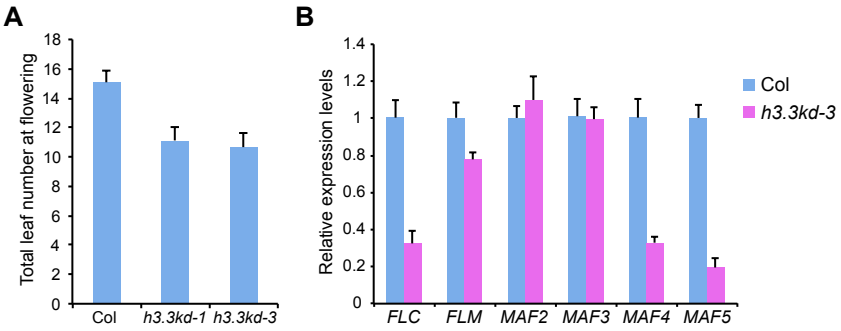
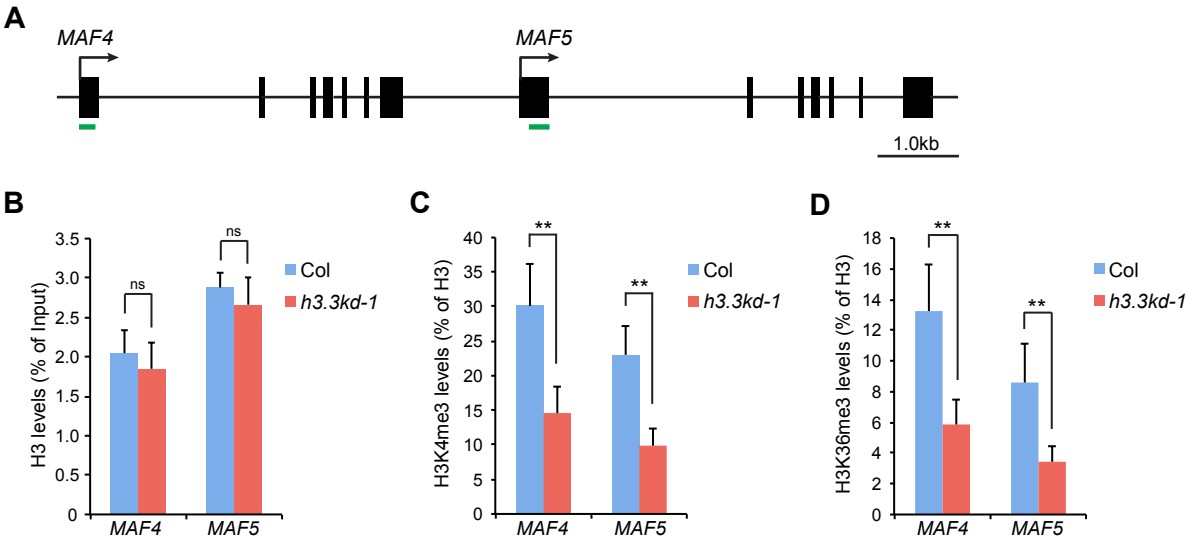
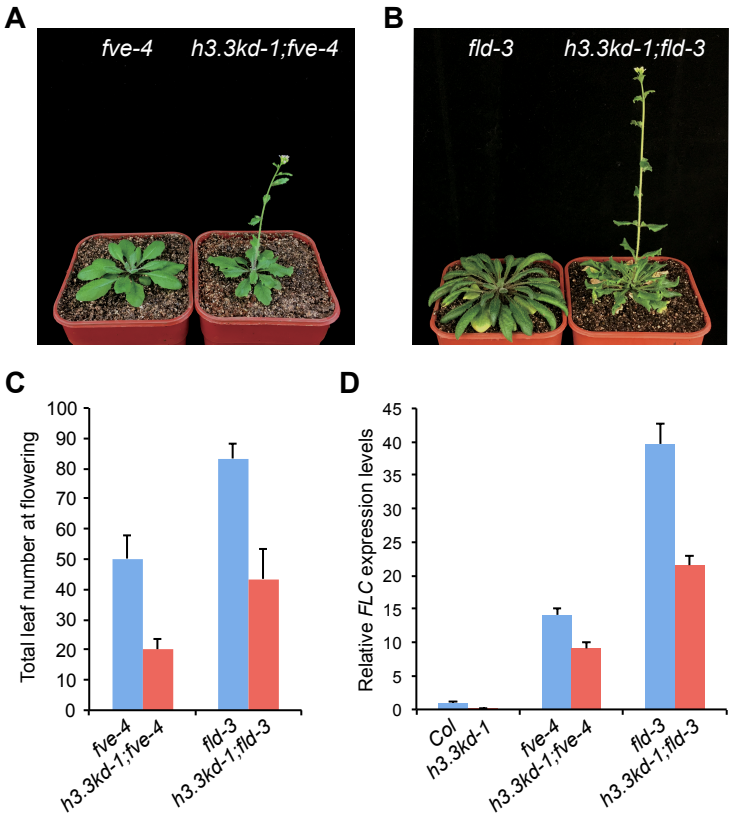


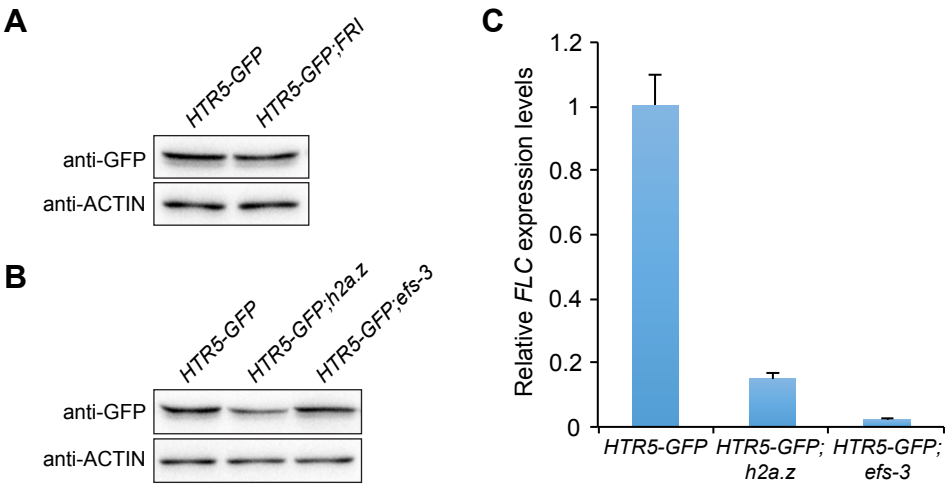

**Supplemental Figure S1. Flowering phenotype and gene expression analyses in *h3.3kd* lines.**
(A) The flowering time of *h3.3kd* lines grown in long days. The total number of primary rosette and cauline leaves at flowering were counted; 12 plants for each line were scored. Values are means ± SD.
(B) Expression profiles of *FLC* and its homologs in Col and *h3.3kd-3* determined by RT-qPCR.*TUB2* was used as an endogenous control. Values are means ± SD of three biological repeats.



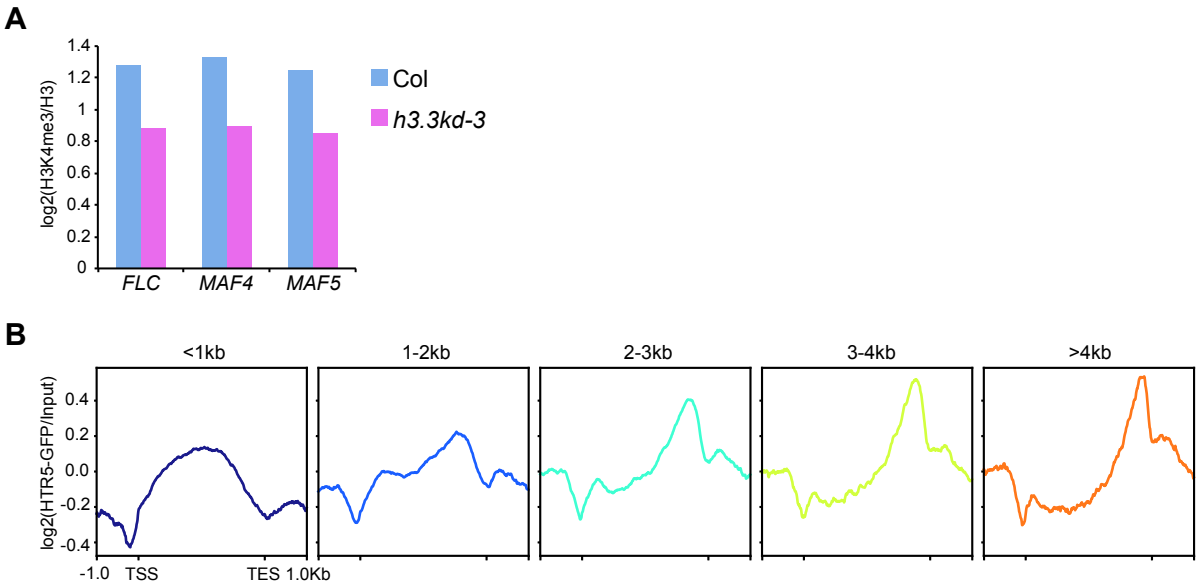

**Supplemental Figure S2. Chromatin modification changes at *MAF4* and *MAF5* in *h3.3kd-1*.**
(A) Schematic structure of *MAF4* and *MAF5*. Filled boxes represent exons; arrows indicate the transcription start sites. ChIP examined regions are indicated by green lines.
(B)-(D) H3 (B), H3K4me3 (C) and H3K36me3 (D) enrichment levels at *MAF4* and *MAF5* transcription start sites determined by ChIP. The amounts of immunoprecipitated DNA fragments were quantified by qPCR, and subsequently normalized to input DNA or H3 antibody-precipitated DNA. Values are means ± SD of three biological repeats. Statistical significance was determined by two-tailed Student's t-test (**, $P<0.01$; ns, not significant, $P>0.05$).




**Supplemental Figure S3. *h3.3kd-1* represses the late flowering phenotypes of *fve-4* and *fld-3*.**
(A) and (B) The flowering phenotypes of *h3.3kd-1;fve-4* (A) and *h3.3kd-1;fld-3* (B) grown in long days.
(C) The flowering time of indicated lines grown in long days. The total number of primary rosette and cauline leaves at flowering were counted; 10 plants were scored for *fve-4* and *fld-3*, 16 plants were scored for *h3.3kd-1;fve-4* and *h3.3kd-1;fld-3*. Values are means ± SD.
(D) Relative *FLC* transcripts determined by RT-qPCR. *TUB2* was used as an endogenous control. Values are means ± SD of three biological repeats.




**Supplemental Figure S4. HTR5-GFP and *FLC* expression in HTR5-GFP-related lines.**
(A) and (B) HTR5-GFP protein expression levels in indicated lines determined by western blot.
(C) Relative transcripts of *FLC* in indicated lines determined by RT-qPCR. *TUB2* was used as an endogenous control. Values are means ± SD of three biological repeats.




**Supplemental Figure S5. ChIP-seq analysis of H3K4me3 and HTR5-GFP distribution.**
(A) Normalized H3K4me3 values over the gene body of *FLC*, *MAF4*, and *MAF5* in Col and *h3.3kd-3* determined by ChIP-seq.
(B) Normalized ChIP-seq profiles of HTR5-GFP enrichment over genes with different lengths.

**Supplemental Table S1.** List of genes at which H3K4me3 changed more than 1.5-fold in *h3.3kd-3*.

| H3K4me3 decreased in *h3.3kd-3* | H3K4me3 increased in *h3.3kd-3* |
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| AT1G04895 | AT1G09815 |
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| AT1G06920 | AT1G15825 |
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| AT1G12190 | AT1G35560 |
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| AT1G13620 | AT1G45165 |
| AT1G13680 | AT1G48940 |
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| AT1G21550 | AT1G79800 |
| AT1G21864 | AT2G10557 |
| AT1G21866 | AT2G12461 |
| AT1G22010 | AT2G15440 |
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| AT1G23645 | AT2G23130 |

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| AT1G27610 | AT2G47130 |
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| AT1G28305 | AT3G02550 |
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| AT1G31255 | AT3G18850 |
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| AT5G39010 |
| AT5G39024 |
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| AT5G39471 |
| AT5G39620 |
| AT5G39630 |
| AT5G39670 |
| AT5G39715 |
| AT5G40350 |
| AT5G40560 |
| AT5G40630 |
| AT5G41080 |
| AT5G41090 |
| AT5G41280 |
| AT5G41510 |

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AT5G42280
AT5G42510
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AT5G43510
AT5G43570
AT5G43650
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AT5G44578
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AT5G45320
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AT5G46140
AT5G46320
AT5G46980
AT5G46990
AT5G47229
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AT5G50423
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AT5G51360
AT5G51390

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|---|
| AT5G51870 |
| AT5G51940 |
| AT5G52130 |
| AT5G52270 |
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| AT5G56325 |
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| AT5G57520 |
| AT5G60810 |
| AT5G60964 |
| AT5G62573 |
| AT5G62750 |
| AT5G64880 |
| AT5G65300 |
| AT5G66890 |

**Supplemental Table S2.** Primer sequences used in this study.

| Experiment | Primers (5' to 3') |
|---|---|
| **RT-qPCR** | |
| qFLC_F | CCGAACTCATGTTGAAGCTTGTTGAG |
| qFLC_R | CGGAGATTTGTCCAGCAGGTG |
| qFLM_F | CGCTGTTGTCGTCGTATCTGC |
| qFLM_R | CAGTCTCAAGTTGTTCCTCCAGAG |
| qMAF2_F | AACTCGGAATTATCTGCCACTCAAAG |
| qMAF2_R | CTTCCCCCATCATTAGTTCTGTCTTC |
| qMAF3_F | GAAAGGGAGAAGTTGCTGATAGAAGAG |
| qMAF3_R | AGCACAAGAACTCTGATATTTGTCTAC |
| qMAF4_F | GCTTCTCCTCAGGTGATAGCATG |
| qMAF4_R | CTGCTCTTCCAGGGACTTTAGAC |
| qMAF5_F | TGTGTCGGAAGAGTGAAGCCAT |
| qMAF5_R | CTGATGATCTTGGCCATGCTGT |
| qTUB2_F | ACTGTCTCCAAGGGTTCCAGG |
| qTUB2_R | AAGAACCATGCACTCATCAGC |
| **ChIP-qPCR** | |
| FLC_a_F | CCTAATTTGATCCTCAGGTTTGGG |
| FLC_a_R | CCGACGAAGAAAAAGTAGATAGGCAC |
| FLC_b_F | CCTTTTGCTGTACATAAACTGGTC |
| FLC_b_R | CCAAACTTCTTGATCCTTTTTACC |
| FLC_c_F | GTGGAAATTCAGATGTGCTACTG |
| FLC_c_R | ACTGGAAACTATGAAACATTGAGAG |
| FLC_d_F | TGGTTGTTATTTGGTGGTGTG |
| FLC_d_R | ATCTCCATCTCAGCTTCTGCTC |
| MAF4_ChIP_F | TTAGGTCAGAAGAATTAGTCGGAG |
| MAF4_ChIP_R | GTGGCAGAGATGATGATAAGAGCG |
| MAF5_ChIP_F | CAGGATCTCCGACCAGTTTATACAGAC |
| MAF5_ChIP_R | GAGGAGTTGTAGAGTTTGCCGGT |
| TUB2_ChIP_F | ATCCGTGAAGAGTACCCAGAT |

| | |
|---|---|
| TUB2_ChIP_R | AAGAACCATGCACTCATCAGC |
| **Pull-down constructs** | |
| HIRA_EcoRI_F | gttgaattcTGATTGCGGAGAAGCCCTTTTGG |
| HIRA_XhoI_R | gttctcgagTCAAGAGCCCGAGTCTCTTGAG |
| FRI_BamHI_F | gccggatccATGTCCAATTATCCACCGACG |
| FRI_EcoRI_R | gttgaattcCTATTTGGGGTCTAATGATG |
| **BiFC and Co-IP constructs** | |
| attB1_HiRA_F | ggggacaagtttgtacaaaaaagcaggcttaATGATTGCGGAGAAGCCCTTT |
| attB2_HiRA_R | ggggaccactttgtacaagaaagctgggttAGAGCCCGAGTCTCTTGAGTTC |
| attB1_FRI_F | ggggacaagtttgtacaaaaaagcaggcttaATGTCCAATTATCCACCGAC |
| attB2_FRI_R | ggggaccactttgtacaagaaagctgggttTTTGGGGTCTAATGATGAGT |