SUPPLEMENTAL MATERIAL

Table S1. Set of transcripts down- and up-regulated in Arabidopsis cell cultures under 30 min of HL stress (adjusted p-value < 0.05). (.xls)

Table S2. GO Biological process terms significantly over-represented in the list of 403 up-regulated transcripts in ACSC under HL stress. (.pdf)

Table S3. Transcription factors up-regulated in ACSC under HL stress. (.pdf)

Table S4. List of transcripts up- and down-regulated in ACSC under HL together with their resulting co-regulated transcripts when compared to key selected Arabidopsis plants (xls)

Table S5. Pearson's correlation between different treatments. (.pdf)

Table S6. Transcripts and their corresponding primers designed for both monitoring ROS-mediated responses in ACSC under HL stress (first four rows) and RT-PCR validation of DNA microarray experiments. (.pdf)

Figure S1. Oxygen evolution rates of ACSC after the HL treatment. LL, control ACSC; HL, ACSC exposes to HL (1,800 μE m^{-2} s^{-1}) for 30 min in the glass vessel and oxygen evolution measured at 300 μE m^{-2} s^{-1} in the oxygen electrode chamber after the treatment; and HL*, ACSC exposes to HL for 30 min and oxygen evolution measured at 1,800 μE m^{-2} s^{-1} in the oxygen electrode chamber after the treatment. (.pdf)

Figure S2. PCA plot of the microarray experiments: ACSC under control (50 μE m^{-2} s^{-1}), 1-h dark and HL (1,800 μE m^{-2} s^{-1}) conditions. (.pdf)

Figure S3. FatiScan over-represented biological processes in ACSC under HL stress. (.pdf)

Figure S4. Validation of the microarray experiments in ACSC under HL stress by RT-PCR. Selected transcripts showed statistically significant changes in expression under the assayed experimental conditions (adjusted *p*-value < 0.05), except the transcripts 2-OXO (At4g10500) and DEF (At2g43510) that did not show significant changes in expression. (.pdf)

Figure S5. Venn Diagrams representing the number of up-regulated transcripts in ACSC at HL that are co-regulated in the $^1O_2$ producing mutants *flu* and *flu*/over-tAPX (panel A) and the (apo)carotenoids deficient mutants *aba1* and *max4* (panel B). (.pdf)

Table S2. *GO Biological process terms significantly over-represented in the list of 403 up-regulated transcripts in ACSC under HL stress.*

Accession code	**Description**	**Adj. *p*-value**
GO:0010200	Response to chitin	4.565E-12
GO:0009743	Response to carbohydrate stimulus	8.727E-10
GO:0010033	Response to organic substance	1.876E-09
GO:0009723	Response to ethylene stimulus	2.717E-05
GO:0006970	Response to osmotic stress	4.517E-04
GO:0009414	Response to water deprivation	4.809E-04
GO:0009628	Response to abiotic stimulus	4.809E-04
GO:0009751	Response to salicylic acid stimulus	4.809E-04
GO:0009651	Response to salt stress	5.463E-04
GO:0009415	Response to water	5.818E-04
GO:0009725	Response to hormone stimulus	1.813E-03
GO:0009753	Response to jasmonic acid stimulus	2.291E-03
GO:0006355	Regulation of transcription, DNA-dependent	5.427E-03
GO:0006952	Defence response	5.427E-03
GO:0051252	Regulation of RNA metabolic process	5.490E-03
GO:0006351	Transcription, DNA-dependent	6.382E-03
GO:0009737	Response to abscisic acid stimulus	6.382E-03
GO:0009409	Response to cold	6.739E-03
GO:0009873	Ethylene mediated signalling pathway	6.739E-03
GO:0009626	Hypersensitive response	1.187E-02
GO:0034050	Host programmed cell death induced by symbiont	1.187E-02
GO:0009266	Response to temperature stimulus	1.503E-02
GO:0009755	Hormone-mediated signalling	1.532E-02
GO:0009863	Salicylic acid mediated signalling pathway	1.632E-02
GO:0000160	Two-component signal transduction system	1.637E-02
GO:0009611	Response to wounding	1.917E-02
GO:0009617	Response to bacterium	1.917E-02
GO:0007242	Intracellular signalling cascade	2.580E-02

Table S3. *Transcription factors up-regulated in ACSC under HL stress.*

Array element	**Gene ID**	**Transcription Factor (TF) Family**
		Redox sensitive
259992_at	AT1G67970	Heat shock TF A8
254592_at	AT4G18880	Heat shock TF A4A
248981_at	AT5G45110	NPR3 (NPR1-like protein 3); protein binding
		Zinc finger
251950_at	AT3G53600	Zinc finger (C2H2 type) family protein
252567_at	AT3G46070	Zinc finger (C2H2 type) family protein
266010_at	AT2G37430	Zinc finger (C2H2 type) family protein (ZAT11)
256356_s_at	AT1G66500	Zinc finger (C2H2-type) family protein
245711_at	AT5G04340	Zinc finger (C2H2-type) 6
265852_at	AT2G42350	Zinc finger (C3HC4-type RING finger) family protein
265853_at	AT2G42360	Zinc finger (C3HC4-type RING finger) family protein
247125_at	AT5G66070	Zinc finger (C3HC4-type RING finger) family protein
252474_at	AT3G46620	Zinc finger (C3HC4-type RING finger) family protein
246777_at	AT5G27420	Zinc finger (C3HC4-type RING finger) family protein
245329_at	AT4G14365	Zinc finger (C3HC4-type RING finger) family protein
256958_at	AT3G13430	Zinc finger (C3HC4-type RING finger) family protein
247708_at	AT5G59550	Zinc finger (C3HC4-type RING finger) family protein
257565_at	AT3G28620	Zinc finger (C3HC4-type RING finger) family protein
256093_at	AT1G20823	Zinc finger (C3HC4-type RING finger) family protein
251745_at	AT3G55980	Zinc finger (CCCH-type) family protein
254922_at	AT4G11370	RHA1A (RING-H2 finger A1A); zinc ion binding
254919_at	AT4G11360	RHA1B (RING-H2 finger A1B); zinc ion binding
262590_at	AT1G15100	RHA2A (RING-H2 finger A2A); zinc ion binding
258436_at	AT3G16720	ATL2; protein binding / zinc ion binding
259312_at	AT3G05200	ATL6; protein binding / zinc ion binding
252009_at	AT3G52800	Zinc finger (AN1-like) family protein
256185_at	AT1G51700	Dof zinc finger protein 1
255381_at	AT4G03510	Ring finger protein with membrane anchor 1

247655_at	AT5G59820	Responsive to high light 41 / zinc ion binding
257022_at	AT3G19580	Zinc-finger protein 2 / zinc ion binding
261648_at	AT1G27730	Salt tolerance zinc finger / zinc ion binding
251861_at	AT3G54810	Blue micropylar end 3-zinc finger
		WRKY DNA-binding protein
267246_at	AT2G30250	WRKY DNA-binding protein 25
255568_at	AT4G01250	WRKY DNA-binding protein 22
245976_at	AT5G13080	WRKY DNA-Binding protein 75
248611_at	AT5G49520	WRKY DNA-binding protein 48
249770_at	AT5G24110	WRKY DNA-binding protein 30
261892_at	AT1G80840	WRKY DNA-binding protein 40
267028_at	AT2G38470	WRKY DNA-binding protein 33
263783_at	AT2G46400	WRKY DNA-binding protein 46
254231_at	AT4G23810	WRKY DNA-binding protein 53
253485_at	AT4G31800	WRKY DNA-binding protein 18
249890_at	AT5G22570	WRKY DNA-binding protein 38
		RAV
260037_at	AT1G68840	Regulator of the ATPase of the Vacuolar membrane
		MYB
250858_at	AT5G04760	MYB family TF
245084_at	AT2G23290	MYB domain protein 70
246253_at	AT4G37260	MYB domain protein 73
246987_at	AT5G67300	MYB domain protein 44
260581_at	AT2G47190	MYB domain protein 2
253067_at	AT4G37780	MYB domain protein 87
257919_at	AT3G23250	MYB domain protein 15
247696_at	AT5G59780	MYB domain protein 59
257140_at	AT3G28910	MYB domain protein 30
252193_at	AT3G50060	MYB domain protein 77
		AP2
255742_at	AT1G25560	AP2 domain-containing TF, putative
263194_at	AT1G36060	AP2 domain-containing TF, putative
253259_at	AT4G34410	AP2 domain-containing TF, putative

259729_at	AT1G77640	AP2 domain-containing TF, putative
248448_at	AT5G51190	AP2 domain-containing TF, putative
259793_at	AT1G64380	AP2 domain-containing TF, putative
256009_at	AT1G19210	AP2 domain-containing TF, putative
261984_at	AT1G33760	AP2 domain-containing TF, putative
261327_at	AT1G44830	AP2 domain-containing TF TINY, putative
253405_at	AT4G32800	AP2 domain-containing TF TINY, putative
		ERF
257053_at	AT3G15210	Ethylene responsive element binding factor 4
266821_at	AT2G44840	Ethylene responsive element binding factor 13
257927_at	AT3G23240	Ethylene responsive element binding factor 1
245250_at	AT4G17490	Ethylene responsive element binding factor 6
245252_at	AT4G17500	Ethylene responsive element binding factor 1
248799_at	AT5G47230	Ethylene responsive element binding factor 5
261470_at	AT1G28370	Ethylene responsive element binding factor 11
252214_at	AT3G50260	ERF#011 cooperatively regulatated by ethylene and jasmonate 1
		NAC
261564_at	AT1G01720	Arabidopsis NAC domain containing protein 2
252681_at	AT3G44350	Arabidopsis NAC domain containing protein 61
249940_at	AT5G22380	Arabidopsis NAC domain containing protein 90
247351_at	AT5G63790	Arabidopsis NAC domain containing protein 102
252278_at	AT3G49530	Arabidopsis NAC domain containing protein 62
		DREB (Dehydration-responsive element binding)
250781_at	AT5G05410	DREB protein 2A
254075_at	AT4G25470	C-Repeat/DREB factor 2
255937_at	AT1G12610	DREB subfamily A-1 of ERF/AP2 TF family
261101_at	AT1G63030	DREB subfamily A-1 of ERF/AP2 TF family
248400_at	AT5G52020	DREB subfamily A-4 of ERF/AP2 TF family
260856_at	AT1G21910	DREB subfamily A-5 of ERF/AP2 TF family

Table S5. *Pearson's correlation between different treatments.*

Mutants or hormone treatments	**Correlation coefficient**	***p*-value**
	Light vs Dark	
flu vs Col-0	0,334	5,48E-09
flu/over tAPX vs Col-0	0,360	2,71E-10
aba1 vs Ler	0,443	2,22E-15
max4 vs Col-0	0,436	7,11E-15
ABA vs mock	-0,017	7,71E-01
SA vs mock	0,037	5,35E-01
Over- tAPX vs Col-0	-0,082	1,63E-01
ACC vs mock	0,106	7,19E-02
MeJA vs mock	0,080	1,72E-01
	flu vs Col-0	
aba1 vs Ler	0,443	2,22E-15
max4 vs Col-0	0,444	1,78E-15
	aba1 vs Ler	
max4 vs Col-0	0,831	2,20E-16

Table S6. *Transcripts and their corresponding primers designed for both monitoring ROS-mediated responses in ACSC under HL stress (first four rows) and RT-PCR validation of DNA microarray experiments.*

Gene ID	Name	Primers
At2g19760	Profilin (PROF)	F: 5´- CCAAGGTGAACAAGGAGCTG -3´ R: 5´- CAAGTTGCATTGACCTCCAG -3´.
At4g10500	2-oxoglutarate-Fe(II) oxidase (2-OXO)	F: 5´- TGCGTGTTCCACTTATGGTTTC -3´ R: 5´- ACTCTTTCGCTCTCGGGTTG -3´
At2g43510	Defensin (DEF)	F: 5´- GGCTATCGTTTCCATCTTCGT -3´ R: 5´- CCAACATCACCTCCGTATTCTT -3´
At5g64870	Nodulin2 (NOD)	F: 5´- GAGGTCTTCAAAGGAACAAAGGAG -3´ R: 5´- CTGCTTCACATTGGCGTTG -3´
At5g45340	CYP707A3; cytochrome P450, oxygen binding.	F: 5´- TCGGCGAAACATTCCAAC-3´ R: 5´- TCGAGATCATCACACATGGAC-3´
At4g11280	ACS6, 1-aminocyclopropane-1-carboxylic acid synthase 6.	F: 5´- CGGCGATGGTTTCTTAGTTC-3´ R: 5´- AGGCTTCCACCGTAATCTTG-3´
At3g25250	AGC2, Oxidative signal-inducible1, kinase.	F: 5´- AGGAAAATGCAATCGGAAAG-3´ R: 5´- TTGGATCATCACATTGTCTGG-3´
At5g63790	NAC102, NAC domain containing protein 102.	F: 5´- CGGAGATGTGCGTCAGAAC-3´ R: 5´- TCCGGTCTCTATGCGAGAAG-3´
At2g26190	CAL, calmodulin-binding family protein.	F: 5´- GACCTTTTTCAAGTCTTCCTTGG-3´ R: 5´- AACACGATCTCTTCCTCCAAAC-3´
At1g19180	JAZ1, Jasmonate-Zim-domain protein 1.	F: 5´- GCTTCTCACAGACGTGTAGTCG-3´ R: 5´- GACGTGAGTTGCCTAAAGTTCC-3´
At1g17380	JAZ5, Jasmonate-Zim-domain protein 5.	F: 5´- ATTCCAGTCTCGCGTTGC-3´ R: 5´- AGGTAGAGGGTTCGCCTTTG-3´
At3g55980	SZF1, Salt inducible Zinc finger family protein 1.	F: 5´- ACCCACCACAACACAATTCC-3´ R: 5´- TTGCTCTTTGGTCCACTGC-3´
At1g66090	TIR-NBS, disease resistance protein.	F: 5´- CCACGCTTTGACCTGTGTG-3´ R: 5´- GATCATGTTTGCCTCATCGTC-3´
At1g80840	WRKY40, WRKY DNA-binding protein 40.	F: 5´- TCTCACTATTGGCGTTACTCG-3´ R: 5´- CGAGAGCTTCTTGTTCTCAGC-3´

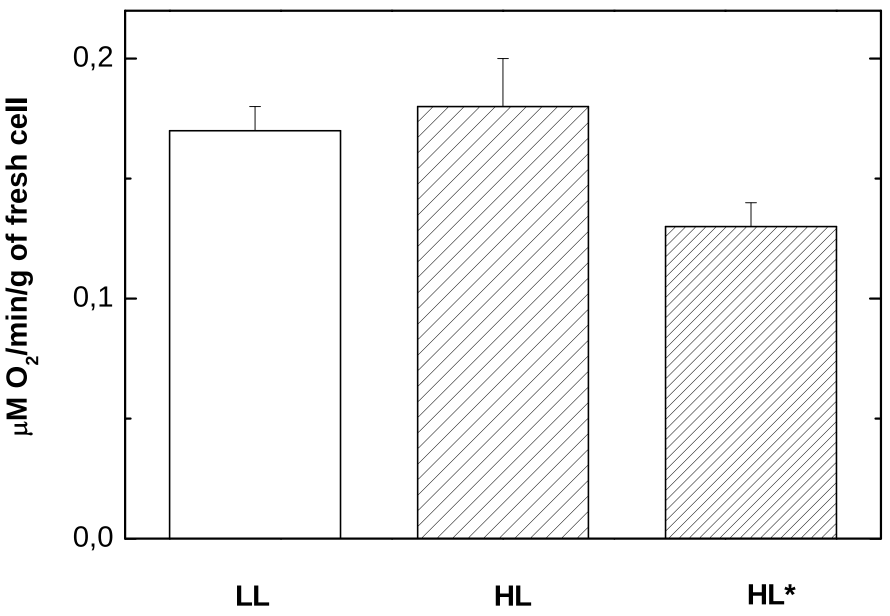

Figure S1. Oxygen evolution rates of ACSC after the HL treatment. LL, control ACSC; HL, ACSC exposes to HL (1,800 μE m^{-2} s^{-1}) for 30 min in the glass vessel and oxygen evolution measured at 300 μE m^{-2} s^{-1} in the oxygen electrode chamber after the treatment; and HL*, ACSC exposes to HL for 30 min and oxygen evolution measured at 1,800 μE m^{-2} s^{-1} in the oxygen electrode chamber after the treatment.

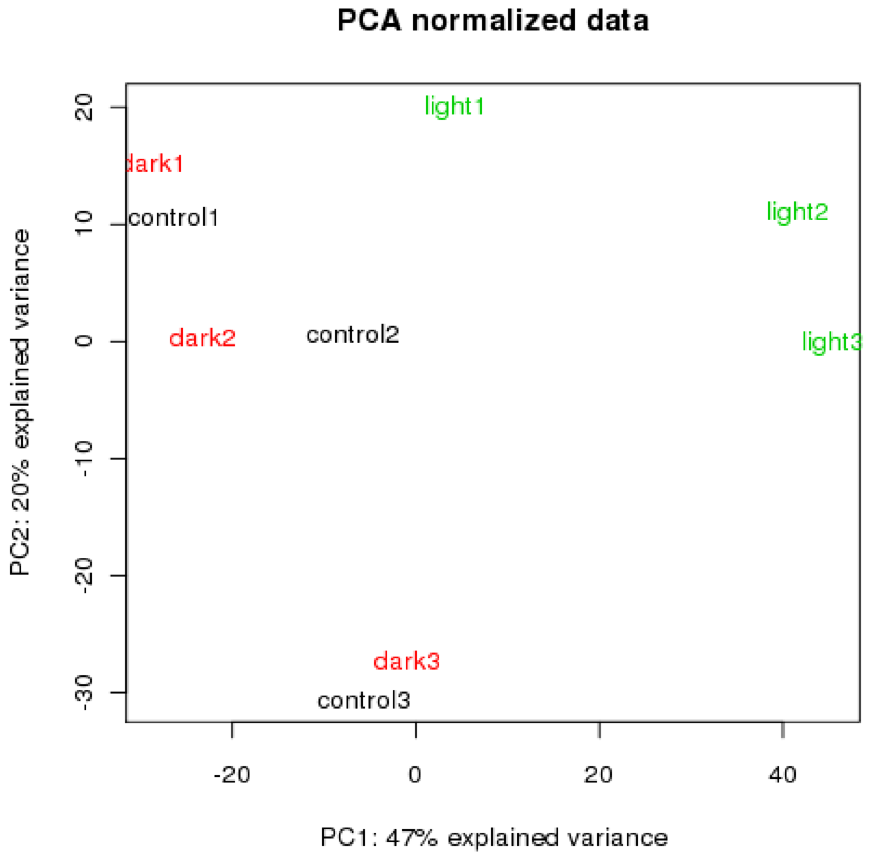

Figure S2. PCA plot of the microarray experiments: ACSC under control (50 µE m^{-2} s^{-1}), 1-h dark and HL (1,800 µE m^{-2} s^{-1}) conditions.

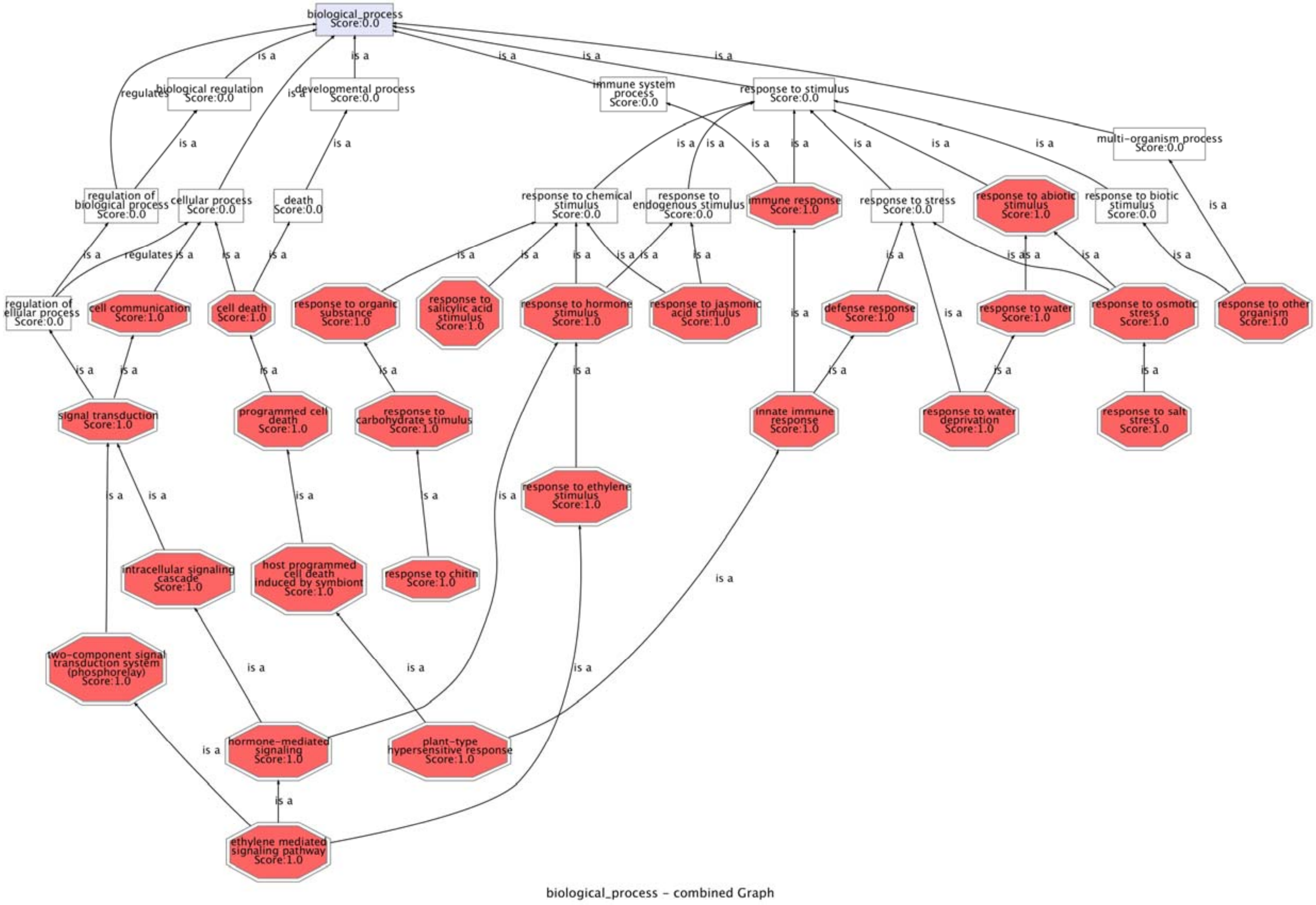

Figure S3. FatiScan over-represented biological processes in ACSC under HL stress.

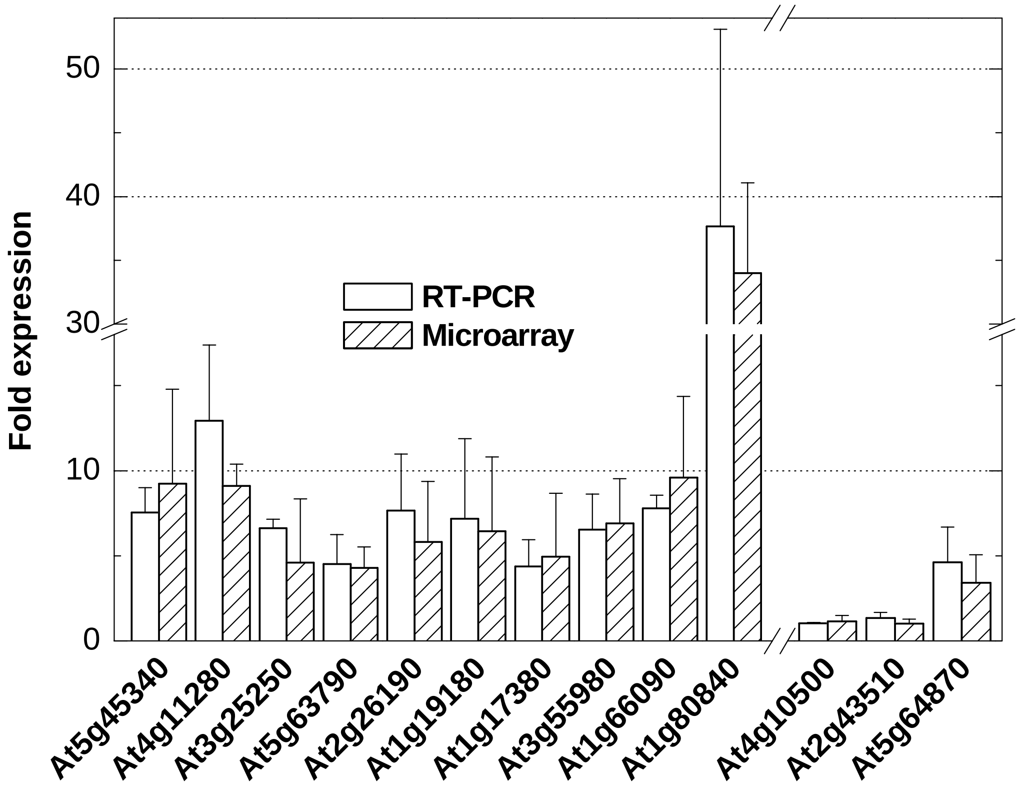

Figure S4. Validation of the microarray experiments in ACSC under HL stress by RT-PCR. Selected transcripts showed statistically significant changes in expression under the assayed experimental conditions (adjusted *p*-value < 0.05), except the transcripts 2-OXO (At4g10500) and DEF (At2g43510) that did not show significant changes in expression.

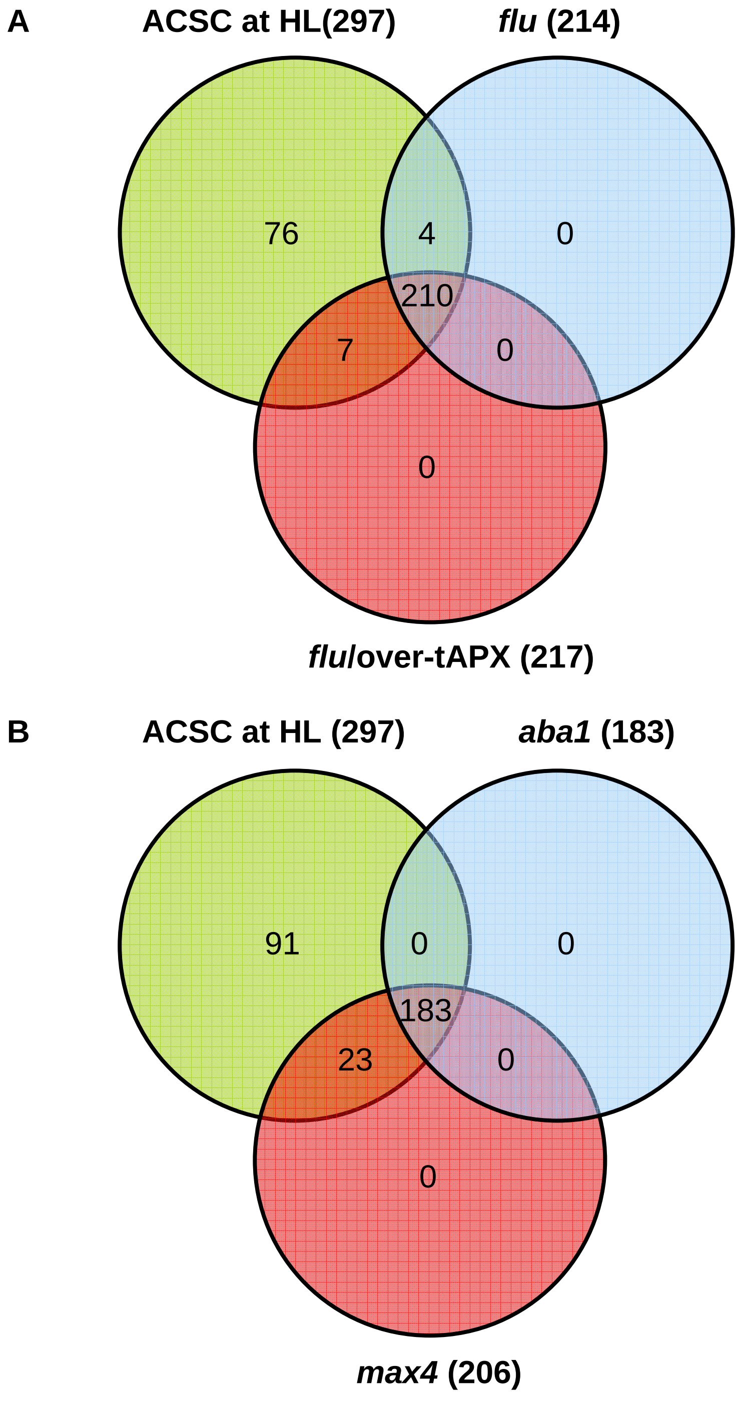

Figure S5. Venn Diagrams representing the number of up-regulated transcripts in ACSC at HL that are co-regulated in the $^1O_2$ producing mutants *flu* and *flu*/over-tAPX (panel A) and the (apo)carotenoids deficient mutants *aba1* and *max4* (panel B).