



SUPPLEMENTARY MATERIAL

INSIGHTS INTO THE RELATIONSHIPS BETWEEN THE DISTRIBUTION OF REPETITIVE DNA SEQUENCES AND THE FLOWERING TIME OF MAIZE

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Supplementary Table 1. Characteristics of the Nested Association Mapping (NAM) lines and reference genomes. Phenotypic data are from MaizeGDB (<https://www.maizegdb.org>). NCBI accession codes for each genome are listed as well as information about DMB and DIS from Buckler et al. (2009).

Genome	Lineage	DMB	DIS	FT	Phenotype
GCF_902167145.1	B73	73.96	75.01	Intermediate	"Stiff Stalk"
GCA_902167175	M37W	79.51	82.32	Intermediate	Seasoned/ Mix
GCA_902167005	NC350	82.09	82.35	Intermediate	Tropical
GCA_902166965	P39	65.15	66.82	Early	Sweet maize
GCA_902167065.1	IL14H	69.57	70.89	Early	Sweet maize
GCA_902166975	CML247	93.46	95.0	Late	Tropical
GCA_902373975	CML52	93.87	98.7	Late	Tropical

DMB = Days for the issue of the maize banner; DIS = Days for issuing stigmas; FT = Flowering time.

Supplementary Table 2. Fourteen genes related to flowering, their respective positions in the maize chromosomes and the accession code in maize.
GDB. L = long arm and S = short arm. CL = Chromosome location.

Genes	CL	Features	Access to MaizeGDB
<i>dwarf8</i>	1L	CO CO-like timing of CAB1 protein domain 14 - transcription factors for gibberellin signaling (Best & Dilke, 2022)	Zm00001eb054480
<i>cct14</i>	2L	Regulation of photoperiodic flowering and salt stress response (Su et al., 2023)	Zm00001eb112080
<i>zfl2</i>	2S	<i>Zea floricaula</i> leafy2 - quantitative control of inflorescence phyllotaxy for maize (Bomblies et al. 2003)	Zm00001eb071990
<i>cca1</i>	4S	Circadian clock associated 1 - Acting on the maize circadian clock (Wang et al., 2011)	Zm00001eb172450
<i>phyC2</i>	5S	PhytochromeC2 - Inhibits flowering on short days by regulating to red light (Franklin et al., 2003; Monte et al., 2003)	Zm00001eb214800
<i>dlf1</i>	7L	delayed flowering1 - Acting in the floral transition (Muszynski et al., 2006)	Zm00001eb331880
<i>cct43</i>	7L	Co CO-Like Timing of CAB1 protein domain 43 - Acting on the maize circadian clock (Dong et al., 2021)	Zm00001eb331630
<i>rap2</i>	8L	rap2.7 orthologue - Negative regulator of the time of flowering (Salvi et al., 2007)	Zm00001eb355240
<i>pebp8</i>	8L	phosphatidylethanolamine-binding protein 8 -Coding for a florigen that integrates endogenous and environmental signals in maize (Jafari et al., 2023)	Zm00001eb353250
<i>mads1</i>	9L	Regulates the fate of the maize ear meristem (Shen et al., 2023)	Zm00001eb403750
<i>mads3</i>	9S	Co-expressed during the development of the ear and tassel in maize (Heuer et al., 2001)	Zm00001eb298680
<i>cct1</i>	10L	Co CO-Like Timing of CAB1 protein domain 1 -Regulator of later flowering (Hung et al., 2012)	Zm00001eb418700
<i>lhy1</i>	10L	Late hypocotyl elongation protein ortholog 1 -Acting on the maize circadian clock (Dwivedi et al., 2024)	Zm00001eb415760
<i>zfl1</i>	10L	<i>Zea floricaula</i> leafy 1 - regulator of the time of flowering (Bomblies et al., 2003)	Zm00001eb430240

Supplementary Table 3. Distribution of FISH signals in composites maizes. DNA 2C values (Mpb), number and size (L = large and S = small) of FISH signals (FS) for K180, TR-1 and CentC probes. MFT = Maize-Flowering Time.

Samples	2C (Mpb)	K180 FS	TR-1 FS	CentC FS	MFT
B73	5,064.34 [5.18 pg]	12 signals (4L e 8S)	4 signals (2L 2S)	16L 4S	Intermediate
C1	5,633.28 [5.79 pg]	18 signals (10L e 8S)	4 signals (2L 2S)	9L 11S	Early
C2	5,418.12 [5.54 pg]	15 signals (15L)	9 signals (4L 5S)	13L 7S	Early
C4	5,728.01 [5.86 pg]	17 signals (15L e 2S)	6 signals (6S)	18L 2S	Late
C6	5,278.34 [5.40 pg]	13 signals (9L e 4S)	6 signals (1L 5S)	8L 12S	Early
C7	5,401.00 [5.52 pg]	13 signals (9L e 4S)	2 signals (2L)	12L 8S	Late

Supplementary Table 4. Distances less than 175 kbp from K180 to gene and number of K180 repeats at annotated position.

zfl1 = *Zea floriculata* / *leafy1*. *dlf1*: *delayed flowering 1*.

CL = Chromosome location. L = long arm. NR = Number of Repeats.

Genome	CL	Gene	Distance (bp)	NR
B73	10L	<i>zfl1</i>	89.800	11
CML247	10L	<i>zfl1</i>	122.371	6
IL14H	10L	<i>zfl1</i>	125.005	31
P39	10L	<i>zfl1</i>	125.007	11
IL14H	7L	<i>dlf1</i>	38.394	2
P39	7L	<i>dlf1</i>	39.461	2

Supplementary Table 5. Distances less than 175 kbp from TR-1 to gene and number of TR-1 repeats at annotated position.

zfl1 = *Zea floriculata* / *leafy1*.

CL = Chromosome location. L = long arm. NR = Number of Repeats.

Genome	CL	Gene	Distance (pb)	NR
B73	10L	<i>zfl1</i>	90.941	4
NC350	10L	<i>zfl1</i>	79.130	2
CML52	10L	<i>zfl1</i>	120.241	1
CML247	10L	<i>zfl1</i>	124.238	1
M37W	10L	<i>zfl1</i>	124.975	1
IL14H	10L	<i>zfl1</i>	126.148	19
P39	10L	<i>zfl1</i>	126.150	19

Supplementary Table 6. Structural analysis of flowering-related genes in different NAM inbred lines genomes. The table shows the total gene size; the number of TEs insertions in exon and intron regions; the total size of these regions; and the number of long non-coding RNA (lncRNA) generators associated with each gene locus.

Gene / Genome	Gene size (bp)	TEs overlaps in exon (pb)	TEs overlaps in intron (pb)	Total size of TEs (pb)	Total size of exon (pb)	Total size of intron (pb)	Number of lncRNAs
cca1_B73	33803	78	25540	25618	2171	31632	13
cct1_B73	2687	0	427	427	723	1964	1
cct14_B73	37753	77	23714	23791	2466	35287	3
cct43_B73	33436	25	23591	23616	2287	31149	15
d8_B73	2908	1054	57	1111	2578	330	4
dlf1_B73	1594	54	95	149	1175	419	0
lhy1_B73	970	30	42	72	564	406	0
mads1_B73	19793	265	10969	11234	713	19080	11
mads3_B73	11292	432	3199	3631	1311	9981	2
pebp8_B73	1794	1	213	214	536	1258	0
phyC2_B73	5040	74	326	400	3416	1624	0
rap2_B73	3876	80	333	413	1167	2709	0
zfl1_B73	3191	328	390	718	1329	1862	2
zfl2_B73	6769	112	1658	1770	1166	5603	0
cca1_M37W	16441	135	9559	9694	2181	14260	5
cct1_M37W	2724	293	1080	1373	622	2102	0
cct14_M37W	15246	77	6563	6640	1626	13620	1
cct43_M37W	34429	25	23909	23934	2291	32138	22
d8_M37W	2908	1100	57	1157	2578	330	4
dlf1_M37W	1228	113	0	113	1124	104	0
lhy1_M37W	17489	345	9921	10266	2135	15354	4
mads1_M37W	22323	319	12231	12550	1162	21161	15
mads3_M37W	11653	245	3417	3662	828	10825	1
pebp8_M37W	4769	1	865	866	536	4233	0
phyC2_M37W	5040	74	326	400	3416	1624	0
rap2_M37W	3736	266	145	411	1446	2290	0
zfl1_M37W	2987	274	352	626	1324	1663	2
zfl2_M37W	6774	285	1683	1968	1169	5605	1
cca1_NC350	16720	135	9547	9682	2181	14539	5
cct1_NC350	2553	0	427	427	723	1830	1
cct14_NC350	4850	77	672	749	1713	3137	0
cct43_NC350	33987	25	23398	23423	2287	31700	21
d8_NC350	2908	1094	57	1151	2578	330	4
dlf1_NC350	2061	107	192	299	1263	798	0
lhy1_NC350	1303	69	39	108	866	437	0
mads1_NC350	19805	292	11457	11749	1168	18637	15
mads3_NC350	11579	245	3675	3920	828	10751	3
pebp8_NC350	4769	0	811	811	348	4421	0
phyC2_NC350	11562	74	1458	1532	3203	8359	1
rap2_NC350	2987	266	115	381	1446	1541	0
zfl1_NC350	2856	347	96	443	1325	1531	1
zfl2_NC350	3369	235	321	130556	1194	2175	0
cca1_P39	22480	135	17935	18070	2178	20302	3
cct1_P39	5042	293	1566	1859	1102	3940	1

cct14_P39	37779	77	23714	23791	1797	35982	0
cct43_P39	27173	93	16160	16253	2287	24886	20
d8_P39	2897	1035	57	1092	2566	331	3
dlf1_P39	1421	107	0	107	1244	177	0
lhy1_P39	17802	351	10098	10449	2179	15623	4
mads1_P39	19766	265	10988	11253	1174	18592	13
mads3_P39	12005	248	4077	4325	836	11169	4
pebp8_P39	1772	1	213	214	536	1236	0
phyC2_P39	7225	1887	708	2595	5339	1886	1
rap2_P39	3742	266	115	381	1446	2296	0
zfl1_P39	17802	242	10097	10339	1371	16431	5
zfl2_P39	3404	62	227	289	1191	2213	0
cca1_IL14H	29405	135	21921	22056	2134	27271	8
cct1_IL14H	2555	0	427	427	723	1832	1
cct14_IL14H	26350	82	12835	12917	1791	24559	2
cct43_IL14H	34516	410	23528	23938	2287	32229	28
d8_IL14H	2897	1035	57	1092	2566	331	3
dlf1_IL14H	1369	202	0	202	1203	166	0
lhy1_IL14H	2058	0	320	320	564	1494	0
mads1_IL14H	15478	319	5436	5755	1168	14310	9
mads3_IL14H	10965	245	2416	2661	833	10132	3
pebp8_IL14H	1794	1	213	214	536	1258	0
phyC2_IL14H	5040	74	326	400	3416	1624	0
rap2_IL14H	3910	103	317	420	1167	2743	0
zfl1_IL14H	14381	242	9597	9839	1316	13065	4
zfl2_IL14H	3735	110	690	800	1098	2637	1
cca1_CML247	1812	114	77	191	1254	558	0
cct1_CML247	1024	0	47	47	501	523	0
cct14_CML247	4740	81	668	749	1441	3299	2
cct43_CML247	34633	55	23881	23936	2017	32616	16
d8_CML247	2908	1100	57	1157	2578	330	3
dlf1_CML247	2512	54	556	610	1244	1268	0
lhy1_CML247	701	32	0	32	564	137	0
mads1_CML247	16490	319	6307	6626	1168	15322	7
mads3_CML247	11394	358	3221	3579	836	10558	2
pebp8_CML247	1688	1	213	214	536	1152	0
phyC2_CML247	5040	74	0	74	3416	1624	0
rap2_CML247	3733	80	256	336	1449	2284	0
zfl1_CML247	3041	274	352	626	1324	1717	2
zfl2_CML247	3518	62	287	349	1191	2327	0
cca1_CML52	25566	135	18360	18495	2181	23385	8
cct1_CML52	2554	0	427	427	723	1831	1
cct14_CML52	2174	209	540	749	1107	1067	1
cct43_CML52	33903	55	23367	23422	2492	31411	10

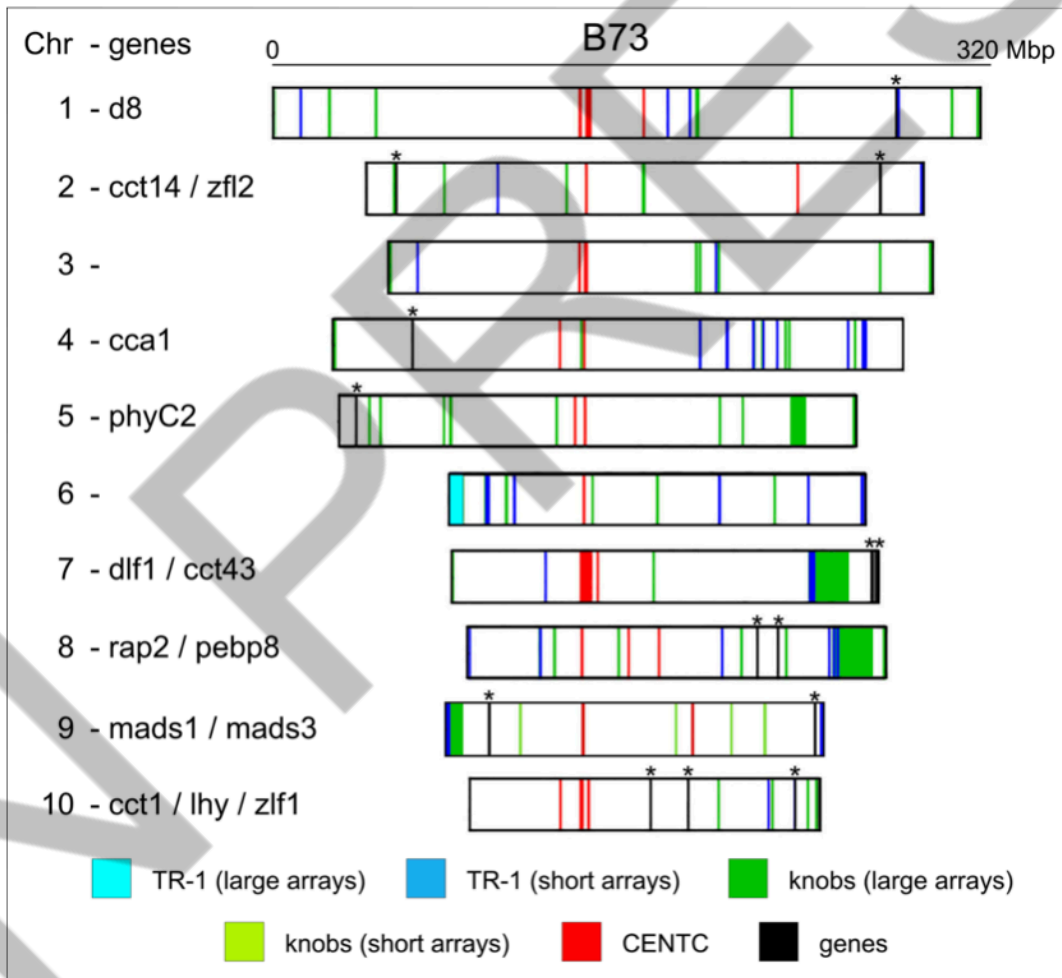
d8_CML52	2907	735	57	792	2577	330	3
dif1_CML52	1713	107	52	159	1323	390	0
lhy1_CML52	736	0	0	0	559	177	0
mads1_CML52	19779	319	11016	11335	1162	18617	10
mads3_CML52	11468	296	3031	3327	833	10635	1
pebp8_CML52	1745	1	171	172	536	1209	0
phyC2_CML52	5060	74	326	400	3353	1707	0
rap2_CML52	3918	21	618	639	1044	2874	0
zfl1_CML52	2817	328	290	618	1302	1515	2
zfl2_CML52	7274	62	1708	1770	1146	6128	0

Supplementary Table 7. Annotation of the best alignments of long non-coding RNAs (lncRNAs) derived from transposable elements (TEs) inserted into flowering-related genes in NAM maize lines.

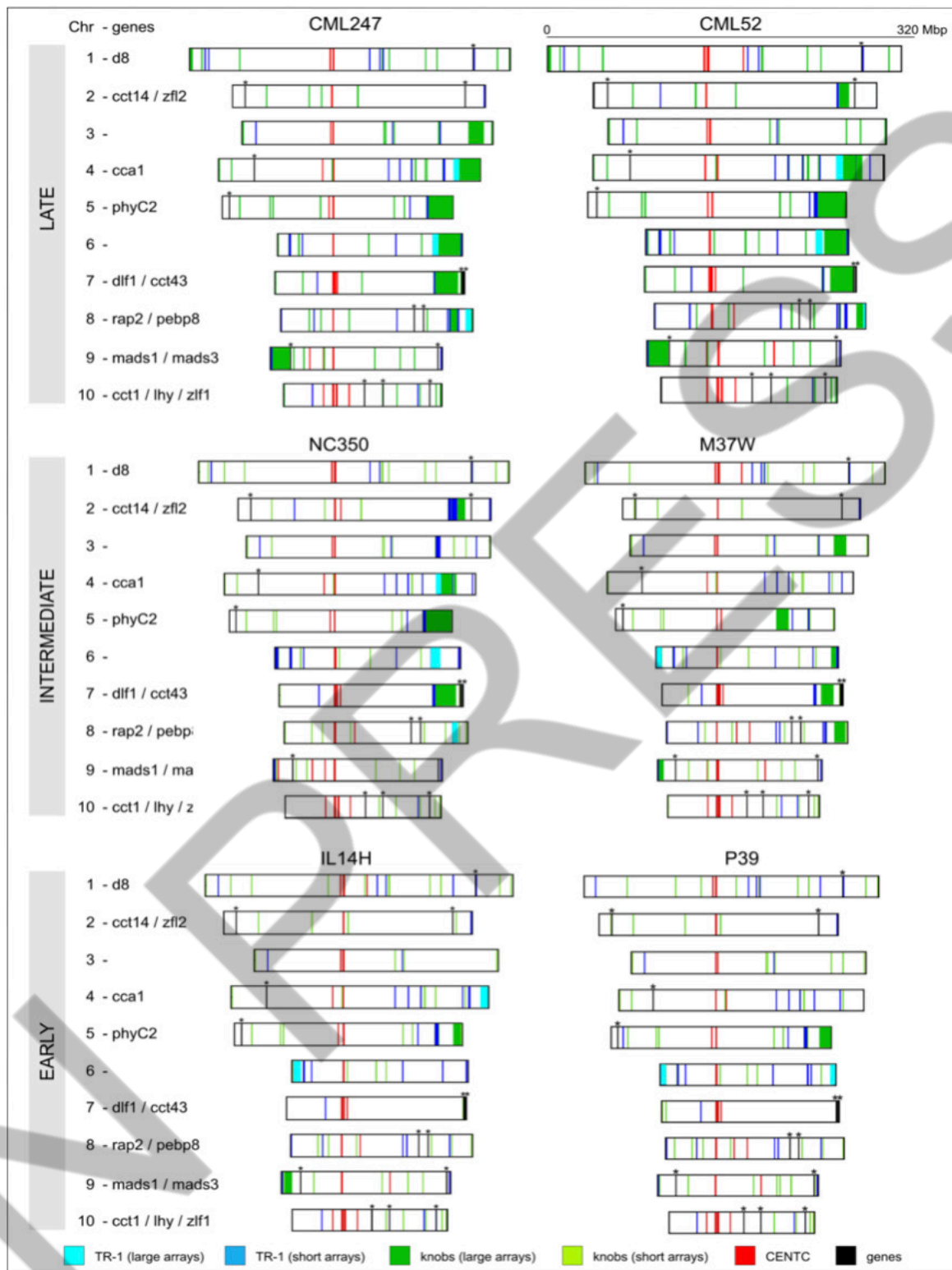
Gene / Genome	Position (bp)	Reference	Sequence
mads1_M37W	2764-7196	URS0002368ED6_4577	<p>CUGGUUAGCGGAAAGCGAGAUCCUGUCUUCUUCUUAACACCCCAUCCACCCCA GCAGCCACCAUACAGCCUCCCAACACCCUCCGCCUCAACCCUACCCGAUCCUGG GCACGCUACCAACUUGCCGACCAACCAUUGGUCGACCUUAGGAGCUAUGGAGU CCUGAAAAACGGAGAUACGACGGAGAUAGGGAGAUAGGACGAGAUAGGCCUCA UAAAGGCGAAGUCGGCCUUCGUAUCUGACUUGGAGGCGGGGUGGUAUGGAGCCU CUGGAGCAGGUAUCGGCCAGGUUCCAGACGUUGGACUUUCCCGUUUUAUUGG CAAGUCUGAUUGAGGCUUUUAUCAAUUGGAGUAGUUGUUUCGUAACAGCG CACC AUGGCCGAGGAGCGUUUGGAGUUGGCCUCAACCCUCAAAGGUAUGCCAC AGAUGUUUUAUGCAACUAGGAGGACGACGACCGCCUUGGGGGGCGAUUCAA AGAUUCUUGAUCUGGAGUUGGAGCGGCGGCGGCGUCCUUGGAGCUUUGGAGCU GACGGAGUCUGGACGACCGACCGGAGGAGUACUACCAACCUUUAUGAGUCU CCUUCUUGCCGUGGGCGGUCGACGAUCCAAAGGAGUCCAGUUCUACAGACAG UCUCUUCCACUCAGCCACCGCUGCCGCUCCACAGUCGGAGACGCGGCGCG GGCUUAGGGAGCCUCCGCAACAAGUUGGAGUUGAUGAACUCGACAGCUGGCGG GGCCUUGGCCAAGCCGGCGCAUCGCGCGCCCGACCGCCGACACAACCGGGG UUGGACAGCCACAGGCGCCCGUUGUCGCGCUAUCGCGACCGCGCGGGAUUCU GCACAGCCGCGGAGAGCGGCAACCGUUUACCGUUAUCCAAGGAAGAUAUGAG GAACGCCACCGGCUCCGGGUCUGUUUUAACUUGAUGGAGGCAUACUUCGCAAGCA CAACUGCAACUUGCGCGCAUCUUCUACGUGGAAGGUGUUGCGUAGGACAGACG ACGAUUGCAUAGGCGUCUGUGUCACGCGGGGAGCCCGCAUUCUCCUUAU CGAGUGCCCGGGUACUACUUCGACACCGUUGGUGUCCGGCGUCCUCCGGGAC AGCAGACUAGUCGCCUUCGACAGGGAGUCGACGCAACAUCUUAUGGAGGAGCGCG AGCGUACCGUCCGGGUCGACAUACAGCGCGCCACCGUCCGCCACUUGGUC AACAGCGAGCGCAUCUUCGCGGGGGUACUCCGACGCGCUAUAUCAAAGUUC AUGGUGAGAGUUCACUUCGACCUUUCGUAUGCCUUGGAGGUAUACCUU GUCCCGGACGAGUUGGUGUAGCCUCCGGGCAUCGUCUGGAGCGUUCGUGU GCGGCAUUGCAGUUCACGCGCGGGGACGCGAUCGUCGUGGACCGGCUUUGCU CUUCGUAUAGCGCGCCUUCUGCGCGGCCAGCGGCAUCCGAGCUGGAGUAGCGCC AACUGGGCGGGAGCCUUCGACGCGCUUUCUUAUCUCCUCCGGAACGUCUUA CGAGCCCGCGGCUCCACCAAGUUAAGCGGAGACUUGCAUACCCUUAAGCG GGAGCGUCCGUAUGGGCGCGUCCGUAACCGGACAGCAACAAGGAGCA GUCGAGCGGACGUCACCGCUAUGAGGAGGCGAUUUCGCGCGGACGACU CGACGUUCUCCUACCGGUAUCUUAUUAAGAGCGGACGCGUCCUGGCAUUC UGCGUCGACUUAUGGGCGGUAACCGGUCACCGUCAAAGGACGCUUCCAAUUC GUGGUGGACGAGCGGCGUAGAGGCUCCAGCGGCAAAUUCUACCAAGCUGCA CAUGCGAUCCGGUACCCAGGUCGGAUGCGCCGAGGACUACCAUAGGAGCG CCUUCGCAACCCAGCGGCUUAUAGUUCGUGUAGCCGUGUCCGGGUGGAGCA CGCCUCCGUGAGCUUCCAGGCUUUGAUGAUGAUGGUCGCGACCGUUUUCUUG CGUUUUCUUGGUCUUCUUGAGCAGCAUUCUUAUCUACUAGGAGGAGCGGAGG AAACUUCGUCACCGCGCGUUCGUAACCGGACUUCAGCGCCUACUAGCGUUC CUAAGCGCAACUAGUUGUUGUUGGGCGAAUGUAGCUGCUACCGCGGACG UGAUUCGAGGCGGCGUCGCAUAGGACCGGCUAAGUUAUGCUAUGGCUAUCGGGA CUGGCCACCGCUAGCAUGAGGCGGUAAGGCUUCCUCCGCGUUGGCGGGG UUAUCGGGAAGUUCGUCCACCAUACCGUACCGUAGCCACGCAUUAACAUCUUG UUGAAGAGGACGGUUCUGGAGGCGGAAAGUUGCGAGCGGCAUUCGAGCAGU CAAGGACCGGUAUCUCCGCUCCUUCUCCGCAUCCUUAUUCUCAAAGUUGU GUCGCGGUGGCGAUGUUCGUCUCCAGGCUUCCGUGCAGUAGGUCAGGACGAG CCACCCCAUCCGUUUUUUUCAGUCGGGCUAUCACACCCGACUACGGGCGUGGGG CCUAACGAGCGGACCCUUGGCGUACUAGGCGGUCGCGACUUGGAGGCUAUC CUUUGGGGACGUGUUCGUGUUAACCGGACUACAGCCUUAUAGUACUUGG GGAUAGUGGUCGCGACAUUCACAACUACGUGGUGGACAAAGCUCUAGGCU UCGAUUCUCCGUGAGUUAAGCCAGUUCGACCAUUGGUGGACGAGUCCGUC UCCCGCAUGACACGCGAGAGUUGCGGAGUUGGCGUCCUUGGCCUUCACAGAC CGCGUUCGACUUCGUGGAGUACUUCGUAAGCGGACUACCGACUCCGCGCCU GUUGCAUGACGAGGUGGAGGCGGCAUCAGGCGCGGCUUUGGGCGGUGG UCGAGGGAUGGUCAGUACGUCAGCGACCCUUAUACCGGCAUUCUACCGGUC CUUCAGGAGCUCUGGAGUUGGACGCGAAAGGCAACGAGGGUCCAGCGCAC GCUCGACCGCUUCGAGCGGACUUCUUCUUAACUAGUAGGAGGUGGUCUCAA AAUAGUAGGAGGUGGCUACCGUCCGAGCGCCACAGUUCGAGGACUUCUACCG GCGGCGUCCUUAUCCUCCGUAUCCGAGGAGUUCGAGGAGUUCGAGGAGU GGACUUCGUAAGCCUCCGCGAGUACGAGAAUUGUUAUCUUAUGGACUUGG UGGACAGGUUACGAAAGUACUUAUUAUUCGCGGACACCAUUAUUGGCG GGAGUCCGUGGUCAGGCGUUCUUCGGAUUAUUGGCGUCCUAGGUGGUGUC GUAGUCCUAGGUGUCGCGACCGGCAUCGUGUUAACCUCAAAGUUCUGGCGG AGCUAUCGCGACUAGUUGGAGCAAUUCUCCACUAGGACUAGGCGUUCACCU CAGUCGACGCGCAUCCGAGUUGGCGGAAACAGAGUUAACCAUAGUACUAGG CCUACGGGUAUCGACACGCAUUGGUGUAGUUGGUCUUCGUGGCGAGAAUUCU CUCAACACCAUACAGGAGUCCUCCGUGACACCGCAUUCGCGGAGUUCGUAUCG CUACGAGCGAUUCUUCUAGUUCGAGUUCGAGGCGGAGGCGGACACGUGUUCU CGUGGCGCAACUAGGAGGAGCGGAGGAGUUCUCCUUGAUGUUGGCGUUCG UCUGGACGCGCCACGUCGUCCAGAAAAGUUAUUAUGACAGGACACCGGUCU CCAUUAUCAGGUGGCAAGUUGGUGUCUCCGCGUCCCGACCGGUCUCCUCCU CCUACAACCGACACCAACGCAAGCUAAAGCCUAGGUAUUAUGGCGGUAACAG UGGUGGAGUAUCAACGAGGUCGUCUCCGCUAAGUACCGGACGAGCCAUUAUC UGUUUUAUGGUGGCGUCCUAAAGUACCAACGACACACUCCCAAGUACGUCG CCCCCGUUCACUAGGCGGCUACCUUUGGAGCCGCGGACGCAACCAAGCUGCC GUGGAGUCCGCGAGUUAUUAUCAGUGGAGGAGGACGUCUCCAGCAUCGAGCU GGAGGAGGACCUUACGCGCAAGUUCUCCCAUUCAGCUCGAGGAGGAGUUGCU CGAGGAGGAGAGA</p>

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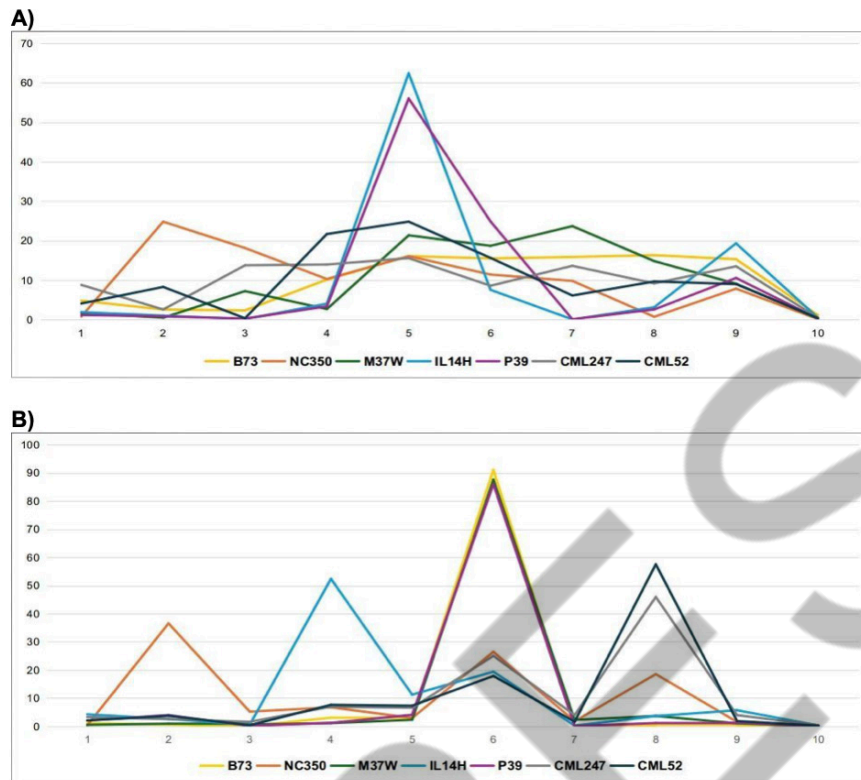
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Supplementary Figure 1. Idiograms of the pseudochromosomes of the B73 NAM line. The pair numbers are followed by the names of the genes related to the flowering time pathway that each pair carries. Asterisks (*) mark the position of each gene.



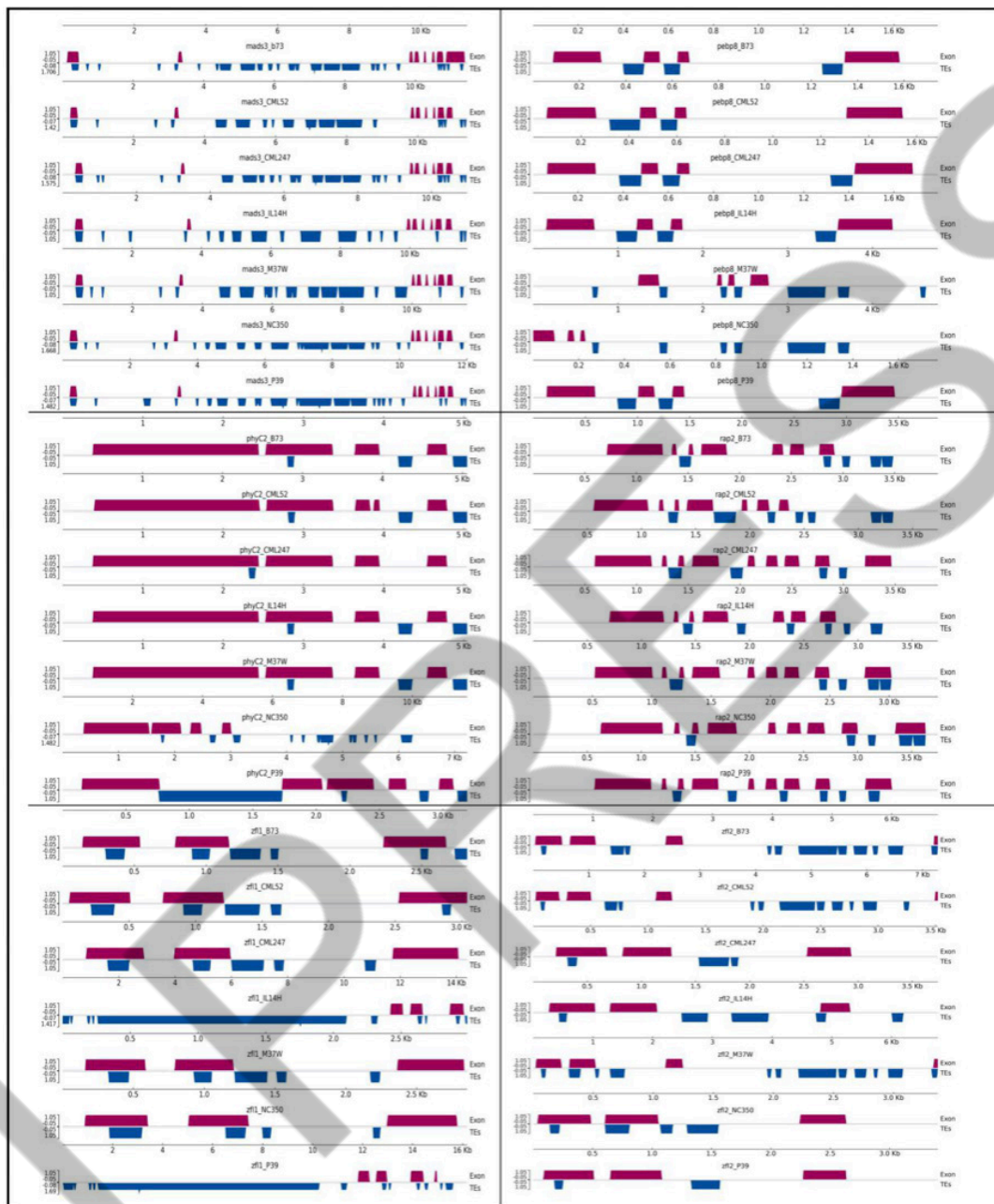
Supplementary Figure 2. Idiograms of the pseudochromosomes of the NAM lines (CML247, CML52, NC350, M37W, IL14H and P39). Pair numbers are followed by the names of the genes related to the flowering time pathway that they carry. Asterisks (*) mark the position of each gene. The pseudochromosomes are centered according to the concentration of CentC arrays. Note that the late flowering lines accumulate more TR-1 than the others. However, the distribution of the blocks was more variable in TR-1. Note also that the TR-1 on chromosome 9 (studied by Carvalho et al. 2022) is close to the *mads1* gene.



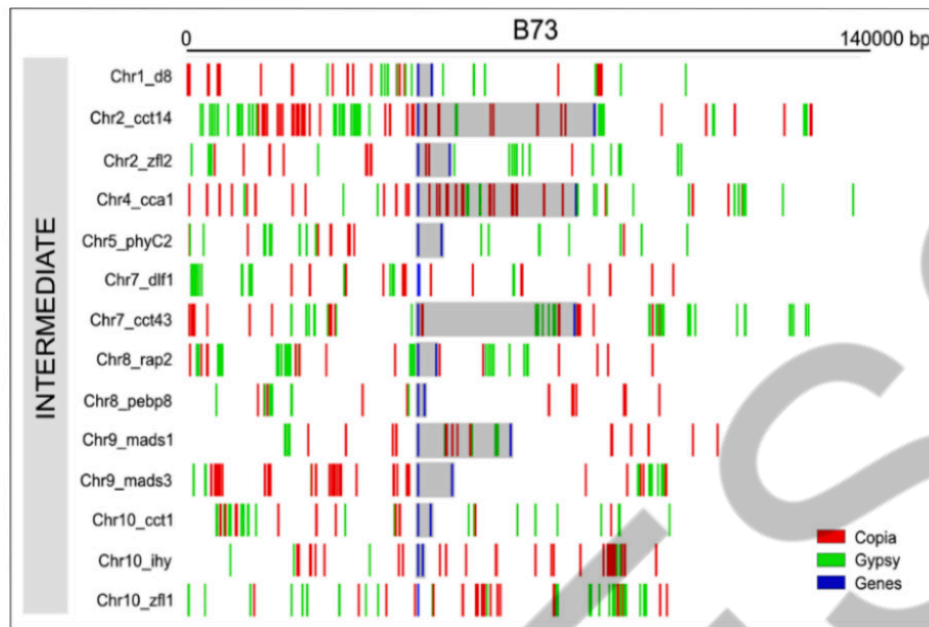
Supplementary Figure 3. Relative amount of K180 (A) and TR-1 (B) monomers in each pseudo-chromosome of NAM lineages. The X-axis represents the chromosomes, and the Y-axis represents the relative amount in percentage (%).



Supplementary Figure 4. Genomic structure of the *cca1*, *cct1*, *cct14*, *cct43*, *d8*, *dlf1*, *lhy1*, and *mads1* genes in seven genomes of NAM maize. Each block (A–H) represents a gene and shows the distribution of exons (magenta) and transposable elements (blue). Scales vary between panels and are indicated in kilobases (kb) or base pairs (bp), as appropriate. Analyses revealed significant variation among genotypes B73, CML52, CM247, IL14H, M37W, NC350, and P39, particularly with regard to gene length, number of exons/introns, and TE presence. Genes such as *cct14*, *cct43*, and *cca1* exhibited greater structural complexity, whereas genes such as *d8*, *dlf1*, and *lhy1* exhibited smaller structures with fewer TE insertions.



Supplementary Figure 5. Genomic structure of the *mads3*, *pebp8*, *phyC2*, *rap2*, *zfl1*, and *zfl2* genes in seven maize genomes. Each block (A–F) show the structural organization of these genes in the following genotypes: B73, CML52, CM247, IL04H, M37W, NC350, and P39. Exons are represented in magenta and TEs in blue. The scale of each panel is presented in kilobases (kb) or base pairs (bp). Analyses reveal wide variation among genotypes, including differences in gene size, the number and position of exons and introns, and TE insertion. Genes such as *rap2* and *mads3* exhibited greater structural complexity, whereas *pebp8*, *zfl1*, and *zfl2* were more conserved and compact. Despite belonging to the same family, *zfl1* and *zfl2* exhibited distinct patterns of exon and TE distribution.



Supplementary Figure 5. Abundance of *Copia* and *Gypsy* retrotransposons in the flanking regions (50,000 bp upstream and downstream) of the 14 flowering time related inbred line NAM B73 genes. The chromosome number is shown on the left, followed by the analyzed gene. The gray shaded region corresponds to the annotated gene region from MaizeGDB. The two blue bars in the analyzed gene regions indicate the start and end of each gene.

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