

1 **Supplementary Information**

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3 **The floral repressor *GmFLC-like* is involved in regulating flowering time
4 mediated by low temperature in soybean**

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6 **This PDF file includes:**

7 Supplementary Fig. 1-2

8 Supplementary Table 1

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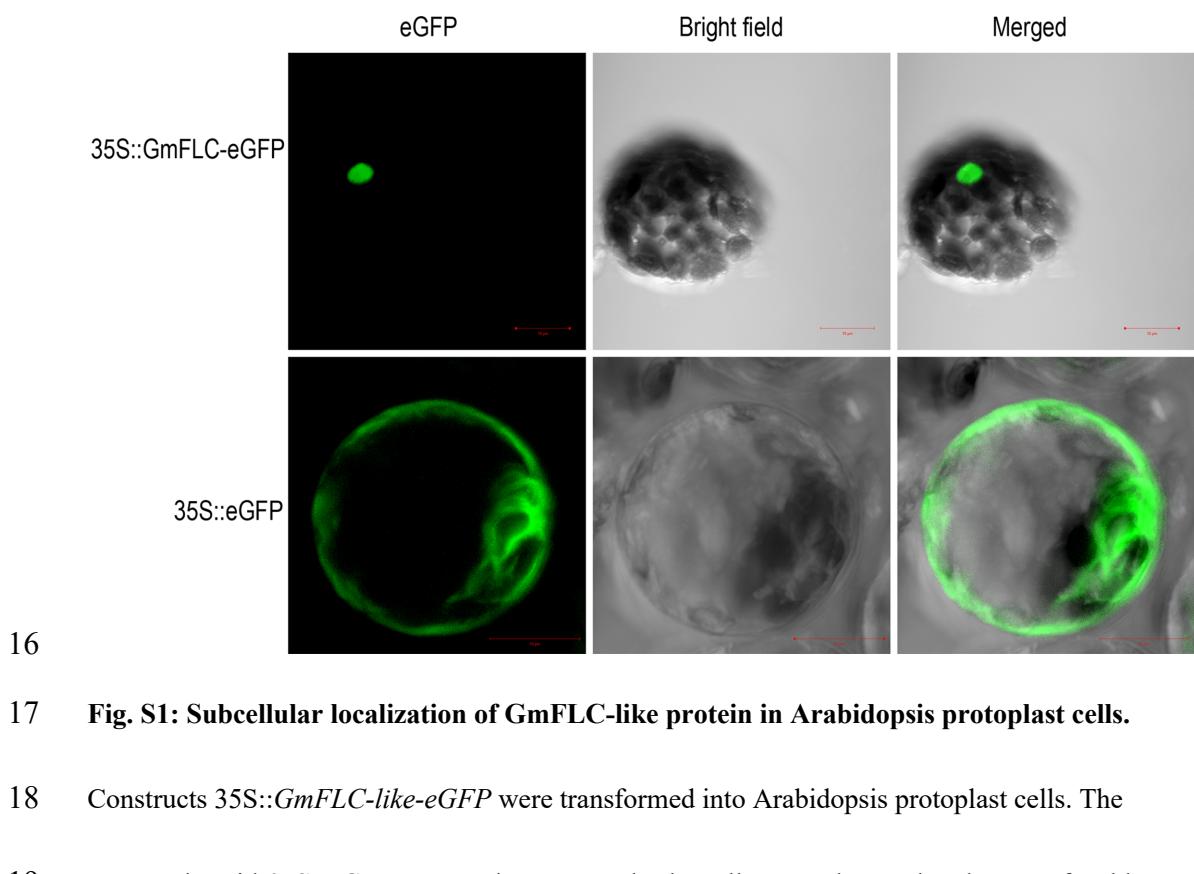
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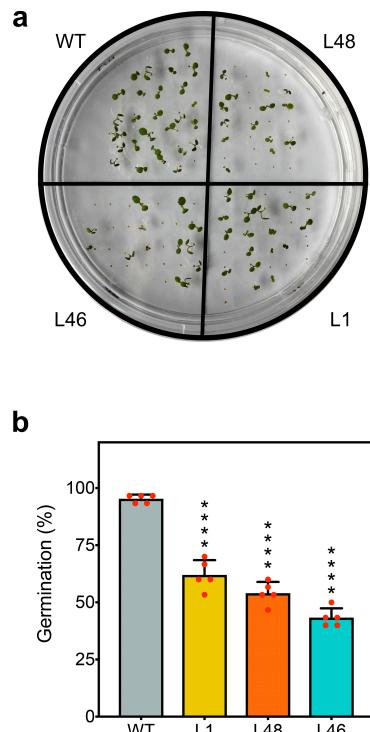
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24 **Fig. S2: Comparative analysis of seed germination rate among four lines of Arabidopsis. a**
 25 Germinating status of WT (Col-0) and three *GmFLC-like* transgenic lines L1, L46, and L48 seeds
 26 on 1/2 MS medium at 3 days after transfer to light. **b** Seed germination rate of WT and three
 27 transgenic lines on 1/2 MS medium. Germination percentage was counted for approximately 30
 28 seeds for each line. Experiments were repeated five times and mean value \pm SD is plotted on the
 29 graph. Significant differences according to the *t*-test are denoted as follows: * $p < 0.05$, ** $p <$
 30 *** $p < 0.01$, **** $p < 0.001$, ***** $p < 0.0001$.

Supplementary Table 1. Primers used in this study

Primers	Sequence
For gene isolation	
<i>K-FLC</i> -F	ATGGGAAAGAAGAAGCTGGAGAT
<i>K-FLC</i> -R	CAACCTCTACCACTAGGCCAATCAT
For vector construction of overexpression in Arabidopsis	
<i>1301-FLC</i> -F	CGCGGATCC(BamHI)ATGGGAAAGAAGCTGG
<i>1301-FLC</i> -R	CGGGTACC(KpnI)TTATTATTACTGAGTTCAAGAATT
For vector construction of subcellular localization	
<i>FLC-GFP</i> -F	CGGGTACC(KpnI)ATGGGAAAGAAGCTGG
<i>FLC-GFP</i> -R	CGGGATCC(BamHI)TTTATTACTGAGTTCAAGAATTGAG
For gene promoter isolation	
<i>Pro-GmFLC</i> -F	TTGCTTCGGTTACTGTTCTTCC
<i>Pro-GmFLC</i> -R	TGTTCTCGATTGCTTTATCTCC
<i>proFT2a-1</i> -F	ATTGGTACCCCGGGTGGGAAGGGCTACT
<i>proFT2a-1</i> -R	ATTCTCGAGAACATTCCCTCCCTCTC
<i>proFT2a-2</i> -F	ATTGGTACCTCCTTTTCACTCAAGTG
<i>proFT2a-2</i> -R	ATTCTCGAGTTACTTATTAAATGGAAACTA
<i>intFT2a-1</i> -F	ATTGGTACCTATGATTTAGTTTCATT
<i>intFT2a-1</i> -R	ATTCTCGAGTAATGGATGCTATATCAT
<i>intFT2a-2</i> -F	ATTGGTACCTTATTATCTATCTCTTT
<i>intFT2a-2</i> -R	ATTCTCGAGTGACTTAAGTCCTATAAAA
For transgenic plants confirmation	
<i>Hpt</i> -F	ACTTCTACACAGCCATCGGTCC
<i>Hpt</i> -R	AGCGAGAGCCTGACCTATTGC
For qRT-PCR analysis	
<i>Gm-FLC</i> -F	TGACGCATAATCTGCTCCCTG
<i>Gm-FLC</i> -R	GCTAAACCATGGCATAGTCCCT
<i>Gm-β-Tublin</i> -F	CCTCGTTGAATTGCGCTTTTG
<i>Gm-β-Tublin</i> -R	CAACTGTCTGTCGCTGGCAT
<i>GmFT1a</i> -F	CCTTTACACCCTGGTTATGG
<i>GmFT1a</i> -R	CCTGGAGGTTGCAGAGTTAGT
<i>GmFT1b</i> -F	GACTTCAGGACCTTTACACCC
<i>GmFT1b</i> -R	GCTCACAAACCTCTTCACCGA
<i>GmFT2a</i> -F	ATCCCGATGCACCTAGCCCA
<i>GmFT2a</i> -R	ACACCAAACGATGAATCCCCA
<i>GmFT2b</i> -F	GACATTCCAGCAACAACGG
<i>GmFT2b</i> -R	ATAGCCTCTTCCACCACAAAC
<i>GmFT3a</i> -F	GGATTCATCGTTCGTGTGTTG
<i>GmFT3a</i> -R	CACCAGAGCCAGTTCCCT
<i>GmFT3b</i> -F	CTATGAAAGCCCACGACCC
<i>GmFT3b</i> -R	TTGAAGAAGACAGCAGCAACC
<i>GmFT4</i> -F	GTGAGTTCAAACCTCCCAAAT
<i>GmFT4</i> -R	CAATCCGATGAATCCCAGAA
<i>GmFT5a</i> -F	ACAGATTATGGTAGCAACGGAA
<i>GmFT5a</i> -R	CAAGGATAGCCAGAAAAGAAAG

<i>GmFT5b</i> -F	CTCAATCCTTTACAATCTCCG
<i>GmFT5b</i> -R	CCTTAGGTCTTCACCACCAACA
<i>At-FT</i> -F	CCCTGCTACAACCTGGAACAAAC
<i>At-FT</i> -R	AAGAACAAAGGTAACCCAATGAAC
<i>At-SOC1</i> -F	AAACGAGAAGCTCTCTGAAAAG
<i>At-SOC1</i> -R	AAGAACAAAGGTAACCCAATGAAC
<i>At-AP1</i> -F	GCAAGCAATGAGCCCTAAAG
<i>At-AP1</i> -R	ACTGCTCCTGTTGAGCCCTA
<i>At-TUB2</i> -F	ATCGATTCCGTTCTCGATGT
<i>At-TUB2</i> -R	ATCCAGTTCCCTCCTCCCAAC
