

Supplemental online Material

of Bruggmann et al., Genome Resesearch #53389

Online Table A

reference point, Mb	BAC	coordinates on pseudomolecule, Kbp	genetic map (rice), cM	markers	genetic map (sorghum), cM	markers (sorghum)
1	OSJNBa0056G13	979,786...1,106,612	2.5	R1468B	60	SOG1733
1.7	P0043E01	1,587,538...1,741,665	7.6	E3445S, S1554, E6157	93.9	SOG2638
	OJ1004C08	1,661,432...1,794,521	7.9	OS		
				E61570S	101.6	SOG0821
2.5	OJ1172F09	2427505...2,533,561	11.5	R2247	n/a	n/a
3.5	OSJNBa0026H19	3,482,348...3,632,967	16.8	S13946, R265A	n/a	n/a
4.5	OSJNBa0042J17	4,394,707...4,566,148	21.2	E2217S, E50348S	n/a	n/a
			21.5	C1051		

Online Table B. FPC minimum tiling path and marker details of the 60 maize BACs on Chr#1 short arm

#	BAC in MTP	fpc size (in bp)	Library	Agarose fpc Contig #	Maize chr #	Physical / genetic marker(s) hitting the BAC on fpc	Comments
1	ZMMBBc0059P07	122,880	EcoRI	Ctg#1	Chr#1	p-pMTY7SC1, SOG1838	fpc was not able to place its simulated digest to any contig
2	ZMMBBb0228P12	98,304	HindIII	Ctg#1	Chr#1	umc1613	
3	ZMMBBb0392A14	131,072	HindIII	Ctg#1	Chr#1		
4	ZMMBBb0504J20	135,168	HindIII	Ctg#1	Chr#1		
5	ZMMBBc0297P24	151,552	Mbol	Ctg#1	Chr#1		
6	ZMMBBb0313O01	147,456	HindIII	Ctg#1	Chr#1		
7	ZMMBBb0290C08	102,400	HindIII	Ctg#3	Chr#1		fpc was not able to place its simulated digest to any contig
8	ZMMBBb0042D08	98,304	HindIII	Ctg#3	Chr#1	dd1718, dd3466, SOG5887	
9	ZMMBBb0112C12	102,400	HindIII	Ctg#3	Chr#1	PCO112869_ov, umc1329.A	fpc was not able to place its simulated digest to any contig. However fpc places Chr#9L BAC c0296C17 here (AC147505) 65,726 bp, phase 2, 2 pieces.
10	ZMMBBb0220A06	106,496	HindIII	Ctg#3	Chr#1	SOG5749	
11	ZMMBBb0521N19	94,208	HindIII	Ctg#3	Chr#1		
12	ZMMBBb0459N17	94,208	HindIII	Ctg#3	Chr#1		
13	ZMMBBc0059O05	159,744	EcoRI	Ctg#3	Chr#1	PCO094675_ov, PCO107031_ov, dd1291, dd1478, si707050H06_ov, PCO108952_ov, CL12851_1_ov, umc1327.A	fpc was not able to place its simulated digest to any contig
14	ZMMBBb0184O23	90,112	HindIII	Ctg#3	Chr#1		fpc was not able to place its simulated digest to any contig
15	ZMMBBb0369D20	86,016	HindIII	Ctg#3	Chr#1		
16	ZMMBBb0222H21	86,016	HindIII	Ctg#3	Chr#1	SOG0909	fpc was not able to place its simulated digest to any contig
17	ZMMBBb0101F20	73,728	HindIII	Ctg#3	Chr#1	si606075G07b_ov, PCO092088_ov, SOG0905	
18	ZMMBBc0062P13	110,592	EcoRI	Ctg#3	Chr#1	SOG5741, SOG1477	fpc was not able to place its simulated digest to any contig
19	ZMMBBb0245N06	135,168	HindIII	Ctg#3	Chr#1		
20	ZMMBBc0161G04	147,456	EcoRI	Ctg#3	Chr#1	CL250_1_ov, CL7875_1_ov, PCo142080_ov, dd3170	fpc was not able to place its simulated digest to any contig
21	ZMMBBc0233L23	135,168	EcoRI	Ctg#3	Chr#1		
22	ZMMBBb0072L05	94,208	HindIII	Ctg#3	Chr#1	Placement markers umc1292 & bnlg1179 (both 48.7 cM), dd2504, dd531, dd808, dd1112, SOG1356, p-umc1292, CL27324_1-ov	
23	ZMMBBc0259F07	143,360	EcoRI	Ctg#3	Chr#1		fpc was not able to place its simulated digest to any contig
24	ZMMBBb0642D14	86,016	HindIII	Ctg#3	Chr#1		
25	ZMMBBb0598C16	77,824	HindIII	Ctg#3	Chr#1		
26	ZMMBBb0048H01	106,496	HindIII	Ctg#3	Chr#1	PCO131983_ov	
27	ZMMBBb0518C23	114,688	HindIII	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig
28	ZMMBBc0031A16	143,360	EcoRI	Ctg#4	Chr#1	PCO087834_ov, SOG5611	
29	ZMMBBb0448P23	102,400	HindIII	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig
30	ZMMBBb0215O13	90,112	HindIII	Ctg#4	Chr#1	Placement markers umc1282 (71.9 cM)	
31	ZMMBBc0056I04	200,704	EcoRI	Ctg#4	Chr#1	PCO110646_ov, PCO113531_ov, dd3185, dd337, GOG1005, SOG5817	
32	ZMMBBc0530H10	147,456	Mbol	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig fpc places the simulated digest on Ctg#201, Chr#4
33	ZMMBBb0531M15	147,456	HindIII	Ctg#4	Chr#1		
34	ZMMBBb0262D19	77,824	HindIII	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig
35	ZMMBBc0477G13	143,360	Mbol	Ctg#4	Chr#1		
36	ZMMBBb0329E12	86,016	HindIII	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig
37	ZMMBBc0302I09	131,072	Mbol	Ctg#4	Chr#1		
38	ZMMBBc0055E07	176,128	EcoRI	Ctg#4	Chr#1	SOG1628, SOG1283	fpc was not able to place its simulated digest to any contig
39	ZMMBBb0451P10	122,880	HindIII	Ctg#4	Chr#1		
40	ZMMBBb0525H21	94,208	HindIII	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig
41	ZMMBBc0161A05	163,840	EcoRI	Ctg#4	Chr#1	PCO132785, gst13	
42	ZMMBBb0467F05	122,880	HindIII	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig
43	ZMMBBc0476C14	167,936	Mbol	Ctg#4	Chr#1		
44	ZMMBBc0391N24	118,784	Mbol	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig
45	ZMMBBc0173B05	102,400	EcoRI	Ctg#4	Chr#1	Framework marker umc1977 (89.2 cM), dd2555, PCO130847_ov	
46	ZMMBBc0283N16	139,264	Mbol	Ctg#309	Chr#7		fpc was not able to place its simulated digest to any contig
47	ZMMBBb0232H17	65,536	HindIII	Ctg#309	Chr#7		
48	ZMMBBc0117E12	114,688	EcoRI	Ctg#309	Chr#7		
49	ZMMBBb0468O14	102,400	HindIII	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig
50	ZMMBBb0597K14	118,784	HindIII	Ctg#4	Chr#1		
51	ZMMBBb0234I10	122,880	HindIII	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig
52	ZMMBBc0364F23	114,688	Mbol	Ctg#4	Chr#1		
53	ZMMBBb0384O05	94,208	HindIII	Ctg#4	Chr#1		fpc was not able to place its simulated digest to any contig
54	ZMMBBc0123F20	131,072	EcoRI	Ctg#4	Chr#1	PCO098394_ov, PCO123869_ov, PCO133818_ov, PCO137008_ov, SOG0842	

Online Table C. Shotgun sequencing, assembly, markers and 3 new SSR mapping details of the 56 maize BACs on Chr#9 long arm

#	BAC in MTP	fpc size (in bp)	Library	Agarose fpc Contig #	Maize chr #	Physical / genetic marker(s) hitting the BAC on fpc	Comments
1	ZMMBBc0079F17	188,557	EcoRI	Ctg#391	Chr#9	Placement marker AY110382 (551.3 cM; Chr#9.07), CL32455_1_ov, CL28586_1_ov, si618065D01_ov, PCO075883_ov, umc1445.A	
2	ZMMBBb0125F17	122,880	HindIII	Ctg#391	Chr#9		
3	ZMMBBb0594O14	94,208	HindIII	Ctg#391	Chr#9	No polymorphism with either Families*	fpc was not able to place its simulated digest to any contig
4	ZMMBBc0383D08	135,168	Mbol	Ctg#391	Chr#9		
5	ZMMBBc0088M21	143,360	EcoRI	Ctg#391	Chr#9	Placement marker mgs2 (589.4 cM; Chr#4), CL222_1_ov, PCO065510_ov, dd472, dd746, dd763, dd2888, SOG5844, CL2558_1_ov	
6	ZMMBBc0046N19	114,688	EcoRI	Ctg#391	Chr#9	PCO065510_ov, dd2888	
7	ZMMBBc0127E02	155,648	EcoRI	Ctg#391	Chr#9	PCO066933_ov, dd123, dd41, si603014E11_ov	
8	ZMMBBb0340I09	106,496	HindIII	Ctg#391	Chr#9		
9	ZMMBBc0241D03		EcoRI	Ctg#391	Chr#9		
10	ZMMBBc0429P12	155,648	Mbol	Ctg#391	Chr#9		
11	ZMMBBb0581M09	69,632	HindIII	Ctg#391	Chr#9		
12	ZMMBBc0256O12	143,360	EcoRI	Ctg#391	Chr#9	Placement marker umc1714 (567.3 cM; Chr#9.07) hits buried clone c0051G01	
13	ZMMBBc0408K22	155,648	Mbol	Ctg#391	Chr#9		
14	ZMMBBc0090N10	167,936	EcoRI	Ctg#391	Chr#9	PCO079938_ov, PCO124016_ov, PCO151039_ov, dd275, PCO100327_ov, AY103770.A	
15	ZMMBBb0281A05	90,112	HindIII	Ctg#391	Chr#9	Placement marker bnlg128 (581.5 cM; Chr#9L), p- bnlg128	
16	ZMMBBb0018A20	98,304	HindIII	Ctg#391	Chr#9		
17	ZMMBBc0496L17	169,861	Mbol	Ctg#391	Chr#9		
18	ZMMBBc0051H21	167,936	EcoRI	Ctg#391	Chr#9	149827_77831 Mapped to Chr#9.07 (Family 2)*	
19	ZMMBBb0185C11	94,208	HindIII	Ctg#391	Chr#9	dd2998	
20	ZMMBBb0305O08	98,304	HindIII	Ctg#391	Chr#9	Framework marker AY106323 (587.9 cM; Chr#9.07) hits buried clone b0060A05	
21	ZMMBBb0309E13	106,496	HindIII	Ctg#391	Chr#9		fpc was not able to place its simulated digest to any contig
22	ZMMBBc0243P06	126,976	EcoRI	Ctg#391	Chr#9	SOG1027, SOG1574	
23	ZMMBBb0403P22	114,688	HindIII	Ctg#391	Chr#9		
24	ZMMBBb0193N08	102,400	HindIII	Ctg#391	Chr#9	CL34420_2_ov, CL4677_2_ov, dd417, dd418	fpc was not able to place its simulated digest to any contig
25	ZMMBBb0159A03	102,400	HindIII	Ctg#391	Chr#9	dd2276	
26	ZMMBBc0307H13	135,168	Mbol	Ctg#391	Chr#9		fpc places the simulated digest on Ctg#250, Chr#5
27	ZMMBBc0269J21	118,784	EcoRI	Ctg#391	Chr#9	SOG0821	
28	ZMMBBb0616O15	98,304	HindIII	Ctg#391	Chr#9		fpc was not able to place its simulated digest to any contig
29	ZMMBBb0500A22	90,112	HindIII	Ctg#391	Chr#9		
30	ZMMBBb0635A02	131,072	HindIII	Ctg#391	Chr#9		
31	ZMMBBb0098N23	90,112	HindIII	Ctg#391	Chr#9	Placement marker umc1942 (604.1 cM; Chr#9.07), p-umc1942, PCO072771_ov, dd615, dd696	
32	ZMMBBb0316C08	81,920	HindIII	Ctg#391	Chr#9		
33	ZMMBBb0516A03	98,304	HindIII	Ctg#391	Chr#9	Placement marker umc1104 (606.6 cM; Chr#9.07) hits buried clone b0001O17	
34	ZMMBBb0589L12	110,592	HindIII	Ctg#391	Chr#9		
35	ZMMBBc0238F04	147,456	EcoRI	Ctg#391	Chr#9	SOG0872, SOG5595, SOG5605, SOG1325	
36	ZMMBBc0536M23	114,688	Mbol	Ctg#391	Chr#9	149832_9847 Mapped to Chr#9.07 (Family 2)*	
37	ZMMBBc0475H06	135,168	Mbol	Ctg#391	Chr#9		
38	ZMMBBc0109E01	147,456	EcoRI	Ctg#391	Chr#9	CL25115_1_ov, SOG1215, SOG5357	
39	ZMMBBb0505J22	98,304	HindIII	Ctg#391	Chr#9		fpc was not able to place its simulated digest to any contig
40	ZMMBBc0414C21	163,840	Mbol	Ctg#391	Chr#9	CL4357_1_ov, CL46210_1_ov, dd811, dd846, dd3164, SOG5603: Framework marker fgp1 (234.3 cM on chr#10) hits buried clone b0159K07	
41	ZMMBBc0141C04	163,840	EcoRI	Ctg#391	Chr#9	Placement marker csu54b (805.1 cM; Chr#9.08) hits buried clone b0253P05	
42	ZMMBBc0475M02	167,936	Mbol	Ctg#391	Chr#9		fpc places the simulated digest on Ctg#422, unanchored
43	ZMMBBc0314A21	159,744	Mbol	Ctg#391	Chr#9		
44	ZMMBBb0141J22	131,072	HindIII	Ctg#391	Chr#9	dd1622, si605054F12_ov, SOG5467: Framework marker umc1505 (635.2 cM; Chr#9.08) hits buried clone b0037O06. Mapped independently to Chr#9.07 (Family 2)*	
45	ZMMBBb0589L20	110,592	HindIII	Ctg#391	Chr#9		
46	ZMMBBc0218F03	126,976	EcoRI	Ctg#391	Chr#9	SOG1856, SOG0987	
47	ZMMBBc0534K21	106,496	Mbol	Ctg#391	Chr#9		
48	ZMMBBb0336K06	143,360	HindIII	Ctg#391	Chr#9		
49	ZMMBBc0294C19	151,552	Mbol	Ctg#391	Chr#9		
50	ZMMBBc0383K04	118,784	Mbol	Ctg#391	Chr#9		
51	ZMMBBc0157L04	147,456	EcoRI	Ctg#391	Chr#9	PCO104488	fpc places the simulated digest on Ctg#375, Chr#9

Online Table D. Shotgun sequencing, assembly and pseudomolecule construction of the 60 maize BACs on Chr#1 short arm

#	FPC MTP		PGIR Assembly				TIGR Assembly			
	BAC in MTP	fpc size (in bp)	Arachne assembly size (in bp)	Arachne status	# of super Ctg	# of Ctg	GenBank accession (TIGR)	TIGR assembly size (in bp)	TIGR assembly status	# of Ctg
1	ZMMBBc0059P07	122,880	175,797	Phase 1	5	15	AC155516	172,391	Phase 1	22
2	ZMMBBb0228P12	98,304	140,876	Phase 1	5	12	AC155425	139,555	Phase 1	11
	No significant overlap*									
3	ZMMBBb0392A14	131,072	154,934	Phase 1	5	11	AC155453	157,143	Phase 1	12
4	ZMMBBb0504J20	135,168	115,931	Phase 1	4	9	AC155462	107,667	Phase 1	12
5	ZMMBBc0297P24	151,552	143,456	Phase 1	2	5	AC155614	150,439	Phase 1	10
	No significant overlap*									
6	ZMMBBb0313001	147,456	159,403	Phase 1	6	23	AC155446	148,996	Phase 1	17
	No significant overlap*									
7	ZMMBBb0290C08	102,400	146,837	Phase 1	4	8	AC155444	134,017	Phase 1	11
8	ZMMBBb0042D08	98,304	174,935	Phase 1	9	24	AC155361	151,170	Phase 1	16
9	ZMMBBb0112C12	102,400	81,672	Phase 1	9	9	AC155372	113,676	Phase 1	8
10	ZMMBBb0220A06	106,496	161,714	Phase 1	6	15	AC155423	123,917	Phase 1	9
11	ZMMBBb0521N19	94,208	150,917	Phase 1	6	16	AC155466	128,254	Phase 1	12
12	ZMMBBb0459N17	94,208	144,493	Phase 1	7	20	AC155458	115,779	Phase 1	12
	No significant overlap*									
13	ZMMBBc0059005	159,744	194,430	Phase 1	6	21	AC155515	161,304	Phase 1	13
14	ZMMBBb0184O23	90,112	145,010	Phase 1	5	14	AC155406	119,483	Phase 1	10
	No significant overlap*									
15	ZMMBBb0369D20	86,016	166,530	Phase 1	2	17	AC155451	148,539	Phase 1	18
16	ZMMBBb0222H21	86,016	122,894	Phase 1	2	9	AC155424	120,813	Phase 1	13
17	ZMMBBb0101F20	73,728	103,250	Phase 1	2	8	AC155369	103,732	Phase 1	9
18	ZMMBBc0062P13	110,592	173,211	Phase 1	5	22	AC155517	148,120	Phase 1	15
19	ZMMBBb0245N06	135,168	96,875	Phase 1	15	25	AC155432	118,677	Phase 1	25
20	ZMMBBc0161G04	147,456	186,213	Phase 1	2	10	AC155554	186,094	Phase 1	13
21	ZMMBBc0233L23	135,168	187,687	Phase 1	3	21	AC155603	184,175	Phase 1	34
	No significant overlap*									
22	ZMMBBb0072L05	94,208	123,393	Phase 1	6	16	AC155364	112,734	Phase 1	13
	No significant overlap*									
23	ZMMBBc0259P07	143,360	159,847	Phase 1	3	11	AC155607	165,688	Phase 1	16
24	ZMMBBb0642D14	86,016	123,756	Phase 1	5	13	AC155476	111,964	Phase 1	13
25	ZMMBBb0598C16	77,824	140,452	Phase 1	7	16	AC155474	134,299	Phase 1	13
26	ZMMBBb0048H01	106,496	150,454	Phase 1	3	9	AC155362	143,862	Phase 1	15
	No significant overlap*									
27	ZMMBBb0518C23	114,688	118,844	Phase 2	1	7	AC155464	119,773	Phase 1	11
28	ZMMBBb0031A16	143,360	165,363	Phase 2	1	9	AC155502	169,818	Phase 1	13
29	ZMMBBb0448P23	102,400	142,296	Phase 1	5	16	AC155456	133,685	Phase 1	15
30	ZMMBBb0215O13	90,112	155,396	Phase 1	7	22	AC155418	132,218	Phase 1	23
31	ZMMBBc0056104	200,704	204,154	Phase 1	8	22	AC155514	212,699	Phase 1	27
	No significant overlap*									
32	ZMMBBc0530H10	147,456	184,237	Phase 1	6	20	AC155632	164,362	Phase 1	17
33	ZMMBBb0531M15	147,456	176,029	Phase 1	3	19	AC155469	168,927	Phase 1	19
34	ZMMBBb0262D19	77,824	104,572	Phase 2	1	4	AC155435	109,422	Phase 1	9
35	ZMMBBc0477G13	143,360	159,269	Phase 2	1	9	AC155630	166,436	Phase 1	20
36	ZMMBBb0329E12	86,016	168,363	Phase 1	3	6	AC155447	167,336	Phase 1	7
37	ZMMBBc0302I09	131,072	162,605	Phase 2	1	4	AC155615	162,487	Phase 1	8
38	ZMMBBc0055E07	176,128	177,472	Phase 1	4	15	AC155512	169,247	Phase 1	19
	No significant overlap*									
39	ZMMBBb0451P10	122,880	139,975	Phase 1	3	5	AC155457	125,371	Phase 1	7
	No significant overlap*									
40	ZMMBBb0525H21	94,208	138,123	Phase 2	1	1	AC155467	138,819	Phase 1	5
41	ZMMBBc0161A05	163,840	187,689	Phase 1	4	14	AC155553	179,212	Phase 1	20
42	ZMMBBb0467F05	122,880	126,429	Phase 2	1	3	AC155459	124,820	Phase 1	7
43	ZMMBBc0476C14	167,936	187,130	Phase 2	1	6	AC155629	183,971	Phase 1	16
44	ZMMBBc0391N24	118,784	150,150	Phase 1	2	10	AC155624	149,282	Phase 1	14
45	ZMMBBc0173B05	102,400	181,566	Phase 1	3	15	AC155699	178,453	Phase 1	23
46	ZMMBBb0468O14	102,400	188,464	Phase 1	6	19	AC155460	152,523	Phase 1	14
	No significant overlap*									
47	ZMMBBb0597K14	118,784	132,012	Phase 1	4	10	AC155473	128,132	Phase 1	8
	No significant overlap*									
48	ZMMBBb0234I10	122,880	163,101	Phase 1	4	10	AC155428	149,271	Phase 1	12
49	ZMMBBc0364F23	114,688	203,232	Phase 1	4	7	AC155621	202,998	Phase 1	10
50	ZMMBBb0384O05	94,208	140,558	Phase 1	2	4	AC155452	130,306	Phase 1	4
51	ZMMBBc0123F20	131,072	151,187	Phase 1	9	23	AC155531	135,914	Phase 1	13
52	ZMMBBb0163H18	86,016	134,093	Phase 1	5	12	AC155396	131,396	Phase 1	9
53	ZMMBBb0157N19	86,016	119,126	Phase 2	1	5	AC155393	122,179	Phase 1	9
	No significant overlap*									
54	ZMMBBc0454E24	159,744	235,303	Phase 1	7	19	AC155627	218,576	Phase 1	16
55	ZMMBBb0548P16	77,824	123,387	Phase 1	3	8	AC155471	118,853	Phase 1	12
56	ZMMBBc0316H01	110,592	109,946	Phase 1	6	16	AC155616	92,733	Phase 1	13
57	ZMMBBb0336N08	86,016	120,906	Phase 1	2	6	AC155448	120,189	Phase 1	8
	No significant overlap*									
58	ZMMBBb0216K18	73,728	113,249	Phase 2	1	5	AC155420	112,809	Phase 1	8
59	ZMMBBb0518K03	106,496	186,522	Phase 1	10	24	AC155465	173,237	Phase 1	20
	No significant overlap*									
60	ZMMBBb0472M17	98,304	175,427	Phase 1	5	16	AC155461	142,627	Phase 1	5
Total		6,938,624	9,151,142	50 Phase 1	259	770	8,690,569		60 Phase 1	813
Average		115,644	152,519	10 Phase 2	4	13	144,843		0 Phase 2	14

*Significant overlap = at least 95% homology over 5 kb

Online Table E. Shotgun sequencing, assembly and pseudomolecule construction of the 56 maize BACs on Chr#9 long arm

#	BAC in MTP	fpc size (in bp)	GenBank accession	Arachne assembly size (in bp)	Arachne assembly status	# of Ctgs
1	ZMMBBc0079F17	188,557	AC149309	192,565	Phase 2	7
2	ZMMBBb0125F17	122,880	AC149812	120,676	Phase 1	14
3	ZMMBBb0594O14	94,208	AC149823	98,669	Phase 1	7
4	ZMMBBc0383D08	135,168	AC149830	137,507	Phase 1	7
5	ZMMBBc0088M21	143,360	AC149034	165,335	Phase 2	1
6	ZMMBBc0046N19	114,688	AC149826	111,575	Phase 1	11
No significant overlap*						
7	ZMMBBc0127E02	155,648	AC149828	189,099	Phase 1	10
8	ZMMBBb0340I09	106,496	AC149817	145,681	Phase 1	9
9	ZMMBBc0241D03	139,264	AC151049	101,767	Phase 1	9
No significant overlap*						
10	ZMMBBc0429P12	155,648	AC150781	172,718	Phase 1	8
11	ZMMBBb0581M09	69,632	AC149822	114,154	Phase 2	3
12	ZMMBBc0256O12	143,360	AC149829	166,063	Phase 2	8
13	ZMMBBc0408K22	155,648	AC149831	173,773	Phase 2	5
14	ZMMBBc0090N10	167,936	AC150253	177,028	Phase 2	2
15	ZMMBBb0281A05	90,112	AC149814	106,434	Phase 1	7
16	ZMMBBb0018A20	98,304	AC149810	156,501	Phase 1	12
No significant overlap*						
17	ZMMBBc0496L17	169,861	AC149836	112,468	Phase 2	2
18	ZMMBBc0051H21	167,936	AC149827	143,793	Phase 1	8
19	ZMMBBb0185C11	94,208	AC149813	110,159	Phase 2	3
No significant overlap*						
20	ZMMBBb0305O08	98,304	AC149815	137,065	Phase 2	9
No significant overlap*						
21	ZMMBBb0309E13	106,496	AC149816	69,497	Phase 2	7
22	ZMMBBc0243P06	126,976	AC151050	134,692	Phase 1	14
23	ZMMBBb0403P22	114,688	AC149818	112,768	Phase 2	4
24	ZMMBBb0193N08	102,400	AC149475	126,765	Phase 2	7
25	ZMMBBb0159A03	102,400	AC150182	137,016	Phase 1	13
26	ZMMBBc0307H13	135,168	AC149308	170,708	Phase 1	4
27	ZMMBBc0269J21	118,784	AC150780	144,005	Phase 2	4
28	ZMMBBb0616O15	98,304	AC149824	90,606	Phase 1	5
29	ZMMBBb0500A22	90,112	AC149819	113,934	Phase 2	5
No significant overlap*						
30	ZMMBBb0635A02	131,072	AC149825	135,553	Phase 2	6
No significant overlap*						
31	ZMMBBb0098N23	90,112	AC149811	111,702	Phase 2	5
32	ZMMBBb0316C08	81,920	AC149476	121,514	Phase 2	4
33	ZMMBBb0516A03	98,304	AC149821	162,194	Phase 2	7
34	ZMMBBb0589L12	110,592	AC149033	124,058	Phase 1	8
35	ZMMBBc0238F04	147,456	AC150630	166,531	Phase 1	10
36	ZMMBBc0536M23	114,688	AC149832	181,233	Phase 2	6
37	ZMMBBc0475H06	135,168	AC150268	175,634	Phase 2	4
No significant overlap*						
38	ZMMBBc0109E01	147,456	AC150631	178,354	Phase 2	9
39	ZMMBBb0505J22	98,304	AC149820	102,959	Phase 1	9
40	ZMMBBc0414C21	163,840	AC149270	190,171	Phase 2	7
41	ZMMBBc0141C04	163,840	AC150183	180,904	Phase 2	15
42	ZMMBBc0475M02	167,936	AC150742	205,299	Phase 1	20
43	ZMMBBc0314A21	159,744	AC150187	143,955	Phase 1	5
44	ZMMBBb0141J22	131,072	AC149632	141,550	Phase 2	11
45	ZMMBBb0589L20	110,592	AC150739	134,226	Phase 1	7
46	ZMMBBc0218F03	126,976	AC149640	187,674	Phase 2	8
47	ZMMBBc0534K21	106,496	AC149633	116,794	Phase 2	3
48	ZMMBBb0336K06	143,360	AC149478	149,228	Phase 1	4
49	ZMMBBc0294C19	151,552	AC150186	154,044	Phase 1	12
50	ZMMBBc0383K04	118,784	AC150189	152,109	Phase 1	11
51	ZMMBBc0157L04	147,456	AC150740	198,073	Phase 1	19
52	ZMMBBc0320B12	172,032	AC150161	179,303	Phase 2	14
53	ZMMBBc0235N17	196,608	AC150185	196,629	Phase 1	14
No significant overlap*						
54	ZMMBBc0188H21	126,976	AC150741	191,261	Phase 2	7
No significant overlap*						
55	ZMMBBc0380G10	159,744	AC150188	166,683	Phase 1	8
56	ZMMBBc0195B11	184,320	AC150184	187,684	Phase 1	7
Total		7,292,946		8,268,340	28 Phase 1	445
Average		130,231		147,649	28 Phase 2	

*Significant overlap = at least 95% homology over 5 kb

Online Table F. Statistics of the two sequenced maize megatiles

Features	ZMMB 1S megatile ^a	ZMMB 9L megatile ^a
Agarose contig(s)	Ctgs#1,3,4	Ctg#391
Chromosomal bin position	bins 1.00 & 1.01	bin 9.07
IBM2 genetic map position & distance	1.8 to 91.5 = 89.7 cM	551.3 to 633.2 = 81.9 cM
F2 populations	29.0 to 46.4 = 17.4 cM	134.8 to 144.04 = 9.24 cM
New SSR markers mapped	0	3
# of BACs	60	56
Assembled to phase 1	50	28
Assembled to phase 2	10	28
Average BAC size	152,519 bp	147,649 bp
Total sequence reads	101,435	95,114
Average read length	925 bp	760 bp
Average sequence coverage	12.35x	8.58x
Total size	9,151,142 bp	8,268,340 bp
Pseudomolecule size	7,822,695 bp	6,560,930 bp
Sequence overlap in MTP	15%	21%

^aZMMB: *Zea mays* ssp. *mays* cv. B73

Online Table G: Summary of coverage of different elements

element type	Met coverage [%]	Cot coverage [%]	total coverage [%]	# of elements
all genes	30	32	49	479
all exons	47	38	65	2938
all introns	21	29	41	2459
genes > 10 kb	13	22	32	28
3 < genes ≤ 10 kb	30	36	53	161
1 < genes ≤ 3 kb	51	38	66	229
genes ≤ 1 kb	48	30	60	61
genes containing introns > 1500 bp	27	19	39	102
genes containing introns 1000-1500 bp	37	33	54	53
genes containing introns ≤1000	38	44	62	280
genes without introns	24	64	71	44

Online Figure 1

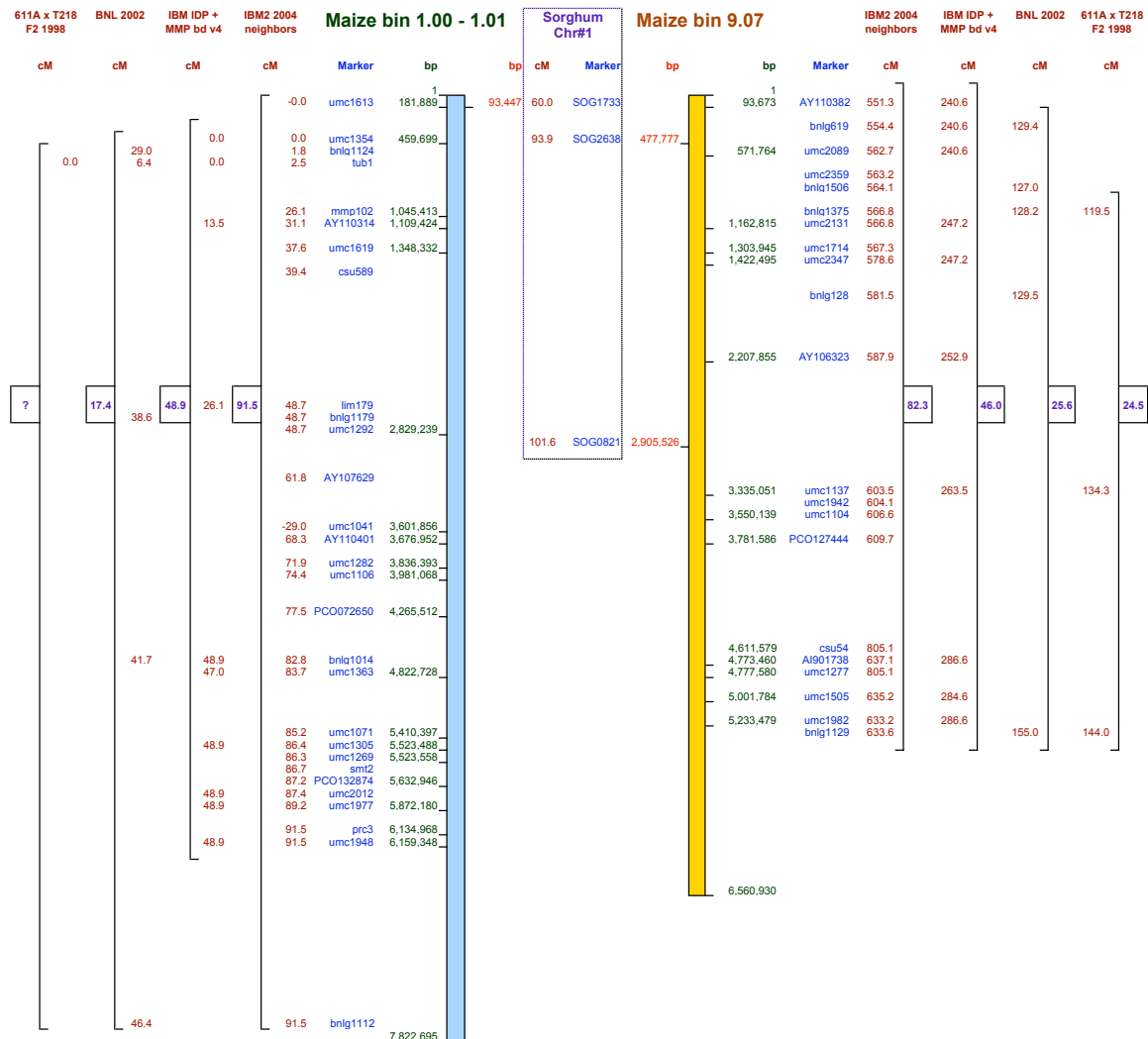
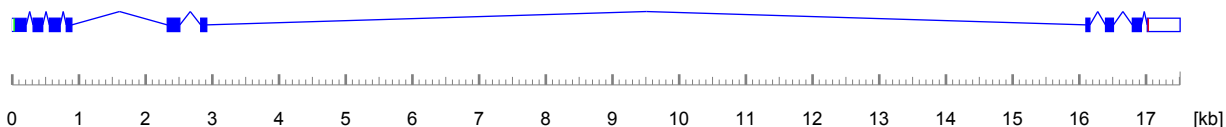


Fig. 1. Alignment of genetic maps to the maize sequences. The sequences of genetic markers were obtained from the respective databases. Sequences were compared to the pseudomolecules by BLASTN. The blue vertical bar represents Zm1S and the yellow Zm9L. Bin map positions are listed above each bar. All known markers are listed in the neighboring column with the nucleotide position marked at each chromosome. The next vertical lines on either side are the respective genetic maps of maize. Each marker known in the respective maps is marked in its position in cM. For comparison mapped sorghum markers from sorghum chromosome 1 are aligned with the physical positions of the two maize chromosomes in the center.

Online Figure 2

A)

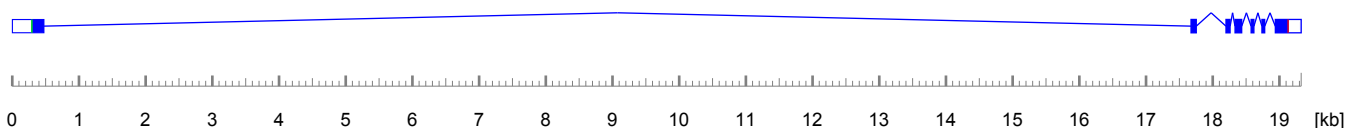
ZM_chr09_CG_01540 (17.511 kb)



The gene model is covered by *Zea mays* TC304850 (TIGR release 16). The size of the large intron is 13182 nt; this intron contains 6 repeats (lengths: 81, 160, 214, 555, 3286 and 4539 nt). The alignment of TC with genomic sequence shows almost 100% identity; one mismatch is found in exon 4, 8 mismatches are found in the 5' UTR within the first 13 bases and 3 mismatches are found in the 3'-UTR. The protein shows homology to a phosphoribosylanthranilate transferase of *Oryza sativa* (87% identity, 91% similarity, 6/393 gaps). The maize protein (393 aa) is shorter than the one of *Oryza sativa* (409 aa; accession: AAM19104).

B)

ZM_chr09_CG_01620 (19.326 kb)



The gene model is covered by *Zea mays* TC281170 (TIGR release 16). The size of the large intron is 17199 nt; this intron contains 12 repeats (lengths: 22, 22, 57, 69, 138, 220, 227, 354, 373, 504, 1189, 4957 nt). The alignment of TC with genomic sequence shows almost 100% identity; only two mismatches are found in the 3' UTR. The protein is identical to MADS box protein 1 of *Zea mays* (accession: AF112148).