Supplementary Table S2 (Ahn et al.)

Accession numbers and amino acid sequences of TFL1 and FT homologs.

TFL1 subfamily
>Cs TFL AY344245 MAARMLEPLAVGGVIGDVIESFTPSIKMSVTYDNKQVCNGHELFPSTVVSKPRVEIQGGDMRSFFTLVMTDPDVPGPSDPYLREHLHWIVTDIPGTTDATFGRELVSYEIPRPNIGIHRFVFVLFKQTRRQTVNPPSSRDHFNTRAFAAENDLGLPVAAVYFNAQRETAARRR
>Nt CET1 AF145259 MASRVVEPLVVARVIGEVVDSFNPSVKLNVIYNGSKQVFNGHELMPAVIAAKPRVEIGGEDMRSAYTLIMTDPDVPGPSDPYLREHLHWIVTDIPGSTDSSFGREIVSYESPKPVIGIHRYVLLLYKQSGRQTVKPAATRDHFNTRRYTAENGLGSPVAAVYFNAQRETAARRR
>Nt CET2 AF145260 MGSKMSDPLVIGRVIGEVVDYFTPSVKMSVTYNSSKHVYNGHELFPSSVTSKPRVEVHGGDLRSFFTMIMIDPDVPGPSDPYLREHLHWIVTDIPGTTDCSFGKEIVGYEMPRPNIGIHRFVFLLFKQKKRQTVLTAPLSRDRFNTRKFAEENELGSPVAAVFFNCQRETAARRR
>Nt CET4 AF145261 MGSKMSDPLVIGRVIGEVVDYFTPSVKMSVTYNSSKHVYNGHELFPSSVTSKPRVEVHGGDLRSFFTLIMIDPDVPGPSDPYLREHLHWIVTDIPGTTDCSFGREIVGYEMPRPNIGIHRFVFLLFKQKKRQTLLSAPLSRDRFNTRKFSEENELGSPVAAAFFNCQRETAARRR
>Nt CET5 AF145262 AVTIRPRVEVQGGDMRTFFTLVITDPDVPGPSDPYLREHVHWIVTDIPGTTDATFGKELVSYEIPRPNIGIHRFVFVLFKQKCRQSVSPPTSRDHFNTRNFANVNDLGPPVAAVFFNA
>Le SP U84140 MASKMCEPLVIGRVIGEVVDYFCPSVKMSVVYNNNKHVYNGHEFFPSSVTSKPRVEVHGGDLRSFFTLIMIDPDVPGPSDPYLREHLHWIVTDIPGTTDCSFGREVVGYEMPRPNIGIHRFVFLLFKQKKRQTISSAPVSRDQFSSRKFSEENELGSPVAAVFFNCQRETAARRR
>Le SP9D AY186738 MARSLEPLIVGRVIGDVIDSFNPTIKMSITYNNKLVCNGHELFPSVVSSRPKVEVQGGDLRTFFTLVMTDPDVPGPSDPYMREHLHWIITDIPGTTDATFGRELVSYETPRPNIGIHRFVFVLFKQKSRSSVSQPTSRDHFNTRNFAQENNLEQPVTAVFFNAQRETAARRR
>Am CEN S81193 MAAKVSSDPLVIGRVIGDVVDHFTSTVKMSVIYNSNNSIKHVYNGHELFPSAVTSTPRVEVHGGDMRSFFTLIMTDPDVPGPSDPYLREHLHWIVTDIPGTTDSSFGKEVVSYEMPRPNIGIHRFVFLLFKQKKRGQAMLSPPVVCRDGFNTRKFTQENELGLPVAAVFFNCQRETAARRR
>Ej EjTFL1 AB162045 MTRALEPLVVGRVIGDVLDSFTATTKMSVTYNTKLVCNGLELFPSVVTAKPRVEIQGGDMRSFFTLVMTDPDFPGPSDPYLREHLHWIVTDIPGTTDATFGREVVSYEMPRPNIGIHRFVFVLFKQNRRQSINTPSSRDHFSTRSFAAENDLGLPVAAVYFNAQRETAARRR
>Md MdTFL1 AB052994 MKRASEPLVVGRVIGDVLDSFTATTKMSVTYNTKLVCNGLELFPSVVTAKPRVEIQGGDMRSFFTLVMTDPDFPGPSDPYLREHLHWIVTDIPGTTDATFGREVVSYEMPKPNIGIHRFVFVLFKQNQRQSINTPSSRDHFSTRSFAAENDLGLPVAAVYFNAQRETAARRR
>Pc PcTFL1 AB162042 MKRASEPLVVGRVIGDVLDSFTATTKMSVTYNTKLVCNGLELFPSVVTAKPRVEIQGGDMRSFFTLVMTDPDFPGPSDPYLREHLHWIVTDIPGTTDATFGREVVSYEMPKPNIGIHRFVFVLFKQNRRQSINTPSSRDHFSTRSFAAENDLGLPVAAVYFNAQRETAARRR
>Pn PnFTL3b AB181240 MANLSDPLVVGRVIGDVIDYFTPNVKMTVTYNSNKQVYNGHELFPSAVTHKPKVEVHGGDMRSFFTLVMTDPDVPGPSDPYLREHLHWIVTDIPGTTDATFGREVVNYEMPRPNIGIHRFVYLLFRQKGRQTVSTPSSRDKFNTRKFAEENELDLPVAAVFFNAQRETAARRR
>Pn PnTFL1c AB104629 MAKMSEPLVVGRVIGDVIDHFTANVKMTVTYQSNRKQVFNGHELFPSAVTHKPKVEVHGGDMRSFFTLVMTDPDVPGPSDPYLREHLHWIVTDIPGTTDATFGREVMNYEMPRPNIGIHRFVFLLFKQKGRQTVTTPASRDKFNTRKFAEENELGLPVAAVFFNAQRETAARKR
>Pn PnFTL1a AB181183 MAKMSEPLVVGRVIGDVIDHFTANVKMTVTYQSSRKQVFNGHELFPSAVTNKPKVEVHGGDMRSFFTLVMTDPDVPGPSDPYLREHLHWIVTDIPGTTDATFGREVMNYEMPRPNIGIHRFVFLLFKQKGRQTVTTPASRDKFNTRKFAEENELGLPVAAVFFNAQRETAARKR

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>Lj CEN1 AY423715
MSKIMSTDPLVVGRVVGDVLDSFTTSMKLTVSFNNKQVFNGHEFFPSTINTKPKVDIGGGDMRSFFTLIMT
DPDVPGPSDPYLKEHLHWMVTDIPGTTDATFGKELVSYEIPKPNIGIHRFVFVLFKQKRRQCVSPPSSRDH
FNTRSFAAQNDLALPVAAVYFNAQRETAARRR
>Ps TFL1a AY340579
MARMAQEPLIVGRVIGEVLDSFTTSMKMTVSYNKKQVFNGHEFFPSTINTKPKVEIDGADMRSFYTLVMTD
PDVPGPSDPYLREHLHWIVTDIPGTTDATFGKEIVSYEIPKPNIGIHRFVFVLFKQRARDSVRATPSSRDH
FNTRSFASQNDLGLPVAAVYFNAQRETAARRR
>At TFL1 U77674
MENMGTRVIEPLIMGRVVGDVLDFFTPTTKMNVSYNKKQVSNGHELFPSSVSSKPRVEIHGGDLRSFFTLV
MIDPDVPGPSDPFLKEHLHWIVTNIPGTTDATFGKEVVSYELPRPSIGIHRFVFVLFRQKQRRVIFPNIPS
RDHFNTRKFAVEYDLGLPVAAVFFNAQRETAARKR
>At ATC AB024714
MARISSDPLMVGRVIGDVVDNCLQAVKMTVTYNSDKQVYNGHELFPSVVTYKPKVEVHGGDMRSFFTLVMT
DPDVPGPSDPYLREHLHWIVTDIPGTTDVSFGKEIIGYEMPRPNIGIHRFVYLLFKQTRRGSVVSVPSYRD
QFNTREFAHENDLGLPVAAVFFNCQRETAARRR
>Os FL cDNA TFL1 AK110622
MSRVLEPLVVGKVIGEVIDNFNPTVKMTATYSSNKQVFNGHELFPSAVVSKPRVEVQGGDLRSFFTLVMTD
PDVPGPSDPYLREHLHWIVTDIPGTTDASFGREVVSYESPKPNIGIHRFVLVLFKQKRRQAVTPPSSRDYF
STRRFAADNDLGLPVAAVYFNAQRETAARRR
>Os FDR1 AF159883
MSRSVEPLVVGRVIGEVIDSFNPCTKMIVTYNSNKLVFNGHEFYPSAVVSKPRVEVQGGDMRSFFTLVMTD
PDVPGPSDPYLREHLHWIVTDIPGTTDASFGREIISYESPKPSIGIHRFVFVLFKQKRRQAVVVPSSRDHF
NTRQFAEENELGLPVAAVYFNAQRETAARRR
>Os FDR2 AF159882
MSRSVEPLVVGRVIGEVLDTFNPCMKMIVTYNSNKLVFNGHELYPSAVVSKPRVEVQGGDLRSFFTLVMTD
PDVPGPSDPYLREHLHWIVTDIPGTTDASFGREVISYESPKPNIGIHRFIFVLFKQKRRQTVIVPSFRDHF
NTRRFAEENDLGLPVAAVYFNAQRETAARRR
>Lp TFL1 AF316419
MSRSVEPLIVGRVIGEVLDPFNPCVKMVATYNSNKLVFNGHELYPSAVVSKPRVEVQGGDLRSLFTLVMTD
PDVPGPSDPYLREHLHWIVSNIPGTTDASFGGEVMSYESPKPNIGIHRFIFVLFKQKRRQTVSVPSFRDHF
NTRQFAVDNDLGLPVAAVYFNCQRETAARRR
>Ta FDR1 AJ577366
VTYSSNKQVFNGHEFFPSAVVSKPRIEVQGGDMRSFFTLVMTDPDVPGPSDPYLREHLHWIVSDIPGTTDA
SFGREVVSYESPKPNIGIHRFTFVLFQQKKRQAMNPPSTRDYFNTRRFANENDLGLPVAAVYFNAQRETAA
RRR
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FT subfamily
>Cu CiFT AB027456 MSSRERDPLIVGRVVGDVLDNFTRTIPMRITYSNKDVNNGRELKPSEVLNQPRAEIGGDDLRTFYTLVMVD PDAPSPSDPSLREYLHWLVTDIPATTGASFGQEIVNYESPRPTMGIHRFVFVLFRQLGRQTVYAPGWRQNF STRDFAELYNLGPPVAAVYFNCQRESGSGGRPVRR
>Le SP3D AY186735 MPRERDPLVVGRVVGDVLDPFTRTIGLRVIYRDREVNNGCELRPSQVINQPRVEVGGDDLRTFFTLVMVDP DAPSPSDPNLREYLHWLVTDIPATTGSSFGQEIVSYESPRPSMGIHRFVFVLFRQLGRQTVYAPGWRQNFN TRDFAELYNLGLPVAAVYFNCQRESGSGGRRRSAD
>Le SP6A AY186737 MPRVDPLIVGRVIGEVLDPFTRSVDLRVVYNNREVNNACVLKPSQVVMQPKVYIGGDDLRTFYTLIMVDPD APSPSNPNLREYLHWLVTDIPATTDTRFGNEIVCYENPTPTMGIHRFVLVLFRQLGRETVYPPGWRQNF
>Md AB161112 MPRDRDPLVVGRVVGDVLDPFTRSVSLRVTYGTKEVNNGCELKPSEVVQQPRADIGGDDLRTFYTLVMVDP DAPSPSDPNLKEYLHWLVTDIPATTAASFGQEIVCYESPRPTVGIHRFVLVVFRQLGRQTVYAPGWRQNFN TRDFAELYNLGLPVSVVYFNCQREGGSGGRRR
>Pn PnFT1b AB161109 MPRDREPLSVGRVIGDVLDPFTRSISLRVNYNSREVNNGCELKPSHVVNQPRVDIGGEDLRTFYTLVMVDP DAPSPSNPNLREYLHWLVTDIPATTGANFGQEVMCYESPRPTAGIHRFVFVLFRQLGRQTVYAPGWRQNFN TRDFAELYNLGSPVAAVYFNCQRESGSGGRRP
>Pn PnFT2c AB110613 MPRDREPLSVGRVIGDVLDPFTRSISLRVNYNSREVNNGCELKPSHVVNQPRVDIGGEDLRTFYTLVMVDP DAPSPSNPNLREYLHWLVTDIPATTGANFGQEVVCYESPRPTAGIHRFVFVLFRQLGRQTVYPPGWRQNFN TRDFAELYNLGSPVAAVYFNCQRESGSGGRRP
>At FT AF152096 MSINIRDPLIVSRVVGDVLDPFNRSITLKVTYGQREVTNGLDLRPSQVQNKPRVEIGGEDLRNFYTLVMVD PDVPSPSNPHLREYLHWLVTDIPATTGTTFGNEIVCYENPSPTAGIHRVVFILFRQLGRQTVYAPGWRQNF NTREFAEIYNLGLPVAAVFYNCQRESGCGGRRL
>At TSF AF152907 MSLSRRDPLVVGSVVGDVLDPFTRLVSLKVTYGHREVTNGLDLRPSQVLNKPIVEIGGDDFRNFYTLVMVD PDVPSPSNPHQREYLHWLVTDIPATTGNAFGNEVVCYESPRPPSGIHRIVLVLFRQLGRQTVYAPGWRQQF NTREFAEIYNLGLPVAASYFNCQRENGCGGRRT
>Os Hd3A AB052941 MAGSGRDRDPLVVGRVVGDVLDAFVRSTNLKVTYGSKTVSNGCELKPSMVTHQPRVEVGGNDMRTFYTLVM VDPDAPSPSDPNLREYLHWLVTDIPGTTAASFGQEVMCYESPRPTMGIHRLVFVLFQQLGRQTVYAPGWRQ NFNTKDFAELYNLGSPVAAVYFNCQREAGSGGRRVYN
>Os FL cDNA FT AK072979 MSGRGRGDPLVLGRVVGDVVDPFVRRVALRVAYGAREVANGCELRPSAVADQPRVAVGGPDMRTFYTLVMV DPDAPSPSDPNLREYLHWLVTDIPATTGVSFGTEVVCYESPRPVLGIHRLVFLLFEQLGRQTVYAPGWRQN FSTRDFAELYNLGLPVAAVYFNCQRESGTGGRRM
>Ta Hd3a TAE577367 MAGRDRDPLVVGRVVGDVLDPFIRTTNLRVTFGNRTVSNGCELKPSMVAQQPRVEVGGNEMRTFYTLVMVD PDAPSPSDPNLREYLHWLVTDIPGTTGASFGQEVMCYESPRPTMGIHRFVLVLFLQLGRQTVYAPGWRQNF NTRDFAELY
>Ta FL cDNA FT BT009051 MHAQRGDPLVVGRVIGDVVDPFVRRVALRVGYASRDVANGCELRPSAIADPPRVEVGGPDMRTFYTLVMVD PDAPSPSDPSLREYLHWLVTDIPATTGVSFGTEVVCYEGPRPVLGIHRLVFLLFQQLGRQTVYAPGWRQNF STRDFAELYNLGLPVAAVYFNCQRETGTGGRRM
>Zm partial FT AY111549 MAGRDREPXXXXXXXXDVLDPFVRTTNLRVSYGARTVSNGCELKPSMVVHQPRVEVXXPDMRTFYTLVMVD PDAPSPSDPNLREYLHWLVTDIPGTTGAAFGQEVICYESPRPTMGIHRFVLVLFQQLGRQTVYAPGWRQNF NTRDFAELYXXXXXXXXXXFNCQREAGSXXRR

BFT and MFT subfamily
>Le SP5G AY186736 MPRDPLIVSGVVGDVVDPFTRCVDFGVVYNNRVVYNGCSLRPSQVVNQPRVDIDGDDLRTFYTLIMVDPDA PNPSNPNLREYLHWLVTDIPAATGATFGNEVVGYESPRPSMGIHRYIFVLYRQLGCDAIDAPDIIDSRQNF NTRDFARFHNLGLPVAAVYFNCNREGGTGGRRL
>Le SP2G AY186734 METSARSVDPLVVGKVIGDVLDMFVPVVDFTVEYASKQISNNGVEIKPAEAAQKPRVHIKGSLHSNNLYTL VMADPDAPSPSEPTFREWLHWIVTDIPEGGDASQGREMVEYMGPKPPAGIHRYVFTLFRQKEAEQVPHKPP QGRSNFKTRQFASDNGLDLPVAALYFNSQKEHAAHH
>Pn AB181241 MAASVDPLVVGRVIGDVVDMFVPAVKMSVYYGSKHVSNGCDIKPSLSVDPPKVTISGHSDELYTLVMTDPD APSPSEPRMREWVHWIVADIPGGTNPTRGKEILSYVGPRPPVGIHRYILVLFQQKMPLGSMVEPPQNRSHF NTRLYAAHLDLGLPVATVYFNAQKEPANKRR
>At BFT NM_125597 MSREIEPLIVGRVIGDVLEMFNPSVTMRVTFNSNTIVSNGHELAPSLLLSKPRVEIGGQDLRSFFTLIMMD PDAPSPSNPYMREYLHWMVTDIPGTTDASFGREIVRYETPKPVAGIHRYVFALFKQRGRQAVKAAPETREC FNTNAFSSYFGLSQPVAAVYFNAQRETAPRRRPSY
>At MFT AF147721 MAASVDPLVVGRVIGDVLDMFIPTANMSVYFGPKHITNGCEIKPSTAVNPPKVNISGHSDELYTLVMTDPD APSPSEPNMREWVHWIVVDIPGGTNPSRGKEILPYMEPRPPVGIHRYILVLFRQNSPVGLMVQQPPSRANF STRMFAGHFDLGLPVATVYFNAQKEPASRRR
>Os FL cDNA MFT AK107056 MASHVDPLVVGRVIGDVVDLFVPTTAMSVRFGTKDLTNGCEIKPSVAAAPPAVQIAGRVNELFALVMTDPD APSPSEPTMREWLHWLVVNIPGGTDPSQGDVVVPYMGPRPPVGIHRYVMVLFQQKARVAAPPPDEDAARAR FSTRAFADRHDLGLPVAALYFNAQKEPAIRRRRY
>Ta FL cDNA MFT BT008995 MAAHVDPLVVGRVIGDVVDMFVPTMPVTVRFGTKDLTNGCEIKPSIADAAPSIQIAGRAGDLFTLVMTDPD APSPSEPTMKEWLHWLVVNIPGGSDPSQGEEVVPYMGPKPPLGIHRYVLVLFQQKARVLAPAPGGDTAASA MRARFSTRAFAERHDLGLPVAAMYFNAQKEPANRRRRY
>Zm Contig425 MFT BT016592 MAAAHVDPLVVGRVIGDVVDLFVPTVAVSARFGAKDLTNGCEIKPSVAAAAPAVLIAGRANDLFTLVMTDP DAPSPSEPTMRELLHWLVVNIPGGADASQGGETVVPYVPPRPPVGIHRYVLVVYQQKARVTAPPSLAPATE ATRARFSNRAFADRHDLGLPVAAMFFNAQKETASRRRHY

Amino acid sequences are given in FASTA format. Species abbreviation: *Am*, *Antirrhinum majus*, *At*, *Arabidopsis thaliana*, *Cs*, *Citrus sinensis*, *Cu*, *Citrus unshiu*, *Ej*, *Eriobotrya japonica*, *Le*, *Lycopersicon esculentum*, *Lj Lotus japonicus*, *Lp*, *Lolium perenne*, *Md*, *Malus domestica*, *Nt*, *Nicotiana tabacum*, *Pc*, *Pyrus communis*, *Pn*, *Populus nigra*, *Ps*, *Pisum sativum*, *Os*, *Oryza sativa*, *Ta*, *Triticum aestivum*, *Zm*, *Zea mays*

The following TFL1 homologs have been confirmed as having the same in vivo activity as *Arabidopsis* TFL1: *Am* CEN (Bradley *et al*, 1996), *Le* SP (Pnueli *et al*, 1998), *At* TFL1 (Bradley *et al*, 1997), *Lp* CEN (Jensen *et al*, 2001), *At* ATC (Mimida *et al*, 2001), *Os* RCN1 and RCN2 (=FDR1 and FDR2) (Nakagawa *et al*, 2002), *Ps* TFL1a (Foucher *et al*, 2003), *Cs* TFL1 (Pillitteri *et al*, 2004).

The following FT homologs have been confirmed in vivo as having the same activity as *Arabidopsis* FT: *At* FT (Kardailsky *et al*, 1999; Kobayashi *et al*, 1999), *Os* Hd3a

(Kojima *et al*, 2002), *At* TSF (Michaels *et al*, 2005)

Bradley D, Carpenter R, Copsey L, Vincent C, Rothstein S, Coen E (1996) Control of inflorescence architecture in *Antirrhinum*. *Nature* **379**: 791-797.

Bradley DJ, Ratcliffe OJ, Vincent C, Carpenter R, Coen ES (1997) Inflorescence commitment and architecture in *Arabidopsis*. *Science* **275**: 80-83.

Foucher F, Morin J, Courtiade J, Cadioux S, Ellis N, Banfield MJ, Rameau C (2003) *DETERMINATE* and *LATE FLOWERING* are two *TERMINAL FLOWER1/CENTRORADIALIS* homologs that control two distinct phases of flowering initiation and development in pea. *Plant Cell* **15**: 2742-2754.

Jensen CS, Salchert K, Nielsen KK (2001) A *TERMINAL FLOWER1*-like gene from perennial ryegrass involved in floral transition and axillary meristem identity. *Plant Physiol* **125**: 1517-1528.

Kardailsky I, Shukla V, Ahn JH, Dagenais N, Christensen SK, Nguyen JT, Chory J, Harrison MJ, Weigel D (1999) Activation tagging of the floral inducer *FT*. *Science* **286**: 1962-1965.

Kobayashi Y, Kaya H, Goto K, Iwabuchi M, Araki T (1999) A pair of related genes with antagonistic roles in mediating flowering signals. *Science* **286**: 1960-1962.

Kojima S, Takahashi Y, Kobayashi Y, Monna L, Sasaki T, Araki T, Yano M (2002) *Hd3a*, a rice ortholog of the *Arabidopsis FT* gene, promotes transition to flowering downstream of *Hd1* under short-day conditions. *Plant Cell Physiol* **43**: 1096-1105.

Michaels SD, Himelblau E, Kim SY, Schomburg FM, Amasino RM (2005) Integration of flowering signals in winter-annual Arabidopsis. *Plant Physiol* **137**: 149-156.

Mimida N, Goto K, Kobayashi Y, Araki T, Ahn JH, Weigel D, Murata M, Motoyoshi F, Sakamoto W (2001) Functional divergence of the *TFL1*-like gene family in *Arabidopsis* revealed by characterization of a novel homologue. *Genes Cells* **6**: 327-336.

Nakagawa M, Shimamoto K, Kyozuka J (2002) Overexpression of *RCN1* and *RCN2*, rice

TERMINAL FLOWER 1/CENTRORADIALIS homologs, confers delay of phase transition and altered panicle morphology in rice. *Plant J* **29**: 743-750.

Pillitteri LJ, Lovatt CJ, Walling LL (2004) Isolation and characterization of a *TERMINAL FLOWER* homolog and its correlation with juvenility in citrus. *Plant Physiol* **135**: 1540-1551.

Pnueli L, Carmel-Goren L, Hareven D, Gutfinger T, Alvarez J, Ganal M, Zamir D, Lifschitz E (1998) The *SELF-PRUNING* gene of tomato regulates vegetative to reproductive switching of sympodial meristems and is the ortholog of *CEN* and *TFL1*. *Development* **125**: 1979-1989.