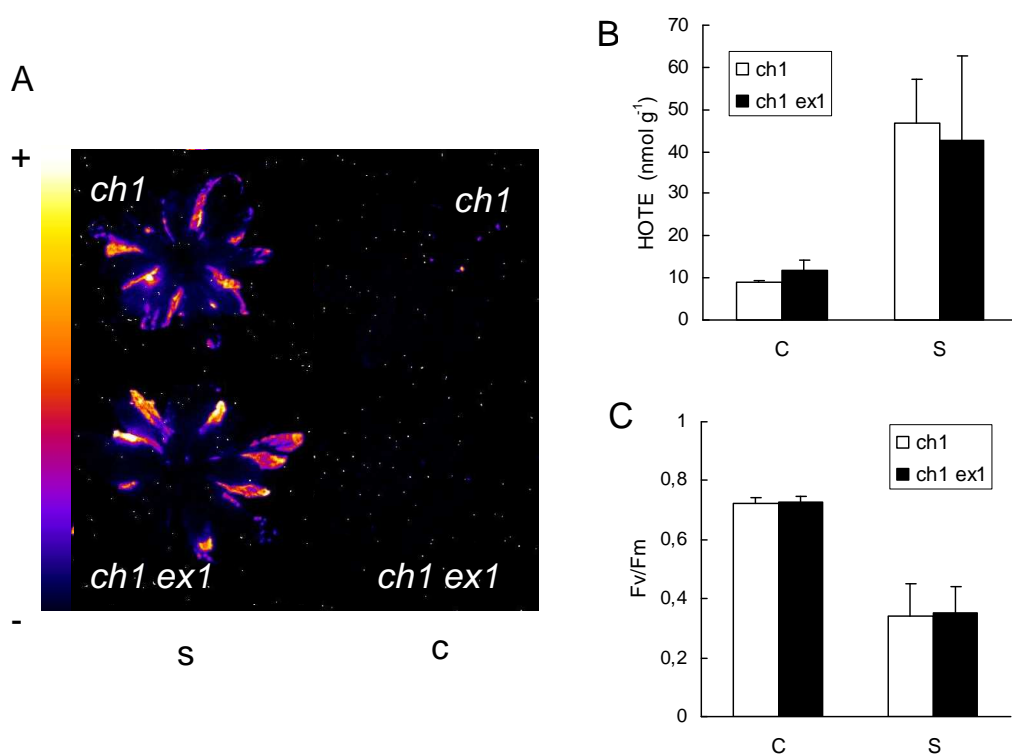
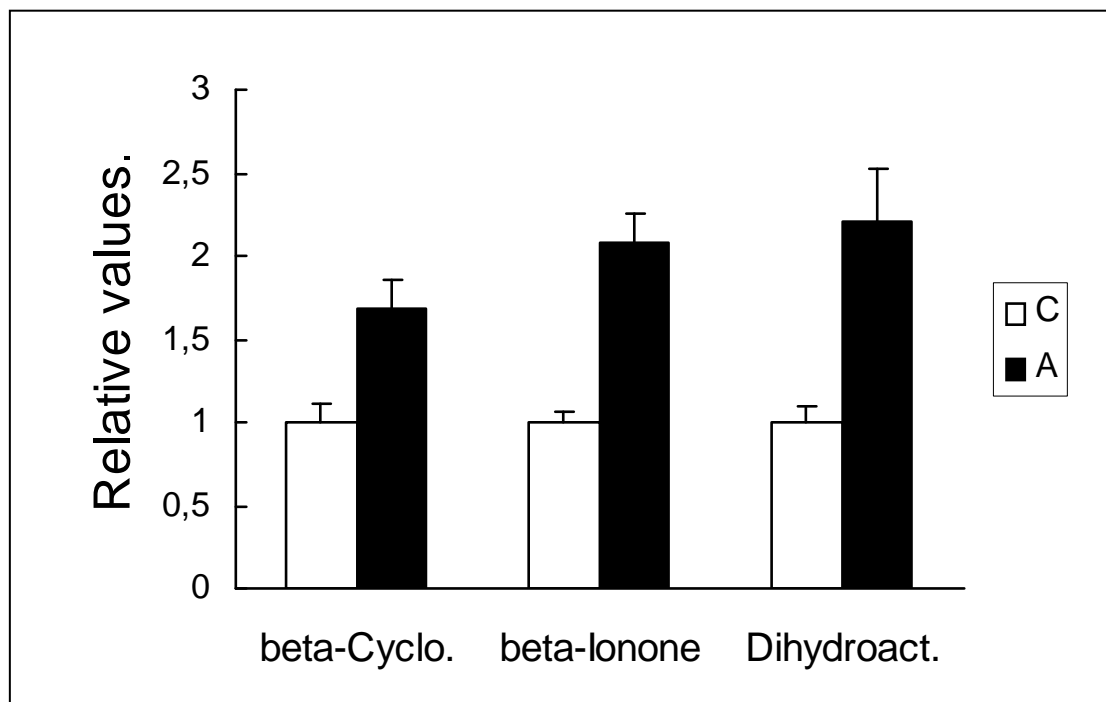


**Supplemental Fig. 1.** Responses to high light stress of the *ch1* single mutant and the *ch1 ex1* double mutant.

A) Autoluminescence imaging of lipid peroxides, B) HOTE levels (in  $\text{nmol g}^{-1}$  fresh weight,  $n=4$ ) and C) PSII photochemical efficiency ( $F_v/F_m$ ).  $n=10$ . C= control; S= stress ( $1000 \mu\text{mol m}^{-2} \text{s}^{-1}$  for 2 d). Data are mean values + SD.



**Supplemental Figure 2.** Levels of different volatile derivatives of  $\beta$ -carotene ( $\beta$ -cyclocitral,  $\beta$ -ionone, dihydroactinidiolide) in *ch1* mutant leaves exposed to acclimatory conditions (A =  $450 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ , 2d). C = control conditions. Data are normalized to the control value (before acclimation) + SD.



**Supplemental Table 1.** List of  $^1\text{O}_2$  specific genes induced in *ch1* mutant leaves during high light stress ( $S=1000 \mu\text{mol photons m}^{-2} \text{s}^{-1}$  for 2 d). For comparison purposes, the gene responses in WT leaves is also shown.

Locus identifier	Description	Fold change		
		WT S/C	<i>ch1</i> S/C	<i>flu</i>
AT1G01260	basic helix-loop-helix (bHLH) family protein	nde	1.591	5.336
AT1G02660	lipase class 3 family protein	nde	2.926	6.059
AT1G03740	kinase	nde	1.881	8.504
AT1G05010	EFE (ethylene forming enzyme)	nde	2.782	5.248
AT1G07500	unknown protein	nde	2.047	13.896
AT1G08930	ERD6 (EARLY RESPONSE TO DEHYDRATION 6); carbohydrate transporter/ sugar porter	nde	2.127	5.080
AT1G09940	HEMA2; glutamyl-tRNA reductase	nde	3.035	16.851
AT1G11960	early-responsive to dehydration protein-related / ERD protein-related	nde	1.472	5.366
AT1G19310	zinc finger (C3HC4-type RING finger) family protein	nde	2.256	10.973
AT1G19770	ATPUP14 (Arabidopsis thaliana purine permease 14); purine transporter	0.65	1.952	7.286
AT1G21000	unknown protein	nde	1.480	5.807
AT1G22280	protein phosphatase 2C, putative / PP2C. putative	nde	2.406	5.064
AT1G25500	choline transporter-related	nde	1.661	11.345
AT1G27130	ATGSTU13 (GLUTATHIONE S-TRANSFERASE 12); glutathione transferase	nde	5.668	5.485
AT1G28380	NSL1 (NECROTIC SPOTTED LESIONS 1)	nde	2.883	5.377
AT1G33590	disease resistance protein-related / LRR protein-related	1.70	3.970	6.818
AT1G50640	ATERF3/ERF3 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 3); DNA binding / protein binding / transcription factor	0.73	1.501	5.649
AT1G51620	protein kinase family protein	nde	1.914	26.597
AT1G63830	proline-rich family protein	nde	1.677	6.839
AT1G69270	RPK1 (RECEPTOR-LIKE PROTEIN KINASE 1); kinase	nde	1.483	5.888
AT1G69500	oxygen binding	0.59	1.633	9.382
AT1G73080	PEPR1 (PEP1 RECEPTOR 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase	nde	2.981	18.878
AT1G74440	unknown protein. MYB95 (myb domain protein 95); DNA binding / transcription factor	nde	1.746	12.664
AT1G74450	unknown protein	nde	2.408	8.089
AT1G74930	AP2 domain-containing transcription factor, putative	nde	1.633	11.963
AT1G75450	CKX5 (CYTOKININ OXIDASE 5); cytokinin dehydrogenase	nde	1.562	5.120
AT1G78080	RAP2.4 (related to AP2 4); DNA binding / transcription factor	nde	1.933	5.459
AT2G04305	magnesium transporter CorA-like protein-related	nde	1.612	5.900
AT2G15960	unknown protein	nde	3.265	5.490
AT2G20340	tyrosine decarboxylase, putative	nde	1.505	7.694
AT2G22300	ethylene-responsive calmodulin-binding protein. putative (SR1)	nde	1.700	6.762
AT2G23450	protein kinase family protein	nde	1.789	7.012
AT2G25625	unknown protein	1.84	1.532	5.366
AT2G27830	unknown protein	nde	1.739	6.620
AT2G29450	ATGSTU5 (Arabidopsis thaliana Glutathione S-transferase (class tau) 5); glutathione transferase	nde	2.267	7.468
AT2G30360	CIPK11 (SNF1-RELATED PROTEIN KINASE 3.22. SOS3-INTERACTING PROTEIN 4); kinase	nde	3.682	13.523
AT2G32240	unknown protein	nde	3.572	5.508
AT2G38400	AGT3 (ALANINE:GLYOXYLATE AMINOTRANSFERASE 3); alanine-glyoxylate transaminase	nde	1.563	8.996
AT2G39200	MLO12 (MILDEW RESISTANCE LOCUS O 12); calmodulin binding	nde	1.901	14.451
AT2G39420	esterase/lipase/thioesterase family protein	nde	1.976	12.631
AT2G43020	ATPAO2 (POLYAMINE OXIDASE 2); amine oxidase. unknown protein	0.65	1.697	5.419

AT2G44840	ATERF13/EREBP (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	nde	3.593	42.082
AT2G46620	AAA-type ATPase family protein	nde	2.107	5.520
AT2G47060	kinase	nde	1.728	6.978
AT3G02140	TMAC2 (TWO OR MORE ABRES-CONTAINING GENE 2)	nde	1.893	11.884
AT3G02875	ILR1 (IAA-LEUCINE RESISTANT 1); metallopeptidase	nde	1.645	6.943
AT3G03480	CHAT (ACETYL COA:(Z)-3-HEXEN-1-OL ACETYLTRANSFERASE); acetyl CoA:(Z)-3-hexen-1-ol acetyltransferase	1.48	1.638	5.723
AT3G05580	serine/threonine protein phosphatase, putative	nde	1.712	5.560
AT3G06490	MYB108 (BOTRYTIS-SUSCEPTIBLE1. myb domain protein 108); DNA binding / transcription factor	nde	1.451	5.775
AT3G09830	protein kinase, putative	nde	1.640	9.284
AT3G16720	ATL2 (Arabidopsis T?xicos en Levadura 2); protein binding / zinc ion binding	nde	1.565	8.794
AT3G17110	pseudogene	0.68	2.161	6.778
AT3G17860	unknown protein	nde	1.639	5.373
AT3G21070	NADK1 (NAD kinase 1); NAD+ kinase	1.46	4.529	7.089
AT3G23220	DNA binding / transcription factor	nde	4.410	6.636
AT3G26980	ubiquitin family protein	nde	2.026	5.331
AT3G44260	CCR4-NOT transcription complex protein. putative	nde	2.549	9.032
AT3G45640	ATMPK3 (MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP kinase/ kinase/ protein kinase	nde	1.474	5.175
AT3G46620	zinc finger (C3HC4-type RING finger) family protein	1.63	2.551	7.820
AT3G46930	protein kinase family protein	nde	2.091	8.514
AT3G47550	zinc finger (C3HC4-type RING finger) family protein	nde	1.453	7.775
AT3G50970	LT130/XERO2 (LOW TEMPERATURE-INDUCED 30)	3.73	5.225	17.689
AT3G53780	rhomboid family protein	1.81	1.877	8.381
AT3G53790	TRFL4 (TRF-LIKE 4); DNA binding	nde	1.498	101.354
AT3G53960	proton-dependent oligopeptide transport (POT) family protein	nde	1.701	5.977
AT3G56260	unknown protein	2.96	1.727	5.964
AT3G57530	CPK32 (CALCIUM-DEPENDENT PROTEIN KINASE 32); calcium- and calmodulin-dependent protein kinase/ kinase	nde	2.296	9.631
AT3G59350	kinase	nde	2.829	24.896
AT4G01010	ATCNGC13 (cyclic nucleotide gated channel 13); calmodulin binding / cyclic nucleotide binding / ion channel	nde	1.699	7.102
AT4G01250	WRKY22 (WRKY DNA-binding protein 22); transcription factor	nde	2.184	9.249
AT4G12410	auxin-responsive family protein	nde	1.675	22.333
AT4G23050	protein kinase, putative	nde	1.512	6.793
AT4G26080	ABI1 (ABA INSENSITIVE 1); calcium ion binding / protein phosphatase type 2C	nde	1.679	12.975
AT4G27657	unknown protein	2.71	3.199	5.102
AT4G27940	mitochondrial substrate carrier family protein	1.79	1.485	6.751
AT4G27970	C4-dicarboxylate transporter/malic acid transport family protein	nde	1.635	6.084
AT4G30210	ATR2 (ARABIDOPSIS P450 REDUCTASE 2)	nde	2.379	5.220
AT4G30350	heat shock protein-related	nde	2.588	6.816
AT4G34410	AP2 domain-containing transcription factor. putative	nde	5.418	96.811
AT4G36500	unknown protein	1.47	3.104	21.796
AT4G39640	GGT1; gamma-glutamyltransferase	nde	3.467	5.066
AT4G39980	DHS1 (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1); 3-deoxy-7-phosphoheptulonate synthase	nde	1.780	5.761
AT5G09440	phosphate-responsive protein, putative	2.36	2.675	5.522
AT5G16970	AT-AER (ALKENAL REDUCTASE); 2-alkenal reductase	nde	2.783	11.142
AT5G24590	TIP (TCV-INTERACTING PROTEIN); transcription factor	nde	1.564	12.375
AT5G26030	ferrochelatase	1.69	3.925	8.635
AT5G42650	AOS (ALLENE OXIDE SYNTHASE); hydro-lyase/ oxygen binding	0.47	1.692	11.540
AT5G43380	TOPP6 (Type one serine/threonine protein phosphatase 6); protein phosphatase type 1	nde	1.498	5.064
AT5G44070	CAD1 (CADMIUM SENSITIVE 1)	nde	1.985	7.179
AT5G47230	ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 5); DNA binding / transcription factor/ transcriptional activator	nde	3.014	8.845
AT5G47240	ATNUDT8 (Arabidopsis thaliana Nudix hydrolase homolog 8); hydrolase	nde	1.777	55.025
AT5G53750	unknown protein	2	5.049	17.198
AT5G53760	MLO11 (MILDEW RESISTANCE LOCUS O 11); calmodulin binding	nde	1.953	6.557

AT5G55120	unknown protein	nde	1.446	5.380
AT5G56980	unknown protein	nde	1.627	24.030
AT5G57630	CIPK21 (CBL-INTERACTING PROTEIN KINASE 21); kinase	nde	1.611	13.027
AT5G58430	AEXO70B1 (exocyst subunit EXO70 family protein B1); protein binding	nde	1.436	8.095
AT5G62620	galactosyltransferase family protein	nde	1.560	5.517
AT5G64310	AGP1 (ARABINOGALACTAN-PROTEIN 1)	nde	3.250	6.882
AT5G67210	nucleic acid binding / pancreatic ribonuclease	nde	1.563	24.511

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nde: not differentially expressed, genes with a Bonferroni *P*-values higher than 5% were considered as being not differentially expressed as described in Lurin *et al.*(2004).

**Supplemental Table 2.** List of  $^1\text{O}_2$  specific genes induced in *ch1* mutant leaves during acclimation (A= 450  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ , 2 d).

Locus identifier	Description	Fold change	
		<i>ch1</i> A/C	<i>flu</i>
AT1G69500	oxygen binding	1.947	9.382
AT2G25625	unknown protein	1.632	5.366
AT3G56260	unknown protein	1.733	5.964
AT4G27657	unknown protein	2.153	5.102
AT4G30210	ATR2 (ARABIDOPSIS P450 REDUCTASE 2)	1.757	5.220
AT4G39980	DHS1 (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1)	1.709	5.761
AT5G16970	AT-AER (ALKENAL REDUCTASE); 2-alkenal reductase	1.485	11.142
AT5G53750	unknown protein	1.594	17.198

**Supplemental Table 3.** Changes in the expression of genes involved in the jasmonate pathway in WT and *chl* leaves during acclimation (A), stress (S) and acclimation followed by S (AS) as measured by microarray-based transcriptomic analyses. C= control conditions.

Locus	Gene description	WT				<i>chl</i>			
		Log <sub>2</sub> (ratio)				Log <sub>2</sub> (ratio)			
		A/C	S/C	S/A	S/AS	A/C	S/C	S/A	S/AS
AT1G02660	lipase class 3 family protein	nde	nde	nde	nde	nde	1.55	1.42	1.10
AT3G45140	LOX2 (LIPOXYGENASE 2)	-0.65	-1.17	nde	nde	nde	1.29	1.43	1.04
AT1G17420	LOX3 (Lipoxygenase 3)	nde	nde	nde	nde	nde	2.40	2.49	2.41
AT5G42650	AOS (ALLENE OXIDE SYNTHASE)	-0.64	-1.09	nde	nde	-0.68	0.76	1.25	1.11
AT3G25760	AOC1 (ALLENE OXIDE CYCLASE 1)	nde	nde	nde	nde	-0.62	2.27	2.54	2.30
AT3G25770	AOC2 (ALLENE OXIDE CYCLASE 2)	nde	nde	nde	nde	-0.69	1.25	1.55	1.43
AT3G25780	AOC3 (ALLENE OXIDE CYCLASE 3)	nde	nde	nde	nde	nde	1.71	1.82	1.77
AT1G13280	AOC4 (ALLENE OXIDE CYCLASE 4)	nde	-0.68	nde	nde	nde	-0.82	nde	nde
AT2G06050	OPR3 (OPDA-REDUCTASE 3)	nde	nde	nde	nde	nde	2.43	2.77	2.60

**Supplemental Table 4.** Functional categories significantly enriched in genes induced or repressed in *ch1* leaves during acclimation to high light stress (A) in comparison with their relative abundance in the genome.

Functional category	Subcategory	<i>Ch1</i> A/C Matches %	Genome Matches %	<i>p</i> -value
<b>Repression</b>				
42 BIOGENESIS OF CELLULAR COMPONENTS	42.01 cell wall	12.1%	0.92%	2.38e-04
70 SUBCELLULAR LOCALIZATION	70.01 cell wall	12.1%	1.51%	1.51e-03
<b>Induction</b>				
01 METABOLISM		35.3%	17.3%	3.72e-04
	01.01 amino acid metabolism	7.69%	1.2%	1.12e-03
	01.01.09 metabolism of the cysteine - aromatic group	6.15%	0.47%	2.71e-04
	01.01.09.04 metabolism of phenylalanine	6.15%	0.11%	9.71e-07
	01.01.09.05 metabolism of tyrosine	3.07%	0.09%	1.74e-03
	01.06.06.11 tetracyclic and pentacyclic triterpenes (cholesterin, steroids and hopanoids) metabolism	3.07%	0.15%	4.58e-03
	01.07 metabolism of vitamins, cofactors, and prosthetic groups	6.15%	0.88%	2.64e-03
	01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups	4.61%	0.44%	3.11e-03
	01.20 secondary metabolism	16.9%	1.49%	3.28e-09
	01.20.35 metabolism of secondary products derived from L-phenylalanine and L-tyrosine	13.8%	0.45%	1.59e-11
	01.20.35.01 metabolism of phenylpropanoids	13.8%	0.41%	6.56e-12
	01.20.35.01.05 metabolism of stilbenes, flavonoids	9.23%	0.16%	9.86e-10
16 PROTEIN WITH BINDING FUNCTION	16.03.01 DNA binding	13.8%	4.90%	4.31e-03
32 CELL RESCUE, DEFENSE AND VIRULENCE		26.1%	5.01%	1.38e-08
	32.01 stress response	23.0%	2.92%	4.68e-10
	32.01.01 oxidative stress response	7.69%	0.70%	9.64e-05
	32.01.06 cold shock response	6.15%	0.58%	5.63e-04
	32.01.13 electromagnetic waves stress response (e.g. UV, X-ray)	3.07%	0.10%	2.01e-03
34 INTERACTION WITH THE ENVIRONMENT		23.0%	5.81%	3.59e-06
	34.11 cellular sensing and response to external stimulus	23.0%	5.24%	1.00e-06
	34.11.01 photoperception and response	7.69%	0.93%	3.56e-04
	34.11.03 chemoperception and response	12.3%	2.95%	6.48e-04
	34.11.09 temperature perception and response	6.15%	0.92%	3.12e-03
36 SYSTEMIC INTERACTION WITH THE ENVIRONMENT		15.3%	2.66%	8.10e-06
	36.20 plant / fungal specific systemic sensing and response	12.3%	2.43%	1.77e-04
	36.20.18 plant hormonal regulation	12.3%	2.07%	5.81e-05
	36.20.18.02 ethylen response	7.69%	0.35%	3.41e-06
	36.25 animal specific systemic sensing and response	4.61%	0.37%	1.91e-03
	36.25.16 immune response	4.61%	0.35%	1.58e-03
	36.25.16.08 response to wounding	4.61%	0.28%	8.28e-04



**Supplemental Table 5.** Gene specific primers and oligonucleotide sequences used for the qRT-PCR analyses.

Name	Locus	Primer sequence 5'-3'	Primer sequence 3'-5'	Length (pb)
Lipase class 3	At1g02660	GAGAAGAACAAAAGTCGCAAGAT	ACGAGAGTGAAGGTAAGAAGCAG	81
MAPKKK18	At1g05100	TAAAATCCGCCGAGTTTCAC	ATCCGATGACGTACGGAGAG	87
AOC4	At1g13280	AGGTCTCTCCACACGAGCA	TCGTAGACGTTAAGCTCTTGGAT	123
LOX3	At1g17420	GCTGATAAAAATTGGTCGAAACA	TCTTCGGCAACTTCGTTTTT	76
Disease resistance protein	At1g57630	GCGTTGTTCAACCATGAAAAT	TAGTGATGACCACCGGAAG	70
OPR3	At2g06050	GGAAAACAGGTGGCGAGTT	CATTCAAAGCAGAAAGGCAAT	122
PRF1	At2g19760	AGAGCGCCAAATTCCTCAG	CCTCCAGGTCCTTCTTCC	169
RD20	At2g33380	GTCCATTCGGATGCTCTGT	GTACGGAACGATTTGGAGGA	86
AOC1	At3g25760	GATTCGTTCCCTTGCCATCAC	AACCTGTCCGTAGGCACCTT	60
AOC2	At3g25770	TTCCTCGCCATCACTGGT	GCTCCAACGGCAAATCAT	136
AOC3	At3g25780	GGAATCTCATCTAACGGTCCAG	TCATACACGTTTAGTTCCTTGGATCTT	149
LOX2	At3g45140	TGACCAGGAAGGCTTACCC	TCCATGTTCTGCGGTCTTATC	73
BAP1	At3g61190	TAAACCGGAGACCCATCAAG	TCGACATTTCTCGTCGATTTT	62
Executer 1	At4g33630	GCTGTCGGGTTTGACAAAAT	TCCTTTCCACCTTCCACTG	147
RRTF1	At4g34410	CAGTTGAAGCAGAGCAATGG	TCATCCACTCCTCCATATTGC	60
AOS	At5g42650	CAAAGACCGTTGGGATTACTTT	CGGATTCGTGATTGAAGAAC	63