

GENETICS

Supporting Information

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Contributions of Flowering Time Genes to Sunflower Domestication and Improvement

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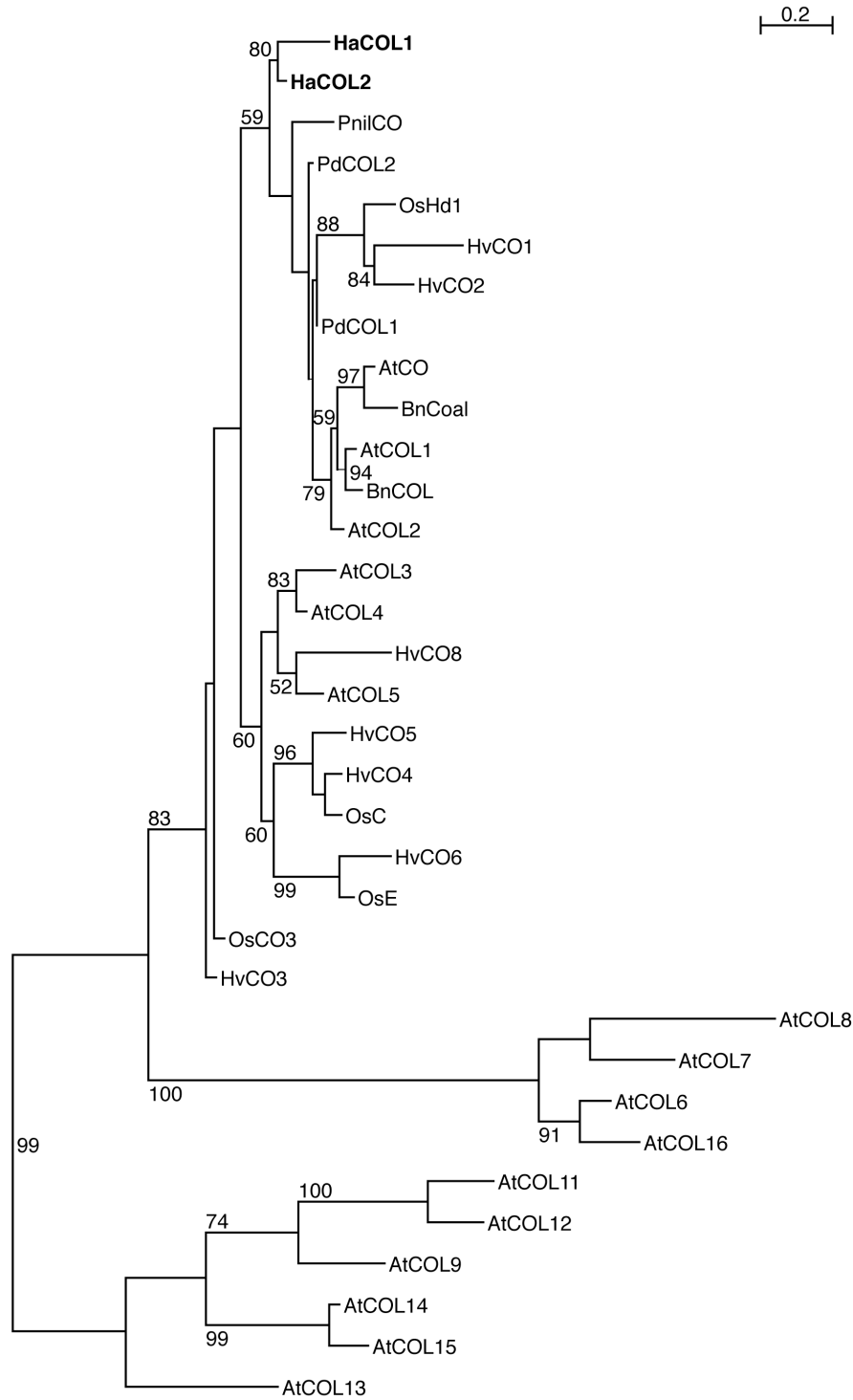


FIGURE S1.—Sunflower COL homologs cluster with the CO-COL1-COL2 clade. The maximum-likelihood phylogeny was constructed with PHYML using the concatenated B-box domains and CCT domains of COL genes from several species and the two full-length COL genes isolated from sunflower (bold). Numbers refer to percent bootstrap support for branches with greater than 50% support. Genes are listed according to the nomenclature in GRIFFITHS 2003 and BOHLENIUS *et al.* 2006.

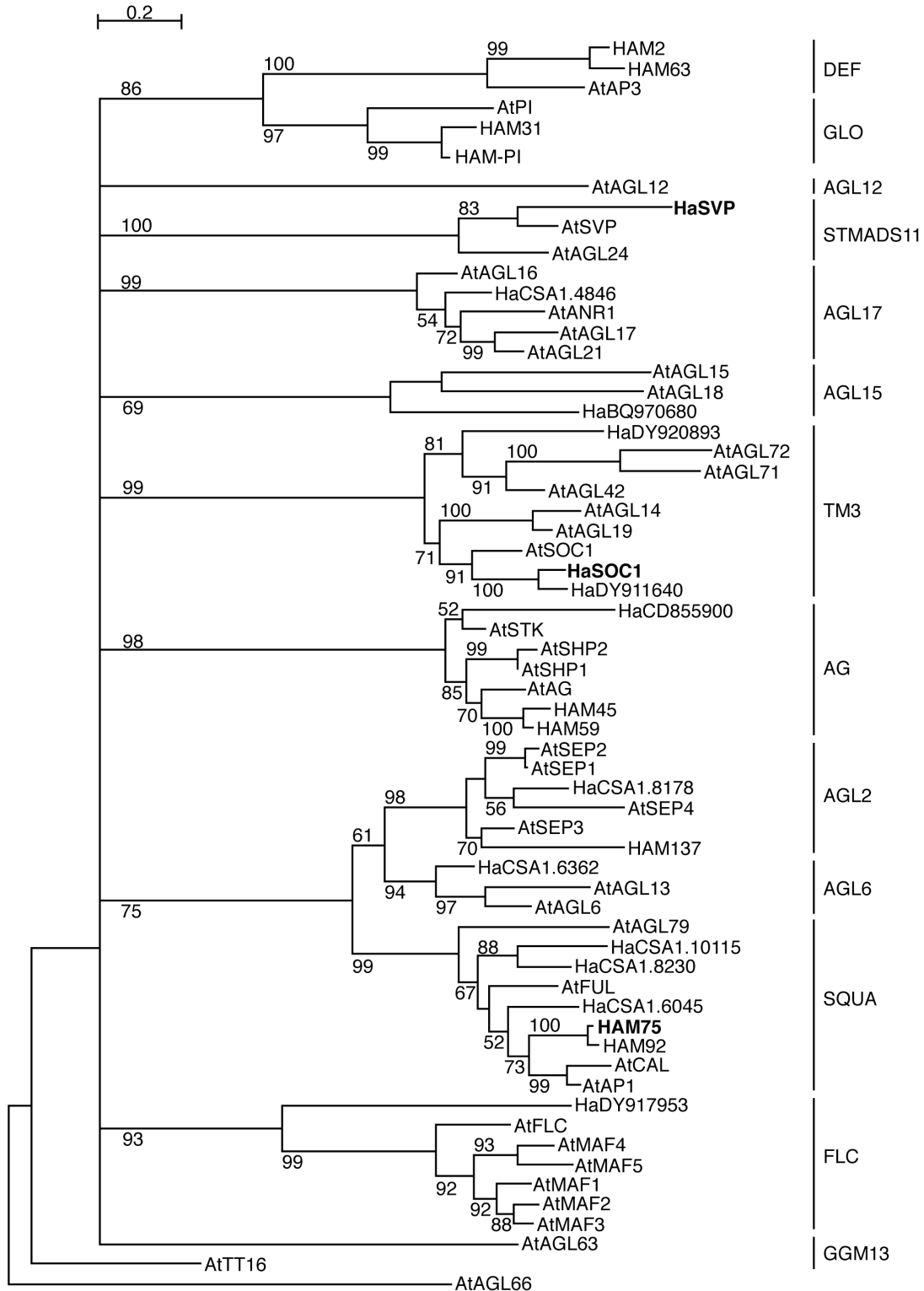


FIGURE S2.—Sunflower Type II MADS-box homologs cluster with all major MADS-box clades. The maximum-likelihood phylogeny was constructed with PHYML using the M, I, and K domains of all known *A. thaliana* (At) type II MADS-box genes and all *H. annuus* ESTs with top BLAST hits to type II MADS-box BLAST hits and complete sequence for these domains. Numbers refer to percent bootstrap support for branches with greater than 50% support. Major clade divisions denoted on the right are listed according to the nomenclature in BECKER and THEISSEN 2003.

FILE S1**Extended Materials and Methods**

Phylogenetic analysis: Few *H. annuus* *CONSTANS*-like (*COL*) ESTs had top BLAST hits to *CO*, *COL1*, or *COL2*, members of the *CO*-containing clade of the *COL* family; however, two full length sequences, *HaCOL1* and *HaCOL2*, obtained from degenerate PCR and BAC library screens match these genes as top hits in a BLASTx search. Of the ESTs that did match a member of this clade, most are identical to *HaCOL2* (Table S5). One of the two exceptional reads contains a short, incomplete CCT domain without convincing *COL* sequence to either side, suggesting this is not a functional *CO* copy. Comparison with *HaCOL2*-like hits from other sunflower libraries suggests the other EST may be a natural variant introduced by hybridization rather than a paralog. Hence, *HaCOL1* and *HaCOL2* appear to be the only members of this clade identifiable from available sequence. To verify *HaCOL1* and *HaCOL2* belong to the *CO-COL1-COL2* clade, all full length *COL* homolog protein sequences from *A. thaliana* and *COL* homologs clustering within the *AtCO-COL5* clade from *Oryza sativa*, *Hordeum vulgare*, *Populus deltoides*, *Pharbitis nil* and *Brassica napá* were aligned with *HaCOL1* and *HaCOL2* using MUSCLE. An edited alignment of the two B-box domains and the CCT domain was produced for phylogenetic analysis. Additional *H. annuus* *COL* homologs were found in the EST assembly, but as none of these contigs or reads contained both B-box domains and the CCT domain, they were excluded from phylogenetic analysis. GenBank accession numbers for these partial *COL* homologs are listed in Table S5.

For the MADS-box phylogeny, the *H. annuus* EST collection BLASTx report was searched by locus ID number. EST contigs in the *H. annuus* assembly whose top BLAST hit was to a type II MADS-box gene and that contained the full M, I, and K domain sequences were included in the phylogeny. GenBank accession numbers for those ESTs included and excluded from the phylogeny are listed in Table S6. Though some excluded sequences likely represent additional MADS-box genes, they may also correspond to unassembled portions of included sequences. An alignment of the M, I, and K domain protein sequences of all *A. thaliana* type II MADS-box genes and *H. annuus* type II MADS-box gene orthologs was then generated with MUSCLE. PHYML v3.0 (GUINDON and GASCUEL 2003) was used to construct maximum-likelihood phylogenies from these alignments assuming the LG substitution model with 4 substitution rate categories and 500 bootstrap replicates.

SUPPORTING REFERENCES

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TABLE S1**Primers**

Gene	Direction	Sequence
<i>Mapping</i>		
HaFT1	Forward	ACGGCCAACAGAATCAATCCCAAG
	Reverse	CACGCTGGCAGTTGAAGTAG
HaFT2	Forward	ATATTCCC GCGACCACTGGAGCACGTTTTGG
	Reverse	CCAGGAAAGACAATATTTTTACTATTAATTAGATGTAG
HaFT3	Forward	TCTCCGTGTCTCCTATCATTGCC
	Reverse	CCAAGGTAGCAAGCGTTGAGCATT
HaFT4	Forward	TTGCGGAGCTCTACAACCTTGGAT
	Reverse	TATAGCCTCCGTTGCCACAGACTA
HaTFL1	Forward	AATTAACTAACAATCATGCATCCCATCG
	Reverse	CCTGTGAATTCCCTATGTTTGGCCTTGG
HaCOL1	Forward	TCCACGTGTCACTCCCTTGATTCT
	Reverse	TTGTGCCTGGAGGAGAGTTTGTTG
HaCOL2	Forward	TGTAATGGGCTTGGGTGTGG
	Reverse	ACTATCCGCATCCGCATACG
HaGI1	Forward	TTCCGGATACTTTCCCAACCTGCT
	Reverse	TTAAGCCGTACGCAGCTTCCCATA
HaGI2	Forward	CAAACACAAACGATGCGAAGCAGG
	Reverse	GCCAACTCAGAAGCATTAAACGGG
HaCDFL1	Forward	CGATATGGGCTACGTTGGGAATCA
	Reverse	CATGCAACACATACACCTTTGCGG
HaPHYB	Forward	TTCCGGCACATGCTCAGTCCTAAA
	Reverse	AATATGGTTCGCCATTACCCCTCC
HaPHYC	Forward	CGATATGTTGACCCGTCTCCGAAT
	Reverse	GCTGTTCTCCACACAACCTCTGATTCC
HaCRY1	Forward	TGGTACGAGAACCAATTCAGCGAG
	Reverse	AGTTTGGGAGAGTTGCCCTCCAGTT
HaCRY2	Forward	AATGCCCTATGTCTGTTCTCCA
	Reverse	CCAGCAGCCTGTTTCAGTTTCTTA
HaZTL	Forward	ACTTTATCAGTGTACGGTGGTTCGG
	Reverse	AGCATCCATTCCCTCACCGGTTTGA
HaFKF1	Forward	AAAGCTAGTGGTTTCAGGTGGGTG
	Reverse	AACCCATTCTTCACCTGTGTGACC
HaSOC1	Forward	TAGGAGCAACCACCATTTGACGAAC
	Reverse	AGGGAGAAAGCCTTCGCCAACATA
HAM75	Forward	AGGGAAAGGCCATACAGGAGCAA
	Reverse	AAGGAAAGCACCTCATGTGGCAAG
HaLFY	Forward	CAGATTCGCTCTCATCGAGCTTGT

	Reverse	AACACCTCCTCTAACCCACCAAGA
HaSVP	Forward	AGCCCATTATGTTGCTATAACCGA
	Reverse	CTAGCAACTCTGGCATGCTTGAAC
HaCPS	Forward	CTCAAGTGCTCTTCCCTGGAGAAA
	Reverse	AATCCAAACATCATCCTCGCCC
HaKO	Forward	AGCCTTCATCACAGCTTCTCTCCT
	Reverse	ATACTCACTGCCATGTGGGACCAA
HaGa2OX	Forward	CAACATGGTGACTGTTTCAAAGCCTC
	Reverse	GTAATCGGATTCGGGTTTGGCGTT
HaGID1B	Forward	TAGATGAACGAACACCCTACCC
	Reverse	ACCTCTTCAAACCAAACATCCA
HaSLY1	Forward	ACGAATCGAGAGAAGCGATAGCGA
	Reverse	AAACTGTTGGCGAATATCGGCTGT
HaDELLA1	Forward	GCGCAATTGGCGGATACGATTCAT
	Reverse	TCTTCCATGGAGCCAACGTCTCAT
HaDELLA2	Forward	TCCGTAAAGTGTTATCGGCGGTGA
	Reverse	TCAACTCGGTGGTTTACTCCGAA
HaSPY	Forward	TAGATCCATGGGAAGGCTTG
	Reverse	CTTCCCATATGCGGGAACTA
HaFCA	Forward	GATAGGGCATACGCGCCTTACAT
	Reverse	GATAGGGCAATACGCGCCTTACAT
HaLD	Forward	AAACCAGCTAATCGCGGTCCACAA
	Reverse	AGCGGTTACAGGTGTCATGCTAGA

Full cDNA Amplification

HaFT1	Forward	CACCATGACGAGGGAGAGGGA
	Reverse	GCTTTC AATATGAGTTGATATAGTCGCCTC
HaFT2	Forward	CACCATGACGAGGGAGAGGGA
	Reverse	AGTCGCCTCTACCATTGACATGCCT
HaFT4	Forward	CACCATGCCGAGGGAACGGGACC
	Reverse	ATCTTACTCTTATCTCCTTCGTCCA
HaTFL1	Forward	GGCAAGAATGTCAGACCCCTCTTGTG
	Reverse	AGTTTCCCTCTGGCAGTTGAAGAAG
HaCOL1	Forward	CACCATGTTAAATGAAGATCTCACTAG
	Reverse	TTTGATCCGGAGCATTGCTTAAA
HaCOL2	Forward	CACCATGTTGGATCACACCGGTACCTTATG
	Reverse	CGTCTTTAAAACGAGGGTACAATTCC
HaCDFL1	Forward	ATGTCGGATCCCGCCATTAAGCTC
	Reverse	CATGCAACACATACACCTTTGCGG
HaPHYB	Forward	GCTCACGGGTCCAGAACCAAC
	Reverse	CTTGCTGTA ACTCTGGGCTTGC
HaFKF1	Forward	CGACGACGGTGATTACACCGATG

	Reverse	ACTTACCAACCAAAGCCCACGC
HaSOC1	Forward	CACCATGGTGAGAGGGAAGACTCAAATG
	Reverse	ACCATGCGTTTACTTTGGTCGTTG
HAM75	Forward	TGAAGATAGCTTGAGAGGGATGGG
	Reverse	GCCAAATAGTCATGAGCAAACACACC
HaLFY	Forward ¹	CAGATTCGCTCTCATCGAGCTTGT
	Reverse ¹	CCAAGTTTCTTGCTCTTCCGTTGC
	Forward ²	ATTCACGGCGGCGTTATCTTCTTG
	Reverse ²	CCCTCAAACGATCACCTAGAAATGCAG
HaCPS	Forward	CTCAAGTGCTCTTCCCTGGAGAAA
	Reverse	GGAGATATGGGCATTAATGGTCTTTGGG
HaSLY1	Forward	CTCACAAAGATCACCTGATCGGCAG
	Reverse	CCAAACATGAAACGAAATCAGCGAATTG
HaDELLA2	Forward	GTCCGTAAAGTGTTATCGGCGGTG
	Reverse	AATCCACCACCACCACTGAGTCAA
HaSPY	Forward	CATCACCAGCACCTGCTCTTTCTA
	Reverse	CCAGCCAGCCAACAACACTCAAAT
HaLD	Forward	GCGATGGAGGTGTGATGATCTTAG
	Reverse	TGGGCTGAACATGAGGTTTAGCG

Expression

HaFT1	Forward	CCTGATGCTCCAAGTCCAAGTG
	Reverse	CGCCTCTATCCATTGATCGACATGC
HaFT2	Forward	CCTGATGCTCCAAGTCCAAGTG
	Reverse	CGCCTCTATCCATTGATCGACATGC
HaFT4	Forward	TTGCGGAGCTCTACAACCTTGGAT
	Reverse	GGTGCAATATTTGCATGCCAGGGA
HaTFL1	Forward	TGATCCGTATCTCAGGGAGCACTT
	Reverse	CAGTTGAAGAAGACACCAGCGACA
HaCOL1	Forward	AGGCAGCCTCATGGCTCATATTTT
	Reverse	CTCCATACCTTTGCTGCTGCTGAA
HaCOL2	Forward	AACTCCAATCTTCCCAACACGAGC
	Reverse	CTCATCACCACCACCATCGTTTGA
HaCDFL1	Forward	CGATATGGGCTACGTTGGGAATCA
	Reverse	CATGCAACACATACACCTTTGCGG
HaPHYB	Forward	ACTCCATCGCCGAACAACAGATGA
	Reverse	CGGGCAAAGCCTGCAAGTTAGAAA
HaFKF1	Forward	CCGTTGGTGGATCCTGTTTGTGTT
	Reverse	CCAGCAGCACATGCACTGAAATTG
HaSOC1	Forward	TAGGAGCAACCACCATTGACGAAC
	Reverse	TGTTGCTTCATTCTCGTCTCTGGC
HAM75	Forward	AGGGAAAGGCCATACAGGAGCAA

	Reverse	AAGGAAAGCACCTCATGTGGCAAG
HaLFY	Forward	GCGGCGTTATCTTCTTGGTTCTGA
	Reverse	CCAAGTTTCTTGCTCTTCCGTTGC
HaCPS	Forward	CTCAAGTGCTCTTCCCTGGAGAAA
	Reverse	AATCCAAACATCATCCTCGCCC
HaSLY1	Forward	ACGAATCGAGAGAAGCGATAGCGA
	Reverse	AAACACTGGGCGAATATCGGCTGT
HaDELLA2	Forward	TCCGTAAAGTGTTATCGGCGGTGA
	Reverse	TCAACTCGGTGGTTTGA CTCCGAA
HaSPY	Forward	TAGATCCATGGGAAGGCTTG
	Reverse	CTTCCCATATGCGGGA ACTA
HaLD	Forward	AAACCAGCTAATCGCGGTCCACAA
	Reverse	AGCGGTTACAGGTGTCATGCTAGA
Ha60S rRNA	Forward	CGGCATGAAGAAGAAAGGAG
	Reverse	TATCAGCTCCAGCACACGAC

Molecular Evolution

HaFT1	Forward ¹	GATCCTGATGCTCCCAGTCCAAGTGACCCTAA
	Reverse ¹	GCCCTGGTGGGAAATGATAGGAAA
	Forward ²	AGAAACCCTTATCACCCAGACTCG
	Reverse ²	CAAACAGTCTTTGTGCGGGATCG
HaFT2	Forward	ACATGTGGCCATCACAAGAGAAAATAGTC
	Reverse	TATCTCCGTTGTCCACCAGATCCACTTTTCACG
HaFT3	Forward	TCTCCGTGTCTCCTATCATTGCCC
	Reverse	CCAAGGTAGCAAGCGTTGAGCATT
HaFT4	Forward	ATATTCCC GCGACCACTGGAGCACGTTTTTG
	Reverse ¹	TATAGCCTCCGTTGCCACAGACTA
	Reverse ²	GGTGCAATATTTGCATGCCAGGGA
HaTFL1	Forward	GATTGTCACAGATATCCCAGGCACAACG
	Reverse ¹	CAGTTGAAGAAGACACCAGCGACA
	Reverse ²	TTAATCTGCGGTGGTGTCTGTAGC
HaCOL1	Forward ¹	AGGCAGCCTCATGGCTCATATTTTC
	Forward ²	AAAGGTATGGAGGTTGCGATGCTG
	Reverse	AAATGAAGGGAAAGTGCAGGATCC
HaCOL2	Forward	TAAAAACTAGTACCACCTGGGCTCGCGTCTGC
	Reverse	ACTCATGGTTCTTCTGAACCGGCACCACACTA
HaCDFL1	Forward	TAACGGTCACCGAACCTGTTCTGG
	Reverse	CATGCAACACATACACCTTTGCGG
HaPHYB	Forward ¹	TGAGCAAAGCCATTGCCAGTACG
	Forward ²	GCTCACGGGTCCAGAACCAAC
	Reverse	TATCATCCTGAACCACACGAACCG
HaSOC1	Forward	CCAAGAACAGATTGAGCAACTACAAGC

	Reverse ¹	ACCATGCGTTTACTTTGGTCGTTG
	Reverse ²	GGTGGCCCGATGAATAGTTCAGTT
HAM75	Forward	AGGGAAAGGCCATACAGGAGCAAA
	Reverse	GCCAAATAGTCATGAGCAAACACACC
HaLFY	Forward	CGAGCTTGTTTAAAGTGGGACACTCG
	Reverse	GACAATCCGGCCAGCTAGTAAA
HaDELLA2	Forward ¹	TCCGTAAAGTGTTATCGGCGGTGA
	Forward ²	GCAGGAGGCCAATCACAATGGAAC
	Reverse	TCAACTCGGTGGTTTACTCCGAA
CGP41	Forward	TTCCGCCTGACAGAGAACCGTTAGATTGGAAC
	Reverse	CCACATTTTGTCTTCTGCAACAGCCCTTTCTC
CGP53	Forward	GGATCTTCAACACTTAATGGACCAAAGGAAGC
	Reverse	CCCAATACAATCATAGTTCATCGTACCCAACA
CGP62	Forward	TCTCTTCTCAAAGGACTCCCGTTAGATCTTCGTC
	Reverse	CTCCCCATCATGCATCGGTGAACACTCATAAT
CGP69	Forward	GGCATACTACCTCGAGAACTTTACCTTACCAATCTT
	Reverse	GATCATGTCCGTAAACGTAAAAATCAACCTC
CGP112	Forward	GATCTTCCAGAGAGACCTGAAGCCCCAGATTG
	Reverse	CCTCAGCAACTGGTATTGAGATGTCTTTTGGGT
PgiC	Forward	GATTCACCAGCTTCAAAAGGA
	Reverse	TATCTCTCCATACGGGTTTTTCC
SCR1	Forward	TTCACTTGCGAAACAAGCTC
	Reverse	GGAATCCTGTCTGCTGATAAGT

Ortholog Isolation

HaCOL2	Forward	GACTCTTGCTTCNCKRTCCAT
	Reverse	AAGCCGGCAYCAACGVGTNCC
HaGI	Forward	CGCCGCCGTGCARYTNGTNGA
	Reverse ¹	GAGGGGTGGCCACGAYDATYTCNNG
	Reverse ²	CGTAGGCGGCCTCCCADATNGT
HaSOC1	Forward	ACGATGGTGAGAGGGAAGACTCAA
	Reverse	TGCTGGTTCCTAATCCTTCTCCCA
HaLFY	Forward	ATGAGGGATGAGGAGCTTGATSANATGATGRA
	Reverse	GCTCCGTCACGATAAANGGRTGYT
HaTFL1	Forward	CCWGATKTTCWGGYCCTAG
	Reverse	CKNGCNGCNGTTTCYCTYTG

Overgo Probes

HaCOL1	Forward	TCCATGTCATCAATGGAAGTTGGA
	Reverse	TCGAATCAGGTACAACCTCCAACCTT
HaSOC1	Forward	TTGACGAACTAGTTCGGATTGAAC
	Reverse	CCCCTTAGCTGTTGTTCAATC
HaTFL1	Forward	CTGTCAATTGTCCACCTTCAAGGC

Reverse CGAGTGTGAAGCCATGCCTTGAA

¹ Primer used in first of two nested PCR reactions.

² Primer used in second of two nested PCR reactions.

TABLE S2**Diversity Panel**

Species	Type	GRIN ID	Line Name or Population Location
<i>H. argophyllus</i>	wild	PI 494571	Corpus Christi, TX
		PI 494572	North Padre Island, TX
		PI 494573	Port Aransas, TX
		PI 494580	Rachal, TX
		PI 494576	Skidmore, TX
		PI 494582	Victoria, TX
<i>H. annuus</i>	elite	PI 552943	RHA280
		PI 599984	HA821
		PI 534655	HA369
		PI 599768	RHA801
		PI 600000	RHA417
		PI 552937	HA292
		PI 578872	HA383
		PI 578873	HA384
		PI 607505	HA414
		PI 633744	HA434
		PI 599773	HA89
		PI 599759	RHA274
		PI 560141	RHA373
		PI 560145	RHA377
		PI 633746	RHA436
		PI 633748	RHA438
		PI 340790	USSR VNIIMK 8931 '66
		PI 650650	Ames7574, Mennonite
	landrace	PI 369357	Arikara
		PI 369360	Seneca
		PI 600717	Mandan #1
		PI 600718	Mandan #2
		PI 600719	Mandan #3
		PI 600720	Hidatsa #1
		PI 600721	Hidatsa #2
		PI 432504	Hopi dye
		PI 432505	Hopi
		PI 432507	Hopi dye
PI 432508	Hopi dye		
PI 432509	Hopi dye		
PI 369358	Havasupapi		
PI 369359	Hopi		

	PI 432510	Hopi dye, Possible hybrid w/Mammoth
	PI 432515	Zuni
	PI 432516	Pueblo
	PI 432521	Anzac Pueblo
	PI 432522	Laguna Pueblo
wild	-	Ann1238, Cedar Point Biological Station, NE
	PI 613750	Dickinson, ND
	PI 592325	Carievale, Saskatchewan
	PI 592316	Keeler, Saskatchewan
	PI 435434	Riviera, TX
	PI 435619	Tulsa, OK
	PI 494567	Skidmore, TX, Ann1811
	PI 468439	Colfax, ND
	PI 586879	Norden, NE
	PI 586872	Axtell, NE
	PI 435616	Topaz, MO
	PI 586869	Silver Creek, NE
	PI 586856	Great Bend, KS
	PI 586849	Colby, KS
	PI 613751	Minot, ND
	PI 613723	Crete, ND
	PI 613722	Onida, SD
	PI 613720	Garden City, KS
	PI 613711	Woonsocket, SD
	PI 592326	Boissevain, Manitoba
	PI 435505	McLoud, OK
	PI 468475	Childress, TX
	PI 597890	Yankton, SD

GRIN ID is the United States Department of Agriculture Germplasm Resources Information Network (<http://www.ars-grin.gov/npgs/>) identification number. Ann1238 lacks a GRIN ID because it was collected directly from the field by the Rieseberg laboratory.

TABLE S3**GenBank Accession Numbers of Deposited Sequences**

GenBank Numbers	Gene	Type of Sequences
GQ884199 - GQ884330	CGP53 (reference gene; homolog of ARABIDOPSIS THALIANA BASIC LEUCINE ZIPPER 11)	Diversity Panel Sequences
GQ884463 - GQ884584	HaFT1	Diversity Panel Sequences
GQ884585 - GQ884716	HaFT3	Diversity Panel Sequences
GQ884717 - GQ884848	PgiC (reference gene; homolog of phosphoglucose isomerase C)	Diversity Panel Sequences
GQ884849 - GQ884980	SCR1 (reference gene; homolog of SCARECROW)	Diversity Panel Sequences
GQ884982, GQ884985 - GQ884987	HaFT1 HaFT2	cDNA sequences from CMSHA89 and Ann1238
GQ884988 - GQ885119	CGP41 (reference gene; homolog of AVRPPHB SUSCEPTIBLE 1)	Diversity Panel Sequences
GU985570 - GU985602	HaCDFL1 HaFT4 HaDELLA2 HaLD HaTFL1 HaPHYB HAM75 HaCOL2 HaCOL1 HaSPY HaSLY1 HaFKF1 HaSOC1 HaLFY HaCPS	cDNA sequences from CMSHA89 and Ann1238
GU985603 - GU985734	HAM75	Diversity Panel Sequences
GU985735 - GU985866	HaCDFL1	Diversity Panel Sequences
GU985867 - GU985994	HaCOL1	Diversity Panel Sequences
GU985995 - GU986126	HaCOL2	Diversity Panel Sequences
GU986127 - GU986258	HaDELLA2	Diversity Panel Sequences
GU986259 - GU986390	HaFT2	Diversity Panel Sequences
GU986391 - GU986522	HaFT4	Diversity Panel Sequences
GU986523 - GU986654	HaLFY	Diversity Panel Sequences
GU986655 - GU986784	HaPHYB	Diversity Panel Sequences
GU986785 - GU986908	HaSOC1	Diversity Panel Sequences
GU986909 - GU987022	HaTFL1	Diversity Panel Sequences
HQ110110-HQ110241	CGP62 (reference gene; homolog of CYCLIC NUCLEOTIDE-GATED CHANNEL 15)	Diversity Panel Sequences
HQ110242-HQ110373	CGP69 (reference gene; homolog of PURPLE ACID PHOSPHATASE 17)	Diversity Panel Sequences
HQ119174-HQ110505	CGP112 (reference gene; homolog of HUA1, ENHANCER OF AG-4 1)	Diversity Panel Sequences

TABLE S4**Helianthus EST Homologs of Additional Flowering Time Genes**

Arabidopsis Homolog	Arabidopsis Locus ID	Helianthus EST GenBank No.
<i>Photoperiod Pathway</i>		
PHYA	AT1G09570	BQ972210
PHYE	AT4G18130	EE611610
PFT1	AT1G25540	BU024741
		BQ974631
		DY910393
PIF3	AT1G09530	DY923270
		DY911026
		DY904925
HRB1	AT5G49230	DY920842
		BQ913451
CDF2	AT5G39660	DY911777
CDF3	AT3G47500	EE607351
CDF4	AT2G34140	<i>DY952008</i>
COG1	AT1G29160	EE659292
FKF1	AT1G68050	EL476501
		EL434899
		EL445080
		BU017506
ZTL	AT5G57360	DY932673
		CD855990
HAP2	AT5G12840	DY908453
		DY920063
	AT3G05690	BQ967481
		BU033934
HAP3	AT2G38880	BU016847
HAP5	AT3G48590	CD856677
	AT1G08970	DY914636
SPA1	AT2G46340	EL453088
		EE623010
SPA2	AT3G15354	BQ970541
SPA3	AT4G11110	EE630648
SPA4	AT1G53090	DY910594
		DY910506
		DY908783
		DY910553
		CD850632

TEM1	AT1G25560	DY905119 DY926039 BQ969581 BQ967030
SPL3	AT2G33810	DY929182 DY931544
TEM2	AT1G68840	CD849387
LOV1	AT2G02450	BQ916716 DY916493 DY910914
TOE1	AT2G28550	DY909965 DY909961
EAT1	AT1G05010	DY922539 CX944177 DY916262 CD850275
LHY	AT1G01060	DY913209 DY914287
CCA	AT2G46830	CD848175 BQ965526
TOC1	AT5G61380	BQ974027 BU025860 DY904043 DY912807 BU034373 BQ973895
FIO1	AT2G21070	DY920550
LWD1	AT1G12910	BU035801 BU020029 BQ968231 BU021577
COP1	AT2G32950	BU027380 BU026944 BQ915272 BQ967989 BU023290 BQ970243
DDB1A	AT4G05420	BU026972 DY908636 DY912301 BU023259

ELF3	AT2G25930	BQ966029 DY903900
LUX	AT3G46640	EL511589
PRR3	AT5G60100	EE635242
PRR5	AT5G24470	DY910187
PRR7	AT5G02810	BU028622 BU028534 BU021703
RFI2	AT2G47700	EL437051
CIB1	AT4G34530	EL463586 EL438160

Meristem Integrators

PNF	AT2G27990	EL481516 EL476702 EE623441 EL451231 EL429724
TFL2	AT5G17690	CD852224
JMJ14		
/PKDM7B	At4g20400	EL413401
ESD7	AT1G08260	AJ829286
EBS	AT4G22140	DY905265 BU020442 CD851270 BQ973283 CX947634 CX947612
FPF1	AT5G24860	DY958609

Autonomous Pathway

FVE	AT2G19520	AJ828273 CD855546 CD850154
FPA	AT2G43410	DY910755
FY	AT5G13480	DY904264
FLK	AT3G04610	BQ971053 DY909732 AJ542175
PEP	AT4G26000	BQ965658 BQ914495

PCFS4	AT4G04885	DY923405 BQ914745 CX947821
REF6	AT3G48430	AJ541136
ELF6	AT5G04240	EE622836
ELF5	AT5G62640	EL418800 EE633730
Polycomb Repressor Complex		
CLF	AT2G23380	DY905029 CD850837
SWN/VRN2	AT4G02020	CX946827
FIE1	AT3G20740	DY922816
EMF2	AT5G51230	DY908914 DY906115 DY922629 CD848472
VIN3	AT5G57380	CD858176
VRN5/VIL1	AT3G24440	EL444144
VEL1	AT4G30200	BU025496
MSI1	AT5G58230	DY923649 BQ913261 AJ828574
<i>PAF1 Complex</i>		
SUF4	AT1G30970	EL428896 EE658922
EFS	AT1G77300	CD850476
VIP3	AT4G29830	EL483190
VIP4	AT5G61150	DY911214 CD855203
VIP5	AT1G61040	DY931343 BU035104
ELF8/VIP6	AT2G06210	BU020760 DY911981 DY914126 DY910652
ELF7	AT1G79730	BQ970281 BQ915613
ATX1	AT2G31650	EE609465

SWR1 Complex

SEF	AT5G37055	CD849314
ARP6/SUF3/E		
SD1	AT3G33520	EL468160
PIE1	AT3G12810	EL425321

Gibberellin Pathway

RGA	AT2G01570	DY907324
CPS	AT4G02780	CX946758 CX948036 CX947384
KS/GA2	AT1G79460	DY925509
KAO	AT1G05160 AT2G32440	CX946829 AJ828411 CX947222 CX947567
GA20ox1	AT4G25420	CX947223 AJ828967
GA20ox2	AT5G51810	EL453670 EE640462 EL442868
GA20ox3	AT5G07200	EL444081 EL485024 EE648243
GA2ox2	AT1G30040	EL513759 EL488304 EL469080 EL448153
GA2ox8	AT4G21200	EL478279 DY954684
GA4/GA3OX	AT1G15550	EE625309 EE634496
GA3OX3	AT4G21690	EL422626
GASA5	AT3G02885	AJ412428 DY930996
GID1A	AT3G05120	EL511883 EL491399
GID1B (additional)	AT3G63010	BQ969049 DY924616 BQ970168

		BQ912656
		BQ978706
		BQ911907
		DY908171
GID1C	AT5G27320	DY905340

TABLE S5**Sunflower COL Gene Sequence Information**

Helianthus CONSTANS- like ESTs	Arabidopsis BLAST hit	Arabidopsis Gene Name	GenBank Number(s)
<i>Partial Sequences Not Included in Tree</i>			
BQ976974	COL9	AT3G07650	BQ976974
CD846649	COL3	AT2G24790	CD846649
CD849374	COL2	AT3G02380	CD849374
CD858413	COL2	AT3G02380	CD858413 same as HaCOL2
CSA1.3680	COL5	AT5G57660	DY929758 DY930347
CSA1.4072	COL9	AT3G07650	DY926712 BU032963 AJ540183
CSA1.4663	COL16	AT1G25440	DY923642 BQ971647
CSA1.5019	COL16	AT1G25440	DY921697 DY910806 DY919231
CSA1.5270	COL4	AT5G24930	DY920421 CD847344
CSA1.6715	COL2	AT3G02380	DY912615 same as HaCOL2 DY914970
CSA1.6725	COL10	AT5G48250	DY912547 DY908417 BU028227
CSA1.983	COL6	AT1G68520	BU024636 BU024138
CX944001	COL5	AT5G57660	CX944001
DY905535	COL16	AT1G25440	DY905535
DY905611	COL6	AT1G68520	DY905611
DY908026	COL5	AT5G57660	DY908026
DY913661	COL9	AT3G07650	DY913661
DY913797	COL9	AT3G07650	DY913797
DY920911	COL10	AT5G48250	DY920911
DY925618	COL1	AT5G15850	DY925618

TABLE S6**Sunflower MADS-Box Gene Sequence Information**

MADS Genes	Arabidopsis BLAST hit	Arabidopsis Gene Name	GenBank Number(s)
<i>Complete Sequences Included in Tree</i>			
HAM - PI	AT5G20240	PI	AY157725
HAM137	AT1G24260	SEP3	AY173072
HAM2	AT3G54340	AP3	EF612597
HAM31	AT5G20240	PI	AY173069
HAM45	AT4G18960	AG	AY173067 AY157724
HAM59	AT4G18960	AG	AY173068
HAM63	AT3G54340	AP3	EF612598
HAM75	AT1G69120	AP1	AF462152
HAM92	AT1G69120	AP1	AY173071
BQ970680	AT3G57390	AGL18	BQ970680
CD855900	AT2G42830	SHP2	CD855900
CSA1.10115	AT1G69120	AP1	CD850624 DY917569
HaSVP (CSA1.10425)	AT2G22540	SVP	CD848608 CD848755 DY916321
CSA1.4524	AT5G20240	PI	DY924373 DY922330 DY924848 DY922807 DY920954 DY924317 DY921819 DY924932 DY917765 DY930490
CSA1.4846	AT3G57230	AGL16	DY922654 DY922206
CSA1.6045	AT1G69120	AGL7	DY916349 DY916807
CSA1.6067	AT2G45660	AGL20	DY916215 DY915850
CSA1.6362	AT2G45650	AGL6	DY914535 DY921092
CSA1.8178	AT5G15800	SEP1	DY904136

			DY926171
CSA1.8230	AT5G60910	FUL	DY903872
			DY917104
			DY917104
			DY924267
HaSOC1	AT2G45660	AGL20	DY911640
DY917953	AT1G69120	AP1	DY917953
DY920893	AT5G62165	AGL42	DY920893

Partial Sequences Not Included in Tree

HAM-AP3	AT3G54340	AP3	AY185363
CD849568	AT5G60910	FUL	CD849568
CD856064	AT5G15800	SEP1	CD856064
CSA1.3783	AT1G30260	AGL79	DY928958
			DY928958
CSA1.5941	AT3G54340	AP3	DY916848
			DY915925
CSA1.6274	AT4G37940	AGL17	DY915024
			DY917918
CSA1.7704	AT1G18750	AGL65	DY906548
			DY906548
DY914595	AT3G02310	SEP2	DY914595
DY917099	AT4G18960	AG	DY917099
DY929352	AT4G18960	AG	DY929352

TABLE S7**Integration of Genetic Maps by Homothetic Projection**

Gene Name or QTL Citation	Linkage Group	Panels Used and Order of Projection
HaPHYB	1	(5 → (3 → 2)) → 4
HaLD	4	(5 → (3 → 2)) → 4
HaSPY	6	(5 → (2 → 3)) → 4
HaSOC1	6	1 → ((5 → (2 → 3)) → 4)
Wills 2007	6	1 → ((5 → (2 → 3)) → 4)
Baack 2008	6	7 → ((5 → (2 → 3)) → 4)
HaAP1	8	(5 → (3 → 2)) → 4
HaLFY	9	(5 → (6 → 1)) → 4
HaSLY1	9	(5 → (6 → 1)) → 4
HaCOL1	9	(5 → (6 → 2)) → 4
Baack 2008	9	7 → ((5 → (3 → 2)) → 4)
HaFT4	14	(3 → 2) → 4
HaCOL2	14	(3 → 2) → 4
Baack 2008	14	7 → ((3 → 2) → 4)
Wills 2007	15	(3 → 1) → 4
HaFKF1	17	2 → 4
HaCPS	17	2 → 4
HaDELLA2	17	2 → 4
Baack 2008	17	7 → (2 → 4)

Candidate gene and QTL positions determined on various panels were projected onto a common map to examine candidate gene-QTL co-localization (Figure 2). Additional maps containing marker that bridge the original map to the target map were first projected onto a locus' original panel (bold). This map was then projected onto the target map, CMSHA89 x Ann1238 F3 panel (BURKE *et al.* 2002). Alternative orders of projection generally yielded similar results. Most maps used can be found in the Sunflower CMap database (<http://sunflower.uga.edu/cmap>). Maps used are numbered as follows: 1) Hopi x Ann1238_Wills & Burke 2007, 2) NMS373 x Ann1811_BC_(in press), 3) RHA280 x RHA801 RIL Tang *et al.* 2002, 4) CMSHA89 x Ann1238_F3_Burke *et al.* 2002, 5) Composite_Burke *et al.* 2004, 6) RHA280 x RHA801_RIL_Tang *et al.* 2006b, 7) CMSHA89 x Ann1238 RIL (data directly from BAACK *et al.* 2008). Projection of LG7 candidate genes and QTL was performed manually because BioMercator always culled the two markers shared between the target map and other maps due to inverted ordering.