4   **Supplementary material**

5   Supplementary material Fig. 1. Alignment of several plant *FT*/*TFL1*-like genes and the *E.*

6   *globulus* putative homologues of *FT* and *TFL1* (*EglFT1* and *EglTFL1*). Shading levels

7   indicate degree of conservation among amino acids: black = 90%, dark grey = 70%, light

8   grey = 50%. Black triangles indicate positions of introns. NCBI/TAIR accession numbers of

9   sequences are given in Accessory Publication Table 1.

10   At, *Arabidopsis thaliana*; Ci, *Citrus unshiu*; Cm, *Cucurbita maxima*; Cr, *Chenopodium rubrum*; Egl, *Eucalyptus globulus*;

11   Eo, *E. occidentalis*; In, *Ipomoea nil*; Le, *Lycopersicon esculentum*; Mc, *Metrosideros collina*; Me, *M. excelsa*; Md, *Malus* x

12   domestica; Mt, *Medicago truncatula*; Pd, *Populus deltoides*; Pn, *P. nigra*; Pt, *P. tremula*; P, *P. trichocarpa*; Ps, *Pisum*

13   *sativum*; Vv, *Vitis vinifera*.

Multiple sequence alignment (three blocks).

Block 1 (ruler: 20, 40, 60, 80):

```
EglFT1   : ----------------------------------------D-----------------      :  29
LeSP3D   : ---MPRE-RD...                                                   :  86
PnFT3b   : ---MSRD-RD...                                                   :  86
PnFT4    : ---MSRD-RD...                                                   :  86
PtFT1    : ---MSRD-RD...                                                   :  86
PnFT1a   : ---MPRD-RE...                                                   :  86
PnFT2a   : ---MPRD-RE...                                                   :  86
PdFT1    : ---MPRD-RE...                                                   :  86
AtFT     : ---MSINIRD...                                                   :  87
AtTSF    : ---MSLSRRD...                                                   :  87
LeSP6A   : ---MPRV--D...                                                   :  85
LeSP5G   : ---MPRD---...                                                   :  84

EglTFL1  : ----------------------------------------------                  :  20
AtCEN    : ---MARISSD...                                                   :  88
LeSP     : ---MASKMCE...                                                   :  88
EoTFL1   : ----------------------------------------------                  :  21
McTFL1   : ----------------------------------------------                  :  21
MeTFL1   : ----------------------------------------------                  :  21
PnTFL1   : ---MA-KMSE...                                                   :  88
PnFTL3a  : ---MA-NLSD...                                                   :  87
LeSP9D   : ----MARSLE...                                                   :  86
AtTFL1   : MENMGTRVIE...                                                   :  90

AtBFT    : ----MSREIE...                                                   :  87
PnFTL1   : ----MSRAME...                                                   :  87

AtMFT    : ----MAASVD...                                                   :  85
PnFTL4a  : ----MAASVD...                                                   :  85
LeSP2G   : -METSARSVD...                                                   :  91
```

Block 3 (ruler: 100, 120, 140, 160, 180):

```
EglFT1   : ... : 113
LeSP3D   : ... : 177
PnFT3b   : ... : 174
PnFT4    : ... : 174
PtFT1    : ... : 174
PnFT1a   : ... : 174
PnFT2a   : ... : 174
PdFT1    : ... : 174
AtFT     : ... : 175
AtTSF    : ... : 175
LeSP6A   : ... : 140
LeSP5G   : ... : 175

EglTFL1  : ... :  53
AtCEN    : ... : 175
LeSP     : ... : 175
EoTFL1   : ... :  61
McTFL1   : ... :  58
MeTFL1   : ... :  58
PnTFL1   : ... : 174
PnFTL3a  : ... : 171
LeSP9D   : ... : 172
AtTFL1   : ... : 177

AtBFT    : ... : 177
PnFTL1   : ... : 173

AtMFT    : ... : 173
PnFTL4a  : ... : 173
LeSP2G   : ... : 178
```

1

2

3

2

1 Supplementary material Fig. 2. Variation in expression of reference and flowering genes in

2 three genotypes (LateA from this study plus two additional genotypes) of *E. globulus*

3 harvested from 1100 h to 1700 h during flower bud initiation in spring 2007: a) *Egl18S* in

4 Leaf 2; b) *Egl18S* in apex; c) *EglFT1* mRNA abundance, relative to *Egl18S*, in Leaf 2; d)

5 *ELF1* mRNA abundance, relative to *Egl18S*, in apex.
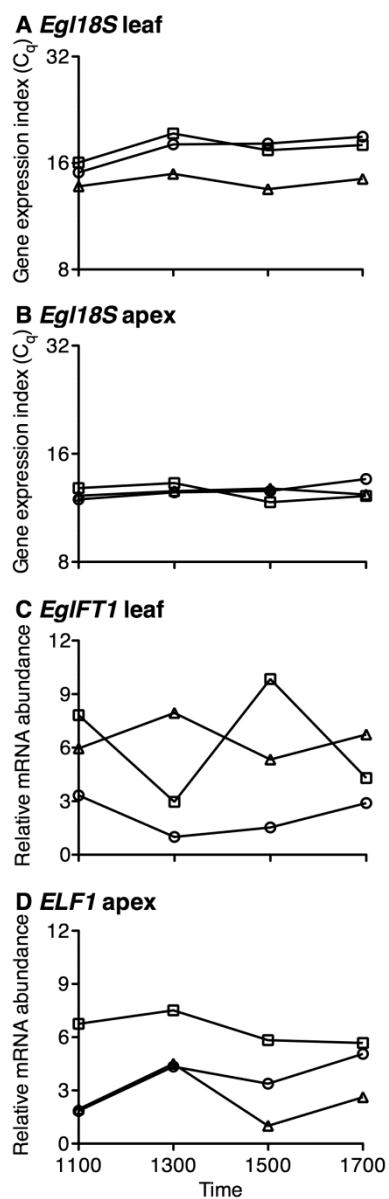
6

7

1 **Table 1. Genes used for phylogenetic analyses of the *FT/TFL1* gene family. Accession**

2 **numbers are NCBI or TAIR accession numbers.**

3 **At,** *Arabidopsis thaliana*; **Ci,** *Citrus unshiu*; **Cm,** *Cucurbita maxima*; **Cr,** *Chenopodium rubrum*; **Egl,**

4 *Eucalyptus globulus*; **Eo,** *E. occidentalis*; **In,** *Ipomoea nil*; **Le,** *Lycopersicon esculentum*; **Mc,** *Metrosideros*

5 *collina*; **Me,** *M. excelsa*; **Md,** *Malus* x domestica; **Mt,** *Medicago truncatula*; **Pd,** *Populus deltoides*; **Pn,** *P.*

6 *nigra*; **Pt,** *P. tremula*; **P,** *P. trichocarpa*; **Ps,** *Pisum sativum*; **Vv,** *Vitis vinifera*.

7

Gene	Accession number
EglFT1	HQ453992
LeSP3D	AY186735
PnFT3b	AB110612
PnFT4	AB369074
PtFT1	DQ387859
PnFT1a	AB106111
PnFT2a	AB109804
PdFT1	AY515152
AtFT	AT1G65480
AtTSF	AT4G20370
LeSP6A	AY186737
LeSP5G	AY186736
EglTFL1	HQ385322
AtCEN	AT2G27550
LeSP	U84140
EoTFL1	EU573981
McTFL1	AY170873
MeTFL1	AY170872
PnTFL1	AB181183
PnFTL3a	AB181185
LeSP9D	AY186738
AtTFL1	AT5G03840
AtBFT	AT5G62040
PnFTL1	AB161110
AtMFT	AT1G18100
PnFTL4a	AB181241
LeSP2G	AY186734