Table 3. MADS-box sequences detected in the *Arabidopsis thaliana* genome

Gene name, symbol, and synonyms	Accession no.	Gene ID	BAC no. identifier (ORF number)	Chromosome	Predicted number of exons	Type of sister paralogon duplication *	Comments and references for functional studies
AGAMOUS / AG	AL021711 / AL161549	At4g18960	F13C5.130	4	8	Interchromosomal †	1
APETALA3 / AP3	AL132971 / AY070397	At3g54340	T12E18_30	3	7	Not duplicated in sister region	2
PISTILLATA / PI	AB035137	At5g20240	F5O24.130	5	6	Not duplicated in sister region	3
AGL1/ SHATTERPROOF1 / SHP1	AL353032	At3g58780	T20N10.130	3	7	Intercrhomosomal	4
AGL2 / SEPALLATA1 / SEP1	M55551	At5g15800	F14F8.180	5	7	Interchromosomal	4, 5
AGL3	AC006836	At2g03710	F19B11.16	2	8	Intrachromosomal	4
AGL4/ SEPALLATA2	AC009755	At3g02310	F14P3.4	3	7	Interchromosomal	4, 5
AGL5 / SHATTERPROOF2 / SHP2	AC006931	At2g42830	F7D19.17	2	7	Interchromosomal	4, 6
AGL6	AC003680	At2g45650	F17K2.18	2	8	Interchromosomal	4
AGL7/ APETALA1 / AP1	AC008262	At1g69120	F4N2.9	1	8	Intrachromosomal	7
AGL8/ FRUITFULL / FUL	AB008269	At5g60910	MSL3.3	5	8	Interchromosomal †	8
AGL9/ SEPALLATA3 / SEP3	AC002396	At1g24260	F3I6.19	1	8	Intrachromosomal †	5
AGL10/ CAULIFLOWER / CAL	P5K112	At1g26310	F28B23.25	1	8	Intrachromosomal	9
AGL11	AL049481 / AL161516	At4g09960	T5L19.90	4	7	Interchromosomal	10
AGL12	AC012654 / AL016163	At1g71692	F14O23.5	1	7	Interchromosomal	10, 11
AGL13	AL137898	At3g61120	T20K12.20	3	8	Interchromosomal	10
AGL14	AL078606 / AL161531 / AL161533	At4g11880	T26M18.90	4	7	Intrachromosomal	10

Gene name, symbol, and synonyms	Accession no.	Gene ID	BAC no. identifier (ORF number)	Chromosome	Predicted number of exons	Type of sister paralogon duplication *	Comments and references for functional studies
AGL15	AB005230	At5g13790	MXE10.8	5	8	Not duplicated is sister region	10
AGL16	AL137080	At3g57230	F28O9.80	3	6	Not duplicated is sister region	12
AGL17	AC006340	At2g22630	T9I22.7	2	7	Interchromosomal	11
AGL18	AL137080 / AF312663	At3g57390	F28O9.240	3	8	Intrachromosomal †	12, ‡
AGL19	AL031018 / AL161558	At4g22950	F7H19.130	4	7	Intrachromosomal	12
AGL20/ SUPRESSOR OF OVEREXPRESSION OF CONSTANS1 / SOC1	AC003680	At2g45660	F17K2.19	2	7	Not duplicated is sister region	13, 14
AGL21	AL035538 / AL161592	At4g37940	F20D10.60	4	7	Interchromosomal	11
AGL22/ SHORT VEGETATIVE PHASE / SVP	AC006592	At2g22540	F14M13.6	2	6	Interchromosomal †	15
AGL23	AC004512	At1g65360	T8F5.14	1	1	Not duplicated is sister region	
AGL24	AL035356 / AL161561	At4g24540	F22K18.260	4	8	Interchromosomal †	16, 17
AGL25/ FLOWERING LOCUS C / FLOWERING LOCUS F / FLC / FLM	AF116528 / AL356332	At5g10140	T31P16_130	5	7	Intrachromosomal	18, 19
AGL26	AF007270	At5g26870	F2P16.19	5	1	Not duplicated is sister region	
AGL27 / FLOWERING LOCUS M / FLM /FK1 / MAF1	AC002291	At1g77080	F22K20.15	1	6	Not duplicated is sister region	12, 20, §
AGL28	Y12776 / AC061957	At1g01530	F22L4.7	1	2	Not duplicated is sister region	
AGL29	AC004077	At2g34440	T31E10.22 (=F13P17.1)	2	2	Interchromosomal †	¶

Gene name, symbol, and synonyms	Accession no.	Gene ID	BAC no. identifier (ORF number)	Chromosome	Predicted number of exons	Type of sister paralogon duplication *	Comments and references for functional studies
AGL30	AC004138	At2g03060	T17M13.23	2	6	Not duplicated is sister region	
AGL31 / MAF2-I	AB019236 /	At5g65050	MXK3.30	5	6	Not duplicated is sister region	12, 21, ‖
AGL32 / TRANSPARENT TESTA 16 / TT16	AB007648	At5g23260	MKD15.12	5	5	Not duplicated is sister region.	22
AGL33	AC004484	At2g26320	T1D16.4	2	2	Not duplicated is sister region.	**
AGL34	AF058914	At5g26575	F21E10.14	5	2	Not duplicated is sister region	
AGL35	AF058914	At5g26625	F21E10.9	5	1	Intrachromosomal †	
AGL36	AF058914	At5g26645	F21E10.10	5	1	Intrachromosomal †	¶
AGL37	AC004512	At1g65330	T8F5.11	1	1	Intrachromosomal †	
AGL38	AC004512	At1g65300	T8F5.8	1	1	Not duplicated is sister region	
AGL39	AF007271	At5g27130	A_TM021B04.16/ T21B4.40	5	1	Not duplicated is sister region	
AGL40	Z99708 / AL161589	At4g36590	C7A10.770	4	2	Not duplicated is sister region	
AGL41	AC005168	At2g26880	F12C20.8	2	2	Intrachromosomal †	
AGL42	AB016880	At5g62165	MTG10.20	5	7	No match found in database	††, ‡ ‡
AGL43	AB010699	At5g40220	MSN9.13	5	1	Interchromosomal †	
AGL44/ ABNORMAL NITRATE RESPONSE / ANR1	AC007210	At2g14210	F15N24.5	2	8	Not duplicated is sister region	24
AGL45	AC012393	At3g05860	F10A16.16	3	2	Not duplicated is sister region	
AGL46	AC007184	At2g28700	T11P11.1	2	1	Not duplicated is sister region	
AGL47	AB009050	At5g55690	MDF20.13	5	1	Not duplicated is sister region	
AGL48	AC018721 / AF085279	At2g40210	T7M7.9	2	1	Interchromosomal	
AGL49	AC005966 / AC007258	At1g60040	T2K10.9	1	1	Not duplicated is sister region	
AGL50	AC007258 / AC005966	At1g59810	F23H11.13	1	1	Not duplicated is sister region	

Gene name, symbol, and synonyms	Accession no.	Gene ID	BAC no. identifier (ORF number)	Chromosome	Predicted number of exons	Type of sister paralogon duplication *	Comments and references for functional studies
AGL51	AF075597 / AL161494	At4g02240	T2H3.15	4	2	Not duplicated is sister region	
AGL52	AL161531	At4g11250	F8L21.40	4	1	Not duplicated is sister region	
AGL53	AF160760	At5g27070	F15P11.40	5	1	Not duplicated is sister region	§§
AGL54	AF160760	At5g27090	F15P11.1	5	1	Not duplicated is sister region	
AGL55	AC018908	At1g60920	T7P1.6	1	1	Not duplicated is sister region	
AGL56	AC018908	At1g60880	T7P1.3	1	1	Not duplicated is sister region	
AGL57	AC016829	At3g04100	T6K12.28	3	1	Not duplicated is sister region	
AGL58	AC010155	At1g28450	F3M18.11	1	1	Not duplicated is sister region	
AGL59	AC010155	At1g28460	F3M18.10	1	1	Not duplicated is sister region	
AGL60	AC016529	At1g72350	T10D10.18	1	1	Intrachromosomal	
AGL61	AC006585	At2g24840	F27C12.24	2	1	Not duplicated is sister region	
AGL62	AB011483	At5g60440	MUF9.24	5	2	Not duplicated is sister region	
AGL63	AC004793	At1g31140	F28K20.7	1	5	Not duplicated is sister region	
AGL64						Not used in this study	¶¶
AGL65	AC011809	At1g18750	F6A14.14	1	7	Not duplicated is sister region	
AGL66	AC009243	At1g77980	F28K19.20	1	9	Intrachromosomal	
AGL67	AC009243	At1g77950	F28K19.16	1	5	Not duplicated is sister region	
AGL68/ FLOWERING C LOCUS1 / FCL1 / MAF5-I	AB02663 (partially) AB013395 (partially) AF214485	At5g65080	F15O5.4	5	6	Not duplicated is sister region	21, ‖‖

Gene name, symbol, and synonyms	Accession no.	Gene ID	BAC no. identifier (ORF number)	Chromosome	Predicted number of exons	Type of sister paralogon duplication *	Comments and references for functional studies
AGL69 / FLOWERING C LOCUS 2 / FCL2 /MAF4	AB026633	At5g65070	F15O5.3	5	8	Intrachromosomal	21
AGL70 / MAF3-I	AB026633	At5g65060	F15O5.2 F15O5(N3)	5	7	Not duplicated is sister region	21, ***
AGL71	AB025623	At5g51870	MJM18.2	5	7	Not duplicated is sister region	
AGL72	AB010074/ AB025623	At5g51860	MIO24.20	5	7	Not duplicated is sister region	† † †
AGL73	AB005231	At5g38620	MBB18.17	5	1	Intrachromosomal †	
AGL74						Not used in this study	¶¶
AGL75	AB010072	At5g41200	MEE6.27	5	1	Intrachromosomal †	
AGL76	AB010699	At5g40120	MSN9.2; MUD12.4	5	1	Not duplicated is sister region	
AGL77	AB011478	At5g38740	MKD10.6	5	1	Not duplicated is sister region	
AGL78	AB011479	At5g65330	MNA5.6	5	1	Not duplicated is sister region	
AGL79	AP001314	At3g3026/At3 g30270	T6J22.1	3	8	Not duplicated is sister region	‡ ‡ ‡
AGL80	AB015468	At5g48670	K15N18.16	5	1	Interchromosomal †	
AGL81	AB016876	At5g39750	MKM21.6	5	1	Interchromosomal †	
AGL82	AB016885	At5g58890	K19M22.9	5	1	Not duplicated is sister region	
AGL83	AB023033	At5g49490	K6M13.3	5	1	Not duplicated is sister region	
AGL84	AB023034	At5g49420	K7J8.9	5	1	Intrachromosomal †	
AGL85	AC005388	At1g54760	T22H22.17	1	1	Not duplicated is sister region	
AGL86	AC074360.1	At1g31630	F27M3_17	1	1	Not duplicated is sister region	
AGL87	AC006551	At1g22590	F12K8.7	1	3	Not duplicated is sister region	
AGL88	AC007045	At2g11990	F23M2.15	2	1	No match	§§§
AGL89	AC007478	At5g27580	F15A18.40	5	1	Intrachromosomal †	
AGL90	AC007627	At5g27960	F15F15.30	5	1	Not duplicated is sister region	¶¶¶

Gene name, symbol, and synonyms	Accession no.	Gene ID	BAC no. identifier (ORF number)	Chromosome	Predicted number of exons	Type of sister paralogon duplication *	Comments and references for functional studies
AGL91	AC036106	At3g66656	T8E24.5	3	1	Interchromosomal †	
AGL92	AC074360.2	At1g31640	F27M3_16	1	2	Intrachromosomal †	
AGL93		At5g26950	F2P16.17	5	1	Intrachromosomal †	‖‖‖
AGL94	NM_105623 / AC073178	At1g69540	F10D13_25	1	8	Not duplicated is sister region	
AGL95						Not used in this study	¶¶
AGL96	AP002543	At5g06500	F15M7.3 (also MHF15.29)	5	1	Not duplicated is sister region	
AGL97						Not used in this study	¶¶
AGL98		At5g39810	MKM21.13	5	2	Not duplicated is sister region	¶¶
AGL99	AL162875	At5g04640	T32M21_240 T1E3.5	5	1	Not duplicated is sister region	
AGL100	AC026479	At1g17310	T13M22.2	1	1	Intrachromosomal	
AGL101	AF160760	At5g27050	F15P11.2	5	1 (varies in different accessions)	Not duplicated is sister region	****
AGL102	AC012463	At1g47760	T2E6.17	1	2	Not duplicated is sister region	
AGL103	AB026654	At3g18650	MVE11.1	3	1	Interchromosomal †	
AGL104	AC069252	At1g22130	F2E2.20	1	10	Intrachromosomal	
AGL105	AP000607	At5g37420	T25O11.7	5	2	Not duplicated is sister region	

Consecutive AGL names for previously unnamed genes were assigned following agreement with Lucia Colombo and collaborators (personal communication).

*From the paralogons in the *A. thaliana* Database (http://wolfe.gen.tcd.ie/athal/dup).

[†] Paralogon contains fewer than seven genes and therefore could be spurious.

[‡] Reported as AGL15 in some GenBank entries.

[§] The MAF1-I splicing form (21) was used for this study.

[¶] Sequence At5g26650 (= AGL36) has been wrongly identified with AGL29.

[‖] The MAF2-I splicing form (21) was used for this study.

**Reported as having eight exons in ref. 23.

[††] T. Nawy, J. E. Malamy, S. Thongrod, J. Jung, and P. N. Benfey, www.arabidopsis2002.com/abstractspublic/abstract_expediente.asp?cdabstract=1147.

[‡‡] There is another MTG10.20 that is not a MADS protein.

[§§] This entry appears to have two MADS-box genes within the same ORF; we have called these AGL53 and AGL101, the former being identical to ORF F15P11.40 (see AGL101).

[¶¶] Personal communication by Lucia Colombo and Lucie Parenicová (not included in this study).

[‖‖] The MAF5-I splicing form (21) was used for this study

***The MAF3-I splicing form (21) was used for this study.

[†††] Also called MJM18.1 (but there is another MJM18.1 that is not a MADS-box gene).

[‡‡‡] In some reports it is wrongly identified as AGL8.

[§§§] Reported as a pseudogene.

[¶¶¶] Reported as synonymous with AGL29 (it is on a different chromosome).

[‖‖‖] Almost identical to F15P11.40 and to half of AGL53.

****Reported as a separate gene but could be part of AGL53 because AGL53 looks like two MADS proteins in the same ORF.

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