

Table S1 Variance analysis of expression level of UVR8 in the wild type (WT) and mutants.

Material name	average value±standard deviation	standard deviation
WT	1.0009±0.04883	a
<i>uvr8-1</i>	0.663±0.03577	b
<i>uvr8-2</i>	0.6061±0.0326	b

Table S2 Details of genes co-expressed by Gh_D10G2310 and Gh_A05G3028.

Gene ID	Annotation
Gh_A05G3863	Chloroplastic enzyme responsible for the synthesis of 16:1 fatty acids from galactolipids and sulpholipids. Uses ferredoxin as electron donor.
Gh_A10G2136	Encodes a temperature sensitive plastidic fatty acid desaturase.
Gh_D05G1179	Chloroplastic enzyme responsible for the synthesis of 16:1 fatty acids from galactolipids and sulpholipids. Uses ferredoxin as electron donor.
Gh_D10G2457	Encodes a temperature sensitive plastidic fatty acid desaturase.
Gh_A08G2526	Similar to ACD1. Leaves of antisense ACD1-like plants turn yellow in darkness like wild-type whereas antisense ACD1 plants remain dark after five days of dark treatment.
Gh_D08G2762	Similar to ACD1. Leaves of antisense ACD1-like plants turn yellow in darkness like wild-type whereas antisense ACD1 plants remain dark after five days of dark treatment.
Gh_D08G2764	Similar to ACD1. Leaves of antisense ACD1-like plants turn yellow in darkness like wild-type whereas antisense ACD1 plants remain dark after five days of dark treatment.
Gh_A02G1698	Encodes a peroxisomal catalase, highly expressed in bolts and leaves. mRNA expression patterns show circadian regulation with mRNA levels being high in the subjective early morning. Loss of function mutations have increased H ₂ O ₂ levels and increased H ₂ O ₂ sensitivity. Mutants accumulate more toxic ions yet show decreased sensitivity to Li ⁺ . This decreased sensitivity is most likely due to an insensitivity to ethylene. Note that in Queval et al. (2007) Plant Journal, 52(4):640, SALK_057998 is named as cat2-1, SALK_076998

	is named as cat2-2; in Bueso et al. (2007) Plant Journal, 52(6):1052, SALK_076998 is named as cat2-1. TAIR has adopted the nomenclature consistent with that in Bueso et al. (2007) after consultation with the authors: SALK_076998 (cat2-1), SALK_057998 (cat2-2).
Gh_A13G1883	Encodes a peroxisomal photorespiratory enzyme that catalyzes transamination reactions with multiple substrates. It is involved in photorespiration.
Gh_D03G0021	Encodes a peroxisomal catalase, highly expressed in bolts and leaves. mRNA expression patterns show circadian regulation with mRNA levels being high in the subjective early morning. Loss of function mutations have increased H ₂ O ₂ levels and increased H ₂ O ₂ sensitivity. Mutants accumulate more toxic ions yet show decreased sensitivity to Li ⁺ . This decreased sensitivity is most likely due to an insensitivity to ethylene. Note that in Queval et al. (2007) Plant Journal, 52(4):640, SALK_057998 is named as cat2-1, SALK_076998 is named as cat2-2; in Bueso et al. (2007) Plant Journal, 52(6):1052, SALK_076998 is named as cat2-1. TAIR has adopted the nomenclature consistent with that in Bueso et al. (2007) after consultation with the authors: SALK_076998 (cat2-1), SALK_057998 (cat2-2).
Gh_D06G0402	Encodes major plastidic long chain acyl-CoA synthetase with a slight substrate preference of oleic acid over any of the other fatty acids.
Gh_A13G1619	Chloroplastic enzyme responsible for the synthesis of 16:2 and 18:2 fatty acids from galactolipids, sulpholipids and phosphatidylglycerol. Uses ferredoxin as electron donor. Gene mutation resulted in reduced level of unsaturated fatty acids leading to susceptibility to photoinhibition.
Gh_D13G1979	Chloroplastic enzyme responsible for the synthesis of 16:2 and 18:2 fatty acids from galactolipids, sulpholipids and phosphatidylglycerol. Uses ferredoxin as electron donor. Gene mutation resulted in reduced level of unsaturated fatty acids leading to susceptibility to photoinhibition.

Gh_A05G2107	Encodes a protein with putative sucrose-phosphate synthase activity.
Gh_D05G2362	Encodes a protein with putative sucrose-phosphate synthase activity.
Gh_D10G1386	Encodes a protein with putative sucrose-phosphate synthase activity.

Table 3. Expression profiles of genes co-expressed by *Gh_D10G2310* and *Gh_A05G3028* under salt stress.

Gene	lea f_1 h_ sal t_1	lea f_1 h_ sal t_2	lea f_1 h_ ck _1	lea f_1 h_ ck _2	lea f_3 h_ sal t_1	lea f_3 h_ sal t_2	lea f_3 h_ ck _1	lea f_3 h_ ck _2	lea f_6 h_ sal t_1	lea f_6 h_ sal t_2	lea f_6 h_ ck _1	lea f_6 h_ ck _2	lea f_1 2h _s alt _1	lea f_1 2h _s alt _2	lea f_1 2h _c k_1	lea f_1 2h _c k_2
Gh_A05G3863	99.3191	97.8727	13.5318	14.5366	35.6287	35.4819	91.5.463	95.5.235	6.61694	6.37459	42.7.54	43.9.121	1.3866	1.30225	26.1.839	27.8.732
Gh_A10G2136	22.6.341	22.5.87	13.32.85	14.32.83	13.5.608	13.6.654	98.3.062	10.33.08	41.148	43.7538	36.4.544	37.4.344	16.7826	16.7336	38.6.707	40.9.47
Gh_D05G179	23.1826	22.9742	30.9.96	32.0.662	10.8248	10.2262	23.3.096	21.7.641	2.46901	2.7011	12.0.667	10.6.734	0.92439	0.97668	89.2239	95.3287
Gh_D08G2762	5.18439	4.72141	89.2843	93.2903	21.0.133	21.4.992	16.7.487	17.0.886	92.5053	91.0629	15.4.289	15.2.292	11.8498	12.6519	39.4635	40.6376

Gh _A 08 G2 52 6	11 9.0 72	11 6.4 58	19 2.5 81	19 9.7 91	71. 65 98	70. 72 1	11 8.8 73	11 9.4 89	21. 48 46	23. 06 48	11 4.1 04	11 1.3 12	0.8 61 39	0.8 82 53	50. 72 65	53. 02 1
Gh _D 08 G2 76 4	90. 70 98	92. 15 81	13 0.4 52	13 6.1 02	2.0 51 41	1.7 46 66	65. 29 19	66. 37 36	0.1 71 28	0.0 93 69 01	21. 27 75	21. 19 32	0.1 50 29 8	0.1 12 92 4	3.2 47 1	3.8 04 33
Gh _D 10 G2 45 7	26 7.5 79	27 4.4 7	25 8.8 32	28 2.3 44	64. 37 23	63. 52 82	74. 33 78	74. 52 83	20. 41 37	19. 98 95	46. 72 17	47. 44 21	1.9 18 55	1.6 76 82	24. 49 86	23. 56 75
Gh _A 02 G1 69 8	20 98. 59	21 32. 87	97. 68 47	10 4.0 47	10 81. 5	11 01. 59	49. 94 47	49. 57 84	38 1.5 88	38 6.4 78	24. 70 55	24. 64 98	15 0.4 43	15 5.8 29	4.9 20 82	5.9 01 44
Gh _A 05 G2 10 7	62. 01 08	63. 47 11	17. 76 76	18. 89 63	24 7.6 52	22 9.4 1	42. 66 66	42. 91 29	44. 57 93	41. 75 85	16. 27 79	15. 45 86	20. 34 49	20. 56 75	7.1 96 27	7.8 03 76
Gh _A 13 G1 61 9	81. 32 09	79. 79 23	56. 84 65	59. 66 9	11 67. 77	11 80. 24	60. 18 47	62. 21 64	37 9.7 03	38 9.2 83	28. 87 55	26. 93 56	92. 67 45	95. 87 38	18. 63 46	17. 68 46
Gh _A 13 G1 88 3	38 9.2 55	35 8.9 03	69. 51 8	72. 85 47	32. 78 51	32. 88 27	23. 09 91	23. 05 75	6.8 44 89	6.6 68 44	6.4 22 83	6.0 49 02	4.9 68 8	5.3 36 33	10. 28 53	10. 41 3
Gh _D	21 27.	21 68.	89. 49	95. 62	50. 37	49. 87	23. 09	23. 05	20. 61	20. 36	6.4 22	6.0 49	7.6 33	8.2 73	10. 28	10. 41

03 G0 02 1	03	49	55	08	32	37	91	75	12	65	83	02	21	88	53	3
Gh _D 05 G2 36 2	46. 98 56	48. 50 41	25. 92 58	25. 36 4	70. 60 88	65. 98 69	19. 07 95	17. 87 88	28. 82 19	26. 76 49	13. 28 04	12. 08 55	8.1 85 36	7.6 22 99	15. 16 22	15. 35 51
Gh _D 06 G0 40 2	72. 15 83	74. 64 01	56. 84 65	59. 66 9	22. 94 32	22. 42 33	7.0 55 09	7.0 32 18	9.9 35 66	9.2 16 32	5.5 70 19	4.9 76 98	5.8 31 18	5.7 87 38	8.9 44 44	10. 35 43
Gh _D 10 G1 38 6	23. 34 11	22. 99 49	4.1 29 26	4.4 26 11	22. 33 65	23. 53 39	12. 56	13. 74 28	6.5 20 54	6.3 60 39	3.4 31 32	3.6 79 07	2.0 29 4	2.2 87 14	3.8 84 86	3.7 42 38
Gh _D 13 G1 97 9	10 1.8 56	98. 24 11	30. 63 1	31. 74 61	8.6 25 31	9.2 22 58	0.6 40 67	1.0 55 94	4.2 43 8	4.3 67 6	1.1 90 18	1.1 16 6	3.4 02 12	3.8 96 37	0.1 12 29	0.2 49 63 2 1

Table S4 Details of all *GhRCCI* family genes.

Gene ID	Principle Transcript ID	Gene Name	Assembly	Species	Description	Chromosome	Start	End	Strand	Length (bp)
Gh_A01	Gh_A01	HE	NAU	Gossy	Probable	A01	1,827,	1,833,	+	5,4

G0184	G0184.1	RC 1		pium hirsut um	E3 ubiquitin -protein ligase HERC1		663	086		24
					Probable					
Gh_A02 G0670	Gh_A02 G0670.1	HE RC 1	NAU	Gossy pium hirsut um	E3 ubiquitin -protein ligase HERC1	A02	11,16 3,214	11,16 9,362	+	6,1 49
					Probable					
Gh_A03 G0868	Gh_A03 G0868.1	HE RC 2	NAU	Gossy pium hirsut um	E3 ubiquitin -protein ligase HERC2	A03	51,19 0,168	51,19 6,727	-	6,5 60
Gh_A03 G1146	Gh_A03 G1146.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	A03	82,09 3,431	82,09 6,182	+	2,7 52
Gh_A04 G0246	Gh_A04 G0246.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	A04	5,216, 030	5,220, 482	-	4,4 53
					Probable					
Gh_A05 G2059	Gh_A05 G2059.1	HE RC 1	NAU	Gossy pium hirsut um	E3 ubiquitin -protein ligase HERC1	A05	22,62 1,736	22,62 8,393	-	6,6 58
Gh_A05 G2188	Gh_A05 G2188.1	rcc2	NAU	Gossy pium hirsut um	Protein RCC2 homolog	A05	25,17 5,332	25,17 9,515	-	4,1 84
Gh_A05 G3028	Gh_A05 G3028.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	A05	77,60 3,269	77,60 8,147	-	4,8 79
Gh_A07 G0164	Gh_A07 G0164.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	A07	2,075, 273	2,077, 370	+	2,0 98
Gh_A08	Gh_A08	HE	NAU	Gossy	Probable	A08	831,6	836,3	-	4,7

G0100	G0100.1	RC 2		pium hirsut um	E3 ubiquitin -protein ligase HERC2		22	52		31
Gh_A08 G0465	Gh_A08 G0465.1	Her c2	NAU	Gossy pium hirsut um	E3 ubiquitin -protein ligase HERC2	A08	6,368, 925	6,373, 210	+	4,2 86
Gh_A09 G0062	Gh_A09 G0062.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	A09	1,367, 420	1,375, 343	-	7,9 24
Gh_A09 G1023	Gh_A09 G1023.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	A09	60,28 7,669	60,29 6,340	-	8,6 72
Gh_A09 G1308	Gh_A09 G1308.1	TH O3	NAU	Gossy pium hirsut um	THO complex subunit 3	A09	65,71 4,420	65,71 8,247	-	3,8 28
Gh_A09 G2009	Gh_A09 G2009.1	HE RC 1	NAU	Gossy pium hirsut um	Probable E3 ubiquitin -protein ligase HERC1	A09	73,28 7,778	73,29 2,152	-	4,3 75
Gh_A10 G0603	Gh_A10 G0603.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	A10	8,602, 138	8,613, 441	-	11, 304
Gh_A10 G1652	Gh_A10 G1652.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	A10	88,05 4,731	88,06 3,481	-	8,7 51
Gh_A10 G2003	Gh_A10 G2003.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	A10	97,80 7,087	97,81 2,175	+	5,0 89
Gh_A11 G0277	Gh_A11 G0277.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	A11	2,556, 265	2,563, 705	-	7,4 41

Gh_A11 G1355	Gh_A11 G1355.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	A11	17,37 3,259	17,37 5,063	-	1,8 05
Gh_A11 G1473	Gh_A11 G1473.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	A11	20,35 5,133	20,35 9,642	-	4,5 10
Gh_A11 G1503	Gh_A11 G1503.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	A11	21,02 0,508	21,02 6,648	+	6,1 41
Gh_A11 G1567	Gh_A11 G1567.1	HE RC1	NAU	Gossypium hirsutum	Probable E3 ubiquitin -protein ligase HERC1	A11	22,78 6,791	22,79 1,697	+	4,9 07
Gh_A11 G2084	Gh_A11 G2084.1	ibtk	NAU	Gossypium hirsutum	Inhibitor of Bruton tyrosine kinase	A11	66,97 9,397	66,98 5,120	+	5,7 24
Gh_A11 G3194	Gh_A11 G3194.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	scaffold29 41_A11	9,171	27,70 7	+	18, 537
Gh_A13 G0645	Gh_A13 G0645.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	A13	18,02 0,525	18,02 4,934	-	4,4 10
Gh_A13 G1460	Gh_A13 G1460.1	ibtk	NAU	Gossypium hirsutum	Inhibitor of Bruton tyrosine kinase	A13	72,44 7,838	72,44 8,784	-	947
Gh_D01 G0233	Gh_D01 G0233.1	HE RC1	NAU	Gossypium hirsutum	Probable E3 ubiquitin -protein ligase HERC1	D01	1,989, 670	1,995, 054	+	5,3 85
Gh_D02 G0718	Gh_D02 G0718.1	HE RC	NAU	Gossypium	Probable E3	D02	10,53 1,951	10,53 7,338	+	5,3 88

		1		hirsutum	ubiquitin-protein ligase HERC1					
Gh_D02 G1249	Gh_D02 G1249.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	D02	40,13 8,479	40,14 4,876	-	6,3 98
Gh_D02 G1578	Gh_D02 G1578.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	D02	54,40 1,729	54,40 6,922	+	5,1 94
Gh_D04 G0616	Gh_D04 G0616.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	D04	11,03 4,497	11,03 9,334	+	4,8 38
Gh_D05 G2301	Gh_D05 G2301.1	HE RC1	NAU	Gossypium hirsutum	Probable E3 ubiquitin-protein ligase HERC1	D05	22,36 4,325	22,37 1,118	-	6,7 94
Gh_D05 G2447	Gh_D05 G2447.1	rcc2	NAU	Gossypium hirsutum	Protein RCC2 homolog	D05	24,54 7,132	24,55 1,323	-	4,1 92
Gh_D05 G3007	Gh_D05 G3007.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	D05	37,81 9,641	37,82 3,344	+	3,7 04
Gh_D05 G3147	Gh_D05 G3147.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	D05	47,18 9,594	47,19 2,537	-	2,9 44
Gh_D05 G3461	Gh_D05 G3461.1	UV R8	NAU	Gossypium hirsutum	Ultraviolet-B receptor UVR8	D05	56,64 1,055	56,64 5,506	+	4,4 52
Gh_D06 G0015	Gh_D06 G0015.1	rcc2	NAU	Gossypium hirsutum	Protein RCC2 homolog	D06	118,7 12	123,9 59	-	5,2 48
Gh_D07	Gh_D07	UV	NAU	Gossypium	Ultraviolet	D07	2,309,	2,311,	+	2,0

G0221	G0221.1	R8		pium hirsut um	et-B receptor UVR8		069	151		83
					Probable					
Gh_D08 G0551	Gh_D08 G0551.1	HE RC 2	NAU	Gossy pium hirsut um	E3 ubiquitin -protein ligase HERC2	D08	6,370, 686	6,374, 970	+	4,2 85
					Probable					
Gh_D08 G2751	Gh_D08 G2751.1	HE RC 1	NAU	Gossy pium hirsut um	E3 ubiquitin -protein ligase HERC1	scaffold43 15_D08	11,87 4	18,90 9	-	7,0 36
Gh_D09 G0059	Gh_D09 G0059.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	D09	1,537, 993	1,545, 883	-	7,8 91
Gh_D09 G1044	Gh_D09 G1044.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	D09	36,46 0,186	36,46 8,799	-	8,6 14
					Probable					
Gh_D09 G2222	Gh_D09 G2222.1	HE RC 1	NAU	Gossy pium hirsut um	E3 ubiquitin -protein ligase HERC1	D09	49,42 3,794	49,42 8,157	-	4,3 64
Gh_D10 G1050	Gh_D10 G1050.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	D10	16,00 6,114	16,01 8,438	-	12, 325
Gh_D10 G1907	Gh_D10 G1907.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	D10	53,24 0,175	53,24 8,825	-	8,6 51
Gh_D10 G2310	Gh_D10 G2310.1	UV R8	NAU	Gossy pium hirsut um	Ultraviol et-B receptor UVR8	D10	61,34 5,236	61,35 0,325	+	5,0 90
Gh_D11 G0331	Gh_D11 G0331.1	UV R8	NAU	Gossy pium hirsut	Ultraviol et-B receptor	D11	2,817, 397	2,824, 509	-	7,1 13

				um	UVR8					
Gh_D11	Gh_D11	UV		Gossypium	Ultraviolet-B		14,94	14,95		1,8
G1503	G1503.1	R8	NAU	hirsutum	receptor	D11	8,548	0,352	-	05
				um	UVR8					
Gh_D11	Gh_D11	UV		Gossypium	Ultraviolet-B		17,21	17,22		4,5
G1630	G1630.1	R8	NAU	hirsutum	receptor	D11	5,939	0,442	-	04
				um	UVR8					
Gh_D11	Gh_D11	UV		Gossypium	Ultraviolet-B		17,83	17,83		6,1
G1664	G1664.1	R8	NAU	hirsutum	receptor	D11	3,298	9,422	-	25
				um	UVR8					
					Probable					
Gh_D11	Gh_D11	HE		Gossypium	E3		18,96	18,96		4,8
G1726	G1726.1	RC1	NAU	hirsutum	ubiquitin-protein ligase	D11	1,594	6,455	-	62
				um	HERC1					
Gh_D11	Gh_D11	UV		Gossypium	Ultraviolet-B		41,12	41,14		13,
G2263	G2263.1	R8	NAU	hirsutum	receptor	D11	6,628	0,544	-	917
				um	UVR8					
Gh_D11	Gh_D11			Gossypium	Inhibitor of		47,66	47,66		5,8
G2399	G2399.1	ibtk	NAU	hirsutum	Bruton tyrosine kinase	D11	0,109	5,938	+	30
				um						
Gh_D13	Gh_D13	UV		Gossypium	Ultraviolet-B		12,54	12,54		4,4
G0764	G0764.1	R8	NAU	hirsutum	receptor	D13	5,537	9,940	-	04
				um	UVR8					
Gh_D13	Gh_D13	IBT		Gossypium	Inhibitor of		52,05	52,06		5,8
G1736	G1736.1	K	NAU	hirsutum	Bruton tyrosine kinase	D13	7,426	3,226	+	01
				um						

Table S5 A list of primers used in this study.

Primers noun	Primer sequences
Gh_A01G0184F	CTCCTGGAAAACCTCATCGCGT
Gh_A01G0184R	AAGCAGCATCGAATCGAGTCCC
Gh_A02G0670F	TTTGGGGATGGTACATTCGGCG
Gh_A02G0670R	CCACATGCCACAGCAATCGTTC

Gh_A03G0868F	GGGCATGGAACTGGAGTCAGTC
Gh_A03G0868R	CCAAATGTGAACAACTGGCCGC
Gh_A03G1146F	TGGGTGGAAAGCTTGGACATGG
Gh_A03G1146R	AACCACCATTGGCTGGAGGTTC
Gh_A04G0246F	ATGTTCTTCGTGTCTCCGCTGG
Gh_A04G0246R	TTGCACAAACCTGCACAGCAAG
Gh_A05G2059F	CTCGGCTTGTAGACAGGCGTTT
Gh_A05G2059R	CGCAAACACGGTAAGGTTTCCC
Gh_A05G2188F	TTGTTCTGTGGCTCCACGTGTT
Gh_A05G2188R	GATATCAACGCCGACGAGAGGG
Gh_A05G3028F	GAAGTGGTGGTGATCAAGCCGA
Gh_A05G3028R	CGAGCTGGCCATACTTGTTCCTA
Gh_A07G0164F	AAGGCTGGAGGAATGACTTCGC
Gh_A07G0164R	GTTGCCACCCCAAGAGTAGCAT
Gh_A08G0100F	ACACGCGAAGAAGTTCACCCTT
Gh_A08G0100R	GCGAAGGTGATCTCCACCATCCT
Gh_A08G0465F	TGGCATTGACAGAGGATGGACA
Gh_A08G0465R	TGGTTTCGGTTTCCAACCACCA
Gh_A09G0062F	GGTGGAAAGCTTTAGCCGACAGT
Gh_A09G0062R	CTTGTTCCATCCCCAGCCGTAG
Gh_A09G1023F	ACGGTCGATTAGGTCATGGGGA
Gh_A09G1023R	AGTGAAGTTGGTGCCACAAGCA
Gh_A09G1308F	GCTTGCTTCCGGTTCTGTTCGAT
Gh_A09G1308R	TGGCCTATGAACTGCTTTCGCA
Gh_A09G2009F	ATCAGTTTGCTCTGGCTGTCTGG
Gh_A09G2009R	TATCGCATAACACGGTGCGGTTT
Gh_A10G0603F	TATGGTTGCTTGTGGATGGCGG
Gh_A10G0603R	TTGACCATACTTGCTCCACCCG
Gh_A10G1652F	CTACTTGTGTTGCCGCTCTGGT
Gh_A10G1652R	GCTTGCCCTCAACTCGGATAGG
Gh_A10G2003F	GGGCGACACAGTGCAGTAATCA
Gh_A10G2003R	TCCTGATGCCCAGTAAGGCAGA
Gh_A11G0277F	TGGTCTTCTAGGGCACGGAAGT
Gh_A11G0277R	ACTTGTGCTACTACGGTCCCCA
Gh_A11G1355F	TCTAACCGCCCATCCTGTGTCT
Gh_A11G1355R	TGTTTCCCCTTCCCATCCCTCA
Gh_A11G1473F	GCACAGCTGCTATTGCAGAACC
Gh_A11G1473R	TCCACAGGACACTTGCGGATA
Gh_A11G1503F	GCTGCTGGGGGTACTCATTCTG
Gh_A11G1503R	AAGTCCCATCCTCCTGGAGAGC
Gh_A11G1567F	GACCCAGAAGGCTCGCAAAAGA
Gh_A11G1567R	GCTCGATTTTCCGTCGGCATTC
Gh_A11G2084F	AGCTGGGCTATACGTCTGTGGA
Gh_A11G2084R	TAGCCAAGTTGACCCTCTCGGT

Gh_A11G3194F	AGAGAGCCGGTTGAAGTTTCGG
Gh_A11G3194R	AGCATTCCACTTTGGTTGGCCT
Gh_A13G0645F	CTCTGCCCCCAAAGTG TAGGTG
Gh_A13G0645R	GGGTTGGAACCTTGCCATCAGT
Gh_A13G1460F	TCTCCTTTCTGGGCCTGTGTTG
Gh_A13G1460R	ACCACTTCCCCAGCTAAACACC
Gh_D01G0233F	TCGGCTTCTTCAACGGCATCAT
Gh_D01G0233R	GGAGGTGCTGCTTCTGTGGTTT
Gh_D02G0718F	ACTGCGGGATGGAAGTAGGGAT
Gh_D02G0718R	CAGTTTGCCAGAAATCGACGC
Gh_D02G1249F	GCTCTAACAACCTCTGGGCGAG
Gh_D02G1249R	TCAACCCGAGTTGGAACCTTGC
Gh_D02G1578F	AGCTCCACCGATTTTCGATCGTC
Gh_D02G1578R	CGGAAAATCGCTGAATCCCCCT
Gh_D04G0616F	GGACGACACAGTGCGGTAATCA
Gh_D04G0616R	GTCCTGCCGCAACAGACACTAT
Gh_D05G2301F	CACGTTTACAGTACCCCCATTCC
Gh_D05G2301R	CTCAACCTGTCCACGCAACGTA
Gh_D05G2447F	GATGAGTGGGTTCCCTCGTCGTG
Gh_D05G2447R	TATACAATTGCCACCGCCTGC
Gh_D05G3007F	GTTAGTGATGCTGGGCGAGTGT
Gh_D05G3007R	GGGGATGTAGGACATCTCATCGCT
Gh_D05G3147F	GCAAATGCAGACCACAGTGCAG
Gh_D05G3147R	TCAGATGTAGCCCCAAACCCTCT
Gh_D05G3461F	GGGTGTCACGATGTTTGTCCCA
Gh_D05G3461R	CCTGCAGAGGTTTGGACCATGT
Gh_D06G0015F	AGTCATCTCCCGTCCGTTGTCT
Gh_D06G0015R	TGGCCAAGCTGACCATACTGTG
Gh_D07G0221F	TTTCCCGGTTTCGGGTCAAGTTC
Gh_D07G0221R	ATTCCTCCAGCCTTGACTGCAC
Gh_D08G0551F	CCTGTGGAGGTTTCATCTTCGGC
Gh_D08G0551R	CGACTGCAACGGATAGCACGTA
Gh_D08G2751F	CGGGGAAGCTATTTACGTGGGG
Gh_D08G2751R	CAACTGTCAGACTGTGTCCGCA
Gh_D09G0059F	GACAGGTCGGGGTTGGTGAAAA
Gh_D09G0059R	TGTGCCTCCATCCACACGAAAC
Gh_D09G1044F	TTCCGATCTTAGCAGAACGGGC
Gh_D09G1044R	CGTACTTCAGCAGGTATGCCCC
Gh_D09G2222F	GGGGCATATCATGTTGCCGTCT
Gh_D09G2222R	TGTCCTAGTCTTCCGTTTGCACC
Gh_D10G1050F	GTACAAATGGACAGCTCGGGCA
Gh_D10G1050R	CTATCTGTTGGCCACTCGAGCC
Gh_D10G1907F	GAGGTTTTCTCTTGGGGAGCCG
Gh_D10G1907R	AAATTGCCTGAGCTACCACCCC

Gh_D10G2310F	TCAGCTTGGTCTTGGTGACGTG
Gh_D10G2310R	CGCATGCGATGTTTTTCGGACT
Gh_D11G0331F	GGGCGATGGGGAAAGCCTAAAT
Gh_D11G0331R	CGGCAGTACGCTGTCCTGATAC
Gh_D11G1503F	CGCAGAGTTGAAGCACTTGCAG
Gh_D11G1503R	TCGGCTGAATAACCCCAGCCTA
Gh_D11G1630F	GCTAGGCAGAGGCGTTACTTCC
Gh_D11G1630R	CACAAGCTCAGGAGCCTCATCC
Gh_D11G1664F	TGTTATTGCTTGGGGCTCAGGTGAAG
Gh_D11G1664R	AACAACCTTGCCATCATCACAAATAG
Gh_D11G1726F	GCAAGCCTTGTCGCGTTTGTA
Gh_D11G1726R	TCTGTGAGACTGAGGCGTCGAT
Gh_D11G2263F	GTTGCAGCTGGGTTGTTGCATT
Gh_D11G2263R	GCATGGTTGCTTTCTTGGCCTC
Gh_D11G2399F	ATTCGAAGGCTTCTAGCGGCTG
Gh_D11G2399R	AGATGACCGAAATGCAGAGCCC
Gh_D13G0764F	AGGCGATTAAAGGAGGTCAGTGC
Gh_D13G0764R	TGTTGGAAGTCTGTTAGCCGCC
Gh_D13G1736F	GCAGCAGAGTGTCTAGTGGAGC
Gh_D13G1736R	GAACATCTGGTGATGCGCTTGC
uvr8-1-LP	TTTGAATATCTCGCTCGATCG
uvr8-1-RP	GGAAACTCGATTAAAGGCCAG
uvr8-2-LP	TTCCAGATCGGATGAAACAAG
uvr8-2-RP	CTTACGAGGAGGAGCCGTAAC
UVR8-RT-U	CTTCCGTTGGATTCTGAAGGT
UVR8-RT-L	ACACAGTTTACAACGCCCAT
LBb1.3	ATTTTGCCGATTTTCGGAAC
A05G3863-RT-U	AAACTCTGGCCATCCAGACTCG
A05G3863-RT-L	AAGCCGACACTTTCCCATTGCT
D05G1179-RT-U	GCAGAGTCCTTTGGGCTCAAGT
D05G1179-RT-L	TGACACCCCATTAGCCAAAGCC
A13G1619-RT-U	TATAGGCCACGATTGCGCTCAC
A13G1619-RT-L	GTGCCTGTCATGCTTAAACCGC
D06G0402-RT-U	GGTGCCACCTTTTCTGAGGTCG
D06G0402-RT-L	AGGCAACCATCAGCGTGAAACT
A02G1698-RT-U	ACTCAAAGGCACCGTCTTGGAC
A02G1698-RT-L	TGCACTTCTCTCTTTTGCCGCT
A13G1883-RT-U	CGCGAAATCGGTTTCGGGTTTTTC
A13G1883-RT-L	CTTCAAGCCCCATGCTTCCACT
D03G0021-RT-U	AAGAGTAGGTGGCGCGAATCAC
D03G0021-RT-L	CAACGGGAAGATGTCCTCTGGC
D06G0402-RT-U	GGTGCCACCTTTTCTGAGGTCG
D06G0402-RT-L	AGGCAACCATCAGCGTGAAACT
A05G2107-RT-U	TGAGGCTTGCTAGGACCGAAGA

A05G2107-RT-L	CTGCGCGAGTGTAGACAAGGTT
D05G2362-RT-U	ACCTTGTCTACACTCACGCAGC
D05G2362-RT-L	GCCACCAAGCAGGTCCTCATAG
D10G1386-RT-U	GTGGCAGTGGCAGTGAAGTGTA
D10G1386-RT-L	AGTATGCAACACAGTGGGCGTT
Gh_A05G3028-CDS-U	acgggggacgagctcggtaccATGAACGGAGAAGGAAAAAAAAAGC
Gh_A05G3028-CDS-L	gcccttgctcaccatgtcgacGCTGGCTGACTCAGCCAGAA
Gh_D10G2310-CDS-U	acgggggacgagctcggtaccATGAATGGAGAAGGAAAAGAAAGT A
Gh_D10G2310-CDS-L	gcccttgctcaccatgtcgacGGTGGGTGATTGAGCCAGAAAG

Table S6 All primers used in the VIGS experiment.

Primers noun	Primer sequences
Gh_A05G3028-CDS-U	acgggggacgagctcggtaccATGAACGGAGAA GGAAAAAAAAAGC
Gh_A05G3028-CDS-L	gcccttgctcaccatgtcgacGCTGGCTGACTCAG CCAGAA
Gh_D10G2310-CDS-U	acgggggacgagctcggtaccATGAATGGAGAA GGAAAAGAAAGTA
Gh_D10G2310-CDS-L	gcccttgctcaccatgtcgacGGTGGGTGATTGAG CCAGAAAG
A02G1698-RT-U	ATTCTGGTGCTCCAGTTTGG
A02G1698-RT-L	ACGTTTCAGGTATGCGTTCTC
A05G2107-RT-U	TCAAGGACGCCAAATTCCAA
A05G2107-RT-L	ACCTTAACCCATGTCCGGTA
A13G1619-RT-U	ATTGGAGAGCCTCTTCCTGA
A13G1619-RT-L	CACATCGTCAATCTCAAACACC
A13G1883-RT-U	ACAAATTAGGAACATTTTGGCCT
A13G1883-RT-L	GCCTTGTTGCTTTGCCTAAA
D03G0021-RT-U	ATGGAGCTATTTTGGATGCAGT
D03G0021-RT-L	AACTGGAGCACCAGAATTGG
D05G1179-RT-U	AGAGTCCTTTGGGCTCAAGT
D05G1179-RT-L	TTTGCTACAACCTGACACCCC
D05G2362-RT-U	GAGGATCGAAGGGGAAGAGT
D05G2362-RT-L	AACTCACTCTGCGTTGTCTC
D06G0402-RT-U	TGTAGGACAGTTTCACGCTG
D06G0402-RT-L	GTCGACATAGGGACTGATGC
D10G1386-RT-U	GTTGAAGAGGTGGTGACAGG
D10G1386-RT-L	CTGGAACCTACGTTCTCTGGC