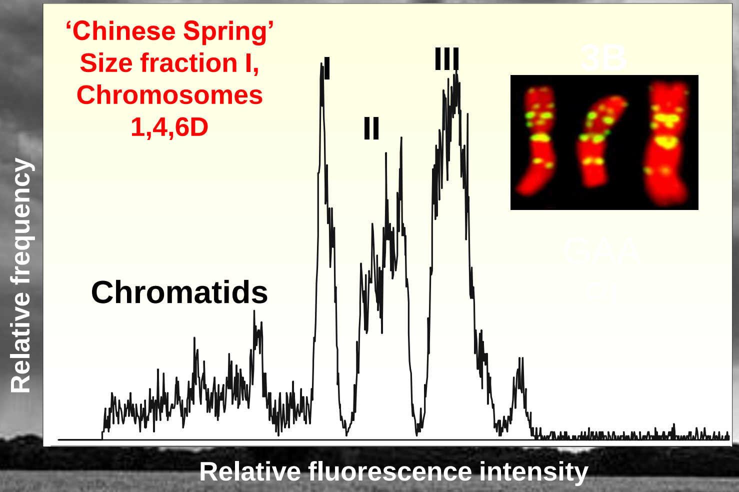
Physical and Genetic Framework of Chromosomes 3A, 1D, 4D, and 6D of Hexaploid Wheat



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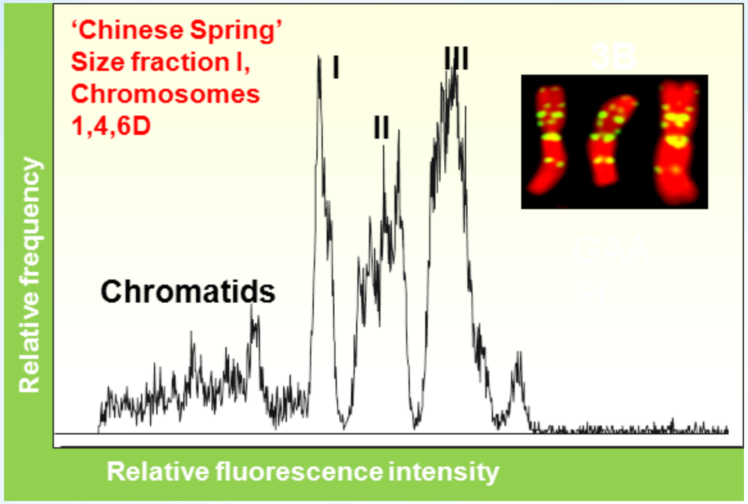
Physical mapping is necessary for complete sequencing of wheat genome primarily because of huge size, largely repetitive DNA, complexity and polyploidy.

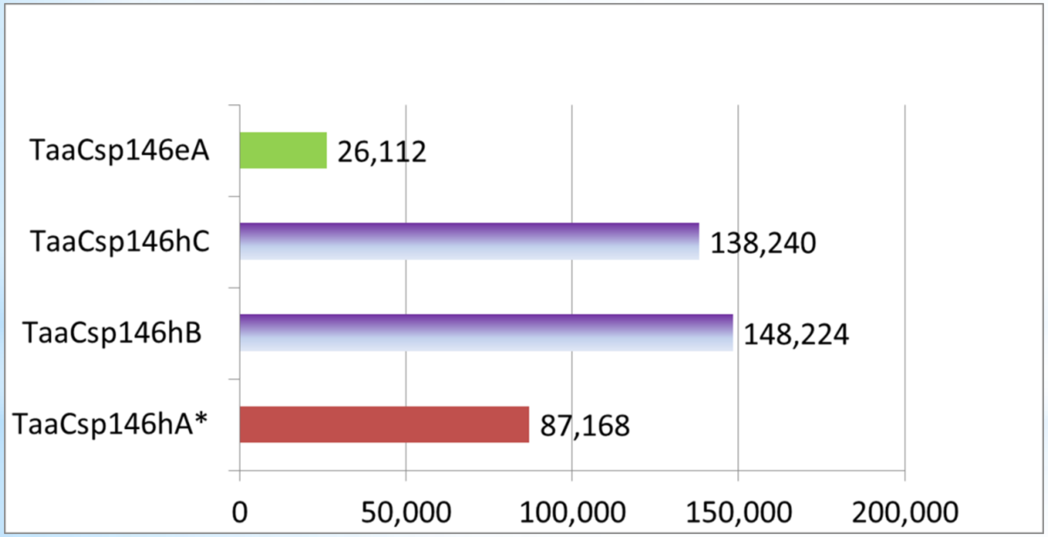
We are making fraction-I physical maps of chromosomes 1D, 4D, and 6D

Chromosome	Size (Mb)	% fraction of wheat genome
1D	604	3.5
4D	648	3.8
6D	712	4.1

BAC Libraries



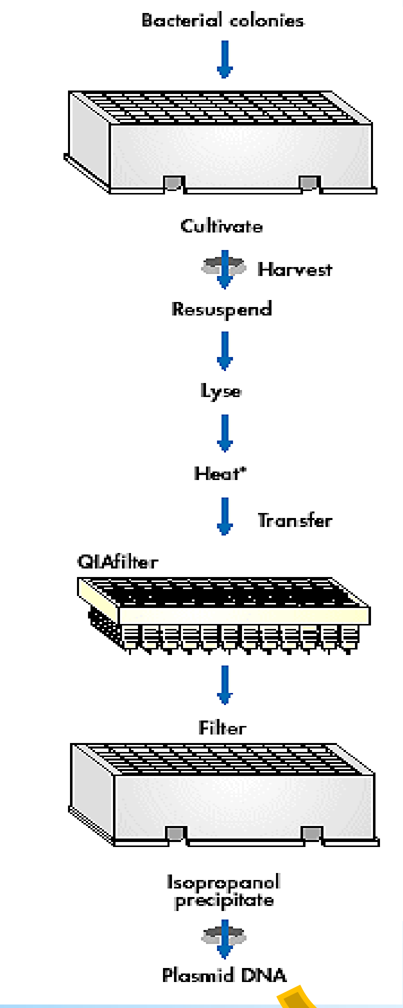
Size: fraction I (1D, 4D, 6D); fraction II (1A, 3A, 6A, 2D, 3D, 5D, 7D); and fraction III (2A, 4A, 5A, 7A, 1B, 2B, 4B, 5B, 6B, 7B); in addition to an individual chromosome 3B



Mean insert size
85 Kb
102 Kb
116 Kb
110 Kb

HICF
(a first step in developing a physical map)

BAC-DNA Isolation



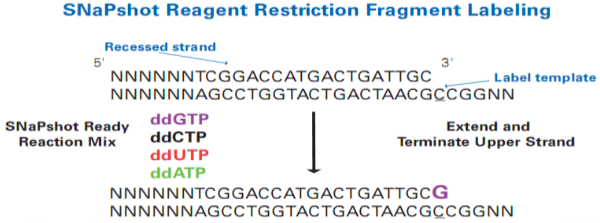
SNaPShot BAC fingerprinting technique

GS1200Liz

Restriction Endonuclease Digestion

Restriction Endonuclease	Restriction Site	ddNTP	Fluorescent Dye Label	Restriction Fragment Color
EcoRI	G↓AATTC	A	dR6G	Green
BamHI	G↓GATCC	G	dR110	Blue
XbaI	T↓CTAGA	C	dTAMRA™	Yellow
XhoI	C↓TCGAG	T	dROX™	Red
HaeIII	GG↓CC	None		

3' end labeling on restricted fragments using SNaPshot chemistry



SNaPshot Reagent Restriction Fragment Labeling

NNNNNNTCGGACCATGACTGATTGC
NNNNNNAGCCTGGTACTGACTAACGCCGGNN

NNNNNNTCGGACCATGACTGATTGCG
NNNNNNAGCCTGGTACTGACTAACGCCGGNN

Size exclusion and signal detection on CE instrument like the 3730/3730*xl*

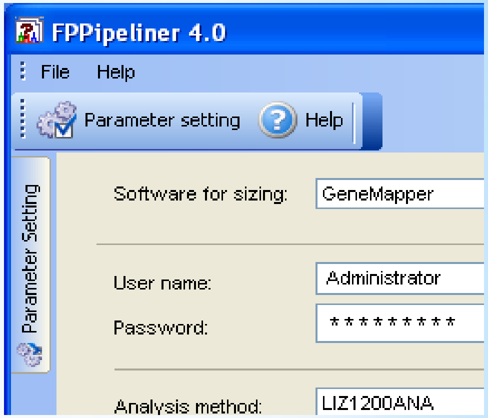
Data processing

DNA Analyzer

Fragment separation

GeneMapper v4.0.lnk

Fragment Sizing



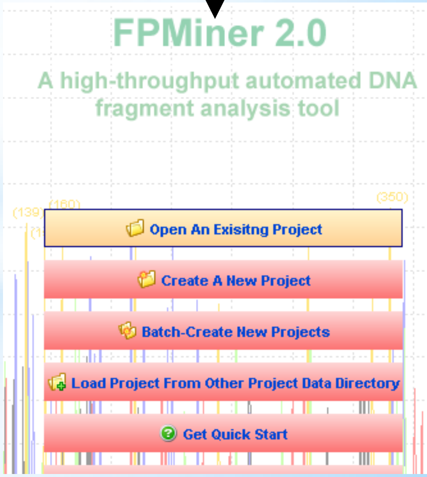
Software for sizing: GeneMapper

User name: Administrator

Password: *********

Analysis method: LIZ1200ANA

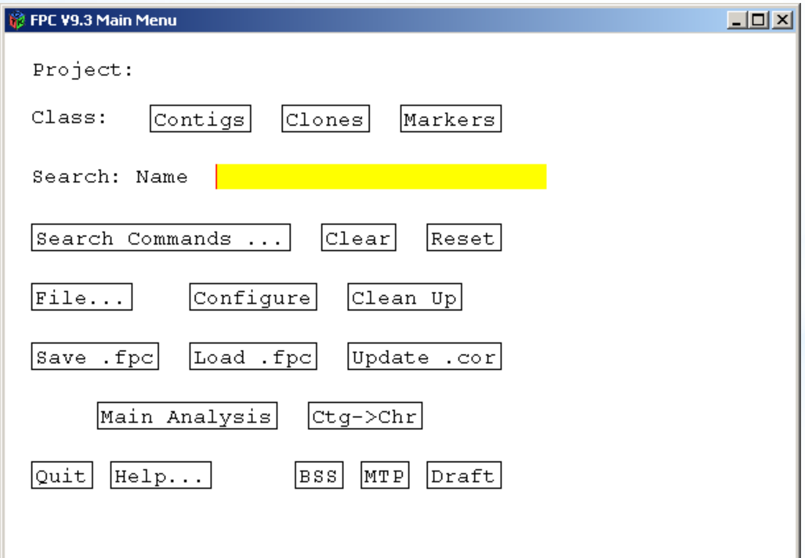
Batch processing



FPMiner 2.0

A high-throughput automated DNA fragment analysis tool

Manual editing, filtering and processing



Contig assembly

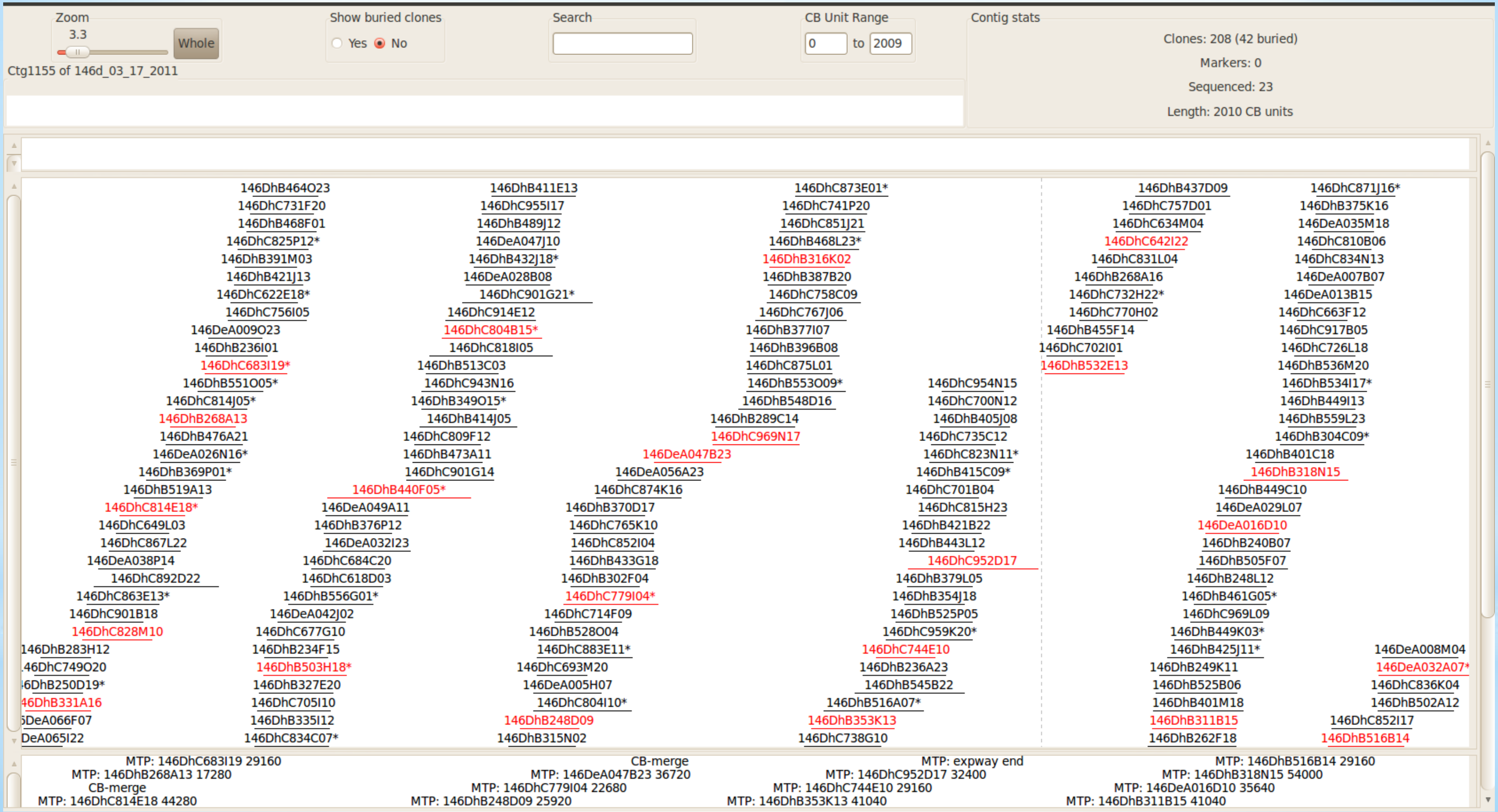
FPC Assembly

- 280,000 BAC clones fingerprinted
- High quality fingerprints from 200,069 clones used in FPC assembly

Features	Statistics
Cutoffs	**1e-45**
Number of clones in contigs	170,368
Singletons	29,701
Total number of contigs (>200 kb)	5,152 (2,411)
Number of contigs >500Kb	1,068
Longest contig (# of clones)	4Mb (517)
400-599clones	4
200-399 clones	89
100-199 clones	350
50-99 clones	714
Average contigs size (Kb)	485
Assembly size (% coverage)	1567Mb (82%)

Selected MTP for Coassembly with *Aegilops tauschii*

A minimum tiling path with MinFPC overlap of 25 was used and 34,350 BACs were identified



CB Unit Range: 0 to 2009

Ctg1155 of 146d_03_17_2011

Clones: 208 (42 buried)
Markers: 0
Sequenced: 23
Length: 2010 CB units

146DhB464O23
146DhC731F20
146DhB468F01
146DhC825P12*
146DhB391M03
146DhB421J13
146DhC622E18*
146DhC756I05
146DeA009O23
146DhB236I01
146DhC683I19*
146DhB551O05*
146DhC814J05*
146DhB268A13
146DhB476A21
146DeA026N16*
146DhB369P01*
146DhB519A13
146DhC814E18*
146DhC649L03
146DhC867L22
146DeA038P14
146DhC892D22
146DhC863E13*
146DhC901B18
146DhC828M10
146DhB283H12
46DhC749O20
6DhB250D19*
46DhB331A16
DeA066F07
DeA065I22

146DhB411E13
146DhC955I17
146DhB489J12
146DeA047J10
146DhB432J18*
146DeA028B08
146DhC901G21*
146DhC914E12
146DhC804B15*
146DhC818I05
146DhB513C03
146DhC943N16
146DhB349O15*
146DhB414J05
146DhC809F12
146DhB473A11
146DhC901G14
146DhB440F05*
146DeA049A11
146DhB376P12
146DeA032I23
146DhC684C20
146DhC618D03
146DhB556G01*
146DeA042J02
146DhC677G10
146DhB234F15
146DhB503H18*
146DhB327E20
146DhC705I10
146DhB335I12
146DhC834C07*

146DhC873E01*
146DhC741P20
146DhC851J21
146DhB468L23*
146DhB316K02
146DhB387B20
146DhC758C09
146DhC767J06
146DhB377I07
146DhB396B08
146DhC875L01
146DhB553O09*
146DhB548D16
146DhB289C14
146DhC969N17
146DeA047B23
146DeA056A23
146DhC874K16
146DhB370D17
146DhC765K10
146DhC852I04
146DhB433G18
146DhB302F04
146DhC779I04*
146DhC714F09
146DhB528O04
146DhC883E11*
146DhC693M20
146DeA005H07
146DhC804I10*
146DhB248D09
146DhB315N02

146DhC954N15
146DhC700N12
146DhB405J08
146DhC735C12
146DhC823N11*
146DhB415C09*
146DhC701B04
146DhC815H23
146DhB421B22
146DhB443L12
146DhC952D17
146DhB379L05
146DhB354J18
146DhB525P05
146DhC959K20*
146DhC744E10
146DhB236A23
146DhB545B22
146DhB516A07*
146DhB353K13
146DhC738G10

146DhB437D09
146DhC757D01
146DhC634M04
146DhC642I22
146DhC831L04
146DhB268A16
146DhC732H22*
146DhC770H02
146DhB455F14
146DhC702I01
146DhB532E13

146DhC871J16*
146DhB375K16
146DeA035M18
146DhC810B06
146DhC834N13
146DeA007B07
146DeA013B15
146DhC663F12
146DhC917B05
146DhC726L18
146DhB536M20
146DhB534I17*
146DhB449I13
146DhB559L23
146DhB304C09*
146DhB401C18
146DhB318N15
146DhB449C10
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146DeA016D10
146DhB240B07
146DhB505F07
146DhB248L12
146DhB461G05*
146DhC969L09
146DhB449K03*
146DhB425J11*
146DhB249K11
146DhB525B06
146DhB401M18
146DhB311B15
146DhB262F18

146DeA008M04
146DeA032A07*
146DhC836K04
146DhB502A12
146DhC852I17
146DhB516B14

MTP: 146DhC683I19 29160
CB-merge
MTP: expway end
MTP: 146DhB516B14 29160
MTP: 146DhB268A13 17280
MTP: 146DeA047B23 36720
MTP: 146DhC952D17 32400
MTP: 146DhB318N15 54000
CB-merge
MTP: 146DhC779I04 22680
MTP: 146DhC744E10 29160
MTP: 146DeA016D10 35640
MTP: 146DhC814E18 44280
MTP: 146DhB248D09 25920
MTP: 146DhB353K13 41040
MTP: 146DhB311B15 41040

BAC anchoring

Random BACs 3-D Pools

Randomly selected 240 384 well plates to develop 3-D BAC pools for anchoring

5x

Total clones= 92,240 clones
Plate Pools= 40
Row Pools= 48
Colum pools=48

MTP BACs 3-D Pools

High confidence MTP selected foe anchoring **and co-assembly with *Aegilops tauschii***

Total clones= 34,350 clones
Plate Pools= 90
Row Pools= 16
Colum pools=24

10K Infinium assay

Selected MTP BACs 3-D Pools

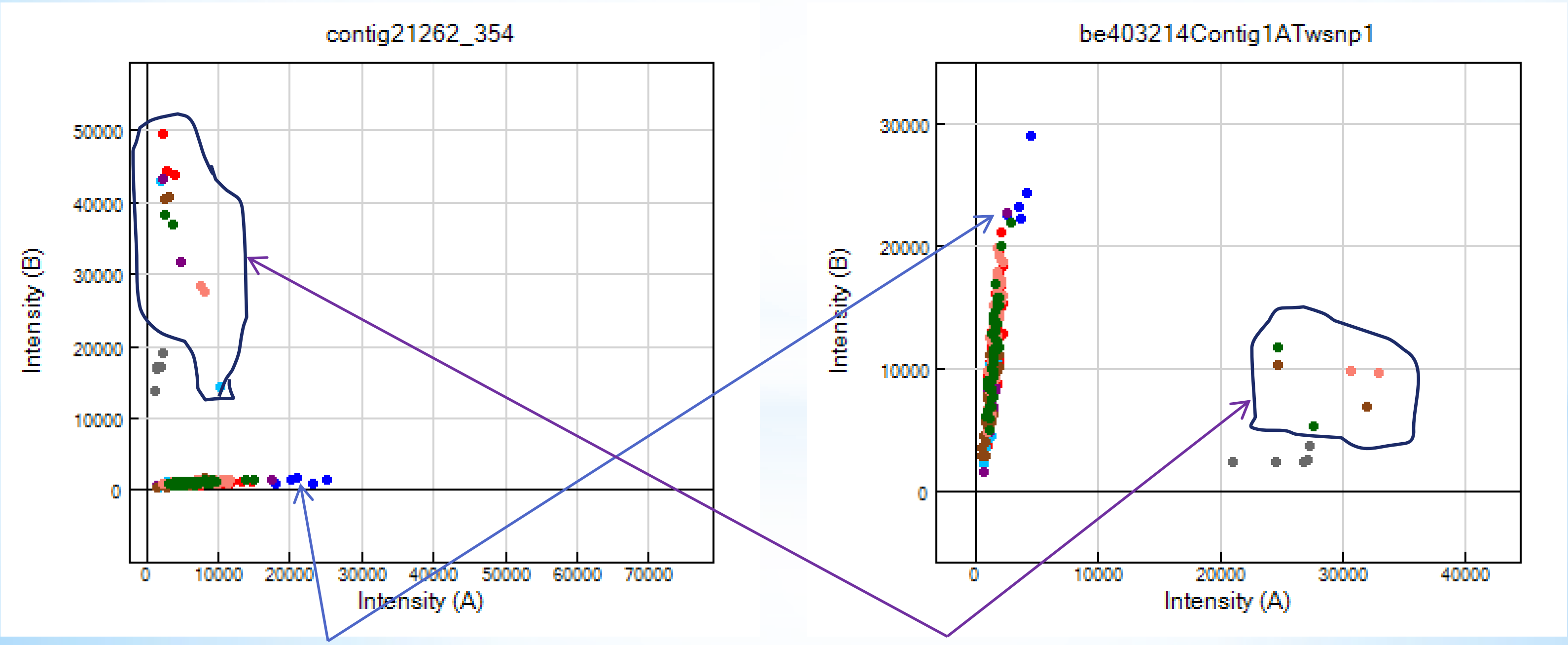
Two border clones from each contigs was selected

Total clones= 7,064 clones
Plate Pools= 19
Row Pools= 16
Colum pools=24

Barcoded BAC pools and Sequenced on HiSeq2000

BAC pool genotyping

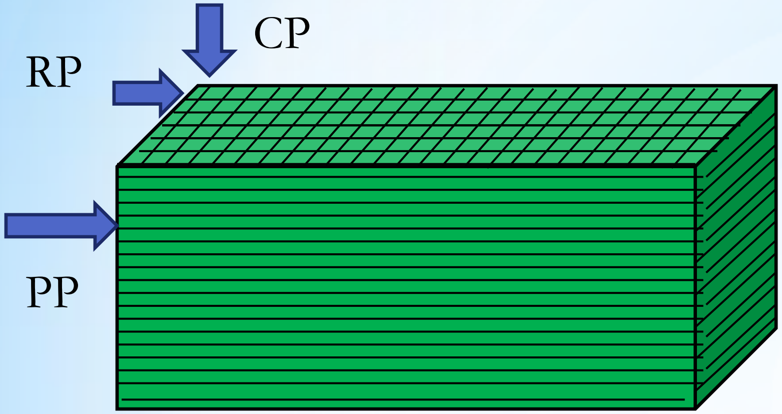
- 10K Infinium was designed based on polymorphism between AL8/78 and AS75 by collaborating group at UC Davis was used for BAC pool genotyping
- SNPs on 1D, 4D, 6D = 2,488
- In absence of target DNA in the pools there was random signal therefore, BAC pools were contaminated with 300 ng of AS75 DNA .



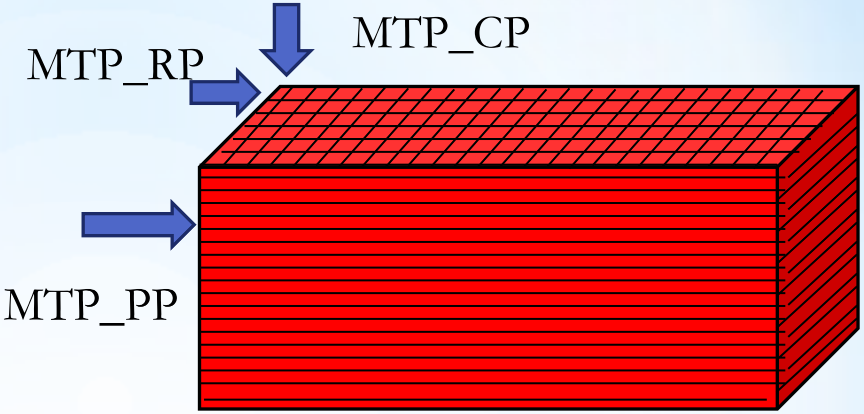
AS 75

Positive Pools

Deconvolution of BAC Pool Genotyping Data



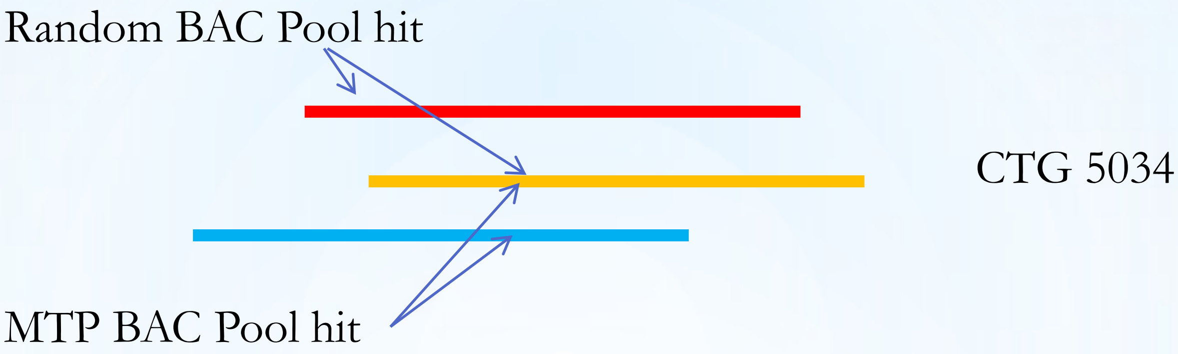
Random BACs 3-D Pools



MTP BACs 3-D Pools

SNP_ID	SNP_Name	Plate Pool hits	Row Pool hits	Column Pool hits	BAC address	Contig
AT6D5706	contig08978_497	RP_PP13	RP_RP26	RP_CP39	146DhB503J15	ctg585
AT6D5706	contig08978_497	RP_PP02	RP_RP38	RP_CP06	146DhC732F06	ctg585
AT6D5706	contig08978_497	RP_PP10	RP_RP33	RP_CP21	146DhC740A21	ctg585
AT6D5706	contig08978_497	RP_PP16	RP_RP35	RP_CP05	146DhC746C05	ctg585
AT6D5706	contig08978_497	RP_PP22	RP_RP47	RP_CP38	146DhC792O14	ctg585
AT6D5706	contig08978_497	MTP_PP82	MTP_RP14	MTP_CP11	146DhC866O20	ctg585

Deconvolution



Random BAC Pool hit

CTG 5034

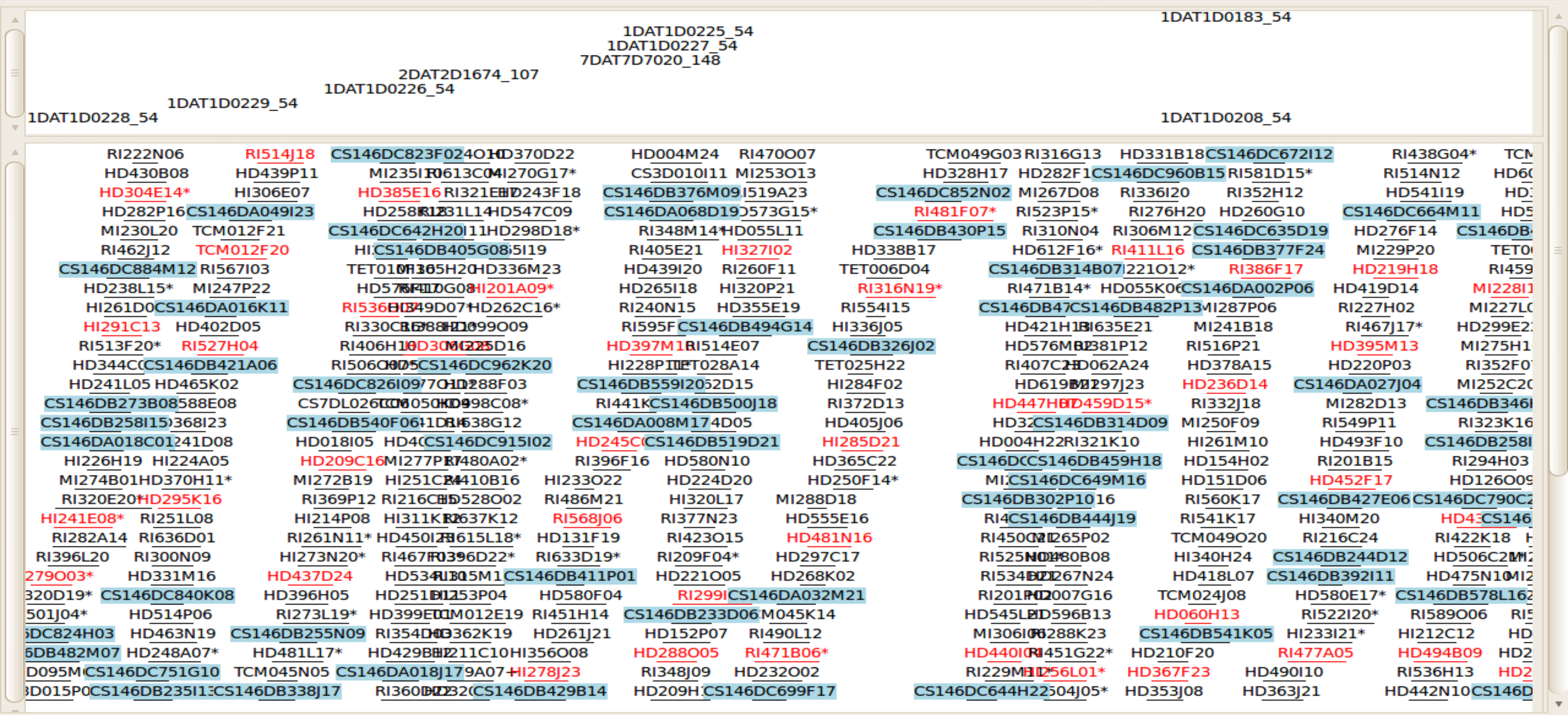
MTP BAC Pool hit

SNP_ID	SNP_Name	Plate Pool hits	Row Pool hits	Column Pool hits	BAC address	Contig
BE403818	BE403818ATwsnp1	MTP_PP43	MTP_RP08	MTP_CP19	146DhB495N02	ctg3671
BE403818	BE403818ATwsnp1	MTP_PP43	MTP_RP08	MTP_CP05	146DhB495L21	ctg4764
BE403818	BE403818ATwsnp1	MTP_PP81	MTP_RP02	MTP_CP13	146DhC860O01	ctg4784
BE403818	BE403818ATwsnp1	MTP_PP81	MTP_RP08	MTP_CP13	146DhC861F24	ctg5034
BE403818	BE403818ATwsnp1	MTP_PP43	MTP_RP02	MTP_CP05	146DhB495F04	ctg5034
BE403818	BE403818ATwsnp1	RP_PP05	RP_RP22	RP_CP28	146DhB495F04	ctg5034
BE403818	BE403818ATwsnp1	RP_PP11	RP_RP21	RP_CP47	146DhB501E23	ctg5034

SNPs anchored = 1,981 using 1D, 4D, 6D BAC pools

BAC anchoring based on Coassembly

Contigs	No. of contigs	Total length (Mb)
After assembly	3153	4756
After editing	3578	4793
CS BACs in contigs	26,525	



SNP markers anchored on BAC contigs

	Number of markers anchored
Total	2,392
Markers anchored based on 3-D pools	1,984
Markers anchored based on Coassembly with *Ae tauschii*	408
Chromosome 1D	869
Chromosome 4D	754
Chromosome 6D	685
Other chromosomes	49

FPC assembly statistics

Contigs	No. of contigs	Total length (Mb)	Average length (kb)	<0.2 Mb	0.2-0.5 Mb	0.5-1 Mb	1-2 Mb	2-5 Mb	>5 Mb
Present assembly	3749	1726	460	2146	604	490	393	113	2
Anchored	964	1047	1087	60	176	295	322	108	2
Unanchored	2785	679	265	2086	428	195	71	5	0

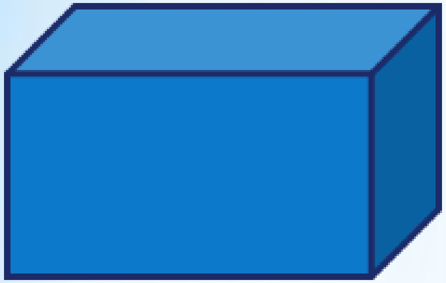
1603 contigs with >0.2 Mb is size of 904 contigs have been anchored making 60 % of the large contigs.

1603 contigs have a physical length of 1403 Mb of which 77 % (1,087Mb) is anchored

Manual editing underway

Editing with support of co-assembly is underway

Sequencing MTP BACs for Anchoring



Two border clones from each contigs was selected

7,064 BACs selected

Plate Pools= 19

Row Pools= 16

Colum pools=24

59 Barcoded libraries were prepared and 100 bp PE sequence was generated by running three lanes of HiSe2000

This generated 18, 21, and 16 Gbp of sequence data from three lanes and a total of 75x coverage.

Individual pools based assemblies were developed and preliminary screened for chromosome 1D 4D 6D sequences were done

Pool	Description	Assembled contigs (contamination cleaned)	Note
S95A	RP11(row pool #11)	19,348 (19,215)	Mixture of 456 (24x19) BACs
S95B	RP9 (row pool #9)	20,144 (19,987)	Mixture of 456 (24x19) BACs
S95C	RP7 (row pool #7)	20,185 (19,790)	Mixture of 456 (24x19) BACs
S95D	CP23 (column pool #23)	18,609 (13,916)	Mixture of 304 (16x19) BACs
S95E	PP3 (plate pool #3)	18,458 (16,667)	Mixture of 384 (24x16) BACs
S95F	PP14 (plate pool #14)	17,195 (17,021)	Mixture of 384 (24x16) BACs

Deconvolution and tracing of contigs individual BACs is underway

Genetic mapping

- A recombinant inbred line population of 311 F_6 individuals, derived by crossing the bread wheat cultivar Prelude (TA2988) with a synthetic wheat (TA8051), was used to develop an integrated genetic map of the D genome of bread wheat.

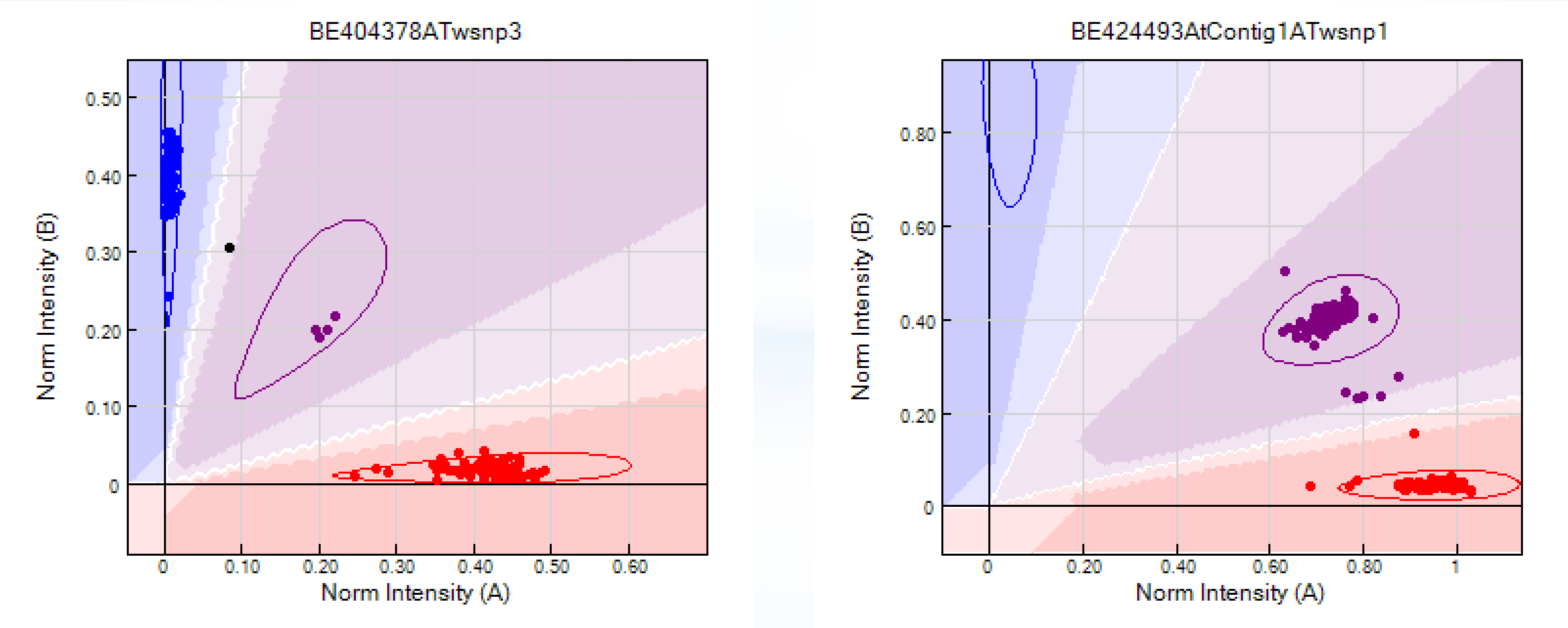
- 187 RILs were genotyped with Illumina10K Infinium HD array (8,609 SNPs) developed for *Ae. tauschii* physical mapping project.

- Same set of 187 RILs were sequenced (GBS) on 6 lanes of Illumina HiSeq2000

Infinium SNP genotyping

10K Infinium genotyping data was analyzed

Data for 8,359 SNPs was obtain and 4,768 high quality polymorphic SNPs were identified and used for development of high density genetic map of D- genome wheat



Genetic Map of Wheat D Genome

Chromosome	No. of SNP markers (10K Infinium)	Total distance (cM)
1D	514	209.3
2D	889	288.5
3D	699	322.1
4D	610	200.6
5D	673	243.6
6D	507	202.4
7D	782	266.1
Total	**4,674**	**1732.6**

Wheat chromosome 1D

515 markers

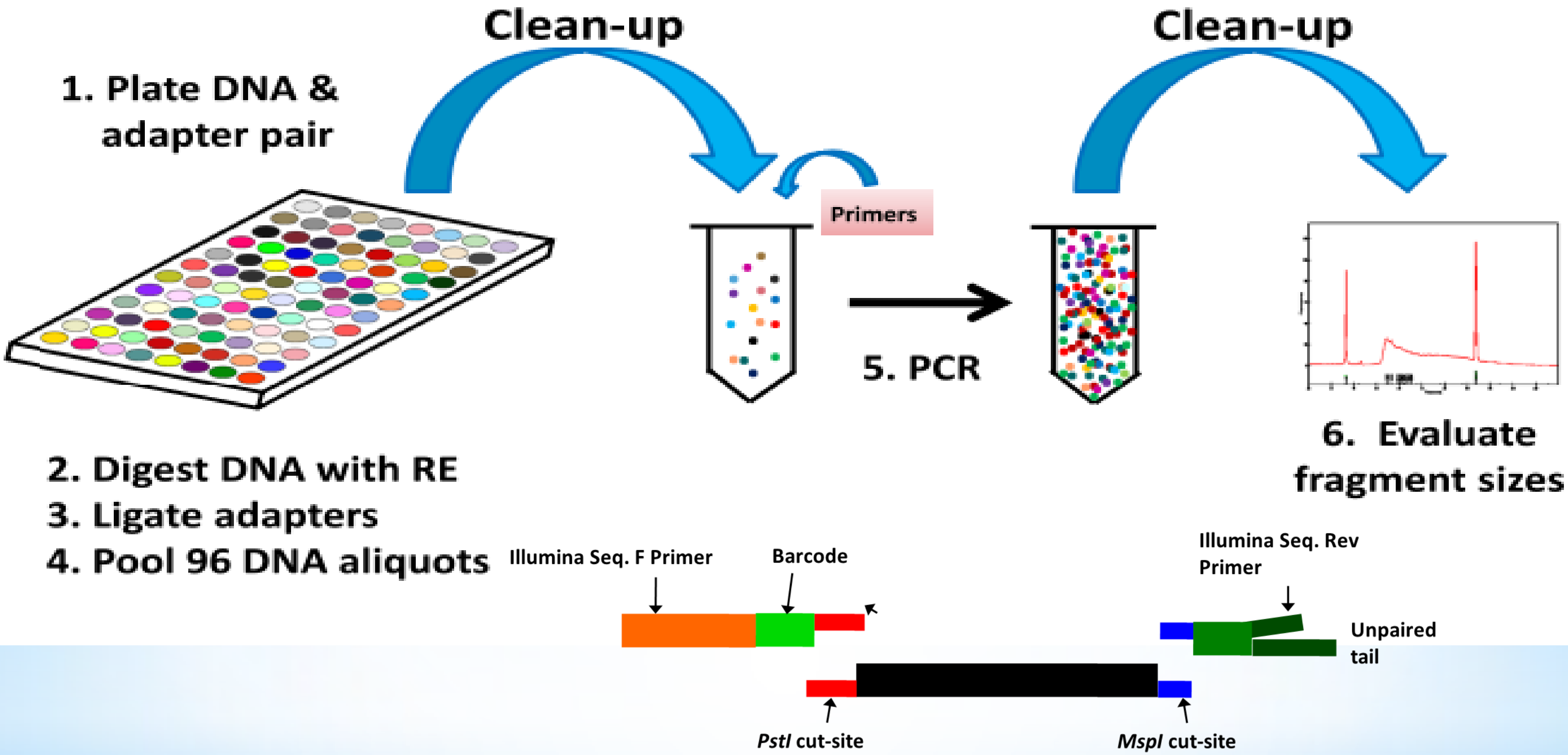
BE443332ATwsnp	115	cM	A	A	A	A	B	B	A	A	A	B	A	B	B	A	B	B	B	A	A	B	A	A	A	A	B	A	B	A	B	B	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0621	115	cM	A	A	A	A	B	B	A	A	A	B	A	B	B	A	B	A	B	A	A	B	A	A	A	A	B	A	B	A	B	B	A	B	A	B	A	A	B	B	B	B	B	A	B	B
BE443930ATwsnp	115	cM	A	A	A	A	B	B	A	A	A	B	A	B	B	A	B	A	B	A	A	B	A	A	A	A	B	A	B	A	B	B	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0632	115	cM	A	A	A	A	B	B	A	A	A	B	A	B	B	A	B	A	B	A	A	B	A	A	A	A	B	A	B	A	B	B	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0644	116	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	A	B	A	B	A	A	B	A	A	A	A	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0656	116	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	A	B	A	B	A	A	B	A	A	A	A	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0659	117	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	A	B	A	B	A	A	A	A	A	A	A	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0661	117	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	A	B	A	B	A	A	A	A	A	A	A	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0667	119	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0669	119	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0674	119	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
F5XZDLF02GD9G	119	cM	A	A	A	A	B	-	A	A	A	B	A	A	-	-	-	A	-	A	A	A	A	A	A	-	-	A	-	A	-	A	A	B	A	B	A	A	-	B	-	B	-	A	-	-
AT1D0676	120	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0683	120	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0686	120	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	-	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0675	120	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0685	120	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0693	120	cM	A	A	A	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0694	121	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0695	121	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	-	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0711	121	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	B	A	B	A	B	A	A	B	A	B	A	A	B	B	B	B	B	A	B	B
AT1D0714	122	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	B	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0721	123	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0723	123	cM	A	A	B	A	B	B	A	-	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0724	123	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0736	124	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0741	124	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0743	124	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0744	124	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0746	124	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0748	124	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
BF484656ATwsnp	124	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0732	124	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0737	124	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0749	125	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	-	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0750	125	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0752	125	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	-	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0756	125	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	A	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0760	125	cM	A	A	B	A	B	B	B	A	A	B	A	A	B	B	B	-	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0766	126	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	A	A	A	A	A	B	A	B	A	A	B	A	B	A	A	B	A	B	A	A	B	B	A	B	B	A	B	B
AT1D0772	127	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	A	A	A	A	A	B	A	B	A	A	B	A	B	A	A	B	A	B	A	A	A	B	A	B	B	A	A	A
AT1D0773	127	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	A	A	A	A	A	B	A	B	A	A	B	A	B	A	A	B	A	B	A	A	A	B	A	B	B	A	A	A
AT1D0776	127	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	-	A	A	A	A	A	B	A	B	A	A	B	A	B	A	A	B	A	B	A	A	A	B	A	B	B	A	A	A
AT1D0777	127	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	A	A	A	A	A	B	A	B	A	A	B	A	B	A	A	B	A	B	A	A	A	B	A	B	B	A	A	A
AT1D0778	128	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	A	A	A	A	A	B	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0782	128	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	A	A	A	A	A	B	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0786	128	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	A	A	A	A	A	B	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	B	A	B	B	A	A	A
GCE8AKX02I2H6	128	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	A	A	A	A	A	A	B	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0792	130	cM	A	A	B	A	B	B	A	A	A	B	A	A	B	B	B	-	A	A	A	A	A	A	A	B	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0797	131	cM	A	A	B	A	B	B	A	B	A	B	A	A	B	B	B	A	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0805	132	cM	A	A	B	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0808	132	cM	A	A	B	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0817	133	cM	A	A	A	A	B	A	A	B	A	B	A	A	B	B	B	-	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0819	133	cM	A	A	A	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	B	B	A	A	A
BE443588ATwsnp	133	cM	A	A	A	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	B	B	A	A	A
GBF1XID01BA2Y	133	cM	A	A	A	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0823	134	cM	A	A	A	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0829	134	cM	A	A	A	A	B	A	A	B	A	-	A	A	-	B	B	-	A	A	A	A	A	A	B	-	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	-	B	A	A	A
AT1D0832	136	cM	A	A	A	A	B	A	A	B	A	B	A	A	B	B	B	-	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	B	B	A	A	A	B	A	B	B	A	A	A
AT1D0835	136	cM	A	A	A	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	A	B	A	A	A	B	A	B	B	A	A	A
AT1D0840	137	cM	A	A	A	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	A	A	A	A	A	B	A	B	B	A	A	A
AT1D0843	138	cM	A	A	A	A	B	A	A	B	A	B	A	A	B	B	B	A	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	A	A	A	A	A	B	A	B	B	A	A	A
AT1D0934	148	cM	A	A	A	B	A	A	B	B	A	A	A	A	B	B	B	B	A	A	A	A	A	A	B	B	A	A	B	A	B	A	A	A	A	B	-	B	A	B	A	B	B	A	A	A

507 markers

Wheat chromosome 6D

AT6D6024	0 cM	B	B	A	A	B	A	A	B	B	A	B	A	A	A	-	B	B	A	A	B	A	B	B	-	A	-	-	A	B	A	A	B	B	-	B	A	-	A	A	B	A	A	A	-	A	A	A	A	B	A
AT6D6015	2.8 cM	B	B	A	A	B	A	A	B	A	A	B	A	A	A	B	B	B	A	A	B	A	B	B	B	A	B	B	A	B	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D6008	7 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	B	B	B	A	A	B	A	B	B	B	A	B	B	A	B	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D6005	7.3 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	H	B	B	A	A	B	A	B	B	B	A	B	B	A	B	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D6006	8.1 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	-	B	B	A	A	B	A	B	B	B	A	B	B	A	B	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
CD454441ATwsnp	8.1 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	A	B	A	B	B	B	A	B	B	A	B	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D6003	8.9 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	B	B	B	A	A	B	A	B	B	B	A	B	B	A	B	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D6004	9.2 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	-	B	B	A	A	B	A	B	B	B	A	B	B	A	B	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D6001	11.8 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	H	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D6000	12.5 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	-	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5994	12.9 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5995	13.2 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5996	14 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5991	16.8 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5990	17.2 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5992	17.2 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5993	18 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	-	B	B	H	A	A	A	B	B	B	B	A	B	-	A	A	A	-	A	B	A	B	-	B	B	A
AT6D5985	20.9 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	-	A
AT6D5986	21.4 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	-	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5987	21.4 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5989	21.4 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5982	22 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5981	22.5 cM	B	A	A	A	B	A	A	B	B	A	B	A	A	A	A	B	B	A	B	B	A	B	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5976	24.2 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	B	A	A	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5972	25 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	B	A	A	B	B	A	B	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5969	26.4 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	B	A	A	B	B	A	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5960	27 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	B	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5961	27 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	B	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5962	27 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	B	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5964	27 cM	B	-	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	B	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5966	27 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	B	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5956	27.8 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	A	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5953	28.1 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	A	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5955	29.2 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	A	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A
AT6D5948	31.2 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	A	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	B	B	B	A
AT6D5950	31.2 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	A	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	B	B	B	A
AT6D5951	31.2 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	A	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	B	B	B	A
AT6D5944	31.4 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	A	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	B	B	B	A
AT6D5946	31.4 cM	B	A	A	A	B	A	A	B	A	A	B	A	A	A	A	B	B	A	B	A	A	A	B	B	B	B	B	A	A	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	B	B	B	A
AT6D5940	32.8 cM	B	A	A	A	B	A	A	B	A	B	B	A	A	A	A	B	B	A	B	A	A	A	B	B	B	B	B	A	B	A	A	B	B	B	A	A	B	A	A	A	A	A	A	B	A	B	B	B	B	A
AT6D5936	34.2 cM	B	A	A	A	B	A	A	B	A	B	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	B	-	A	A	B	A	A	A	B	A	A	B	A	B	B	B	B	A
AT6D5933	35.3 cM	B	A	A	A	B	A	A	B	A	B	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	B	H	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
be517715Contig1/	35.3 cM	B	A	A	A	B	A	A	B	A	B	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	B	B	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5924	36.4 cM	B	A	A	B	B	A	A	B	A	B	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	B	H	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5930	37.5 cM	B	A	A	A	B	A	A	B	A	B	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	B	-	A	A	B	A	A	A	B	A	A	B	A	A	B	B	-	A
AT6D5931	37.5 cM	B	A	A	A	B	A	A	B	A	B	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	B	B	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
BE637911ATwsnp	37.5 cM	B	A	A	A	B	A	A	B	A	B	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	B	B	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5934	39.2 cM	B	A	A	A	B	A	A	B	A	B	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	B	A	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
GB5Y7FA02H663I	39.2 cM	B	A	A	A	B	A	A	B	A	B	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	B	A	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5917	43.8 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	-	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5912	44.3 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	A	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5913	44.3 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	-	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5915	44.3 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	A	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5911	44.9 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	A	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5908	45.2 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	-	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
CD490964ATwsnp	45.2 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	A	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5914	47.7 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5906	48.6 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	H	A	A	B	A	A	A	B	A	A	B	A	A	B	B	B	A
AT6D5903	50.2 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	A	A	B	A	A	B	A	A	A	B	A	A	A	A	A	B	B	B	A
AT6D5899	50.5 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	A	A	B	A	A	B	A	A	A	B	A	A	A	A	A	B	B	B	A
AT6D5900	50.5 cM	B	A	B	B	B	B	A	B	A	B	B	A	A	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	A	A	H	A	A	B	A	A	A	B	A	A	A	A	A	B	B	B	A
bq171182Contig1/	52.5 cM	B	A	B	B	B	A	A	B	A	B	B	A	B	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	A	A	A	A	A	B	A	A	A	B	A	A	A	A	A	B	B	B	A
AT6D5897	54.3 cM	B	A	B	B	B	A	A	B	A	B	B	A	B	B	A	B	B	A	B	A	B	B	B	B	B	B	B	A	B	A	A	A	A	-	A	A	B	A	A	A	B	A	A	A	A	A	B	B	B	A
AT6D5895	57.7 cM	B	A	B	B	B	A	A	B	A	B	B	A	B	B	A	B	B	A	B	B	B	B	B	B	B	B	B	A	B	A	A	A	A	B	A	A	B	A	A	A	B	A	A	A	A	A	A	B	B	A

Genotyping By Sequencing



Clean-up

Clean-up

1. Plate DNA & adapter pair

Primers

5. PCR

6. Evaluate fragment sizes

2. Digest DNA with RE
3. Ligate adapters
4. Pool 96 DNA aliquots

Illumina Seq. F Primer

Barcode

Illumina Seq. Rev Primer

Unpaired tail

PstI cut-site

MspI cut-site

Plant ID	Barcode	Population
11-1-1	TGACGCCA	PreludeTA2988SyntheticTA8051F5P01
11-1-71	CAGATA	PreludeTA2988SyntheticTA8051F5P01
11-1-92	GAAGTG	PreludeTA2988SyntheticTA8051F5P01
11-1-144	TAGCGGAT	PreludeTA2988SyntheticTA8051F5P01
11-1-177	TATTCGCAT	PreludeTA2988SyntheticTA8051F5P01
11-1-216	ATAGAT	PreludeTA2988SyntheticTA8051F5P01
11-1-256	CCGAACA	PreludeTA2988SyntheticTA8051F5P01
11-1-281	GGAAGACAT	PreludeTA2988SyntheticTA8051F5P01
11-1-6	GGCTTA	PreludeTA2988SyntheticTA8051F5P01
11-1-74	AACGCACATT	PreludeTA2988SyntheticTA8051F5P01

6 lane HiSeq 2000

60 Gb of sequence data from 187 RILs and 2 parents

Adapted from Elshire et al 2011

Genetic map of D genome of wheat

More than 30,000 SNPs identified

7,743 SNPs with less that 30% missing data

More than 19,000 mapped to seven D genome chromosomes

Chromosome	No. of SNP markers (Infinium)	No. of SNP markers (GBS)	Total distance (cM)
1D	514	2,104	205
2D	889	2,103	288.5
3D	699	3,781	322.1
4D	610	2,205	200.6
5D	673	3,460	243.6
6D	507	2,768	202.4
7D	782	3,149	266.1
Total	**4,674**	**19,570**	**1732.6**

Infinium and GBS based SNP Map

1029 Markers

Chromosome 6D

AT6D5328	70.2	B	B	B	B	B	A	B	A	A	B	B	B	B	B	B	A	B	B	A	A	A	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	A	B	B	A	B	A	A	A	A	A	A	B	B	B
AT6D5330	70.2	B	B	B	B	B	A	B	A	A	B	B	B	B	B	B	A	B	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	B	A	A	A	A	A	A	B	B	B
wxs_snp2148	70.2	-	-	B	B	B	A	B	A	A	-	B	B	B	B	B	A	-	B	A	A	-	A	-	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	-	A	B	B	A	B	B	-	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	B	-	-	A	A	A	A	B	B	B
wxs_snp2899	70.2	-	-	B	B	B	A	B	A	A	B	B	B	B	B	B	-	B	B	A	A	A	A	B	A	B	-	A	B	-	A	B	B	A	B	B	B	B	A	B	-	-	A	B	B	-	B	B	B	A	B	A	-	-	-	A	-	-	A	B	-	B	B	A	B	-	-	-	A	A	A	B	B	B
wxs_snp4106	70.2	B	B	B	-	B	A	B	A	A	B	B	B	B	B	B	A	B	B	A	A	-	A	B	A	B	-	A	B	-	A	B	B	A	B	B	B	B	A	B	-	B	-	B	B	A	-	B	B	A	B	A	B	-	-	A	-	-	A	B	-	B	B	A	-	A	-	A	A	A	A	B	B	B
wxs_snp5261	70.2	-	B	B	B	B	A	B	A	-	B	B	B	B	B	B	A	B	B	A	A	-	A	B	A	B	-	A	B	-	A	B	B	A	B	B	B	B	A	-	-	B	-	-	B	A	-	B	B	-	B	-	B	-	-	A	A	-	A	B	-	B	-	A	B	A	-	-	A	A	A	B	-	B
wxs_snp6140	70.2	-	B	B	-	-	A	B	A	A	B	B	B	-	B	B	A	-	B	A	A	-	A	B	A	B	A	A	B	-	A	B	-	A	B	B	-	B	A	B	-	B	-	B	B	-	-	B	B	A	B	A	-	-	-	A	-	A	A	B	-	B	-	A	-	A	-	-	A	A	A	B	B	B
wxs_snp6744	70.2	-	B	B	B	B	A	B	-	A	B	B	B	B	B	B	A	B	B	A	A	-	A	B	A	-	-	A	B	-	A	B	B	A	B	B	-	B	A	-	B	-	-	B	B	A	-	B	B	-	B	A	-	-	-	A	A	-	A	B	-	B	-	A	-	-	-	-	A	A	A	B	B	B
wxs_snp5424	70.6	-	B	B	B	-	-	-	A	-	B	B	-	-	B	B	A	-	B	A	A	-	A	B	A	B	A	-	B	-	A	B	B	A	B	B	B	B	A	-	-	B	-	B	B	-	-	B	B	-	B	A	B	A	-	A	A	A	-	B	-	B	-	A	-	-	-	A	-	A	A	B	-	B
wxs_snp4490	71	-	-	B	A	B	A	B	A	A	B	B	B	B	B	B	A	-	B	A	A	-	A	B	A	-	-	-	B	B	A	B	B	A	B	B	B	B	A	-	B	-	-	B	B	A	-	B	B	-	B	A	-	A	-	A	A	A	A	B	-	B	B	A	B	-	-	-	-	A	A	B	B	B
AT6D5335	71.3	B	B	B	A	B	A	B	A	A	B	B	B	B	B	B	A	A	B	A	A	A	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	B	A	A	A	A	B	A	B	B	B
AT6D5339	71.9	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	B	A	A	A	A	B	A	B	B	B
AT6D5348	71.9	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	A	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	A	B	B	A	B	A	A	A	A	B	A	B	B	B
AT6D5343	71.9	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	A	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	A	B	B	A	B	A	A	A	A	B	A	B	B	B
AT6D5345	71.9	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	B	A	A	A	A	B	A	B	B	B
AT6D5337	71.9	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	B	A	A	A	A	B	A	B	B	B
AT6D5344	71.9	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	A	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	B	A	A	A	A	B	A	B	B	B
wxs_snp0676	71.9	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	-	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	-	B	-	B	B	A	-	B	B	A	B	A	B	A	-	A	A	A	A	B	-	B	B	A	B	A	-	-	A	B	A	B	B	B
wxs_snp0709	71.9	-	B	B	A	-	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	-	B	B	A	B	B	B	A	B	B	A	-	B	B	A	B	A	B	-	B	-	A	A	A	B	-	B	B	A	-	A	-	A	A	B	A	B	B	B
wxs_snp2065	71.9	-	-	B	A	B	A	A	A	A	B	B	B	-	B	B	A	-	B	A	A	-	A	B	A	-	-	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	-	-	B	B	-	B	A	-	-	-	A	A	A	A	B	-	B	B	A	B	A	-	-	A	B	A	B	B	B
wxs_snp3331	71.9	-	B	B	A	-	A	A	A	A	-	-	B	B	B	B	A	A	B	A	A	-	A	B	A	B	A	A	-	-	A	B	-	A	B	B	B	B	A	-	-	-	A	B	B	A	B	B	B	A	B	A	B	A	-	-	A	A	A	B	-	B	-	A	B	-	-	A	A	B	A	B	-	B
wxs_snp3720	71.9	-	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	-	-	A	A	-	A	B	A	-	-	A	B	A	A	B	B	A	B	B	B	B	A	B	-	B	-	B	B	-	-	B	B	A	B	A	B	-	B	A	A	A	A	B	-	B	-	A	-	-	-	-	A	B	A	B	B	B
wxs_snp5022	72.3	B	B	B	-	B	A	A	-	-	B	B	B	B	B	B	A	-	B	A	A	-	A	B	-	B	A	A	B	-	A	B	B	-	B	B	B	B	A	B	-	B	A	B	B	-	-	B	B	A	B	A	B	-	B	-	-	-	A	B	-	B	B	-	-	A	-	-	A	B	A	B	B	B
wxs_snp6203	72.3	B	-	B	-	B	A	A	A	A	B	B	B	B	-	B	A	A	B	A	A	A	A	B	A	B	A	A	B	-	A	B	B	A	B	B	-	B	A	-	-	B	-	B	B	-	-	B	B	-	-	A	-	-	-	A	A	A	A	B	-	-	-	A	-	-	-	-	A	B	A	B	B	B
wxs_snp1233	72.7	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	-	A	B	-	B	-	B	B	A	-	B	B	A	B	A	B	A	-	A	A	A	A	B	-	B	B	A	B	-	-	A	A	B	A	B	-	B
AT6D5349	73	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	B	B	B	A	B	A	A	A	A	B	A	B	B	B
AT6D5350	73.9	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	B	A	A	A	A	B	A	B	B	B
wxs_snp0731	73.9	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	-	A	B	B	B	A	B	B	-	B	B	B	A	B	A	B	-	B	A	A	A	A	B	-	B	B	A	B	A	-	-	A	B	A	B	B	B
wxs_snp3751	73.9	B	B	B	A	B	A	A	A	A	B	B	B	B	B	B	A	A	B	A	A	-	A	B	A	-	A	-	B	-	-	B	B	A	B	B	B	B	A	B	-	-	-	B	B	A	-	B	B	A	B	A	B	A	-	A	A	A	A	B	-	B	B	A	-	-	-	A	-	B	A	B	B	B
wxs_snp6151	74.7	-	-	B	A	-	A	A	A	A	-	B	-	B	-	B	A	-	B	A	A	A	A	B	A	-	-	A	-	A	-	B	B	A	B	-	B	B	A	-	-	-	-	B	B	-	-	-	B	A	B	A	B	A	-	A	A	A	-	B	A	B	-	A	B	-	-	A	-	B	A	-	B	B
wxs_snp2541	75.2	-	-	B	A	B	A	A	A	A	B	B	B	B	B	B	A	-	B	A	A	-	A	B	A	B	A	A	B	-	-	B	B	A	B	B	B	B	A	B	-	B	-	B	B	A	B	B	B	A	B	A	B	A	-	A	A	A	A	B	-	B	B	A	B	A	-	A	A	B	A	B	B	B
wxs_snp7675	75.2	-	-	B	A	-	A	A	A	A	B	B	-	B	B	B	A	-	B	A	-	-	A	B	A	B	-	-	B	-	A	B	B	A	B	B	B	B	A	-	-	B	-	B	B	A	-	B	B	-	B	A	B	-	B	A	-	-	A	B	-	B	-	-	-	-	-	-	-	B	-	B	-	B
wxs_snp6733	75.6	B	-	B	A	B	A	A	A	A	B	B	B	-	B	-	A	-	B	A	A	-	A	B	A	B	-	A	B	-	A	B	B	A	B	B	B	B	A	-	-	B	A	B	B	-	-	B	B	-	-	A	-	-	-	A	A	A	A	B	-	B	B	A	B	-	-	-	-	B	A	B	B	B
wxs_snp3673	76	B	B	B	A	B	A	-	B	A	B	B	B	B	-	B	A	A	-	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	-	-	-	B	B	A	B	B	B	A	B	A	B	A	-	A	A	-	A	B	-	B	B	A	B	A	-	-	-	B	A	B	B	B
AT6D5357	76.4	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	B	A	A	A	A	B	A	B	B	B
wxs_snp3691	76.4	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	-	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	-	-	A	B	B	-	-	B	B	-	B	A	B	-	-	A	A	-	A	B	-	B	-	A	-	-	-	A	A	B	A	B	B	B
AT6D5371	77	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	A	A	A	A	A	B	A	B	B	B
AT6D5363	77.6	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	A	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	A	B	B	A	A	A	A	A	A	B	A	B	B	B
AT6D5369	78.4	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	B	B	B	A	A	A	A	A	A	B	A	B	B	B
AT6D5368	78.4	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	B	B	B	A	A	A	A	A	A	B	A	B	B	B
AT6D5364	78.4	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	A	A	A	A	A	B	A	B	B	B
AT6D5366	78.4	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	A	A	A	A	A	B	A	B	B	B
wxs_snp0444	78.4	B	B	B	A	-	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	-	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	-	-	A	A	A	A	B	-	B	B	A	A	-	-	A	A	B	A	B	B	B
wxs_snp0526	78.4	B	B	B	A	-	A	A	B	A	B	B	B	B	B	B	B	A	B	-	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	-	B	B	A	A	A	-	A	A	B	A	B	B	B
wxs_snp2563	78.4	-	B	B	A	B	A	A	B	A	B	B	B	-	B	B	B	-	B	A	A	B	A	B	A	B	-	A	B	A	A	B	B	A	B	B	B	B	A	B	-	B	A	B	B	A	-	B	B	-	-	A	B	-	-	-	-	A	A	B	-	B	B	A	A	A	-	-	A	B	A	B	B	B
wxs_snp2840	78.4	-	B	B	-	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	-	B	A	A	B	A	A	B	B	A	B	B	-	B	A	B	-	B	A	B	B	A	-	B	B	A	B	A	B	-	B	A	A	A	A	B	-	B	-	A	A	-	-	A	A	B	A	B	B	B
wxs_snp3239	79.2	-	-	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	-	-	A	B	B	-	-	B	B	-	B	A	B	A	-	A	A	A	A	B	-	-	-	A	-	-	-	A	A	B	A	B	B	B
AT6D5362	79.6	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	A	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	A	B	B	A	A	A	A	A	A	B	A	B	B	B
wxs_snp5546	79.6	-	-	B	A	B	A	A	B	A	B	B	B	B	B	-	B	A	B	A	A	-	A	B	A	-	A	A	B	-	A	B	B	A	B	B	-	-	A	-	-	-	A	B	B	A	B	B	B	A	B	A	B	A	-	A	-	A	A	B	-	B	-	A	A	-	A	A	-	B	A	B	-	B
wxs_snp5552	79.6	B	-	B	A	B	A	A	B	A	-	B	-	-	B	-	-	A	B	A	A	B	A	B	A	-	A	-	B	A	A	B	B	A	-	B	-	B	A	-	-	-	A	B	B	A	-	-	B	A	B	A	-	A	-	A	A	A	A	B	A	B	-	A	-	A	-	-	A	-	A	B	-	B
wxs_snp6889	79.6	B	-	B	A	-	A	A	B	A	-	B	-	B	B	-	-	A	B	A	A	-	A	-	A	-	A	A	-	A	A	B	B	A	B	-	-	B	A	-	-	B	A	-	B	A	B	-	B	A	B	A	B	A	-	-	A	A	A	B	-	B	B	A	A	A	-	A	A	B	A	-	-	B
AT6D5359	80.4	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	A	A	B	A	B	A	A	B	-	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	B	A	A	A	A	B	B	B	B	A	A	A	A	A	A	B	A	B	B	B
wxs_snp6831	81.6	B	B	B	A	-	A	A	B	A	B	B	B	B	-	B	B	-	B	A	A	B	-	B	A	B	-	A	B	A	B	B	B	A	B	B	B	B	A	-	-	B	A	B	B	-	-	B	B	A	B	-	-	-	-	A	A	A	A	B	-	B	B	A	-	-	-	-	A	B	A	B	-	B
AT6D5401	83.2	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	A	A	A	A	A	B	-	B	B	A	A	A	A	A	A	B	A	B	B	B
AT6D5392	83.8	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	A	A	A	A	A	B	B	B	B	A	A	A	A	A	A	B	A	B	B	B
AT6D5394	83.8	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	A	A	A	A	A	B	-	B	B	A	A	A	A	A	A	B	A	B	B	B
AT6D5391	83.8	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	A	A	A	A	A	B	B	B	B	A	A	A	A	A	A	B	A	B	B	B
AT6D5393	85.2	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	A	A	A	A	A	B	A	B	B	A	A	A	A	A	A	B	A	B	B	B
contig33076_213	85.2	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	A	A	A	A	A	B	A	B	B	A	A	A	A	A	A	B	A	B	B	B
AT6D5396	85.2	B	B	B	A	B	A	A	B	A	B	B	B	B	B	B	B	A	B	A	A	B	A	B	A	B	A	A	B	A	A	B	B	A	B	B	B	B	A	B	B	B	A	B	B	A	B	B	B	A	B	A	B	A	A	A	A	A	A	B	A	B	B	A	A	A	A	A	A	B	A	B	B	B

Integrated Genetic and Physical Map

1D

AT1D0008	0	cM	ctg3191
AT1D0004	0.8	cM	ctg3191
AT1D0009	0.8	cM	ctg3191
AT1D0001	1.1	cM	ctg3191
AT1D0002	1.1	cM	ctg3191
AT1D0003	1.1	cM	ctg3191
AT1D0005	1.1	cM	ctg3191
AT1D0006	1.1	cM	ctg3191
AT1D0007	1.1	cM	ctg3191
AT1D0016	4.7	cM	ctg4040
AT1D0020	4.7	cM	ctg3703
GDEEGVY0	4.7	cM	
AT1D0022	5.4	cM	ctg150
AT1D0024	5.8	cM	ctg150
AT1D0025	6.3	cM	ctg4
AT1D0026	6.3	cM	ctg4
AT1D0031	10.4	cM	ctg50
AT1D0034	12.9	cM	
AT1D0038	16.7	cM	ctg1768
AT1D0036	17.2	cM	ctg1768
AT1D0041	19.6	cM	ctg14106
AT1D0044	24.8	cM	ctg14106
AT1D0048	30.8	cM	ctg3279
AT1D0052	32.3	cM	ctg1544
AT1D0053	32.9	cM	
AT1D0061	35	cM	
AT1D0057	35.6	cM	ctg1704
AT1D0062	37.5	cM	ctg1589
AT1D0066	38.1	cM	ctg241
AT1D0071	42.2	cM	
contig69241	44.9	cM	
AT1D0082	46.4	cM	ctg1699
AT1D0077	47.7	cM	ctg1699
AT1D0076	49.8	cM	ctg14071
AT1D0078	50.6	cM	ctg1699
AT1D0081	50.6	cM	ctg1699
AT1D0084	51.4	cM	ctg14135
AT1D0086	51.4	cM	ctg14135
AT1D0088	51.7	cM	ctg140
AT1D0091	51.7	cM	ctg140
AT1D0090	52.3	cM	ctg13569
AT1D0095	53.7	cM	ctg1403
GB5Y7FA02	53.9	cM	
AT1D0098	54.2	cM	ctg309
AT1D0102	54.7	cM	
AT1D0105	55.3	cM	ctg13988
AT1D0116	57	cM	ctg159
AT1D0123	59.7	cM	ctg1695
AT1D0122	60	cM	ctg1695
AT1D0100	67.4	cM	ctg309
AT1D0099	68.2	cM	ctg309
AT1D0103	68.2	cM	ctg309

	Number of markers physical map	Number of marker on Genetic map
Total	2,392	4,674
Chromosome 1D	869	514
Chromosome 4D	754	610
Chromosome 6D	685	507

61 % of FPC assembly anchored

6D

AT6D5445	144.5	cM	ctg14081
AT6D5446	144.5	cM	ctg14081
AT6D5447	144.5	cM	ctg14081
AT6D5442	145.5	cM	ctg14081
AT6D5441	146.4	cM	ctg332
AT6D5439	147.5	cM	ctg14150
AT6D5436	148.9	cM	ctg797
AT6D5435	149.2	cM	ctg797
bg262421C	149.2	cM	
AT6D5429	149.7	cM	
AT6D5431	149.7	cM	ctg1658
AT6D5424	150	cM	ctg380
AT6D5426	150	cM	ctg380
AT6D5416	150.6	cM	ctg809
AT6D5417	150.6	cM	ctg809
bg495635C	150.6	cM	
AT6D5411	150.8	cM	ctg462
AT6D5412	150.8	cM	ctg14
ca643341C	150.8	cM	
AT6D5432	154.7	cM	ctg1658
AT6D5433	154.7	cM	ctg1658
AT6D5427	155.3	cM	ctg380
bf483025Co	155.3	cM	
bg604419C	155.3	cM	
AT6D5423	155.8	cM	ctg380
AT6D5419	156.1	cM	ctg177
AT6D5420	156.1	cM	ctg177
AT6D5422	156.1	cM	ctg72
AT6D5418	156.3	cM	ctg809
AT6D5413	156.6	cM	ctg809
AT6D5404	158.3	cM	ctg405
AT6D5792	158.6	cM	ctg123
contig30284	159.4	cM	
AT6D5362	161.7	cM	ctg2106
AT6D5371	162	cM	ctg826
AT6D5380	162.8	cM	ctg14043
AT6D5387	162.8	cM	ctg295
be424523C	162.8	cM	
AT6D5396	163.1	cM	ctg696
AT6D5393	163.1	cM	ctg1669
contig33076	163.1	cM	
AT6D5401	163.9	cM	ctg1669
GA8KES402	166.3	cM	
AT6D5395	167	cM	ctg300
AT6D5402	167	cM	ctg3293
AT6D5403	167	cM	ctg728
AT6D5391	168.1	cM	ctg1669
AT6D5392	168.1	cM	ctg183
AT6D5394	168.1	cM	ctg474
AT6D5372	168.4	cM	
AT6D5374	168.4	cM	ctg14043
AT6D5376	168.4	cM	ctg14043

Deconvolute pooled BAC sequence contigs to individual BACs

Finalize the integrated GBS and 10K Infinium map

Integration of CS data with *Ae. tauschii* data

Final integration of the Physical and Genetic map

Genomic resources

- Chromosome 3A: ~827 Mb
- 3AS: ~355 Mb,
- 3AL: ~472 Mb

Library code	Chromosome Arm	Number of clones	Mean insert size	Coverage
TaaCsp3AShA	3AS	55,296	80 kb	11.2 x
TaaCsp3AShB	3AS	55,296	115 kb	16.1 x
	3AS	110,592		27.7x
TaaCsp3ALhA	3AL	55,296	106 kb	11.4 x
TaaCsp3ALhB	3AL	24,576	114 kb	5.4 x
	3AL	79,872		16.8x

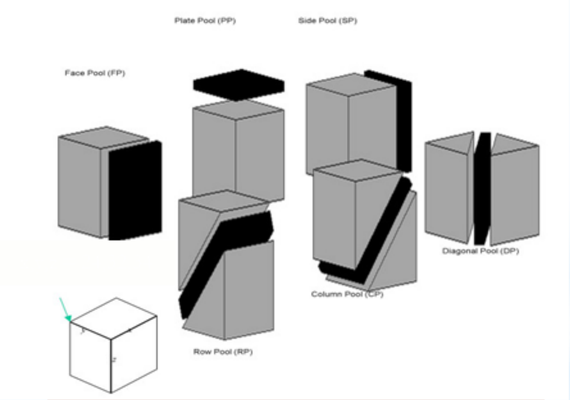
Chromosome 3A FPC assembly

Library	Clones (coverage)	# of clones in contigs	Singletons	Total # of contigs (contigs >500kb)	Longest contig (clones)	Assembly size (% arm coverage with contigs >2clones)
3AS (Phase-I)	55,296 (11.2x)	35,124	11,939	1,677 (199) 1e-15	2.7 kb (417)	327Mb (91 %)
3AS (Phase-II)	65,677 (20.2x)	45,739	11,938	1325 (288) 1e-30	4.99 kb (650)	340Mb (95%)
3AL (Phase-I)	79,872 (16.8x)	51,405	12,064	1417 (273) 1e-25	4.46 (594)	391 Mb (87%)

Chromosome arm	3AS	3AL
FPC assembly	16.8x arm coverage	13.6x arm coverage
Contig assembly	15x arm coverage	12.2x arm coverage
MTP	5,397 clones	5,754 clones
Pools	Six-dimensional random pools Three-dimensional of MTP BAC pools	Three-dimensional of MTP BAC pools

Marker discovery and BAC anchoring

Markers	Identified	Primers designed	Primesr tested	Primers amplified (CS)	# of unique contigs anchored
SSRs	1,057	758 180 (class I)	180	156 (88%)	201
ISBPs	2,736	695	96	92 (95%)	172
Genic	519	240	96	84 (85%)	126



6-dimensional pools

Marker	# of primers designed	# of primers amplified (3AS super pool)	# of markers anchored to BAC
NSF-ESTs	198	135	135
ESTs (Barley/Rice/*Brachypodium*)	1,170	460	366
Total	1,368	595	501

Genetic Mapping

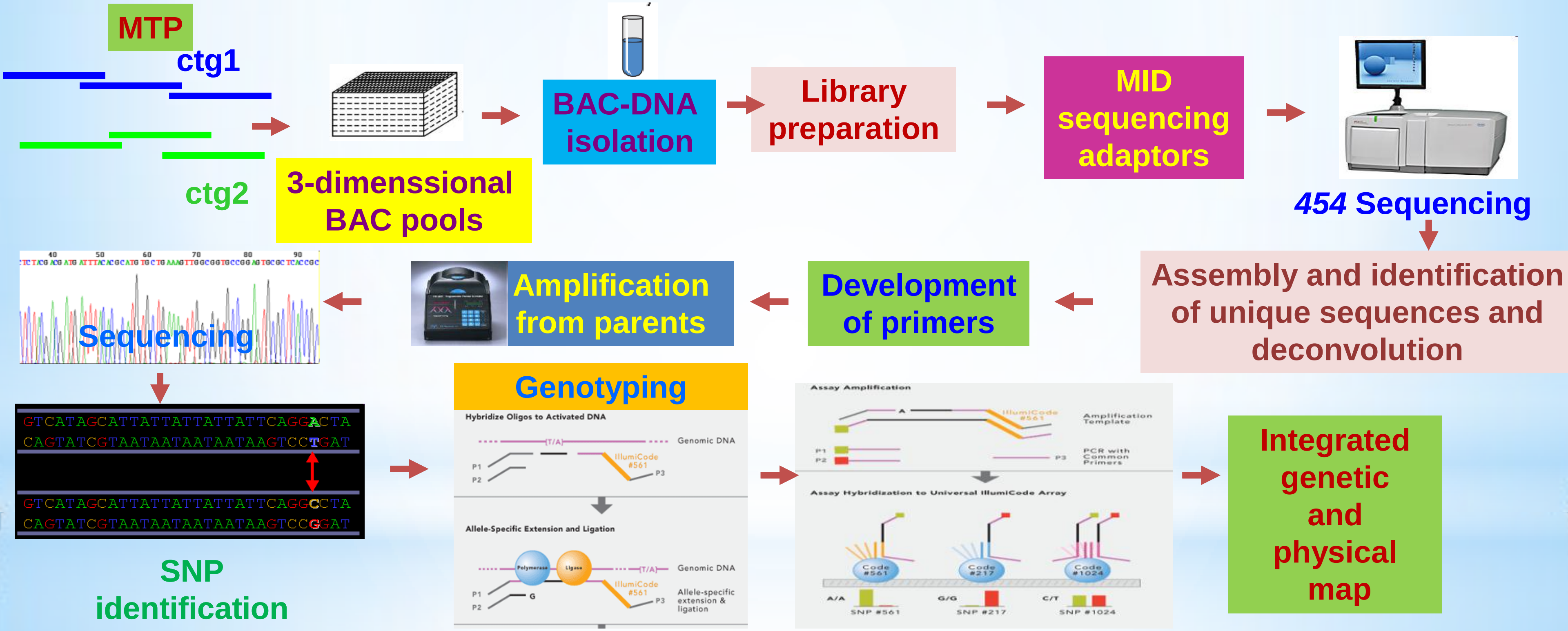
T. monococcum subsp. *aegilopoides* /
T. monococcum subsp. *monococcum*
1,200 F_6 RILs

T. monococcum (>100x sequence generated by collaborators at CSHL, PE, MP 2kb 5kb)

T. aegilopoides (~30x sequence being generated at KSU, PE, MP 2 kb, 5 kb, 10 kb)

Marker discovery

2,743 BAC clones (2-6 per contig) from 3A MTP



MTP

ctg1

ctg2

3-dimenssional BAC pools

BAC-DNA isolation

Library preparation

MID sequencing adaptors

***454* Sequencing**

Assembly and identification of unique sequences and deconvolution

Development of primers

Amplification from parents

Sequencing

SNP identification

Genotyping

Integrated genetic and physical map

Marker discovery

The sequences was assembled into 194,000 contigs (228 Mb) and deconvoluted and analyzed for unique sequences.

Nearly, 55% of the 194,000 contigs and over 70% of the gene containing contigs were traced back to individual BAC clones.

From the parents of the diploid mapping population, 2,908 primers (from genic and low-copy sequences) were designed and amplified.

Of these, ~2,100 primers amplifying one unique band were pooled and sequenced on 454 for SNP identification.

We have identified 2,262 SNPs with minimum base consensus ration 0.9 and read depth of 5.

The SNPs were traced back to 750 genes

To further increase the marker coverage we identified *T. monococcum* contigs (20,646) repeated masked shotgun sequence of chromosome 3A and 3B unigenes.

Marker discovery

We sequence the second parent *T. monococcum* subsp. *aegilopoides* depth of 12x

T. monococcum subsp. *aegilopoides* was aligned to *T. monococcum* subsp. *monococcum contigs* and SNPs discovery

Number of SNPs identified	42,021
Number SNPs with minimum 5 reads , 0.9 base consensus ratio and reference length of >150bp	26,211
Number SNPs with no neighboring SNP in 50bp and within or <200bp flanking the gene	1,710
Number of genes covered	1,182

Illumina GoldenGate design is underway for developing high density integrated and genetic map

GBS based SNP map

376 RILs from the mapping population were genotyped by GBS *T. monococcum* subsp. *aegilopoides* / *T. monococcum* subsp. *monococcum*

6 lanes on Hiseq2000 (4more lanes HiSeq 2000 are underway)

61 Gb of sequence data generated

Initial analysis showed 21,454 SNPs with 2,698 SNPs with less than 30% missing data

GBS based map is underway and would be used to integrated 2,743 BACs sequenced (108,000 contigs) from the MTP of chromosome 3A

T. aegilopoides / T. monococcum denovo GBS map

Tm_snp005	0	-	A	B	A	A	A	A	-	B	-	A	A	A	A	A	A	A	A	B	B	A	B	B	A	B	A	A	A	A	A	A	A	A	B	-	B	B	A	A	A	B	B	A	A	B	A	A	B	B	A	B	A	B	B	B	A	A	A	A	A	A	B	B	A	A	B	-	A	A	A	B	B	A	A	A	B	A	A	A	A	A	B
Tm_snp014	0.45	B	A	B	A	A	A	A	-	B	A	A	A	A	A	A	A	A	A	B	-	A	-	-	A	-	A	A	A	A	A	A	A	A	B	A	B	A	A	A	A	B	B	A	A	B	A	A	B	B	A	-	A	B	B	B	A	-	-	A	A	A	B	B	A	A	B	B	A	A	A	B	B	-	-	A	B	A	A	A	-	A	B
Tm_snp027	1.41	-	A	B	A	A	-	A	B	B	-	A	A	-	A	A	A	A	A	B	B	-	B	B	A	B	A	A	A	-	A	A	A	A	B	-	B	-	A	A	A	B	B	A	A	B	A	A	B	-	A	-	A	B	B	B	A	A	A	A	A	A	B	-	A	A	B	B	A	A	A	-	B	A	A	A	-	A	A	A	A	A	B
Tm_snp027	1.87	-	A	B	A	A	A	A	-	B	-	A	A	-	A	A	A	A	A	B	B	A	B	B	A	B	A	A	A	A	A	A	A	A	B	-	B	-	A	A	A	B	B	A	A	B	A	A	B	B	A	-	A	B	B	B	A	A	A	A	A	A	B	-	A	A	B	B	A	A	A	B	B	A	A	A	-	A	A	-	-	A	B
Tm_snp029	1.87	B	A	B	A	A	A	A	-	B	B	A	A	A	A	-	-	A	-	B	B	-	B	B	A	B	A	A	A	A	A	A	A	A	B	A	B	B	A	A	A	B	B	A	A	B	-	A	B	B	A	-	A	B	B	B	A	A	A	-	A	A	B	-	A	A	B	-	A	A	A	B	B	A	A	A	B	A	A	A	A	A	B
Tm_snp045	2.85	-	-	B	A	A	A	A	B	-	-	A	A	-	A	-	A	A	A	B	B	A	B	B	A	B	A	A	A	A	A	A	A	A	B	A	B	B	A	A	A	B	B	A	-	B	A	A	B	B	A	-	-	B	B	B	A	-	A	A	A	A	B	B	A	A	B	A	A	-	A	B	B	A	A	A	B	A	A	A	A	A	B
Tm_snp063	2.85	-	A	B	A	A	-	A	B	B	-	A	A	A	A	A	A	-	A	B	B	A	-	B	A	B	A	A	A	A	A	A	A	A	-	A	B	B	A	A	A	-	B	A	A	B	A	A	B	B	A	-	A	B	B	B	A	A	A	A	A	A	B	B	A	A	B	-	A	A	A	B	-	-	A	A	B	-	A	-	A	A	B
Tm_snp063	3.86	-	A	B	A	A	A	A	B	B	-	A	-	-	A	-	A	-	A	B	B	-	B	B	A	-	A	A	A	A	A	A	A	A	B	A	B	B	A	A	A	B	B	A	A	B	A	A	B	B	A	B	A	B	-	B	A	A	A	A	A	A	B	B	A	A	B	-	A	A	-	-	B	A	-	A	B	-	A	A	A	A	B
Tm_snp072	4.92	-	A	-	A	A	-	A	B	B	-	A	A	A	A	A	A	A	A	B	B	-	B	B	A	B	A	A	A	A	A	A	A	A	-	-	B	B	A	-	-	B	B	A	A	B	A	A	B	B	A	B	A	B	B	B	A	A	-	A	A	A	-	B	A	A	B	-	A	A	A	B	B	A	A	A	-	A	A	A	A	A	B
Tm_snp073	4.92	-	A	B	A	A	-	A	B	B	-	A	-	-	A	-	A	A	A	B	B	A	-	-	A	B	A	A	A	A	A	-	A	A	B	A	B	-	A	A	A	B	B	-	A	-	A	A	-	B	A	B	A	B	-	B	A	A	A	A	A	A	B	B	A	A	B	B	A	A	A	B	B	A	A	A	B	A	A	A	A	A	B
Tm_snp084	4.92	B	-	B	A	A	A	A	-	B	A	A	A	-	A	-	A	-	A	B	B	A	-	B	A	B	A	A	A	A	A	-	A	-	B	A	B	-	A	A	A	B	B	A	A	B	A	A	B	B	-	B	A	B	B	B	A	A	A	A	A	A	B	B	A	A	B	B	-	A	A	B	B	A	-	-	B	A	A	A	A	A	B
Tm_snp093	4.92	-	A	B	A	A	A	A	-	B	-	A	A	A	A	A	A	A	A	B	B	A	A	-	A	B	A	A	A	A	A	A	A	A	B	A	B	-	A	A	A	B	B	A	A	B	A	A	-	B	A	B	A	B	-	B	-	A	A	A	A	A	B	B	A	A	-	B	A	A	A	-	B	-	A	A	-	A	A	-	A	A	B
Tm_snp094	6	-	-	B	A	A	A	A	-	B	-	A	A	-	A	A	-	-	A	B	B	A	-	B	A	B	A	A	A	A	A	A	A	A	B	A	B	-	A	A	A	B	B	A	A	B	A	A	B	B	A	B	A	B	B	B	-	A	A	A	A	A	B	B	A	A	-	-	A	A	A	B	B	A	-	A	B	A	A	A	A	-	B
Tm_snp104	7.75	B	A	B	A	A	A	A	A	B	-	A	A	A	A	A	A	A	A	B	B	-	B	B	A	B	A	A	A	-	A	A	A	-	-	A	A	-	A	A	-	B	B	A	A	-	A	-	B	B	A	B	A	-	B	B	A	B	A	A	A	A	B	-	A	-	B	A	A	A	A	B	B	A	A	A	B	A	A	-	-	A	B
Tm_snp106	9.97	-	A	B	A	A	A	A	B	B	-	A	A	A	A	-	A	A	A	B	B	A	B	B	A	-	A	A	A	A	A	-	A	-	B	A	A	-	A	A	A	B	B	A	A	B	A	A	B	B	A	B	A	B	B	B	A	B	A	A	A	A	-	B	A	A	B	B	-	A	A	-	B	A	-	A	-	A	A	A	-	A	B
Tm_snp106	11	-	A	B	-	A	-	A	A	B	-	A	A	-	A	A	A	A	A	B	B	A	-	B	A	B	-	-	A	A	-	A	A	A	B	A	-	-	A	A	A	-	B	A	-	B	A	A	B	B	A	B	A	B	B	B	A	B	-	A	A	A	B	B	A	A	B	A	A	A	A	B	B	A	-	A	-	A	A	A	A	A	B
Tm_snp106	12.08	-	A	B	A	A	-	A	A	B	-	-	A	A	A	A	-	-	A	B	B	A	-	B	A	B	A	A	A	A	A	A	-	A	B	A	B	B	A	A	A	B	B	A	A	B	A	A	B	B	-	B	A	B	B	B	A	A	A	A	-	A	B	B	A	A	B	-	A	A	A	B	B	A	A	-	B	A	A	A	A	A	-
Tm_snp107	14.97	B	A	B	A	A	-	A	B	-	-	A	A	-	A	A	-	-	A	B	B	A	B	B	A	-	-	-	A	A	A	A	A	A	B	A	A	A	A	A	A	B	B	-	A	B	-	A	B	B	A	-	-	B	B	B	-	B	A	A	A	A	B	B	-	-	B	-	A	A	A	B	B	A	A	A	B	A	A	A	A	A	B
Tm_snp117	16.69	-	A	B	A	A	A	A	A	-	-	A	A	A	A	A	-	-	-	B	B	A	B	B	A	-	A	A	A	A	-	A	A	-	-	A	A	-	A	A	A	B	B	A	A	B	A	A	B	-	-	B	A	-	B	B	A	B	A	A	A	A	-	B	A	-	B	B	-	A	A	-	B	A	A	A	-	A	A	A	A	A	B
Tm_snp118	18.48	-	A	B	A	-	A	A	-	B	-	-	-	-	A	A	A	A	A	B	B	A	-	B	A	B	A	A	A	A	A	-	A	A	B	-	B	-	A	A	A	B	B	A	A	-	A	A	B	B	A	B	A	B	-	B	A	A	A	A	A	A	B	B	A	A	B	B	A	A	A	B	-	A	A	A	B	A	A	A	-	A	B
Tm_snp119	19.05	A	-	B	A	A	A	A	-	-	B	A	A	A	A	A	A	A	-	B	B	A	B	-	A	B	-	A	A	A	A	A	A	A	-	-	B	B	A	A	-	B	B	A	A	B	A	A	B	B	-	B	A	B	B	B	A	A	A	A	A	A	-	B	A	A	B	-	A	A	A	-	B	A	A	A	-	-	A	A	A	A	B
Tm_snp131	20.18	B	A	-	A	A	A	A	-	B	B	A	A	A	A	-	A	-	A	B	B	A	B	B	A	-	A	A	A	A	-	A	A	A	B	A	B	-	A	A	A	B	B	A	A	B	A	A	B	B	A	B	A	-	B	B	A	A	A	A	A	A	B	B	A	-	B	-	-	A	A	B	-	A	A	A	-	-	A	-	A	-	B
Tm_snp142	22.65	A	A	-	A	A	A	A	-	-	B	A	A	A	-	A	A	A	A	B	-	A	-	-	A	B	-	A	-	A	-	A	A	A	-	A	-	-	A	-	A	B	B	A	A	B	-	A	B	B	-	B	A	B	B	B	A	A	A	A	A	A	B	-	A	A	B	B	-	A	A	B	-	A	A	-	B	-	A	A	-	A	B
Tm_snp156	25.06	A	A	B	A	A	A	-	-	B	-	-	A	A	A	A	A	A	A	B	-	A	B	-	-	B	A	A	A	A	A	A	A	A	B	A	B	-	A	A	A	B	B	A	A	B	A	A	B	B	-	B	A	-	B	B	B	A	A	A	A	A	-	B	A	A	B	A	-	A	A	-	B	A	-	A	B	-	A	A	A	A	B
Tm_snp156	27.42	A	A	B	A	A	-	-	B	B	A	A	A	A	A	-	A	A	-	B	B	-	B	B	-	B	A	A	-	A	A	A	A	A	B	A	A	-	A	A	A	B	-	A	A	-	-	A	B	B	A	B	A	B	-	B	A	B	A	A	A	A	-	-	A	A	-	-	A	A	A	B	B	A	-	A	B	-	A	A	A	A	B
Tm_snp158	30.69	B	A	B	A	A	A	A	B	B	-	A	A	-	A	-	-	A	A	B	B	A	-	A	A	B	A	A	A	A	A	-	A	-	B	A	-	-	A	-	A	-	B	A	A	B	A	A	B	B	A	B	A	B	B	B	-	A	-	A	-	A	B	B	A	A	B	B	A	A	A	B	-	-	-	-	B	A	A	A	-	A	B
Tm_snp169	33.79	A	A	B	A	A	A	A	A	B	-	A	A	-	A	A	-	A	A	B	B	A	-	B	A	B	A	A	A	A	A	A	-	A	-	-	A	-	A	A	A	-	B	A	A	B	A	-	B	B	A	-	A	B	B	B	-	B	A	A	A	A	B	B	-	A	-	-	A	A	A	-	B	A	A	A	B	A	A	-	A	A	B
Tm_snp182	34.38	-	A	B	A	A	-	A	-	B	-	A	A	-	A	A	A	-	-	B	B	A	B	B	A	B	A	A	A	A	A	A	-	A	B	A	-	A	-	A	-	B	B	-	A	-	A	A	B	B	-	-	A	B	B	-	A	-	A	A	A	A	B	B	A	A	B	-	A	A	A	-	B	A	A	A	B	A	-	A	A	A	B
Tm_snp183	34.38	A	A	-	-	-	A	A	-	B	-	A	A	-	A	-	A	-	A	B	-	A	-	B	A	B	A	A	A	A	-	A	A	A	-	A	B	-	A	-	A	B	B	A	A	B	A	A	B	B	A	-	A	B	B	B	A	A	A	-	A	A	B	B	A	-	B	B	A	A	A	B	B	-	A	A	B	A	A	A	A	A	B
Tm_snp194	36.34	-	A	B	A	A	A	A	-	B	-	A	A	A	A	A	A	-	-	B	B	A	B	-	A	B	A	-	-	A	A	B	A	A	B	A	-	A	-	A	A	B	B	A	A	-	A	A	B	B	-	B	A	B	B	B	A	-	-	A	A	A	B	B	-	A	B	-	A	A	A	-	B	A	A	-	-	-	A	A	A	A	B
Tm_snp195	38.36	-	A	B	A	-	A	-	B	B	-	A	A	-	A	A	A	A	A	B	B	-	B	B	A	-	A	A	A	A	A	A	A	A	B	-	B	-	A	A	A	B	B	A	A	B	-	A	B	-	A	B	-	B	B	B	-	A	A	A	-	A	B	B	A	A	-	A	A	A	A	-	B	-	A	-	-	A	A	A	A	-	B
Tm_snp207	39.73	-	A	B	-	A	-	A	-	-	-	A	A	A	A	A	-	-	-	B	B	A	-	B	-	B	A	A	A	A	A	A	A	A	B	A	B	B	A	A	A	B	B	A	-	-	A	A	B	B	A	B	A	B	-	B	A	-	A	-	A	A	B	B	A	-	B	-	-	A	A	B	B	A	A	A	B	A	A	-	A	A	B
Tm_snp208	41.01	-	A	B	A	A	A	-	-	B	-	-	A	-	A	B	A	-	-	B	B	A	-	B	A	-	A	A	A	A	A	A	-	-	-	-	B	B	A	-	A	B	-	-	A	-	A	A	-	B	-	B	A	B	B	B	A	A	A	-	-	A	B	B	A	A	B	-	A	A	A	B	B	A	A	A	B	A	A	A	A	A	B
Tm_snp209	42.92	-	A	B	A	A	A	-	B	B	B	A	A	-	A	A	A	-	-	-	B	A	-	-	-	B	A	A	A	A	-	A	A	A	B	A	B	-	A	-	A	B	B	A	A	-	-	A	B	B	-	B	-	B	B	B	A	A	A	A	A	A	B	B	A	-	B	B	A	A	A	-	-	-	A	A	B	A	A	A	A	A	B
Tm_snp221	44.2	B	-	B	A	A	-	A	-	B	B	A	A	-	A	A	-	-	A	B	-	A	-	B	-	B	A	A	A	A	A	A	A	A	B	A	B	-	A	-	A	B	B	A	A	B	A	A	B	B	-	-	A	B	-	B	A	A	-	A	A	A	B	-	A	A	B	-	-	A	A	B	-	A	A	A	-	-	A	A	A	A	B
Tm_snp222	46.07	-	A	B	A	A	-	A	-	B	B	A	A	-	A	-	A	-	-	B	-	A	B	B	-	B	-	A	A	A	A	A	A	A	B	A	A	-	A	-	A	B	B	A	-	B	A	A	B	B	-	B	A	B	B	B	A	B	A	A	A	-	B	B	A	A	-	-	A	A	A	B	B	A	A	-	B	-	A	A	A	A	B
Tm_snp235	48.05	-	A	B	A	A	A	-	-	B	-	-	-	-	A	A	A	A	A	B	-	A	-	B	A	B	A	A	A	A	A	A	-	A	-	A	B	A	A	A	A	B	B	A	A	B	A	A	B	B	A	B	A	B	B	B	A	A	-	A	-	A	-	B	A	A	-	B	-	A	A	B	B	A	A	A	B	A	A	A	A	-	B
Tm_snp235	50.1	-	A	B	A	A	A	-	B	B	-	A	-	-	A	-	A	A	-	B	B	-	B	-	-	B	A	A	A	A	A	A	-	A	B	A	-	B	A	A	A	-	B	A	A	-	A	-	B	B	A	-	A	B	B	B	A	A	A	A	A	-	B	-	A	A	B	-	A	A	A	B	B	-	-	-	B	-	A	A	-	A	B
Tm_snp237	52.01	B	A	B	A	A	A	A	B	B	-	-	A	-	A	A	A	-	-	B	B	-	B	-	A	-	A	A	A	-	-	A	A	-	B	A	B	-	A	A	-	-	B	A	A	B	A	A	-	B	-	B	A	B	B	B	A	A	A	A	A	-	B	-	A	-	B	-	-	A	A	B	B	A	-	-	-	A	A	-	-	A	B
Tm_snp259	53.99	-	A	B	A	A	A	-	-	B	-	A	A	-	A	A	-	-	-	B	B	A	B	B	A	B	A	A	A	A	-	-	A	A	-	A	A	-	A	A	-	B	B	A	A	-	A	A	B	B	A	B	A	B	-	B	A	B	A	A	-	A	B	-	A	-	-	-	A	A	A	B	-	-	A	A	B	A	A	A	-	A	-
Tm_snp261	58	-	A	B	-	A	-	A	B	B	A	A	-	A	A	-	A	A	-	B	B	A	B	B	-	B	A	A	A	A	A	A	A	A	B	-	B	-	-	-	A	B	-	A	A	-	A	A	-	B	-	B	-	B	B	B	A	A	A	-	A	A	B	-	A	-	B	B	-	A	A	B	B	-	A	-	B	A	A	A	A	A	B
Tm_snp259	58.7	A	A	B	A	A	-	A	B	B	-	A	A	-	-	A	A	-	A	B	B	A	B	B	A	B	A	A	A	A	-	A	A	A	B	A	A	B	A	A	-	B	-	A	A	-	-	-	B	B	A	B	A	B	-	B	-	B	A	A	A	-	-	-	A	A	-	-	-	A	A	B	B	A	A	A	B	-	A	-	-	A	B
Tm_snp261	58.7	-	A	B	A	A	A	A	B	B	-	-	A	A	A	-	A	A	A	B	B	-	-	B	A	B	A	A	A	A	A	A	-	A	B	-	-	B	A	-	-	B	-	A	A	A	A	-	B	-	-	B	A	B	B	B	A	-	A	A	-	-	B	B	-	A	B	-	A	A	-	B	B	A	A	A	-	A	A	-	A	-	B
Tm_snp010	59.83	-	A	B	A	A	A	A	A	B	-	A	A	A	A	A	A	A	A	B	B	A	B	B	A	B	A	A	A	A	A	A	A	A	B	A	A	-	A	-	A	-	B	A	A	B	A	A	B	B	A	B	A	B	B	B	A	B	A	A	A	A	B	B	A	A	B	-	-	A	A	-	-	A	A	A	B	A	-	A	A	A	B
Tm_snp052	61.28	-	A	B	A	A	A	A	B	B	-	A	A	-	A	-	A	A	A	-	B	-	B	B	A	B	A	A	A	A	A	A	A	A	B	-	A	A	A	A	A	B	-	A	A	-	-	A	B	B	A	B	A	B	B	B	A	B	A	A	A	A	B	B	A	-	B	-	A	A	A	B	B	A	-	A	B	A	A	A	A	A	B

2,698 SNPs with <30% missing data used

More genotyping underway for better coverage

D-Genome

K-STATE
Kansas State University

Bikram S. Gill
Gaganpreet Kaur

UC DAVIS
UNIVERSITY OF CALIFORNIA

Jan Dvorak
Ming-Cheng Luo
Karin R. Deal
Yaqin Ma
Patrick E. McGuire

USDA ars

Olin D. Anderson
Yong Q. Gu
Frank M. You

CSH
COLD SPRING HARBOR LABORATORY

Doreen H. Ware

UNIVERSITY OF SASKATCHEWAN

Curtis Pozniak

USDA ars

Jesse Poland

IEB

Jaroslav Dolezel
Jan Safar
Hana Simkova

National Research Council Canada

Andrew Sharpe

NSF

Chromosome 3A

Bikram S. Gill
Eduard Akhunov
Gaganpreet Kaur

Ming-Cheng Luo
Yaqin Ma

Justin D.Faris
Leela Reddy

Wanlong Li

Pablo Rabinowicz

Katrien Devos

Jaroslav Dolezel
Jan Safar
Hana Simkova