

MiFT1-Shelly	MSWEGCCSDRDPLVVGRVIGDVIDNFNTSISRNVSYGNRDVGNGVELKPSVVANHPRVDI	60
MiFT-Irwin	MSWEGCCSDRDPLVVGRVIGDVIDNFNTSISRNVSYGNRDVGNGVELKPSVVANHPRVDI	60
MiFT1-Alphonso	MSWEGCCSDRDPLVVGRVIGDVIDNFNTSISRNVSYGNRDVGNGVELKPSVVANHPRVDI	60
MiFT1-SiJiMi	MSWEGSCSNRDPLVVGRVIGDVINNFNRSVSLNVSYGNRDVNNGVELKPAVVANHPRVDI	60
	*****.*.*:*****:*** *.* *****.*:*****	
MiFT1-Shelly	GGTDLRTFYTLVMVDPDAPSPSNPGLREY LHWLVTDIPGSTGASFGQEIVNYESPRPTLG	120
MiFT-Irwin	GGTDLRTFYTLVMVDPDAPSPSNPSLREY LHWLVTDIPGSTGASFGQEIVNYESPRPTLG	120
MiFT1-Alphonso	GGTDLRTFYPLVMMDPDAPSPSNPSLREY LHWLVTDIPGSTGASFGQEIVNYESPRPTLG	120
MiFT1-SiJiMi	GGTDLRTFYTLVMVDPDAPSPSNPSLRFY LHWLVTDIPGSTGASFGQEIVNYESPRPTIG	120
	*****.*.*:*****.* *****:*****.*	
MiFT1-Shelly	IHRFVFMLFRQLGRQTVYAPAWRQNFITRDAELYNLGSPAAAVYFNCQKETGSGGRRRQ	180
MiFT-Irwin	IHRFVFMLFRQLGRQTVYAPAWRQNFITRDAELYNLGSPVAAVYFNCQKETGSGGRRRQ	180
MiFT1-Alphonso	IHRFVFMLFRQLGRQTVYAPAWRQNFITRDAELYNLGSPVAAVYFNCQKETGSGGRRRQ	180
MiFT1-SiJiMi	IHRFVFLFRQLGRQTVYAPAWRQNFITRDAELYNLGSPVAAVYFNCQKETGSGGRRR	179
	*****.*:*****.* *****.*:*****	

**Figure S1. (A)** Amino acid sequence comparison and structural features of mango cv. Shelly *MiFT1* (accession number: OP341600). Comparison of deduced amino acid sequence of *MiFT1* from 'Shelly' (this study) to *MiFT* from 'Irwin' (accession number [ac]: AB671587.1), *MiFT1* from 'Alphonso' (ac: JX177434.1), and *MiFT1* from 'SiJiMi' (ac: MT419778). The two conserved amino acids Tyr-89 and Gln-144 (corresponding to Tyr-85 and Gln-140 in *AtFT*), required for FT activity, are highlighted in purple. The conserved amino acid sequence in *AtFT1* C-terminal region, with Ala-141 corresponding to Gly-137 in *AtFT*, is highlighted in yellow. The three conserved amino acids Val-74, Ser-80 and Arg-87 (corresponding to Val-70, Ser-76 and Arg-83 in *AtFT*), which are suggested to play an essential role in regulating *AtFT* transport, are highlighted in green.

MiFT2-Shelly	MDGEDYGESASRETRESASRDPLVVGRVVGVDVLDNFTKSIAFTASYGHKLEVHNGVLLKP	60
MiFT-like-Keitt/TA	MDGEDYGESASRETRESASRDPLVVGRVVGVDVLDNFTKSIAFTASYGHKLEVHNGVLLKP	60
MiFT3-SiJiMi	MDGEGYGESASRETRESASRDPLVVGRVVGVDVLDNFTKSIAFTASYGHKLEVHNGVLLKP	60
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MiFT2-Shelly	SQVAKQPRVSIIGGSDFRNFYTLVMVDPDAPSPSDPHLKEYLHVLVIDIPESTGATYGKEV	120
MiFT-like-Keitt/TA	SQVAKQPRVSIIGGSDFRNFYTLVMVDPDAPSPSDPHLKEYLHVLVIDIPESTGATYGKEV	120
MiFT3-SiJiMi	SQVAKQPRVSIIGGSDFRNFYTLVMVDPDAPSPSDPHLKEYLHVLVIDIPESTGATYGKEV	120
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MiFT2-Shelly	VSYESPKPTVGIHRFVFLFRQPGKQPVYAPGWRQNFVTRDFAELYNLGSPVAALFFNCQ	180
MiFT-like-Keitt/TA	VSYESPKPTVGIHRFVFLFRQPGKQPVYAPGWRQNFVTRDFAELYNLGSPVAALFFNCQ	180
MiFT3-SiJiMi	VSYESPKPTVGIHRFVFLFRQPGKQPVYAPGWRQNFVTRDFAELYNLGSPVAALFFNCQ	180
	*****	
MiFT2-Shelly	KETKTSTSSSSSSRRR	197
MiFT-like-Keitt/TA	KETKTSTSSSSSSRRR	197
MiFT3-SiJiMi	KETKTSTSSSSSSRRR	197
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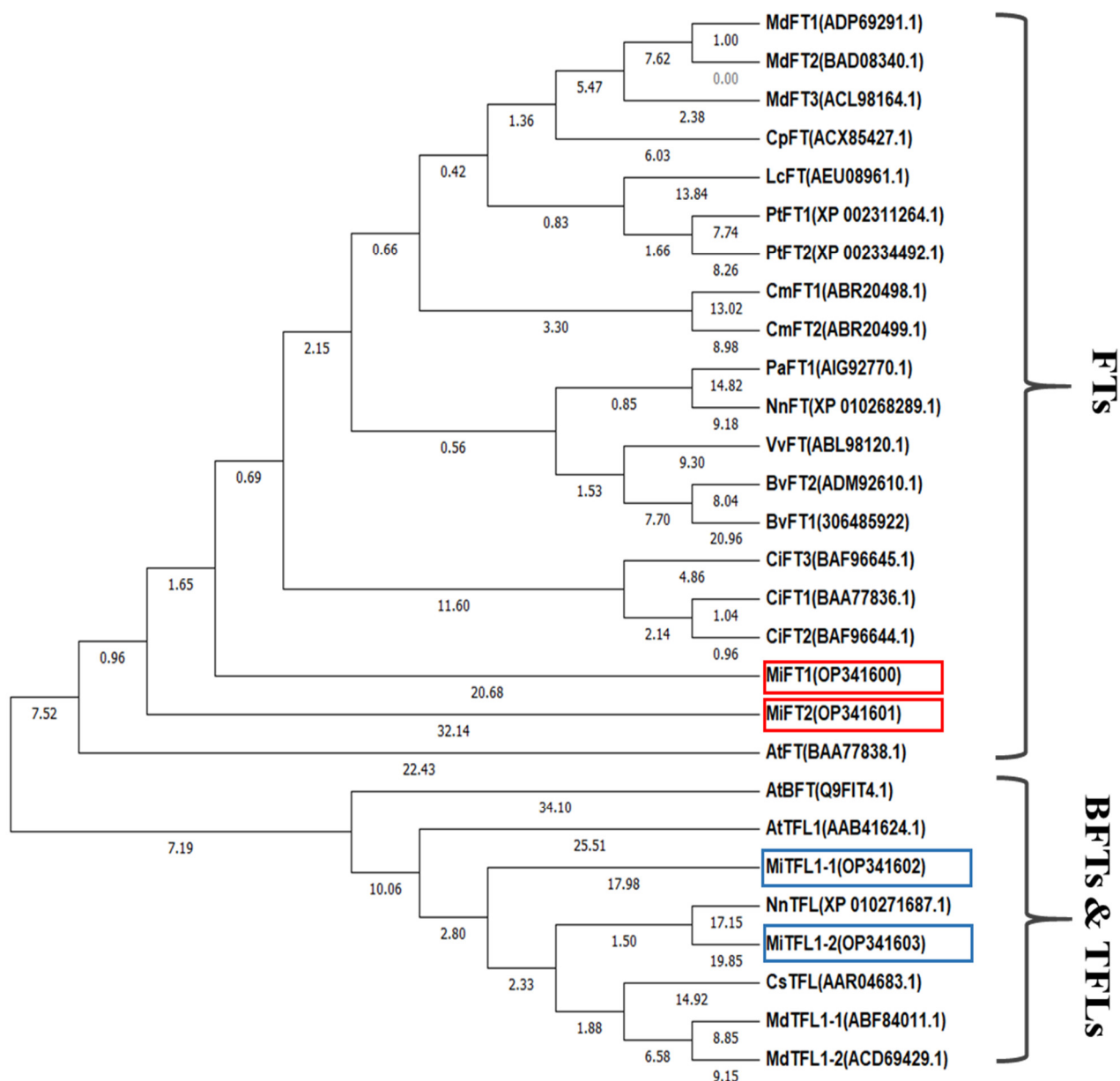
**Figure S1. (B)** Amino acid sequence comparison and structural features of 'Shelly' *MiFT2* (accession number: OP341601). Comparison of deduced amino acid sequence of *MiFT2* from 'Shelly' (this study) to *MiFT*-like from 'Keitt' and 'Tommy Atkins'(Keitt/TA) (transcriptome data base; mango\_rep\_c5502) and *MiFT3* from 'SiJiMi' (ac: JQ700254.1). The two conserved amino acids Tyr-89 and Gln-144 (corresponding to Tyr-85 and Gln-140 in *AtFT*), required for *AtFT* activity, are highlighted in purple. The semi-conserved amino acid sequence, found in the C-terminal region of the proteins, with Pro-143, Lys-145 and Pro-147 (highlighted in gray) instead of Leu-128, Arg-130 and Thr-132 in *AtFT*, is highlighted in yellow. Two out of three conserved amino acids: Val-74 and Ser-80 (corresponding to Val-70 and Ser-76 in *AtFT*), which are suggested to play an essential role in regulating FT transport, are highlighted in green.

MiTFL1-1-Shelly	MARIVDPLVVGRVIGDVLDVSFSPTITMFVSYNRRQVCNGHELLPSTVSFRPRVEIQGGDM	60
MiTFL $\alpha$ -Alphonso	MARIVDPLVVGRVIGDVLDVSFSPTITMFVSYNRRQVCNGHELLPSTVSFRPRVEIQGGDM	60
MiTFL1-1-SiJiMi	MARIVDPLVVGRVIGDVLDVSFSPTITMFVSYNRRQVCNGHELLPSTVSFRPRVEIQGGDM	60
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MiTFL1-1-Shelly	RTFFTLVMTDPDVPGPSDPYLREHLHLWLVANIPGTTDVTFGRELVSYEIPRPNIGIHRFV	120
MiTFL $\alpha$ -Alphonso	RTFFTLVMTDPDVPGPSDPYLREHLHWPVANIPGTTDVTFGRELVSYEIPRPNIGIHRFV	120
MiTFL1-1-SiJiMi	RTFFTLVMTDPDVPGPSDPYLREHLHLWLVANIPGTTDVTFGRELVSYEIPRPNIGIHRFA	120
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MiTFL1-1-Shelly	FALFRQKGRQIFNPPSSRDNFSTRIFAAENDLGPPVAAVYFNAQRETAARRR	172
MiTFL $\alpha$ -Alphonso	FALFRQKGRQIFNPPSSRDNFSTRIFAAENDLGPPVAAVYFNAQRETAARRR	172
MiTFL1-1-SiJiMi	FALFRQKGRQIFNPPSSRDNFSTRIFAAENDLGPPVAAVYFNAQRETAARR	171
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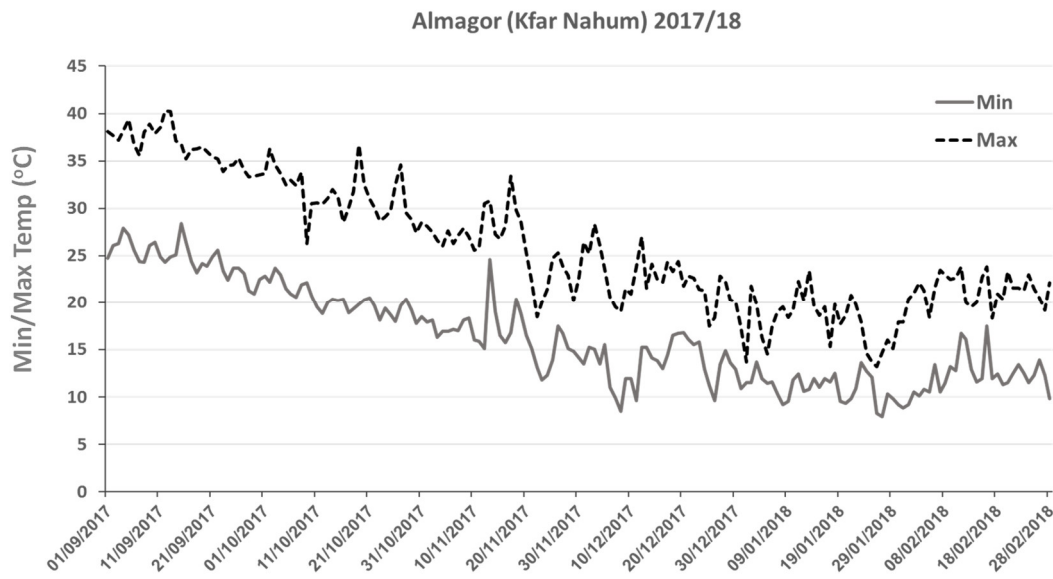
**Figure S1. (C)** Amino acid sequence comparison and structural features of 'Shelly' *MiTFL1-1* (accession number: OP341602). Comparison of deduced amino acid sequence of *MiTFL1-1* from 'Shelly' (this study) to *MiTFL $\alpha$*  from 'Alphonso' (ac: AND81244.1) and *MiTFL1-1* from 'SiJiMi' (Wang et al., 2021). The two crucial conserved amino acid residues His-85 and Asp-140 (corresponding to *AtTFL1*), which are required for TFL1 anti-florigenic function, are highlighted in purple.

MiTFL1-2-Shelly	MARMPDPLVVGRVIGDVVDCCDQTVKMAVTYNSSKQVYNGHELFPSSVTVPKPKEVHGG	60
MiTFL1-2-SiJiMi	MARMPDPLVVGRVIGDVVDCCDQTVKMAVTYNSSKQVYNGHELFPSSVTVPKPKEVHGG	60
MiTFL1-Alphonso	MARMPDPLVVGRVIGDVVDCCDQTVKMAVTYNSSKQVYNGHELFPSSVTVPKPKEVHGG	60
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MiTFL1-2-Shelly	DMRSFFTLIMTDPDVPGPSDPYLREHLHWVVDIPGTTDATFGRELVNYEMPRNIGIHR	120
MiTFL1-2-SiJiMi	DMRSFFTLIMTDPDVPGPSDPYLREHLHWVVDIPGTTDATFGRELVNYEMPRNIGIHR	120
MiTFL1-Alphonso	DMRSFFTLIMTDPDVPGPSDPYLREHLHWVVDIPGTTDATFGKELVNYEMPRNIGIHR	120
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MiTFL1-2-Shelly	FVLLFRQKRRQTVISIPSSRDGFNTRKFAEDNDLGQPVAAVFFNAQRETAARRR	176
MiTFL1-2-SiJiMi	FVLLFRQKRRQTVISIPSSRDGFNTRKFAEDNDLGQPVAAVFFNAQRETAARR	176
MiTFL1-Alphonso	FVLLFRQKRRQTVISIPSSRDGFNTRKFAEDNDLGQPVAAVFFNAQRETAARRR	175
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**Figure S1. (D)** Amino acid sequence comparison and structural features of 'Shelly' *MiTFL1-2* (accession number: OP341603). Comparison of deduced amino acid sequence of *MiTFL1-2* from 'Shelly' (this study) to *MiTFL1-2* from 'SiJiMi' (Wang et al., 2021) and *MiTFL1* from 'Alphonso' (ac: AGW23412.1). The two crucial conserved amino acid residues His-85 and Asp-140 (corresponding to *AtTFL1*), which are required for TFL1 anti-florigenic function, are highlighted in purple.



**Figure S2.** Phylogeny of FT, TFL and BFT proteins. Conserved amino acid sequences of MiFT/TFL1 proteins (boxed) and FT, TFL and BFT proteins from various plant species (Vv, *Vitis vinifera*; At, *Arabidopsis thaliana*; Pt, *Populus trichocarpa*; Mi, *Mangifera Indica*; Cs, *Citrus sinensis*; Md, *Malus domestica*; Nn, *Nelumbo nucifera*; Ci, *Citrus unshiu*; Cm, *Cucurbita moschata*; Lc, *Litchi chinensis*; Cp, *Carica papaya*; Pa, *Persea Americana*; Bv, *Beta vulgaris*). Database accession numbers are given. Bootstrap consensus trees were inferred from 1000 replicates and graphically designed with iTOL (Interactive Tree of Life, V5). Branch lengths are indicated.



**Figure S3.** Minimal and maximal temperatures recorded from September 2017 through February 2018 at Kfar Nahum near Almagor, where experimental 'Shelly' trees were grown.