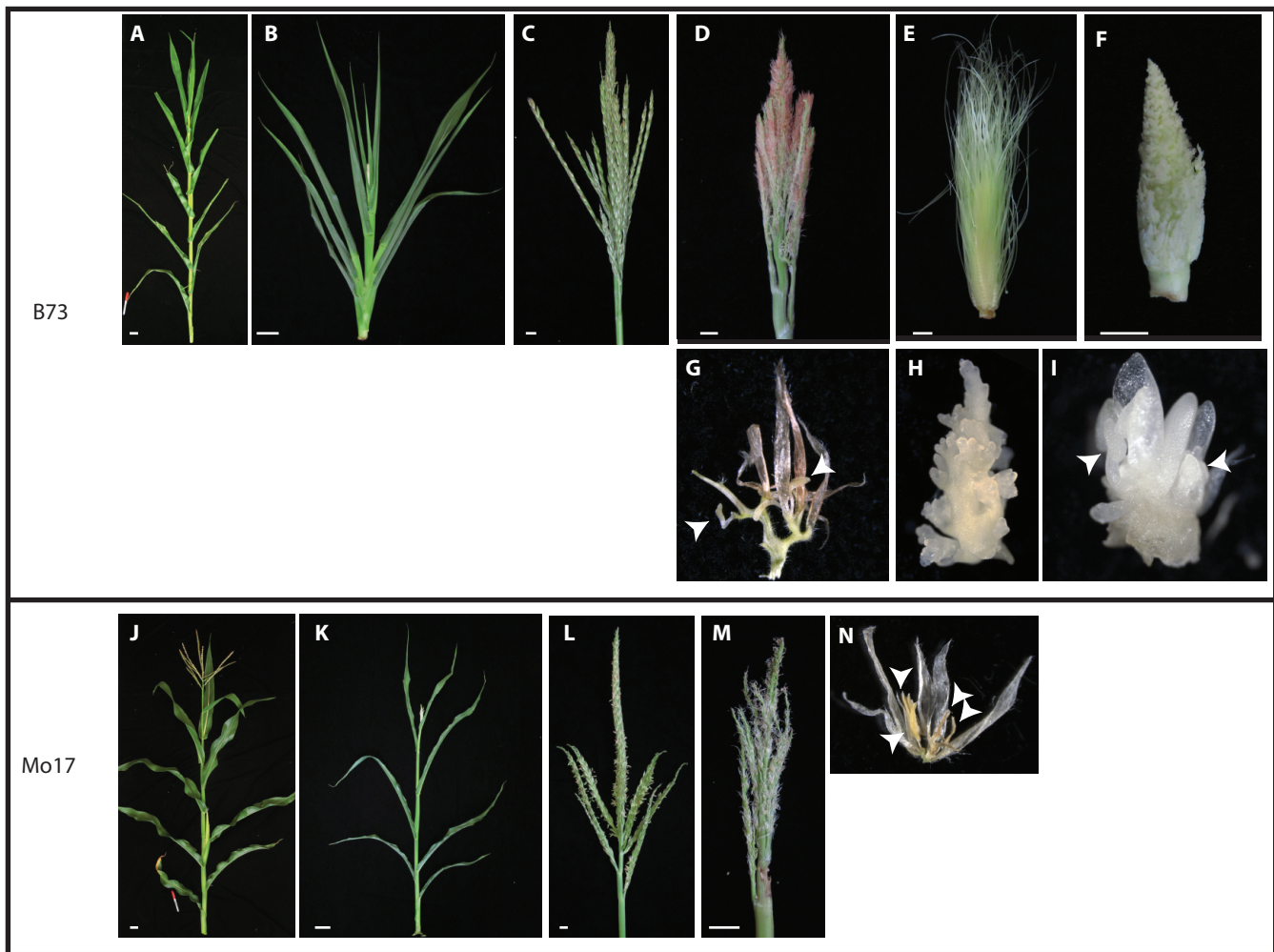
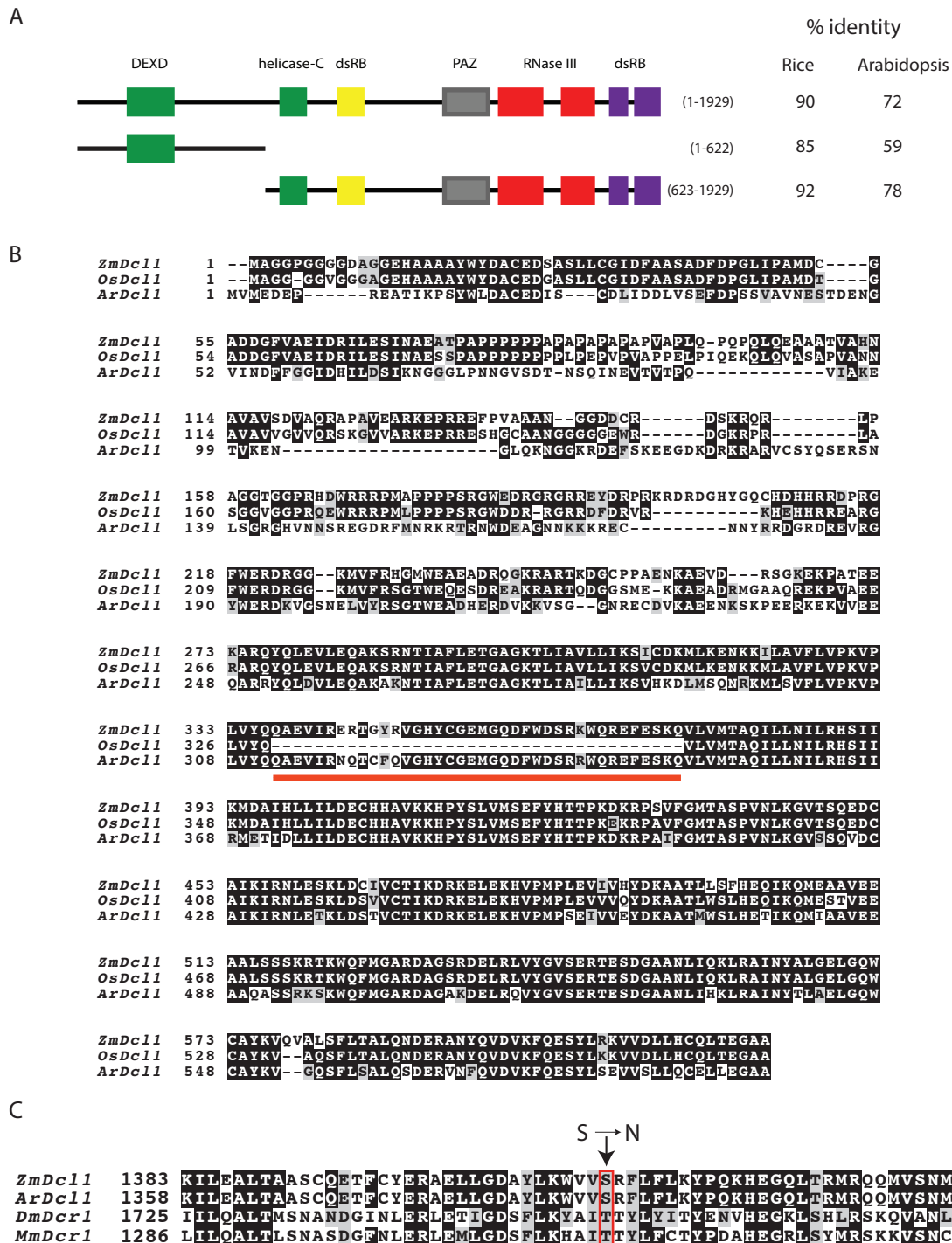


**Supplemental Figure 1.** Additional phenotypic characterization of *fzt* plants.

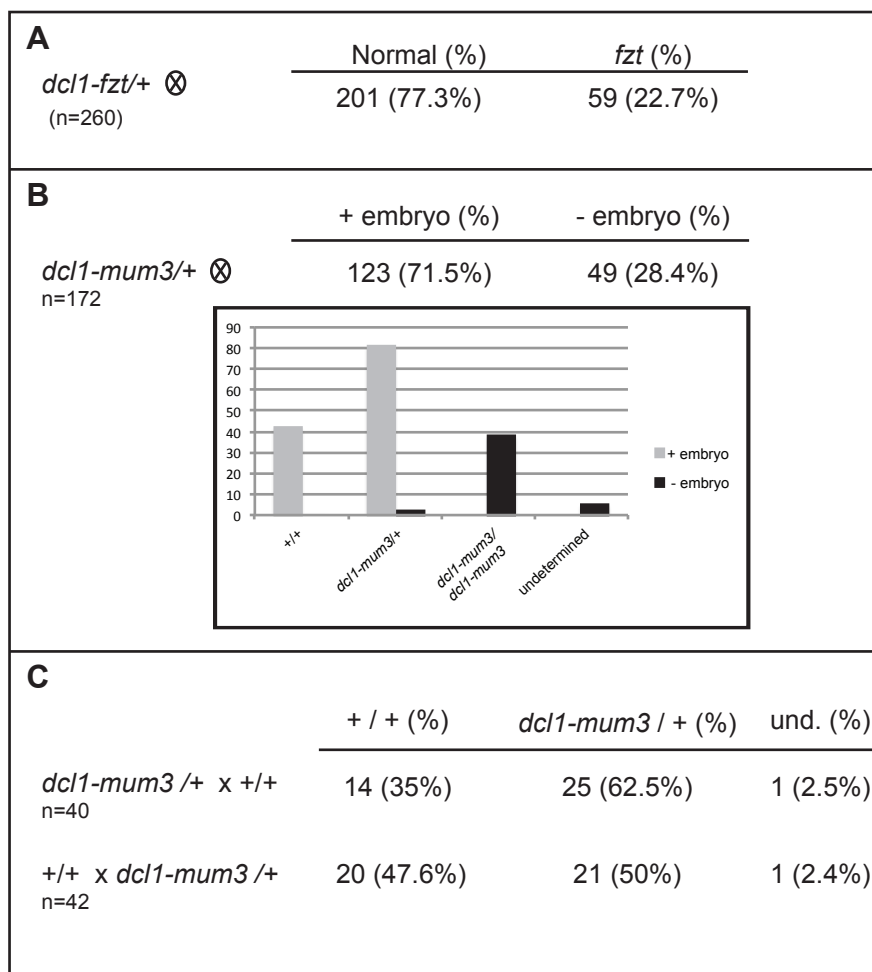
(A) *fzt* plants are shorter than normal siblings. (B) *fzt* plants make fewer leaves than normal siblings. (C) *fzt* plants have fewer nodes than normal siblings. (D) Internode length is reduced in *fzt* plants compared to normal siblings. *fzt* plants have shorter (E) and narrower (F) leaves than normal siblings. (G) Cell number/unit area in *fzt* and normal leaves. Cell number/unit area was slightly reduced in *fzt* and normal leaves, indicating that cell size is slightly increased in *fzt* compared to normal leaves. Leaf samples were taken from the middle of the blade of leaf 9. (H) *fzt* plants make fewer tassel branches than normal siblings. Data for (A), (B), (E), (F) and (H) are from field grown plants; data for (C), (D), and (G) are from greenhouse grown plants. Error bars indicate standard error. \*\* indicates  $p < 0.05$  and \* indicates  $p < 0.01$  in a 2-tailed student t-test.



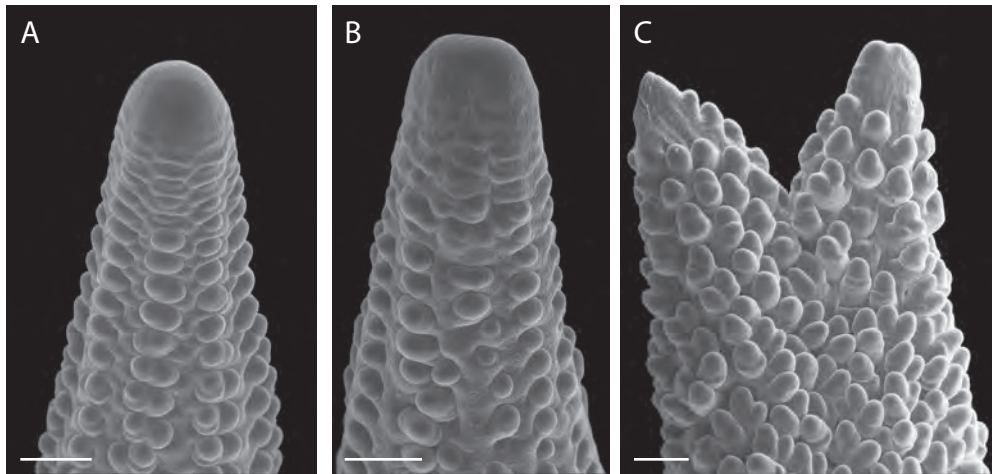
**Supplemental Figure 2.** *fzt* phenotypes introgressed into the B73 and Mo17 inbreds. (A-I) *fzt* and normal control plants introgressed into the B73 inbred background (5x) and (J-N) *fzt* and normal control plants introgressed into the Mo17 inbred background (5x). Normal plants (A) are much taller than *fzt* [B73] mutants (B). Normal tassel (C) compared to *fzt* [B73] tassel (D). *fzt* [B73] tassels are smaller than normal controls and are highly branched. Normal ear (E) compared to *fzt* [B73] ear (F). *fzt* [B73] ears are highly branched and contain few floral organs. *fzt* [B73] tassel “spikelets” (G) contain an excess of palea/lemma-like organs and a few immature and abnormal stamens (arrowheads). (H) Branch from ear in (F) initiates meristems in a disordered manner. (I) Spikelet from ear in (F) contains immature stamens (arrowheads). Normal plants (J) are much taller than *fzt* [Mo17] mutants (K). Normal tassel (L) compared to *fzt* [Mo17] tassel (M). *fzt* [Mo17] tassels are smaller than normal controls and are highly branched. *fzt* [Mo17] tassel spikelets (N) contain lemma/palea-like organs and immature and abnormal stamens (arrowheads). *fzt* [Mo17] plants rarely make ears. Scale bars: A-B, J-K = 5cm; C-E, L-M = 1cm; F = 0.5cm.

**Supplemental Figure 3. Genomic structure of maize *dcl1*.**

(A) The predicted maize full-length DCL1 protein is 1929 amino acids and contains a two part helicase domain (green boxes), a novel double stranded RNA-binding domain (yellow), PAZ domain (gray), two RNase III domains (red) and two C-terminal double stranded RNA binding domains (purple). The gene model GRMZM2G040762 corresponds to amino acids 623-1929 and lacks the conserved DEXD helicase domain at the N-terminus. The N-terminus of ZmDCL1 was predicted based on similarity to ArDCL1 and OsDCL1. Percent amino acid identity of ZmDCL1 to rice and Arabidopsis DCL1 full-length and partial proteins is indicated. (B) Amino acid alignment of the predicted N-terminus of ZmDCL1 (aa 1-622) to OsDCL1 and ArDCL1 is indicated. The red underlined amino acids are annotated as intronic sequences in rice, but exonic sequences in Arabidopsis. The high degree of conservation between Arabidopsis and maize suggest this sequence is exonic in both Arabidopsis and maize. (C) Alignment of part of the RNase IIIa domain, with the *fzt* mutation indicated. Alignments were performed using ClustalW2 (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>) and shaded with BOXSHADE 3.21 ([http://www.ch.embnet.org/software/BOX\\_form.html](http://www.ch.embnet.org/software/BOX_form.html)).

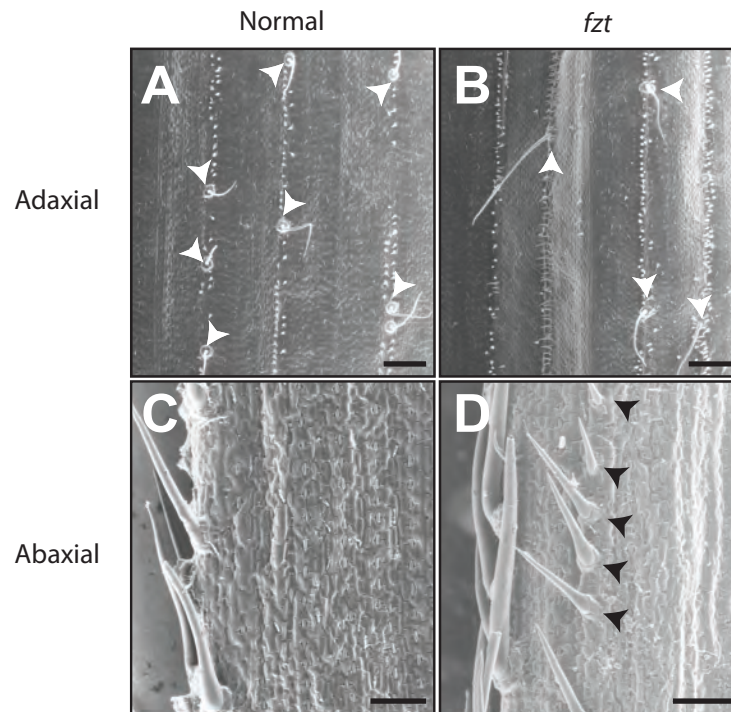


**Supplemental Figure 4.** *dcl1* alleles are transmitted in Mendelian ratios **(A)** One quarter of *dcl1-fzt*/<sup>+</sup> self progeny are *dcl1-fzt* homozygotes. **(B)** *dcl1-mum-3* homozygous seeds lack a recognizable embryo. Seeds were allowed to germinate on wet paper towels and embryos dissected for genotyping. For seeds that lacked an embryo, the whole seed including the endosperm was genotyped. **(C)** *dcl1-mum3* is transmitted normally through both the male and female gametophyte in reciprocal crosses. The genotypes of a few seeds were undetermined (und.) due to PCR failure.

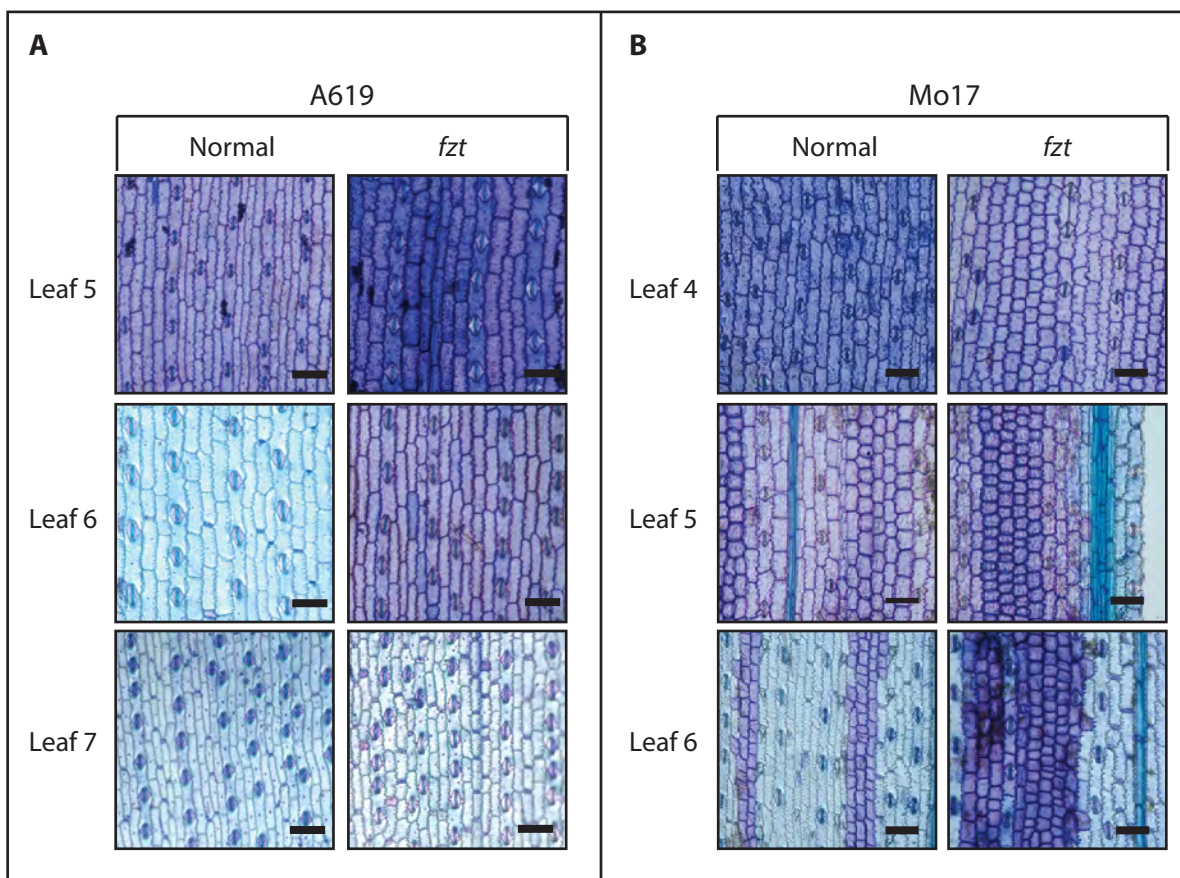


**Supplemental Figure 5.** Inflorescence meristems are fasciated in *dcl1-fzt* mutants.

(A) IM from normal ear forms a dome shape and grows as a single apex. (B) IM from young *dcl1-fzt* ear is broader and flatter than normal, indicative of mild fasciation. (C) IM from older *dcl1-fzt* ear has split into two apices, indicative of severe fasciation. Scale bars = 250 $\mu$ m.

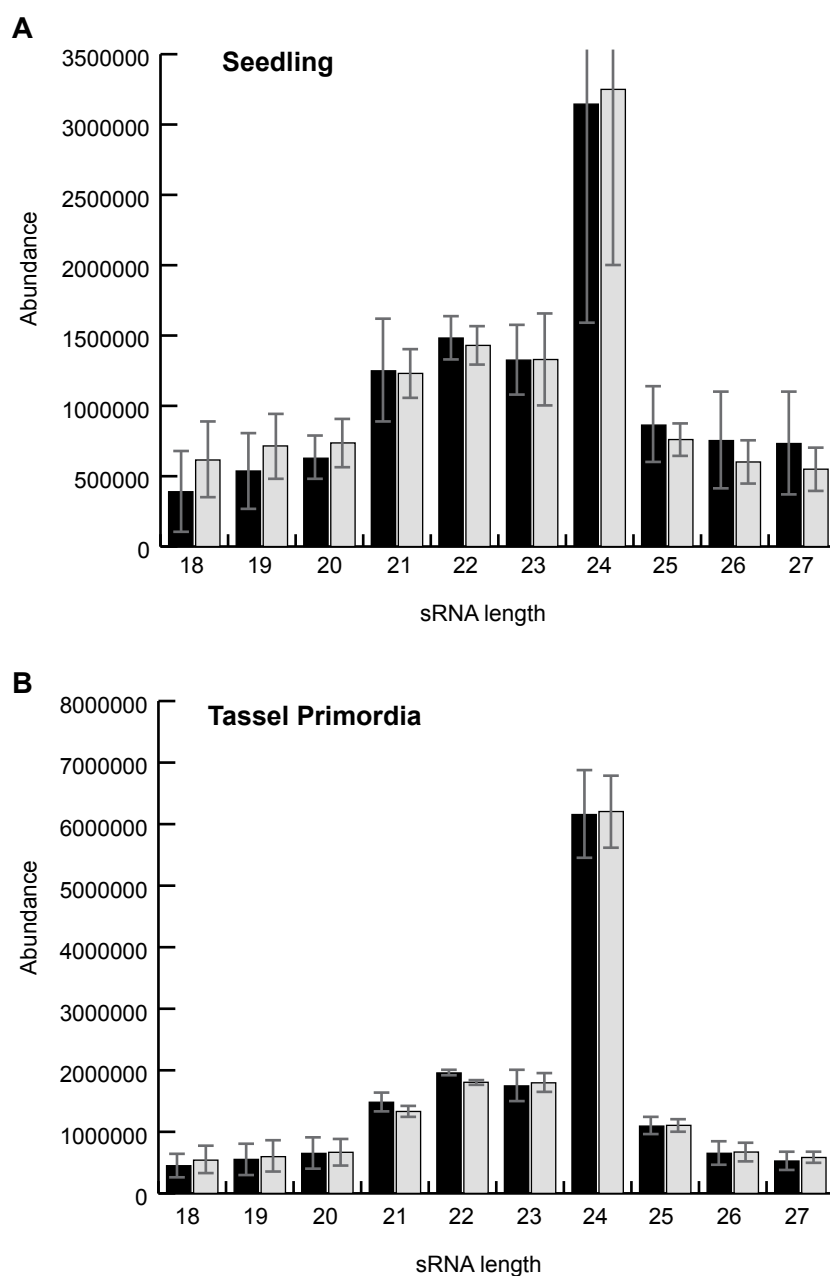


**Supplemental Figure 6.** *dcl1-fzt* leaf polarity defects in the A619 inbred. In normal leaves, macrohairs (arrowheads) are present on the adaxial blade (**A**), but not on the abaxial blade (**C**). In *dcl1-fzt* [A619] leaves, fewer macrohairs are present on the adaxial blade (**B**), and extend onto the abaxial blade near the margin (**D**). Arrowheads indicate macrohairs. Scale bars = 1mm A-B; 0.5 mm C-D.



**Supplemental Figure 7.** *dcl1-fzt* plants have phase change defects.

**(A)** Toluidine Blue staining of epidermal peels from *dcl1-fzt* [A619] and normal leaves. Violet color indicates juvenile leaf waxes and light blue indicates adult waxes. *dcl1-fzt* [A619] plants transition to the adult phase ~1 leaf later than normal siblings. **(B)** Toluidine Blue staining of epidermal peels from *dcl1-fzt* [Mo17] and normal leaves. *dcl1-fzt* [Mo17] plants begin to transition ~1 leaf earlier than normal siblings. The violet stained cells in adult leaves are bulliform cells. Scale bars = 100  $\mu$ m.

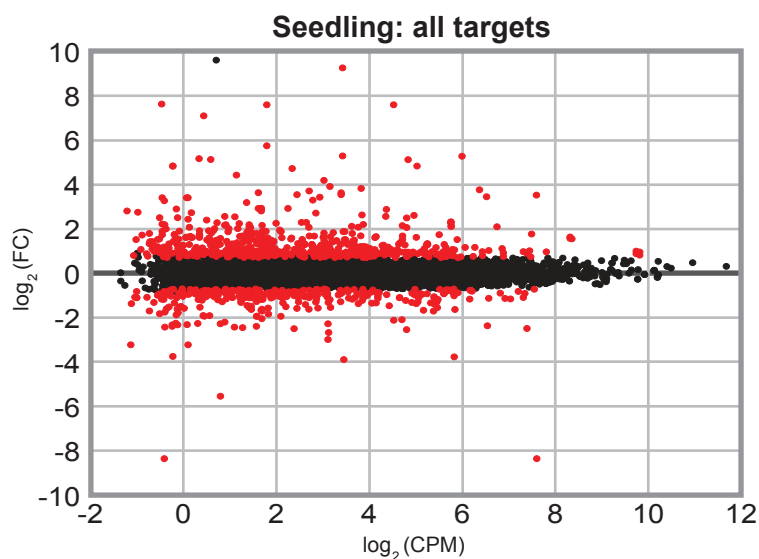
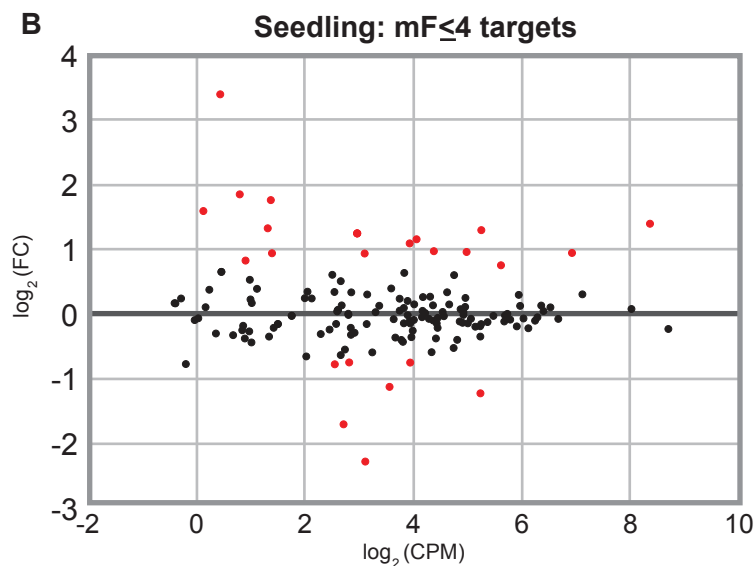


**Supplemental Figure 8.** Size distribution of small RNAs in *dcl1-fzt* and normal control plants.

**(A)** Size distribution of small RNAs in *dcl1-fzt* and A619 14 day old seedlings in three biological replicates. **(B)** Size distribution of small RNAs in *dcl1-fzt* and normal sibling control tassel primordia. There is no statistical difference in the abundance of 21-nt small RNAs, which are predominantly miRNAs, in *dcl1-fzt* and normal controls. Error bars indicate standard error.





**A****B**

**Supplemental Figure 10:** Analysis of predicted miRNA targets in seedlings. **(A)** MA plot showing all predicted miRNA targets ( $mF \leq 7$ ) for miRNAs decreased in *dcl1-fzt* seedlings. Red dots indicate miRNA targets differentially expressed in *dcl1-fzt* mutants ( $p < 0.05$  and  $FDR < 0.05$ ) and black dots indicate mRNAs that are not differentially expressed. MiRNA targets are not broadly increased in *dcl1-fzt* mutants. **(B)** MA plot showing predicted miRNA targets with  $mF \leq 4$  in seedling. Dot color indicates statistical significance as in **(A)**. Of the differentially expressed targets, the majority (19/26) are increased in *dcl1-fzt* seedlings. FC=fold change; CPM=counts per million.

**Supplemental Figure 11.** Maize *dcl1* genomic sequence

Reconstructed genomic sequence of *dcl1*-containing region (from BACs. AC155424, AC191351 and AC191256). Exon sequences are highlighted in yellow. START and STOP codons are highlighted in red. We are coordinating with MaizeGDB to update the B73 reference genome (<http://curation.maizegdb.org/curation/cgi-bin/displaylocusrecord.cgi?id=974366>).

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CATGGACGTGTGTTGTTTGGCAACAACGACGCAACCAGCACGGACAAGAAGGGGGGACATG  
CAGTCTCTCGAAACCTGTCCTATACAATTAGAAAGAAAAAAAAAGAGGGAAAATAAAAGGAA  
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**Supplemental Table 1.** Summary statistics of sequence-by-synthesis (SBS) small RNA and RNA-seq libraries used in this study.**(A) Number of small RNA reads from maize seedling and tassel primordium libraries by SBS sequencing.**

Library	SBS reads*	Genome-matched reads†	Distinct, genome-matched reads‡	Structural RNA - matched read§
<b>Seedling libraries</b>				
A619 rep1 (1_A619)	19,957,581	14,067,731	3,175,417	580,505
A619 rep2 (2_A619)	26,611,750	17,062,800	3,212,249	3,355,354
A619 rep3 (3_A619)	15,413,702	13,098,107	1,483,837	598,764
<i>fzt</i> rep1 (1_fzt)	18,893,333	13,063,256	3,012,437	656,996
<i>fzt</i> rep2 (2_fzt)	16,146,074	9,308,443	2,242,646	2,746,804
<i>fzt</i> rep3 (3_fzt)	15,010,707	12,805,536	1,195,641	648,198
<b>Tassel primordia libraries</b>				
Normal sib rep1 (1T_Nsib)	25,417,120	19,300,805	4,573,444	368,094
Normal sib rep2 (2T_Nsib)	39,914,118	32,701,207	4,747,414	1,164,269
Normal sib rep3 (3T_Nsib)	31,949,641	25,972,929	5,223,978	680,557
<i>fzt</i> rep1 (1T_fzt)	26,803,810	19,912,137	3,847,192	470,647
<i>fzt</i> rep2 (2T_fzt)	42,999,370	35,204,539	4,673,353	1,109,735
<i>fzt</i> rep3 (3T_fzt)	31,817,065	25,180,384	5,171,764	612,867

**(B) Number of RNA-seq reads from maize seedling and tassel primordium libraries by SBS sequencing.**

Library	SBS reads*	Genome-matched reads†	Distinct, genome-matched reads‡
<b>Seedling libraries</b>			
A619 rep1 (A619_mRNA_1)	48,390,153	32,986,739	13,802,327
A619 rep2 (A619_mRNA_2)	39,199,346	26,991,654	11,018,284
A619 rep3 (A619_mRNA_3)	53,171,397	32,877,538	16,772,561
A619 rep4 (A619_mRNA_4)	48,833,687	30,467,909	15,048,583
<i>fzt</i> rep1 ( <i>fzt</i> _mRNA_1)	46,273,586	31,177,203	13,413,861
<i>fzt</i> rep2 ( <i>fzt</i> _mRNA_2)	35,970,700	22,306,804	10,943,978
<i>fzt</i> rep3 ( <i>fzt</i> _mRNA_3)	51,084,786	31,971,552	15,327,774
<i>fzt</i> rep4 ( <i>fzt</i> _mRNA_4)	49,832,138	30,464,416	16,195,059
<b>Tassel primordia libraries</b>			
Normal sib rep1 (1Tm_Nsib)	32,848,281	21,331,466	10,499,351
Normal sib rep2 (2Tm_Nsib)	44,923,665	24,888,262	14,794,347
Normal sib rep3 (3Tm_Nsib)	43,640,888	23,985,211	15,120,652
<i>fzt</i> rep1 (1Tm_fzt)	28,419,244	18,620,103	9,603,233
<i>fzt</i> rep2 (2Tm_fzt)	39,022,802	21,538,920	12,758,730
<i>fzt</i> rep3 (3Tm_fzt)	37,558,567	21,220,372	11,704,614

\* Reads  $\geq$  18 bp in length (after trimming of the 3' adapter) from SBS sequencing reactions.

† Number of sequences which are matched to the genome sequence of Maize Genome Project 5b.60 AGPv2.

‡ Number of genome-matched sequences which are uniquely found within the set, excluding sequences matched to structural RNAs (*t/r/sn/snoRNAs*).§ Numbers of sequences matched to structural RNAs (*t/r/sn/snoRNAs*).



**Supplemental Table 2.** Abundance of miRNAs in seedling and tassel primordium

libraries. (A) miRNA abundances in seedling libraries.

miRNA	A619_1S	A619_2S	A619_3S	<i>ft</i> _1S	<i>ft</i> _2S	<i>ft</i> _3S	Fold Change	p-value
miR398b-5p	7.11	1.16	3.21	0.00	0.00	0.07	-101.38	0.000016
miR408a-b-3p	186.20	44.36	134.16	5.27	1.53	1.18	-45.83	0.000038
miR408b-5p	7.33	0.41	1.52	0.12	0.00	0.00	-73.97	0.000156
miR394a-b-5p	193.90	4.50	15.41	2.22	0.08	0.29	-82.75	0.000168
miR167c-3p	33.14	5.04	7.38	1.17	0.32	0.37	-24.58	0.000274
miR156a-3p	6.13	3.00	4.41	0.59	0.08	0.00	-21.10	0.000795
miR167b-3p	8.98	1.77	1.85	0.47	0.00	0.07	-23.83	0.000952
miR319b,d-5p	140.64	16.42	25.28	6.32	3.70	0.59	-17.20	0.001780
miR169i-k-5p	30.30	1.84	5.94	1.52	0.40	0.29	-17.25	0.001807
miR167a-d-5p	76.16	2.93	6.74	3.51	0.48	0.59	-18.80	0.002656
miR168b-3p	53.71	3.00	7.06	2.81	0.64	0.15	-17.81	0.003027
miR168a-3p	80.05	1.36	6.02	3.04	0.16	0.07	-26.85	0.003412
miR156d,g-f-3p	108.70	18.26	35.22	9.48	2.81	1.40	-11.86	0.003446
miR398a-b-3p	27.75	10.83	32.26	5.62	0.88	1.70	-8.67	0.006280
miR528a-b-3p	50.79	2.45	9.79	4.68	0.56	0.66	-10.71	0.009762
miR156e-3p	14.14	2.11	4.65	1.76	0.40	0.22	-8.87	0.009971
miR397a-b-5p	3.52	1.91	4.97	0.94	0.08	0.37	-7.57	0.012040
miR159a-5p	26.78	1.64	2.81	2.57	0.32	0.37	-9.63	0.014022
miR2118b	15.93	2.45	2.89	1.40	1.29	0.29	-7.11	0.016870
miR399e, i-j-3p	44.29	2.79	6.82	5.15	1.45	1.33	-6.81	0.024005
miR160a-e, g-5p	648.59	10.63	27.52	56.40	3.38	6.93	-10.30	0.028673
miR398a-5p	26.56	0.48	2.65	3.28	0.40	0.22	-7.65	0.037656
miR156l-3p	57.98	13.22	21.42	12.87	4.74	4.13	-4.26	0.051517
miR156k-3p	7.78	3.75	4.73	2.11	0.64	1.25	-4.07	0.052957
miR164b-3p	15.49	0.61	2.09	2.46	0.64	0.52	-5.05	0.063800
miR164c,h-3p	15.34	0.07	2.81	1.40	1.37	0.00	-6.55	0.072312
miR167e-3p	12.04	1.02	2.09	2.81	0.40	0.44	-4.18	0.093978
miR166j-k,n-3p	411.15	15.81	82.57	71.73	33.21	7.96	-4.51	0.094014
miR444a-b	183.06	9.06	22.95	36.86	7.96	2.06	-4.59	0.096759
miR159a-b,f,j-k-3p	247.54	52.95	88.66	72.67	22.60	10.03	-3.70	0.108699
miR396a-b-3p	4.19	2.52	6.18	1.87	1.61	0.66	-3.11	0.110868
miR319a-d-3p	411.97	13.76	24.63	63.19	30.31	2.29	-4.70	0.112358
miR166a-5p	3.74	4.91	6.74	2.11	1.77	1.25	-3.00	0.114763
miR827-3p	996.60	30.46	43.81	190.85	17.77	17.84	-4.73	0.118812
miR169f-h-5p	10.85	0.48	1.20	2.81	0.32	0.29	-3.69	0.147126
miR169c-3p	16.53	6.95	19.74	8.78	4.50	1.99	-2.83	0.150224
miR160g-b-3p	10.10	0.34	0.64	2.22	0.48	0.37	-3.62	0.152030
miR156k-5p	28.13	4.16	14.04	9.83	2.49	4.13	-2.82	0.167111

<b>miR156h-3p</b>	7.41	1.02	1.36	1.52	1.53	0.15	-3.06	0.169994
<b>miR164a-d,g-5p</b>	116.18	1.91	8.10	31.83	3.70	2.80	-3.29	0.204619
<b>miR171d-e,i,j-3p</b>	95.61	6.61	20.86	33.11	6.83	4.20	-2.79	0.215852
<b>miR167e-j-5p</b>	345.69	53.15	86.90	119.94	33.29	25.07	-2.72	0.219239
<b>miR166g-5p</b>	3.82	0.14	0.80	5.38	8.20	0.37	2.92	0.223596
<b>miR528a-b-5p</b>	37.40	7.09	26.64	21.76	4.50	2.51	-2.48	0.241688
<b>miR168a-b-5p</b>	5793.92	459.07	641.51	1622.98	615.95	246.84	-2.77	0.254964
<b>miR390a-b-5p</b>	329.01	10.63	69.73	106.48	33.85	13.79	-2.66	0.267478
<b>miR396a-b-5p</b>	258.76	16.42	52.48	65.64	51.95	14.08	-2.49	0.273774
<b>miR166c-5p</b>	6.88	2.93	5.46	3.28	3.22	1.11	-2.01	0.321000
<b>miR171d-e-5p</b>	40.17	0.07	4.49	11.82	5.39	0.37	-2.55	0.347901
<b>miR393a,c-5p</b>	5.31	0.68	1.52	2.11	1.13	0.59	-1.97	0.371809
<b>miR529-3p</b>	8.90	0.20	0.88	2.34	2.17	0.37	-2.05	0.409106
<b>miR169c,r-5p</b>	10.32	0.61	1.20	5.27	0.40	0.07	-2.13	0.422256
<b>miR156a-i,l-5p</b>	2729.61	416.82	1265.69	1076.52	951.58	301.77	-1.89	0.433263
<b>miR166b,d-5p</b>	76.16	34.34	44.69	47.39	31.36	14.52	-1.66	0.480683
<b>miR396e-f-5p</b>	99.20	22.08	91.95	188.98	107.75	51.98	1.64	0.521011
<b>miR156b-3p</b>	49.45	3.88	10.27	19.31	17.61	0.44	-1.70	0.535738
<b>miR529-5p</b>	882.37	18.60	43.97	254.97	276.29	11.72	-1.74	0.566813
<b>miR166l-m-3p</b>	444.14	16.22	81.44	213.67	118.20	33.40	-1.48	0.647884
<b>miR166n-5p</b>	4.49	0.00	1.28	1.64	2.89	0.00	-1.27	0.813295
<b>miR166a-3p</b>	41600.11	11994.81	20767.72	38845.89	29647.07	11135.22	1.07	0.934536
<b>miR396f-3p</b>	2.17	0.27	1.69	2.22	1.85	0.29	1.05	0.946778
<b>miR166m-5p</b>	5.01	0.00	0.24	2.11	2.89	0.00	-1.05	0.962411
<b>miR166b-i-3p</b>	406.81	44.63	115.79	311.02	182.05	56.33	-1.03	0.968487

**(B)** miRNA abundances in tassal primordium libraries.

<b>miRNA</b>	<b>Normal_1T</b>	<b>Normal_2T</b>	<b>Normal_3T</b>	<b><i>fzt</i>_1T</b>	<b><i>fzt</i>_2T</b>	<b><i>fzt</i>_3T</b>	<b>Fold Change</b>	<b>p-value</b>
<b>miR167d-3p</b>	6.89	3.92	4.96	0.22	0.04	0.09	-45.32	1.00E-05
<b>miR167a-d-5p</b>	63.01	58.56	58.52	2.91	1.57	1.53	-29.98	1.11E-05
<b>miR172e</b>	5.45	3.40	2.61	0.15	0.12	0.09	-30.68	2.74E-05
<b>miR408a-b-3p</b>	1.36	35.03	22.82	0.22	0.20	0.74	-49.87	6.87E-05
<b>miR398b-5p</b>	0.00	4.38	6.42	0.07	0.00	0.09	-60.85	0.000371
<b>miR394a-b-5p</b>	41.20	24.90	33.45	4.14	0.56	0.79	-18.21	0.000421
<b>miR167c-3p</b>	41.50	50.99	73.81	2.62	6.05	6.54	-10.91	0.001073
<b>miR398a-b-3p</b>	0.23	33.75	32.74	0.15	1.33	2.27	-17.63	0.004924
<b>miR319a-d-3p</b>	307.12	170.02	181.97	70.76	12.78	9.00	-7.12	0.009999
<b>miR159a-b,f,j-k-3p</b>	240.92	327.02	219.73	27.53	91.81	45.35	-4.78	0.021724
<b>miR528a-b-5p</b>	6.06	52.82	34.00	0.58	5.32	8.39	-6.48	0.023661
<b>miR160a-e,g-5p</b>	18.78	15.19	10.03	1.96	3.79	3.34	-4.82	0.028341
<b>miR166j-k,n-3p</b>	1063.06	759.47	709.03	310.14	211.85	230.71	-3.36	0.038039
<b>miR159a-5p</b>	141.78	11.24	14.99	23.32	0.73	2.55	-6.32	0.045364

<b>miR444a-b</b>	20.30	11.83	11.98	3.71	3.39	5.56	-3.48	0.076749
<b>miR399e,i,j-3p</b>	24.92	0.38	0.80	4.36	0.40	0.14	-5.34	0.101966
<b>miR528a-b-3p</b>	0.23	14.51	9.68	0.00	2.74	3.66	-3.80	0.171741
<b>miR529-5p</b>	28586.87	5313.93	2203.75	13007.52	1168.54	1340.79	-2.33	0.196562
<b>miR166c-5p</b>	13.78	5.92	4.41	5.96	2.34	1.21	-2.54	0.201334
<b>miR166a-3p</b>	57911.96	13792.38	7356.52	29633.78	5468.07	4890.56	-1.98	0.212390
<b>miR168a-3p</b>	15.75	0.47	0.35	4.07	0.77	0.00	-3.43	0.241722
<b>miR166b,d-5p</b>	109.74	54.99	24.32	60.88	13.47	11.22	-2.21	0.280910
<b>miR171d-e,i,j-3p</b>	16.81	11.49	9.88	8.86	4.80	5.84	-1.96	0.330129
<b>miR390a-b-5p</b>	166.02	26.17	28.78	78.24	9.84	15.07	-2.14	0.330370
<b>miR397a-b-5p</b>	0.08	4.85	4.21	0.00	1.77	2.27	-2.25	0.383805
<b>miR171d-e-5p</b>	20.15	8.13	8.57	12.64	3.79	4.59	-1.75	0.432998
<b>miR164g-3p</b>	22.27	4.89	12.79	49.18	7.94	9.78	1.67	0.487308
<b>miR168b-3p</b>	19.31	0.47	0.30	9.44	0.44	0.05	-2.02	0.505393
<b>miR166n-5p</b>	176.32	37.66	40.57	127.06	9.84	17.39	-1.65	0.525309
<b>miR396a-b-5p</b>	79.15	2.98	2.61	43.01	1.49	1.81	-1.83	0.525607
<b>miR156a-i,l-5p</b>	2.50	1.28	1.30	2.62	0.20	0.14	-1.73	0.535494
<b>miR319b,d-5p</b>	3.48	0.04	0.15	6.54	0.04	0.00	1.79	0.617197
<b>miR166k-5p</b>	76.95	9.45	10.68	54.56	4.64	6.12	-1.49	0.625897
<b>miR529-3p</b>	604.77	15.24	12.69	983.89	6.81	7.47	1.58	0.660026
<b>miR390a-b-3p</b>	4.47	1.79	0.80	3.85	1.01	0.70	-1.27	0.741551
<b>miR160b,g-3p</b>	12.95	0.98	1.60	10.53	0.52	0.70	-1.32	0.751210
<b>miR166l-m-3p</b>	1619.05	816.50	659.43	1492.73	577.35	539.46	-1.19	0.765345
<b>miR166b-3p</b>	1039.80	172.07	100.94	905.21	70.64	75.08	-1.25	0.774307
<b>miR827-3p</b>	58.24	40.60	91.66	88.12	31.61	42.85	-1.17	0.814654
<b>miR164a-3p</b>	9.47	0.94	1.45	9.08	0.81	0.51	-1.14	0.876787
<b>miR166m-5p</b>	34.69	16.60	10.03	46.79	13.43	8.21	1.12	0.877797
<b>miR396e-f-5p</b>	1.59	0.51	1.50	2.03	0.32	1.72	1.13	0.883789
<b>miR164a-d,g-5p</b>	15.15	8.30	6.62	19.11	3.67	4.54	-1.10	0.894511
<b>miR166a-5p</b>	20.90	9.62	5.37	28.04	6.17	4.92	1.09	0.907698
<b>miR168a-b-5p</b>	319.69	159.43	141.10	435.17	107.13	96.78	1.03	0.964328

**Supplemental Table 3. Abundance of pri-miRNAs in seedling and tassel primordium**

libraries. (A) pri-miRNA abundances in seedling libraries.

pri-miRNA	A619 1S	A619 2S	A619 4S	A619 5S	<i>fzt_1S</i>	<i>fzt_2S</i>	<i>fzt_4S</i>	<i>fzt_5S</i>	log <sub>2</sub> FC	p-value	FDR
pri-miRNA 528b	0.09	1.72	1.50	1.58	4.67	7.86	18.50	5.60	2.91	2.33E-23	5.99E-21
pri-miRNA 156b	3.46	1.08	0.20	0.52	5.24	7.82	0.39	20.88	2.71	8.06E-21	1.66E-18
pri-miRNA 319b	1.13	1.96	5.51	3.45	10.97	7.59	15.29	20.44	2.17	3.47E-15	4.47E-13
pri-miRNA 167d	0.07	0.46	0.64	0.28	1.62	1.65	1.58	3.51	2.51	2.64E-14	3.12E-12
pri-miRNA 167c	0.06	0.08	0.31	0.11	0.56	0.20	1.72	1.24	2.68	1.19E-11	9.92E-10
pri-miRNA 528a	0.03	1.41	1.07	1.54	2.20	4.05	7.88	1.81	1.98	1.27E-11	1.05E-09
pri-miRNA 159a	16.33	17.71	16.23	13.57	42.27	32.64	44.41	93.96	1.74	4.66E-11	3.52E-09
pri-miRNA 408b	0.17	2.28	2.17	3.83	6.02	7.51	12.39	3.02	1.77	1.53E-10	1.08E-08
pri-miRNA 169c	1.22	2.12	7.69	13.30	5.62	8.49	33.64	19.24	1.46	3.99E-08	1.84E-06
pri-miRNA 168b	4.10	4.16	5.16	4.02	8.81	7.67	15.55	14.48	1.41	1.34E-07	5.60E-06
pri-miRNA 172c	1.60	3.60	2.12	1.90	4.70	3.95	6.48	8.98	1.39	4.53E-07	1.69E-05
pri-miRNA 159f	2.82	3.52	4.13	5.33	8.68	6.76	11.38	12.14	1.30	1.24E-06	4.15E-05
pri-miRNA 398b	0.29	8.63	6.50	13.98	7.60	17.19	36.90	7.28	1.23	3.12E-06	9.42E-05
pri-miRNA 166h	2.06	0.88	0.47	0.49	1.95	3.28	0.82	3.67	1.32	7.69E-06	0.000207
pri-miRNA 156f	16.62	14.67	23.86	20.61	37.97	24.78	47.51	52.22	1.10	2.33E-05	0.000555
pri-miRNA 168a	12.03	12.03	22.52	16.02	34.70	28.81	35.71	33.85	1.09	2.99E-05	0.000685
pri-miRNA 397a	0.67	1.28	0.02	1.11	0.31	0.75	0.00	0.56	-0.91	0.007992	0.075175
pri-miRNA 156g	20.95	32.45	39.62	39.46	71.34	42.29	44.08	47.38	0.63	0.014359	0.117918
pri-miRNA 169d	0.09	1.72	9.87	8.48	2.75	2.81	19.10	5.13	0.56	0.033946	0.218638
pri-miRNA 169b	0.09	1.32	1.50	1.50	0.43	2.53	2.42	1.22	0.59	0.046887	0.270172
pri-miRNA 156l	0.65	0.50	0.43	1.06	0.67	1.93	1.06	0.12	0.52	0.102654	0.440367
pri-miRNA 162	1.74	1.68	3.59	4.89	1.70	0.75	3.86	2.63	-0.41	0.134327	0.512222
pri-miRNA 164b	3.63	3.48	5.29	4.98	3.46	5.61	7.32	6.40	0.39	0.142310	0.528950
pri-miRNA 167b	1.83	1.68	3.66	2.42	2.35	2.65	5.77	1.36	0.34	0.220493	0.658025
pri-miRNA 399g	62.62	70.74	109.74	138.01	47.67	90.11	70.95	98.00	-0.31	0.220984	0.658383
pri-miRNA 396d	0.87	2.20	1.81	4.30	2.44	1.98	3.63	3.48	0.33	0.232499	0.674695
pri-miRNA 169h	0.33	0.71	1.53	0.88	0.65	0.21	1.36	0.57	-0.31	0.327345	0.770845
pri-miRNA 396c	0.41	0.53	1.71	2.39	1.10	0.83	2.19	1.87	0.25	0.398249	0.820271
pri-miRNA 396a	1.51	1.80	1.81	2.23	1.85	2.25	2.42	2.08	0.23	0.420679	0.836266
pri-miRNA 169i	1.05	2.24	7.43	8.27	4.48	2.57	11.86	3.09	0.21	0.426833	0.839534
pri-miRNA 156d	31.58	21.66	20.84	21.46	36.00	22.31	29.63	19.61	0.17	0.506920	0.881953
pri-miRNA 171i	0.67	0.48	2.39	1.85	1.17	0.40	2.42	2.17	0.19	0.519809	0.887347
pri-miRNA 166d	0.78	1.40	2.14	1.60	0.93	0.91	1.92	2.80	0.14	0.624142	0.925777
pri-miRNA 166l	0.17	0.36	2.86	2.07	0.74	0.40	3.94	0.88	0.12	0.677706	0.941492
pri-miRNA 169e	3.48	2.96	3.98	3.71	3.09	2.88	6.21	2.76	0.08	0.766577	0.962968
pri-miRNA 2275d	56.23	57.27	75.85	86.50	56.08	64.58	60.02	83.11	-0.06	0.800611	0.971546
pri-miRNA 171f	1.92	0.60	3.66	1.71	1.98	2.06	1.66	2.19	-0.01	0.981092	0.997767
pri-miRNA 156k	22.07	17.64	31.45	32.20	19.08	14.68	47.56	21.86	0.00	0.992717	0.999578

## (B) pri-miRNA abundances in tassel primordium libraries.

pri-miRNA	Normal 1T	Normal 2T	Normal 3T	<i>fst_1T</i>	<i>fst_2T</i>	<i>fst_3T</i>	log <sub>2</sub> FC	p-value	FDR
pri-miRNA 167d	20.19	16.23	36.04	130.87	196.14	248.56	2.99	7.18E-21	4.63E-18
pri-miRNA 167c	4.78	4.99	14.90	29.32	56.98	80.05	2.75	6.09E-18	2.46E-15
pri-miRNA 172e	13.93	12.60	33.98	63.05	155.75	152.14	2.62	9.18E-17	3.36E-14
pri-miRNA 168a	1.83	2.14	4.33	7.25	19.02	17.58	2.40	1.38E-13	3.39E-11
pri-miRNA 156f	1.95	1.44	0.77	0.34	0.03	0.07	-3.24	1.19E-11	2.08E-09
pri-miRNA 408b	0.21	14.28	22.72	0.29	76.97	73.26	2.02	7.27E-11	1.15E-08
pri-miRNA 528b	0.33	25.50	53.77	0.19	108.26	206.55	1.98	1.05E-10	1.61E-08
pri-miRNA 319d	0.08	0.18	0.03	0.72	1.08	1.17	3.29	3.86E-10	5.42E-08
pri-miRNA 159f	15.22	7.61	11.88	38.19	42.45	42.62	1.83	2.92E-09	3.53E-07
pri-miRNA 166k, m	1.83	2.56	4.47	4.37	15.44	12.12	1.85	7.45E-09	8.55E-07
pri-miRNA 159d	0.46	0.15	0.18	1.97	1.53	0.77	2.44	1.55E-08	1.72E-06
pri-miRNA 156d	2.08	1.94	0.59	0.48	0.24	0.17	-2.36	2.03E-08	2.20E-06
pri-miRNA 528a	0.04	18.82	21.73	0.10	50.31	69.68	1.56	3.01E-07	2.61E-05
pri-miRNA 171e	0.12	0.03	0.44	0.48	1.36	1.10	2.29	8.43E-07	6.60E-05
pri-miRNA 394a	3.45	5.11	6.16	7.53	16.10	17.68	1.49	1.81E-06	0.000133
pri-miRNA 172c	14.30	12.87	16.77	41.74	44.61	32.58	1.44	2.32E-06	0.000167
pri-miRNA 159a	163.54	142.56	271.55	331.21	480.47	649.41	1.34	8.05E-06	0.000503
pri-miRNA 169b	2.04	2.44	2.22	0.72	0.80	0.80	-1.52	2.69E-05	0.001462
pri-miRNA 168b	7.44	7.00	8.98	14.84	20.18	18.92	1.20	8.46E-05	0.004029
pri-miRNA 398b	0.25	132.54	121.23	0.10	291.83	277.80	1.17	9.79E-05	0.004559
pri-miRNA 166d	6.65	3.88	3.41	1.87	2.89	2.38	-0.96	0.002889	0.079827
pri-miRNA 319a	0.58	0.71	1.42	1.49	1.67	2.52	1.06	0.003106	0.084519
pri-miRNA 390a	3.41	3.06	5.48	4.70	9.91	7.80	0.91	0.003675	0.096527
pri-miRNA 171j	1.00	0.76	1.75	1.82	2.02	3.15	0.99	0.004325	0.110282
pri-miRNA 319c	0.30	0.50	0.53	0.48	1.39	1.05	1.13	0.005876	0.139716
pri-miRNA 156k	6.95	9.79	5.51	4.27	4.00	4.29	-0.83	0.008170	0.181083
pri-miRNA 394b	1.95	1.38	1.54	1.44	3.23	2.80	0.62	0.066206	0.760186
pri-miRNA 164d	0.62	0.73	0.53	0.48	1.46	1.07	0.67	0.084092	0.869147
pri-miRNA 169h	2.48	1.26	1.17	3.02	2.17	2.00	0.55	0.103341	0.967291
pri-miRNA 156g	1.91	1.94	1.21	1.44	1.11	0.90	-0.55	0.118805	0.999993
pri-miRNA 395d,f,g	0.08	0.29	2.67	0.10	0.80	1.17	-0.55	0.154137	0.999993
pri-miRNA 167b	8.03	7.23	6.19	8.97	11.61	8.07	0.42	0.170673	0.999993
pri-miRNA 171d	0.67	1.18	1.60	0.29	0.97	1.21	-0.48	0.203909	0.999993
pri-miRNA 395a	0.46	0.94	3.79	0.24	1.70	1.94	-0.41	0.238072	0.999993
pri-miRNA 169e	14.82	6.87	6.83	16.75	11.32	7.78	0.33	0.276094	0.999993
pri-miRNA 399g	178.64	191.45	167.18	151.38	211.38	124.65	-0.14	0.634086	0.999993
pri-miRNA 2275d	91.36	75.33	69.59	76.19	83.93	59.56	-0.10	0.722512	0.999993
pri-miRNA 529	24.42	20.04	15.46	27.87	10.27	25.89	0.10	0.750200	0.999993
pri-miRNA 162	3.59	9.81	10.55	4.27	7.27	12.94	0.03	0.921054	0.999993

**Supplemental Table 4:** Summary of predicted miRNA targets based on conserved biological function in *dcl1-fzt* and normal tassel primordia. Differentially expressed targets are indicated in bold

Gene ID	Locus	mF Score	Log(2) CPM	Log(2) FC	P value	FDR
<b>miR159a-b,f,j-k-3p (PF00249: Myb-like DNA binding domain)</b>						
<b>GRMZM2G423833</b>	<i>myb115</i>	2	2.8753	<b>1.0470</b>	<b>0.00082</b>	<b>.01443</b>
GRMZM2G093789	<i>mmyb59</i>	2.5	4.4846	0.8587	0.00427	0.0565
GRMZM2G004090	<i>myb87</i>	2.5	-0.007	0.5005	0.20567	0.7919
GRMZM2G028054	<i>myb74</i>	3	3.2294	-0.0257	0.93313	0.9999
<b>GRMZM2G139688</b>	<i>myb138</i>	3.5	3.4013	<b>1.7189</b>	<b>4.75E-08</b>	<b>2.38E-06</b>
GRMZM2G049194	<i>mybr67</i>	5.5	1.5715	-0.7996	0.01646	0.1581
<b>GRMZM2G050550</b>	<i>myb153</i>	6	2.8898	<b>1.7955</b>	<b>2.19E-08</b>	<b>1.17E-06</b>
GRMZM2G130149	<i>myb56</i>	6.5	3.3538	-0.1965	0.51900	0.9999
<b>miR160a-e,g-50 (PF02309; PF02362; PF06507: B3 DNA binding domain; Auxin response factor; AUX/IAA family)</b>						
GRMZM2G153233	<i>arftf2</i>	1	5.3861	5.3861	0.5516	0.0641
GRMZM2G159399	<i>arftf17</i>	1	5.4598	0.4698	0.1144	0.5796
AC207656.3_FG002	<i>arftf19</i>	1	0.9716	-0.2670	0.4416	0.9999
GRMZM5G808366	<i>arftf5</i>		1.2607	-0.1147	0.7338	0.9999
GRMZM2G081406	<i>arftf15</i>	2	4.1355	0.6909	0.0222	0.1967
GRMZM2G338259	<i>arftf10</i>	6.5	8.6898	0.1590	0.5895	0.9999
GRMZM5G874163	<i>arftf26</i>	7	6.15093	0.07146	0.8092	0.9999
<b>miR167a-d-5p (PF02309; PF02362; PF06507: B3 DNA binding domain; Auxin response factor; AUX/IAA family)</b>						
GRMZM2G475882	<i>arftf30</i>	4	6.5423	0.6427	0.0304	0.2458
GRMZM2G078274	<i>arftf3</i>	4	7.6643	0.3617	0.2208	0.8131
<b>GRMZM2G081158</b>	<i>arftf34</i>	<b>5</b>	<b>8.4320</b>	<b>1.6456</b>	<b>5.33E-08</b>	<b>2.65E-06</b>
<b>GRMZM2G073750</b>	<i>arftf9</i>	<b>5</b>	<b>6.4322</b>	<b>1.0271</b>	<b>0.0006</b>	<b>0.0109</b>
GRMZM2G089640	<i>arftf22</i>	5	6.4787	0.6851	0.0211	0.1898
GRMZM2G028980	<i>arftf16</i>	5	7.3120	0.4336	0.1426	0.6586
GRMZM2G035405	<i>arftf18</i>	5	7.1127	0.02455	0.93374	0.9999
GRMZM2G086949	<i>arftf29</i>	5.5	4.6541	-0.8669	0.0040	0.05343
<b>GRMZM2G034840</b>	<i>arftf4</i>	<b>6.5</b>	<b>5.0653</b>	<b>-1.4576</b>	<b>1.67E-06</b>	<b>6.19E-05</b>
<b>miR172e (PF0847: AP2 domain)</b>						
<b>GRMZM2G160730</b>	<i>gl15</i>	2	<b>0.02606</b>	<b>1.2209</b>	<b>0.0017</b>	<b>0.0265</b>

Gene ID	Locus	mF Score	Log(2) CPM	Log(2) FC	P value	FDR
<b>GRMZM5G862109</b>	<i>ids1</i>	<b>2.5</b>	<b>5.5508</b>	<b>0.9674</b>	<b>0.0012</b>	<b>0.0206</b>
GRMZM2G176175	<i>ereb121</i>	2.5	4.7519	0.8321	0.0056	0.0701
<b>GRMZM2G174784</b>	<i>ereb197</i>	<b>3</b>	<b>3.2165</b>	<b>1.0892</b>	<b>0.0004</b>	<b>0.0086</b>
GRMZM2G076602	<i>ereb212</i>	3	0.7817	0.5001	0.1586	0.6973
GRMZM2G124524	<i>wri1</i>	4	2.4794	0.09893	0.7521	0.9999
GRMZM2G020054	<i>ereb54</i>	6.5	1.3410	-0.0462	0.8904	0.9999
<b>miR319a-d-3p (PF03634: TCP family transcription factor)</b>						
GRMZM2G148022	<i>tcptf29</i>	2.5	0.8043	-0.9688	0.0069	0.0811
GRMZM2G089361	<i>tcptf44</i>	2.5	2.0622	0.2813	0.3791	0.9689
GRMZM2G115516	<i>tcptf5</i>	2.5	2.5601	0.1603	0.6077	0.9999
GRMZM2G020805	<i>tcptf43</i>	3	2.1055	0.4581	0.1516	0.6816
GRMZM2G015037	<i>tcptf24</i>	4	3.1169	0.1239	0.6860	0.9999
<b>miR394a-b-5p (PF00646: F-box domain)</b>						
<b>GRMZM2G119650</b>		<b>0</b>	<b>6.7312</b>	<b>1.0151</b>	<b>0.0007</b>	<b>0.0122</b>
<b>GRMZM2G064954</b>		<b>0</b>	<b>6.0225</b>	<b>0.8676</b>	<b>0.0036</b>	<b>0.0495</b>
<b>miR408a-b-3p (PF2298, PF00732: plastocyanin-like domain, multicopper oxidase)</b>						
GRMZM2G004012		2.5	5.3719	0.4958	0.0959	0.5205
GRMZM2G352678		3.5	1.4754	-0.5048	0.1295	0.6231
GRMZM2G076225		5	2.0026	-0.1700	0.5956	0.9999
GRMZM2G177934		6.5	1.2213	0.2870	0.3966	0.9796

**Supplemental Table 5.** Summary of predicted miRNA targets based on conserved biological function in *dcl1-fzt* and normal seedlings. Differentially expressed targets are indicated in bold.

Gene ID	Locus	mF Score	Log(2) CPM	Log(2) FC	P value	FDR
<b>miR160a-e,g-50 (PF02309; PF02362; PF06507:</b>						
<b>B3 DNA binding domain; Auxin response factor; AUX/IAA family)</b>						
<b>GRMZM2G153233</b>	<i>arftf2</i>	<b>1</b>	<b>4.9775</b>	<b>0.9625</b>	<b>0.0002</b>	<b>0.0029</b>
GRMZM2G159399	<i>arftf17</i>	1	4.7477	0.6050	0.01925	0.1126
<b>AC207656.3_FG002</b>	<i>arftf19</i>	<b>1</b>	<b>4.3744</b>	<b>0.9749</b>	<b>0.0002</b>	<b>0.0026</b>
GRMZM2G390641	<i>arftf21</i>	1	0.8911	-0.3745	0.1970	0.5211
GRMZM5G808366	<i>arftf5</i>	1.5	-0.3870	0.1681	0.6166	0.8655
<b>GRMZM2G081406</b>	<i>arftf15</i>	<b>2</b>	<b>2.7105</b>	<b>-1.701</b>	<b>5.60E-10</b>	<b>2.61E-08</b>
GRMZM2G328742	<i>abi40</i>	4	1.0133	-0.4354	0.1300	0.4117
GRMZM2G338259	<i>arftf10</i>	6.5	7.3086	0.0565	0.8250	0.9500
GRMZM5G874163	<i>arftf26</i>	7	5.0434	0.2918	0.02567	0.5990
<b>miR167a-d-5p (PF02309; PF02362; PF06507:</b>						
<b>B3 DNA binding domain; Auxin response factor; AUX/IAA family)</b>						
GRMZM2G475882	<i>arftf30</i>	4	4.6187	0.3398	0.1878	0.5064
GRMZM2G078274	<i>arftf3</i>	4	5.9387	0.2996	0.2425	0.5816
<b>GRMZM2G035405</b>	<i>arftf18</i>	<b>5</b>	<b>5.9680</b>	<b>0.7376</b>	<b>0.0042</b>	<b>0.0349</b>
GRMZM2G081158	<i>arftf34</i>	5	5.966	0.3969	0.1218	0.3957
GRMZM2G073750	<i>arftf9</i>	5	4.4693	-0.3912	0.1300	0.4118
GRMZM2G089640	<i>arftf22</i>	5	4.6208	0.0912	0.7235	0.9119
GRMZM2G028980	<i>arftf16</i>	5	6.0209	0.3570	0.1638	0.4707
GRMZM2G086949	<i>arftf29</i>	5.5	0.6835	0.1894	0.5202	0.8158
<b>GRMZM2G034840</b>	<i>arftf4</i>	6.5	1.764	-0.3944	0.1510	0.4501
<b>miR169i-k5p (PF002045: CCAAT-binding transcription factor)</b>						
GRMZM5G857944	<i>ca2p13</i>	2	3.8294	0.6390	0.0143	0.0897
<b>GRMZM2G091964</b>	<i>ca2p16</i>	<b>3</b>	<b>4.0559</b>	<b>1.1589</b>	<b>1.03E-05</b>	<b>0.0002</b>
<b>GRMZM2G000686</b>	<i>ca2p11</i>	<b>3</b>	<b>3.0994</b>	<b>0.9387</b>	<b>0.0004</b>	<b>0.0050</b>
GRMZM2G165488	<i>ca2p10</i>	3	0.9833	0.5327	0.0648	0.2668
GRMZM5G829103	<i>ca2p6</i>	3	0.2371	0.3788	0.2201	0.5544
GRMZM5G853836	<i>ca2p5</i>	3	2.9136	-0.2861	0.2784	0.6231
GRMZM2G037630	<i>ca2p3</i>	3.5	2.123	0.2441	0.3661	0.7076
<b>GRMZM2G040349</b>	<i>ca2p4</i>	<b>4</b>	<b>0.9044</b>	<b>0.8296</b>	<b>0.0045</b>	<b>0.0371</b>
GRMZM2G038303	<i>ca2p15</i>	4	0.9956	0.2292	0.4249	0.7537
<b>miR394a-b-5p (PF00646: F-box domain)</b>						
<b>GRMZM2G119650</b>		<b>0</b>	<b>6.9199</b>	<b>0.9476</b>	<b>0.0002</b>	<b>0.0032</b>
<b>GRMZM2G064954</b>		<b>0</b>	<b>5.611</b>	<b>0.7569</b>	<b>0.0033</b>	<b>0.0291</b>
<b>miR397a-b-5p (PF007732, PF00394, PF7731: Multicopper oxidase)</b>						
GRMZM2G072808		<b>0</b>	<b>5.2327</b>	<b>-1.222</b>	<b>2.79E-06</b>	<b>6.48E-05</b>



Gene ID	Locus	mF Score	Log(2) CPM	Log(2) FC	P value	FDR
GRMZM2G305526		4	3.1111	-2.2761	2.62E-16	2.59E-14
GRMZM2G447271		4	3.5578	-1.1218	2.19E-05	0.0004
GRMZM2G146152		4.5	4.7830	-0.9074	0.0005	0.0057
GRMZM2G132169		6	7.0000	-0.2284	0.3717	0.7120
GRMZM2G336337		6	5.4715	-0.0256	0.9206	0.9798
GRMZM2G367668		7	5.3805	-1.5703	2.35E-09	9.90E-08
GRMZM2G388587		7	1.1616	-0.7611	0.0063	0.0479
GRMZM2G094375		7	3.3346	-0.5501	0.0362	0.1773
<b>miR408a-b-3p (PF2298, PF00732: plastocyanin-like domain, multicopper oxidase)</b>						
GRMZM5G866053		2	2.0237	-0.65174	0.0167	0.1013
GRMZM2G004012		2.5	2.0464	0.3490	0.1981	0.5225
GRMZM2G023847		3	6.3529	0.1348	0.5985	0.8558
GRMZM2G352678		3.5	3.9382	-0.7466	0.0042	0.0352
GRMZM2G097851		3.5	5.2463	-0.1514	0.5553	0.8347
GRMZM5G814718		4	3.9293	-0.1072	0.6794	0.8935
GRMZM2G336337		4	5.4715	-0.2557	0.9206	0.9798
GRMZM2G132169		4.5	7.0003	-0.2284	0.3717	0.7120
GRMZM2G076225		5	0.8160	-0.7983	0.0067	0.05037
GRMZM2G043300		5	4.0512	-0.5639	0.0300	0.1555
GRMZM2G053779		5	4.6357	0.1549	0.5479	0.8310
GRMZM2G039381		6	1.8140	-0.3881	0.1566	0.4561
<b>GRMZM2G177934</b>		<b>6.5</b>	<b>0.3775</b>	<b>0.9964</b>	<b>0.0012</b>	<b>0.0130</b>

**Supplemental Table 6:** Primers used in this study.

<b>Primer Name</b>	<b>Sequence</b>
ZmGAPDF-5F	CCTGCTTCTCATGGATGGTT
ZmGAPDF-6R	TGGTAGCAGGAAGGGAAACA
GRMZM2G475882-2F	TGTCGCATCGAAATCTTCAG
GRMZM2G475882-2R	TTGCAGTTCATCGTCGAAAG
GRMZM2G078274-2F	TGTGTTCGCATCAGGATCTTC
GRMZM2G078274-2R	TTGCAGTTCATCGTCGAAAG
GRMZM2G119650-4F	TGACAAGTTCTGCGAAAACG
GRMZM2G119650-4R	ACTCAGCTCTGGGCAGGTAA
GRMZM2G004012-5F	CGTGTAGGCTCAGTCAGTCG
GRMZM2G004012-5R	CGTCAAGCAATTTGTCATGG
GRMZM2G423833-1F	G TTCCTGAGCAGCAGTTTCC
GRMZM2G423833-2R	GCTCATCATCCCAGCAAAGT
GRMZM2G150893-1F	TGATTAATCCACGACGACGA
GRMZM2G150893-1R	CGCTAGTGCACTCTTGCTTG
GRMZM5G832582-2F	TCGTGGAAAGACTGGGATTC
GRMZM5G832582-1R	GTCAGCAAGGCAACTCTTCC
GRMZM2G074238-2F	TCCAGGTCGTCACGTGTAGT
GRMZM2G074238-2R	GCATCCTAGCTACAACGCTAGA
GRMZM2G081158-3F	CAGGCAAGGCAAGAATTGAT
GRMZM2G081158-2R	GAAAGAATCGGCAAAGGTGA
GRMZM2G139688- 2F	CAGGTGCAGCAGCTACCATA
GRMZM2G139688- 2R	TGACAGGGTTGACAAAAACG
GRMZM2G352678-2F	TCGTGTGGCATACTCGTACC
GRMZM2G352678-2R	CCATCAGCCACACGTACATC
GRMZM5G899308-2F	GTCCGGCGTAGTTTCTTGAG
GRMZM5G899308-2R	TGGATTATTGGTTCGGCTTC
GRMZM5G803935-2F	TTGATGATGCTGCATTGGAT
GRMZM5G803935-2R	TAGCAAGCCTGGAAGGAAGA