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New SSR markers for barley derived from the EST database

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Introduction

There are currently 1,196 microsatellite [or simple sequence repeat (SSR)] marker primer sets that have been developed for barley (from both genomic libraries and EST databases) of which 504 have been mapped (Saghai Maroof et al., 1994; Becker and Heun, 1995; Liu et al., 1996; Struss and Plieske, 1998; Ramsay et al., 2000; Pillen et al., 2000; Holton et al., 2002; Thiel et al., 2003; Li et al., 2003; Yu et al., 2005). Unfortunately, the available SSR markers provide uneven coverage of the barley genome and are concentrated near the centromeres. We have compared the available mapped SSRs and identified 62 BINs out of the total of 99 barley BINs (http://barleygenomics.wsu.edu/; http://rye.pw.usda.gov/cgi-bin/gbrowse/BarleyBinMaps) that have poor coverage. Although this represents, 63% of the barley genome, only 31% of the available SSRs map to these BINs. Additional SSR markers are needed to increase coverage in these BINs. Moreover, some of the SSR markers recently published are restricted from being used to develop new barley varieties, thus there is still a need for additional publicly available SSR markers that can be used without restrictions.

Materials and Methods

Barley ESTs used for primer development were selected by using either rice BAC or wheat EST sequences in a BLASTn search for publicly available barley ESTs with the low complexity filter turned off (BLASTn searches were completed between October, 2002 and October, 2004) (http://www.ncbi.nih.gov/BLAST/). Matches with e-values between 0 and 1e-2 were used. The resulting barley ESTs were processed through the Tandem repeats finder which measures the rate at which the actual EST sequence matches a perfect repeat sequence (Benson, 1999; http://tandem.bu.edu/trf/trf.submit.options.html). Primers were designed for SSRs with 85-100% matches to the perfect repeat sequence. Primer pairs were designed to flank SSR motifs using Primer3 software (Rozen and Skaletsky, 2000; http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi) and screened on a set of mapping parents to identify which population(s) were appropriate for mapping. Primer pairs were tested using two to four PCR protocols to identify a protocol that resulted in clear products (Tables 1 and 2). Products were separated on 6% polyacrylamide gels and visualized using silver staining.

Newly developed SSR markers were mapped on the appropriate mapping population(s) including: Steptoe x Morex (Kleinhofs et al., 1993), Chevron x M69 (Canci et al., 2003), Frederickson x Stander (Mesfin et al., 2003), or Atahualpa x M81 (unpublished). We used JoinMap 3.0 for map construction (Van Ooijen and Voorrips, 2001). Assignment to BINs was based on adjacent mapped markers that have been previously assigned to BINs (http://barleygenomics.wsu.edu/; http://rye.pw.usda.gov/cgi-bin/gbrowse/BarleyBinMaps). Wheat STS markers were mapped on the barley populations to increase the coverage of chromosome 3 (3H) (Liu and Anderson, 2003).

Results and Discussion

A total of 76 new markers were developed that produce between two to six alleles per locus among the twelve mapping parents: Atahualpa, M81, Chevron, M69, Frederickson, Stander, Harrington, OUH602, Hor211, Lacey, Steptoe and Morex (Table 3). Sixty of the markers were mapped using the Steptoe x Morex, Chevron x M69, Frederickson x Stander, and Atahualpa x M81populations (Figure 1 and Table 3). Of the 60 mapped markers, 41 (68%) have mapped to BIN positions that were previously identified as being poorly covered with the currently available SSR markers. These markers should provide additional tools for barley genetic mapping and marker-assisted selection.

Acknowledgements

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Table 1. PCR recipes for UMB SSR markers

PCR recipe	A	B	C
dNTPs (1.25 mM each)	1.0	1.0	1.0
$MgCl_2^2$ (25 mM)	1.0	1.0	0.5
10 X buffer *	1.0	1.0	1.0
Forward Primer (5µM)	0.6	0.6	1.0
Reverse Primer (5µM)	0.6	0.6	1.0
Betaine (5 M)	0	2.0	0
DMSO (100%)	0	0.5	0
Taq polymerase*	0.075	0.075	0.075
H_2O	2.725	0.225	2.425
DNA (10 ng/µL)	3.0	3.0	3.0
Total	10.0	10.0	10.0

* 10 X buffer is provided with purchase of Taq polymerase

Table 2. PCR programs for UMB SSR markers

Stage	Temp. (°C)	Time (min.)	Cycles	Stage	Temp. (°C)	Time (min.)	Cycles
Program A*				Program F*			
Initial Hold	95	9:00	1	Initial Hold	-	-	-
Thermal Cycles-1	94 64 72	1:00 0:30 1:00	18	Pre-PCR	95 58 72	9:00 1:00 1:00	1
Thermal Cycles-2	94 55 72	1:00 1:00 1:00	30	Thermal Cycles	94 58 72	0:30 0:30 0:30	30
Ending Hold	72	5:00	1	Ending Hold	72	5:00	1
Final Hold	4	∞	1	Final Hold	4	∞	1
Program J*				Program L58			
Initial Hold	95	8:00	1	Initial Hold	95	9:00	1
Thermal Cycles	94 60 72	1:00 1:00 2:00	35	Thermal Cycles	94 58 72	0:10 0:20 0:45	30
Ending Hold	72	5:00	1	Ending Hold	72	2:30	1
Final Hold	4	∞	1	Final Hold	4	∞	1

* Programs A, F and J are as in Ramsay et al., 2000.

Table 3. PCR and mapping information for UMB markers.

Name	Chr.	BIN[1]	Population[2] Polymorphism	Population[2] Mapped	Quality Score[3]	Alleles[4]	PCR Program	PCR Recipe
UMB101	1 (7H)	11-12	A/M; F/S; H/O; H/L; S/M	A/M; F/S; S/M	2	3	L58	A
UMB102	1 (7H)	11-12	A/M; H/O; H/L; S/M	S/M	2.5	2	L58	A
UMB103	1 (7H)	13	A/M; F/S; H/O; H/L; S/M	A/M; F/S; S/M	2	4	L58	A
UMB104	1 (7H)	7-8	C/M; F/S; H/O; H/L; S/M	F/S; S/M	1.5	2	F	A
UMB105	1 (7H)	10-11	A/M; C/M; H/O	A/M; C/M	3	2	L58	A
UMB106	1 (7H)	**4-5**	C/M; H/L; S/M	C/M; S/M	2	2	L58	A
UMB107	1 (7H)	**4-5**	F/S; H/O	F/S	3	4	J	C
UMB108	1 (7H)	2	A/M; F/S; H/O; H/L; S/M	F/S; S/M	1	3	A	B
UMB201	2 (2H)	6-7	C/M; F/S; H/O; H/L; S/M	C/M; F/S; S/M	2.5	4	L58	A
UMB202	2 (2H)	6-7	A/M; C/M; F/S; H/O; S/M	A/M; C/M; F/S; S/M	2	2	F	A
UMB203	2 (2H)	4-5	C/M; H/L	C/M	2	2	J	C
UMB204	2 (2H)	7-8	F/S; H/O	F/S	2.5	2	L58	A
UMB205a	2 (2H)	4-5	C/M	C/M	1	2	J	C
UMB205b	2 (2H)	4-5	A/M; C/M; H/O	C/M	1	3	J	C
UMB206	2 (2H)	**2-3**	C/M; F/S; H/O; H/L; S/M	F/S; S/M	2	3	L58	B
UMB301	3 (3H)	**1-2**	C/M; F/S; H/L; S/M	C/M; F/S; S/M	3	3	F	A
UMB302	3 (3H)	**4-6**	A/M; C/M; F/S; H/O; S/M	A/M; C/M; F/S; S/M	1	4	L58	A
UMB303	3 (3H)	**4-6**	A/M; C/M; F/S; H/O; S/M	A/M; C/M; F/S; S/M	2	6	L58	A
UMB304	3 (3H)	**4-6**	A/M; C/M; F/S; H/L; S/M	A/M; C/M; S/M	1	4	J	C
UMB305	3 (3H)	**2-4**	A/M; H/O; H/L	A/M	1	2	F	A
UMB306	3 (3H)	**2-4**	A/M; H/O; H/L	A/M	1	3	F	A
UMB307	3 (3H)	**2-4**	A/M; H/O; H/L	A/M	1	3	L58	A
UMB308	3 (3H)	**1-2**	A/M; C/M; F/S; H/O; S/M	F/S; S/M	2.5	2	F	B
UMB309	3 (3H)	**4-6**	A/M; C/M; F/S; S/M	S/M	3	4	J	B
UMB310	3 (3H)	**4-6**	A/M; C/M; F/S; H/L; S/M	C/M; S/M	2	3	L58	B
UMB311	3 (3H)	**16**	CM; F/S; H/L	C/M	3	3	J	B
UMB401	4 (4H)	**4-5**	H/O; H/L; S/M	S/M	1	2	J	B
UMB402	4 (4H)	**2-3**	H/O; H/L; S/M	S/M	1	2	L58	A

Table 3 cont. PCR and mapping information for UMB markers.

Name	Chr.	BIN[1]	Population[2] Polymorphism	Mapped	Quality Score[3]	Alleles[4]	PCR Program	PCR Recipe
UMB403	4 (4H)	**4-5**	A/M; C/M; H/O; H/L; S/M	C/M; S/M	2	4	L58	B
UMB404	4 (4H)	5-6	C/M; H/O; S/M	C/M; S/M	1	2	J	B
UMB501a	5 (1H)	6	C/M; F/S	C/M; F/S	2	2	L58	B
UMB501b	5 (1H)	6	C/M; F/S	C/M; F/S	3	2	L58	A
UMB502	5 (1H)	**12-13**	A/M; F/S; H/O	A/M; F/S	1	3	L58	A
UMB503	5 (1H)	**2**	A/M; C/M; F/S; H/O; H/L; S/M	C/M; S/M	2	6	L58	A
UMB504	5 (1H)	**11-12**	A/M; F/S; H/O; H/L; S/M	F/S; S/M	2	4	L58	B
UMB505	5 (1H)	**2**	A/M; C/M; H/O; H/L; S/M	S/M	3	3	J	B
UMB506	5 (1H)	6	C/M; F/S; H/O; H/L	C/M; F/S	2	2	J	B
UMB507	5 (1H)	6	C/M; F/S; H/O; H/L	C/M; F/S	1	3	L58	B
UMB508	5 (1H)	**14**	A/M; C/M; F/S; H/O; H/L	C/M	2.5	3	L58	B
UMB601	6 (6H)	**13-14**	A/M; F/S; S/M	A/M; F/S; S/M	1	2	F	B
UMB602	6 (6H)	**11-13**	A/M; C/M; F/S; H/O; H/L	A/M; C/M; F/S	2	4	F	A
UMB603	6 (6H)	**13-14**	A/M; C/M; F/S; H/O; H/L; S/M	A/M; C/M; F/S; S/M	2	4	L58	A
UMB604	6 (6H)	7-9	A/M; C/M; F/S; H/O; H/L; S/M	C/M; F/S; S/M	1	5	L58	A
UMB605	6 (6H)	**14**	A/M; C/M; F/S; H/O; H/L	C/M; F/S	1	2	L58	B
UMB606	6(6H)	**1**	A/M; C/M; F/S; H/O; H/L; S/M	S/M	3	3	F	B
UMB701	7 (5H)	**9**	A/M; F/S; H/O	F/S	2	2	J	B
UMB702	7 (5H)	**10-11**	C/M; H/O; H/L	C/M	1	3	F	A
UMB703	7 (5H)	**7-8**	A/M; S/M	S/M	1.5	2	L58	A
UMB704	7 (5H)	2-4	A/M; F/S; H/O; H/L	A/M; F/S	1	4	L58	A
UMB705	7 (5H)	**5-6**	F/S; H/O	F/S	1.5	3	L58	A
UMB706	7 (5H)	**9**	A/M; C/M; H/O; H/L	A/M; C/M	1	2	L58	A
UMB707	7 (5H)	**6-7**	A/M; F/S; H/O; S/M	A/M; S/M	1	3	L58	A
UMB708	7 (5H)	**10-11**	A/M; H/O	A/M	1	2	F	A
UMB709	7 (5H)	**10-11**		A/M; H/O; S/M	S/M	2	2	F
UMB710	7 (5H)	**11-12**		S/M	S/M	2	2	L58
UMB711	7 (5H)	**11-12**		A/M; F/S; H/O;	F/S; S/M	2	3	L58

Table 3 cont. PCR and mapping information for UMB markers.

Name	Chr.	BIN[1]	Population[2] Polymorphism	Mapped	Quality Score[3]	Alleles[4]	PCR Program	PCR Recipe
UMB712	7 (5H)	**13-14**	A/M; F/S; H/O; H/L; S/M	F/S; S/M	2	3	F	B
UMB713	7 (5H)	**13-14**	A/M; F/S; H/O; S/M	S/M	2	4	L58	B
UMB714	7 (5H)	**13-14**	A/M; F/S; H/O; H/L; S/M	F/S	3	2	F	B
UMB715	7 (5H)	**13**	A/M; F/S; H/O	F/S	2	5	J	B
UMB001			H/L		2	3	L58	B
UMB002			H/O		3	2	F	A
UMB003			H/O		2	4	F	A
UMB004			H/O; H/L		3	2	J	C
UMB005			H/O		1.5	2	L58	A
UMB006			H/O		3	2	L58	A
UMB007			H/O; H/L		2	3	L58	A
UMB008			H/O; H/L		1	3	A	C
UMB009			H/O		2	3	L58	A
UMB010			A/M; H/O; H/L; S/M		2.5	3	F	A
UMB011			A/M; H/O		1	3	L58	B
UMB012			H/O		1	2	L58	B
UMB013			H/L		2	2	L58	B
UMB014			A/M; C/M; H/O; H/L		2	3	J	B
UMB015			C/M; H/O; H/L; S/M		3	5	F	B
UMB016			H/O		1	2	A	B

[1] Bold type indicates BINs with poor SSR marker coverage

[2] Mapping populations: A/M=Atahualpa x M81; C/M=Chevron x M69; F/S=Frederickson x Stander; H/O=Harrington x OUH602; H/L=Hor211 x Lacey; S/M=Steptoe x Morex

[3] Scale from 1-5 where 1=Very easy to score and 5=Very hard to score

[4] Number of Alleles based on the twelve mapping parents

Table 4. Design information for UMB primers.

Name	EST Accession[1]	Forward Primer	Reverse Primer
UMB101	BE421034	CGGGTTCCATTGAGAAGAAC	CACAAATACAGATGCCGCAC
UMB102	CB881209	TTGTGTTTGAGATATCCTGTACTTTTC	ACCTTTTGCCGGCTTTTATT
UMB103	BQ762328	TGCCCATGAAGCCTCTTTAC	GGAACGGAGGGAGTATTAAGC
UMB104	CB881555	GGAAAAATAAACTATTCAACATCCTG	CAGCGCATGTGTTCTCAGAT
UMB105	BJ485220	GCCCCTGGTAAGAACTCCAT	CTGGGAACCGTACAGTGTTG
UMB106	AL502019	AGCATAAAGCCGCAAAAGAA	GCGTCCTGATGAAGAGGTGT
UMB107	CB873957	ACGCACGGGCATTTGTACT	GCCTGCATCATTTGTTTGTG
UMB108	CV055381	TCAAGCTGCTGCATTGCT	AGCCCAAACCCTTTTGTTTT
UMB201	BJ480735	GCTCCTGAAAAGGACCTCAG	TCTCCGCCACCTACACATAG
UMB202	BG299528	GGTCGGCTCCCTCTTCTACT	CGAGCGACATGAGGAACAT
UMB203	CB873608	TTTCATTGCTGTGACGGATG	AGCCTCACCCGGACTACC
UMB204	BM371159	GAATCCTCGGCCTTCTCAAC	GCGGAGCTTGACCTCGAC
UMB205a	CB881957	CGGTCGTAGAACGGAATCAG	GCACTTCCACCACAAGAAGC
UMB205b	CB881957	CGGTCGTAGAACGGAATCAG	GCACTTCCACCACAAGAAGC
UMB206	CB863325	GCGCTAGCTATCCACACAAA	AACATTAAGGGCGACAAGGA
UMB301	AV944239	CTTCACATGTCTGGGAAAACA	GACATGTTGGAAGGTGGCTT
UMB302	CD663662	ACCACAGGTAACCTCGCAAC	AAAGTGCTGGGAGCTTGAAA
UMB303	BU979287	CACGAGGGATGCTCTTGAGT	TGTATATTTCAAGCTCCCAGCA
UMB304	BM443659	CTTCGCTTACCGCTTTCG	TTTCAAGCTCCCAGCACTTT
UMB305	BJ484842	CAGAGCGGGCTCAACGTA	ACTTGCTGTCATCCTTGCTG
UMB306	BJ467519	GCAGAGCTGGCTCAACGTA	TTCACTGATCGACCACTTGC
UMB307	BJ461914	CTGCAGAGCTGGCTAACGTA	TTCACTGATCGACCACTTGC
UMB308	CB859861	CCCCTCAGGTTGTTCATCAT	AGCAGCAGCAACAACAACAG
UMB309	BF265771	GCTCGACTTCGAGGACACC	ATTCTTGCGGAACGACCTC
UMB310	CB879994	CTCCCAGCACTTTCACCATC	CCGATGCTCTTGAGTCGTG
UMB311	CA592691	ATCCAGTTTCAGCCACCAAC	ACCGCAGTGATCAGTGACAA
UMB401	AL507067	CGTCTTCGTACTCGCCTCTC	ATCGAGATGCACTCCCTCAT
UMB402	BQ466542	TCGATCCATCCAAACATGAG	CGTGTCACGTGTGTGTGTGT

Table 4 cont. Ordering and design information for UMB primers.

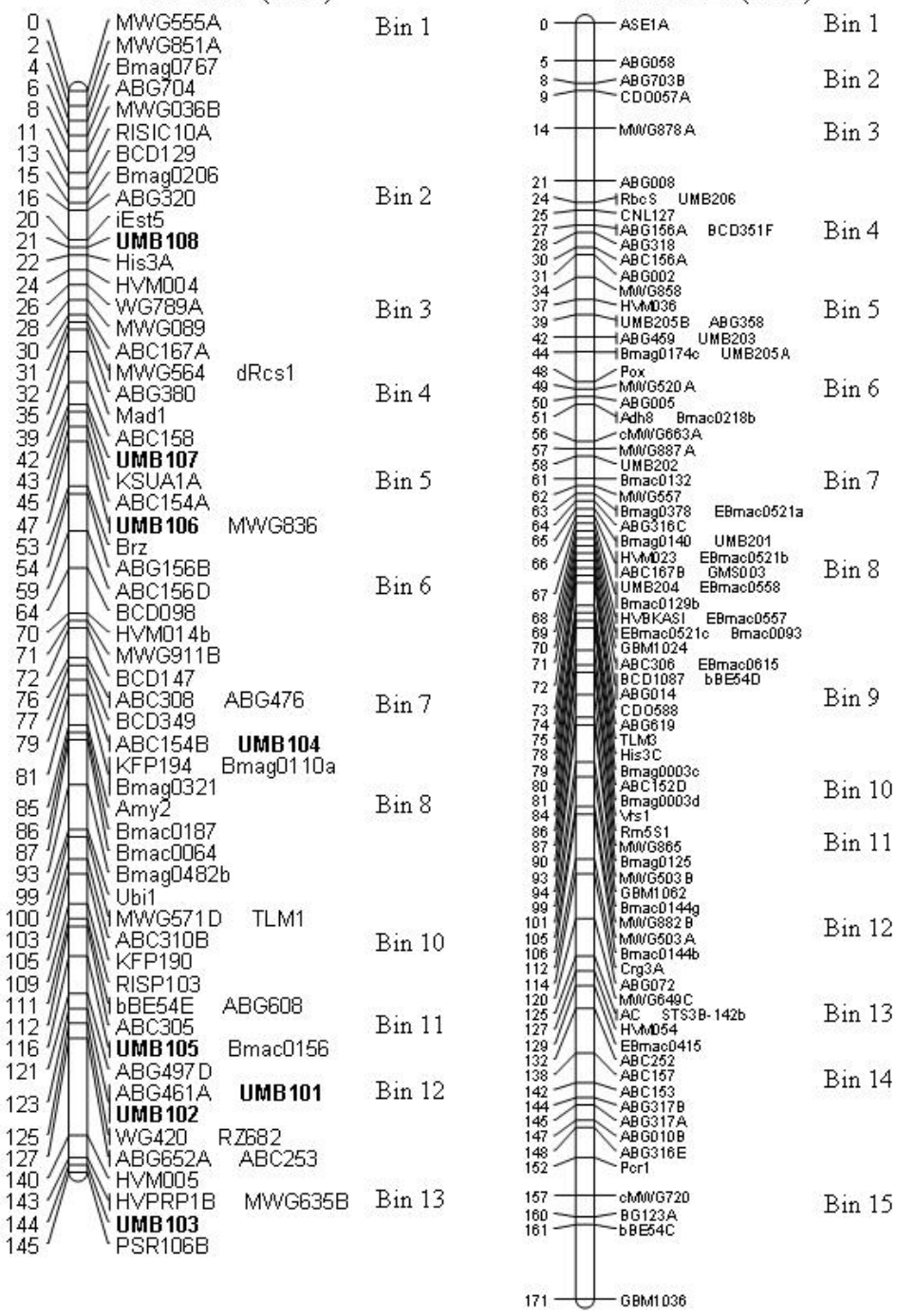
Name	EST Accession[1]	Forward Primer	Reverse Primer
UMB403	BM372825	TTCCGCAGATTCATTTCCAC	GCTGGACAGGCGTTAAAAAG
UMB404	AJ475924	GGAGGCAAGAACACTTGACAG	GCTCGATCTCCTCCTTGTTG
UMB501a	BE421033	CACACAGGCGACCATTTTC	CAGCTAGACGCTATGAGCCA
UMB501b	BE421033	CACACAGGCGACCATTTTC	CAGCTAGACGCTATGAGCCA
UMB502	BI953342	ATCCCATCTCCCTCCTCCTA	TGGAGTGCTCCTCCCAGTAG
UMB503	BQ766039	TCCCGGTGCCATATACAAAT	TTTGATGAAACGAAGGGAAA
UMB504	CV054443	CAAAGTGCGCGTGAGAAATA	AATCACCACCAGCTTCTTGG
UMB505	BE195848	ATGTTGCAGCAGAGCAGTTG	ATTGTTGGGGTTGTTCTTGC
UMB506	CD663377	CTCTTCCGTGAAACGAAACC	CGAGCAAGGACGTGGTAGAT
UMB507	CD663377	ATGTTTCAACAGGCCATTCC	CATGAAAACAGATGACGATGC
UMB508	BF621983	GATTAAGGCGTCCAATTCCA	TCGGGATGTGAAGAAGGAAC
UMB601	BJ486149	AAATACCGTATGGAGGGTGCT	CTACCCCTACGTCCGAGATG
UMB602	CB877685	AGGAGTGGGTCTCAGGTTTG	CAAGCAGATGCAACTACACCA
UMB603	CA006980	ATGAAACATCGCGAACTGTG	ACTGCAGTGAGGGAAGCTGT
UMB604	CA004840	GAGCAATCCCCTCATCCAAT	TCTTTGGTTTCCTCGTGTCC
UMB605	CD053629	GAGGCTTGTTCCTCAGACCA	ATGAGGAAGAGCGGGATCAG
UMB606	CV056304	CGAGCAGCAGCAGATCGT	CTCCTGCGCTTGGAGAAG
UMB701	BE421177	ACGTCGTGGATCAACGTGTA	TTACATTGCGCACAGCTAGG
UMB702	BF265777	CAGCATCCATCAGCAATGAA	CATGTTTGGCTTCTTCGTCC
UMB703	CA025623	GCCGCCTCTTACTCTTTGC	GGAGATGCCGAGGGACTT
UMB704	AV942720	ATCCTCCAACGAGGCACATA	GAGTCCATTTCACGGAGACC
UMB705	CB876579	TGCTGAGACACACACACACC	CGATGCACGAAAAGCTGTAG
UMB706	CB875298	TCAACAGATGACGTGCATGA	TCACACATTGAGGGAGGACA
UMB707	CB876579	TGCTGAGACACACACACACC	CGATGCACGAAAAGCTGTAG
UMB708	BE421505	CTCCTCAGCTCTGGAATGGA	GCGCATATACAAGCCAAACA
UMB709	CV063649	ACGACAAGACTATGGCAGCA	AAGGTTTCCTCAGCCTGTGA
UMB710	CV063745	ACAGTTCCCAACTTCCAAGC	CAGCACATCAGCCCGTACT
UMB711	BJ553047	GCAACGACACGTCTAAACCA	GTGGTGTGGTGTCCTTCCTC

Table 4 cont. Design information for UMB primers.

Name	EST Accession[1]	Forward Primer	Reverse Primer
UMB712	CB881537	CAAGAAGGAACGAAGCCAAG	TGCTAGTTTTTCCGGCTGAT
UMB713	CB881537	ATCAGCCGGAAAAACTAGCA	CAAGCGAAGAGGAAGAGGAA
UMB714	CB881537	GCAAGCAAATCACACTCTGG	GCGTCATCTACGGCTGATTC
UMB715	CB879524	CCGCGCCTAATTAACAAAAA	AGCTGACTGCTGACCAACCT
UMB001	BI949870	TTCTCCATGTTCGGCTTCTT	ATCAGCAATGAAGTTGTCGG
UMB002	BJ481660	GGCAAGTGAGCTCAACCTCT	GCCCTCACATGCAACATCTA
UMB003	CB881957	TCAGTGGTGACCGTGGTATC	GCACTTCCACCACAAGAAGC
UMB004	BG309433	ACCACGTCCACCACCATC	CTCTTTCTCCGCTCATCACC
UMB005	BQ763410	AAGAAAGCCCGGAAGAGAAG	ATGGTGCCATCCTGATTGAT
UMB006	BQ662872	CGGAGTCGCTTTCGAGATT	ACTGACAGCAACGGTGGTAG
UMB007	CB881851	CGCAATAAAATCGCAGGAAT	ACGGAAGACCGGGATAGTTT
UMB008	BU996005	CTGGAGCCTAGCTTGGAGTG	CTCCACCGTTCTTCACGTTT
UMB009	BI954579	CATCCCCATCCAGATCCA	GTCGAGAGGTGCGAGGATT
UMB010	BF621983	GCCACAGCCAAGAAAGCTAC	GATGGGATCTGCTTGGAGAG
UMB011	AV918630	TCTTCTCGCTAGCATCAGCA	CAAAGAAGGAGGTGGCTTCA
UMB012	BI960225	ATAGCGACGTGCTCCAGAGA	AGCAGCGACTTCCTTAGCAG
UMB013	CB873614	GAGCAAGCACGCACGTATTA	GGGACCTCGAGATGATCAAG
UMB014	CB882192	CAGGAGATCCGCGCTCTT	CGAGCAGTGAACGATGTACG
UMB015	CA030737	CGGACGAGGTTTACTCCAAA	AGCACAGGAGGATGAGGATG
UMB016	CA032410	CCATCACCCATTTCTTCCTC	GATGGATTTGTCCGTCCAAG

[1] EST accession from which the primers were designed (http://www.ncbi.nih.gov/)

Figure 1. Map locations of the UMB markers on consensus maps of the Steptoe x Morex (S/M), Frederickson x Stander (F/S) and Chevron x M69 (C/M) populations. Chromosome 7 (5H) is presented as a consensus map of the F/S and C/M populations with the S/M population separate. UMB508 (denoted with '✦') has had its location inferred from the C/M population (C/M is included in the consensus but the inferred marker did not map in the consensus). Markers denoted with '▶' have had their location inferred from the Atahualpa x M81 (A/M) population. Marker "ABG497D" [chr. 1 (7H), BIN 11], was named "ABG497B" in Canci et al. (2003), but the "ABG497B" locus should map to chr. 1 (7H), BIN 4, therefore we have designated a new locus name.


Chr. 1 (7H)
0 MWG555A
2 MWG851A
4 Bmag0767
6 ABG704
8 MWG036B
11 RISIC10A
13 BCD129
15 Bmag0206
16 ABG320
20 iEst5
21 UMB108
22 His3A
24 HVM004
26 WG789A
28 MWG089
30 ABC167A
31 MWG564 dRcs1
32 ABG380
35 Mad1
39 ABC158
42 UMB107
43 KSUA1A
45 ABC154A
47 UMB106 MWG836
53 Brz
54 ABG156B
59 ABC156D
64 BCD098
70 HVM014b
71 MWG911B
72 BCD147
76 ABC308 ABG476
77 BCD349
79 ABC154B UMB104
81 KFP194 Bmag0110a
Bmag0321
85 Amy2
86 Bmac0187
87 Bmac0064
93 Bmag0482b
99 Ubi1
100 MWG571D TLM1
103 ABC310B
105 KFP190
109 RISP103
111 bBE54E ABG608
112 ABC305
116 UMB105 Bmac0156
121 ABG497D
123 ABG461A UMB101
UMB102
125 WG420 RZ682
127 ABG652A ABC253
140 HVM005
143 HVPRP1B MWG635B
144 UMB103
145 PSR106B
Bin 1
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Chr. 2 (2H)
0 ASE1A
5 ABG058
8 ABG703B
9 CDO057A
14 MWG878A
21 ABG008
24 RbcS UMB206
25 CNL127
27 ABG156A BCD351F
28 ABG318
30 ABC156A
31 ABG002
34 MWG858
37 HVM036
39 UMB205B ABG358
42 ABG459 UMB203
44 Bmag0174c UMB205A
48 Pox
49 MWG520A
50 ABG005
51 Adh8 Bmac0218b
56 cMWG663A
57 MWG887A
58 UMB202
61 Bmac0132
62 MWG557
63 Bmag0378 EBmac0521a
64 ABG316C
65 Bmag0140 UMB201
66 HVM023 EBmac0521b
ABC167B GMS003
67 UMB204 EBmac0558
Bmac0129b
68 HVBKASI EBmac0557
69 EBmac0521c Bmac0093
70 GBM1024
71 ABC306 EBmac0615
72 BCD1087 bBE54D
ABG014
73 CDO588
74 ABG619
75 TLM3
78 His3C
79 Bmag0003c
80 ABC152D
81 Bmag0003d
84 Vrs1
86 Rm5S1
87 MWG865
90 Bmag0125
93 MWG503B
94 GBM1062
99 Bmac0144g
101 MWG882B
105 MWG503A
106 Bmac0144b
112 Crg3A
114 ABG072
120 MWG649C
125 IAC STS3B-142b
127 HVM054
129 EBmac0415
132 ABC252
138 ABC157
142 ABC153
144 ABG317B
145 ABG317A
147 ABG010B
148 ABG316E
152 Pcr1
157 cMWG720
160 BG123A
161 bBE54C
171 GBM1036
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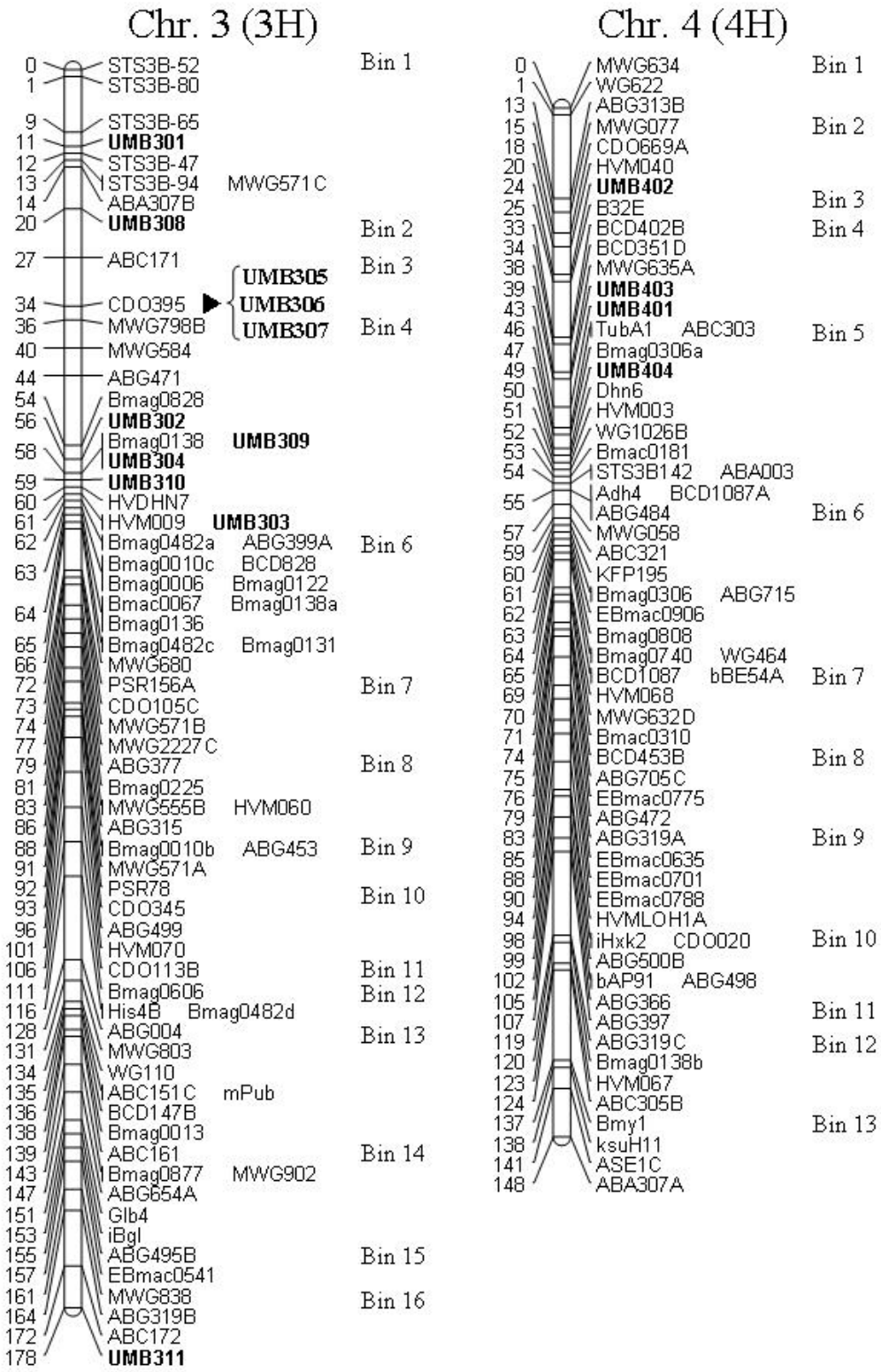
Chr. 3 (3H)
0 STS3B-52
1 STS3B-80
9 STS3B-65
11 UMB301
12 STS3B-47
13 STS3B-94 MWG571C
14 ABA307B
20 UMB308
27 ABC171
34 CDO395
36 MWG798B
40 MWG584
44 ABG471
54 Bmag0828
56 UMB302
58 Bmag0138
UMB309
UMB304
59 UMB310
60 HVDHN7
61 HVM009 UMB303
62 Bmag0482a ABG399A
63 Bmag0010c BCD828
Bmag0006 Bmag0122
Bmac0067 Bmag0138a
64 Bmag0136
65 Bmag0482c Bmag0131
66 MWG680
72 PSR156A
73 CDO105C
74 MWG571B
77 MWG2227C
79 ABG377
81 Bmag0225
83 MWG555B HVM060
86 ABG315
88 Bmag0010b ABG453
91 MWG571A
92 PSR78
93 CDO345
96 ABG499
101 HVM070
106 CDO113B
111 Bmag0606
116 His4B Bmag0482d
128 ABG004
131 MWG803
134 WG110
135 ABC151C mPub
136 BCD147B
138 Bmag0013
139 ABC161
143 Bmag0877 MWG902
147 ABG654A
151 Glb4
153 iBgl
155 ABG495B
157 EBmac0541
161 MWG838
164 ABG319B
172 ABC172
178 UMB311
UMB305
UMB306
UMB307
Bin 1
Bin 2
Bin 3
Bin 4
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Bin 10
Bin 11
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Bin 14
Bin 15
Bin 16
Chr. 4 (4H)
0 MWG634
1 WG622
13 ABG313B
15 MWG077
18 CDO669A
20 HVM040
24 UMB402
25 B32E
33 BCD402B
34 BCD351D
38 MWG635A
39 UMB403
43 UMB401
46 TubA1 ABC303
47 Bmag0306a
49 UMB404
50 Dhn6
51 HVM003
52 WG1026B
53 Bmac0181
54 STS3B142 ABA003
Adh4 BCD1087A
55 ABG484
57 MWG058
59 ABC321
60 KFP195
61 Bmag0306 ABG715
62 EBmac0906
63 Bmag0808
64 Bmag0740 WG464
65 BCD1087 bBE54A
69 HVM068
70 MWG632D
71 Bmac0310
74 BCD453B
75 ABG705C
76 EBmac0775
79 ABG472
83 ABG319A
85 EBmac0635
88 EBmac0701
90 EBmac0788
94 HVMLOH1A
98 iHxk2 CDO020
99 ABG500B
102 bAP91 ABG498
105 ABG366
107 ABG397
119 ABG319C
120 Bmag0138b
123 HVM067
124 ABC305B
137 Bmy1
138 ksuH11
141 ASE1C
148 ABA307A
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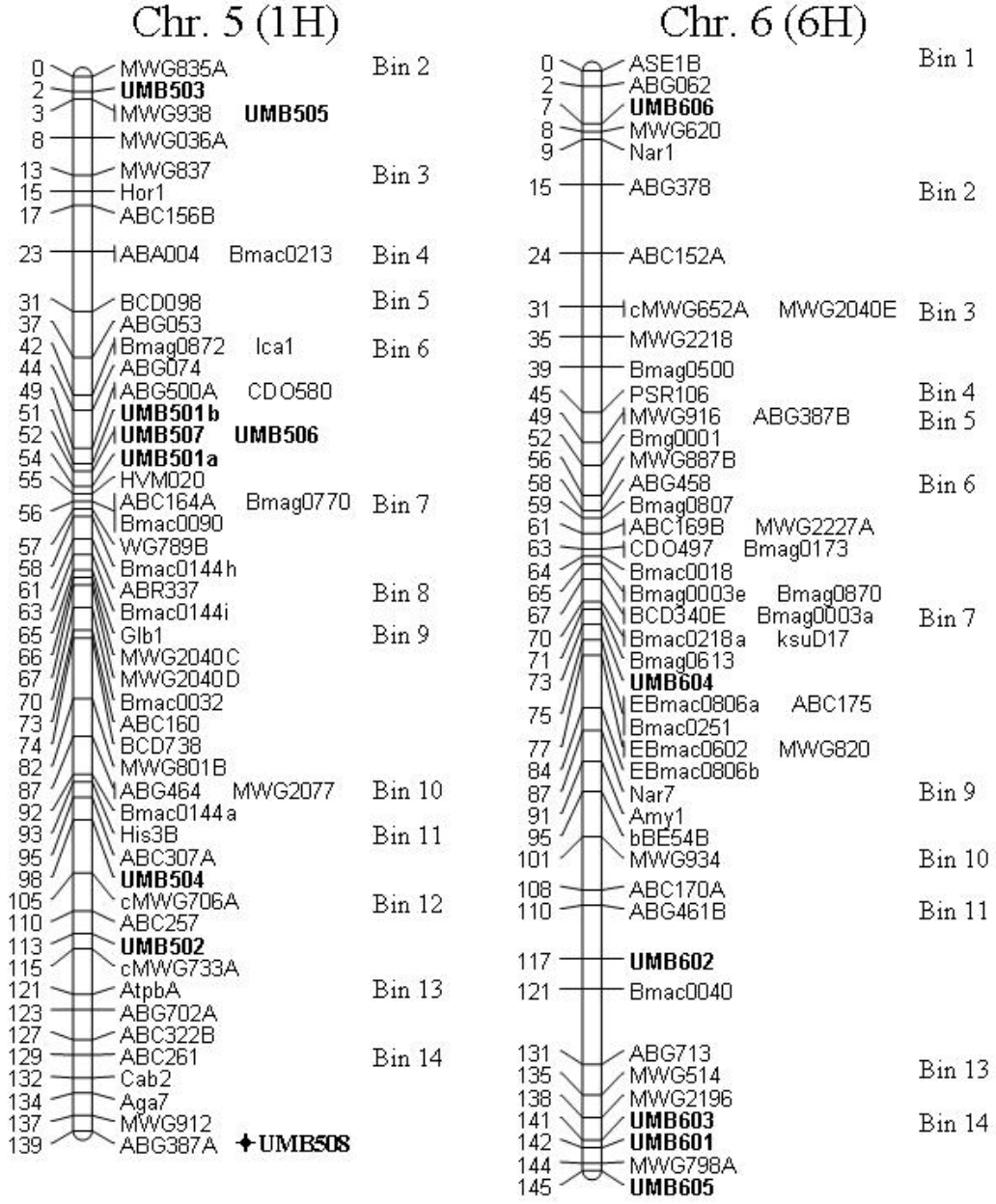
Chr. 5 (1H)
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2 UMB503
3 MWG938 UMB505
8 MWG036A
13 MWG837
15 Hor1
17 ABC156B
23 ABA004 Bmac0213
31 BCD098
37 ABG053
42 Bmag0872 Ica1
44 ABG074
49 ABG500A CDO580
51 UMB501b
52 UMB507 UMB506
54 UMB501a
55 HVM020
56 ABC164A Bmag0770
Bmac0090
57 WG789B
58 Bmac0144h
61 ABR337
63 Bmac0144i
65 Glb1
66 MWG2040C
67 MWG2040D
70 Bmac0032
73 ABC160
74 BCD738
82 MWG801B
87 ABG464 MWG2077
92 Bmac0144a
93 His3B
95 ABC307A
98 UMB504
105 cMWG706A
110 ABC257
113 UMB502
115 cMWG733A
121 AtpbA
123 ABG702A
127 ABC322B
129 ABC261
132 Cab2
134 Aga7
137 MWG912
139 ABG387A ✦UMB508
Bin 2
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Chr. 6 (6H)
0 ASE1B
2 ABG062
7 UMB606
8 MWG620
9 Nar1
15 ABG378
24 ABC152A
31 cMWG652A MWG2040E
35 MWG2218
39 Bmag0500
45 PSR106
49 MWG916 ABG387B
52 Bmg0001
56 MWG887B
58 ABG458
59 Bmag0807
61 ABC169B MWG2227A
63 CDO497 Bmag0173
64 Bmac0018
65 Bmag0003e Bmag0870
67 BCD340E Bmag0003a
70 Bmac0218a ksuD17
71 Bmag0613
73 UMB604
75 EBmac0806a ABC175
Bmac0251
77 EBmac0602 MWG820
84 EBmac0806b
87 Nar7
91 Amy1
95 bBE54B
101 MWG934
108 ABC170A
110 ABG461B
117 UMB602
121 Bmac0040
131 ABG713
135 MWG514
138 MWG2196
141 UMB603
142 UMB601
144 MWG798A
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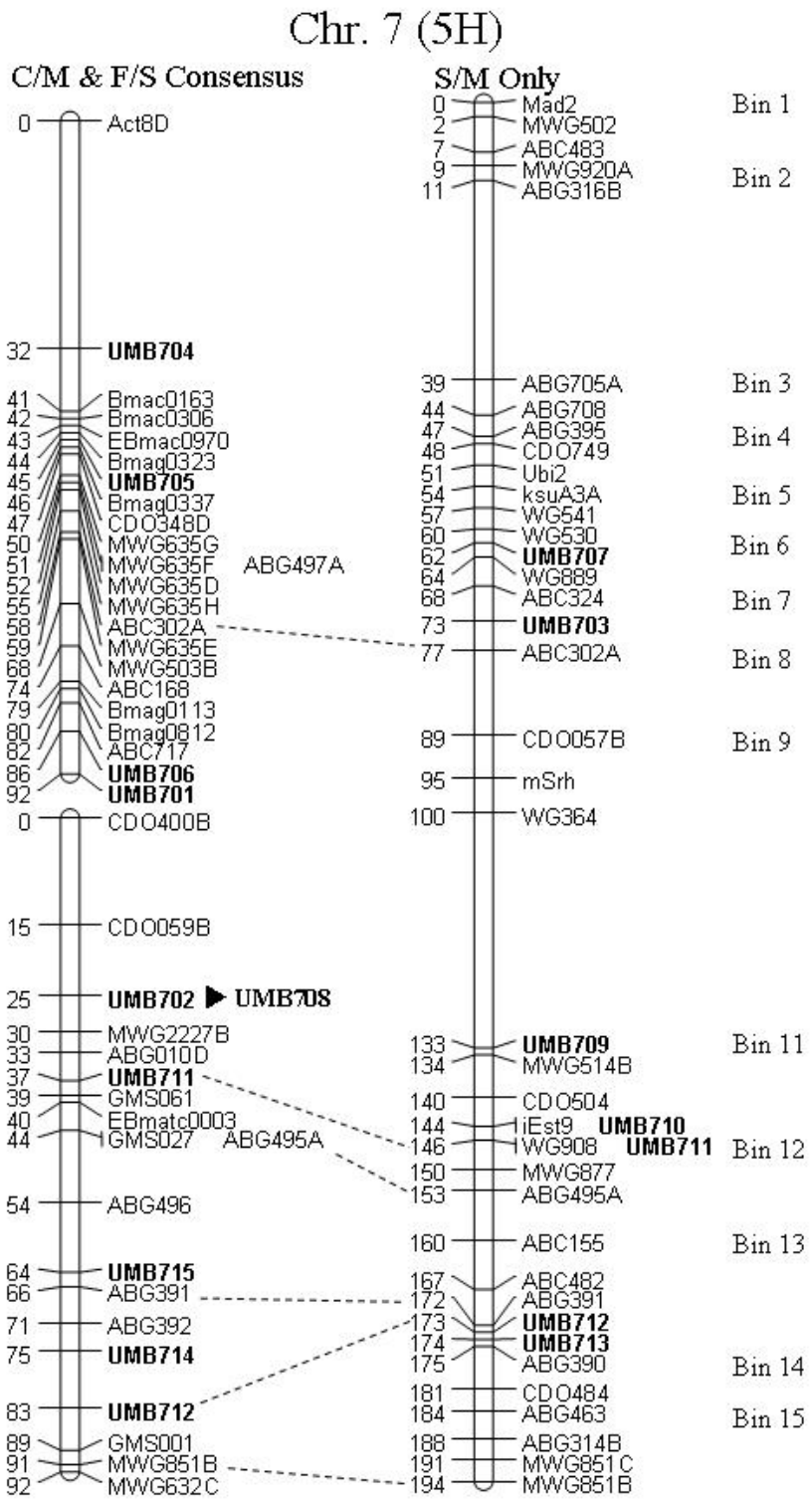
Chr. 7 (5H)
C/M & F/S Consensus
S/M Only
0 Act8D
32 UMB704
41 Bmac0163
42 Bmac0306
43 EBmac0970
44 Bmag0323
45 UMB705
46 Bmag0337
47 CDO348D
50 MWG635G
51 MWG635F
52 MWG635D
55 MWG635H
58 ABC302A
59 MWG635E
68 MWG503B
74 ABC168
79 Bmag0113
80 Bmag0812
82 ABC717
86 UMB706
92 UMB701
ABG497A
0 CDO400B
15 CDO059B
25 UMB702 ▶ UMB708
30 MWG2227B
33 ABG010D
37 UMB711
39 GMS061
40 EBmatc0003
44 GMS027
ABG495A
54 ABG496
64 UMB715
66 ABG391
71 ABG392
75 UMB714
83 UMB712
89 GMS001
91 MWG851B
92 MWG632C
0 Mad2
2 MWG502
7 ABC483
9 MWG920A
11 ABG316B
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39 ABG705A
44 ABG708
47 ABG395
48 CDO749
51 Ubi2
54 ksuA3A
57 WG541
60 WG530
62 UMB707
64 WG889
68 ABC324
73 UMB703
77 ABC302A
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89 CDO057B
95 mSrh
100 WG364
Bin 9
133 UMB709
134 MWG514B
140 CDO504
144 iEst9
146 WG908
UMB710
UMB711
150 MWG877
153 ABG495A
160 ABC155
167 ABC482
172 ABG391
173 UMB712
174 UMB713
175 ABG390
181 CDO484
184 ABG463
188 ABG314B
191 MWG851C
194 MWG851B
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