Supplemental Figures:

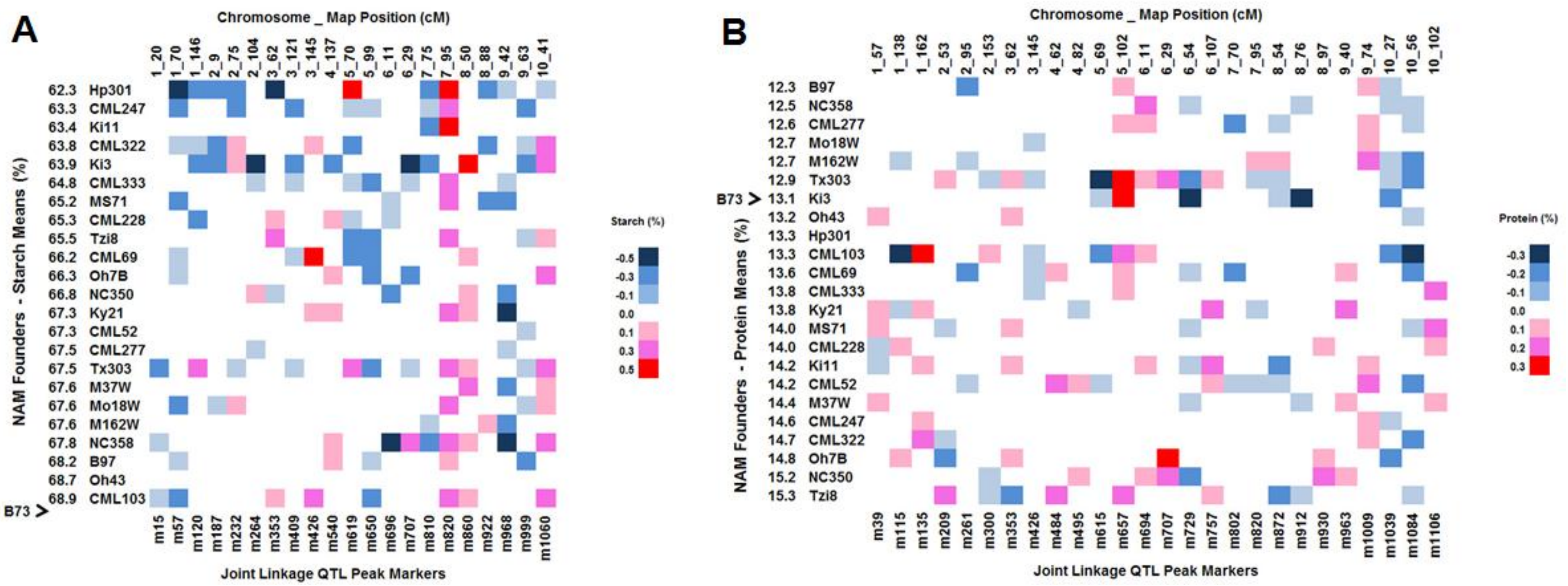

Fig. S1. Heat map displaying additive allelic effects for (A) starch and (B) protein percent kernel content on a dry matter basis QTL for the 23 NAM founders relative to B73. The horizontal top horizontal axis lists the chromosome and genetic map position for each QTL peak, and the bottom axis shows the NAM map SNP selected by stepwise regression. The vertical axis displays the 23 inbred NAM founder lines sorted in increasing (A) starch and (B) protein content. Allelic effects are color coded based on (A) 0.2% increments for starch and (B) 0.1% increments for protein.

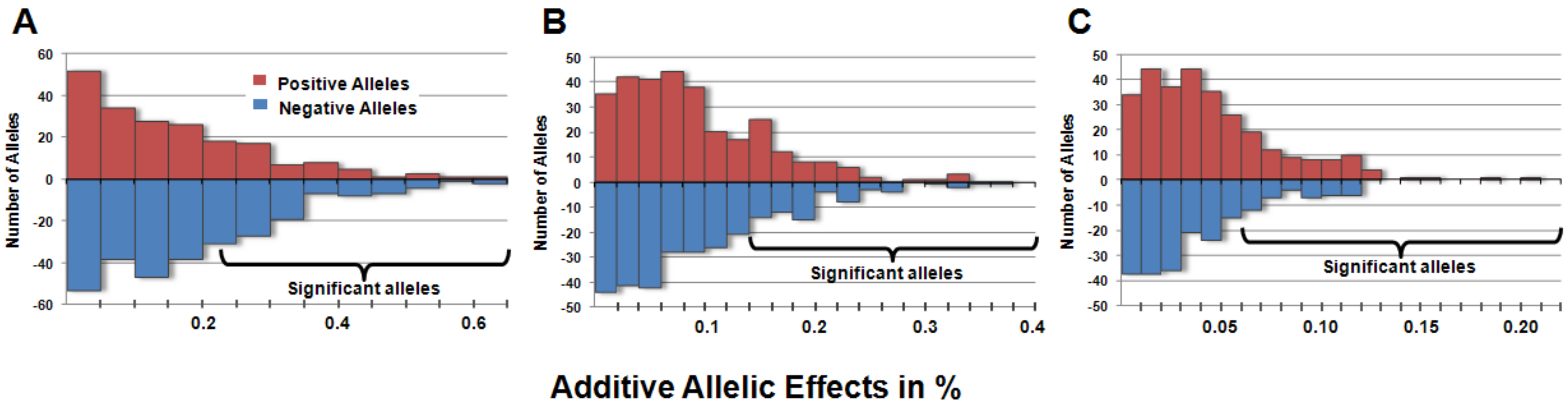

Fig. S2. Distribution of allele effect size derived from joint-linkage mapping in NAM for percent (A) starch, (B) protein, and (C) oil kernel content on a dry matter basis relative to B73. Significant alleles after a 5% FDR correction are indicated.

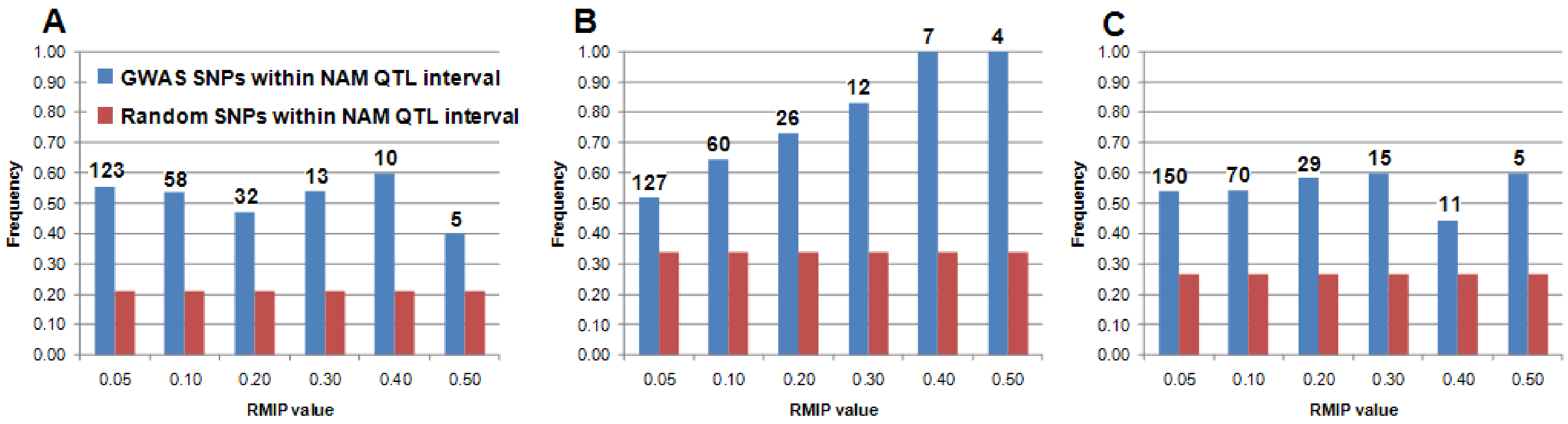

Fig. S3. Significant SNPs from the NAM sub-sampling GWAS method overlapped with NAM joint-linkage QTL intervals. Proportion of associated SNPs within QTL support intervals were calculated for multiple RMIP values. Expected proportion by chance was obtained by calculating the proportion of the number of HapMap.v1 SNPs within the QTL support intervals. The number of associated SNPs for each RMIP value is displayed above the GWAS bars. (A) Starch. (B) Protein. (C) Oil.

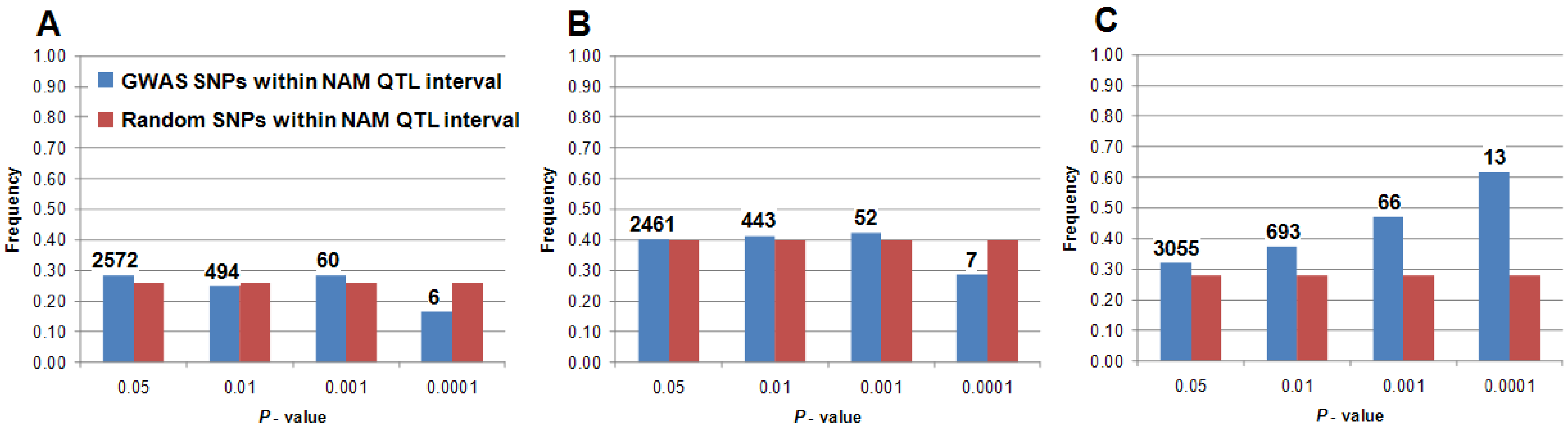

Fig. S4. Significant SNP overlap from 282 inbred association panel genome scan overlapped with NAM joint-linkage QTL intervals. Proportion of SNPs within QTL support intervals were calculated for multiple *P*-value thresholds. Expected proportion by chance was obtained by calculating the proportion of the number of MaizeSNP50 BeadChip SNPs within the QTL support intervals. The number of SNPs for each P-value threshold is displayed above the GWAS bars. (A) Starch. (B) Protein. (C) Oil.

Supplemental Tables:

Table S1: Means and ranges for percent starch, protein, and oil kernel composition BLUPS on a dry matter basis in each nested association mapping (NAM) family and parental lines.

			RIL BLUPs		
Family	Trait	Parental BLUP (%)	Mean (%)	Min (%)	Max (%)
B73	Starch	69.6	--	--	--
B73	Protein	13.1	--	--	--
B73	Oil	3.6	--	--	--
B97	Starch	68.2	69.0	64.9	71.5
B97	Protein	12.3	13.0	11.1	14.9
B97	Oil	4.0	4.0	3.3	4.7
CML103	Starch	68.9	68.5	64.5	71.6
CML103	Protein	13.3	13.2	10.9	15.8
CML103	Oil	4.3	4.3	3.4	5.4
CML228	Starch	65.3	66.4	62.8	69.2
CML228	Protein	14.0	14.4	12.8	16.1
CML228	Oil	5.1	4.7	3.5	5.9
CML247	Starch	63.3	66.7	62.0	69.9
CML247	Protein	14.6	14.0	12.3	15.9
CML247	Oil	3.6	4.1	3.4	4.7
CML277	Starch	67.5	68.3	64.3	71.4
CML277	Protein	12.6	13.3	11.5	15.2
CML277	Oil	4.0	4.0	3.0	4.8
CML322	Starch	63.8	67.5	62.5	70.9
CML322	Protein	14.7	13.6	11.5	15.4
CML322	Oil	5.4	4.5	3.6	5.5
CML333	Starch	64.8	67.0	63.1	71.0
CML333	Protein	13.8	13.6	12.3	15.1
CML333	Oil	5.5	4.8	3.9	5.8

Table S1: (continued…)

			RIL BLUPs		
Family	Trait	Parental BLUP (%)	Mean (%)	Min (%)	Max (%)
CML52	Starch	67.3	67.2	64.9	69.8
CML52	Protein	14.2	14.3	12.0	16.4
CML52	Oil	4.4	4.5	3.7	5.6
CML69	Starch	66.2	67.9	64.0	72.3
CML69	Protein	13.6	13.9	12.3	16.0
CML69	Oil	4.6	4.2	3.2	5.2
Hp301	Starch	62.3	66.4	59.7	70.9
Hp301	Protein	13.3	13.5	12.2	14.9
Hp301	Oil	4.2	4.5	3.7	5.4
Ki11	Starch	63.4	67.3	64.1	70.2
Ki11	Protein	14.2	13.2	11.5	15.5
Ki11	Oil	4.7	4.1	3.5	4.8
Ki3	Starch	63.9	66.6	60.6	71.4
Ki3	Protein	13.1	13.8	11.1	16.1
Ki3	Oil	4.6	4.3	3.6	5.6
Ky21	Starch	67.3	69.0	64.2	71.3
Ky21	Protein	13.8	13.0	11.1	15.6
Ky21	Oil	3.6	3.8	3.1	4.8
M162W	Starch	67.6	68.5	63.9	72.2
M162W	Protein	12.7	13.2	11.4	15.8
M162W	Oil	4.4	4.0	3.1	5.1
M37W	Starch	67.6	69.3	66.0	73.0
M37W	Protein	14.4	13.0	10.8	15.1
M37W	Oil	3.6	3.6	2.9	4.4
Mo18W	Starch	67.6	67.7	63.5	70.3
Mo18W	Protein	12.7	13.4	11.8	14.8
Mo18W	Oil	4.1	4.3	3.6	5.0

Table S1: (continued…)

			RIL BLUPs		
Family	Trait	Parental BLUP (%)	Mean (%)	Min (%)	Max (%)
MS71	Starch	65.2	67.5	64.0	70.8
MS71	Protein	14.0	13.4	11.6	15.7
MS71	Oil	4.2	4.0	3.4	5.0
NC350	Starch	66.8	68.4	64.0	71.2
NC350	Protein	15.2	13.8	11.7	16.6
NC350	Oil	5.3	4.4	3.5	5.8
NC358	Starch	67.8	67.6	63.8	72.4
NC358	Protein	12.5	13.4	11.0	15.5
NC358	Oil	3.9	4.0	3.4	4.9
Oh43	Starch	68.7	68.3	66.2	70.6
Oh43	Protein	13.2	14.0	12.7	15.6
Oh43	Oil	3.5	3.8	3.0	4.7
Oh7B	Starch	66.3	68.0	62.8	70.8
Oh7B	Protein	14.8	13.8	11.9	16.8
Oh7B	Oil	5.3	4.5	3.6	5.5
Tx303	Starch	67.5	68.3	64.2	72.8
Tx303	Protein	12.9	13.6	11.2	16.0
Tx303	Oil	3.9	4.0	2.8	5.8
Tzi8	Starch	65.5	66.3	61.8	70.4
Tzi8	Protein	15.3	14.6	12.3	17.7
Tzi8	Oil	5.2	4.8	3.8	6.4

Table S2: NAM joint-linkage mapping analysis summary for percent starch content on a dry matter basis

QTL	Marker ID	Chr	cM	AGP_v1 (bp)	SS	df	MS	F	*P*-value	R^2	Support interval (cM)[a]	Interval Length (cM)	Support Interval AGP_v1 (bp)	Interval Length AGP_v1 (bp)
m15	PZA00106.10	1	20.1	10,068,913	23	88	3.81	3.10	9.1E-07	0.01	11.5 - 24.4	12.9	6,220,629 - 12,208,717	5,988,088
m57	PZB01062.3	1	70.3	56,846,393	23	287	12.46	10.14	1.8E-35	0.03	69.1 - 73.3	4.2	54,049,352 - 63,913,678	9,864,326
m120	PZA03064.6	1	146.0	248,503,059	23	109	4.73	3.84	1.8E-09	0.01	129.8 - 146.6	16.8	222,427,674 - 251,142,743	28,715,069
m187	PZB01233.1	2	8.5	3,375,793	23	121	5.25	4.27	4.1E-11	0.01	5.7 - 11.5	5.8	2,484,113 - 4,180,858	1,696,745
m232	PHM3457.6	2	74.8	62,804,386	23	127	5.52	4.49	5.8E-12	0.01	70.9 - 82.5	11.6	48,526,009 - 161,878,369	113,352,360
m264	PHM3055.9	2	103.7	192,601,949	23	99	4.29	3.49	3.7E-08	0.01	103.7 - 109.9	6.2	192,601,949 - 202,113,283	9,511,334
m353	PZD00016.4	3	62.4	133,481,025	23	155	6.75	5.49	6.3E-16	0.01	61.2 - 65.5	4.3	130,082,268 - 145,421,390	15,339,122
m409	PZA02616.1	3	120.7	210,161,705	23	106	4.62	3.76	3.8E-09	0.01	104 - 132.8	28.8	196,870,259 - 216,915,146	20,044,887
m426	PZA01688.3	3	145.3	223,670,206	23	112	4.87	3.96	6.2E-10	0.01	136.8 - 146.8	10.0	219,859,786 - 224,184,332	4,324,546
m540	PZA01905.12	4	136.6	244,087,628	23	98	4.26	3.46	4.5E-08	0.01	135.6 - 136.6	1.0	243,937,276 - 244,087,628	150,352
m619	PZA02164.16	5	70.0	112,180,088	23	166	7.23	5.88	1.6E-17	0.01	70.0 - 75.6	5.6	97,952,577 - 160,321,863	62,369,286
m650	PZA02383.1	5	98.8	189,143,714	23	306	13.32	10.84	1.8E-38	0.03	90.2 - 100.2	10.0	179,952,918 - 191,075,482	11,122,564
m696	PZA00543.12	6	11.3	80,533,790	23	184	8.01	6.52	3.7E-20	0.02	6.9 - 22.1	15.2	20,837,695 - 95,788,878	74,951,183
m707	PZB01658.1	6	28.7	102,953,989	23	102	4.44	3.61	1.3E-08	0.01	27.8 - 28.7	0.9	102,565,657 - 102,953,989	388,332
m810	PZA03728.1	7	75.3	138,551,744	23	100	4.35	3.54	2.4E-08	0.01	75.3 - 77.0	1.7	137,207,831 - 138,551,744	1,343,913
m820	PZA02386.2	7	95.2	154,593,844	23	205	8.93	7.27	2.9E-23	0.02	95.2	0.0	0.0	-
m860	PZA00758.1	8	49.9	23,796,614	23	220	9.57	7.79	1.8E-25	0.02	48.6 - 56.0	7.4	22,422,862 - 90,837,884	68,415,022
m922	PHM3465.6	8	88.2	159,478,175	23	155	6.74	5.48	6.6E-16	0.01	80.2 - 94.1	13.9	151,452,478 - 163,067,046	11,614,568
m968	PZB01110.6	9	41.8	24,028,939	23	423	18.37	14.95	3.7E-56	0.04	39.4 - 45.2	5.8	22,041,392 - 37,421,647	15,380,255
m999	PZA00213.19	9	62.9	126,584,775	23	132	5.76	4.69	1.0E-12	0.01	54.0 - 69.4	15.4	109,910,040 - 133,450,589	23,540,549
m1060	PHM12990.15	10	40.8	86,998,024	23	198	8.61	7.00	3.7E-22	0.02	33.9 - 47.1	13.2	18,903,610 - 117,796,659	98,893,049
Population					22	3262	148.26	120.62	0	0.29		9.1		
Error					3809	4682	1.23							

[a] *P*<0.05 support interval for each QTL

Table S3: NAM joint-linkage mapping analysis summary for percent protein content on a dry matter basis.

QTL	Marker ID	Chr	cM	AGP_v1 (bp)	SS	df	MS	F	*P*-value	R^2	Support interval (cM)[a]	Interval Length (cM)	Support Interval AGP_v1 (bp)	Interval Length AGP_v1 (bp)
m39	PZA02271.1	1	56.5	38,608,085	23	24	1.04	2.91	4.0E-06	0.01	54.0 - 70.3	16.3	34,476,379 - 56,846,393	22,370,014
m115	PZA03001.15	1	137.6	231,037,638	23	47	2.06	5.77	4.7E-17	0.01	132.9 - 140.2	7.3	224,518,354 - 237,638,987	13,120,633
m135	PZB00895.1	1	162.2	268,369,738	23	39	1.71	4.78	4.3E-13	0.01	156.5 - 169.2	12.7	260,297,447 - 276,644,729	16,347,282
m209	PZA00590.1	2	53.3	21,991,096	23	38	1.64	4.59	2.4E-12	0.01	53.3 - 64.1	10.8	21,991,096 - 40,814,002	18,822,906
m261	PZA00755.2	2	94.9	-	23	45	1.94	5.42	1.2E-15	0.01	81.7 - 98.9	17.2	155,867,789 - 187,225,285	31,357,496
m300	PZA03321.4	2	153.4	234,574,710	23	26	1.15	3.22	3.4E-07	0.01	151.6 - 155.7	4.1	231,190,534 - 233,128,413	1,937,879
m353	PZD00016.4	3	62.4	133,481,025	23	38	1.67	4.68	1.1E-12	0.01	55.5 - 74.3	18.8	37,537,206 - 161,515,805	123,978,599
m426	PZA01688.3	3	145.1	223,670,206	23	35	1.52	4.26	4.5E-11	0.01	145.1 - 145.3	0.2	223,670,047 - 223,670,206	159
m484	PZA03152.3	4	61.8	147,045,311	23	47	2.06	5.75	5.5E-17	0.01	55.2 - 69.8	14.6	49,713,730 - 158,126,226	108,412,496
m495	PZA01658.1	4	81.7	172,269,404	23	23	0.99	2.76	1.3E-05	0.01	80.6 - 89.1	8.5	171,613,479 - 177,666,469	6,052,990
m615	PZA01693.1	5	68.7	83,544,179	23	33	1.42	3.97	5.7E-10	0.01	67.5 - 81.7	14.2	77,679,856 - 169,719,924	92,040,068
m657	PHM532.23	5	101.9	193,208,486	23	70	3.04	8.51	1.7E-28	0.02	90.2 - 114.0	23.8	179,952,918 - 207,274,028	27,321,110
m694	PZA00355.2	6	11.1	78,756,246	23	46	2.02	5.65	1.4E-16	0.01	0 - 22.1	22.1	9,561,985 - 95,788,878	86,226,893
m707	PZB01658.1	6	28.7	102,953,989	23	22	0.98	2.73	1.7E-05	0.01	11.8 - 28.7	16.9	82,066,479 - 102,953,989	20,887,510
m729	PZA02187.1/2	6	54	139,105,837	23	42	1.84	5.16	1.3E-14	0.01	50.0 - 55.7	5.7	131,405,672 - 142,648,551	11,242,879
m757	PZA00910.1	6	106.6	166,688,135	23	33	1.45	4.06	2.8E-10	0.01	94.0 - 109.7	15.7	163,119,951 - 167,884,169	4,764,218
m802	PZA03583.1	7	69.8	128,404,190	23	30	1.31	3.68	7.4E-09	0.01	61.4 - 81.2	19.8	121,400,796 - 143,285,623	21,884,827
m820	PZA02386.2	7	95.2	154,593,844	23	57	2.50	7.00	4.1E-22	0.02	95.2 - 112.3	17.1	143,285,623 - 162,173,913	18,888,290
m872	PZA01470.1	8	53.9	72,801,634	23	76	3.30	9.23	1.5E-31	0.02	52.7 - 54.7	2.0	64,422,612 - 82,582,808	18,160,196
m912	PZA03651.1	8	76.1	146,342,392	23	32	1.38	3.85	1.7E-09	0.01	64.1 - 88.5	24.4	118,438,603 - 159,897,609	41,459,006
m930	PZA00362.1	8	96.5	163,939,260	23	26	1.14	3.19	4.2E-07	0.01	95.6 - 106.9	11.3	163,565,258 - 166,984,210	3,418,952
m963	PZB00540.3	9	40	23,217,547	23	31	1.33	3.71	5.5E-09	0.01	30.4 - 44.6	14.2	16,979,604 - 37,421,647	20,442,043
m1009	PHM1766.1	9	74	136,401,562	23	90	3.91	10.94	7.1E-39	0.03	62.2 - 89.3	27.1	124,619,263 - 142,925,131	18,305,868
m1039	PZB01301.5	10	26.8	9,747,844	23	37	1.60	4.49	6.1E-12	0.01	15.2 - 40.1	24.9	5,118,792 - 84,002,545	78,883,753
m1084	PZA02320.1	10	56.1	132,256,686	23	164	7.15	20.01	1.1E-77	0.05	43.4 - 69.2	25.8	99,471,497 - 139,616,869	40,145,372
m1106	PZA02527.2	10	101.9	148,488,798	23	29	1.25	3.51	3.1E-08	0.01	101.9	0.0	0.0	-
Population					22	878	39.92	111.70	0	0.26		14.44230769		
Error					3694	1320	0.36							

[a] *P*<0.05 support interval for each QTL

Table S4: NAM joint-linkage mapping analysis summary for percent oil content on a dry matter basis.

QTL	Marker ID	Chr	cM	AGP_v1 (bp)	SS	df	MS	F	*P*-value	R^2	Support interval (cM)[a]	Interval Length (cM)	Support Interval AGP_v1 (bp)	Interval Length AGP_v1 (bp)
m23	PZA02393.2	1	33.1	16,530,728	23	11	0.49	6.41	1.03E-19	0.01	21.9 - 47.3	25.4	10,934,471 - 28,526,284	17,591,813
m94	PHM5480.17	1	116.5	204,199,175	23	13	0.57	7.41	7.55E-24	0.01	116.2 - 123.7	7.5	203,035,528 - 212,356,112	9,320,584
m118	PZA03301.2	1	141.9	240,574,106	23	5	0.23	3.05	1.38E-06	0.01	127.6 - 153.4	25.8	216,926,935 - 257,414,765	40,487,830
m170	PZA00856.2	1	199.4	295,785,390	23	10	0.46	5.93	9.92E-18	0.01	197.2 - 202.4	5.2	294,646,513 - 298,082,932	3,436,419
m221	PZA01993.7	2	64.2	-	23	8	0.33	4.30	3.30E-11	0.01	52.0 - 72.1	20.1	21,203,379 - 51,780,232	30,576,853
m240	PZA02626.1	2	79.8	144,527,767	23	14	0.59	7.66	6.75E-25	0.01	76.5 - 84.2	7.7	103,493,675 - 170,899,948	67,406,273
m266	PHM3668.12	2	106.1	195,555,727	23	6	0.24	3.17	5.16E-07	0.01	105.3 - 107.1	1.8	193,997,108 - 197,109,711	3,112,603
m330	PZA03070.9	3	56.0	43,868,335	23	8	0.34	4.42	1.08E-11	0.01	54.7 - 61.8	7.1	31,695,641 - 132,192,350	100,496,709
m401	PZA01457.1	3	104.0	196,870,259	23	10	0.45	5.80	3.41E-17	0.01	96.7 - 120.7	24.0	185,290,988 - 210,161,705	24,870,717
m474	PZA03203.2	4	57.4	90,204,048	23	14	0.61	7.92	5.17E-26	0.01	56.3 - 61.8	5.5	76,123,299 - 148,400,968	72,277,669
m492	PHM3155.14	4	78.4	170,467,696	23	7	0.30	3.92	9.49E-10	0.01	77.2 - 93.2	16.0	169,608,734 - 180,309,837	10,701,103
m538	PHM4125.11	4	129.3	242,313,396	23	7	0.29	3.78	3.19E-09	0.01	0	0.0	0.00	-
m553	PHM13122.43	5	13.3	4,191,020	23	5	0.22	2.83	8.03E-06	0.01	7.2 - 30.3	23.1	2,690,777 - 8,220,095	5,529,318
m565	PZA01284.6	5	37.9	11,989,892	23	7	0.31	4.04	3.33E-10	0.01	30.2 - 51.8	21.6	7,945,833 - 21,771,520	13,825,687
m591	PZA02207.1	5	60.6	49,203,578	23	24	1.03	13.35	2.95E-49	0.02	58.0 -63.6	5.6	34,587,147 - 61,405,377	26,818,230
m638	PZA03714.1	5	87.2	175,463,122	23	6	0.26	3.34	1.23E-07	0.01	87.2 - 99.3	12.1	175,460,187 - 190,025,819	14,565,632
m708	PZA03461.1	6	33.4	107,548,161	23	41	1.80	23.43	2.89E-92	0.04	18.6 - 42.1	23.5	91,704,263 - 117,238,757	25,534,494
m739	PZA01342.2	6	61.4	148,798,933	23	6	0.26	3.35	1.18E-07	0.01	54.7 - 61.8	7.1	141,111,493 - 149,251,127	8,139,634
m793	PZA02236.1	7	51.2	101,321,689	23	5	0.23	2.95	2.97E-06	0.01	49.1 - 64.9	15.8	46,238,062 - 124,599,116	78,361,054
m918	PHM15278.6	8	82.3	155,483,712	23	16	0.72	9.30	6.97E-32	0.02	76.1 - 88.2	12.1	146,341,811 - 159,478,175	13,136,364
m995	PZA02325.4	9	57.7	117,870,517	23	12	0.52	6.78	3.29E-21	0.01	57.3 - 64.3	7.0	116,763,624 - 128,514,657	11,751,033
m1085	PZB01111.8	10	58.4	134,034,340	23	8	0.36	4.62	1.81E-12	0.01	44.8 - 58.4	13.6	111,608,632 - 134,034,340	22,425,708
Population					22	428	19.43	252.75	0	0.44		13.1		
Error					3786	291	0.08							

[a] *P*<0.05 support interval for each QTL

Table S5: NAM joint-linkage mapping analysis QTL allelic effects summary for percent starch content on a dry matter basis.

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m15	B97	-0.07	0.478	0.669
Starch	m15	CML103	-0.25	0.006	0.028*
Starch	m15	CML228	0.20	0.022	0.073
Starch	m15	CML247	-0.10	0.265	0.432
Starch	m15	CML277	-0.08	0.371	0.548
Starch	m15	CML322	-0.13	0.132	0.264
Starch	m15	CML333	0.11	0.197	0.352
Starch	m15	CML52	-0.13	0.126	0.256
Starch	m15	CML69	-0.21	0.019	0.062
Starch	m15	HP301	-0.11	0.204	0.362
Starch	m15	Ki11	-0.14	0.124	0.256
Starch	m15	Ki3	0.00	1.000	1.000
Starch	m15	Ky21	-0.02	0.817	0.910
Starch	m15	M162W	-0.13	0.164	0.306
Starch	m15	M37W	-0.13	0.124	0.256
Starch	m15	Mo18W	-0.08	0.358	0.533
Starch	m15	MS71	-0.16	0.058	0.147
Starch	m15	NC350	0.04	0.664	0.814
Starch	m15	NC358	-0.26	0.004	0.021*
Starch	m15	Oh43	0.15	0.104	0.225
Starch	m15	Oh7B	-0.22	0.018	0.060
Starch	m15	Tx303	-0.30	0.001	0.006*
Starch	m15	Tzi8	-0.16	0.073	0.176
Starch	m57	B97	-0.24	0.007	0.031*
Starch	m57	CML103	-0.32	0.000	0.004*
Starch	m57	CML228	-0.03	0.716	0.850
Starch	m57	CML247	-0.31	0.000	0.004*
Starch	m57	CML277	-0.17	0.056	0.146
Starch	m57	CML322	-0.27	0.002	0.013*
Starch	m57	CML333	-0.17	0.058	0.147
Starch	m57	CML52	-0.06	0.523	0.705
Starch	m57	CML69	-0.25	0.007	0.030*
Starch	m57	HP301	-0.52	0.000	0.001**
Starch	m57	Ki11	-0.02	0.851	0.932
Starch	m57	Ki3	-0.24	0.033	0.098
Starch	m57	Ky21	-0.20	0.034	0.099

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m57	M162W	0.20	0.032	0.096
Starch	m57	M37W	-0.18	0.052	0.137
Starch	m57	Mo18W	-0.34	0.000	0.001**
Starch	m57	MS71	-0.37	0.000	0.001**
Starch	m57	NC350	0.08	0.386	0.567
Starch	m57	NC358	-0.06	0.481	0.671
Starch	m57	Oh43	-0.03	0.778	0.886
Starch	m57	Oh7B	-0.28	0.002	0.015*
Starch	m57	Tx303	0.13	0.177	0.323
Starch	m57	Tzi8	-0.12	0.183	0.332
Starch	m120	B97	-0.01	0.916	0.960
Starch	m120	CML103	-0.12	0.174	0.321
Starch	m120	CML228	-0.32	0.000	0.003*
Starch	m120	CML247	-0.15	0.079	0.184
Starch	m120	CML277	0.10	0.248	0.408
Starch	m120	CML322	-0.26	0.003	0.018*
Starch	m120	CML333	0.03	0.735	0.860
Starch	m120	CML52	-0.09	0.327	0.505
Starch	m120	CML69	-0.01	0.944	0.975
Starch	m120	HP301	-0.32	0.000	0.003*
Starch	m120	Ki11	0.05	0.551	0.726
Starch	m120	Ki3	-0.40	0.000	0.003*
Starch	m120	Ky21	0.05	0.608	0.766
Starch	m120	M162W	0.21	0.017	0.057
Starch	m120	M37W	-0.04	0.645	0.802
Starch	m120	Mo18W	0.00	0.980	0.984
Starch	m120	MS71	-0.20	0.027	0.084
Starch	m120	NC350	0.00	0.967	0.980
Starch	m120	NC358	-0.12	0.200	0.356
Starch	m120	Oh43	-0.05	0.562	0.733
Starch	m120	Oh7B	-0.01	0.887	0.936
Starch	m120	Tx303	0.34	0.000	0.003*
Starch	m120	Tzi8	-0.06	0.478	0.669
Starch	m187	B97	0.09	0.275	0.441
Starch	m187	CML103	0.00	0.958	0.980
Starch	m187	CML228	0.11	0.209	0.366
Starch	m187	CML247	0.13	0.147	0.286

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m187	CML277	-0.01	0.932	0.971
Starch	m187	CML322	-0.46	0.000	0.001**
Starch	m187	CML333	0.01	0.882	0.936
Starch	m187	CML52	-0.14	0.099	0.217
Starch	m187	CML69	-0.17	0.076	0.180
Starch	m187	HP301	-0.30	0.001	0.007*
Starch	m187	Ki11	0.05	0.556	0.727
Starch	m187	Ki3	-0.41	0.000	0.004*
Starch	m187	Ky21	0.00	0.971	0.980
Starch	m187	M162W	-0.18	0.056	0.145
Starch	m187	M37W	-0.10	0.244	0.403
Starch	m187	Mo18W	-0.28	0.002	0.011*
Starch	m187	MS71	-0.11	0.216	0.371
Starch	m187	NC350	-0.16	0.084	0.192
Starch	m187	NC358	-0.17	0.057	0.146
Starch	m187	Oh43	-0.05	0.542	0.717
Starch	m187	Oh7B	0.06	0.475	0.668
Starch	m187	Tx303	-0.08	0.422	0.607
Starch	m187	Tzi8	0.02	0.801	0.900
Starch	m232	B97	0.20	0.034	0.099
Starch	m232	CML103	0.02	0.858	0.934
Starch	m232	CML228	0.02	0.835	0.921
Starch	m232	CML247	-0.45	0.000	0.001**
Starch	m232	CML277	0.10	0.272	0.438
Starch	m232	CML322	0.25	0.008	0.032*
Starch	m232	CML333	0.04	0.713	0.850
Starch	m232	CML52	-0.11	0.254	0.415
Starch	m232	CML69	0.14	0.153	0.291
Starch	m232	HP301	-0.34	0.000	0.003
Starch	m232	Ki11	0.01	0.948	0.975
Starch	m232	Ki3	0.29	0.009	0.038*
Starch	m232	Ky21	-0.03	0.758	0.869
Starch	m232	M162W	0.04	0.711	0.850
Starch	m232	M37W	0.07	0.491	0.679
Starch	m232	Mo18W	0.28	0.004	0.021*
Starch	m232	MS71	0.16	0.118	0.247
Starch	m232	NC350	-0.18	0.051	0.135

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m232	NC358	0.09	0.288	0.454
Starch	m232	Oh43	0.05	0.599	0.765
Starch	m232	Oh7B	-0.12	0.272	0.438
Starch	m232	Tx303	-0.25	0.009	0.036*
Starch	m232	Tzi8	-0.11	0.314	0.488
Starch	m264	B97	0.15	0.122	0.252
Starch	m264	CML103	-0.12	0.215	0.371
Starch	m264	CML228	0.02	0.800	0.900
Starch	m264	CML247	0.13	0.207	0.363
Starch	m264	CML277	-0.27	0.004	0.020*
Starch	m264	CML322	0.14	0.135	0.267
Starch	m264	CML333	-0.28	0.003	0.018*
Starch	m264	CML52	-0.02	0.855	0.932
Starch	m264	CML69	-0.07	0.439	0.629
Starch	m264	HP301	-0.17	0.081	0.188
Starch	m264	Ki11	-0.11	0.283	0.449
Starch	m264	Ki3	-0.62	0.000	0.001**
Starch	m264	Ky21	0.00	0.967	0.980
Starch	m264	M162W	-0.16	0.105	0.227
Starch	m264	M37W	-0.04	0.699	0.842
Starch	m264	Mo18W	0.03	0.715	0.850
Starch	m264	MS71	-0.21	0.040	0.112
Starch	m264	NC350	0.26	0.007	0.030*
Starch	m264	NC358	-0.13	0.215	0.371
Starch	m264	Oh43	0.06	0.563	0.733
Starch	m264	Oh7B	-0.01	0.921	0.963
Starch	m264	Tx303	-0.13	0.175	0.321
Starch	m264	Tzi8	0.01	0.965	0.980
Starch	m353	B97	-0.04	0.693	0.837
Starch	m353	CML103	0.27	0.002	0.012*
Starch	m353	CML228	0.28	0.002	0.014*
Starch	m353	CML247	0.03	0.736	0.860
Starch	m353	CML277	0.16	0.079	0.184
Starch	m353	CML322	-0.12	0.160	0.300
Starch	m353	CML333	0.01	0.880	0.936
Starch	m353	CML52	-0.03	0.715	0.850
Starch	m353	CML69	-0.04	0.664	0.814

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m353	HP301	-0.55	0.000	0.001**
Starch	m353	Ki11	0.05	0.522	0.705
Starch	m353	Ki3	0.03	0.801	0.900
Starch	m353	Ky21	0.19	0.032	0.096
Starch	m353	M162W	0.16	0.094	0.209
Starch	m353	M37W	-0.17	0.062	0.154
Starch	m353	Mo18W	-0.04	0.653	0.807
Starch	m353	MS71	0.02	0.792	0.896
Starch	m353	NC350	-0.26	0.003	0.019*
Starch	m353	NC358	-0.14	0.135	0.267
Starch	m353	Oh43	-0.20	0.025	0.078
Starch	m353	Oh7B	-0.04	0.650	0.807
Starch	m353	Tx303	0.02	0.803	0.900
Starch	m353	Tzi8	0.43	0.000	0.001**
Starch	m409	B97	-0.05	0.600	0.765
Starch	m409	CML103	-0.22	0.015	0.054
Starch	m409	CML228	-0.09	0.332	0.511
Starch	m409	CML247	-0.35	0.000	0.003*
Starch	m409	CML277	-0.14	0.193	0.347
Starch	m409	CML322	-0.06	0.533	0.717
Starch	m409	CML333	-0.25	0.012	0.045*
Starch	m409	CML52	0.02	0.852	0.932
Starch	m409	CML69	-0.25	0.009	0.038*
Starch	m409	HP301	-0.11	0.243	0.403
Starch	m409	Ki11	-0.11	0.222	0.379
Starch	m409	Ki3	-0.42	0.000	0.003*
Starch	m409	Ky21	-0.19	0.050	0.134
Starch	m409	M162W	0.00	0.966	0.980
Starch	m409	M37W	-0.13	0.207	0.363
Starch	m409	Mo18W	-0.01	0.897	0.942
Starch	m409	MS71	0.01	0.933	0.971
Starch	m409	NC350	-0.06	0.536	0.717
Starch	m409	NC358	-0.20	0.067	0.163
Starch	m409	Oh43	-0.17	0.083	0.191
Starch	m409	Oh7B	-0.21	0.038	0.109
Starch	m409	Tx303	-0.25	0.013	0.048*
Starch	m409	Tzi8	-0.14	0.157	0.296

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m426	B97	0.10	0.291	0.457
Starch	m426	CML103	0.43	0.000	0.001**
Starch	m426	CML228	0.19	0.051	0.135
Starch	m426	CML247	0.14	0.125	0.256
Starch	m426	CML277	-0.09	0.345	0.522
Starch	m426	CML322	0.25	0.007	0.031*
Starch	m426	CML333	0.13	0.149	0.287
Starch	m426	CML52	-0.06	0.454	0.645
Starch	m426	CML69	0.50	0.000	0.001**
Starch	m426	HP301	0.17	0.062	0.154
Starch	m426	Ki11	-0.05	0.595	0.765
Starch	m426	Ki3	-0.09	0.419	0.605
Starch	m426	Ky21	0.29	0.003	0.015*
Starch	m426	M162W	0.10	0.276	0.441
Starch	m426	M37W	0.07	0.507	0.694
Starch	m426	Mo18W	0.16	0.080	0.185
Starch	m426	MS71	0.12	0.226	0.384
Starch	m426	NC350	0.13	0.154	0.292
Starch	m426	NC358	0.10	0.340	0.520
Starch	m426	Oh43	0.01	0.943	0.975
Starch	m426	Oh7B	0.24	0.016	0.055
Starch	m426	Tx303	0.22	0.017	0.057
Starch	m426	Tzi8	0.23	0.017	0.057
Starch	m540	B97	0.22	0.014	0.049*
Starch	m540	CML103	-0.07	0.413	0.598
Starch	m540	CML228	0.29	0.001	0.005*
Starch	m540	CML247	0.05	0.582	0.750
Starch	m540	CML277	0.13	0.165	0.307
Starch	m540	CML322	0.07	0.484	0.672
Starch	m540	CML333	0.08	0.391	0.572
Starch	m540	CML52	0.00	0.974	0.980
Starch	m540	CML69	0.20	0.031	0.095
Starch	m540	HP301	0.06	0.484	0.672
Starch	m540	Ki11	0.06	0.499	0.686
Starch	m540	Ki3	-0.33	0.002	0.014*
Starch	m540	Ky21	0.26	0.004	0.019*
Starch	m540	M162W	0.16	0.063	0.155

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m540	M37W	0.10	0.243	0.403
Starch	m540	Mo18W	0.13	0.147	0.286
Starch	m540	MS71	-0.14	0.118	0.247
Starch	m540	NC350	0.20	0.024	0.077
Starch	m540	NC358	0.25	0.007	0.030*
Starch	m540	Oh43	0.02	0.844	0.929
Starch	m540	Oh7B	0.27	0.004	0.022*
Starch	m540	Tx303	0.08	0.400	0.582
Starch	m540	Tzi8	0.16	0.090	0.202
Starch	m619	B97	0.03	0.754	0.867
Starch	m619	CML103	-0.01	0.939	0.975
Starch	m619	CML228	-0.25	0.009	0.038*
Starch	m619	CML247	-0.25	0.007	0.031*
Starch	m619	CML277	-0.16	0.074	0.176
Starch	m619	CML322	-0.44	0.000	0.001**
Starch	m619	CML333	-0.23	0.013	0.048*
Starch	m619	CML52	0.12	0.172	0.318
Starch	m619	CML69	-0.32	0.000	0.003*
Starch	m619	HP301	0.56	0.000	0.001**
Starch	m619	Ki11	-0.14	0.129	0.260
Starch	m619	Ki3	-0.19	0.085	0.193
Starch	m619	Ky21	-0.02	0.814	0.910
Starch	m619	M162W	-0.06	0.569	0.738
Starch	m619	M37W	-0.09	0.345	0.522
Starch	m619	Mo18W	-0.04	0.693	0.837
Starch	m619	MS71	0.06	0.497	0.686
Starch	m619	NC350	-0.07	0.462	0.653
Starch	m619	NC358	0.04	0.652	0.807
Starch	m619	Oh43	0.04	0.688	0.835
Starch	m619	Oh7B	0.18	0.070	0.170
Starch	m619	Tx303	0.40	0.000	0.001*
Starch	m619	Tzi8	-0.40	0.000	0.001**
Starch	m650	B97	-0.27	0.007	0.031*
Starch	m650	CML103	-0.37	0.000	0.002*
Starch	m650	CML228	-0.24	0.016	0.054
Starch	m650	CML247	-0.30	0.001	0.008*
Starch	m650	CML277	-0.14	0.104	0.225

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m650	CML322	0.03	0.759	0.869
Starch	m650	CML333	-0.41	0.000	0.001**
Starch	m650	CML52	0.06	0.508	0.694
Starch	m650	CML69	-0.50	0.000	0.001**
Starch	m650	HP301	0.05	0.576	0.743
Starch	m650	Ki11	-0.09	0.295	0.463
Starch	m650	Ki3	-0.23	0.034	0.099
Starch	m650	Ky21	-0.03	0.752	0.867
Starch	m650	M162W	0.12	0.214	0.371
Starch	m650	M37W	-0.09	0.336	0.516
Starch	m650	Mo18W	0.02	0.866	0.936
Starch	m650	MS71	-0.22	0.022	0.073
Starch	m650	NC350	-0.20	0.030	0.092
Starch	m650	NC358	-0.11	0.242	0.403
Starch	m650	Oh43	0.01	0.879	0.936
Starch	m650	Oh7B	-0.38	0.000	0.002*
Starch	m650	Tx303	-0.47	0.000	0.001**
Starch	m650	Tzi8	-0.47	0.000	0.001**
Starch	m696	B97	-0.15	0.137	0.270
Starch	m696	CML103	-0.15	0.109	0.234
Starch	m696	CML228	-0.26	0.007	0.031*
Starch	m696	CML247	-0.19	0.058	0.147
Starch	m696	CML277	-0.22	0.032	0.096
Starch	m696	CML322	-0.06	0.537	0.717
Starch	m696	CML333	0.11	0.283	0.449
Starch	m696	CML52	-0.04	0.670	0.818
Starch	m696	CML69	-0.14	0.150	0.287
Starch	m696	HP301	-0.08	0.451	0.645
Starch	m696	Ki11	-0.06	0.521	0.705
Starch	m696	Ki3	-0.15	0.241	0.403
Starch	m696	Ky21	0.02	0.865	0.936
Starch	m696	M162W	-0.18	0.092	0.207
Starch	m696	M37W	0.01	0.949	0.975
Starch	m696	Mo18W	-0.05	0.642	0.802
Starch	m696	MS71	-0.26	0.006	0.029*
Starch	m696	NC350	-0.47	0.000	0.001**
Starch	m696	NC358	-0.55	0.000	0.001**

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m696	Oh43	0.02	0.881	0.936
Starch	m696	Oh7B	0.01	0.948	0.975
Starch	m696	Tx303	-0.20	0.073	0.176
Starch	m696	Tzi8	0.03	0.741	0.860
Starch	m707	B97	-0.06	0.541	0.717
Starch	m707	CML103	-0.16	0.096	0.212
Starch	m707	CML228	-0.23	0.015	0.054
Starch	m707	CML247	0.02	0.854	0.932
Starch	m707	CML277	0.16	0.118	0.247
Starch	m707	CML322	-0.10	0.347	0.524
Starch	m707	CML333	-0.25	0.012	0.046*
Starch	m707	CML52	0.00	0.997	0.999
Starch	m707	CML69	-0.03	0.740	0.860
Starch	m707	HP301	0.12	0.283	0.449
Starch	m707	Ki11	-0.02	0.872	0.936
Starch	m707	Ki3	-0.61	0.000	0.001**
Starch	m707	Ky21	-0.15	0.177	0.323
Starch	m707	M162W	-0.21	0.071	0.172
Starch	m707	M37W	0.00	0.972	0.980
Starch	m707	Mo18W	-0.23	0.023	0.075
Starch	m707	MS71	0.16	0.132	0.264
Starch	m707	NC350	0.00	0.972	0.980
Starch	m707	NC358	0.34	0.001	0.005*
Starch	m707	Oh43	0.09	0.407	0.590
Starch	m707	Oh7B	-0.46	0.000	0.001**
Starch	m707	Tx303	-0.27	0.012	0.044*
Starch	m707	Tzi8	-0.15	0.152	0.289
Starch	m810	B97	-0.11	0.318	0.492
Starch	m810	CML103	-0.11	0.348	0.524
Starch	m810	CML228	0.01	0.897	0.942
Starch	m810	CML247	-0.28	0.004	0.020*
Starch	m810	CML277	0.23	0.034	0.099
Starch	m810	CML322	-0.16	0.127	0.256
Starch	m810	CML333	-0.15	0.148	0.286
Starch	m810	CML52	-0.05	0.671	0.818
Starch	m810	CML69	0.16	0.089	0.201
Starch	m810	HP301	-0.33	0.001	0.006*

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m810	Ki11	-0.38	0.001	0.005*
Starch	m810	Ki3	-0.33	0.006	0.029*
Starch	m810	Ky21	-0.11	0.271	0.438
Starch	m810	M162W	-0.29	0.003	0.016*
Starch	m810	M37W	-0.06	0.607	0.766
Starch	m810	Mo18W	-0.23	0.032	0.096
Starch	m810	MS71	-0.03	0.739	0.860
Starch	m810	NC350	0.09	0.361	0.537
Starch	m810	NC358	-0.31	0.001	0.010*
Starch	m810	Oh43	0.04	0.730	0.860
Starch	m810	Oh7B	0.21	0.059	0.148
Starch	m810	Tx303	-0.03	0.745	0.863
Starch	m810	Tzi8	-0.19	0.074	0.176
Starch	m820	B97	0.30	0.011	0.042*
Starch	m820	CML103	0.43	0.001	0.004*
Starch	m820	CML228	-0.02	0.881	0.936
Starch	m820	CML247	0.47	0.000	0.001**
Starch	m820	CML277	0.07	0.541	0.717
Starch	m820	CML322	0.07	0.543	0.717
Starch	m820	CML333	0.36	0.001	0.007*
Starch	m820	CML52	0.23	0.065	0.160
Starch	m820	CML69	0.22	0.031	0.095
Starch	m820	HP301	0.51	0.000	0.001**
Starch	m820	Ki11	0.50	0.000	0.002*
Starch	m820	Ki3	0.28	0.035	0.103
Starch	m820	Ky21	0.31	0.003	0.016*
Starch	m820	M162W	0.14	0.188	0.340
Starch	m820	M37W	-0.04	0.719	0.852
Starch	m820	Mo18W	0.36	0.002	0.011*
Starch	m820	MS71	0.39	0.000	0.001*
Starch	m820	NC350	0.22	0.056	0.145
Starch	m820	NC358	0.38	0.000	0.002*
Starch	m820	Oh43	0.17	0.232	0.394
Starch	m820	Oh7B	0.11	0.349	0.524
Starch	m820	Tx303	0.31	0.003	0.015*
Starch	m820	Tzi8	0.38	0.000	0.004*
Starch	m860	B97	0.06	0.570	0.738

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m860	CML103	0.27	0.005	0.023*
Starch	m860	CML228	0.01	0.886	0.936
Starch	m860	CML247	-0.03	0.735	0.860
Starch	m860	CML277	-0.01	0.868	0.936
Starch	m860	CML322	0.19	0.037	0.106
Starch	m860	CML333	0.03	0.752	0.867
Starch	m860	CML52	0.08	0.344	0.522
Starch	m860	CML69	0.24	0.009	0.038*
Starch	m860	HP301	0.17	0.051	0.135
Starch	m860	Ki11	0.11	0.234	0.395
Starch	m860	Ki3	0.65	0.000	0.001*
Starch	m860	Ky21	0.28	0.002	0.014*
Starch	m860	M162W	0.06	0.509	0.694
Starch	m860	M37W	0.30	0.001	0.005*
Starch	m860	Mo18W	0.03	0.773	0.882
Starch	m860	MS71	-0.11	0.210	0.366
Starch	m860	NC350	0.27	0.005	0.024*
Starch	m860	NC358	0.26	0.004	0.022*
Starch	m860	Oh43	0.01	0.884	0.936
Starch	m860	Oh7B	0.01	0.956	0.980
Starch	m860	Tx303	0.25	0.007	0.031*
Starch	m860	Tzi8	-0.02	0.822	0.911
Starch	m922	B97	0.03	0.791	0.896
Starch	m922	CML103	-0.23	0.014	0.050
Starch	m922	CML228	-0.19	0.039	0.110
Starch	m922	CML247	0.07	0.460	0.651
Starch	m922	CML277	0.08	0.398	0.581
Starch	m922	CML322	-0.33	0.000	0.003*
Starch	m922	CML333	-0.13	0.127	0.256
Starch	m922	CML52	-0.13	0.142	0.278
Starch	m922	CML69	-0.02	0.832	0.919
Starch	m922	HP301	-0.38	0.000	0.001**
Starch	m922	Ki11	-0.22	0.016	0.055
Starch	m922	Ki3	0.20	0.086	0.195
Starch	m922	Ky21	-0.10	0.249	0.409
Starch	m922	M162W	0.23	0.009	0.038*
Starch	m922	M37W	-0.09	0.305	0.475

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m922	Mo18W	-0.06	0.554	0.727
Starch	m922	MS71	-0.45	0.000	0.001**
Starch	m922	NC350	-0.21	0.024	0.076
Starch	m922	NC358	0.19	0.050	0.134
Starch	m922	Oh43	-0.06	0.538	0.717
Starch	m922	Oh7B	-0.16	0.112	0.238
Starch	m922	Tx303	-0.13	0.139	0.274
Starch	m922	Tzi8	0.03	0.782	0.888
Starch	m968	B97	-0.17	0.111	0.237
Starch	m968	CML103	-0.13	0.250	0.409
Starch	m968	CML228	-0.05	0.643	0.802
Starch	m968	CML247	-0.22	0.015	0.054
Starch	m968	CML277	-0.27	0.006	0.027*
Starch	m968	CML322	-0.13	0.160	0.300
Starch	m968	CML333	-0.26	0.005	0.023*
Starch	m968	CML52	-0.02	0.821	0.911
Starch	m968	CML69	-0.25	0.021	0.070
Starch	m968	HP301	-0.26	0.006	0.029*
Starch	m968	Ki11	-0.20	0.047	0.130
Starch	m968	Ki3	-0.18	0.122	0.252
Starch	m968	Ky21	-0.52	0.000	0.001**
Starch	m968	M162W	-0.43	0.000	0.001*
Starch	m968	M37W	-0.35	0.000	0.003*
Starch	m968	Mo18W	0.02	0.866	0.936
Starch	m968	MS71	-0.34	0.003	0.015*
Starch	m968	NC350	-0.32	0.001	0.007*
Starch	m968	NC358	-0.55	0.000	0.001**
Starch	m968	Oh43	-0.09	0.386	0.567
Starch	m968	Oh7B	-0.04	0.702	0.843
Starch	m968	Tx303	-0.23	0.037	0.107
Starch	m968	Tzi8	-0.09	0.369	0.546
Starch	m999	B97	-0.34	0.002	0.015*
Starch	m999	CML103	0.13	0.236	0.397
Starch	m999	CML228	-0.21	0.026	0.082
Starch	m999	CML247	-0.34	0.000	0.002*
Starch	m999	CML277	-0.05	0.604	0.766
Starch	m999	CML322	-0.28	0.003	0.017*

Table S5: (continued…Starch)

Trait	QTL	Population	Effect^{a} (%)	Raw *P-value*	FDR *P-value*
Starch	m999	CML333	-0.17	0.058	0.147
Starch	m999	CML52	-0.25	0.012	0.046*
Starch	m999	CML69	-0.02	0.818	0.910
Starch	m999	HP301	-0.20	0.039	0.110
Starch	m999	Ki11	-0.17	0.096	0.212
Starch	m999	Ki3	-0.39	0.001	0.005*
Starch	m999	Ky21	0.13	0.178	0.323
Starch	m999	M162W	-0.04	0.681	0.829
Starch	m999	M37W	-0.05	0.604	0.766
Starch	m999	Mo18W	-0.29	0.003	0.016*
Starch	m999	MS71	-0.05	0.644	0.802
Starch	m999	NC350	-0.03	0.736	0.860
Starch	m999	NC358	-0.21	0.043	0.118
Starch	m999	Oh43	-0.12	0.221	0.379
Starch	m999	Oh7B	-0.14	0.205	0.362
Starch	m999	Tx303	-0.29	0.010	0.039*
Starch	m999	Tzi8	-0.27	0.010	0.040*
Starch	m1060	B97	0.04	0.658	0.811
Starch	m1060	CML103	0.36	0.000	0.001**
Starch	m1060	CML228	0.19	0.039	0.110
Starch	m1060	CML247	-0.01	0.886	0.936
Starch	m1060	CML277	0.14	0.112	0.238
Starch	m1060	CML322	0.42	0.000	0.001**
Starch	m1060	CML333	0.06	0.453	0.645
Starch	m1060	CML52	0.17	0.049	0.134
Starch	m1060	CML69	0.06	0.510	0.694

Table S5: (continued…Starch)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Starch	m1060	HP301	-0.26	0.003	0.016*
Starch	m1060	Ki11	-0.04	0.630	0.793
Starch	m1060	Ki3	0.39	0.000	0.004*
Starch	m1060	Ky21	0.09	0.304	0.475
Starch	m1060	M162W	0.15	0.094	0.209
Starch	m1060	M37W	0.25	0.004	0.021*
Starch	m1060	Mo18W	0.22	0.011	0.042*
Starch	m1060	MS71	0.18	0.048	0.130
Starch	m1060	NC350	-0.05	0.598	0.765
Starch	m1060	NC358	0.35	0.000	0.002*
Starch	m1060	Oh43	0.08	0.355	0.530
Starch	m1060	Oh7B	0.40	0.000	0.001**
Starch	m1060	Tx303	0.33	0.000	0.002*
Starch	m1060	Tzi8	0.23	0.010	0.039*

[a] Percent starch kernel composition on a dry matter basis relative to B73.

* FDR: $P \leq 0.05$

** FDR: $P \leq 0.001$

Table S6: NAM joint-linkage mapping analysis QTL allelic effects summary for percent protein content on a dry matter basis.

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m39	B97	-0.04	0.414	0.586
Protein	m39	CML103	-0.12	0.015	0.063
Protein	m39	CML228	-0.15	0.003	0.018*
Protein	m39	CML247	0.05	0.315	0.503
Protein	m39	CML277	0.06	0.208	0.378
Protein	m39	CML322	-0.02	0.623	0.743
Protein	m39	CML333	-0.04	0.378	0.559
Protein	m39	CML52	-0.04	0.361	0.546
Protein	m39	CML69	0.03	0.496	0.657
Protein	m39	HP301	-0.04	0.478	0.644
Protein	m39	Ki11	-0.15	0.003	0.018*
Protein	m39	Ki3	-0.01	0.846	0.905
Protein	m39	Ky21	0.13	0.009	0.043*
Protein	m39	M162W	-0.02	0.714	0.815
Protein	m39	M37W	0.17	0.001	0.007*
Protein	m39	Mo18W	-0.02	0.629	0.745
Protein	m39	MS71	0.12	0.010	0.045
Protein	m39	NC350	-0.03	0.584	0.715
Protein	m39	NC358	0.03	0.544	0.691
Protein	m39	Oh43	0.15	0.002	0.012*
Protein	m39	Oh7B	-0.02	0.763	0.856
Protein	m39	Tx303	-0.08	0.082	0.201
Protein	m39	Tzi8	-0.06	0.249	0.431
Protein	m115	B97	-0.03	0.511	0.666
Protein	m115	CML103	-0.34	0.000	0.001**
Protein	m115	CML228	0.15	0.003	0.019*
Protein	m115	CML247	0.10	0.065	0.171
Protein	m115	CML277	-0.03	0.621	0.742
Protein	m115	CML322	0.09	0.101	0.230
Protein	m115	CML333	-0.02	0.717	0.815
Protein	m115	CML52	0.05	0.329	0.519
Protein	m115	CML69	0.01	0.862	0.920
Protein	m115	HP301	0.02	0.732	0.827
Protein	m115	Ki11	0.00	0.965	0.976
Protein	m115	Ki3	0.15	0.031	0.106
Protein	m115	Ky21	-0.15	0.003	0.017*

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m115	M162W	-0.18	0.001	0.009*
Protein	m115	M37W	-0.06	0.265	0.446
Protein	m115	Mo18W	-0.03	0.547	0.691
Protein	m115	MS71	0.06	0.305	0.488
Protein	m115	NC350	-0.11	0.037	0.118
Protein	m115	NC358	0.00	0.933	0.956
Protein	m115	Oh43	0.07	0.231	0.407
Protein	m115	Oh7B	0.17	0.004	0.024*
Protein	m115	Tx303	-0.09	0.079	0.197
Protein	m115	Tzi8	0.11	0.037	0.118
Protein	m135	B97	0.07	0.144	0.300
Protein	m135	CML103	0.34	0.000	0.001**
Protein	m135	CML228	0.04	0.511	0.666
Protein	m135	CML247	0.19	0.000	0.001*
Protein	m135	CML277	0.03	0.615	0.739
Protein	m135	CML322	0.20	0.000	0.002*
Protein	m135	CML333	-0.08	0.160	0.317
Protein	m135	CML52	0.06	0.215	0.386
Protein	m135	CML69	0.05	0.377	0.559
Protein	m135	HP301	0.02	0.700	0.804
Protein	m135	Ki11	0.15	0.006	0.029*
Protein	m135	Ki3	0.13	0.062	0.168
Protein	m135	Ky21	0.13	0.008	0.040*
Protein	m135	M162W	0.07	0.226	0.401
Protein	m135	M37W	0.02	0.619	0.742
Protein	m135	Mo18W	0.06	0.261	0.443
Protein	m135	MS71	0.04	0.475	0.642
Protein	m135	NC350	-0.01	0.870	0.924
Protein	m135	NC358	0.08	0.098	0.229
Protein	m135	Oh43	0.04	0.488	0.651
Protein	m135	Oh7B	-0.05	0.343	0.532
Protein	m135	Tx303	0.01	0.792	0.877
Protein	m135	Tzi8	-0.07	0.195	0.364
Protein	m209	B97	0.02	0.697	0.803
Protein	m209	CML103	0.12	0.023	0.090
Protein	m209	CML228	-0.04	0.367	0.554

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m209	CML247	0.13	0.014	0.058
Protein	m209	CML277	-0.02	0.667	0.776
Protein	m209	CML322	-0.14	0.003	0.020*
Protein	m209	CML333	-0.02	0.635	0.750
Protein	m209	CML52	0.06	0.236	0.414
Protein	m209	CML69	0.07	0.152	0.313
Protein	m209	HP301	0.01	0.790	0.876
Protein	m209	Ki11	0.06	0.212	0.384
Protein	m209	Ki3	-0.01	0.822	0.890
Protein	m209	Ky21	0.03	0.641	0.755
Protein	m209	M162W	0.10	0.060	0.165
Protein	m209	M37W	-0.03	0.572	0.706
Protein	m209	Mo18W	0.04	0.383	0.559
Protein	m209	MS71	-0.13	0.009	0.041*
Protein	m209	NC350	0.09	0.077	0.194
Protein	m209	NC358	-0.03	0.552	0.693
Protein	m209	Oh43	0.10	0.044	0.132
Protein	m209	Oh7B	-0.22	0.000	0.001**
Protein	m209	Tx303	0.15	0.001	0.011*
Protein	m209	Tzi8	0.24	0.000	0.001**
Protein	m261	B97	-0.27	0.000	0.001**
Protein	m261	CML103	-0.08	0.129	0.276
Protein	m261	CML228	-0.01	0.821	0.890
Protein	m261	CML247	-0.03	0.558	0.698
Protein	m261	CML277	-0.03	0.574	0.708
Protein	m261	CML322	-0.11	0.036	0.118
Protein	m261	CML333	0.04	0.464	0.630
Protein	m261	CML52	-0.15	0.002	0.015*
Protein	m261	CML69	-0.22	0.000	0.001**
Protein	m261	HP301	-0.04	0.400	0.572
Protein	m261	Ki11	-0.03	0.521	0.672
Protein	m261	Ki3	0.01	0.872	0.924
Protein	m261	Ky21	-0.13	0.019	0.076
Protein	m261	M162W	-0.18	0.001	0.011*
Protein	m261	M37W	0.10	0.117	0.257
Protein	m261	Mo18W	-0.10	0.038	0.121

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m261	MS71	0.05	0.320	0.508
Protein	m261	NC350	-0.07	0.158	0.316
Protein	m261	NC358	-0.07	0.133	0.283
Protein	m261	Oh43	-0.05	0.294	0.478
Protein	m261	Oh7B	-0.06	0.292	0.478
Protein	m261	Tx303	0.08	0.104	0.235
Protein	m261	Tzi8	-0.08	0.158	0.316
Protein	m300	B97	-0.08	0.085	0.209
Protein	m300	CML103	0.14	0.002	0.015*
Protein	m300	CML228	-0.04	0.418	0.588
Protein	m300	CML247	-0.08	0.124	0.270
Protein	m300	CML277	-0.10	0.044	0.132
Protein	m300	CML322	-0.08	0.103	0.234
Protein	m300	CML333	-0.11	0.015	0.062
Protein	m300	CML52	-0.07	0.159	0.317
Protein	m300	CML69	0.03	0.587	0.717
Protein	m300	HP301	-0.05	0.317	0.506
Protein	m300	Ki11	0.02	0.653	0.766
Protein	m300	Ki3	0.11	0.064	0.170
Protein	m300	Ky21	0.02	0.708	0.810
Protein	m300	M162W	-0.05	0.342	0.531
Protein	m300	M37W	-0.03	0.570	0.705
Protein	m300	Mo18W	-0.06	0.200	0.367
Protein	m300	MS71	-0.10	0.040	0.125
Protein	m300	NC350	-0.16	0.001	0.008*
Protein	m300	NC358	-0.03	0.529	0.678
Protein	m300	Oh43	0.01	0.913	0.946
Protein	m300	Oh7B	0.00	0.992	0.995
Protein	m300	Tx303	-0.19	0.000	0.002*
Protein	m300	Tzi8	-0.14	0.004	0.023*
Protein	m353	B97	0.03	0.597	0.726
Protein	m353	CML103	0.03	0.470	0.637
Protein	m353	CML228	-0.02	0.660	0.772
Protein	m353	CML247	0.04	0.338	0.527
Protein	m353	CML277	-0.09	0.055	0.154
Protein	m353	CML322	0.02	0.663	0.773

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m353	CML333	-0.01	0.838	0.903
Protein	m353	CML52	0.10	0.026	0.096
Protein	m353	CML69	0.02	0.695	0.802
Protein	m353	HP301	0.10	0.051	0.146
Protein	m353	Ki11	0.12	0.009	0.043*
Protein	m353	Ki3	-0.02	0.723	0.821
Protein	m353	Ky21	0.00	0.948	0.967
Protein	m353	M162W	-0.08	0.116	0.256
Protein	m353	M37W	0.10	0.036	0.118
Protein	m353	Mo18W	-0.04	0.486	0.651
Protein	m353	MS71	0.15	0.001	0.009*
Protein	m353	NC350	0.09	0.054	0.152
Protein	m353	NC358	0.08	0.092	0.220
Protein	m353	Oh43	0.17	0.001	0.007*
Protein	m353	Oh7B	0.15	0.002	0.012*
Protein	m353	Tx303	0.15	0.003	0.017*
Protein	m353	Tzi8	-0.27	0.000	0.001**
Protein	m426	B97	-0.10	0.042	0.127
Protein	m426	CML103	-0.13	0.005	0.026*
Protein	m426	CML228	-0.11	0.022	0.085
Protein	m426	CML247	-0.08	0.080	0.199
Protein	m426	CML277	0.03	0.532	0.678
Protein	m426	CML322	-0.07	0.141	0.296
Protein	m426	CML333	-0.12	0.010	0.043*
Protein	m426	CML52	0.10	0.042	0.127
Protein	m426	CML69	-0.19	0.000	0.001*
Protein	m426	HP301	0.04	0.405	0.576
Protein	m426	Ki11	-0.03	0.586	0.716
Protein	m426	Ki3	0.02	0.761	0.855
Protein	m426	Ky21	-0.02	0.607	0.736
Protein	m426	M162W	0.02	0.612	0.736
Protein	m426	M37W	-0.02	0.611	0.736
Protein	m426	Mo18W	-0.12	0.010	0.045*
Protein	m426	MS71	-0.06	0.214	0.386
Protein	m426	NC350	-0.08	0.089	0.216
Protein	m426	NC358	-0.07	0.154	0.313

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m426	Oh43	0.04	0.375	0.558
Protein	m426	Oh7B	-0.05	0.271	0.452
Protein	m426	Tx303	-0.16	0.001	0.007*
Protein	m426	Tzi8	-0.02	0.753	0.848
Protein	m484	B97	-0.04	0.436	0.601
Protein	m484	CML103	-0.01	0.811	0.887
Protein	m484	CML228	0.12	0.034	0.114
Protein	m484	CML247	0.11	0.036	0.118
Protein	m484	CML277	0.04	0.420	0.590
Protein	m484	CML322	0.12	0.014	0.059
Protein	m484	CML333	-0.05	0.357	0.543
Protein	m484	CML52	0.23	0.000	0.001*
Protein	m484	CML69	0.20	0.000	0.003*
Protein	m484	HP301	0.10	0.079	0.197
Protein	m484	Ki11	0.11	0.040	0.125
Protein	m484	Ki3	0.05	0.428	0.598
Protein	m484	Ky21	0.04	0.380	0.559
Protein	m484	M162W	0.08	0.123	0.268
Protein	m484	M37W	0.10	0.063	0.168
Protein	m484	Mo18W	0.09	0.100	0.230
Protein	m484	MS71	-0.07	0.243	0.422
Protein	m484	NC350	0.08	0.185	0.349
Protein	m484	NC358	0.10	0.080	0.199
Protein	m484	Oh43	0.10	0.065	0.171
Protein	m484	Oh7B	0.14	0.050	0.145
Protein	m484	Tx303	0.09	0.100	0.230
Protein	m484	Tzi8	0.25	0.000	0.001**
Protein	m495	B97	0.03	0.549	0.692
Protein	m495	CML103	-0.01	0.904	0.943
Protein	m495	CML228	-0.08	0.154	0.313
Protein	m495	CML247	0.10	0.063	0.168
Protein	m495	CML277	-0.03	0.567	0.705
Protein	m495	CML322	0.06	0.214	0.386
Protein	m495	CML333	0.07	0.180	0.344
Protein	m495	CML52	0.20	0.000	0.003*
Protein	m495	CML69	0.01	0.821	0.890

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m495	HP301	-0.05	0.337	0.527
Protein	m495	Ki11	0.09	0.089	0.216
Protein	m495	Ki3	0.10	0.142	0.296
Protein	m495	Ky21	-0.20	0.000	0.002*
Protein	m495	M162W	0.01	0.878	0.928
Protein	m495	M37W	0.08	0.155	0.314
Protein	m495	Mo18W	-0.04	0.518	0.671
Protein	m495	MS71	0.12	0.037	0.118
Protein	m495	NC350	0.17	0.003	0.019*
Protein	m495	NC358	-0.01	0.842	0.904
Protein	m495	Oh43	-0.03	0.547	0.691
Protein	m495	Oh7B	-0.12	0.103	0.234
Protein	m495	Tx303	-0.05	0.404	0.576
Protein	m495	Tzi8	-0.05	0.447	0.612
Protein	m615	B97	-0.03	0.514	0.669
Protein	m615	CML103	-0.20	0.000	0.002*
Protein	m615	CML228	0.13	0.012	0.051
Protein	m615	CML247	0.08	0.114	0.253
Protein	m615	CML277	0.10	0.039	0.123
Protein	m615	CML322	-0.01	0.819	0.890
Protein	m615	CML333	0.04	0.413	0.585
Protein	m615	CML52	-0.13	0.009	0.043*
Protein	m615	CML69	0.07	0.148	0.306
Protein	m615	HP301	-0.11	0.023	0.089
Protein	m615	Ki11	-0.11	0.026	0.096
Protein	m615	Ki3	-0.19	0.003	0.019*
Protein	m615	Ky21	-0.01	0.808	0.886
Protein	m615	M162W	-0.01	0.863	0.920
Protein	m615	M37W	0.02	0.715	0.815
Protein	m615	Mo18W	-0.01	0.809	0.886
Protein	m615	MS71	-0.09	0.073	0.186
Protein	m615	NC350	0.07	0.156	0.315
Protein	m615	NC358	0.03	0.594	0.723
Protein	m615	Oh43	0.02	0.753	0.848
Protein	m615	Oh7B	-0.13	0.012	0.052
Protein	m615	Tx303	-0.34	0.000	0.001**

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m615	Tzi8	-0.03	0.546	0.691
Protein	m657	B97	0.18	0.001	0.007*
Protein	m657	CML103	0.21	0.000	0.001*
Protein	m657	CML228	-0.02	0.771	0.859
Protein	m657	CML247	0.04	0.407	0.578
Protein	m657	CML277	0.15	0.002	0.014*
Protein	m657	CML322	0.04	0.505	0.662
Protein	m657	CML333	0.15	0.006	0.029*
Protein	m657	CML52	0.05	0.372	0.557
Protein	m657	CML69	0.15	0.003	0.018*
Protein	m657	HP301	0.04	0.417	0.588
Protein	m657	Ki11	0.07	0.154	0.313
Protein	m657	Ki3	0.33	0.000	0.001**
Protein	m657	Ky21	0.10	0.047	0.139
Protein	m657	M162W	-0.09	0.062	0.168
Protein	m657	M37W	0.03	0.621	0.742
Protein	m657	Mo18W	0.11	0.021	0.084
Protein	m657	MS71	0.07	0.150	0.309
Protein	m657	NC350	0.04	0.391	0.566
Protein	m657	NC358	0.00	0.924	0.955
Protein	m657	Oh43	0.01	0.883	0.928
Protein	m657	Oh7B	0.08	0.118	0.257
Protein	m657	Tx303	0.32	0.000	0.001**
Protein	m657	Tzi8	0.23	0.000	0.001**
Protein	m694	B97	0.10	0.056	0.157
Protein	m694	CML103	0.16	0.002	0.012*
Protein	m694	CML228	0.04	0.459	0.627
Protein	m694	CML247	0.07	0.222	0.397
Protein	m694	CML277	0.16	0.005	0.026*
Protein	m694	CML322	0.07	0.209	0.381
Protein	m694	CML333	-0.05	0.391	0.566
Protein	m694	CML52	-0.02	0.777	0.863
Protein	m694	CML69	0.08	0.171	0.334
Protein	m694	HP301	0.06	0.304	0.488
Protein	m694	Ki11	0.14	0.011	0.047*
Protein	m694	Ki3	0.16	0.026	0.096

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m694	Ky21	0.03	0.583	0.715
Protein	m694	M162W	0.06	0.285	0.470
Protein	m694	M37W	0.00	0.999	0.999
Protein	m694	Mo18W	0.08	0.170	0.333
Protein	m694	MS71	0.05	0.350	0.536
Protein	m694	NC350	0.18	0.001	0.009*
Protein	m694	NC358	0.22	0.000	0.001*
Protein	m694	Oh43	-0.09	0.126	0.271
Protein	m694	Oh7B	-0.05	0.394	0.569
Protein	m694	Tx303	0.18	0.002	0.014*
Protein	m694	Tzi8	0.09	0.090	0.216
Protein	m707	B97	-0.12	0.068	0.177
Protein	m707	CML103	0.05	0.436	0.601
Protein	m707	CML228	0.05	0.382	0.559
Protein	m707	CML247	-0.01	0.843	0.904
Protein	m707	CML277	-0.11	0.063	0.169
Protein	m707	CML322	-0.03	0.610	0.736
Protein	m707	CML333	0.04	0.563	0.702
Protein	m707	CML52	-0.02	0.771	0.859
Protein	m707	CML69	0.05	0.352	0.539
Protein	m707	HP301	-0.09	0.153	0.313
Protein	m707	Ki11	0.06	0.334	0.525
Protein	m707	Ki3	0.13	0.073	0.186
Protein	m707	Ky21	0.13	0.041	0.127
Protein	m707	M162W	0.01	0.864	0.920
Protein	m707	M37W	0.10	0.128	0.274
Protein	m707	Mo18W	0.02	0.700	0.804
Protein	m707	MS71	0.01	0.933	0.956
Protein	m707	NC350	0.20	0.008	0.038*
Protein	m707	NC358	-0.05	0.349	0.536
Protein	m707	Oh43	0.00	0.951	0.968
Protein	m707	Oh7B	0.32	0.000	0.001**
Protein	m707	Tx303	0.21	0.001	0.008*
Protein	m707	Tzi8	0.07	0.252	0.433
Protein	m729	B97	0.01	0.880	0.928
Protein	m729	CML103	-0.08	0.134	0.283

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m729	CML228	-0.06	0.220	0.393
Protein	m729	CML247	-0.08	0.147	0.305
Protein	m729	CML277	-0.10	0.051	0.146
Protein	m729	CML322	-0.05	0.380	0.559
Protein	m729	CML333	-0.06	0.292	0.478
Protein	m729	CML52	-0.07	0.131	0.280
Protein	m729	CML69	-0.18	0.000	0.003*
Protein	m729	HP301	0.00	0.994	0.995
Protein	m729	Ki11	-0.17	0.003	0.019*
Protein	m729	Ki3	-0.38	0.000	0.001**
Protein	m729	Ky21	0.00	0.926	0.955
Protein	m729	M162W	-0.07	0.181	0.344
Protein	m729	M37W	-0.16	0.002	0.014*
Protein	m729	Mo18W	0.07	0.201	0.367
Protein	m729	MS71	-0.19	0.000	0.003*
Protein	m729	NC350	-0.22	0.000	0.005*
Protein	m729	NC358	-0.17	0.001	0.011*
Protein	m729	Oh43	-0.02	0.628	0.745
Protein	m729	Oh7B	-0.07	0.264	0.446
Protein	m729	Tx303	-0.20	0.000	0.002*
Protein	m729	Tzi8	0.03	0.560	0.699
Protein	m757	B97	0.08	0.086	0.210
Protein	m757	CML103	0.09	0.096	0.225
Protein	m757	CML228	0.04	0.437	0.601
Protein	m757	CML247	0.00	0.967	0.976
Protein	m757	CML277	-0.01	0.824	0.891
Protein	m757	CML322	0.07	0.160	0.317
Protein	m757	CML333	0.06	0.199	0.366
Protein	m757	CML52	0.12	0.008	0.039*
Protein	m757	CML69	-0.03	0.548	0.691
Protein	m757	HP301	0.06	0.185	0.349
Protein	m757	Ki11	0.20	0.000	0.001**
Protein	m757	Ki3	0.02	0.796	0.879
Protein	m757	Ky21	0.20	0.000	0.001**
Protein	m757	M162W	0.00	0.930	0.955
Protein	m757	M37W	-0.02	0.651	0.765

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m757	Mo18W	0.08	0.113	0.253
Protein	m757	MS71	-0.05	0.290	0.477
Protein	m757	NC350	-0.01	0.908	0.943
Protein	m757	NC358	0.09	0.072	0.184
Protein	m757	Oh43	0.00	0.955	0.970
Protein	m757	Oh7B	-0.03	0.517	0.670
Protein	m757	Tx303	0.17	0.000	0.005*
Protein	m757	Tzi8	0.13	0.008	0.039*
Protein	m802	B97	-0.02	0.799	0.879
Protein	m802	CML103	-0.04	0.502	0.661
Protein	m802	CML228	-0.07	0.135	0.285
Protein	m802	CML247	-0.06	0.256	0.436
Protein	m802	CML277	-0.25	0.000	0.001**
Protein	m802	CML322	-0.04	0.436	0.601
Protein	m802	CML333	-0.05	0.375	0.558
Protein	m802	CML52	-0.19	0.000	0.002*
Protein	m802	CML69	-0.25	0.000	0.001**
Protein	m802	HP301	-0.04	0.496	0.657
Protein	m802	Ki11	0.04	0.499	0.658
Protein	m802	Ki3	-0.07	0.263	0.446
Protein	m802	Ky21	-0.05	0.303	0.488
Protein	m802	M162W	0.00	0.959	0.972
Protein	m802	M37W	0.03	0.521	0.672
Protein	m802	Mo18W	-0.07	0.180	0.344
Protein	m802	MS71	-0.01	0.843	0.904
Protein	m802	NC350	-0.11	0.034	0.114
Protein	m802	NC358	-0.02	0.726	0.822
Protein	m802	Oh43	-0.11	0.058	0.161
Protein	m802	Oh7B	-0.12	0.050	0.145
Protein	m802	Tx303	0.05	0.347	0.536
Protein	m802	Tzi8	0.13	0.015	0.061
Protein	m820	B97	-0.15	0.012	0.051
Protein	m820	CML103	-0.07	0.285	0.470
Protein	m820	CML228	-0.12	0.033	0.112
Protein	m820	CML247	-0.11	0.045	0.133
Protein	m820	CML277	-0.05	0.433	0.601

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m820	CML322	0.08	0.164	0.324
Protein	m820	CML333	-0.09	0.095	0.224
Protein	m820	CML52	-0.18	0.003	0.017*
Protein	m820	CML69	-0.07	0.172	0.334
Protein	m820	HP301	-0.07	0.252	0.433
Protein	m820	Ki11	-0.11	0.091	0.217
Protein	m820	Ki3	-0.12	0.090	0.216
Protein	m820	Ky21	-0.18	0.001	0.011*
Protein	m820	M162W	0.16	0.003	0.019*
Protein	m820	M37W	0.07	0.231	0.407
Protein	m820	Mo18W	-0.13	0.036	0.118
Protein	m820	MS71	-0.09	0.086	0.209
Protein	m820	NC350	0.01	0.909	0.943
Protein	m820	NC358	-0.07	0.166	0.327
Protein	m820	Oh43	0.02	0.799	0.879
Protein	m820	Oh7B	0.01	0.930	0.955
Protein	m820	Tx303	-0.17	0.002	0.012*
Protein	m820	Tzi8	-0.14	0.012	0.051
Protein	m872	B97	-0.10	0.114	0.253
Protein	m872	CML103	-0.13	0.025	0.094
Protein	m872	CML228	-0.01	0.881	0.928
Protein	m872	CML247	-0.12	0.031	0.106
Protein	m872	CML277	-0.13	0.009	0.043*
Protein	m872	CML322	-0.11	0.027	0.098
Protein	m872	CML333	0.02	0.684	0.791
Protein	m872	CML52	-0.14	0.006	0.029*
Protein	m872	CML69	-0.11	0.033	0.112
Protein	m872	HP301	-0.05	0.319	0.508
Protein	m872	Ki11	-0.23	0.000	0.002*
Protein	m872	Ki3	-0.19	0.009	0.042*
Protein	m872	Ky21	-0.13	0.029	0.101
Protein	m872	M162W	0.15	0.005	0.027*
Protein	m872	M37W	-0.10	0.070	0.182
Protein	m872	Mo18W	-0.05	0.387	0.563
Protein	m872	MS71	-0.02	0.767	0.859
Protein	m872	NC350	-0.07	0.179	0.344

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m872	NC358	-0.09	0.101	0.230
Protein	m872	Oh43	-0.05	0.383	0.559
Protein	m872	Oh7B	-0.04	0.568	0.705
Protein	m872	Tx303	-0.15	0.006	0.031*
Protein	m872	Tzi8	-0.20	0.000	0.002*
Protein	m912	B97	0.09	0.172	0.334
Protein	m912	CML103	-0.05	0.464	0.630
Protein	m912	CML228	-0.13	0.028	0.099
Protein	m912	CML247	-0.08	0.185	0.349
Protein	m912	CML277	0.01	0.838	0.903
Protein	m912	CML322	0.05	0.398	0.572
Protein	m912	CML333	0.02	0.678	0.786
Protein	m912	CML52	-0.11	0.047	0.139
Protein	m912	CML69	0.14	0.035	0.115
Protein	m912	HP301	0.07	0.266	0.446
Protein	m912	Ki11	0.08	0.227	0.402
Protein	m912	Ki3	-0.36	0.000	0.003*
Protein	m912	Ky21	0.00	0.977	0.985
Protein	m912	M162W	-0.15	0.024	0.092
Protein	m912	M37W	-0.18	0.003	0.020*
Protein	m912	Mo18W	-0.02	0.770	0.859
Protein	m912	MS71	0.14	0.012	0.051
Protein	m912	NC350	-0.07	0.254	0.435
Protein	m912	NC358	-0.18	0.004	0.021*
Protein	m912	Oh43	-0.09	0.114	0.253
Protein	m912	Oh7B	0.16	0.031	0.106
Protein	m912	Tx303	0.06	0.293	0.478
Protein	m912	Tzi8	-0.17	0.002	0.014*
Protein	m930	B97	-0.03	0.612	0.736
Protein	m930	CML103	0.13	0.027	0.099
Protein	m930	CML228	0.19	0.000	0.004*
Protein	m930	CML247	0.01	0.796	0.879
Protein	m930	CML277	-0.12	0.025	0.094
Protein	m930	CML322	0.10	0.054	0.154
Protein	m930	CML333	-0.03	0.672	0.781
Protein	m930	CML52	0.05	0.331	0.521

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m930	CML69	-0.08	0.181	0.344
Protein	m930	HP301	0.04	0.532	0.678
Protein	m930	Ki11	-0.01	0.908	0.943
Protein	m930	Ki3	0.16	0.055	0.154
Protein	m930	Ky21	-0.05	0.341	0.531
Protein	m930	M162W	-0.09	0.101	0.230
Protein	m930	M37W	0.05	0.381	0.559
Protein	m930	Mo18W	0.04	0.455	0.623
Protein	m930	MS71	0.07	0.192	0.361
Protein	m930	NC350	0.22	0.000	0.002*
Protein	m930	NC358	0.05	0.368	0.554
Protein	m930	Oh43	-0.05	0.372	0.557
Protein	m930	Oh7B	0.18	0.001	0.007*
Protein	m930	Tx303	0.03	0.629	0.745
Protein	m930	Tzi8	0.08	0.126	0.271
Protein	m963	B97	0.09	0.081	0.201
Protein	m963	CML103	0.01	0.893	0.937
Protein	m963	CML228	0.04	0.399	0.572
Protein	m963	CML247	0.11	0.028	0.099
Protein	m963	CML277	0.06	0.192	0.361
Protein	m963	CML322	-0.01	0.895	0.937
Protein	m963	CML333	0.08	0.106	0.238
Protein	m963	CML52	0.02	0.663	0.773
Protein	m963	CML69	0.18	0.000	0.003*
Protein	m963	HP301	0.02	0.642	0.755
Protein	m963	Ki11	0.00	0.986	0.993
Protein	m963	Ki3	0.15	0.018	0.073
Protein	m963	Ky21	0.29	0.000	0.001**
Protein	m963	M162W	0.12	0.025	0.095
Protein	m963	M37W	0.13	0.010	0.043*
Protein	m963	Mo18W	0.02	0.702	0.804
Protein	m963	MS71	0.10	0.054	0.152
Protein	m963	NC350	0.16	0.001	0.005*
Protein	m963	NC358	0.11	0.030	0.105
Protein	m963	Oh43	0.05	0.349	0.536
Protein	m963	Oh7B	0.06	0.271	0.452

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m963	Tx303	0.10	0.066	0.171
Protein	m963	Tzi8	0.04	0.491	0.652
Protein	m1009	B97	0.15	0.003	0.018*
Protein	m1009	CML103	0.11	0.032	0.110
Protein	m1009	CML228	0.10	0.062	0.168
Protein	m1009	CML247	0.19	0.001	0.007*
Protein	m1009	CML277	0.15	0.003	0.020*
Protein	m1009	CML322	0.18	0.000	0.003*
Protein	m1009	CML333	0.05	0.302	0.488
Protein	m1009	CML52	0.22	0.000	0.001**
Protein	m1009	CML69	-0.07	0.197	0.365
Protein	m1009	HP301	0.10	0.042	0.128
Protein	m1009	Ki11	0.15	0.004	0.021*
Protein	m1009	Ki3	0.07	0.279	0.464
Protein	m1009	Ky21	-0.01	0.882	0.928
Protein	m1009	M162W	0.23	0.000	0.001**
Protein	m1009	M37W	0.04	0.489	0.652
Protein	m1009	Mo18W	0.13	0.011	0.048*
Protein	m1009	MS71	0.00	0.991	0.995
Protein	m1009	NC350	0.05	0.329	0.519
Protein	m1009	NC358	0.07	0.197	0.365
Protein	m1009	Oh43	0.10	0.046	0.136
Protein	m1009	Oh7B	0.06	0.266	0.446
Protein	m1009	Tx303	0.00	0.941	0.962
Protein	m1009	Tzi8	0.09	0.071	0.183
Protein	m1039	B97	-0.20	0.000	0.002*
Protein	m1039	CML103	-0.23	0.000	0.001**
Protein	m1039	CML228	0.03	0.511	0.666
Protein	m1039	CML247	-0.17	0.001	0.007*
Protein	m1039	CML277	0.09	0.058	0.160
Protein	m1039	CML322	0.05	0.354	0.541
Protein	m1039	CML333	0.06	0.249	0.431
Protein	m1039	CML52	0.06	0.282	0.468
Protein	m1039	CML69	0.04	0.433	0.601
Protein	m1039	HP301	0.01	0.903	0.943
Protein	m1039	Ki11	-0.09	0.096	0.225

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m1039	Ki3	-0.22	0.001	0.011*
Protein	m1039	Ky21	-0.01	0.819	0.890
Protein	m1039	M162W	-0.16	0.003	0.019*
Protein	m1039	M37W	-0.12	0.026	0.097
Protein	m1039	Mo18W	-0.04	0.483	0.649
Protein	m1039	MS71	-0.05	0.370	0.556
Protein	m1039	NC350	0.07	0.199	0.366
Protein	m1039	NC358	-0.18	0.000	0.005*
Protein	m1039	Oh43	-0.05	0.304	0.488
Protein	m1039	Oh7B	-0.24	0.000	0.001*
Protein	m1039	Tx303	-0.18	0.001	0.007*
Protein	m1039	Tzi8	-0.05	0.399	0.572
Protein	m1084	B97	-0.11	0.040	0.126
Protein	m1084	CML103	-0.31	0.000	0.001**
Protein	m1084	CML228	-0.10	0.061	0.165
Protein	m1084	CML247	0.04	0.486	0.651
Protein	m1084	CML277	-0.18	0.001	0.011*
Protein	m1084	CML322	-0.23	0.000	0.001**
Protein	m1084	CML333	-0.12	0.028	0.099
Protein	m1084	CML52	-0.26	0.000	0.001**
Protein	m1084	CML69	-0.27	0.000	0.001**
Protein	m1084	HP301	-0.06	0.255	0.436
Protein	m1084	Ki11	-0.13	0.030	0.106
Protein	m1084	Ki3	-0.12	0.074	0.187
Protein	m1084	Ky21	-0.15	0.012	0.052
Protein	m1084	M162W	-0.22	0.000	0.001**
Protein	m1084	M37W	-0.13	0.041	0.126
Protein	m1084	Mo18W	-0.13	0.020	0.078
Protein	m1084	MS71	-0.17	0.004	0.021*
Protein	m1084	NC350	-0.12	0.022	0.086
Protein	m1084	NC358	-0.15	0.006	0.029*
Protein	m1084	Oh43	-0.16	0.005	0.026*
Protein	m1084	Oh7B	-0.12	0.047	0.138
Protein	m1084	Tx303	-0.22	0.000	0.001*
Protein	m1084	Tzi8	-0.18	0.002	0.012*
Protein	m1106	B97	0.05	0.427	0.598

Table S6: (continued…Protein)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Protein	m1106	CML103	0.06	0.240	0.418
Protein	m1106	CML228	0.15	0.002	0.015*
Protein	m1106	CML247	0.03	0.553	0.694
Protein	m1106	CML277	-0.06	0.237	0.415
Protein	m1106	CML322	0.06	0.225	0.401
Protein	m1106	CML333	0.21	0.000	0.004*
Protein	m1106	CML52	-0.08	0.178	0.344
Protein	m1106	CML69	0.09	0.118	0.257
Protein	m1106	HP301	-0.04	0.478	0.644
Protein	m1106	Ki11	-0.01	0.928	0.955
Protein	m1106	Ki3	0.04	0.504	0.662
Protein	m1106	Ky21	-0.04	0.360	0.546
Protein	m1106	M162W	0.12	0.050	0.145
Protein	m1106	M37W	0.19	0.000	0.002*
Protein	m1106	Mo18W	0.03	0.583	0.715
Protein	m1106	MS71	0.24	0.000	0.001**
Protein	m1106	NC350	0.08	0.095	0.224
Protein	m1106	NC358	0.06	0.196	0.364
Protein	m1106	Oh43	0.05	0.434	0.601
Protein	m1106	Oh7B	0.03	0.531	0.678
Protein	m1106	Tx303	0.00	0.953	0.969
Protein	m1106	Tzi8	0.04	0.527	0.678

[a] Percent oil kernel composition on a dry matter basis relative to B73.

* FDR: $P \leq 0.05$

** FDR: $P \leq 0.001$

Table S7: NAM joint-linkage mapping analysis QTL allelic effects summary for percent oil content on a dry matter basis.

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m23	B97	0.06	0.003	0.020*
Oil	m23	CML103	0.01	0.751	0.837
Oil	m23	CML228	0.05	0.018	0.072
Oil	m23	CML247	-0.03	0.233	0.405
Oil	m23	CML277	0.01	0.538	0.696
Oil	m23	CML322	0.03	0.142	0.287
Oil	m23	CML333	0.04	0.107	0.243
Oil	m23	CML52	0.10	0.000	0.001**
Oil	m23	CML69	0.10	0.000	0.001**
Oil	m23	HP301	-0.01	0.654	0.768
Oil	m23	Ki11	-0.01	0.642	0.765
Oil	m23	Ki3	0.02	0.566	0.720
Oil	m23	Ky21	0.03	0.140	0.286
Oil	m23	M162W	0.04	0.062	0.166
Oil	m23	M37W	0.05	0.013	0.058
Oil	m23	Mo18W	0.04	0.049	0.142
Oil	m23	MS71	-0.06	0.009	0.042*
Oil	m23	NC350	0.03	0.242	0.419
Oil	m23	NC358	0.02	0.372	0.549
Oil	m23	Oh43	-0.04	0.104	0.238
Oil	m23	Oh7B	0.01	0.766	0.848
Oil	m23	Tx303	0.10	0.000	0.001**
Oil	m23	Tzi8	0.10	0.000	0.001**
Oil	m94	B97	-0.02	0.375	0.549
Oil	m94	CML103	0.00	0.843	0.903
Oil	m94	CML228	0.11	0.000	0.001**
Oil	m94	CML247	-0.02	0.408	0.583
Oil	m94	CML277	0.06	0.018	0.074
Oil	m94	CML322	0.08	0.001	0.006*
Oil	m94	CML333	0.12	0.000	0.001**
Oil	m94	CML52	0.07	0.002	0.016*
Oil	m94	CML69	0.04	0.086	0.204
Oil	m94	HP301	0.03	0.163	0.317
Oil	m94	Ki11	0.04	0.065	0.171
Oil	m94	Ki3	0.05	0.066	0.171
Oil	m94	Ky21	0.04	0.044	0.132

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m94	M162W	0.01	0.572	0.724
Oil	m94	M37W	0.05	0.053	0.149
Oil	m94	Mo18W	0.02	0.499	0.661
Oil	m94	MS71	0.03	0.234	0.405
Oil	m94	NC350	0.05	0.042	0.129
Oil	m94	NC358	0.04	0.122	0.261
Oil	m94	Oh43	0.00	0.912	0.943
Oil	m94	Oh7B	-0.04	0.142	0.287
Oil	m94	Tx303	0.05	0.035	0.112
Oil	m94	Tzi8	0.06	0.013	0.057
Oil	m118	B97	0.04	0.055	0.152
Oil	m118	CML103	-0.04	0.079	0.194
Oil	m118	CML228	0.05	0.079	0.194
Oil	m118	CML247	0.03	0.255	0.434
Oil	m118	CML277	0.04	0.101	0.234
Oil	m118	CML322	-0.04	0.083	0.201
Oil	m118	CML333	-0.03	0.360	0.545
Oil	m118	CML52	-0.05	0.023	0.086
Oil	m118	CML69	-0.02	0.530	0.689
Oil	m118	HP301	0.05	0.044	0.132
Oil	m118	Ki11	-0.08	0.001	0.007*
Oil	m118	Ki3	0.07	0.017	0.070
Oil	m118	Ky21	0.04	0.118	0.261
Oil	m118	M162W	-0.05	0.034	0.112
Oil	m118	M37W	-0.04	0.075	0.187
Oil	m118	Mo18W	0.05	0.056	0.153
Oil	m118	MS71	0.01	0.656	0.768
Oil	m118	NC350	0.00	0.973	0.985
Oil	m118	NC358	-0.01	0.555	0.711
Oil	m118	Oh43	0.02	0.486	0.651
Oil	m118	Oh7B	0.08	0.001	0.010*
Oil	m118	Tx303	0.01	0.605	0.736
Oil	m118	Tzi8	0.03	0.191	0.354
Oil	m170	B97	0.03	0.122	0.261
Oil	m170	CML103	0.03	0.124	0.264
Oil	m170	CML228	0.00	0.951	0.971
Oil	m170	CML247	0.05	0.034	0.112

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m170	CML277	0.00	0.946	0.968
Oil	m170	CML322	0.04	0.099	0.231
Oil	m170	CML333	0.04	0.062	0.166
Oil	m170	CML52	0.04	0.054	0.150
Oil	m170	CML69	0.02	0.293	0.475
Oil	m170	HP301	0.07	0.001	0.008*
Oil	m170	Ki11	0.04	0.119	0.261
Oil	m170	Ki3	0.02	0.479	0.650
Oil	m170	Ky21	0.01	0.602	0.736
Oil	m170	M162W	0.07	0.003	0.016*
Oil	m170	M37W	0.02	0.260	0.436
Oil	m170	Mo18W	0.05	0.026	0.094
Oil	m170	MS71	0.06	0.003	0.018*
Oil	m170	NC350	0.04	0.055	0.152
Oil	m170	NC358	0.04	0.124	0.264
Oil	m170	Oh43	0.11	0.000	0.001**
Oil	m170	Oh7B	0.06	0.010	0.046*
Oil	m170	Tx303	0.06	0.005	0.028*
Oil	m170	Tzi8	0.03	0.260	0.436
Oil	m221	B97	0.02	0.431	0.605
Oil	m221	CML103	0.02	0.591	0.734
Oil	m221	CML228	-0.07	0.007	0.033*
Oil	m221	CML247	-0.02	0.417	0.593
Oil	m221	CML277	-0.08	0.001	0.010*
Oil	m221	CML322	-0.06	0.016	0.067
Oil	m221	CML333	-0.10	0.000	0.003*
Oil	m221	CML52	-0.03	0.260	0.436
Oil	m221	CML69	-0.01	0.680	0.791
Oil	m221	HP301	-0.10	0.000	0.001**
Oil	m221	Ki11	0.02	0.327	0.514
Oil	m221	Ki3	-0.01	0.826	0.889
Oil	m221	Ky21	0.00	0.947	0.968
Oil	m221	M162W	0.04	0.172	0.330
Oil	m221	M37W	-0.06	0.040	0.125
Oil	m221	Mo18W	0.02	0.541	0.698
Oil	m221	MS71	-0.10	0.000	0.004*
Oil	m221	NC350	-0.01	0.645	0.765

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m221	NC358	-0.03	0.308	0.490
Oil	m221	Oh43	-0.03	0.230	0.402
Oil	m221	Oh7B	-0.06	0.030	0.103
Oil	m221	Tx303	0.01	0.729	0.821
Oil	m221	Tzi8	-0.07	0.022	0.085
Oil	m240	B97	-0.04	0.106	0.241
Oil	m240	CML103	-0.10	0.001	0.005*
Oil	m240	CML228	0.06	0.022	0.084
Oil	m240	CML247	0.00	0.891	0.929
Oil	m240	CML277	0.03	0.226	0.398
Oil	m240	CML322	-0.02	0.482	0.650
Oil	m240	CML333	0.01	0.585	0.731
Oil	m240	CML52	-0.09	0.001	0.007*
Oil	m240	CML69	-0.11	0.000	0.001**
Oil	m240	HP301	0.00	0.945	0.968
Oil	m240	Ki11	-0.02	0.467	0.637
Oil	m240	Ki3	0.01	0.823	0.888
Oil	m240	Ky21	-0.05	0.158	0.308
Oil	m240	M162W	-0.11	0.000	0.002*
Oil	m240	M37W	0.03	0.329	0.514
Oil	m240	Mo18W	0.05	0.120	0.261
Oil	m240	MS71	0.05	0.126	0.266
Oil	m240	NC350	-0.10	0.001	0.005*
Oil	m240	NC358	-0.02	0.435	0.608
Oil	m240	Oh43	-0.05	0.053	0.149
Oil	m240	Oh7B	-0.01	0.637	0.764
Oil	m240	Tx303	0.01	0.822	0.888
Oil	m240	Tzi8	0.06	0.069	0.174
Oil	m266	B97	0.01	0.647	0.765
Oil	m266	CML103	0.03	0.266	0.440
Oil	m266	CML228	0.07	0.001	0.007*
Oil	m266	CML247	0.01	0.683	0.792
Oil	m266	CML277	0.00	0.963	0.979
Oil	m266	CML322	-0.04	0.082	0.200
Oil	m266	CML333	0.07	0.002	0.011*
Oil	m266	CML52	-0.03	0.145	0.290
Oil	m266	CML69	0.02	0.325	0.513

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m266	HP301	-0.01	0.696	0.797
Oil	m266	Ki11	0.01	0.737	0.827
Oil	m266	Ki3	0.04	0.118	0.261
Oil	m266	Ky21	-0.07	0.005	0.025*
Oil	m266	M162W	0.03	0.248	0.424
Oil	m266	M37W	-0.01	0.578	0.730
Oil	m266	Mo18W	-0.04	0.083	0.201
Oil	m266	MS71	-0.04	0.121	0.261
Oil	m266	NC350	0.02	0.500	0.661
Oil	m266	NC358	-0.05	0.034	0.112
Oil	m266	Oh43	-0.02	0.303	0.485
Oil	m266	Oh7B	0.01	0.656	0.768
Oil	m266	Tx303	-0.09	0.000	0.001**
Oil	m266	Tzi8	-0.03	0.211	0.382
Oil	m330	B97	0.02	0.366	0.549
Oil	m330	CML103	-0.01	0.644	0.765
Oil	m330	CML228	0.06	0.006	0.032*
Oil	m330	CML247	-0.03	0.108	0.243
Oil	m330	CML277	-0.04	0.051	0.145
Oil	m330	CML322	0.05	0.018	0.074
Oil	m330	CML333	0.00	0.894	0.929
Oil	m330	CML52	0.01	0.599	0.736
Oil	m330	CML69	-0.05	0.024	0.089
Oil	m330	HP301	0.06	0.005	0.026*
Oil	m330	Ki11	0.00	0.990	0.994
Oil	m330	Ki3	-0.07	0.008	0.040*
Oil	m330	Ky21	-0.08	0.000	0.002*
Oil	m330	M162W	-0.05	0.051	0.145
Oil	m330	M37W	-0.02	0.383	0.556
Oil	m330	Mo18W	-0.04	0.067	0.171
Oil	m330	MS71	0.00	0.820	0.888
Oil	m330	NC350	0.06	0.008	0.040*
Oil	m330	NC358	-0.01	0.530	0.689
Oil	m330	Oh43	-0.10	0.000	0.001**
Oil	m330	Oh7B	-0.05	0.029	0.102
Oil	m330	Tx303	0.02	0.494	0.658
Oil	m330	Tzi8	0.05	0.017	0.071

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m401	B97	0.04	0.127	0.268
Oil	m401	CML103	0.04	0.065	0.171
Oil	m401	CML228	0.05	0.014	0.059
Oil	m401	CML247	0.03	0.129	0.269
Oil	m401	CML277	0.11	0.000	0.001**
Oil	m401	CML322	0.11	0.000	0.001**
Oil	m401	CML333	0.08	0.001	0.005*
Oil	m401	CML52	-0.01	0.788	0.868
Oil	m401	CML69	0.04	0.055	0.152
Oil	m401	HP301	-0.02	0.293	0.475
Oil	m401	Ki11	0.04	0.042	0.129
Oil	m401	Ki3	0.07	0.010	0.047*
Oil	m401	Ky21	-0.02	0.429	0.603
Oil	m401	M162W	-0.05	0.032	0.109
Oil	m401	M37W	0.06	0.011	0.048*
Oil	m401	Mo18W	0.04	0.103	0.238
Oil	m401	MS71	-0.02	0.420	0.593
Oil	m401	NC350	-0.01	0.583	0.731
Oil	m401	NC358	-0.03	0.245	0.422
Oil	m401	Oh43	0.00	0.863	0.915
Oil	m401	Oh7B	0.00	0.910	0.943
Oil	m401	Tx303	0.06	0.004	0.023*
Oil	m401	Tzi8	0.02	0.491	0.656
Oil	m474	B97	0.03	0.200	0.369
Oil	m474	CML103	0.01	0.685	0.792
Oil	m474	CML228	0.10	0.000	0.001**
Oil	m474	CML247	0.02	0.508	0.666
Oil	m474	CML277	-0.01	0.657	0.768
Oil	m474	CML322	0.11	0.000	0.001**
Oil	m474	CML333	0.00	0.980	0.988
Oil	m474	CML52	0.01	0.571	0.724
Oil	m474	CML69	0.03	0.224	0.398
Oil	m474	HP301	0.03	0.295	0.475
Oil	m474	Ki11	-0.01	0.684	0.792
Oil	m474	Ki3	0.07	0.026	0.095
Oil	m474	Ky21	-0.02	0.344	0.531
Oil	m474	M162W	0.02	0.421	0.593

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m474	M37W	-0.05	0.042	0.129
Oil	m474	Mo18W	-0.02	0.403	0.581
Oil	m474	MS71	-0.06	0.021	0.083
Oil	m474	NC350	0.04	0.103	0.238
Oil	m474	NC358	0.03	0.297	0.478
Oil	m474	Oh43	-0.04	0.088	0.207
Oil	m474	Oh7B	0.12	0.001	0.006*
Oil	m474	Tx303	0.02	0.449	0.622
Oil	m474	Tzi8	0.12	0.000	0.001**
Oil	m492	B97	0.04	0.150	0.297
Oil	m492	CML103	0.06	0.022	0.084
Oil	m492	CML228	0.10	0.000	0.001**
Oil	m492	CML247	0.02	0.457	0.629
Oil	m492	CML277	0.02	0.375	0.549
Oil	m492	CML322	0.03	0.153	0.300
Oil	m492	CML333	0.05	0.061	0.166
Oil	m492	CML52	0.03	0.225	0.398
Oil	m492	CML69	0.03	0.175	0.332
Oil	m492	HP301	0.01	0.819	0.888
Oil	m492	Ki11	0.06	0.033	0.110
Oil	m492	Ki3	0.06	0.065	0.171
Oil	m492	Ky21	-0.03	0.262	0.437
Oil	m492	M162W	-0.03	0.337	0.521
Oil	m492	M37W	-0.01	0.557	0.711
Oil	m492	Mo18W	0.03	0.308	0.490
Oil	m492	MS71	0.02	0.407	0.583
Oil	m492	NC350	0.06	0.009	0.043*
Oil	m492	NC358	0.11	0.000	0.001**
Oil	m492	Oh43	0.02	0.329	0.514
Oil	m492	Oh7B	-0.01	0.873	0.918
Oil	m492	Tx303	0.00	0.867	0.916
Oil	m492	Tzi8	-0.03	0.270	0.445
Oil	m538	B97	0.03	0.209	0.381
Oil	m538	CML103	-0.02	0.372	0.549
Oil	m538	CML228	-0.01	0.818	0.888
Oil	m538	CML247	-0.06	0.010	0.047*
Oil	m538	CML277	-0.07	0.001	0.007*

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m538	CML322	-0.10	0.000	0.001**
Oil	m538	CML333	-0.04	0.047	0.138
Oil	m538	CML52	-0.05	0.024	0.090
Oil	m538	CML69	-0.03	0.222	0.396
Oil	m538	HP301	0.01	0.592	0.734
Oil	m538	Ki11	-0.01	0.588	0.733
Oil	m538	Ki3	0.00	0.954	0.972
Oil	m538	Ky21	-0.04	0.049	0.142
Oil	m538	M162W	0.00	0.865	0.915
Oil	m538	M37W	-0.05	0.023	0.088
Oil	m538	Mo18W	-0.05	0.036	0.115
Oil	m538	MS71	-0.01	0.663	0.773
Oil	m538	NC350	-0.05	0.018	0.074
Oil	m538	NC358	-0.03	0.179	0.338
Oil	m538	Oh43	-0.04	0.083	0.201
Oil	m538	Oh7B	0.01	0.723	0.818
Oil	m538	Tx303	-0.07	0.003	0.016*
Oil	m538	Tzi8	0.00	0.991	0.994
Oil	m553	B97	0.00	0.888	0.929
Oil	m553	CML103	-0.03	0.190	0.354
Oil	m553	CML228	0.03	0.265	0.439
Oil	m553	CML247	0.07	0.001	0.008*
Oil	m553	CML277	0.01	0.744	0.831
Oil	m553	CML322	0.10	0.000	0.001**
Oil	m553	CML333	0.04	0.093	0.218
Oil	m553	CML52	0.00	0.992	0.994
Oil	m553	CML69	0.04	0.066	0.171
Oil	m553	HP301	0.04	0.153	0.300
Oil	m553	Ki11	-0.01	0.653	0.768
Oil	m553	Ki3	0.02	0.470	0.639
Oil	m553	Ky21	0.02	0.404	0.581
Oil	m553	M162W	-0.02	0.351	0.538
Oil	m553	M37W	0.05	0.037	0.116
Oil	m553	Mo18W	0.05	0.029	0.102
Oil	m553	MS71	-0.02	0.361	0.545
Oil	m553	NC350	0.04	0.068	0.174
Oil	m553	NC358	-0.02	0.542	0.698

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m553	Oh43	0.00	0.942	0.968
Oil	m553	Oh7B	-0.03	0.201	0.369
Oil	m553	Tx303	0.06	0.014	0.060
Oil	m553	Tzi8	-0.02	0.358	0.544
Oil	m565	B97	0.03	0.369	0.549
Oil	m565	CML103	-0.01	0.801	0.879
Oil	m565	CML228	0.02	0.455	0.628
Oil	m565	CML247	-0.02	0.334	0.518
Oil	m565	CML277	-0.02	0.444	0.619
Oil	m565	CML322	-0.01	0.692	0.797
Oil	m565	CML333	-0.06	0.028	0.100
Oil	m565	CML52	-0.02	0.375	0.549
Oil	m565	CML69	-0.04	0.149	0.296
Oil	m565	HP301	-0.02	0.632	0.761
Oil	m565	Ki11	-0.03	0.400	0.580
Oil	m565	Ki3	0.01	0.809	0.886
Oil	m565	Ky21	-0.11	0.000	0.001**
Oil	m565	M162W	-0.04	0.177	0.335
Oil	m565	M37W	-0.11	0.000	0.001**
Oil	m565	Mo18W	0.02	0.508	0.666
Oil	m565	MS71	-0.05	0.027	0.098
Oil	m565	NC350	-0.02	0.466	0.637
Oil	m565	NC358	-0.05	0.050	0.145
Oil	m565	Oh43	-0.09	0.001	0.008*
Oil	m565	Oh7B	0.01	0.764	0.848
Oil	m565	Tx303	-0.12	0.000	0.001**
Oil	m565	Tzi8	-0.02	0.371	0.549
Oil	m591	B97	-0.04	0.085	0.204
Oil	m591	CML103	0.12	0.000	0.001**
Oil	m591	CML228	0.13	0.000	0.001**
Oil	m591	CML247	0.04	0.087	0.207
Oil	m591	CML277	0.05	0.040	0.126
Oil	m591	CML322	0.03	0.282	0.462
Oil	m591	CML333	0.05	0.067	0.171
Oil	m591	CML52	0.05	0.043	0.130
Oil	m591	CML69	0.12	0.000	0.001**
Oil	m591	HP301	0.00	0.929	0.959

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m591	Ki11	0.06	0.050	0.145
Oil	m591	Ki3	0.03	0.446	0.620
Oil	m591	Ky21	0.02	0.420	0.593
Oil	m591	M162W	0.07	0.010	0.046*
Oil	m591	M37W	0.08	0.004	0.022*
Oil	m591	Mo18W	0.04	0.166	0.320
Oil	m591	MS71	-0.01	0.580	0.730
Oil	m591	NC350	0.14	0.000	0.001**
Oil	m591	NC358	0.06	0.022	0.084
Oil	m591	Oh43	0.04	0.141	0.286
Oil	m591	Oh7B	0.12	0.000	0.002*
Oil	m591	Tx303	0.09	0.002	0.011*
Oil	m591	Tzi8	0.09	0.001	0.008*
Oil	m638	B97	0.02	0.510	0.667
Oil	m638	CML103	0.04	0.173	0.330
Oil	m638	CML228	-0.01	0.798	0.878
Oil	m638	CML247	-0.02	0.367	0.549
Oil	m638	CML277	0.01	0.698	0.797
Oil	m638	CML322	0.05	0.025	0.091
Oil	m638	CML333	0.08	0.001	0.007*
Oil	m638	CML52	-0.03	0.178	0.336
Oil	m638	CML69	0.03	0.233	0.405
Oil	m638	HP301	0.04	0.116	0.260
Oil	m638	Ki11	0.01	0.584	0.731
Oil	m638	Ki3	0.07	0.019	0.077
Oil	m638	Ky21	0.10	0.000	0.001*
Oil	m638	M162W	0.05	0.056	0.154
Oil	m638	M37W	-0.03	0.191	0.354
Oil	m638	Mo18W	0.03	0.184	0.344
Oil	m638	MS71	-0.02	0.556	0.711
Oil	m638	NC350	0.03	0.164	0.317
Oil	m638	NC358	0.01	0.639	0.764
Oil	m638	Oh43	0.01	0.636	0.764
Oil	m638	Oh7B	0.04	0.219	0.394
Oil	m638	Tx303	-0.02	0.462	0.633
Oil	m638	Tzi8	0.07	0.002	0.015*
Oil	m708	B97	-0.02	0.506	0.666

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m708	CML103	-0.04	0.153	0.300
Oil	m708	CML228	0.10	0.000	0.001**
Oil	m708	CML247	0.02	0.455	0.628
Oil	m708	CML277	0.01	0.604	0.736
Oil	m708	CML322	-0.02	0.353	0.539
Oil	m708	CML333	0.05	0.038	0.121
Oil	m708	CML52	0.08	0.000	0.002*
Oil	m708	CML69	0.00	0.996	0.996
Oil	m708	HP301	-0.02	0.351	0.538
Oil	m708	Ki11	0.01	0.696	0.797
Oil	m708	Ki3	0.09	0.002	0.014*
Oil	m708	Ky21	0.18	0.000	0.001**
Oil	m708	M162W	0.12	0.000	0.001**
Oil	m708	M37W	-0.05	0.032	0.108
Oil	m708	Mo18W	0.03	0.290	0.473
Oil	m708	MS71	-0.02	0.401	0.580
Oil	m708	NC350	0.09	0.001	0.010*
Oil	m708	NC358	-0.01	0.814	0.888
Oil	m708	Oh43	-0.04	0.126	0.266
Oil	m708	Oh7B	0.16	0.000	0.001**
Oil	m708	Tx303	0.21	0.000	0.001**
Oil	m708	Tzi8	0.12	0.000	0.001**
Oil	m739	B97	0.01	0.557	0.711
Oil	m739	CML103	0.00	0.947	0.968
Oil	m739	CML228	0.02	0.416	0.593
Oil	m739	CML247	-0.04	0.141	0.286
Oil	m739	CML277	0.03	0.144	0.289
Oil	m739	CML322	0.00	0.893	0.929
Oil	m739	CML333	0.03	0.217	0.391
Oil	m739	CML52	0.02	0.265	0.439
Oil	m739	CML69	-0.03	0.132	0.274
Oil	m739	HP301	0.05	0.030	0.103
Oil	m739	Ki11	0.00	0.967	0.981
Oil	m739	Ki3	-0.07	0.011	0.048*
Oil	m739	Ky21	0.04	0.094	0.221
Oil	m739	M162W	-0.01	0.743	0.831
Oil	m739	M37W	-0.02	0.378	0.551

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m739	Mo18W	0.04	0.140	0.286
Oil	m739	MS71	0.03	0.134	0.276
Oil	m739	NC350	-0.01	0.627	0.757
Oil	m739	NC358	-0.03	0.260	0.436
Oil	m739	Oh43	0.05	0.034	0.112
Oil	m739	Oh7B	0.06	0.031	0.105
Oil	m739	Tx303	0.07	0.005	0.026*
Oil	m739	Tzi8	0.12	0.000	0.001**
Oil	m793	B97	-0.02	0.484	0.650
Oil	m793	CML103	0.02	0.255	0.434
Oil	m793	CML228	0.06	0.006	0.029*
Oil	m793	CML247	0.01	0.535	0.694
Oil	m793	CML277	0.05	0.022	0.084
Oil	m793	CML322	-0.02	0.274	0.450
Oil	m793	CML333	0.01	0.645	0.765
Oil	m793	CML52	0.04	0.045	0.132
Oil	m793	CML69	0.03	0.181	0.340
Oil	m793	HP301	0.01	0.612	0.742
Oil	m793	Ki11	0.04	0.074	0.185
Oil	m793	Ki3	0.08	0.004	0.023*
Oil	m793	Ky21	0.03	0.128	0.268
Oil	m793	M162W	0.04	0.067	0.171
Oil	m793	M37W	-0.01	0.732	0.823
Oil	m793	Mo18W	0.00	0.873	0.918
Oil	m793	MS71	0.08	0.000	0.004*
Oil	m793	NC350	0.04	0.073	0.184
Oil	m793	NC358	0.07	0.001	0.008*
Oil	m793	Oh43	0.01	0.752	0.837
Oil	m793	Oh7B	0.03	0.224	0.398
Oil	m793	Tx303	0.02	0.294	0.475
Oil	m793	Tzi8	0.01	0.712	0.810
Oil	m918	B97	-0.01	0.595	0.734
Oil	m918	CML103	0.00	0.844	0.903
Oil	m918	CML228	0.06	0.006	0.032*
Oil	m918	CML247	0.01	0.713	0.810
Oil	m918	CML277	-0.01	0.600	0.736
Oil	m918	CML322	0.10	0.000	0.001**

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m918	CML333	0.11	0.000	0.001**
Oil	m918	CML52	0.08	0.000	0.003*
Oil	m918	CML69	0.12	0.000	0.001**
Oil	m918	HP301	0.03	0.119	0.261
Oil	m918	Ki11	0.00	0.862	0.915
Oil	m918	Ki3	-0.02	0.368	0.549
Oil	m918	Ky21	-0.02	0.366	0.549
Oil	m918	M162W	-0.06	0.009	0.043*
Oil	m918	M37W	0.01	0.604	0.736
Oil	m918	Mo18W	0.04	0.062	0.166
Oil	m918	MS71	0.06	0.010	0.046*
Oil	m918	NC350	0.10	0.000	0.001**
Oil	m918	NC358	0.07	0.006	0.029*
Oil	m918	Oh43	0.02	0.318	0.504
Oil	m918	Oh7B	0.00	0.859	0.915
Oil	m918	Tx303	0.02	0.484	0.650
Oil	m918	Tzi8	0.08	0.000	0.003*
Oil	m995	B97	-0.06	0.003	0.019*
Oil	m995	CML103	-0.04	0.044	0.132
Oil	m995	CML228	-0.11	0.000	0.001**
Oil	m995	CML247	-0.03	0.246	0.422
Oil	m995	CML277	0.01	0.496	0.659
Oil	m995	CML322	-0.03	0.213	0.385
Oil	m995	CML333	-0.04	0.041	0.127
Oil	m995	CML52	0.01	0.728	0.821
Oil	m995	CML69	0.04	0.111	0.249
Oil	m995	HP301	0.06	0.004	0.022*
Oil	m995	Ki11	0.03	0.148	0.295
Oil	m995	Ki3	0.03	0.309	0.490
Oil	m995	Ky21	-0.06	0.002	0.014*
Oil	m995	M162W	-0.04	0.118	0.261
Oil	m995	M37W	-0.04	0.077	0.192
Oil	m995	Mo18W	-0.07	0.001	0.008*
Oil	m995	MS71	-0.01	0.715	0.811
Oil	m995	NC350	-0.06	0.005	0.026*
Oil	m995	NC358	0.03	0.228	0.400
Oil	m995	Oh43	0.00	0.878	0.921

Table S7: (continued…Oil)

Trait	QTL	Population	Effect[a] (%)	Raw *P-value*	FDR *P-value*
Oil	m995	Oh7B	0.00	0.976	0.986
Oil	m995	Tx303	-0.09	0.000	0.002*
Oil	m995	Tzi8	-0.10	0.000	0.001**
Oil	m1085	B97	-0.01	0.693	0.797
Oil	m1085	CML103	-0.06	0.003	0.020*
Oil	m1085	CML228	-0.03	0.120	0.261
Oil	m1085	CML247	-0.01	0.812	0.887
Oil	m1085	CML277	-0.07	0.006	0.030*
Oil	m1085	CML322	0.00	0.888	0.929
Oil	m1085	CML333	0.00	0.828	0.889
Oil	m1085	CML52	-0.09	0.000	0.001**
Oil	m1085	CML69	-0.06	0.013	0.057
Oil	m1085	HP301	-0.01	0.594	0.734
Oil	m1085	Ki11	0.02	0.483	0.650
Oil	m1085	Ki3	-0.06	0.030	0.104
Oil	m1085	Ky21	-0.11	0.000	0.001**
Oil	m1085	M162W	-0.03	0.202	0.369
Oil	m1085	M37W	0.01	0.768	0.848
Oil	m1085	Mo18W	-0.02	0.333	0.518
Oil	m1085	MS71	0.00	0.862	0.915
Oil	m1085	NC350	-0.06	0.004	0.023*
Oil	m1085	NC358	-0.05	0.031	0.107
Oil	m1085	Oh43	0.01	0.621	0.752
Oil	m1085	Oh7B	-0.02	0.355	0.542
Oil	m1085	Tx303	-0.07	0.002	0.012*
Oil	m1085	Tzi8	-0.10	0.000	0.001**

[a] Percent oil kernel composition on a dry matter basis relative to B73.

* FDR: $P \leq 0.05$

** FDR: $P \leq 0.001$

Table S8: Pleitropy between percent starch, protein, and oil kernel content on a dry matter basis NAM QTL.

	Joint-linkage QTL Marker [cM]			Correlations		
Chr	Starch	Protein	Oil	S/P	S/O	P/O
---	Phenotypic			-066***	-0.41***	0.32***
---	All Overlapping QTL			-0.59***	-0.27***	0.29***
1	m120 [146]	m115 [137.6]	m118 [141.9]	-0.51*	-0.25	0.43*
2	---	m209 [53.3]	m221 [64.2]	---	---	0.46*
2	m232 [74.8]	m261 [94.9]	m240 [79.8]	-0.20	0.05	0.62**
3	m353 [62.4]	m353 [62.4]	m330 [56]	-0.62**	-0.10	-0.10
3	m426 [145.3]	m425 [145.1]	---	-0.69**	---	---
4	---	m484 [61.8]	m474 [57.4]	---	---	0.46*
5	m619 [70]	m615 [68.7]	---	-0.57**	---	---
5	m650 [98.8]	m657 [101.9]	m638 [87.2]	-0.63**	-0.04	0.24
6	m696 [11.3]	m694 [11.1]	m708 [33.4]	-0.70**	0.06	0.01
6	m707 [28.7]	m707 [28.7]	m708 [33.4]	-0.61**	-0.59**	0.65**
6	---	m729 [54]	m739 [61.4]	---	---	0.61*
7	m810 [75.3]	m802 [69.8]	---	-0.60**	---	---
7	m820 [95.2]	m820 [95.2]	---	-0.52**	---	---
8	m922 [88.2]	m912 [76.1]	m918 [82.3]	-0.58**	-0.35	0.15
9	m968 [41.8]	m963 [40]	---	-0.68**	---	---
10	m1060 [40.8]	m1084 [56.1]	m1085 [58.4]	-0.45*	-0.22	0.42*

* Significant at $P \leq 0.05$

** Significant at $P \leq 0.01$

*** Significant at $P \leq 0.0001$

Table S9: NAM GWAS Stepwise Forward Regression associations overlap with NAM joint-linkage QTL intervals, and NAM multiple SNP model GWAS for percent starch on a dry matter basis.

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	Joint-Linkage QTL Interval[b]	Multiple SNP Model[c]	Candidate Gene[d]
01	pze0109178815	9,178,815	17.71	-0.17	5.55E-11	Yes	Yes	Unknown
01	pze0158650146	58,650,146	71.21	-0.25	6.81E-19	Yes	Yes	
01	pze01117997538	117,997,538	89.26	-0.23	3.60E-09	No	Yes	
01	pze01201990714	201,990,714	115.48	-0.18	2.00E-09	No	Yes	*MKL1* (transmembrane kinase-like 1)
02	pze0202620319	2,620,319	6.01	-0.35	3.70E-13	Yes	Yes	*ATEHD1* (EPS15 Homology Domain 1)
02	pze02141337051	141,337,051	79.39	-0.28	6.99E-11	Yes	Yes	Unknown
02	pze02192606911	192,606,911	103.71	-0.63	3.33E-08	Yes	Yes	Subtilisin homologue
03	pze0356089855	56,089,855	57.48	-0.70	9.37E-13	Yes	Yes	
03	pze03123153166	123,153,166	60.36	-0.19	1.15E-07	No	No	
03	pze03140000571	140,000,571	63.78	0.25	5.79E-15	Yes	Yes	Unknown
03	pze03211988248	211,988,248	122.98	-0.22	7.87E-10	Yes	Yes	
03	pze03226480885	226,480,885	150.48	0.30	3.62E-14	Yes	Yes	
04	pze04170737403	170,737,403	78.92	-0.21	2.96E-09	Yes	Yes	

Table S9: (continued…Starch)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	Joint-Linkage QTL Interval[b]	Multiple SNP Model[c]	Candidate Gene[d]
04	pze04244714059	244,714,059	138.08	0.16	5.22E-11	Yes	Yes	*BMY2* (Beta-Amylase 2)
05	pze0510452325	10,452,325	33.52	0.23	4.40E-07	No	Yes	*MKK-4* (MAP kinase)
05	pze0552385845	52,385,845	61.25	0.61	1.41E-07	No	No	
05	pze05142118751	142,118,751	71.87	-0.23	9.86E-15	Yes	Yes	
05	pze05186099665	186,099,665	95.67	-0.27	1.10E-19	Yes	Yes	
05	pze05204759530	204,759,530	116.92	-0.33	7.23E-12	No	Yes	GDSL-like lipase/acylhydrolase
06	pze0685049949	85,049,949	13.07	-0.16	1.35E-11	Yes	Yes	Unknown
06	pze06105019334	105,019,334	30.81	-0.33	3.04E-13	No	Yes	*DGAT1-2* (type I acyl-CoA:diacylglycerol acyltransferase)
06	pze06137691479	137,691,479	53.31	0.14	4.27E-08	No	Yes	
07	pze07125162082	125,162,082	65.63	-0.19	3.66E-09	No	Yes	
07	pze07155752329	155,752,329	97.60	0.28	1.15E-31	Yes	Yes	
08	pze0822633514	22,633,514	48.80	0.28	4.39E-10	No	No	
08	pze0844345061	44,345,061	52.07	0.34	1.33E-14	Yes	Yes	

Table S9: (continued…Starch)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	Joint-Linkage QTL Interval[b]	Multiple SNP Model[c]	Candidate Gene[d]
08	pze08144928072	144,928,072	74.76	-0.44	5.66E-11	No	Yes	
08	pze08163605070	163,605,070	95.70	-0.18	3.07E-08	No	No	
09	pze0926889502	26,889,502	43.53	-0.19	6.57E-12	Yes	Yes	Expansin precursor
09	pze09105200196	105,200,196	52.21	-0.19	4.32E-05	No	Yes	
09	pze09126531474	126,531,474	62.88	-0.16	5.42E-07	Yes	Yes	
10	pze1009087858	9,087,858	25.14	0.19	1.61E-07	No	No	
10	pze1091042082	91,042,082	41.73	0.16	1.39E-12	Yes	Yes	

[a] Percent oil kernel composition on a dry matter basis relative to B73.

[b] 'Yes' = associated SNP is positioned in a NAM joint-linkage QTL interval, and 'No' = associated SNP is located outside NAM joint-linkage QTL intervals.

[c] 'Yes' = associated stepwise forward regression SNP was selected by the multiple SNP model (RMIP ≥ 0.05) ,and 'No' = associated stepwise forward regression SNP was not selected by the multiple SNP model (RMIP ≥ 0.05)

[d] Candidate gene described if associated marker is located within the gene.

Table S10: NAM GWAS Stepwise Forward Regression associations, overlap with NAM joint-linkage QTL intervals, and NAM multiple SNP model GWAS for percent protein on a dry matter basis.

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	Joint-Linkage QTL Interval[b]	Multiple SNP Model[c]	Candidate Gene[d]
01	pze0141569344	41,569,344	59.1	0.16	2.70E-08	Yes	Yes	Unknown
01	pze01214607570	214,607,570	125.8	-0.14	2.41E-09	No	Yes	
01	pze01233597309	233,597,309	138.6	-0.11	1.22E-07	No	No	
01	pze01264586209	264,586,209	159.2	0.11	1.72E-18	Yes	Yes	
02	pze0206003320	6,003,320	18.5	0.08	2.95E-07	No	Yes	
02	pze0218286061	18,286,061	48.0	0.14	3.03E-07	No	Yes	Unknown
02	pze02184529536	184,529,536	95.0	-0.10	3.57E-12	Yes	Yes	
02	pze02234059444	234,059,444	156.6	-0.08	2.65E-09	No	Yes	*KNAT1* (Knotted-like from *Arabidopsis thaliana*, transcription factor)
03	pze03107736175	107,736,175	58.7	0.14	1.17E-14	Yes	Yes	
03	pze03225917080	225,917,080	149.6	-0.09	8.26E-12	No	Yes	
04	pze04152317836	152,317,836	64.0	0.14	3.69E-15	Yes	Yes	
04	pze04175740882	175,740,882	86.8	0.20	8.11E-08	Yes	Yes	Subtilase family protein
05	pze0588027712	88,027,712	69.4	-0.16	7.57E-10	Yes	Yes	

Table S10: (continued…Protein)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	Joint-Linkage QTL Interval[b]	Multiple SNP Model[c]	Candidate Gene[d]
05	pze05197933894	197,933,894	105.8	0.15	2.03E-26	Yes	Yes	
06	pze0673924500	73,924,500	10.4	0.15	6.56E-15	Yes	Yes	Phosphate translocator-related
06	pze06106474383	106,474,383	32.3	0.12	6.19E-08	No	No	
06	pze06137612791	137,612,791	53.3	-0.14	1.09E-17	Yes	Yes	
06	pze06164950817	164,950,817	100.7	0.09	1.87E-11	Yes	Yes	
07	pze07128349130	128,349,130	69.8	-0.12	1.44E-09	Yes	Yes	
07	pze07149948232	149,948,232	87.8	-0.10	1.18E-12	No	Yes	
08	pze0873822546	73,822,546	54.0	-0.12	1.50E-21	Yes	Yes	Unknown
08	pze08145172472	145,172,472	75.0	-0.16	1.47E-11	Yes	Yes	Carbonic anhydrase
08	pze08163510712	163,510,712	95.4	0.18	4.69E-09	Yes	Yes	
09	pze098323233	8,323,233	11.8	0.11	6.50E-07	No	Yes	
09	pze09102494203	102,494,203	51.1	0.09	2.21E-11	No	Yes	
09	pze09135383651	135,383,651	72.4	0.10	1.40E-13	Yes	Yes	*TRFL1* (TRF-Like 1)

Table S10: (continued…Protein)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	Joint-Linkage QTL Interval[b]	Multiple SNP Model[c]	Candidate Gene[d]
09	pze09142950644	142,950,644	89.4	0.19	1.29E-07	Yes	Yes	Zinc finger (C3HC4-type RING finger) family protein
10	pze1050061312	50,061,312	36.3	-0.14	6.34E-13	Yes	Yes	
10	pze10131716806	131,716,806	55.2	-0.15	7.67E-35	Yes	Yes	
10	pze10143096411	143,096,411	80.1	-0.11	2.61E-08	No	Yes	
10	pze10148028746	148,028,746	99.5	0.14	4.06E-12	Yes	Yes	

[a] Percent oil kernel composition on a dry matter basis relative to B73.

[b] 'Yes' = associated SNP is positioned in a NAM joint-linkage QTL interval, and 'No' = associated SNP is located outside NAM joint-linkage QTL intervals.

[c] 'Yes' = associated stepwise forward regression SNP was selected by the multiple SNP model (RMIP ≥ 0.05) ,and 'No' = associated stepwise forward regression SNP was not selected by the multiple SNP model (RMIP ≥ 0.05)

[d] Candidate gene described if associated marker is located within the gene.

Table S11: NAM GWAS Stepwise Forward Regression associations, overlap with NAM joint-linkage QTL intervals, and NAM multiple SNP model GWAS for percent oil on a dry matter basis.

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	Joint-Linkage QTL Interval[b]	Multiple SNP Model[c]	Candidate Gene[d]
01	pze0118568101	18,568,101	35.1	0.04	7.67E-08	Yes	Yes	
01	pze0127054049	27,054,049	44.6	0.07	5.46E-10	Yes	Yes	
01	pze0174517643	74,517,643	79.1	-0.06	2.45E-07	No	Yes	
01	pze01198964527	198,964,527	112.3	0.06	1.35E-14	No	Yes	
01	pze01210953214	210,953,214	122.6	0.05	7.82E-10	Yes	Yes	
01	pze01295769034	295,769,034	199.4	0.05	9.64E-19	Yes	Yes	
02	pze0212864473	12,864,473	36.8	0.10	1.26E-08	No	No	
02	pze0220327496	20,327,496	51.1	-0.06	1.35E-11	No	Yes	*CNX5* (Co-Factor for Nitrate Reductase and Xanthine Dehydrogenas 5)
02	pze0244884255	44,884,255	69.7	-0.04	6.24E-12	Yes	Yes	*ABA1* (ABA Deficient 1, zeaxanthin epoxidase)
02	pze02173076399	173,076,399	85.2	-0.07	3.09E-08	No	Yes	*SCPL18* (Serine carboxypeptidase-like 18)
02	pze02188225260	188,225,260	99.8	0.09	4.17E-10	No	Yes	
02	pze02216096302	216,096,302	129.0	-0.06	4.63E-07	No	No	
03	pze0302103927	2,103,927	4.5	-0.05	9.37E-09	No	Yes	

Table S11: (continued…Oil)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	Joint-Linkage QTL Interval[b]	Multiple SNP Model[c]	Candidate Gene[d]
03	pze0358388350	58,388,350	57.7	-0.07	3.98E-13	Yes	Yes	Serine/threonine protein kinase
03	pze03101264408	101,264,408	58.3	0.07	1.38E-07	Yes	No	
03	pze03173206531	173,206,531	83.5	-0.06	9.48E-07	No	No	
03	pze03179938275	179,938,275	92.0	0.05	3.52E-16	No	Yes	
03	pze03211146687	211,146,687	121.9	0.06	1.40E-11	No	Yes	
03	pze03220908923	220,908,923	139.1	-0.03	3.88E-08	No	No	
04	pze0422895076	22,895,076	46.3	0.08	1.37E-10	No	Yes	
04	pze04163300645	163,300,645	73.4	0.07	5.43E-08	No	Yes	
04	pze04172891298	172,891,298	82.7	0.04	1.39E-07	Yes	Yes	*ERF* (Ethylene Response Factor B-6 of ERF/AP2 transcription factor)
04	pze04209879846	209,879,846	109.4	-0.06	3.44E-11	No	Yes	
04	pze04242648433	242,648,433	130.6	-0.04	3.52E-07	No	Yes	Sugar isomerase (SIS) domain-containing protein
05	pze0504091479	4,091,479	12.9	0.06	4.80E-12	Yes	Yes	Histone H1.2
05	pze0511879036	11,879,036	37.3	-0.06	9.67E-16	Yes	Yes	
05	pze0547696011	47,696,011	60.3	0.07	3.00E-08	No	No	
05	pze0551583383	51,583,383	61.1	0.06	9.74E-17	Yes	Yes	Iron ion binding / oxidoreductase
05	pze05177086187	177,086,187	88.2	0.04	2.71E-08	No	No	
05	pze05212800876	212,800,876	142.3	-0.05	3.24E-08	No	Yes	

Table S11: (continued…Oil)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	Joint-Linkage QTL Interval[b]	Multiple SNP Model[c]	Candidate Gene[d]
06	pze06105019473	105,019,473	30.8	0.12	6.32E-22	Yes	Yes	*DGAT1-2* (type I acyl-CoA:diacylglycerol acyltransferase)
06	pze06106914732	106,914,732	32.8	0.05	1.76E-08	Yes	Yes	
06	pze06112065791	112,065,791	39.0	0.12	7.71E-14	Yes	Yes	
06	pze06131405628	131,405,628	50.0	-0.11	8.35E-09	No	Yes	*ATGA2OX3* (gibberellin 2-oxidase 3)
06	pze06166173995	166,173,995	104.9	0.10	1.46E-09	No	Yes	Transcription factor
07	pze0798745124	98,745,124	50.8	0.04	5.78E-10	Yes	Yes	
08	pze08140964810	140,964,810	72.1	0.07	2.32E-07	No	No	
08	pze08155478230	155,478,230	82.3	0.08	2.47E-23	Yes	Yes	
09	pze0921983416	21,983,416	38.8	0.13	2.45E-08	No	Yes	
09	pze0923229673	23,229,673	40.0	-0.07	1.10E-06	No	No	
09	pze09117897621	117,897,621	57.7	-0.07	2.11E-11	Yes	Yes	*SUS4* (Sucrose Synthase)
09	pze09141771810	141,771,810	86.9	-0.06	4.09E-08	No	Yes	
10	pze10134625388	134,625,388	59.4	-0.05	5.12E-15	Yes	Yes	

[a] Percent oil kernel composition on a dry matter basis relative to B73.

[b] 'Yes' = associated SNP is positioned in a NAM joint-linkage QTL interval, and 'No' = associated SNP is located outside NAM joint-linkage QTL intervals.

[c] 'Yes' = associated stepwise forward regression SNP was selected by the multiple SNP model (RMIP ≥ 0.05) ,and 'No' = associated stepwise forward regression SNP was not selected by the multiple SNP model (RMIP ≥ 0.05)

[d] Candidate gene described if associated marker is located within the gene.

Table S12: NAM multiple SNP model GWAS associations (RMIP ≥ 0.05) and overlap with NAM joint-linkage QTL intervals for percent starch content on a dry matter basis.

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
01	pze0109178815	9,178,815	17.7	-0.18	3.62E-09	0.66	Yes	Unknown
01	pze0158650146	58,650,146	71.2	-0.27	3.74E-17	0.19	Yes	
01	pze0159830429	59,830,429	71.8	-0.29	7.14E-23	0.06	Yes	Zinc finger (B-box type) family protein
01	pze0168727976	68,727,976	76.2	-0.29	2.20E-21	0.06	No	
01	pze0169444334	69,444,334	76.5	-0.26	2.33E-18	0.13	No	
01	pze0171186169	71,186,169	77.4	-0.36	1.09E-16	0.28	No	*LBD40* (Lob Domain-Containing Protein 40)
01	pze0171187215	71,187,215	77.4	-0.23	1.33E-14	0.12	No	*LBD40* (Lob Domain-Containing Protein 40)
01	pze01116549619	116,549,619	89.2	-0.29	1.06E-08	0.05	No	
01	pze01117997538	117,997,538	89.3	-0.26	2.51E-10	0.12	No	
01	pze01191979771	191,979,771	105.6	-0.32	1.57E-08	0.08	No	*RABA5E* (Rab GTPAse Homolog A5E)
01	pze01199483749	199,483,749	112.9	-0.32	1.01E-07	0.06	No	*AMY1* (Alpha-Amylase-Like)
01	pze01200084192	200,084,192	113.6	-0.22	4.63E-11	0.05	No	Patatin
01	pze01201990714	201,990,714	115.5	-0.21	7.18E-11	0.06	No	*MKL1* (transmembrane kinase-like 1)
01	pze01202136346	202,136,346	115.6	-0.25	3.04E-13	0.06	No	
01	pze01240044380	240,044,380	141.6	-0.36	1.01E-08	0.10	Yes	
01	pze01240049862	240,049,862	141.6	-0.27	1.61E-07	0.05	Yes	
01	pze01248398421	248,398,421	145.9	-0.24	3.54E-08	0.09	Yes	

Table S12: (continued…Starch)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
02	pze0201639448	1,639,448	1.9	-0.34	6.96E-08	0.08	No	
02	pze0202619241	2,619,241	6.0	-0.57	7.88E-13	0.10	Yes	*ATEHD1* (EPS15 Homology Domain 1)
02	pze0202620319	2,620,319	6.0	-0.37	1.56E-17	0.29	Yes	*ATEHD1* (EPS15 Homology Domain 1)
02	pze0203736479	3,736,479	10.4	-0.57	5.24E-17	0.07	Yes	*NRT1.6* (Nitrate Transporter 1.6)
02	pze0203736494	3,736,494	10.4	-0.55	7.08E-16	0.07	Yes	*NRT1.6* (Nitrate Transporter 1.6)
02	pze0203851757	3,851,757	10.7	-0.20	1.88E-12	0.09	Yes	
02	pze0205342144	5,342,144	15.9	-0.32	9.86E-14	0.21	No	
02	pze0205687767	5,687,767	17.2	-0.32	6.76E-12	0.09	No	*ATEME1A* (Arabidopsis Essential Meiotic Endonuclease 1A)
02	pze0220521754	20,521,754	51.3	-0.29	2.37E-07	0.05	No	
02	pze0223242982	23,242,982	55.3	-0.26	1.10E-09	0.12	No	
02	pze02141337051	141,337,051	79.4	-0.30	1.51E-09	0.23	Yes	Unknown
02	pze02190583445	190,583,445	101.9	-0.42	9.31E-10	0.18	No	
02	pze02192124279	192,124,279	103.3	-0.39	2.44E-08	0.09	Yes	*CYP78A9* (Cytochrome P450 78A9)
02	pze02192606911	192,606,911	103.7	-0.75	2.33E-13	0.16	Yes	Subtilisin homologue
02	pze02193309684	193,309,684	104.5	-0.33	3.98E-12	0.12	Yes	
02	pze02214677037	214,677,037	127.3	-0.67	7.85E-10	0.05	No	Unknown
03	pze0343868037	43,868,037	56.0	-0.73	1.21E-10	0.23	No	Pyruvate kinase

Table S12: (continued…Starch)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
03	pze0356089855	56,089,855	57.5	-0.84	1.65E-11	0.27	No	
03	pze0357223756	57,223,756	57.6	-0.72	8.17E-09	0.05	No	
03	pze0357884496	57,884,496	57.7	-0.73	1.16E-08	0.05	No	
03	pze0360227357	60,227,357	57.8	-0.40	4.64E-10	0.08	No	
03	pze03140000024	140,000,024	63.8	0.23	7.00E-08	0.16	Yes	Unknown
03	pze03140000571	140,000,571	63.8	0.20	1.20E-07	0.12	Yes	Unknown
03	pze03140397085	140,397,085	63.8	0.32	3.59E-10	0.16	Yes	
03	pze03151971302	151,971,302	67.7	0.23	5.41E-10	0.06	No	
03	pze03207655069	207,655,069	117.3	-0.25	1.96E-09	0.05	Yes	
03	pze03208168922	208,168,922	118.4	-0.71	2.53E-12	0.09	Yes	
03	pze03208402374	208,402,374	118.7	-0.19	7.73E-08	0.07	Yes	
03	pze03210621010	210,621,010	121.3	-0.17	2.10E-10	0.05	Yes	*GBF3* (G-Box Binding Factor 3)
03	pze03211142389	211,142,389	121.9	-0.32	1.56E-14	0.05	Yes	
03	pze03211151474	211,151,474	121.9	-0.26	2.20E-08	0.13	Yes	
03	pze03211988248	211,988,248	123.0	-0.26	6.14E-12	0.08	Yes	
03	pze03225230331	225,230,331	148.5	0.19	3.42E-09	0.06	Yes	Unknown
03	pze03225299207	225,299,207	148.6	0.30	5.67E-11	0.25	Yes	

Table S12: (continued…Starch)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
03	pze03226480885	226,480,885	150.5	0.30	1.44E-10	0.36	Yes	
04	pze04170736886	170,736,886	78.9	-0.21	8.94E-09	0.05	No	
04	pze04170737403	170,737,403	78.9	-0.23	1.26E-07	0.38	No	
04	pze04243222819	243,222,819	132.8	0.20	5.56E-08	0.19	No	*RPN1A* (26S Proteasome Regulatory Subunit S2 1A)
04	pze04244042011	244,042,011	136.3	0.19	9.45E-10	0.07	Yes	*CDC2* (Cell Division Control 2)
04	pze04244714059	244,714,059	138.1	0.17	1.76E-09	0.20	No	*BMY2* (Beta-Amylase 2)
04	pze04244768564	244,768,564	138.4	0.15	7.78E-09	0.08	No	
04	pze04245058429	245,058,429	140.1	0.25	3.10E-08	0.09	No	*ATMPK17* (MAP kinase)
04	pze04246797805	246,797,805	150.3	0.16	3.53E-08	0.24	No	
05	pze0510452325	10,452,325	33.5	0.29	2.86E-08	0.06	No	*MKK-4* (MAP kinase)
05	pze0549013626	49,013,626	60.6	0.66	4.98E-09	0.10	No	
05	pze0556090439	56,090,439	62.0	0.46	6.11E-10	0.05	No	
05	pze05133562850	133,562,850	71.1	-0.23	7.70E-10	0.07	Yes	
05	pze05135149153	135,149,153	71.2	0.39	1.01E-10	0.11	Yes	Lectin protein kinase
05	pze05142118751	142,118,751	71.9	-0.26	3.49E-12	0.49	Yes	
05	pze05142203995	142,203,995	71.9	-0.31	3.68E-10	0.13	Yes	
05	pze05186099279	186,099,279	95.7	-0.29	2.89E-23	0.16	Yes	

Table S12: (continued…Starch)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
05	pze05186099665	186,099,665	95.7	-0.28	2.66E-27	0.53	Yes	
05	pze05186318478	186,318,478	95.9	-0.37	3.60E-24	0.05	Yes	
05	pze05186323199	186,323,199	95.9	-0.22	4.21E-28	0.05	Yes	
05	pze05204759425	204,759,425	116.9	-0.35	2.35E-11	0.10	No	GDSL-like lipase/acylhydrolase
05	pze05204759530	204,759,530	116.9	-0.35	8.20E-10	0.29	No	GDSL-like lipase/acylhydrolase
05	pze05204955808	204,955,808	117.6	-0.33	1.23E-09	0.06	No	Unknown
05	pze05205834648	205,834,648	120.4	-0.41	3.46E-08	0.26	No	Unknown
06	pze0679020378	79,020,378	11.1	-0.19	4.44E-16	0.05	Yes	
06	pze0683224185	83,224,185	12.2	-0.38	7.91E-11	0.07	Yes	
06	pze0683624290	83,624,290	12.4	-0.19	2.26E-11	0.13	Yes	*Apetala 3* (Transcription Factor)
06	pze0685049949	85,049,949	13.1	-0.19	1.15E-19	0.23	Yes	Unknown
06	pze0687588096	87,588,096	15.1	-0.20	3.20E-16	0.10	Yes	
06	pze0687590851	87,590,851	15.1	-0.19	6.31E-18	0.05	Yes	
06	pze06103124221	103,124,221	28.9	-0.76	3.59E-13	0.15	Yes	
06	pze06104825402	104,825,402	30.6	-0.37	1.62E-08	0.10	No	Leucine-rich repeat family protein / protein kinase family protein
06	pze06105019334	105,019,334	30.8	-0.38	3.92E-17	0.51	No	*DGAT1-2* (type I acyl-CoA:diacylglycerol acyltransferase)
06	pze06105019473	105,019,473	30.8	-0.31	2.00E-09	0.11	No	*DGAT1-2* (type I acyl-CoA:diacylglycerol acyltransferase)

Table S12: (continued…Starch)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
06	pze06137558184	137,558,184	53.2	0.19	1.24E-07	0.06	No	
06	pze06137691479	137,691,479	53.3	0.15	1.06E-08	0.12	No	
06	pze06137691806	137,691,806	53.3	0.16	3.62E-09	0.07	No	
07	pze0700041894	41,894	-2.6	0.62	4.42E-10	0.17	No	
07	pze07125162082	125,162,082	65.6	-0.21	2.50E-11	0.16	No	
07	pze07125723935	125,723,935	66.4	-0.23	4.17E-09	0.09	No	
07	pze07131916751	131,916,751	71.6	-0.19	2.40E-09	0.09	No	
07	pze07135133066	135,133,066	73.5	-0.17	2.38E-07	0.05	Yes	Unknown
07	pze07155187710	155,187,710	96.4	0.31	2.06E-20	0.19	Yes	
07	pze07155752329	155,752,329	97.6	0.28	4.95E-23	0.39	Yes	
07	pze07156689774	156,689,774	99.5	0.27	1.50E-20	0.06	Yes	
07	pze07157016301	157,016,301	100.2	0.26	2.57E-21	0.08	Yes	
08	pze0814982196	14,982,196	37.4	0.16	2.55E-11	0.05	No	Hydrolase
08	pze0822538190	22,538,190	48.7	0.82	1.63E-12	0.05	Yes	
08	pze0822624701	22,624,701	48.8	0.28	1.33E-10	0.08	Yes	Unknown
08	pze0822625418	22,625,418	48.8	0.25	2.92E-16	0.07	Yes	
08	pze0823124377	23,124,377	49.3	0.87	5.54E-10	0.08	Yes	

Table S12: (continued…Starch)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
08	pze0823558987	23,558,987	49.7	0.75	2.43E-16	0.08	Yes	
08	pze0844345061	44,345,061	52.1	0.34	3.94E-14	0.25	Yes	
08	pze0844895265	44,895,265	52.1	0.24	4.36E-12	0.11	Yes	
08	pze0868350516	68,350,516	53.2	0.21	1.95E-13	0.05	Yes	
08	pze08142382170	142,382,170	73.0	-0.56	1.15E-07	0.09	No	
08	pze08144928072	144,928,072	74.8	-0.53	7.90E-11	0.44	No	
08	pze08149060169	149,060,169	78.3	-0.37	1.12E-12	0.22	No	
08	pze08163606566	163,606,566	95.7	-0.22	4.25E-13	0.06	Yes	
09	pze0925024800	25,024,800	42.4	-0.21	4.81E-10	0.05	Yes	
09	pze0925474814	25,474,814	42.7	-0.23	7.95E-10	0.09	Yes	Folic acid binding / transferase
09	pze0925696839	25,696,839	42.8	-0.22	1.07E-09	0.06	Yes	
09	pze0926763799	26,763,799	43.5	-0.24	1.88E-39	0.05	Yes	Haloacid dehalogenase-like hydrolase family protein
09	pze0926772667	26,772,667	43.5	-0.19	2.80E-10	0.14	Yes	Nodulin MtN21 family protein
09	pze0926889502	26,889,502	43.5	-0.23	3.17E-09	0.16	Yes	Expansin precursor
09	pze09103060309	103,060,309	51.3	-0.22	2.48E-39	0.09	No	
09	pze09105200196	105,200,196	52.2	-0.22	4.51E-39	0.52	No	
09	pze09126531474	126,531,474	62.9	-0.21	4.01E-11	0.10	Yes	

Table S12: (continued…Starch)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
09	pze09126623782	126,623,782	62.9	-0.19	1.07E-11	0.10	Yes	Catalytic/ metal ion binding / metalloendopeptidase/ zinc ion binding
09	pze09126792692	126,792,692	62.9	-0.18	3.90E-12	0.05	Yes	
10	pze1001442529	1,442,529	-1.5	0.22	2.71E-07	0.07	No	*ACA11* (autoinhibited Ca2+-ATPase 11)
10	pze1010103670	10,103,670	27.7	0.36	1.14E-08	0.14	No	Disease resistance response protein
10	pze1083322810	83,322,810	39.9	0.23	8.31E-19	0.32	Yes	
10	pze1083752598	83,752,598	40.0	0.19	1.42E-17	0.10	Yes	
10	pze1086726985	86,726,985	40.7	0.20	1.77E-20	0.09	Yes	
10	pze1091042082	91,042,082	41.7	0.19	5.11E-18	0.26	Yes	

[a] Percent oil kernel composition on a dry matter basis relative to B73.

[b] 'Yes' = associated SNP is positioned in a NAM joint-linkage QTL interval, and 'No' = associated SNP is located outside a NAM joint-linkage QTL intervals.

[c] Candidate gene described if associated marker is located within the gene.

Table S13: NAM multiple SNP model GWAS associations (RMIP ≥ 0.05) and overlap with NAM joint-linkage QTL intervals for percent protein on a dry matter basis.

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
01	pze0141569344	41,569,344	59.1	0.18	5.45E-08	0.23	Yes	Unknown
01	pze01174097456	174,097,456	94.4	-0.11	8.17E-08	0.06	No	Putative Na+/H+ antiporter family
01	pze01191729382	191,729,382	105.4	-0.15	5.98E-10	0.14	No	*FRAGILE FIBER3* (inositol or phosphatidylinositol phosphatase activity)
01	pze01191729419	191,729,419	105.4	-0.17	2.07E-10	0.06	No	*FRAGILE FIBER3* (inositol or phosphatidylinositol phosphatase activity)
01	pze01214607570	214,607,570	125.8	-0.17	7.49E-11	0.30	No	
01	pze01214607581	214,607,581	125.8	-0.17	1.76E-10	0.10	No	
01	pze01224419429	224,419,429	132.8	-0.16	1.17E-12	0.05	Yes	*YABBY3* (protein binding / transcription factor)
01	pze01233488715	233,488,715	138.6	-0.16	1.20E-08	0.07	Yes	
01	pze01233488765	233,488,765	138.6	-0.17	4.51E-11	0.05	Yes	
01	pze01261647632	261,647,632	156.9	0.10	1.39E-09	0.13	Yes	Glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein
01	pze01261647745	261,647,745	156.9	0.15	6.13E-11	0.36	Yes	Glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein
01	pze01263215117	263,215,117	158.1	0.12	7.28E-13	0.05	Yes	
01	pze01264586209	264,586,209	159.2	0.11	8.98E-12	0.21	Yes	
02	pze0205903537	5,903,537	18.2	0.10	1.16E-07	0.09	No	
02	pze0206003320	6,003,320	18.5	0.09	8.92E-08	0.07	No	
02	pze0218286061	18,286,061	48.0	0.18	1.64E-10	0.29	No	Unknown
02	pze02173762551	173,762,551	85.5	-0.17	3.37E-08	0.07	Yes	Unknown

Table S13: (continued…Protein)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
02	pze02184529536	184,529,536	95.0	-0.11	1.01E-12	0.40	Yes	
02	pze02192531858	192,531,858	103.6	-0.13	3.92E-10	0.06	No	
02	pze02195678917	195,678,917	106.1	-0.13	3.86E-11	0.15	No	
02	pze02195938470	195,938,470	106.3	-0.13	3.89E-08	0.09	No	PAZ and PIWI-domain containing protein
02	pze02229979130	229,979,130	148.3	-0.17	4.80E-08	0.10	No	
02	pze02230780427	230,780,427	150.5	-0.08	1.32E-07	0.11	No	
02	pze02234059444	234,059,444	156.6	-0.09	7.43E-10	0.11	No	*KNAT1* (Knotted-like from *Arabidopsis thaliana*, transcription factor)
02	pze02234059448	234,059,448	156.6	-0.09	4.27E-08	0.07	No	*KNAT1* (Knotted-like from *Arabidopsis thaliana*, transcription factor)
02	pze02234064898	234,064,898	156.6	-0.10	7.04E-09	0.05	No	
03	pze0321965052	21,965,052	50.8	-0.15	1.70E-07	0.06	No	
03	pze03107736175	107,736,175	58.7	0.14	2.82E-14	0.88	Yes	
03	pze03223101410	223,101,410	144.2	-0.09	8.90E-11	0.17	Yes	
03	pze03225299207	225,299,207	148.6	-0.15	6.87E-09	0.23	No	
03	pze03225917080	225,917,080	149.6	-0.10	4.23E-08	0.12	No	
03	pze03227465051	227,465,051	152.1	-0.25	7.81E-08	0.05	No	Unknown
03	pze03227520838	227,520,838	152.1	-0.12	2.28E-10	0.07	No	Unknown
03	pze03227520964	227,520,964	152.1	-0.12	3.16E-11	0.16	No	
04	pze0405875549	5,875,549	20.0	0.13	4.44E-08	0.05	No	Cytochrome P450

Table S13: (continued…Protein)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
04	pze04139123563	139,123,563	59.8	0.11	1.69E-14	0.21	Yes	ATP binding / ATP-dependent helicase/ DNA helicase
04	pze04146879810	146,879,810	61.7	0.11	2.18E-17	0.13	Yes	
04	pze04152317836	152,317,836	64.0	0.16	4.05E-18	0.38	Yes	
04	pze04155357655	155,357,655	66.3	0.11	2.72E-13	0.06	Yes	
04	pze04175740882	175,740,882	86.8	0.23	3.89E-08	0.05	Yes	Subtilase family protein
04	pze04176743530	176,743,530	88.0	0.19	3.83E-09	0.07	Yes	Nitrate reductase
05	pze0569077652	69,077,652	65.3	-0.14	2.69E-08	0.16	No	
05	pze0588027712	88,027,712	69.4	-0.17	1.37E-09	0.39	Yes	
05	pze05191372077	191,372,077	100.7	0.16	1.33E-23	0.07	Yes	
05	pze05194861680	194,861,680	103.3	0.13	5.39E-20	0.05	Yes	
05	pze05197933894	197,933,894	105.8	0.14	2.30E-21	0.70	Yes	
06	pze0672858614	72,858,614	10.3	0.12	3.00E-14	0.10	Yes	Transferase family protein
06	pze0673924500	73,924,500	10.4	0.16	3.14E-16	0.35	Yes	Phosphate translocator-related
06	pze0673925144	73,925,144	10.4	0.15	1.54E-13	0.12	Yes	Phosphate translocator-related
06	pze0685180180	85,180,180	13.1	0.13	1.79E-18	0.18	Yes	*LEUCINE-RICH REPEAT/EXTENSIN 2*
06	pze0687784687	87,784,687	15.3	0.15	1.00E-07	0.07	Yes	Cysteine Proteinase
06	pze06132243413	132,243,413	50.6	-0.12	2.94E-11	0.17	Yes	Meiotic recombination Spo11
06	pze06137612791	137,612,791	53.3	-0.13	1.68E-11	0.22	Yes	

Table S13: (continued…Protein)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
06	pze06137618280	137,618,280	53.3	-0.13	3.56E-13	0.08	Yes	
06	pze06137783057	137,783,057	53.4	-0.10	7.87E-12	0.09	Yes	
06	pze06137825948	137,825,948	53.4	-0.20	5.67E-14	0.08	Yes	*BGLU1* (Beta Glucosidase 1)
06	pze06139630511	139,630,511	54.2	-0.10	6.88E-09	0.06	Yes	
06	pze06144893470	144,893,470	56.7	-0.10	1.40E-10	0.05	No	
06	pze06164886922	164,886,922	100.3	0.10	1.81E-11	0.05	Yes	
06	pze06164950817	164,950,817	100.7	0.10	1.07E-09	0.16	Yes	
06	pze06164952310	164,952,310	100.7	0.09	1.98E-09	0.15	Yes	
06	pze06165669774	165,669,774	103.2	0.14	4.46E-08	0.09	Yes	
06	pze06166173090	166,173,090	104.9	0.12	1.05E-09	0.08	Yes	Zinc Finger (GATA type) family protein
06	pze06166614008	166,614,008	106.6	0.13	1.30E-11	0.21	Yes	Rad21 / Rec8 like protein
07	pze07114949129	114,949,129	58.1	-0.19	1.37E-09	0.19	No	
07	pze07126431538	126,431,538	67.3	-0.16	1.54E-09	0.06	Yes	
07	pze07128349130	128,349,130	69.8	-0.13	7.00E-08	0.11	Yes	
07	pze07136002039	136,002,039	74.3	-0.14	1.43E-07	0.14	Yes	
07	pze07140392751	140,392,751	78.7	-0.19	2.50E-16	0.06	Yes	*PHT4;5* (inorganic phosphate transmembrane transporter)
07	pze07140662870	140,662,870	79.0	-0.16	1.71E-16	0.06	Yes	

Table S13: (continued…Protein)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
07	pze07149948232	149,948,232	87.8	-0.12	1.54E-17	0.27	No	
07	pze07154373209	154,373,209	94.8	-0.12	9.24E-16	0.17	Yes	
07	pze07155187710	155,187,710	96.4	-0.11	2.76E-08	0.07	Yes	
07	pze07156274680	156,274,680	98.7	-0.14	7.98E-18	0.14	Yes	
07	pze07156275259	156,275,259	98.7	-0.12	3.18E-16	0.06	Yes	
08	pze0873822546	73,822,546	54.0	-0.12	3.98E-23	0.68	Yes	Unknown
08	pze0889215231	89,215,231	55.8	-0.15	8.96E-24	0.09	No	
08	pze0889804861	89,804,861	55.8	-0.12	1.60E-24	0.19	No	
08	pze08130270260	130,270,260	68.6	-0.16	9.28E-11	0.07	Yes	
08	pze08145172472	145,172,472	75.0	-0.18	6.26E-09	0.59	Yes	Carbonic anhydrase
08	pze08149198460	149,198,460	78.4	-0.21	5.30E-11	0.11	Yes	IAA8 transcription factor
08	pze08163510712	163,510,712	95.4	0.19	8.75E-09	0.37	Yes	
08	pze08164298281	164,298,281	98.8	0.09	1.27E-08	0.06	Yes	
08	pze08165335641	165,335,641	102.1	0.09	2.20E-08	0.09	Yes	
09	pze0908323233	8,323,233	11.8	0.14	1.67E-07	0.07	No	
09	pze09102186205	102,186,205	51.0	0.11	2.28E-11	0.06	No	
09	pze09102433519	102,433,519	51.1	0.12	6.15E-32	0.06	No	

Table S13: (continued…Protein)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
09	pze09102433540	102,433,540	51.1	0.11	8.99E-12	0.10	No	
09	pze09102452830	102,452,830	51.1	0.10	8.22E-12	0.13	No	NC domain-containing protein
09	pze09102494203	102,494,203	51.1	0.10	2.57E-11	0.15	No	
09	pze09103811965	103,811,965	51.6	0.11	3.81E-27	0.08	No	
09	pze09134852827	134,852,827	71.6	0.10	2.79E-26	0.06	Yes	*PAB7* (Poly(A) Binding Protein 7)
09	pze09135383651	135,383,651	72.4	0.11	2.27E-30	0.42	Yes	*TRFL1* (TRF-Like 1)
09	pze09135401487	135,401,487	72.4	0.11	2.65E-26	0.19	Yes	
09	pze09138490691	138,490,691	79.2	0.12	2.61E-29	0.11	Yes	
09	pze09138761646	138,761,646	79.9	0.13	1.42E-15	0.14	Yes	
09	pze09142010824	142,010,824	87.2	0.22	4.55E-08	0.07	Yes	Leucine-rich repeat transmembrane protein kinase
09	pze09142950644	142,950,644	89.4	0.23	1.63E-07	0.12	Yes	Zinc finger (C3HC4-type RING finger) family protein
10	pze1000647587	647,587	-4.3	-0.31	1.14E-07	0.07	No	
10	pze1049739669	49,739,669	36.3	-0.14	1.35E-12	0.26	Yes	
10	pze1050061312	50,061,312	36.3	-0.15	1.42E-13	0.05	Yes	
10	pze1077008373	77,008,373	38.5	-0.12	7.00E-12	0.19	Yes	
10	pze1077258298	77,258,298	38.5	-0.20	8.47E-14	0.06	Yes	
10	pze1083433186	83,433,186	40.0	-0.15	9.60E-12	0.05	Yes	

Table S13: (continued…Protein)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
10	pze10128879017	128,879,017	51.7	-0.14	2.13E-48	0.06	Yes	
10	pze10128879122	128,879,122	51.7	-0.15	3.23E-49	0.07	Yes	
10	pze10130522512	130,522,512	53.3	-0.14	4.40E-46	0.09	Yes	
10	pze10131425475	131,425,475	54.8	-0.14	6.01E-47	0.11	Yes	Cytokinin dehydrogenase precursor
10	pze10131716490	131,716,490	55.2	-0.16	1.56E-50	0.23	Yes	
10	pze10131716806	131,716,806	55.2	-0.14	2.03E-45	0.19	Yes	
10	pze10131789724	131,789,724	55.3	-0.17	5.95E-47	0.09	Yes	
10	pze10141182124	141,182,124	73.6	-0.14	5.03E-08	0.14	No	
10	pze10143096411	143,096,411	80.1	-0.13	1.25E-08	0.12	No	
10	pze10146018487	146,018,487	89.1	0.15	2.00E-08	0.10	No	
10	pze10147958625	147,958,625	99.1	0.17	1.03E-08	0.22	No	Zinc finger, RING-type
10	pze10148028746	148,028,746	99.5	0.13	4.23E-08	0.24	No	
10	pze10148052043	148,052,043	99.6	0.13	6.34E-08	0.07	No	C2 domain-containing protein
10	pze10148507725	148,507,725	102.2	0.17	2.33E-09	0.05	No	Nodulin

[a] Percent oil kernel composition on a dry matter basis relative to B73.

[b] 'Yes' = associated SNP is positioned in a NAM joint-linkage QTL interval, and 'No' = associated SNP is located outside a NAM joint-linkage QTL intervals.

[c] Candidate gene described if associated marker is located within the gene.

Table S14: NAM multiple SNP model GWAS associations (RMIP ≥ 0.05) and overlap with NAM joint-linkage QTL intervals for percent oil on a dry matter basis.

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
01	pze0116416350	16,416,350	32.9	0.10	9.36E-13	0.07	Yes	
01	pze0118568101	18,568,101	35.1	0.06	2.45E-14	0.18	Yes	
01	pze0119034013	19,034,013	35.6	0.08	7.14E-08	0.11	Yes	
01	pze0122489200	22,489,200	39.4	0.06	6.68E-14	0.07	Yes	
01	pze0125332530	25,332,530	42.2	0.06	1.92E-18	0.05	Yes	*MIPS2* (Myo-Inositol-1-Phosphate Synthase 2)
01	pze0125468628	25,468,628	42.4	0.06	7.78E-12	0.13	Yes	
01	pze0127054049	27,054,049	44.6	0.08	1.74E-07	0.26	Yes	
01	pze0174517643	74,517,643	79.1	-0.07	2.05E-08	0.13	No	
01	pze01198964527	198,964,527	112.3	0.07	4.99E-20	0.39	No	
01	pze01200550540	200,550,540	114.1	0.09	1.99E-18	0.25	No	
01	pze01203289133	203,289,133	116.3	0.06	4.96E-15	0.11	Yes	
01	pze01210953214	210,953,214	122.6	0.05	1.01E-07	0.06	Yes	
01	pze01240495541	240,495,541	141.9	0.05	6.18E-08	0.09	Yes	
01	pze01240496258	240,496,258	141.9	0.06	1.19E-08	0.08	Yes	
01	pze01294901080	294,901,080	198.0	0.06	4.00E-14	0.05	Yes	
01	pze01295090084	295,090,084	198.3	0.07	5.91E-15	0.09	Yes	
01	pze01295763463	295,763,463	199.4	0.05	2.11E-16	0.11	Yes	

Table S14: (continued…Oil)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
01	pze01295769034	295,769,034	199.4	0.05	4.04E-15	0.34	Yes	
02	pze0211679968	11,679,968	33.6	0.12	1.79E-08	0.05	No	
02	pze0220326346	20,326,346	51.1	-0.07	5.08E-09	0.16	No	*CNX5* (Co-Factor for Nitrate Reductase and Xanthine Dehydrogenas 5)
02	pze0220326432	20,326,432	51.1	-0.07	7.31E-13	0.05	No	*CNX5* (Co-Factor for Nitrate Reductase and Xanthine Dehydrogenas 5)
02	pze0220327496	20,327,496	51.1	-0.06	1.13E-08	0.64	No	*CNX5* (Co-Factor for Nitrate Reductase and Xanthine Dehydrogenas 5)
02	pze0239068567	39,068,567	66.8	-0.05	1.67E-20	0.10	Yes	
02	pze0244884255	44,884,255	69.7	-0.05	1.27E-19	0.23	Yes	*ABA1* (ABA Deficient 1, zeaxanthin epoxidase)
02	pze0249122012	49,122,012	71.3	-0.05	2.70E-18	0.14	Yes	U-box domain containing protein
02	pze0249125290	49,125,290	71.3	-0.05	1.44E-19	0.14	Yes	
02	pze02125195471	125,195,471	77.4	-0.07	3.41E-11	0.20	Yes	
02	pze02172957702	172,957,702	85.1	-0.06	2.18E-07	0.05	No	
02	pze02173076399	173,076,399	85.2	-0.08	3.46E-09	0.05	No	*SCPL18* (Serine carboxypeptidase-like 18)
02	pze02183780201	183,780,201	94.0	0.10	3.13E-09	0.06	No	
02	pze02188225260	188,225,260	99.8	0.10	7.69E-08	0.19	No	
02	pze02201845456	201,845,456	109.6	0.10	5.74E-08	0.18	No	
03	pze0302103927	2,103,927	4.5	-0.06	1.56E-08	0.21	No	
03	pze0302105219	2,105,219	4.5	-0.07	3.77E-09	0.05	No	

Table S14: (continued…Oil)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
03	pze0308839067	8,839,067	31.7	-0.07	1.04E-08	0.14	No	PHD finger family protein
03	pze0316337497	16,337,497	44.0	-0.08	8.92E-13	0.12	No	
03	pze0335980205	35,980,205	55.3	-0.07	8.08E-12	0.08	Yes	
03	pze0342757479	42,757,479	55.9	0.02	1.95E-09	0.09	Yes	G protein-coupled receptor GPR1
03	pze0358388350	58,388,350	57.7	-0.07	1.66E-11	0.23	Yes	Serine/threonine protein kinase
03	pze03111141904	111,141,904	58.9	-0.08	2.74E-13	0.11	Yes	
03	pze03179802623	179,802,623	91.7	0.07	5.59E-16	0.17	No	
03	pze03179804597	179,804,597	91.7	0.06	1.52E-13	0.13	No	
03	pze03179938275	179,938,275	92.0	0.06	1.36E-15	0.21	No	
03	pze03194187278	194,187,278	102.3	0.05	1.19E-07	0.07	Yes	
03	pze03194648926	194,648,926	103.0	0.06	2.61E-16	0.08	Yes	
03	pze03198398046	198,398,046	105.5	0.07	1.90E-13	0.05	Yes	UDP-glucoronosyl/UDP-glucosyl transferase family protein
03	pze03205226976	205,226,976	113.7	0.07	5.40E-08	0.10	Yes	
03	pze03211146687	211,146,687	121.9	0.06	9.31E-08	0.15	No	
03	pze03211151474	211,151,474	121.9	0.06	1.51E-07	0.09	No	
03	pze03220114561	220,114,561	137.4	-0.05	2.78E-07	0.06	No	*ALDH2C4 (*3-chloroallyl aldehyde dehydrogenase)
04	pze0406032338	6,032,338	20.4	0.08	9.92E-08	0.15	No	

Table S14: (continued…Oil)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
04	pze0422895076	22,895,076	46.3	0.08	1.83E-08	0.07	No	
04	pze0492992084	92,992,084	57.6	0.06	2.77E-08	0.09	Yes	
04	pze04108097627	108,097,627	58.0	0.10	1.43E-10	0.07	Yes	
04	pze04120561643	120,561,643	58.3	0.06	2.73E-19	0.08	Yes	
04	pze04123294754	123,294,754	58.3	0.07	4.02E-10	0.10	Yes	
04	pze04123329276	123,329,276	58.3	0.06	1.14E-17	0.14	Yes	
04	pze04123343028	123,343,028	58.3	0.06	5.71E-19	0.11	Yes	
04	pze04163300645	163,300,645	73.4	0.07	1.11E-18	0.35	No	
04	pze04163338800	163,338,800	73.4	0.06	1.81E-18	0.08	No	
04	pze04172652992	172,652,992	82.3	0.05	4.73E-11	0.05	Yes	
04	pze04172658360	172,658,360	82.3	0.08	4.12E-11	0.05	Yes	
04	pze04172891298	172,891,298	82.7	0.05	2.91E-07	0.05	Yes	*ERF* (Ethylene Response Factor B-6 of ERF/AP2 transcription factor family)
04	pze04173560682	173,560,682	83.8	0.08	1.15E-17	0.16	Yes	
04	pze04205693464	205,693,464	108.2	-0.05	2.86E-11	0.08	No	
04	pze04209879821	209,879,821	109.4	-0.06	3.20E-11	0.19	No	
04	pze04209879846	209,879,846	109.4	-0.06	6.00E-13	0.39	No	
04	pze04242018671	242,018,671	128.1	-0.06	3.41E-12	0.05	No	

Table S14: (continued…Oil)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
04	pze04242648433	242,648,433	130.6	-0.05	1.23E-11	0.23	No	Sugar isomerase (SIS) domain-containing protein
05	pze0503525173	3,525,173	10.9	0.07	5.48E-10	0.05	Yes	*PSAD-2* (photosystem I subunit D-2)
05	pze0504091479	4,091,479	12.9	0.06	8.64E-09	0.63	Yes	Histone H1.2
05	pze0504901650	4,901,650	16.9	0.07	2.70E-10	0.11	Yes	
05	pze0505307997	5,307,997	19.0	0.05	6.24E-11	0.07	Yes	
05	pze0511742915	11,742,915	36.5	-0.06	1.08E-10	0.18	Yes	
05	pze0511879036	11,879,036	37.3	-0.06	1.19E-12	0.46	Yes	
05	pze0511879078	11,879,078	37.3	-0.06	6.72E-09	0.18	Yes	
05	pze0546081614	46,081,614	60.0	0.09	2.68E-08	0.06	Yes	
05	pze0547984914	47,984,914	60.3	0.08	9.04E-29	0.07	Yes	
05	pze0551583383	51,583,383	61.1	0.07	1.15E-31	0.38	Yes	Iron ion binding / oxidoreductase
05	pze0551720445	51,720,445	61.1	0.07	4.13E-30	0.11	Yes	Unknown
05	pze0552059382	52,059,382	61.2	0.07	2.34E-25	0.07	Yes	*RPA2* (Replicon Protein A2)
05	pze0552835376	52,835,376	61.3	0.08	8.80E-26	0.14	Yes	
05	pze0557934465	57,934,465	62.4	0.07	2.42E-29	0.10	Yes	Chloroplast thylakoid lumen protein
05	pze05173565198	173,565,198	85.1	0.07	2.38E-09	0.08	No	
05	pze05174885784	174,885,784	86.6	0.08	5.81E-09	0.08	No	Unknown

Table S14: (continued…Oil)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
05	pze05175579810	175,579,810	87.3	0.04	3.14E-08	0.06	Yes	
05	pze05187894128	187,894,128	97.7	0.05	1.36E-08	0.08	Yes	Unknown
05	pze05212800876	212,800,876	142.3	-0.06	6.43E-08	0.28	No	
06	pze06103555835	103,555,835	29.3	0.10	3.04E-21	0.05	Yes	
06	pze06103696732	103,696,732	29.5	0.13	6.23E-14	0.05	Yes	
06	pze06103835279	103,835,279	29.6	0.11	6.88E-17	0.06	Yes	
06	pze06105014855	105,014,855	30.8	0.18	8.91E-43	0.31	Yes	*DGAT1-2* (type I acyl-CoA:diacylglycerol acyltransferase)
06	pze06105019473	105,019,473	30.8	0.13	4.31E-49	0.67	Yes	*DGAT1-2* (type I acyl-CoA:diacylglycerol acyltransferase)
06	pze06106914732	106,914,732	32.8	0.05	2.69E-07	0.08	Yes	
06	pze06110008048	110,008,048	36.5	0.10	3.69E-16	0.06	Yes	
06	pze06110413739	110,413,739	37.0	0.16	1.79E-12	0.11	Yes	
06	pze06110952436	110,952,436	37.7	0.08	5.76E-14	0.09	Yes	
06	pze06112065791	112,065,791	39.0	0.13	2.82E-16	0.58	Yes	
06	pze06131405628	131,405,628	50.0	-0.12	2.45E-08	0.69	No	*ATGA2OX3* (gibberellin 2-oxidase 3)
06	pze06146638392	146,638,392	58.3	0.05	2.05E-07	0.06	Yes	CUE domain containing protein
06	pze06146859183	146,859,183	58.6	0.07	1.10E-08	0.05	Yes	*PTR2* (Peptide transporter)
06	pze06151712033	151,712,033	65.8	0.07	9.81E-10	0.05	No	

Table S14: (continued…Oil)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
06	pze06153418317	153,418,317	68.6	0.05	2.49E-08	0.08	No	
06	pze06153910135	153,910,135	69.4	0.04	2.57E-09	0.17	No	Allergen-related
06	pze06164606481	164,606,481	98.5	0.09	1.68E-09	0.11	No	
06	pze06166173995	166,173,995	104.9	0.11	8.79E-10	0.18	No	Transcription factor
06	pze06169226283	169,226,283	108.7	0.08	8.36E-09	0.17	No	
07	pze0786521550	86,521,550	50.0	0.04	4.38E-10	0.05	Yes	
07	pze0790011130	90,011,130	50.1	0.05	2.65E-08	0.06	Yes	
07	pze0798440879	98,440,879	50.8	0.04	2.32E-09	0.14	Yes	Armadillo/beta-catenin repeat family protein / U-box domain-containing protein
07	pze0798745124	98,745,124	50.8	0.04	4.28E-10	0.27	Yes	
07	pze0798963774	98,963,774	50.8	0.05	3.70E-09	0.06	Yes	
07	pze07106530799	106,530,799	53.8	0.05	5.15E-09	0.05	Yes	
07	pze07109178008	109,178,008	55.2	0.04	1.33E-08	0.09	Yes	
08	pze08151664284	151,664,284	80.4	0.07	6.17E-19	0.05	Yes	
08	pze08153813784	153,813,784	81.3	0.08	2.13E-20	0.17	Yes	*BRI1* (Brassinosteroid Insensitive 1)
08	pze08153813786	153,813,786	81.3	0.09	1.40E-18	0.06	Yes	*BRI1* (Brassinosteroid Insensitive 1)
08	pze08155478153	155,478,153	82.3	0.08	3.95E-19	0.14	Yes	
08	pze08155478230	155,478,230	82.3	0.08	2.71E-18	0.53	Yes	

Table S14: (continued…Oil)

Chr	Marker ID	AGP_v1 (bp)	cM	Effect[a] (%)	*P*-Value	RMIP	Joint-Linkage QTL Interval[b]	Candidate Gene[c]
09	pze0921934769	21,934,769	38.7	0.09	4.07E-08	0.05	No	
09	pze0921983416	21,983,416	38.8	0.15	5.54E-08	0.09	No	
09	pze0926515022	26,515,022	43.3	0.09	2.25E-07	0.08	No	
09	pze09113469332	113,469,332	56.0	-0.12	6.18E-14	0.05	No	
09	pze09117897621	117,897,621	57.7	-0.08	9.99E-14	0.36	Yes	*SUS4* (Sucrose Synthase)
09	pze09118277164	118,277,164	58.0	-0.08	1.63E-13	0.11	Yes	Unknown
09	pze09120796850	120,796,850	59.7	-0.09	3.16E-11	0.07	Yes	
09	pze09122959898	122,959,898	61.2	-0.05	2.87E-10	0.08	Yes	*CYP709B2 (*electron carrier)
09	pze09123776478	123,776,478	61.8	-0.06	2.29E-08	0.05	Yes	
09	pze09129555959	129,555,959	64.6	-0.06	6.25E-11	0.13	Yes	ABC transporter, ATP-binding protein
09	pze09141771810	141,771,810	86.9	-0.06	2.01E-08	0.19	No	
10	pze10134625388	134,625,388	59.4	-0.05	1.87E-12	0.21	Yes	
10	pze10134625403	134,625,403	59.4	-0.06	5.16E-12	0.12	Yes	
10	pze10136116629	136,116,629	62.0	-0.09	9.16E-12	0.14	No	
10	pze10137549553	137,549,553	64.8	-0.06	5.25E-14	0.11	No	
10	pze10137660662	137,660,662	64.9	-0.06	6.34E-12	0.05	No	

[a] Percent oil kernel composition on a dry matter basis relative to B73.

[b] 'Yes' = associated SNP is positioned in a NAM joint-linkage QTL interval, and 'No' = associated SNP is located outside a NAM joint-linkage QTL intervals.

[c] Candidate gene described if associated marker is located within the gene.

Table S15: Overlap between NAM Joint-linkage QTL and previously identified biparental QTL.

Trait	Chr.Bin	Marker/Interval	NAM-QTL Overlap	Population Parentals(Reference)
Starch	1.01	*php20689*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	1.01/02	*php20689–bnlg1429*	Yes	Illinois High Oil x B73[2]
Starch	1.02	*bmc1953*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	1.02/03	*bnlg1429–bnl12.06*	No	Illinois High Oil x Mo17[2]
Starch	1.03	*bmc1866*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	1.04	*npi262*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	1.04	*npi262*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	1.06	*umc67a*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	1.07	*umc23a*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	1.07/08	*umc33a–dupssr12*	No	Illinois High Oil x B73[2]
Starch	1.08	*umc128*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	1.08	*bmc1643*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	1.11	*npi238*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	2.03	*umc6a*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	2.04	*bnl12.09*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	2.05	*dupssr21*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	2.06/07	*npi337*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	2.07	*umc5a*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	2.08	*npi298*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	2.08	*umc125*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	2.10	*bnl17.14*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	3.02	*bmc1144*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	3.03	*php20042*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	3.03	*bmc1523*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	3.03	*npi269*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	3.04	*umc154*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	3.04	*umc10*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	3.04	*npi249*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	3.04	*phi036–bnlg1019a*	No	Illinois High Oil x B73[2]
Starch	3.05	*phi073*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	3.06	*bnl5.37b*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	3.06/07	*bnlg1047a–bnlg1605*	No	Illinois High Oil x B73[2]
Starch	3.06/07	*bnlg1605–bnlg197*	No	Illinois High Oil x B73[2]

Table S15: (continued…)

Trait	Chr.Bin	Marker/Interval	NAM-QTL Overlap	Population Parentals(Reference)
Starch	3.07	*bnl5.33b*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	3.07	*umc16*	Yes	Illinois High Protein x Illinois Low Protein[5]
Starch	3.08	*umc16a*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	3.08	*npi432*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	3.08	*umc17*	Yes	Illinois High Protein x Illinois Low Protein[5]
Starch	3.09	*php20726*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	3.09	*sh2*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	3.09	*umc63a*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	3.09	*umc96*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	3.09	*Sh2*	Yes	Illinois High Protein x Illinois Low Protein[5]
Starch	3.09	*umc63*	Yes	Illinois High Protein x Illinois Low Protein[5]
Starch	3.09	*umc96*	Yes	Illinois High Protein x Illinois Low Protein[5]
Starch	4.03/05	*nc004–phi026*	No	Illinois High Oil x Mo17[2]
Starch	4.04/05	*phi096–nc005*	No	Illinois High Oil x B73[2]
Starch	5.01	*umc72A*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	5.02	*umc90*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	5.03	*php20872*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	5.03	*umc1*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	5.03	*php15018– CO7CO2CD*	No	Illinois High Oil x B73[2]
Starch	5.03	*CO7BO2CD– php10014*	?	Illinois High Oil x Mo17[2]
Starch	5.05	*npi237*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	5.07	*php20053–phi048*	No	Illinois High Oil x Mo17[2]
Starch	6.00/01	*phi126–y1ssr*	Yes	Illinois High Oil x Mo17[2]
Starch	6.05	*umc21*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	7.03	*php20746*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	7.04	*bnl8.39*	Yes	Illinois High Protein x Illinois Low Protein[5]
Starch	7.06	*php20020*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	7L	*P200746*	?	Illinois High Protein x Illinois Low Protein[5]
Starch	8.02	*bnl09.11a*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	8.03	*npi260b*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	8.03/04	*bnl9.08*	Yes	Illinois High Protein x Illinois Low Protein[1]

Table S15: (continued…)

Trait	Chr.Bin	Marker/Interval	NAM-QTL Overlap	Population Parentals(Reference)
Starch	8.05	*umc2c*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	8.05	*bnlg162–bnlg1599*	No	Illinois High Oil x B73[2]
Starch	8.08	*umc7*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	9.03	*php20075b*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	9.03	*phi027–umc81*	Yes	Illinois High Oil x Mo17[2]
Starch	9.05	*npi443*	No	Illinois High Protein x Illinois Low Protein[5]
Starch	10.00	*phi118*	?	Illinois High Protein x Illinois Low Protein[1]
Starch	10.00	*bnl10.17a*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	10.02	*npi285a*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	10.03	*umc130*	Yes	Illinois High Protein x Illinois Low Protein[1]
Starch	10.07	*npi320*	No	Illinois High Protein x Illinois Low Protein[1]
Starch	10.07	*bmc1185*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	1.01	*php20689*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	1.02	*bmc1953*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	1.02/03	*bnlg1429–bnl1206*	No	Illinois High Oil x Mo17[2]
Protein	1.03	*bmc1866*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	1.04	*npi262*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	1.06	*umc67a*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	1.07	*umc23a*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	1.07	*npi447*	Yes	Illinois High Protein x Illinois Low Protein[5]
Protein	1.07	*cfbbi58–php20668*	?	Illinois High Oil x B73[2]
Protein	1.08	*umc128*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	1.08	*bmc1643*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	1.11	*npi238*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	2.03	*umc6a*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	2.03	*npi269*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	2.04	*bnl12.09*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	2.05	*dupssr21*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	2.06	*umc1156*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	2.06/07	*npi337*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	2.07	*umc5a*	Yes	Illinois High Protein x Illinois Low Protein[1]

Table S15: (continued…)

Trait	Chr.Bin	Marker/Interval	NAM-QTL Overlap	Population Parentals(Reference)
Protein	2.08	*npi298*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	2.08	*umc125*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	2.10	*bnl17.14*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	3.01	*umc121*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.03	*php20042*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.03	*bmc1144*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.03	*bmc1523*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.04	*umc154*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.04	*npi249*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	3.04	*umc10*	Yes	Illinois High Protein x Illinois Low Protein[5]
Protein	3.05	*phi073*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	3.06	*bnl5.37b*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.07	*bnl5.33b*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.07	*umc16*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	3.08	*php10080*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.08	*umc17*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	3.08	*npi432*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	3.09	*php20726*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.09	*sh2*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.09	*umc63a*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	3.09	*Sh2*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	3.09	*umc63*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	3L	*P10080*	?	Illinois High Protein x Illinois Low Protein[5]
Protein	4.03/05	*nc004–phi026*	No	Illinois High Oil x Mo17[2]
Protein	5.01	*umc72A*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	5.01/03	*nc007–phi113*	No	Illinois High Oil x Mo17[2]
Protein	5.02	*umc90*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	5.03	*php20872*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	5.03	*umc43*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	5.03	*umc1*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	5.03	*phi113–php150018*	Yes	Illinois High Oil x B73[2]

Table S15: (continued…)

Trait	Chr.Bin	Marker/Interval	NAM-QTL Overlap	Population Parentals(Reference)
Protein	5.05	*npi237*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	5.08	*umc104B*	No	Illinois High Protein x Illinois Low Protein[5]
Protein	6.01/02	*y1ssr–umc1006*	Yes	Illinois High Oil x Mo17[2]
Protein	6.04/05	*nc009–umc21*	No	Illinois High Oil x B73[2]
Protein	6.05/06	*phi129–dupssr15*	Yes	Illinois High Oil x B73[2]
Protein	7.03	*php20746*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	7.03	*npi455*	Yes	Illinois High Protein x Illinois Low Protein[5]
Protein	7.03	*dupssr009–bnlg1805*	No	Illinois High Oil x Mo17[2]
Protein	7.04	*bnl8.39*	Yes	Illinois High Protein x Illinois Low Protein[5]
Protein	7.06	*php20020*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	7L	*P200746*	?	Illinois High Protein x Illinois Low Protein[5]
Protein	8.02	*bnl9.11a*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	8.03	*npi260b*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	8.03/04	*bnl9.08*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	8.05/08	*umc1130–bnlg1056*	Yes	Illinois High Oil x B73[2]
Protein	8.05	*umc2c*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	8.05	*bnlg1599–umc1130*	Yes	Illinoise High Oil x B73[2]
Protein	9.03	*php20075b*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	9.03	*phi027–umc81*	Yes	Illinois High Oil x B73[2]
Protein	9.05	*npi443*	Yes	Illinois High Protein x Illinois Low Protein[5]
Protein	9.07	*umc20–npi291*	Yes	Illinois High Oil x B73[2]
Protein	10.00	*phi118*	?	Illinois High Protein x Illinois Low Protein[1]
Protein	10.00	*bnl10.17a*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	10.02	*npi285a*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	10.02	*phi059*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	10.03	*umc130*	Yes	Illinois High Protein x Illinois Low Protein[1]
Protein	10.07	*npi320*	No	Illinois High Protein x Illinois Low Protein[1]
Protein	10.07	*bmc1185*	Yes	Illinois High Protein x Illinois Low Protein[1]
Oil	1.04/07	*bnlg2086-umc1122*	No	By804 x B73[3]
Oil	1.07	*npi447*	Yes	Illinois High Protein x Illinois Low Protein[4]
Oil	1.08	*mmc0041–phi053*	Yes	Illinois High Oil x Mo17[2]
Oil	2.04	*umc134*	Yes	Illinois High Protein x Illinois Low Protein[4]

Table S15: (continued…)

Trait	Chr.Bin	Marker/Interval	NAM-QTL Overlap	Population Parentals(Reference)
Oil	2.04/05	*bnlg108-phi092*	Yes	By804 x B73[3]
Oil	2.06	*npi456*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	2.08	*umc125*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	3.04	*umc10*	Yes	Illinois High Protein x Illinois Low Protein[4]
Oil	3.04	*bnlg1019–npi247*	Yes	Illinois High Oil x B73[2]
Oil	3.04	*phi036–bnlg1019*	No	Illinois High Oil x Mo17[2]
Oil	3.09	*npi420*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	4.01/04	*phi213984-phi096*	No	By804 x B73[3]
Oil	4.04/05	*phi096-bnlg1755*	Yes	By804 x B73[3]
Oil	4.07	*umc104*	Yes	Illinois High Protein x Illinois Low Protein[4]
Oil	4.08	*npi270*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	4.08	*npi410*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	5.04	*CO7CO2CD– php100014*	?	Illinois High Oil x B73[2]
Oil	6.01	*umc85*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	6.02	*npi377*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	6.04	*umc65–nc009*	Yes	Illinois High Oil x B73[2]
Oil	6.04/05	*nc009–umc21*	Yes	Illinois High Oil x Mo17[2]
Oil	6.05	*bnl5.47*	Yes	Illinois High Protein x Illinois Low Protein[4]
Oil	6.05	*umc2319-phi129*	No	By804 x B73[3]
Oil	6.06	*npi280*	No	Illinois High Protein x Illinois Low Protein[4]

Table S15: (continued…)

Trait	Chr.Bin	Marker/Interval	NAM-QTL Overlap	Population Parentals(Reference)
Oil	6.08	*umc38*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	7.03	*umc116*	Yes	Illinois High Protein x Illinois Low Protein[4]
Oil	7.03	*bnlg1070–phi091*	No	Illinois High Oil x B73[2]
Oil	7.04	*bnl8.32T*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	8.02	*npi276*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	8.02/03	*phi119-umc1360*	No	By804 x B73[3]
Oil	8.03	*npi260*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	8.03/04	*bnl9.08*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	8.05	*umc93*	No	Illinois High Protein x Illinois Low Protein[4]
Oil	8.05	*bnlg162–bnlg1599*	No	Illinois High Oil x B73[2]
Oil	10.05	*npi232*	Yes	Illinois High Protein x Illinois Low Protein[4]

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[2] Wassom J.J., Wong J.C., Martinez E., King J.J., DeBaene J., Hotchkiss J.R., Mikkilineni V., Bohn M.O., Rocheford T.R. (2008) QTL Associated with Maize Kernel Oil, Protein, and Starch Concentrations; Kernel Mass; and Grain Yield in Illinois High Oil x B73 Backcross-Derived Lines. Crop Sci 48:243-252.

[3] Zhang J., Lu X., Song X., Yan J., Song T., Dai J., Rocheford T., Li J. (2008) Mapping quantitative trait loci for oil, starch, and protein concentrations in grain with high-oil maize by SSR markers. Euphytica 162:335-344.

[4] Goldman I.L., Rocheford T.R., Dudley J.W. (1994) Molecular Markers Associated with Maize Kernel Oil Concentration in an Illinois High Protein x Illinois Low Protein Cross. Crop Sci 34:908-915.

[5] Goldman I.L., Rocheford T.R., Dudley J.W. (1993) Quantitative trait loci influencing protein and starch concentration in the Illinois Long Term Selection maize strains. TAG Theoretical and Applied Genetics 87:217-224.