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Genome-wide analysis and gene expression studies revealed putative homeotic genes with a role in flower formation in sesame (*Sesamum indicum* L.)

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SUPPLEMENTARY MATERIAL

Table S1. Classification of the floral bud development into 5 distinct stages.

Floral Stage	Description of flower formation in different stages
Stage 1	The stage is characterized by the adjoined sepals at the anterior end of the bud.
Stage 2	The sepals separate at the anterior ends while remaining wrapped around the petals.
Stage 3	The petals are free from each other and as well as from the sepals.
Stage 4	The stage is characterized by closed petals that are longer than the sepals i.e., pre-anthesis.
Stage 5	The petals finally open up and the flower blooms, i.e., anthesis.

Table S2. Primers used for Reverse Transcriptase (RT-PCR)-based gene expression studies.

Primer Name	Class	Nucleotide Sequences (5’-3’)	Annealing Temperature (^oC)	Amplicon size (bp)
SiAP1	A	ATGGGAAGAGGAAAGGTACAGC CACAAACAGTCATAATCATGCAGC	56	790
SiAP2	A	ATGAGCAATCTAACAAAGGAGG	52	883

		GGATTAGGATTAGGATTAGGAG		
SiSQUA	A	TGACTTCTTCACTGGCTATGAG	57	606
		CACACAGGTTACATATAGATCG		
SiPFG	A	TGGAGGAGGAACACAAGCAAC	50	382
		CGAAGGGCAAATGGCATCTG		
SiAP3	B	ATGGCTCGTGGGAAGATCCAGA	56	798
		CATGAAACACGACATCAAACACAC		
SiDFE	B	ACATGGACAACTCTCTGAGG	57	986
		GAAATCCAAGGACAGAATTG		
SiTM6	B	GCAGGAAGAGGGTGAGGAAC	54	845
		GCCATAGCAGAGTTGAAATGTCC		
SiPI	B	TGGGCTAAGTCGGAAGGA	52	680
		GTGATAAACCCCAACTGCC		
SiGLO	B	TTATCTGCAAACAAAAACAAGAGAGA	53	288
		TTAGACAACCGATGGCTGGG		
SiGLO1	B	AATGAGGTTCTGAGGATGATGAGG	56	590
		CTTCGCCAATTTCTCCCATATTCC		
SiMADS2	B	CCAGAACATAGCCAAGGAGC	58	352
		AATGGCAAGACGAGGATGTG		
SiAG	C	ATGGAATTCCCTAGTGATC	49	735
		CAAGCTAGCTAATTGCTCAT		
SiPLENA	C	TGAAGAGGAGAGTGAATTTGACAAGG	58	576
		TGTGCTTCTAAGATAACTTG		
SiMADS3	C	TTCTTGGTGAATCTCTTGCTG	54	718
		GGTAATGGTTGTTGGTCTGC		
SiFBP6	C	ACCATGCCGATTCCACAAGTA	52	420
		CCTCTCCAACAATTTGCCTGTTA		
SiSTK	D	ATG GGA AGA GGA AAG ATA GAA ATA	50	579
		GAT CAG AGT AAG AAC CTC CA		
SiFBP7	D	CATGCTTCCCAAGTAAGTCCTCAC	47	364
		GAGATTACTCCAACTTCATAAGTTCAACAC		
SiFBP11	D	GCTGGAGAAAGAAATCTGCTCTTAG	59	372
		GAGAAAAGCTGACGAGTTCACCA		
SiSEP1	E	ATGATCCAGCTACTTCAAGCCAA	56	391
		TATGGTACATTCACAGCATCCAAC		
SiSEP2	E	GGACCAAGAGAGGAAAGGGA	50	691
		ATTAACGTTGTGTGCGGACA		
SiSEP3	E	ATGGGAAGGGGGAGAGTTGA	54	629
		TAGCCCACGTCCTGAGCATT		
SiDEF49	E	ATCATGACCAGCAAGCACGACTCA	55	596
		CTTAGCTCTTTCTCGGTCCACCTT		
SFBP2	E	GTGGCAGCAAAATGCACAAG	57	507
		TTGGCCCTGCTCCTCCTAC		
SiLFY	TF	TTACTGATGGGGTGAGCACA	54	620
		GCAAGCATGTTACAAGCCCT		
SiFLO	TF	TTGCAAGATCACAACAATTCGCTTCTC	54	997
		GAGAGTTTGGTTCCGTCAACGACGATG		
SiALF	TF	ATGGACCCAGAGGCTTTCTCA	55	635
		CTAATTCCTCCACCACCCTCAT		
SiWUS	TF	GAGACCTGCTAATTCCGTCAACG	50	232
		GTTCAGACGTAGCTCAAGAGAAGC		

SiTER	TF	CGAGGCCATATTCTCTTCACTC TCAAGAGAAGCTCTAGCAGCAG	52	625
SiUFO	TF	ATGGATTCAACTGTGTTCATCAAT AGCAGTCTTAACTGCAGAAGTGG	48	313
SiFIM	TF	TCCATGGAAACTGGTGTTGTGC TTGCAGGGTCAGGTTGTTGCTC	51.5	372
SiDOT	TF	TGCCACCAACTTTAAGGCCTAG AATCATCACCAGCCACAGCTAAG	56	995
SiSOC1	TF	ATAGGAACATGCTCAATCGAGGAGCTG TTTCTTGAAGAACAAGGTAACCCAATG	60	962
SiUBQ		CACCAAGCCGAAGAAGATCAAG CCTCAGCCTCTGCACCTTTC	68	100

Table S3. Primers used for Real Time-quantitative PCR (RT-qPCR).

Primer Name	**Forward primer sequence (5'→ 3')**	**Annealing Temperature (°C)**
SiAP1-RT-F	ATAAGAGGTACAAAGGGGCAGG	68
SiAP1-RT-R	GTGCCAGTCACACAAAGCAT	
SiAP3-RT-F	TTTGATGCAAGACAGGAGGA	68
SiAP3-R -R	AATGTGGTGAGGTCTGAGGC	
SiAG-RT-F	GAAACTGCGTGCTCAAATCA	67
SiAG-RT-R	TAATTCCTCGTTCGACCCTG	
SiSTK-RT-F	ACGCGCAGAAAAGGGAGATTGAGC	69
SiSTK-RT-R	TGTCGGGATCAGAGTAAGAACCTCC	
SiSEP3-RT-F	CACGGACTCAAGCTATGCTG	68
SiSEP3-RT-R	CTGAGCATTTGGGTTCCACT	
**SiACT*-RT-F	CTCCCTTTATGCCAGTGGTCGT	68
SiACT-RT R	GCTCAGCTGTTGTAGTGAAGGA	
**SiDNAJ*-RT-F	TGGTGACCTCAACCACCTCAT	68
SiDNAJ-RT-R	TGACAGCGAGTTTCCTGAGATC	
**SiUBQ6*-RT-F	CACCAAGCCGAAGAAGATCAAG	69
SiUBQ6-RT-R	CCTCAGCCTCTGCACCTTTC	

*Primers used for amplifying genes as internal controls (Wei et al., 2013)

Table S4. The partial cDNA sequences of all 32 putative homeotic genes of sesame in comparison to the reported homeotic genes from other model plant species.

Gene Name	**Partial cDNA sequence (bp)**	**Domain**[e]	**Query sequences (Acsession No.)**	***Petunia hybrida* (%)**	***Antirrhinum majus* (%)**	***Arabidopsis thaliana* (%)**
SiLFY	620	FLO-LFY SP	OQ092330	92	89	95
SiFLO	997	FLO-LFY SP	OQ092333	85	87	90
SiALF	635	FLO-LFY SP	OQ092335	86	83	89
SiWUS	232	Homeodomain	OQ092336	91	93	87
SiTER	625	Homeodomain	OQ092332	86	97	97
SiUFO	313	F-box	OQ092337	91	89	82
SiFIM	372	F-box	OQ092334	89	96	94
SiDOT	995	F-box	OQ092353	93	85	93
SiSOC1	962	MADS	OQ092331	80	86	96
SiAP1	790	MADS	KM677186	99	98	100
SiSQUA	606	MADS	OQ092352	92	99	97
SiPFG	382	MADS	OQ092338	86	92	93
SiAP2	883	AP2 Superfamily	KM190074	91	94	98
SiAP3	798	MADS	KM190075	93	95	100
SiDEF	986	MADS	OQ033392	82	91	90
SiTM6	846	MADS	OQ092344	89	90	82
SiPI	680	MADS	OQ092350	96	83	91
SiGLO	288	MADS	OQ092349	93	89	85
SiGLO1	590	MADS	OQ092340	96	98	89
SiMADS2	352	MADS	OQ092348	82	96	92
SiAG	735	MADS	KM190076	98	99	100
SiPLE	576	MADS	OQ092347	92	95	90
SiMADS3	718	MADS	OQ092421	99	89	86
SiFBP6	420	MADS	OQ092343	97	94	83
SiSTK	579	MADS	OQ198411	95	90	99
SiFBP7	364	MADS	OQ092342	83	86	81
SiFBP11	372	MADS	OQ092345	93	96	82
SiSEP1	391	MADS	OQ092352	98	96	97
SiSEP2	691	MADS	OQ092351	92	93	96
SiSEP3	629	MADS	KF601336	100	99	100
SiDEFH49	596	MADS	OQ092346	97	89	88
SiFBP2	501	MADS	OQ092339	94	96	90

SUPPLEMENTARY FIGURES

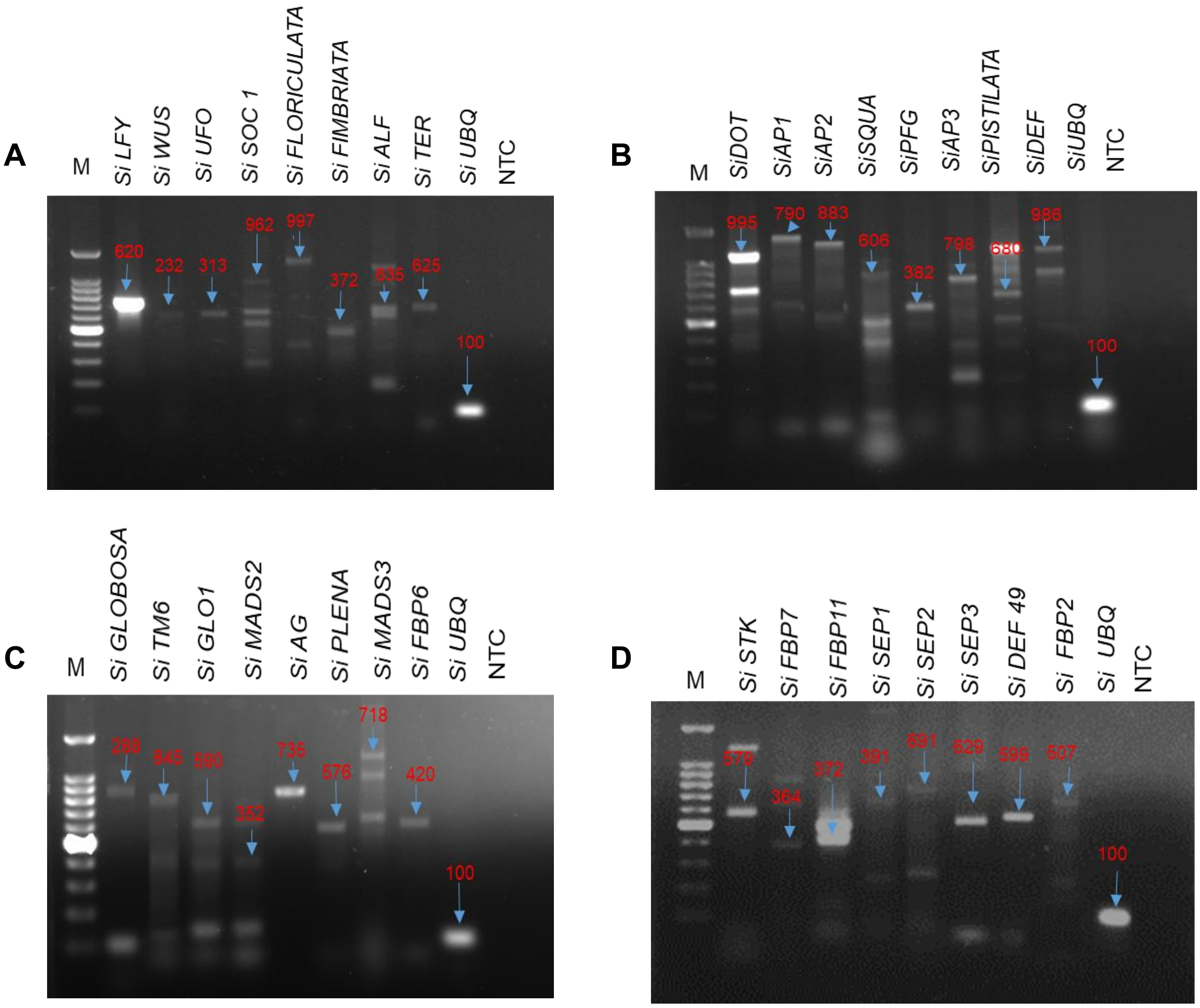

Figure S1. Genomic PCR confirming the presence of all 32 putative homeotic genes in sesame. The *Ubiquitin* gene, *SiUBQ* served as an internal control and non-template control (NTC) served as negative control. A-D: The 32 genes with 8 genes per gel are presented. The arrows indicate the expected amplicon size for each of the putative homeotic genes. M: 1 Kb Ladder.

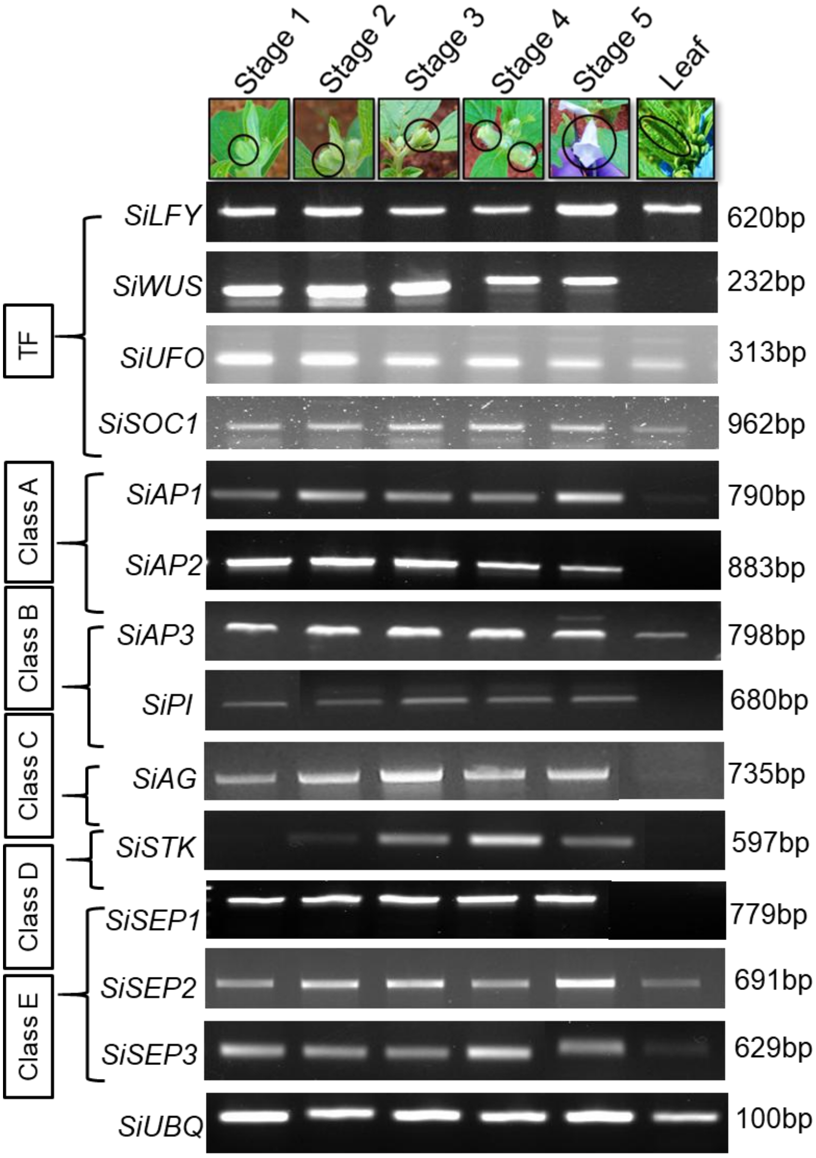

Figure S2. Gene expression analysis of putative floral homeotic genes in sesame that are homologous to ABCDE gene classes of *Arabidopsis thaliana* by RT-PCR. The mRNA transcript accumulation of the putative sesame floral homeotic genes was compared at different stages of flower formation with leaf tissue. The ubiquitin gene, *SiUBQ* served as an internal control.

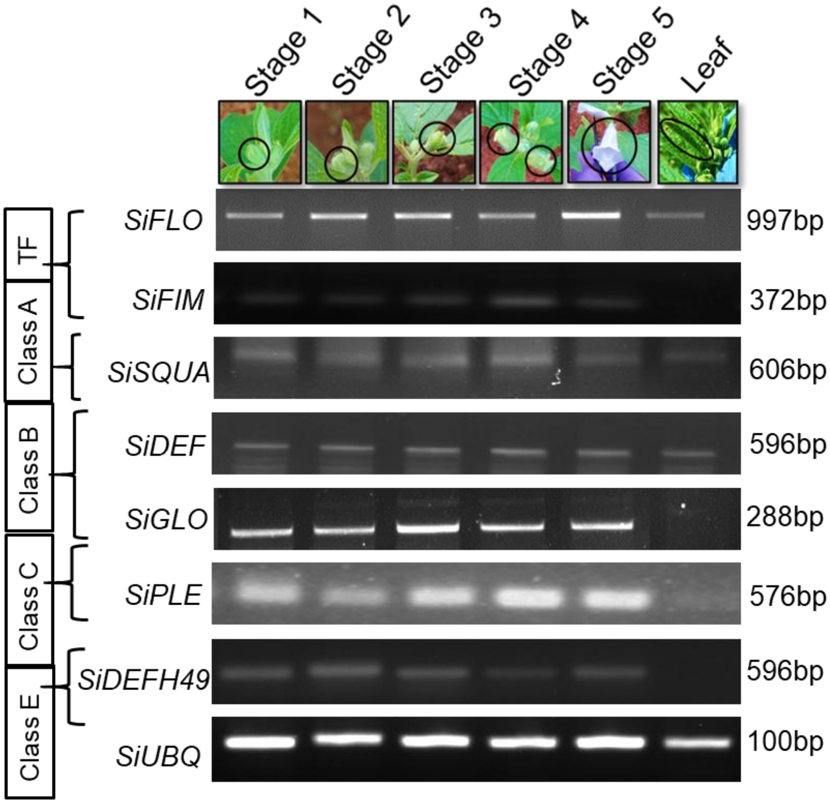

Figure S3. Gene expression analysis of putative floral homeotic genes in sesame that are homologous to ABCDE gene classes of *Antirrhinum majus* by RT-PCR. The mRNA transcript accumulation of the putative sesame floral homeotic genes was compared at different stages of floral bud formation with leaf tissue. The ubiquitin gene, *SiUBQ* served as an internal control.

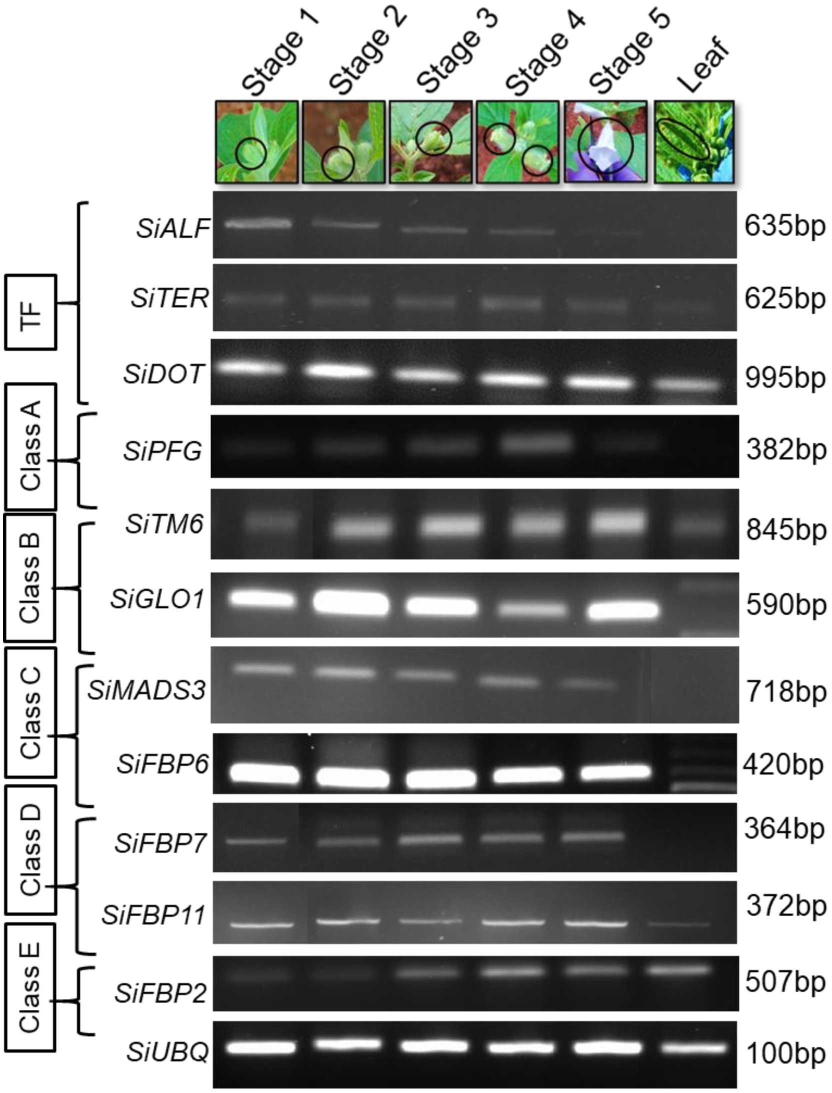

Figure S4. Gene expression analysis of putative floral homeotic genes in sesame that are homologous to ABCDE gene classes of *Petunia hybrida* by RT-PCR. The mRNA transcript accumulation of the putative sesame floral homeotic genes was compared at different stages of floral bud formation with leaf tissue. The ubiquitin gene, *SiUBQ* served as an internal control.