## SUPPLEMENTARY DATA

| Sample types               | Sample description                                     | Sampling date |
|----------------------------|--|---------------|
| Vegetative                 | Shoot tips with/without inflorescence primordia        | 8/11/2002     |
| tissue +/-<br>reproductive | Shoot tips with/without inflorescence primordia        | 8/01/2003     |
| structures                 | Shoot tips with/without inflorescence primordia        | 24/02/2003    |
|                            | Shoot tips with/without inflorescence primordia        | 4/04/2003     |
|                            | Shoot tips without inflorescence primordia             | 1/05/2003     |
|                            | Shoot tips with inflorescence primordia                | 1/05/2003     |
|                            | Fully expanded leaves                                  | 16/05/2003    |
|                            | Shoot tips with/without inflorescence primordia        | 4/07/2003     |
|                            | Shoot tips with/without inflorescence primordia        | 17/09/2003    |
| Reproductive               | Inflorescences (1–2 mm)                                | 1/05/2003     |
| structures                 | Inflorescences (15–20 mm)                              | 28/01/2003    |
|                            | Inflorescences (15–20 mm)                              | 24/02/2003    |
|                            | Inflorescences (15–20 mm)                              | 4/04/2003     |
|                            | Inflorescences (15–20 mm)                              | 30/04/2003    |
|                            | Inflorescences (15–20 mm)                              | 11/06/2003    |
|                            | Inflorescences (25–35 mm) with flower buds around 1 mm | 11/06/2003    |
|                            | Flower buds (2–3 mm)                                   | 11/06/2003    |
|                            | Flower buds (2–3 mm)                                   | 24/07/2003    |
|                            | Flower buds (5–7 mm)                                   | 11/06/2003    |
|                            | Flower buds (10–12 mm) showing petal tip               | 15/08/2003    |
|                            | Flower buds (10–12 mm) showing petal tip               | 26/09/2003    |
|                            | Sepals from flower buds showing petal tip              | 26/09/2003    |
|                            | Petals from flower buds showing petal tip              | 26/09/2003    |
|                            | Stamens from flower buds showing petal tip             | 26/09/2003    |
|                            | Carpels from flower buds showing petal tip             | 26/09/2003    |
|                            | Mature flower buds before open                         | 18/09/2003    |
|                            | Mature flower buds before open                         | 26/09/2003    |
|                            | Fully opened flowers before senescence                 | 26/09/2003    |
|                            | Young seed pods 2 weeks after flower senescence        | 7/10/2003     |
|                            |  | i i           |

TABLE S1. Tissue samples of *Clianthus maximus* 'Kaka King'<sup>®</sup> for RNA isolation

| Homologues        | Gene names       | Species                                  | Accession No.      |
|-------------------|------------------|--|--------------------|
|                   | CmLFY            | Clianthus maximus                        | DQ418756           |
| LFY/FLO           | LEAFY            | Arabidopsis thaliana                     | NM125579           |
|                   | FLO              | Antirrhinum majus                        | AAA62574           |
|                   | UNIFOLIATA (UNI) | Pisum sativum                            | AAB88139           |
|                   | LcLFY            | Lotus corniculatus var. japonicus        | AAX13294           |
|                   | MtUNI            | Medicago truncatula                      | AY928184           |
|                   | <b>StLFY</b>     | Sophora tetraptera                       | DO418760           |
|                   | BoLFY            | Brassica oleracea                        | 005536             |
|                   | NFL2             | Nicotiana tabacum                        | AAC48986           |
|                   | PtLF             | Populus trichocarpa                      | AAB51533           |
|                   | VvLFY            | Vitis vinifera                           | AAM46141           |
|                   | 7FI 1            | Zea mays                                 | ΔΔΩ/3175           |
|                   | NEEDI V          | Dinus radiata                            | AAB68601           |
|                   |                  | Clianthus maximus                        | DO418757           |
| A class           |                  | Arabidonsis thaliana                     | 716421             |
| MADS-box          |                  | Anabidopsis thaliana                     | Z10421<br>NM102205 |
| genes             | SOUA             | Arabiaopsis inaliana<br>Antimbinum maius | CAA45228           |
|                   | SQUA<br>DEAMA    | Antirrhinum majus                        | CAA45228           |
| (AP1/SQUA,        | PEAM4            | Pisum sativum                            | AJ291298           |
| CAL, euFUL)       |                  | Medicago truncatula                      | DQ139345           |
|                   | StAP1            | Sophora tetraptera                       | DQ418/61           |
|                   | LcAPIa           | Lotus corniculatus var. japonicus        | AY770395           |
|                   | LcAP1b           | Lotus corniculatus var. japonicus        | AY770396           |
|                   | MdAP1            | Malus x domestica                        | AY071921           |
|                   | MdCAL            | Malus x domestica                        | GU983665           |
|                   | PtAP1-1          | Populus trichocarpa                      | AAT39554           |
|                   | FRUITFULL        | Antirrhinum majus                        | AY306139           |
|                   | NAP1             | Nicotiana tabacum                        | AAD01421           |
|                   | EAP1             | Eucalyptus globulus                      | AAG24909           |
|                   | MdMADS2          | Malus x domestica                        | U78948             |
|                   | PsFUL            | Pisum sativum                            | AY884287           |
|                   | AGL8             | Arabidopsis thaliana                     | NM125484           |
|                   | LpMADS1          | Lolium perenne                           | AY198326           |
|                   | PrMADS2          | Pinus radiata                            | AAD09207           |
|                   | CmPI             | Clianthus maximus                        | DO418758           |
| B class           | PI               | Arabidopsis thaliana                     | D30807             |
| MADS-box          | GLO              | Antirrhinum maius                        | X68831             |
| genes             | PEAM1            | Pisum sativum                            | AAW29099           |
|                   | MtPI             | Medicago truncatula                      | FI403468           |
| (PI/GLO, AD2/DEE) | StPI             | Sonhora tetrantera                       | DO418762           |
| AP3/DEF)          | I cPIa           | Lotus corniculatus var japonicus         | AY770398           |
|                   | LePh             | Lotus corniculatus var. japonicus        | ΔΥ770399           |
|                   | VvPI             | Vitis vinifora                           | D0059750           |
|                   | FRPI             | Patunia hybrida                          | 003/88             |
|                   | ΩsPI             | Oryza satiya                             | 1 37577            |
|                   |                  | Chuaina mar                              | L3/32/<br>AV210202 |
|                   |                  | Giycine max                              | A I 310303         |
|                   | LCAFJ            | Loius corniculatus var. japonicus        | AI//0400           |
|                   | DEF              | Antirrhinum majus                        | X62810             |
|                   | VvAP3            | Vitis vinifera                           | EF418603           |
|                   | AP3              | Arabidopsis thaliana                     | NM115294           |
|                   | PrDGL            | Pinus radiata                            | AF120097           |

TABLE S2. Floral identity gene homologues used for multiple alignment and phylogenetic analysis

|              | CmAG            | Clianthus maximus                 | DQ418759    |
|--------------|-----------------|-----------------------------------|-------------|
| C class      | AG              | Arabidopsis thaliana              | X53579      |
| MADS-box     | StAG            | Sophora tetraptera                | DQ418763    |
| genes        | PsM7            | Pisum sativum                     | AY884291    |
| (AC/FAR      | LcAGa           | Lotus corniculatus var. japonicus | AY770402    |
| PLE/SHP      | LcAGb           | Lotus corniculatus var. japonicus | AY770403    |
| 1 LL/ 5111 ) | NAG1            | Nicotiana tabacum                 | Q43585      |
|              | VvAG            | Vitis vinifera                    | GU133631    |
|              | PtAG1           | Populus trichocarpa               | AF052570    |
|              | PtAG2           | Populus trichocarpa               | AF052571    |
|              | BnAG            | Brassica napus                    | Q01540      |
|              | FARINELLI (FAR) | Antirrhinum majus                 | AB516405    |
|              | PLENA (PLE)     | Antirrhinum majus                 | S53900      |
|              | PsM8            | Pisum sativum                     | AY884292    |
|              | LcAGL1          | Lotus corniculatus var. japonicus | AY770404    |
|              | SHP1            | Arabidopsis thaliana              | AY727644    |
|              | SHP2            | Arabidopsis thaliana              | AY727669    |
|              | OsMADS3         | Oryza sativa                      | FJ750940    |
|              | ZAG1            | Zea mays                          | NM001111851 |
|              | ZAG2            | Zea mays                          | NM001111908 |
|              | PrMADS9         | Pinus radiata                     | PRU90344    |

TABLE S3. Real-time PCR primers for expression analysis of floral identity genes and housekeeping genes in *Clianthus* 

| Genes          | Primer seque | ences (5 <sup>to 3<sup>t</sup></sup> ) |
|----------------|--------------|--|
| LEAFY          | Forward      | ACG ATC AAT GCC GTG AGT TC             |
|                | Reverse      | TCT AAC TGC TGC TCC AGA CTT TG         |
| APETALA1       | Forward      | ATG CTG AGG TTG CTT TGA TTG            |
|                | Reverse      | TCT AAC TGC TGT TCC AGA CTT TG         |
| PISTALLATA     | Forward      | AGA ACA CAA GCA ACA GGC AAG T          |
|                | Reverse      | GTG CCT GAG CTC AAT TTG CAT            |
| AGAMOUS        | Forward      | TGG TCG CCT CTA TGA ATA TGC TA         |
|                | Reverse      | GTT TGT CTG CTT CTT GCT GGT AA         |
| $\beta$ -Actin | Forward      | GAG CTA TGA GCT GCC TGA TGG ACA        |
|                | Reverse      | GTA ATC TCC TTG CTC ATC CTA TCA        |
| GAPDH          | Forward      | ATG ACA GRT TTG GMA TTG TTG A          |
|                | Reverse      | TGC CCT CAG AYT CYT CCT TGA            |
| 18S rRNA       | Forward      | TAC CGT CCT AGT CTC AAC CAT AA         |
|                | Reverse      | AGA ACA TCT AAG GGC ATC ACA            |

FIG. S1. Comparison of amino acid sequences of CmLFY with representative FLO/LFY-like proteins

|                 |       | 301 360  |
|-----------------|-------|--|
| CmLFY           | (1)   | PGEVARCKKNGLDYLFHLYDQCREFLIQVQTIAKDRGEKCPTKVTNQVFR   |
| LcLFY           | (233) | QREHPFIVTE <mark>PGEVAR</mark> GKKNGLDYLF <mark>HLY</mark> EQCREFLIQVQAIAKDRGEKCPTKVTNQVFR   |
| UNI             | (223) | QREHPFIVTE <mark>PAEVAR</mark> GKKNGLDYLF <mark>HLY</mark> EQCREFLIQVQAIAK <mark>ERGEK</mark> CPTKVTNQVFR                                |
| MtUNI           | (220) | QREHPFIVTE <mark>PGEVAR</mark> GKKNGLDYLF <mark>HLY</mark> EQCREFLIQVQAIAK <mark>ERGEK</mark> CPTKVTNQVFR                                |
| GmFLY           | (235) | QREHPFIVTE <mark>PGEVAR</mark> GKKNGLDYLFHLYEQCREFLMQVQAIAKDRGEKCPTKVTNQVFR  |
| PTLF            | (205) | QREHPFIVTE <mark>PGEVAR</mark> GKKNGLDYLFHLYEQCRDFLIQVQSIAKER <mark>GE</mark> KCPTKVTNQVFR   |
| NFL2            | (237) | QREHPFIVTE <mark>PGEVAR</mark> GKKNGLDYLF <mark>HLY</mark> EQCRDFLIQVQNIAK <mark>ERGEK</mark> CPTKVTNQVFR                                |
| FLO             | (220) | QREHPFIVTE <mark>PGEVAR</mark> GKKNGLDYLF <mark>HLY</mark> EQCRDFLIQVQTIAK <mark>ERGEK</mark> CPTKVTNQVFR                                |
| LFY             | (232) | QREHPFIVTE <mark>PGEVAR</mark> GKKNGLDYLF <mark>HLY</mark> EQCREFLLQVQTIAKDRGEKCPTKVTNQVFR   |
| Bolfy           | (233) | QREHPFIVTE <mark>PGEVAR</mark> GKKNGLDYLF <mark>HLY</mark> EQCREFLLQVQTIAKDRGEKCPTKVTNQVFR   |
| ZFL1            | (220) | QREHPFVVTE <mark>PGEVAR</mark> AKKNGLDYLF <mark>HLY</mark> EQCRVFLLQVQSIAKLG <mark>GHK</mark> SPTKVTNQVFR                                |
| NEEDLY          | (245) | PREHPFIVTEPGELARCKKNGLDYLFDLYEQCGKFLLEVQRIAKEKGEKCPTKVTNQVFR   |
|                 |       |  |
| Om T EV         | (E1)  |  |
| UNLF I          | (202) | IARRAGASI INRPAMRHIVHUQVALHOLDEEASNELRKAFKERGENVGAWKQACINPLVAL   |
| LCLFI<br>UNT    | (293) | IARRAGASI INRPAMRHI VHCIALHCLDEE VSNELRRGFRERGEN VGAWRQACI RPLVAI  |
| UN I<br>M+IINIT | (203) | IARRAGASI INREMMENTI UCIALICLEEV SNELRAGERED CEMUCAMDOA CYMDI WAT  |
| CMELV           | (200) | IARRAGASI INRPRIMENTI UNCIALICEDEE VSNELRAGI RERGEN VGAWRQACI NELVAT   |
| СШЕ ЦІ<br>ППТ Б | (295) | IARAAGASI INAPAMAHI VACIALACIDEE VSNELRAAPARGEN VGAWAQACIAPIDVAI   |
| ГІЦГ<br>NET 2   | (203) | TARAAGASTINAPAMAATIYACTABACLDEDASNABAAATABAGENVGAWAQACTAPBVAT  |
| FLO             | (297) | YAKKACANYTNKEKMENYUHCYATHCIDEA ASNALERATKERGENVGAWROACYKEI VAT   |
| LEA             | (200) | YAKKSGASYTNKRKMRHYVHCYALHCLDEFASNALRRAFKERGENVGAWKQACTNI LVAT  |
| BOLEV           | (293) | VAKKSCANVINKOKMOHVUHCVAIHCIDEEASNAIDSAEKUDCENVOSWKOACIAIDUUT   |
| ZFL1            | (233) | YANKCCASY INKRIMINI VIICIALIICEDEEAONALIRAAYKVRGENVGSWKQACINI LVDI<br>YANKCCASY INKRIMINI VIICIALIICEDEEAONALIRAAYKSRCENVCAWROACYA PLVEI |
| NEEDLY          | (200) | HAKHNGAVYINKPKMRHYVHCYALHCLDSEOSNHLBRLYKERGENVGAWROACYYPLVAT   |
|                 | (000) |  |
|                 |       | 421 480  |
| CmLFY           | (111) | AARQGWDIDAIFNAHPRISIWYV  |
| LCLFY           | (353) | AARQGWDIDAIFNAHPRISIWYVPTKLRQLCHAERNSAAASSSVSVGTAHLPF  |
| UNI             | (343) | AARQGWDIDAIFNAHPRISIWYGPTKLRQLCHAERNGAAASSSVSFGTTHLPF  |
| MtUNI           | (340) | AARQGWDIDAIFNAHPRISIWYVPTKLRQLCHAERNSAAASSSVSVGTAHLPF  |
| GmFLY           | (355) | AARQGWDIDAI NAHPRUSIWYVPTKLRQLCHAERNSVSASSSVSAGSAHLPF  |
| PTLF            | (325) | ASRQGWDIDSIFNAHPRIAIWYVPTKLRQLCYAERNSATSSSSVSGTGGHLPF  |
| NFL2            | (357) | AARQGWDIDTIFNAHPRIAIWYVPTKLRQLCHSERSNAAAAAASSSVSGGGGGGDHLPHF   |
| FLO             | (340) | AARQGWDIDTIFNAHPRISIWYVPTKLRQLCHAERSSAAVAATSSITGGGPADHLPF  |
| LFY             | (352) | ACRHGWDIDAV NAHPRUSIWYVPTKLRQLCHLERNNAVAAAAALVGGISCTGSSTSGRG   |
| Bolfy           | (353) | ACRHGWD1DAVENAHPRUSIWYVPTKLRQLCHLERNNAEAAAATLVGGISCRDRLRLDAL   |
| ZFL1            | (340) | AARHGFDIDAVRAAHPRIAVWYVPTRLRQLCHQARGSHAHAAAGLPPPPMF  |
| NEEDLY          | (365) | ARENNWDLEGIGNRNEKLKIWYVPTKLROLCHMERSKECO   |

Identical and conserved amino acids are shaded. Sequence segments not covered by the CmLFY fragments were not included. ▼ intron/exon split site. E2 and E3: exon 2 and exon 3. Corresponding species names are listed in Table S2.

FIG. S2.. Neighbor-joining phylogenetic tree of representative FLO/LFY orthologues generated with 1000 bootstrap replicates





FIG. S3. Deduced gene structure of CmLFY, CmAP1, CmPI and CmAG fragments in C. maximus

*LFY: Arabidopsis thaliana LEAFY* gene (AF466791); *PEAM4: Pisum sativum AP1* homologue (AJ291298); *MdPI: Malus domestica PI* homologue (AJ291491); *PTAG1: Populus trichocarpa AG* homologue (AF052570).

FIG. S4. Comparison of amino acid sequences of CmAP1 with representative class A MADS-box gene proteins

|   |  | MADS-box   |
|---|--|--|
|   |  |  |
|   |  | 1 60   |
| CmAP1   | (1)  | NKINRQVTFSKRRAGLLKKAHEI <mark>SVLCDA</mark> EVALIVFSNKGKLFEYATD  |
| PEAM4   | (⊥)<br>(1)   | MGRGRVQLKRIENKINRQVTFSKRRAGLLKKAHEISVLCDAEVALIVFSHKGKLFEYATD   |
| LCAPIA  | (⊥)<br>(1)   | MGRGRVQLKKIENKINKQVTFSKKRAGLLKKAHEISVLCDAEVALIVFSHKGKLFEYATD   |
| SQUA<br>1 1 A M   | (⊥)<br>(1)   |  |
| PIAPI-I<br>ND1  | (1)<br>(1)   | MCCCDIOL RD TENKTNDOUTECRDDACI I KRAUETSVLCDAEVALI VE SHAGALFEISIN   |
| Periii.   | (1)  | MGRGRVQLKRIENKINKQVIISKRAAGLEKRAHEISVLCDAEVALVVISHRGRLFEISID   |
| FUI.  | (1)  | RHEMSVLCDADVGLIVESTKGKLEEYATD  |
| LoMADS1   | (1)  | MGRGKVOLKRIENKINROVTESKRRSGLLKKAHEISVLCDAEVGLITESTKGKLYEFATD   |
|   | (-)  |  |
|   |  | <mark>┌──</mark> ► K-box   |
|   | E  | E2▼E3 E3▼E4  |
|   |  | 61 120   |
| CmAP1   | (49)   | SCMERILLERY BRY SYADRQLVANDSESQGNWTIEYTRIKAKIDLLQRNYRHYMGEDIGSM  |
| PEAM4   | (61)   | SCMEKILLERYERYSYADRQLVANDSESQGNWTIEYTRIKAKIDLLQRNYRHYMGEDIGTM  |
| LcAPla  | (61)   | SCMEKILERYERYAYABRQLVANDSESQGNWTIEYTRIKAKIDLLQRNHRHYMGEDUGSM   |
| SQUA<br>DERDI 1   | (61)   | SCMDRILLEKYERYSFAERQLVSNEPQSPANWTLEYSKIKARIELLQRNHRHYMGEDLDSM  |
| PTAPI-I   | (61)   |  |
| API   | (01)   |  |
| PSFUL   | (20)   |  |
| LoMADS1   | (61)   | SCMERT HERTERY STARRY  |
| пыппрот   | (01)   |  |
|   |  |  |
|   |  | K-box ← → C terminal   |
|   |  | K-box ← → C terminal   |
|   |  | K-box $\leftarrow$ → C terminal<br>E4 V E5 E5 V E6 E6 V E7   |
| CmAP1   | (109)  | K-box ← → C terminal<br>E4 ▼ E5 E5 ▼ E6 E6 ▼ E7<br>121 180<br>SLKELOSLEOOLDTALKOIRTRNOLMYESISELOKKEKVIOEONNMLAKKIKEKEKIAA  |
| CmAP1<br>PEAM4  | (109)<br>(121)   | K-box ← C terminal<br>E4 V E5 E5 V E6 E6 V E7<br>121 180<br>SLKELQSLEQQLDTALKQIRTRRNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SLKELQSLEQQLDTALKLIRTRRNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA   |
| CmAP1<br>PEAM4<br>LcAP1a  | (109)<br>(121)<br>(121)  | K-box<br>C terminal<br>E4 VE5 E5 VE6 E6 VE7<br>121<br>SLKELQSLEQQLDTALKQIRTRRNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA<br>SLKELQSLEQQLDTALKLIRTRRNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA<br>SLKELQSLEQQLDTALKHIRTRRNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA  |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA  | (109)<br>(121)<br>(121)<br>(121)   | K-box - C terminal<br>E4 VE5 E5 VE6 E6 VE7<br>121 180<br>SLKELQSLEQOLDTALKQIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SLKELQSLEQOLDTALKLIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SLKELQSLEQOLDTALKHIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SLKELQSLEQOLDTALKHIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA  |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1   | (109)<br>(121)<br>(121)<br>(121)<br>(121)  | K-box ← C terminal<br>E4 VE5 E5 VE6 E6 VE7<br>121 180<br>SLKELQSLEQQLDTALKQIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SLKELQSLEQQLDTALKLIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SLKELQSLEQQLDTALKHIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SLKELQSLEQQLDTALKHIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SLKELQSLEQQLDTALKHIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SLKELQSLEQQLDTALKHIRTERNQLYDSISELQHKEKAIQEQNTMLAKKIKEKEKIAA   |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1  | (109)<br>(121)<br>(121)<br>(121)<br>(121)<br>(121)   | K-box - C terminal<br>E4 V E5 E5 V E6 E6 V E7<br>121 E6 V E0 LDTALKQIRTRRNQLMYESI SELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SIKELQSIEQQIDTALKIIRTRRNQLMYESI SELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SIKELQSIEQQIDTALKIIRTRRNQLMYESI SELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SIKELQSIEQQIDTALKIIRTRRNQLMYESI SELQKKEKVIQEQNNMLAKKIKEKEKIAA<br>SIKELQSIEQQIDTALKIIRTRRNQLMYESI SELQKKEKVIQEQNTMLAKKIKEKEKIAA<br>SIKELQSIEQQIDTALKIIRTRKNQLLYDSI SELQKKEKAIQEQNTMLAKKIKEKEKAA<br>SIKELQNIEQQIDTALKIIRTRKNQLLYDSI SELQIKEKAIQEQNTMLAKKIKEKEKAA<br>SIKELQNIEQQIDTALKIIRTRKNQLMYESI NELQKKEKAIQEQNSMLSKQIKEREKILR   |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PsFUL   | (109)<br>(121)<br>(121)<br>(121)<br>(121)<br>(121)<br>(121)<br>(86)  | K-box ← C terminal<br>E4 VE5 E5 VE6 E6 VE7<br>121 180<br>SLKELQSLEQQLDTALKQIRTRRNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA<br>SLKELQSLEQQLDTALKLIRTRRNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA<br>SLKELQSLEQQLDTALKHIRTRRNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA<br>SLKELQSLEQQLDTALKHIRTRRNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA<br>SLKELQSLEQQLDTALKHIRTRRNQLMYESISELQKKEKAIQEQNTMLAKKIKEKEK IAA<br>SLKELQNLEQQLDTALKLIRERKNHLMYQSISELQIKEKAIQEQNTMLAKKIKEKEKALA<br>SPKELQNLEQQLDTALKHIRTRKNQLMYESINELQKKEKAIQEQNSMLSKQIKEREKILR<br>SMKELQNLEQQLDTALKHIRTRKNQLMYESINELQKKEKAIQEQNSMLSKQIKEREKILR   |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PSFUL<br>FUL  | (109)<br>(121)<br>(121)<br>(121)<br>(121)<br>(121)<br>(121)<br>(86)<br>(90)  | K-box       C terminal         E4 V E5       E5 V E6       C terminal         121       180         SLKELQSLEQQLDTALKQIRTRENQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA         SLKELQSLEQQLDTALKLIRTRENQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA         SLQSLEQQLDTALKHIRTRENQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA         SLQSLEQQLDTALKHIRTRENQLMYESISELQKKEKVIQEQNNMLAKKIKEKEK IAA         SLQSLEQQLDTALKHIRTRENQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKEIA         SLQSLEQQLDTALKHIRTRENQLMYESISELQKKEKAIQEQNMLAKKIKEKEKEIA         SLQSLEQQLDTALKHIRTRENQLMYESISELQKKEKAIQEQNMLVKQIKEKEKAIA         SLQSLEQQLDTALKHIRTRENQLMYESISELQKKEKAIQEQNMLVKQIKEKEKAIA         SLQSLEQQLDTALKHIRTRENQLMYESISELQKKEKAIQEQNMLVKQIKEKEKAIA         SLQSLEQQLDTALKHIRTRENQLMYESISELQKKEKAIQEQNMLVKQIKEKEKAIA         SLQSLEQQLDTALKHIRTRENQLMYESISELQKKEKAIQEQNMLVKQIKEKEKAIA         SLQSLEQQLDTALKHIRTRENQLMYESISELQKKEKAIQEQNMLVKQIKEKEKAIA         SKELQNLEQQLDTALKHIRTRENQLMYESISELQKKEKAIQEQNMLVKQIKEKEKAIA         SKELQNLEQQLDTALKHIRTRENQLMHETISELQKKEKAIQEQNMLVKQIKEKEKAIA   |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PsFUL<br>FUL<br>LpMADS1   | <pre>(109) (121) (121) (121) (121) (121) (121) (121) (86) (90) (121)</pre>   | K-box       C terminal         E4 V E5       E5 V E6       E6 V E7         121       180         SLKELQSLEQOLDTALKQIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA         SLKELQSLEQOLDTALKLIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA         SLKELQSLEQOLDTALKLIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA         SLKELQSLEQOLDTALKLIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA         SLKELQSLEQOLDTALKNIRTERNQLMYESISELQKKEKVIQEQNNMLAKKIKEKEKIAA         SLKELQSLEQOLDTALKNIRTERNQLMYESISELQKKEKAIQEQNNMLAKKIKEKEKIAA         SLKELQNLEQOLDTALKNIRTERNQLMYESISELQKKEKAIQEQNMLVKQIKEKEKAIA         SLKELQNLEQOLDTALKNIRTERNQLMYESINELQKKEKAIQEQNSMLSKQIKEREKILR         SKELQNLEQOLDTALKNIRTERNQLMYESINELQKKEKAIQEQNSMLSKQIKEREKILR         SKELQNLEQOLDTALKNIRTERNQLMYESINELQKKEKAIQEQNSMLSKQIKEREKILR         SKELQNLEQOLDTALKHIRTERNQLMYESINELQKKEKAIQEQNSMLSKQIKEREKILR         SKELQNLEQOLDTALKHIRTERNQLMYESISELQKKEKAIQEQNSMLSKQIKEREKILR         SKELQNLEQOLDTALKHIRTERNQLMYESISELQKKEKAIQEQNSMLSKQIKEREKILR         SKELQNLEQOLDTALKHIRTERNQLMYESISELQKKEKAIQEQNNLLAKKIKEREQEFA         NLKELQQLEQOLESSIKHIRARKNQLMHETISELQKKERSIQEENKILQKELIEKQKAHT   |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PSFUL<br>FUL<br>LpMADS1   | <pre>(109) (121) (121) (121) (121) (121) (121) (86) (90) (121)</pre>   | K-box - Cterminal<br>E4 VE5 E5 VE6 E6 VE7<br>121 180<br>SIKELOSLEOOLDTALKOIRTERNOLMYESISELOKKEKVIQEONNMLAKKIKEKEKIAA<br>SIKELOSLEOOLDTALKUIRTERNOLMYESISELOKKEKVIQEONNMLAKKIKEKEKIAA<br>SIKELOSLEOOLDTALKUIRTERNOLMYESISELOKKEKVIQEONNMLAKKIKEKEKIAA<br>SIKELOSLEOOLDTALKUIRTERNOLMYESISELOKKEKVIQEONNMLAKKIKEKEKIAA<br>SIKELOSLEOOLDTALKUIRTERNOLMYESISELOKKEKVIQEONNMLAKKIKEKEKIAA<br>SIKELONLEOOLDTALKUIRTERNOLMYESISELOKKEKAIQEONNMLAKKIKEKEKALA<br>SIKELONLEOOLDTALKUIRERKNHLMYOSISELOKKEKAIQEONSMLSKOIKEREKILE<br>SMKELONLEOOLDTALKUIRERKNHLMYOSISELOKKEKAIQEONSMLSKOIKEREKILE<br>SMKELONLEOOLDTALKUIRSEKNOLMHETISELOKKEKAIQEONNLLAKKIKEREQEFA<br>NLKELONLEOOLESSIKHIRAEKNOLMHESISELOKKERSLOEENKILOKELIEKOKAH  |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PSFUL<br>FUL<br>LpMADS1   | (109)<br>(121)<br>(121)<br>(121)<br>(121)<br>(121)<br>(86)<br>(90)<br>(121)  | $\begin{array}{c c} K-box & \leftarrow C terminal\\ E4 \lor E5 & E5 \lor E6 & E6 \lor E7 \end{array}$  |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PsFUL<br>FUL<br>LpMADS1   | <pre>(109) (121) (121) (121) (121) (121) (121) (86) (90) (121)</pre>   | $\begin{array}{c c} K-box & \leftarrow C terminal \\ E4 \lor E5 & E5 \lor E6 & E6 \lor E7 \\ \hline 121 & 180 \\ Sikelosieoldtalkoirternolmyesiselokkekvioeonnmlakkikekekiaa \\ sikelosieoldtalkiirternolmyesiselokkekvioeonnmlakkikekekiaa \\ sikelosieoldtalkiirternolmyesiselokkekvioeonnmlakkikekekiaa \\ sikelosieoldtalkiirternolmyesiselokkekvioeonnmlakkikekekiaa \\ sikelosieoldtalkiirternolmyesiselokkekaioeonnmlakkikekekeia \\ sikelonieoldtalkiirternolmyesiselokkekaioeonnmlokkikekekeia \\ sikelonieoldtalkiirternolmyesiselokkekaioeonnmlokkikekekeia \\ sikelonieoldtalkiirternolmyesiselokkekaioeonnmlokoikekekaia \\ sikelonieoldtalkiirternolmyesiselokkekaioeonnmlokoikekekaia \\ sikelonieoldtalkiirternolmyesiselokkekaioeonnmlokoikekekaia \\ hikelonieoldtalkiirternolmyesiselokkekaioeonnilakkikereeta \\ metalonieoloolessikiirterenommetaselokkeresioeenkilokeliekokaia \\ outoreolessikiirterenommetaselokkeresioeenkilokeliekokai$  |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PsFUL<br>FUL<br>LpMADS1<br>CmAP1<br>PEAM4   | <pre>(109) (121) (121) (121) (121) (121) (121) (121) (86) (90) (121) (169) (181)</pre>   | $\begin{array}{c c} K-box & \leftarrow C terminal \\ E4 \lor E5 & E5 \lor E6 & E6 \lor E7 \end{array}$   |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PsFUL<br>FUL<br>LpMADS1<br>CmAP1<br>PEAM4<br>LcAP1a   | <pre>(109) (121) (121) (121) (121) (121) (121) (86) (90) (121) (169) (181) (181)</pre>   | $\begin{array}{c c} K \best{black} b \best{black} c \best{black} c \best{black} b \best{black} c \bst{black} c \bst{black} c \bst{black} c \bst{black} c$ |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PSFUL<br>FUL<br>LpMADS1<br>CmAP1<br>PEAM4<br>LcAP1a<br>SQUA   | <pre>(109) (121) (121) (121) (121) (121) (121) (121) (121) (121) (169) (121) (169) (181) (181) (181)</pre>   | $\begin{array}{c c} K \ box \$ |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PsFUL<br>FUL<br>LpMADS1<br>CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1  | <pre>(109) (121) (121) (121) (121) (121) (121) (121) (121) (121) (121) (121) (181) (181) (181) (181)</pre>   | $\begin{array}{c c} K \cdot box & \leftarrow C \ terminal\\ E4 \lor E5 & E5 \lor E6 & C \ e7 \lor e7 \cr e7 \lor e7 \lor$   |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PSFUL<br>FUL<br>LpMADS1<br>CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1   | <pre>(109) (121)</pre>   | $\begin{array}{c c} K \ box \$ |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PSFUL<br>FUL<br>LpMADS1<br>CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PSFUL  | <pre>(109) (121) (121) (121) (121) (121) (121) (86) (90) (121) (169) (181) (181) (181) (181) (181) (186)</pre>   | $\begin{array}{c c} K-box & \leftarrow C terminal \\ E4 VE5 & E5 VE6 & E6 VE7 \\ \hline \\ 121 & & & & & & & & & & & & & & & & & &$  |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PsFUL<br>FUL<br>LpMADS1<br>CmAP1<br>PUL<br>EAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PsFUL<br>FUL                               | <pre>(109) (121) (</pre> | $\begin{tabular}{lllllllllllllllllllllllllllllllllll$  |
| CmAP1<br>PEAM4<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PsFUL<br>FUL<br>LpMADS1<br>CmAP1<br>FUL<br>LpMADS1<br>CmAP1<br>FUL<br>LcAP1a<br>SQUA<br>PTAP1-1<br>AP1<br>PsFUL<br>FUL<br>LpMADS1 | <pre>(109) (121) (121) (121) (121) (121) (121) (121) (121) (121) (121) (181) (181) (181) (181) (181) (181) (181) (181) (181) (181) (181) (181)</pre>   | $\begin{tabular}{lllllllllllllllllllllllllllllllllll$  |

Identical and conserved amino acids were shaded. Sequence segments not covered by CmAP1 were not included.

▼ split sites of intron/exon. E1-E8: exon 1-8. Corresponding species names are listed in Table S2.

FIG. S5. Neighbor-joining phylogenetic tree of representative representative class A MADS-box gene proteins generated with 1000 bootstrap replicates



FIG. S6. Comparison of amino acid sequences of CmPI with representative class B MADS-box gene proteins

|  |  |  | MADS-box  |  |
|--|--|--|---|--|
|  |  | 1  |   | 60   |
| CmPI   | (1)  | MG <mark>RGKI</mark> EIKRIENTS   | S <mark>NRQVTYSKR</mark> KN <mark>GILKKA</mark> KEIS  | VLCD <mark>AQLSLII</mark> FGAS <mark>GK</mark> MHEYISP   |
| StPI   | (1)  | MG <mark>RGKI</mark> EIKRIENTS   | S <mark>NRQVT</mark> Y <mark>SKR</mark> KN <mark>G</mark> IL <mark>KKA</mark> KEII  | VLCD <mark>AQVSLII</mark> FGSS <mark>GK</mark> MHEYISP   |
| PEAM1  | (1)  | MG <mark>RGKI</mark> EIKRIEN <mark>SS</mark>   | S <mark>NRQVTYSKR</mark> KN <mark>GILKKA</mark> KEIS  | VLCD <mark>AQVSLIL</mark> FGAS <mark>GK</mark> MHEYISP   |
| MtPI   | (1)  | MG <mark>RGKI</mark> EIKRIENSS   | S <mark>NRQVTYSKR</mark> KN <mark>GILKKA</mark> KEIS  | VLCD <mark>AQVSLIL</mark> FGAS <mark>GK</mark> MHEYISP   |
| LcPIb  | (1)  | MG <mark>RGKI</mark> EIKRIEN <mark>SS</mark>   | S <mark>NRQVTYSKR</mark> KNGILKKAKEIS   | VLCD <mark>AQVSLII</mark> FGSS <mark>GK</mark> MHEYISP   |
| LcPIa  | (1)  | MG <mark>RGKI</mark> EIKRIEN <mark>SS</mark>   | S <mark>NRQVTYSKR</mark> KN <mark>GILKKA</mark> KEII  | VLCD <mark>AQVSLII</mark> FAAS <mark>GK</mark> MHDYISP   |
| VvPI   | (1)  | MG <mark>RGKI</mark> EIKRIENSS   | S <mark>NRQVT</mark> Y <mark>SKR</mark> RN <b>G</b> IM <mark>KKA</mark> KEII  | VLCDAHVSLVIFASS <mark>GK</mark> MHEYCSP  |
| GLO  | (1)  | M <mark>GRGKI</mark> EIKRIEN <mark>SS</mark>   | S <mark>NRQVTYSKR</mark> RNGIM <mark>KKA</mark> KEIS  | VLCDAHVSVII <mark>F</mark> ASS <mark>GK</mark> MHEFCSP   |
| PI   | (1)  | MG <mark>RGKI</mark> EIKRIENAN   | JNRVVTFSKRRNGLVKKAKEII  | VLCDAKVALIIFASN <mark>GK</mark> MIDYCCP  |
| OsPI   | (1)  | MG <mark>RGKI</mark> EIKRIENSI   | I <mark>NRQVT</mark> F <mark>SKR</mark> RS <mark>G</mark> IL <mark>KKA</mark> REIG  | G <mark>VLCD</mark> REVGVVIFSSA <mark>GK</mark> LSDYCTP  |
| LcAP3  | (1)  | MARGKIQIKRIENTI  | NRQVTYSKRRNGLFKKANELI   | VLCDAKVSIIMFSST <mark>GK</mark> LHEYISP  |
|  |  |  |   |  |
|  |  |  |   |  |
|  |  |  |   |  |
|  |  |  | ⊢→ K-b  | DX   |
|  |  | E1▼E2  | F2▼E3   | ox<br>E3▼E4  |
|  |  | <b>E1▼E2</b><br><sup>61</sup>  | F2▼E3   | E3▼E4  |
| CmPI   | (61)   | <b>E1 V E2</b><br>61<br>STTLIDILDR <mark>¥</mark> QRAS   | K-b<br>E2▼E3<br>KTIMDTKHENLSNEIDRIKE  | OX<br>E3▼E4<br>120<br>KENDSMQIELRHLK   |
| CmPI<br>StPI   | (61)<br>(61)   | <b>E1▼E2</b><br>61<br>STTLIDILDR¥QRAS<br>STTLIDILDR¥HKAS   | E2▼E3<br>GKTIMDTKHENLSNEIDRIKH<br>KRLMDAKHENLSNEIDRVKH  | OX<br>E3▼E4<br>120<br>KENDSMQIELRHLK   |
| CmPI<br>StPI<br>PEAM1  | (61)<br>(61)<br>(61)   | E1VE2<br>61<br>STTLIDILDRYQRAS<br>STTLIDILDRYHKAS<br>STTLIDVLDRYQRAS   | K-b<br>E2▼E3<br>CKTIWDTKHENLSNEIDRIKE<br>CKRLWDAKHENLSNEIDRVKE<br>CKTLWDAKHENLSNEIDRIQE   | OX<br>E3▼E4<br>120<br>KENDSMQIELRHLK<br>KENDSMQIELRH<br>KENDSMQIELRHLKGEDITSLNYKE  |
| CmPI<br>StPI<br>PEAM1<br>MtPI  | (61)<br>(61)<br>(61)<br>(61)                                 | E1VE2<br>61<br>STTLIDILDRYQRAS<br>STTLIDILDRYHKAS<br>STTLIDVLDRYQRAS<br>STTLIDILDRYQRAS  | K-b<br>E2▼E3<br>CKTIWDTKHENLSNEIDRIKK<br>CKRLWDAKHENLSNEIDRVKK<br>CKTLWDAKHENLSNEIDRIQF<br>CKTLWDAKHENLSNEIDRIKF  | E3▼E4<br>120<br>KENDSMQIELRHLK<br>KENDSMQIELRH<br>KENDSMQIELRHLKGEDITSLNYKE<br>KENDSMQIDLRHLKGEDITSLNYKE   |
| CmPI<br>StPI<br>PEAM1<br>MtPI<br>LcPIb                                       | (61)<br>(61)<br>(61)<br>(61)<br>(61)                         | E1 VE2<br>61<br>STTLIDILDRYQRAS<br>STTLIDILDRYHKAS<br>STTLIDVLDRYQRAS<br>STTLIDILDRYQRAS<br>STTLIDVLDRYQRAS  | K-b<br>E2▼E3<br>CKTIWDTKHENLSNEIDRIK<br>CKRLWDAKHENLSNEIDRVK<br>CKTLWDAKHENLSNEIDRIK<br>CKTLWDAKHENLSNEIDRIK<br>CKTLWDAEHENLSNEIDRVK  | E3▼E4<br>120<br>KENDSMQIELRHLK<br>KENDSMQIELRH<br>KENDSMQIELRHLKGEDITSLNYKE<br>KENDSMQIDLRHLKGEDITSLNYKE<br>KENDSMQIELRHLKGDDITSLNYKE  |
| CmPI<br>StPI<br>PEAM1<br>MtPI<br>LcPIb<br>LcPIa                              | (61)<br>(61)<br>(61)<br>(61)<br>(61)<br>(61)                 | E1VE2<br>61<br>STTLIDILDRYQRAS<br>STTLIDILDRYHKAS<br>STTLIDVLDRYQRAS<br>STTLIDILDRYQRAS<br>STTLIDVLDRYQRAS<br>STTLIDVLDRYQRAS  | K-b<br>E2 V E3<br>CKTIWDTKHENLSNEIDRIK<br>CKRLWDAKHENLSNEIDRVK<br>CKTLWDAKHENLSNEIDRIK<br>CKTLWDAEHENLSNEIDRVK<br>CKTLWDAEHENLSNEIDRVK<br>CKRLWDAKHENLNGEIERLK  | E3▼E4<br>120<br>KENDSMQIELRHLK<br>KENDSMQIELRHLKGEDITSLNYKE<br>KENDSMQIDLRHLKGEDITSLNYKE<br>KENDSMQIELRHLKGDDITSLNYKE<br>KENDSMQIELRHLKGDDITSLNYKE<br>KENDGMQIELRHLKGDDINSLNYKE  |
| CmPI<br>StPI<br>PEAM1<br>MtPI<br>LcPIb<br>LcPIa<br>VvPI                      | (61)<br>(61)<br>(61)<br>(61)<br>(61)<br>(61)<br>(61)         | E1VE2<br>61<br>STTLIDILDRYQRAS<br>STTLIDILDRYHKAS<br>STTLIDVLDRYQRAS<br>STTLIDILDRYQRAS<br>STTLIDVLDRYQRAS<br>STTLIDVLDRYHKTS<br>STTLIDILDRYHKTS   | K-b<br>E2 VE3<br>CKTIWDTKHENLSNEIDRIK<br>CKRLWDAKHENLSNEIDRVK<br>CKTLWDAKHENLSNEIDRIK<br>CKTLWDAEHENLSNEIDRVK<br>CKRLWDAEHENLSNEIDRVK<br>CKRLWDAKHENLSNEIDRIK<br>CKRLWDAKHENLSNELDRIK   | E3▼E4<br>120<br>KENDSMQIELBHLK<br>KENDSMQIELBH<br>KENDSMQIELBHLKGEDITSLNYKE<br>KENDSMQIELBHLKGDDITSLNYKE<br>KENDSMQIELBHLKGDDITSLNYKE<br>KENDGMQIELBHLKGDDINSLNYKE<br>KENDSMQIELBHLKGDDINSLNYKE<br>KENDSMQIELBHLKGDDINSLNYKE                                 |
| CmPI<br>StPI<br>PEAM1<br>MtPI<br>LcPIb<br>LcPIa<br>VvPI<br>GLO               | (61)<br>(61)<br>(61)<br>(61)<br>(61)<br>(61)<br>(61)<br>(61) | E1VE2<br>61<br>STTLIDILDRYQRAS<br>STTLIDILDRYHKAS<br>STTLIDVLDRYQRAS<br>STTLIDVLDRYQRAS<br>STTLIDVLDRYQRAS<br>STTLVDMLERYHKTS<br>STTLIDILDRYHKQS<br>STTLVDMLDHYHKLS  | K-b<br>E2 VE3<br>CKTIWDTKHENLSNEIDRIKH<br>CKRLWDAKHENLSNEIDRVKH<br>CKTLWDAKHENLSNEIDRIKH<br>CKTLWDAKHENLSNEIDRVKH<br>CKRLWDAKHENLNGEIERLKH<br>CKRLWDAKHENLSNELDRIKH<br>CKRLWDAKHENLSNELDRIKH<br>CKRLWDAKHENLSNELDRIKH<br>CKRLWDPKHEHLDNEINRVKH  | E3 VE4<br>120<br>ENDSMQIELRHLK<br>ENDSMQIELRHLKGEDITSLNYKE<br>ENDSMQIELRHLKGEDITSLNYKE<br>ENDSMQIELRHLKGDDITSLNYKE<br>ENDSMQIELRHLKGDDINSLNYKE<br>ENDSMQIELRHLKGEDISSLHHKE<br>ENDSMQIELRHLKGEDISSLHKE  |
| CmPI<br>StPI<br>PEAM1<br>MtPI<br>LcPIb<br>LcPIa<br>VvPI<br>GLO<br>PI         | (61)<br>(61)<br>(61)<br>(61)<br>(61)<br>(61)<br>(61)<br>(61) | E1VE2<br>61<br>STTLIDILDRYQRAS<br>STTLIDILDRYHKAS<br>STTLIDVLDRYQRAS<br>STTLIDVLDRYQRAS<br>STTLIDVLDRYQRAS<br>STTLIVDMLERYHKTS<br>STTLIDILDRYHKQS<br>STTLVDMLDHYHKLS<br>SMDLGAMLDQYQKLS                                      | K-b<br>E2 VE3<br>CKTIWDTKHENLSNEIDRIKH<br>CKRLWDAKHENLSNEIDRVKH<br>CKTLWDAKHENLSNEIDRIKH<br>CKTLWDAEHENLSNEIDRVKH<br>CKRLWDAKHENLSNEIDRIKH<br>CKRLWDAKHENLSNEIDRIKH<br>CKRLWDAKHENLSNEIDRIKH<br>CKRLWDAKHENLSNEIDRIKH<br>CKRLWDAKHENLSNEIDRIKH  | E3 VE4<br>120<br>ENDSMQIELRHLK<br>ENDSMQIELRHLKGEDITSLNYKE<br>ENDSMQIELRHLKGEDITSLNYKE<br>ENDSMQIELRHLKGEDITSLNYKE<br>ENDSMQIELRHLKGEDISSLHKE<br>ENDSMQIELRHLKGEDISSLHKE<br>ENDSMQIELRHLKGEDITTLNYKE<br>ENDSMQIELRHLKGEDITTLNYKE<br>ENDSLQLELRHLKGEDIQSLNLKN |
| CmPI<br>StPI<br>PEAM1<br>MtPI<br>LcPIb<br>LcPIa<br>VvPI<br>GLO<br>PI<br>OSPI | <pre>(61) (61) (61) (61) (61) (61) (61) (61)</pre>           | E1VE2<br>61<br>STTLIDILDRYQRAS<br>STTLIDILDRYHKAS<br>STTLIDVLDRYQRAS<br>STTLIDVLDRYQRAS<br>STTLIDVLDRYQRAS<br>STTLIDVLDRYHKTS<br>STTLIDILDRYHKTS<br>STTLVDMLCHYHKLS<br>STTLVDMLDHYHKLS<br>SMDLGAMLDQYQKLS<br>KTTLSRILEKYQTNS | K-b<br>E2 VE3<br>CKTIWDTKHENLSNEIDRIKH<br>CKRLWDAKHENLSNEIDRVKH<br>CKTLWDAKHENLSNEIDRVKH<br>CKTLWDAKHENLSNEIDRVKH<br>CKRLWDAKHENLSNEIDRVKH<br>CKRLWDAKHENLSNEIDRIKH<br>CKRLWDAKHENLSNEIDRIKH<br>CKRLWDAKHENLSNEIDRIKH<br>CKLLWDAKHENLSNEIDRIKH<br>CKLLWDAKHENLSNEIDRIKH<br>CKLLWDAKHENLSNEIDRIKH<br>CKLLWDAKHENLSNEIDRIKH | E3 VE4<br>120<br>ENDSMQIELRHLK<br>ENDSMQIELRHLKGEDITSLNYKE<br>ENDSMQIELRHLKGEDITSLNYKE<br>ENDSMQIELRHLKGEDITSLNYKE<br>ENDSMQIELRHLKGEDISSLHKE<br>ENDSMQIELRHLKGEDISSLHKE<br>ENDSMQIELRHLKGEDITTLNYKE<br>ENDSLQLELRHLKGEDIQSLNLKN<br>ENDNMQIELRHKGEDLNSLQPKE  |

Identical and conserved amino acids were shaded. Sequence segments not covered by CmPI were not included.

▼ split sites of intron/exon. E1-E4: exon 1- 4. Corresponding species names are listed in Table S2.

FIG. S7. Neighbor-joining phylogenetic tree of representative representative class B MADS-box gene proteins generated with 1000 bootstrap replicates.



FIG. S8. Comparison of amino acid sequences of CmAG with representative class C MADS-box gene proteins



Identical and conserved amino acids were shaded. Sequence segments not covered by CmAG were not included.

▼ split sites of intron/exon. E2-E6: exon 2- 6. Corresponding species names are listed in Table S2.

FIG. S9. Neighbor-joining phylogenetic tree of representative representative class C MADS-box gene proteins generated with 1000 bootstrap replicates

