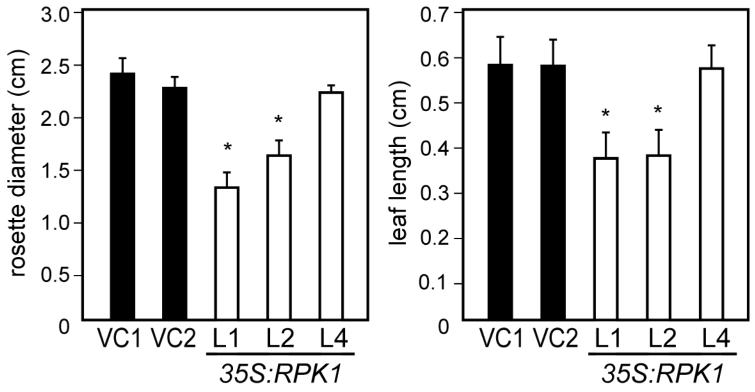
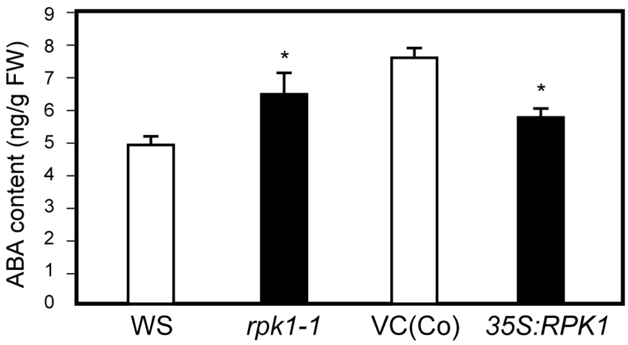
SUPPLEMENTAL FIGURES



Supplemental Figure 1. Rosette sizes and leaf lengths of 35S:*RPK1* grown on GM-agar for 2-weeks. Similar results were obtained 5 times independent experiments. Values are means ±SD of 20 measurements. Student's *t* test; *P < 0.0005.



Supplemental Figure 2. ABA contents (ng/g fresh weight) in the leaves of WS, *rpk1-1*, 35S:*RPK1* L2, and the control plants (vector control: VC) grown on soil pots for 5-weeks. Values are means ±SD of three independent replicates of leaves pooled from five independent plants. Student's *t* test; *P < 0.05, **P < 0.001.

Supplemental Table 1. Primer pairs used in quantitative real-time PCR

Gene		Forword primer	Reverse primer
RPK1	At1g69270	actggtgtggctggaacatt	cgagactcggcatgtcatt
rd29a	At5g52310	tggatctgaagaacgaatctgatatc	ggtcttcccttcgccagaa
cor15a	At2g42540	cagttcgtcgtcgtttctca	cgcagctttctcagcttctt
kin2	At5g15970	aaggccaaggatgctgct	actgccgcatccgatatact
AtrbohD	AT5g47910	aactctccgctgattccaac	tcattcctaagcattcccaaa
FRK	At2g19190	tgagactccttacgatgcactt	gaagttttcccgttttgctg
AtGLR2.7	At2g29120	agatagctagggatatcgggatg	gcgtcattccattggtcatt
18SrRNA		cctacggaaaccttgttacga	cgcgagaagtccactaaacc

Supplementary Table 2. The upregulated genes in the microarray analysis of 35S:RPK1 plants with fold change of >2 (35SRPK1/wild-type control).

		Fold change*		**P value**			
Locus	**Gene name**	Average Ratio	S.D.	lineL1 cy3	lineL1 cy5	lineL2 cy3	lineL2 cy5
At1g69270.1	leucine-rich repeat family protein	12.2	4	8.82E-31	6.45E-32	6.09E-28	1.18E-28
At2g42540.1	cold-responsive protein / cold-regulated protein (cor15a)	5.4	3.5	6.26E-09	2.81E-11	4.21E-27	1.04E-27
At5g50200.1	expressed protein similar to unknown protein	5.2	4.2	3.13E-27	1.26E-28	6.77E-04	5.93E-04
At2g43620.1	chitinase, putative similar to basic endochitinase CHB4 precursor	5.1	3.1	9.71E-27	5.77E-27	8.18E-09	6.51E-08
At1g25560.1	AP2 domain-containing transcription factor, putative similar to DNA-binding protein RAV2	4.4	1.0	7.67E-22	5.19E-24	2.81E-17	2.02E-19
At5g39670.1	calcium-binding EF hand family protein	4.2	2.3	3.70E-25	1.69E-24	1.84E-09	9.67E-09
At2g20142.1	expressed protein	4.2	2.0	9.59E-23	2.02E-24	7.91E-09	4.22E-09
At1g09350.1	galactinol synthase, glycosyl transferase family 8	4.0	1.7	2.73E-10	1.22E-09	5.48E-22	5.90E-19
At1g13260.1	DNA-binding protein RAV1 (RAV1)	3.9	1.0	5.78E-20	6.33E-23	5.71E-14	8.25E-18
At1g68840.1	DNA-binding protein RAV2 (RAV2) / AP2 domain-containing protein RAP2.8	3.9	0.4	9.17E-19	3.12E-21	1.54E-17	3.12E-19
At4g23810.1	WRKY family transcription factor AR411	3.9	0.3	2.28E-17	1.63E-18	2.10E-19	5.33E-20
At1g75900.1	family II extracellular lipase 3 (EXL3) EXL3	3.8	0.7	5.99E-12	5.99E-12	1.15E-17	3.80E-18
At3g09440.1	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)	3.7	1.2	3.38E-22	4.77E-22	3.13E-13	4.37E-13
At2g17040.1	no apical meristem (NAM) family protein contains	3.6	0.5	1.54E-15	1.25E-16	1.02E-19	3.41E-19
At1g64400.1	long-chain-fatty-acid--CoA ligase, putative / long-chain acyl-CoA synthetase	3.6	2.3	4.81E-24	4.81E-24	1.18E-04	7.73E-04
At5g62070.1	calmodulin-binding family protein	3.5	0.3	9.19E-14	4.20E-16	3.75E-16	1.36E-16
At5g52310.1	desiccation-responsive protein 29A (RD29A)	3.5	1.0	7.50E-13	1.15E-12	4.43E-21	9.06E-21
At4g30650.1	low temperature and salt responsive protein	3.4	0.7	1.38E-13	4.90E-13	4.73E-19	3.25E-17
At5g52640.1	heat shock protein 81-1 (HSP81-1) / heat shock protein 83 (HSP83)	3.4	1.5	9.94E-22	8.19E-22	2.79E-10	5.10E-06
At2g24600.1	ankyrin repeat family protein	3.4	1.4	9.43E-10	5.36E-09	1.19E-21	6.06E-21
At3g52430.1	phytoalexin-deficient 4 protein (PAD4)	3.4	1.6	3.30E-22	1.40E-21	6.23E-08	6.12E-08
At5g56010.1	Heat shock protein 81-2 (HSP81-2)	3.3	0.8	3.85E-19	4.10E-20	6.04E-12	9.94E-15
At3g44870.1	S-adenosyl-L-methionine:carboxyl methyltransferase family protein	3.2	1.5	5.00E-22	6.07E-20	2.66E-08	2.60E-05
At2g42530.1	cold-responsive protein / cold-regulated protein (cor15b)	3.2	1.2	4.81E-09	2.32E-09	3.41E-21	2.18E-19
At4g38560.1	expressed protein	3.1	1.2	7.62E-19	4.13E-20	1.66E-07	7.17E-06
At2g41090.1	calmodulin-like calcium-binding protein, 22 kDa (CaBP-22)	3.0	1.7	6.54E-22	4.86E-20	7.58E-05	4.19E-04
At3g12580.1	heat shock protein 70, putative / HSP70	3.0	0.8	6.35E-17	6.40E-18	2.65E-09	4.92E-08
At5g23240.1	DNAJ heat shock N-terminal domain-containing protein	3.0	0.9	2.36E-16	1.36E-18	1.23E-07	4.95E-07
At5g25610.1	dehydration-responsive protein (RD22)	2.9	0.5	4.94E-11	1.59E-13	8.27E-16	1.14E-17
At5g56030.1	heat shock protein 81-2 (HSP81-2)	2.9	0.6	9.45E-18	5.91E-17	6.34E-11	6.36E-11
At1g45010.1	expressed protein	2.8	0.2	3.79E-09	8.11E-04	1.90E-15	9.79E-13
At1g56660.1	expressed protein	2.8	1.2	4.37E-11	8.18E-11	1.27E-12	1.55E-11
At4g18440.1	adenylosuccinate lyase	2.8	0.7	6.29E-07	5.25E-13	3.61E-12	8.22E-16
At1g59590.1	expressed protein	2.8	1.0	5.83E-18	4.17E-19	3.76E-05	1.23E-04
At2g29120.1	glutamate receptor family protein (GLR2.7)	2.8	1.1	1.13E-18	2.90E-18	1.15E-06	1.93E-06
At4g31500.1	cytochrome P450 83B1 (CYP83B1)	2.8	1.1	7.42E-20	1.68E-17	5.50E-08	3.10E-06
At4g32650.1	inward rectifying potassium channel, putative (KAT3)	2.8	1.4	4.29E-17	2.46E-20	8.32E-04	8.20E-04

Supplementary Table 2. The upregulated genes in the microarray analysis of 35S:RPK1 plants with fold change of >2 (35SRPK1/wild-type control).

		Fold change*		**P value**			
Locus	**Gene name**	Average Ratio	S.D.	lineL1 cy3	lineL1 cy5	lineL2 cy3	lineL2 cy5
At5g52320.1	cytochrome P450, putative	2.7	0.1	2.33E-12	7.80E-13	2.42E-10	1.68E-09
At4g33050.1	calmodulin-binding family protein	2.6	0.6	5.92E-15	4.56E-17	5.89E-08	1.19E-10
At1g66090.1	disease resistance protein (TIR-NBS class)	2.6	0.9	3.14E-17	1.83E-17	1.76E-06	5.33E-07
At1g06000.1	UDP-glucoronosyl/UDP-glucosyl transferase family protein	2.6	0.7	3.05E-15	1.29E-14	6.24E-08	4.57E-05
At1g72930.1	Toll-Interleukin-Resistance (TIR) domain-containing protein	2.6	1.0	1.82E-15	5.34E-19	4.19E-05	9.82E-09
At3g16460.1	jacalin lectin family protein	2.6	0.6	2.90E-07	7.13E-08	8.64E-13	1.13E-12
At4g12720.1	MutT/nudix family protein	2.6	0.1	2.32E-12	2.89E-12	1.59E-13	2.29E-12
At2g37710.1	lectin protein kinase	2.6	1.0	1.57E-17	1.57E-17	7.80E-06	7.03E-06
At2g46430.1	cyclic nucleotide-regulated ion channel	2.6	1.0	1.94E-18	1.94E-18	1.04E-07	1.21E-04
At3g07390.1	auxin-responsive protein / auxin-induced protein (AIR12)	2.6	0.7	3.07E-16	3.07E-16	1.58E-08	2.57E-07
At3g45860.1	receptor-like protein kinase, putative similar to receptor-like protein kinase 4	2.5	1.1	5.21E-18	5.21E-18	4.27E-04	4.56E-04
At5g47910.1	respiratory burst oxidase protein D (RbohD) / NADPH oxidase	2.5	0.5	3.28E-09	6.46E-09	5.16E-15	1.01E-12
At5g44580.1	expressed protein	2.5	0.6	2.49E-11	7.94E-17	8.25E-07	4.53E-12
At1g80840.1	WRKY family transcription factor	2.5	0.6	3.16E-07	5.90E-08	7.56E-14	3.93E-13
At5g27420.1	zinc finger (C3HC4-type RING finger) family protein similar to RING-H2 zinc finger protein ATL6	2.5	0.6	2.54E-14	1.09E-15	2.05E-07	1.06E-07
At5g15970.1	stress-responsive protein (KIN2) / cold-responsive protein (COR6.6)	2.4	0.7	2.79E-06	2.16E-09	1.08E-12	6.29E-17
At1g24140.1	matrixin family protein similar to matrix metalloproteinase	2.4	0.8	1.25E-15	3.8E-16	9.93E-06	5.31E-05
At4g34150.1	C2 domain-containing protein similar to calcium-dependent protein kinase	2.4	0.2	5.05E-11	2.04E-09	9.17E-12	2.58E-13
At1g70820.1	phosphoglucomutase, putative / glucose phosphomutase	2.4	0.5	4.13E-08	1.3E-07	1.26E-14	1.17E-13
At1g20510.1	4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	2.4	0.1	1.38E-11	4.86E-12	7.55E-11	4.03E-10
At1g71880.1	sucrose transporter / sucrose-proton symporter (SUC1)	2.4	0.2	8.34E-13	2.1E-12	1.25E-09	2.57E-09
At1g67330.1	expressed protein	2.3	0.5	4.34E-13	2.24E-13	1.19E-06	1.86E-05
At3g55130.1	ABC transporter family protein breast cancer resistance protein 1 BCRP1	2.3	0.3	1.46E-11	1.51E-10	1.3E-12	9.84E-08
At1g22250.1	expressed protein	2.3	0.3	7.02E-06	5.59E-08	1.43E-08	1.48E-08
At4g16860.1	disease resistance protein (TIR-NBS-LRR class)	2.3	0.1	2.19E-11	7.95E-10	3.37E-11	1.08E-09
At3g55980.1	zinc finger (CCCH-type) family protein	2.3	0.6	1.22E-06	1.07E-05	1.32E-14	1.39E-13
At4g02330.1	pectinesterase family protein	2.3	0.5	5.57E-13	9.03E-14	1.4E-06	9.42E-06
At2g26190.1	calmodulin-binding family protein	2.3	0.1	7.65E-11	9.23E-12	3.8E-09	9.02E-10
At1g13080.1	cytochrome P450 family protein	2.3	0.2	7.26E-10	9.02E-13	2.16E-09	3.35E-09
At3g46600.1	scarecrow transcription factor family protein scarecrow-like 11	2.2	0.1	7.89E-11	2.33E-09	3.91E-11	1.84E-09
At4g39330.1	mannitol dehydrogenase	2.2	0.5	5.58E-06	1.65E-06	6.13E-14	1.23E-12
At3g24500.1	ethylene-responsive transcriptional coactivator	2.2	0.7	1.01E-13	1.77E-14	5.52E-05	0.000147
At5g01540.1	lectin protein kinase, putative similar to receptor lectin kinase 3	2.2	0.5	9.48E-13	6.42E-13	5.74E-06	1.77E-06
At5g54190.1	protochlorophyllide reductase A, chloroplast / PCR A / NADPH-protochlorophyllide oxidoreductase A (PORA)	2.2	0.1	6.68E-10	2.54E-09	1.43E-08	3.18E-07
At5g13200.1	GRAM domain-containing protein / ABA-responsive protein-related	2.2	0.4	3.04E-11	9.29E-13	1.03E-05	6.94E-08
At4g38620.1	myb family transcription factor (MYB4)	2.2	0.3	4.08E-12	1.3E-09	5.16E-10	3.71E-06
At5g11790.1	Ndr family protein	2.2	0.2	1.81E-07	1.19E-08	6.41E-11	5.93E-09
At1g68520.1	zinc finger (B-box type) family protein	2.2	0.1	2.44E-08	9.86E-10	6.35E-11	5.81E-10

Supplementary Table 2. The upregulated genes in the microarray analysis of 35S:RPK1 plants with fold change of >2 (35SRPK1/wild-type control).

		Fold change*		**P value**			
Locus	**Gene name**	Average Ratio	S.D.	lineL1 cy3	lineL1 cy5	lineL2 cy3	lineL2 cy5
At5g41750.1	disease resistance protein (TIR-NBS-LRR class)	2.2	0.3	2.59E-12	3.34E-09	3.65E-09	7.31E-06
At3g52470.1	harpin-induced family protein / HIN1 family protein	2.2	0.3	7.38E-07	4.6E-12	1.67E-05	9.79E-08
At2g30870.1	glutathione S-transferase	2.1	0.3	2.54E-12	8.93E-11	5.5E-08	9.37E-07
At3g50970.1	dehydrin xero2 (XERO2) / low-temperature-induced protein LTI30 (LTI30)	2.1	0.5	0.000518	1.85E-05	1.93E-09	3.93E-10
At1g66920.1	serine/threonine protein kinase	2.1	0.6	1.42E-12	7.76E-13	5.94E-06	0.000296
At5g19240.1	expressed protein	2.1	0.5	1.93E-13	2.16E-11	2.72E-06	4.85E-05
At1g01420.1	UDP-glucoronosyl/UDP-glucosyl transferase family protein	2.1	0.3	1.04E-10	4.7E-07	1.11E-11	1.86E-06
At2g41870.1	remorin family protein	2.1	0.5	3.61E-06	1.4E-05	1.33E-13	4.63E-10
At5g56000.1	heat shock protein 81-4 (HSP81-4) , hsp81.4 [Arabidopsis thaliana]	2.1	0.3	8.14E-11	1.47E-10	2.06E-07	1.13E-06
At1g18570.1	myb family transcription factor (MYB51)	2.1	0.3	9.92E-10	2.62E-11	7.84E-06	3.2E-06
At4g01250.1	WRKY family transcription factor	2.1	0.5	1.15E-11	9.17E-13	0.000219	9.66E-06
At3g13080.1	ABC transporter family protein	2.1	0.5	1.53E-10	1.15E-12	0.000697	3.35E-05
At5g49910.1	heat shock protein 70 / HSP70 (HSC70-7)	2.1	0.8	1.5E-09	1.29E-08	0.000675	0.0003
At2g23340.1	AP2 domain-containing transcription factor	2.0	0.2	2.85E-08	3.21E-10	5.69E-08	1.34E-06
At1g74940.1	senescence-associated protein-related SAG102_	2.0	0.2	1.14E-07	2.38E-07	6.85E-11	1.53E-08
At4g30470.1	cinnamoyl-CoA reductase-related protein	2.0	0.1	6.49E-08	9.69E-08	6.77E-10	5.25E-08
At1g80270.1	DNA-binding protein	2.0	0.4	0.000189	4.11E-06	2.4E-09	1.93E-10
At3g04710.1	ankyrin repeat family protein	2.0	0.1	3.87E-07	1.81E-06	1.99E-07	4.95E-06
At1g55450.1	embryo-abundant protein-related	2.0	0.3	5.06E-05	1.11E-07	1.72E-10	1.65E-10
At4g31550.2	WRKY family transcription factor	2.0	0.1	9.27E-08	2.31E-07	3.04E-09	6.73E-09

*Fold change was defined as the fluorescence intensity (>1000) of each cDNA of 35S:RPK1/fluorescence intensity of each cDNA of the wild-type vector control line with P value <0.001.

Supplementary Table 3. The downregulated genes in the microarray analysis of 35S:RPK1 plants with fold change of >3 (wild-type control/35SRPK1).

Locus	Gene name	Fold change*		P value			
		Average Ratio	S.D.	lineL1 cy3	lineL1 cy5	lineL2 cy3	lineL2 cy5
At1g61390.1	S-locus protein kinase, putative contains protein kinase domain	11.9	1.5	2.39E-30	9.93E-30	8.04E-30	1.83E-28
At2g33380.1	calcium-binding RD20 protein (RD20) induced by abscisic acid during dehydration	8.3	0.4	1.92E-27	3.23E-27	1.28E-27	5.45E-28
At5g61160.1	malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from Perilla frutescens	7.8	0.6	2.93E-22	2.43E-24	4.16E-22	6.77E-20
At3g10320.1	expressed protein	7.5	6.5	1.90E-05	2.61E-07	1.94E-23	3.48E-22
At3g61930.1	expressed protein	7.4	5.4	9.06E-15	1.87E-14	2.70E-24	1.15E-19
At4g37430.1	cytochrome P450 81F1 (CYP81F1) (CYP91A2)	6.4	3.7	6.23E-19	3.51E-16	1.32E-29	2.20E-26
At5g44420.1	plant defensin protein, putative (PDF1.2a) plant defensin protein family member	5.9	1.7	1.75E-18	1.58E-19	2.78E-22	1.69E-19
At1g74010.1	strictosidine synthase family protein similar to strictosidine synthase [Rauvolfia serpentina]	5.6	4.8	7.29E-04	1.72E-04	1.41E-29	8.50E-28
At3g60140.1	glycosyl hydrolase family 1 protein contains	5.3	3.8	3.33E-06	2.12E-09	1.04E-24	1.48E-23
At1g19050.1	two-component responsive regulator / response regulator 7 (ARR7)	5.1	1.7	5.40E-25	4.15E-26	2.95E-18	1.71E-18
At4g25480.1	DRE-binding protein (DREB1A) / CRT/DRE-binding factor 3 (CBF3) identical to DREB1A	4.9	0.9	6.40E-24	4.62E-22	8.98E-21	8.08E-18
At1g05680.1	UDP-glucoronosyl/UDP-glucosyl transferase family protein	4.4	0.4	1.10E-18	9.43E-21	3.17E-21	1.08E-20
At4g23750.1	AP2 domain-containing transcription factor	4.3	2.5	5.54E-09	8.34E-09	3.78E-24	3.39E-21
At2g14620.1	xyloglucan:xyloglucosyl transferase	4.2	2.7	6.18E-04	8.62E-08	7.38E-14	2.77E-14
At1g52400.1	glycosyl hydrolase family 1 protein / beta-glucosidase, putative	4.2	0.9	5.46E-22	4.99E-21	9.62E-14	6.04E-21
At1g17170.1	glutathione S-transferase	4.1	2.3	2.92E-24	1.69E-24	5.78E-08	3.81E-10
At1g02640.1	glycosyl hydrolase family 3 protein similar to beta-xylosidase	4.0	1.9	1.16E-11	2.94E-11	1.25E-24	7.42E-23
At5g62920.1	two-component responsive regulator / response regulator 6 (ARR6)	4.0	2.0	1.34E-22	1.44E-24	1.86E-09	4.98E-11
At3g16670.1	expressed protein	3.9	0.5	6.07E-21	6.50E-20	1.58E-18	9.91E-17
At4g26150.1	zinc finger (GATA type) family protein	3.7	0.9	1.10E-13	1.18E-15	4.69E-20	2.08E-20
At1g74890.1	two-component responsive regulator / response regulator 15 (ARR15)	3.6	0.1	5.95E-19	7.07E-18	1.04E-18	1.09E-17
At3g21150.1	zinc finger (B-box type) family protein	3.6	0.1	6.90E-18	1.54E-18	8.91E-17	2.45E-17
At5g49360.1	glycosyl hydrolase family 3 protein	3.6	0.5	7.37E-19	2.01E-19	1.07E-15	3.03E-14
At5g02760.1	protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6)	3.6	0.5	8.50E-19	7.68E-19	4.06E-15	9.68E-15
At3g28740.1	cytochrome P450 family protein	3.5	1.8	9.24E-21	4.47E-23	3.53E-07	5.83E-09
At5g56870.1	beta-galactosidase, putative / lactase	3.5	0.2	5.64E-15	5.30E-16	4.32E-16	4.50E-13
At5g59220.1	protein phosphatase 2C, putative / PP2C, putative ABA induced protein phosphatase 2C	3.4	0.5	3.46E-15	1.86E-15	6.21E-19	1.20E-19
At4g25470.1	DRE-binding protein (DREB1C) / CRT/DRE-binding factor 2 (CBF2) identical to DREB1C	3.4	0.4	5.94E-18	2.91E-19	3.09E-15	1.20E-15
At5g40690.1	expressed protein	3.3	0.5	2.24E-17	2.90E-19	2.41E-13	1.21E-14
At4g36850.1	PQ-loop repeat family protein / transmembrane family protein	3.3	1.9	3.57E-04	1.23E-06	4.26E-19	2.73E-18
At1g52890.1	no apical meristem (NAM) family protein	3.2	0.7	2.31E-13	3.37E-13	7.56E-20	5.78E-18
At3g05730.1	expressed protein	3.2	1.1	2.25E-09	2.92E-10	5.02E-20	1.00E-19
At2g29490.1	glutathione S-transferase, putative similar to glutathione S-transferase 103-1A	3.2	1.1	2.93E-09	1.51E-11	5.09E-20	2.67E-16
At5g13180.1	no apical meristem (NAM) family protein : hypothetical protein SENU5	3.2	0.9	1.65E-14	6.43E-10	2.53E-20	9.31E-16
At4g08290.1	nodulin MtN21 family protein	3.1	0.0	4.82E-15	3.97E-15	4.74E-15	5.59E-15
At4g28040.1	nodulin MtN21 family protein	3.1	0.9	1.42E-18	9.60E-20	4.84E-10	1.49E-10
At5g60890.1	receptor-like protein kinase (ATR1); identical to cDNA putative transcription factor (MYB34)	3.0	0.4	1.49E-12	6.18E-14	2.89E-17	1.79E-17
At1g69570.1	Dof-type zinc finger domain-containing protein nearly identical to H-protein promoter binding factor-2b	3.0	0.4	1.10E-16	1.51E-17	7.82E-13	1.17E-13
At1g17020.1	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase	3.0	0.2	7.64E-14	8.21E-16	2.36E-14	2.07E-15

*Fold change was defined as the fluorescence intensity (>1000) of each cDNA of the wild-type vector control /fluorescence intensity of each cDNA of 35S:RPK1 line with P value <0.001.