Supplementary Table 1. The genomic location, statistical significance, allele frequency, and implicated genes of the identified TASs underlying five maize quantitative traits from the merged SNP dataset.

Trait	Ch	Position	-log$_{10}P$	-log$_{10}Q$	R^2	Freq[a]	Effect[b]	Gene	Annotation
Length	1	7,353,770	8.7	5.6	0.0087	0.04	12.12	GRMZM2G059428	No apical meristem protein
	1	15,122,404	4.6	1.5	0.0046	0.02	-16.17	-	-
	1	30,809,304	5.6	2.2	0.0053	0.16	-6.62	GRMZM2G072292	Expressed protein
	1	52,242,177	12.1	8.8	0.0133	0.29	6.69	GRMZM2G174896	Protein kinase
	1	85,130,587	20.7	17.9	0.0233	0.36	7.39	-	-
	1	244,100,533	23.7	21	0.0269	0.11	-13.68	GRMZM2G145458	ZIM domain
	1	283,982,913	7.6	4.9	0.0088	0.06	9.74	GRMZM2G361220	Clathrin adaptor complex small chain domain
	2	2,618,178	8.9	6.1	0.0106	0.04	-13.09	GRMZM2G065012	Expressed protein
	2	13,245,188	16.8	13.7	0.0185	0.37	-6.12	-	-
	2	59,584,754	21	17.4	0.0239	0.07	14.36	GRMZM2G134235	Expressed protein
	2	210,128,410	10	7.4	0.0103	0.41	4.35	-	-
	2	229,511,399	8.1	4.6	0.0074	0.30	-4.33	GRMZM2G444533	F-box and FBD domain
	3	8,019,525	7.7	5.5	0.0082	0.02	22.64	-	-
	3	22,034,011	10.9	7.1	0.0113	0.19	-7.87	GRMZM2G129777	AP2 domain
	3	177,565,419	5.8	2.3	0.0055	0.16	5.01	-	-
	3	212,248,700	46.8	43.4	0.0496	0.42	8.96	GRMZM2G047129	GDSL-like lipase
	4	3,248,688	21.7	18.5	0.0253	0.38	6.58	GRMZM2G097981	Tropinone reductase
	4	151,524,406	9.6	6.3	0.0096	0.06	-10.11	GRMZM2G323719	Amino acid kinase
	4	197,993,592	10.5	7.3	0.0114	0.05	-10.82	-	-
	5	3,062,680	12	9.1	0.0132	0.28	-5.50	GRMZM2G096165	Ribosomal protein
	5	74,510,491	17.8	14.8	0.0192	0.16	-11.19	-	-
	5	202,073,473	23.9	21.1	0.0261	0.45	-6.00	-	-
	6	23,864,967	7.4	5	0.0076	0.02	-15.71	GRMZM2G459581	MAP kinase phosphatase
	6	105,119,528	7.4	4	0.0074	0.07	8.85	GRMZM2G331283	Amino acid transporter
	6	152,684,138	8	4.3	0.0085	0.28	-4.46	GRMZM2G069737	F-box domain
	7	17,118,117	6.8	2.7	0.0073	0.10	-7.25	-	-
	7	150,990,249	6.5	3.6	0.0071	0.11	-7.05	-	-
	7	161,864,686	10.5	6.5	0.0122	0.26	5.69	-	-
	8	5,776,641	7.5	4.5	0.0073	0.04	-10.98	GRMZM2G155260	Protein kinase
	8	121,054,240	18.2	15.1	0.0209	0.14	-10.86	-	-
	8	164,043,117	6.7	3.6	0.0074	0.08	8.08	-	-
	9	13,032,982	10.5	7.5	0.0112	0.22	5.89	-	-
	9	104,339,779	12	8.6	0.0127	0.15	9.09	-	-
	9	131,683,423	24.5	21.8	0.0288	0.31	9.17	-	-
	10	13,610,740	6.7	4.2	0.0056	0.08	-6.73	GRMZM2G125931	Expressed protein
	10	132,894,369	13.5	10.4	0.0145	0.12	-10.71	GRMZM2G425072	Auxin-responsive SAUR gene
	10	148,546,034	9.8	6.6	0.0108	0.21	-5.31	GRMZM2G039011	Expressed protein
Width	1	21,725,298	32.4	29.7	0.0125	0.19	1.33	-	-
	1	23,250,177	30.4	27.2	0.0016	0.36	0.40	-	-
	1	55,604,358	10.6	7.8	0.0112	0.29	0.85	GRMZM2G075262	Expressed protein
	1	160,331,991	6.9	3.6	0.0070	0.04	2.05	-	-
	1	210,399,194	5.1	2.1	0.0055	0.04	-1.44	-	-
	1	277,518,310	16.2	12.9	0.0172	0.18	1.45	GRMZM2G330218	Expressed protein
	1	298,083,583	7	3.9	0.0078	0.17	-0.81	GRMZM2G417843	4-nitrophenylphosphatas

	2	10,679,395	7.7	4.8	0.0080	0.10	-0.98	-	-
	2	57,602,831	106.1	104.1	0.1153	0.44	1.90	AC191050.3_FG003	Globulin-1 S allele
	2	124,883,226	106.7	104.3	0.1161	0.42	1.95	-	-
	2	214,076,426	12.3	9.4	0.0131	0.37	0.64	GRMZM2G030646	Eukaryotic translation initiation factor 2
	3	5,633,931	6.7	3.3	0.0077	0.04	-1.68	-	-
	3	31,698,831	34.3	30.6	0.0376	0.39	1.26	GRMZM2G049672	Zinc finger, C3HC4 type
	3	163,889,745	24.8	21.7	0.0273	0.29	-1.30	-	-
	3	194,352,239	10.2	7.4	0.0107	0.21	-0.90	-	-
	3	204,956,307	11.5	7.7	0.0013	0.07	-0.62	-	-
	4	156,002,632	12.9	9.1	0.0134	0.11	-1.31	-	-
	4	201,525,973	11.2	9	0.0125	0.13	-1.06	GRMZM2G163709	Phospholipase C
	5	6,130,146	26.7	23.6	0.0291	0.36	-1.01	GRMZM2G171468	MYB transcription factor
	5	31,528,232	69.6	64.5	0.0776	0.48	-1.56	GRMZM2G337048	UDP-glucosyl transferase
	5	185,911,974	5.1	1.6	0.0055	0.08	-0.97	-	-
	5	213,362,996	12	8.6	0.0139	0.09	1.35	GRMZM2G083812	Heparanase-like
	6	119,603,988	25.7	23.6	0.0283	0.27	-1.39	GRMZM2G075710	Embryogenesis transmembrane protein
	6	147,218,755	19.1	16.3	0.0209	0.34	-1.17	-	-
	6	157,675,994	7.2	3.6	0.0069	0.11	1.08	-	-
	6	165,339,108	9	6.2	0.0088	0.35	-0.62	-	-
	7	3,576,083	13.8	10	0.0159	0.06	1.72	-	-
	7	121,502,283	10.7	6.8	0.0109	0.25	0.74	GRMZM2G072218	Serine Carboxypeptidase
	7	165,920,367	11.5	8.3	0.0133	0.18	0.88	GRMZM2G137064	PPR repeat domain
	8	22,860,690	9.8	6.6	0.0100	0.21	-0.88	-	-
	8	121,052,910	13	10.1	0.0147	0.17	1.24	-	-
	8	167,519,904	7.9	4.4	0.0083	0.17	-0.78	-	-
	9	121,382,512	32.8	30.2	0.0359	0.28	1.31	GRMZM2G131221	Expressed protein
	10	124,313,332	11.9	10	0.0124	0.02	2.65	-	-
	10	124,863,499	12.1	10.2	0.0125	0.02	2.66	-	-
	10	147,266,926	18.9	15.7	0.0214	0.40	-0.80	GRMZM2G475882	Auxin response factor
Angle	1	30,342,426	29.7	26.7	0.0315	0.47	-0.83	-	-
	1	251,379,569	20.1	16.5	0.0208	0.38	0.82	GRMZM2G014392	9-cis-epoxycarotenoid dioxygenase
	1	281,810,922	6.4	3.1	0.0064	0.18	-0.62	GRMZM2G068158	Methyltransferase
	2	4,156,772	42.9	40.1	0.0452	0.42	-1.11	GRMZM2G039532	Expressed protein
	2	14,696,322	13.5	10.2	0.0130	0.31	0.68	-	-
	2	49,478,060	7.1	4.1	0.0067	0.02	-1.73	-	-
	2	209,607,885	5.2	2.2	0.0049	0.18	0.49	GRMZM2G064630	MYB transcription factor
	3	31,703,959	20.6	17	0.0213	0.42	0.82	-	-
	3	158,616,899	22.9	20.6	0.0237	0.06	-2.49	-	-
	3	175,048,356	51.8	49.4	0.0557	0.36	-1.60	GRMZM2G060216	Liguleless 2
	3	202,365,265	5.2	1.9	0.0040	0.10	0.62	-	-
	4	129,385,200	21.3	18.2	0.0217	0.13	-1.30	GRMZM2G104118	Glycosyl transferase
	4	180,859,297	5.3	1.9	0.0055	0.04	1.20	-	-
	4	242,646,294	8.5	5.4	0.0082	0.08	1.00	GRMZM2G012143	SETH3-like
	5	3,193,230	13.1	9.9	0.0137	0.23	-0.75	-	-
	5	33,281,655	61.1	59.4	0.0643	0.15	-2.22	GRMZM2G075150	Exocyst complex component
	5	74,060,756	48.9	46.5	0.0527	0.31	-1.40	-	-
	5	199,130,596	20	17.4	0.0209	0.40	-0.70	-	-
	6	16,432,104	5.8	2.6	0.0053	0.11	0.81	-	-

	6	91,074,658	25.4	22.2	0.0133	0.06	2.02	-	-
	7	128,396,999	11.5	9.1	0.0115	0.13	-0.89	-	-
	8	112,526,887	29.5	27	0.0306	0.02	-3.87	GRMZM2G139574	Glycosyltransferase
	8	117,449,528	27.4	25.2	0.0283	0.02	-3.80	GRMZM2G113554	Expressed protein
	8	166,486,198	13.8	11	0.0142	0.36	-0.62	-	-
	9	105,203,693	23.3	20.8	0.0253	0.02	-3.68	-	-
	9	142,011,299	21.4	17.5	0.0227	0.29	-0.91	GRMZM2G045981	Leucine-rich repeat protein
	10	116,704,001	6.3	3.3	0.0056	0.07	-0.87	-	-
	10	143,270,554	7.6	4.8	0.0080	0.33	-0.49	GRMZM2G180471	Phosphatase 2C
DTA	1	15,859,601	11.2	7.9	0.0129	0.11	0.38	GRMZM2G000741	Mitochondrial carrier
	1	45,309,466	14	11	0.0157	0.40	0.23	-	-
	1	198,503,585	8.4	5.2	0.0080	0.35	-0.19	GRMZM2G001803	Expressed protein
	1	223,148,600	6.6	3.8	0.0071	0.14	0.26	-	-
	1	285,088,949	10.1	7	0.0114	0.19	-0.25	GRMZM2G174136	Expressed protein
	2	13,183,762	12.6	9.4	0.0139	0.22	-0.27	GRMZM2G035719	RNA recognition motif
	2	71,694,864	23.3	19.8	0.0252	0.04	0.79	GRMZM2G000980	Putative uncharacterized protein
	2	196,646,460	7.3	4.1	0.0074	0.13	0.29	-	-
	2	215,685,793	34.1	31.4	0.0347	0.29	0.39	-	-
	3	33,704,604	30.7	27.8	0.0323	0.36	0.37	-	-
	3	109,874,104	32.9	31.1	0.0373	0.28	0.49	-	-
	3	157,651,234	19.6	16.5	0.0237	0.23	-0.47	GRMZM2G171600	Calmodulin-binding transcription activator
	3	197,449,919	21.8	19.3	0.0246	0.31	0.34	GRMZM2G177906	Hexokinase
	3	213,247,367	25.3	22.1	0.0253	0.41	0.30	GRMZM2G067583	Tat pathway signal sequence family
	4	39,171,288	10.8	8.8	0.0097	0.08	0.36	GRMZM2G005583	Esterase
	4	218,097,053	9.4	6.2	0.0103	0.03	0.54	-	-
	5	3,379,634	13.4	10.6	0.0127	0.33	-0.21	-	-
	5	129,802,132	17.2	14.1	0.0214	0.19	0.35	-	-
	6	58,682,095	7.8	5.1	0.0071	0.04	-0.41	-	-
	6	155,742,011	5.9	2	0.0051	0.11	0.25	GRMZM2G116258	Glutamate-1-semialdehyde-2,1-aminomutase
	6	162,708,977	17.6	14.7	0.0192	0.17	0.38	GRMZM2G061663	Zinc finger transcription factor
	7	145,739,720	10.9	7.7	0.0135	0.14	-0.33	-	-
	7	168,992,525	12.3	9	0.0136	0.36	0.20	GRMZM2G134341	PRM5
	8	121,051,703	36.1	33.6	0.0399	0.25	0.48	GRMZM2G527250	Expressed protein
	8	160,241,887	10.3	7.8	0.0107	0.25	0.25	-	-
	9	26,551,727	5.2	2.3	0.0051	0.04	0.48	-	-
	9	113,530,209	62.3	60	0.0320	0.31	0.45	-	-
	9	124,069,745	39.6	37.5	0.0404	0.47	0.40	-	-
	9	142,535,940	6.3	3.6	0.0057	0.05	-0.38	-	-
	10	8,398,599	6.4	3	0.0064	0.20	0.21	GRMZM2G136910	Abscisic stress-ripening
	10	87,615,338	42.5	39.6	0.0452	0.07	0.92	GRMZM2G062541	Helix-loop-helix DNA-binding domain
	10	144,082,871	11.6	8.8	0.0121	0.31	-0.21	GRMZM2G445575	Transcription factor
DTS	1	21,691,747	8.7	5.8	0.0077	0.22	0.25	GRMZM2G016922	Terpene synthase
	1	42,970,480	11.5	8.4	0.0124	0.10	0.52	-	-
	1	196,441,970	5.8	2.5	0.0048	0.15	-0.24	GRMZM2G045135	Haloacid dehalogenase-like hydrolase
	1	236,344,417	8.7	5.1	0.0087	0.22	0.26	GRMZM2G141256	3-oxoacyl-reductase
	1	286,872,569	10.7	7.7	0.0127	0.08	0.47	-	-

2	13,183,762	20	16.5	0.0210	0.22	-0.38	GRMZM2G035719	RNA recognition motif
2	56,512,014	26.4	23.4	0.0284	0.29	0.38	GRMZM2G434669	Expressed protein
2	205,195,986	6.1	3.2	0.0058	0.08	0.44	GRMZM2G403800	Expressed protein
2	215,685,793	25.1	21.8	0.0268	0.29	0.41	-	-
3	23,542,690	17.1	13.8	0.0003	0.30	0.07	GRMZM2G114552	BBTI1
3	158,221,870	15.2	11.7	0.0188	0.12	-0.56	-	-
3	211,703,629	58.2	56.5	0.0142	0.48	0.27	-	-
3	212,725,952	58.2	56.4	0.0142	0.48	0.27	-	-
4	17,307,125	12.8	9.6	0.0123	0.04	0.78	-	-
4	155,219,577	8.1	5	0.0082	0.09	-0.42	GRMZM2G003514	Zea agamous5
4	221,605,444	10	8	0.0095	0.01	0.85	-	-
5	2,583,875	12.8	9.7	0.0133	0.31	-0.25	-	-
5	159,438,987	11	7.7	0.0114	0.09	0.41	-	-
5	207,746,609	9.2	6.2	0.0086	0.08	0.40	-	-
6	103,280,254	8.6	6.2	0.0063	0.04	0.50	-	-
6	160,828,364	14.1	11	0.0146	0.11	0.46	GRMZM2G474546	Protein kinase
6	166,267,781	7.9	4.8	0.0078	0.31	0.21	GRMZM2G114578	AMP-binding enzyme
7	138,927,147	13	9.8	0.0140	0.33	-0.25	-	-
7	168,992,525	7.3	4.3	0.0085	0.36	0.18	GRMZM2G134341	PRM5
8	6,989,621	9.7	7.6	0.0087	0.48	-0.16	GRMZM2G109627	No apical meristem protein
8	161,249,047	16.5	13.4	0.0185	0.24	0.36	-	-
9	93,250,059	8.7	5.1	0.0097	0.06	0.60	GRMZM2G141256	3-oxoacyl-reductase
9	124,365,160	43.9	41.4	0.0473	0.31	0.61	GRMZM2G095124	Adapitin protein
9	142,281,937	7.5	4.2	0.0082	0.14	-0.31	GRMZM2G102218	YABBY domain
10	87,615,338	58.7	55.9	0.0657	0.07	1.13	GRMZM2G062541	Helix-loop-helix DNA-binding domain
10	144,836,415	10.9	7.9	0.0132	0.28	-0.25	GRMZM2G421033	AP2 domain

[a] Frequency of non-B73 allele within the maize NAM population. The range of the theoretical frequency for non-B73 allele is 2% - 50% with the NAM design. [b] Genetic effect as compared with B73 allele. Leaf length, mm; leaf width, mm; leaf angle, degree; DTA, days to anthesis, day; and DTS, days to silking, day.