene (AGI code)	Primer name	Primer sequence (5' to 3')	Tm	GC (%)	Product size (bp)
<i>ULP2a</i> (At4g33620)	ULP2A RT F	CTTTTGACTGTGGCCTCTT	49.6	47.4	183
	ULP2A RT R	CTTTGTGGAGTTGTAAAGC	49.1	45.0	
<i>ULP2b</i> (At1g09730)	ULP2B RT F	GGAAGAAGAAATGGAAGGTC	47.8	45.0	152
	ULP2B RT R	CTAAATGGTCAGTGGTTTCC	48.2	45.0	
<i>XTH6</i> (At5g65730)	XTH6 RT Fw1	TGATCAGAGCACTGGATGTGG	59.8	52.4	153
	XTH6 RT Rv1	TCTAGCTCGTCTCACCCT	59.8	55.0	
<i>CAD7</i> (At4g37980)	CAD7 RT F1	TTTCCTCTCATCTTTGGGCG	57.9	50.0	144
	CAD7 RT R1	GGCGGTGTTGACATAATCCG	59.3	55.0	
<i>SOC1</i> (At2g45660)	SOC1 RT F1	GAGCAGCTCAAGCAAAGGAGA	61.1	50.0	137
	SOC1 RT R1	GGGCTACTCTTCATCACCTC	59.6	54.6	
<i>NIA1</i> (At1g77760)	NIA1 RT F1	CCACCAGGAGAAACCGAACA	59.9	55.0	167
	NIA1 RT R1	TCATCCCCATGAGGTTCCAG	58.9	55.0	
<i>XTH31</i> (At3g44990)	XTH31 RT F1	TCCACTGGGAGTGGGTTCA	60.1	57.9	191
	XTH31 RT R1	GAATAAGGCTTCCCTGGCGT	60.1	55.0	
<i>PER1</i> (At1g48130)	PER1 RT F1	TTCGCCAATTCTTGACCGT	60.2	50.0	199
	PER1 RT R1	CCTTGCTTCCGTGATTAAGGC	60.2	50.0	
<i>KNAT1</i> (At4g08150)	KNAT1 RT F1	AGTGGCCATATCCTTCTGAGTC	59.3	50.0	181
	KNAT1 RT R1	TCCATGTACAGAGCTGCGTG	60.1	55.0	
<i>ACT2</i> (At3g18780)	ActinF	CTAAGCTCTCAAGATCAAAGGCTTA	52.7	40.0	211
	ActinR	ACTAAAACGCAAAACGAAAGCGGTT	57.2	40.0	

*Tm* - Melting temperature; *bp* - Base pair

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