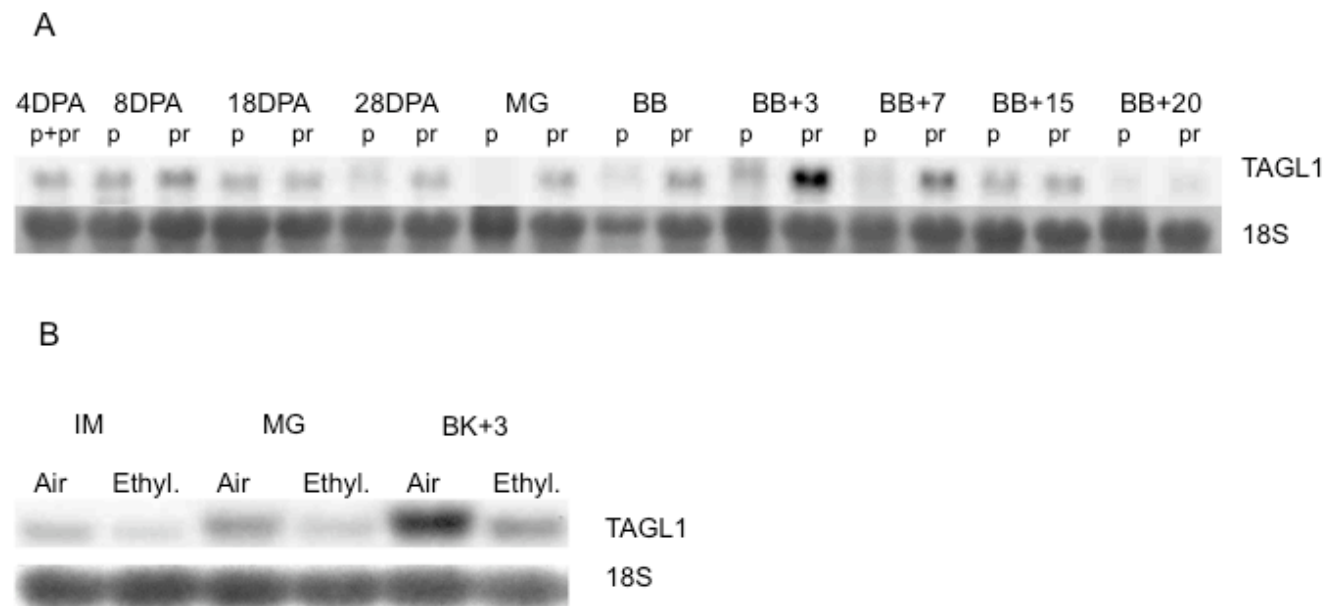


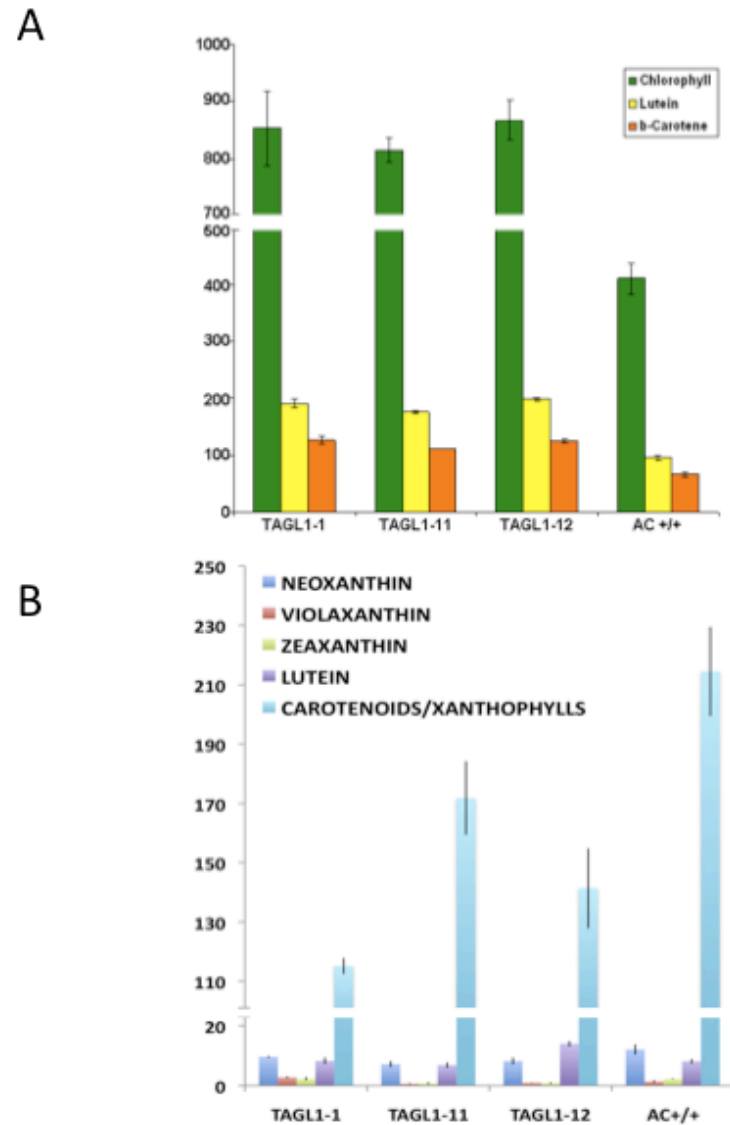
Supplemental Figure 1. *TAGL1* hybridization to tomato genomic DNA. Wild-type tomato genomic DNA (Ailsa Craig) was digested with the indicated six restriction enzymes and the resulting DNA gel-blot hybridized to a probe representing the *TAGL1* RNAi sequence. The *TAGL1* probe sequence includes an internal *DraI* restriction site that explains 2 bands in the *DraI* lane.



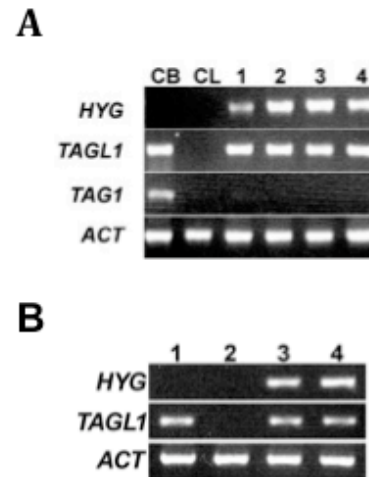
Supplemental Figure 2.

Total RNA gel-blot analysis of *TAGL1* and *18S* rRNA (control)

- A.** Expression of the *TAGL1* gene in pulp and pericarp of developing tomato fruit . Total fruit RNA isolated from pulp (p) and pericarp (pr) was analyzed via gel-blot analysis from the wild-type cultivar Ailsa Craig at the indicated fruit stages. Only at the 4 days post-anthesis stage (4DPA) was RNA isolated from the whole fruit (p+pr) due to the difficulty in separating the tissues at this young stage.
- B.** Expression of the *TAGL1* gene in response to exogenous ethylene treatment. Total RNA was isolated from from wild-type cultivar Ailsa Craig fruit at IM (immature stage, 28DPA), MG (mature green) and BK+3 (3 days post-breaker) treated with air or 20ppm ethylene (Ethyl).



Supplemental Figure 3. Chlorophyll and carotenoid accumulation in sepal and petals of *TAGL1* repressed lines. Three individual pools of separated anthesis stage sepals and petals were harvested and frozen in liquid nitrogen. All values reflect percentages of non-transformed controls and are derived from duplicate samplings of each of the three pooled samples for a total of six data points per sample. **A)** HPLC analysis of the major sepal pigments, chlorophyll, lutein and β -carotene. **B)** HPLC of the predominant petal pigments in addition to analysis of total carotenoids.



Supplemental Figure 4. *TAGL1* expression in *TAGL1* overexpression lines.

(A) *TAGL1* expression levels in *TAGL1* overexpression lines generated in the cultivar Microtom. RT-PCR in control buds at anthesis (CB), control leaves (CL) and leaves from four *35S::TAGL1* lines, of *HYG* (Hygromycin antibiotic resistance marker), *TAGL1*, *TAG1* and *ACT* (actin). *TAG1* levels are unaffected in the *35S::TAGL1* lines.

(B) Sepal expression at different stages. RT-PCR on control buds at anthesis (1), WT sepals (2), *35S::TAGL1* green sepals (3) and *35S::TAGL1* red sepals (4). In *35S::TAGL1* plants, *TAGL1* expression is consistently high in sepals throughout development.

Supplemental Table 1. List of species and accession numbers of coding regions used for phylogenetic analysis.

Species	Loci	Accession #
Asterids		
<i>Antirrhinum majus</i>	PLENA	S53900
	FARINELLI	AJ239057
<i>Petunia hybrida</i>	FBP6	X68675
	PMADS3	X72912
	FBP7	X81651
	FBP11	X81852
<i>Petunia inflata</i>	PAGL1	L33973
<i>Nicotiana tabacum</i>	NAG	L23925
	PLE36	U63163
<i>Solanum lycopersicon</i>	TAG1	L26295
	TAGL1	AY098735
	TAGL11	AY098736
	MBP3	TC156476
<i>Daucus carota</i>	DcMADS4	AJ271150
<i>Panax ginseng</i>	GAG2	Z46612
<i>Gerbera hybrida</i>	GAGA1	AJ009722
	GAGA2	AJ009723
<i>Helianthus annuus</i>	HaAG	AY157724
	HAM59	AY173068
<i>Chrysanthemum x morifolium</i>	CDM37	AY173059
<i>Ipomoea nil</i>	CDNA	AB006182
	CDNA2	AB006183
<i>Eustoma grandiflorum</i>	MADS1	AY522501
Rosids		
<i>Arabidopsis thaliana</i>	AG	X53579
	SHP1	M55550
	SHP2	M55553
	STK	U20182
<i>Brassica napus</i>	BnSHP1	AY036062
	BAG1	M99415
<i>Brassica rapa</i>	AG	AY162471
<i>Cucumis sativus</i>	CAG1	AF022377
	CAG2	AF022378
	CAG3	AF022379
	M1	AJ312773
<i>Rosa rugosa</i>	D1	AB025643
	C1	AB025644
	C2	AB025645
	C3	AB025646
<i>Rosa hybrida</i>	RAG	U43372
<i>Malus domestica</i>	MdMADS14	AJ251117
	MdMADS15	AJ251118
	MdMADS10	AJ000762
	AGL	AF401637

<i>Juglans regia</i>	JrAG	AJ313088
<i>Corylus avellana</i>	CaMADS1	AF027376
<i>Betula pendula</i>	BpMADS6	AJ252071
<i>Gossypium hirsutum</i>	AP3L	AY083173
	GhMADS2	AF538966
<i>Fragaria x ananassa</i>	STAG	AF168468
<i>Populus trichocarpa</i>	PTAG1	AF052570
	PTAG2	AF052571
	PtMADS43	EEE99912
	PtMADS51	EEE78119
<i>Momordica charantia</i>	McAG	AY178837
Vitaceae		
<i>Vitis vinifera</i>	VvMADS1	AF265562
	VvMADS5	AF373604
Caryophyllales		
<i>Silene latifolia</i>	SLM1	X80488
<i>Rumex acetosa</i>	RAP1	X89107
<i>Phytolacca americana</i>	PhaAG1	AY464093
	PhaAG2	AY464118
Saxifragales		
<i>Saxifraga caryana</i>	SxcAG1	AY464117
	SxcAG2	AY464116
<i>Liquidamber styraciflua</i>	LAG	AF103903
Sabiaceae		
<i>Meliosma dilleniifolia</i>	MdAG2	AY464105
Ranunculales		
<i>Ranunculales ficaria</i>	RfAG1	AY464114
	RfAG2	AY464115
<i>Helleborus orientalis</i>	HoAG1a	AY464109
	HoAG1b	AY464108
<i>Clematis integrifolia</i>	CliAG1	AY464113
	CliAG2	AY464112
<i>Aquilegia alpina</i>	AqaAG1	AY464111
	AqaAG2	AY464110
<i>Thalictrum dioicum</i>	TdAG1	AY464095
	ThdAGL2	Ay464094
<i>Berberis gilgiana</i>	BgAG	AY464106
<i>Akebia quinata</i>	AkqAG	AY464107
<i>Sanguinaria canadensis</i>	ScAG	AY464097
Magnoliales		
<i>Magnolia precossimina</i>	MpMADS2	AB050644

	MpMADS11	AB050653
Piperales		
<i>Saruma henryii</i>	SrhAG	AY464101
<i>Houttuynia cordata</i>	HtcAG	AY464096
<i>Asarum caudigerum</i>	MADS544	AJ419958
Chloranthaceae		
<i>Chloranthus spicatus</i>	CsAG1	AY464100
	CsAG2	AY464099
Liliales		
<i>Lilium longiflorum</i>	AG1	AY500376
	AG2	AY500377
	MADS2	AY522502
Asparagales		
<i>Phalaenopsis equestris</i>	PeMADS1	AF234617
<i>Hyacinthus orientalis</i>	HAG1	AF099937
	MADS1	AF194335
<i>Agapanthus praecox</i>	ApMADS2	AB079260
<i>Asparagus virgatus</i>	AVAG1	AB125347
<i>Crocus sativus</i>	AG1	AY555579
Poales		
<i>Hordeum vulgare</i>	HvAG1	AF486648
	HvAG2	AF486649
<i>Triticum aestivum</i>	WAG	AB084577
<i>Oryza sativa</i>	OsMADS3	L37528
	OsMADS13	AF151693
	RMADS207	AY551913
	RMADS206	AY551912
<i>Zea mays</i>	ZAG1	L18924
	ZAG2	L18925
	ZMM1	X81199
	ZMM23	AJ430637
	ZMM25	AJ430639
	AG	L81162
	MAF1	AY332475
Nymphaeales		
<i>Nymphaea sp.</i>	NymAG1	AY464104
	NymAG2	AY464103
	NymAG3	AY464102
Ginkgoales		
<i>Ginkgo biloba</i>	M5	AY114304
Cycadales		
<i>Cycas edentata</i>	AG	AF492455

Gnetales*Gnetum gnemon*

GGM3

AJ132219

Coniferales*Picea mariana*

SAG1

U69482

Pinus resinosa

MADS

AF006210

Supplemental Table 2. DNA Primer Sequences.

18SF

5'-CTGGTTGATCCTGCCAGTAGT-3'

18SR

5'GGTTGAGGTACGCAAACCTG-3'

35S2

5'-CCTCTATATAAGGAAGTTCATTTCA-3'

ACO1F

5'-ACCO1TGATCCAATTGCAAGTGCTTAG-3'

ACO1R

5'-TGATACATATGCAGCAAATCACA-3'

ACS2F

5'-GAGGTTTCGTAGGTGTTGAGAAAAG-3'

ACS2R

5'-GAACTAATGGTGAGGGAGGAATAG-3'

ACS4F

5'-CGATGATCAAACAATGGAGATCGCACTTG-3'

ACS4R

5'-CAATAATTTTGTGGCTCGCACTA-3'

ACT1

5'-GATGGATCCTCCAATCCAGACACTGTA-3'

ACT2

5'-GTATTGTGTTGGACTCTGGTGATGGTGT-3'

cLEG9L5For

5'-GCAGAACGCCAACATGTATCTA-3'

cLEG9L5Rev

5'-CATTCTTAATTAACAGATGACTGAAT-3'

CNRF

5'-CTGTCAATTCCCGGATTTCTAA-3'

CNRR

5'-ACCTCATAAAGTGAGTTGGAATGTC-3'

CYC-BF

5'- GGCTCAATTGACGTGATCA-3'

CYC-BR

5'- AGAGTGGTGAAGGGTCAACACA-3'

E4F

5'-ACCAGCAATATCTAGAGAAGGGTG-3'

E4R

5'-ATCATTGTCATGTTTATTCAAATTTAAAG-3'

E8F

5'-GAATAAGAATAATAATGTTATCTATTATTAC-3'

E8R

5'-ATGTAATATTATTTAATGTTTTAAACAAC-3'

HB1F

5'-GTTGTTTCATTGATGGAAAAGTTACA-3'

HB1R

5'-ACGACACTTATTTTCATCATACAAAGC-3'

HYG1-F

5'-GTTGCGTCCGTCATCTACTCTATTC-3'

HYG1-R

5'-TCGGCTCCAACAATGTCCTGAC-3'

LSUF

5'-ATAATTGACAAGAACGCAAAGATAGG-3'

LSUR

5'-GTTTCATCAAGTCCAAGAAAGTGAAT-3'

LYC-BF

5'- CGAAATCCATGTTGATATGCAA-3'

LYC-BR

LCY-B Rev 5'- GAACAAGAGATCTAGAGAAGCCAG-3';

NRF

5'-AGGTAACATTTGGATTGAGAGTGAGG-3'

NRR
5'-CTCCAGTACTCACTTTACGAGCATTG-3'

PG2AF
5'-ACAAACTTTCCATGTGAAGGAATTA-3'

PG2AR
5'-TATACAAAAGAGCTTCATCCTCTGAA-3'

PGMF
5'-AAGTTAATAAAGGGAATCCGTTTCTGAA-3'

PGMR
5'-ACATTTCAAACCTCCAGACAGAAGAGT-3'

PSY1F
5'-TCAGAATGTCTGTTGCCTTGTTA-3'

PSY1R
5'-TGGTAGATCTCAGTTGCCTCTTC-3'

RINF
5'-ATTCATCATTGAGGCAAATTAGGT-3'

RINR
5'-ATACTCCAAATTCAAAGCATCCAT-3'

SAIF
5'-TATGGTAGTTCAGTACCTGTGTTGGA-3'

SAIR
5'-TGCATATATTTGCTGAGCTTTCTTAG-3'

SSYF
5'-GTCGGATTTAATGTTCCAGTTTCTC-3'

SSYR
5'-TGTATCTCGTTTGCATTTTTACTTGA-3'

SHP1FL-F
5'-AGTCATCTAGAATGGAGGAAGGTGGGAGTAG-3'

SHP1FL-R
5'-TGCATGGATCCTTACACAAGTTGAAGAGGAG-3'

SHP2FL-F

5'-AGTCATCTAGAATGGAGGGTGGTGCGAGTAA-3'

SHP2FL-R

5'-TGCATGGATCCTCAAACAAGTTGCAGAGGTG-3'

TAG1-F

5'-AGCTCTTGCTGGAATGAAAC-3'

TAG1-R

5'-AAGCTCATGATAGTTTGATG-3'

TAGL1-F

5'-GCATTGGGCAGTTTAAGCCC-3'

TAGL1-R

5'-TCGCGACGAGAGTAATGAGG-3'

TAGL1FLFB1

5'GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGTTTTTCCTATTAATCA-3'

TAGL1FLR-B2

5'GGGGACCACTTTGTACAAGAAAGCTGGGTCTCAGACAAGCTGGAGAGGAG-3'

TAGL1FL-F

5'-AGTCATCTAGAATGGTTTTTCCTATTAATCA-3'

TAGL1FL-R

5'-TGCATGGATCCTCAGACAAGCTGGAGAGGAG-3'

TAGL1FLF0

5'-ATGGTTTTTCCTATTAATCA-3'

TAGL1R7

5'-CTTAATACGACTCACTATAGGGCATTGCTCTTGCTCTCT-3'

TAGL1UR7

5'-CTTAATACGACTCACTATAGGGGCATATTATTTATATAAGGC-3'

TDR4F

5'-AGAGGTGGCACAGCAAATC-3'

TDR4R

5'-GCATGTCTTTGAAAGCAAGTACAC-3'