

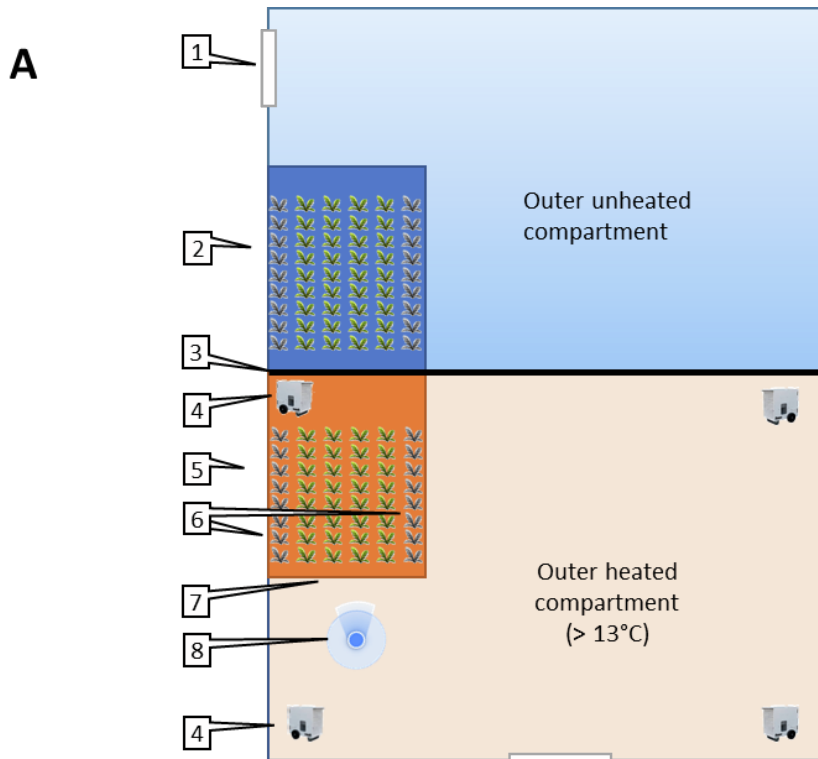
Supplemental information

A reduced vernalization requirement is a key component of the early-bolting trait in globe artichoke (*Cynara cardunculus* var. *scolymus*)

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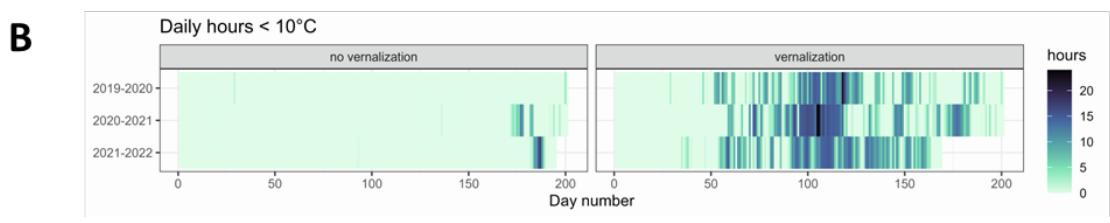
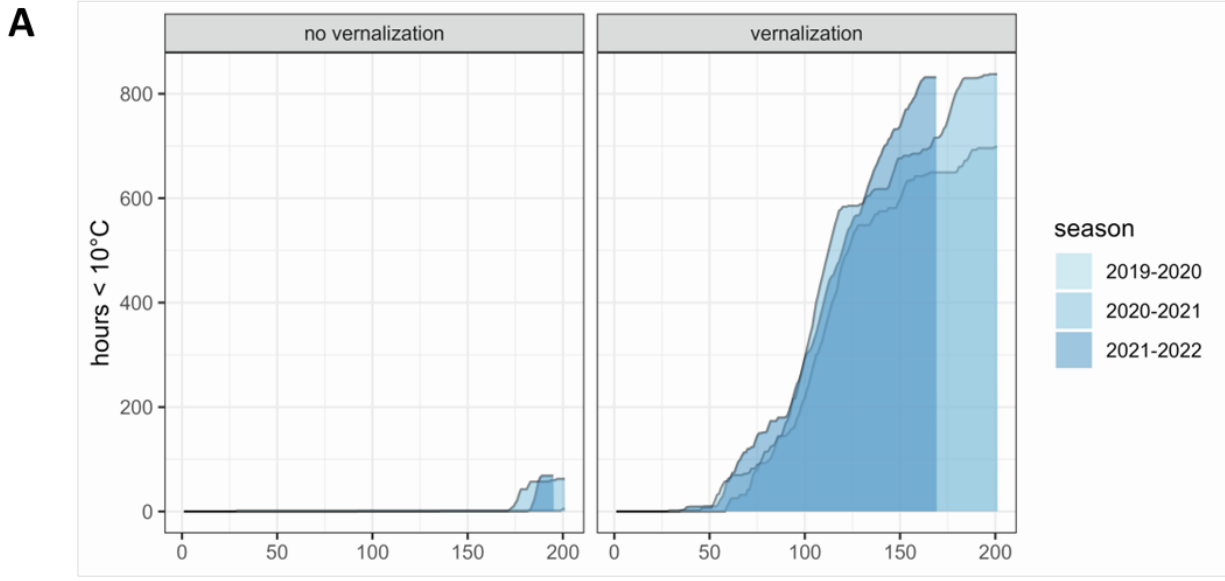
1 Supplementary Figures

2



3

4 **Supplementary Figure S1: Schematic representation and photographic illustration of experimental**
 5 **conditions. Related to STAR METHODS (Experimental design and treatment).** A. Schematic
 6 representation of the experiment. 1 = access door in outer wall, 2 = cold compartment (vernalization /
 7 control) (blue fill), 3 = double wall separating heated and non-heated sectors, 4 = heater, 5 = heated
 8 compartment (red fill), 6 = border rows (grey), 7 = inner compartment wall, 8 = viewpoint for the
 9 photograph below. B. Photograph of the heated compartment from the viewpoint indicated by marker
 10 (8). The inner compartment wall facing the camera has been raised while the lateral inner wall and outer
 11 wall are still lowered for comparison. In the back of the image is the double wall separating the sectors,
 12 behind which is the cold compartment. Yellow bands along the outer wall serve as pest control. The table
 13 and tools illustrate the scale of the image.

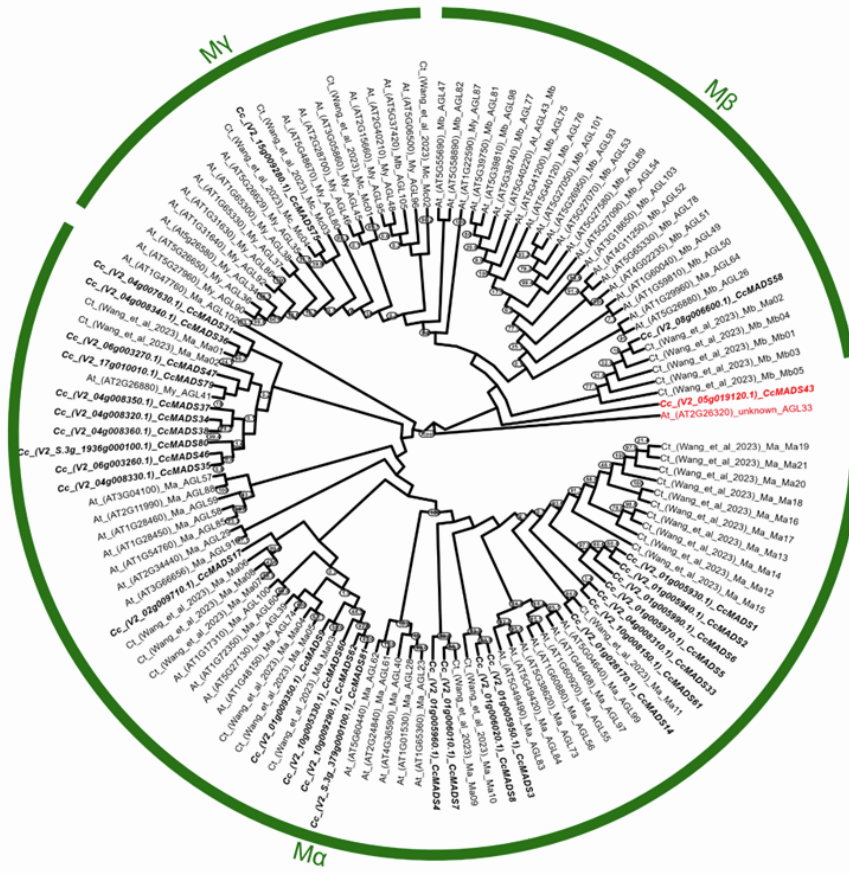
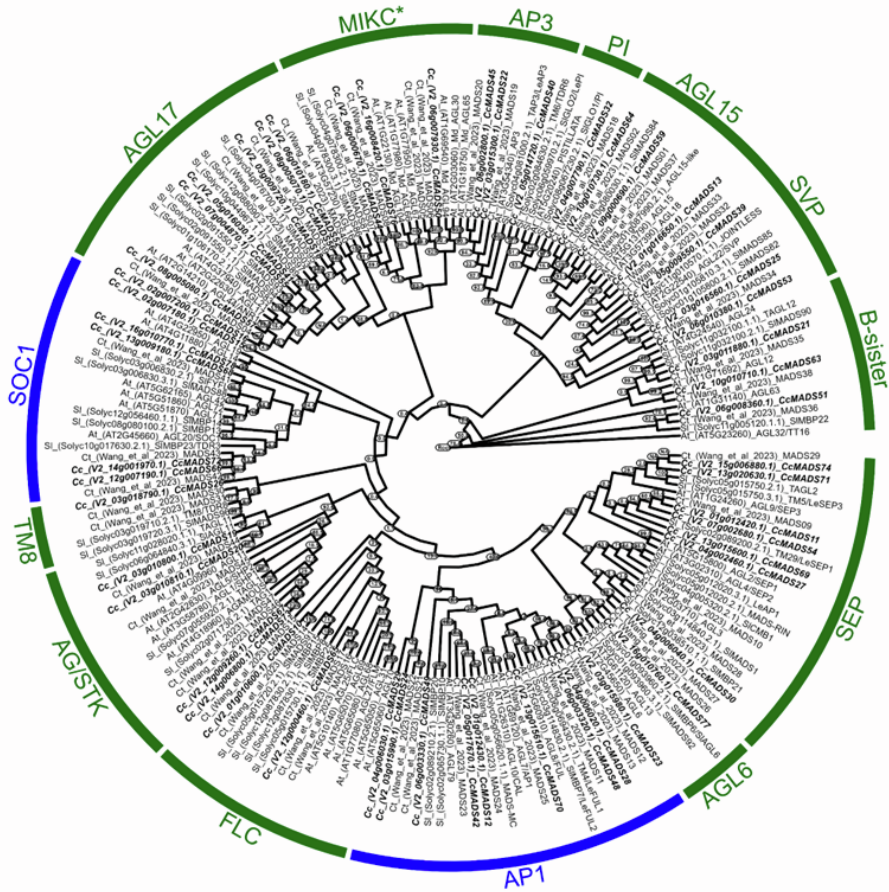


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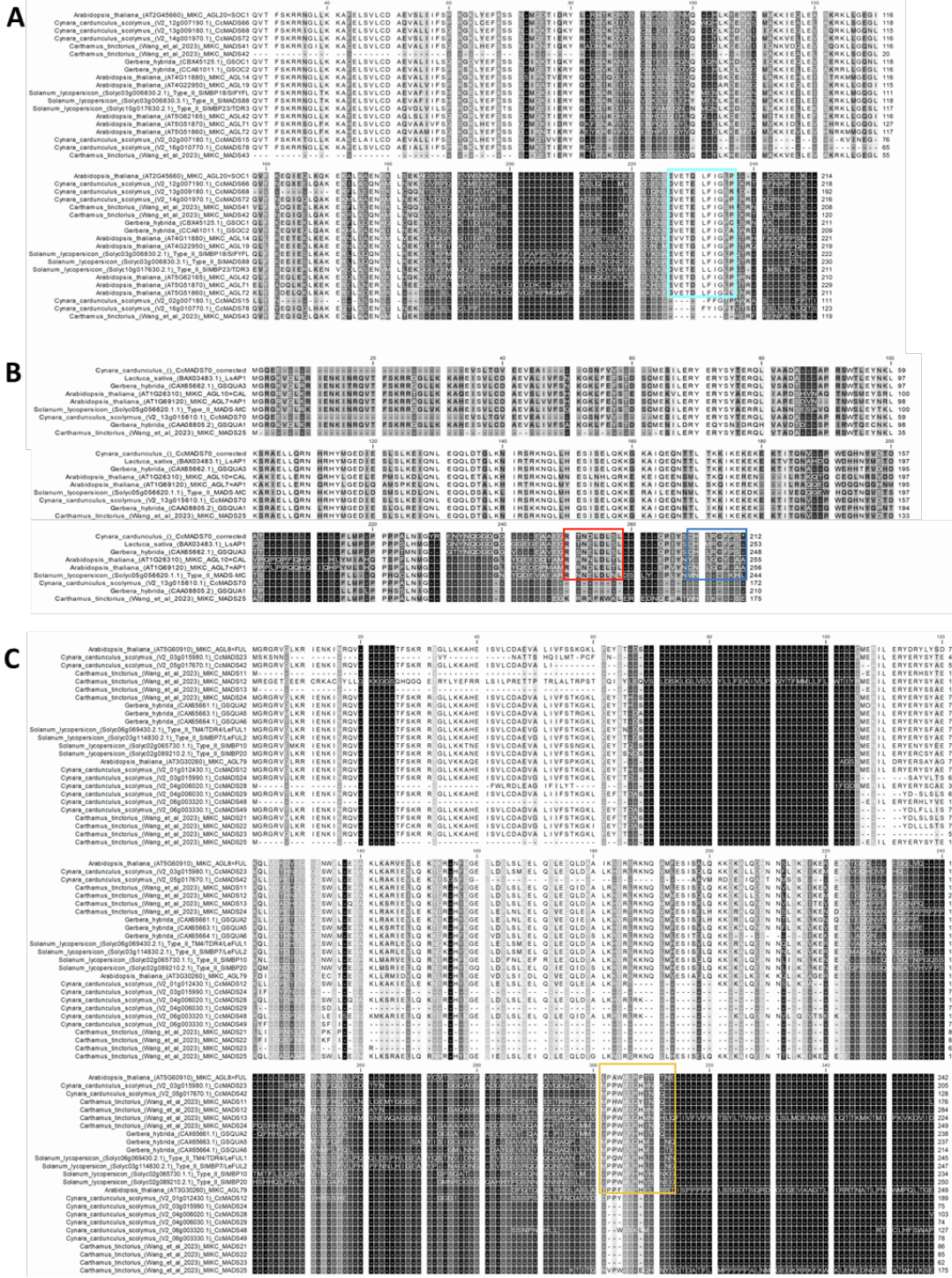
15 **Supplementary Figure S2: Accumulation and distribution of hours < 10°C. Related to Figure 2. A**

16 Accumulated numbers of hours < 10°C for each season in the no-vernalization and vernalization

17 compartments. **B** Number of hours < 10°C for each individual day. Data from three seasons.

A**B**

19 **Supplementary Figure S3: ML cladograms of Type I and Type II MADS box genes. Related to STAR**
20 **METHODS (Identification of MADS box genes in globe artichoke).** **A** Type I MADS box genes from
21 globe artichoke and Arabidopsis. Red tip names indicate ungrouped genes. **B** Type II MADS box genes
22 from globe artichoke (Cc), Arabidopsis (At), tomato (Sl) and safflower (Ct). Green strips annotate
23 subclades for both Type I and Type II cladograms, with the AP1 and SOC1 subclades highlighted in
24 blue.



25
 26 **Supplementary Figure S4: Protein sequence alignments for SOC1, AP1 and FUL subfamilies. Related**
 27 **to Figure 4. Genes used in the phylogenetic study. A** SOC1 subfamily, TM3/SOC1 motifs marked with a
 28 cyan box. **B** AP1 subfamily. Red box denotes the euAP1 acidic domain and the blue box the farnesylation
 29 motif. **C** FUL subfamily. The euFUL/paleoAP1 domain is marked by a yellow box.

30 **Supplementary tables**

31 **Supplementary Table S1: Comparison between phenological stages around the time of floral transition**
 32 **and the stages added to describe morphological changes. Related to Figure 1. Grey fill accentuates**
 33 **the positioning of the added bolting stages in relation to the existing scales.**

phenological stages according to BBCH scale (Archontoulis et al., 2009)	phenological stages according to (Foury, 1967) and (Pesce and Mauromicale, 2019) (modified)		phenological stages added to describe morphological changes at the microscopic level	
stage	stage	description	developmental stage	description
Principal growth stage 4: development of vegetative plant parts (Codes 41-49)	bolting stage 0	No signs of bolting on macroscopic scale (if no dissection of apex)	pre-bolting stage 0	Apex round, later flat at dissection.
	bolting stage R	caulinar apex in transition from the vegetative to reproductive phase	pre-bolting stage 1	Apex assuming a pointed shape at dissection.
Principal growth stage 5: inflorescence emergence and development, code 501	bolting stage A	Primary inflorescence perceptible by palpation	pre-bolting stage 2	Primordial primary head visible to the naked eye at dissection of apex
Principal growth stage 5: inflorescence emergence and development, code 501	bolting stage B	Top of primary inflorescence visible in center of the rosette	pre-bolting stage 3	Primary head developing, height ± 1 cm at dissection of apex.
Principal growth stage 5: inflorescence emergence and development, codes 501-503	bolting stage C	Primary inflorescence more than 10 cm above center of rosette.	pre-bolting stage 4	Primary head fully developed, secondary primordial heads visible to naked eye at dissection. First inflorescence stem elongation.

34

35 Supplementary Table S2: Environmental data calculated and collected during the experiments.
 36 Related to Table 1.

season	treatment	n_days	daily mean (°C)			accumulated
			min	mean	max	hours < 10°C
2019-2020	no vernalization	201	19.1	14.4	28.3	5
2020-2021	no vernalization	201	18.1	13.4	27.4	62
2021-2022	no vernalization	195	17.6	13.6	26.2	69
2019-2020	vernalization	201	16.7	10.6	27.5	698
2020-2021	vernalization	201	16.1	9.9	26.8	837
2021-2022	vernalization	169	15.8	9.9	27.5	832

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38

39 **Supplementary Table S3: Wald tests for non-zero predictors. Related to Figure 2.** Wald tests for models
 40 per genotype (genotypes c1, c70, c20, and c154) and per category (early-bolting genotypes c1 and c70
 41 vs late-bolting genotypes c20 and c154).

42

model^a	source	Df^b	denDF^c	F.inc^d	Pr^e
per genotype	(Intercept)	1	100.6	94810	1.85E-151
	genotype	6	107.3	615.1	1.16E-80
	treatment	1	99.8	271.8	3.01E-30
	season	2	51.6	1.537	2.25E-01
	genotype:treatment	6	106.8	6.383	9.09E-06
	season:treatment	2	52.5	7.253	1.66E-03
	per category	(Intercept)	1	154.7	24030
earliness		1	147.7	718.6	1.29E-58
treatment		1	154.6	48.21	9.95E-11
season		2	74.2	0.3074	7.36E-01
earliness:treatment		1	146.9	14.47	2.08E-04
treatment:season		2	74.1	6.669	2.17E-03

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44 ^a Model used: "per genotype", each genotype, "per category", early-bolting vs late-bolting genotypes

45 ^b Df: Degrees of freedom

46 ^c denDF: denominator degrees of freedom

47 ^d F.inc: F-statistic value

48 ^e Pr = p-value

49

50 Supplementary Table S4: MADS box genes from globe artichoke. Related to STAR METHODS
 51 (Identification of MADS box genes in globe artichoke).

Name	Gene	GeneID	Length (a.a)	Domains	Genomic position	CDS length	Exons	Group	Classification	
									Subfamily	
CcMADS1		V2_01g005930.1	682	SRF, SRF, SRF, SRF	Chr_01:6563154-6579934	2049	4	Ma	-	-
CcMADS2		V2_01g005940.1	755	SRF, SRF	Chr_01:6592245-6612897	2268	13	Ma	-	-
CcMADS3		V2_01g005950.1	470	SRF, SRF	Chr_01:6636827-6645096	1413	5	Ma	-	-
CcMADS4		V2_01g005960.1	184	SRF	Chr_01:6643236-6644793	555	4	Ma	-	-
CcMADS5		V2_01g005970.1	196	SRF	Chr_01:6645121-6645711	591	1	Ma	-	-
CcMADS6		V2_01g005990.1	89	SRF	Chr_01:6659102-6659371	270	1	Ma	-	-
CcMADS7		V2_01g006010.1	219	SRF	Chr_01:6672187-6672849	663	1	Ma	-	-
CcMADS8		V2_01g006020.1	267	SRF	Chr_01:6673382-6674418	804	2	Ma	-	-
CcMADS9		V2_01g009350.1	233	SRF	Chr_01:10447026-10447727	702	1	Ma	-	-
CcMADS10		V2_01g010600.1	126	SRF	Chr_01:11863297-11864466	381	2	MIKC ^G	-	FLC
CcMADS11		V2_01g012420.1	190	SRF, K-box	Chr_01:13776558-13782784	573	5	MIKC ^G	-	SEP
CcMADS12		V2_01g012430.1	189	SRF, K-box	Chr_01:13817078-13825390	570	6	MIKC ^G	-	AP1
CcMADS13		V2_01g016650.1	171	SRF	Chr_01:19062272-19066258	516	5	MIKC ^G	-	SVP
CcMADS14		V2_01g026170.1	199	SRF	Chr_01:49764431-49765030	600	1	Ma	-	-
CcMADS15	CcSOC1Like-C	V2_02g007180.1	111	SRF	Chr_02:8995755-9004272	344	2	MIKC ^G	-	SOC1
CcMADS16		V2_02g007200.1	198	SRF, K-box	Chr_02:9035643-9049722	597	6	MIKC ^G	-	AGL17
CcMADS17		V2_02g009710.1	127	SRF	Chr_02:14659672-14660193	384	2	Ma	-	-
CcMADS18		V2_03g009720.1	170	K-box	Chr_03:17696857-17702624	515	6	MIKC,SRF incomplete	-	AGL17
CcMADS19		V2_03g010800.1	239	K-box	Chr_03:32010378-32016725	720	6	MIKC,SRF incomplete	-	AG/STK
CcMADS20		V2_03g010810.1	78	SRF	Chr_03:32026348-32027307	237	2	MIKC ^G	-	AG/STK
CcMADS21		V2_03g011880.1	176	SRF	Chr_03:46733984-46739542	531	6	MIKC ^G	-	B-sister
CcMADS22		V2_03g015300.1	229	SRF, K-box	Chr_03:59976194-59980703	690	7	MIKC ^G	-	AP3 (DEF/GLO)
CcMADS23	CcFULLike-B	V2_03g015980.1	205	K-box	Chr_03:61174353-61180637	816	9	MIKC,SRF incomplete	-	AP1
CcMADS24		V2_03g015990.1	75	SRF	Chr_03:61198079-61198306	228	1	MIKC ^G	-	AP1
CcMADS25		V2_03g016560.1	252	SRF, K-box	Chr_03:61999323-62016372	759	11	MIKC ^G	-	SVP
CcMADS26		V2_03g018790.1	115	K-box	Chr_03:64996337-64997256	348	5	MIKC,SRF incomplete	-	TM8
CcMADS27		V2_04g002460.1	107	SRF	Chr_04:2743621-2750447	658	7	MIKC ^G	-	SEP
CcMADS28		V2_04g006020.1	103	K-box	Chr_04:7740034-7740917	312	3	MIKC,SRF incomplete	-	AP1
CcMADS29		V2_04g006030.1	74	SRF	Chr_04:7758582-7758806	225	1	MIKC ^G	-	AP1
CcMADS30		V2_04g006040.1	248	SRF, K-box	Chr_04:7777716-7780938	765	8	MIKC ^G	-	SEP
CcMADS31		V2_04g007630.1	193	SRF	Chr_04:10649060-10649641	582	1	Ma	-	-
CcMADS32		V2_04g007790.1	170	SRF, K-box	Chr_04:11094347-11095508	513	4	MIKC ^G	-	PI (DEF/GLO)
CcMADS33		V2_04g008310.1	357	SRF	Chr_04:12663996-12673567	1321	6	Ma	-	-
CcMADS34		V2_04g008320.1	292	SRF	Chr_04:12664285-12671674	879	4	Ma	-	-
CcMADS35		V2_04g008330.1	607	SRF	Chr_04:12700422-12716552	1824	6	Ma	-	-
CcMADS36		V2_04g008340.1	193	SRF	Chr_04:12717490-12718071	582	1	Ma	-	-
CcMADS37		V2_04g008350.1	313	SRF	Chr_04:12736542-12748071	942	3	Ma	-	-
CcMADS38		V2_04g008360.1	120	SRF	Chr_04:12745559-12746192	634	1	Ma	-	-
CcMADS39		V2_05g009550.1	220	SRF, K-box	Chr_05:16157678-16162664	663	7	MIKC ^G	-	SVP
CcMADS40		V2_05g014720.1	139	SRF	Chr_05:56612198-56616210	420	3	MIKC ^G	-	AP3 (DEF/GLO)
CcMADS41	CcFULLike-A	V2_05g016030.1	137	SRF, K-box	Chr_05:58719144-58728679	414	5	MIKC ^G	-	AGL17
CcMADS42		V2_05g017670.1	128	SRF	Chr_05:61226372-61236507	387	4	MIKC ^G	-	AP1
CcMADS43		V2_05g019120.1	437	SRF	Chr_05:63006208-63007521	1314	1	Mβ	-	-
CcMADS44		V2_06g000670.1	200	SRF	Chr_06:2542888-2546558	603	6	MIKC* / Mδ	-	MIKC*
CcMADS45		V2_06g002800.1	232	SRF, K-box	Chr_06:10366962-10371671	699	7	MIKC ^G	-	AP3 (DEF/GLO)
CcMADS46		V2_06g003260.1	241	SRF	Chr_06:11217724-11221447	726	2	Ma	-	-
CcMADS47		V2_06g003270.1	106	SRF	Chr_06:11221157-11221776	620	1	Ma	-	-
CcMADS48		V2_06g003320.1	127	K-box	Chr_06:11289297-11291933	384	5	MIKC,SRF incomplete	-	AP1
CcMADS49		V2_06g003330.1	78	SRF	Chr_06:11303009-11303245	237	1	MIKC ^G	-	AP1
CcMADS50		V2_06g007930.1	365	SRF	Chr_06:17105260-17109803	1098	10	MIKC* / Mδ	-	MIKC*
CcMADS51		V2_06g008360.1	325	SRF, K-box	Chr_06:18606119-18608510	1036	7	MIKC ^G	-	B-sister
CcMADS52		V2_06g010180.1	453	SRF, K-box	Chr_06:23081934-23106721	1370	14	MIKC ^G	-	AGL17
CcMADS53		V2_06g010380.1	174	SRF, K-box	Chr_06:23474053-23479848	525	3	MIKC ^G	-	SVP
CcMADS54		V2_07g002680.1	142	SRF, K-box	Chr_07:2665138-2669869	429	4	MIKC ^G	-	SEP
CcMADS55		V2_07g004870.1	123	SRF	Chr_07:5959657-5962387	372	3	MIKC ^G	-	AGL17
CcMADS56		V2_08g005070.1	93	SRF	Chr_08:6179130-6180671	282	2	MIKC ^G	-	AGL17
CcMADS57		V2_08g005080.1	191	K-box	Chr_08:6193002-6199425	576	7	MIKC ^G	-	AGL17
CcMADS58		V2_08g006600.1	333	SRF	Chr_08:8157232-8158233	1002	1	My	-	-
CcMADS59		V2_09g000690.1	234	SRF, K-box	Chr_09:1966147-1970271	705	6	MIKC ^G	-	AGL15
CcMADS60		V2_10g005330.1	236	SRF	Chr_10:5839834-5840544	711	1	Ma	-	-
CcMADS61		V2_10g008150.1	241	SRF, SRF	Chr_10:9337223-9338186	792	2	Ma	-	-
CcMADS62		V2_10g009290.1	232	SRF	Chr_10:11534672-11535370	699	1	Ma	-	-
CcMADS63		V2_10g010710.1	156	SRF	Chr_10:14465025-14466948	471	5	MIKC ^G	-	B-sister
CcMADS64		V2_10g010730.1	198	SRF, K-box	Chr_10:14543135-14547905	597	6	MIKC ^G	-	AGL15
CcMADS65		V2_12g000460.1	318	SRF	Chr_12:433937-449367	957	10	MIKC ^G	-	FLC
CcMADS66	CcSOC1b	V2_12g007190.1	218	SRF, K-box	Chr_12:9071115-9075949	657	7	MIKC ^G	-	SOC1
CcMADS67		V2_12g009260.1	211	SRF, K-box	Chr_12:12648980-12655523	692	6	MIKC ^G	-	AG/STK
CcMADS68	CcSOC1Like-B	V2_13g009180.1	192	SRF, K-box	Chr_13:28823008-28829911	579	6	MIKC ^G	-	SOC1
CcMADS69		V2_13g015600.1	137	SRF	Chr_13:38196053-38199798	414	3	MIKC ^G	-	SEP
CcMADS70	(CcAP1)	V2_13g015610.1	172	K-box	Chr_13:38268961-38273174	519	7	MIKC,SRF incomplete	-	AP1
CcMADS70_corrected	CcAP1	-	211	K-box	Chr_13:38268961-38273724	636	8	MIKC,SRF incomplete	-	AP1
CcMADS71		V2_13g020630.1	215	SRF, K-box	Chr_13:44604397-44610355	648	7	MIKC ^G	-	SEP
CcMADS72	CcSOC1a	V2_14g001970.1	216	SRF, K-box	Chr_14:2757551-2762802	666	7	MIKC ^G	-	SOC1
CcMADS73		V2_14g006800.1	192	SRF, K-box	Chr_14:23531833-23539409	579	4	MIKC ^G	-	AG/STK
CcMADS74		V2_15g006880.1	227	SRF, K-box	Chr_15:7887245-7897105	704	6	MIKC ^G	-	SEP
CcMADS75		V2_15g009280.1	249	SRF	Chr_15:10879232-10879981	750	1	My	-	-
CcMADS76		V2_16g008420.1	203	SRF	Chr_16:22853005-22856757	612	6	MIKC* / Mδ	-	MIKC*
CcMADS77		V2_16g010760.1	156	K-box	Chr_16:28395469-28404407	471	7	MIKC ^G	-	AGL6
CcMADS78	CcSOC1Like-A	V2_16g010770.1	123	SRF	Chr_16:28415914-28421188	372	4	MIKC ^G	-	SOC1
CcMADS79		V2_17g010010.1	254	K-box	Chr_17:31971253-31978191	762	3	MIKC ^G	-	-
CcMADS80		V2_ScYrq3g_1936g000100.1	190	SRF	ScYrq3g_1936:2832-3401	570	1	Ma	-	-
CcMADS81		V2_ScYrq3g_379g000100.1	232	SRF	ScYrq3g_379:2561-3259	699	1	Ma	-	-

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53

54 Supplementary Table S5: Primers developed. Related to Figure 5.

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Primer name	Sequence	F/R	Target	Fragment length (bp) ^a
ORB_7	TCCCAGGCTGATTGTGCTGTCCTTATTAT	F	CcElf1 α	90
ORB_8	ATGCTCACGGGTCTGACCATCCTTA	R	CcElf1 α	90
ORB_57	TGGAAGAAGGTCGAGCAAGT	F	CcSOC1A	98
ORB_58	CCTGGTCCGTTTTTCGGGTA	R	CcSOC1A	98
ORB_59	TGTTGAGCCCGAAAGATGC	F	CcSOC1B	120
ORB_60	TGGTCCGTTTGGACTAGGCA	R	CcSOC1B	120
ORB_105	CTTGAACCTGCCTCGGGT	F	CcFULLike-B	145
ORB_106	GAGAAAGAAGTAGGGCAGCA	R	CcFULLike-B	145
ORB_113	CTGCTTACTGCACCTGAA	F	CcFULLike-A	74
ORB_114	TCATCCCTCATCACTGCT	R	CcFULLike-A	74
ORB_119	TCCCTTCAGCTGCTTCTCC	F	CcAP1 (CcMADS70)	95
ORB_120	AACCTTCCTCATGCCACC	R	CcAP1 (CcMADS70)	95

56

57 ^a Fragment when amplified from cDNA

58