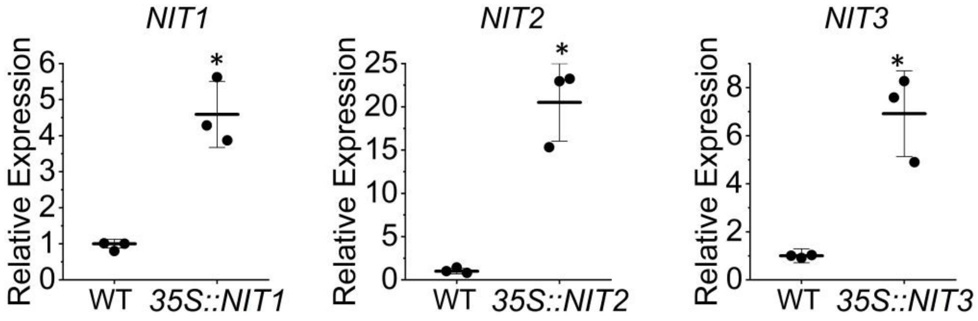

Figure S1. Relative expression levels of *NIT1/2/3* in transgenic lines. The error bars represent the standard error (three biological repeats). The asterisks at the top of the bar indicate significant differences between *35S::NIT1/2/3* and wild type (WT), $P < 0.05$(*) or $P < 0.01$(**) by Student's *t* test.

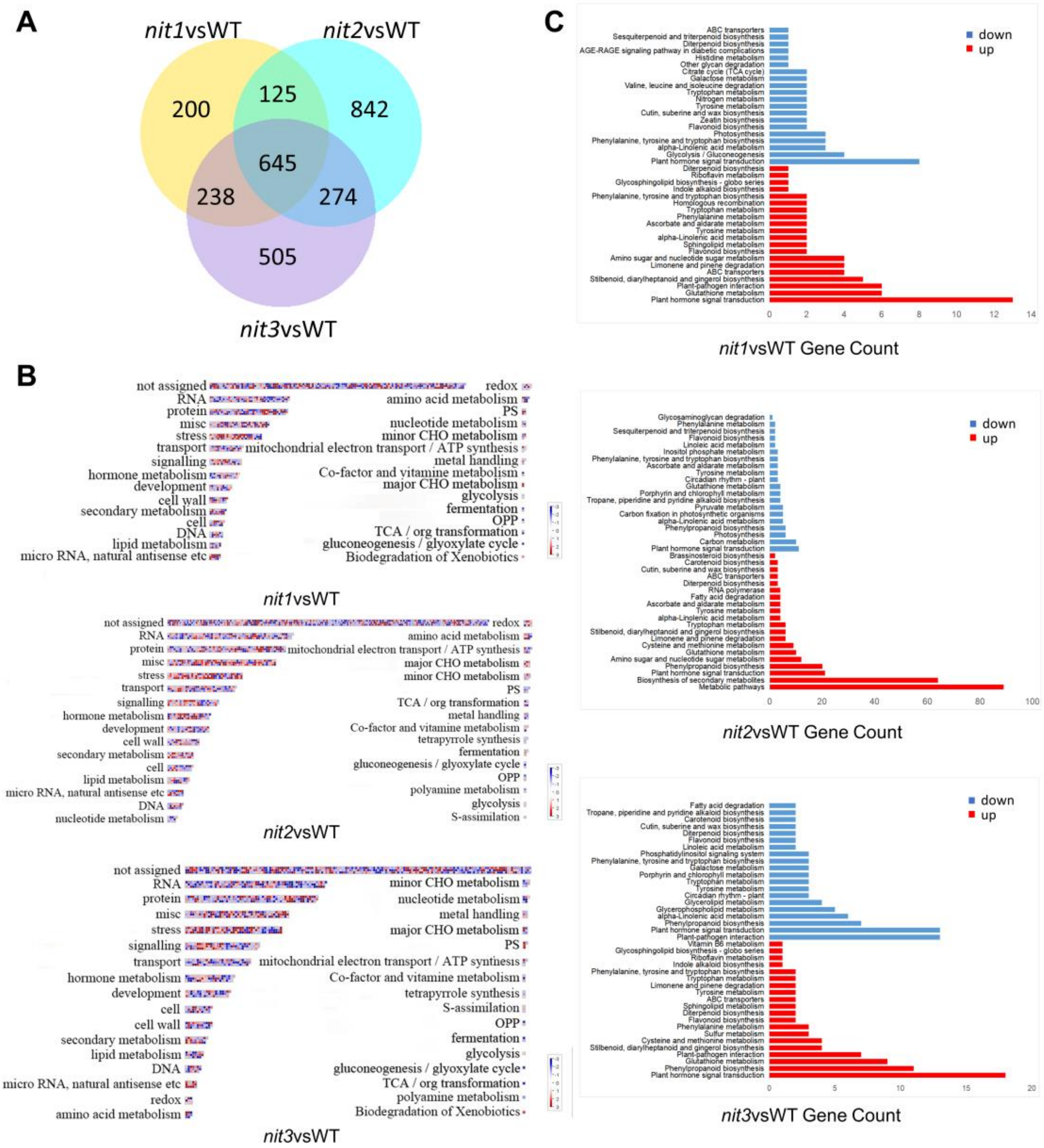

Figure S2. Transcriptome analysis of *nit1*/*nit2*/*nit3* in Arabidopsis. (A) Venn diagram showing overlapped differentially expressed genes (DEGs) between *nit1*, *nit2* and *nit3*. (B) GO enrichment analysis of the DEGs in *nit1*/*nit2*/*nit3* compared to wild type. Red squares represent up-regulated and blue squares represent down-regulated genes. (C) The top 40 (20 up-regulated, 20 down-regulated) enriched Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway terms of DEGs.

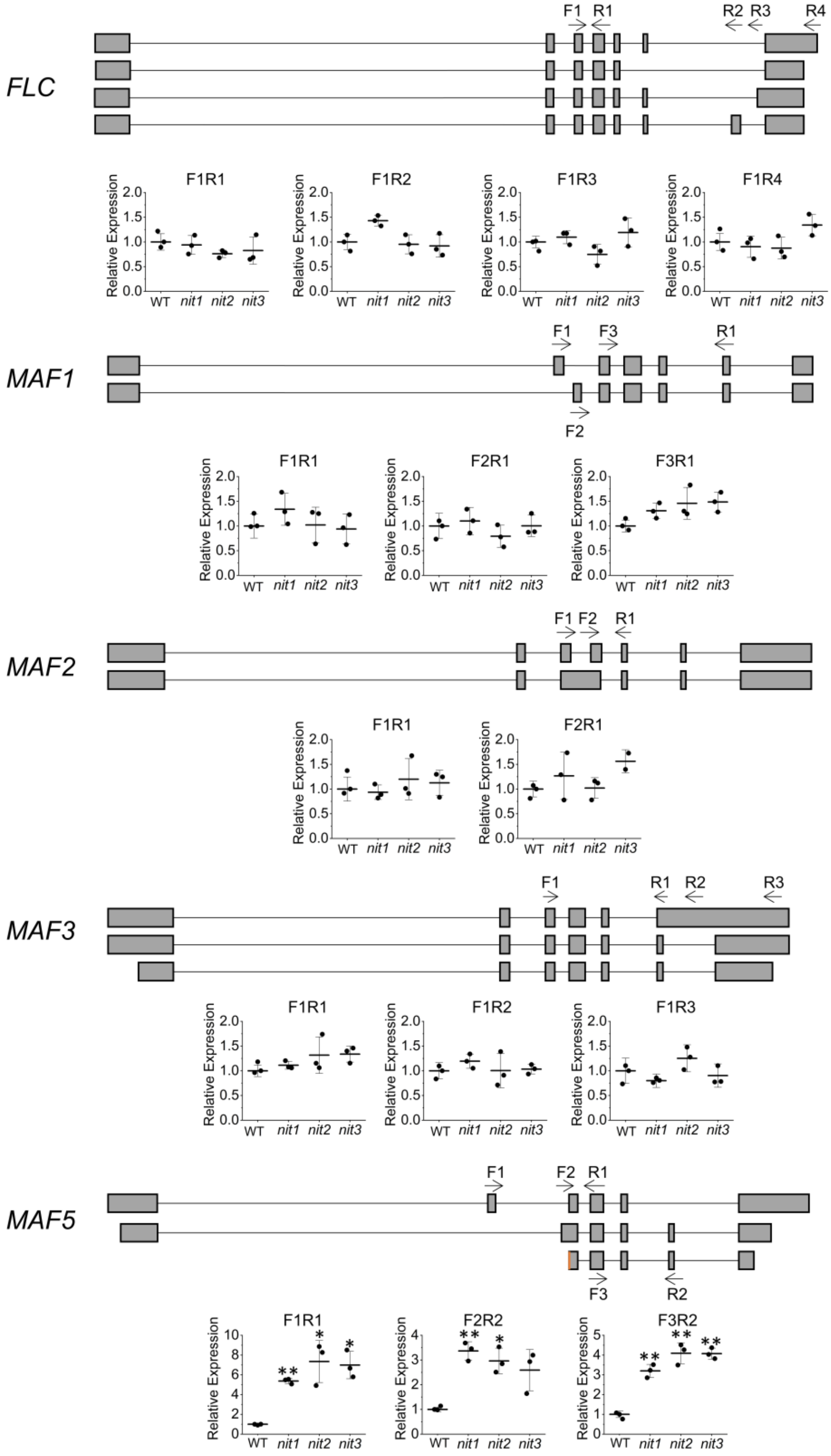

Figure S3. Relative expression levels of *FLC, MAF1, MAF2, MAF3* and *MAF5* splicing variants. Squares and lines represent exons and introns respectively. F means forward primer and R means reverse primer. Arrow indicates primer direction. The error bars represent the standard error (three biological repeats). The asterisks at the top of the bar indicate significant differences between *nit1/2/3* and wild type (WT), *P* < 0.05(*) or *P* < 0.01(**) by Student's *t* test.

Supplemental Table 1. Sequences of primers used in this study

Name	Sequence
NIT1-F	ATGTCTAGTACTAAAGATATGTCAACTGTC
NIT1-R	CTATTTGTTTGAGTCATCCTCAGC
NIT2-F	ATGTCAACTTCAGAAAACACTCC
NIT2-R	TTACTTGTTTGAGTCATCTTCCG
NIT3-F	ATGTCTAGTACTGAAGAAATGTCATCA
NIT3-R	CTATTTGTTTGATTCATCCTCTGC
NIT1p-F	AATCTTCTTTAGTTTTTATCTTAGGCT
NIT1p-R	CGAGTCTTTGTTTTTTACTTTGG
NIT2p-F	GATTGAGTCGACAGTAATACGAGAC
NIT2p-R	ACTTGAGCTTTAGTCTTACTTCGAT
NIT3p-F	AATGTATTTGGCTTGTCTTGTGTC
NIT3p-R	ACTCGAGTCTTTGTTTTTACTTTATAC
LBb1.3	ATTTTGCCGATTTCGGAAC
nit1-L	AAATAGGAGCCAAACTCACATTTC
nit1-R	CGCTAAACCGAACCTAAAACC
nit2-L	TGAGATGGTATACCACGGATG
nit2-R	AAACGGGTATCTTTCGGTTTG
nit3-L	GGTATTGCAGAACGAACC
nit3-R	GAGACTTGGGAGGCATT
maf4-L	TGATTACATATGCATGCGACC
maf4-R	TGAGTTATTGGGTCTCATGGG
ACTIN2-F	TTACCCGATGGGCAAGTC
ACTIN2-R	GCTCATACGGTCAGCGATAC
FKF1-F	GGAGGGTGTGGAAGACAAGG
FKF1-R	AGAAGGTGTCGCTGAGAAGC
TOC1-F	ATCCACATTCCCTTGAGCGG
TOC1-R	TTTGGTGCAGAGAAACCCGA
CDF3-F	TTGGTCTCGAAGCTCAGCAG
CDF3-R	ACAAGCCGTTGATCCGCTAA
CO-F	TCCCCCGTAGCTCGTCTGTGGTA
CO-R	GCGTGCTCCGGCTGCTTTTT
PHYA-F	TGATTCAGCCCTTCGGTTGT
PHYA-R	GACGCACTAGGAGCAGTGAA
FT-F	CTAGCAACCCTCACCTCCGA
FT-R	TCGTAACACACAATCTCATTGCCAAA
SOC1-F	GCTCATTGATGGACTCGTACATAAGTTGGT
SOC1-R	TTGACCAAACTTCGCTTTCA
AP1-F	CCAGAGGCATTATCTTGGGGAAGACTTG
AP1-R	GCTCATTGATGGACTCGTACATAAGTTGGT
LFY-F	TCATTTGCTACTCTCCGCCGCT
LFY-R	CATTTTTCGCCACGGTCTTTAG

FLC-F	TGTGGATAGCAAGCTTGTGG
FLC-R	TAGTCACGGAGAGGGCAGTC
MAF1-F1	ACATGCTGATGAACTTAGAGCCT
MAF1-F2	AGCCGGAGAAACCTCAATGT
MAF1-F3	CCACACAAGGAGTTACTAGAAACAGTCC
MAF1-R1	GCCAGAACCTGGTTCTCTTCTCTCAG
MAF2-F1	CTTGCAGAAAAAACTCGGAATTATCTGCCAC
MAF2-F2	TAGCACAAAGACACTTTTATCTCCCTC
MAF2-R1	CCTAGCTCTAGTTACGGACAGAGCAGTC
MAF3-F1	TCGGAATTATCTTCCACACAAGGAG
MAF3-R1	GCCAGAATCTGGTTCTCTTCTATCAGC
MAF3-R2	GCCTAGCTTCCATCAAACTCCT
MAF3-R3	CCAGAAACGTCTTCTTCCCCA
MAF4-F1	TTGTGAATCCTCCGTCGCTC
MAF4-F2	TCTTGATCTCTCCAGCATGGC
MAF4-F3	TGGCCAAGATCCTCAGTCGTTATGA
MAF4-F4	TCCAAGAGCAGTGTTTGGGT
MAF4-F5	GGAGCTTGTGAAGACCCATCA
MAF4-R1	TGGCCATGAAATCTACCGGG
MAF4-R2	TGCTGGTCTCTCTCCACAATG
MAF4-R3	TCTAGCAACTCCTTGTGCGAA
MAF4-R4	GCTGCTCTTCCAGGGACTTTAGACA
MAF4-R5	GCATAGCTAGGGATGGCGAA
MAF4-R6	TACTTGAGAAGCAGGAGAGTCTCC
MAF5-F1	TCCATGGAAGAGCAGCTCAA
MAF5-F2	GATGGAGCTTGTGAAGAACCTTCAGG
MAF5-F3	ACAAGCTGATGATCCTGAAACCT
MAF5-R1	CCACCTCGCTAGCTAGAACC
MAF5-R2	CAGCCGTTGATGATTGGTGGTTACTTG
MAF5-R3	ACAGACAGAGCACTCTTGAGC
MAS-F	GTGATGGTGGTTACTTGAGAAGCA
MAS-R	AACTGAATAAAGTTGTGATGGTG
MAF4-ChIP-F1	GGCAGAAAAAGACTTGTCGAGGCTGG
MAF4-ChIP-R1	GTGTGTTTTCCAAAAATCCAAAAATTTGAACCGAG
MAF4-ChIP-F2	CAAACGAATTGAGAACAAAAGCTCTCGACAAGT
MAF4-ChIP-R2	GCTGTAGAGTCTTCCGGTGGCAGA
MAF4-ChIP-F3	CAGTGGAAGAAAATAGCATGTGTACACATTGAGTAGC
MAF4-ChIP-R3	CGTACCAAATGTTTGTAGAGACTCAGTTTCTTTGG
MAF4-ChIP-F4	TTTCTTACAGATGGGGAAGATGAAGAAGTCTG
MAF4-ChIP-R4	GGTGATGGTGGTTACTTGAGAAGCAGGAG
MAF5-ChIP-F1	GCCCAGATTCGGCCCATTTA
MAF5-ChIP-R1	TGTCAATCGCGTACCCTGAA
MAF5-ChIP-F2	TCGGAAGAGTGAAGCCATGG
MAF5-ChIP-R2	ACGATGAAAAGAGCGACGGA

MAF5-ChIP-F3	GGGCCAAAAAGAGGTACCGA
MAF5-ChIP-R3	AGTGACAAGGACATCCCCAT

Supplemental Table 2. Proteins involved in regulation of *FLC* clade members

Gene	Locus	Function	Reference
FRI	AT4G00650	activates the transcription of *FLC*. FRI acts as a scaffold protein interacting with FRL1, FES1, SUF4, and FLX to form a transcription activator complex.	(Johanson et al., 2000; Choi et al., 2011)
FRL1	AT5G16320	family member of FRI-related genes that is required for the winter-annual habit.	(Michaels et al., 2004)
FRL2	AT1G31814		
SUF4	AT1G30970	component of FRI complex.	(Kim et al., 2006)
FLX	AT2G30120	component of FRI complex, required for FRI-dependent activation of *FLC* expression.	(Andersson et al., 2008)
FES1	AT2G33835	component of FRI complex.	(Schmitz et al., 2005)
ABH1/ CBP20	AT2G13540	suppress *FLC* expression.	(Bezerra et al., 2004)
SWR1 complex		chromatin remodeling complex promotes the substitution of H2A by H2A.Z (the histone variant promotes transcription) at *FLC*, *MAF4*, and *MAF5* chromatin	(Cui et al., 2017)
SKIP	AT1G77180	activate the expression of *FLC* and *MAF4/5*.	
PIE1	AT3G33520	component of the SWR1 complex.	
ARP	AT2G41460	component of the SWR1 complex.	
SEF	AT5G37055	component of the SWR1 complex.	
FER	AT3G51550	positively regulates the transcription of *FLC/MAF*.	(Wang et al., 2020)
HEN4	AT5G64390	promotes transcription of *FLC* and *MAF4*.	(Ortuño-Miquel et al., 2019)
VOZ1	AT1G28520	inhibit transcription of *FLC/MAF*.	(Yasui and Kohchi, 2014)
VOZ2	AT2G42400	inhibit transcription of *FLC/MAF*.	
FLY	AT1G33680	promotes transcription of *FLC* and *MAF*.	(Dai et al., 2020)
HUB1	AT2G44950	HUB1 and HUB2 interact with each other and with UBC1 and UBC2 to monoubiquitinate histone H2B and enhance H3K4 and H3K36	(Cao et al., 2008)
HUB2	AT1G55250		
UBC1	AT1G14400		

UBC2	AT2G02760	hypermethylation, increased *FLC/MAF* expression.	
HDA6	AT5G63110	binds to the chromatin of FLC/MAF4.	(Yu et al., 2011)
TOP1α	AT5G55300	binds to the genomic regions of *FLC*, *MAF4*, and *MAF5*, facilitating the expression of *FLC*, *MAF4*, and *MAF5*.	(Gong et al., 2017)
MLK4	AT3G13670	phosphorylates histone H3T3, repressing the transcription of *FLC/MAF*.	(Wang et al., 2021)
DEK3 DEK4	AT4G26630 AT5G55660	directly associate with chromatin of *FLC*, *MAF4* and *MAF5*, to promote their expression.	(Zong et al., 2021)
COMPASS-like		The H3K4 methyltransferase including the core components Ash2, RbBP5 and WDR5 deposits H3K4me3 and promotes the expression of *FLC*, *MAF4* and *MAF5*.	(Jiang et al., 2011)
Ash2R	AT1G51450	component of COMPASS-like complex.	
RbBP5	AT3G21060	component of COMPASS-like complex.	
WDR5	AT3G49660	component of COMPASS-like complex.	