Supplementary Tables and Figures

Table S1 Primers for the markers used in this study

Marker	Position	Primers			Haplotype	
KASP [a]		**FAM**	**VIC**	**COM**	**A10**	**D10**
3A-117.82	117,828,272	CTCGTCGCCGTCCACCT**T**	CTCGTCGCCGTCCACCT**C**	CTCCCTTGGACATTCCCTCC	FAM	VIC
3A-118.6-R1	118,623,070	CTCCTCCTCAGGCCACG**G**	CTCCTCCTCAGGCCACG**A**	CAGGTGAGACAACGAGCAGG	FAM	VIC
3A-120.2	120,227,651	GTGACCTACGACGTTGGCA**T**	GTGACCTACGACGTTGGCA**G**	AGTTTTCTCTGGTCCGCTCG	FAM	VIC
3A-121.4	121,482,459	CTACCTCCGCCACTGTGA**G**	CTACCTCCGCCACTGTGA**A**	GGACCTTCACTGTAGCCGAC	FAM	VIC
3A-122.540	122,540,617	GTCGGATCTGTCGAGTTCTC**C**	GTCGGATCTGTCGAGTTCTC**T**	TGACAATGACGACGTGGACTA	VIC	FAM
3A-125.4-R1	125,402,254	TCATGGACCTTGTCGATGCT**A**	TCATGGACCTTGTCGATGCT**G**	CCCAGCACCGACCTCACA	VIC	FAM
3A-126.5-L4	126,567,437	GTCTAGCCGTCGCCGAT**C**	GTCTAGCCGTCGCCGAT**G**	TGCACCCATCTCAAATTTCCG	VIC	FAM
3A-127.8	127,821,835	TAAGGAAGAAGAAGGCCCC**A**	TAAGGAAGAAGAAGGCCCC**G**	AAGACGCTCATCGCCCGT	FAM	VIC
CAPS		**Forward**	**Reverse**	**Restriction enzyme**	**Band**	**Band**
3A-121.64	121,646,195	GGGTTCTTTGATACTGGCAATGT	AGCTTCGGGGTACTGCTGT	*BssH*II [b]	Low	High
FT-A2-L4	122,542,102	GAGTCCTGTTTCCGTCTTCCCT	GTGTTGCCCATCTCGAATAT	*Sac*II [c]	Low	High
FT-A2-D10A	124,172,909	CCGGACAGAGCAATGGACTT	TGAGTAAGCAGTCTAGGAGCAT	*Apa*I [d]	Low	High
FTA2-R1	125,094,949	TCGTCGTCGTCGTCATCATC	AGTGGATTCGTTTCACGCCT	*Hinf*I [e]	Low	High

[a] 94 °C for 15 min, 10 cycles of: 94 °C 20 s, -0.8 °C touch down from 65 to 57 °C 1 min, and 30 cycles of: 94 °C 20s, 57 °C 1 min.

[b] 94 °C for 5 min, 35 cycles of: 94 °C 30 s, 55 °C 30 s, 72 °C 30 s, and a final cycle of: 72 °C for 5 min.

[c] 94 °C for 5 min, 35 cycles of: 94 °C 30 s, 55 °C 30 s, 72 °C 40 s, and a final cycle of: 72 °C for 5 min.

[d] 94 °C for 5 min, 10 cycles of: 94 °C 30 s, -0.8 °C touch down from 65 to 57 °C 20 s, 72 °C 30 s, followed by 30 cycles of: 94 °C 30 s, 57°C for 20 s, 72 °C for 30 s, and a final cycle of: 72 °C for 5 min.

[e] 94 °C for 5 min, 35 cycles of: 94 °C for 30 s, 55 °C 20s, 72 °C 30 s, and a final cycle of: 72 °C for 5 min.

Table S2 ANOVAS for *FT-A2* and flanking markers in the winter wheat population LA95135 (D10 allele) x SS-MVP57 (A10 allele)

Dependent variable: SNS

Marker S3A_116,149,133 (96.4 cM)

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	5	736.44	147.29	75.55	<.0001
Error	1622	3162.29	1.95		
Corrected Total	1627	3898.73			

R-Square: 0.188893

Source	DF	Type III SS	Mean S	F Value	Pr > F
Env	4	665.32	166.33	85.31	<.0001
FTA1	1	71.19	71.19	36.51	<.0001

FT-A2 3AS 124,172,909 bp (97.9 cM)

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	5	749.69	149.94	77.23	<.0001
Error	1622	3149.04	1.94		
Corrected Total	1627	3898.73			

R-Square: 0.192291

Source	DF	Type III SS	Mean S	F Value	Pr > F
Env	4	665.33	166.33	85.67	<.0001
FTA2	1	84.44	84.44	43.49	<.0001

Dependent Variable: SNS. Marker S3A_194,830,543 (101.4 cM)

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	5	727.21	145.44	75.20	<.0001
Error	1602	3098.23	1.93		
Corrected Total	1607	3825.45			

R-Square: 0.190099

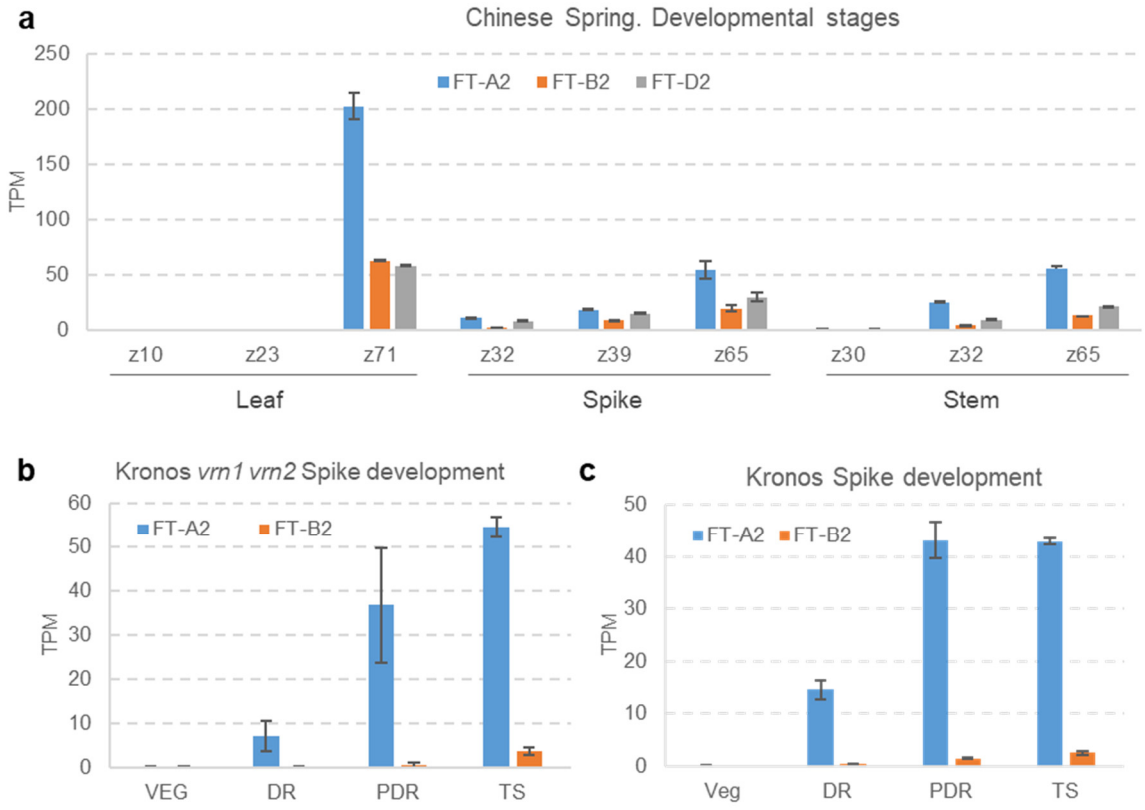
Source	DF	Type III SS	Mean S	F Value	Pr > F
Env	4	654.97	163.74	84.67	<.0001
FTA3	1	72.30	72.30	37.38	<.0001

Table S3 Evaluation of $BC_1F_{3:5}$ homozygous sister lines from recombinant line H2-14-18-5 in a field experiment performed at UC Davis in 2021. H2-14-18-5-#3-3 was homozygous for the recombinant chromosome and H2-14-18-5-#3-3 for the non-recombinant chromosome, and both carry the *FT-A2* A10 (G) allele. Control lines H2-14-#16-2 and K, H2-14-#1-4 are separate lines from family H2-14 homozygous for the *FT-A2* D10 (K) or the *FT-A2* A10 (G) alleles, respectively.

Marker	Chr. 3AS CS	H2-14-18-5 #3-3	H2-14-18-5 #3-5	H2-14 #16-2	H2-14 #1-4
3A-117.82	117,828,272	K	G	K	G
3A-120.23	120,227,651	K	G	K	G
3A-121.48	121,482,459	G	G	K	G
FT-A2	124,172,909	G	G	K	G
SNS PHENO.		G	G	K	G
3A-127.8	127,821,835	G	G	K	G
Number of plants		30	48	49	38
SNS Avg		22.69	23.23	21.72	23.19
P values D10 (K) vs A10 (G)		0.8056		< 0.0001	

Supplementary Figures

Fig. S1 Expression levels of *FT2* homeologs in hexaploid (Chinese Spring) and tetraploid wheat (Kronos) **a** Transcript levels of *FT-A2*, *FT-B2* and *FT-D2* in leaves, spikes and stems and three developmental stages (Choulet et al. 2014). Developmental stages are based on Zadok's scale z10= seedling, z23= three tillers, z30= spike 1 cm, z32= two nodes, z39= meiosis, z65= anthesis, z71= two days after anthesis (Zadok et al. 1974). **b** Quant-Seq data from developing spikes of Kronos spring line *vrn1 vrn2* (Li et al. 2020). **c** Unpublished RNAseq from our lab at the same spike development stages in Kronos wild type (*Vrn-A1*). VEG = vegetative stage, DR = double ridge, PDR = post-double ridge, and TS = terminal spikelet stage. TPM= transcripts per million. Values are transcripts per million based on four biological replications per stage in each experiments and error bars are s.e.m.



References Fig. S1

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Fig. S2 Yeast-two-hybrid interactions between FT-A2 and six 14-3-3 proteins. FT-A2 alleles D10 and A10 were used as baits and the six different 14-3-3 proteins as preys. Selection for yeast transformants containing both bait and prey vectors was performed in SD medium lacking Leucine and Tryptophan (-L-W). Interaction strength was tested on SD media lacking Leucine, Tryptophan, Histidine and Adenine (-L-W-H-A). As positive control, we used FT1 as bait and 14-3-3A as pray. As negative controls we tested the FT-A2 alleles D10 and A10 against the empty vector LAW11.