

Flowering time in banana (*Musa spp.*), a day neutral plant, is controlled by at least four putative *FLOWERING LOCUS T* homologues

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Supplementary Tables and figures

Supplementary Table S1. The details and coordinates of 14 *FT/TSF*-like genes of banana taken from banana genome database (<http://banana-genome.cirad.fr>).

Banana Genome Annotation (Gene/Locus)	Chr	Start	End	Strand	Query Coverage	Name given in this study	Amino Acid Residues (n)
GSMUA_Achr9T07900_001~ Protein HEADING DATE 3A~ HD3A~	chr9	5067756	5068866	-	99.91	MaFT1	172
GSMUA_Achr10T21780_001~ Protein HEADING DATE 3A~ HD3A~	chr10	27215563	27216458	+	99.89	MaFT2	174
GSMUA_Achr5T06600_001~ Protein HEADING DATE 3A~ HD3A~	chr5	4856092	4856954	+	99.88	MaFT3	175
GSMUA_Achr2T19360_001~ Protein FLOWERING LOCUS T~ FT~	chr2	19463406	19464372	-	99.90	MaFT4	177
GSMUA_Achr4T08540_001~ Protein HEADING DATE 3A~ HD3A~	chr4	6274754	6275889	-	99.91	MaFT5	179
GSMUA_Achr2T19310_001~ Protein HEADING DATE 3A~ HD3A~	chr2	19414161	19416534	-	99.96	MaFT6	175
GSMUA_Achr2T05870_001~ Protein FLOWERING LOCUS T~ FT~	chr2	10806987	10808797	+	99.94	MaFT7	173
GSMUA_Achr10T16460_001~ Protein HEADING DATE 3A~ HD3A~	chr10	23980518	23982407	+	99.95	MaFT8	180
GSMUA_Achr3T02730_001~ Protein FLOWERING LOCUS T~ FT~	chr3	1776128	1779521	-	99.97	MaFT9	178
GSMUA_Achr2T20900_001~ Protein HEADING DATE 3A~ HD3A~	chr2	20579763	20581731	+	99.95	MaFT10	180
GSMUA_Achr10T21760_001~ Protein HEADING DATE 3A~ HD3A~	chr10	27212259	27213048	+	99.87	MaFT11	177
GSMUA_Achr5T06420_001~ Protein FLOWERING LOCUS T~ FT~	chr5	4708329	4709190	-	99.88	MaFT12	175
GSMUA_Achr1T17050_001~ Protein TWIN SISTER OF FT~ TSF~	chr1	12729700	12733006	+	99.91	MaTSF1	173
GSMUA_Achr3T21510_001~ Protein TWIN SISTER OF FT~ TSF~	Chr3	22452853	22457385	-	99.98	MaTSF2	174

Supplementary Table S2. Identity (upper triangle in bold) and similarity (lower triangle) percentage of putative banana FT/TSF-like proteins. The results were generated by MatGat software with default parameters.

	MaF T1	MaF T2	MaF T3	MaF T4	MaF T5	MaF T6	MaF T7	MaF T8	MaF T9	MaF T10	MaF T11	MaF T12	MaTS F1	MaTS F2
MaFT 1	–	67.8	62.5	59.0	63.7	67.4	87.9	79.4	82.1	81.6	68.4	61.9	68.4	72.4
MaFT 2	79.9	–	68.8	66.9	77.7	81.9	69.5	63.9	94.8	66.7	78.0	68.2	60.8	63.6
MaFT 3	78.3	81.7	–	82.5	68.2	63.7	64.8	62.8	62.0	61.4	65.2	98.9	59.6	59.6
MaFT 4	76.8	79.1	92.1	–	67.8	60.2	61.2	60.0	59.2	60.7	62.2	83.1	60.0	56.1
MaFT 5	79.3	82.1	86.0	82.1	–	71.1	65.4	62.6	60.8	62.6	78.2	68.7	58.1	59.2
MaFT 6	79.4	89.7	79.4	75.1	81.0	–	66.5	61.7	63.2	65.0	75.8	63.1	61.7	61.1
MaFT 7	93.6	80.5	78.9	78.5	79.3	79.4	–	80.0	80.4	82.2	68.4	64.2	68.0	70.3
MaFT 8	87.2	77.8	76.1	76.7	78.9	77.2	89.4	–	85.6	78.9	64.8	62.2	66.5	67.0
MaFT 9	88.8	78.7	77.0	75.8	78.2	78.7	89.9	91.7	–	84.4	66.9	61.7	68.5	69.1
MaFT 10	89.1	79.9	76.6	76.8	78.2	77.7	91.4	88.3	92.1	–	68.9	60.8	71.1	72.2
MaFT 11	79.1	84.7	80.8	79.1	87.7	82.5	81.4	81.1	82.0	81.4	–	64.6	59.3	62.7
MaFT 12	78.3	81.7	99.4	92.1	86.0	79.4	78.9	76.1	77.0	76.6	80.8	–	59.6	59.0
MaTS F1	83.8	78.7	77.1	76.3	74.9	80.0	86.7	81.1	83.1	83.9	77.4	77.7	–	78.7
MaTS F2	85.1	79.3	78.3	76.3	77.7	77.7	86.8	81.7	83.1	84.5	78.0	78.9	91.4	–

Supplementary Table S3. Identity and similarity percentage of putative banana FT/TSF-like proteins with Arabidopsis (AtFT), rice (Hd3a) and maize (ZCN8) functional proteins.

Gene	Identity / Similarity (%)			
	AtFT	AtTSF	Hd3a	ZCN8
MaFT1	68.8 / 81.1	66.9 / 79.4	68.2 / 79.9	55.1 / 71.4
MaFT2	71.2 / 82.9	70.6 / 81.7	76.0 / 83.8	61.4 / 76.6
MaFT3	63.7 / 81.7	64.8 / 80.0	64.6 / 81.6	60.2 / 82.9
MaFT4	63.0 / 79.1	61.9 / 80.2	61.2 / 78.2	56.7 / 79.1
MaFT5	71.7 / 83.8	70.6 / 81.6	76.9 / 87.7	60.9 / 75.4
MaFT6	69.3 / 81.7	68.8 / 77.1	73.1 / 83.2	57.3 / 71.4
MaFT7	71.0 / 85.1	69.3 / 82.9	67.0 / 80.4	57.4 / 72.6
MaFT8	63.4 / 78.9	64.5 / 78.9	66.5 / 80.0	54.1 / 70.6
MaFT9	67.0 / 80.9	65.9 / 80.9	65.2 / 81.6	53.3 / 71.3
MaFT10	68.9 / 81.7	66.7 / 81.7	67.6 / 81.0	52.8 / 70.9
MaFT11	71.3 / 85.3	70.2 / 81.4	78.9 / 91.6	58.8 / 72.9
MaFT12	64.2 / 81.7	64.2 / 80.0	64.1 / 81.6	59.7 / 82.9
MaTSF1	63.4 / 78.9	65.1 / 79.4	59.2 / 76.5	52.5 / 71.4
MaTSF2	64.0 / 79.4	66.3 / 77.7	62.0 / 77.1	51.4 / 70.3

Supplementary Table S4: Flowering time analysis of individual plants over-expressing various banana *FT/TSF*-like genes in an *ft-10* mutant background. Values are means $\pm$ SE calculated using Tukey-Kramer multiple comparison test. Asterisks indicate a statistically significant difference between plants in the same column (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ respectively).

Line	LD conditions (16 h light/8 h dark period)				
	No. of Plants	Days to Flower	Rosette leaves	Cauline leaves	Total leaves
<i>ft-10</i>	12	48.50 $\pm$ 1.0	32.17 $\pm$ 0.6	7.34 $\pm$ 0.3	39.50 $\pm$ 0.8
VC(<i>ft-10</i>)	12	47.58 $\pm$ 1.0	31.75 $\pm$ 0.6	7.17 $\pm$ 0.2	38.91 $\pm$ 0.7
Wt (Col)	12	27.84 $\pm$ 0.5***	11.08 $\pm$ 0.3***	2.58 $\pm$ 0.2***	13.67 $\pm$ 0.4***
VC/Wt (Col)	12	27.25 $\pm$ 0.5***	11.33 $\pm$ 0.3***	2.50 $\pm$ 0.2***	13.84 $\pm$ 0.5***
35S::<i>MaFT1/ft-10</i>					
#6	12	30.33 $\pm$ 0.6***	12.75 $\pm$ 0.6***	2.33 $\pm$ 0.1***	15.08 $\pm$ 0.5***
#9	12	29.17 $\pm$ 0.7***	12.25 $\pm$ 0.6***	2.16 $\pm$ 0.2***	14.42 $\pm$ 0.7***
#10	12	30.50 $\pm$ 0.7***	12.60 $\pm$ 0.7***	2.08 $\pm$ 0.2***	14.70 $\pm$ 0.7***
#11	12	29.83 $\pm$ 0.8***	12.33 $\pm$ 0.6***	2.25 $\pm$ 0.2***	14.58 $\pm$ 0.8***
35S::<i>MaFT2/ft-10</i>					
#3	12	27.17 $\pm$ 0.6***	12.50 $\pm$ 0.5***	1.75 $\pm$ 0.2***	14.25 $\pm$ 0.5***
#4	12	28.75 $\pm$ 1.0***	11.25 $\pm$ 0.4***	1.84 $\pm$ 0.3***	13.08 $\pm$ 0.5***
#5	12	28.08 $\pm$ 0.9***	11.67 $\pm$ 0.6***	2.41 $\pm$ 0.2***	14.08 $\pm$ 0.6***
#7	12	27.30 $\pm$ 0.9***	11.30 $\pm$ 0.6***	2.17 $\pm$ 0.2***	13.50 $\pm$ 0.7***
#8	12	29.10 $\pm$ 0.8***	12.40 $\pm$ 0.6***	2.58 $\pm$ 0.2***	15.00 $\pm$ 0.6***
35S::<i>MaFT3/ft-10</i>					
#8	12	31.08 $\pm$ 0.8***	12.67 $\pm$ 0.5***	2.84 $\pm$ 0.3***	15.50 $\pm$ 0.4***
#9	12	30.84 $\pm$ 0.9***	12.17 $\pm$ 0.5***	2.08 $\pm$ 0.3***	14.25 $\pm$ 0.6***
#10	12	29.67 $\pm$ 0.7***	12.25 $\pm$ 0.5***	2.75 $\pm$ 0.3***	15.00 $\pm$ 0.5***
#12	12	30.42 $\pm$ 0.5***	13.08 $\pm$ 0.5***	2.42 $\pm$ 0.3***	15.50 $\pm$ 0.6***
35S::<i>MaFT4/ft-10</i>					
#1	12	28.83 $\pm$ 0.2***	11.75 $\pm$ 0.6***	2.16 $\pm$ 0.1***	13.92 $\pm$ 0.6***
#2	12	32.58 $\pm$ 0.7***	15.50 $\pm$ 0.7***	2.84 $\pm$ 0.2***	18.34 $\pm$ 0.9***
#4	12	28.17 $\pm$ 0.4***	11.67 $\pm$ 0.6***	2.16 $\pm$ 0.2***	13.84 $\pm$ 0.6***
#5	12	27.34 $\pm$ 0.8***	11.42 $\pm$ 0.5***	2.50 $\pm$ 0.2***	13.92 $\pm$ 0.6***
#6	12	26.84 $\pm$ 0.7***	11.00 $\pm$ 0.5***	1.75 $\pm$ 0.2***	12.75 $\pm$ 0.6***
#10	12	27.67 $\pm$ 0.7***	11.67 $\pm$ 0.5***	1.91 $\pm$ 0.2***	13.58 $\pm$ 0.6***
#14	12	26.84 $\pm$ 0.7***	10.42 $\pm$ 0.5***	1.75 $\pm$ 0.2***	12.17 $\pm$ 0.5***
#15	12	27.17 $\pm$ 0.7***	11.42 $\pm$ 0.5***	2.34 $\pm$ 0.1***	13.75 $\pm$ 0.6***
35S::<i>MaFT5/ft-10</i>					
#4	12	20.75 $\pm$ 0.7***	7.58 $\pm$ 0.3***	1.16 $\pm$ 0.2***	8.75 $\pm$ 0.5***
#5	12	19.92 $\pm$ 0.5***	6.75 $\pm$ 0.4***	1.25 $\pm$ 0.1***	8.00 $\pm$ 0.4***
#6	12	21.08 $\pm$ 0.6***	8.00 $\pm$ 0.4***	1.00 $\pm$ 0.2***	9.00 $\pm$ 0.5***
#7	12	25.17 $\pm$ 0.7***	10.00 $\pm$ 0.8***	1.41 $\pm$ 0.2***	11.42 $\pm$ 0.7***
#10	12	24.25 $\pm$ 0.4***	10.08 $\pm$ 0.4***	1.34 $\pm$ 0.1***	11.42 $\pm$ 0.6***
#11	12	24.50 $\pm$ 0.4***	9.50 $\pm$ 0.4***	1.58 $\pm$ 0.1***	11.08 $\pm$ 0.5***
#12	12	20.92 $\pm$ 0.3***	6.91 $\pm$ 0.1***	1.08 $\pm$ 0.2***	8.00 $\pm$ 0.2***
#17	12	26.08 $\pm$ 0.6***	11.58 $\pm$ 0.5***	1.75 $\pm$ 0.2***	13.34 $\pm$ 0.6***
35S::<i>MaFT6/ft-10</i>					
#1	12	45.58 $\pm$ 1.0	30.34 $\pm$ 0.7	7.08 $\pm$ 0.4	37.42 $\pm$ 0.8
#2	12	45.00 $\pm$ 1.3	30.92 $\pm$ 0.5	7.00 $\pm$ 0.3	37.92 $\pm$ 0.6
#3	12	46.67 $\pm$ 1.1	31.58 $\pm$ 0.7	7.25 $\pm$ 0.3	38.84 $\pm$ 0.8
#4	12	47.17 $\pm$ 1.2	32.08 $\pm$ 1.0	7.25 $\pm$ 0.4	39.34 $\pm$ 1.1
#6	12	45.08 $\pm$ 1.1	31.42 $\pm$ 0.5	7.75 $\pm$ 0.3	39.17 $\pm$ 0.6
#11	12	46.84 $\pm$ 1.2	32.67 $\pm$ 0.6	7.25 $\pm$ 0.4	39.92 $\pm$ 0.8
#14	12	47.00 $\pm$ 1.0	31.92 $\pm$ 0.7	7.84 $\pm$ 0.3	39.75 $\pm$ 0.8
#17	12	48.17 $\pm$ 1.1	32.17 $\pm$ 0.8	7.75 $\pm$ 0.3	39.92 $\pm$ 0.7

Table S4: Continued

Line	LD conditions (16 h light/8 h dark period)				
	No. of Plants	Days to Flower	Rosette leaves	Cauline leaves	Total leaves
35S::MaFT7/ <i>ft-10</i>					
#5	12	37.83±1.0***	24.42±1.0***	6.16±0.3	30.58±1.3***
#6	12	38.42±1.2***	26.00±0.8***	6.58±0.4	32.58±1.1***
#8	12	38.17±0.9***	23.42±0.8***	5.58±0.2**	29.00±0.9***
#9	12	36.25±0.8***	20.25±0.8***	4.66±0.2***	24.92±0.7***
35S::MaFT8/ <i>ft-10</i>					
#1	12	28.25±0.6***	10.92±0.5***	2.42±0.2***	13.33±0.5***
#2	12	28.75±0.4***	11.17±0.6***	2.50±0.2***	13.67±0.7***
#3	12	28.25±0.5***	11.17±0.7***	2.33±0.1***	13.50±0.8***
#4	12	27.20±0.5***	11.40±0.5***	2.42±0.2***	13.80±0.5***
#5	12	28.67±0.6***	11.25±0.6***	2.50±0.2***	13.75±0.6***
#6	12	27.08±0.5***	11.17±0.5***	2.50±0.2***	13.67±0.5***
#7	12	27.83±0.4***	10.92±0.4***	2.58±0.1***	13.50±0.6***
#8	12	27.10±0.5***	11.20±0.5***	2.42±0.2***	13.58±0.5***
35S::MaFT9/ <i>ft-10</i>					
#1	12	47.33±0.8	32.92±0.9	7.17±0.4	40.08±1.0
#2	12	48.42±1.0	33.08±0.8	7.25±0.3	40.33±0.8
#3	12	46.42±1.1	30.83±1.0	7.25±0.3	38.08±1.1
#4	12	46.17±0.7	31.67±0.9	7.58±0.2	39.25±0.8
#5	12	45.50±1.2	31.42±0.7	7.08±0.4	38.50±0.9
#6	12	47.92±0.7	31.50±0.9	7.16±0.3	38.67±1.1
#7	12	48.08±0.9	32.42±0.7	7.50±0.3	39.92±0.6
#8	12	48.17±1.0	31.58±0.6	7.58±0.3	39.17±0.6
35S::MaFT12/ <i>ft-10</i>					
#1	12	31.17±0.8***	13.00±0.6***	2.17±0.3***	15.17±0.6***
#2	12	31.50±0.7***	12.08±0.6***	2.25±0.3***	14.34±0.6***
#3	12	30.17±0.7***	11.34±0.6***	2.58±0.2***	13.92±0.7***
#5	12	29.34±0.7***	12.25±0.5***	2.92±0.3***	15.17±0.6***
#6	12	29.92±0.5***	12.58±0.5***	2.84±0.3***	15.42±0.5***
#7	12	31.08±1.0	13.00±0.9	6.84±0.2	37.92±1.0
#8	12	30.25±0.7***	12.67±0.6***	2.75±0.4***	15.42±0.5***
35S::MaTSF1/ <i>ft-10</i>					
#1	12	26.67±0.8***	12.34±0.5***	2.17±0.3***	14.50±0.6***
#2	12	27.17±0.9***	12.08±0.6***	2.25±0.3***	14.34±0.6***
#6	12	28.50±0.6***	11.34±0.6***	2.58±0.2***	13.92±0.7***
#9	12	28.58±0.8***	12.08±1.6***	2.75±0.3***	14.84±0.5***
#13	12	29.00±0.6***	11.92±0.6***	2.84±0.3***	14.75±0.6***
#18	12	29.83±0.6***	11.75±0.6***	2.84±0.3***	14.58±0.4***
35S::MaTSF2/ <i>ft-10</i>					
#1	12	48.34±1.1	32.25±0.7	6.17±0.3	38.42±0.8
#2	12	48.58±1.2	31.25±0.7	6.25±0.3	37.50±0.7
#3	12	47.67±0.9	31.00±0.7	6.58±0.2	37.58±0.7
#4	12	47.42±1.3	32.08±0.9	6.17±0.4	38.25±1.1
#5	12	49.08±0.7	31.83±0.7	6.92±0.3	38.75±0.8
#8	12	48.25±0.8	31.75±0.7	6.83±0.3	38.58±0.7
#11	12	47.67±1.5	30.83±1.0	7.08±0.2	37.92±1.0
#18	12	48.17±0.9	32.50±0.7	6.75±0.4	39.25±0.6

Supplementary Table S5: Flowering time analysis of individual plants over-expressing various banana *FT/TSF*-like genes in a Col-0 background. Values are means $\pm$ SE calculated using Tukey-Kramer multiple comparison test. Asterisks indicate a statistically significant difference between plants in the same column (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ respectively).

Line	LD conditions (16 h light/8 h dark period)				
	No. of Plants	Days to Flower	Rosette leaves	Cauline leaves	Total leaves
Wt (Col)	12	27.84 $\pm$ 0.5	11.08 $\pm$ 0.3	2.58 $\pm$ 0.2	13.67 $\pm$ 0.4
VC/Wt (Col)	12	27.25 $\pm$ 0.5	11.33 $\pm$ 0.3	2.50 $\pm$ 0.2	13.84 $\pm$ 0.5
35S::MaFT1/wt					
#5	12	22.92 $\pm$ 0.5***	7.84 $\pm$ 0.5***	1.75 $\pm$ 0.2*	9.58 $\pm$ 0.5***
#6	12	23.17 $\pm$ 0.6***	8.08 $\pm$ 0.5***	1.67 $\pm$ 0.2	9.75 $\pm$ 0.5***
#7	12	22.67 $\pm$ 0.6***	7.58 $\pm$ 0.4***	1.84 $\pm$ 0.2	9.42 $\pm$ 0.4***
#8	12	23.08 $\pm$ 0.7***	8.17 $\pm$ 0.5***	1.75 $\pm$ 0.1	9.92 $\pm$ 0.6***
#9	12	22.75 $\pm$ 0.7***	7.66 $\pm$ 0.4***	1.75 $\pm$ 0.2	9.42 $\pm$ 0.5***
35S::MaFT2/wt					
#1	12	19.17 $\pm$ 0.5***	6.91 $\pm$ 0.2***	1.50 $\pm$ 0.2*	8.41 $\pm$ 0.3***
#2	12	19.34 $\pm$ 0.4***	6.84 $\pm$ 0.4***	1.58 $\pm$ 0.2*	8.41 $\pm$ 0.5***
#3	12	19.84 $\pm$ 0.6***	7.00 $\pm$ 0.3***	1.41 $\pm$ 0.1**	8.41 $\pm$ 0.4***
#7	12	18.92 $\pm$ 0.3***	6.67 $\pm$ 0.4***	1.34 $\pm$ 0.1***	8.00 $\pm$ 0.4***
#9	12	19.25 $\pm$ 0.6***	6.50 $\pm$ 0.4***	1.58 $\pm$ 0.1*	8.08 $\pm$ 0.4***
#10	12	18.84 $\pm$ 0.4***	6.75 $\pm$ 0.4***	1.34 $\pm$ 0.1***	8.08 $\pm$ 0.4***
35S::MaFT3/wt					
#6	12	23.92 $\pm$ 0.7**	7.58 $\pm$ 0.6***	1.75 $\pm$ 0.2	9.33 $\pm$ 0.6***
#7	12	22.50 $\pm$ 0.7***	7.66 $\pm$ 0.5***	1.58 $\pm$ 0.2*	9.25 $\pm$ 0.5***
#8	12	23.25 $\pm$ 0.8***	7.41 $\pm$ 0.4***	1.83 $\pm$ 0.2	9.08 $\pm$ 0.5***
#9	12	22.25 $\pm$ 0.6***	7.25 $\pm$ 0.4***	1.66 $\pm$ 0.2	8.91 $\pm$ 0.6***
35S::MaFT4/wt					
#1	12	19.84 $\pm$ 0.4***	7.41 $\pm$ 0.3***	1.67 $\pm$ 0.1	9.03 $\pm$ 0.4***
#2	12	17.92 $\pm$ 0.3***	7.08 $\pm$ 0.3***	1.84 $\pm$ 0.1	8.91 $\pm$ 0.3***
#3	12	18.58 $\pm$ 0.5***	7.58 $\pm$ 0.2***	1.25 $\pm$ 0.1***	8.84 $\pm$ 0.2***
#4	12	18.42 $\pm$ 0.4***	6.84 $\pm$ 0.4***	1.50 $\pm$ 0.2*	8.84 $\pm$ 0.5***
#9	12	18.50 $\pm$ 0.3***	6.34 $\pm$ 0.4***	1.67 $\pm$ 0.2	8.00 $\pm$ 0.4***
#14	12	19.08 $\pm$ 0.4***	6.34 $\pm$ 0.4***	1.91 $\pm$ 0.2	8.25 $\pm$ 0.6***
35S::MaFT5/wt					
#3	12	16.34 $\pm$ 0.5***	5.41 $\pm$ 0.3***	1.41 $\pm$ 0.1**	6.84 $\pm$ 0.3***
#6	12	15.67 $\pm$ 0.4***	5.25 $\pm$ 0.3***	1.34 $\pm$ 0.1***	6.58 $\pm$ 0.3***
#7	12	14.42 $\pm$ 0.4***	4.84 $\pm$ 0.2***	1.25 $\pm$ 0.1***	6.08 $\pm$ 0.4***
#8	12	15.75 $\pm$ 0.5***	5.16 $\pm$ 0.2***	1.58 $\pm$ 0.1*	6.75 $\pm$ 0.3***
#9	12	14.67 $\pm$ 0.5***	4.84 $\pm$ 0.2***	1.41 $\pm$ 0.1***	6.25 $\pm$ 0.3***
#10	12	16.00 $\pm$ 0.5***	5.34 $\pm$ 0.3***	1.25 $\pm$ 0.1***	6.58 $\pm$ 0.4***
35S::MaFT6/wt					
#1	12	28.08 $\pm$ 0.6	11.50 $\pm$ 0.5	2.25 $\pm$ 0.3	13.75 $\pm$ 0.6
#2	12	27.17 $\pm$ 0.5	10.84 $\pm$ 0.4	2.67 $\pm$ 0.2	13.50 $\pm$ 0.4
#3	12	28.75 $\pm$ 0.6	11.17 $\pm$ 0.5	2.75 $\pm$ 0.1	13.92 $\pm$ 0.5
#6	12	29.08 $\pm$ 0.7	11.50 $\pm$ 0.5	2.67 $\pm$ 0.1	14.17 $\pm$ 0.5
#9	12	27.75 $\pm$ 0.8	11.50 $\pm$ 0.5	2.25 $\pm$ 0.1	13.75 $\pm$ 0.5
#10	12	29.17 $\pm$ 0.5	11.58 $\pm$ 0.5	2.83 $\pm$ 0.1	14.42 $\pm$ 0.5
#12	12	28.75 $\pm$ 0.8	11.42 $\pm$ 0.5	2.41 $\pm$ 0.1	13.83 $\pm$ 0.5
#13	12	28.42 $\pm$ 0.6	12.00 $\pm$ 0.5	2.33 $\pm$ 0.1	14.33 $\pm$ 0.5

Table S5: Continued

Line	LD conditions (16 h light/8 h dark period)				
	No. of Plants	Days to Flower	Rosette leaves	Cauline leaves	Total leaves
35S::<i>MaFT7</i>/wt					
#1	12	28.25±0.8	12.08±0.6	2.50±0.2	14.58±0.5
#2	12	27.00±0.6	11.75±0.6	2.08±0.2	13.83±0.4
#4	12	26.68±0.5	12.08±0.6	2.25±0.2	14.33±0.6
#5	12	25.08±0.5	8.91±0.6*	2.08±0.2	11.00±0.6**
#6	12	23.92±0.7**	8.16±0.7***	1.91±0.3	10.08±0.7***
#7	12	24.58±0.8	8.33±0.5**	1.83±0.2	10.17±0.5***
#8	12	24.33±0.6*	8.41±0.5**	1.91±0.2	10.33±0.5***
#9	12	24.08±0.5*	8.25±0.4**	2.08±0.2	10.33±0.4***
35S::<i>MaFT8</i>/wt					
#1	12	22.25±0.5***	7.83±0.4***	1.67±0.2	9.50±0.5***
#2	12	22.67±0.6***	7.91±0.3***	1.91±0.2	9.83±0.4***
#3	12	23.25±0.7**	8.08±0.5***	1.83±0.2	9.91±0.5***
#5	12	22.08±0.7***	7.91±0.5***	1.91±0.2	9.83±0.6***
#6	12	23.17±0.8***	8.16±0.7***	1.83±0.2	10.00±0.6***
#7	12	22.58±0.6***	8.08±0.5***	1.58±0.2	9.66±0.4***
#8	12	23.08±0.9***	8.16±0.5***	1.83±0.2	9.75±0.6***
#9	12	22.33±0.6***	8.25±0.4***	1.66±0.2	9.91±0.5***
35S::<i>MaFT9</i>/wt					
#1	12	27.92±0.6	11.25±0.5	2.16±0.2	13.42±0.6
#2	12	27.08±0.5	10.75±0.5	2.58±0.2	13.33±0.4
#3	12	28.42±0.6	10.83±0.5	2.66±0.1	13.50±0.6
#4	12	28.67±0.7	11.25±0.6	2.58±0.2	13.83±0.6
#5	12	27.83±0.7	11.50±0.5	2.25±0.1	13.75±0.5
#6	12	28.83±0.6	11.50±0.6	2.41±0.2	13.92±0.7
#7	12	28.58±0.8	11.42±0.5	2.33±0.1	13.75±0.5
#9	12	28.25±0.6	11.75±0.6	2.25±0.2	14.00±0.6
35S::<i>MaTSF1</i>/wt					
#1	12	19.58±0.8***	5.84±0.5***	1.67±0.2	7.50±0.4***
#2	12	20.92±0.8***	6.08±0.4***	1.75±0.2	7.84±0.5***
#4	12	21.58±0.9***	6.17±0.4***	1.75±0.2	7.92±0.5***
#6	12	19.84±0.7***	5.58±0.5***	1.84±0.2	7.42±0.5***
#7	12	19.67±0.5***	5.84±0.4***	1.75±0.2	7.58±0.4***
#9	12	21.34±0.9***	6.00±0.5***	1.67±0.2	7.67±0.6***
35S::<i>MaTSF2</i>/wt					
#1	12	27.75±0.8	11.42±0.6	2.17±0.3	13.58±0.5
#3	12	27.42±0.8	11.58±0.5	2.25±0.3	13.84±0.5
#4	12	28.50±0.9	11.50±0.5	2.58±0.2	14.08±0.6
#8	12	27.50±0.8	11.42±0.6	2.34±0.2	13.75±0.4
#9	12	28.75±1.0	11.58±0.6	2.67±0.3	14.25±0.6
#15	12	28.84±0.8	12.17±0.5	2.58±0.3	14.75±0.5
#19	12	28.92±0.8	12.75±0.5	2.25±0.2	15.00±0.6
#25	12	27.34±0.9	12.00±0.5	2.42±0.4	14.42±0.6

Supplementary Table_S6. List of oligonucleotide primers used in this study. (GW = genome walking).

Name	Sequence	Purpose
FT-A9-F	GCACTGGCTGGTGacngayathcc	Gene isolation
FT-B6-R	GGACTCCCGCTGGcarttrwarwa	Gene isolation
FT-A19-F	GCGGACCTTCTACACCytnngnatggt	Gene isolation
MaFT1-F1	ATTCAACACCAAGGACTTCTCCGCT	Gene completion
MaFT1-F2	GGGGATCCCGTCGCTGCCATG	Gene completion
MaFT1-R1	CTTGGTGTTGAAGTTCTGCCTCCAC	Gene completion
MaFT1-R2	GCGTAGATCGTCTGCCGGACCGAT	Gene completion
MaFT2-F1	ATTCAACACCAGGGACTTCGCCGAG	Gene completion
MaFT2-F2	GGCTCGCCTGTGGCTGCCGTC	Gene completion
MaFT2-R1	CCTGGTGTTGAAGTTTTGCCGCCAG	Gene completion
MaFT2-R2	GTGTACACCGTCTGCCGACCCAAC	Gene completion
MaFT3-F1	ATTCAGCACCAGAAGGTTCTGTGCTG	Gene completion
MaFT3-F2	ACCTGGCGCCTGTGCGCCGCCAC	Gene completion
MaFT3-R1	CTGGTGCTGAAGTTGTGGCGCATC	Gene completion
MaFT3-R2	GCGAACACCGTCCCCCTCCCCATC	Gene completion
MaFT2-GW-F1	GAAGAGACCAATCTAATCACTAGAAG	GW Intron specific
MaFT2-GW-F2	ATGAGACGGATGCATGAAAGGAAGGA	GW Intron specific
MaFT2-GW-R1	GCAAGTTAGCTTAAGCAGATATACTGG	GW Intron specific
MaFT2-GW-R2	AATAGAGCAGCAGCGGCAGGGCATG	GW Intron specific
MaFT3-GW-F1	ATAGGCATCTCTAGAATTTCTCGTCC	GW Intron specific
MaFT3-GW-F2	GAAAAAGCTGCTGCTGATGATGATG	GW Intron specific
MaFT3-GW-R1	CCAAGTTGCAGAAAACCTACGTACTC	GW Intron specific
MaFT3-GW-R2	AAACCATCAGTTCAGATCTATCAAC	GW Intron specific
MaFT4-GW-F1	ACGCCAACATGACATCGTTCCTCAG	GW Intron specific
MaFT4-GW-F2	ATTAAGTGTGATGTTGGTGACACAGG	GW Intron specific
MaFT4-GW-R1	CATCAGTTAAAGATCCGTCAGCTCT	GW Intron specific
MaFT4-GW-R2	CGCTAAGGGACTCACCTAACGTGT	GW Intron specific
MaFT1-5'UTR-F	GTTGCCAGTGACTCCTGCAATCC	Full Gene amplification
MaFT1-3'UTR-R	TCAGCCATCCTCTTCACGGTCCACA	Full Gene amplification
MaFT1-0F	ATCTAGAATGTGCGAGGGATCCTCTTG	Full Gene amplification
MaFT1-0R	ATCTAGACCACAGCCATTAGTACCTTCTTCC	Full Gene amplification
MaFT2-5'UTR-F	CTGACCATTTGCACCTCGAGAG	Full Gene amplification
MaFT2-3'UTR-R	GGGAAGGGAGGAGAAGTGTGA	Full Gene amplification
MaFT2-0F	ATCTAGAATGCAAAGAGATTCTTTGACTG	Full Gene amplification
MaFT2-0R	ATCTAGATGCAGGCCTCACCATAGC	Full Gene amplification
MaFT3-5'UTR-F	GAAGAAGCTTGTGCTCCTTCCTG	Full Gene amplification
MaFT3-3'UTR-R	GGCATGCATTTATTTACGGATTCA	Full Gene amplification
MaFT3-0F	ATCTAGAATGTGCGAGGGACCCTCTG	Full Gene amplification
MaFT3-0R	ATCTAGAGTCGTCTCCCCGAAACCTT	Full Gene amplification
MaFT4-5'UTR-F	TGGAAAGAAGCTTCGGTCACAGA	Full Gene amplification
MaFT4-3'UTR-R	TGCCTTGAAACGCTAATACAGCTT	Full Gene amplification
MaFT4-0F	ATCTAGAATGTGCGAGGGATCCGCTAAT	Full Gene amplification
MaFT4-0R	ATCTAGATATTGCTCTCAGCATCGGTC	Full Gene amplification
MaFT5-5'UTR-F	TCACTCACCATGAGTAGGGAGAC	Full Gene amplification
MaFT5-3'UTR-R	GGAGGAGGTGTACGAAATGAGAC	Full Gene amplification
MaFT5-0F	ATCTAGAATGAGTAGGGAGACTGATCCAC	Full Gene amplification
MaFT5-0R	ATCTAGAGTTCTGGAAGAGGTACATGCG	Full Gene amplification
MaFT6-5'UTR-F	TCAGTCCATTTGCACCCAGAGAA	Full Gene amplification

MaFT6-3'UTR-R	CCTCACCAGAGCCTGTATTGTATA	Full Gene amplification
MaFT6-0F	ATCTAGAATGCAAAGAGACAGGGATTCTT	Full Gene amplification
MaFT6-0R	ATCTAGAGCATATCCAAGCTACATCCTC	Full Gene amplification
MaFT7-5'UTR-F	CCAGTAGCTCTTCTCGTCACTAAT	Full Gene amplification
MaFT7-3'UTR-R	TGAAAATTGTTATCTTAACTCTGTTGGTC	Full Gene amplification
MaFT7-0F	ATCTAGAATGTGCGAGGGATCCGCTT	Full Gene amplification
MaFT7-0R	ATCTAGATCTGTTGGTCAAATCAAACGC	Full Gene amplification
MaFT8-5'UTR-F	GTCTCCTTTTTCTCTGTGTTGTTTGA	Full Gene amplification
MaFT8-3'UTR-R	CATTATGTTTTAGATGAAGTTGAGCTCT	Full Gene amplification
MaFT8-3'UTR-R1	GCAGTCCAAAGAAGACCATCATCA	Full Gene amplification
MaFT8-0F	ATCTAGAATGTGCGAGGGATCCGCTAGT	Full Gene amplification
MaFT8-0R	ATCTAGACTCTATTGATCTGATATGTAGTACC	Full Gene amplification
MaFT8-0R1	ATCTAGAAGACCATCATCACATCCATCC	Full Gene amplification
MaFT9-5'UTR-F	TTACCGAGAAGCTCTCTTCTGCT	Full Gene amplification
MaFT9-3'UTR-R	AGATAATTTGCATGAGTTAGTTGAACCC	Full Gene amplification
MaFT9-3'UTR-R1	CCCTAATGAGTATTGACTTACTCTC	Full Gene amplification
MaFT9-0F	ATCTAGAATGTGCGAGGGACGCCCT	Full Gene amplification
MaFT9-0R	ATCTAGAGTTGAACCCTATTATTGTTCTGATG	Full Gene amplification
MaFT9-0R1	ATCTAGACAGTCATCACGTCCATCCA	Full Gene amplification
MaFT10-5'UTR-F	ACCGTGGTGGTAGTTAGTCCATT	Full Gene amplification
MaFT10-3'UTR-R	CTTGGAAGTTTAGGCAGGTGTTATAT	Full Gene amplification
MaFT10-3'UTR-R1	CCATAACCGTTGCAGTTTAAAGAAGA	Full Gene amplification
MaFT10-0F	ATCTAGAATGTGCGAGGGACCCACTT	Full Gene amplification
MaFT10-0R	ATCTAGAATCTGATATACCTTCTTCCACCA	Full Gene amplification
MaFT10-0R1	ATCTAGAAAGAAGACCATCACATCCATCCG	Full Gene amplification
MaFT11-5'UTR-F	CTGCGTACTAATGAGCAGGGAA	Full Gene amplification
MaFT11-3'UTR-R	AGTAGTGTTCAAGTGGCGAGTAG	Full Gene amplification
MaFT11-3'UTR-R1	AGTAGTGTTCAAGTGGCGAGTAG	Full Gene amplification
MaFT11-0F	ATCTAGAATGAGCAGGGAAAGGGATC	Full Gene amplification
MaFT11-0R	ATCTAGACAGCTACATGGGATACATCC	Full Gene amplification
MaFT11-0R1	ATCTAGACAGCTACATGGGATACATCC	Full Gene amplification
MaFT12-5'UTR-F	GAAGAAGTTTGTGCTCCTTCCTG	Full Gene amplification
MaFT12-3'UTR-R	GTATATCTCCTCTCAGCATCAGTCGTC	Full Gene amplification
MaFT12-0F	ATCTAGAATGTGCGAGGGGCCCTCTG	Full Gene amplification
MaFT12-0R	ATCTAGAGTCGTCTCCCCGAAACCTT	Full Gene amplification
MaTSF1-5'UTR-F	TTACAGCGCATTAGCAGGCAG	Full Gene amplification
Ma TSF1-3'UTR-R	CTAGATGATGGAGTTCTTAGTGTG	Full Gene amplification
Ma TSF1-0F	ATCTAGAATGTGACGAGGAAGGGATC	Full Gene amplification
Ma TSF1-0R	ATCTAGAGTTCTTAGTGTGTTATTTACTACC	Full Gene amplification
MaTSF2-5'UTR-F	CTTCTTCCATCACAGCTTCAACTTGT	Full Gene amplification
Ma TSF2-3'UTR-R	TGATTCATGTGCGTAAGCAATGACTTTTG	Full Gene amplification
Ma TSF2-0F	ATCTAGAATGCCCCAAGGAAGGGAT	Full Gene amplification
Ma TSF2-0R	TGACTTTTGTTTATTACCTTCGTCCC	Full Gene amplification
MaFT1-qRT-F	CAATGGATCCGAGCTCAAAC	qRT-PCR
MaFT1-qRT-R	CACCAGCGTGTACAGAGTCC	qRT-PCR
MaFT2-qRT-F	GGCAGGAGATCGTGTGCTAT	qRT-PCR
MaFT2-qRT-R	GTTGTAGAGCTCGGCGAAGT	qRT-PCR
MaFT3-qRT-F	CCACAACTTCAGCACGAGAA	qRT-PCR
MaFT3-qRT-R	TCTCCTCTCAGCATCAGTCG	qRT-PCR
MaFT4-qRT-F	TTCGGTCACAGAATGTGCGAG	qRT-PCR
MaFT4-qRT-R	CAGCAGACGGCTTGAACCTC	qRT-PCR
MaFT5-qRT-F	CGCCAAAACCTTCAACACCAG	qRT-PCR

MaFT5-qRT-R	TGGAAGAGATACATGCGCCTA	qRT-PCR
MaFT6-qRT-F	ACGTCTTCGTGCTCTTCAGG	qRT-PCR
MaFT6-qRT-R	GCGATCCGAGGTTATAGAGC	qRT-PCR
MaFT7-qRT-F	GTTTGTGTTGTTCCGGCAAT	qRT-PCR
MaFT7-qRT-R	CCTTCTTCCACCACAACCAT	qRT-PCR
MaFT8-qRT-F	TCTCTGGAATCCATCGCTTT	qRT-PCR
MaFT8-qRT-R	GAACATGGCAGCAACAGGAT	qRT-PCR
MaFT9-qRT-F	GTGTTGTTCCGGCAGTCC	qRT-PCR
MaFT9-qRT-R	CCCCTAGGTTGTAAACTGCTG	qRT-PCR
MaFT11-qRT-F	CAACTCTGGGGATCCATCG	qRT-PCR
MaFT11-qRT-R	GTTGTAGAGCTCGGCGAAGT	qRT-PCR
MaFT12-qRT-F	TGGTTGCTTCGAGTGTCTTG	qRT-PCR
MaFT12-qRT-R	GCGGATGGTTTGAAGTCG	qRT-PCR
Ma TSF1-qRT-F	AGCCGGGATTCACCGTAT	qRT-PCR
Ma TSF1-qRT-R	CAGCAGGGAGTCCAAGGTTA	qRT-PCR
Ma TSF1-qRT-F	GCAGGGATTCATCGTATCGT	qRT-PCR
Ma TSF1-qRT-R	CCATTCTCTCTTTGGCAGTTG	qRT-PCR
RPS-qRT-F	CGGGATTGCCTGATATTGTG	qRT-PCR
RPS-qRT-R	CCCTCACAAATTGCGGATAC	qRT-PCR
AtAP1-qRT-F	AGGAGCAGTGGGATCAGCAG	qRT-PCR
AtAP1-qRT-F	TTGATACAGACCACCCATGTT	qRT-PCR
AtSAND-qRT-F	TTGATCCACTTGCAGACAAGGC	qRT-PCR
AtSAND-qRT-F	TACCCTTTGGCACACCTGATTG	qRT-PCR

Supplementary Table S7. Accession numbers / Sequence identifiers used for phylogenetic analysis of *FT/TSF*-like gene family. (RGA, Rice Genome Annotation)

Plant	Common Name	Gene Name	Accession Numbers / Sequence Identifiers	Database
<i>Arabidopsis thaliana</i>	Thale Cress	FT	NP_176726	NCBI
<i>Arabidopsis thaliana</i>	Thale Cress	TSF	NP_193770	NCBI
<i>Oryza sativa</i>	Rice	OsFTL1	LOC_Os01g11940	RGA
<i>Oryza sativa</i>	Rice	OsFTL2 (Hd3a)	LOC_Os06g06320	RGA
<i>Oryza sativa</i>	Rice	OsFTL3 (RFT1)	LOC_Os06g06300	RGA
<i>Oryza sativa</i>	Rice	OsFTL4	LOC_Os09g33850	RGA
<i>Oryza sativa</i>	Rice	OsFTL5	LOC_Os02g39064	RGA
<i>Oryza sativa</i>	Rice	OsFTL6	LOC_Os04g41130	RGA
<i>Oryza sativa</i>	Rice	OsFTL9	LOC_Os01g54490	RGA
<i>Oryza sativa</i>	Rice	OsFTL10	LOC_Os05g44180	RGA
<i>Oryza sativa</i>	Rice	OsFTL11	LOC_Os11g18870	RGA
<i>Oryza sativa</i>	Rice	OsFTL12	LOC_Os06g35940	RGA
<i>Oryza sativa</i>	Rice	OsFTL13	LOC_Os02g13830	RGA
<i>Zea mays</i>	Maize	ZCN7	EU241899	NCBI
<i>Zea mays</i>	Maize	ZCN8	EU241900	NCBI
<i>Zea mays</i>	Maize	ZCN12	EU241903	NCBI
<i>Zea mays</i>	Maize	ZCN13	EU241904	NCBI
<i>Zea mays</i>	Maize	ZCN14	EU241905	NCBI
<i>Zea mays</i>	Maize	ZCN15	EU241906	NCBI
<i>Zea mays</i>	Maize	ZCN16	EU241907	NCBI
<i>Zea mays</i>	Maize	ZCN17	EU241908	NCBI
<i>Zea mays</i>	Maize	ZCN18	EU241909	NCBI
<i>Zea mays</i>	Maize	ZCN19	EU241910	NCBI
<i>Zea mays</i>	Maize	ZCN20	EU241911	NCBI
<i>Zea mays</i>	Maize	ZCN21	EU241912	NCBI
<i>Zea mays</i>	Maize	ZCN24	EU241914	NCBI
<i>Zea mays</i>	Maize	ZCN25	EU241915	NCBI
<i>Zea mays</i>	Maize	ZCN25	EU241916	NCBI
<i>Allium cepa</i>	Onion	AcFT1	KC485348	NCBI
<i>Allium cepa</i>	Onion	AcFT2	KC485349	NCBI
<i>Allium cepa</i>	Onion	AcFT3	KC485350	NCBI
<i>Allium cepa</i>	Onion	AcFT4	KC485351	NCBI
<i>Allium cepa</i>	Onion	AcFT5	KC485352	NCBI
<i>Allium cepa</i>	Onion	AcFT6	KC485353	NCBI
<i>Hordeum vulgare</i>	Barley	HvFT1	DQ100327	NCBI
<i>Hordeum vulgare</i>	Barley	HvFT2	DQ297407	NCBI
<i>Hordeum vulgare</i>	Barley	HvFT3	DQ411319	NCBI
<i>Hordeum vulgare</i>	Barley	HvFT4	DQ411320	NCBI
<i>Hordeum vulgare</i>	Barley	HvFT5	EF012202	NCBI

Supplementary Table S8. Accession numbers (genomic and mRNA) in the NCBI database for various banana *FT/TSF* genes identified in this study.

Gene name	Accession No (genomic)	Accession No (mRNA)
<i>MaFT1</i>	KC296753	KC296755
<i>MaFT2</i>	JX842683	JX842681
<i>MaFT3</i>	JX842678	HQ425707
<i>MaFT4</i>	JX842677	JX842676
<i>MaFT5</i>	KF853462	KF853467
<i>MaFT6</i>	KF853463	KF853468
<i>MaFT7</i>	KF853464	KF853469
<i>MaFT8</i>	KF853465	KF853470
<i>MaFT9</i>	KF853466	KF853471
<i>MaFT10</i>	KM042900	--
<i>MaFT11</i>	KM042901	KM054874
<i>MaFT12</i>	KM042902	KM054874
<i>MaTSF1</i>	KM487739	KF853460
<i>MaTSF2</i>	KM487740	KF853461

Supplementary figures

Figure S1. Phylogenetic analysis of Banana FT/TSF-like family proteins with Arabidopsis FT and TSF proteins. The functional FT proteins of rice (Hd3a) and maize (ZCN8) are also included. The accession numbers are provided in methods.

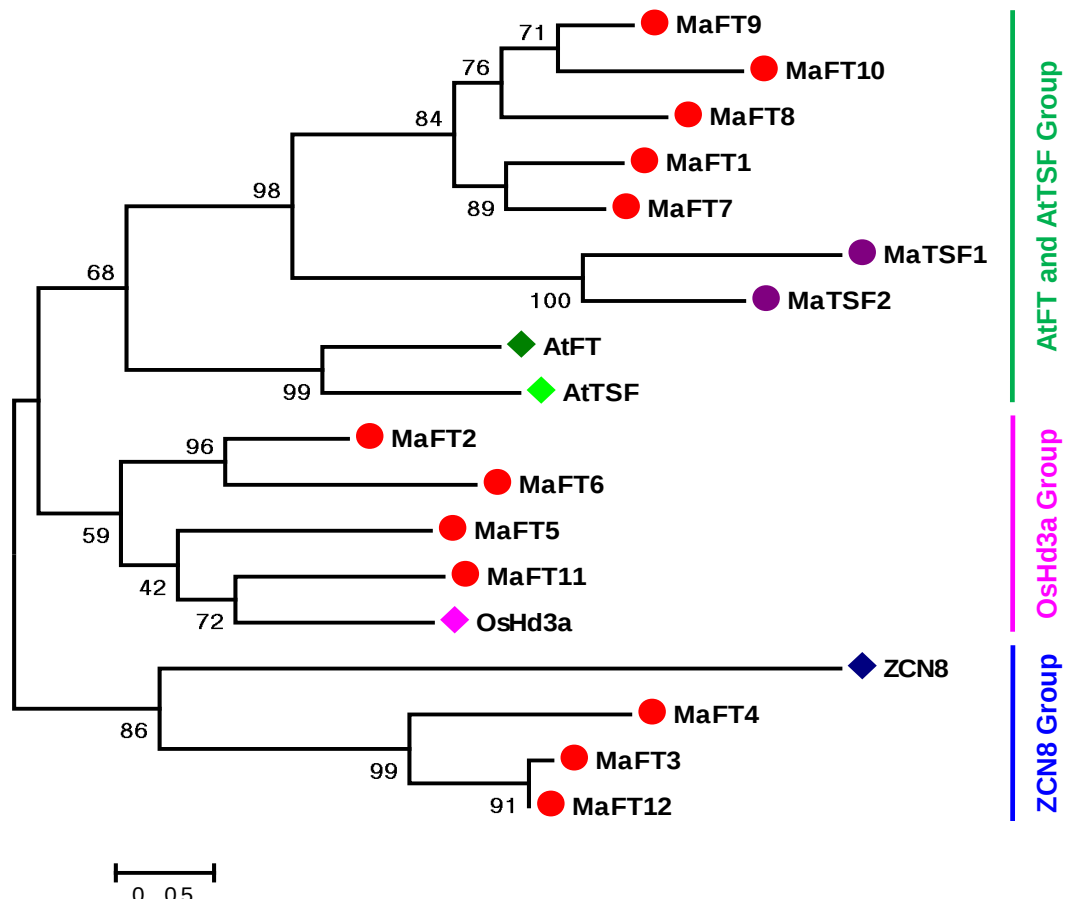


Figure S1

Figure S2. Reversion of the late flowering phenotype of the *Arabidopsis ft-10* mutant upon ectopic expression of various banana *FT/TSF* genes.

- (A) Early flowering upon expression of *MaFT2*, *MaFT3*, *MaFT4*, *MaFT5* and *MaFT12* in *ft-10* mutant
- (B) Early flowering upon expression of *MaFT1*, *MaFT8*, *MaTSF1* and *MaFT7* genes in *ft-10* mutant. The photographs A and B were taken 45 days and 38 days after planting respectively.

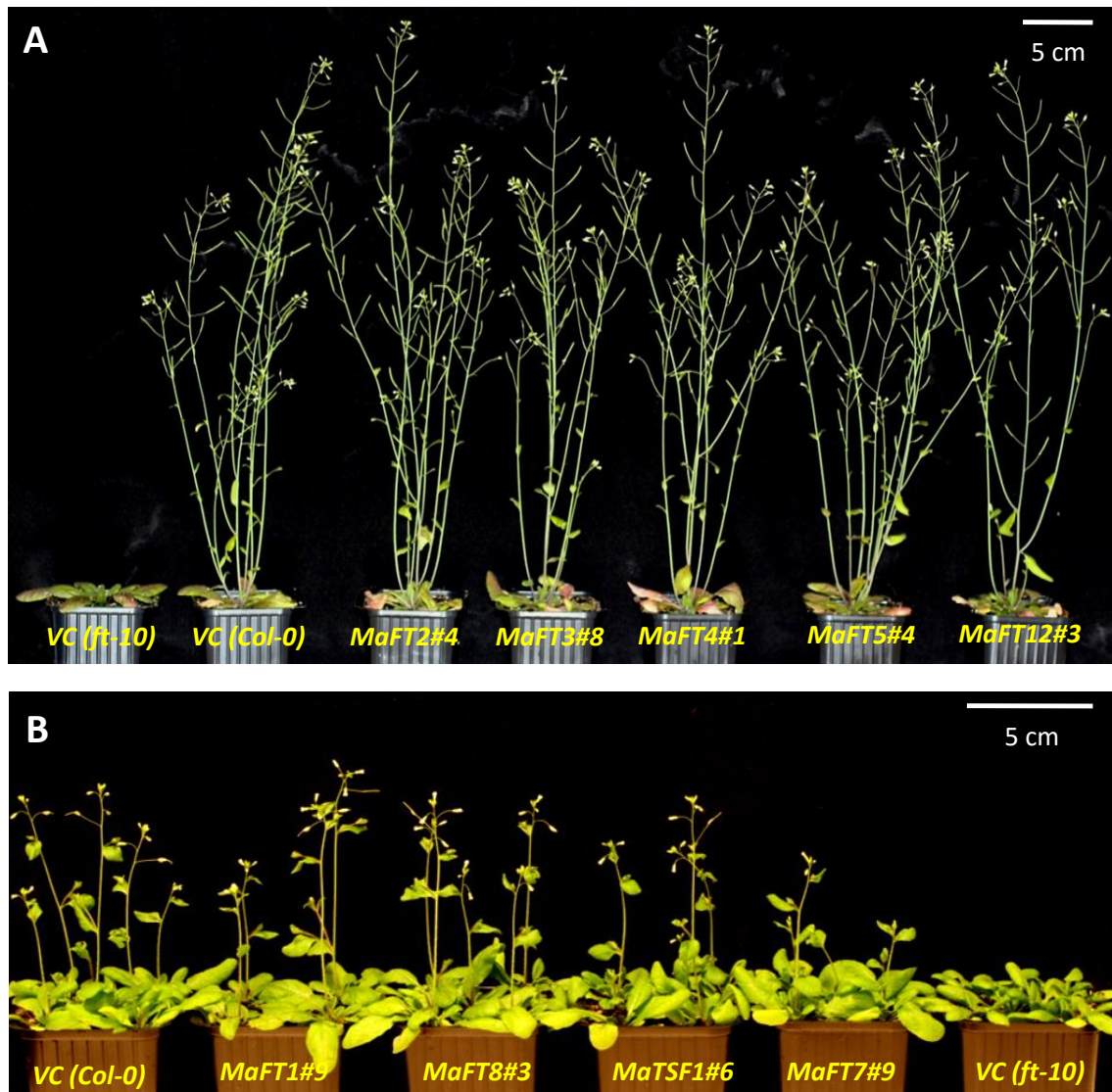


Figure S2

Figure S3. Early flowering in *Arabidopsis* Col-0 induced by over-expression of various banana *FT/TSF*-like genes. Except *MaFT6*, *MaFT9* and *MaTSF2*, all genes showed early flowering compared to vector control (VC) wild type plants. The photographs were taken 38 days after planting.

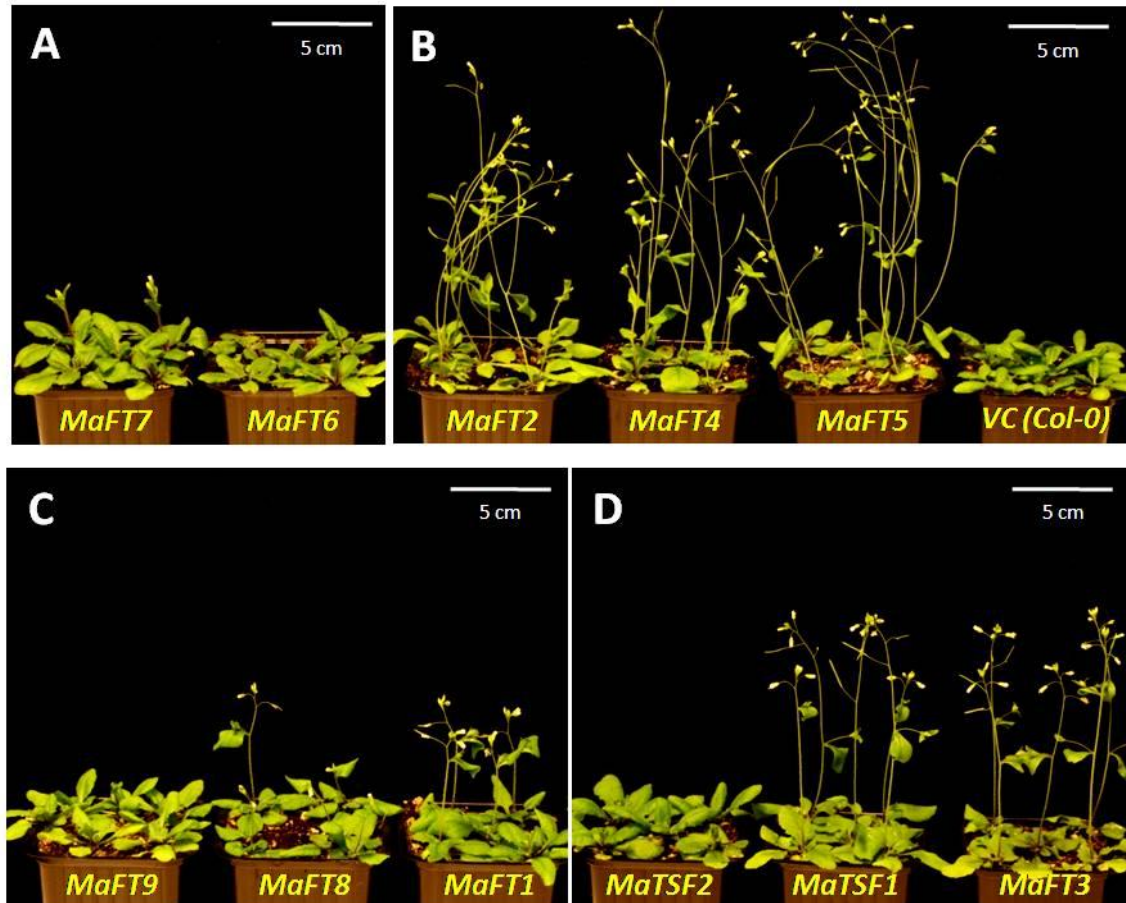


Figure S3

Figure S4. Relative transcript level of *MaFT*/*TSF*-like genes in transgenic *Arabidopsis* lines ectopically expressing various banana genes. The *SAND* (AT2G28390) gene of *Arabidopsis* is used as reference gene.

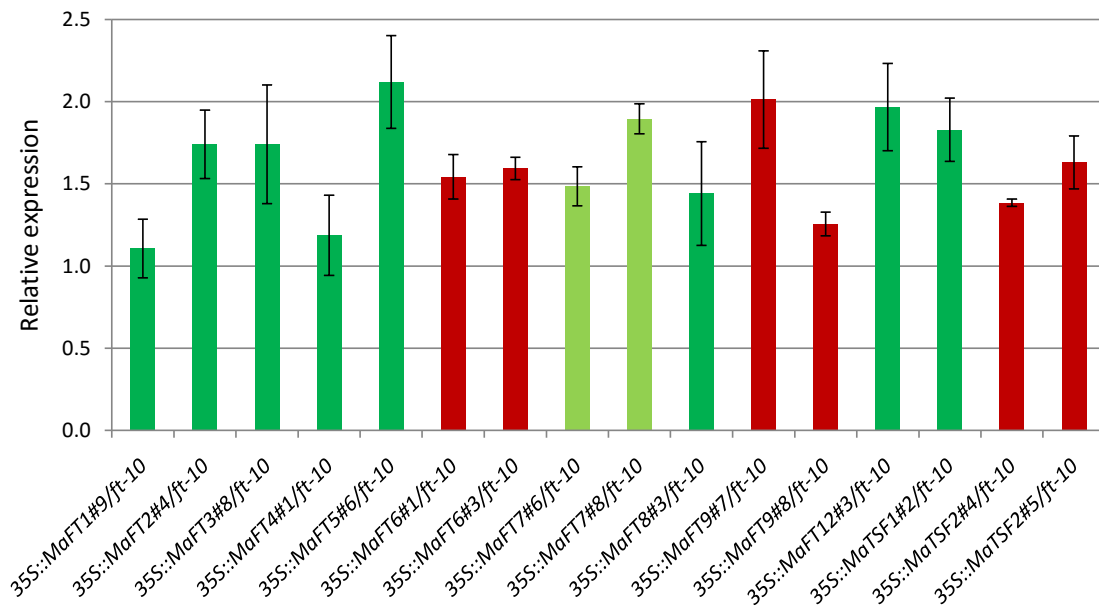


Figure S4

Figure S5. Various field parameters during growth of banana

Day length (top), Temperature (middle) and Humidity (bottom) (data taken from JISL weather station)

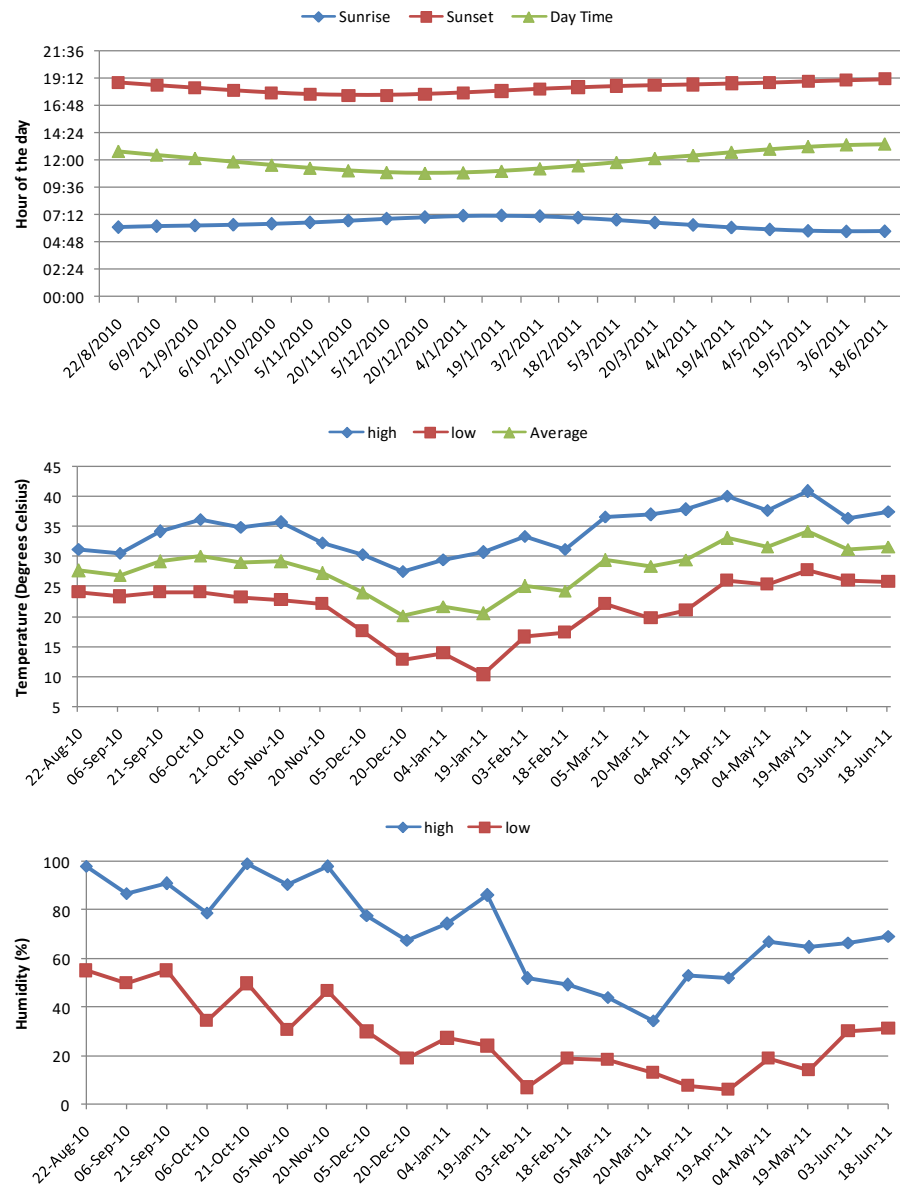


Figure S5