Table S1. 35 *Mutator* mutant alleles isolated from the UniformMu population in maize. Mutant allele transcriptome data obtained, transcript abundance, and transcriptome assembly predicted transcript structure. UniformMu Mu ID and Stock, Pos: Mu insertion position within the gene, genotyping primers used to isolate the homozygous mutant, and Pedi: pedigree of the mutant stock sampled for RNA-seq (BC = backcross, S = self). RNA-seq CPM and FPKM for mutant and wild type W22, DE data averaged across biological replicates (N), log2fc: log2 fold change of mutant to control, lfcSE: log fold change standard error and FDR adjusted p-value. Transcript assembly transcript structure references categories described in Figure 3A.

						Genotyping Primers		RNA-seq Transcriptome Data			Gene Normalized Read Count						Differential Expression				Transcript Assembly Transcript Structure - Figure 3A	
											Mutant			W22 Control								
TF Name	W22 gid	Mutant Allele	Mu ID	UFMu Stock	Pos.	F_ID	R_ID	Pedi.	Tissue	Illumina	FPKM	CPM	N	FPKM	CPM	N	log2fc	lfcSE	p-value	DE	5' of Mu	3' of Mu
BAF60.21	Zm00004b012791	*baf60.21-m1*	mu1034781	UFMu-03236	5' UTR	BAF60.21-F3	BAF60.21-R3	BC2S2	tassel_stem	PE150	45.60	37.49	3	32.79	26.96	3	0.480	0.114	8.22E-04	Not_DE	NA	Mu TSS
BAF60.21	Zm00004b012791	*baf60.21-m2*	mu1092086	UFMu-11153	CDS	BAF60.21-F3	BAF60.21-R3	BC2S2	tassel_stem	PE150	18.52	15.22	3	32.79	26.96	3	-0.829	0.118	1.16E-09	Not_DE	NA	Mu TSS
BSD10	Zm00004b040474	*bsd10-m2*	mu1072546	UFMu-03453	5' UTR	BSD8-F1	BSD8-R1	S2	imbibed_embryo	PE150	12.62	22.79	3	16.19	29.24	4	-0.438	0.108	4.86E-04	Not_DE	NA	Mu TSS
BZIP76	Zm00004b029476	*bzip76-m2*	mu1083967	UFMu-10010	Intron	bZIP76-F5	bZIP76-R5	BC2S2	imbibed_embryo	PE150	4.31	7.92	3	4.04	7.41	4	0.064	0.217	9.01E-01	Not_DE	NA	Mu TSS
BZIP76	Zm00004b029476	*bzip76-m3*	mu1081677	UFMu-09463	Intron	bZIP76-F6	bZIP76-R6	BC2S2	imbibed_embryo	PE150	2.07	3.80	3	4.04	7.41	4	-0.954	0.237	1.10E-03	Not_DE	NA	gene exon partial
C3H42	Zm00004b024707	*c3h42-m1*	mu1068676	UFMu-08608	Intron	C3H42-F1	C3H42-R1	BC2S2	tassel_stem	PE150	7.20	5.05	3	5.31	3.73	3	0.443	0.173	6.28E-02	Not_DE	gene TSS-Mu	Mu TSS
E2F13	Zm00004b023063	*e2f13-m1*	mu1086360	UFMu-11121	CDS	ump020	ump104	S3	coleoptile_tip	PE150	3.15	5.77	3	4.86	8.90	4	-0.607	0.159	3.62E-03	Not_DE	gene TSS-Mu	Mu TSS
E2F19	Zm00004b000391	*e2f19-m1*	mu1040458	UFMu-04300; UFMu-13849	5' UTR	E2F19-F2	E2F19-R1	BC2S2	seedling_leaf	PE150	2.43	4.13	3	5.43	9.22	4	-1.125	0.217	8.47E-06	DE_Down	NA	gene exon partial
E2F19	Zm00004b000391	*e2f19-m2*	mu1080409	UFMu-09504	5' UTR	E2F19-F2	E2F19-R1	BC2S2	seedling_leaf	PE150	4.01	6.82	3	5.43	9.22	4	-0.471	0.203	1.13E-01	Not_DE	NA	gene exon partial
GRAS52	Zm00004b006535	*gras52-m1*	mu1037818	UFMu-03743	CDS	ump190	ump191	S3	imbibed_embryo	PE150	0.38	0.72	2	6.59	12.33	4	-4.072	0.355	4.83E-28	DE_Down	gene TSS-Mu	gene exon partial
GRAS75	Zm00004b009784	*gras75-m1*	mu1080849	UFMu-09435	CDS	ump173	ump174	S2	imbibed_embryo	PE150	32.49	54.10	3	78.36	130.48	4	-1.266	0.142	4.06E-17	DE_Down	gene TSS-Mu	NA
HSF13	Zm00004b000433	*hsf13-m1*	mu1085337	UFMu-10587	CDS	ump188	ump189	S3	seedling_leaf	PE150	31.24	45.52	3	63.51	92.53	4	-0.989	0.110	4.03E-17	Not_DE	gene TSS-Mu	Mu TSS
HSF18	Zm00004b013608	*hsf18-m1*	mu1086526	UFMu-10749	CDS	ump056	ump139	S3	imbibed_embryo	PE150	5.40	7.69	3	1.98	2.83	4	1.373	0.290	2.90E-05	DE_Up	gene TSS partial	Mu TSS
HSF20	Zm00004b040094	*hsf20-m1*	mu1085720	UFMu-10752	CDS	ump210	ump211	S3	imbibed_embryo	PE150	0.71	0.89	3	0.49	0.61	4	0.514	0.692	6.33E-01	Not_DE	gene TSS-Mu	gene exon partial
HSF24	Zm00004b004268	*hsf24-m3*	mu1065831	UFMu-08727	5' UTR	HSF24-F5	HSF24-R5	BC2S2	tassel	SE50	21.03	51.22	3	16.89	41.15	3	0.045	0.168	8.73E-01	Not_DE	gene TSS-Mu	gene exon partial
HSF24	Zm00004b004268	*hsf24-m4*	mu1037205	UFMu-03655	CDS	HSF24-F5	HSF24-R5	BC2S2	tassel	SE50	8.72	21.24	3	16.89	41.15	3	-1.104	0.172	9.37E-09	DE_Down	NA	gene exon partial
HSF29	Zm00004b013825	*hsf29-m1*	mu1023451	UFMu-02314	5' UTR	ump194	ump195	S3	imbibed_embryo	PE150	17.78	32.75	3	15.11	27.83	4	0.201	0.168	4.41E-01	Not_DE	NA	Mu TSS
HSF29	Zm00004b013825	*hsf29-m2*	mu1083642	UFMu-10398	CDS	ump194	ump195	S3	imbibed_embryo	PE150	15.17	27.94	3	15.11	27.83	4	-0.025	0.169	9.36E-01	Not_DE	NA	gene exon partial
HSF6	Zm00004b013941	*hsf6-m1*	mu1048425	UFMu-06347	CDS	ump067	ump149	S3	imbibed_embryo	PE150	0.02	0.04	3	0.20	0.48	4	-3.748	1.245	1.58E-02	DE_Down	NA	NA
HSF6	Zm00004b013941	*hsf6-m2*	mu1056797	UFMu-07611	CDS	ump068	ump150	S2	imbibed_embryo	PE150	0.14	0.34	3	0.20	0.48	4	-0.479	0.772	7.28E-01	Not_DE	NA	NA
JMJ13	Zm00004b023587	*jmj13-m4*	mu1081210	UFMu-09466	CDS	JMJ13-F7	JMJ13-R7	BC2S2	tassel_stem	PE150	4.24	8.90	3	6.73	14.14	3	-0.669	0.133	1.13E-04	Not_DE	gene TSS-Mu	Mu TSS
JMJ13	Zm00004b023587	*jmj13-m7*	mu1041192	UFMu-04767	5' UTR	JMJ13-F9	JMJ13m7-R9	BC2S2	tassel_stem	PE150	7.54	15.85	3	6.73	14.14	3	0.162	0.128	6.00E-01	Not_DE	NA	Mu TSS
MYB40	Zm00004b016719	*myb40-m1*	mu1090929	UFMu-11189	Intron	MYB40-F1	MYB40-R3	BC2S2	coleoptile_tip	PE150	7.95	13.17	3	6.98	11.57	4	0.184	0.147	8.98E-01	Not_DE	gene TSS-Mu	Mu TSS
MYB40	Zm00004b016719	*myb40-m2*	mu1043293	UFMu-04991	Intron	MYB40-F2	MYB40-R2	BC2S2	coleoptile_tip	PE150	5.29	8.76	3	6.98	11.57	4	-0.372	0.151	3.42E-01	Not_DE	NA	gene exon partial
MYBR21	Zm00004b024904	*mybr21-m1*	mu1042351	UFMu-04838	CDS	ump060	ump143	S3	imbibed_embryo	PE150	4.56	14.29	3	19.42	60.91	4	-2.075	0.129	1.64E-55	DE_Down	gene TSS-Mu	gene exon partial
MYBR32	Zm00004b002134	*mybr32-m1*	mu1076168	UFMu-09083	CDS	ump042	ump125	S2	seedling_leaf	PE150	37.42	61.19	3	86.66	141.69	4	-1.187	0.083	2.06E-43	DE_Down	gene TSS-Mu	Mu TSS
ORPHAN249	Zm00004b031116	*orphan249-m2*	mu1029949	UFMu-02921; UFMu-06508	5' UTR	Orph249-F9	Orph249-R9	BC1S2	imbibed_embryo	PE150	7.71	17.17	3	6.23	13.86	4	0.298	0.239	4.11E-01	Not_DE	NA	Mu TSS
SBP20	Zm00004b024383	*sbp20-m2*	mu1086430	UFMu-10892	CDS	ump083	ump165	S3	imbibed_embryo	PE150	3.55	9.39	3	5.31	14.03	4	-0.620	0.160	8.08E-04	Not_DE	gene TSS-Mu	Mu TSS
SBP20	Zm00004b024383	*sbp20-m3*	mu1091327	UFMu-11256	CDS	ump084	ump166	S2	imbibed_embryo	PE150	5.63	14.90	3	5.31	14.03	4	0.065	0.160	8.24E-01	Not_DE	gene TSS-Mu	Mu TSS
WRKY2	Zm00004b013450	*wrky2-m2*	mu1025953	UFMu-11813	CDS	ump065	ump147	S3	coleoptile_tip	PE150	1.23	2.21	3	1.28	2.29	4	-0.059	0.258	9.86E-01	Not_DE	gene TSS partial	Mu TSS
WRKY8	Zm00004b023980	*wrky8-m1*	mu1048159	UFMu-06456	CDS	ump200	ump201	S3	imbibed_embryo	PE150	10.99	19.28	3	4.08	7.15	4	1.452	0.295	2.40E-05	DE_Up	gene TSS-Mu	Mu TSS
WRKY8	Zm00004b023980	*wrky8-m2*	mu1077370	UFMu-08953	CDS	ump080	ump163	S3	imbibed_embryo	PE150	3.07	5.38	3	4.08	7.15	4	-0.330	0.301	5.12E-01	Not_DE	gene TSS-Mu	Mu TSS
WRKY82	Zm00004b031112	*wrky82-m1*	mu1081611	UFMu-09469	CDS	ump018	ump102	S3	imbibed_embryo	PE150	4.40	7.19	3	21.01	34.36	4	-2.297	0.262	8.04E-17	DE_Down	gene TSS-Mu	NA
WRKY87	Zm00004b023521	*wrky87-m1*	mu1067257	UFMu-08437	CDS	ump059	ump142	S3	imbibed_embryo	PE150	3.39	8.83	3	2.30	5.99	4	0.535	0.252	1.07E-01	Not_DE	gene TSS-Mu	Mu TSS
WRKY87	Zm00004b023521	*wrky87-m2*	mu1091217	UFMu-12044	CDS	ump058	ump141	S3	imbibed_embryo	PE150	3.40	8.84	3	2.30	5.99	4	0.571	0.252	7.39E-02	Not_DE	gene TSS-Mu	Mu TSS

Table S2. Gene expression values for 24 transcription factor genes in different tissues. The expression value (CPM) for each of the 22 TFs was assessed based on prior sampling of tissues or developmental stages in B73 (Zhou et al. 2019). Values highlighted indicate the predicted expression level of TF genes in tissues sampled for RNA-seq in this study.

			24 h		6 DAS		seedling 11 DAS				v12			v14			0 DAP					14 DAP		27 DAP
TF	B73v4_gid	RNAseq Tissue	imbibed embryo	coleoptile tip	radicle root	leaf	root	meristem	blade leaf	sheath	internode	tassel	auricle	ear	silk	spikelet	husk	tassel stem	floret	flag leaf	root	kernel	endosperm	embryo	endosperm
WRKY2	Zm00001d016052	coleoptile_tip	3.0	11.9	6.2	1.4	3.7	6.2	0.6	0.9	1.7	2.5	1.2	1.5	1.4	2.1	1.3	2.6	0.9	1.2	0.3	3.1	2.4	3.9	1.3
MYB40	Zm00001d040621	coleoptile_tip	4.9	45.7	21.2	7.9	1.6	19.1	5.7	4.1	0.8	14.1	12.8	10.4	6.8	9.8	4.0	1.3	8.5	59.8	2.0	22.3	23.9	5.5	26.2
E2F13	Zm00001d052288	coleoptile_tip	0.1	20.7	9.6	0.0	6.1	34.2	0.0	0.0	0.0	5.9	0.0	34.8	0.1	2.9	0.1	0.1	0.1	0.1	2.3	1.1	0.5	6.5	0.0
GRAS52	Zm00001d002573	imbibed_embryo	114.8	5.2	5.4	23.7	13.7	10.5	9.0	17.9	16.2	12.3	20.5	9.7	3.9	12.9	13.8	28.8	12.4	23.6	10.5	8.6	11.8	5.0	48.5
GRAS75	Zm00001d006701	imbibed_embryo	163.0	32.4	21.9	17.7	7.3	14.8	32.9	27.0	9.6	7.3	18.2	18.3	12.5	16.4	16.1	61.0	19.8	71.3	4.4	47.6	62.1	20.8	58.2
MYBR21	Zm00001d008602	imbibed_embryo	183.3	16.9	28.7	66.4	101.0	20.6	28.1	42.5	55.7	15.2	31.5	23.5	29.4	27.3	31.0	71.9	35.7	40.9	26.3	21.1	20.6	4.8	29.7
HSF18	Zm00001d016255	imbibed_embryo	74.2	10.2	2.5	22.0	34.7	7.0	0.8	5.4	6.1	0.2	3.8	0.1	0.7	0.3	0.2	0.4	0.5	1.3	63.7	2.3	4.4	8.4	7.3
HSF29	Zm00001d016520	imbibed_embryo	15.1	15.2	15.7	15.1	20.9	11.3	23.2	26.5	40.2	22.3	25.8	13.2	30.2	24.5	32.1	29.1	17.7	13.2	21.1	14.5	8.2	14.1	9.8
HSF6	Zm00001d016674	imbibed_embryo	175.7	0.8	5.3	1.7	1.1	0.5	32.4	21.3	10.3	5.3	11.7	4.7	11.0	6.2	7.9	16.8	7.8	45.0	12.0	3.9	2.4	16.1	3.0
HSF20	Zm00001d026094	imbibed_embryo	14.0	1.1	0.4	15.7	7.7	9.7	28.2	11.9	9.6	9.0	13.6	4.7	4.8	5.3	4.7	4.0	5.6	23.4	2.4	4.3	12.4	3.0	10.0
WRKY82	Zm00001d038843	imbibed_embryo	43.5	7.0	15.8	31.0	16.6	1.5	7.7	12.3	18.3	1.5	11.9	0.5	1.4	2.7	8.9	14.3	5.3	10.8	43.6	4.1	0.1	0.2	0.6
WRKY87	Zm00001d052847	imbibed_embryo	40.1	0.4	0.1	12.0	0.5	0.3	9.5	2.0	0.4	0.2	1.4	0.3	0.0	0.1	1.6	1.1	1.6	14.1	0.2	0.3	0.1	0.6	0.1
WRKY8	Zm00001d053369	imbibed_embryo	6.2	3.9	3.1	0.9	4.7	4.6	0.9	2.3	2.6	1.9	3.4	2.6	2.6	1.7	1.6	3.1	1.2	2.7	1.1	1.3	1.0	4.7	0.6
SBP20	Zm00001d053890	imbibed_embryo	37.5	11.8	13.5	5.3	11.0	23.5	1.4	10.4	18.7	16.9	7.5	11.8	2.2	8.5	4.8	17.0	7.9	1.7	37.3	3.7	2.3	6.1	0.8
BZIP76	Zm00001d036736	imbibed_embryo	10.8	2.7	5.2	13.0	2.6	2.0	2.3	1.5	6.7	2.9	0.6	3.1	13.8	5.0	1.4	7.0	4.3	5.3	5.8	2.9	2.2	1.4	1.6
BSD10	Zm00001d026518	imbibed_embryo	19.0	8.3	8.7	8.3	10.2	8.5	12.7	13.5	8.8	11.4	11.8	13.9	12.6	15.0	10.8	8.7	8.4	6.2	10.9	11.3	14.5	15.4	17.2
ORPHAN249	Zm00001d038846	imbibed_embryo	57.0	7.5	26.6	34.5	30.0	7.8	28.6	38.1	24.7	14.3	30.8	20.4	28.2	27.0	14.7	31.3	22.9	61.5	38.9	8.5	2.8	4.4	1.9
E2F19	Zm00001d027709	seedling_leaf	15.8	9.7	10.3	17.0	9.9	15.8	13.5	13.5	11.7	12.6	11.0	23.1	14.6	14.6	10.0	15.2	8.8	22.0	11.4	14.7	14.1	13.0	19.9
HSF13	Zm00001d027757	seedling_leaf	12.4	2.6	5.2	454.1	11.4	1.7	418.9	374.1	9.7	1.1	111.3	1.6	21.2	1.2	99.3	73.6	46.1	650.7	11.2	1.0	0.0	0.2	0.3
MYBR32	Zm00001d029963	seedling_leaf	25.4	22.4	40.5	299.6	136.9	29.4	35.4	158.2	486.2	25.6	189.4	71.8	208.4	55.4	199.4	233.8	114.5	89.7	263.6	20.6	3.1	37.4	5.3
HSF24	Zm00001d032923	tassel	61.0	32.3	39.4	76.4	52.7	120.3	457.3	250.3	292.2	96.7	188.4	80.7	82.7	100.1	73.7	109.6	89.0	400.1	155.9	167.1	208.2	265.2	121.1
C3H42	Zm00001d008356	tassel_stem	3.9	7.4	10.4	2.2	4.6	9.5	3.5	5.2	27.3	7.5	3.9	6.9	8.2	7.2	6.7	9.6	2.8	4.7	7.8	9.1	11.2	4.9	6.5
BAF60.21	Zm00001d015127	tassel_stem	14.6	22.8	20.9	4.2	12.8	40.2	14.1	14.7	8.2	11.7	14.1	19.8	14.1	10.8	13.3	16.3	11.3	24.1	14.9	7.5	6.1	16.7	3.9
JMJ13	Zm00001d052933	tassel_stem	27.5	19.5	14.9	0.9	11.5	21.1	6.1	8.2	6.9	7.0	7.0	18.3	10.7	11.4	6.6	6.8	6.5	7.8	8.1	20.1	23.5	13.9	16.0

Table S3. Mutant allele *Mu* element identity and orientation by gDNA PCR. Table follows the format of Figure S2 with primer sets not tested—gray, and tested primer sets resulting in amplification—blue, no amplification—pink.

		Forward				Reverse				
		F : Mu 5'		Mu 3' : R		F : Mu 3'		Mu 5' : R		
Allele	***Mu***	**F**	**Mu 5'**	**Mu 3'**	**R**	**F**	**Mu 3'**	**Mu 5'**	**R**	**Orientation**
sbp20-m2	*Mu3*	gsp01	qrp28	qrp21	gsp02					**F**
wrky87-m2	*Mu3*	gsp03	qrp28	qrp21	gsp04					**F**
sbp20-m3	*Mu7*	qrp11	qrp36	qrp62	qrp12					**F**
jmj13-m4	*Mu7*	gsp08	qrp36	qrp62	gsp07					**F**
wrky87-m1	*Mu7*	qrp05	qrp36	qrp62	gsp06					**F**
wrky8-m1	*Mu1.7*	gsp09	qrp41	qrp43	gsp10					**F**
hsf13-m1	*Mu1.7*	qrp41	gsp11	mtp02	gsp12	qrp43	gsp11	qrp41	gsp12	**F**
e2f13-m1	*Mu8*	ump220	mtp10					ump221	mtp10	**F**
hsf18-m1	*Mu8*	ump139	mtp10					ump056	mtp10	**R**
mybr32-m1	*Mu8*	ump042	mtp10					ump125	mtp10	**R**
wrky2-m2	*Mu7*			ump065	qrp63	ump147	qrp63			**F**
wrky8-m2	*Mu8*	ump080	mtp10					ump163	mtp10	**R**
baf60.21-m1	*Mu1.7*	BAF60.21-F3	qrp41					qrp41	BAF60.21-R3	**R**
baf60.21-m2	*Mu1.7*	BAF60.21-F3	qrp41					qrp41	BAF60.21-R3	**F**
jmj13-m7	*Mu1.7*	JMJ13-F9	qrp41					qrp41	JMJ13-m7R9	**F**
myb40-m1	*Mu7*			qrp62	MYB40-R3	MYB40-F1	qrp62			**F**
orphan249-m2	*Mu8*	Orphan249-R9	mtp10					mtp10	Orphan249-F9	**F**
c3h42-m1	*Mu1.7*	C3H42-R1	qrp41	mtp01	C3H42-F1	C3H42-R1	mtp01	qrp41	C3H42-F1	**F**
bsd10-m2	*Mu1*			mtp01	BSD8-R1	BSD8-F1	mtp01			**R**

Table S4. Mutant allele transcript boundaries and potential for *Mu* read-through tested by RT-PCR. Transcript boundaries of gene promoter-*Mu* and *Mu* promoter transcripts: Table follows format of Figure 5B with *Mu*-specific primers listed above the *Mu* sequence amplified (bp) and the gene-specific primer used for each allele in the corresponding row. Tan; RT-PCR amplification, Pink; absence of RT-PCR amplification and the region where the transcript terminates, Black; absence of RT-PCR amplification. Some *Mu*-specific primers used have specificity to both 5' and 3' *Mu* TIRs. The three alleles tested with gene-specific primers flanking *Mu* are included (Figure 2C).

gene TSS-*Mu*

Allele	*Mu*	gene primer	*Mu* primer 1	2	3	4	5	6	7
wrky8-m1	*Mu1.7*	gsp09	qrp44.2 109	qrp40 208	qrp41 252	qrp80 336			
sbp20-m2	*Mu3*	gsp01	qrp25 135	qrp27-rc 168	qrp28 215	qrp68 456	qrp69 565	qrp70 734	qrp61 883
wrky87-m2	*Mu3*	gsp03	qrp25 135	qrp27-rc 168	qrp28 215	qrp68 456	qrp69 565	qrp70 734	qrp61 883
jmj13-m4	*Mu7*	gsp08	qrp34 108	qrp64 322	qrp65 428	qrp66 528	qrp74 663		
sbp20-m3	*Mu7*	qrp11	qrp33 51	qrp34 108	qrp64 322	qrp66 528	qrp74 663	qrp75 779	
wrky87-m1	*Mu7*	gsp05	qrp37 34	qrp33 51	qrp34 108	qrp64 322	qrp65 428	qrp36 462	qrp66 528

***Mu* TSS**

gene primer	*Mu* primer 8	7	6	5	4	3	2	1
gsp10		qrp83 775	qrp82 623	mtp01 393	qrp40 250	qrp44.2 118	qrp42 59	qrp43 31
gsp02		qrp73 941	qrp72 790	qrp71 663	qrp24 543	qrp23 473	qrp22 396	qrp21 323
gsp04			qrp73 941	qrp71 663	qrp24 543	qrp23 473	qrp22 396	qrp21 323
gsp07	qrp79 722	qrp78 580	qrp77 470	qrp63 343	qrp62 261	qrp32 171	qrp31 122	qrp30 79
qrp12			qrp63 343	qrp62 261	qrp32 171	qrp31 122	qrp30 79	qrp29 39
gsp06		qrp77 470	qrp63 343	qrp62 261	qrp32 171	qrp31 122	qrp30 79	qrp29 39

Table S5. Transcript abundance for shared exon sequence between mutant and wild type transcripts. Counts per million (CPM) per fragment calculated for each mutant allele transcript, gene promoter partial or *Mu* promoter, and the corresponding wild type W22 transcript(s) is shown—see Methods for calculation and normalization. The distance in bp of the *Mu* insertion from the annotated W22 TSS is listed: bp_TSS. Gene promoter refers to gene promoter partial or gene promoter-Mu transcripts.

		CPM/Fragment			
		Gene TSS		*Mu* TSS	
Allele	**bp_TSS**	**Mutant**	**W22**	**Mutant**	**W22**
baf60.21-m1	137	NA	NA	64.94	44.19
baf60.21-m2	238	NA	NA	19.70	28.83
bsd10-m2	95	NA	NA	14.35	11.79
e2f13-m1	655	2.20	4.30	6.86	10.77
gras52-m1	293	0.08	1.67	NA	NA
gras75-m1	1362	52.18	110.59	NA	NA
hsf13-m1	869	22.02	35.97	3.50	33.13
hsf18-m1	476	3.58	1.38	6.29	2.48
hsf20-m1	414	0.51	0.32	NA	NA
hsf29-m1	1	NA	NA	35.18	30.54
jmj13-m4	616	3.01	4.39	5.67	11.11
jmj13-m7	51	NA	NA	16.41	14.77
myb40-m1	527	2.63	3.56	12.69	10.77
mybr21-m1	939	13.08	38.45	NA	NA
mybr32-m1	827	83.77	187.83	13.92	39.68
orphan249-m2	400	NA	NA	12.14	8.86
sbp20-m2	891	5.32	7.33	12.52	19.57
sbp20-m3	1267	11.26	11.66	15.70	15.23
wrky2-m2	745	0.54	0.86	1.83	1.76
wrky8-m1	422	5.54	3.08	25.05	7.58
wrky8-m2	822	4.08	6.35	3.23	3.69
wrky82-m1	882	8.94	43.58	NA	NA
wrky87-m1	1380	7.44	4.74	2.65	2.41
wrky87-m2	1778	5.65	3.80	5.94	4.07

Table S6. Tissue-specific expression patterns for mutant and wild type W22 transcripts tested by RT-qPCR. The average delta Ct +/- standard deviation for biological replicates of each mutant allele and W22 transcript in the 6 tissues tested: coleoptile tip, root, shoot, flag leaf, ear spikelet and tassel stem. RT-qPCR primers used are listed: F_ID and R_ID.

Allele	Treatment	Transcript	F_ID	R_ID	coleoptile_tip	root	shoot	flag_leaf	spikelet	tassel_stem
baf60.21-m1	mutant	Mu TSS	qrp51	qrp52	-2.99 ± 0.27	-3.5 ± 0.68	-2.46 ± 0.2	-1.57 ± 0.25	-4.19 ± 0.12	-3.69 ± 0.45
baf60.21-m1	W22	Mu TSS	qrp51	qrp52	-2 ± 0.22	-1.64 ± 0.32	-0.63 ± 0.26	-0.76 ± 0.34	-1.91 ± 0.39	-1.86 ± 0.08
baf60.21-m2	mutant	Mu TSS	qrp51	qrp52	-2.84 ± 0.31	-2.42 ± 0.24	-2.54 ± 0.52	-0.92 ± 0.37	-2.12 ± 0.47	-2.69 ± 0.48
baf60.21-m2	W22	Mu TSS	qrp51	qrp52	-2 ± 0.22	-1.64 ± 0.32	-0.63 ± 0.26	-0.76 ± 0.34	-1.91 ± 0.39	-1.86 ± 0.08
jmj13-m4	mutant	gene TSS	qrp01	qrp02	4.94 ± 0.17	5.74 ± 0.38	7.24 ± 0.36	6.72 ± 0.71	4.82 ± 1.37	5.04 ± 0.56
jmj13-m4	W22	gene TSS	qrp01	qrp02	3.76 ± 0.6	3.67 ± 0.77	6.43 ± 0.28	5.94 ± 0.16	3.48 ± 0.39	4.93 ± 0.11
jmj13-m4	mutant	Mu TSS	qrp03	qrp04	4.18 ± 0.16	4.33 ± 0.04	4.7 ± 0.24	4.98 ± 0.43	3.93 ± 1.1	3.8 ± 0.38
jmj13-m4	W22	Mu TSS	qrp03	qrp04	0.93 ± 0.14	1 ± 0.43	2.49 ± 0.42	2.84 ± 0.21	0.98 ± 0.48	1.85 ± 0.11
jmj13-m7	mutant	Mu TSS	qrp03	qrp04	1.34 ± 0.3	1.53 ± 0.25	1.67 ± 0.27	2.89 ± 0.38	1.73 ± 0.11	1.29 ± 0.42
jmj13-m7	W22	Mu TSS	qrp03	qrp04	0.93 ± 0.14	1 ± 0.43	2.49 ± 0.42	2.84 ± 0.34	0.8 ± 0.38	2.14 ± 0.22
sbp20-m2	mutant	gene TSS	qrp09	qrp10	0.62 ± 0.33	1.16 ± 0.37	1.93 ± 0.47	8.07 ± 0.09	1.61 ± 0.39	0.98 ± 0.54
sbp20-m2	W22	gene TSS	qrp09	qrp10	0.31 ± 0.56	0.76 ± 0.23	2.68 ± 0.23	7.1 ± 0.26	1.53 ± 0.26	0.51 ± 0.22
sbp20-m2	mutant	Mu TSS	qrp15	qrp16	1.51 ± 0.22	1.72 ± 0.23	2.78 ± 0.33	5.81 ± 0.12	1.56 ± 0.42	0.44 ± 0.15
sbp20-m2	W22	Mu TSS	qrp15	qrp16	-0.25 ± 0.22	0.23 ± 0.23	2.18 ± 0.28	6.23 ± 0.24	1.4 ± 0.35	0.02 ± 0.18
sbp20-m3	mutant	gene TSS	qrp13	qrp14	-0.5 ± 0.19	-0.27 ± 0.39	1.38 ± 0.24	6.1 ± 0.34	1.49 ± 0.28	0.38 ± 0.58
sbp20-m3	W22	gene TSS	qrp13	qrp14	-0.65 ± 0.14	-0.34 ± 0.12	1.59 ± 0.27	6.43 ± 0.56	1.56 ± 0.59	0.64 ± 0.05
sbp20-m3	mutant	Mu TSS	qrp15	qrp16	0.15 ± 0.13	0.8 ± 0.15	2.54 ± 0.11	6.21 ± 0.2	1.54 ± 0.17	-0.03 ± 0.08
sbp20-m3	W22	Mu TSS	qrp15	qrp16	-0.25 ± 0.22	0.23 ± 0.23	2.18 ± 0.28	6.23 ± 0.24	1.4 ± 0.35	0.02 ± 0.18
wrky8-m1	mutant	gene TSS	qrp53	qrp54	2.79 ± 0.45	1.71 ± 0.18	4.83 ± 0.28	6.6 ± 0.74	4.8 ± 0.85	4.61 ± 0.31
wrky8-m1	W22	gene TSS	qrp53	qrp54	3.28 ± 0.57	1.28 ± 0.28	5.12 ± 0.13	7.61 ± 0.47	4.55 ± 0.42	5.58 ± 0.21
wrky8-m1	mutant	Mu TSS	qrp55	qrp56	4.65 ± 0.63	3.26 ± 0.22	6.48 ± 0.4	7.2 ± 0.77	5.74 ± 0.15	6.04 ± 0.09
wrky8-m1	W22	Mu TSS	qrp55	qrp56	5.74 ± 0.5	4 ± 0.64	6.93 ± 0.58	9.47 ± 0.2	6.41 ± 0.67	8.14 ± 0.76
wrky8-m2	mutant	gene TSS	qrp59	qrp60	4.89 ± 0.43	4.11 ± 0.52	7.37 ± 0.21	9.95 ± 0.19	9.76 ± 1.28	8.2 ± 1.42
wrky8-m2	W22	gene TSS	qrp59	qrp60	5.5 ± 0.62	3.64 ± 0.47	7.47 ± 0.33	9.27 ± 0.43	6.61 ± 0.39	7.82 ± 0.38
wrky8-m2	mutant	Mu TSS	qrp57	qrp58	6.17 ± 0.14	4.83 ± 0.29	8.17 ± 0.47	10.02 ± 0.69	8.23 ± 0.75	7.55 ± 0.64
wrky8-m2	W22	Mu TSS	qrp57	qrp58	6.76 ± 0.38	5.06 ± 0.46	8.64 ± 0.54	10.79 ± 0.6	8.74 ± 0.68	9.24 ± 1.32
wrky87-m1	mutant	gene TSS	qrp45	qrp46	4.88 ± 0.5	6.13 ± 0.35	2.15 ± 0.29	3.16 ± 0.63	7.47 ± 0.78	4.94 ± 1.02
wrky87-m1	W22	gene TSS	qrp45	qrp46	3.12 ± 0.91	5.09 ± 0.25	2.31 ± 0.27	2.65 ± 0.15	6.06 ± 0.88	4.69 ± 0.71
wrky87-m1	mutant	Mu TSS	qrp17	qrp18	3.58 ± 0.48	7.19 ± 0.1	2.58 ± 0.19	6.66 ± 0.07	6.79 ± 0.9	6.2 ± 0.56
wrky87-m1	W22	Mu TSS	qrp17	qrp18	1.93 ± 0.43	5.72 ± 0.29	2.26 ± 0.14	5.09 ± 0.27	4.7 ± 0.6	6.25 ± 0.16
wrky87-m2	mutant	gene TSS	qrp49	qrp50	6.72 ± 0.31	6.53 ± 0.34	3.43 ± 0.12	5.58 ± 0.6	7.85 ± 1.48	6.97 ± 1.27
wrky87-m2	W22	gene TSS	qrp49	qrp50	4.74 ± 0.76	5.12 ± 0.13	2.25 ± 0.13	2.59 ± 0.15	6.25 ± 0.65	4.43 ± 0.62
wrky87-m2	mutant	Mu TSS	qrp17	qrp18	3.04 ± 0.11	6.52 ± 0.25	2.98 ± 0.26	7.51 ± 0.26	6.49 ± 0.51	6.86 ± 0.65
wrky87-m2	W22	Mu TSS	qrp17	qrp18	1.93 ± 0.43	5.72 ± 0.29	2.26 ± 0.14	5.09 ± 0.27	4.7 ± 0.6	6.25 ± 0.16